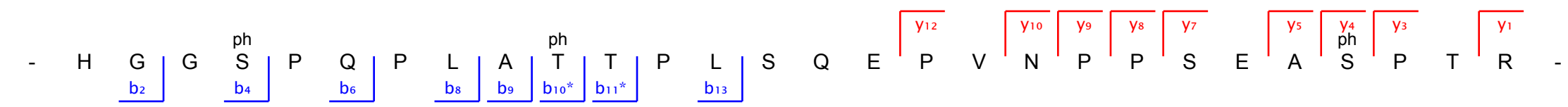
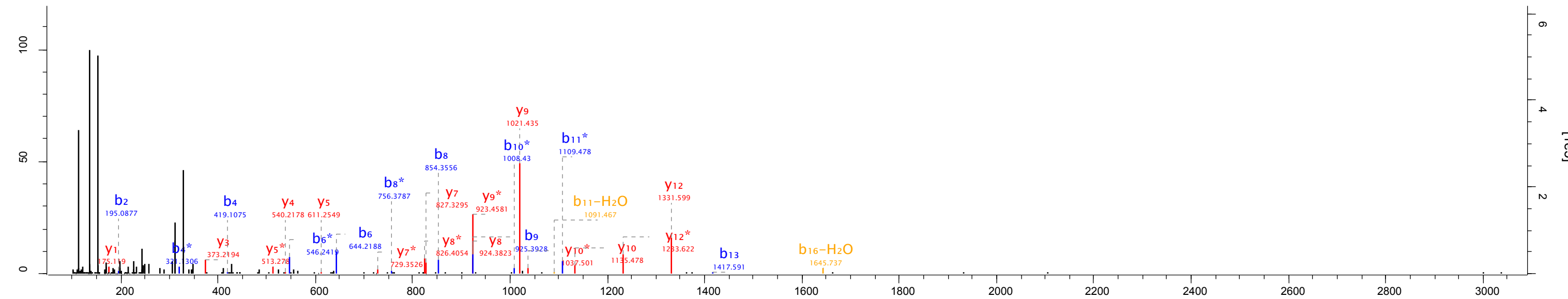
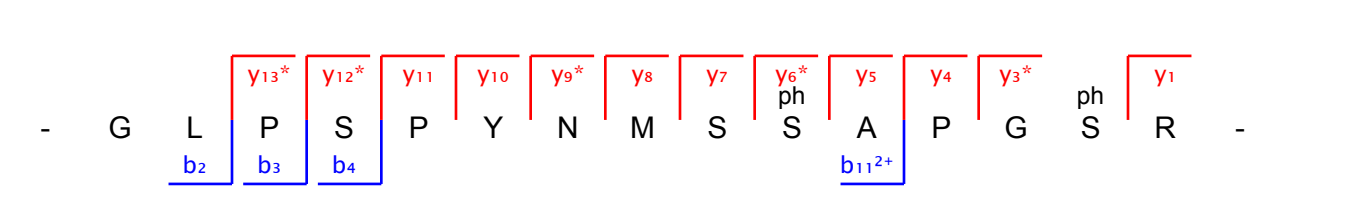
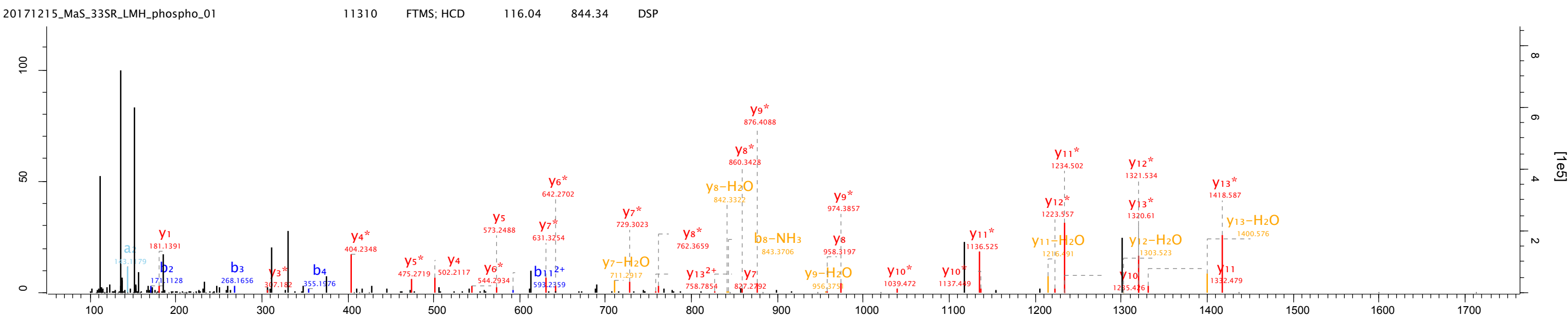


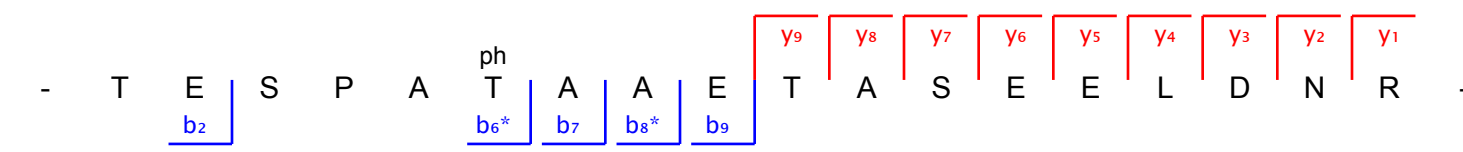
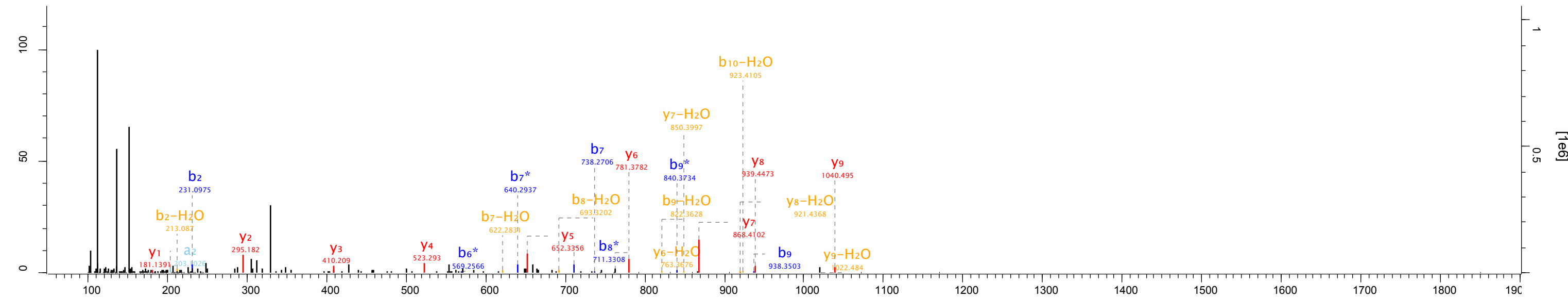
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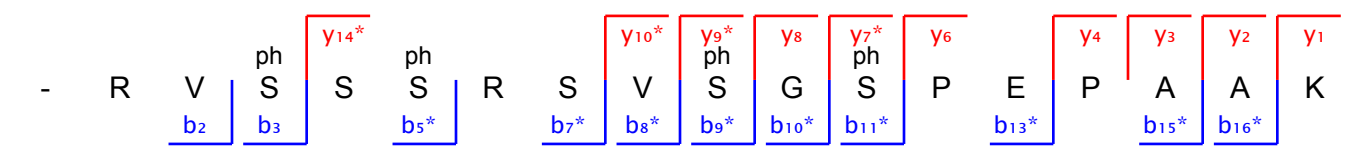
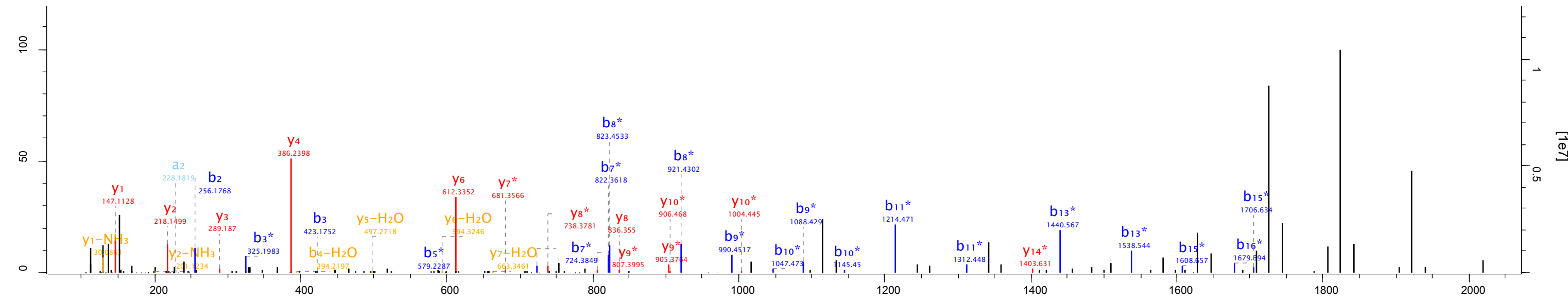
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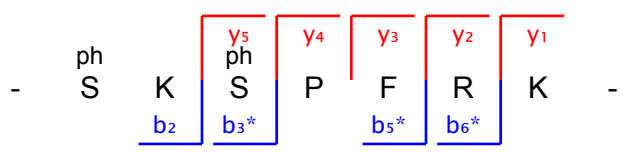
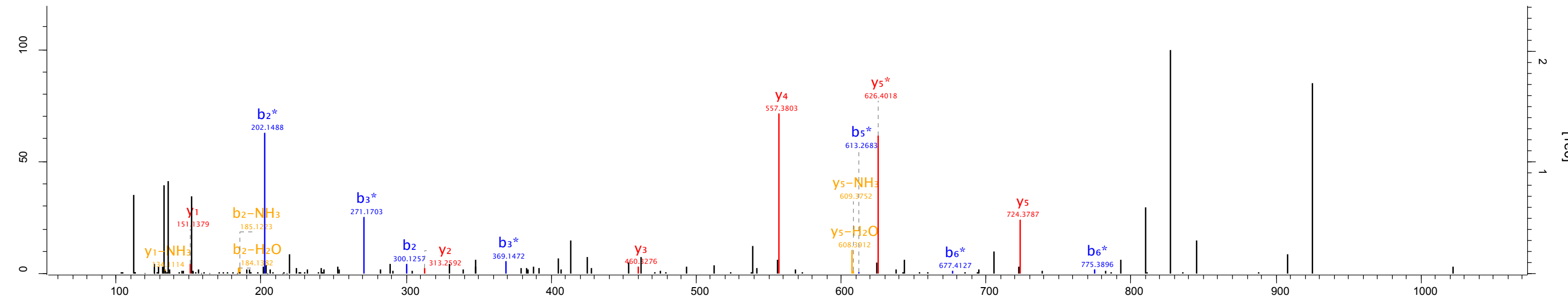
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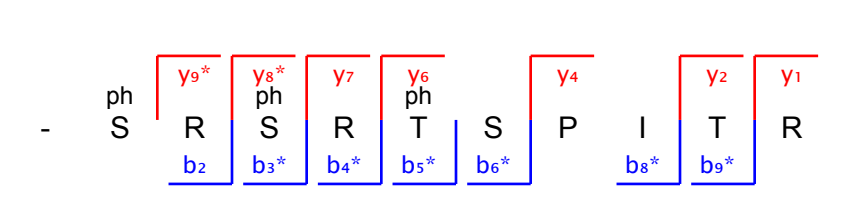
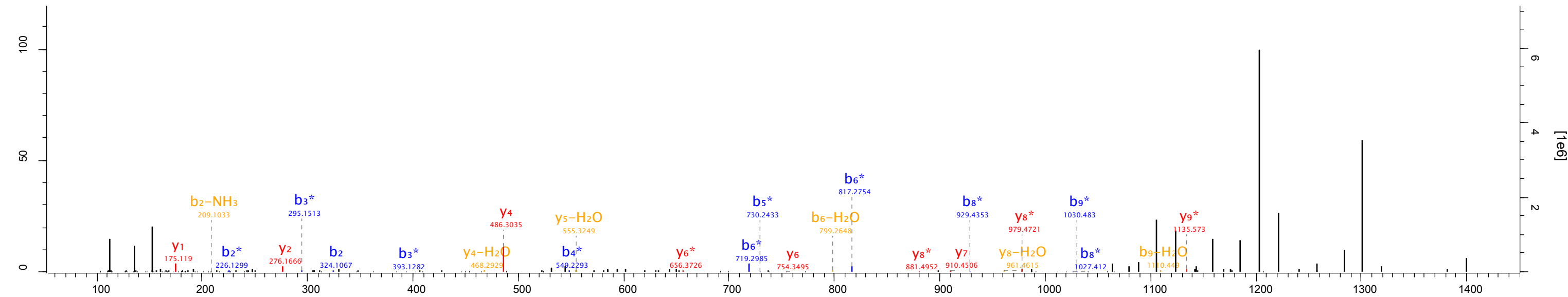
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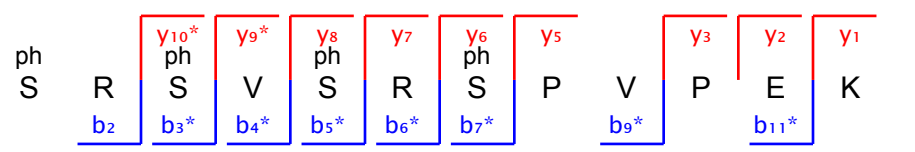
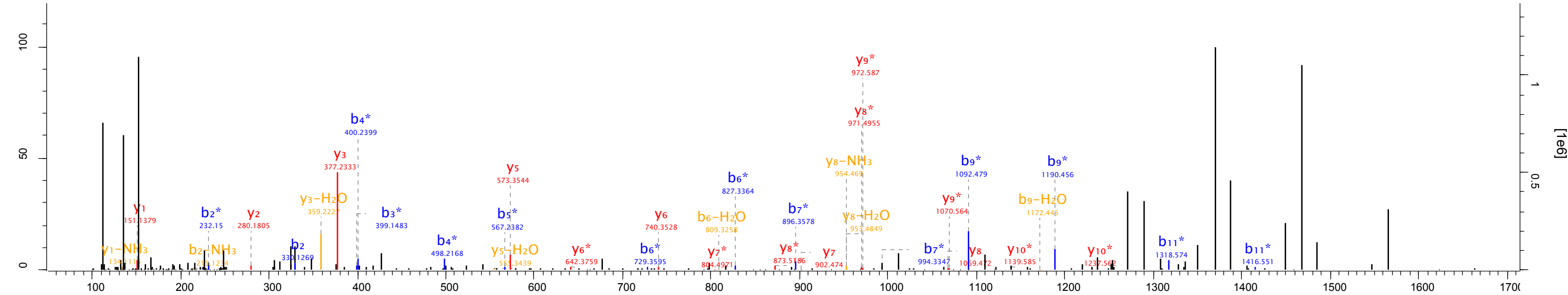


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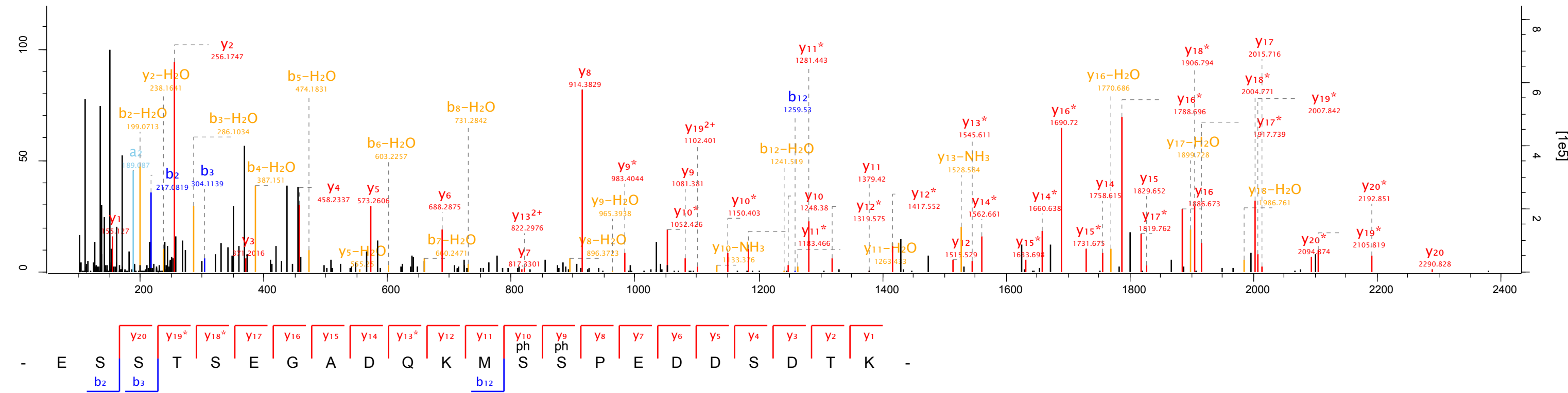


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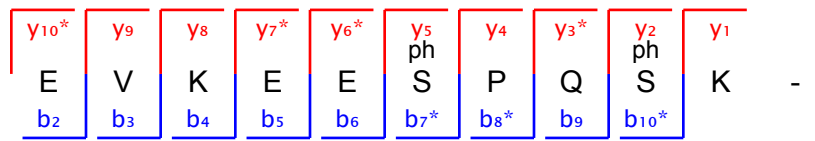
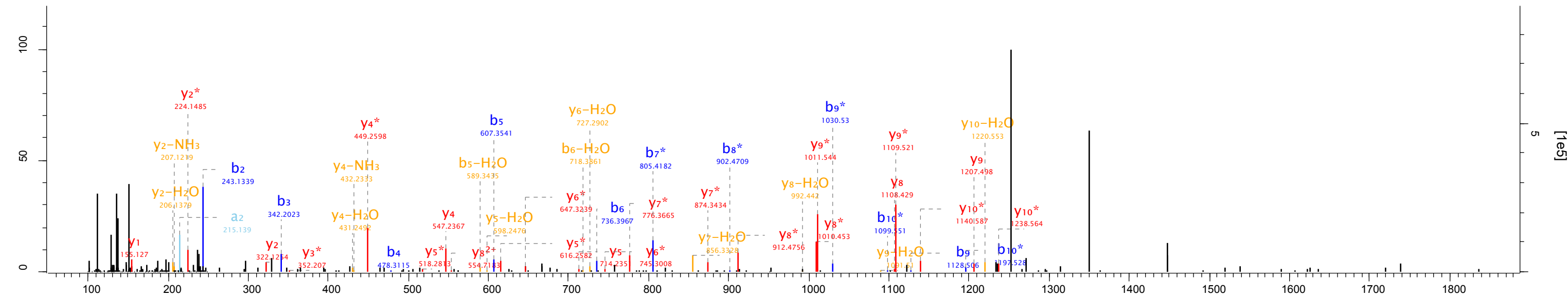
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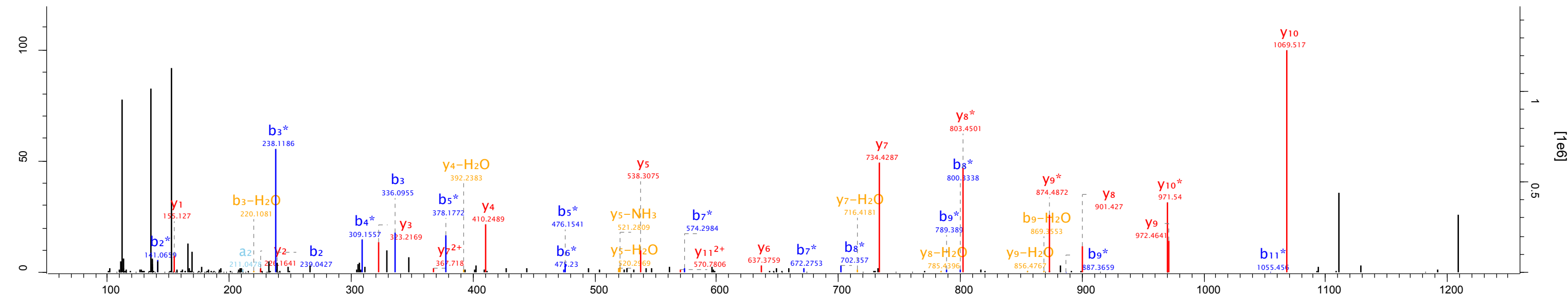
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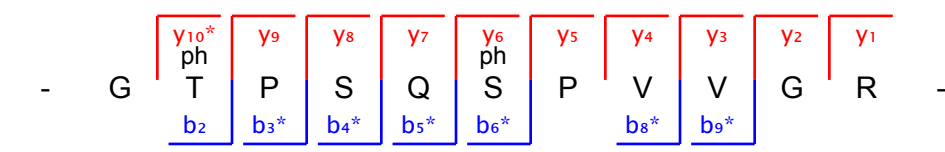
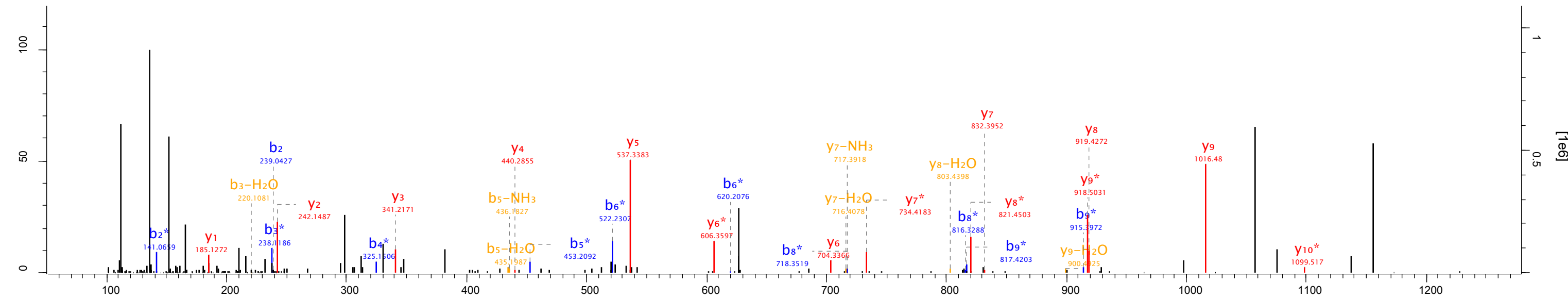


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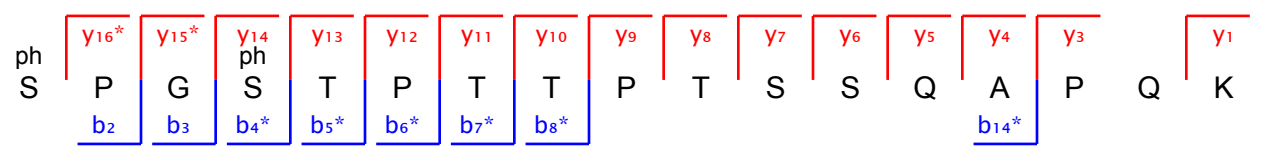
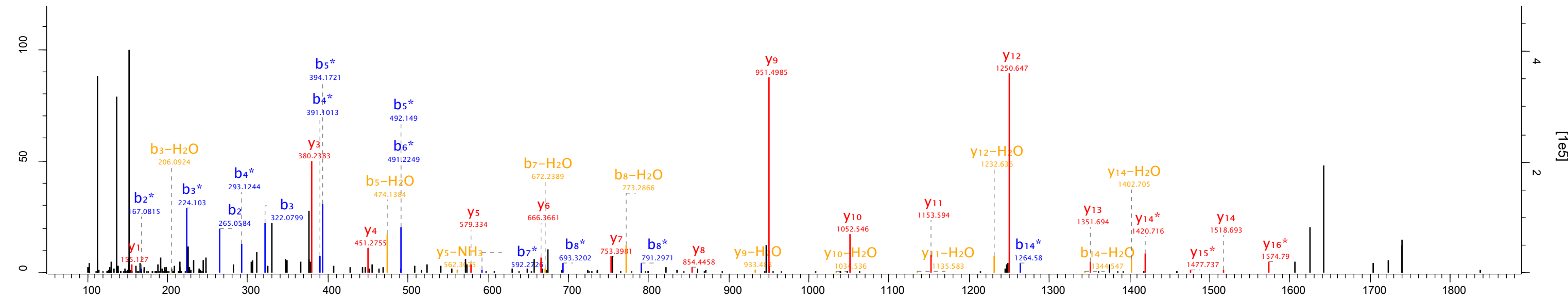
y ₁₁ ²⁺	y ₁₀	y ₉	y ₈ ^{ph}	y ₇	y ₆	y ₅	y ₄	y ₃	y ₂	y ₁
A	P	A	S	P	V	Q	S	P	A	K
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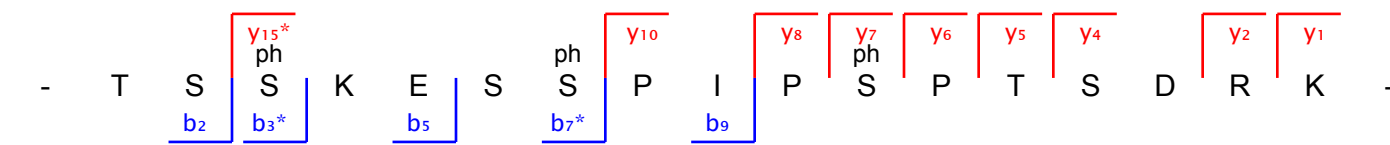
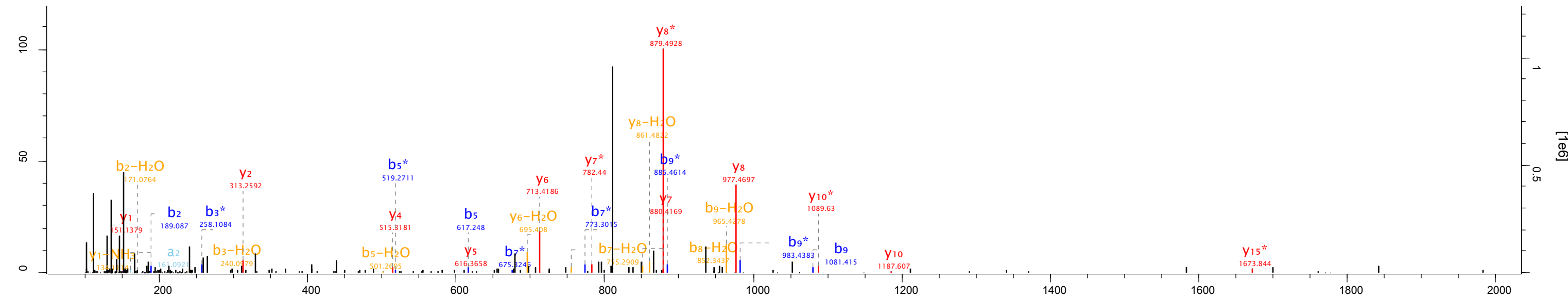
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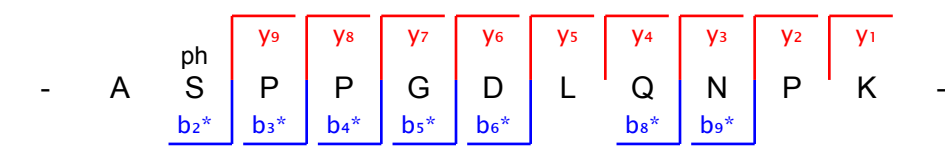
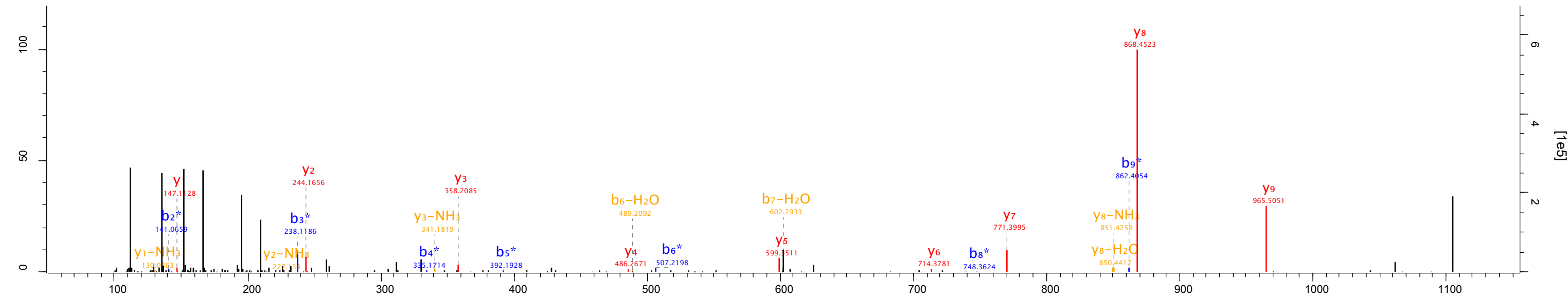


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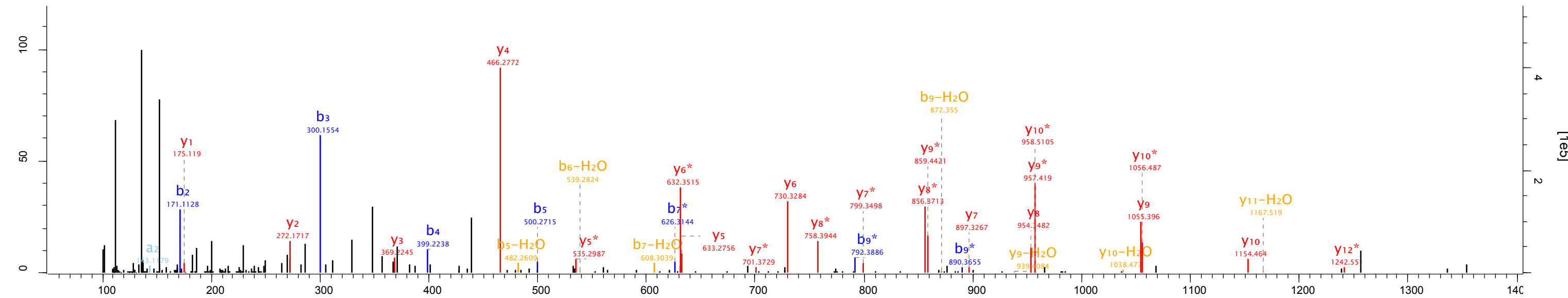




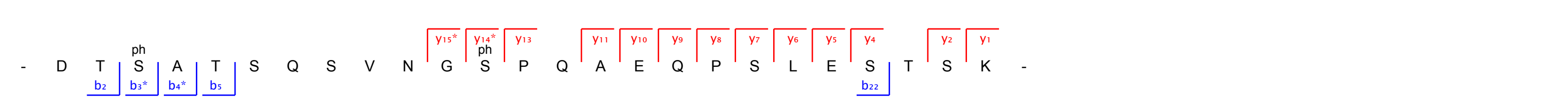
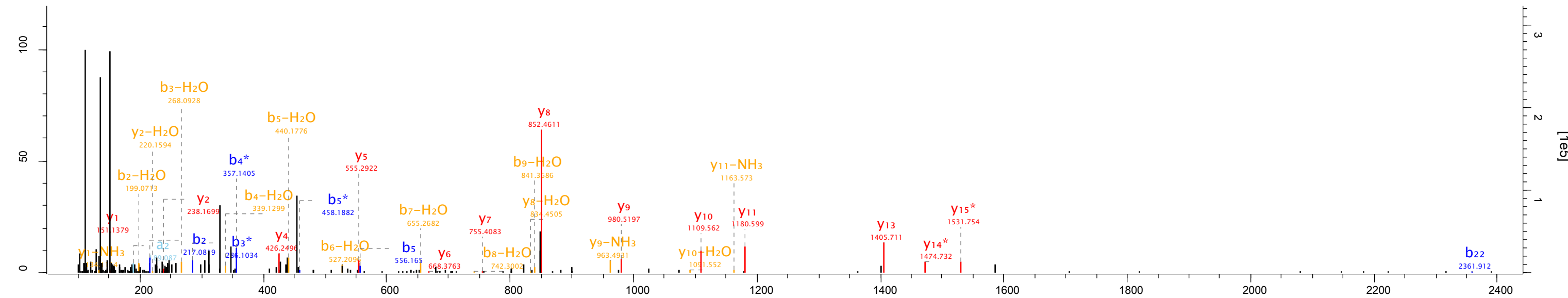
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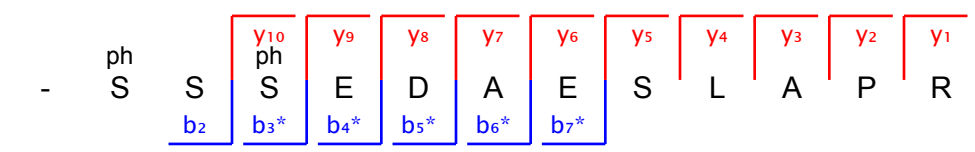
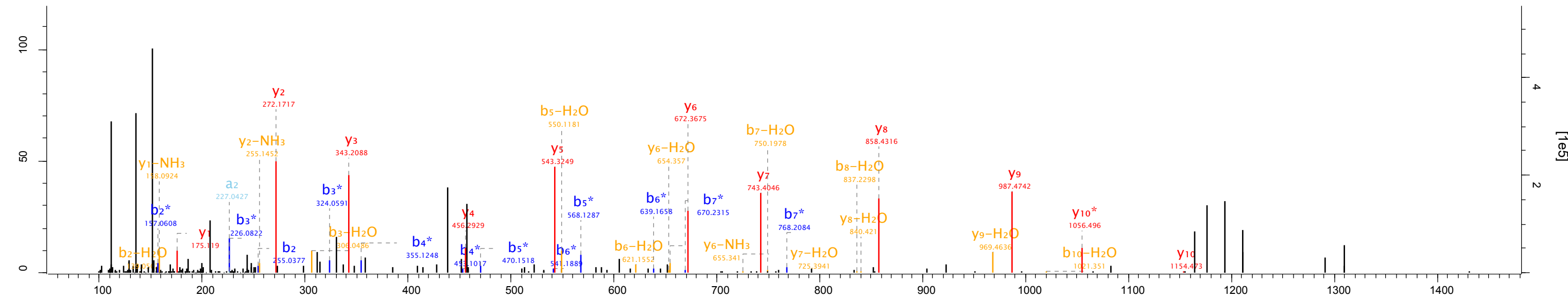
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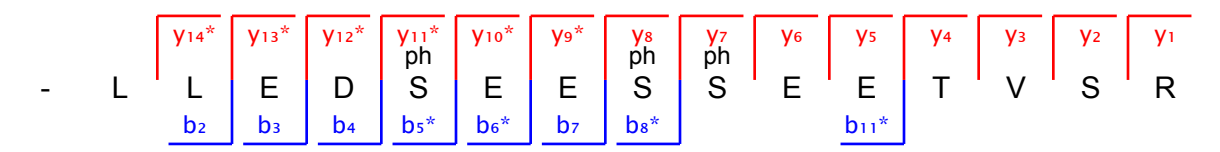
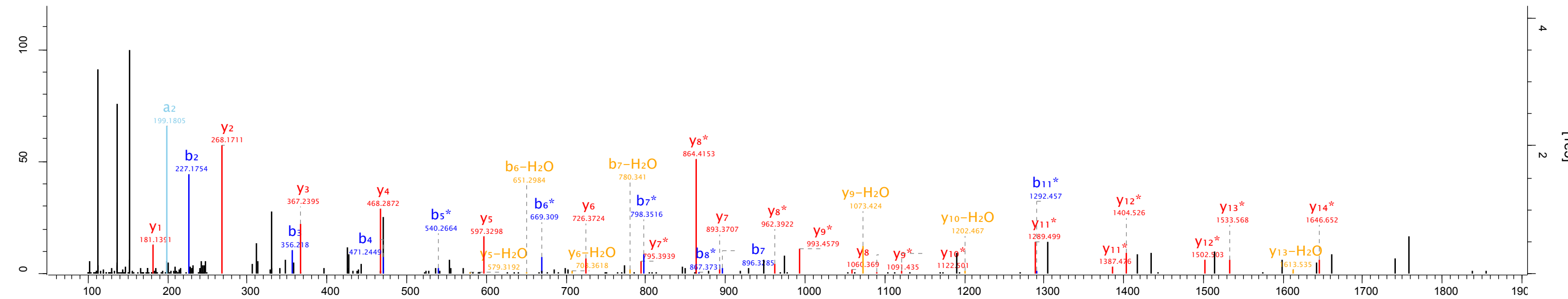
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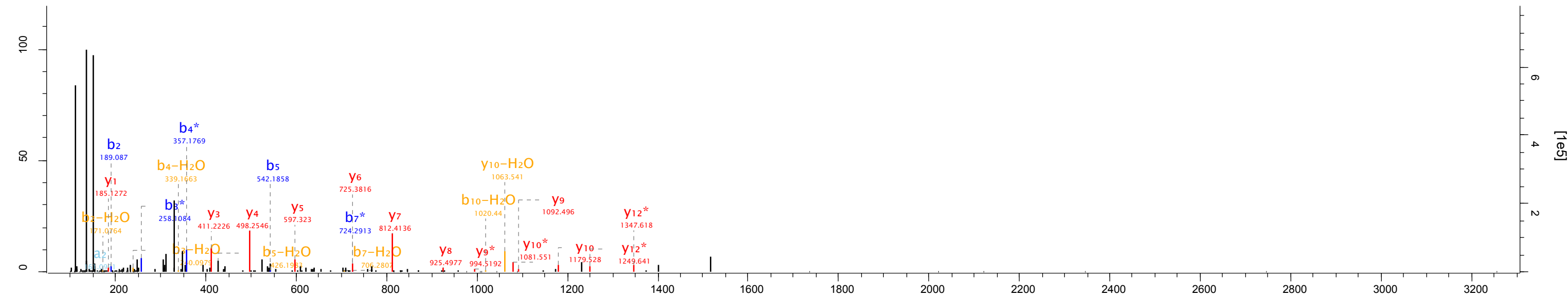
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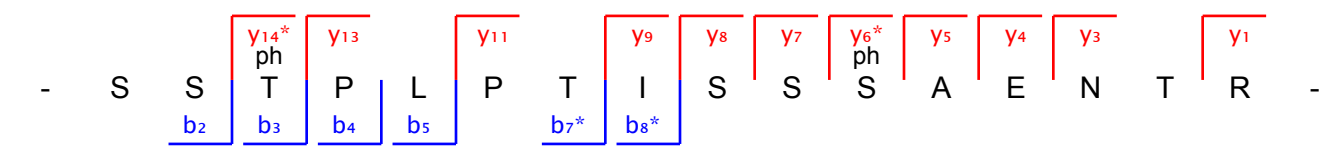
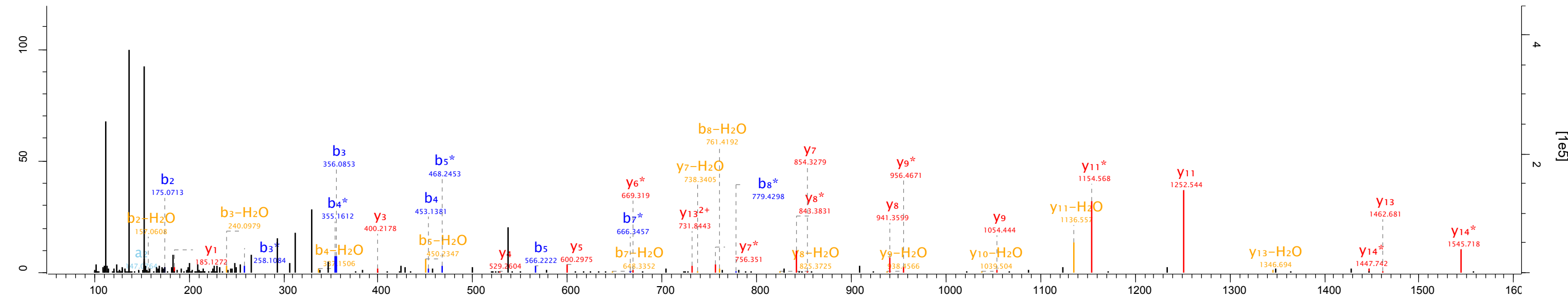
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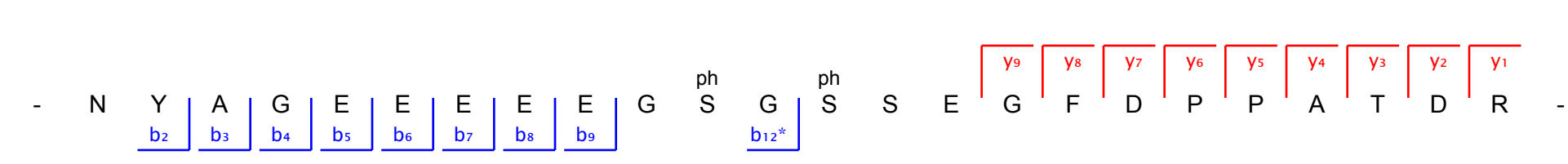
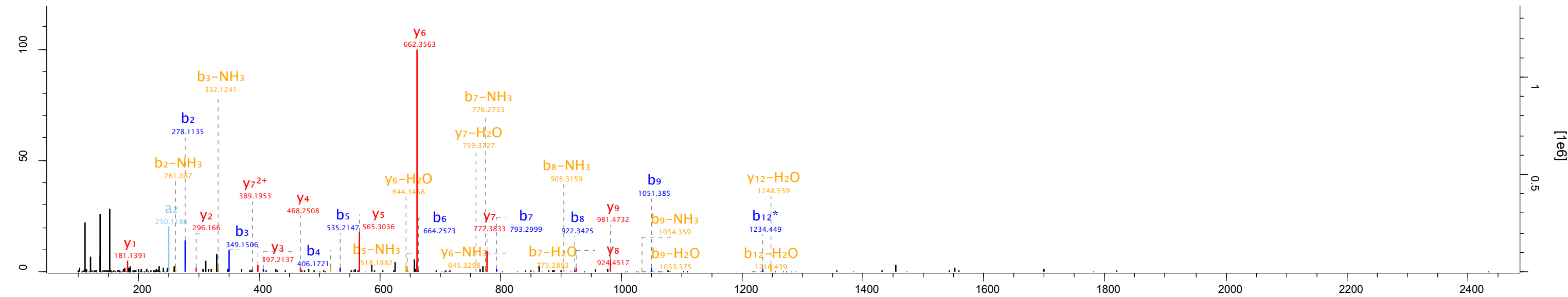
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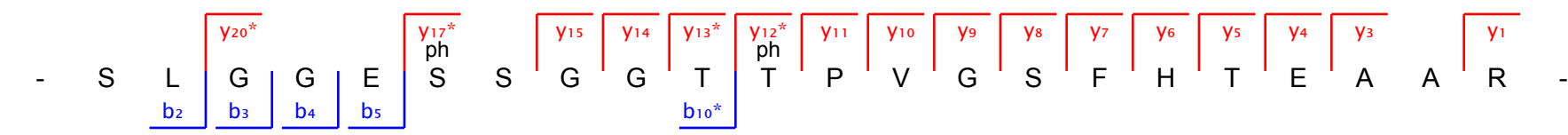
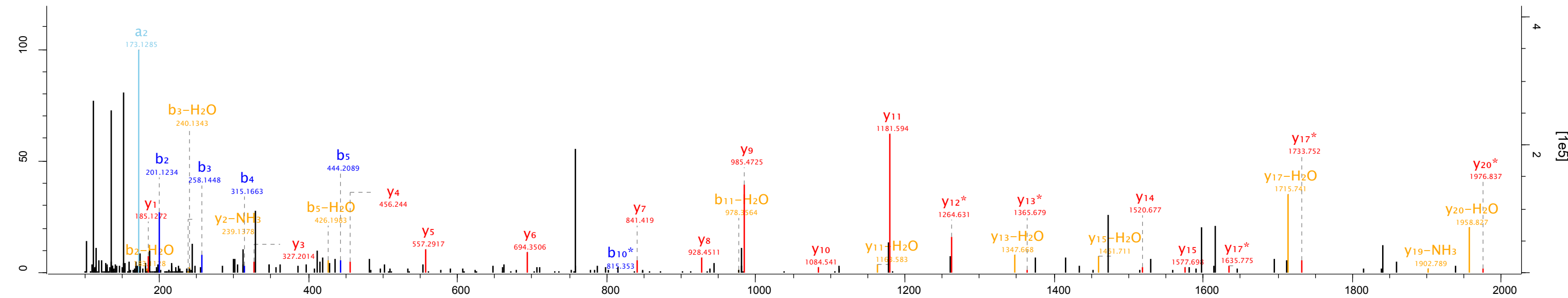
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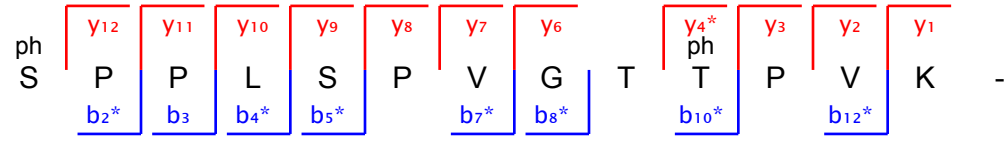
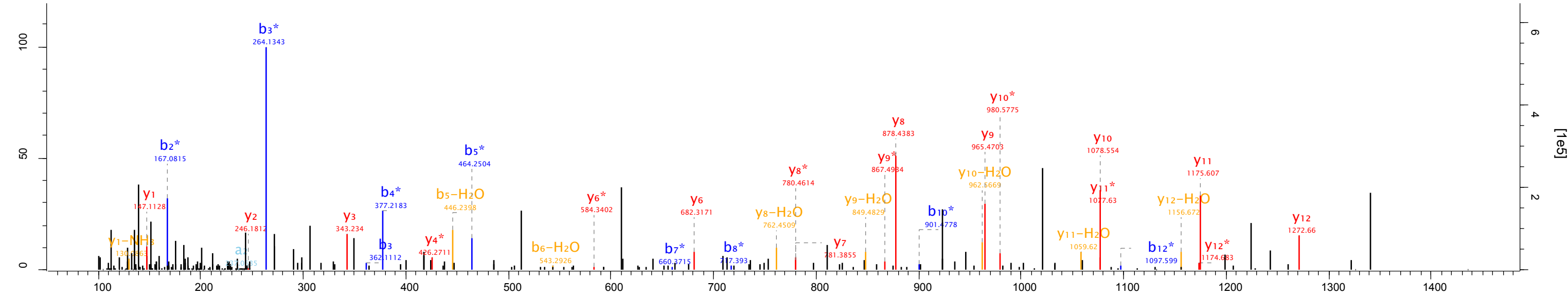
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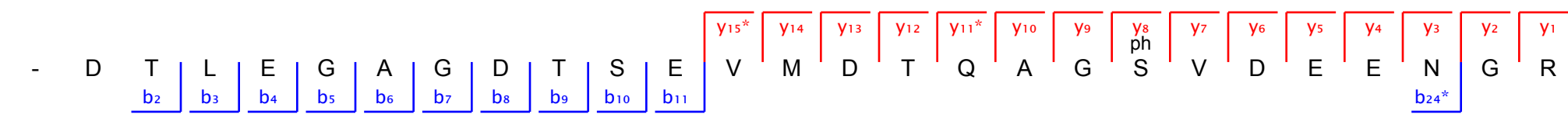
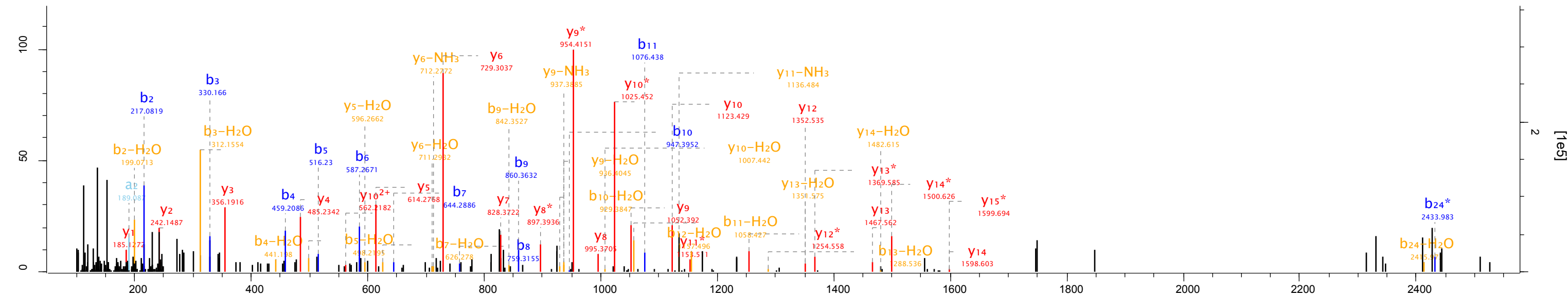
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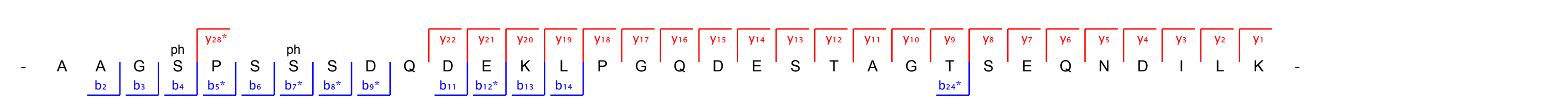
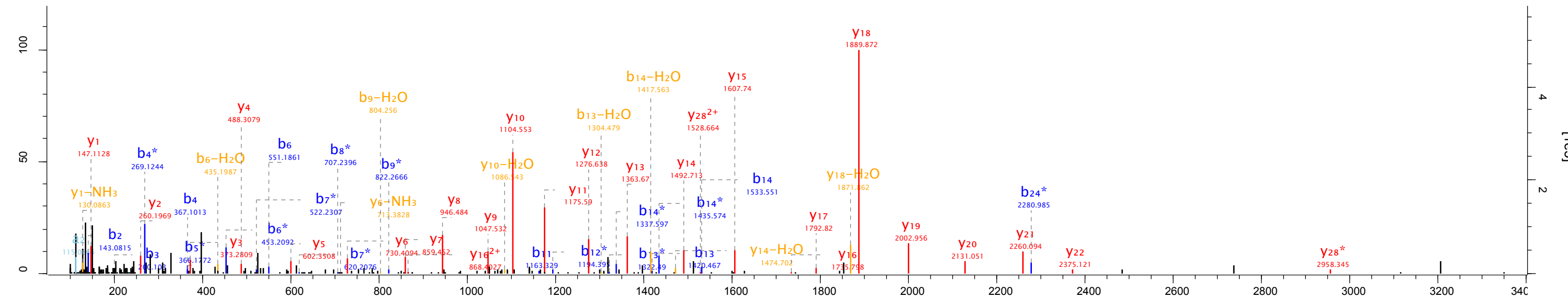
20171215_MaS_33SR_LMH_phospho_02 10690 FTMS; HCD 107.41 720.33 C2orf49



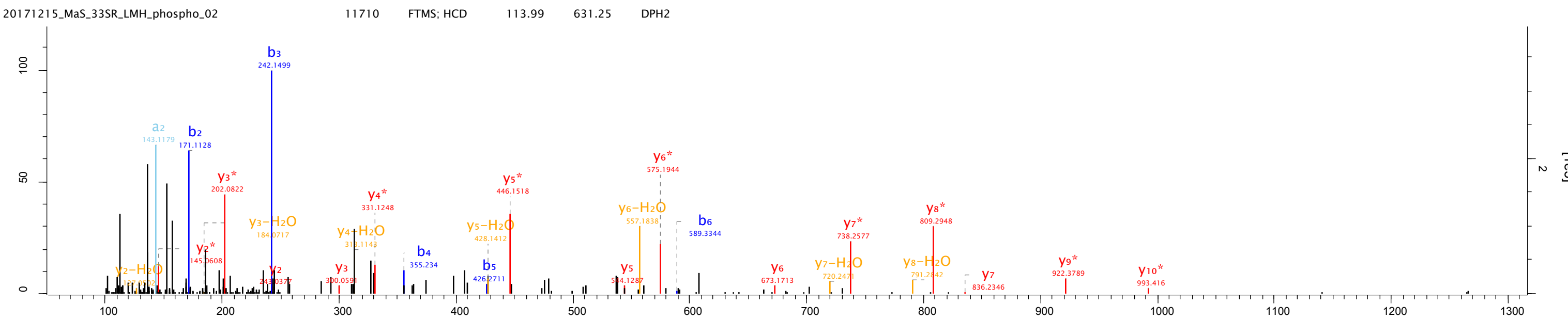
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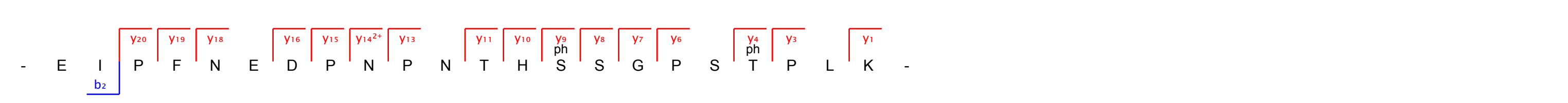
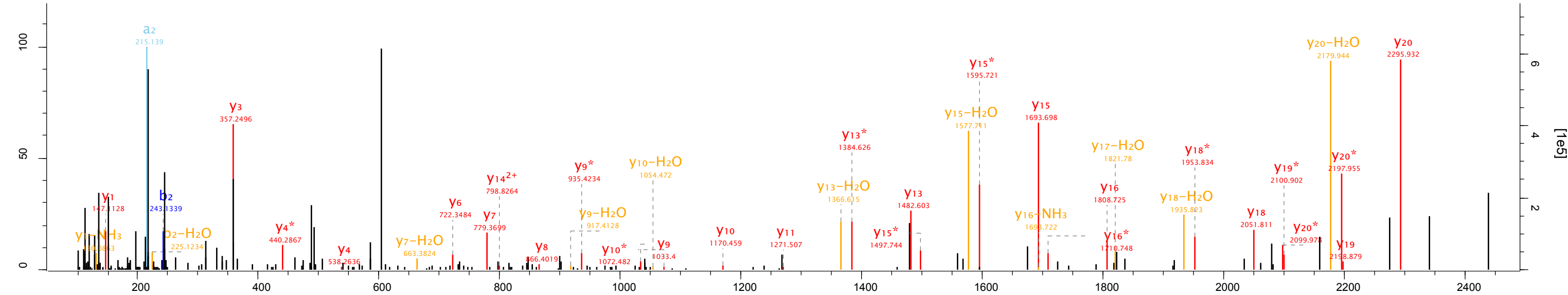
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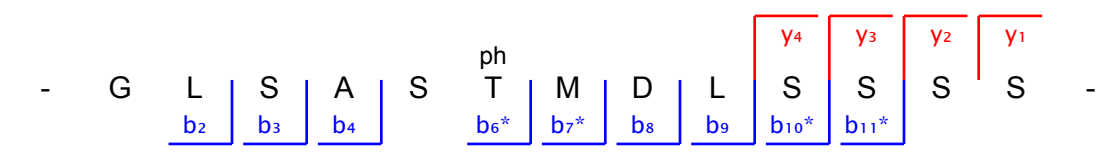
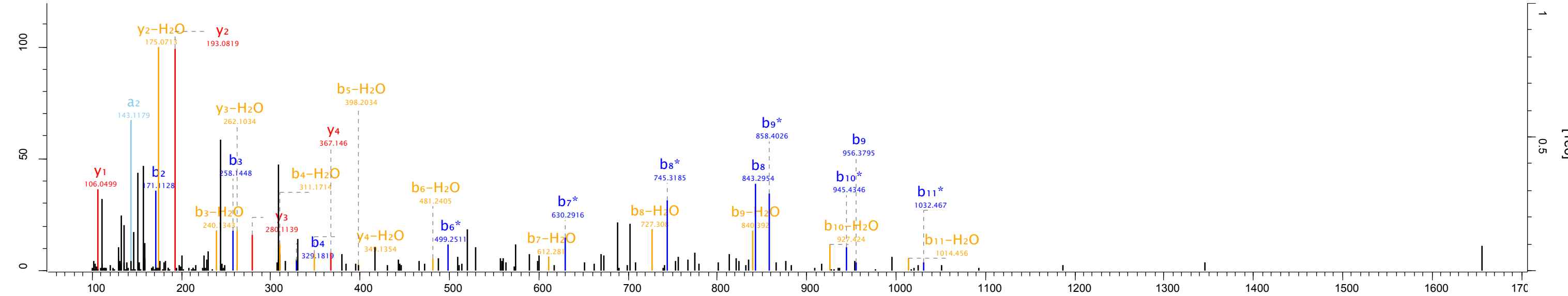
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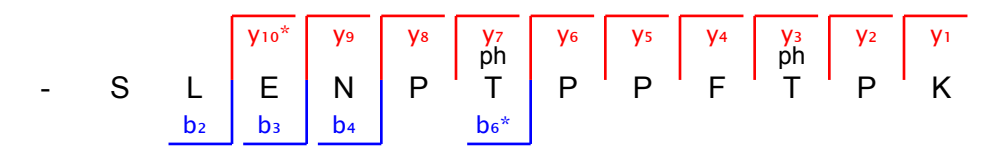
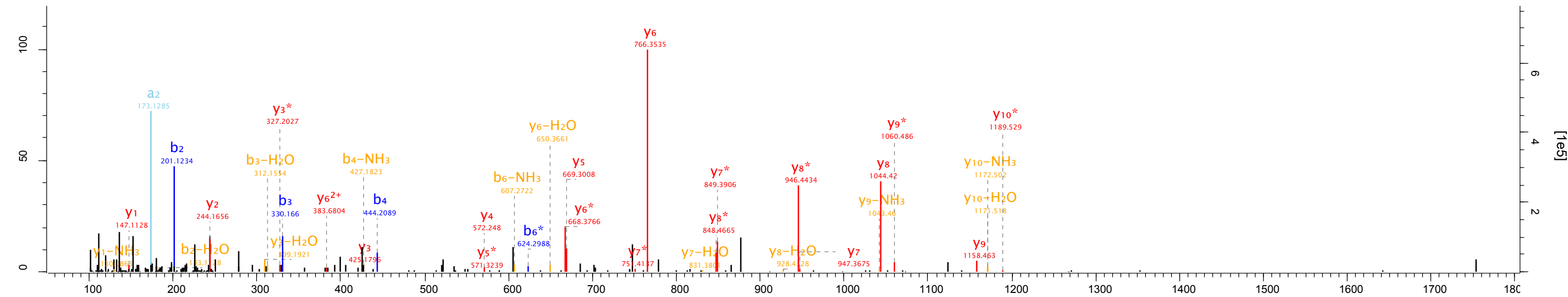
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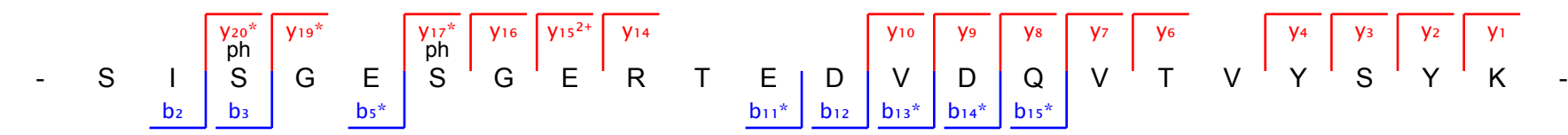
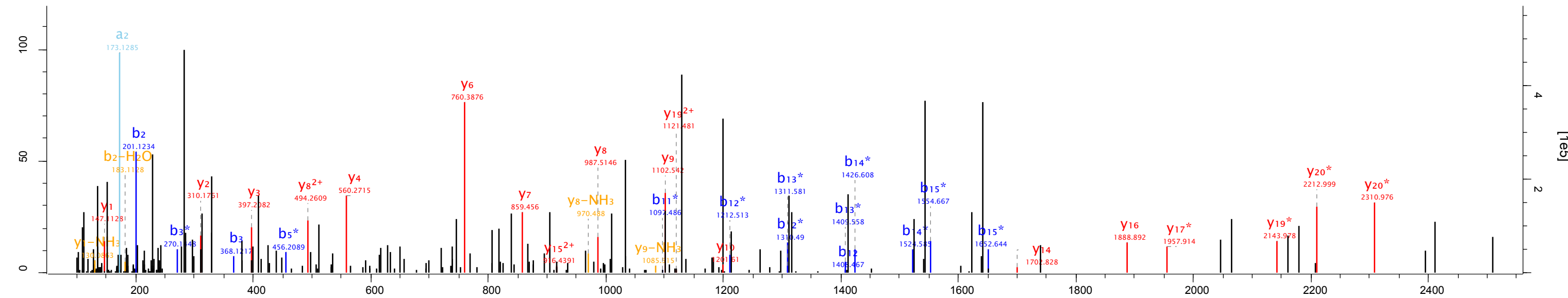
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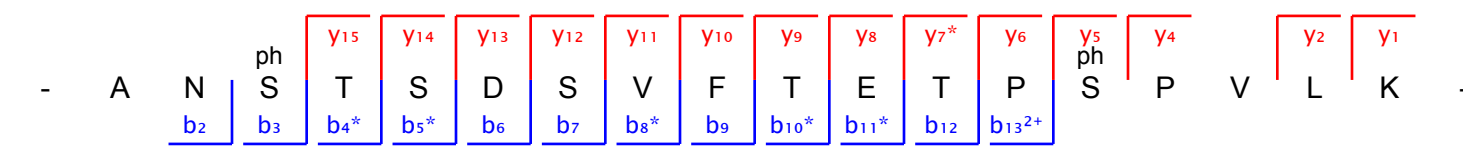
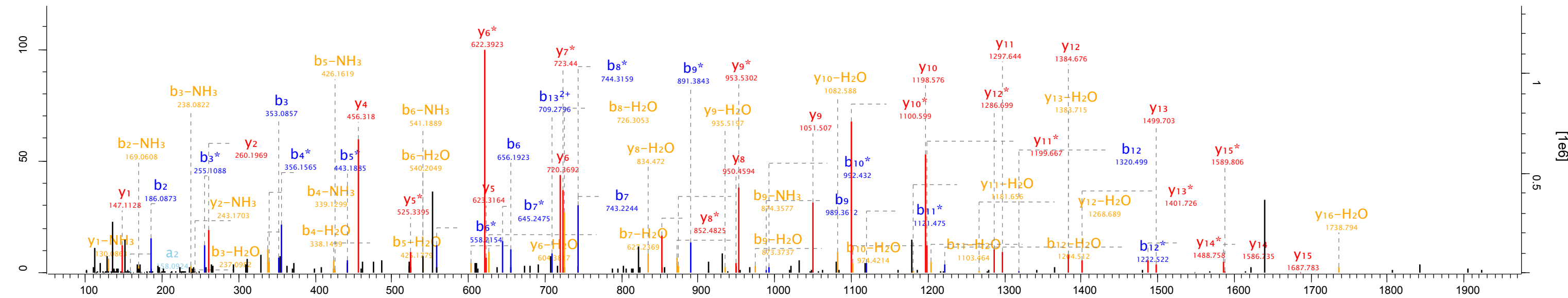
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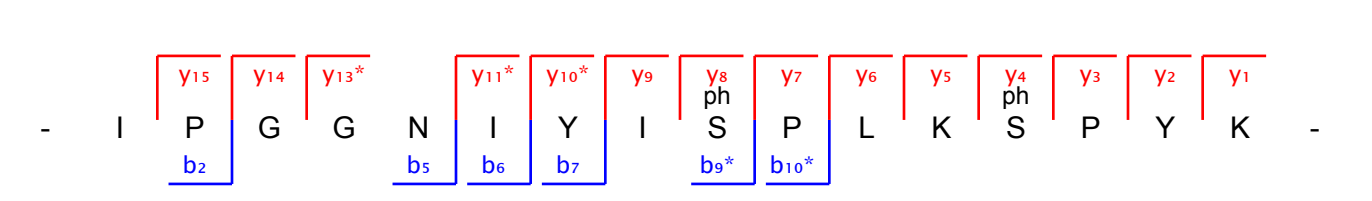
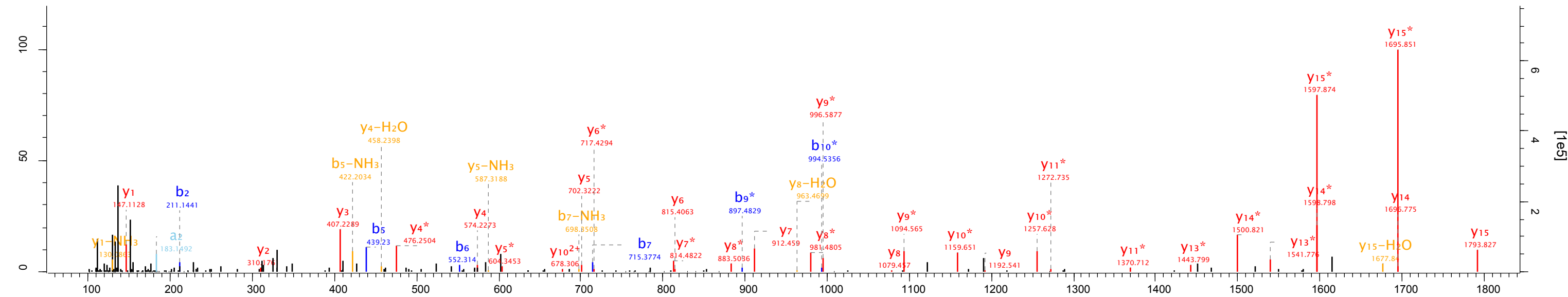
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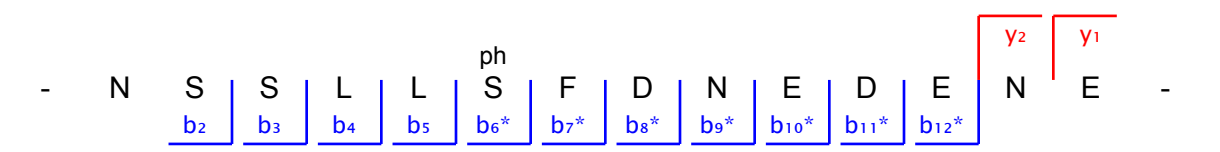
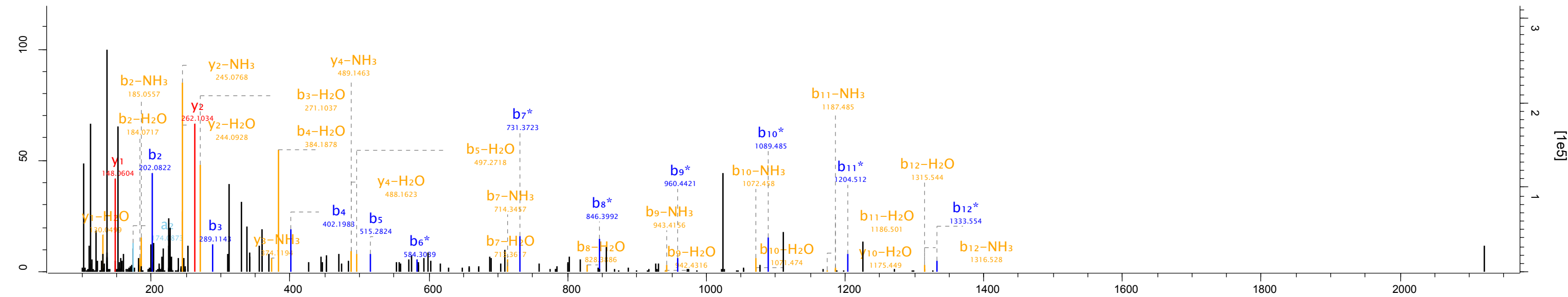
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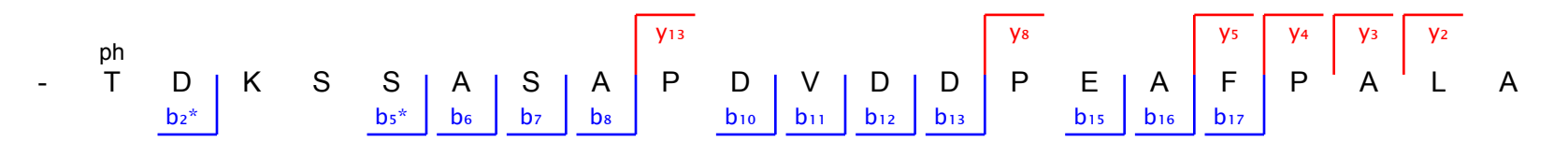
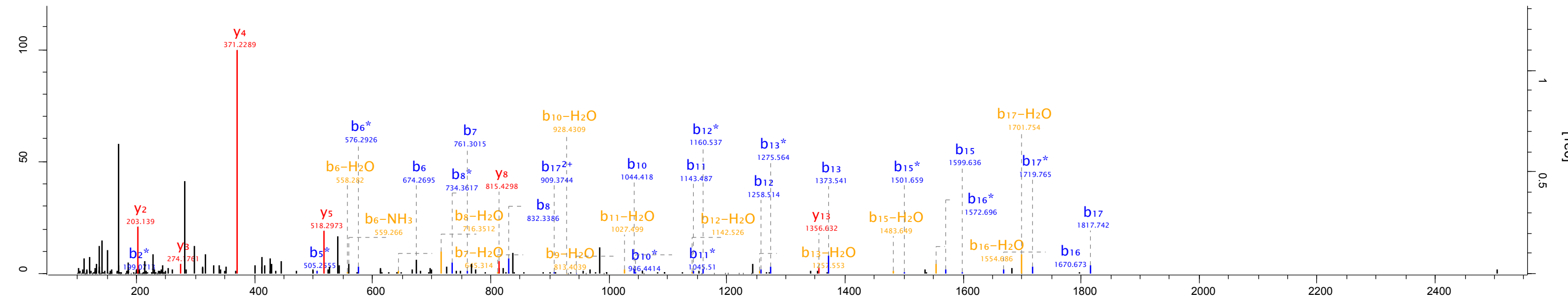
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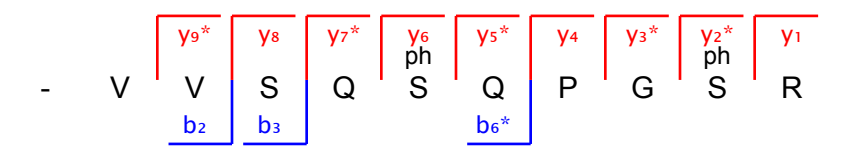
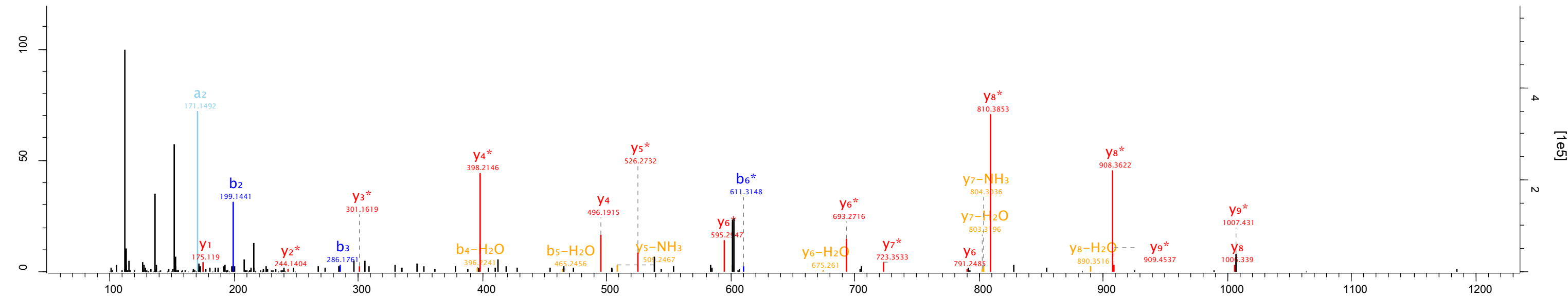
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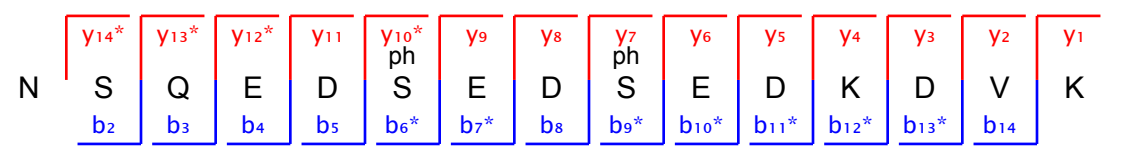
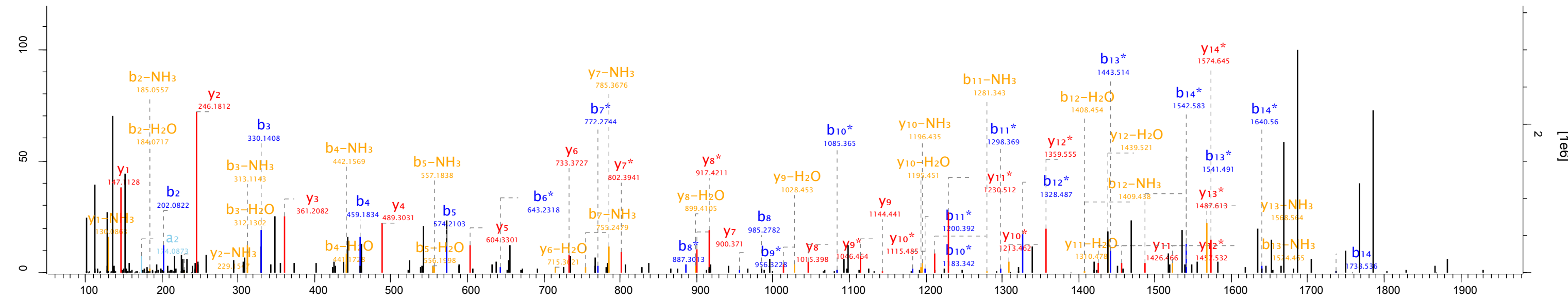
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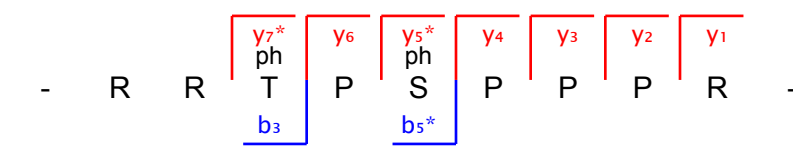
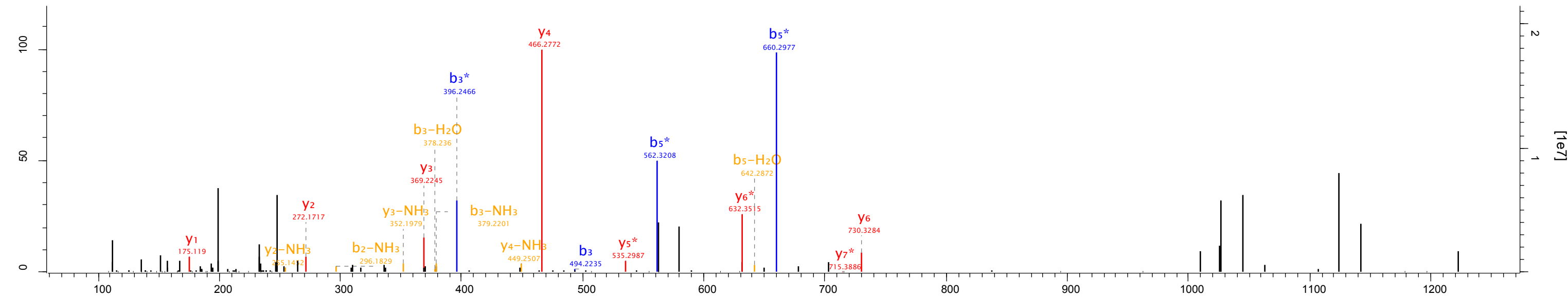
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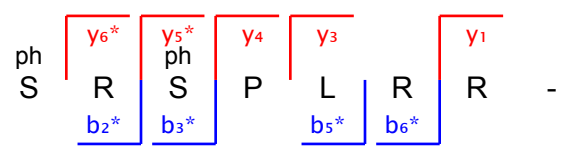
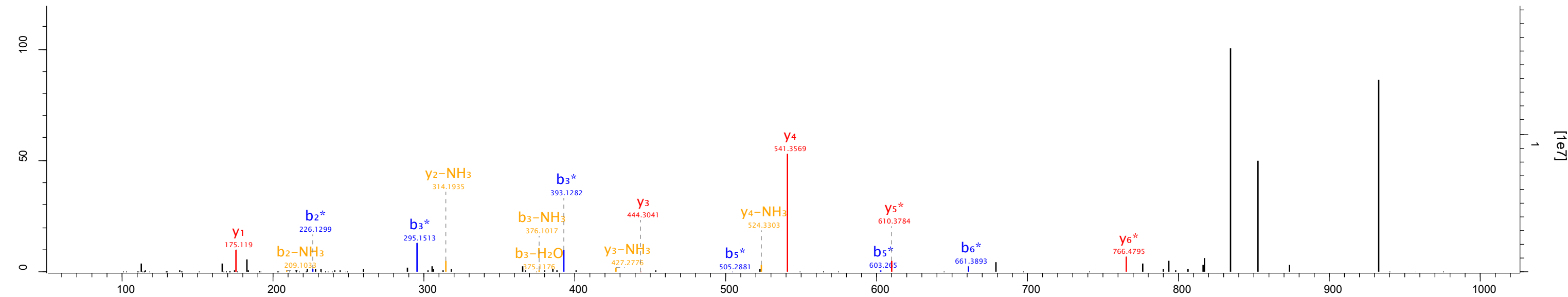
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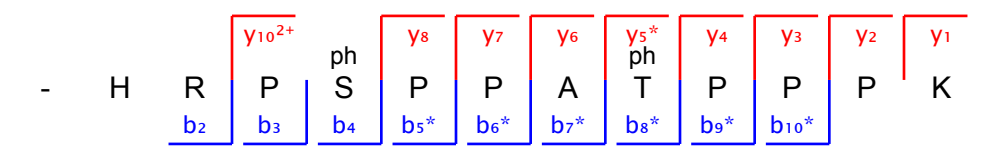
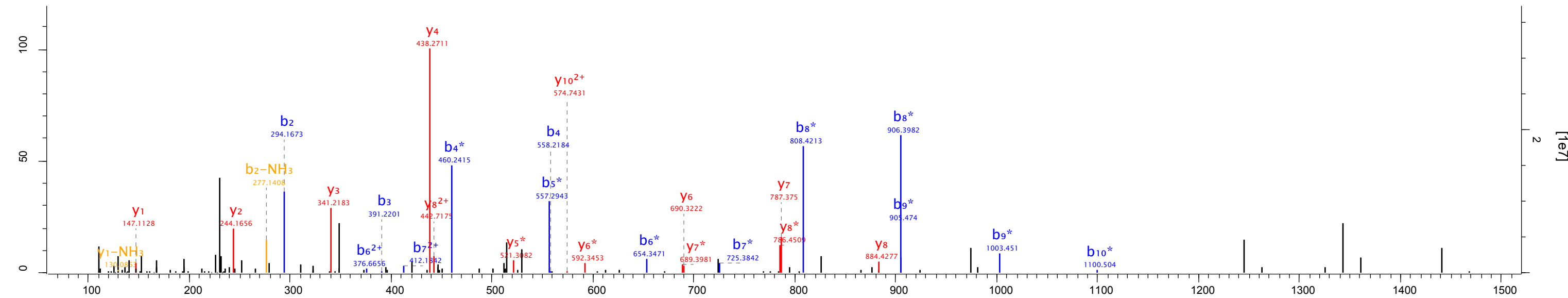
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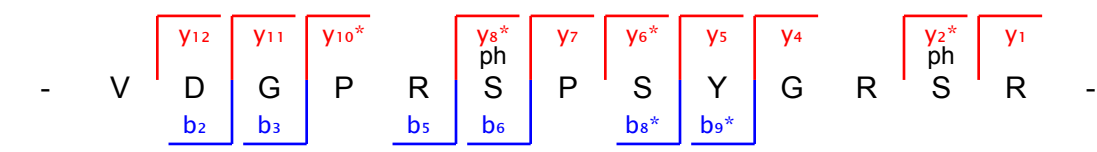
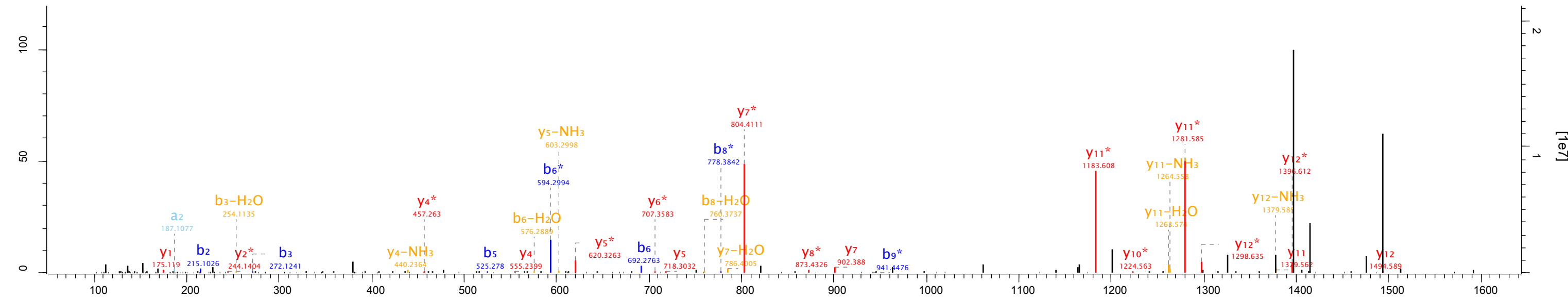
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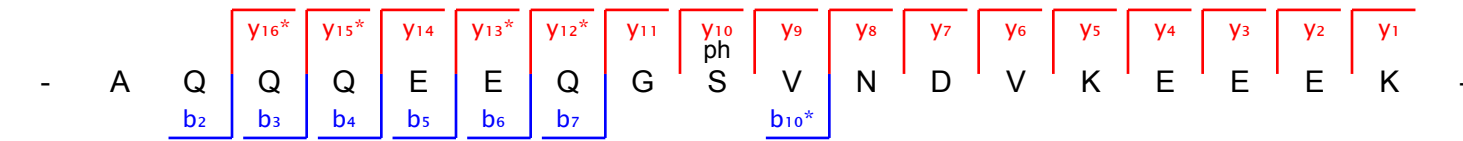
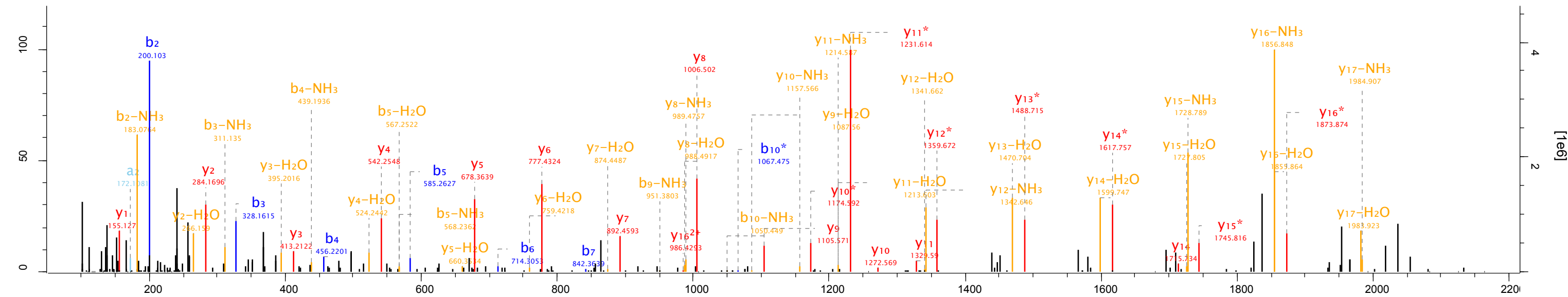


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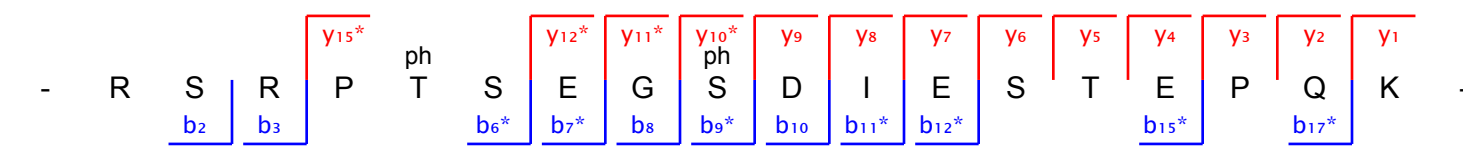
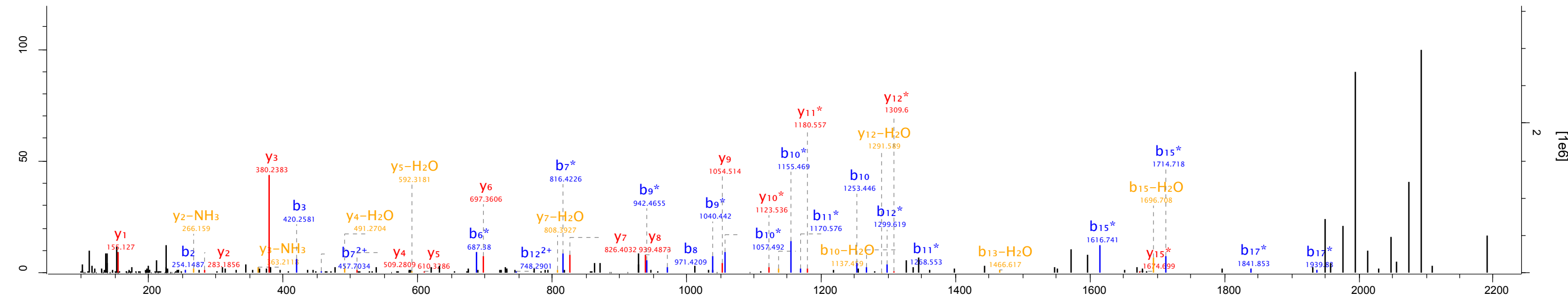


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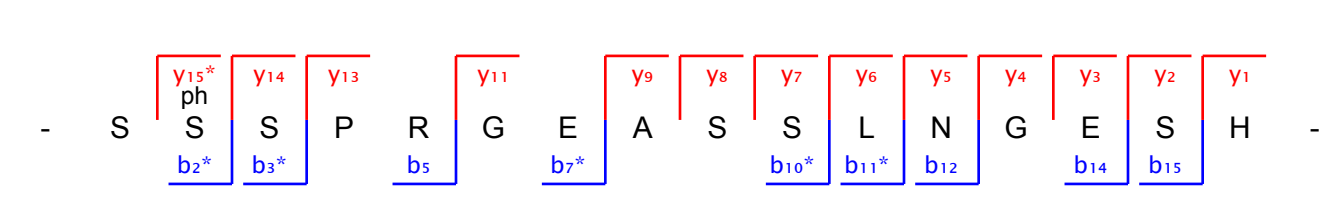
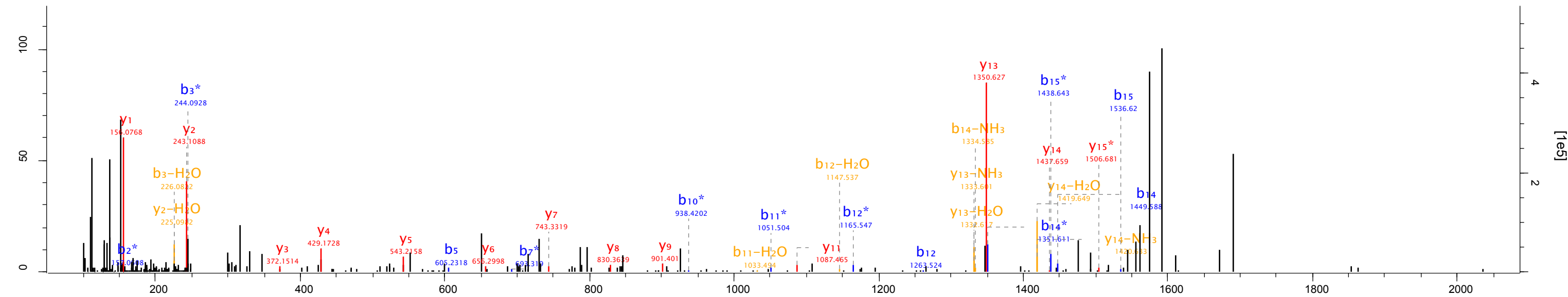




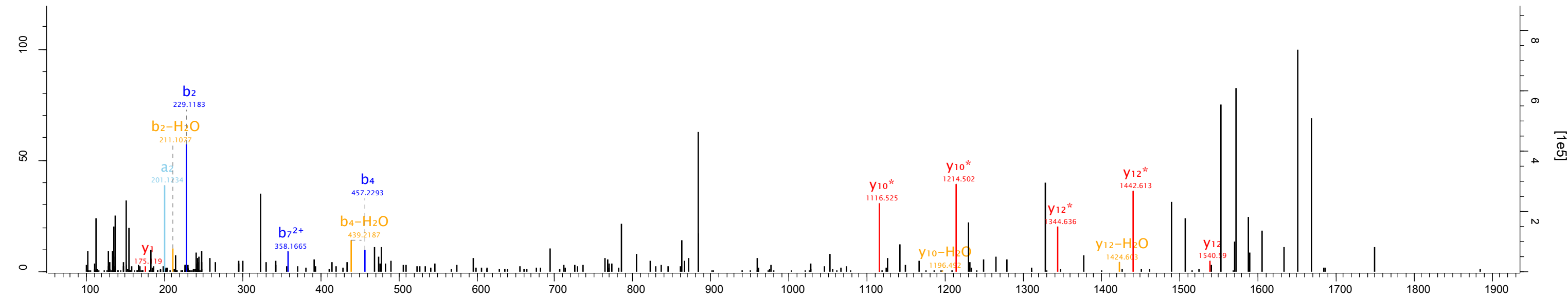
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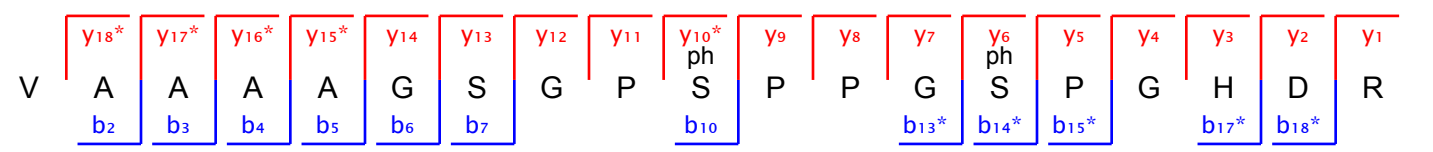
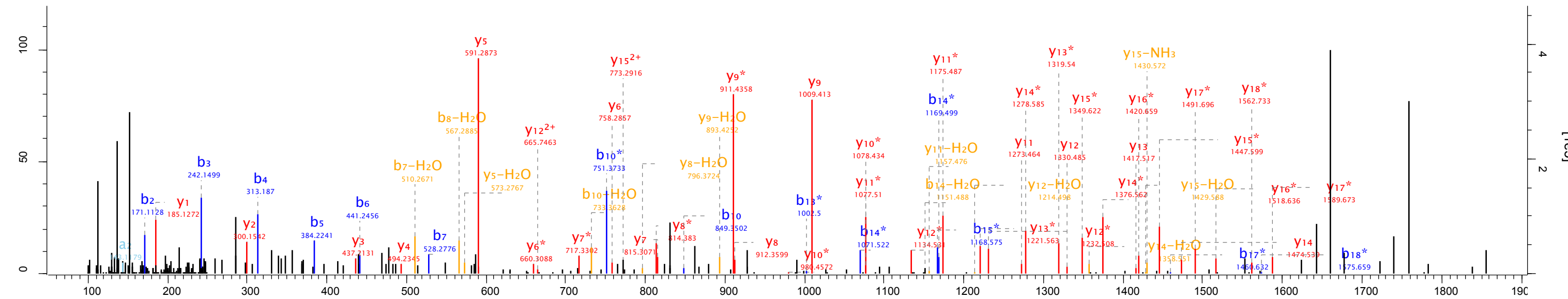
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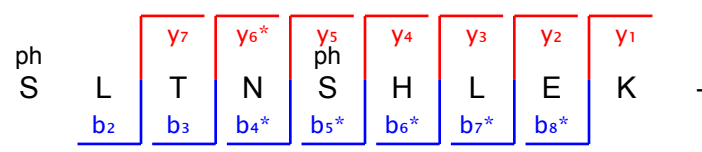
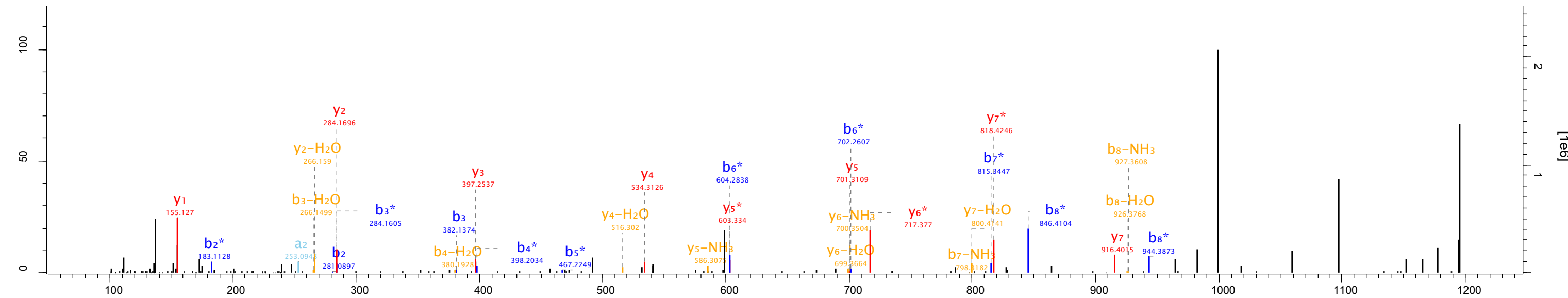
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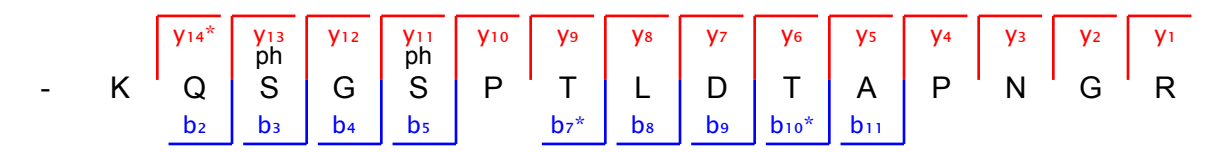
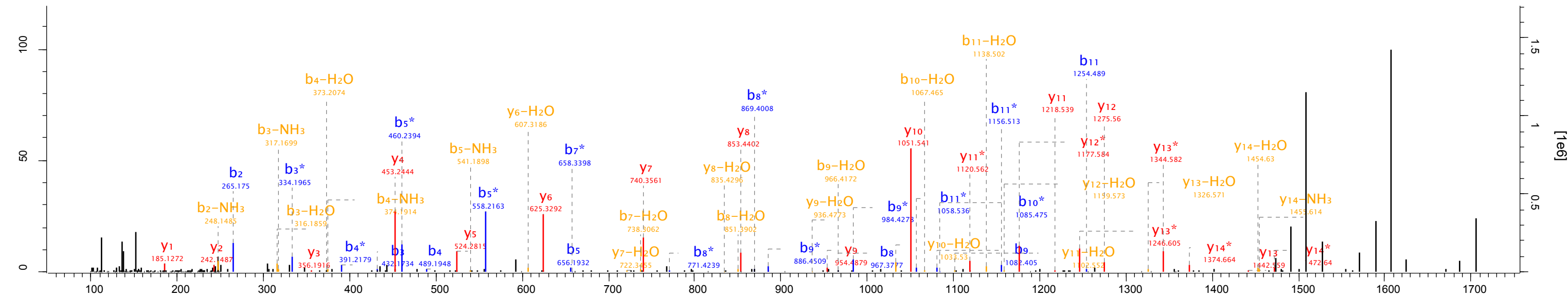
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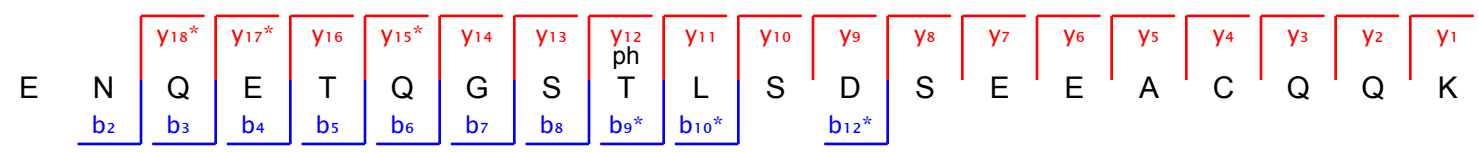
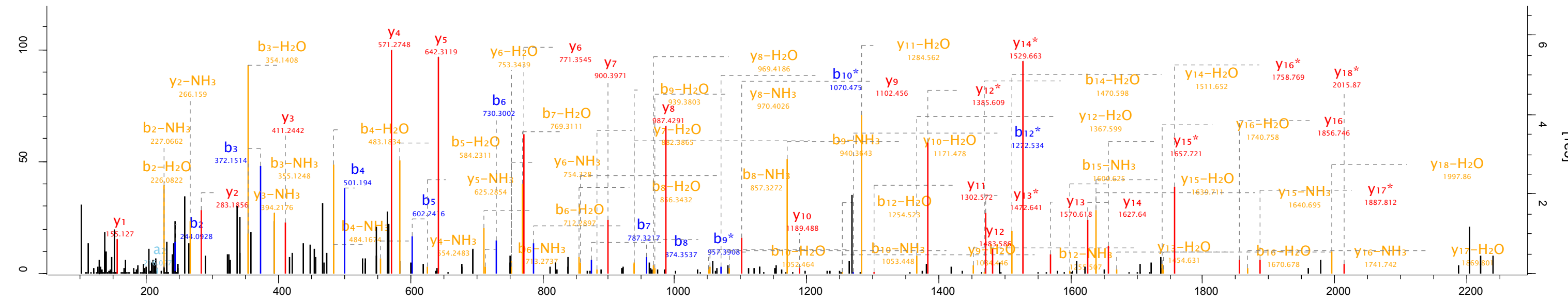
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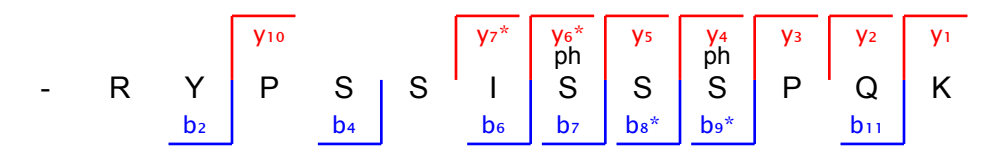
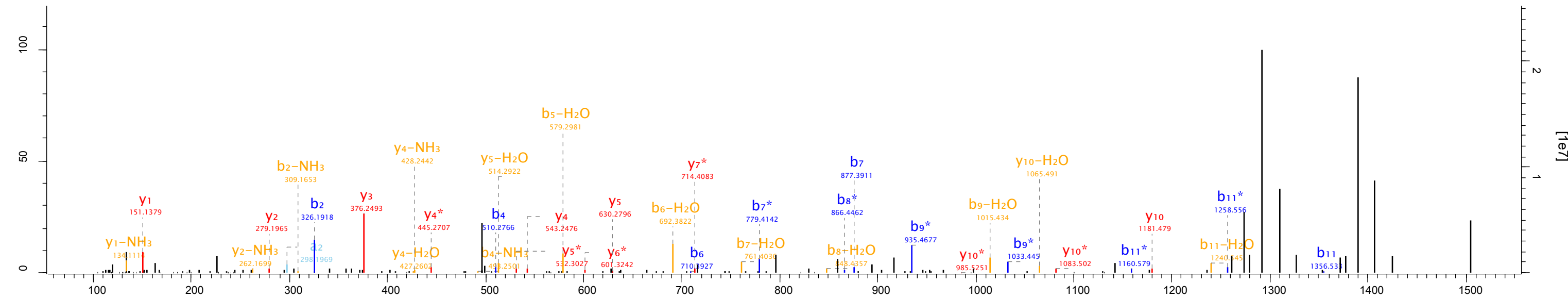
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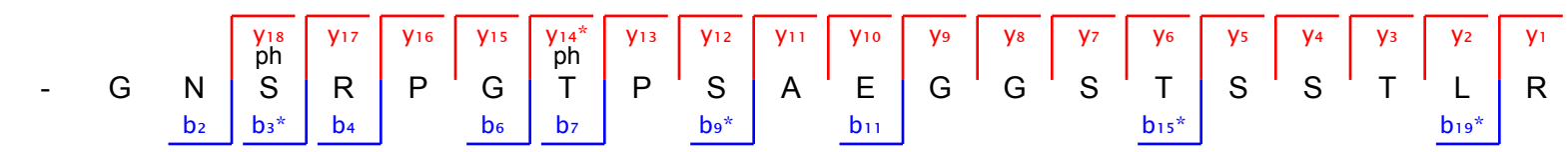
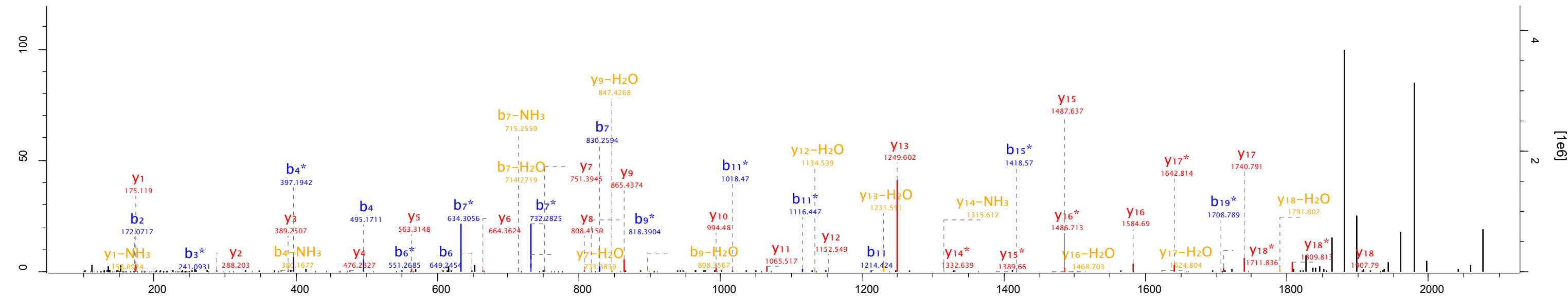
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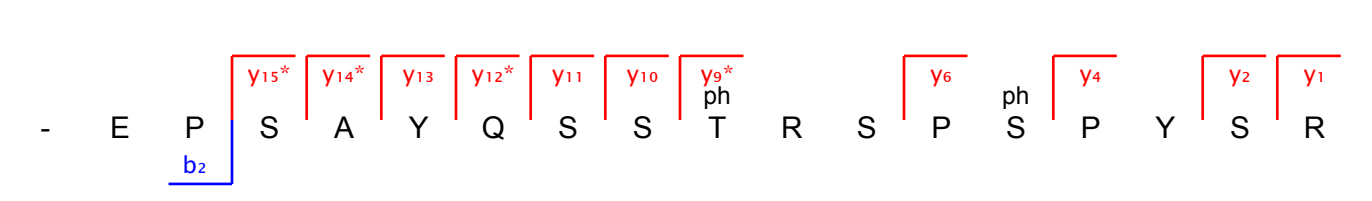
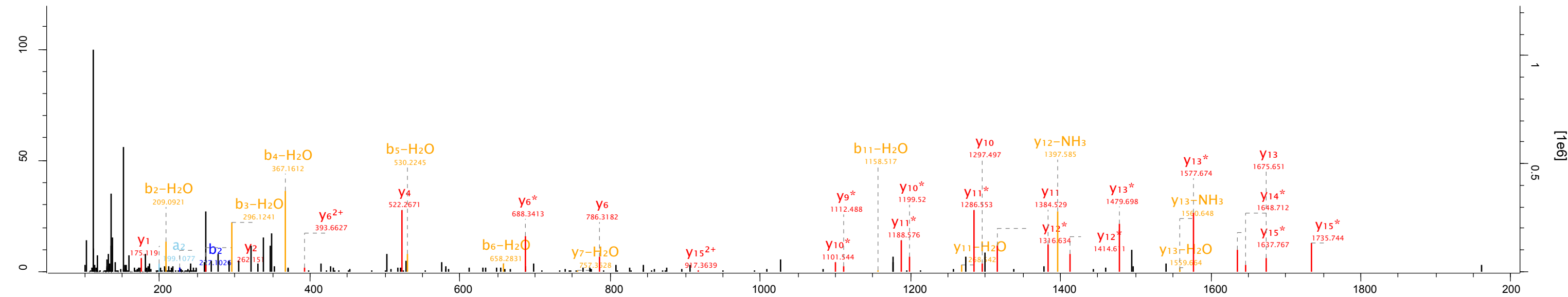
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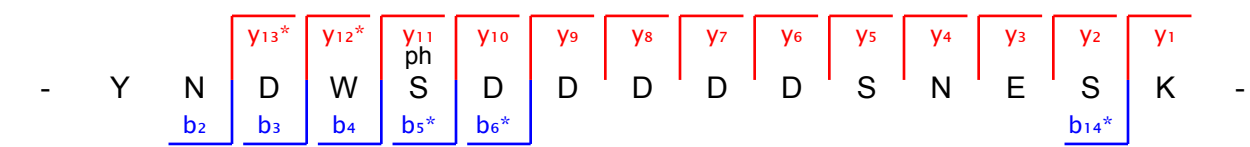
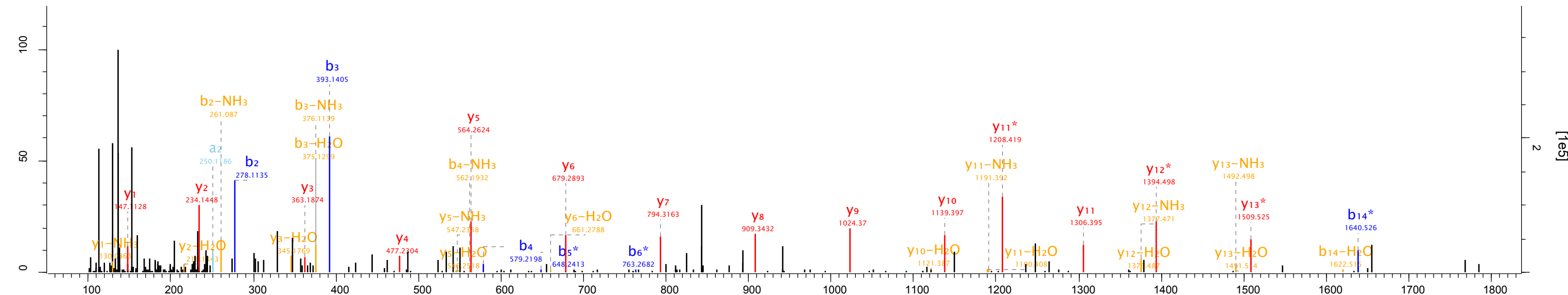
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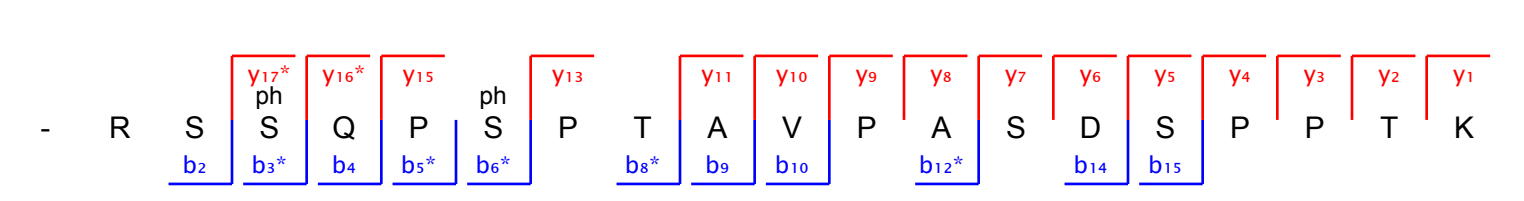
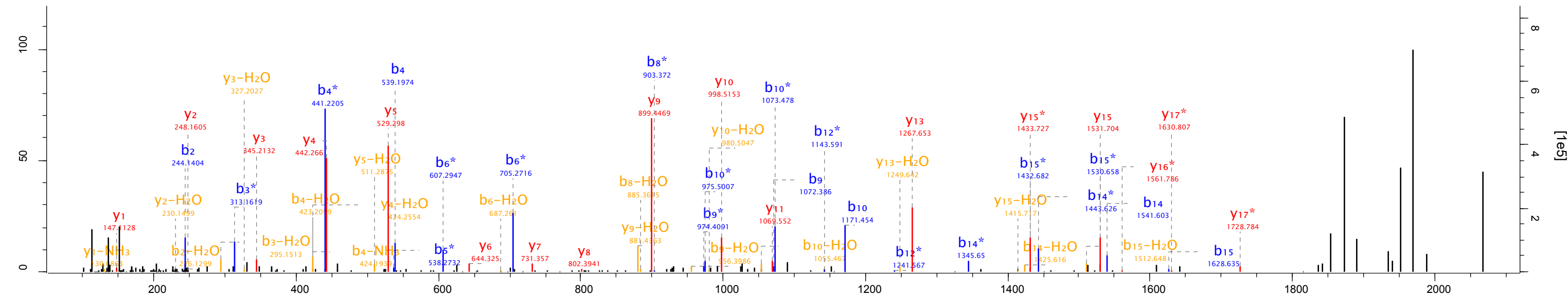
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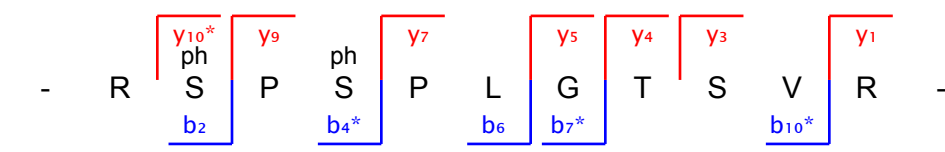
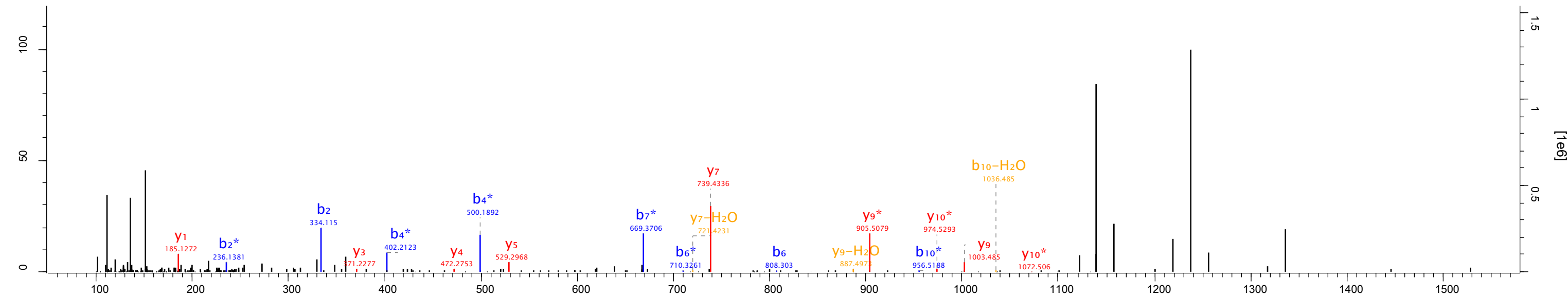
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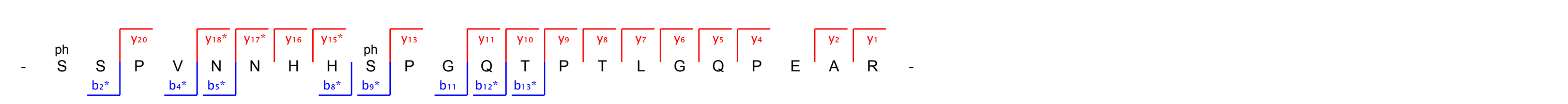
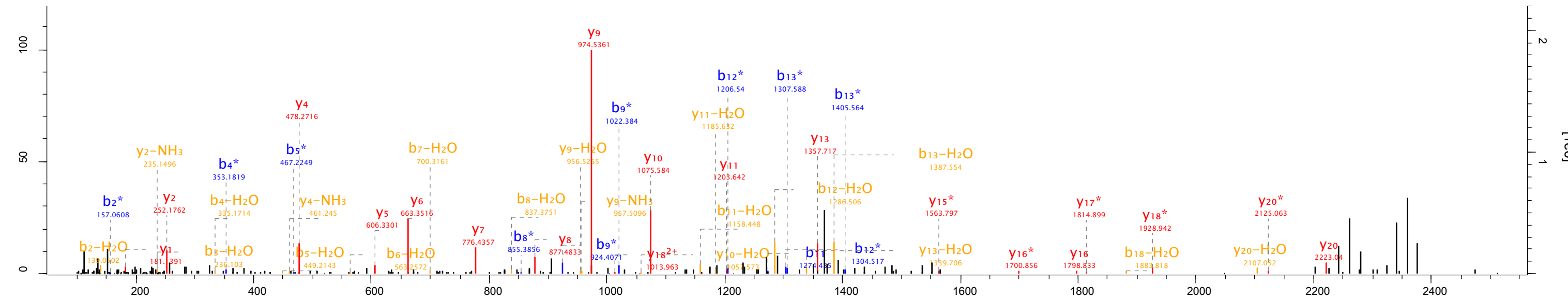
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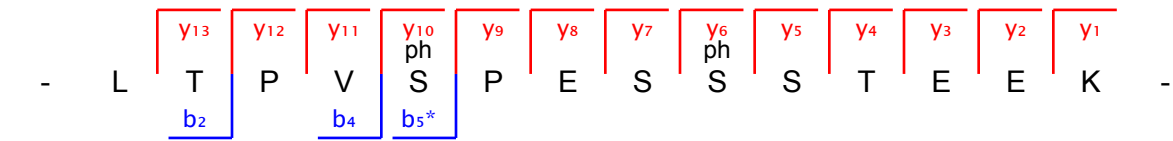
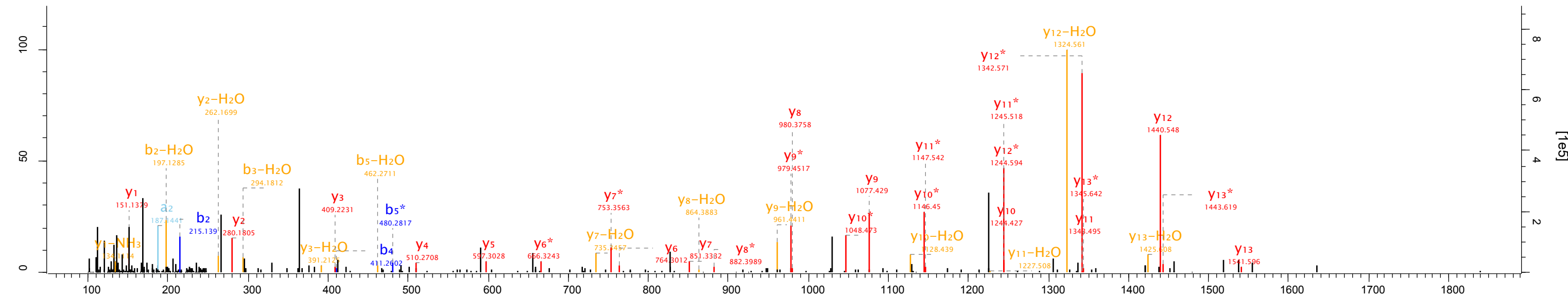


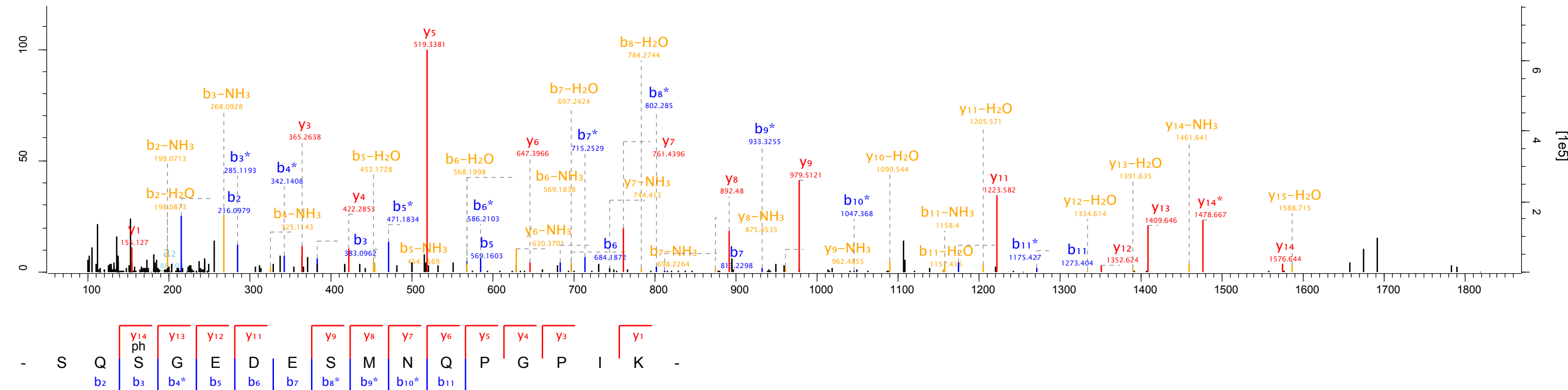
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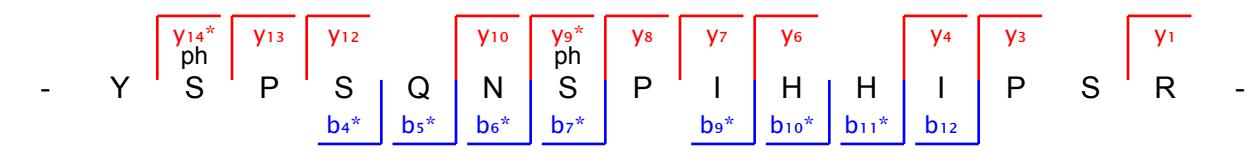
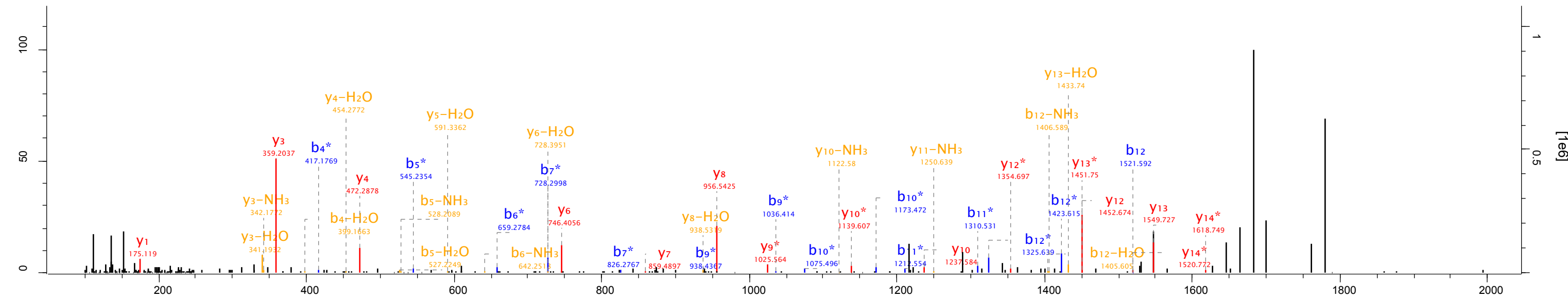
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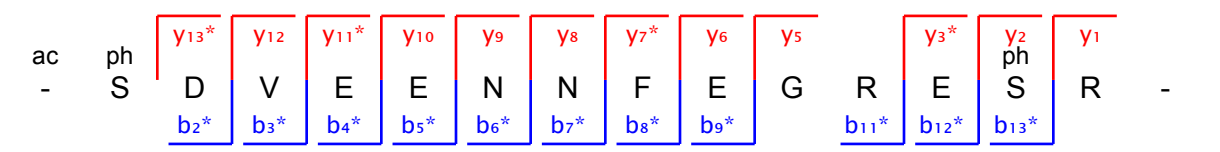
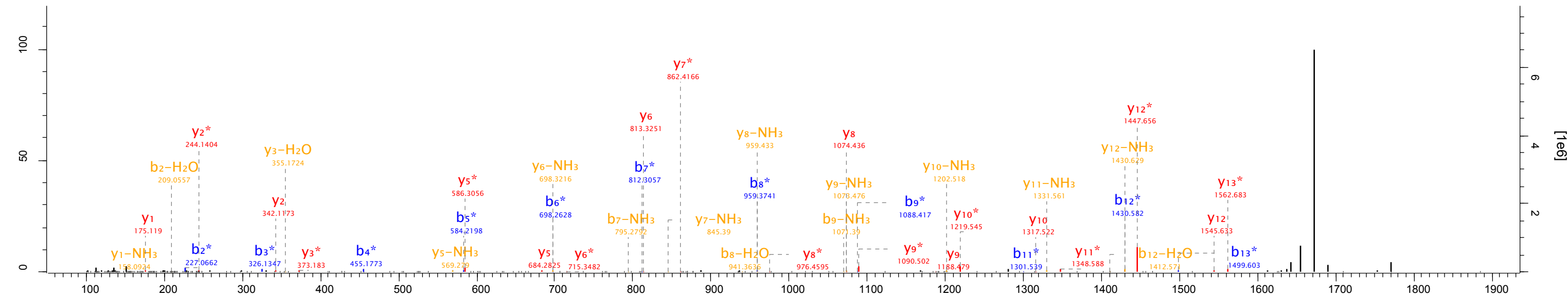


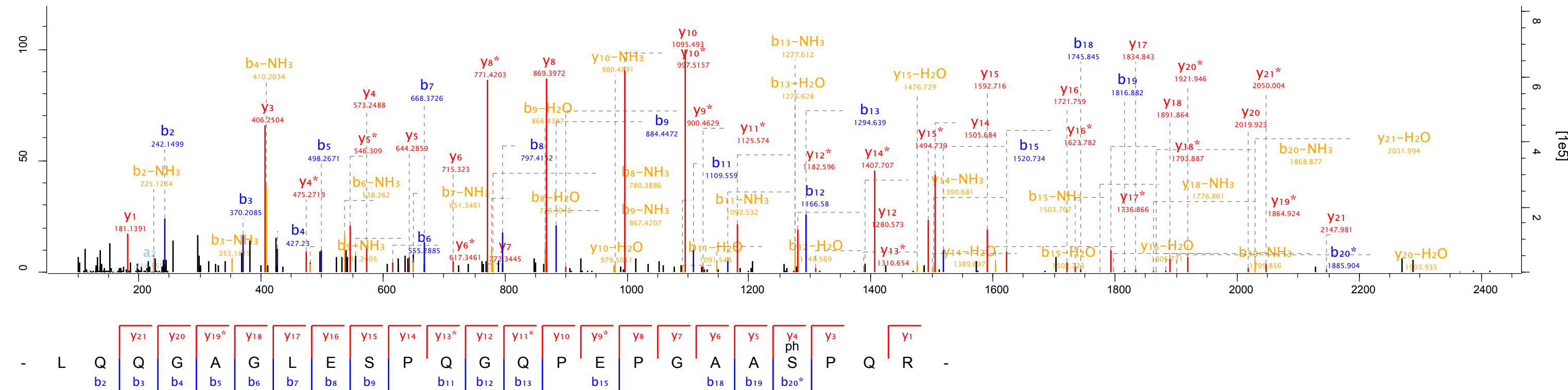


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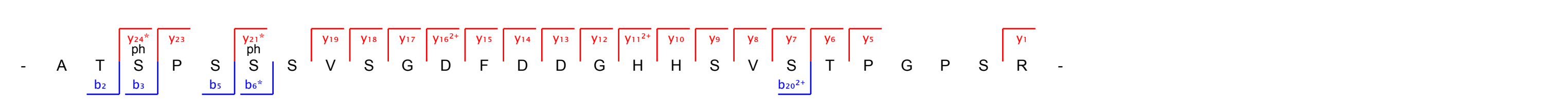
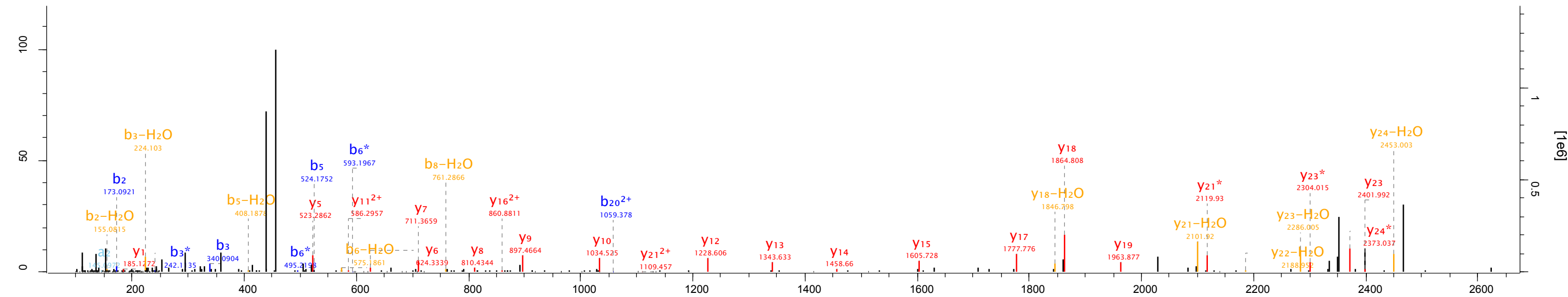


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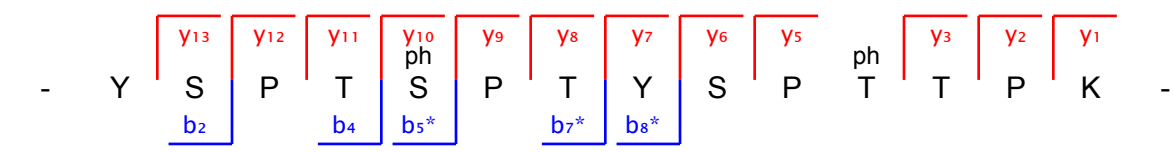
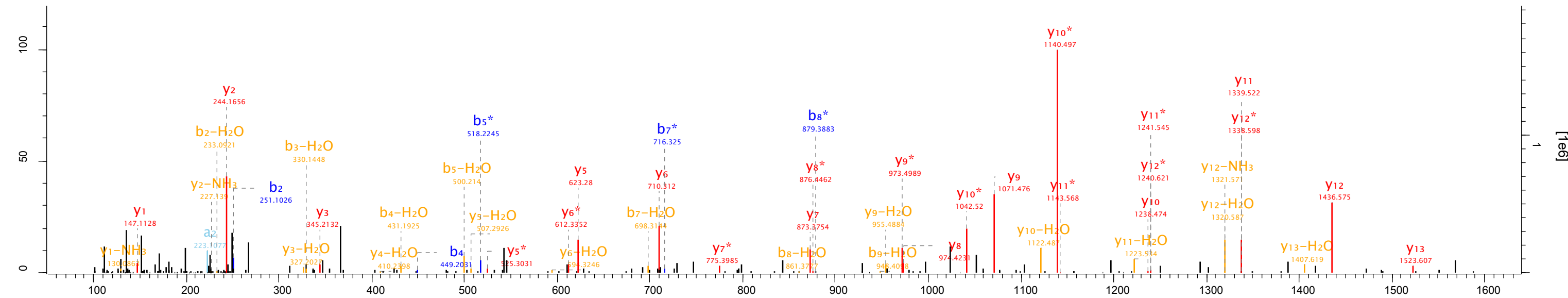




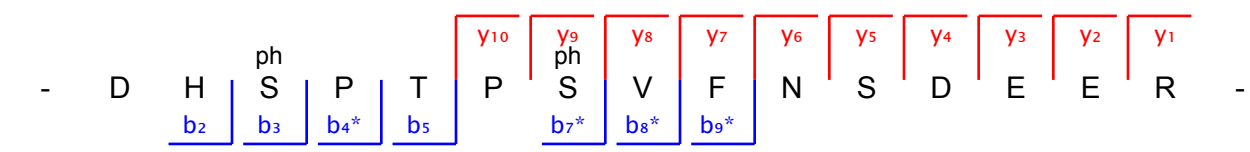
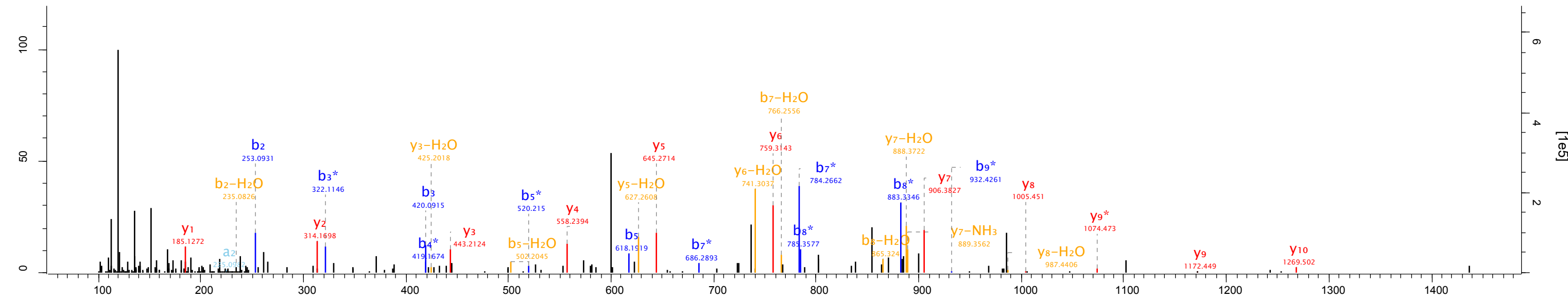
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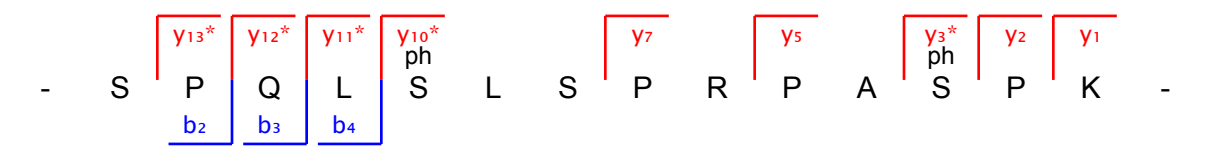
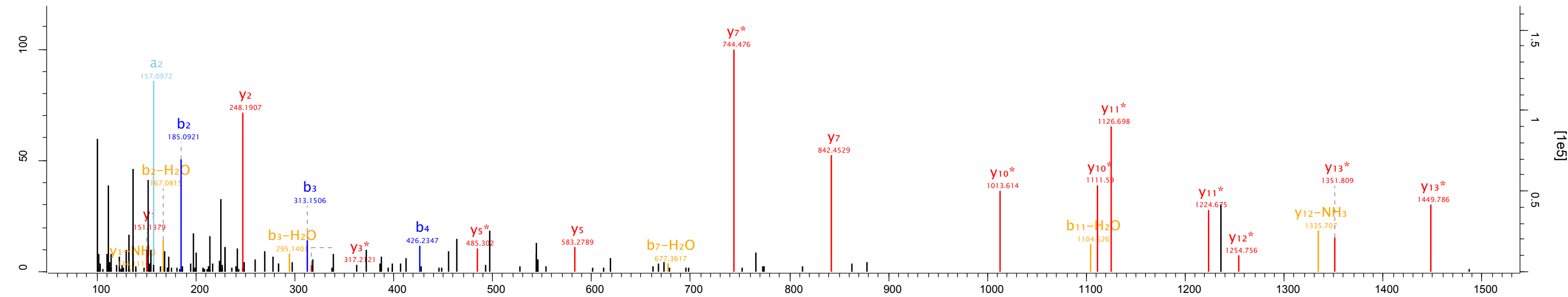
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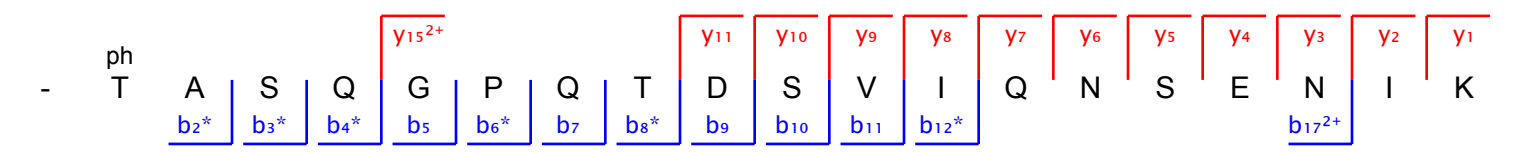
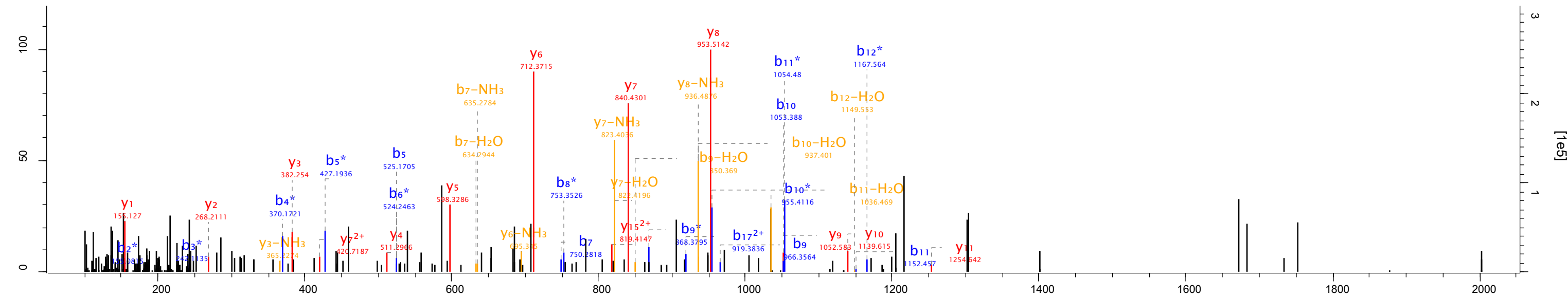
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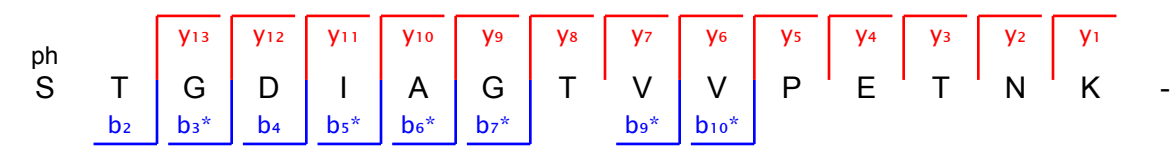
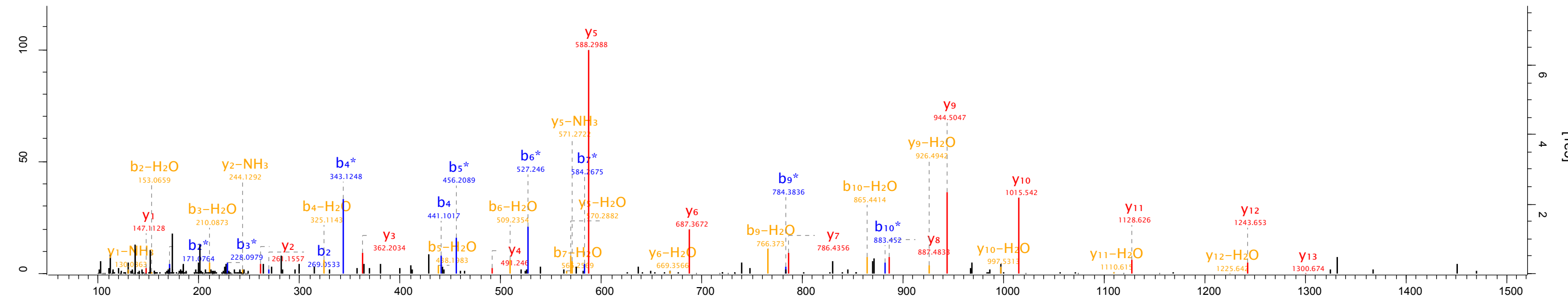
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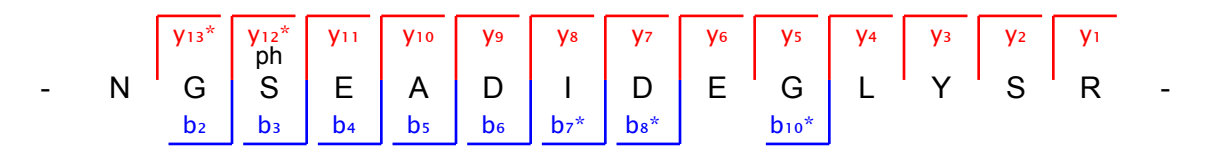
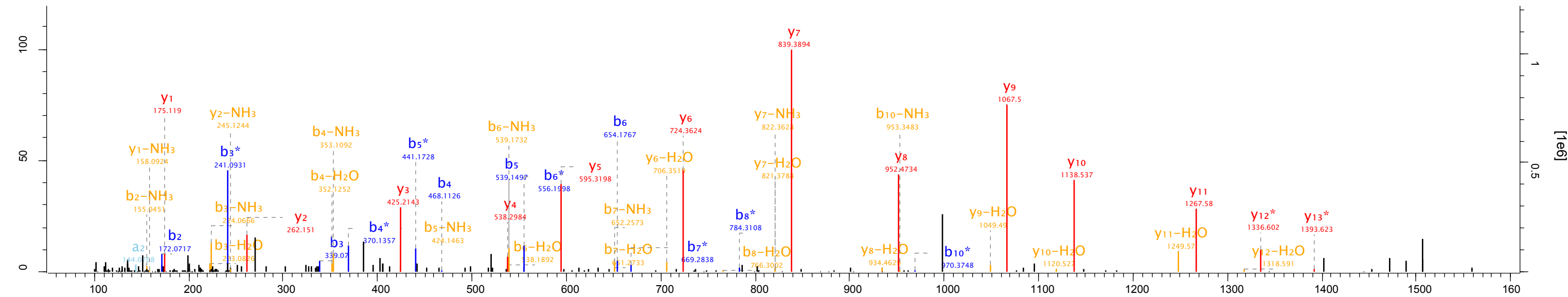
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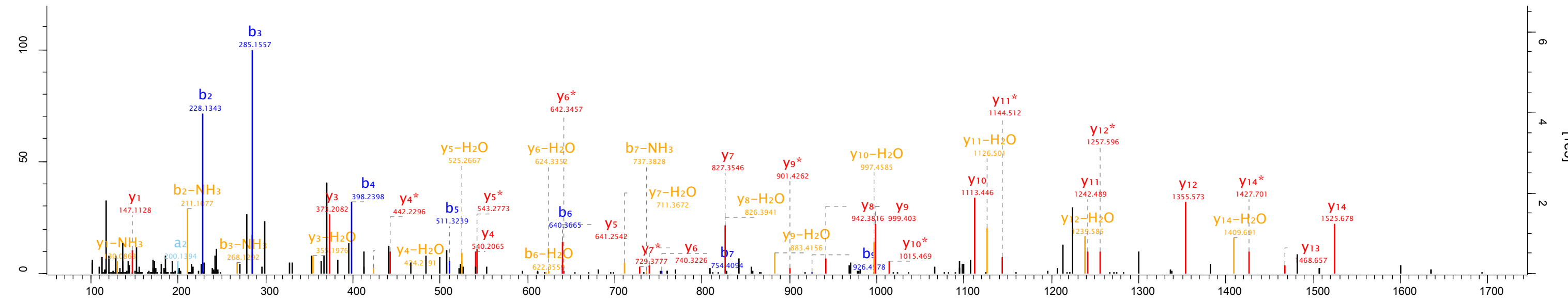
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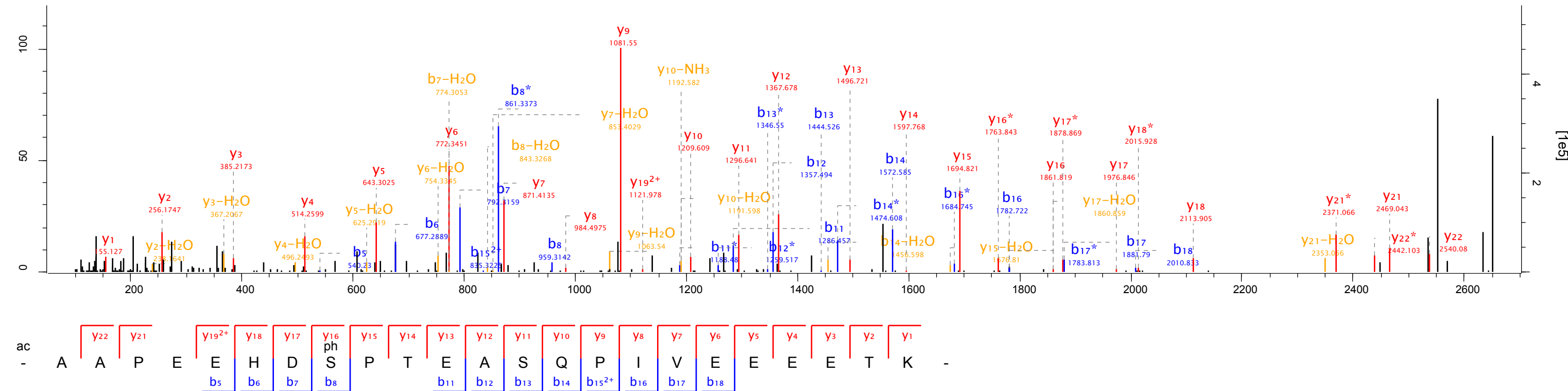
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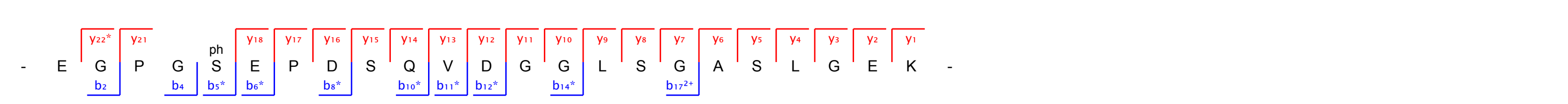
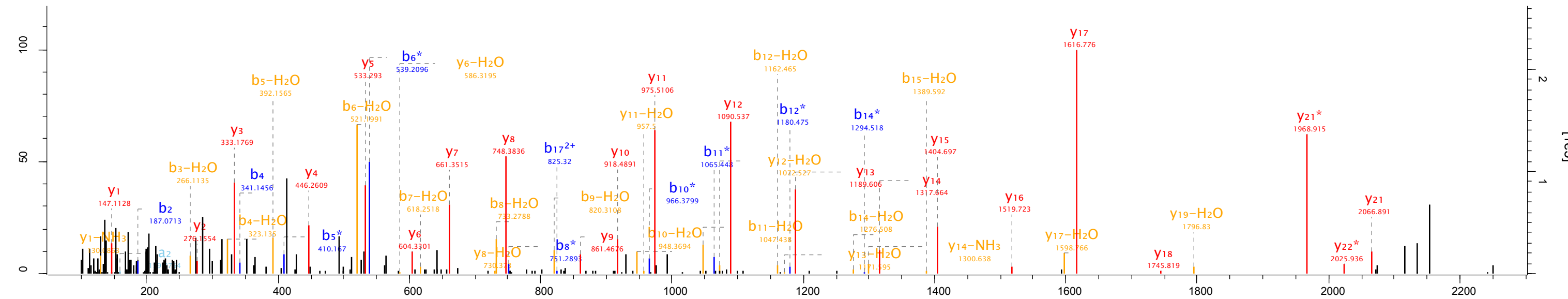
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Fragmentation sites are indicated by brackets below the sequence:

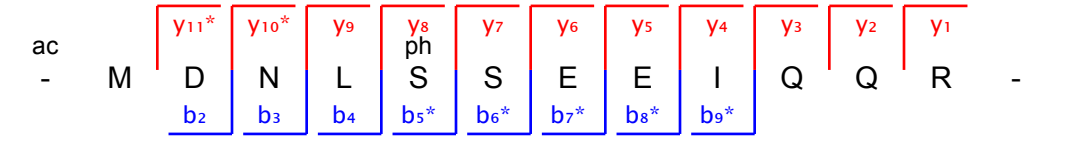
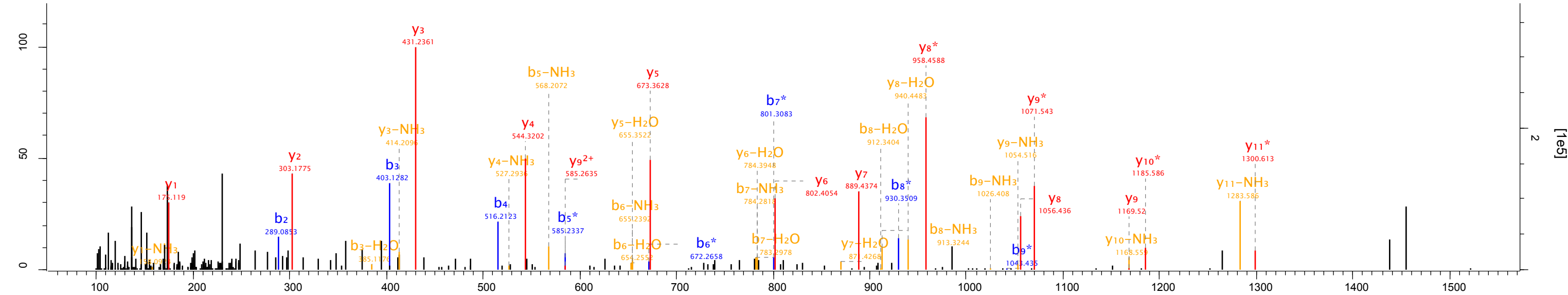
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- b₃ (under G)
- b₄ (under L)
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- y₁ (under K)
- y₃ (under P)
- y₄ (under S)
- y₅ (under T)
- y₆ (under V)
- y₇ (under S)
- y₈ (under D)
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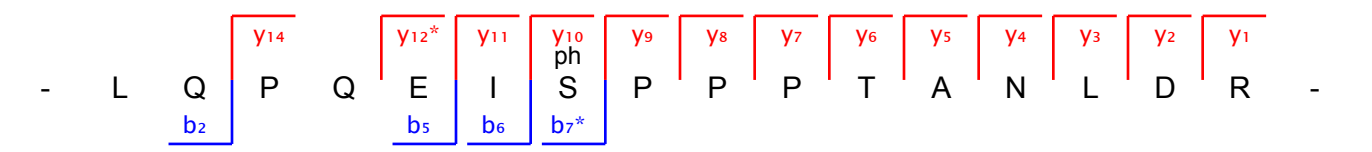
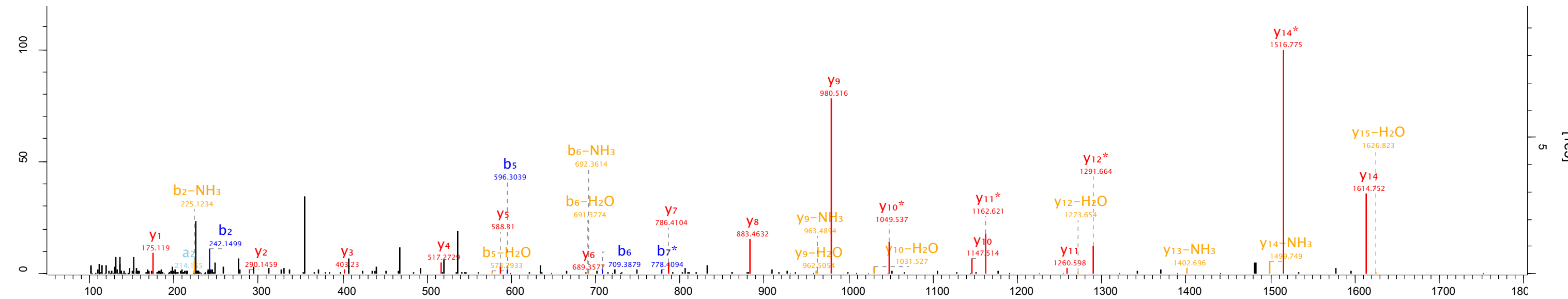
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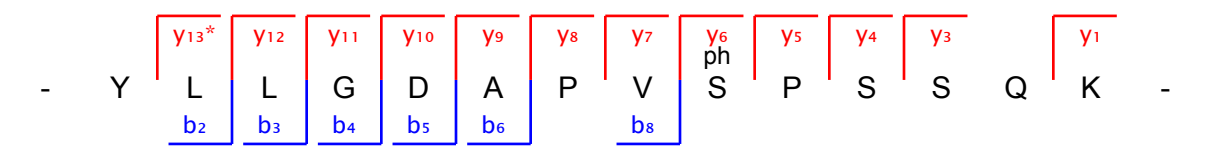
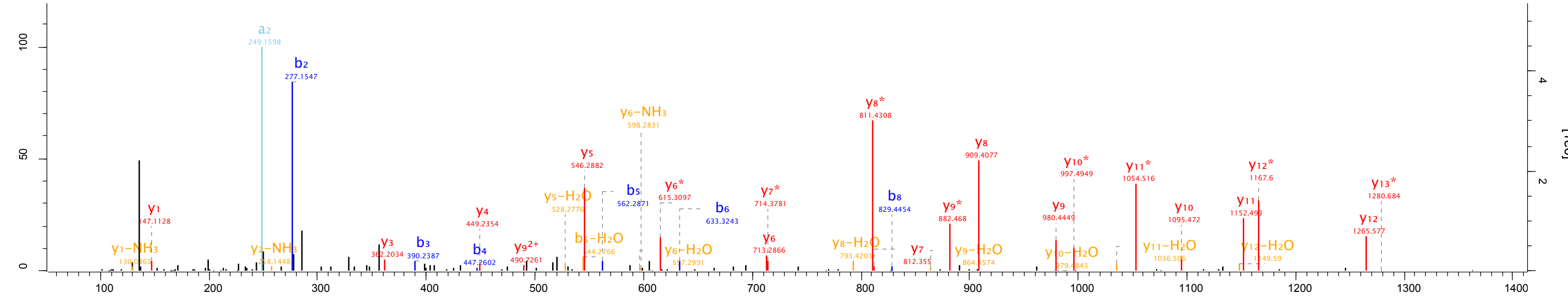
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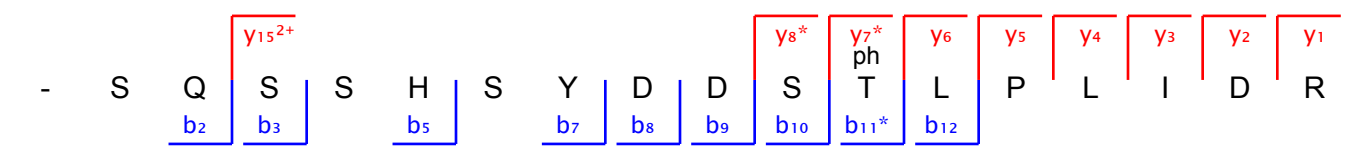
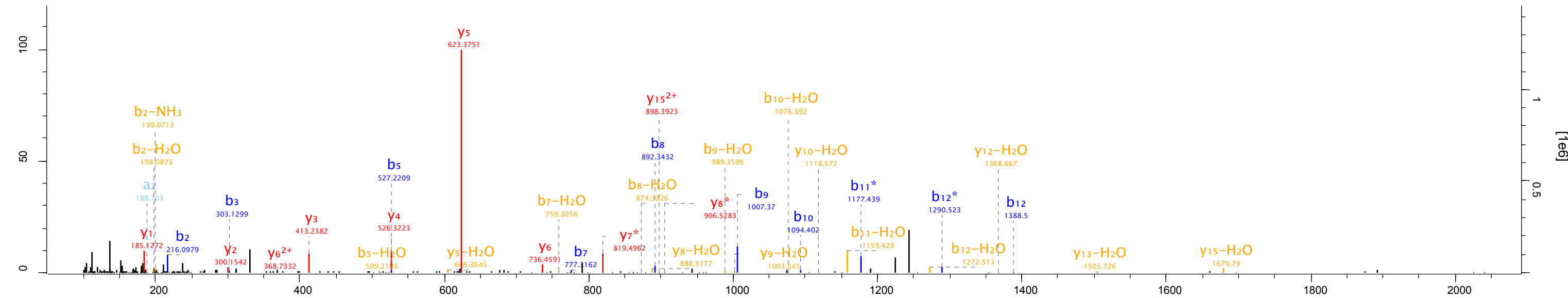
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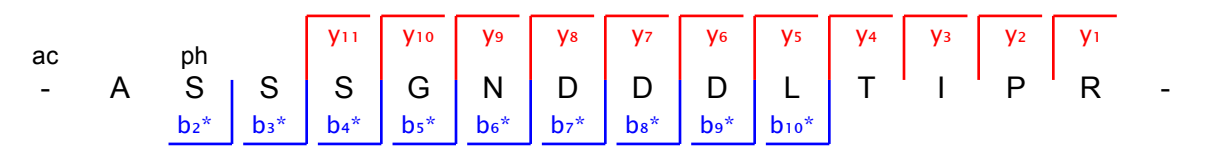
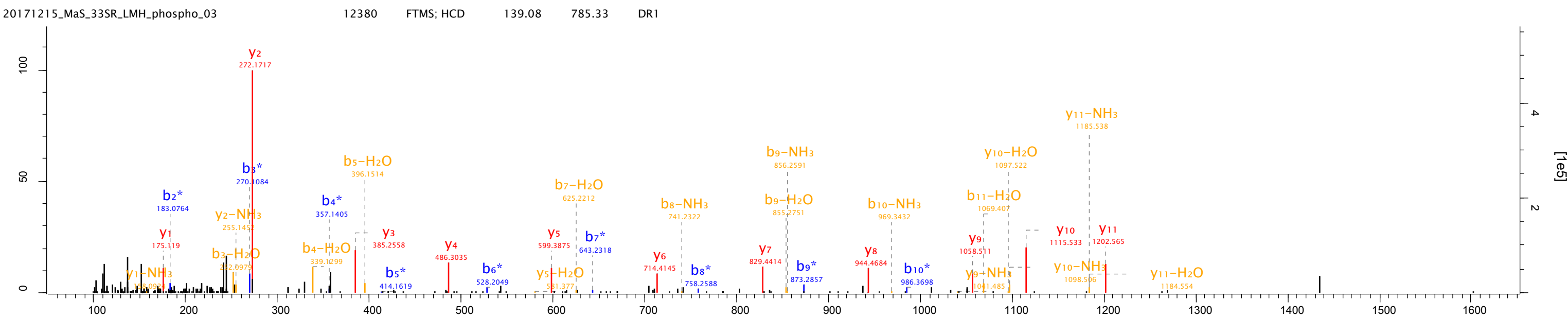
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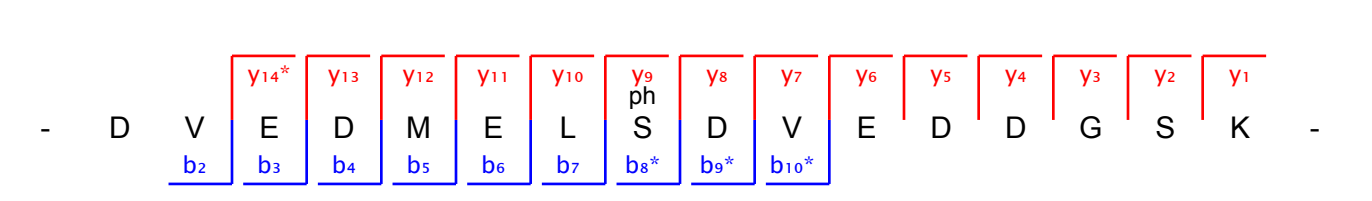
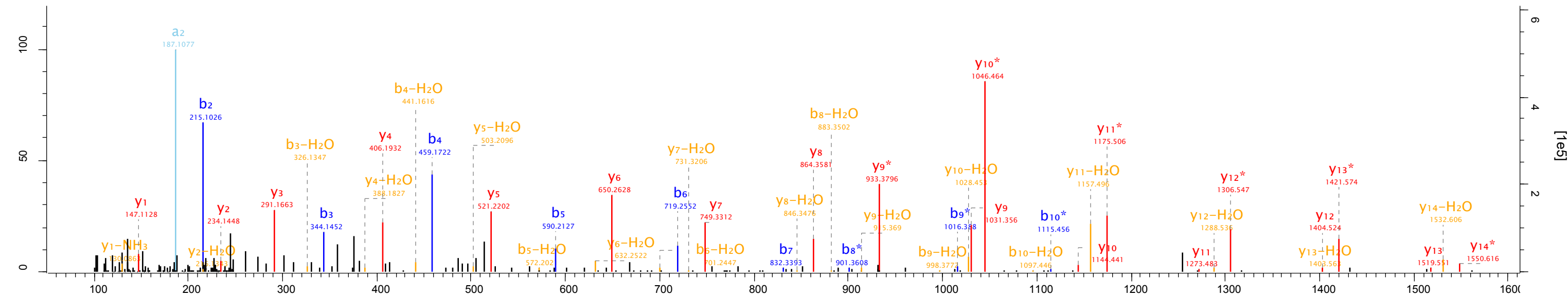
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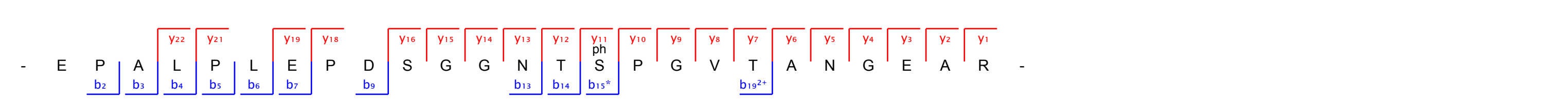
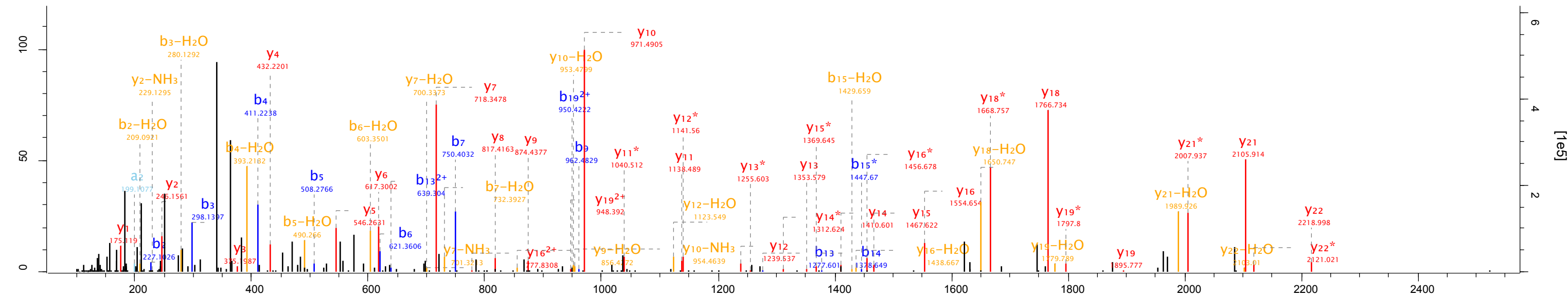
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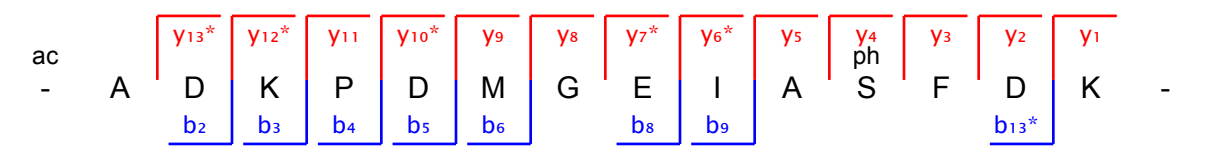
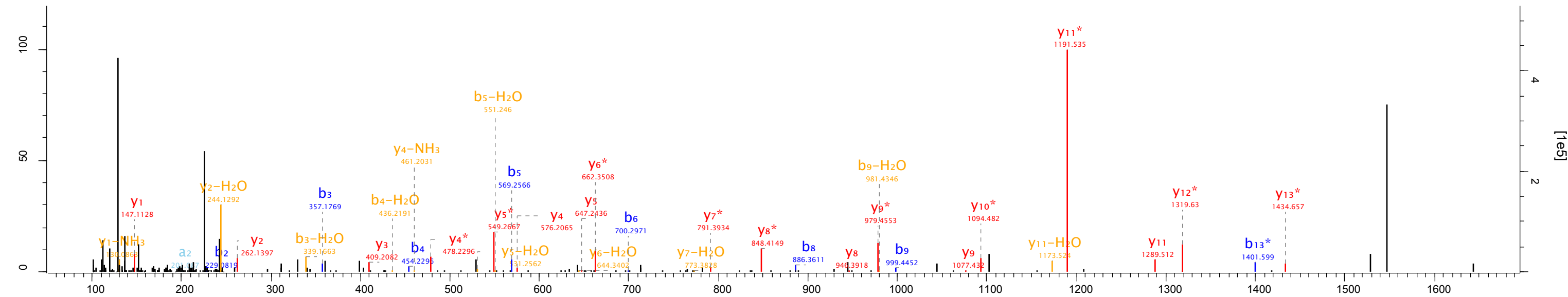
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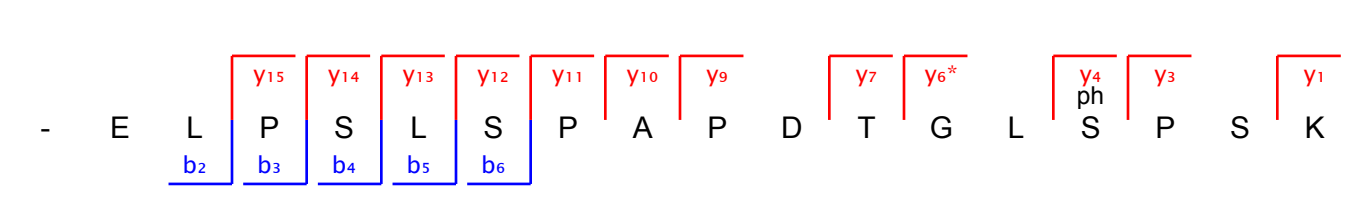
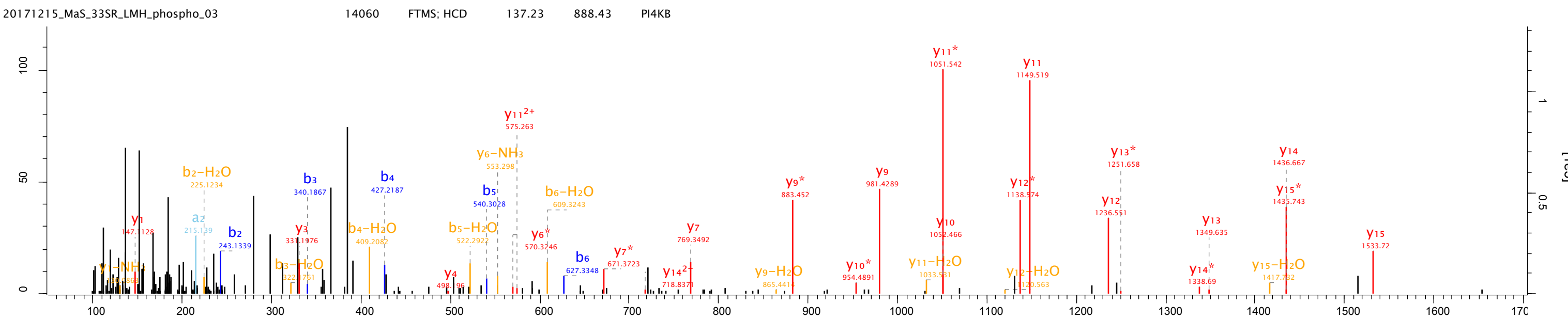
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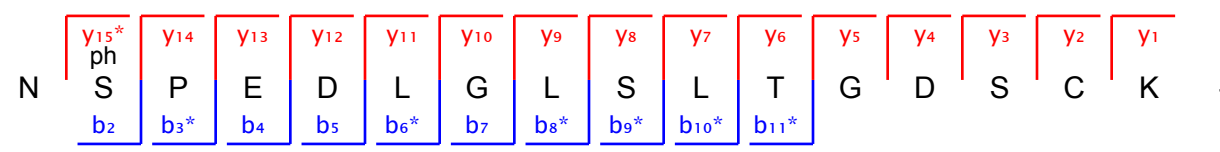
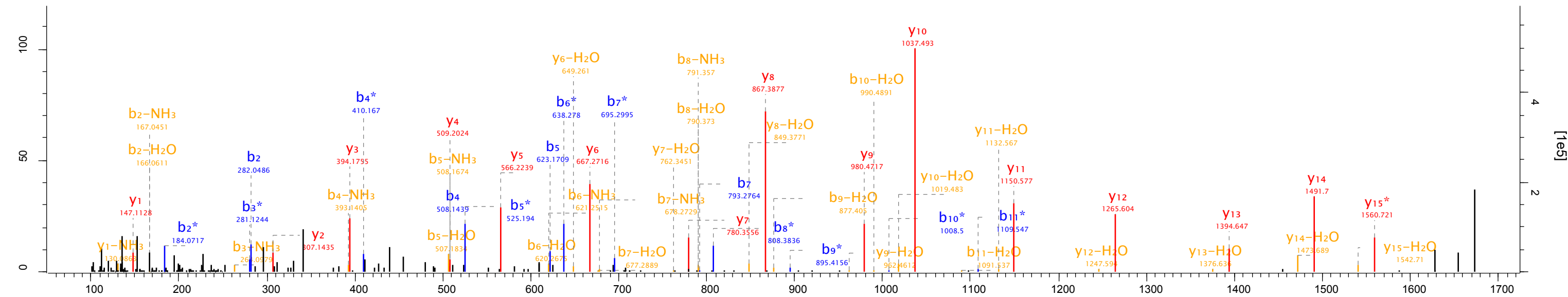
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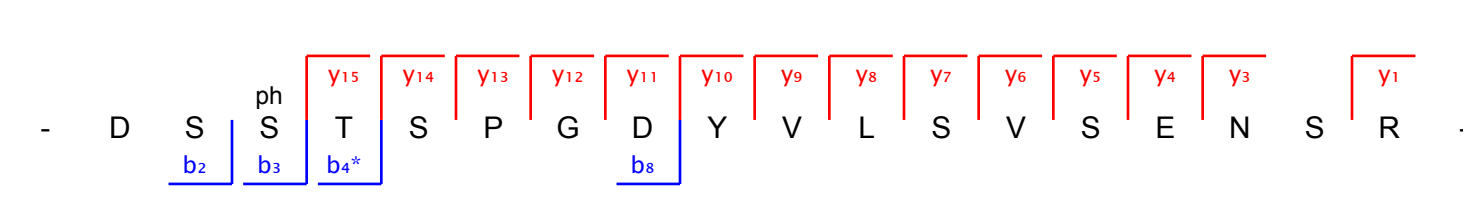
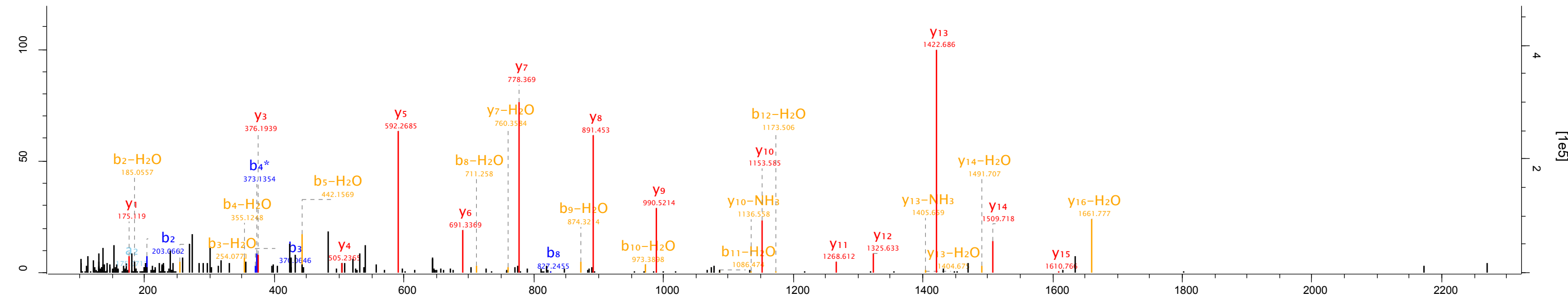
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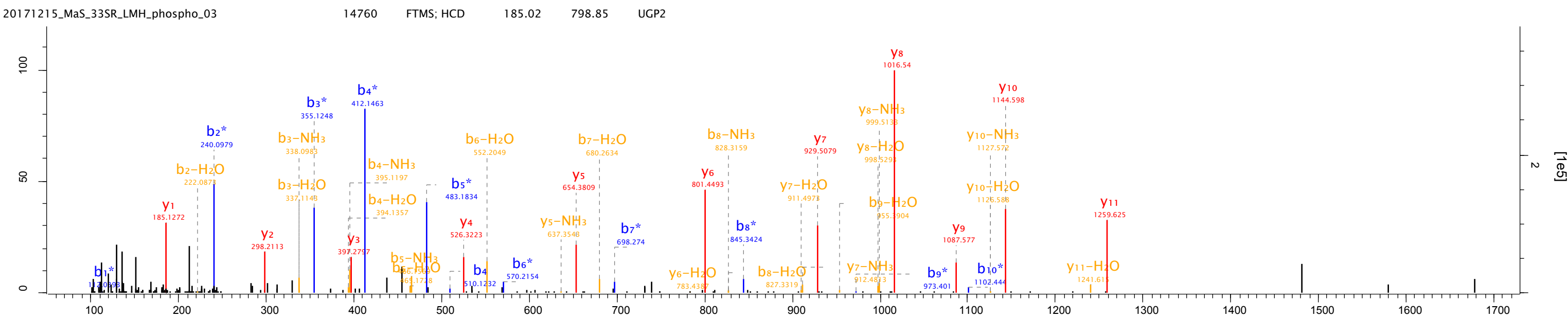
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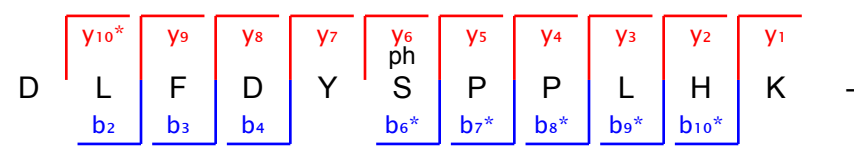
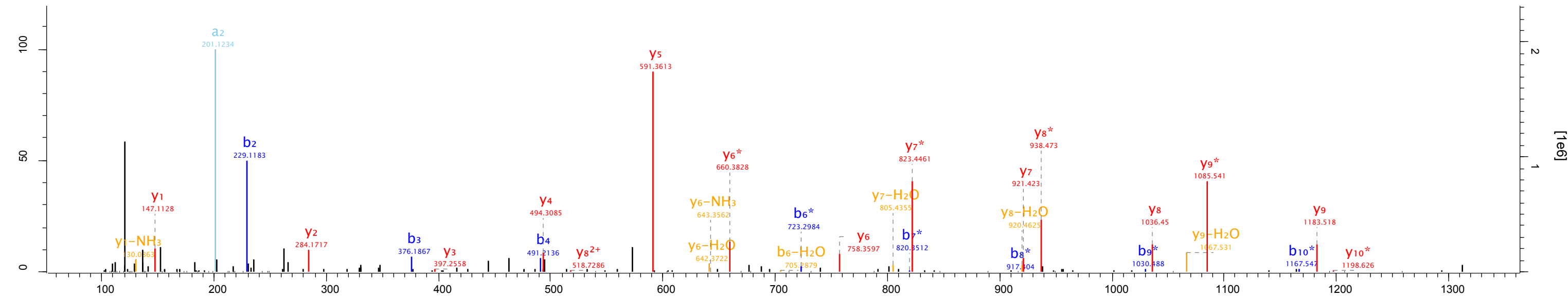
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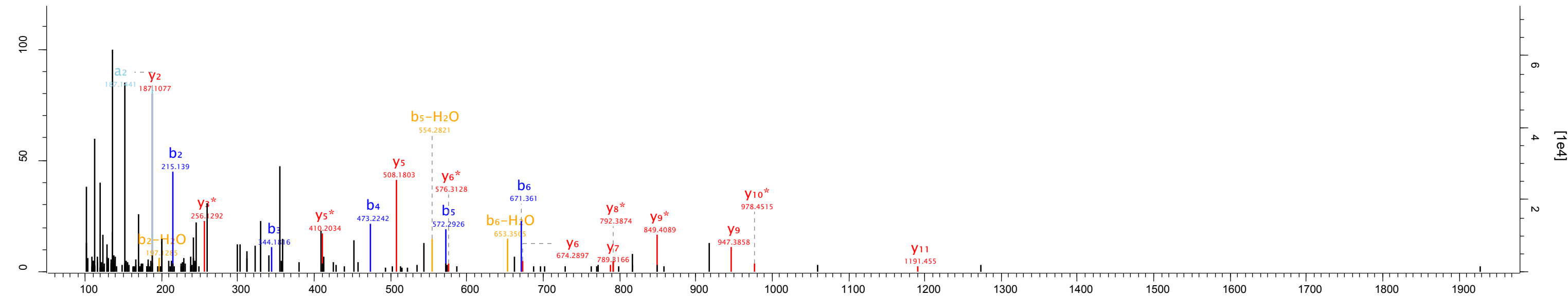
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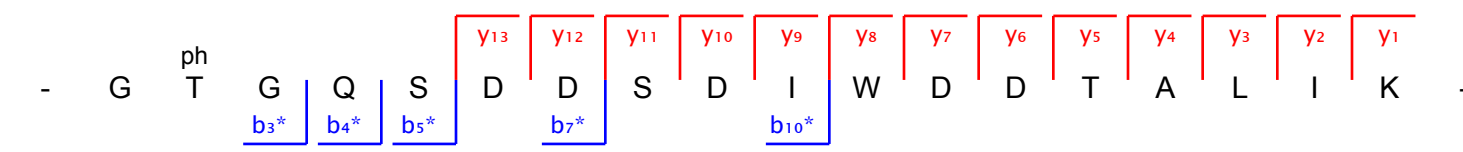
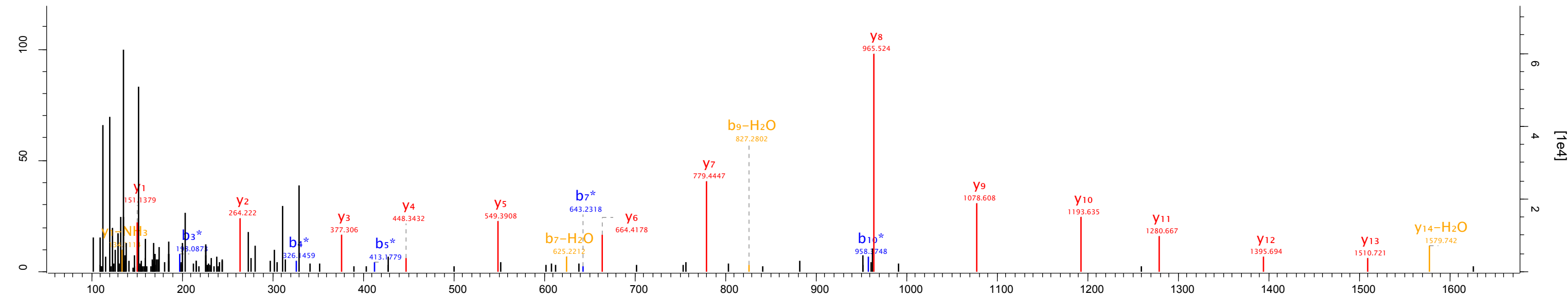
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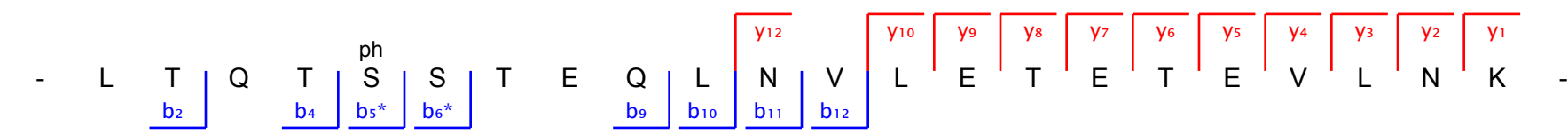
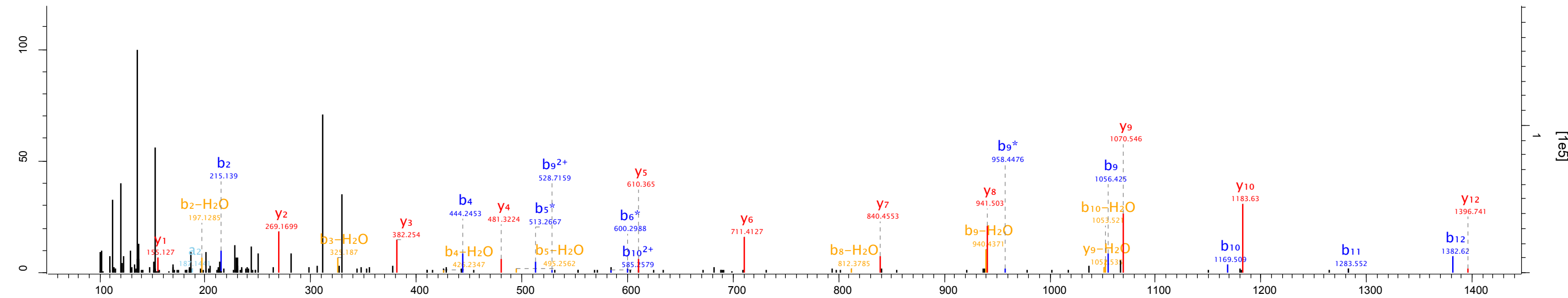
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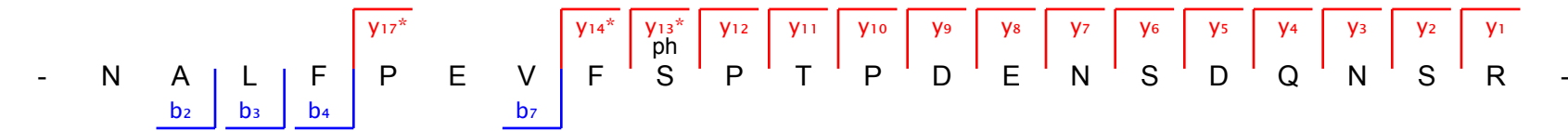
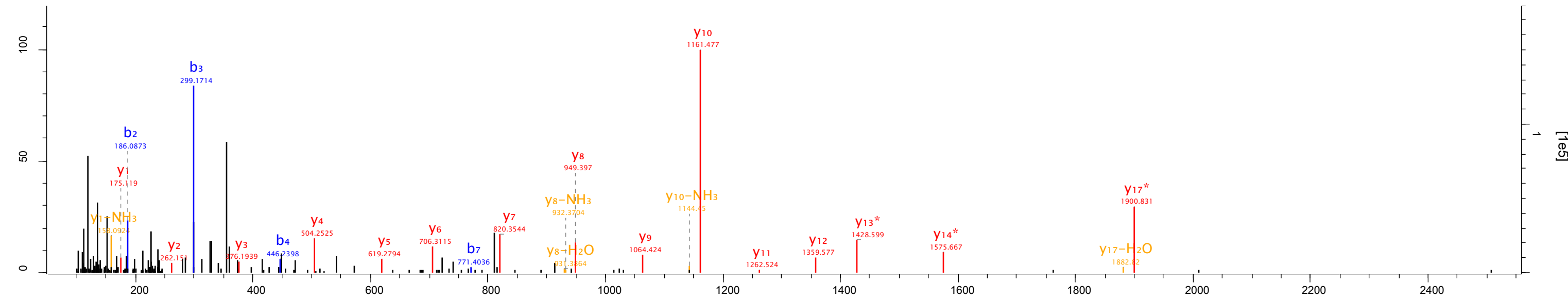


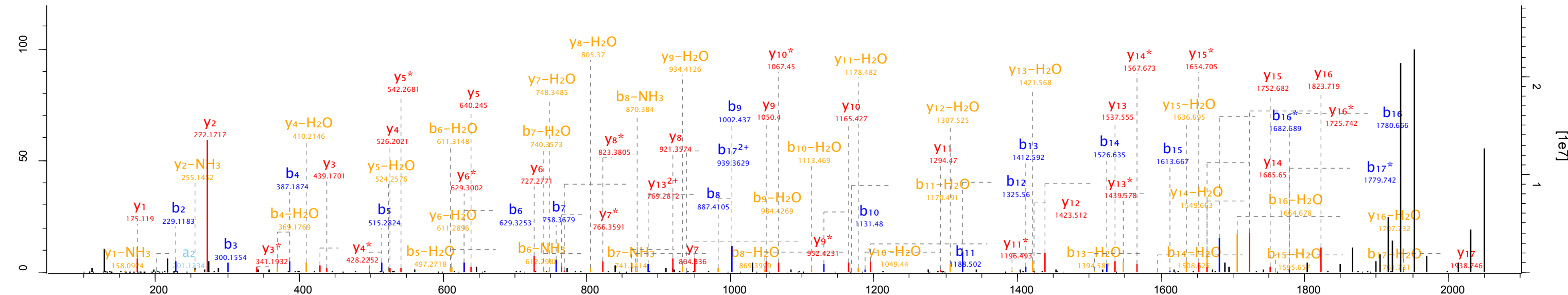
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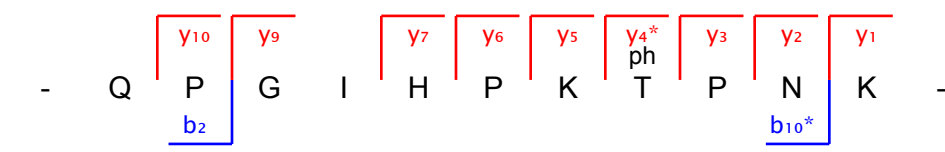
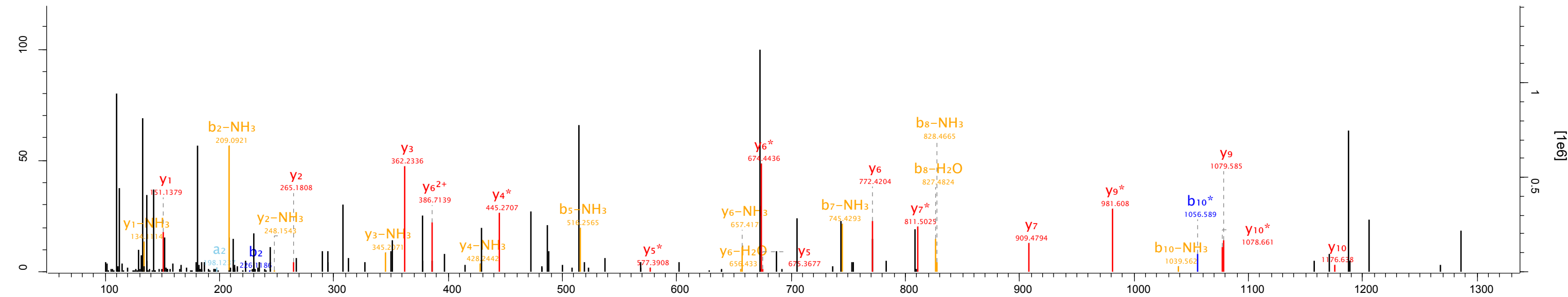




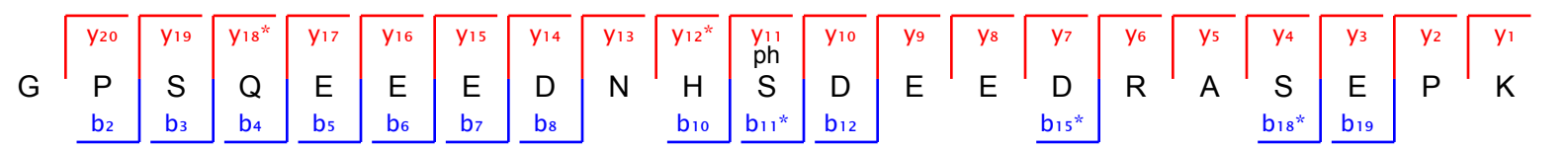
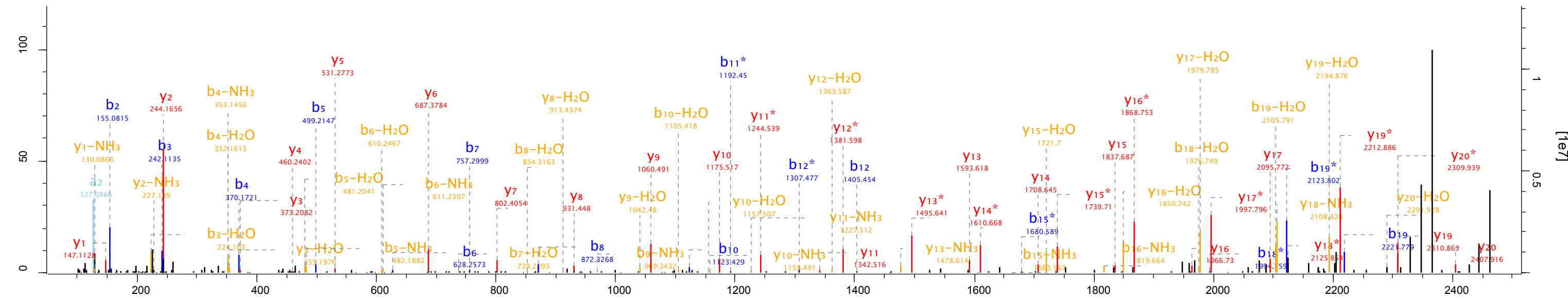


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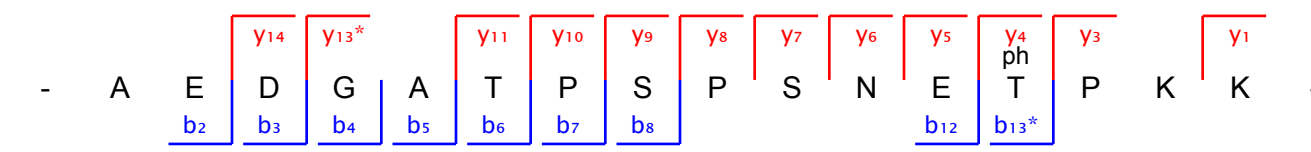
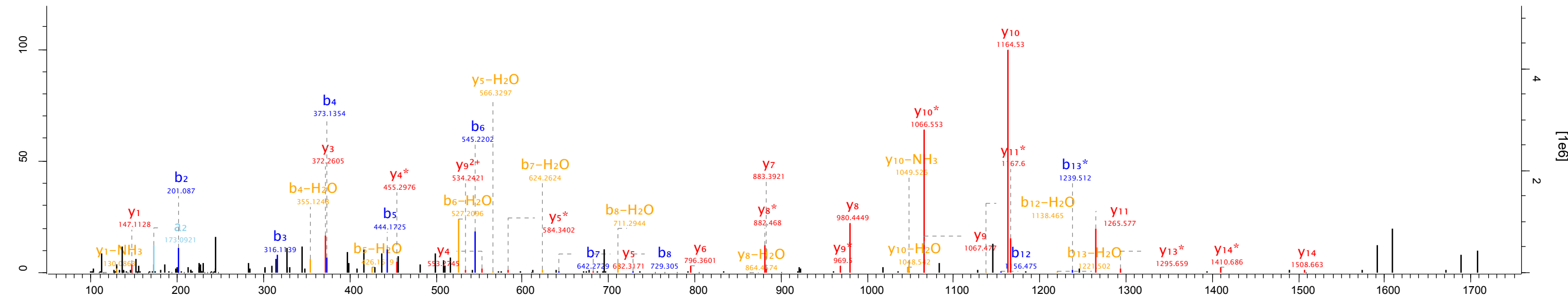
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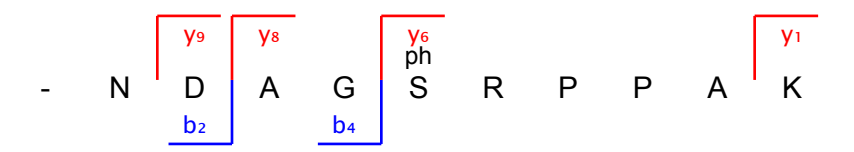
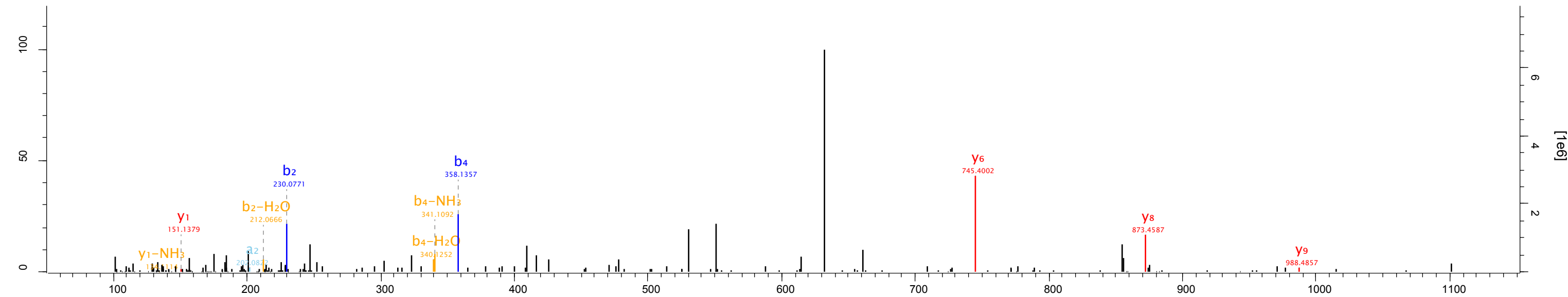
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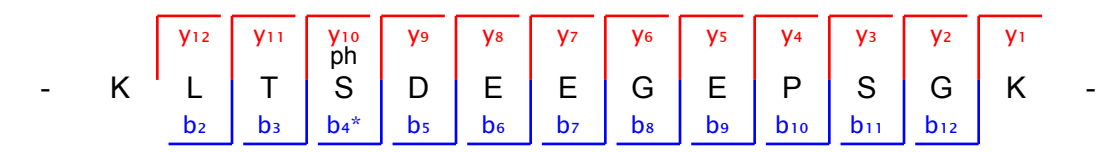
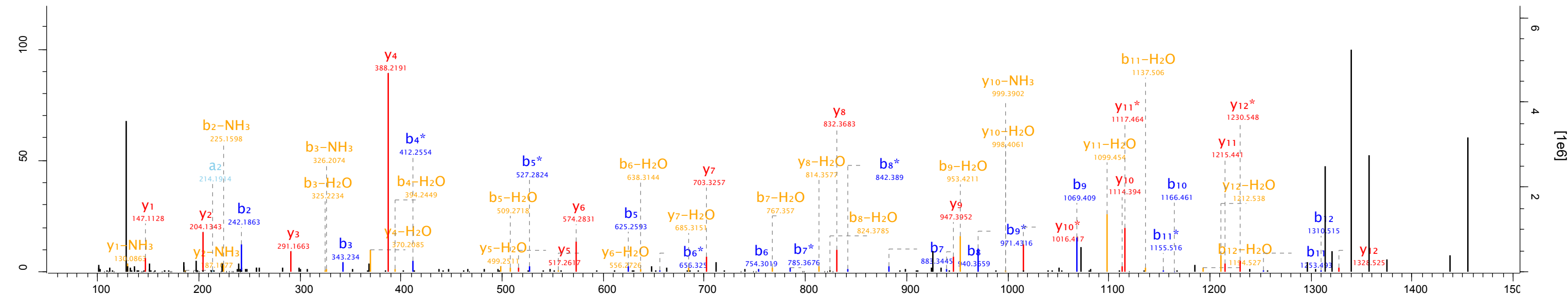


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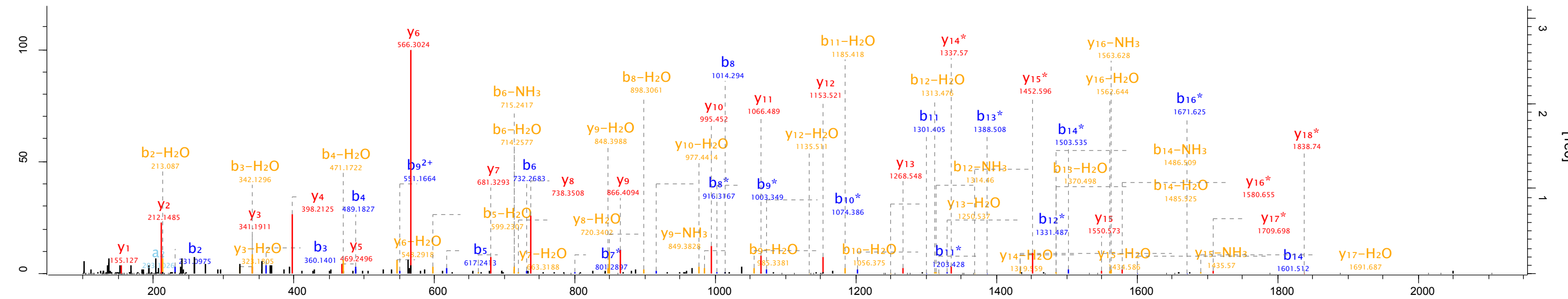


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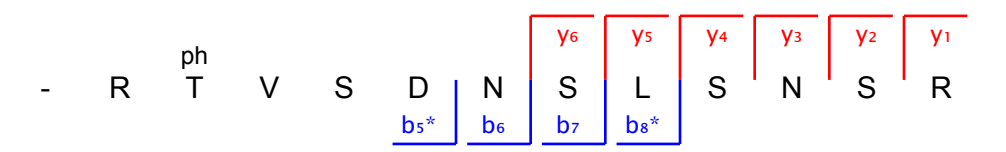
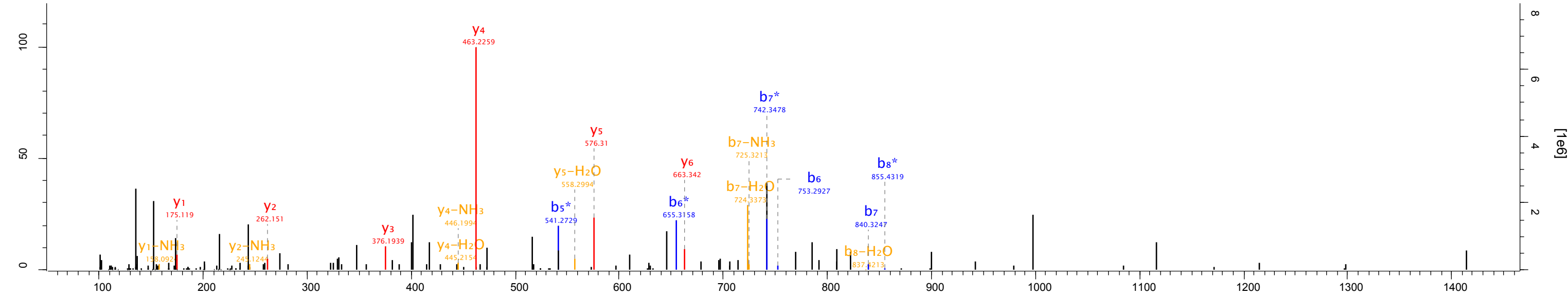
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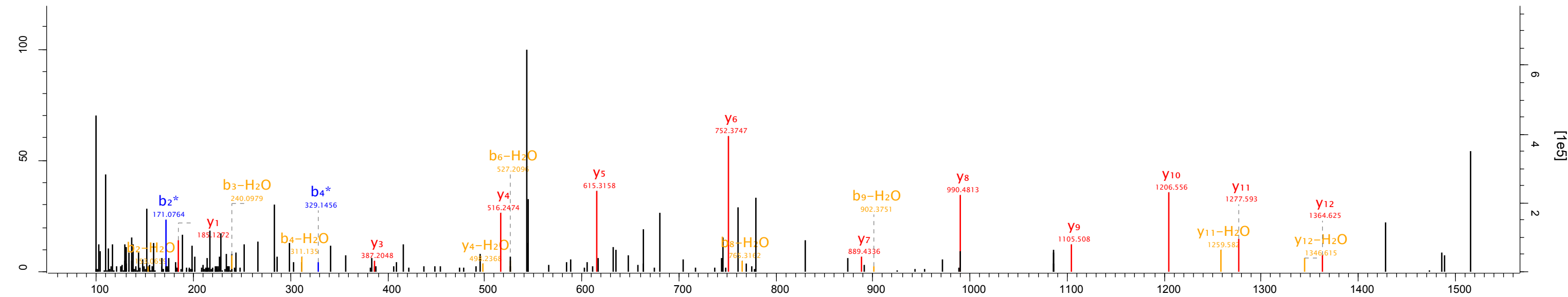
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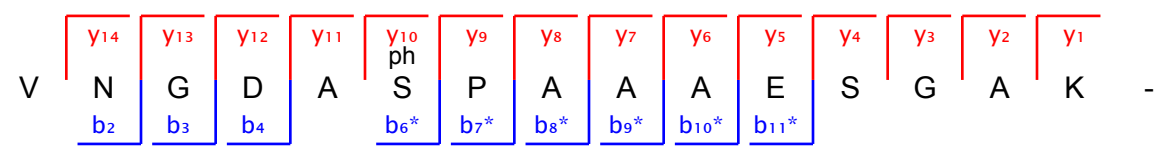
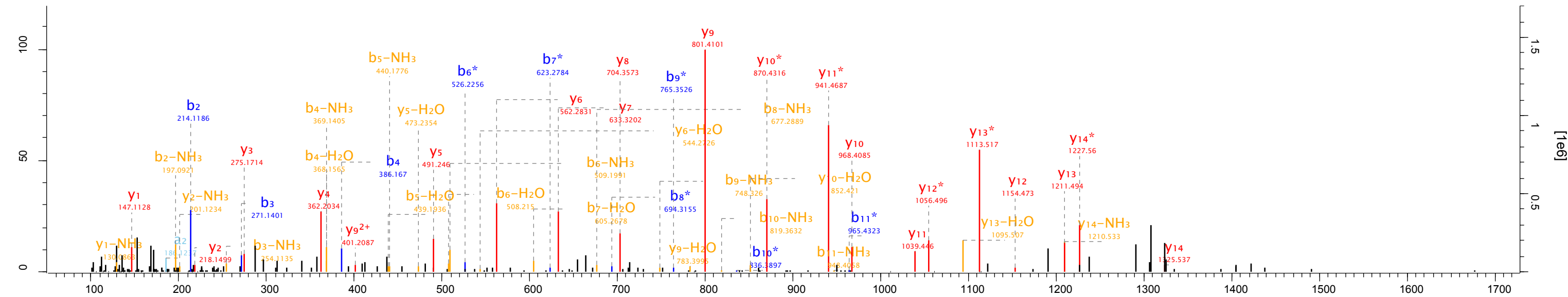
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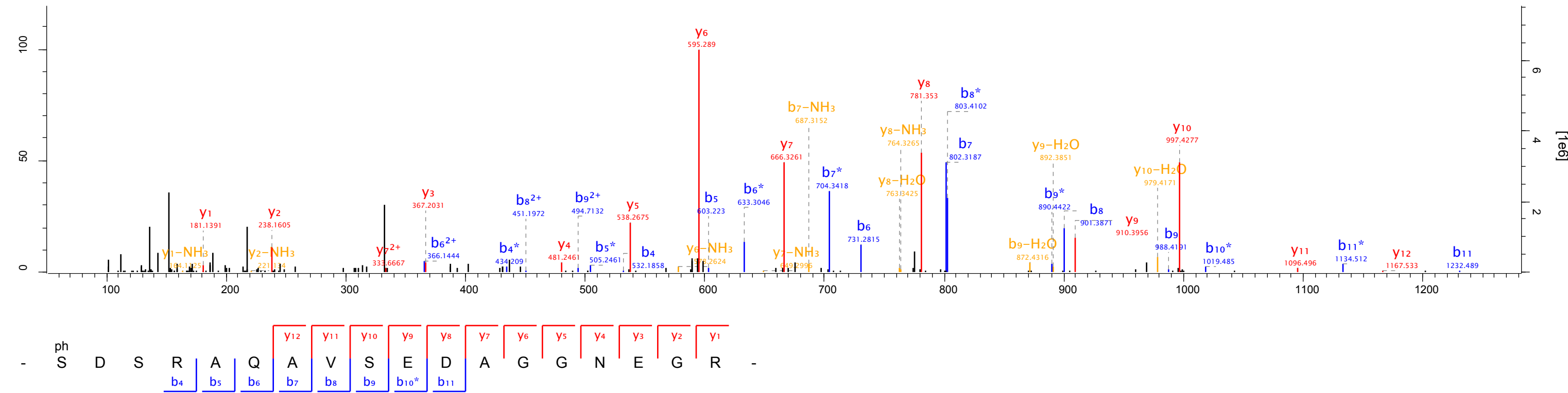


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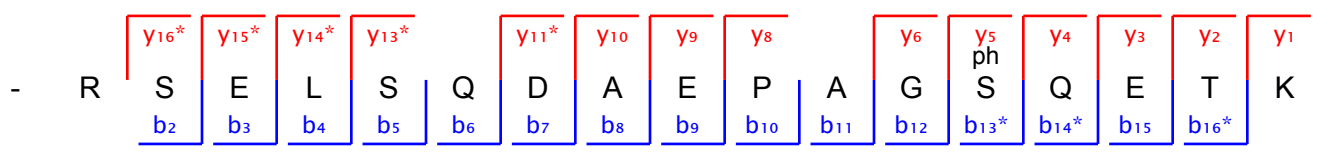
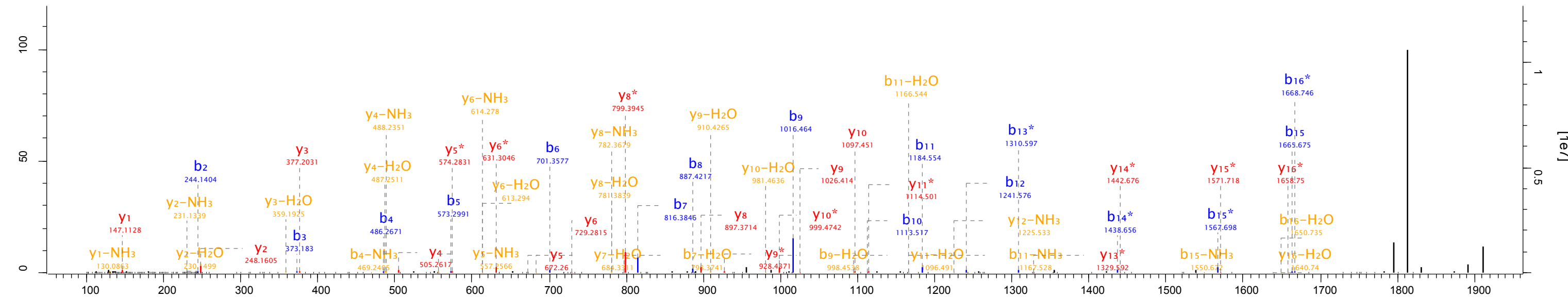


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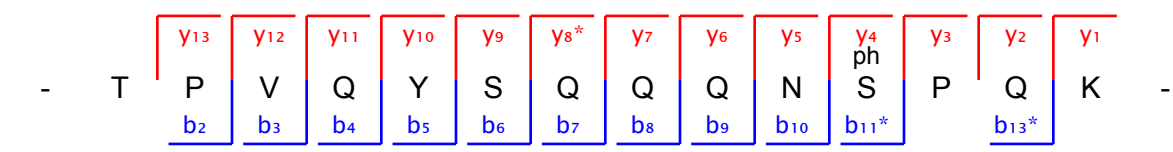
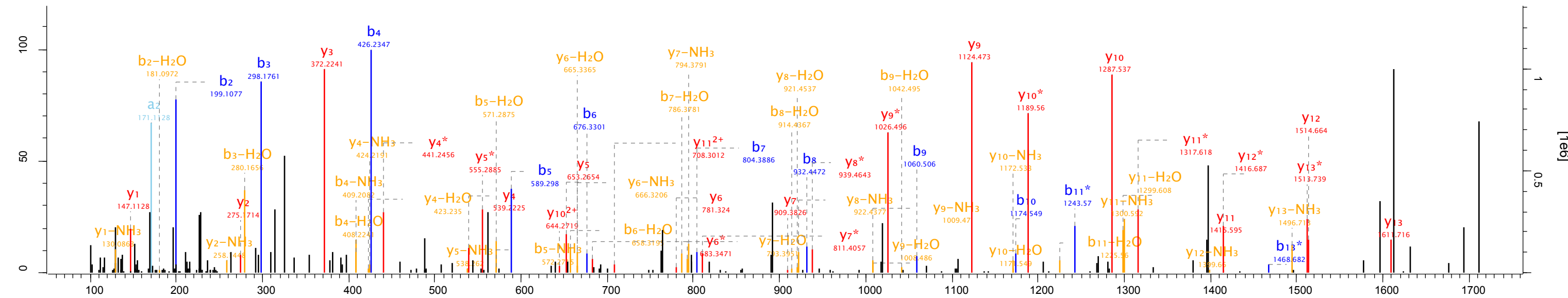




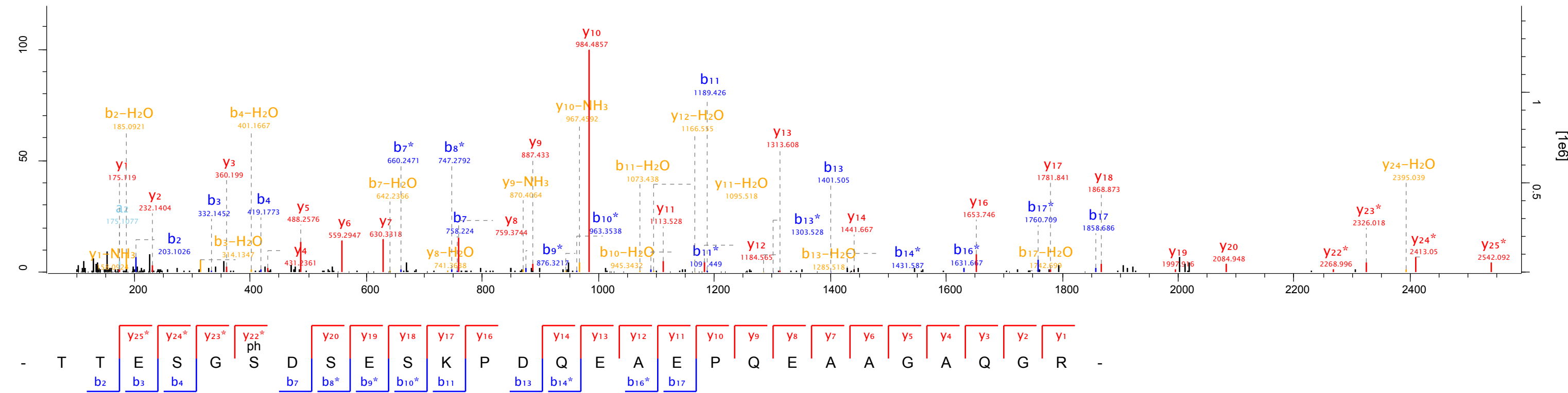
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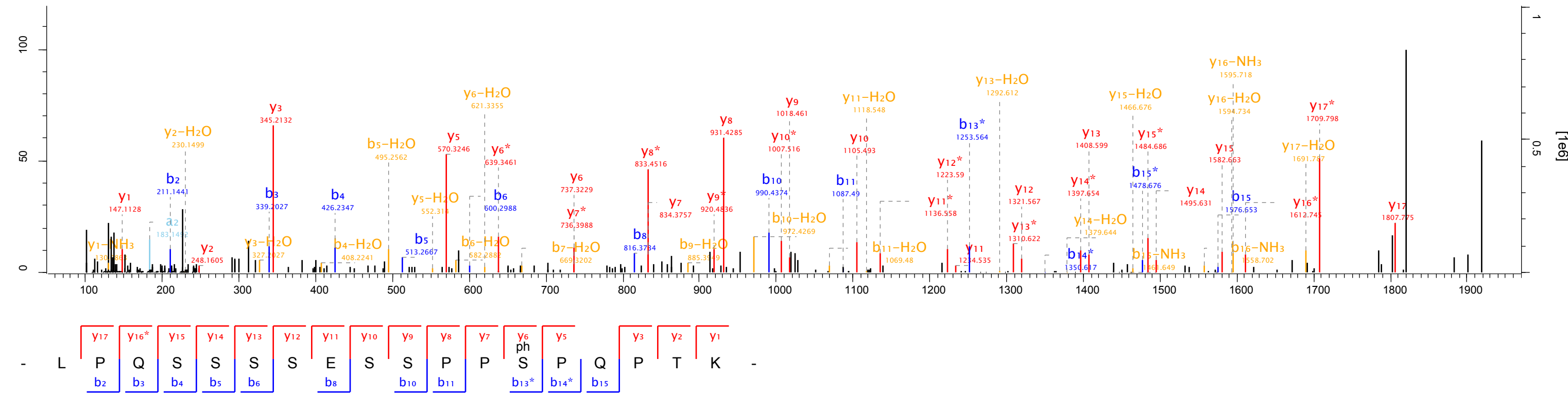


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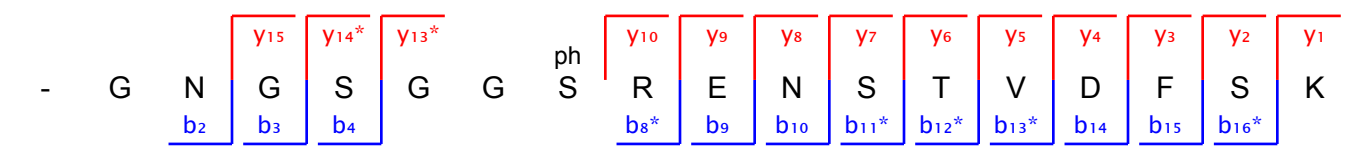
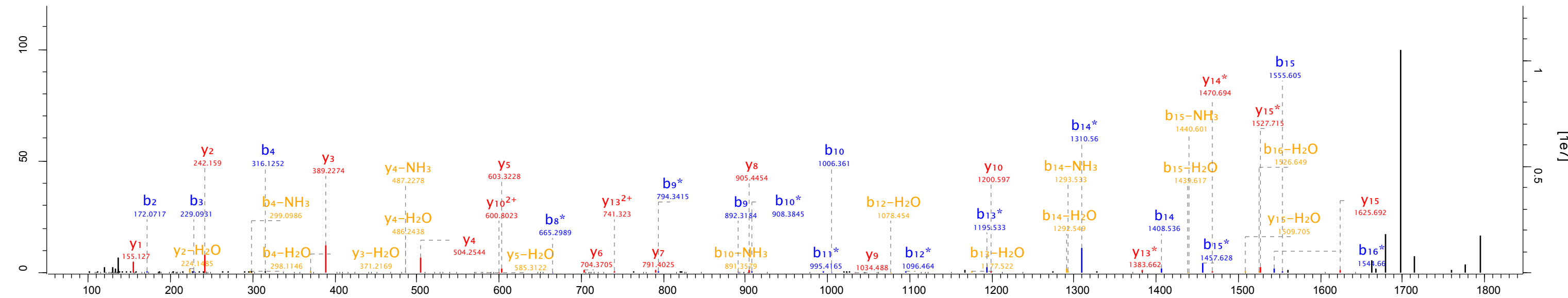


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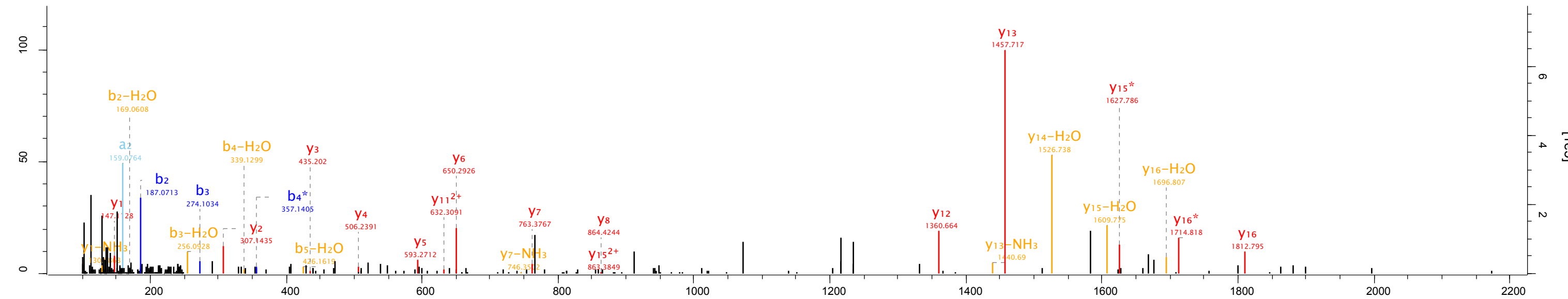




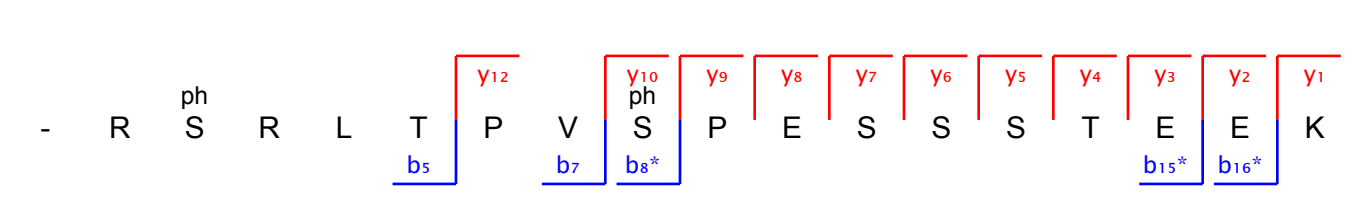
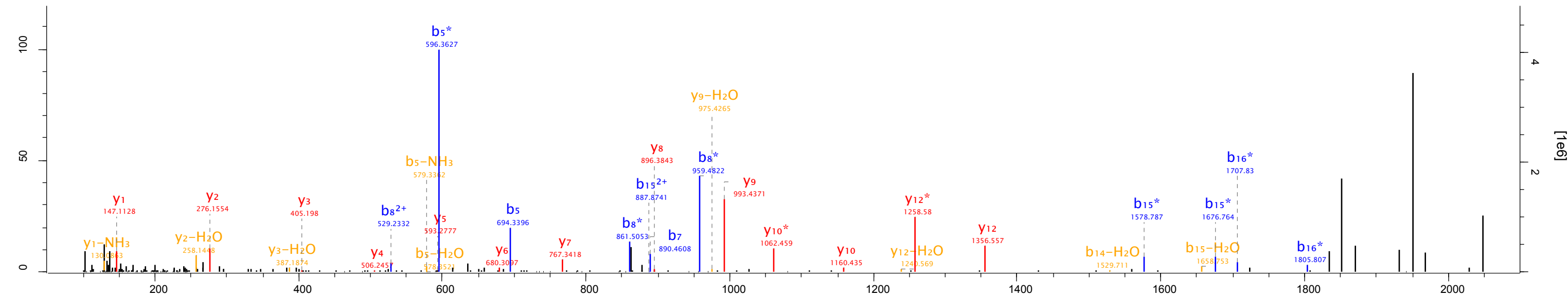
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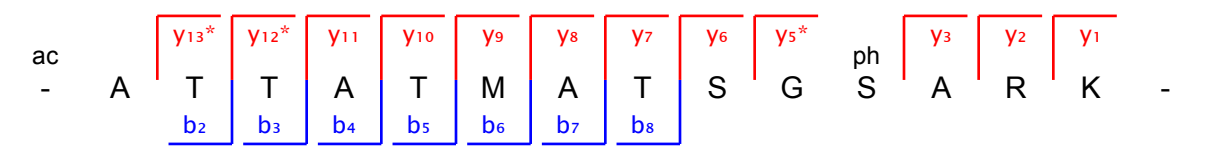
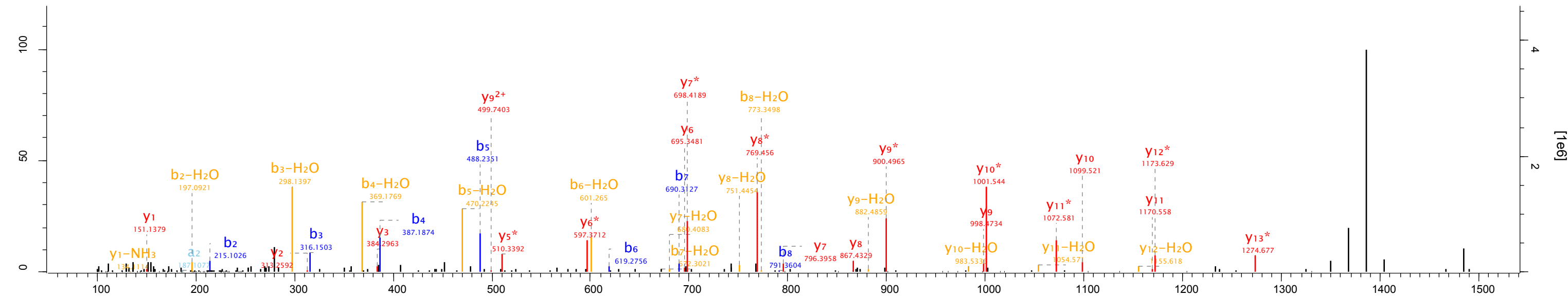
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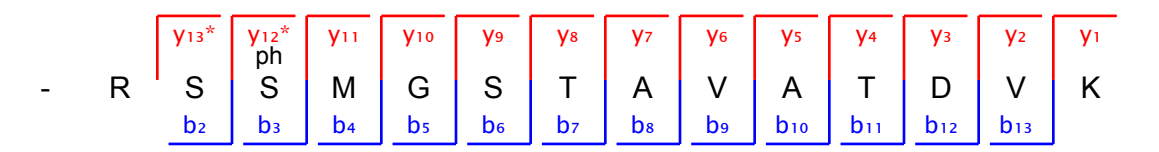
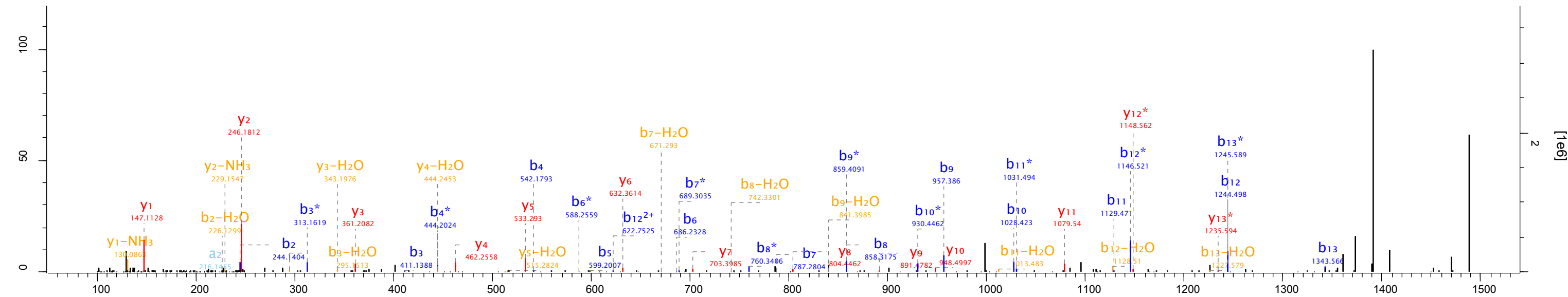
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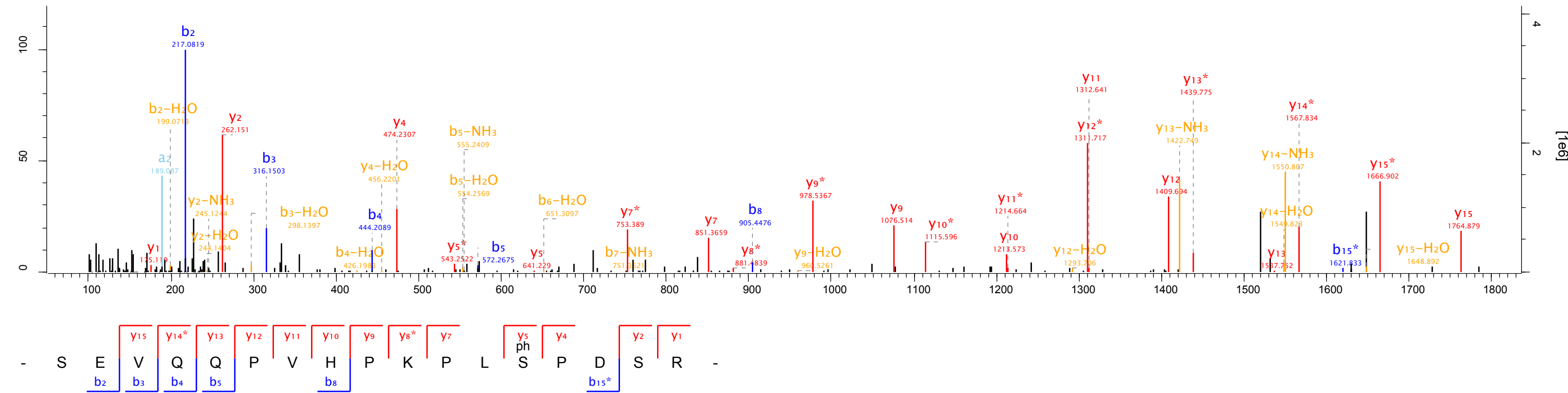


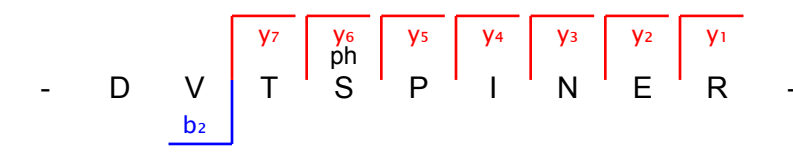
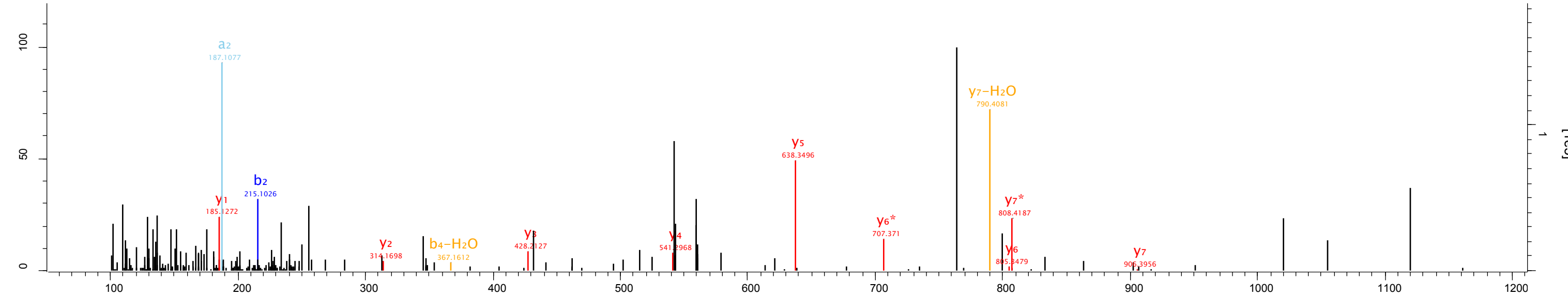
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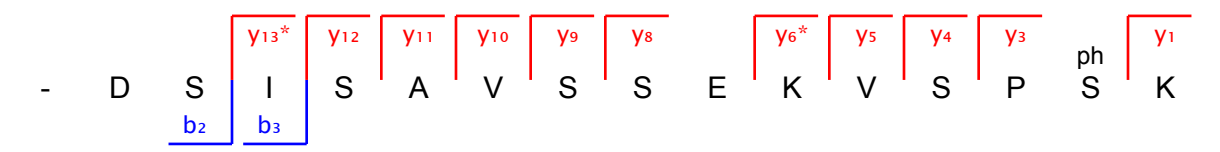
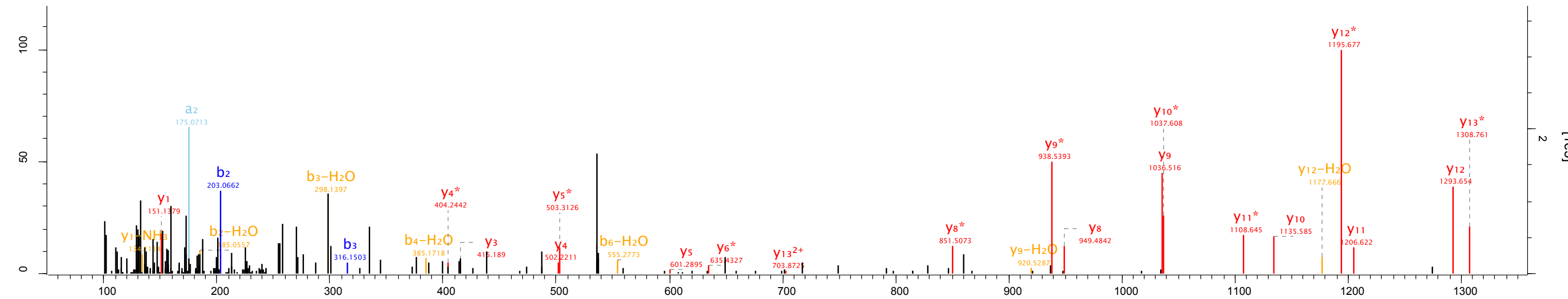
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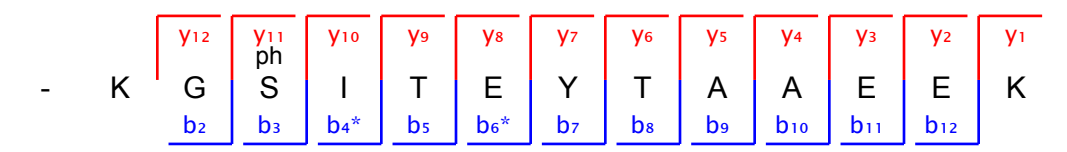
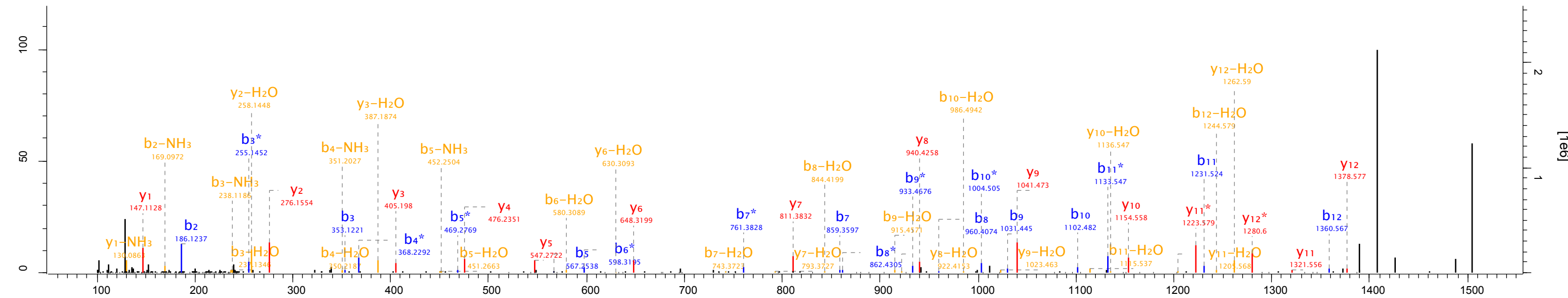




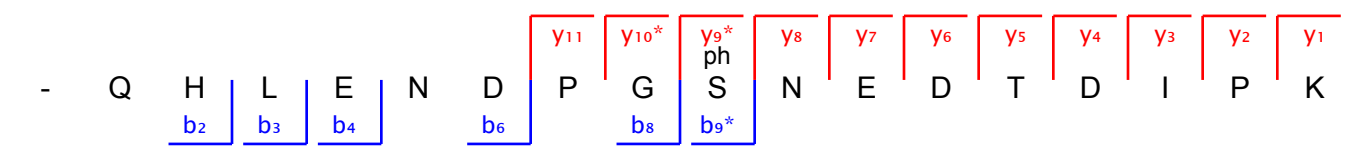
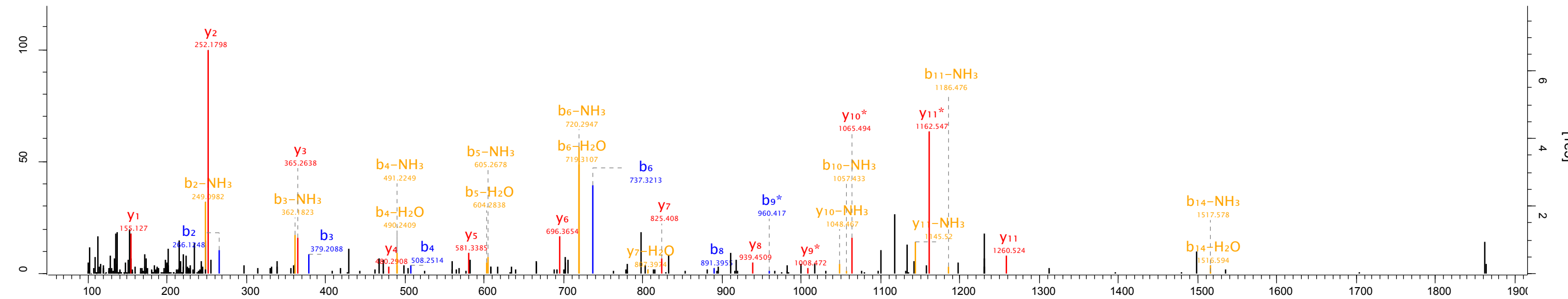
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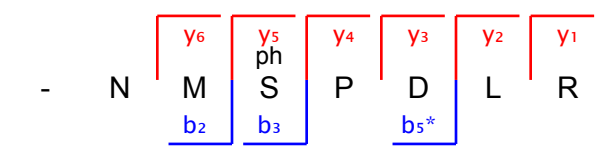
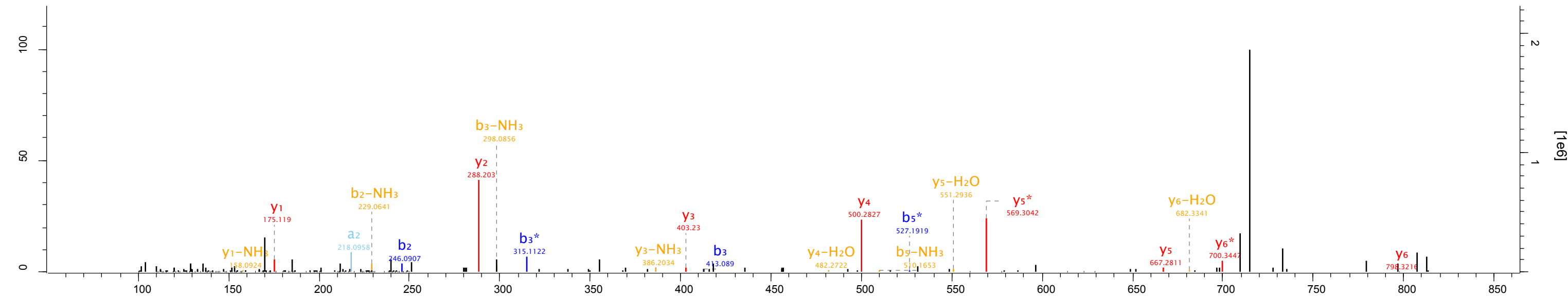
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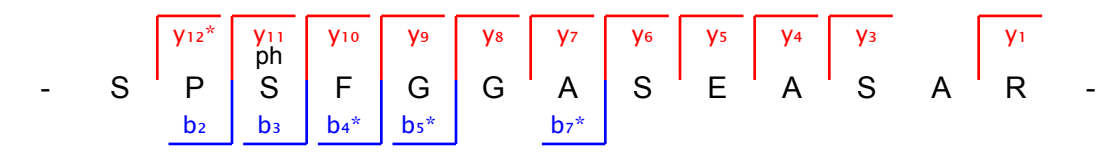
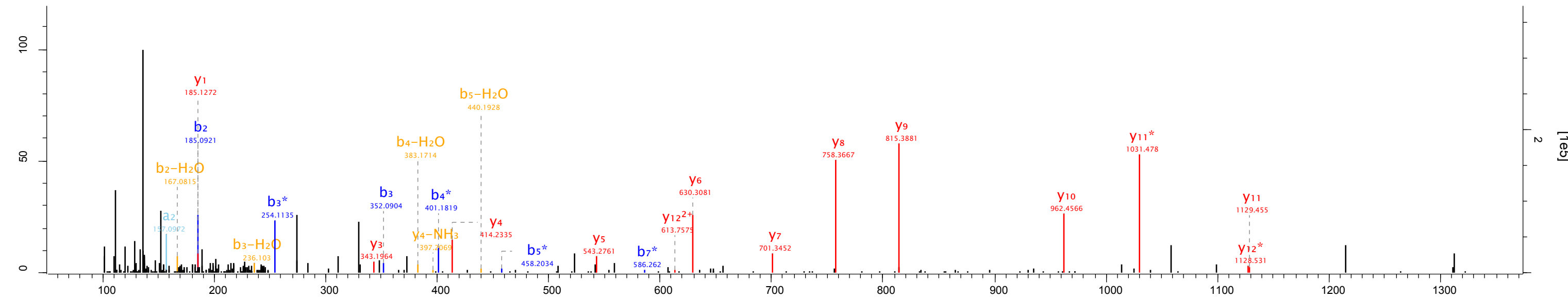
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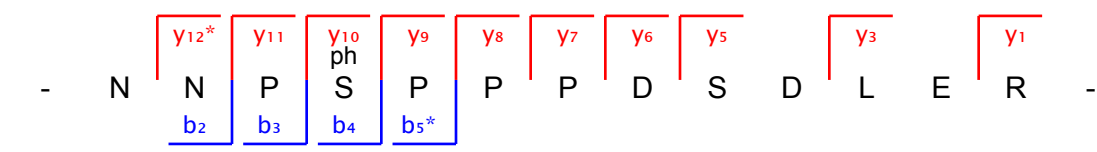
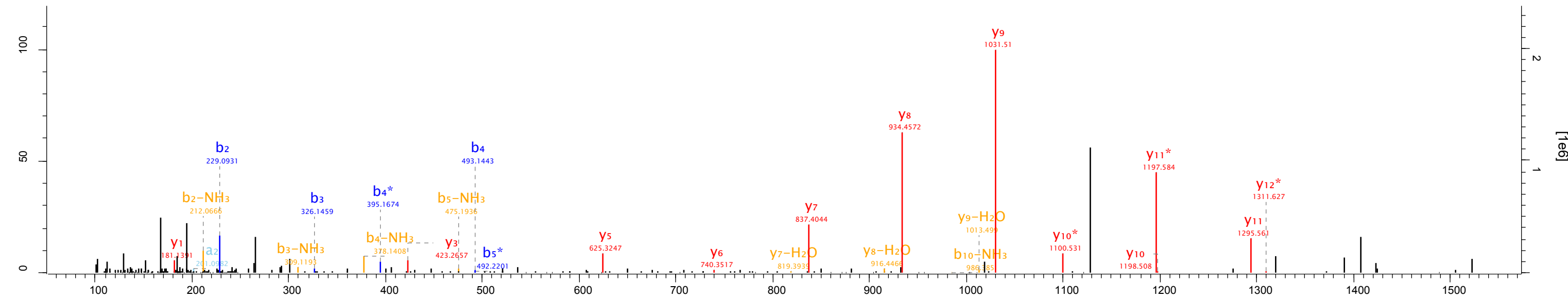
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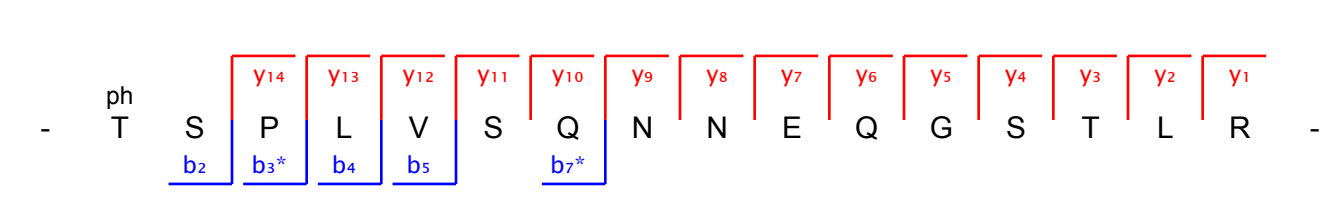
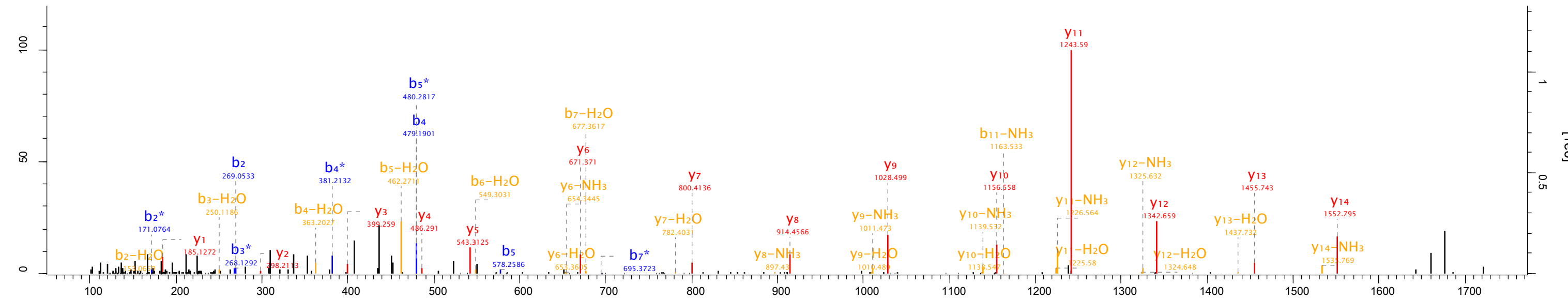
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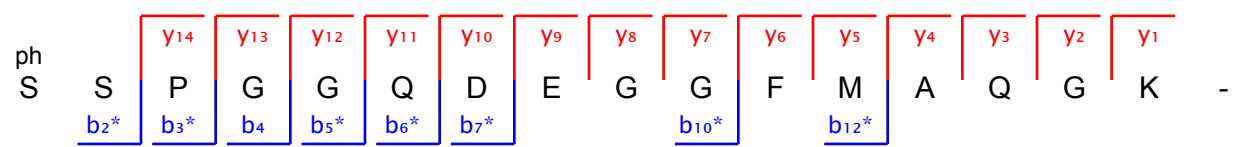
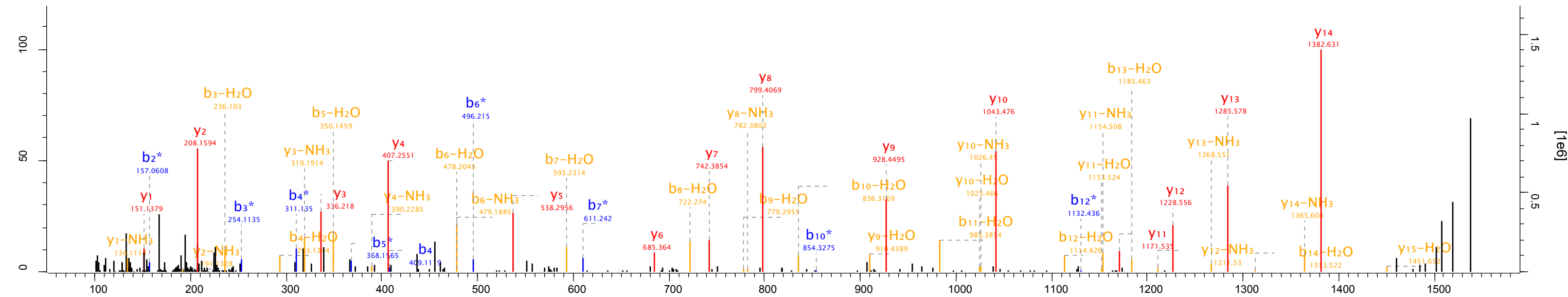
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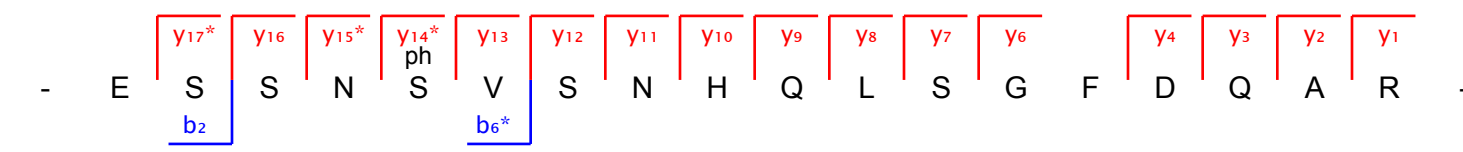
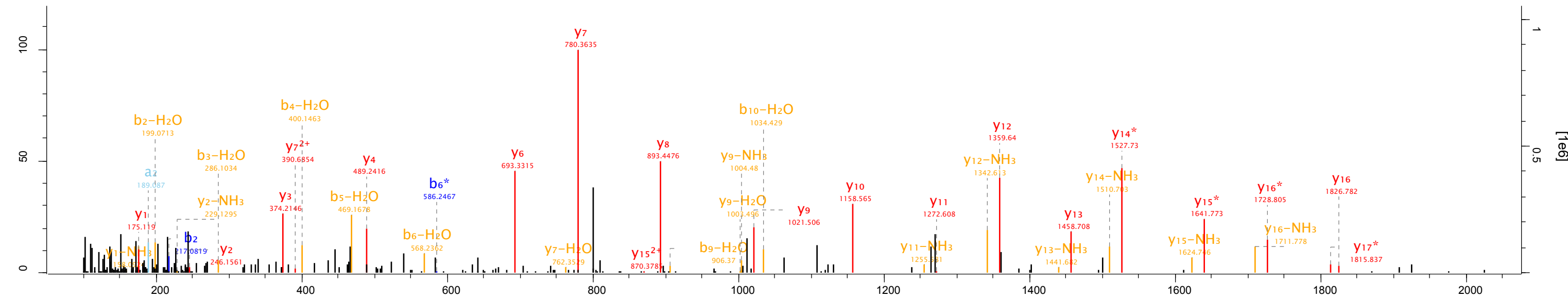
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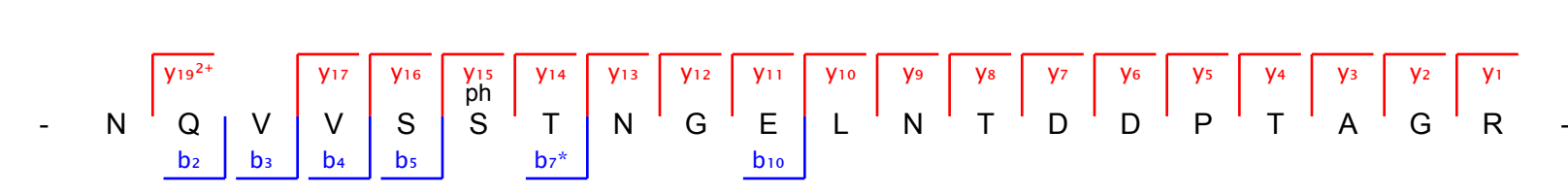
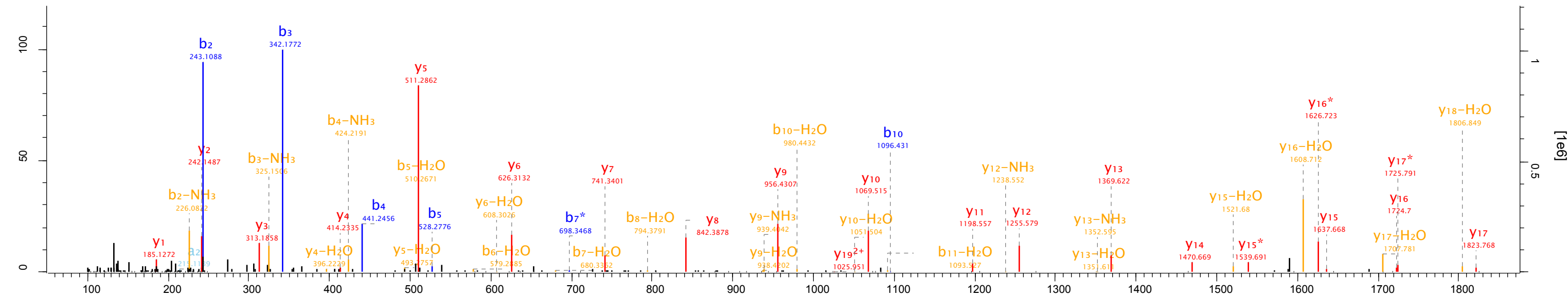
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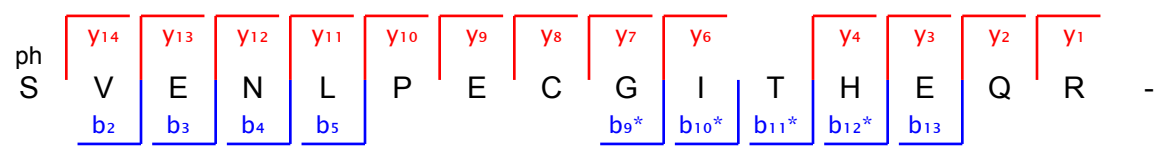
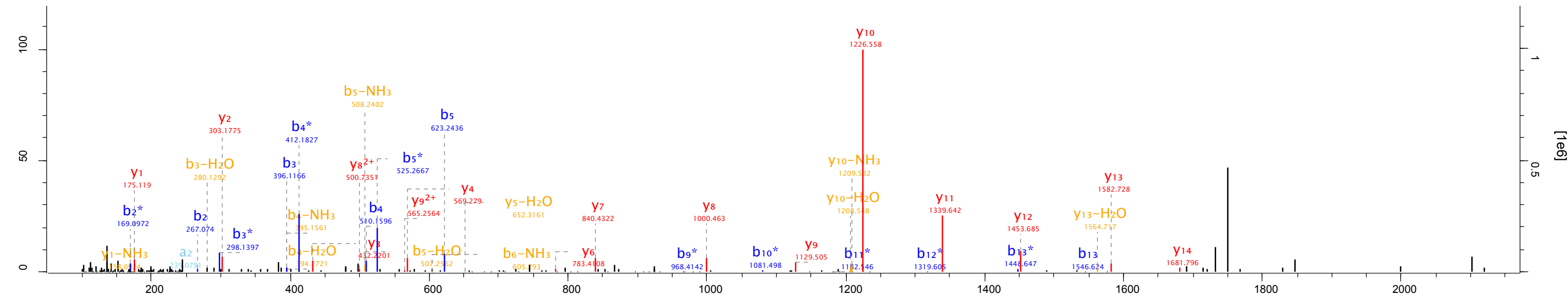
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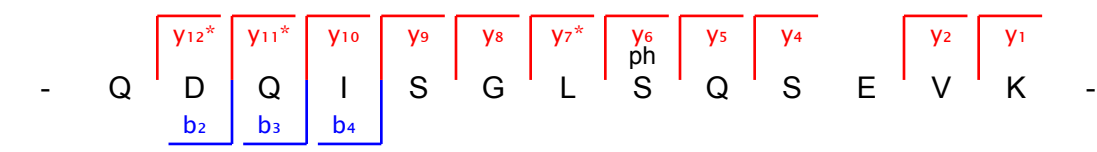
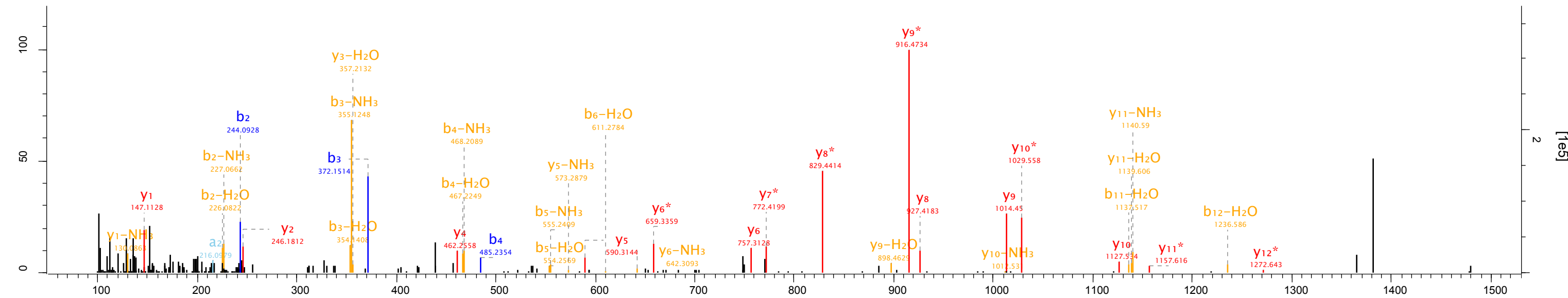
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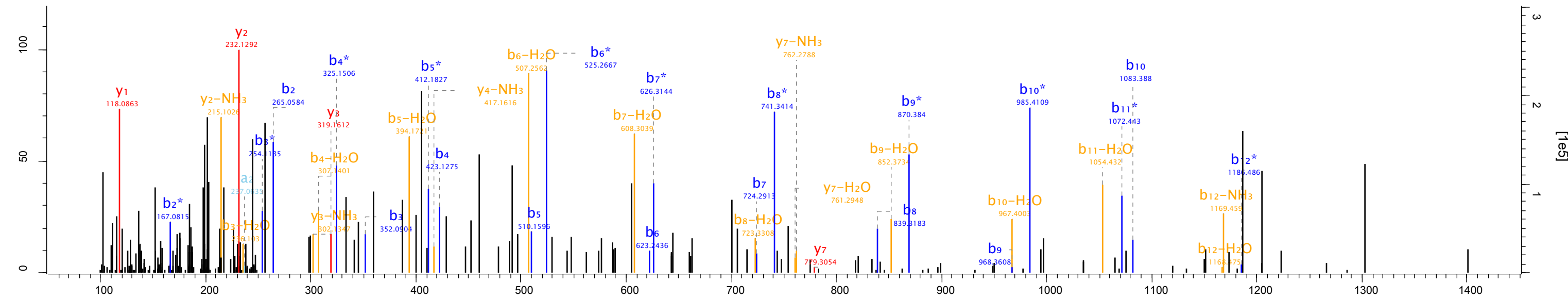
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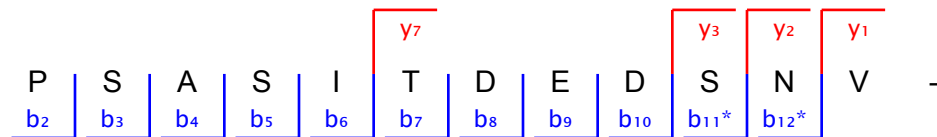
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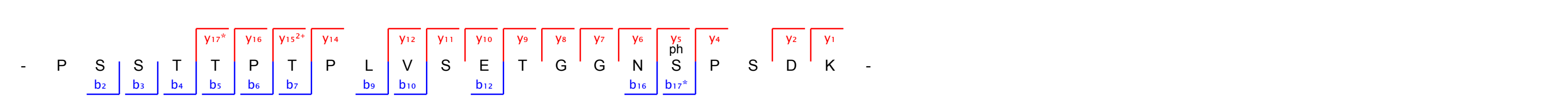
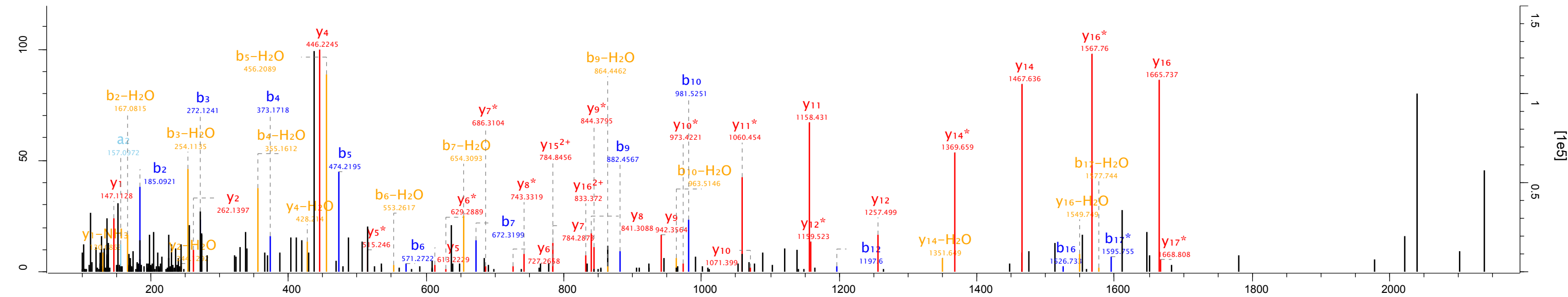
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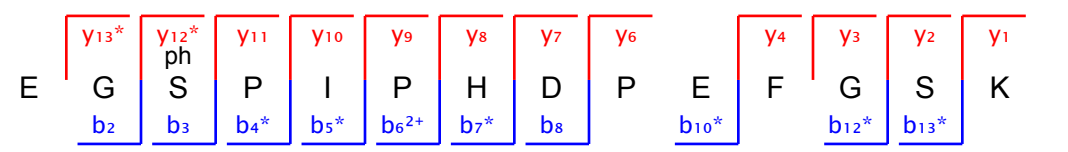
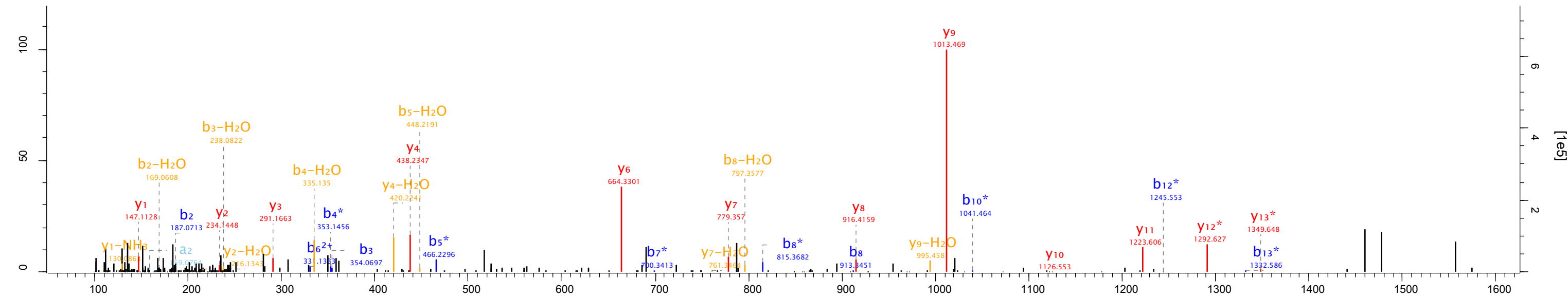
ph
S



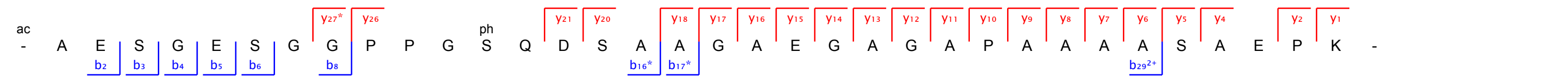
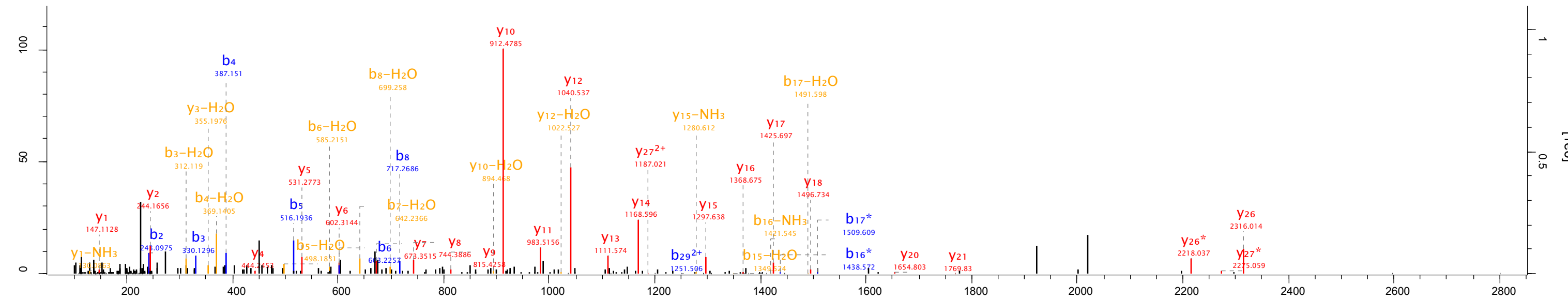
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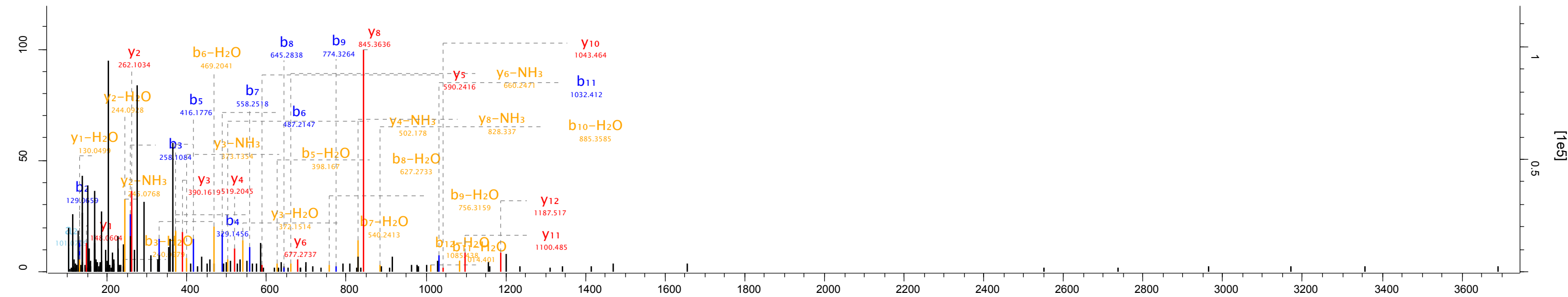
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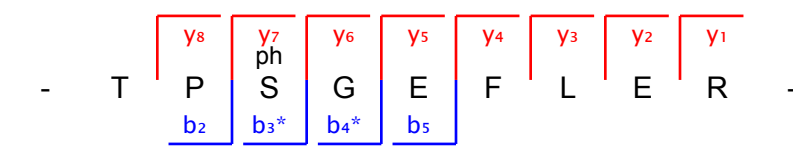
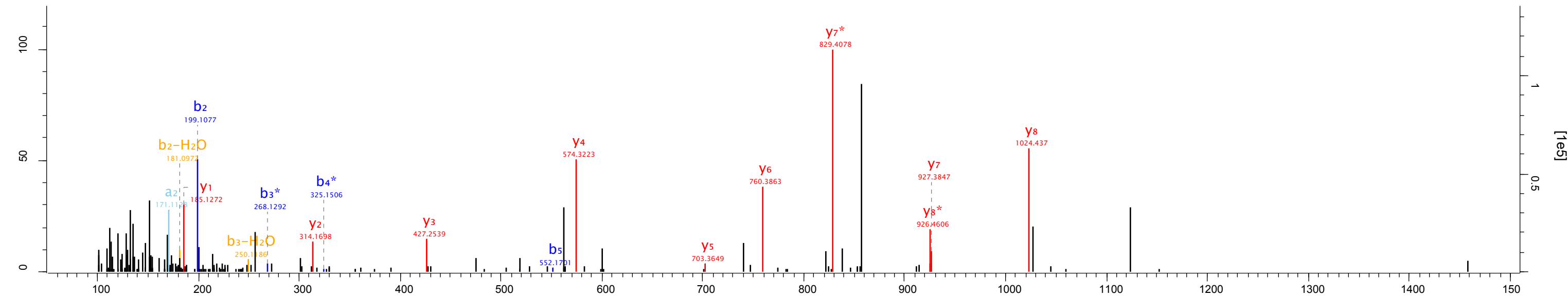
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 Scan: 9440 Method: FTMS; HCD Score: 85.04 m/z: 1011.43 Gene names: UBQLN1



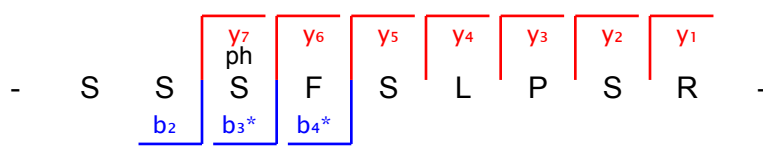
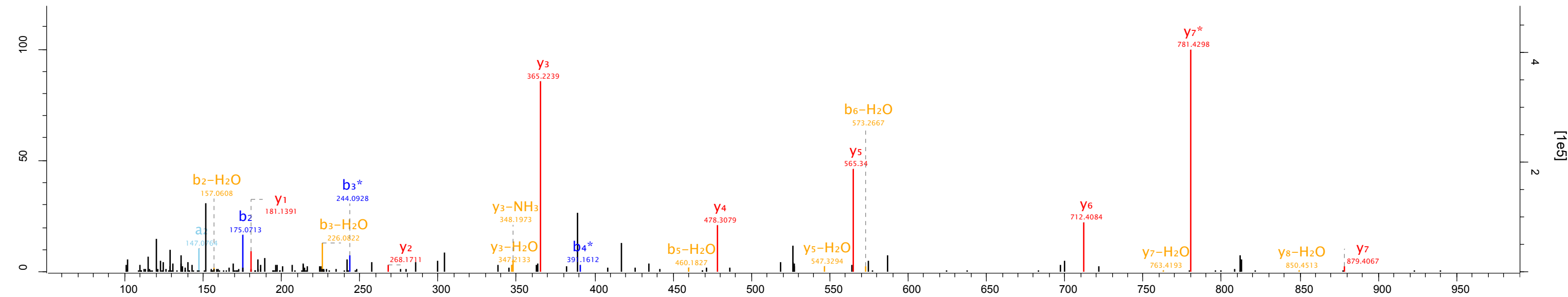
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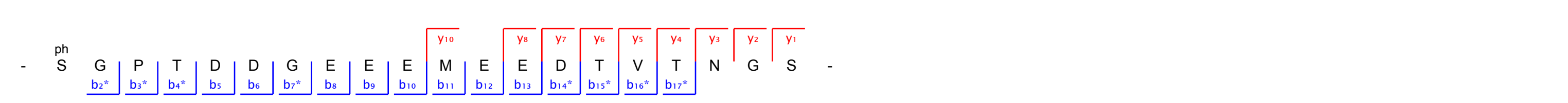
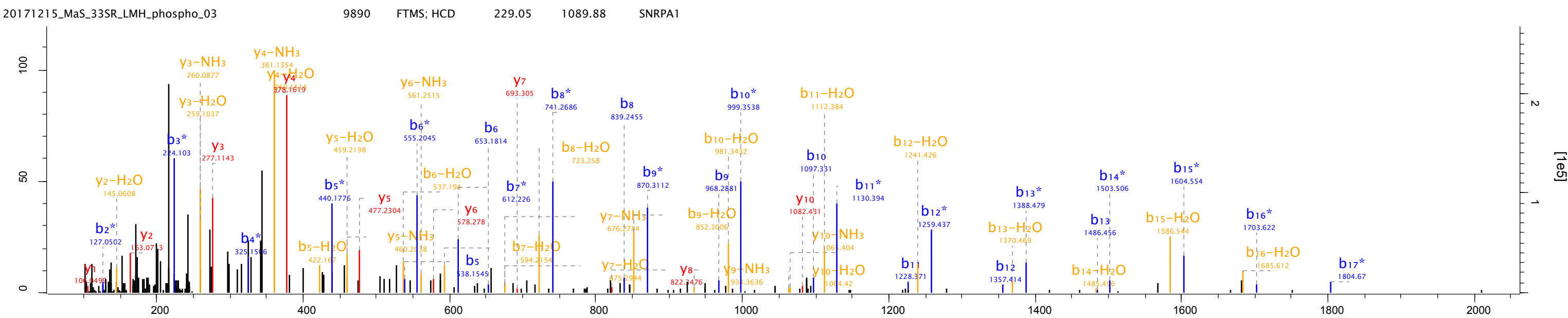


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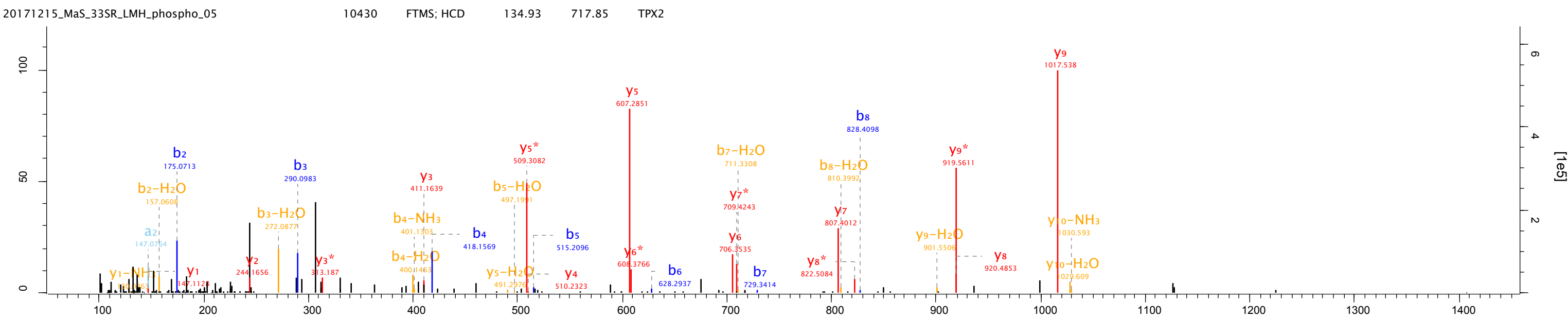


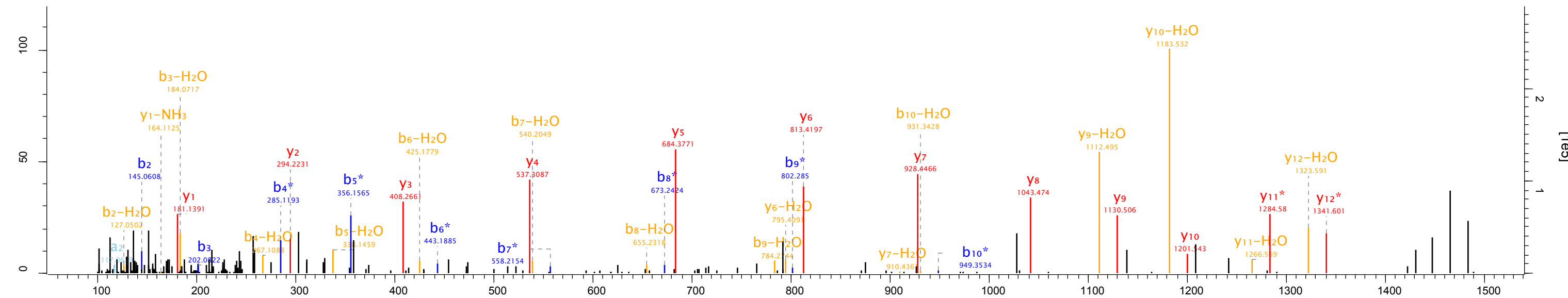
Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 9820 Method FTMS; HCD Score 62.8 m/z 527.24 Gene names FAM53B





Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 10430 Method FTMS; HCD Score 134.93 m/z 717.85 Gene names TPX2





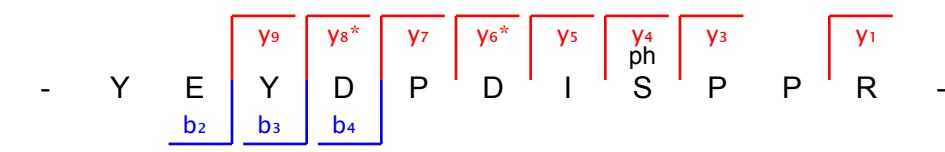
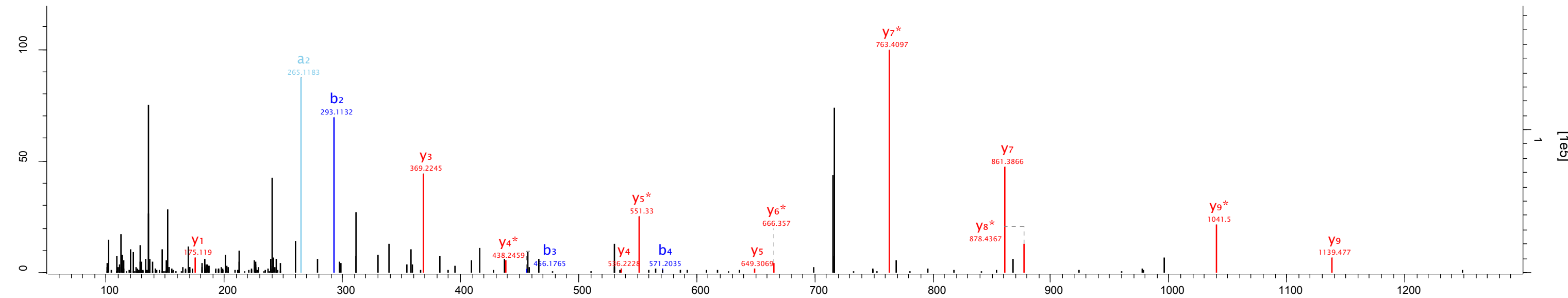
- G S G T A S D D E F E N L R -

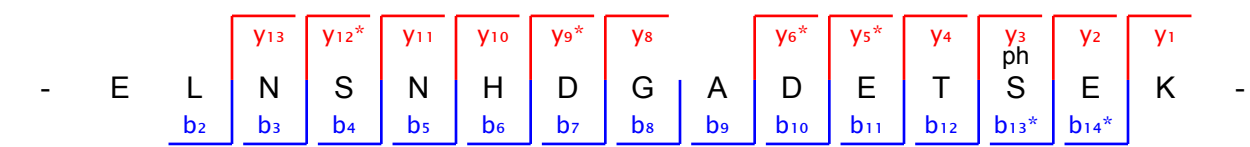
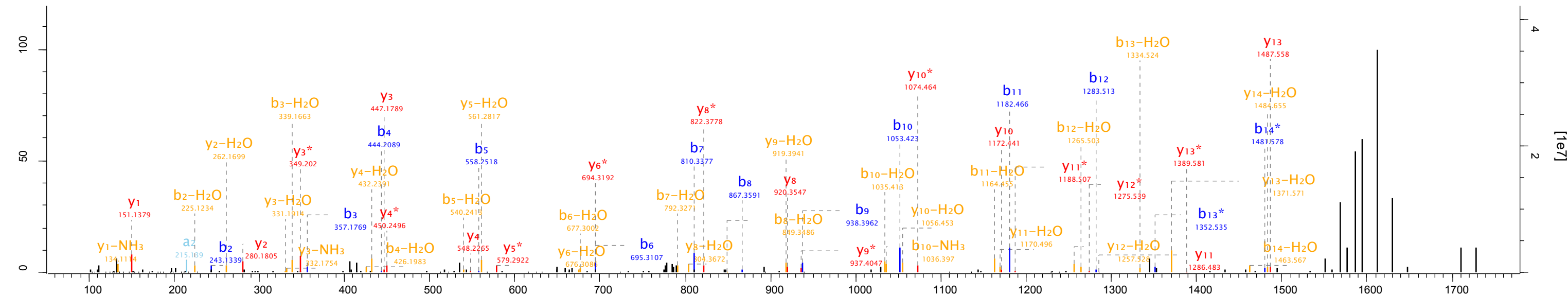
b₂ b₃ b₄* b₅* b₆* b₇* b₈* b₉* b₁₀*

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

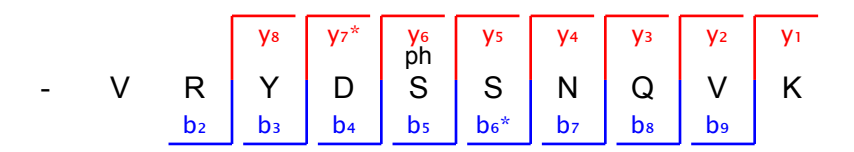
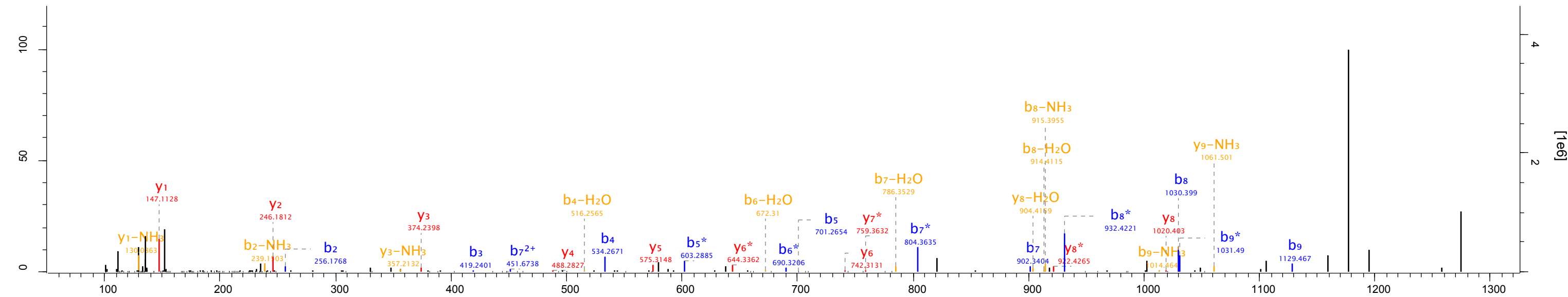
ph

Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 11120 Method FTMS; HCD Score 50.3 m/z 716.8 Gene names BUD13

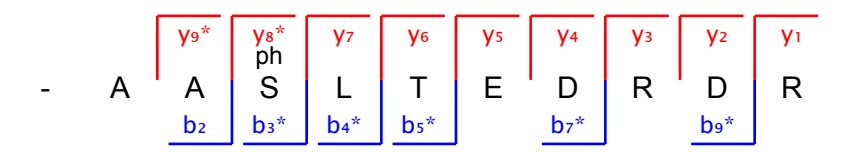
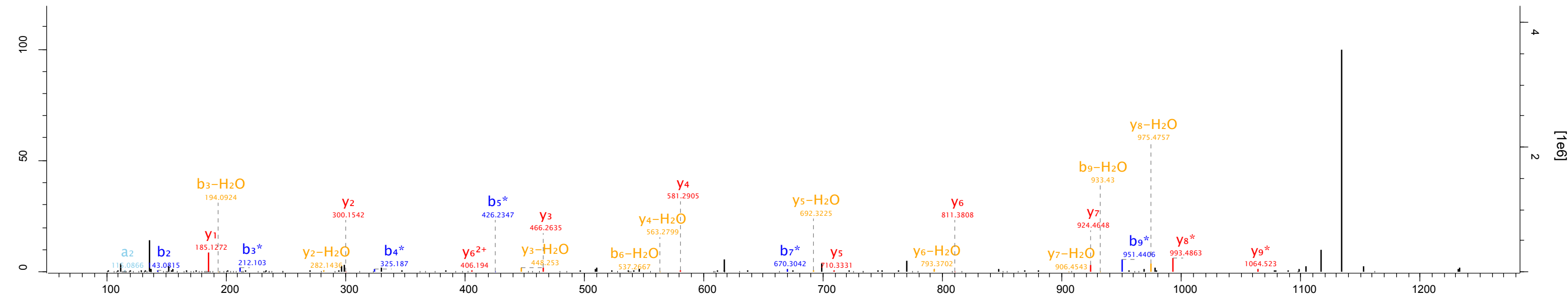




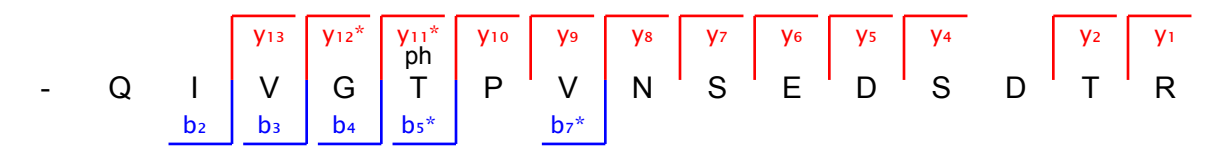
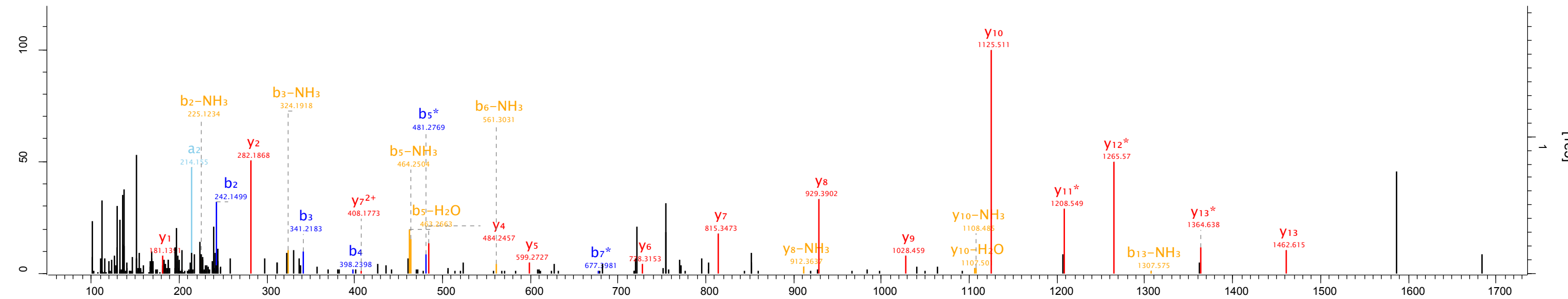
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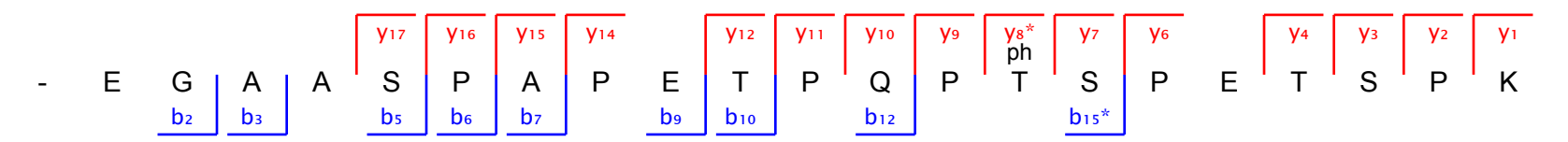
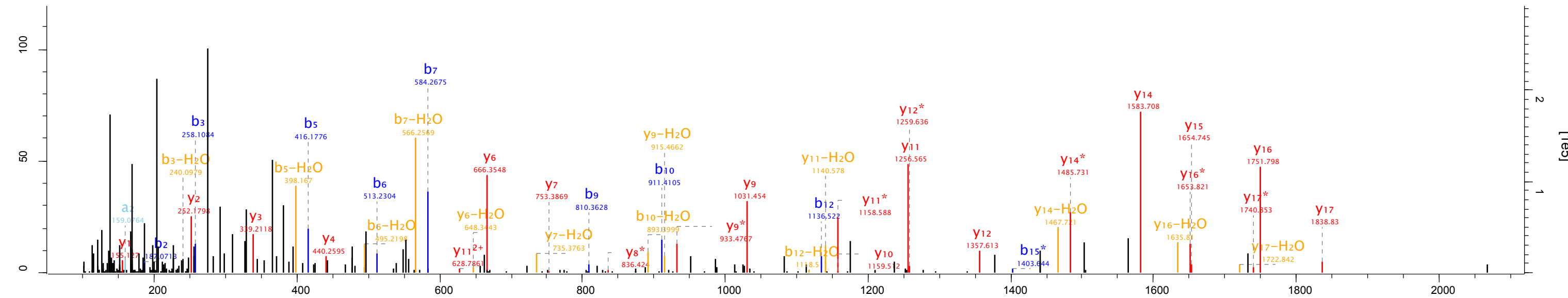


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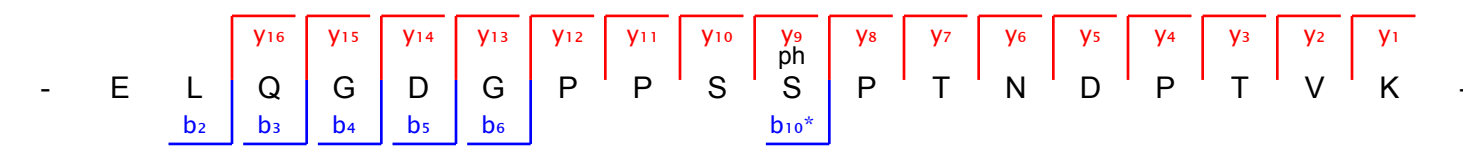
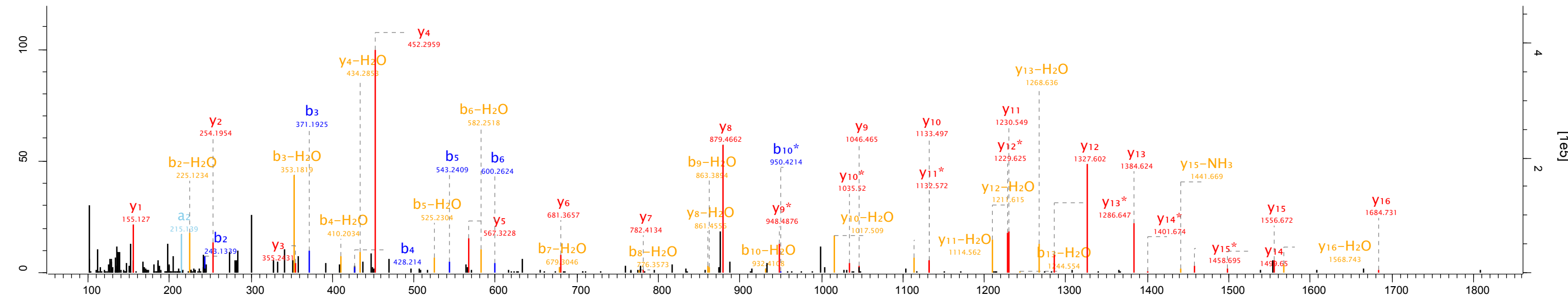


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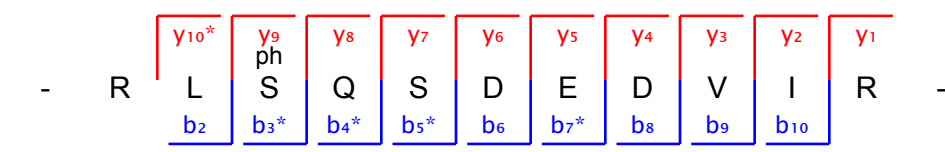
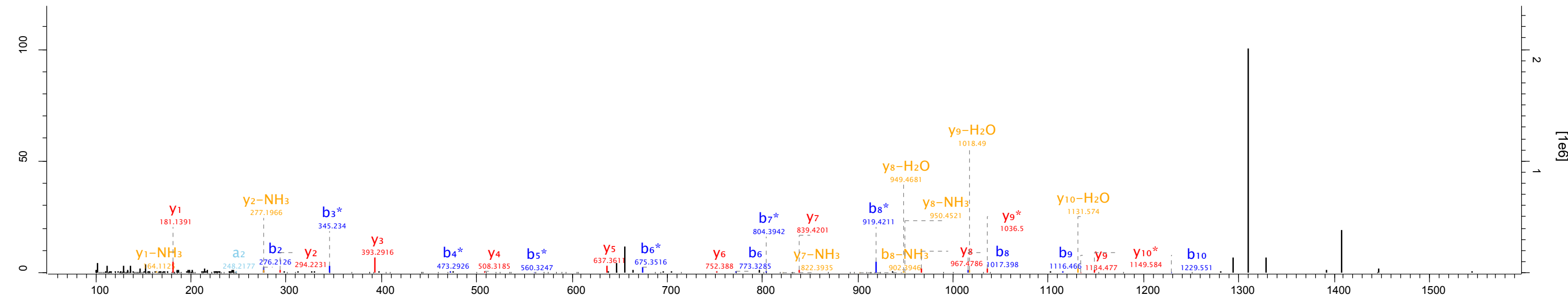




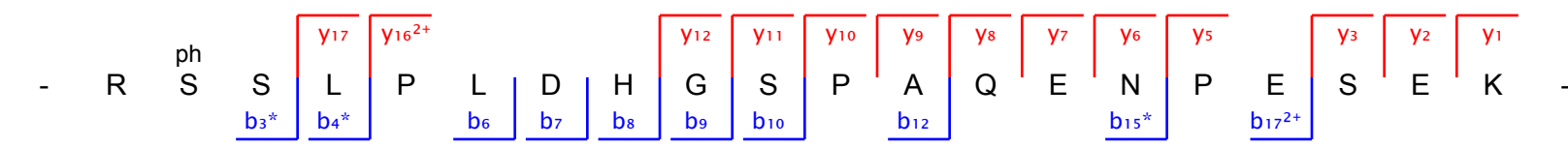
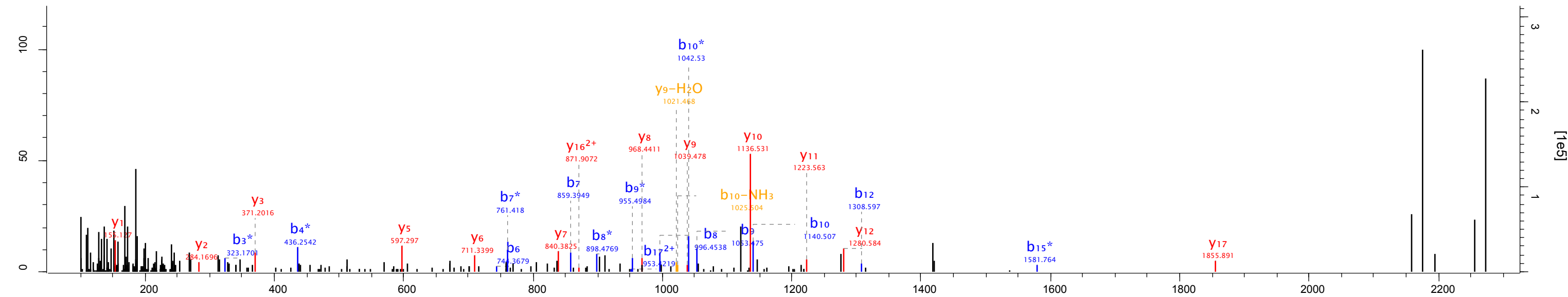
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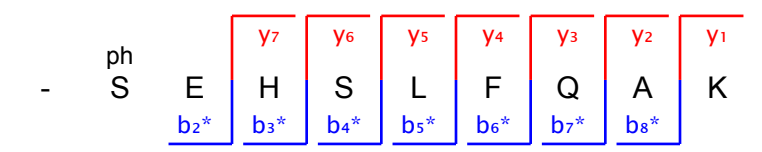
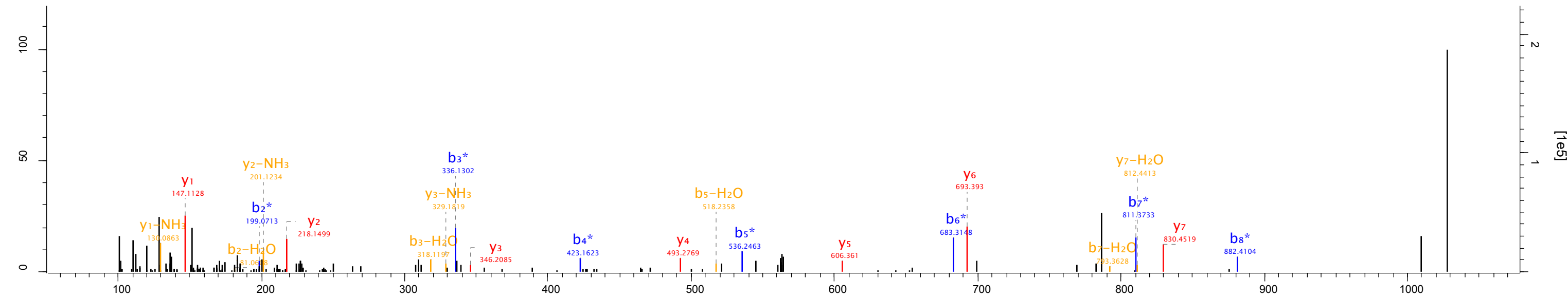
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 Scan: 6530 Method: FTMS; HCD Score: 154.46 m/z: 705.35 Gene names: WDR26



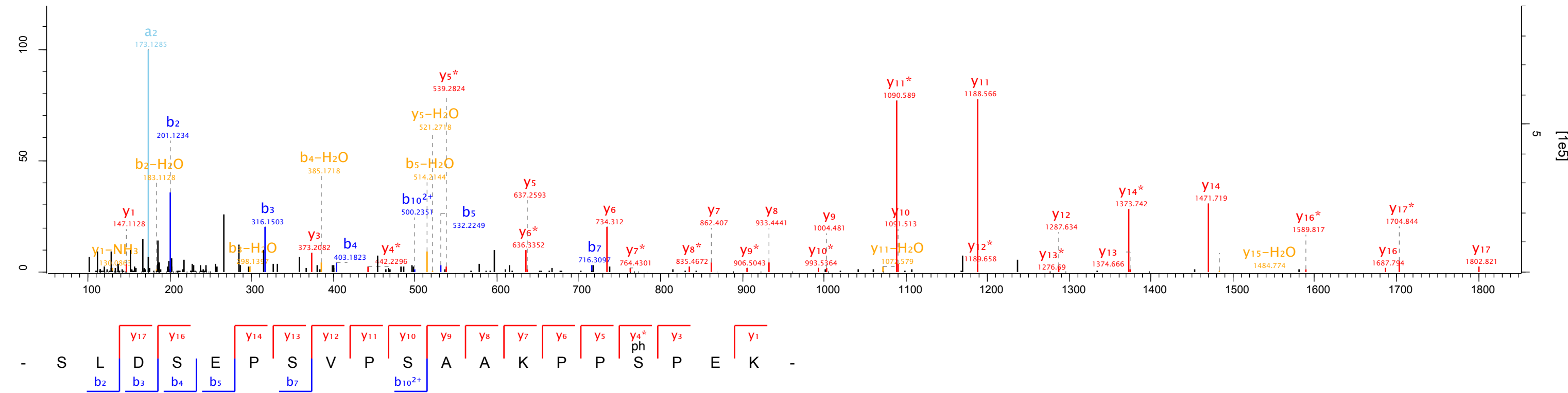
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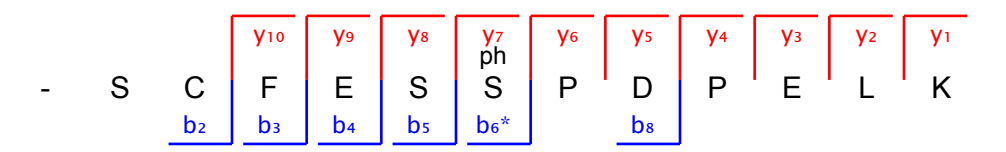
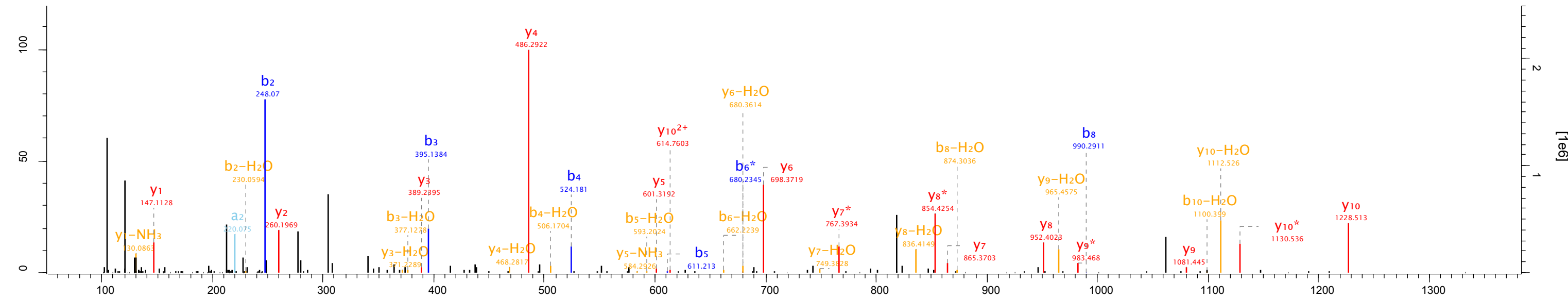
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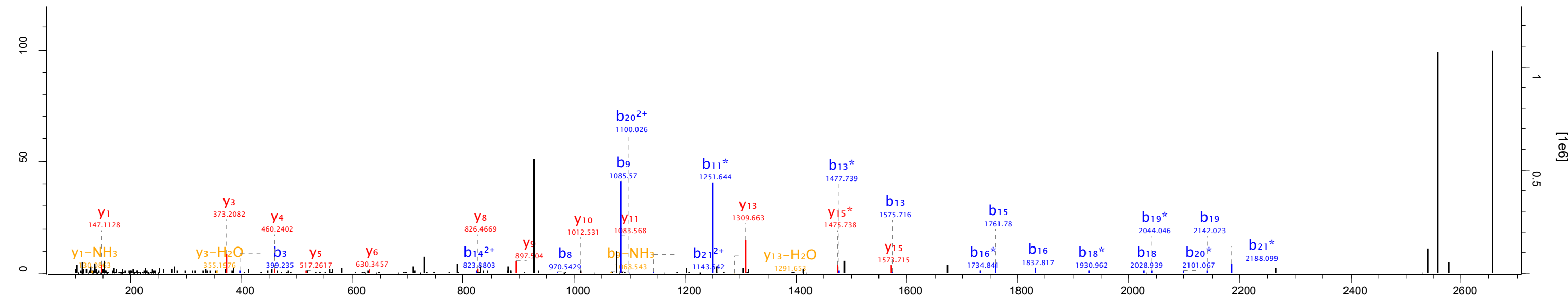
Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 8750 Method FTMS; HCD Score 143.32 m/z 668.32 Gene names POGZ



Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 8830 Method FTMS; HCD Score 175.66 m/z 738.29 Gene names SRRM2



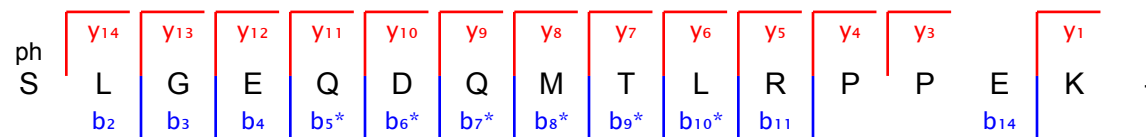
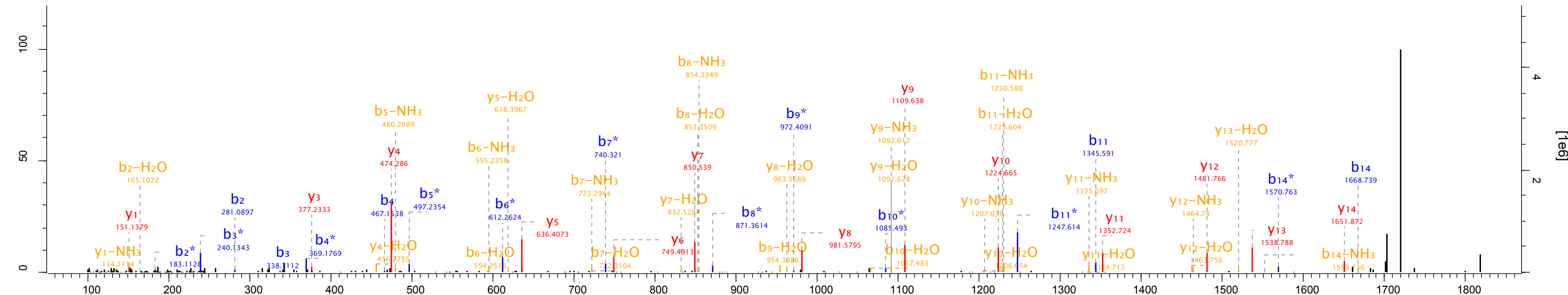
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 10380 Method FTMS; HCD Score 70.06 m/z 887.1 Gene names CASC3



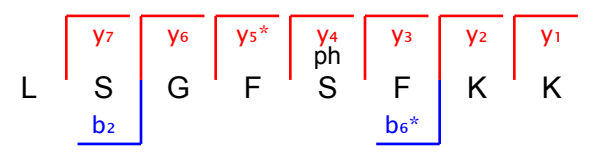
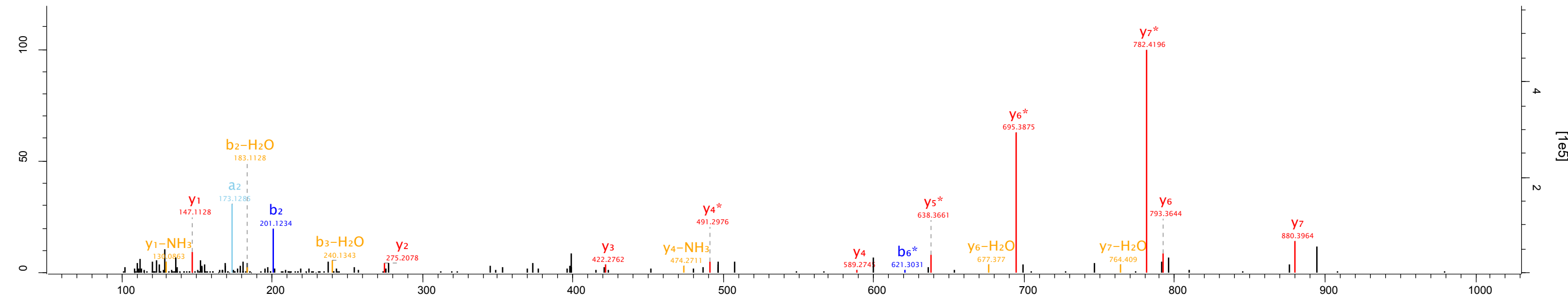
- R L E Q T S V R D P S P E A D A P V L G S P E K -

Fragmentation sites are indicated by brackets below the sequence:

- Red brackets (y-series): y15 (D-P), y13 (P-E), y11 (A-D), y10 (D-A), y9 (A-P), y8 (P-V), y6 (L-G), y5 (G-S), y4 (S-P), y3 (P-E), y1 (E-K)
- Blue brackets (b-series): b3 (E-Q), b8 (R-D), b9 (D-P), b11* (S-P), b13 (E-A), b14²⁺ (A-D), b15 (D-A), b16 (A-P), b18 (V-L), b19 (L-G), b20* (G-S), b21* (S-P)

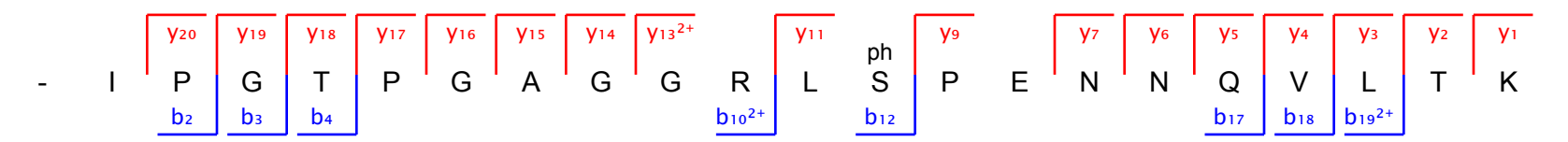
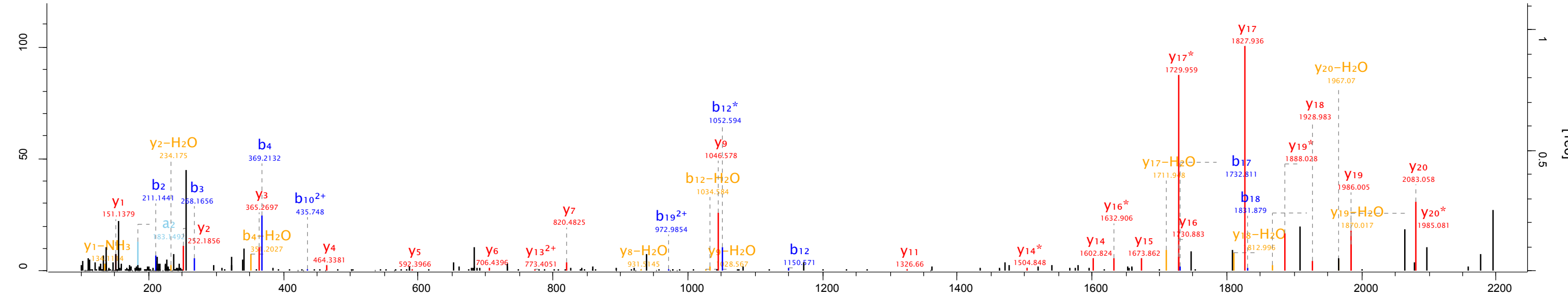


Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 10780 Method FTMS; HCD Score 76.84 m/z 497.24 Gene names MARCKS

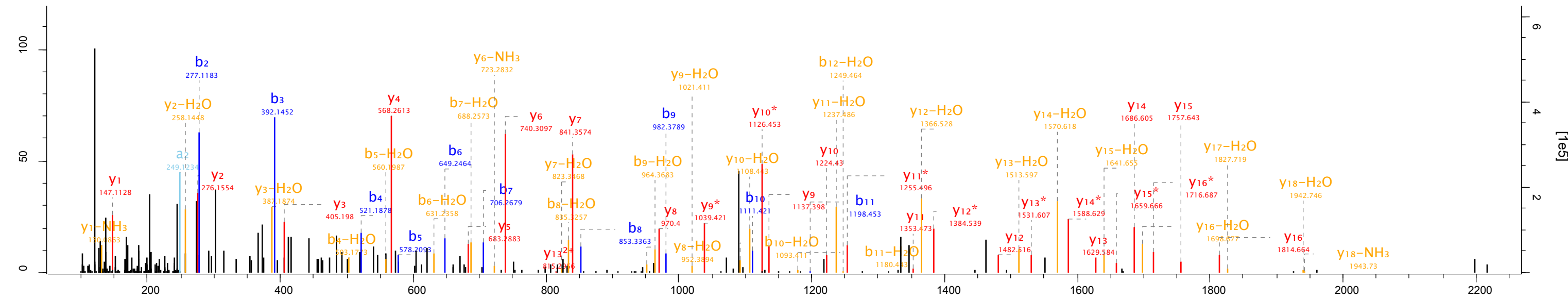


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho_06 10990 FTMS; HCD 146.65 733.05 TAF12



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

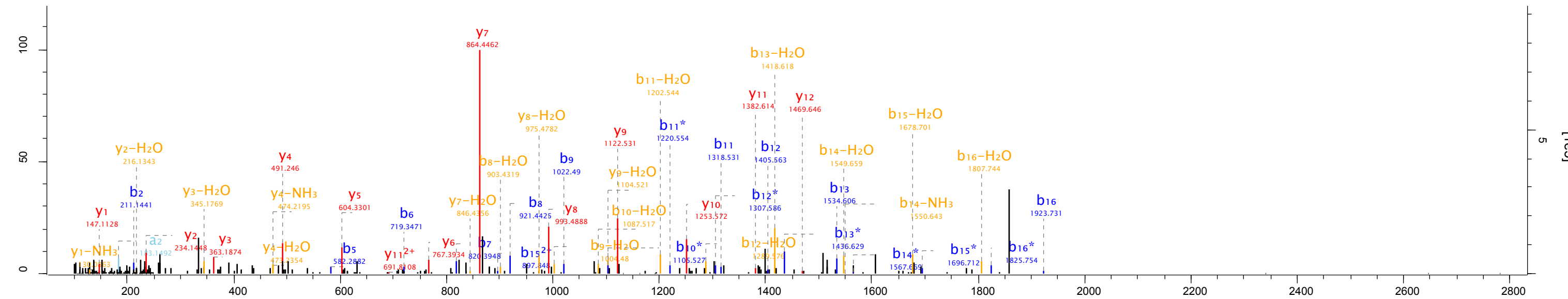


- F E D E G A G F E E S S E T G D Y E E K -

b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ b₁₀ b₁₁ y_{ph} y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11280 Method FTMS; HCD Score 148.19 m/z 930.4 Gene names PHC2



- L P Q Q D H T T T T D S E M E E P Y L Q E S K -

Peptide sequence: L P Q Q D H T T T T D S E M E E P Y L Q E S K

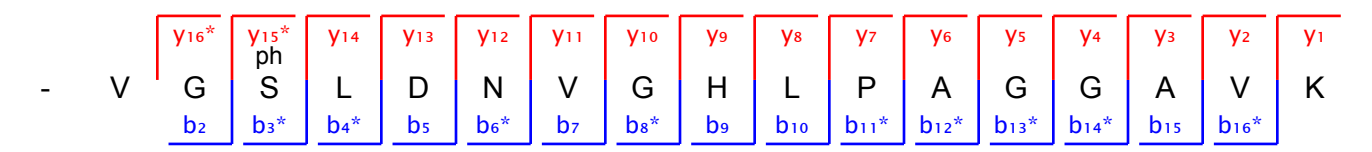
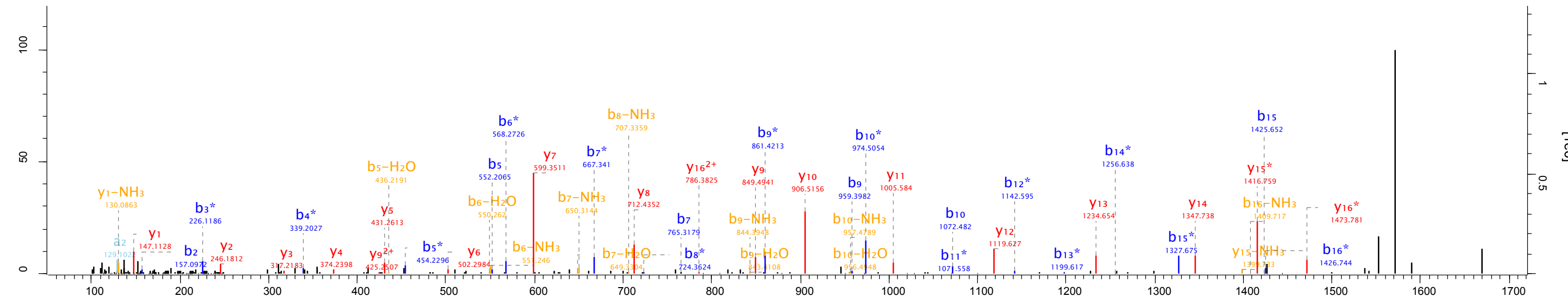
Fragmentation sites (b and y ions) are indicated by brackets below the sequence:

- b₂ (L-P)
- b₅ (D-H)
- b₆ (H-T)
- b₇ (T-T)
- b₈ (T-T)
- b₉ (T-T)
- b₁₀^{*} (T-T)
- b₁₁ (T-D)
- b₁₂ (D-S)
- b₁₃ (S-E)
- b₁₄^{*} (E-M)
- b₁₅^{*} (M-E)
- b₁₆ (E-E)

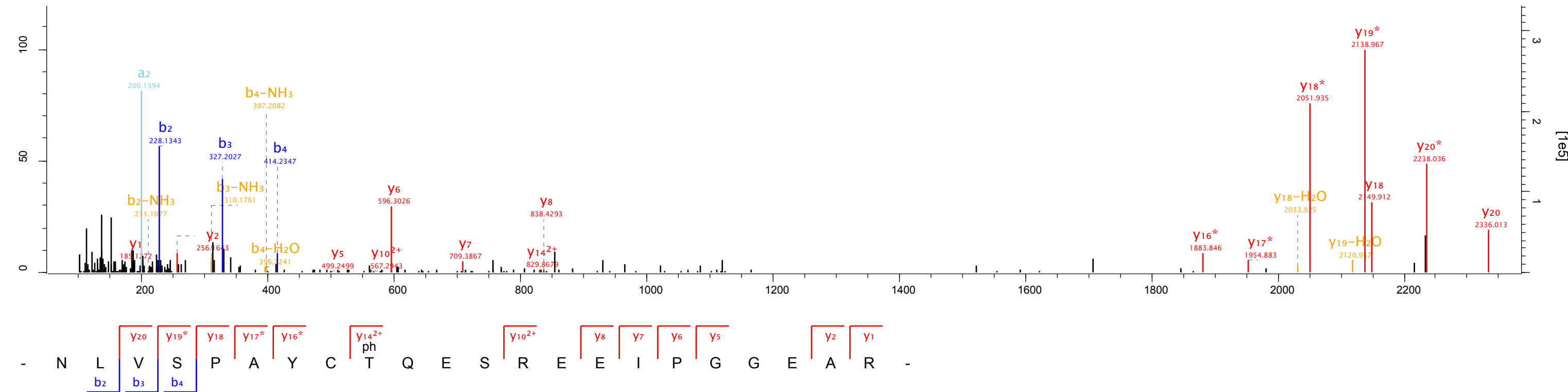
Corresponding y ions (y₁ to y₁₂) are shown above the sequence, with y₁ to y₁₂ corresponding to the amino acids P, Q, Q, D, H, T, T, T, T, D, S, E, M, E, E, P, Y, L, Q, E, S, K respectively.

Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11680 Method FTMS; HCD Score 185.16 m/z 835.92 Gene names MAP4

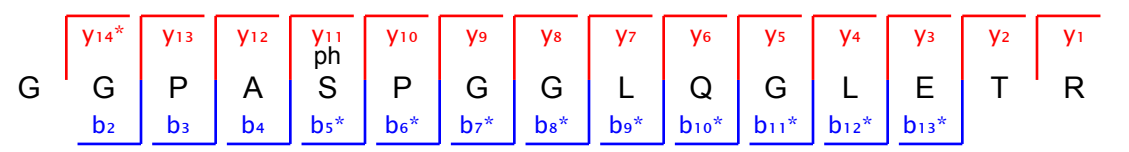
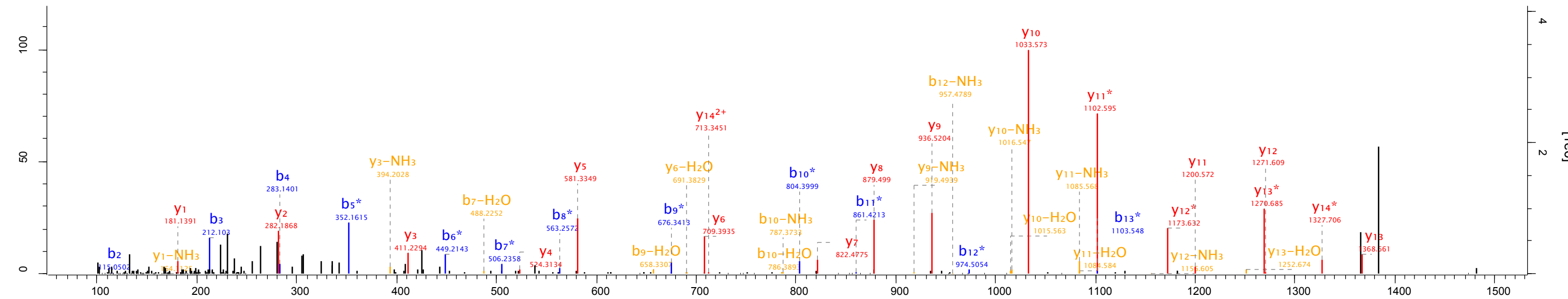
20171215_MaS_33SR_LMH_phospho_06



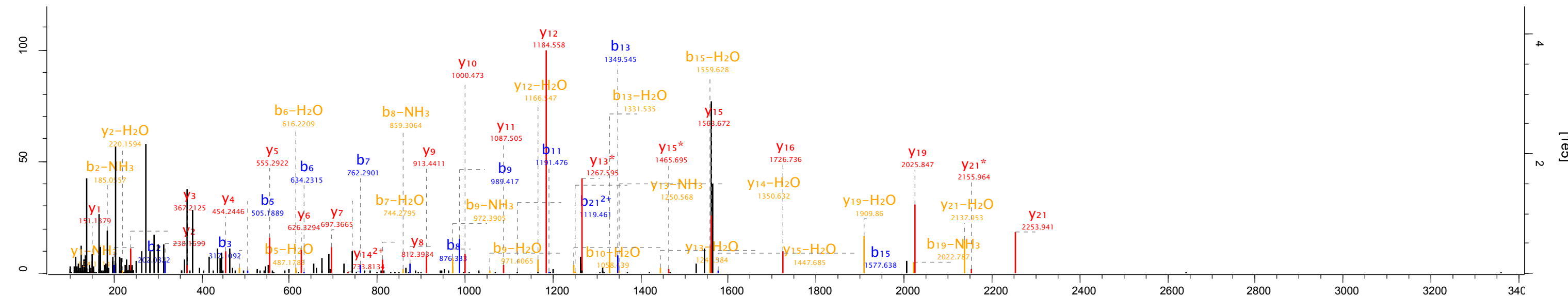
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11690 Method FTMS; HCD Score 50.5 m/z 855.38 Gene names TXLNG



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11810 Method FTMS; HCD Score 189.55 m/z 741.85 Gene names HJURP



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11950 Method FTMS; HCD Score 82.77 m/z 1201.83 Gene names HUWE1

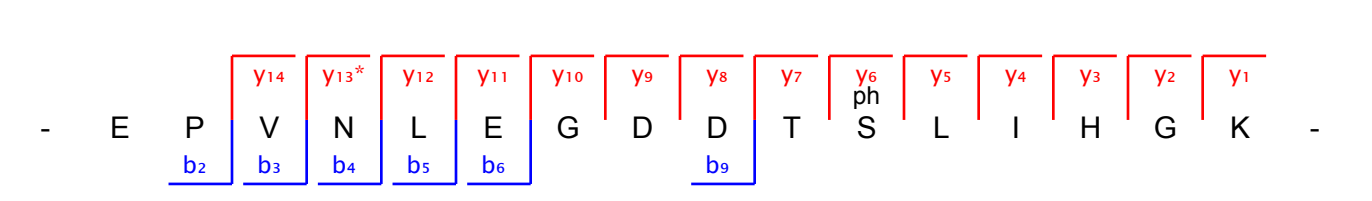
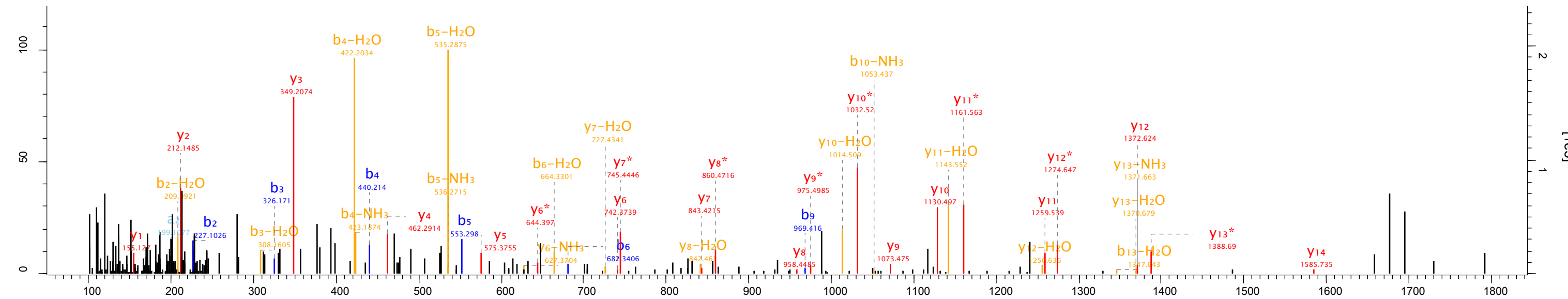


- S N D S T E Q N L S D G T P M P D S Y P T ph T P S S T D A A T S E S K -

b₂ b₃ b₅ b₆ b₇ b₈ b₉ b₁₁ b₁₃ b₁₅ b₂₁²⁺

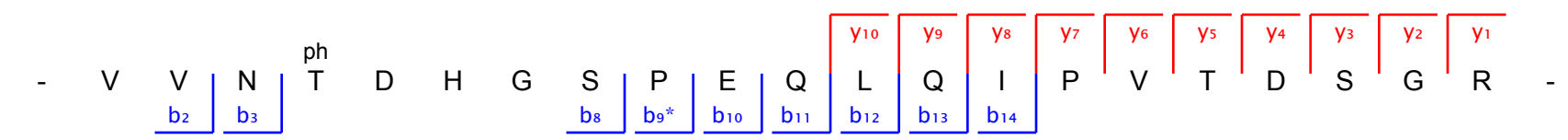
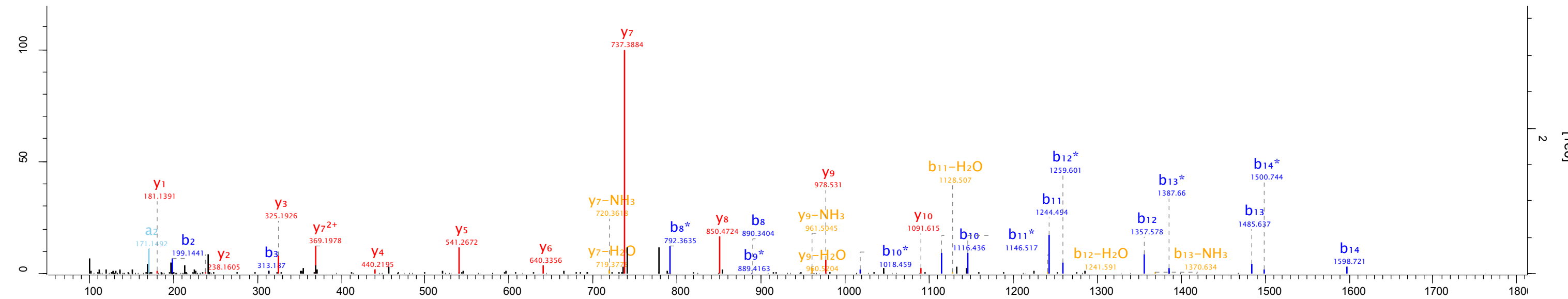
y₂₁ y₁₉ y₁₆ y₁₅ y₁₄²⁺ y₁₃^{*} y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

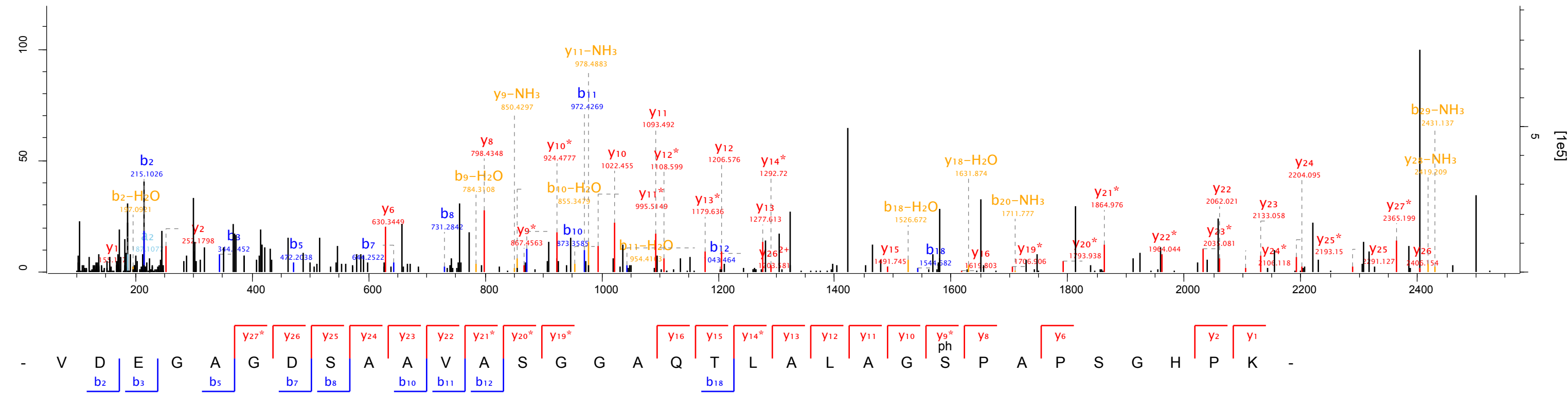
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 Scan: 11970 Method: FTMS; HCD Score: 156.44 m/z: 906.42 Gene names: SLC6A15



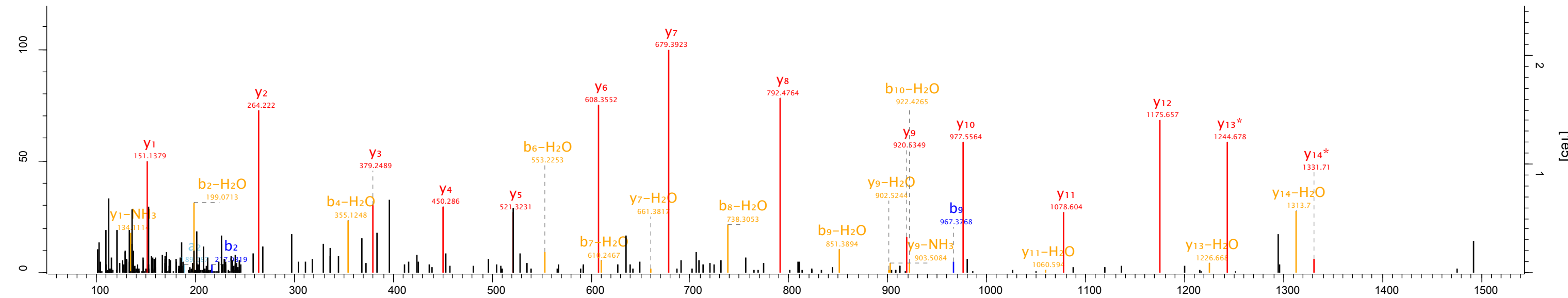
Raw file
20171215_MaS_33SR_LMH_phospho_06

Scan 12020 Method FTMS; HCD Score 105.79 m/z 779.7 Gene names SDE2





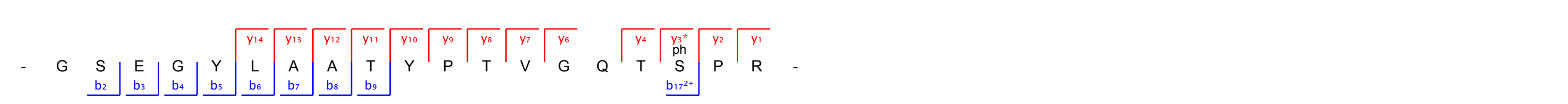
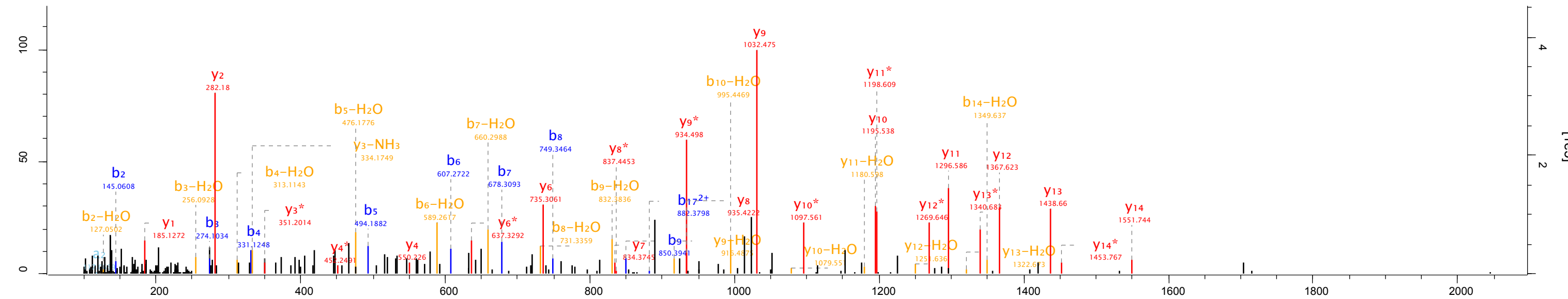
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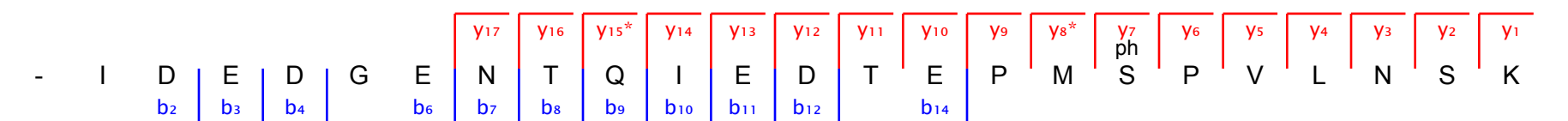
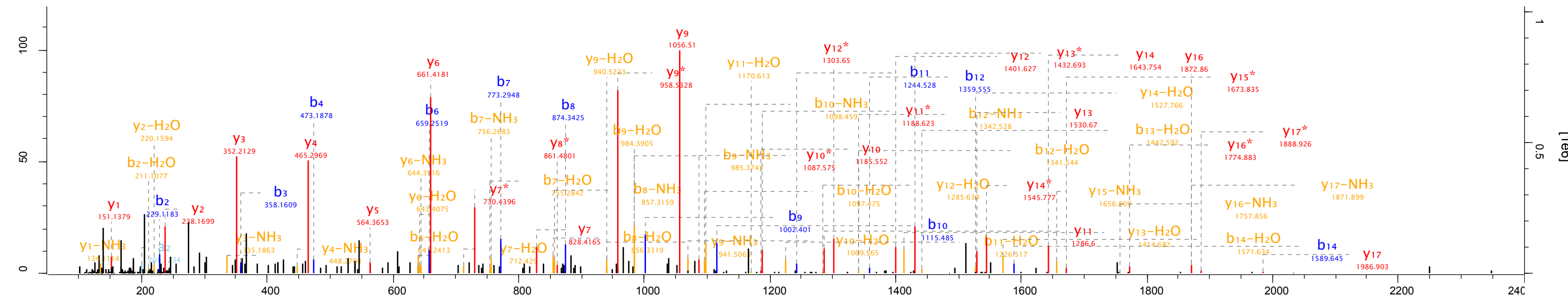
ac - S S S S P T G Q I A S A A D I K -

Fragmentation mapping: b2 (under the second S), b9 (under the I), and y14* (under the first S), y13* (under the second S), y12 (under P), y11 (under T), y10 (under G), y9 (under Q), y8 (under I), y7 (under A), y6 (under S), y5 (under A), y4 (under A), y3 (under D), y2 (under I), y1 (under K).

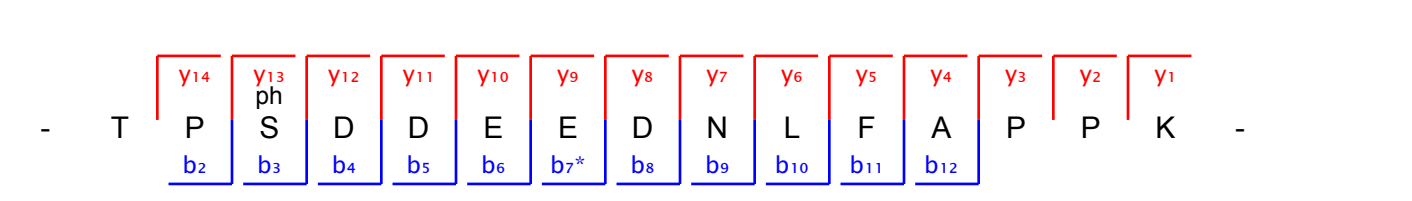
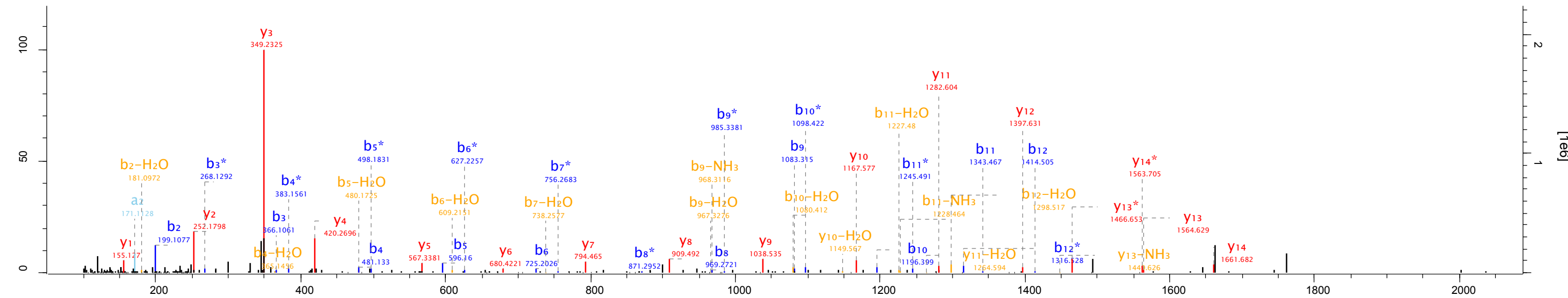
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 13630 Method FTMS; HCD Score 183.07 m/z 1023.47 Gene names NF1



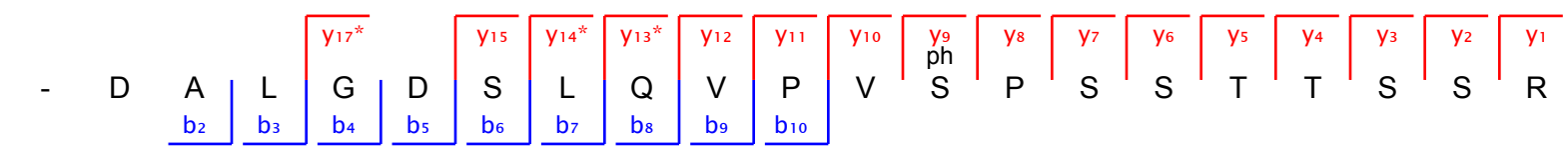
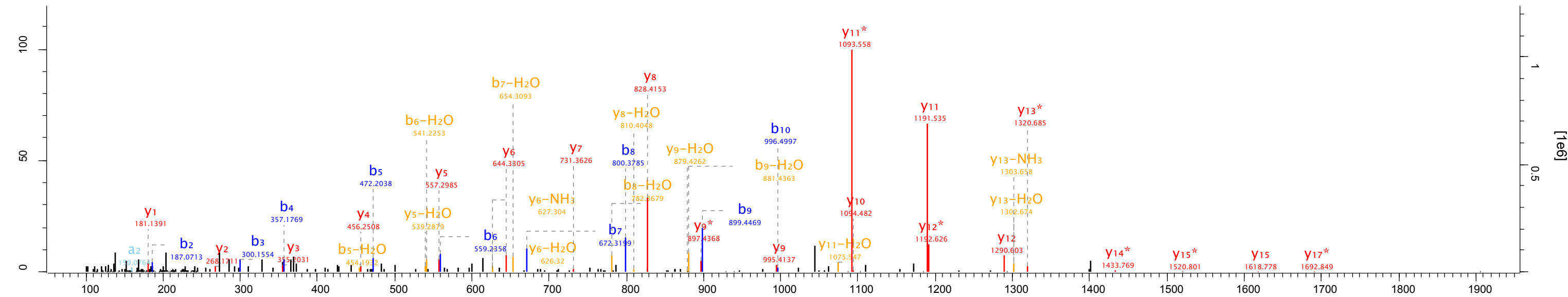
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 13850 Method FTMS; HCD Score 298.97 m/z 1323.58 Gene names TP53BP1



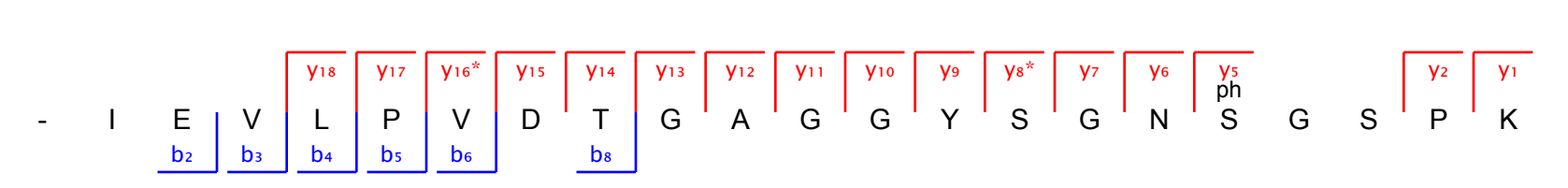
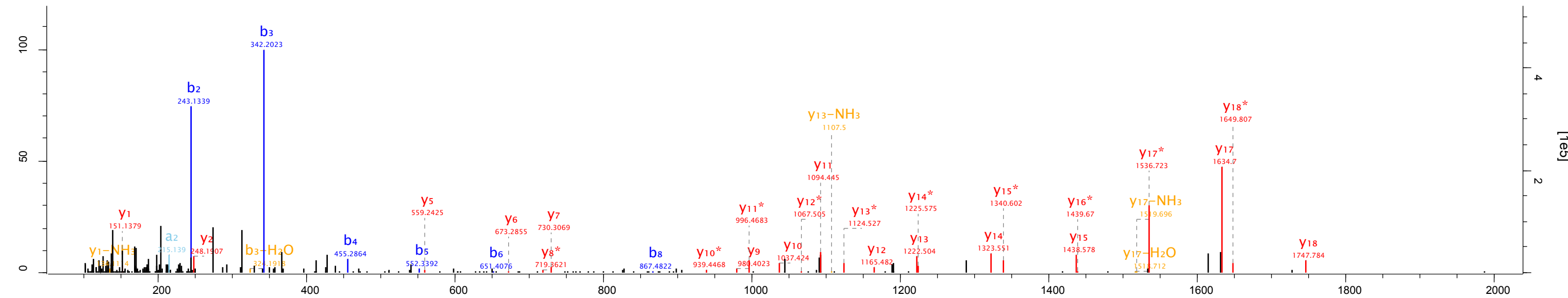
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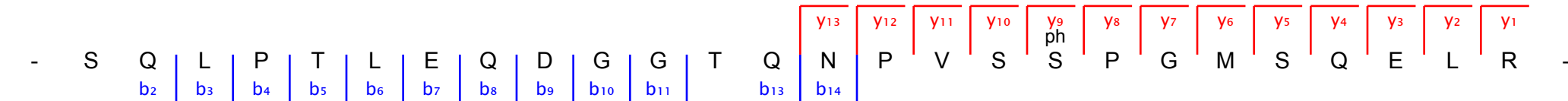
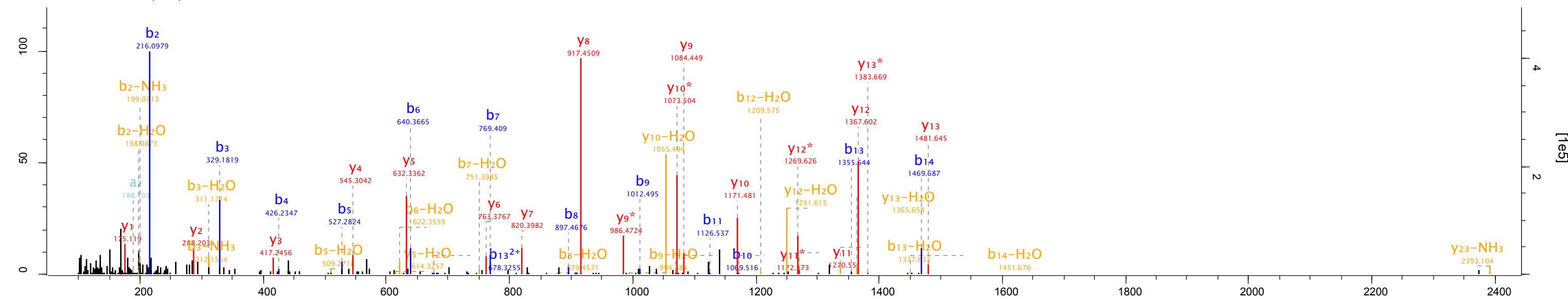


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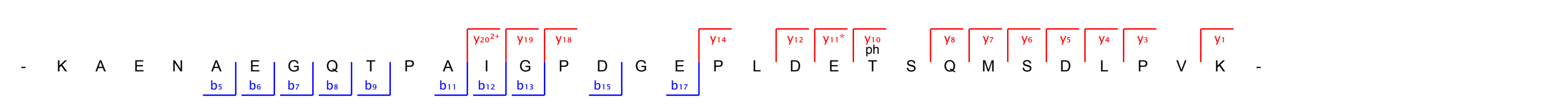
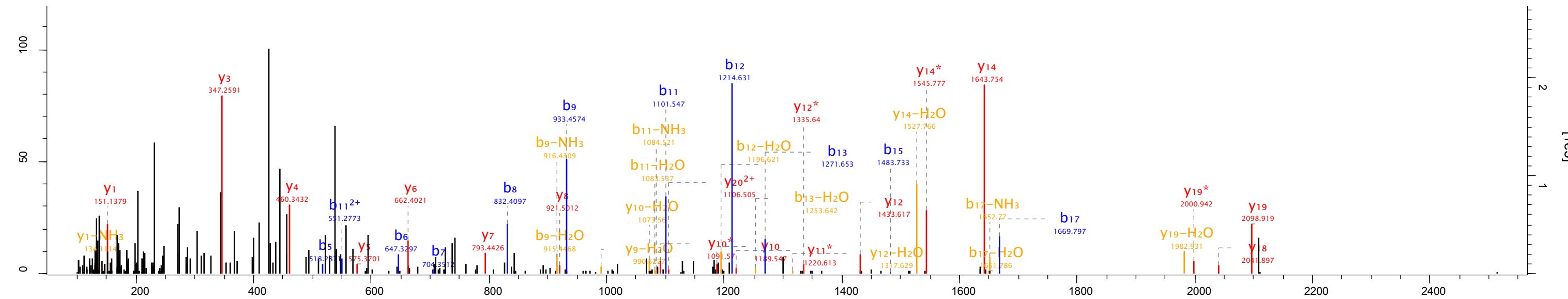


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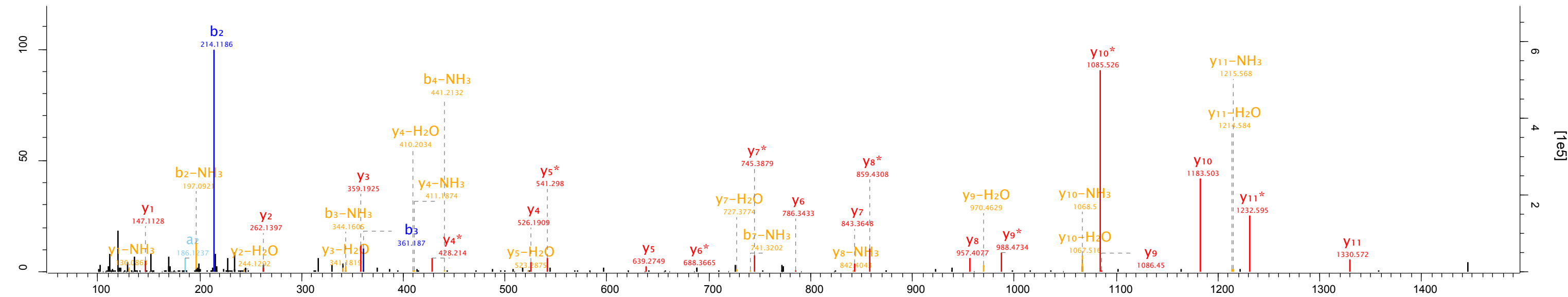


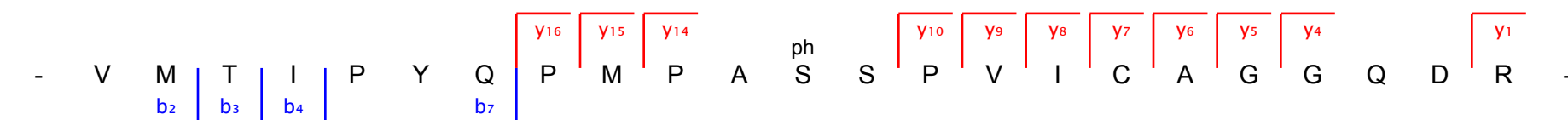
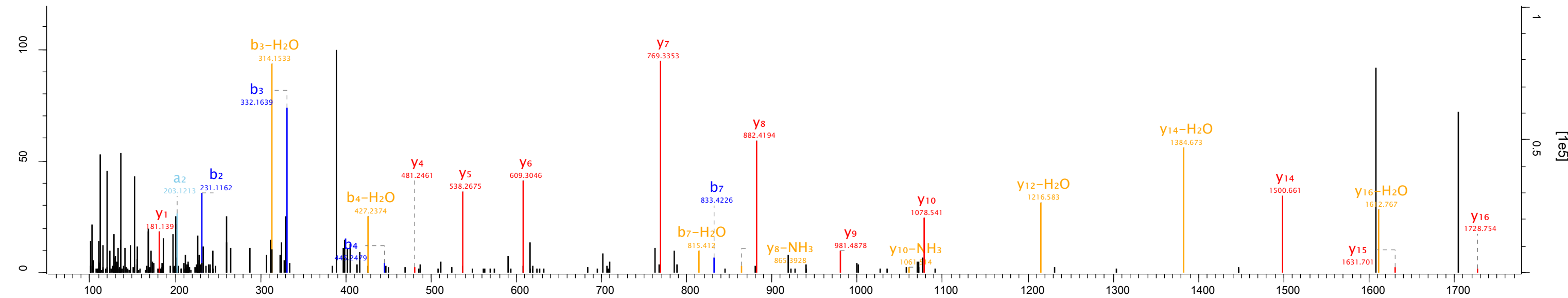


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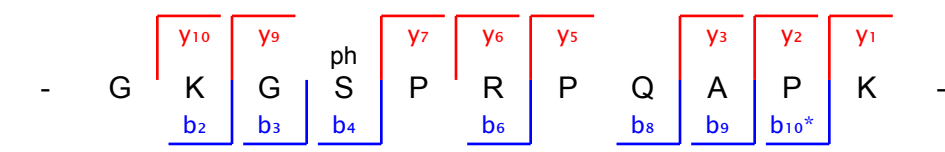
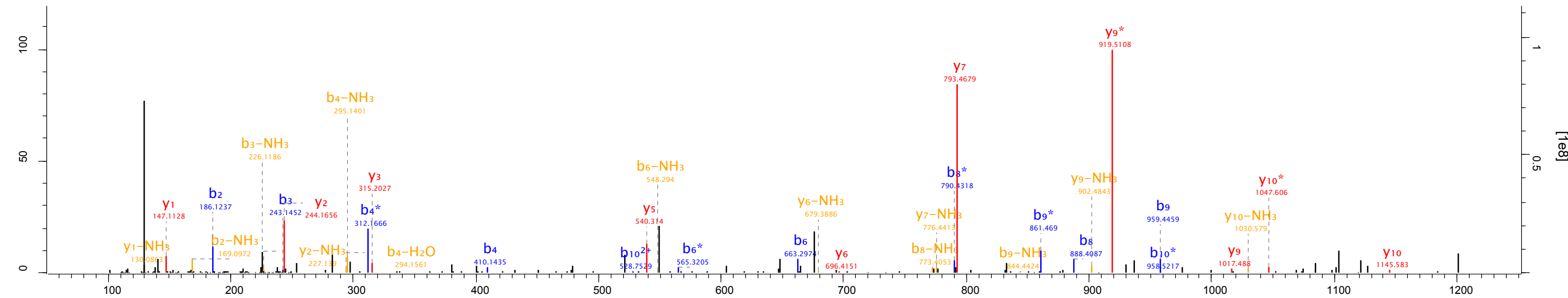


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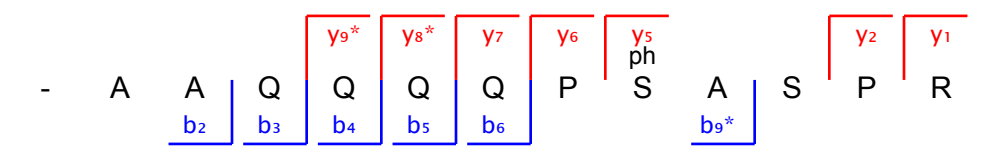
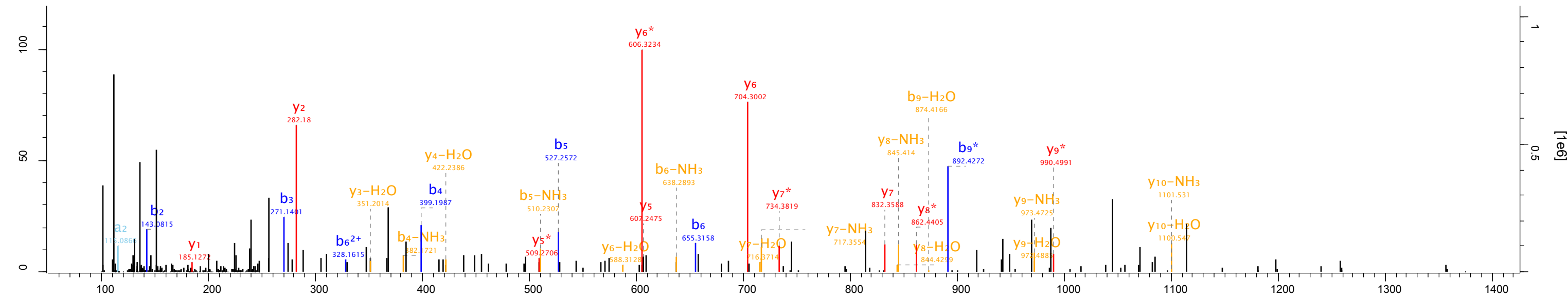




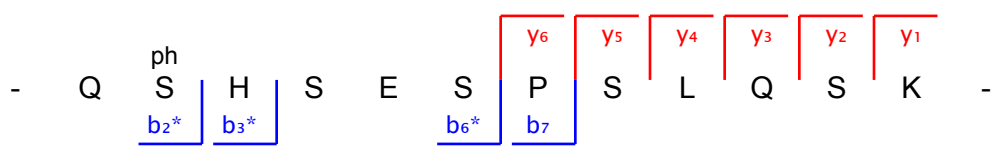
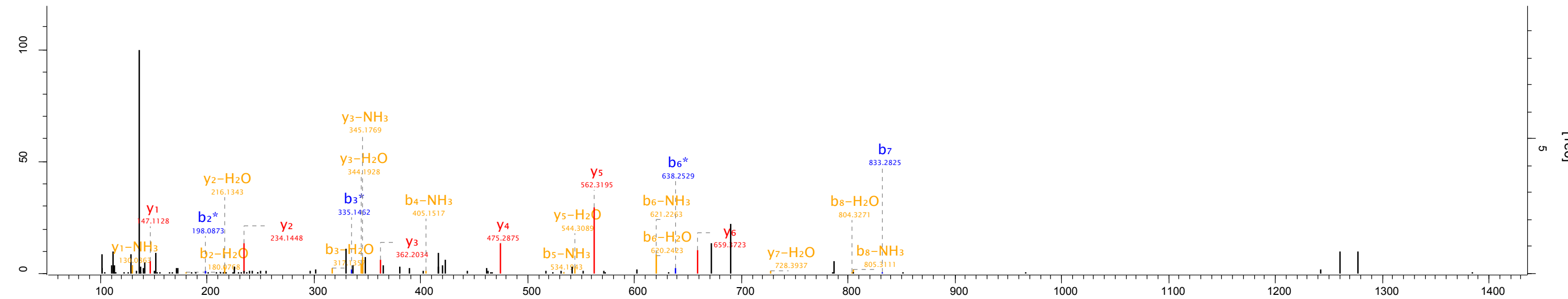
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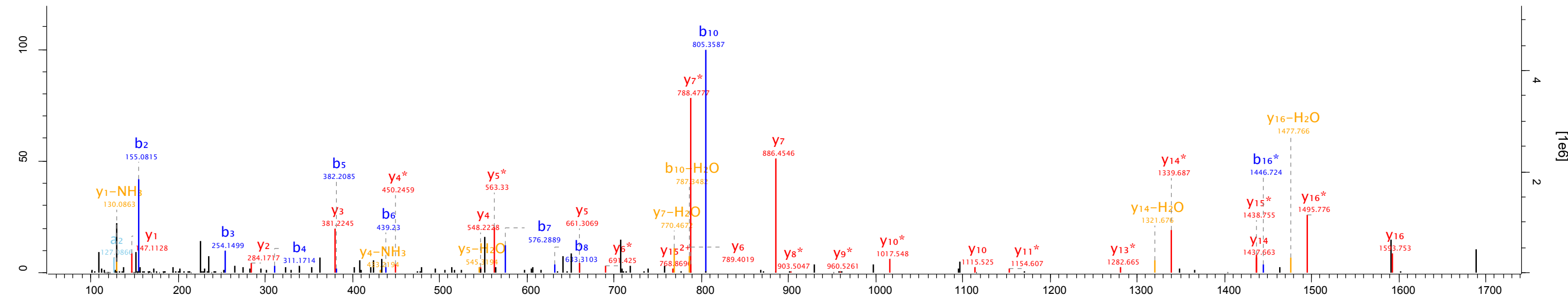
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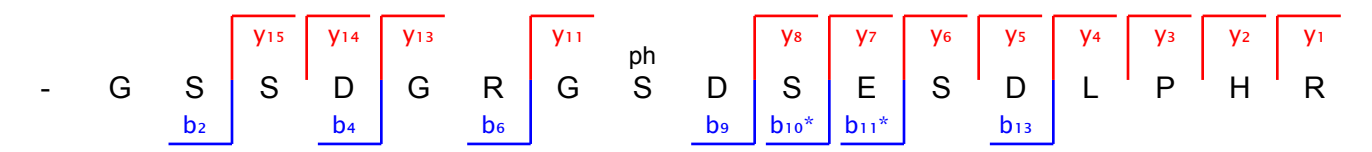
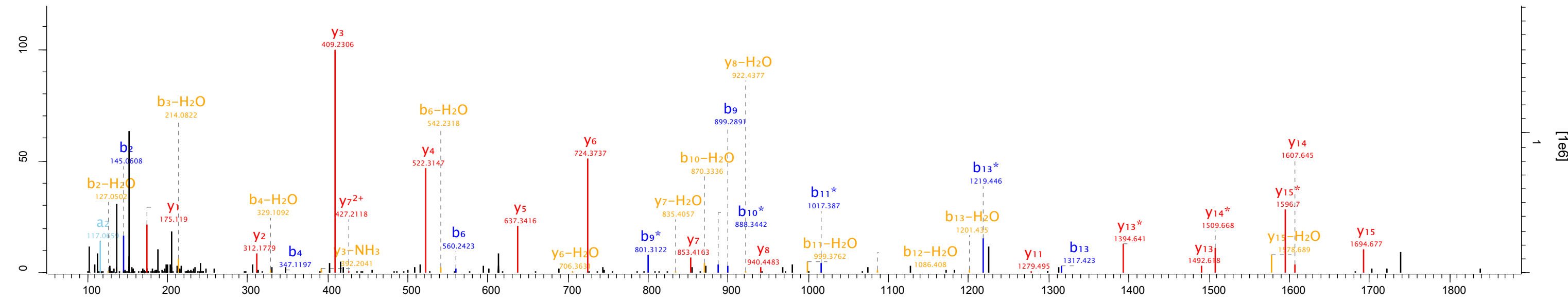
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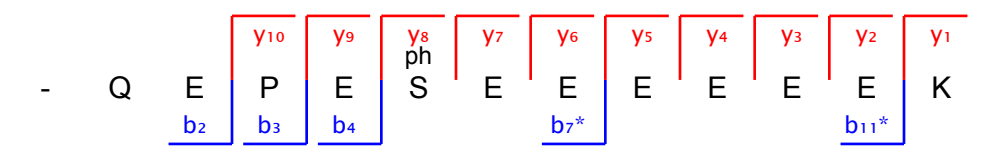
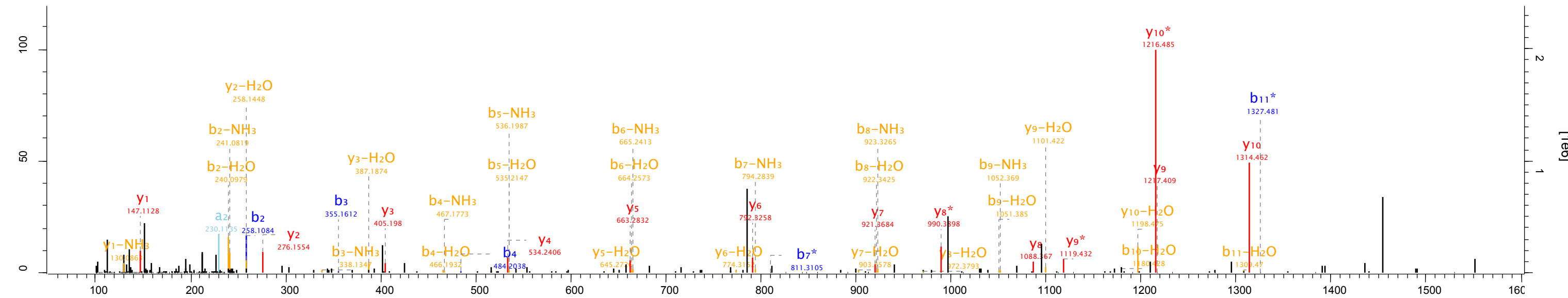
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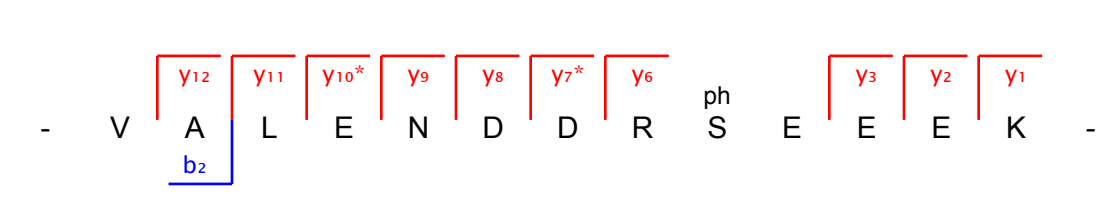
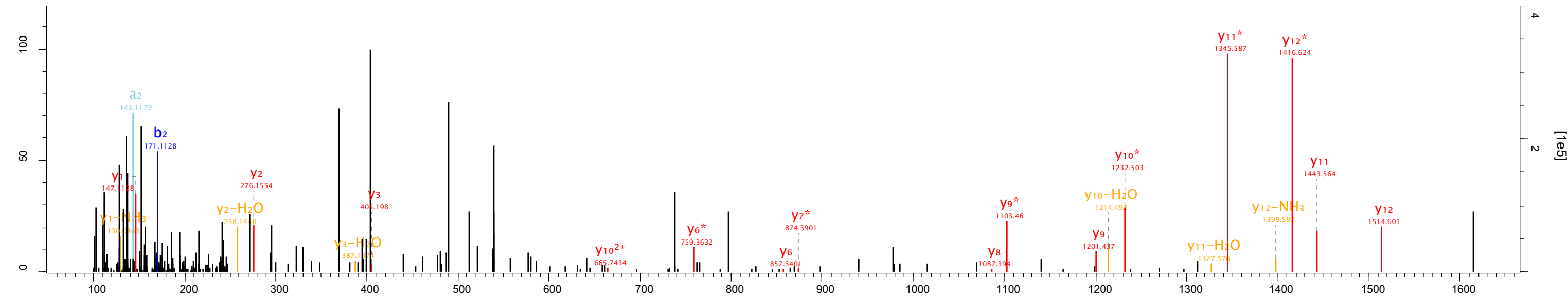
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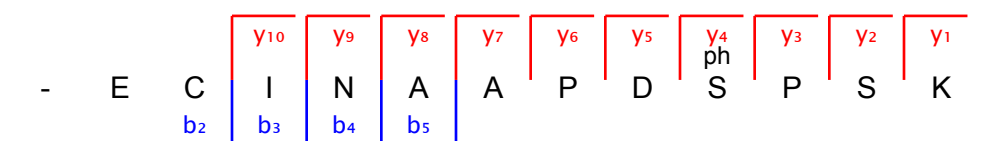
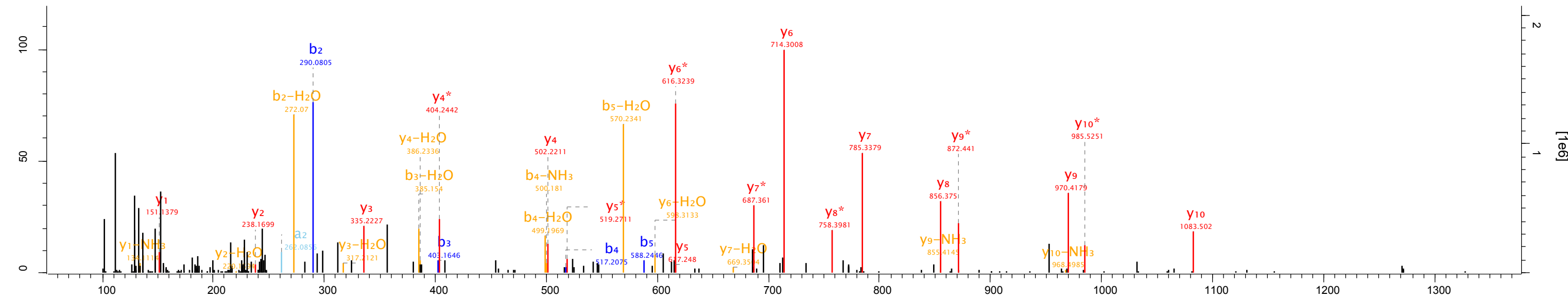
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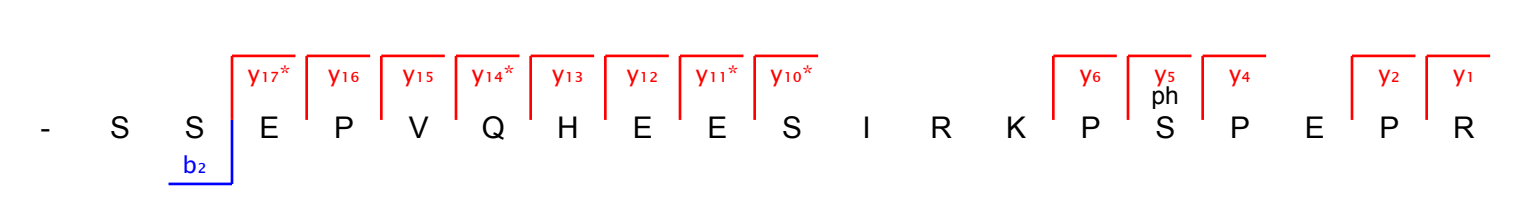
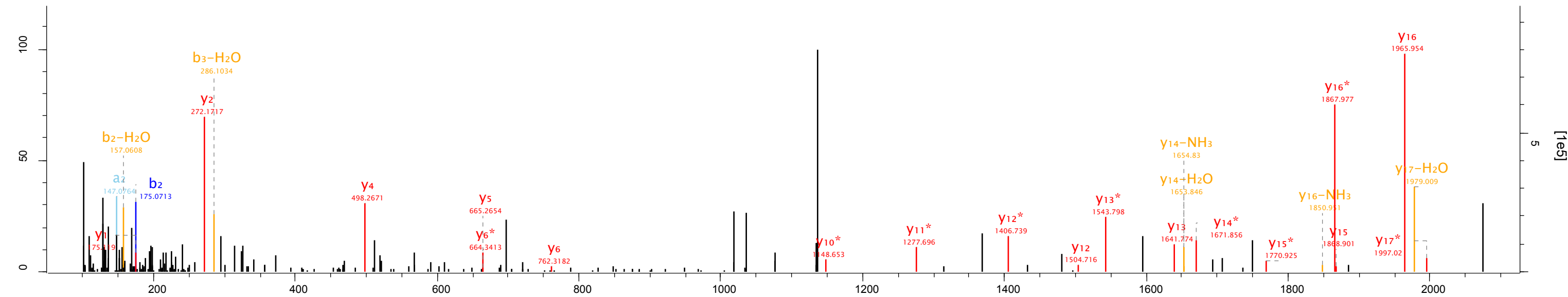
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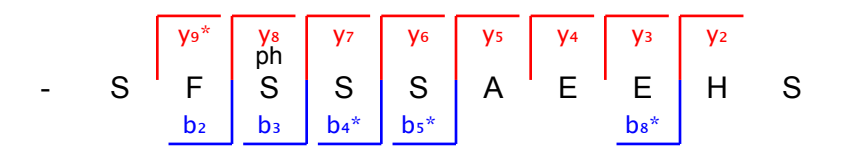
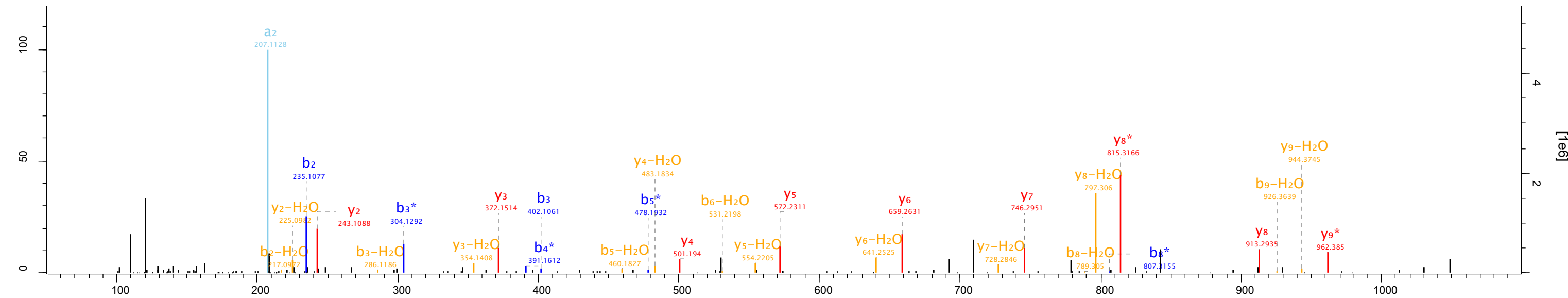
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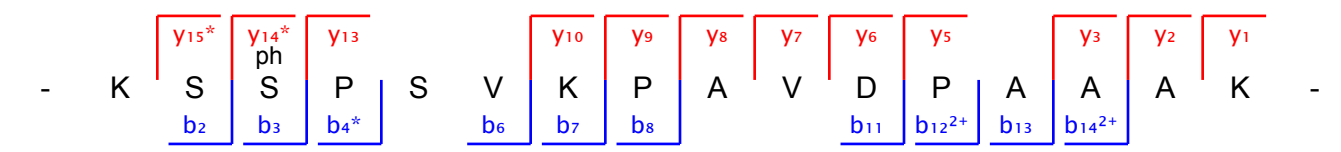
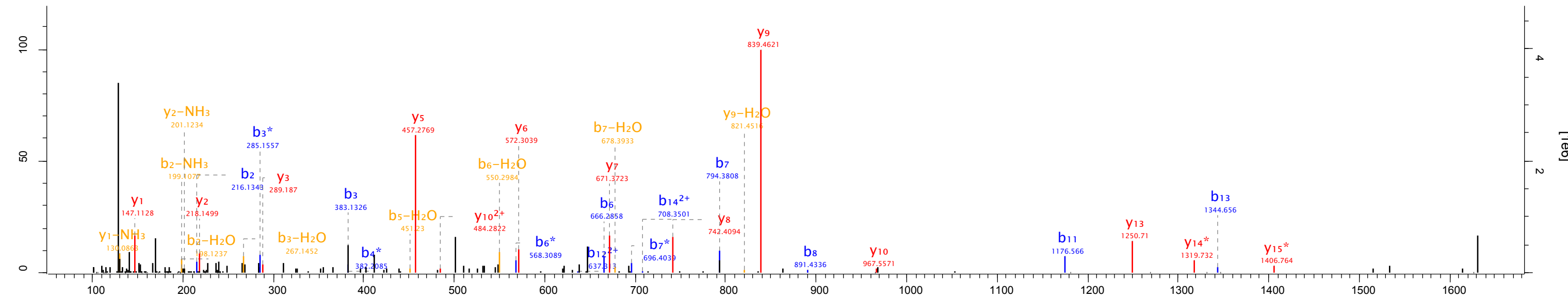
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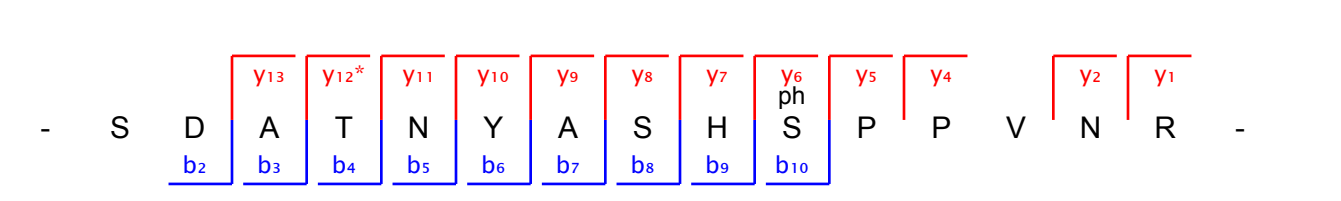
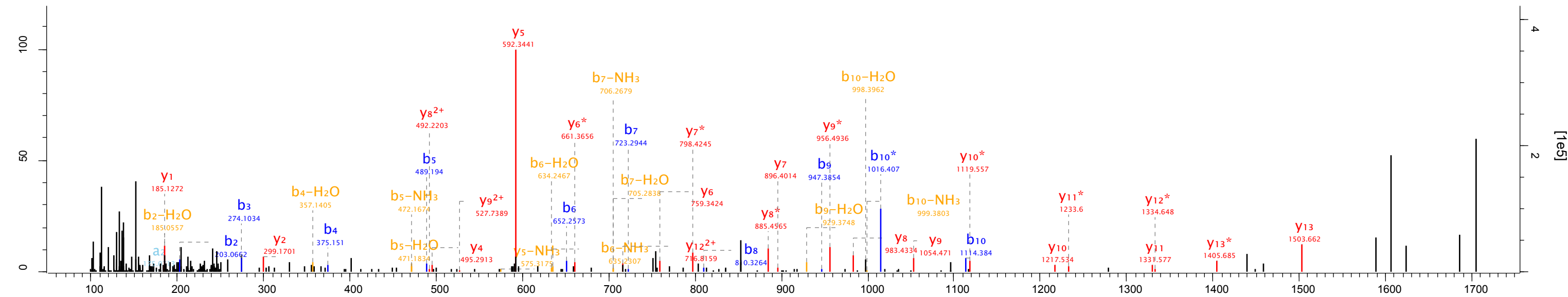
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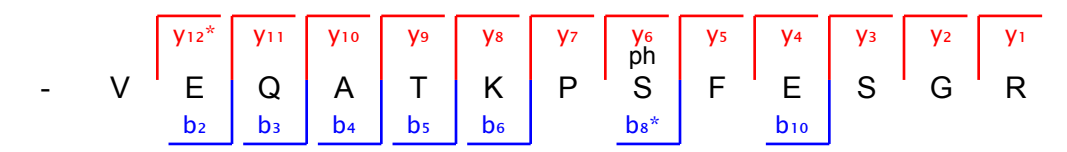
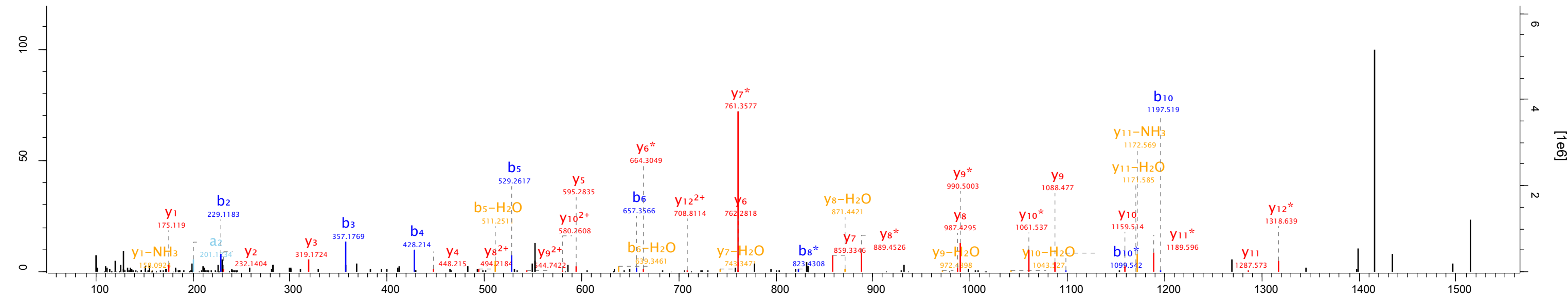
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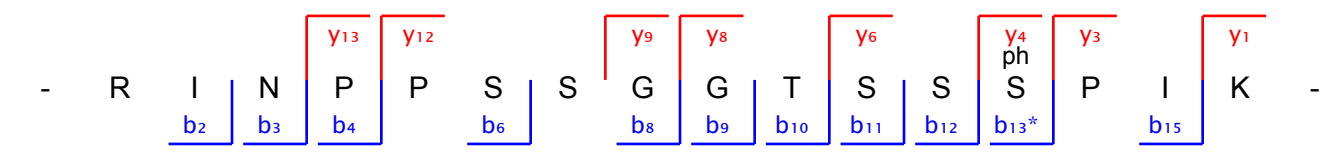
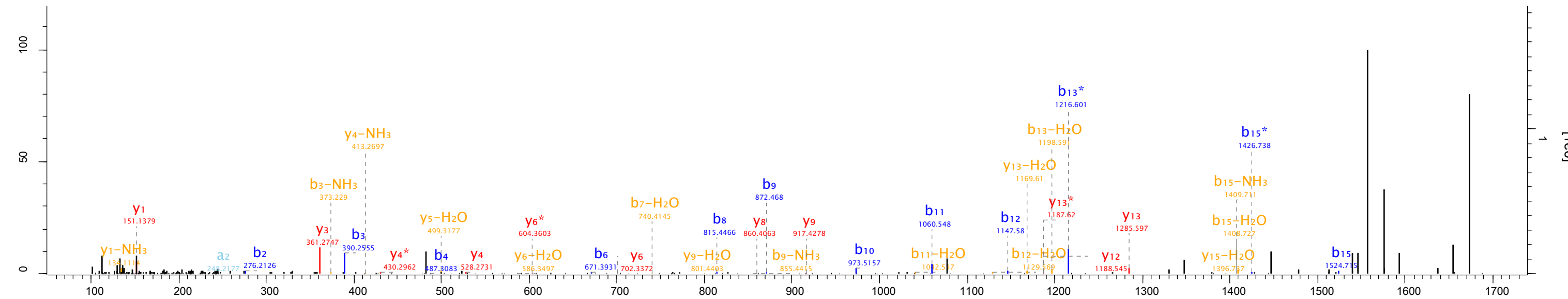
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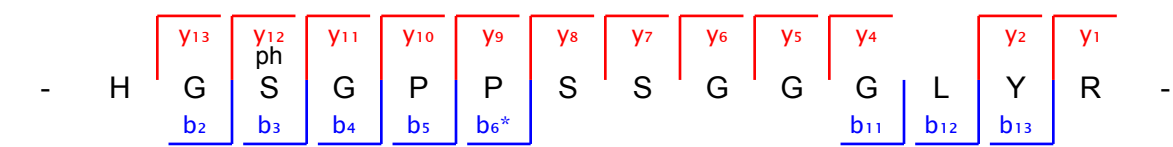
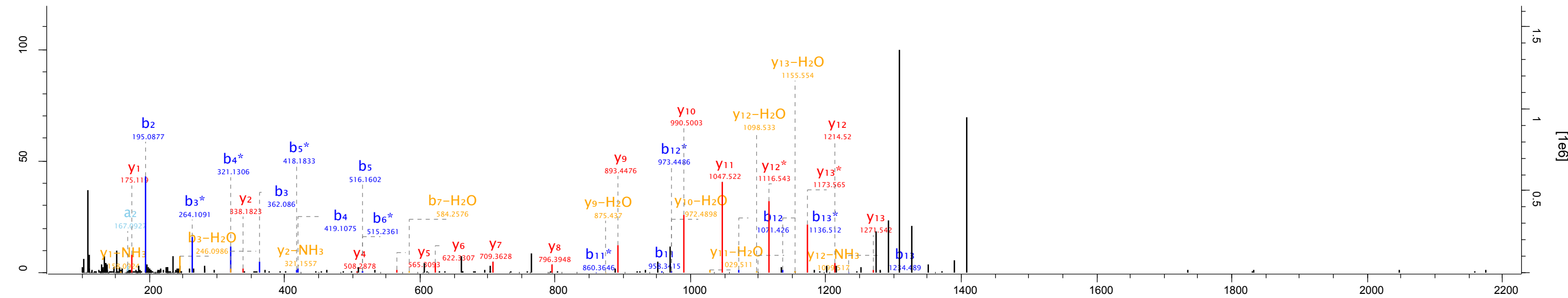
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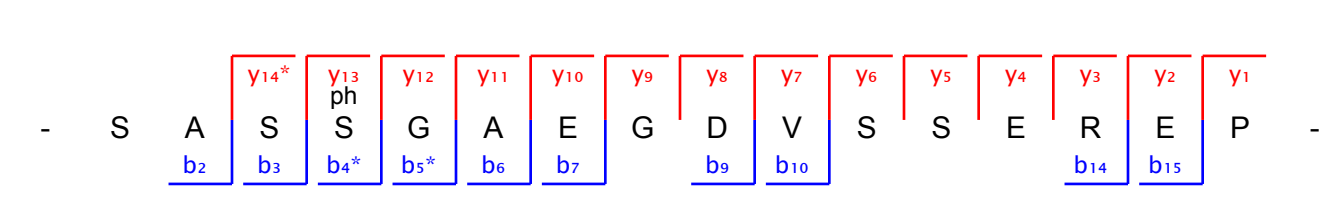
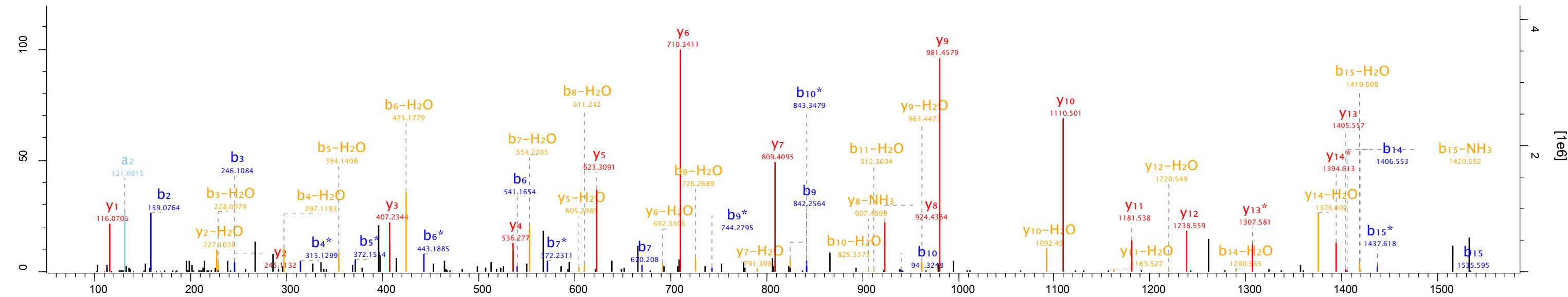
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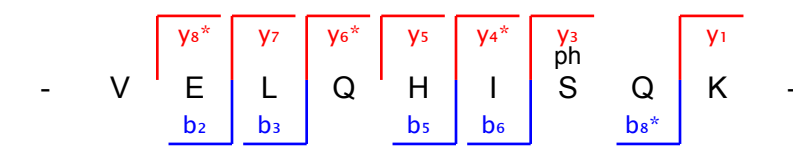
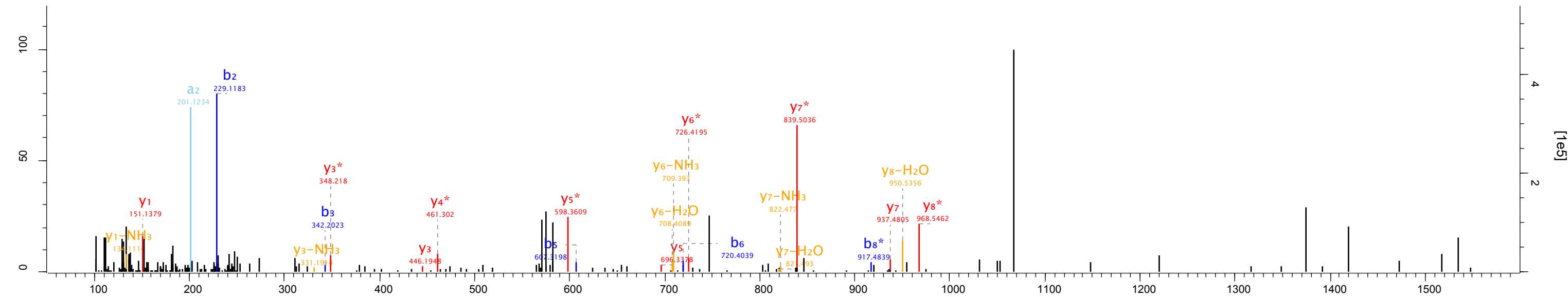
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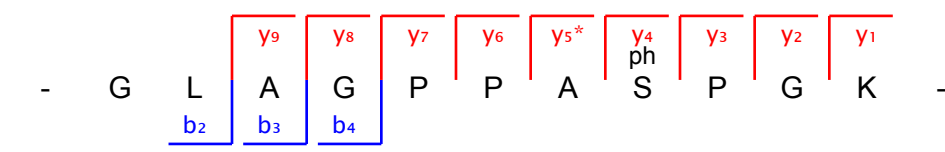
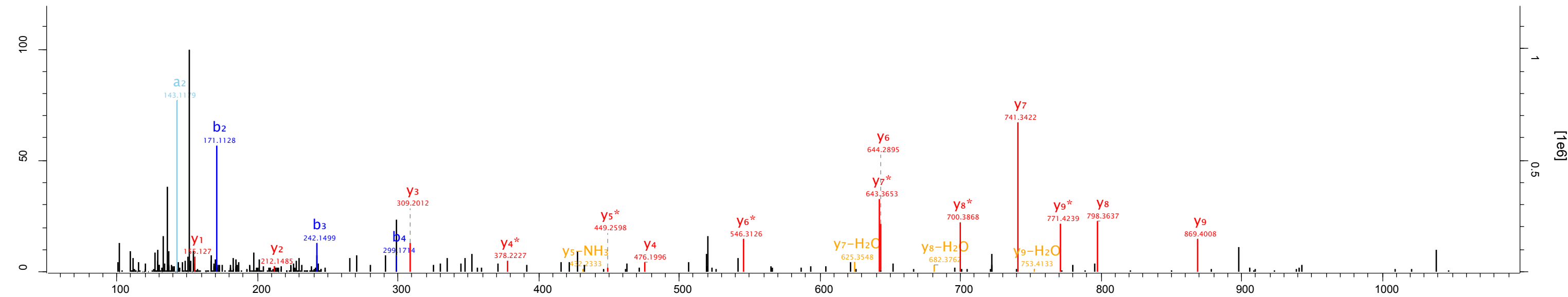
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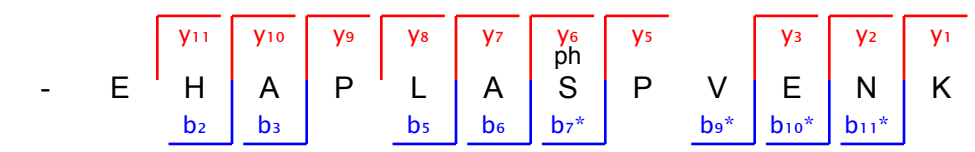
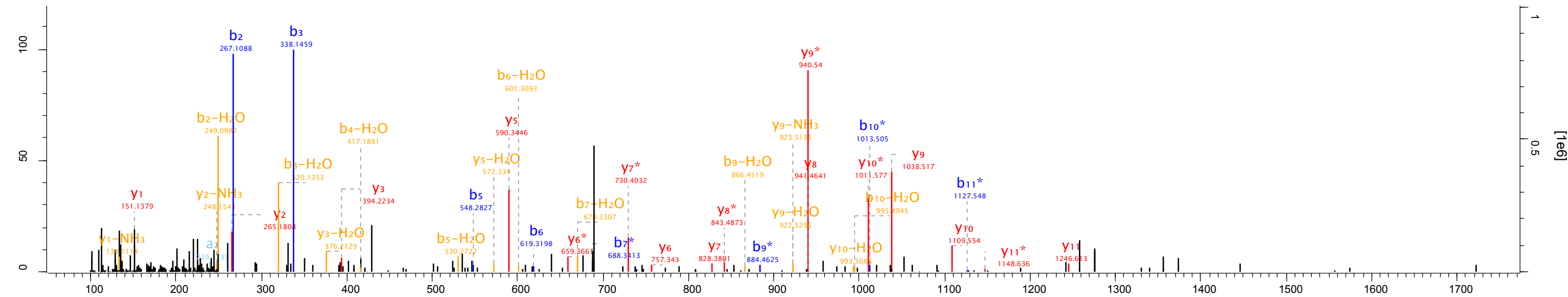
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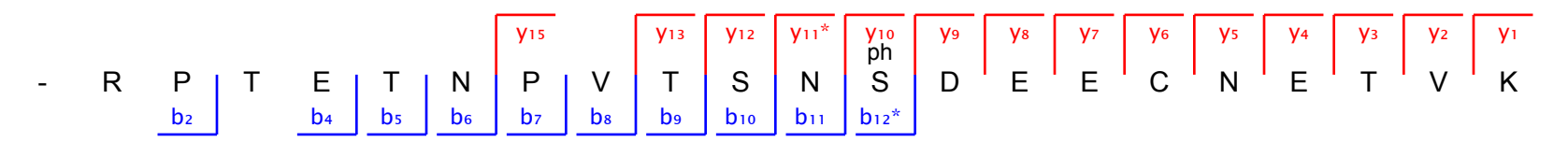
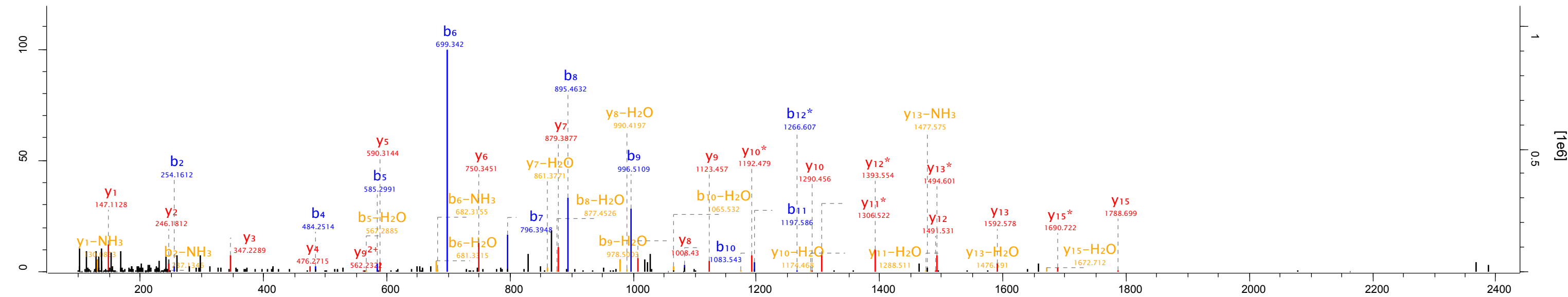
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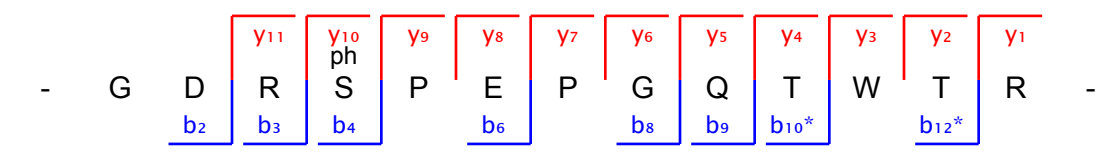
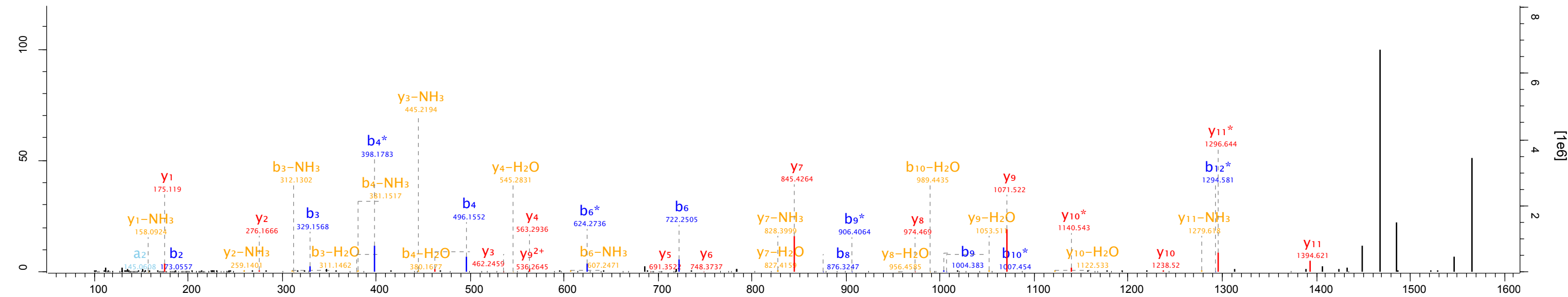
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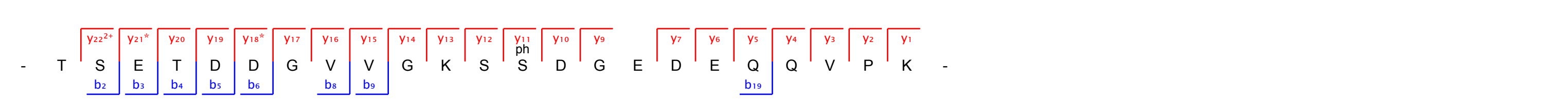
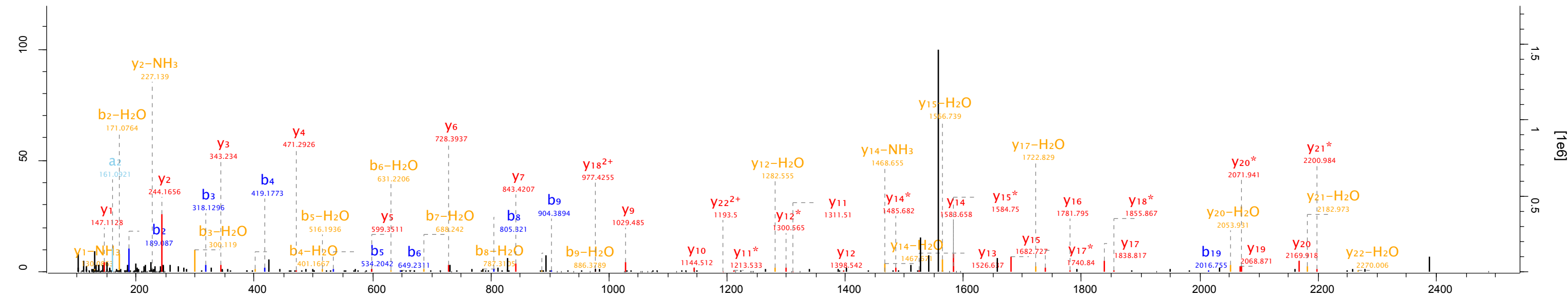
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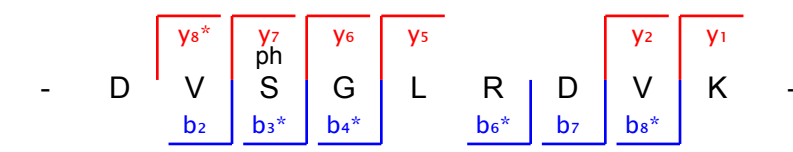
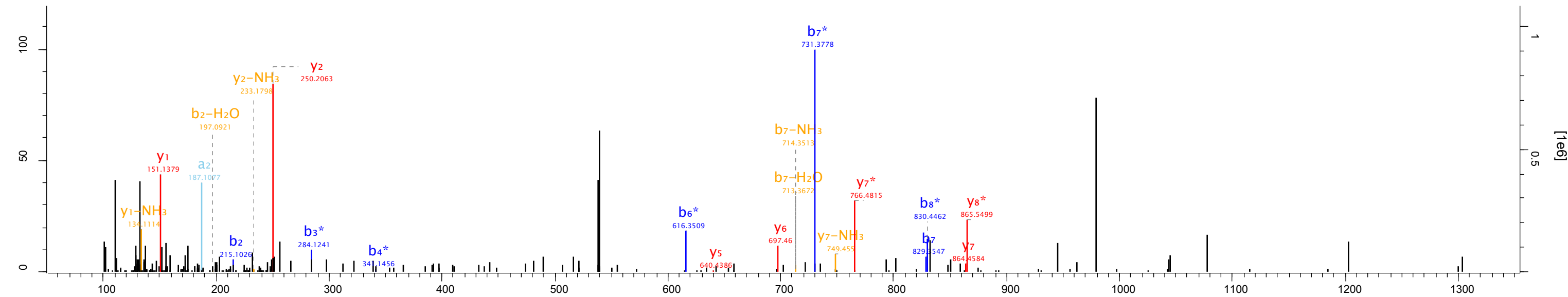
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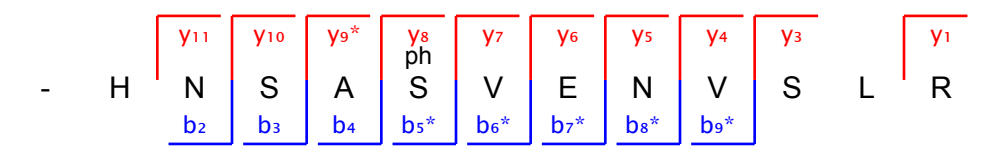
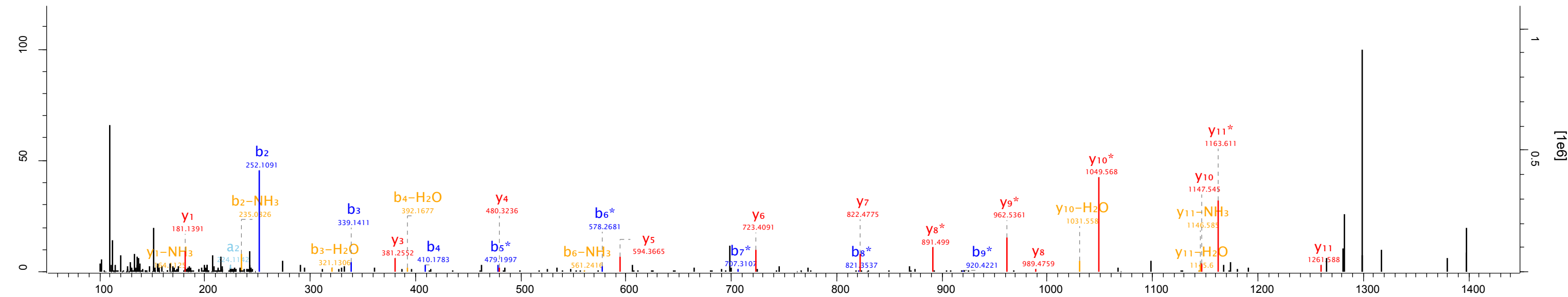
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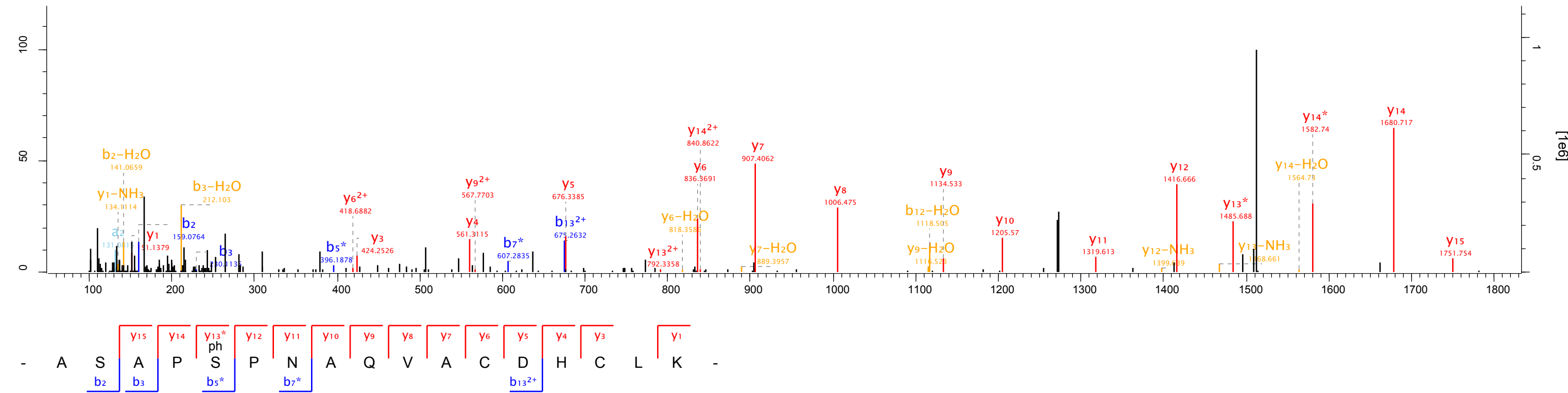


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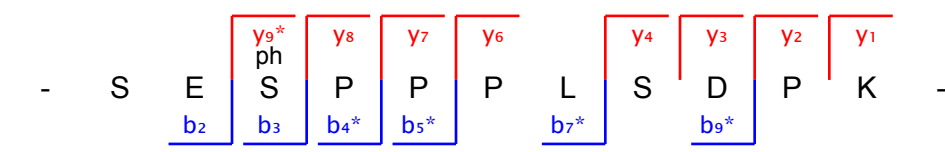
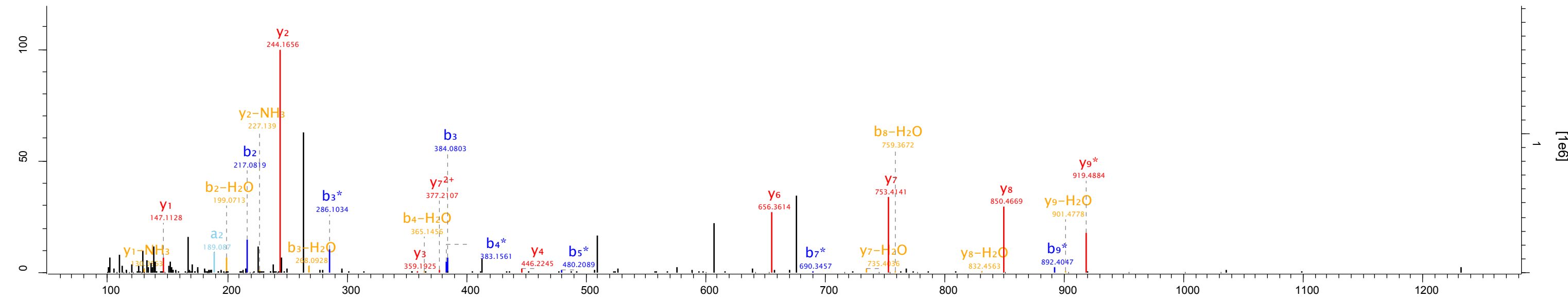


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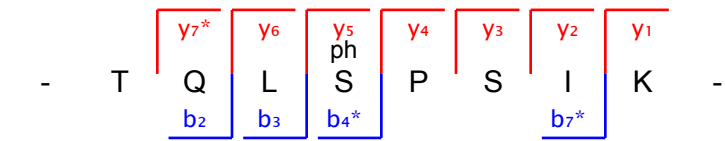
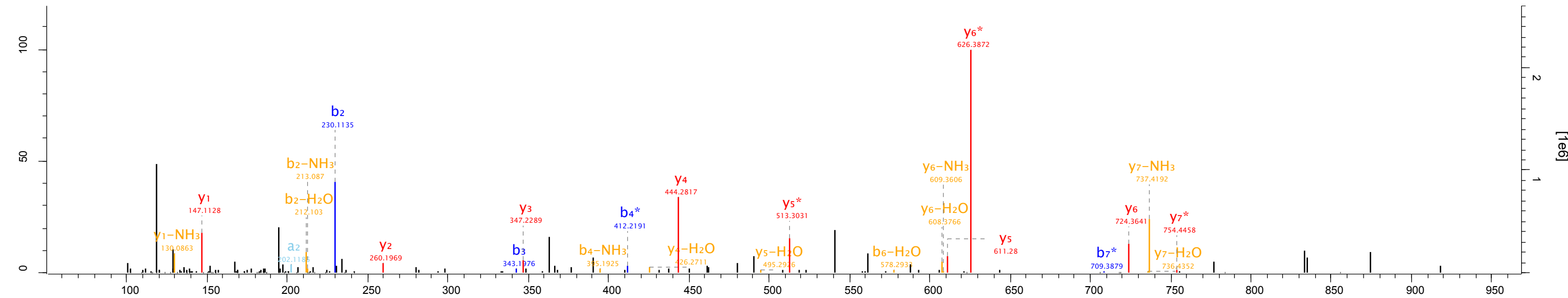




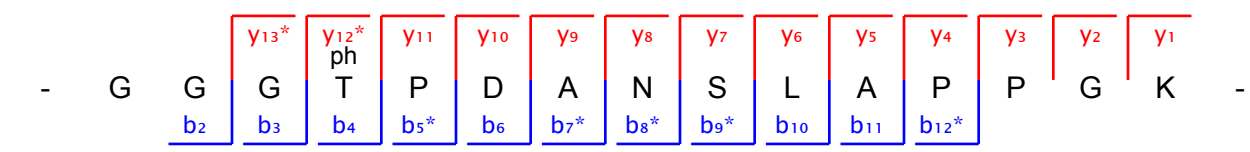
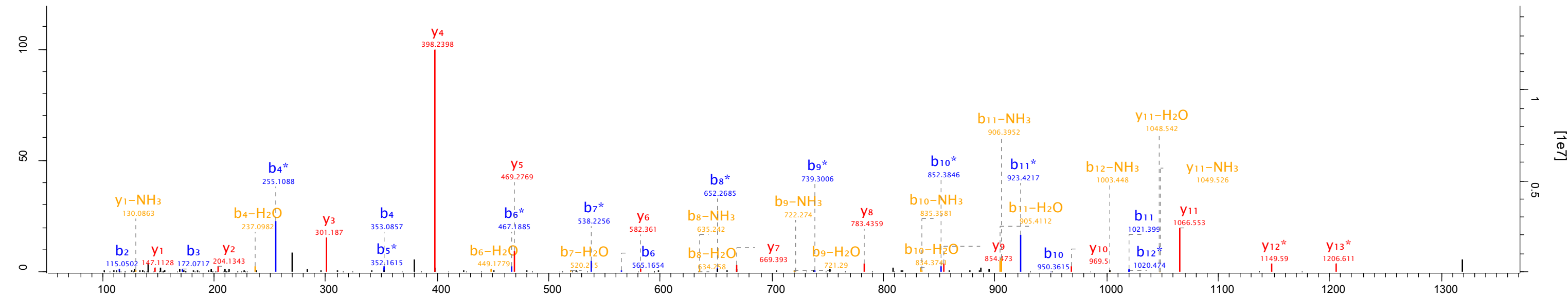
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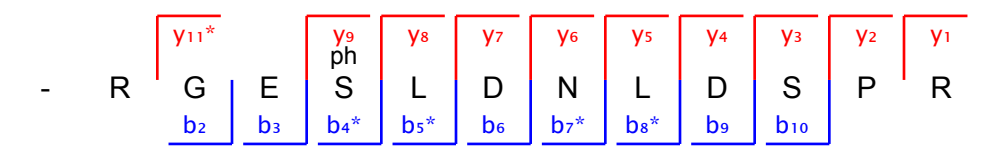
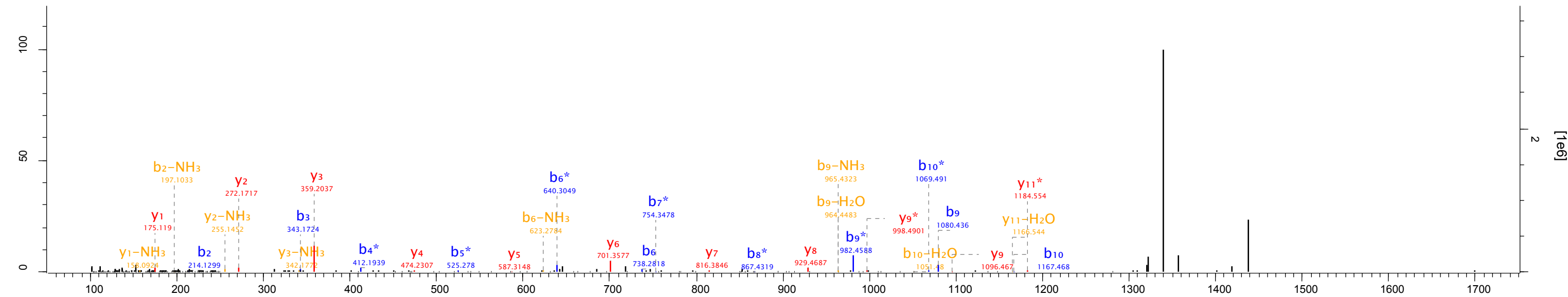
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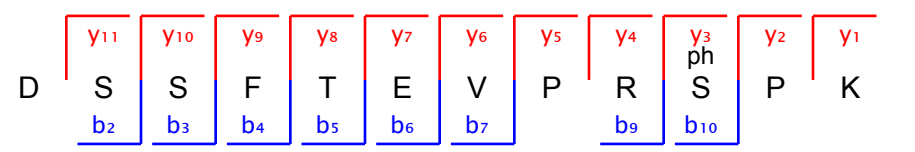
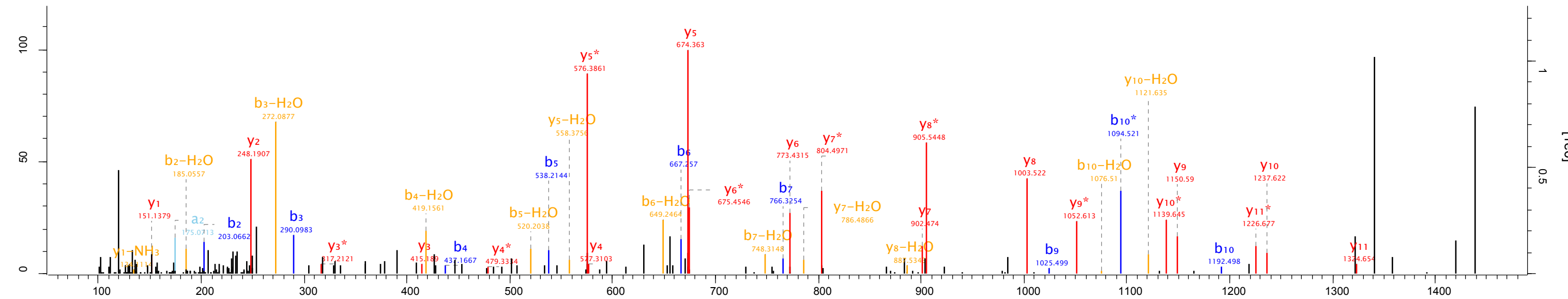
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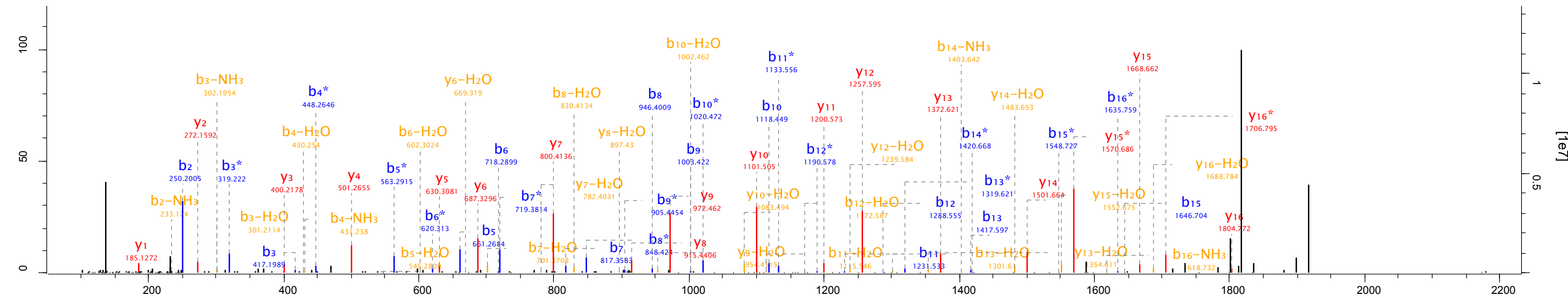


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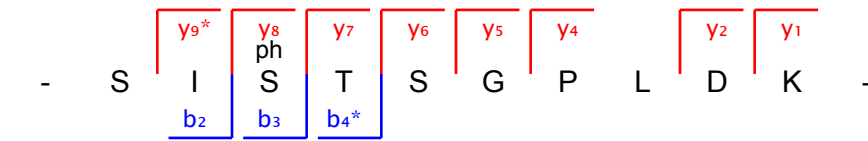
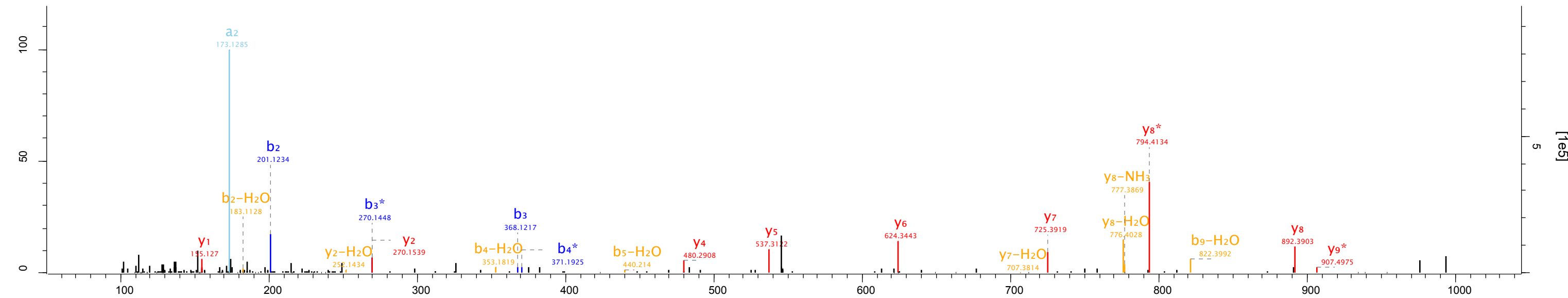
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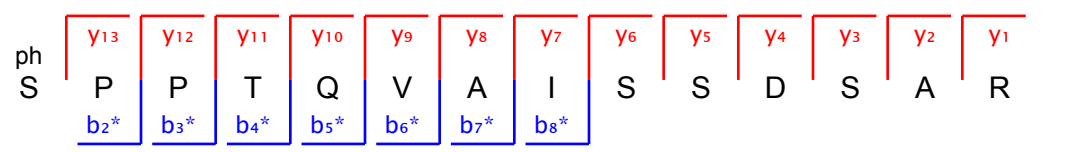
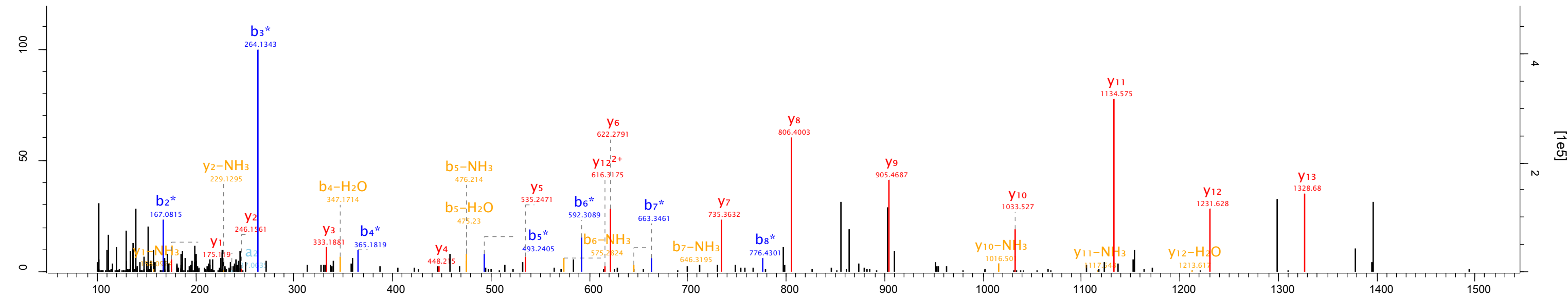
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20171215_MaS_33SR_LMH_phospho_06

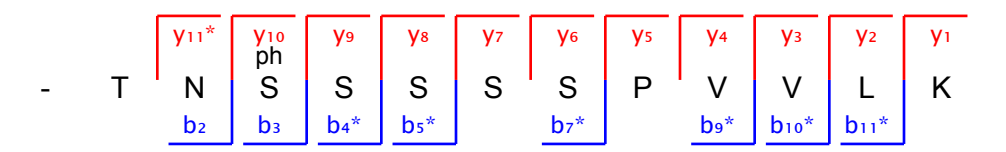
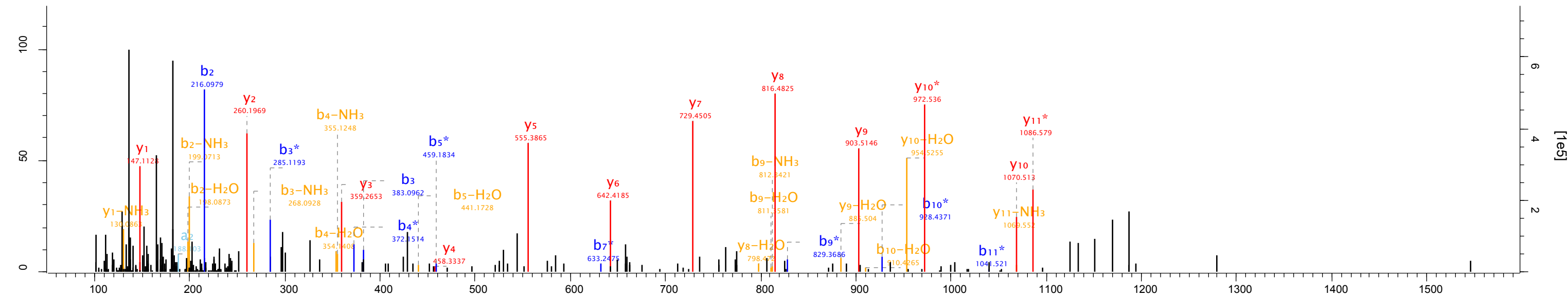
Scan	Method	Score	m/z	Gene names
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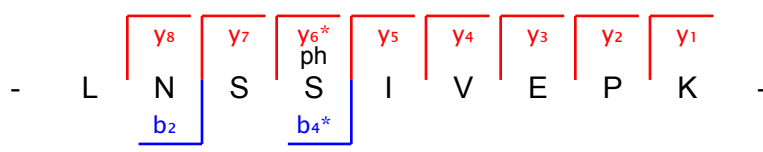
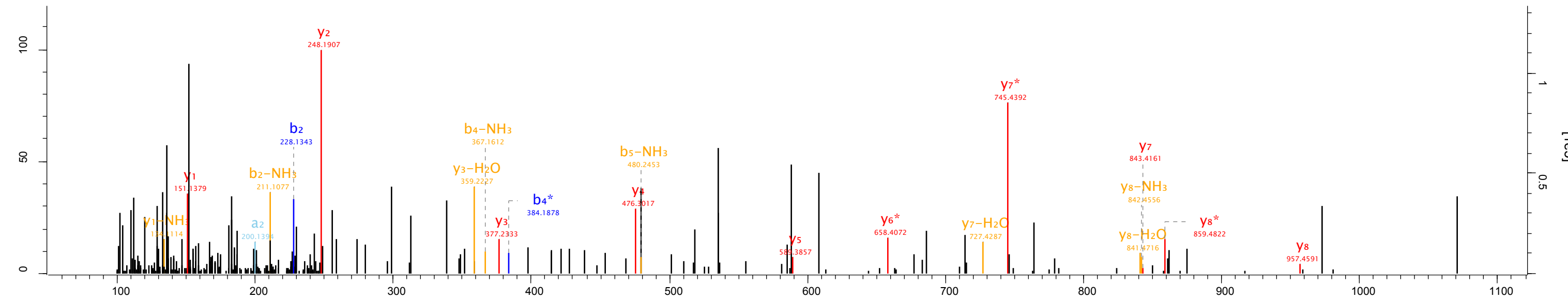
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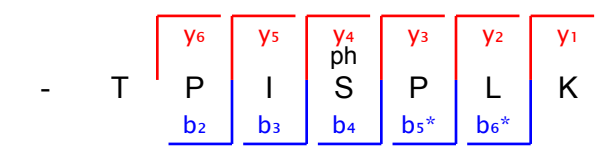
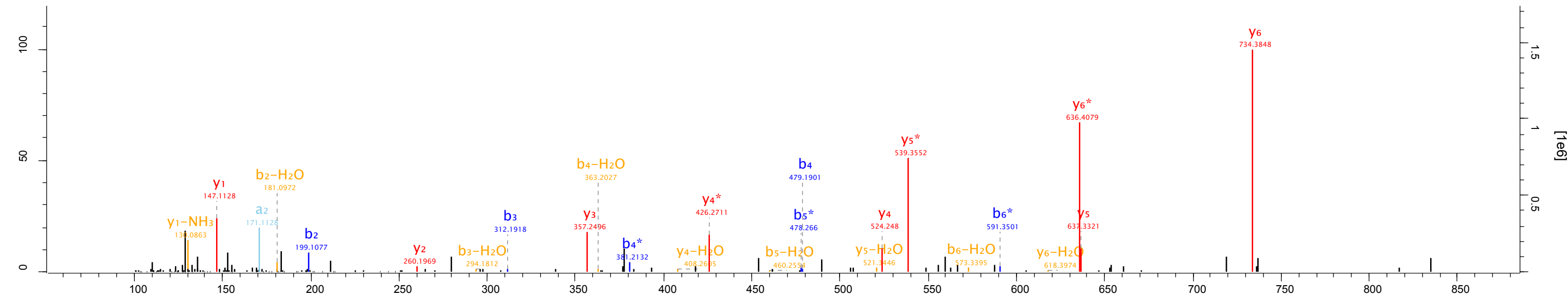
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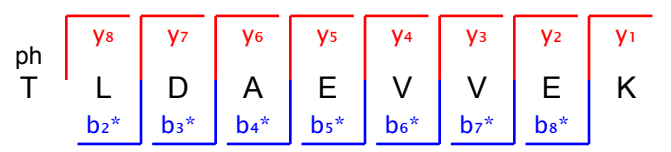
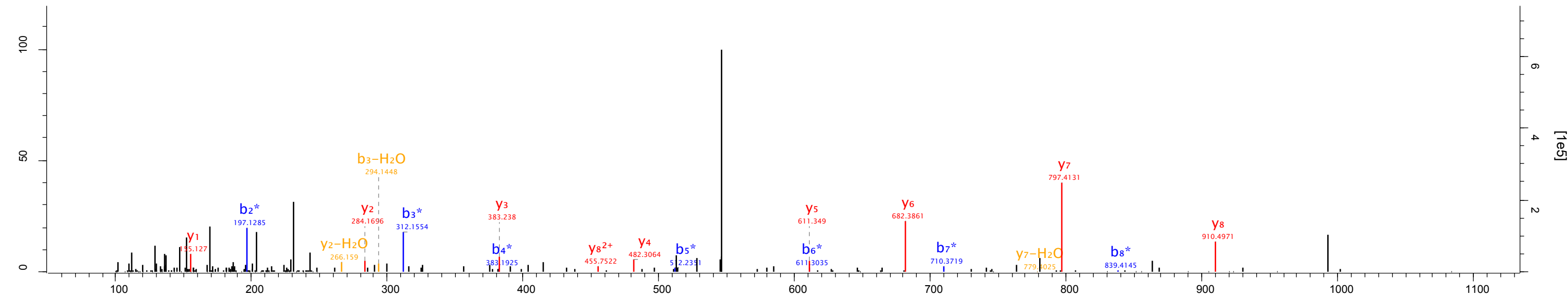
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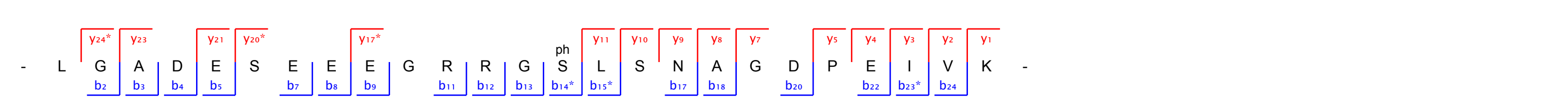
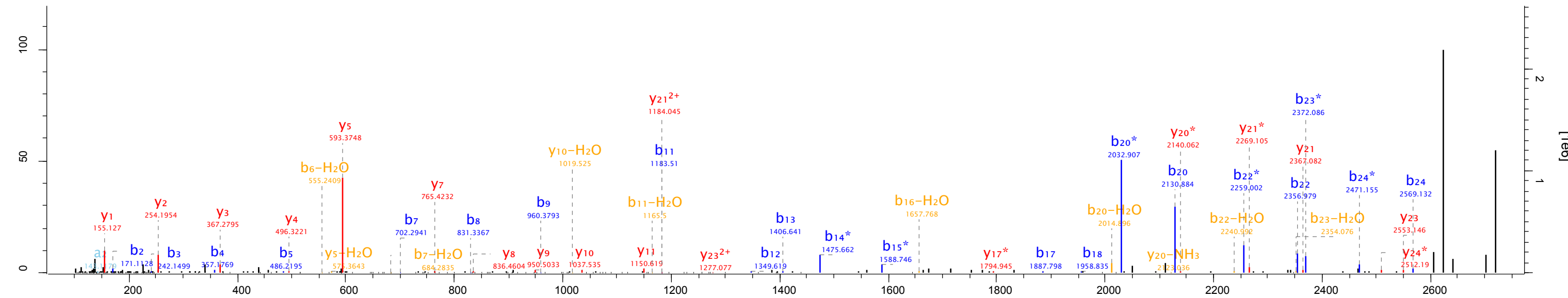
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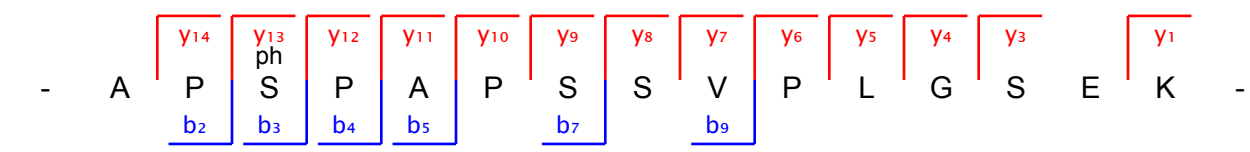
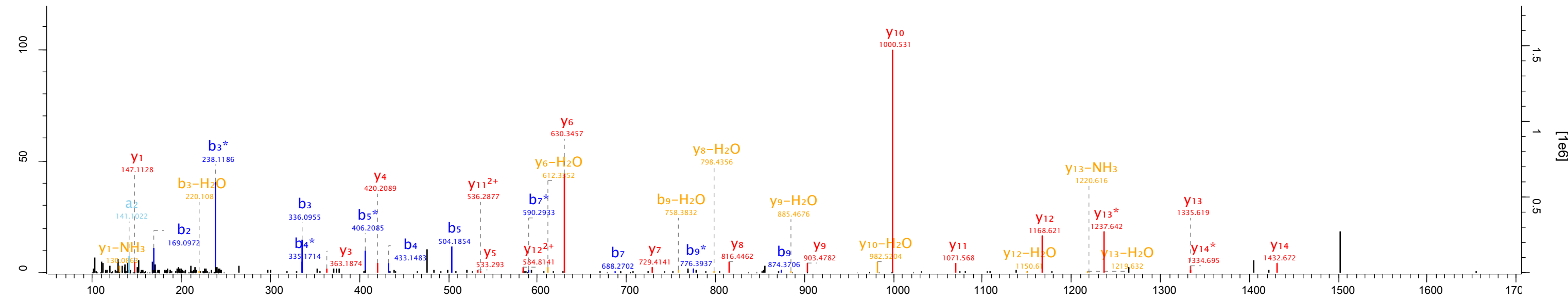
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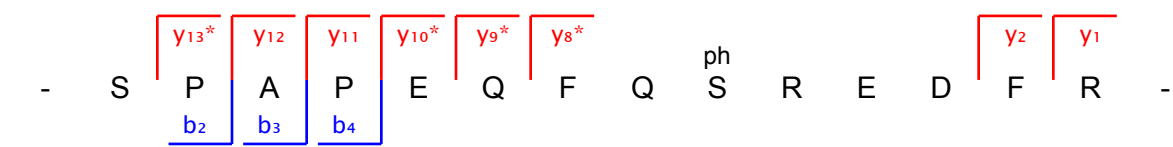
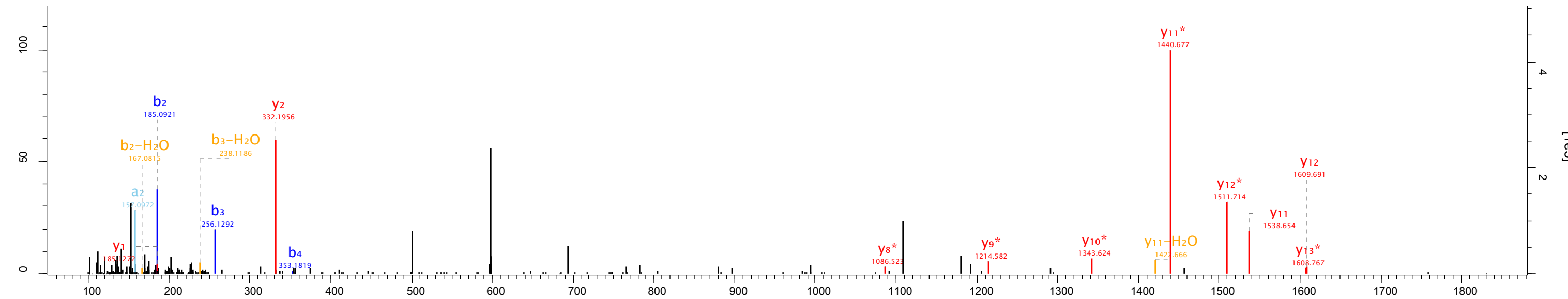
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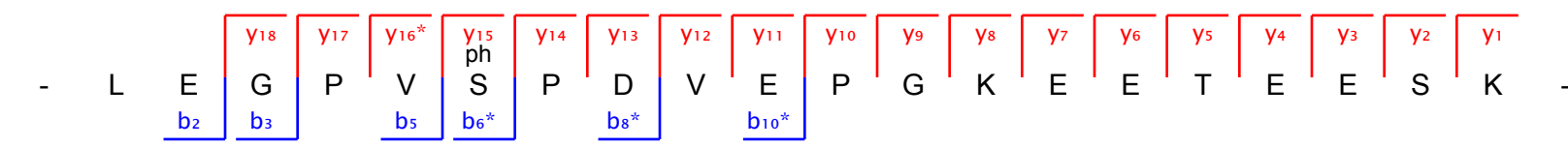
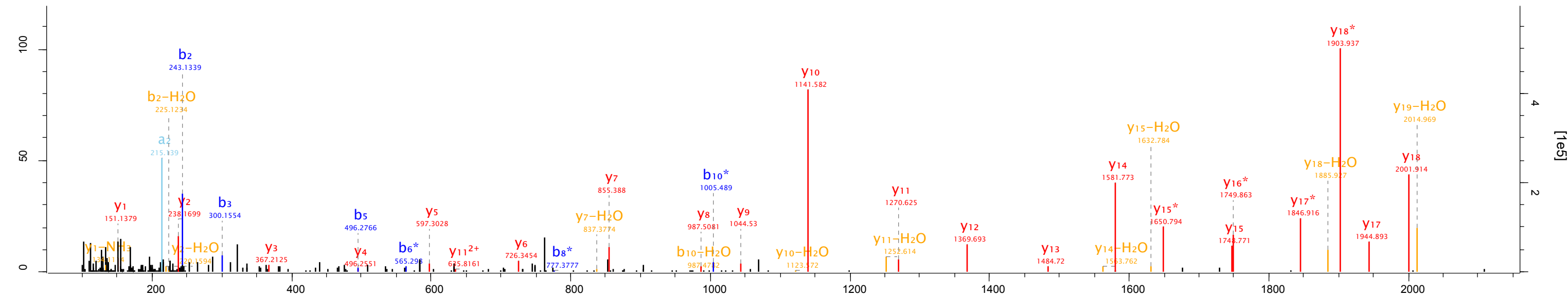
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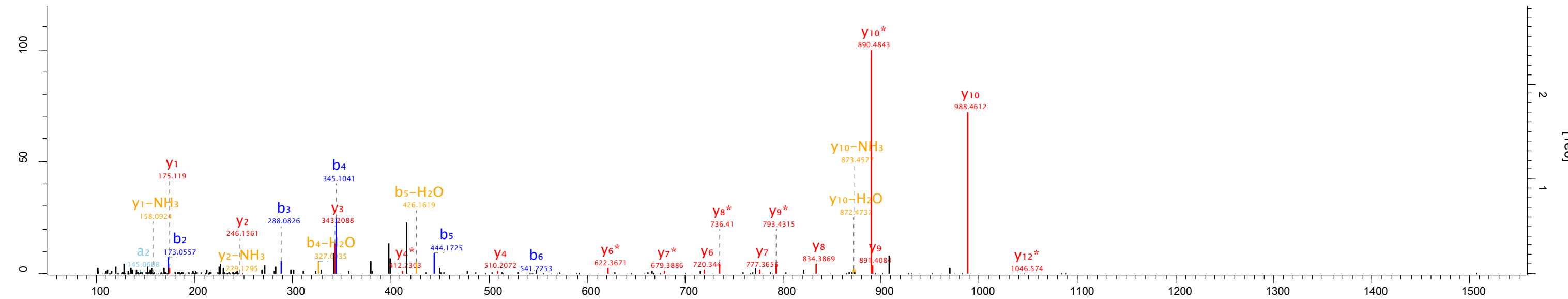
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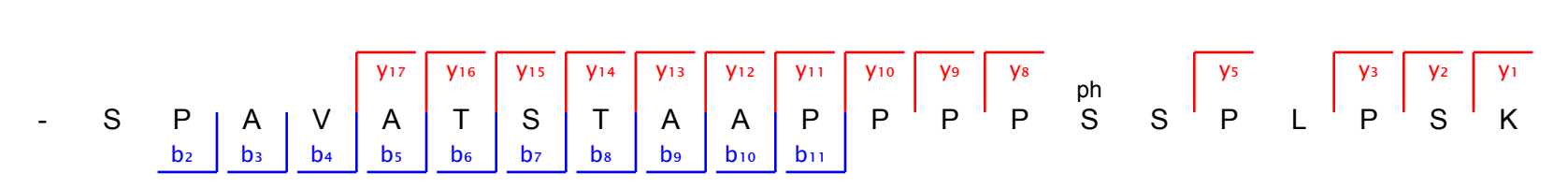
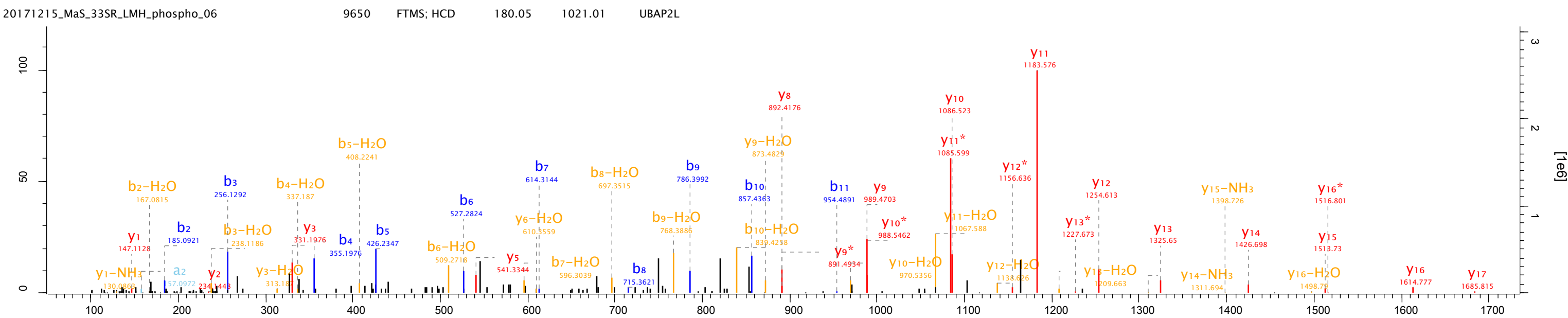
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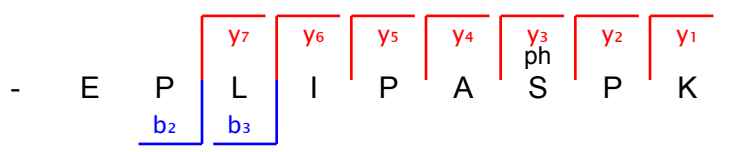
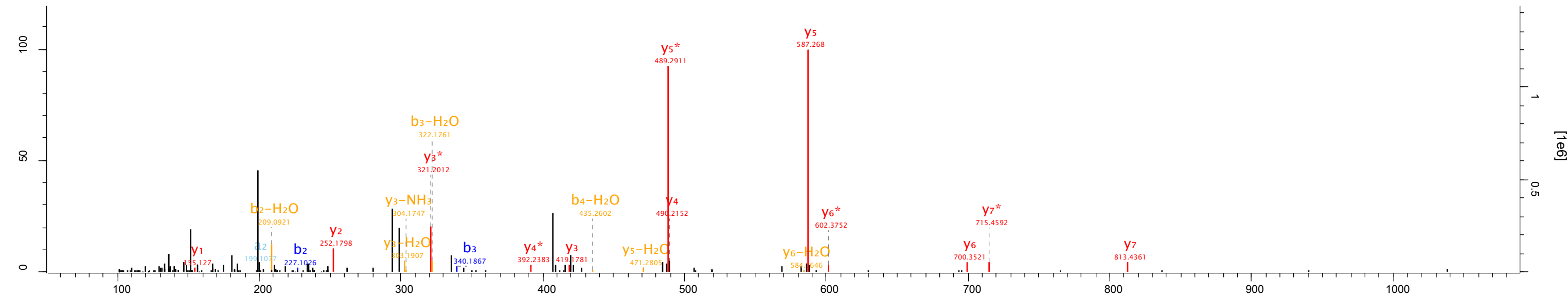
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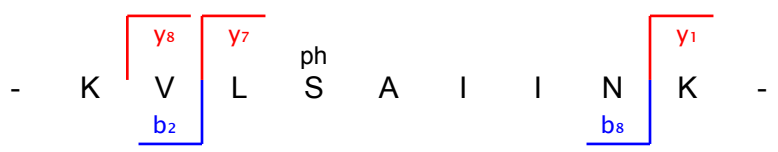
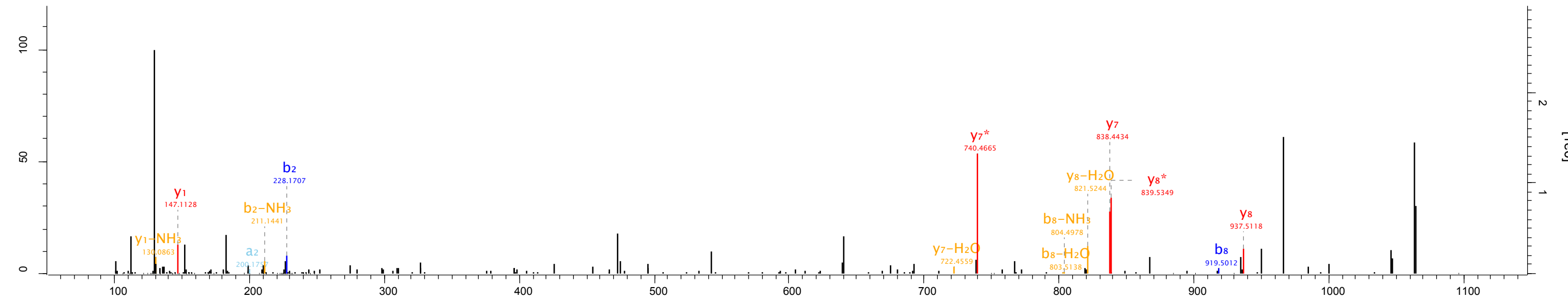
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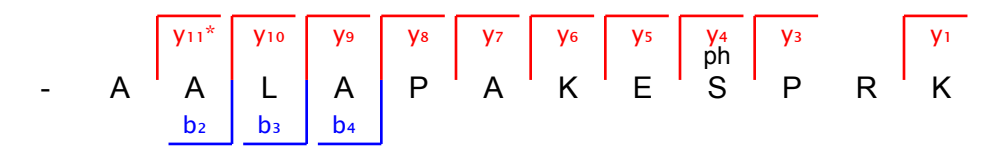
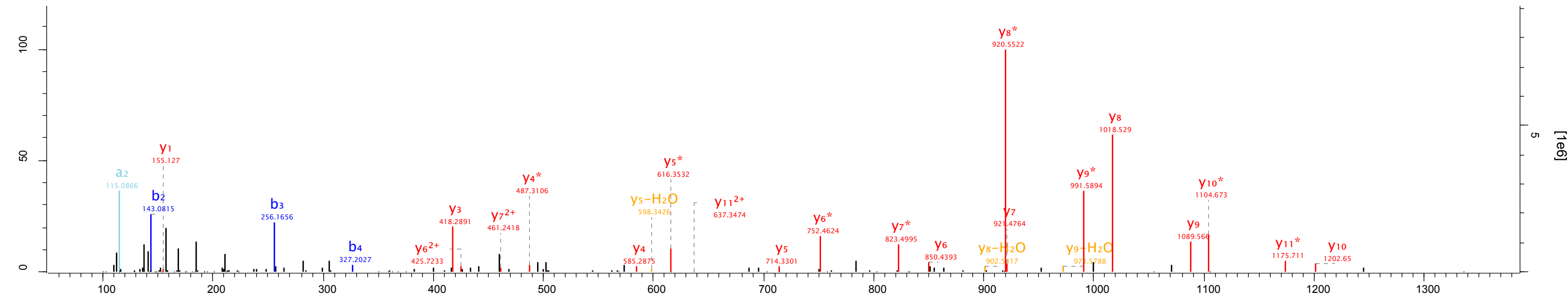
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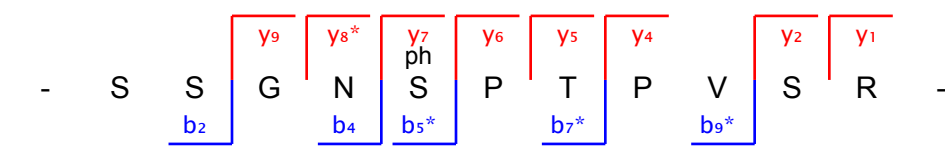
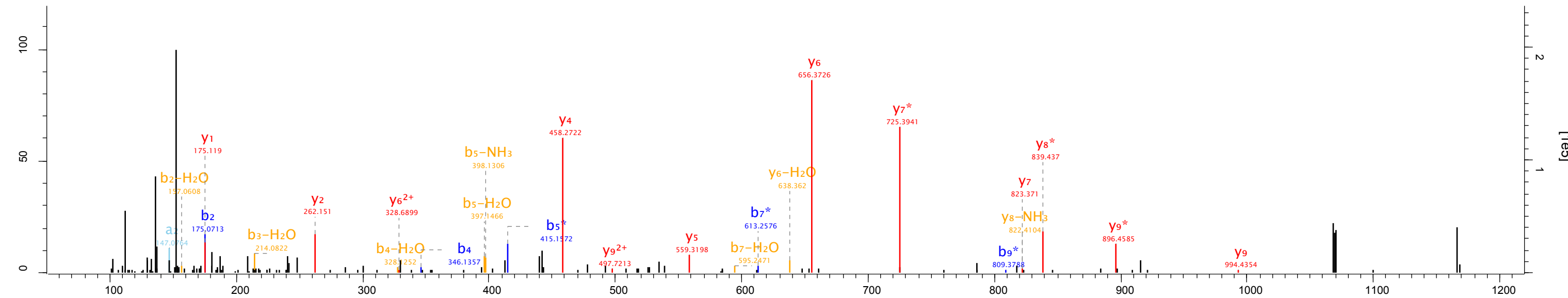


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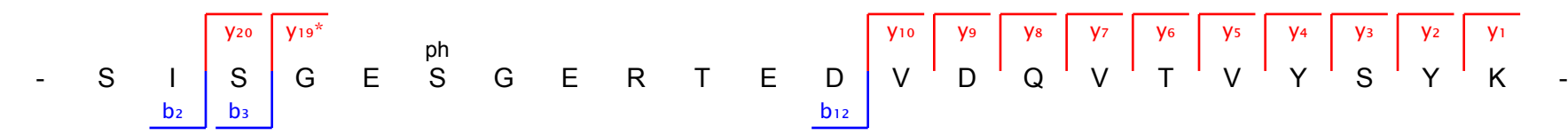
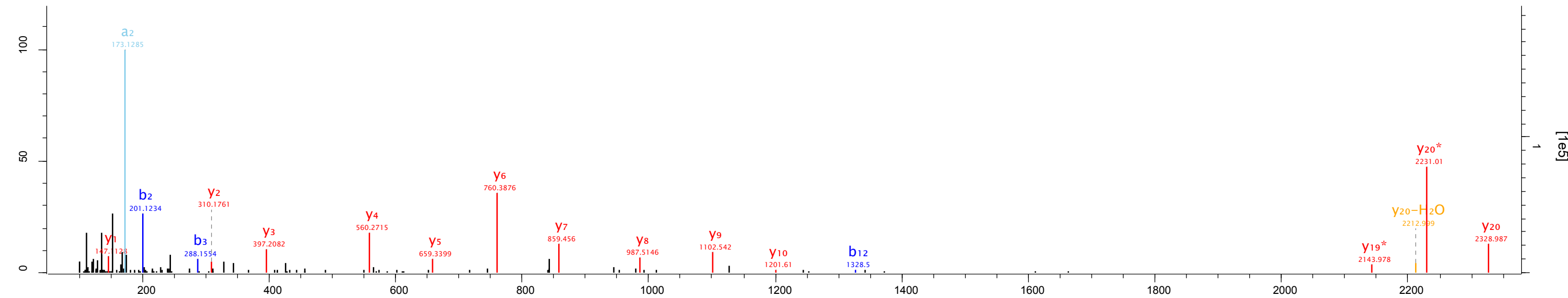


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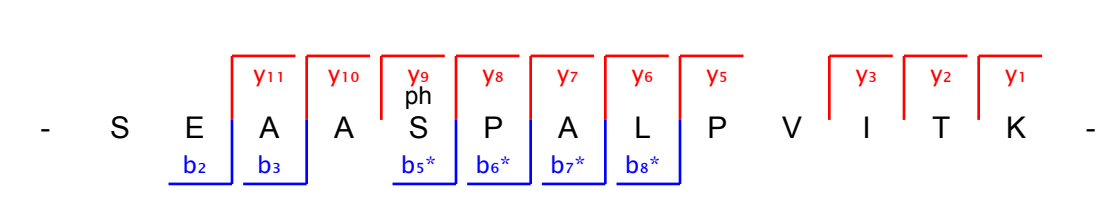
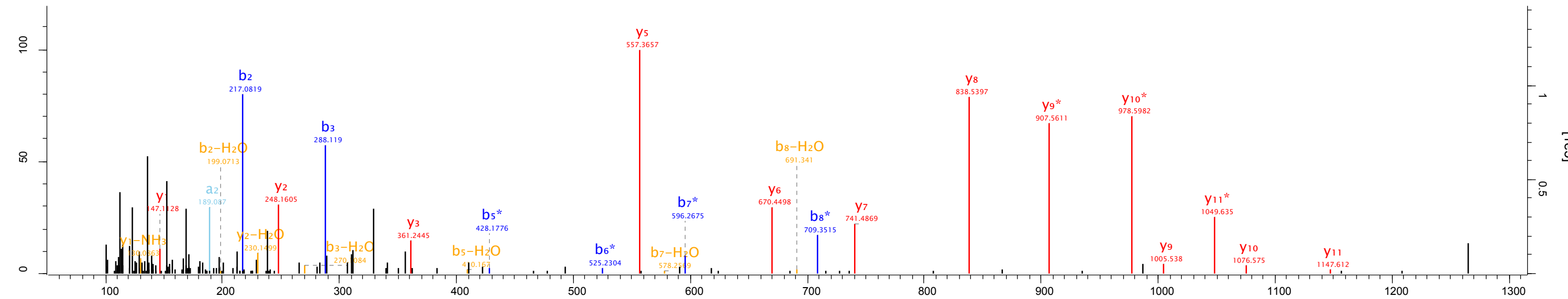




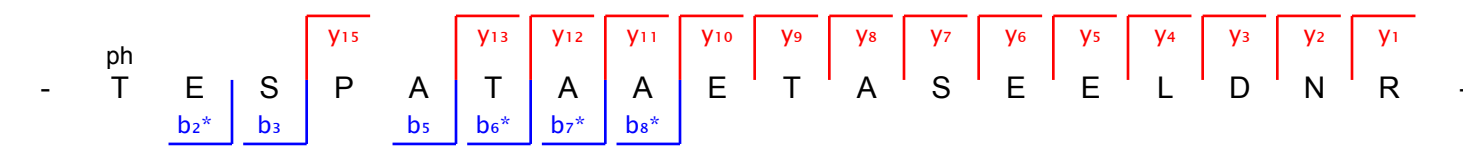
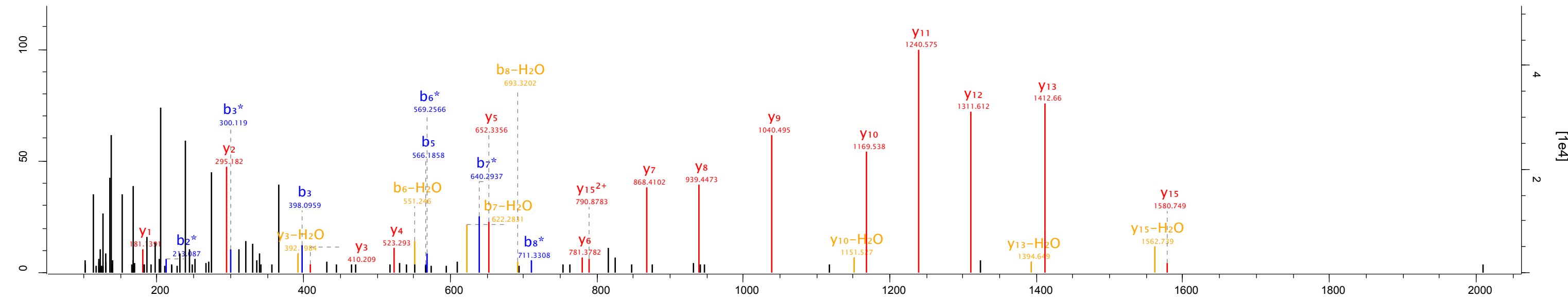
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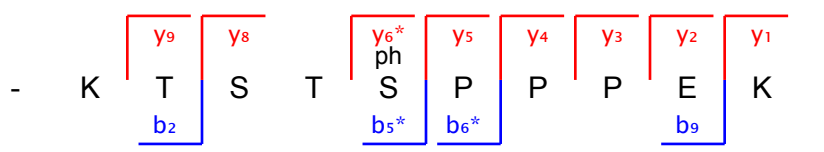
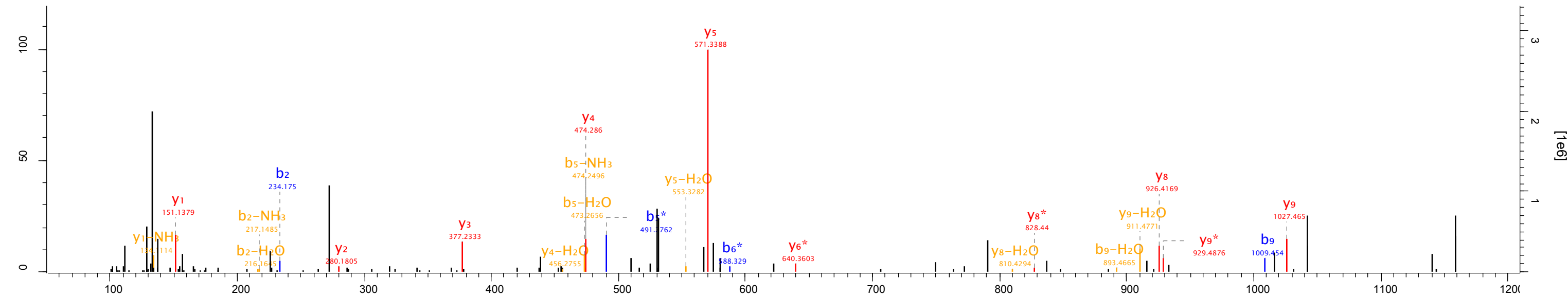
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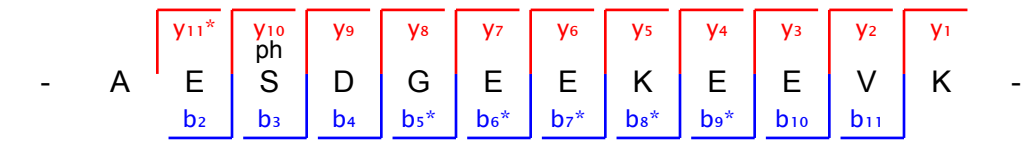
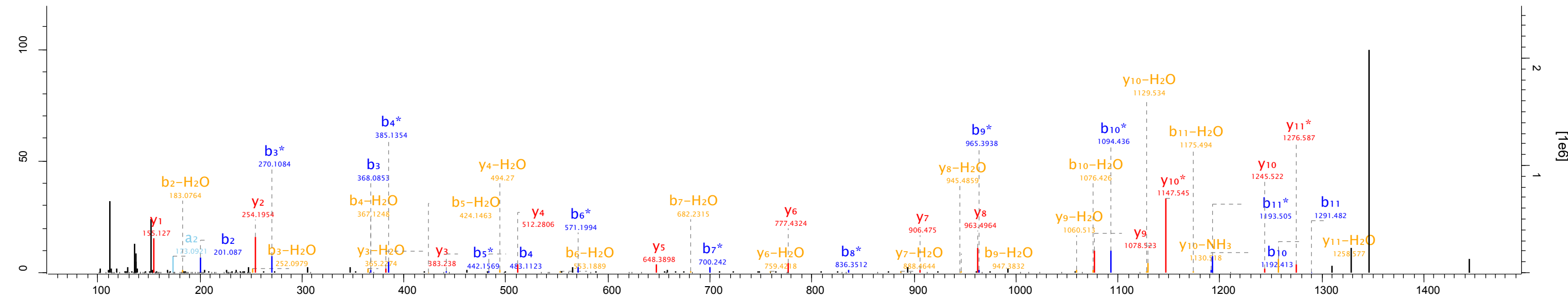
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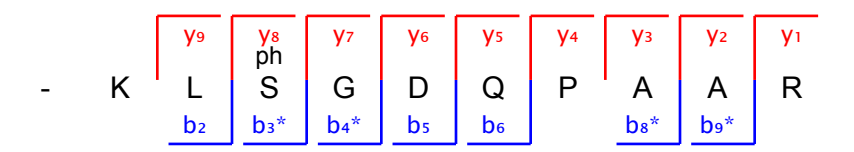
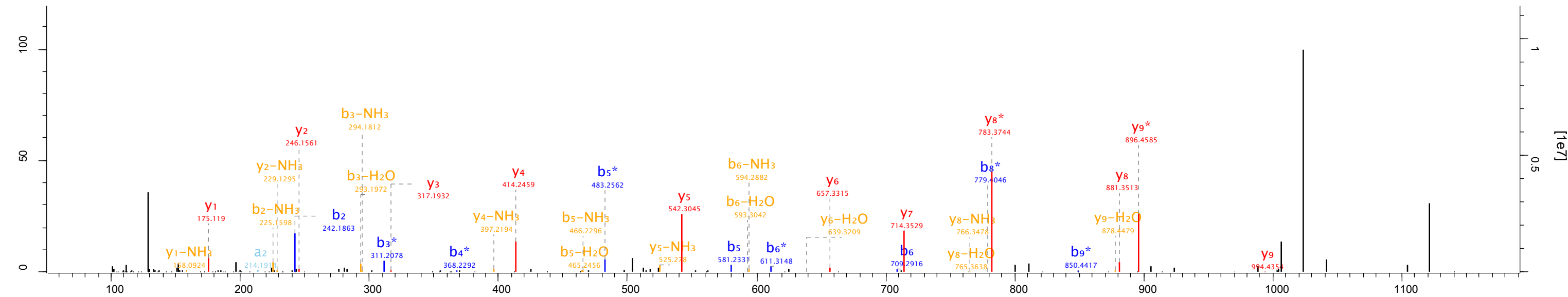
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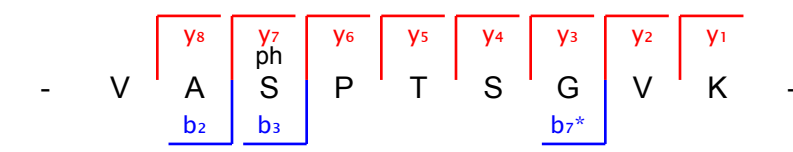
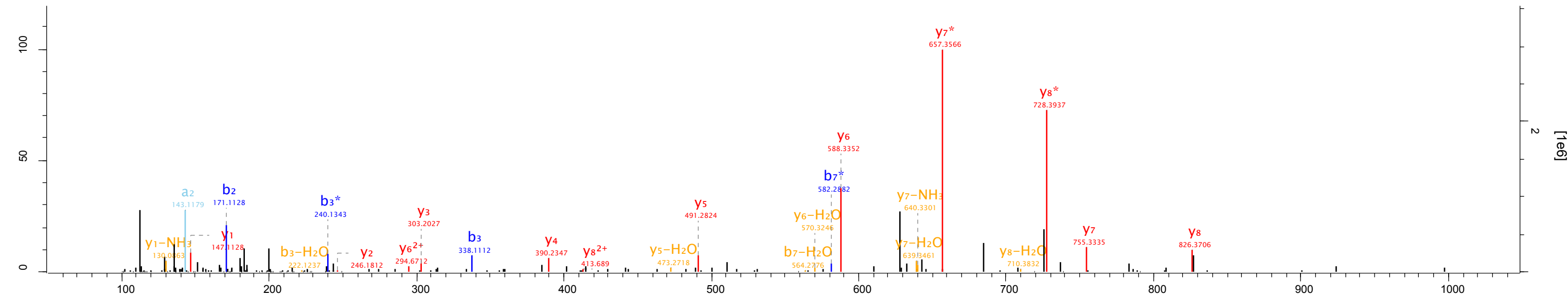
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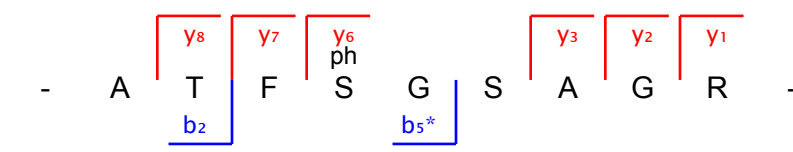
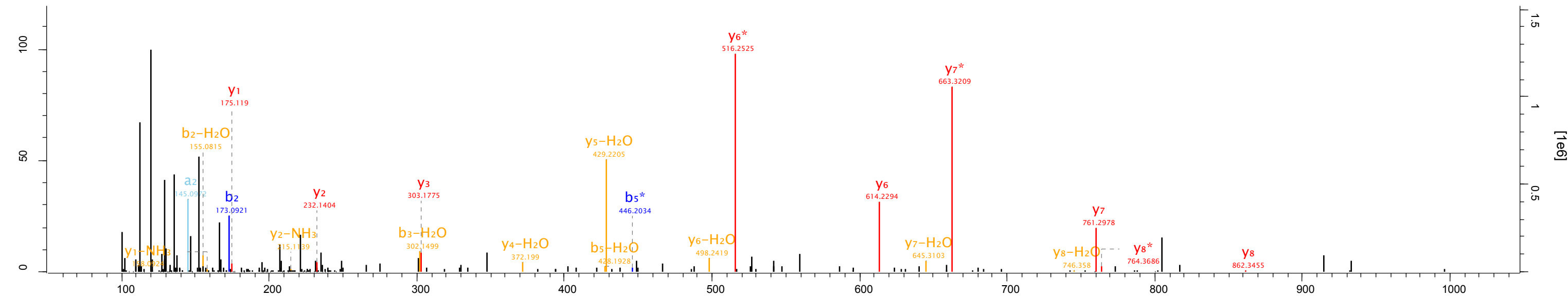
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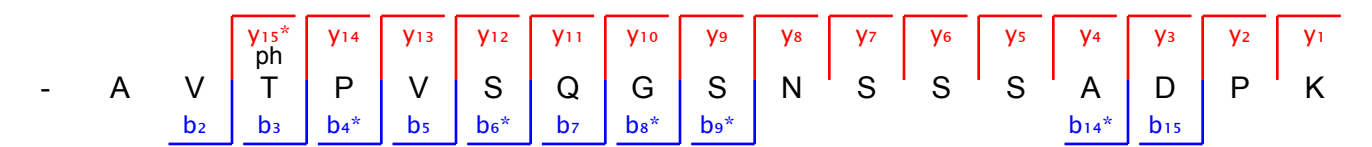
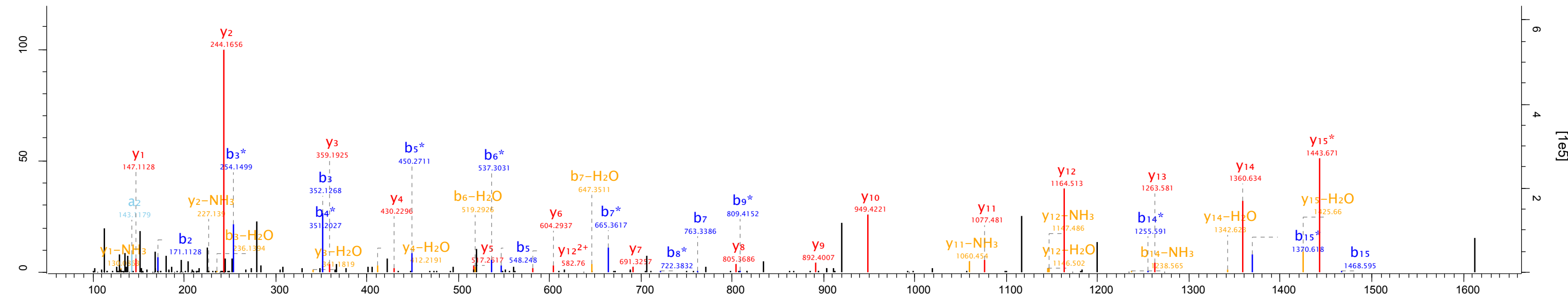
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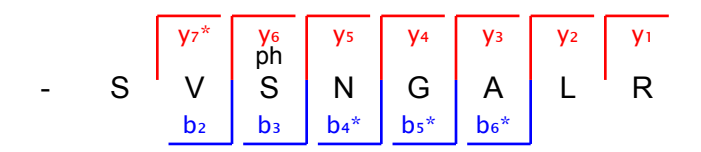
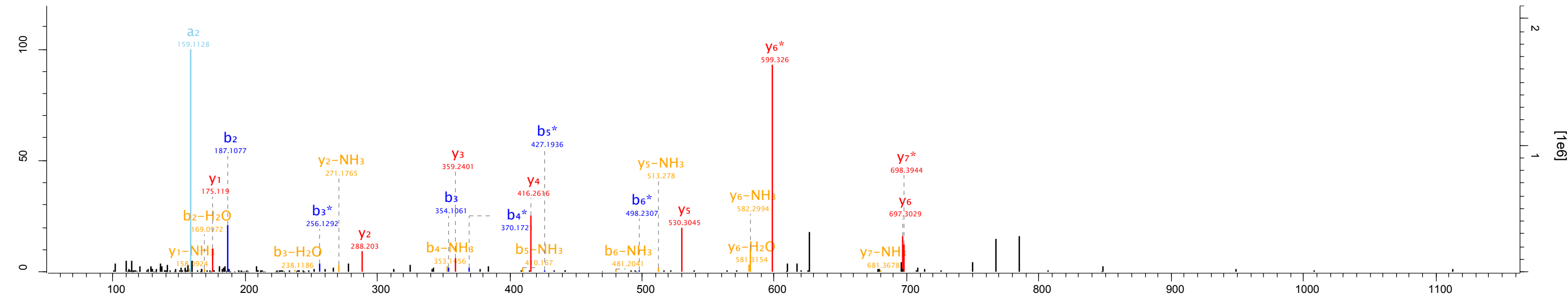
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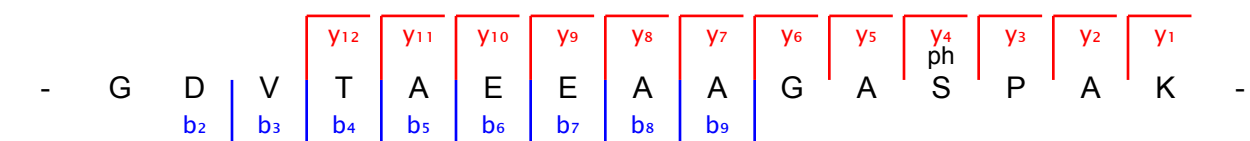
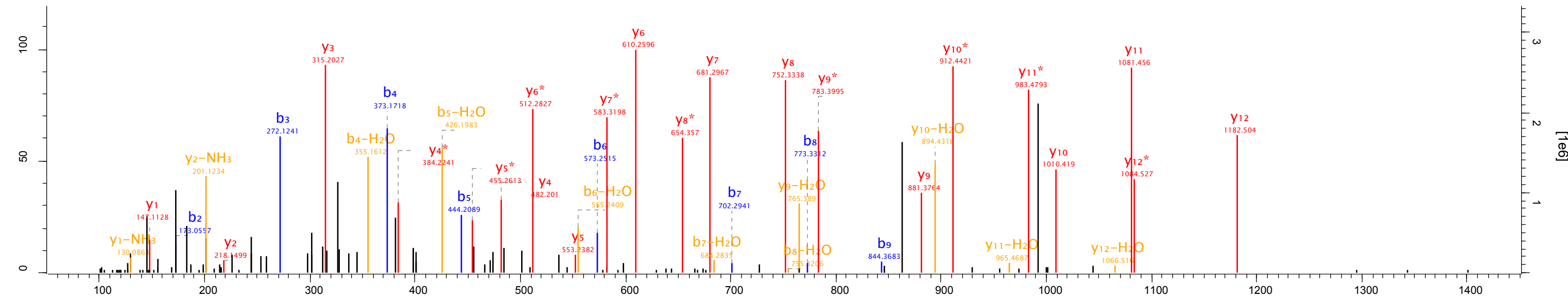


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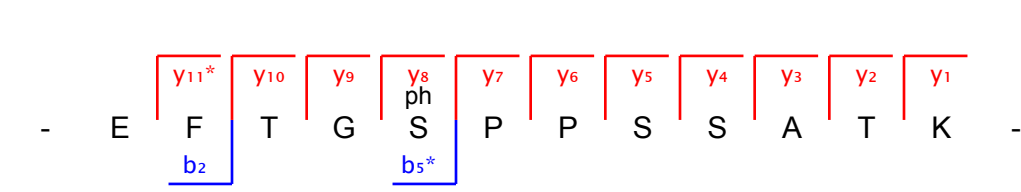
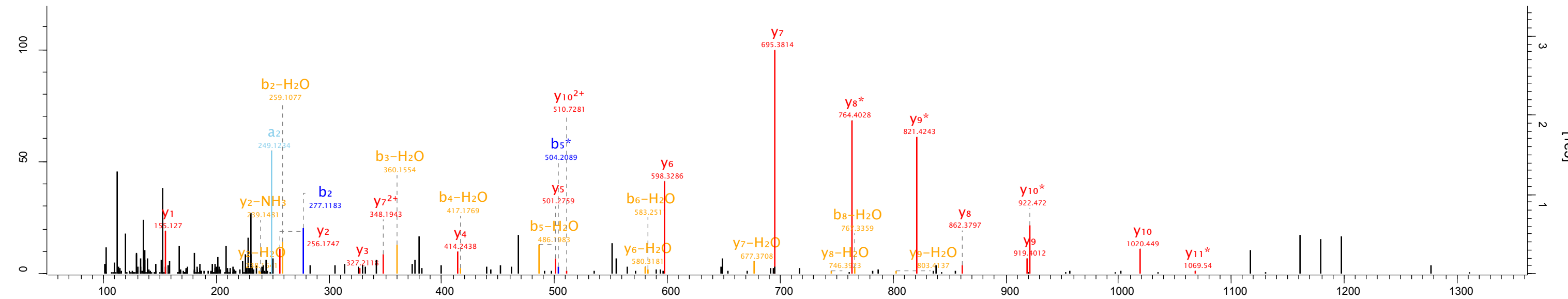


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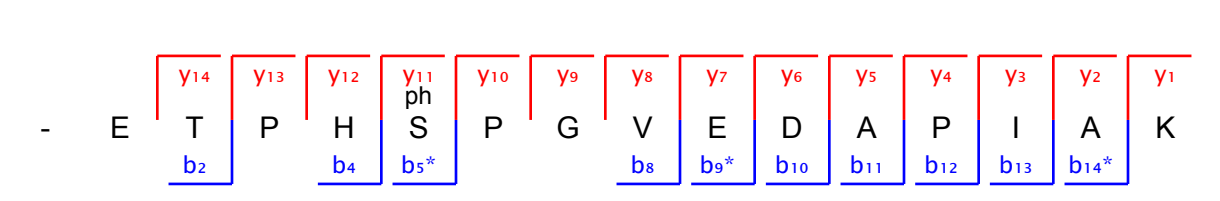
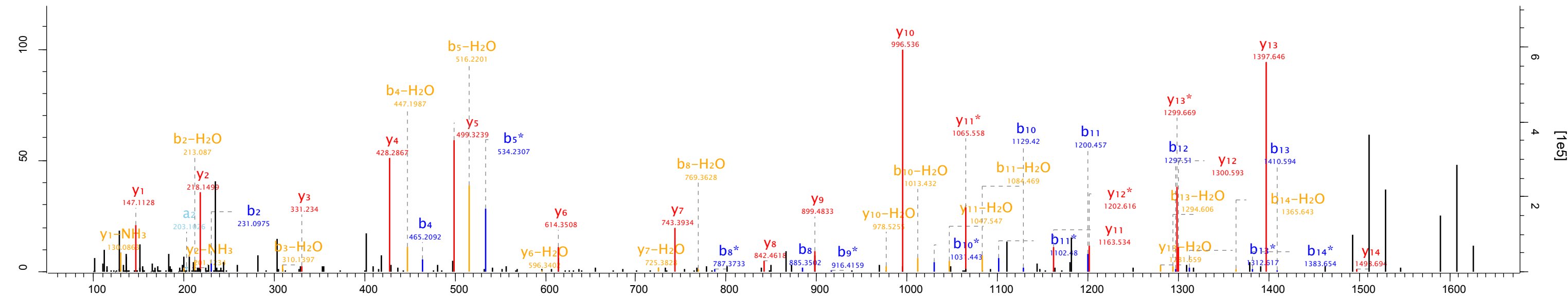




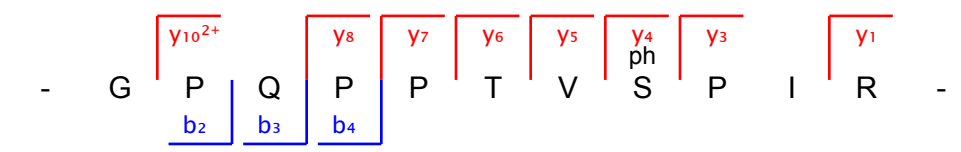
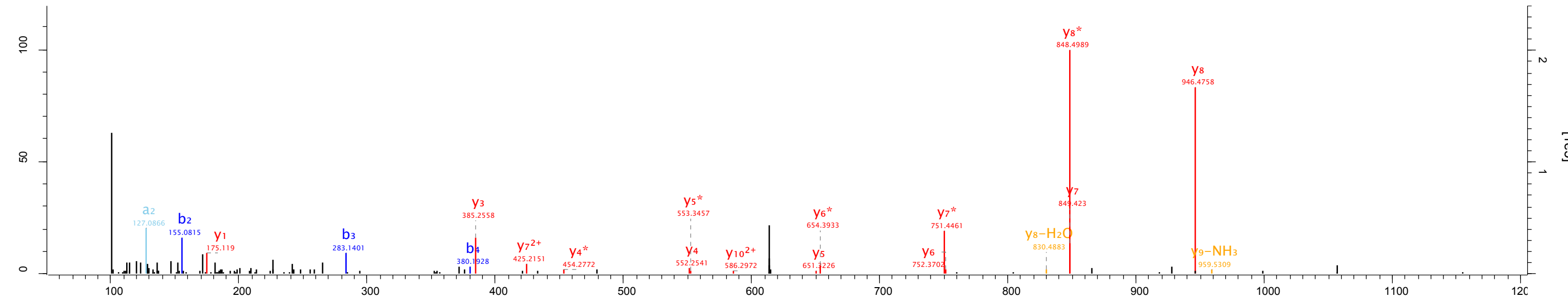
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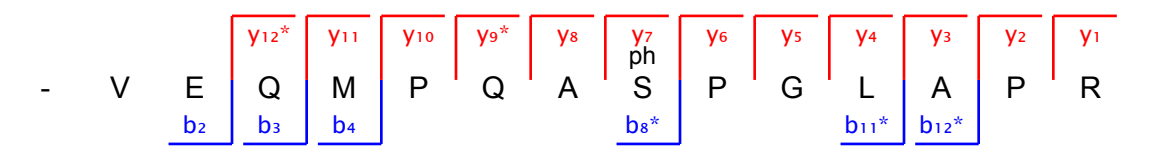
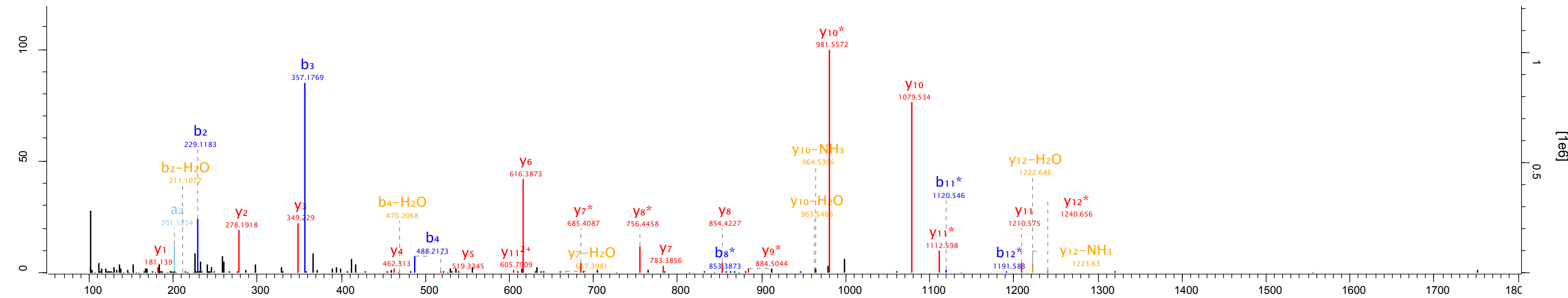
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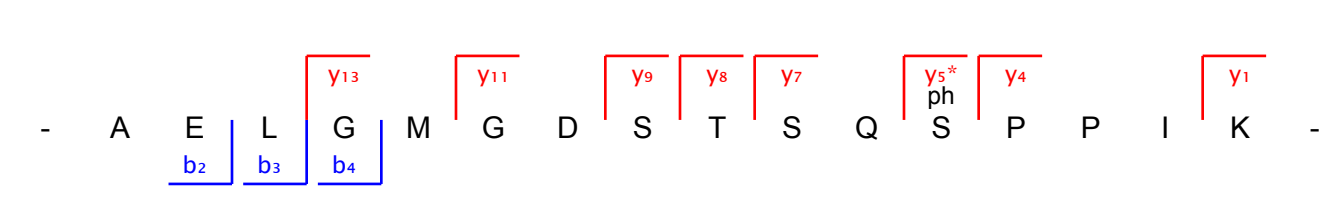
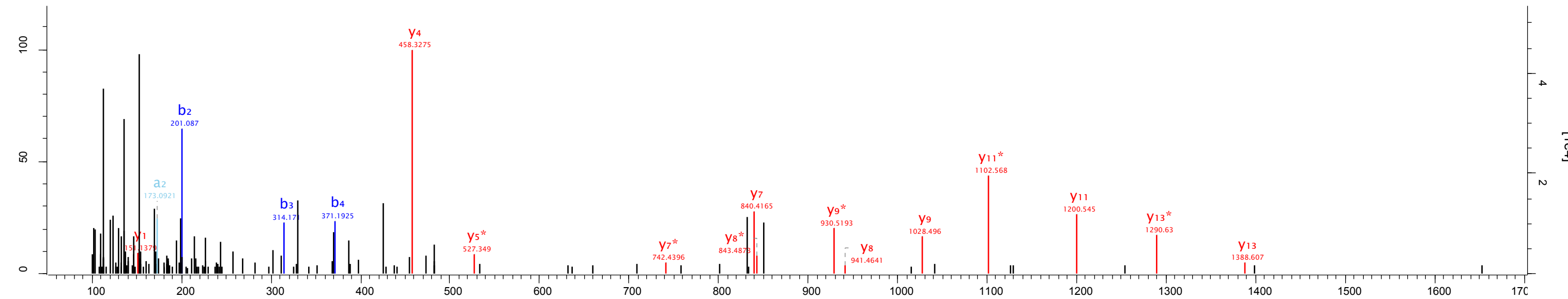
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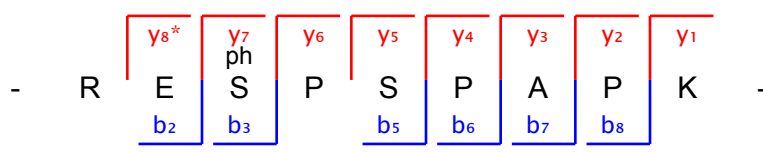
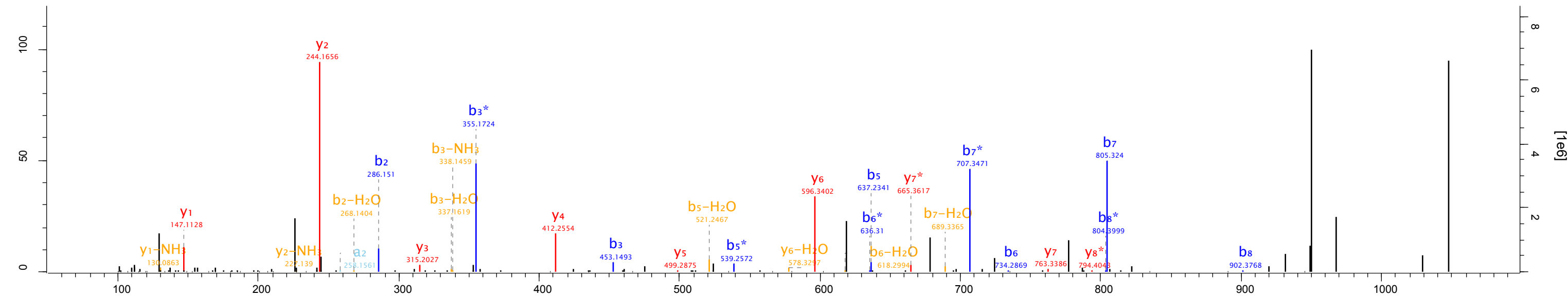
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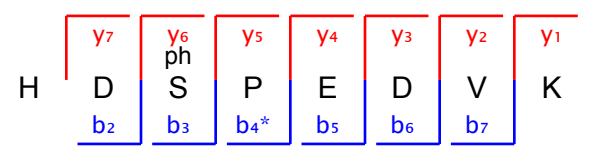
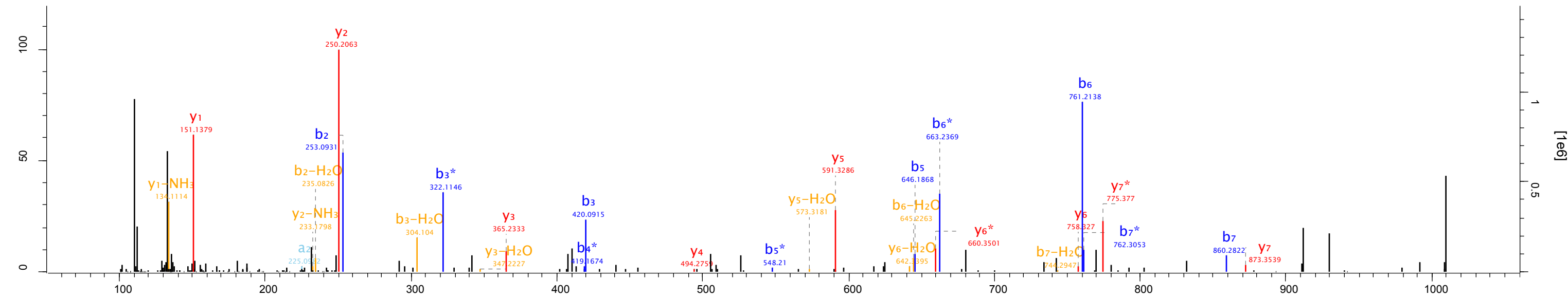
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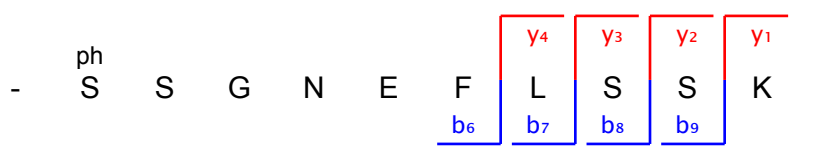
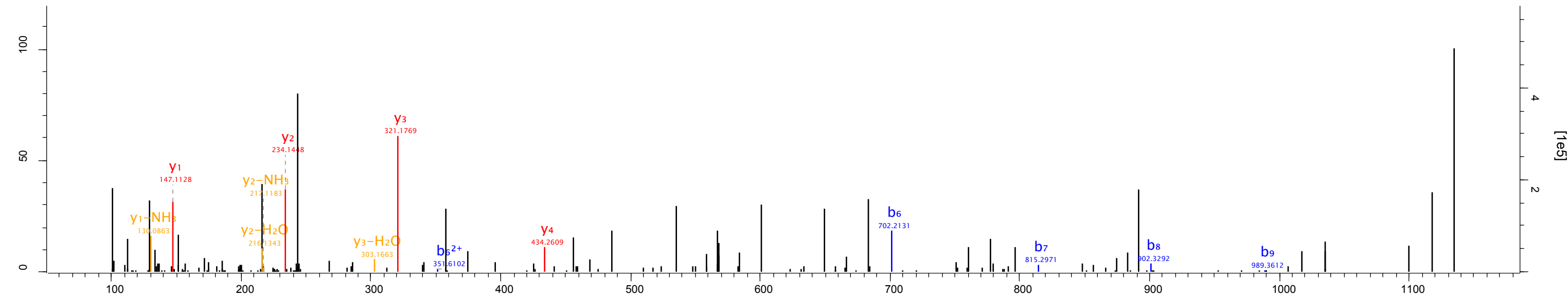
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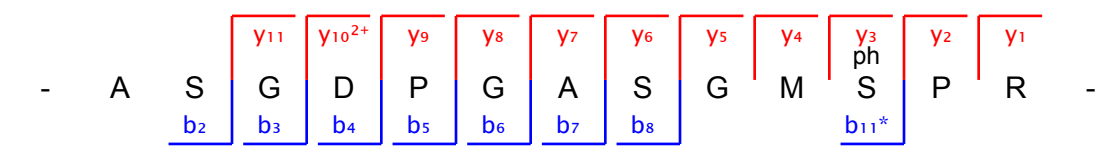
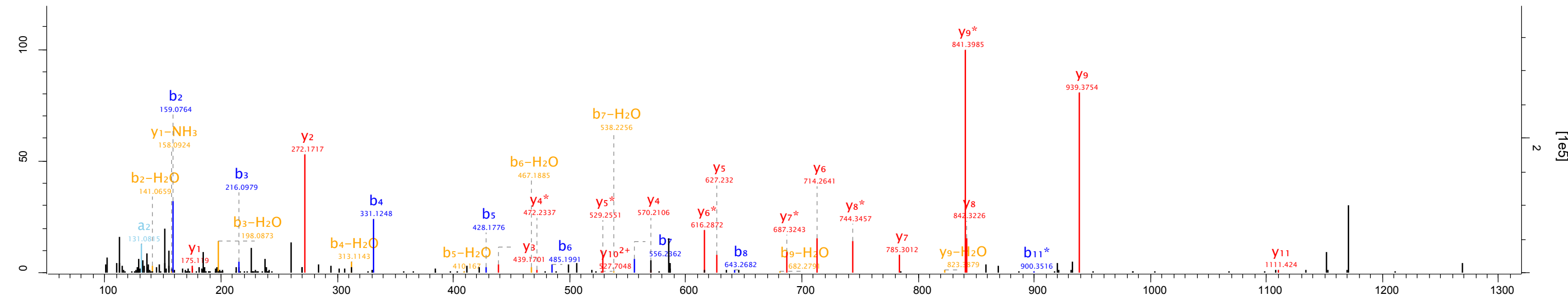
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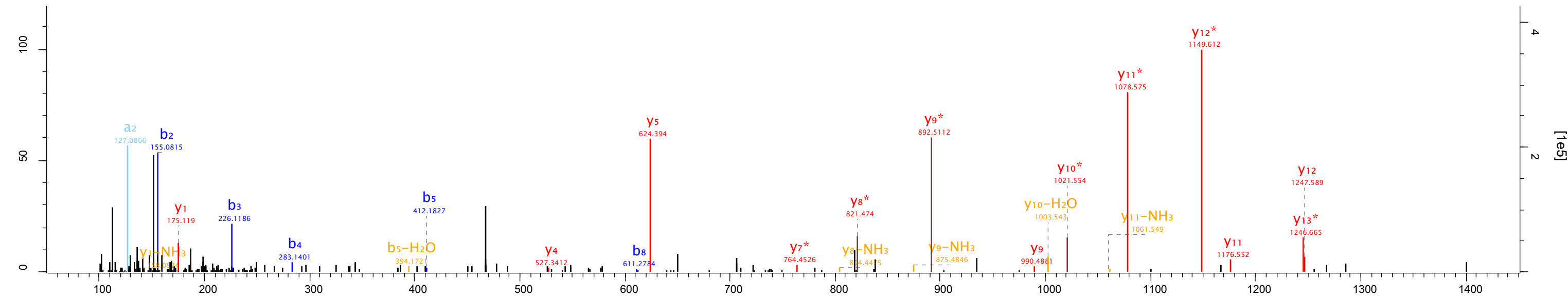
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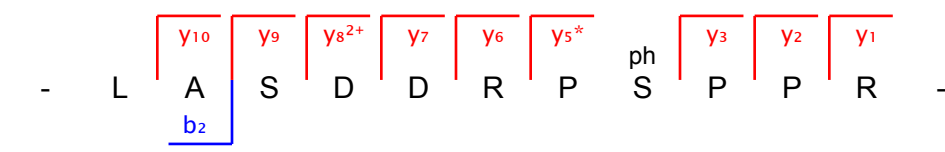
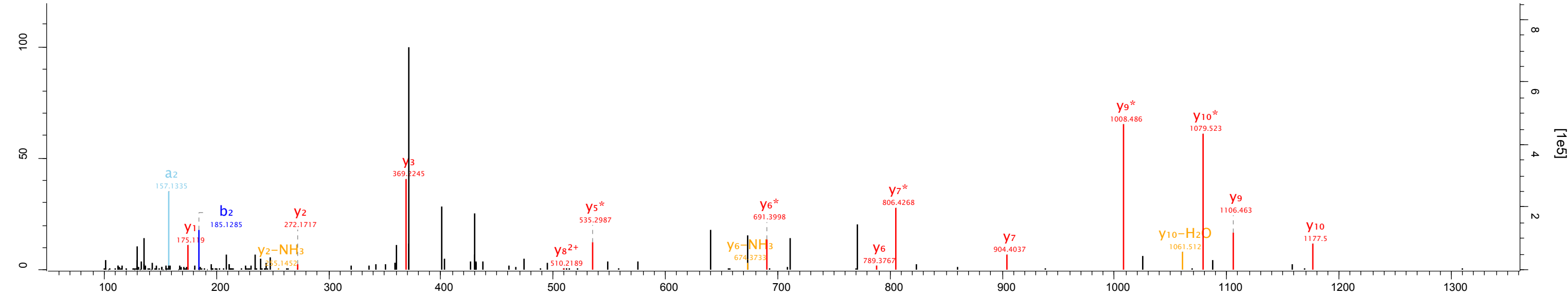
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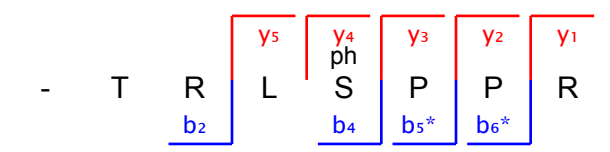
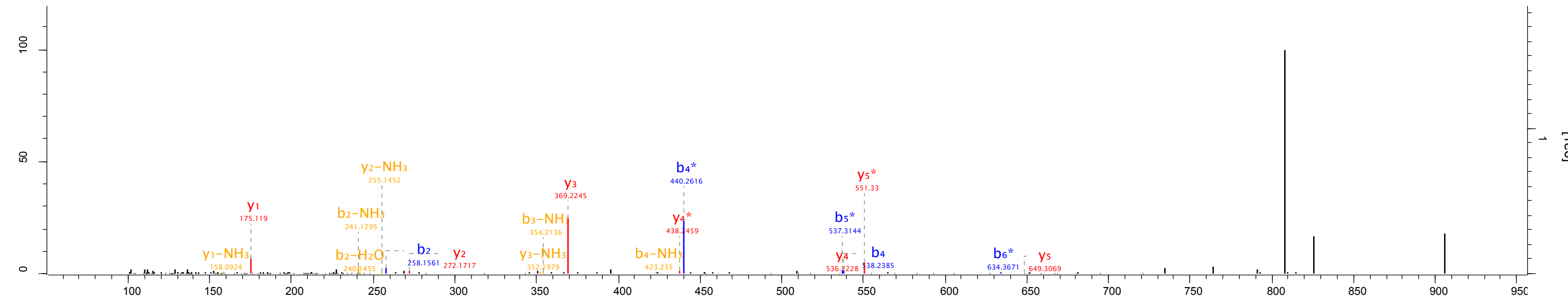
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20171215_MaS_33SR_LMH_phospho_09

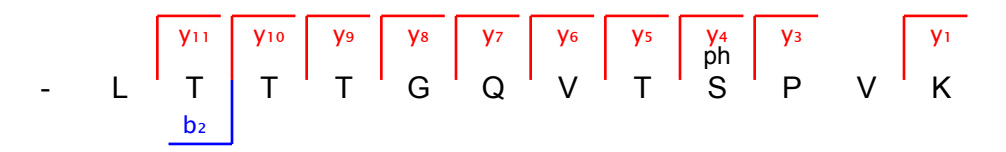
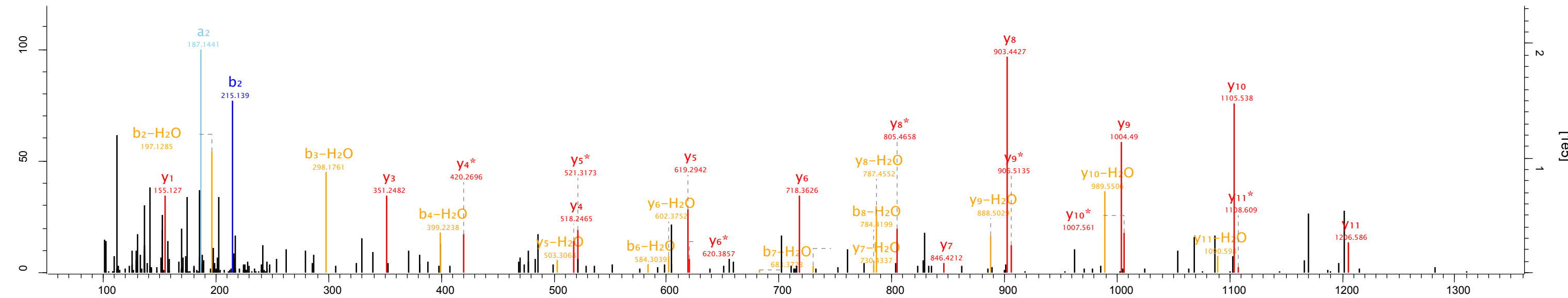
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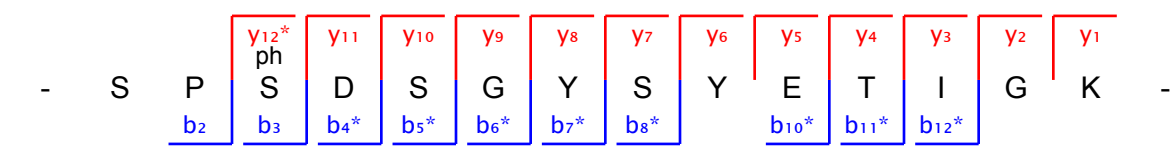
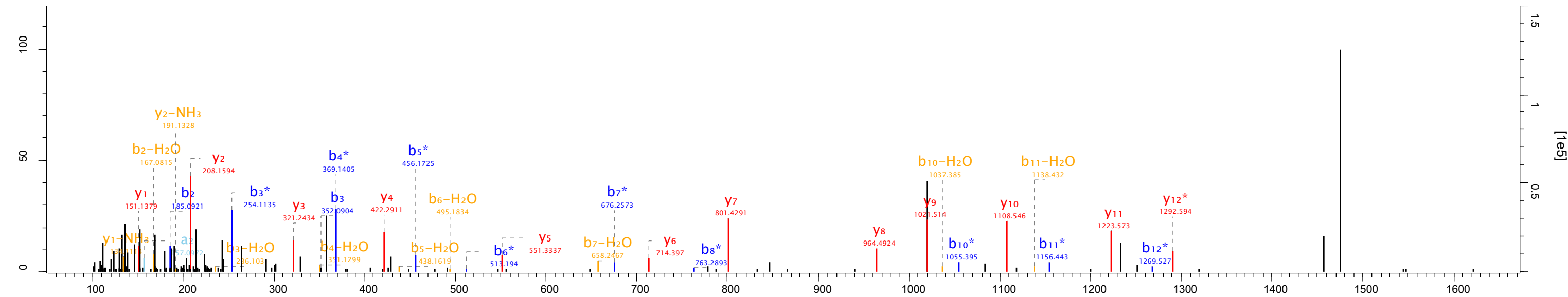
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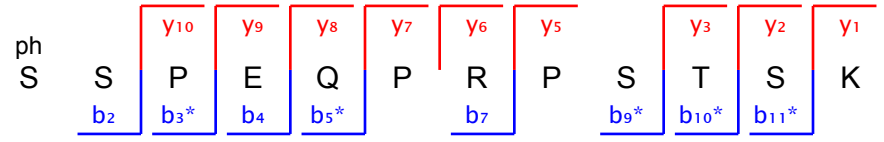
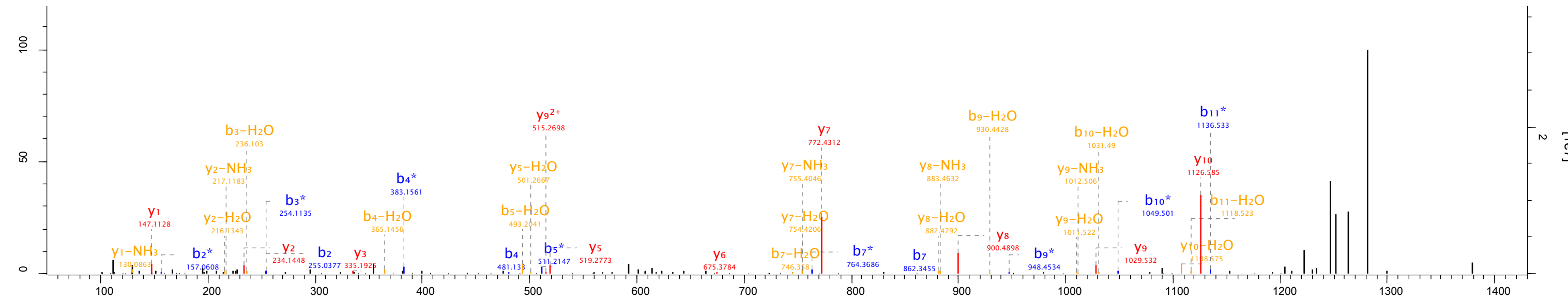


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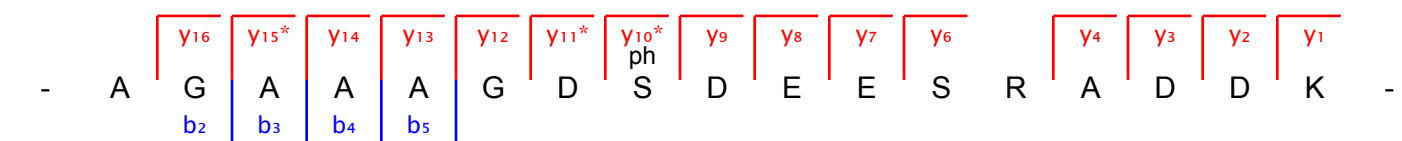
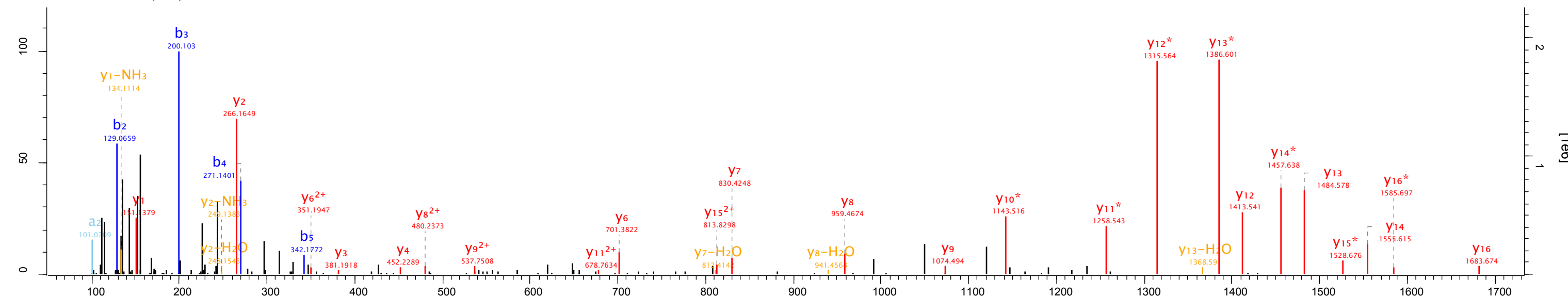
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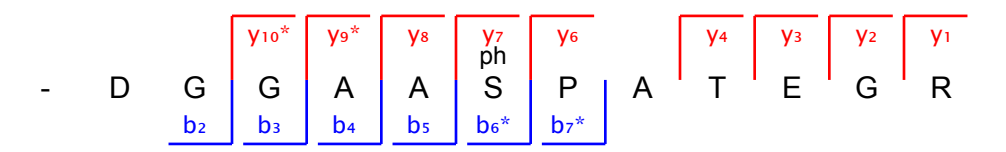
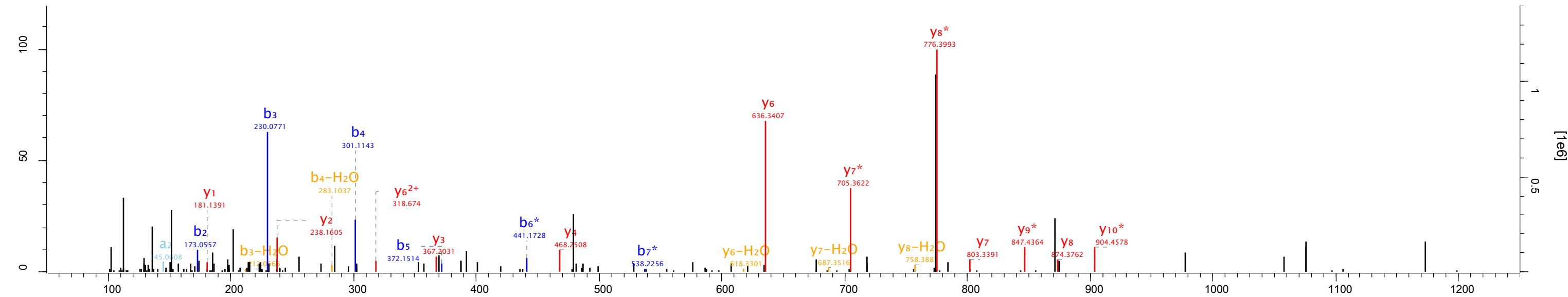


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20171215_MaS_33SR_LMH_phospho2_01

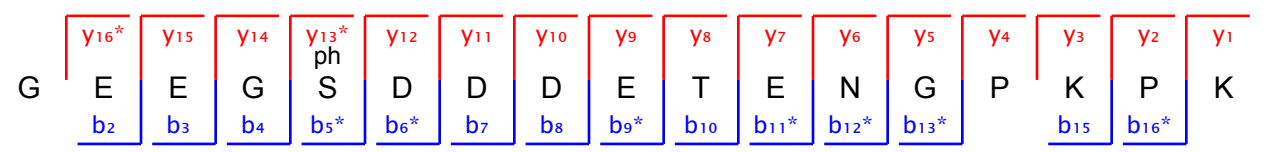
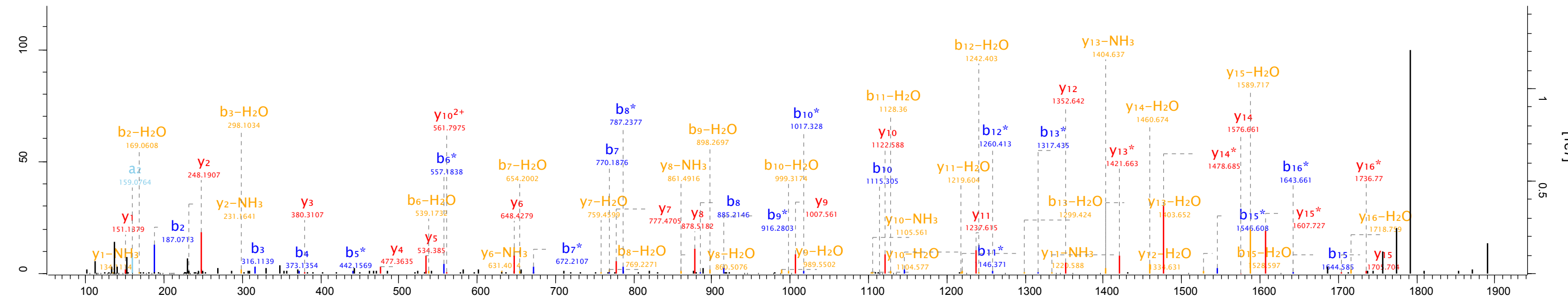
Scan 2060 Method FTMS; HCD Score 148.38 m/z 585.58 Gene names ZBTB7A



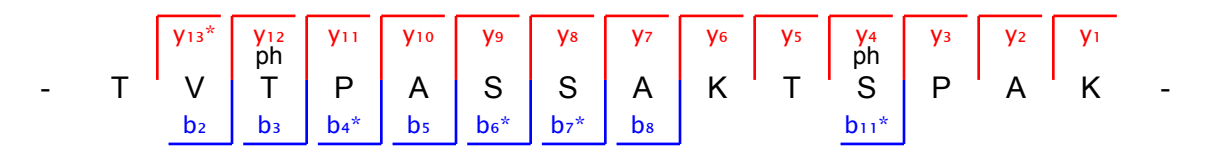
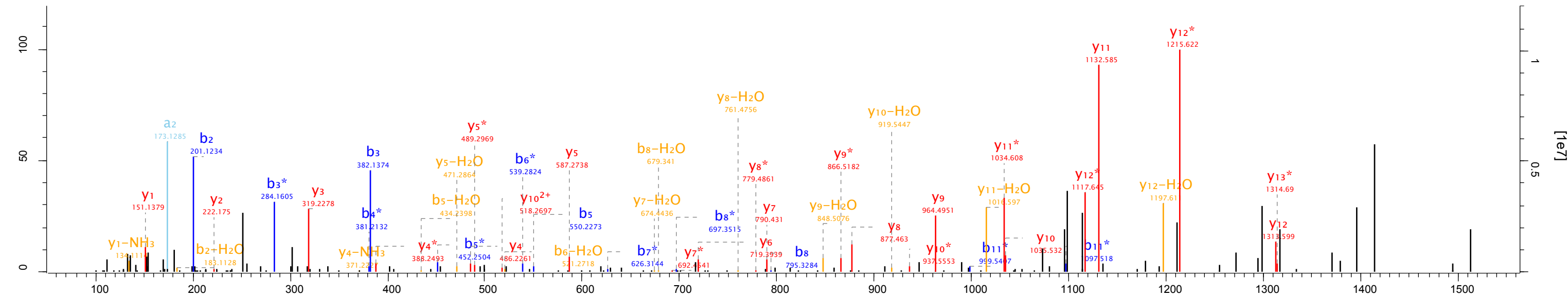
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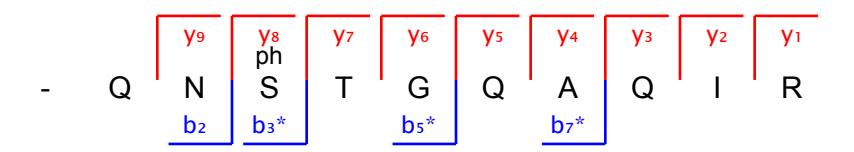
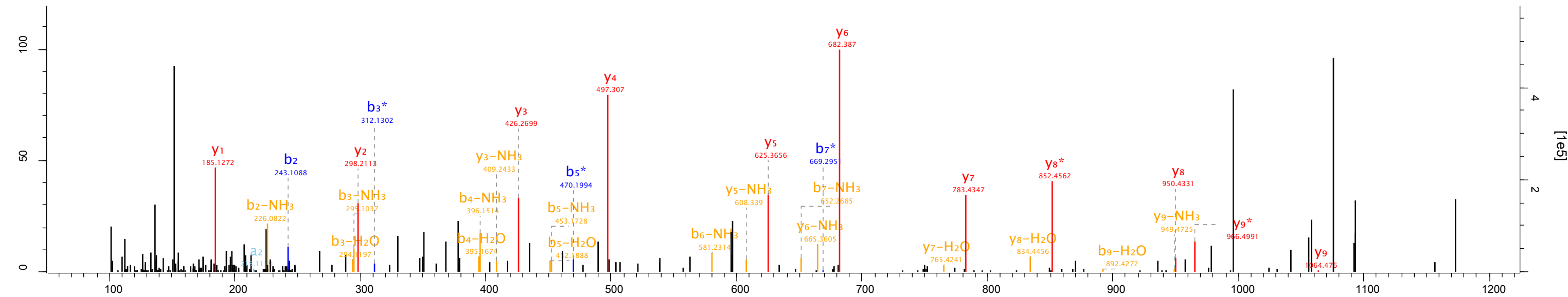
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 Scan: 2380 Method: FTMS; HCD Score: 321.88 m/z: 946.39 Gene names: CTR9

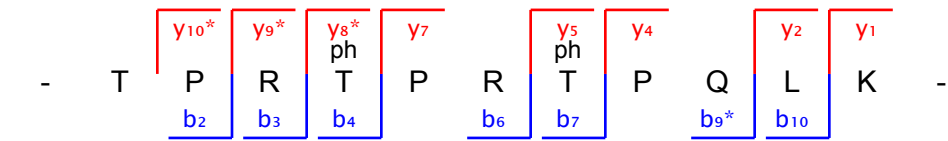
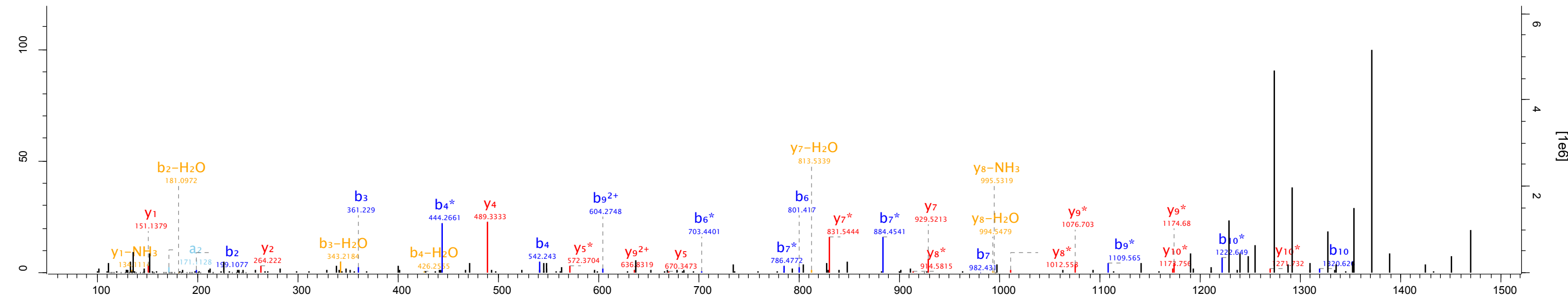


Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 2530 Method FTMS; HCD Score 167.35 m/z 757.36 Gene names DPYSL2



Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 2980 Method FTMS; HCD Score 92.97 m/z 596.77 Gene names RASAL2

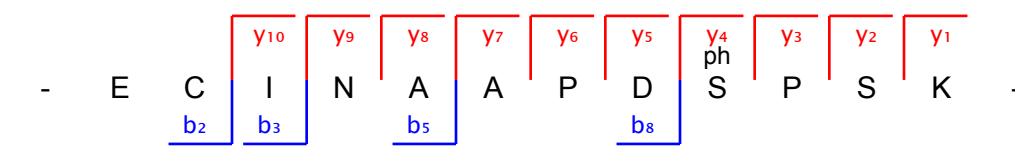
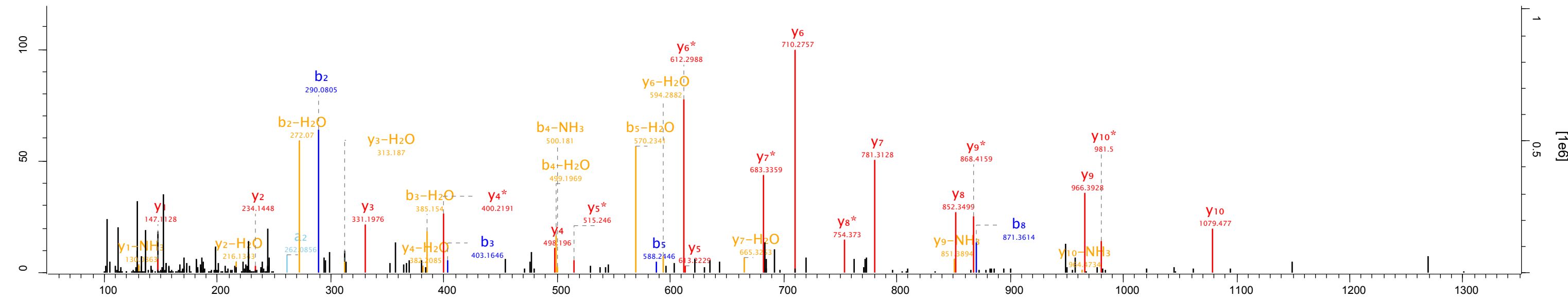




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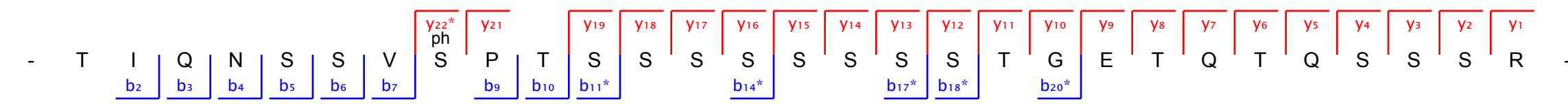
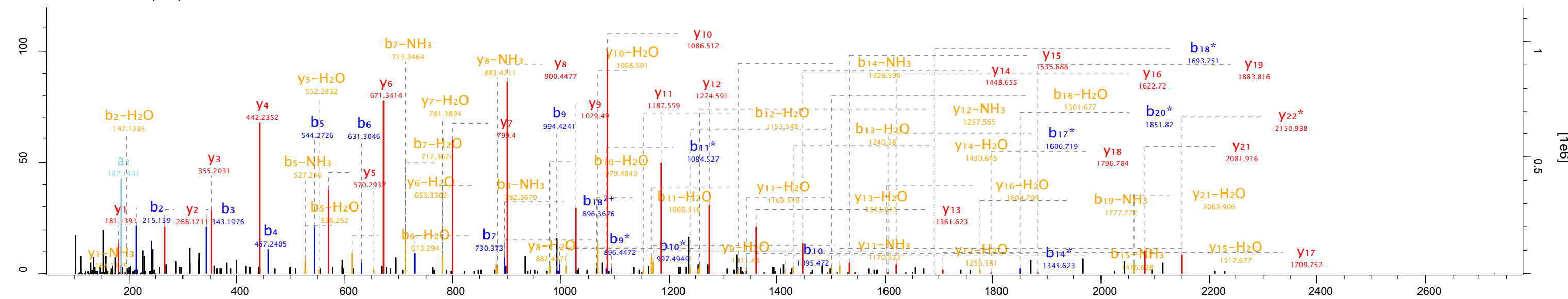
20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
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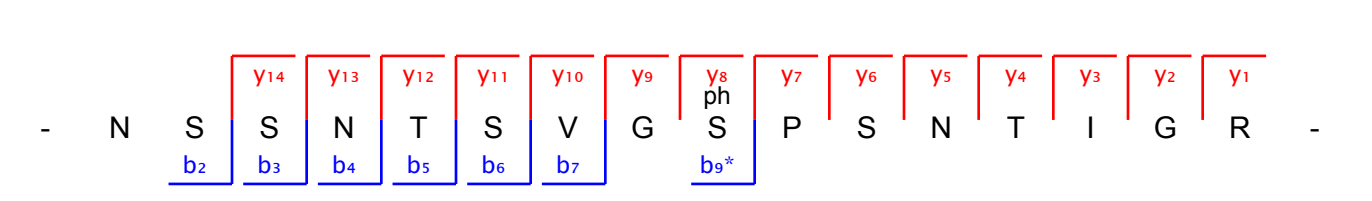
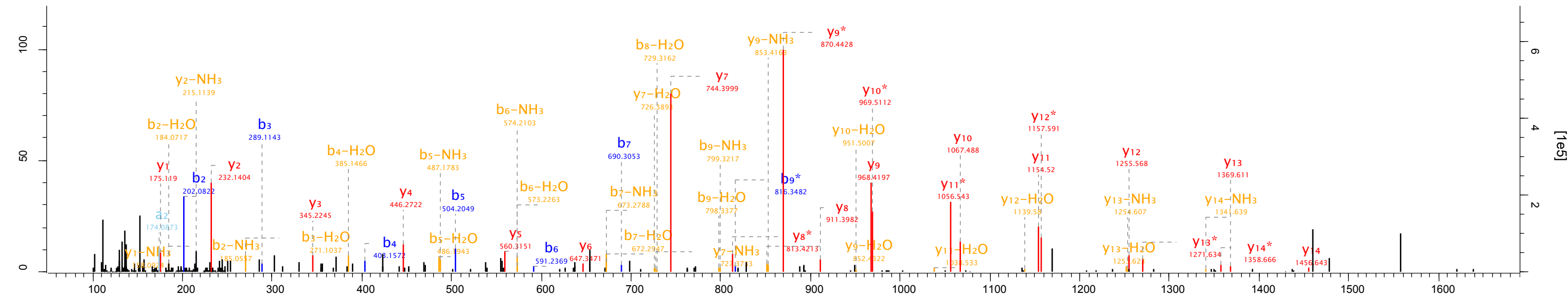


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20171215_MaS_33SR_LMH_phospho2_01

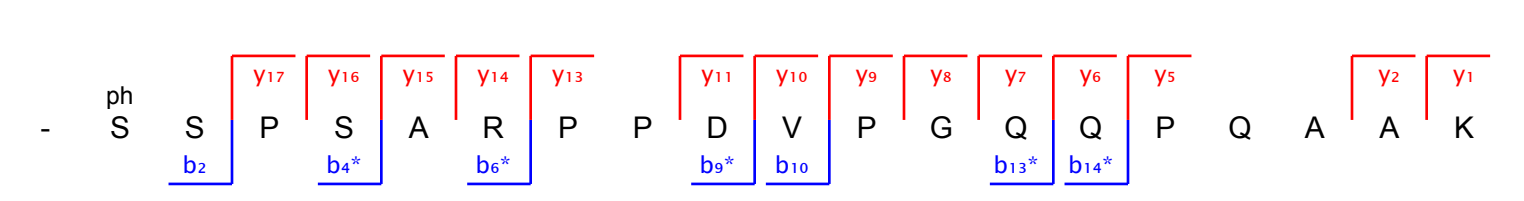
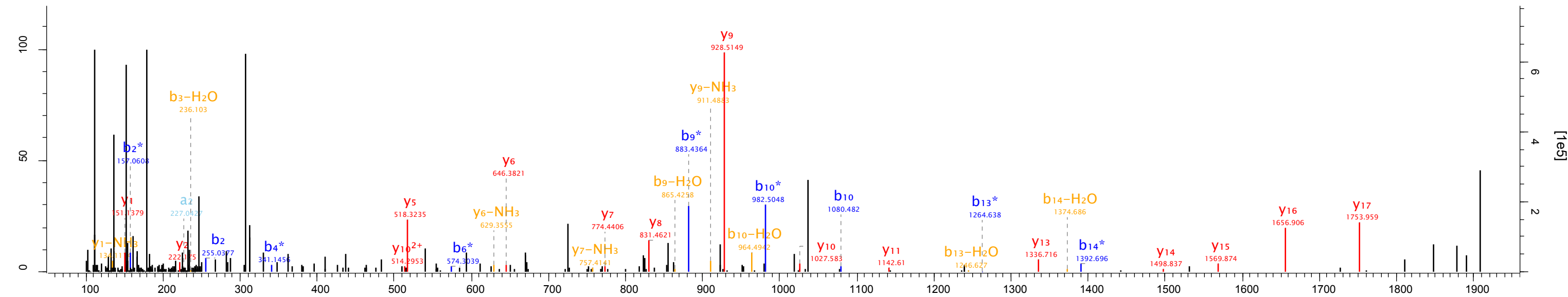
Scan 4050 Method FTMS; HCD Score 179.54 m/z 993.77 Gene names NUFIP2



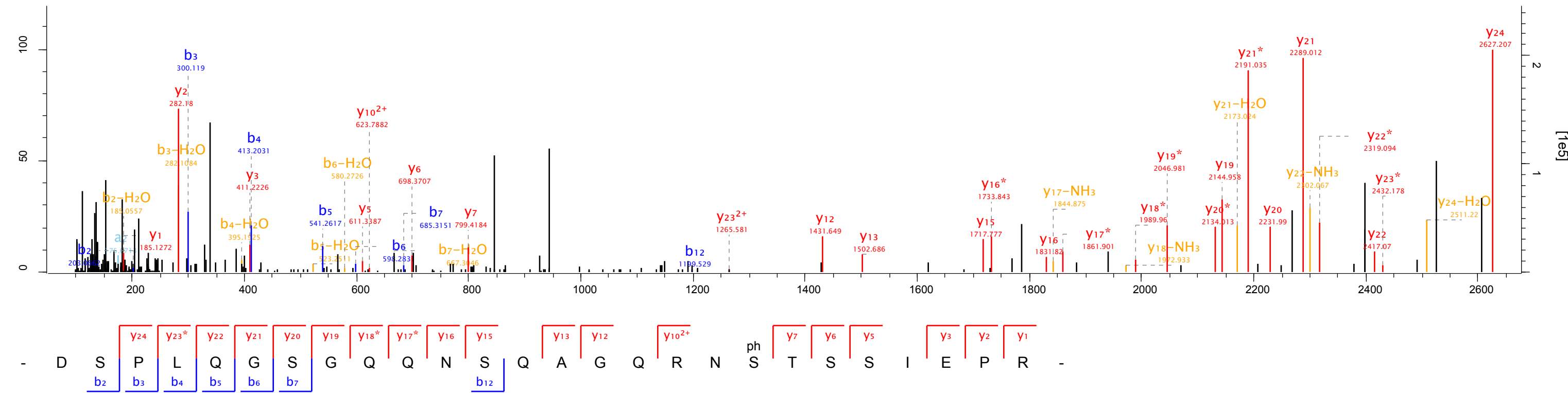
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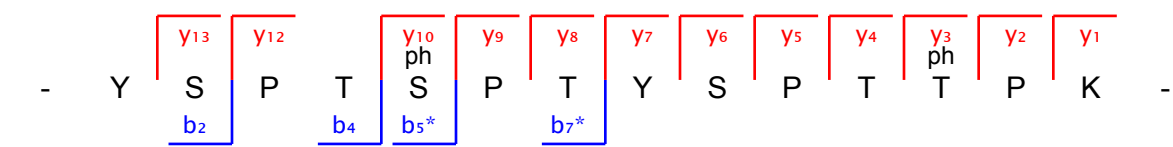
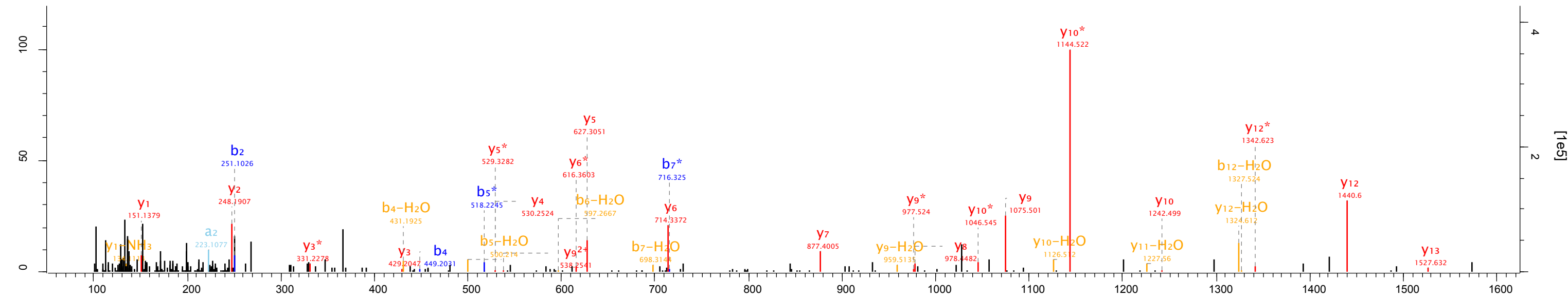


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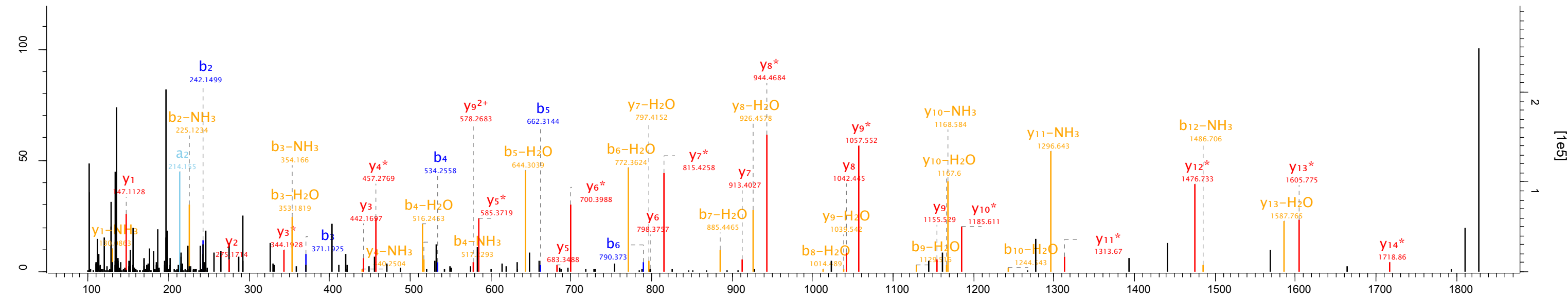


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Raw file: 20171215_MaS_33SR_LMH_phospho2_02
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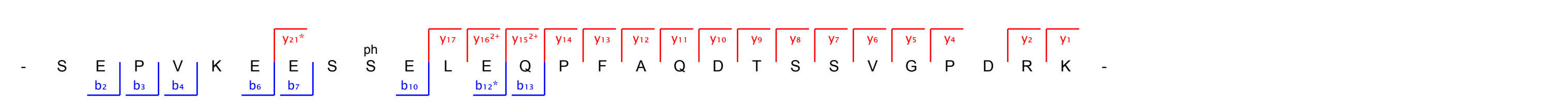
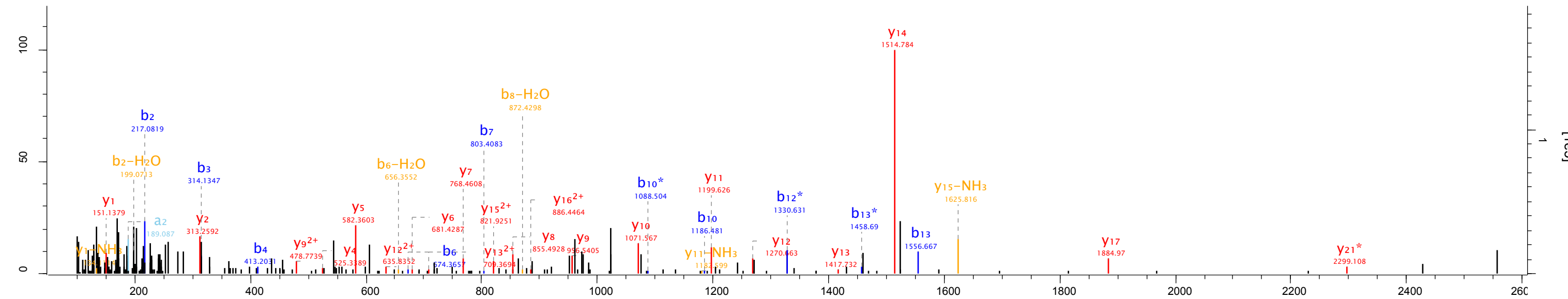


Peptide sequence: - Q L E Y Q Q L E D D K L S Q K -

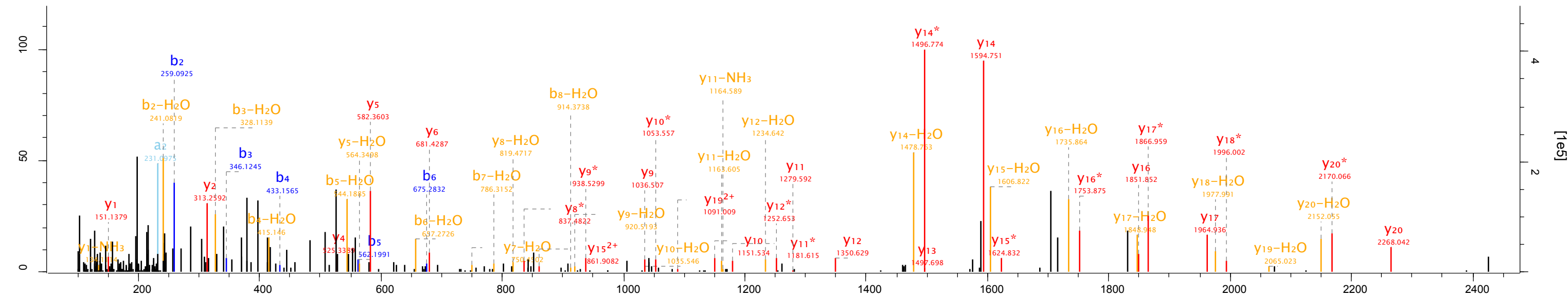
Fragmentation mapping (b and y ions):

- Red boxes (y ions): y14* (L), y13* (E), y12* (Y), y11* (Q), y10* (Q), y9 (L), y8 (E), y7 (D), y6 (D), y5 (K), y4* (L), y3_{ph} (S), y2 (Q), y1 (K)
- Blue boxes (b ions): b2 (L), b3 (E), b4 (Y), b5 (Q), b6 (Q)

Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 10890 Method FTMS; HCD Score 49.43 m/z 1024.49 Gene names SAFB;SAFB2



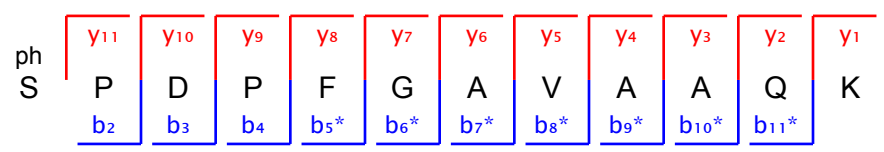
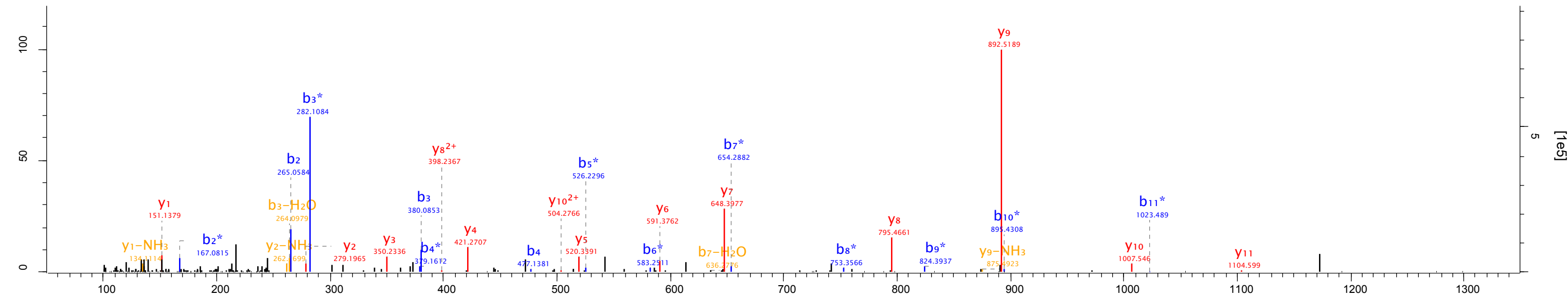
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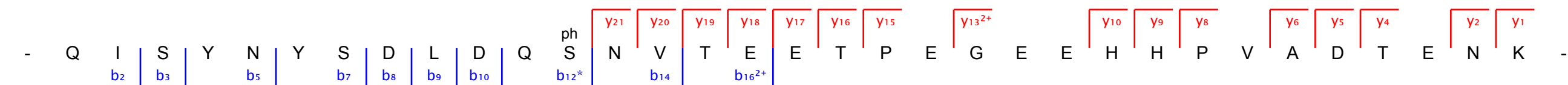
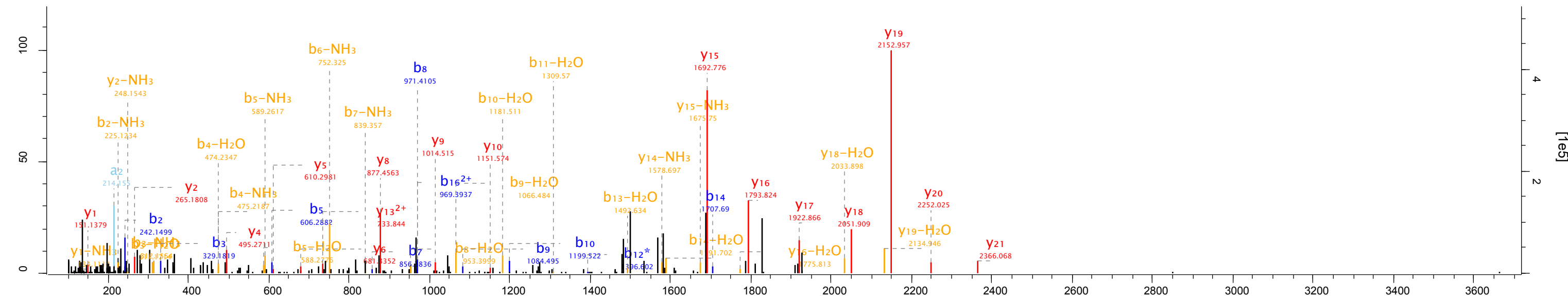
- E E S S E L E Q P F A Q D T S S V G P D R K -

b₂
b₃
b₄
b₅
b₆
y₂₀
y₁₉²⁺
y₁₈^{*}
y₁₇
y₁₆
y₁₅^{*}
y₁₄
y₁₃
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y₂
y₁

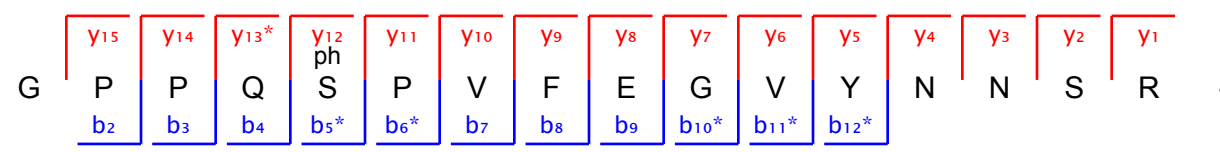
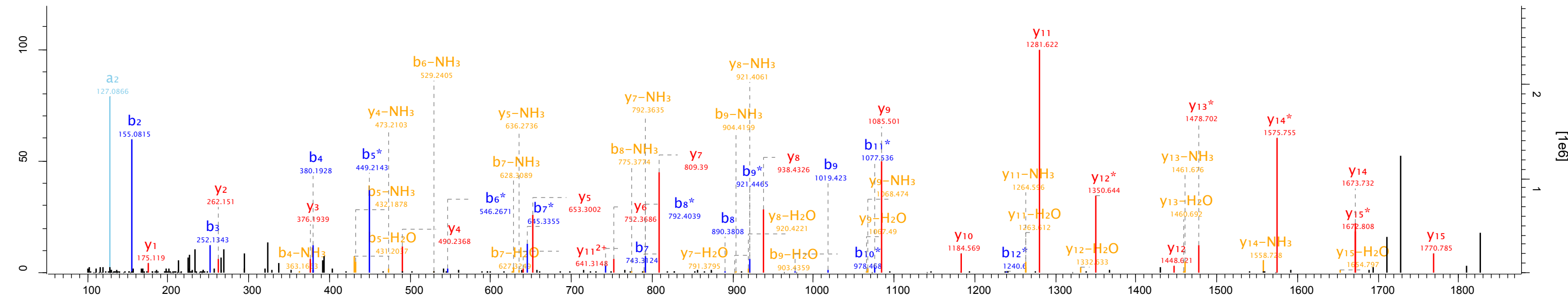
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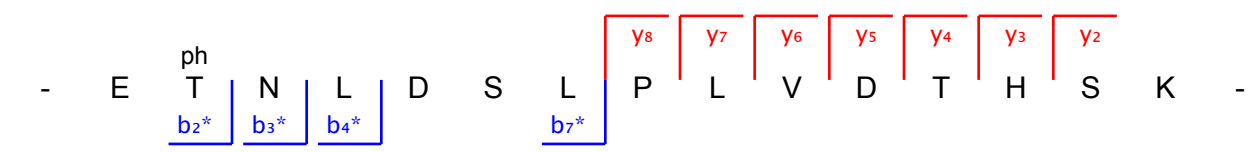
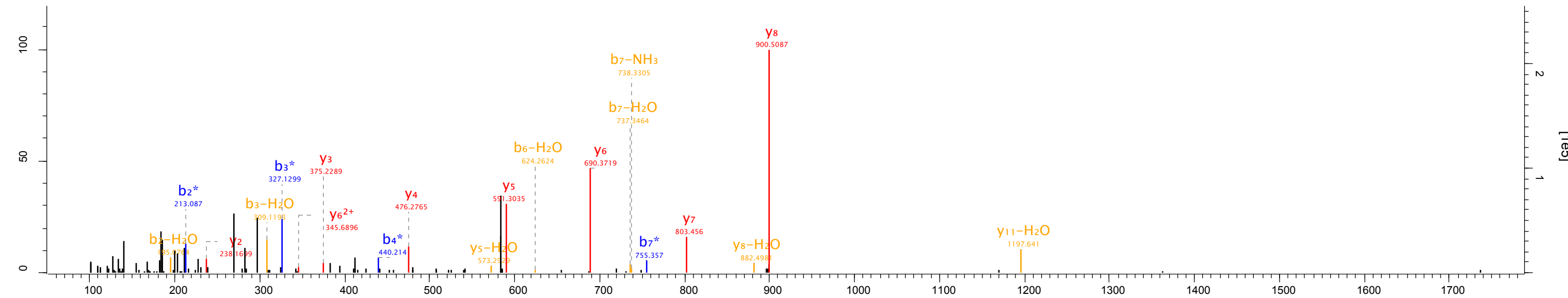


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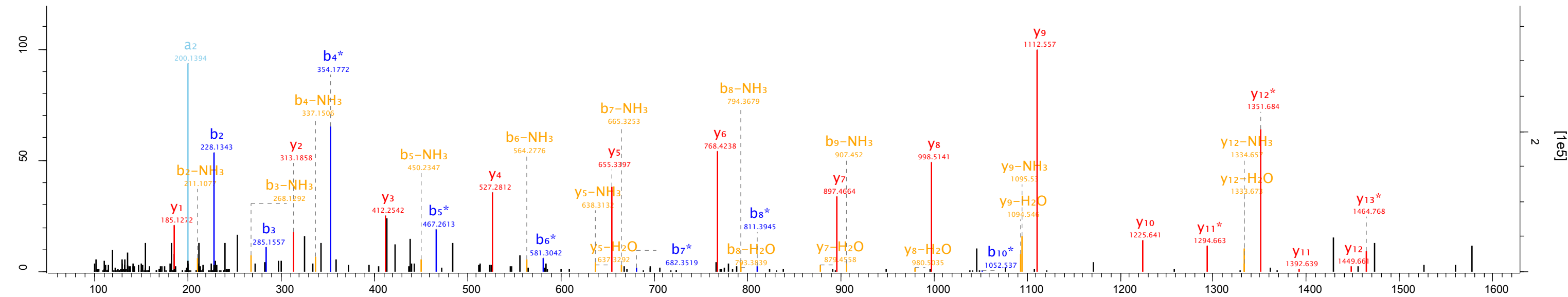


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20171215_MaS_33SR_LMH_phospho2_02

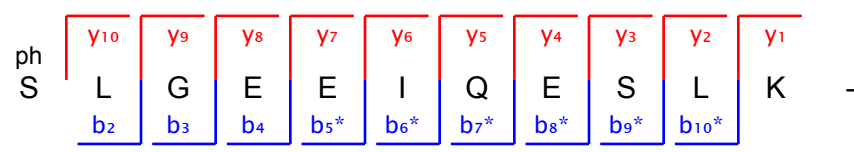
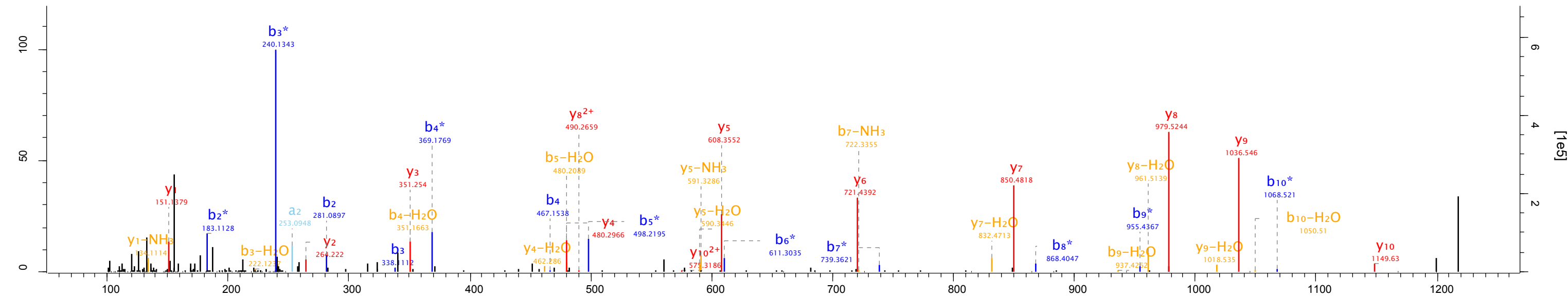
Scan 13830 Method FTMS; HCD Score 54.1 m/z 584.95 Gene names VIM



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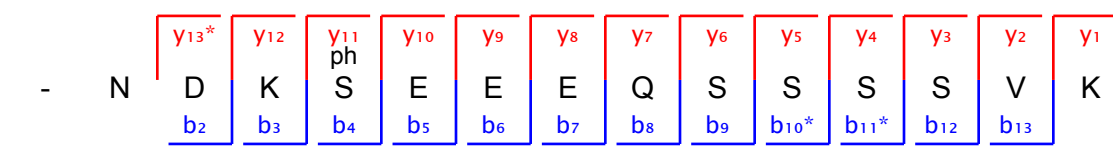
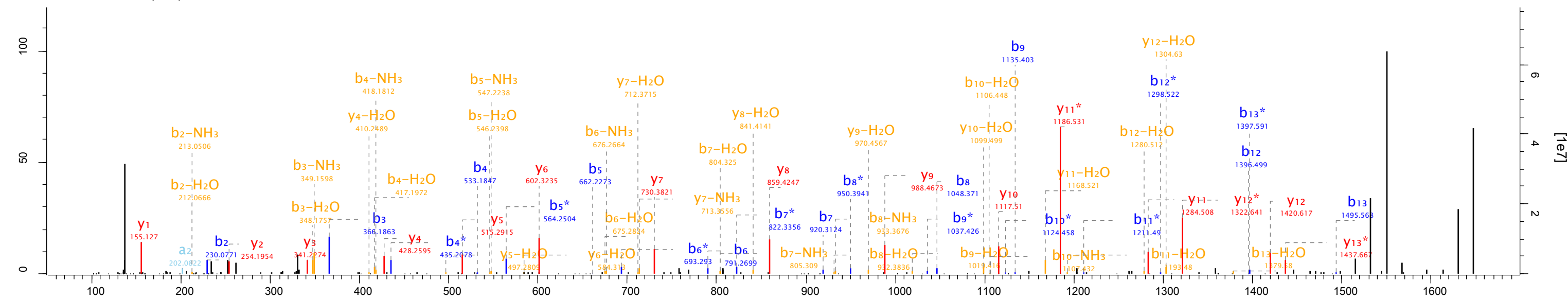


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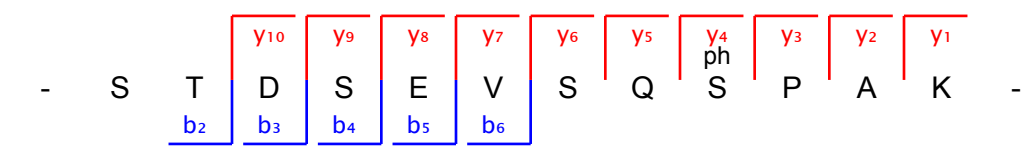
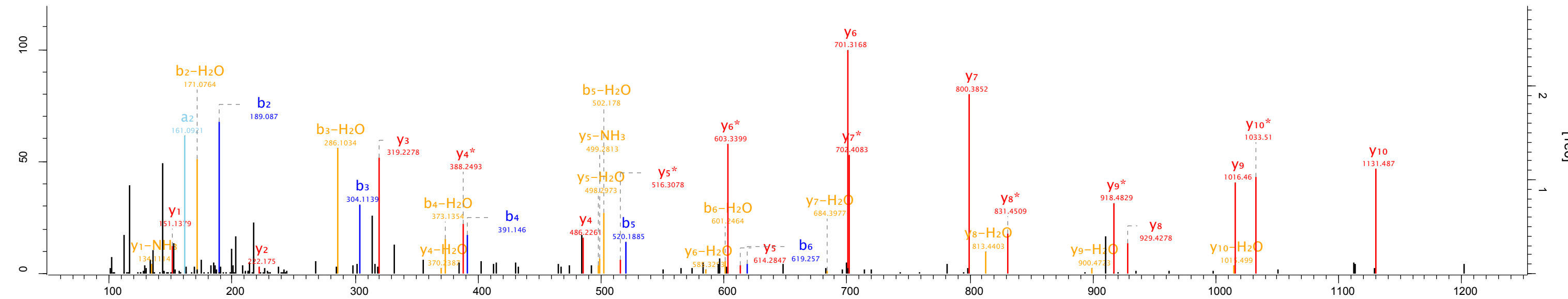


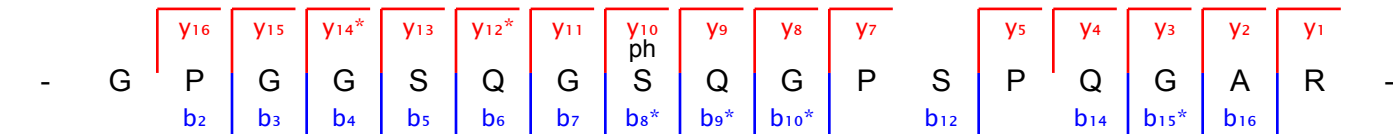
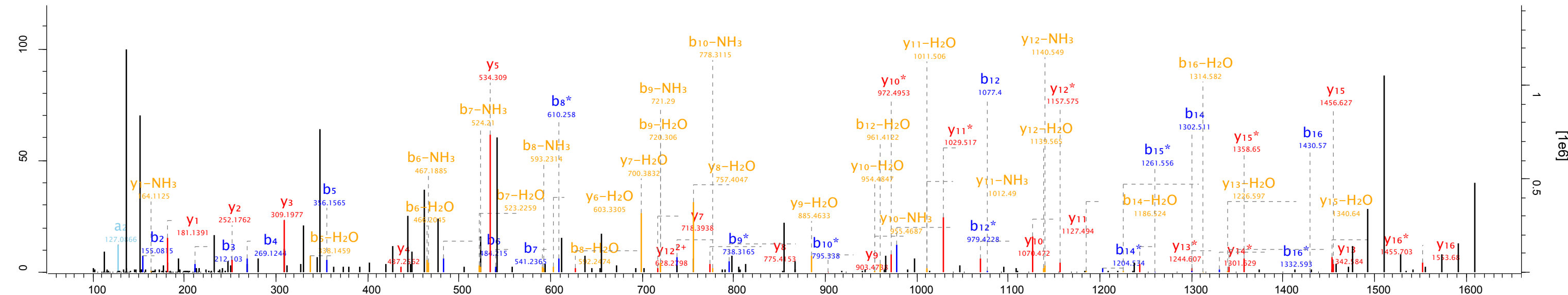
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20171215_MaS_33SR_LMH_phospho2_02

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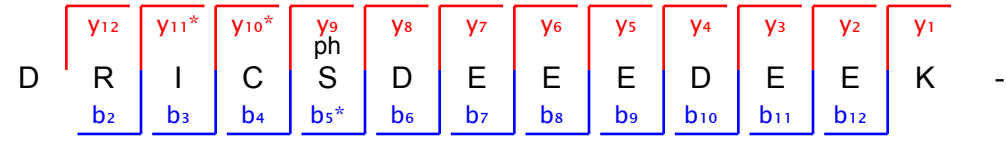
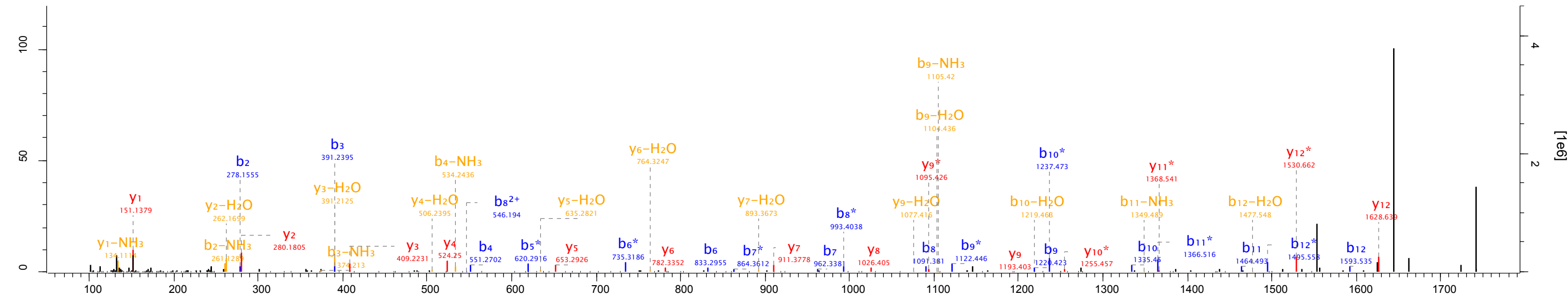


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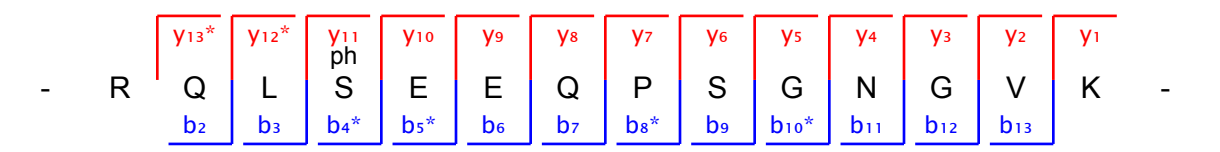
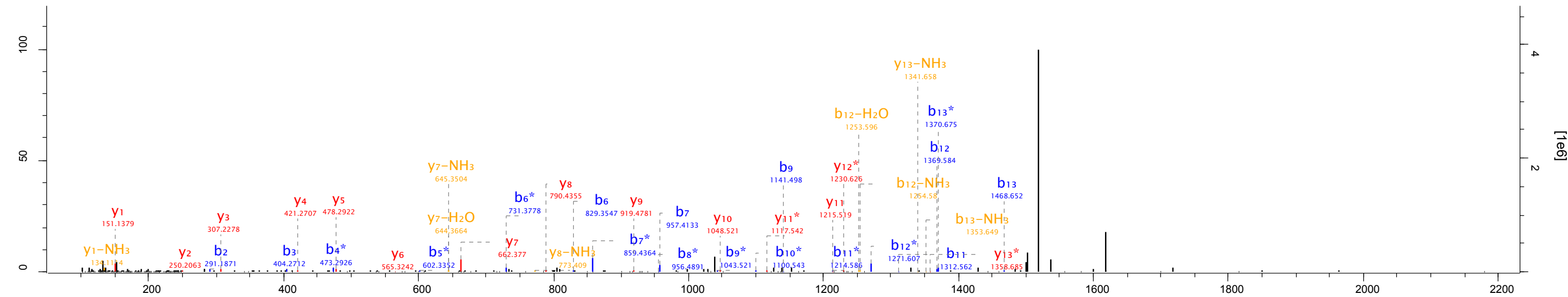


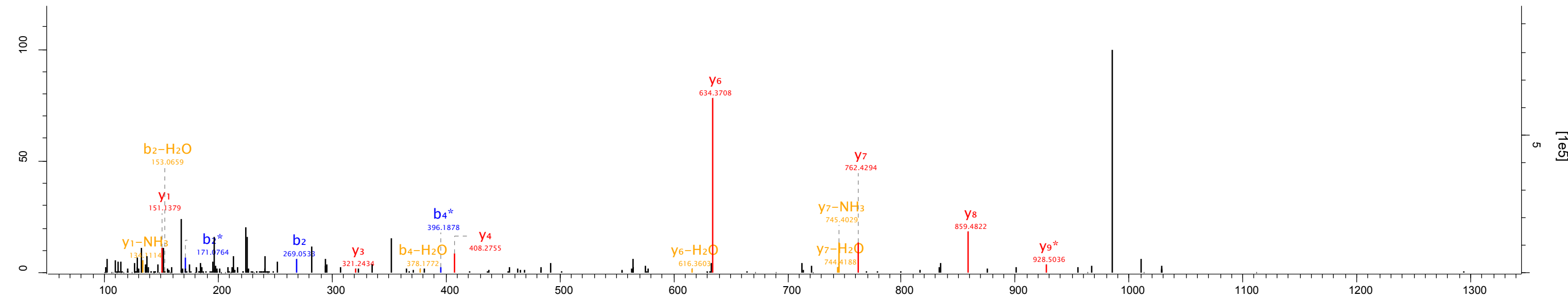


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3340 Method FTMS; HCD Score 220.36 m/z 872.34 Gene names UBN1



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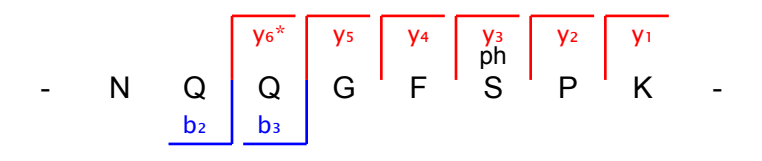
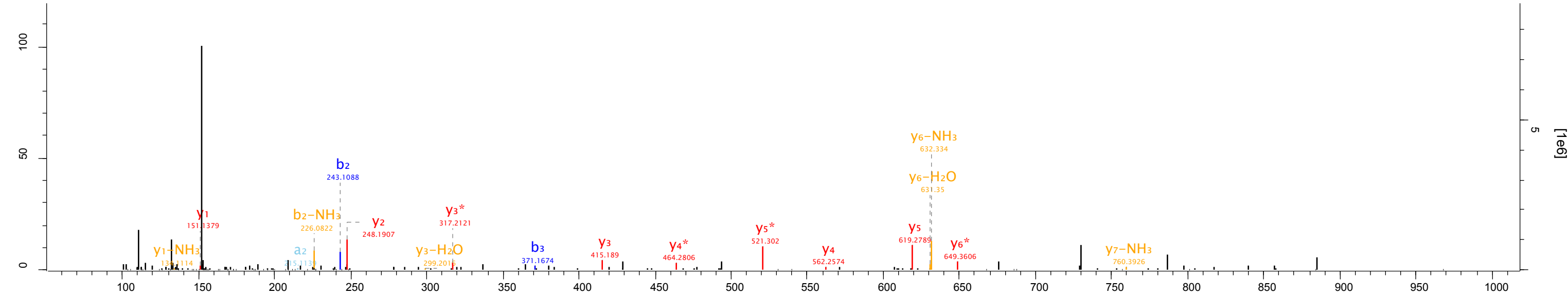
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b₂ y₈ P y₇ y₆ P E y₄ y₃ I y₁ K -

b₄*

Raw file

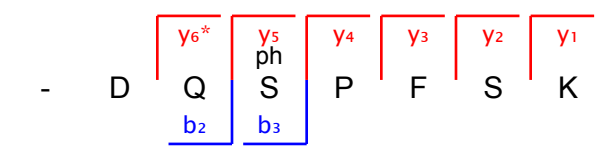
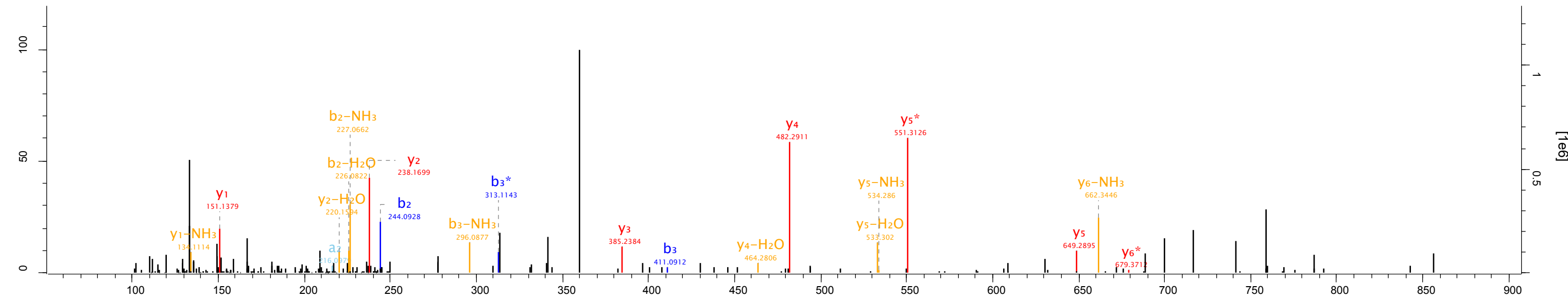
20171215_MaS_33SR_LMH_phospho2_02

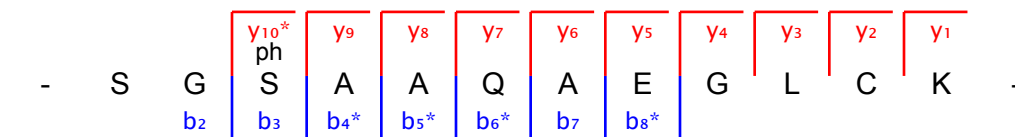
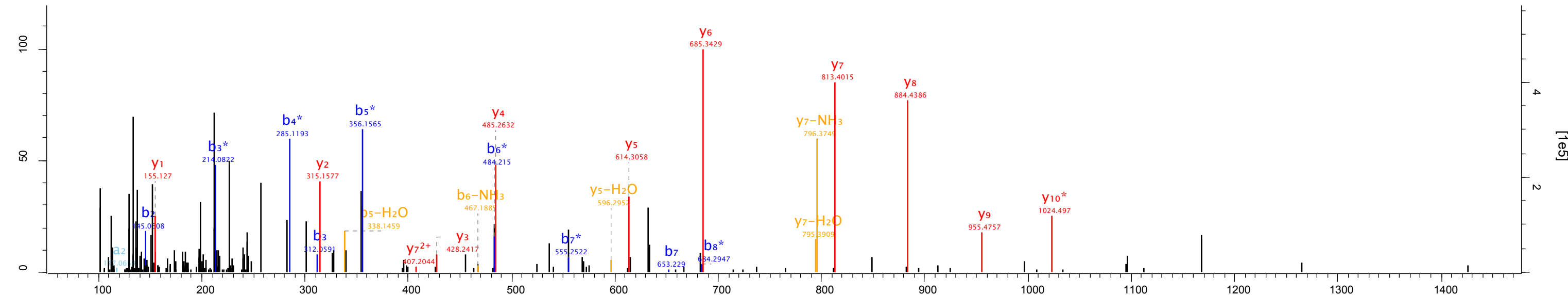
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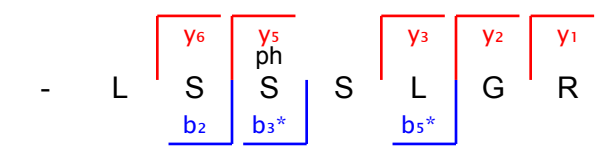
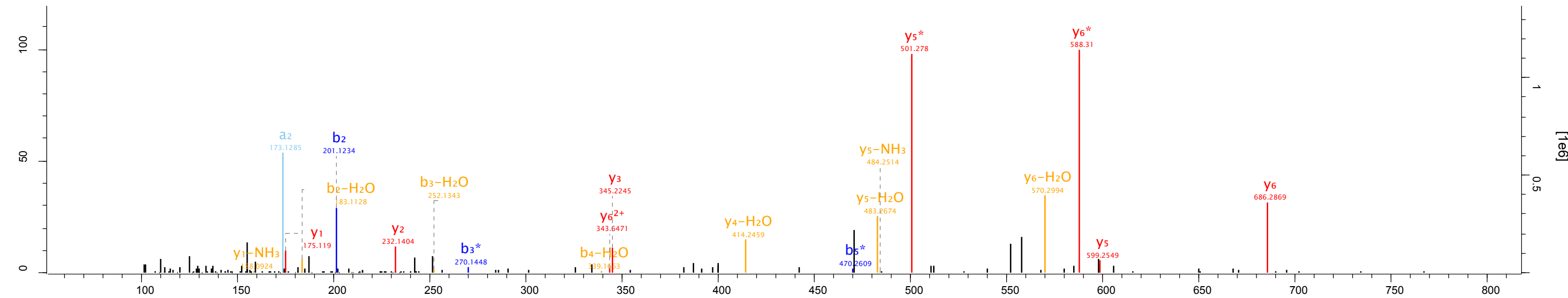
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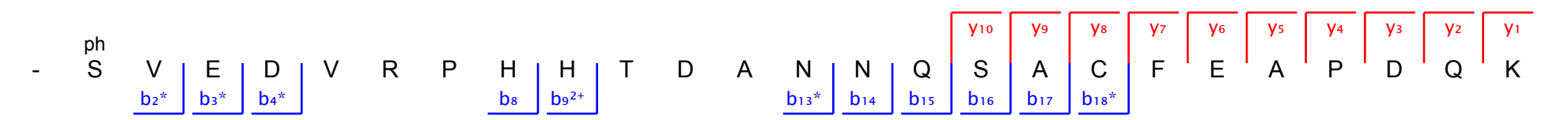
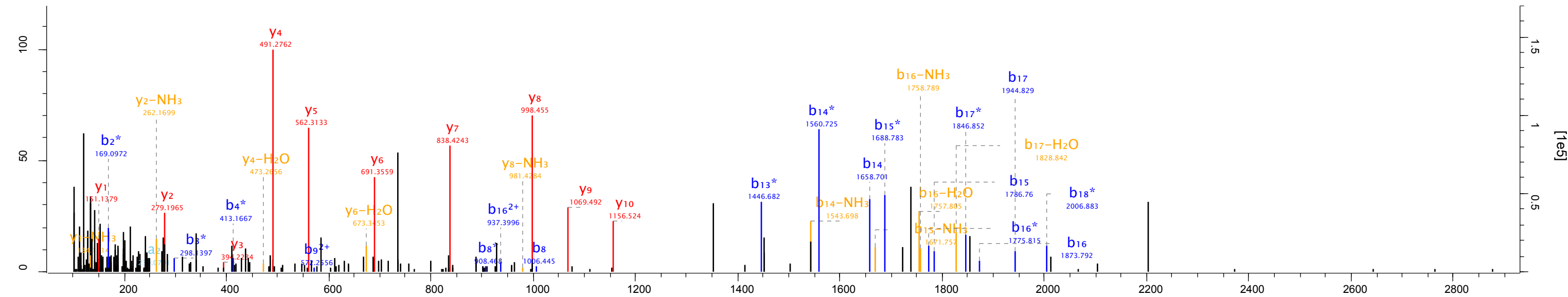


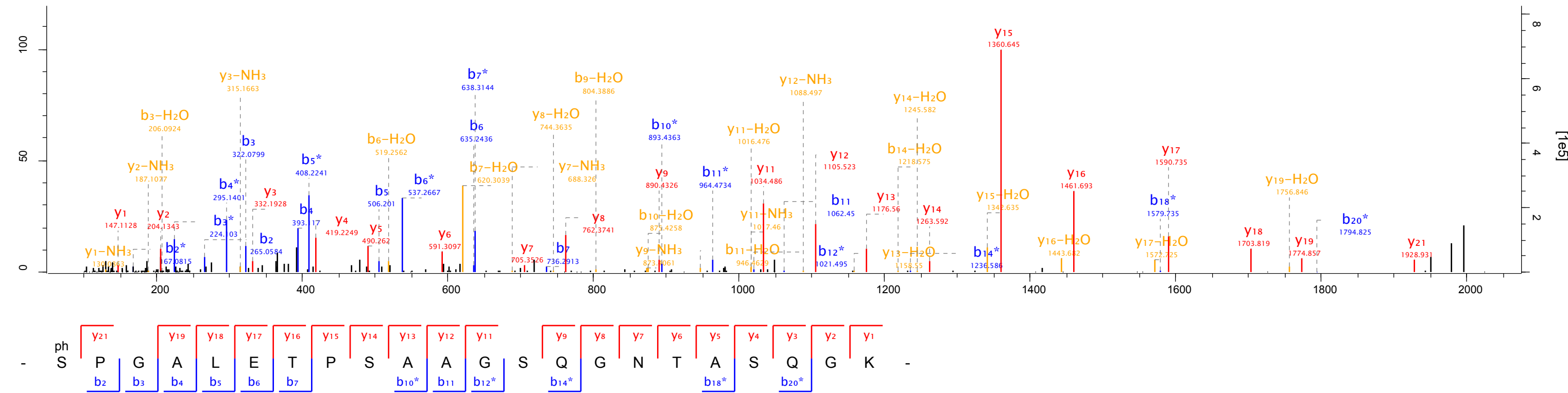


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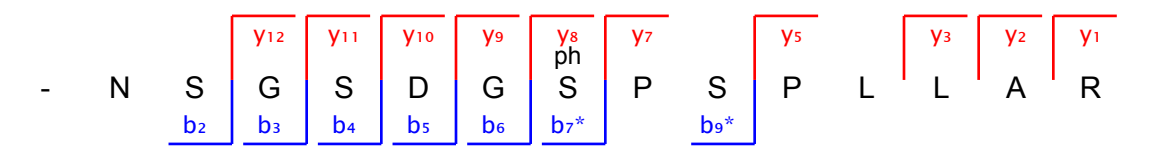
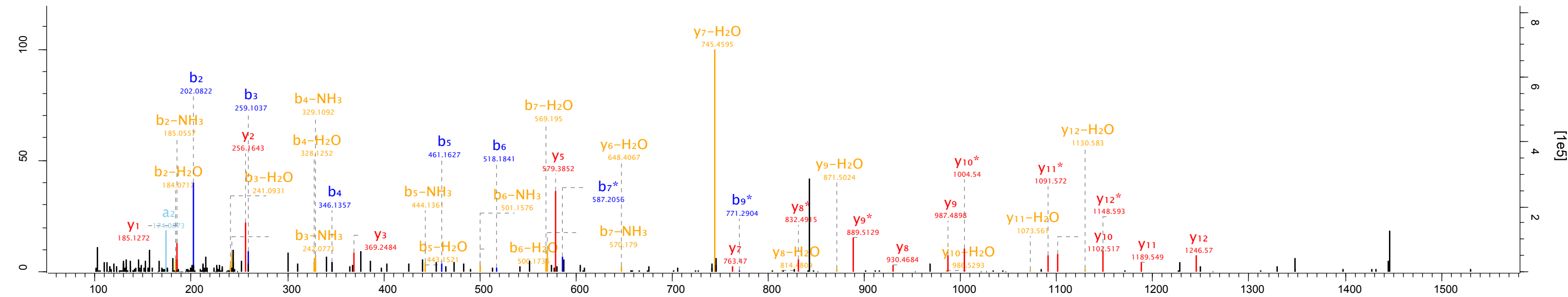
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Raw file
20171215_MaS_33SR_LMH_phospho2_02

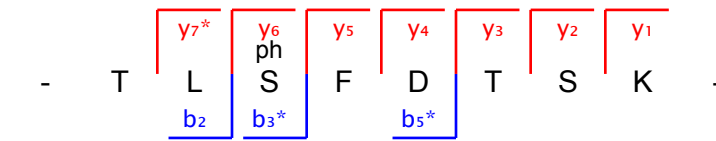
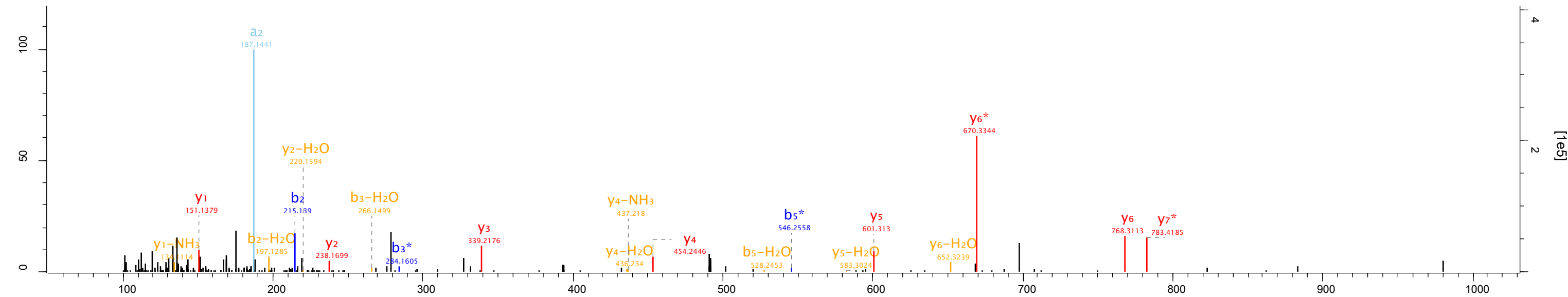
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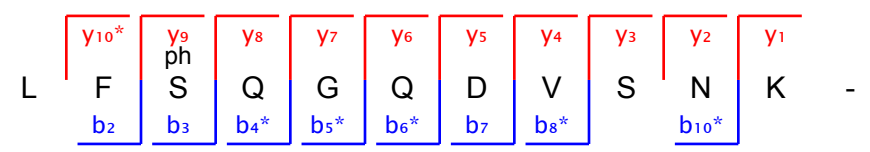
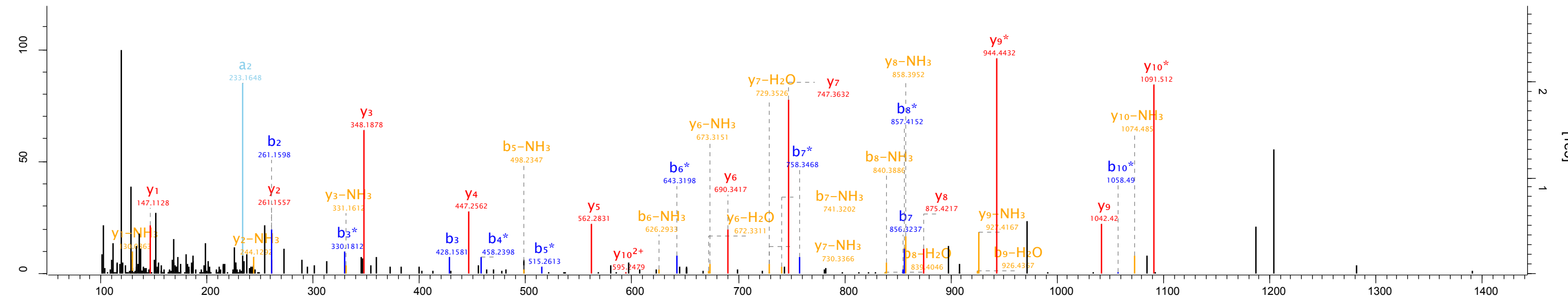
Raw file

20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
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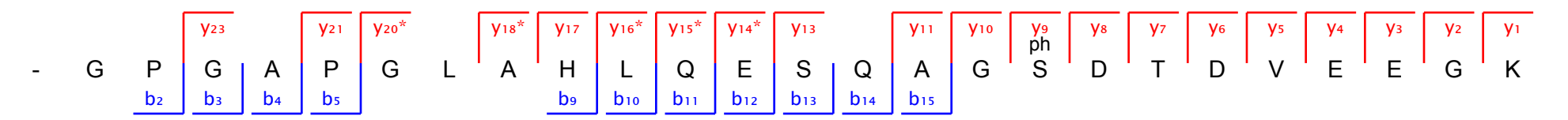
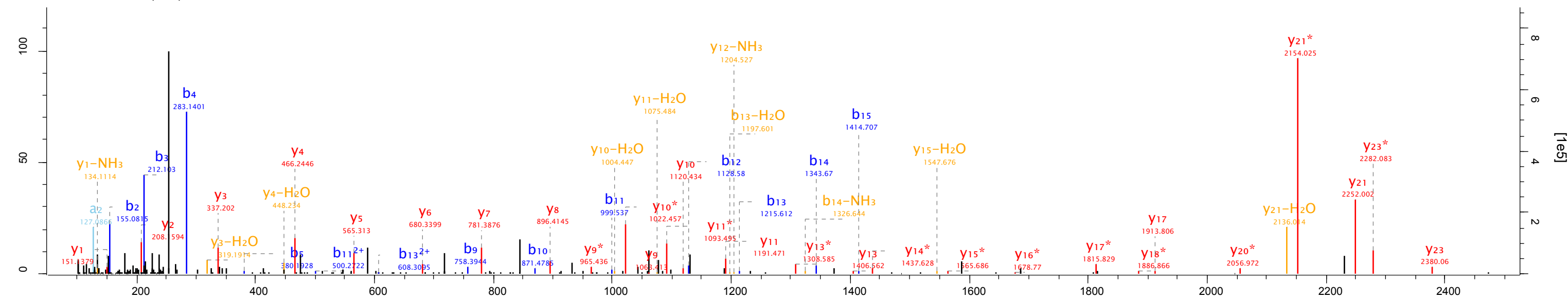


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 8900 Method: FTMS; HCD Score: 153.41 m/z: 651.79 Gene names: MLLT4

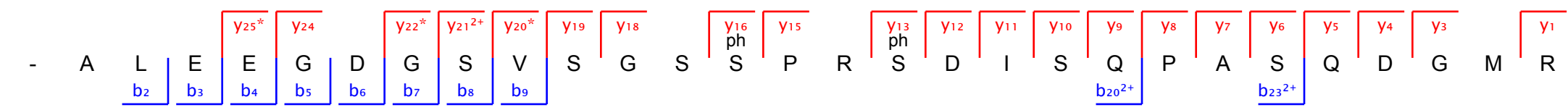
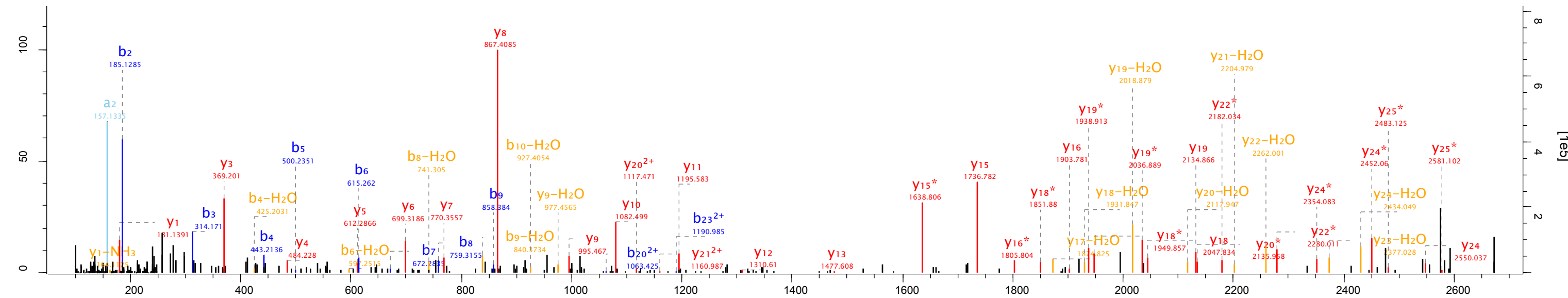


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20171215_MaS_33SR_LMH_phospho2_02

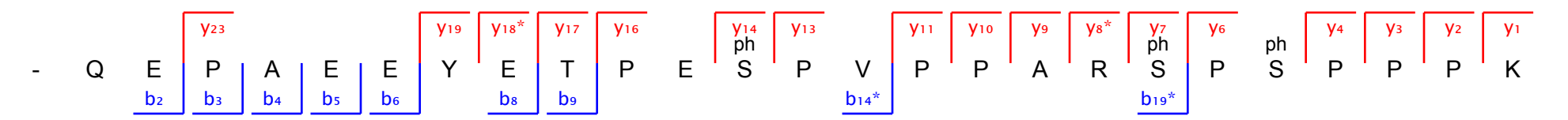
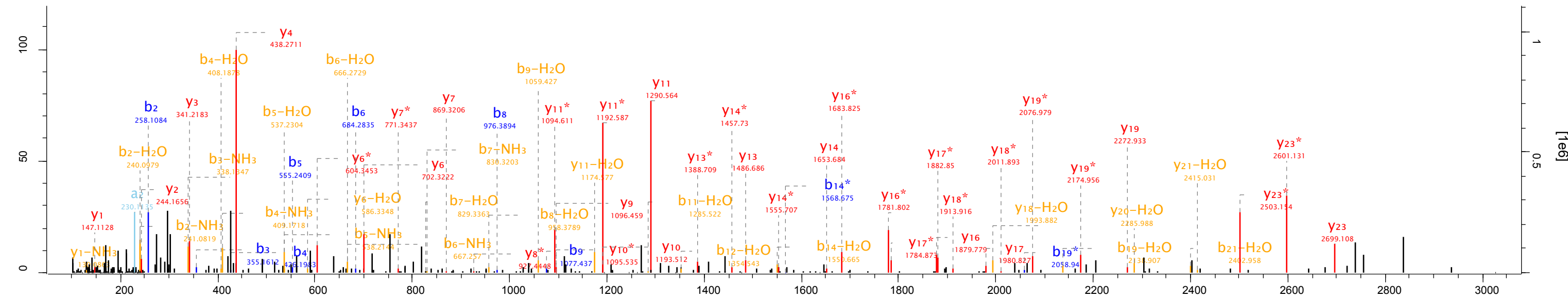
Scan 9710 Method FTMS; HCD Score 180.6 m/z 845.72 Gene names MDC1



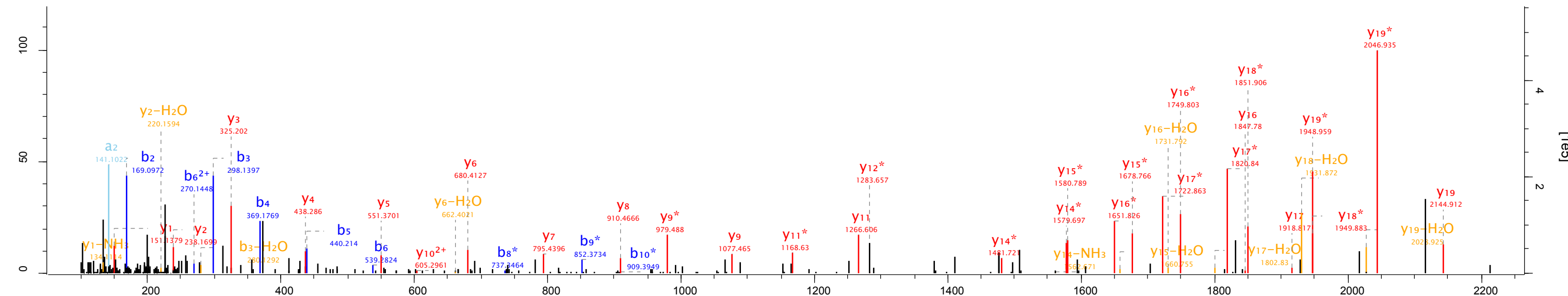
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10000 Method FTMS; HCD Score 140.4 m/z 998.42 Gene names FNBP4



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10110 Method FTMS; HCD Score 127.35 m/z 986.41 Gene names ATN1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10200 Method FTMS; HCD Score 149.16 m/z 739.65 Gene names NAV1



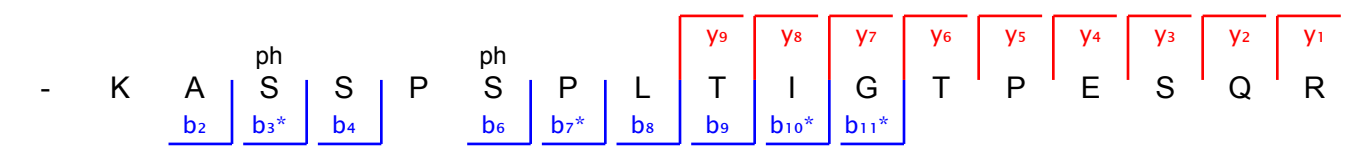
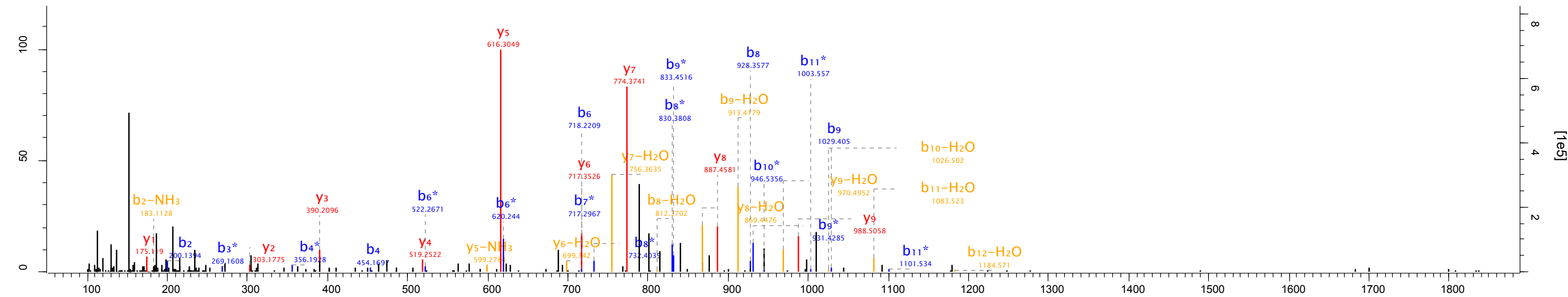
- A P E A A V S E D G K S D D E L L S S K -

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

- Red boxes above the sequence indicate y ions: y19, y18*, y17, y16, y15*, y14*ph, y12*, y11, y10²⁺, y_{ph}, y8, y7, y6, y5, y4, y3, y2, y1.
- Blue boxes below the sequence indicate b ions: b2, b3, b4, b5, b6, b8*, b9*, b10*.

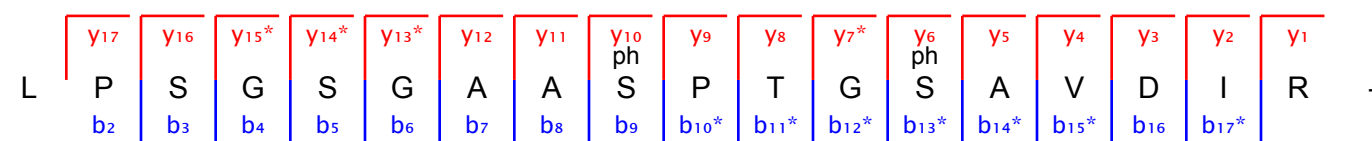
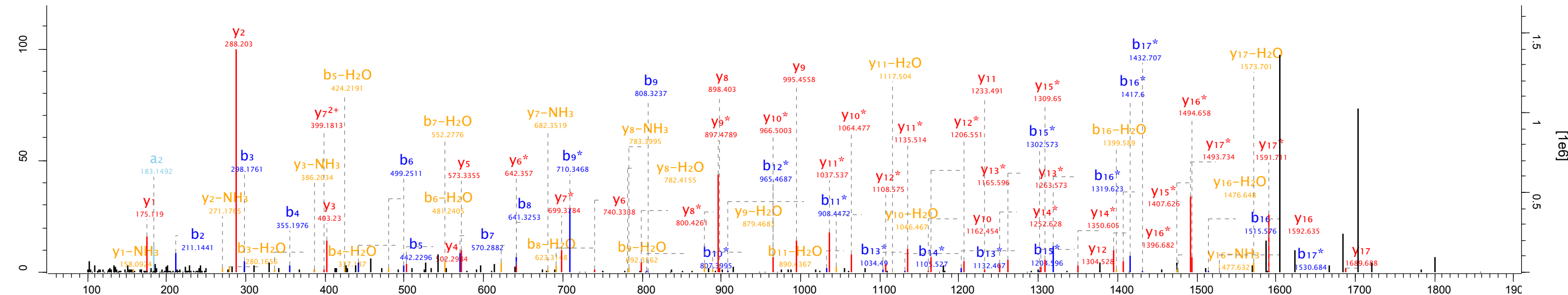
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20171215_MaS_33SR_LMH_phospho2_03

Scan 10250 Method FTMS; HCD Score 73.43 m/z 639.96 Gene names DCP1A

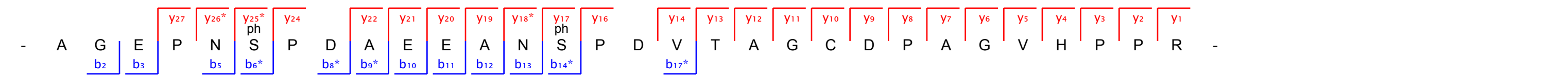
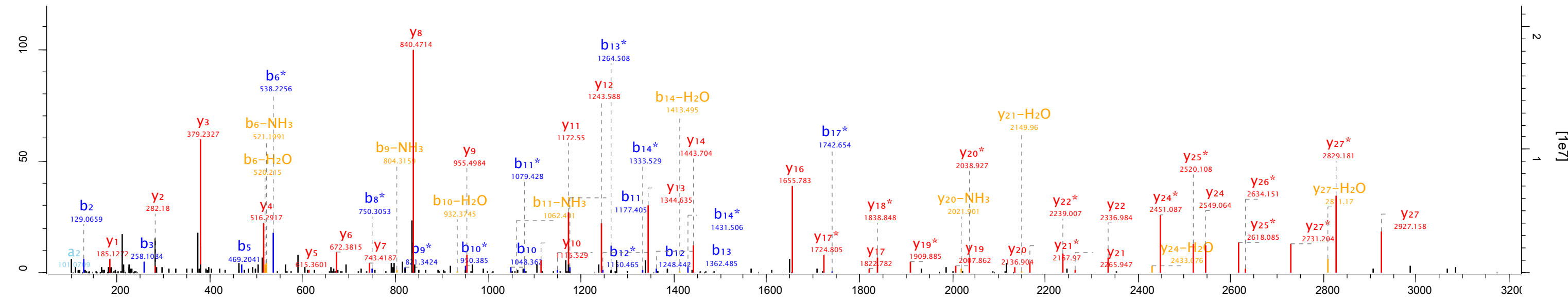


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20171215_MaS_33SR_LMH_phospho2_03

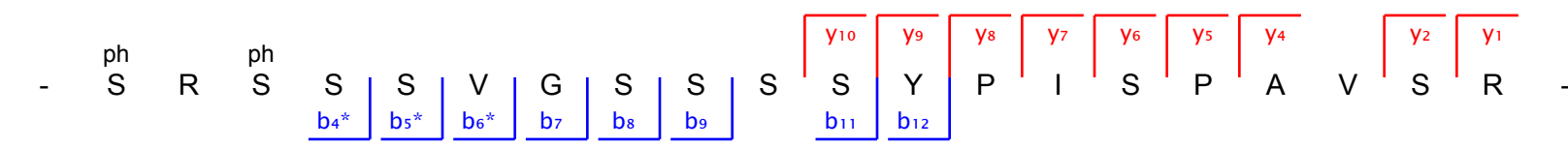
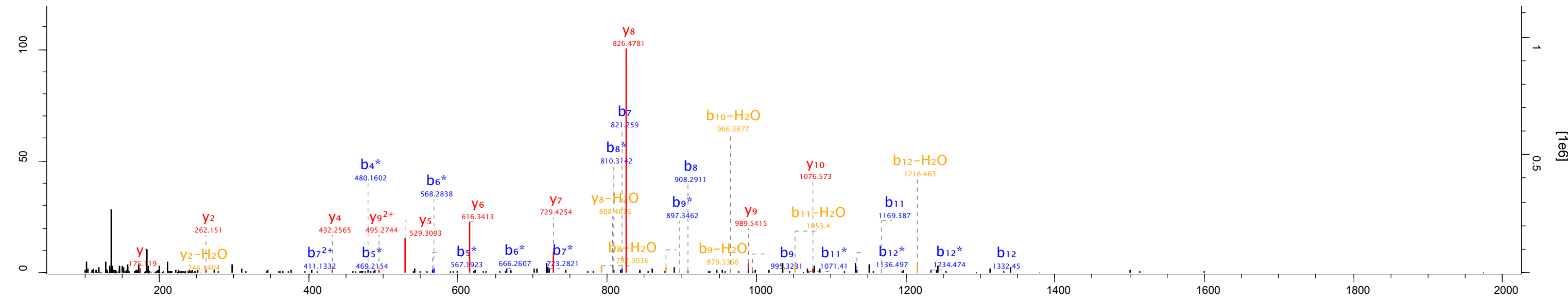
Scan 10340 Method FTMS; HCD Score 269.46 m/z 902.39 Gene names AHNAK



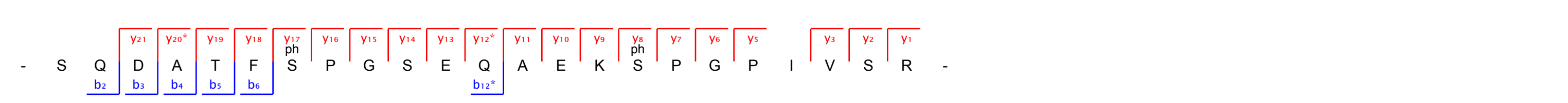
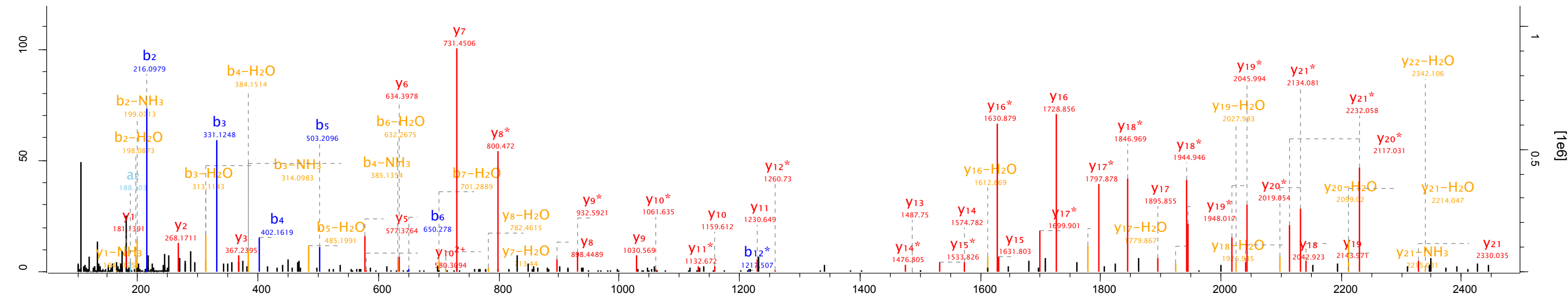
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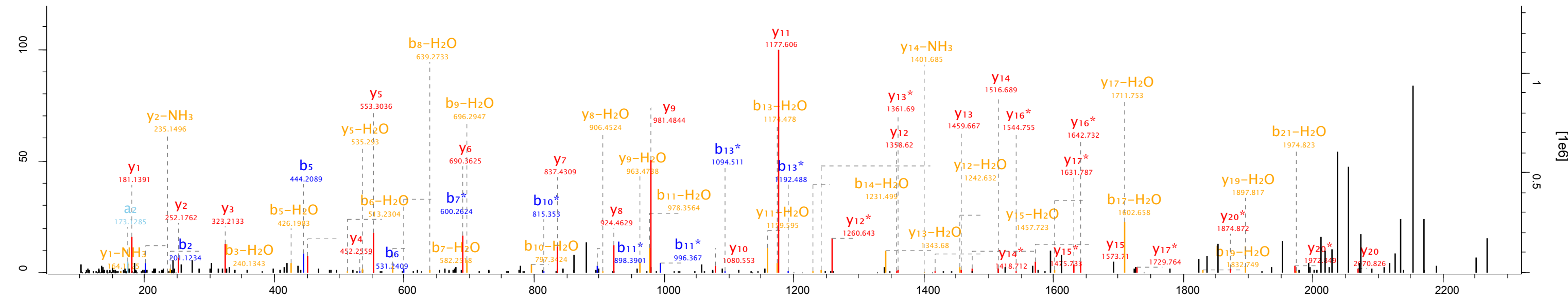
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Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10660 Method: FTMS; HCD Score: 225.07 m/z: 849.71 Gene names: ZC3HC1



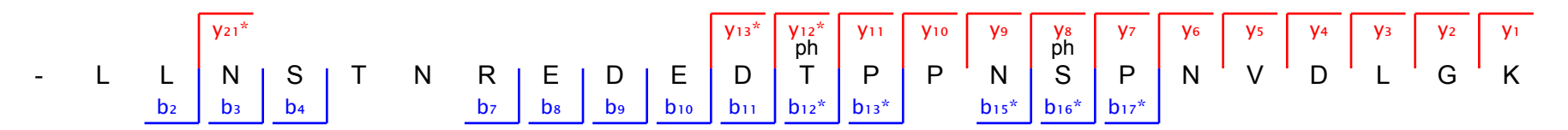
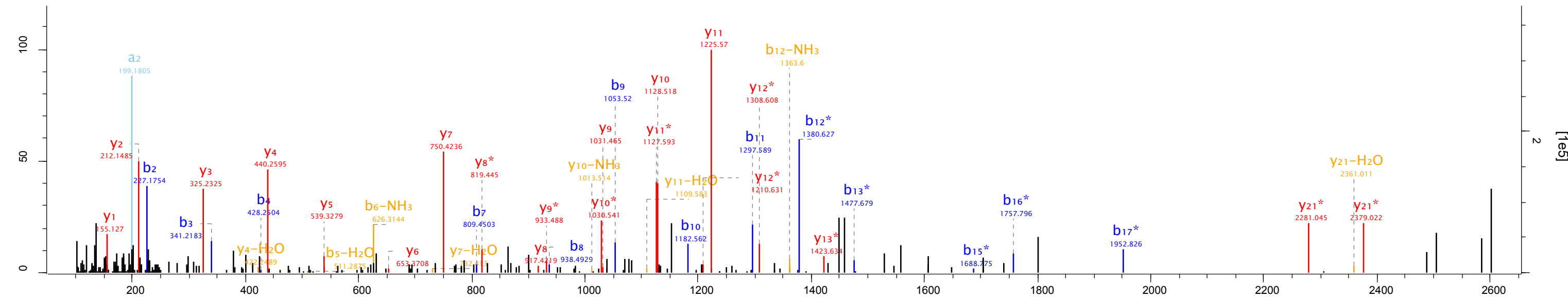
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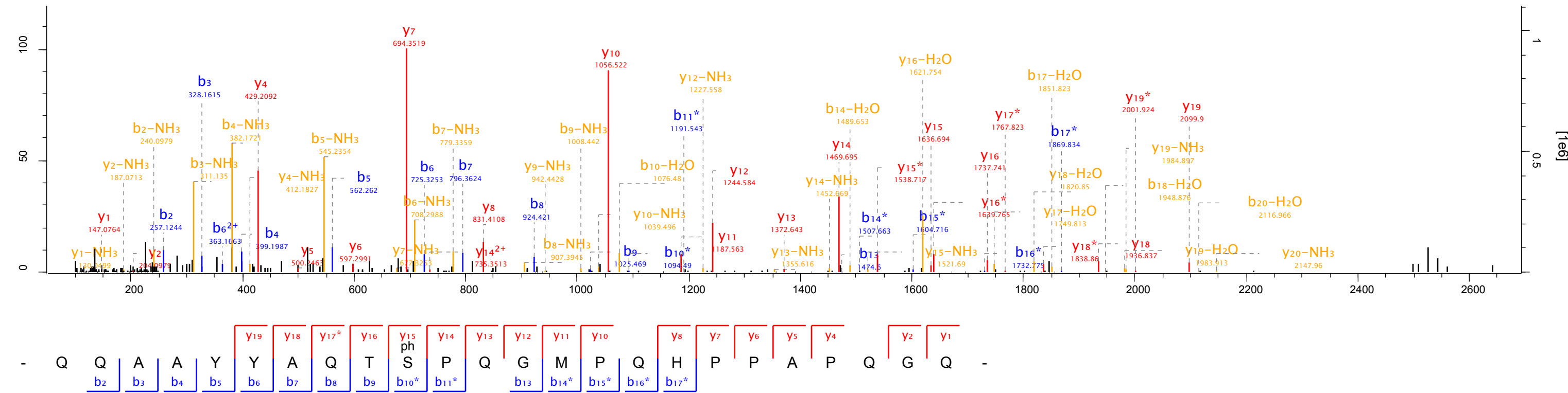


- S L G G E S S G G T T P V G S F H T E A A R -

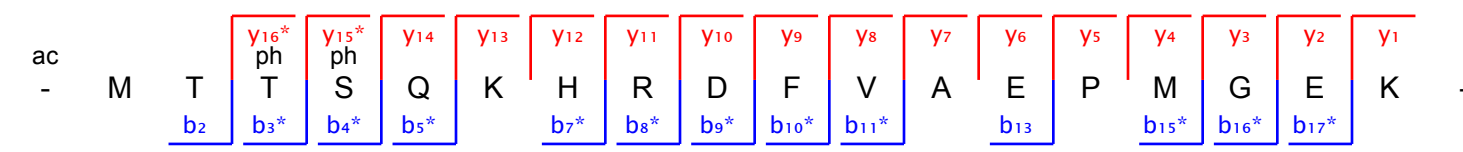
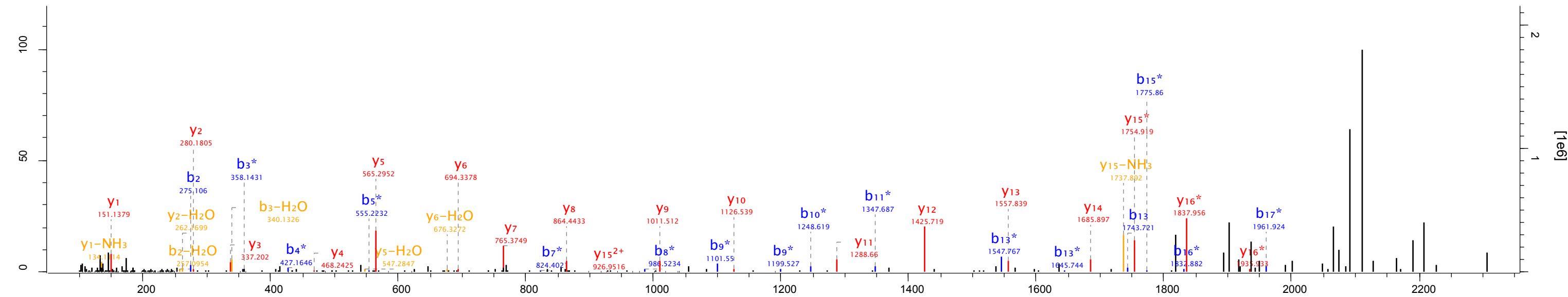
b₂
b₅
b₆
b₇*
b₁₀*
b₁₁*
b₁₃*
y₂₀
y₁₇*
y₁₆*
ph
y₁₅
y₁₄
y₁₃
y₁₂
ph
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10700 Method FTMS; HCD Score 86 m/z 902.4 Gene names FGD1

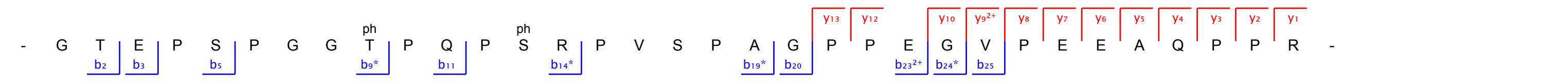
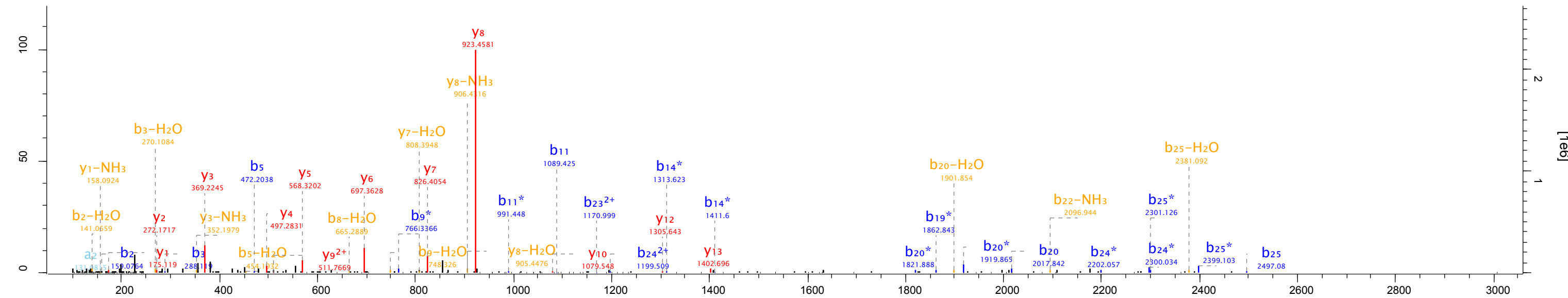




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 Scan: 11120 Method: FTMS; HCD Score: 143.35 m/z: 770.01 Gene names: BANF1

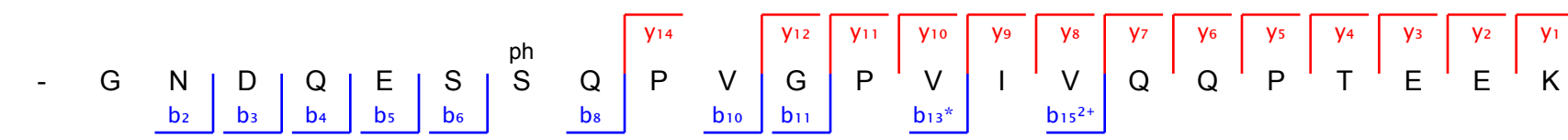
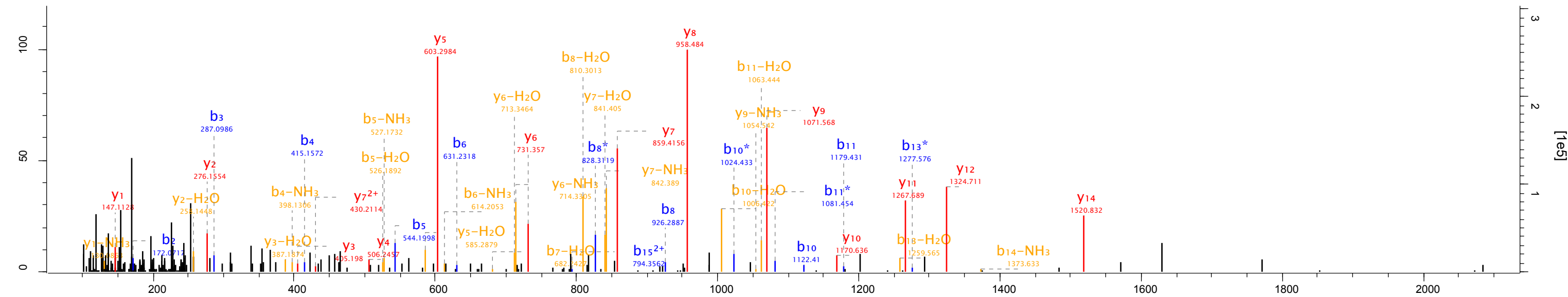


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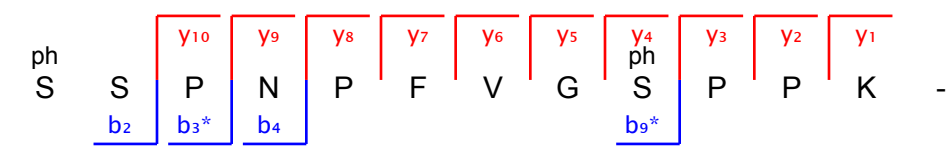
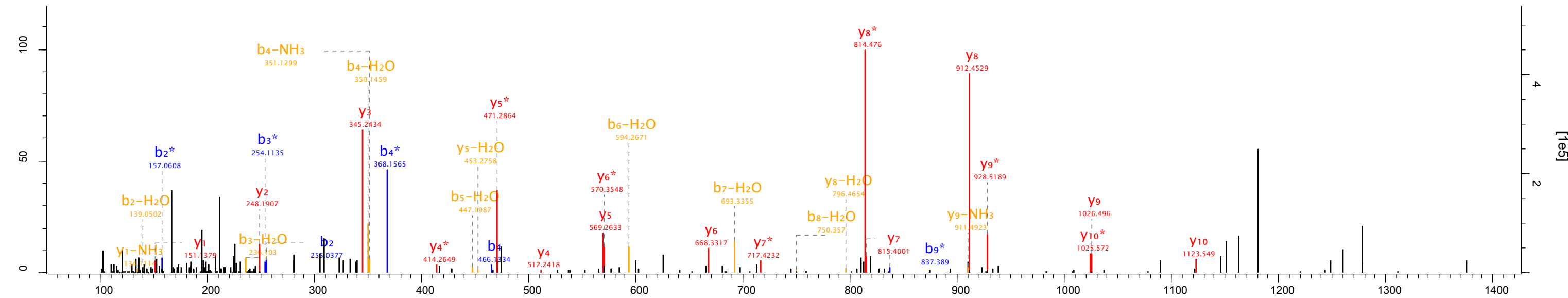


Raw file
20171215_MaS_33SR_LMH_phospho2_03

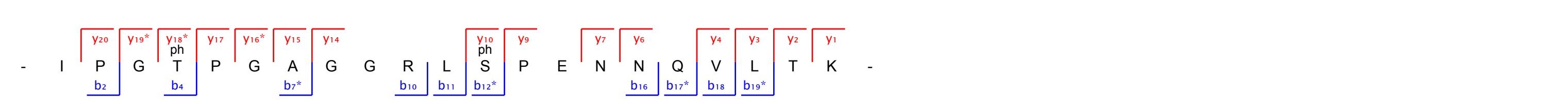
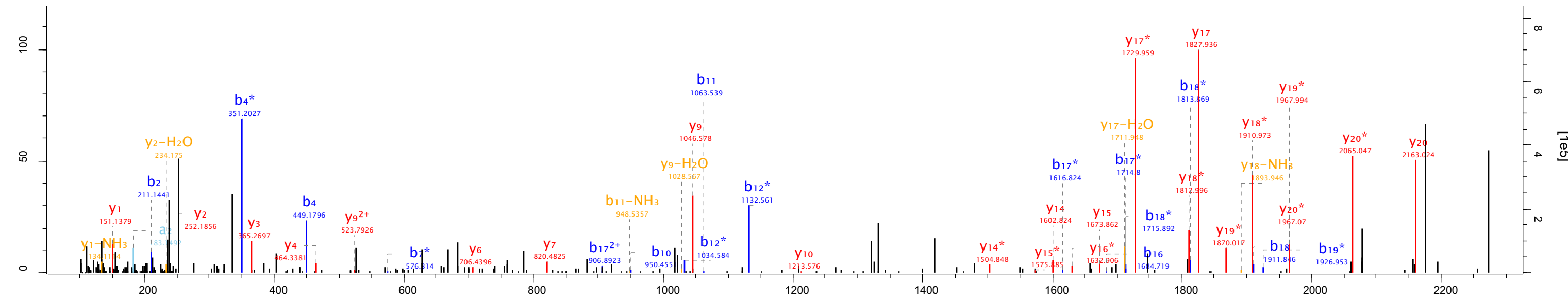
Scan 11450 Method FTMS; HCD Score 102.66 m/z 816.38 Gene names PAGE5



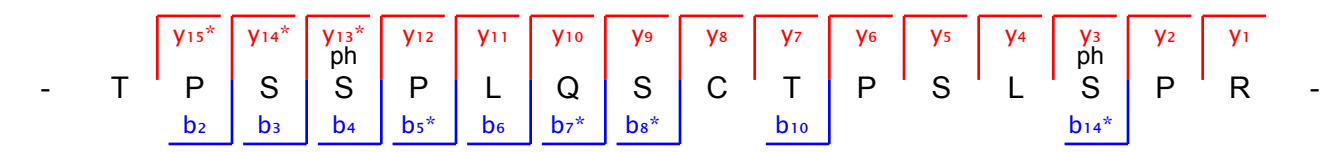
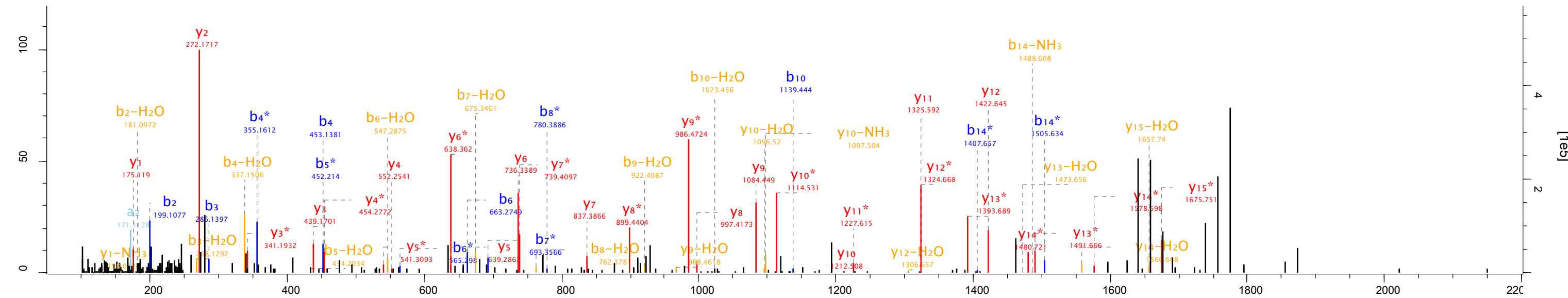
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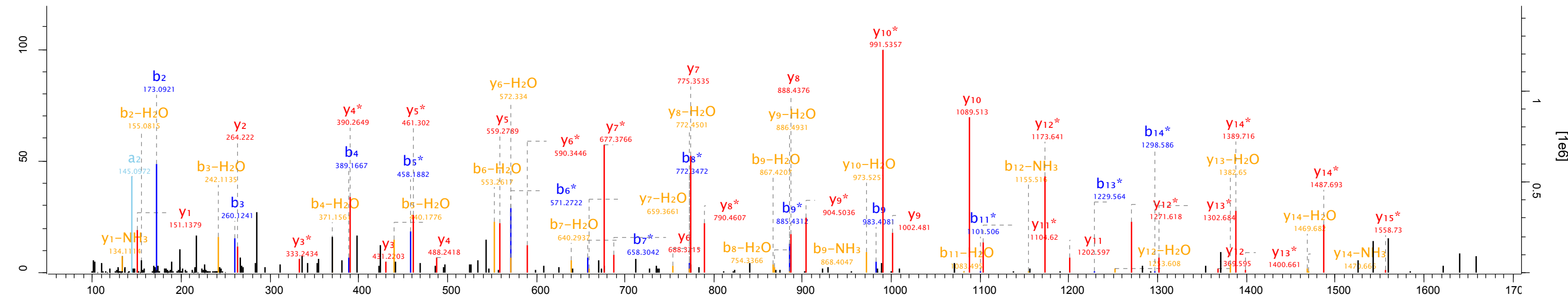
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11650 Method FTMS; HCD Score 215.45 m/z 938.4 Gene names ACD



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11780 Method FTMS; HCD Score 277.07 m/z 879.38 Gene names CLIP1

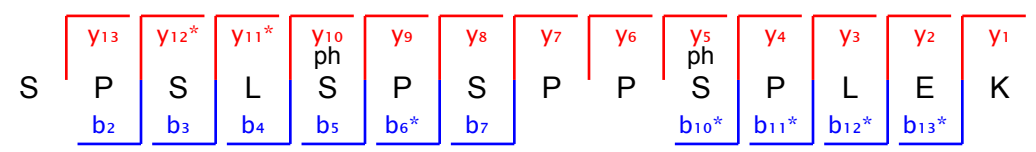
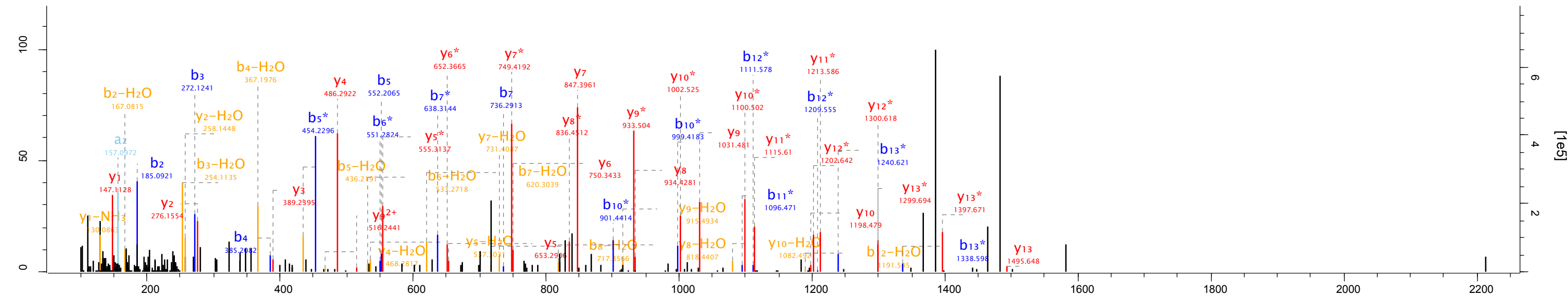


- T A S E I S N L S E A G S I K -

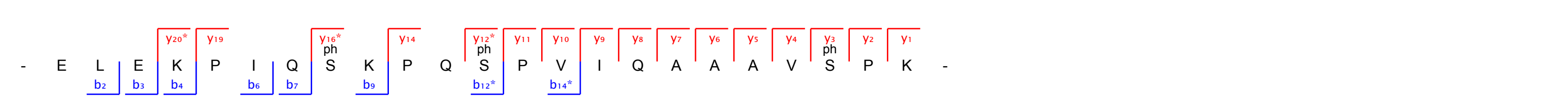
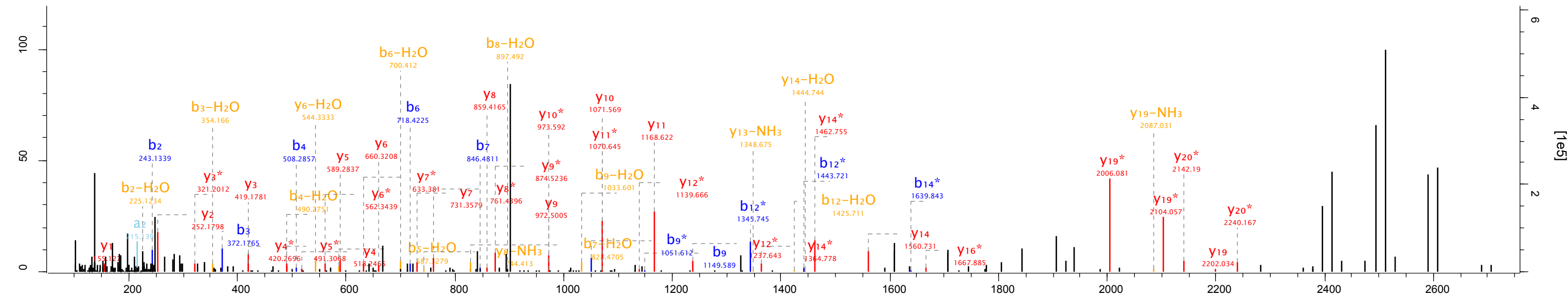
Fragmentation mapping (b and y ions) is shown below the sequence:

- b2 (A), b3 (S), b4 (E), b5* (S), b6* (I), b7* (S), b8* (N), b9 (L), b11* (S), b13* (A), b14* (G)
- y1 (K), y2 (I), y3 (S), y4 (N), y5 (L), y6 (E), y7 (S), y8 (L), y9 (N), y10 (S), y11 (I), y12 (S), y13* (E), y14* (A), y15* (G)

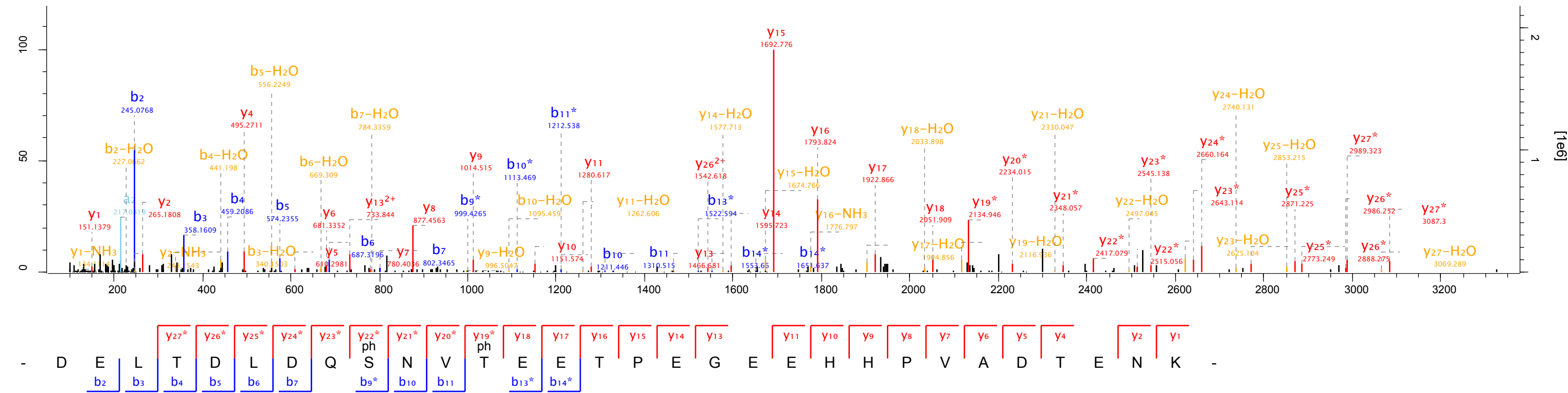
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 Scan: 11810 Method: FTMS; HCD Score: 288.69 m/z: 792.34 Gene names: MAP1B

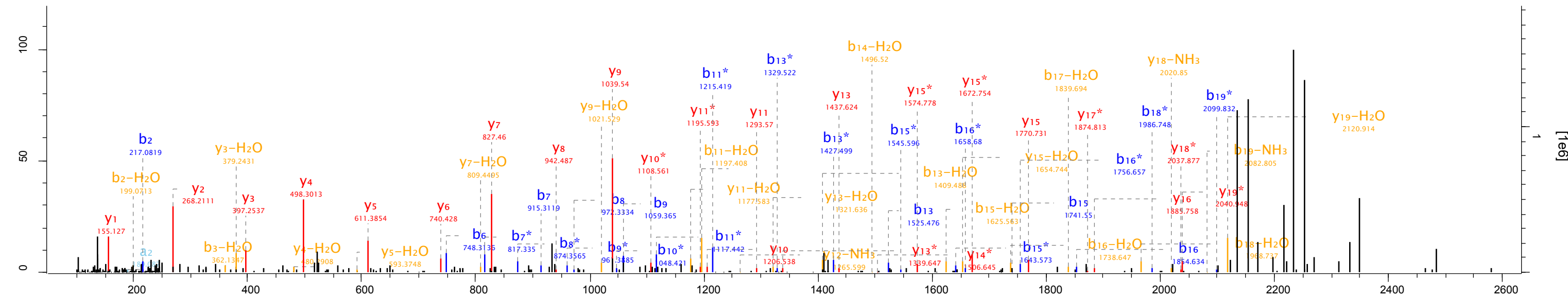


Raw file
 20171215_MaS_33SR_LMH_phospho2_03
 Scan 11820 Method FTMS; HCD Score 155.11 m/z 904.11 Gene names ARFGEF2



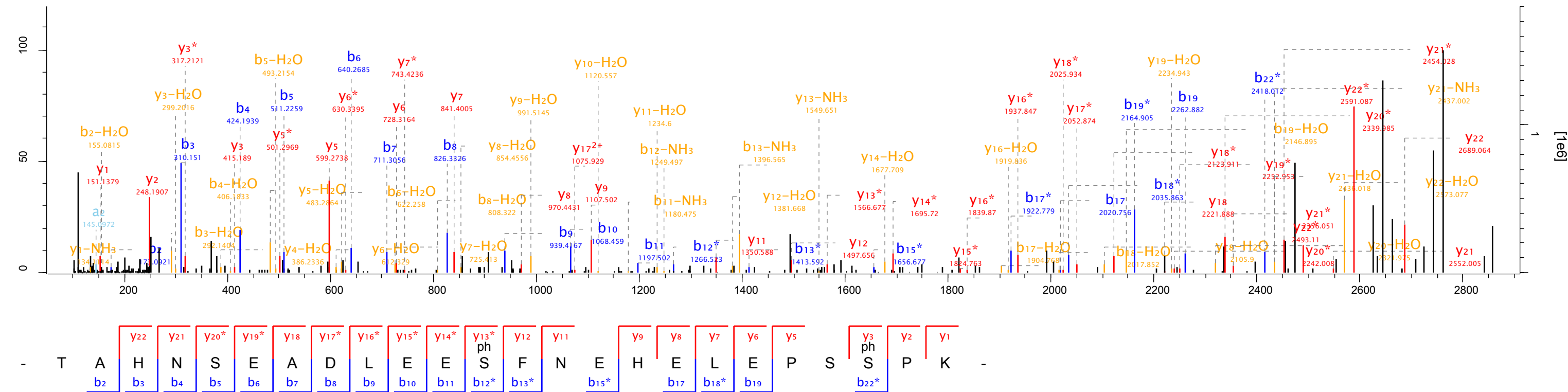
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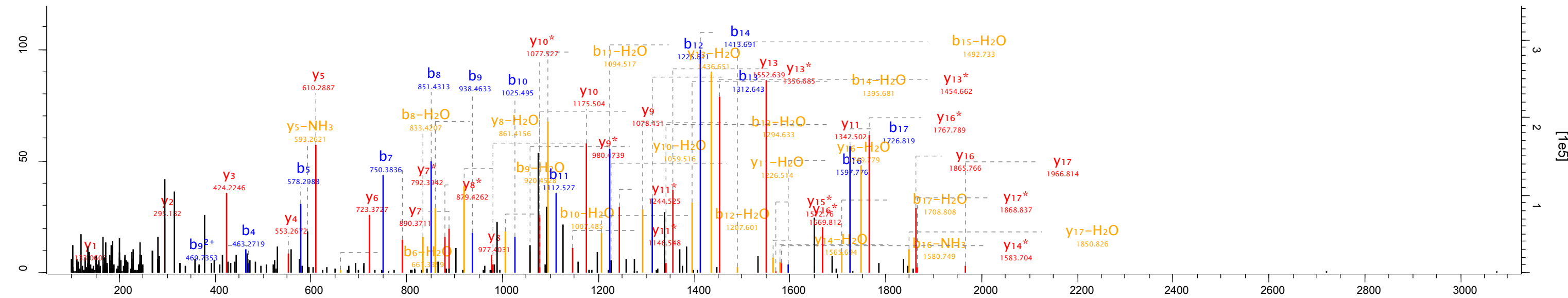


- D T Y S D R S G S S S P D S E I T E L K -
 b₂ b₆ b₇ b₈ b₉ b₁₀* b₁₁* b₁₃ b₁₅ b₁₆ b₁₈* b₁₉*

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 12310 Method: FTMS; HCD Score: 233.93 m/z: 954.72 Gene names: PHF6



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12470 Method FTMS; HCD Score 147.37 m/z 1093.82 Gene names GYS1

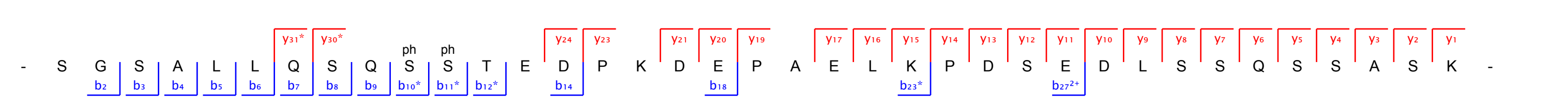
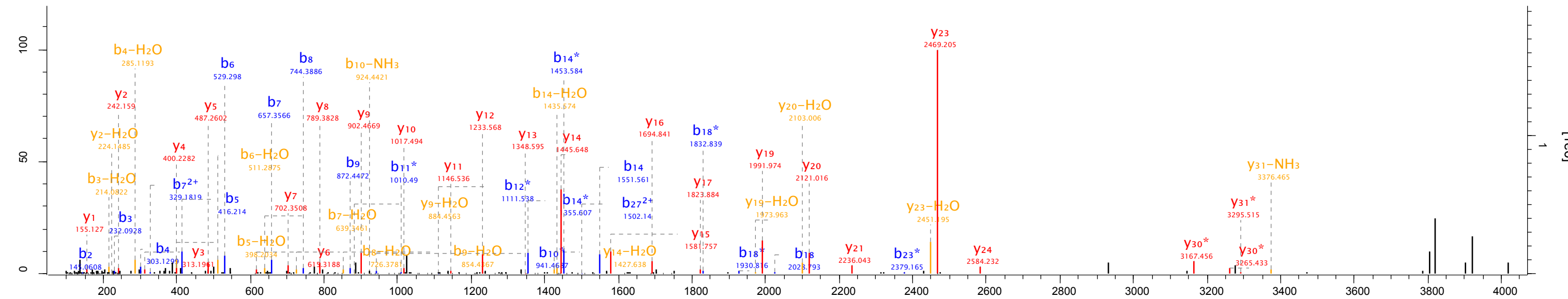


- R N S V D T A T S S S L S T P S E P L S P T S S L G E E R N -

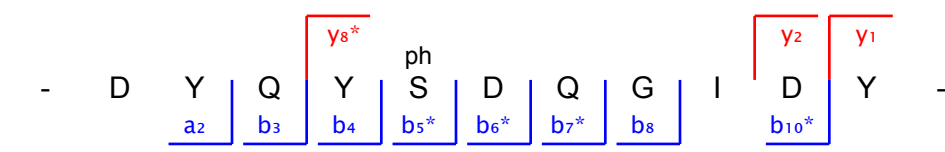
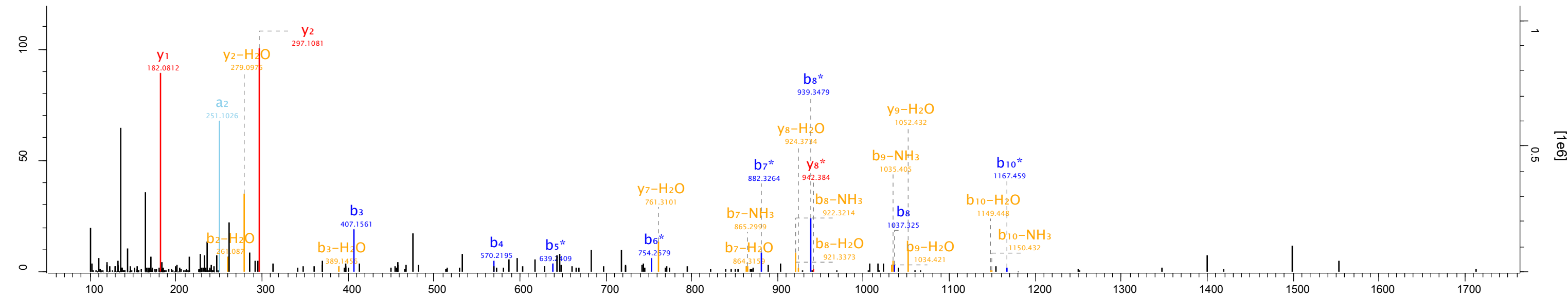
Fragmentation mapping below the sequence:

- Red boxes: y17, y16, y15*, y14*, y13, y11 ph, y10, y9, y8, y7 ph, y6, y5, y4, y3, y2, y1
- Blue boxes: b4, b5, b7, b8, b9, b10, b11, b12, b13, b14, b16, b17

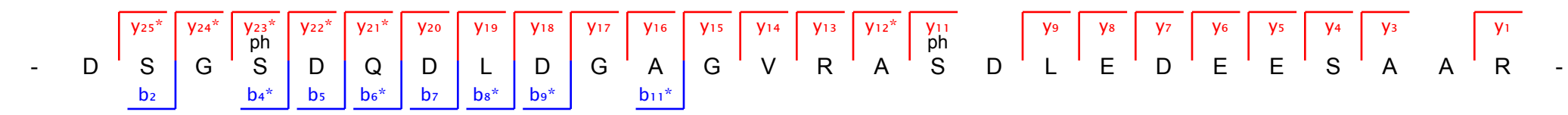
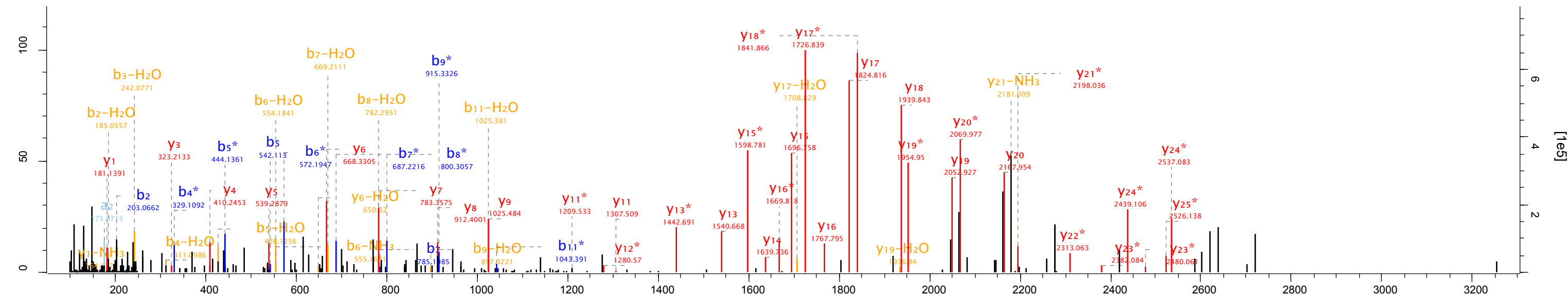
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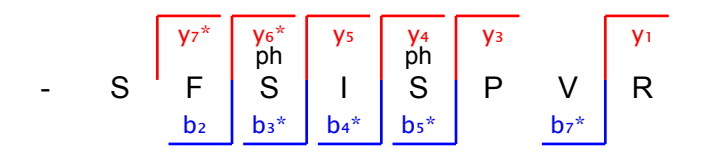
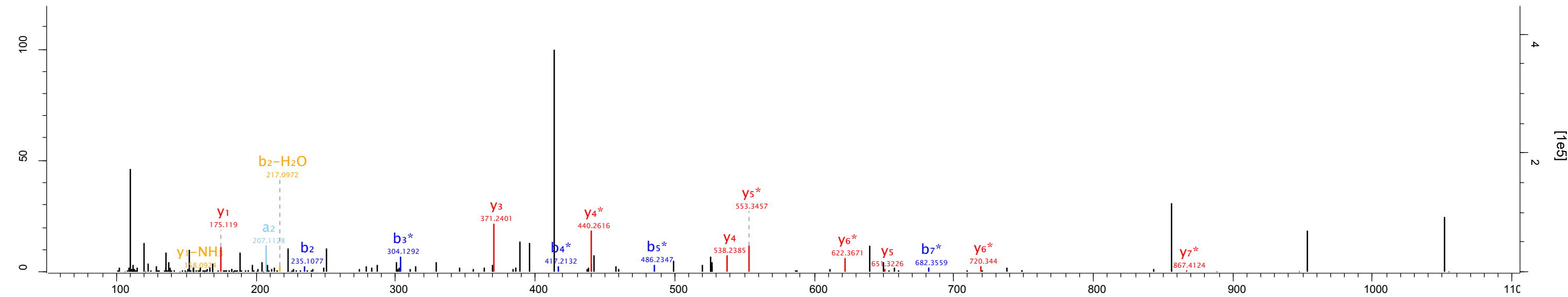
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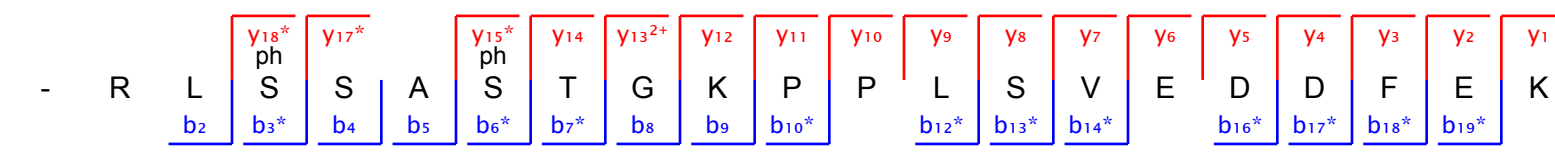
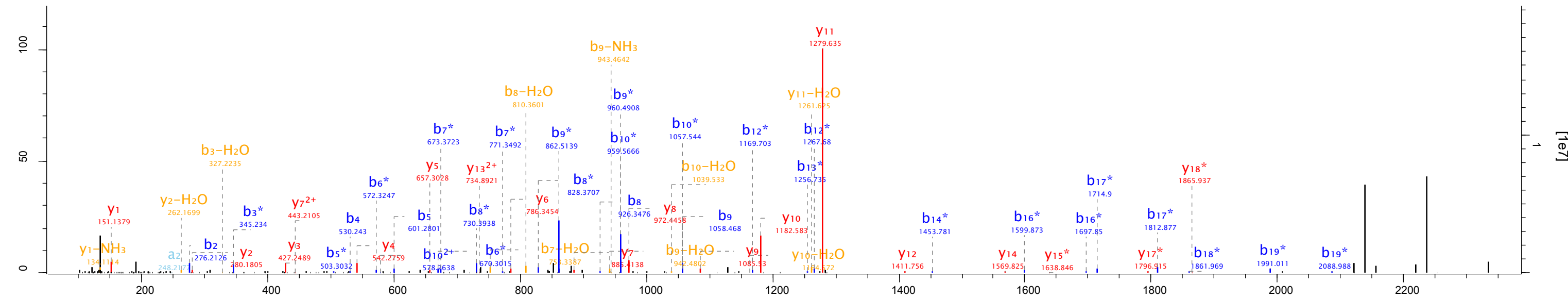
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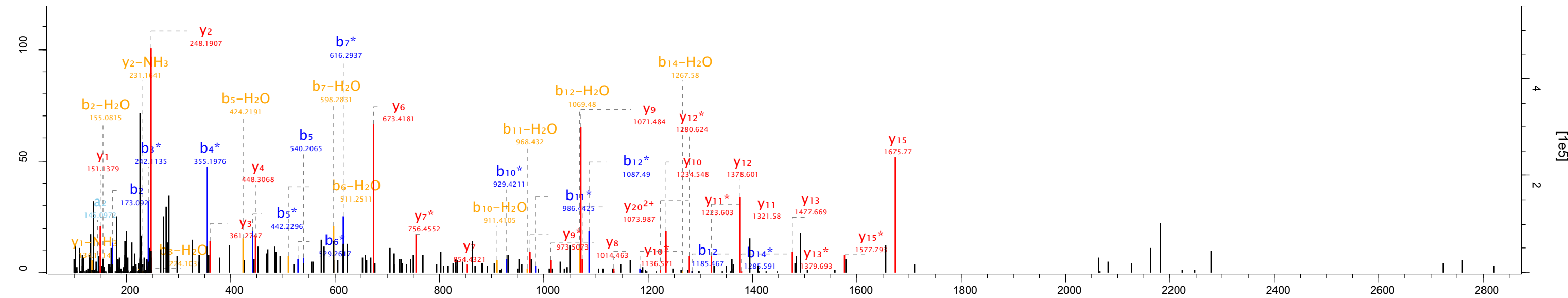


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13340 Method FTMS; HCD Score 55.26 m/z 526.71 Gene names SON



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13420 Method FTMS; HCD Score 209.46 m/z 780.04 Gene names ZC3H11A





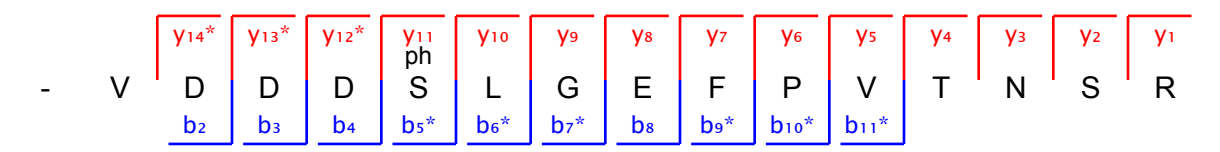
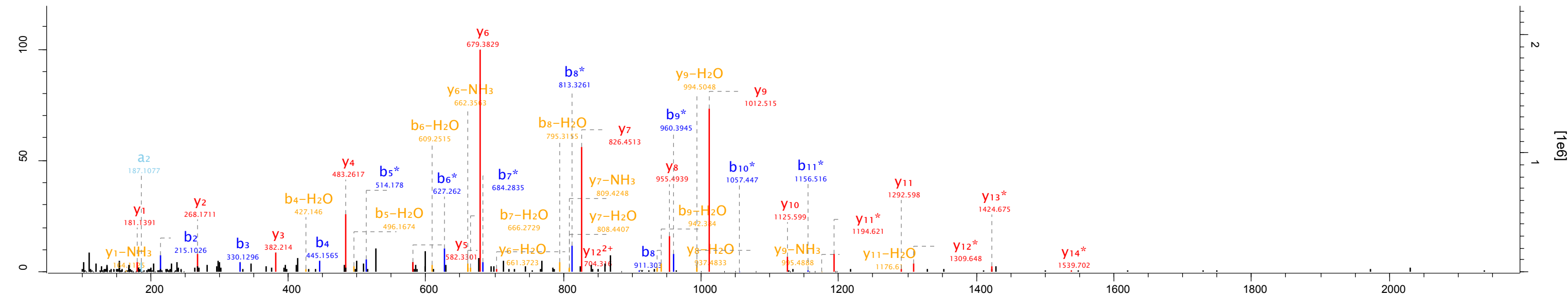
- T A S I S S S P S E G T P T V G S Y G C T P Q S L P K -

ph

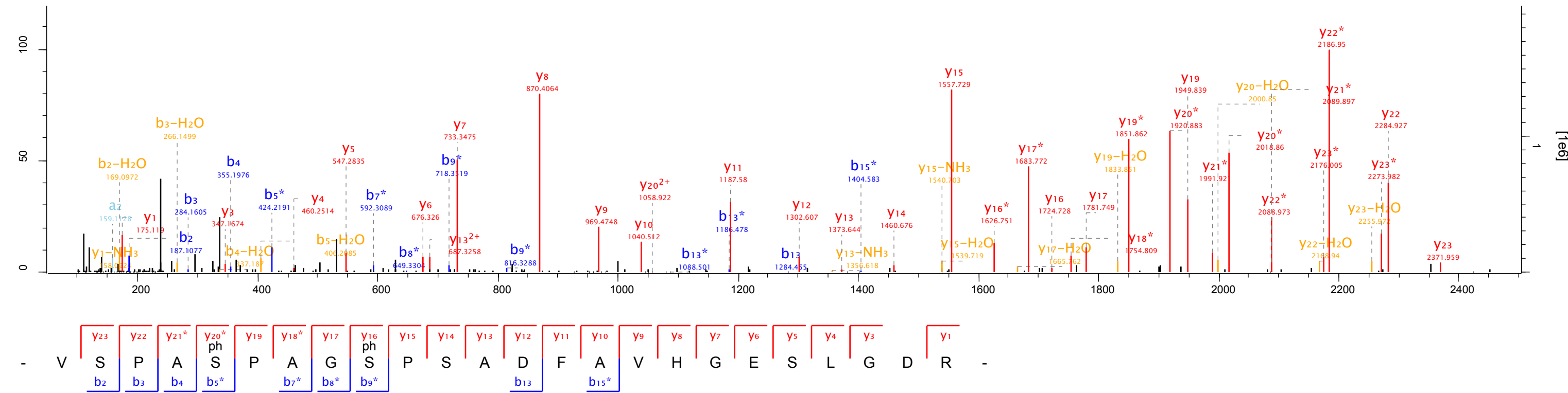
b₂ b₃^{*} b₄^{*} b₅ b₆^{*} b₇^{*} y₂₀²⁺ y₁₅ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₄ y₃ y₂ y₁

ph

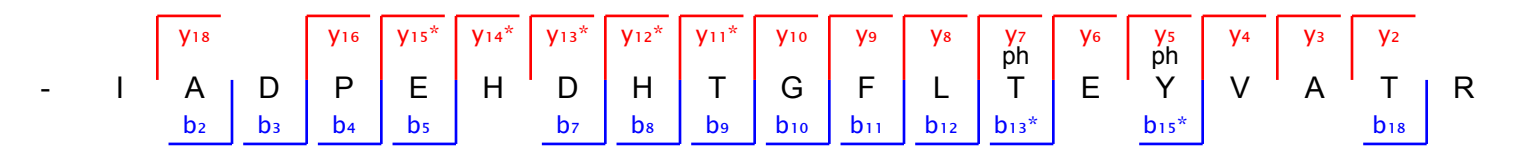
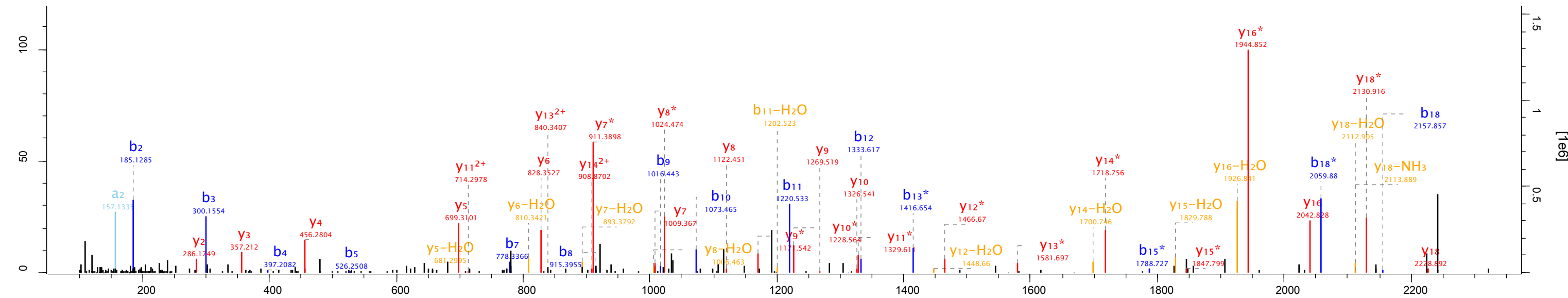
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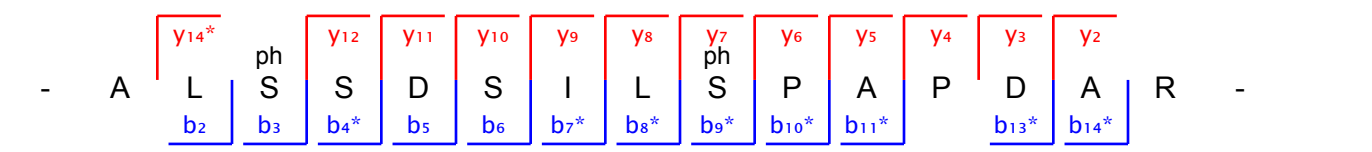
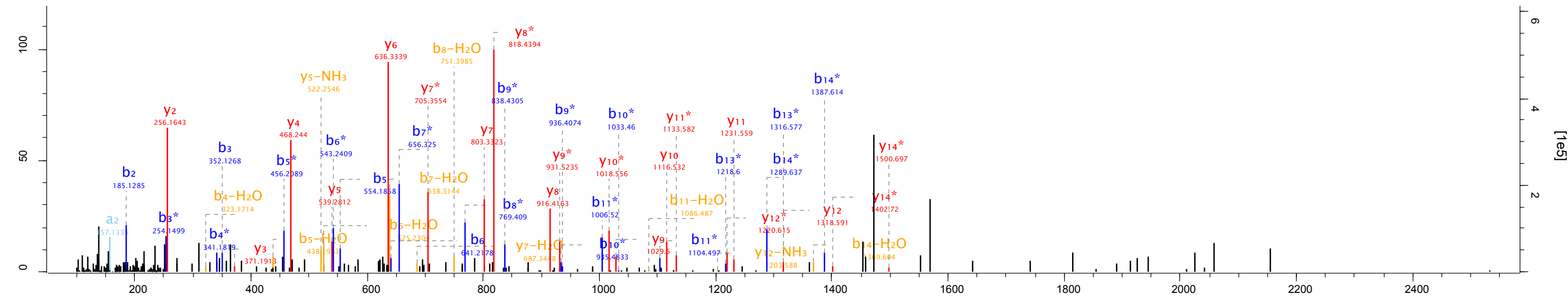
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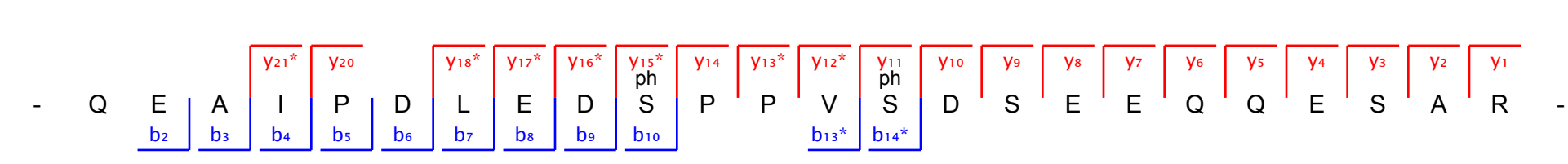
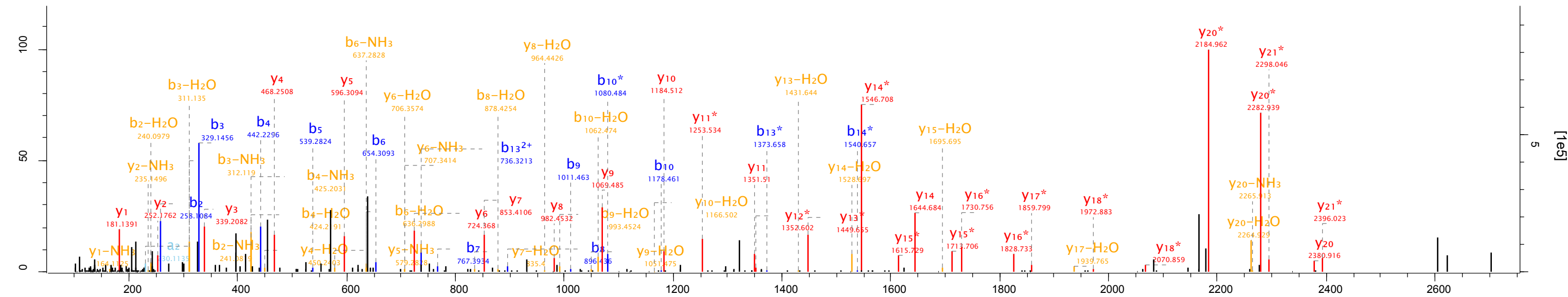
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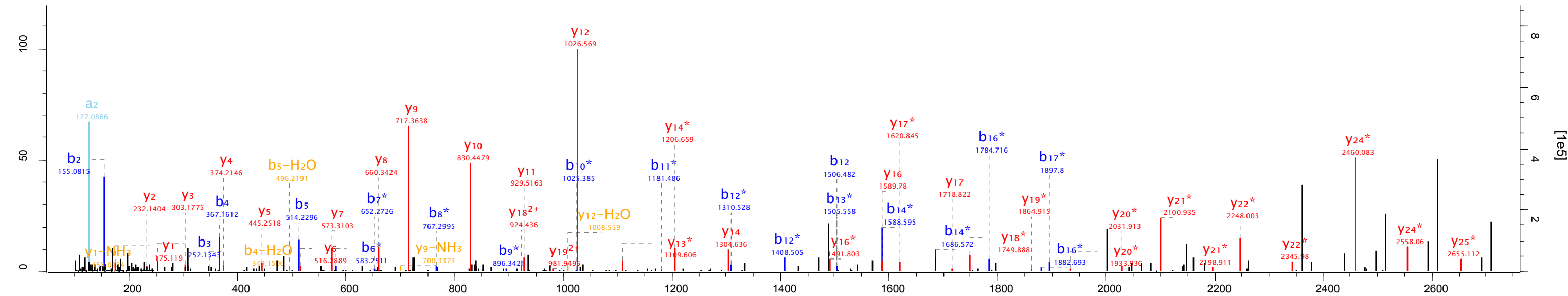


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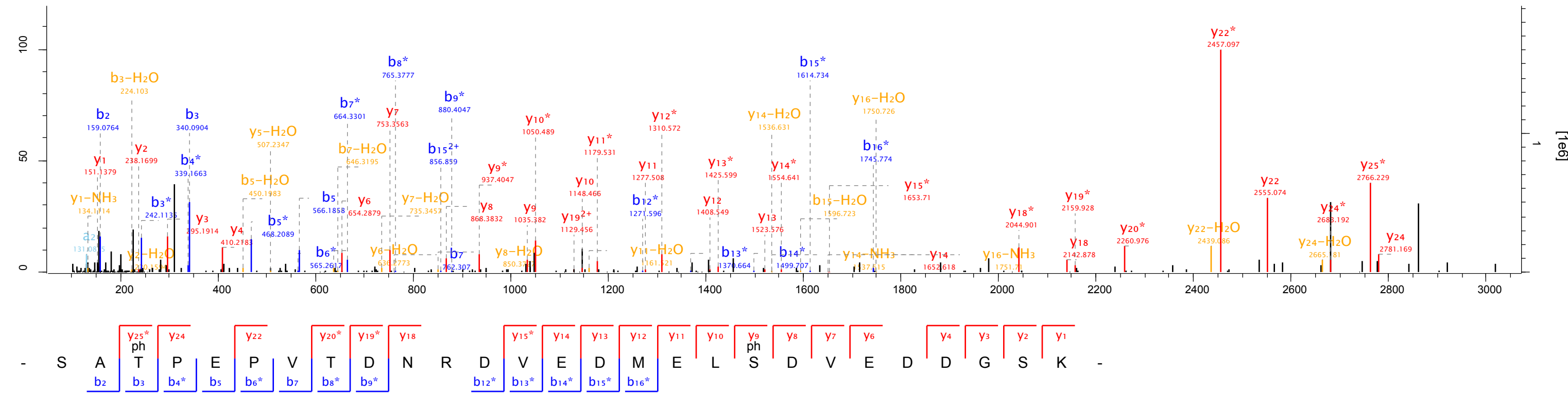
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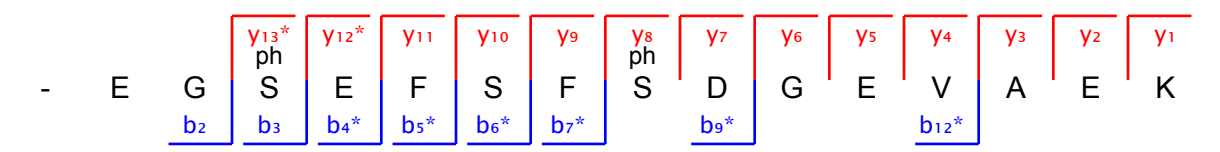
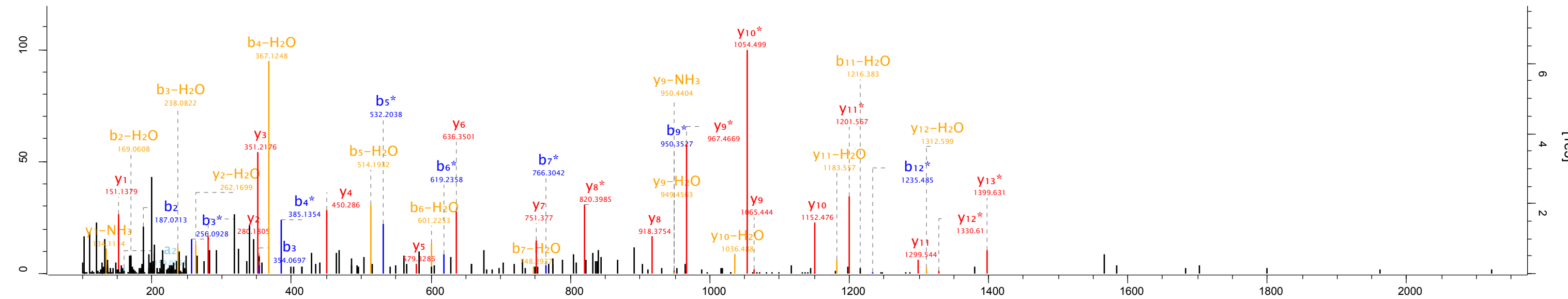


- G P P D F S S D E E R E P T P V L G S G A A A A G R -
 b₂ b₃ b₄ b₅ b₆^{*} b₇^{*} b₈^{*} b₉^{*} b₁₀^{*} b₁₁^{*} b₁₂ b₁₃^{*} b₁₄^{*} b₁₆^{*} b₁₇^{*}
 y₂₅^{*} y₂₄^{*} y₂₂^{*} y₂₁^{*} y₂₀^{*} y₁₉^{*} y₁₈^{*} y₁₇ y₁₆ y₁₄ y₁₃^{*} y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

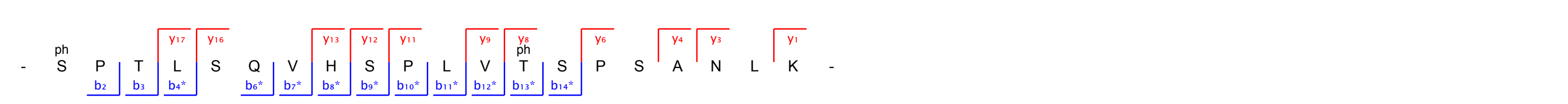
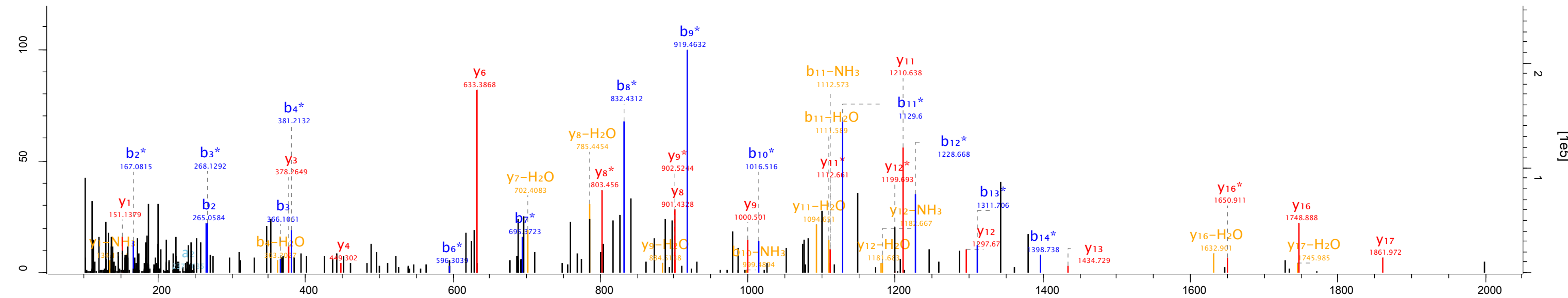
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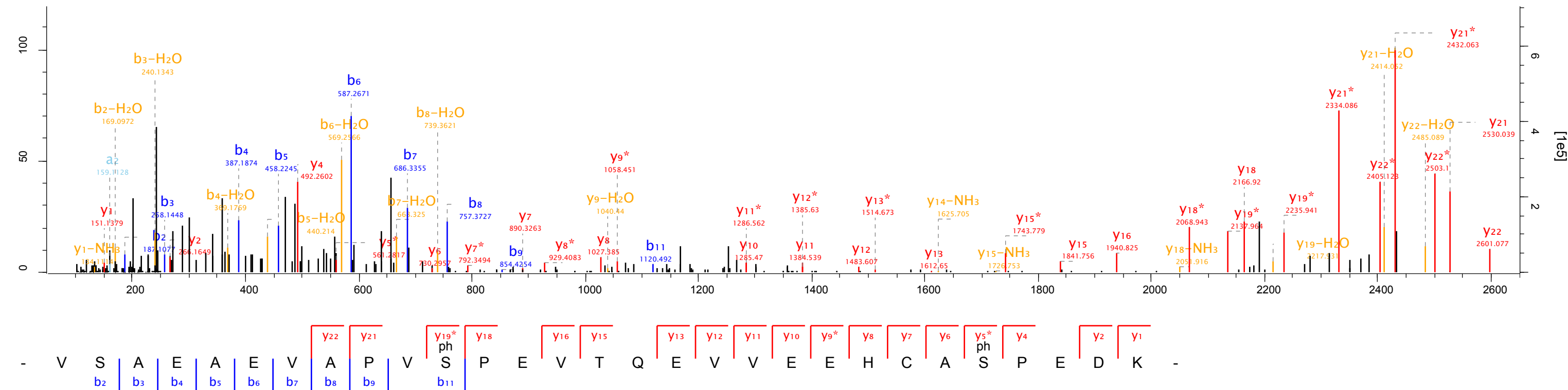
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 Scan: 14830 Method: FTMS; HCD Score: 125.23 m/z: 891.33 Gene names: RIOK2



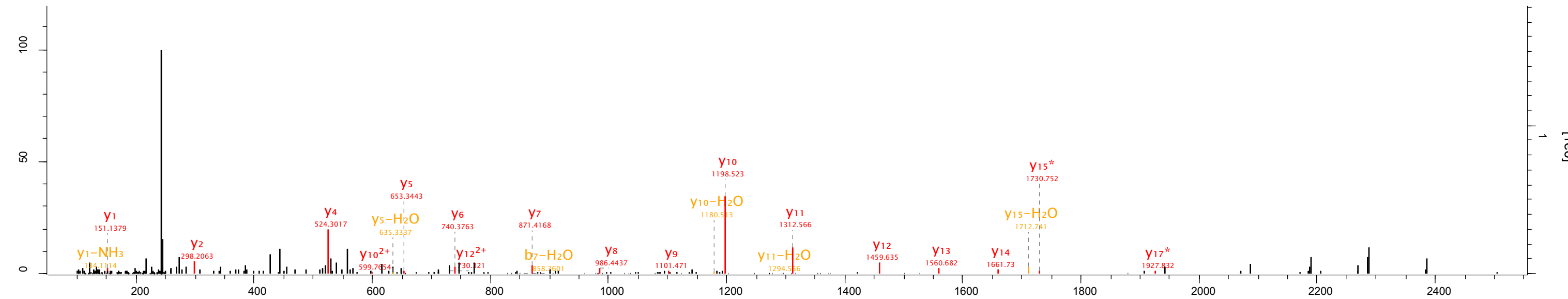
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Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 15270 Method: FTMS; HCD Score: 156.18 m/z: 1096.8 Gene names: MAP1B

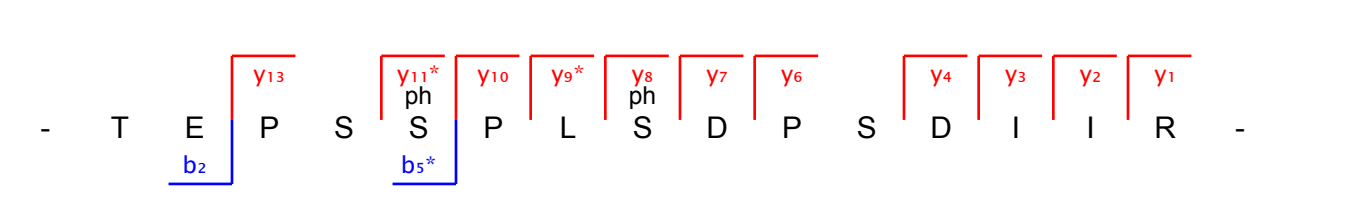
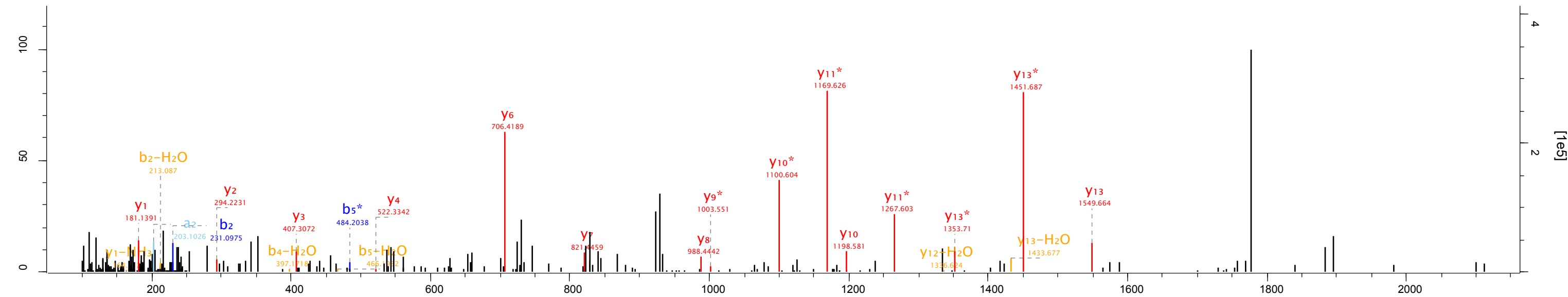


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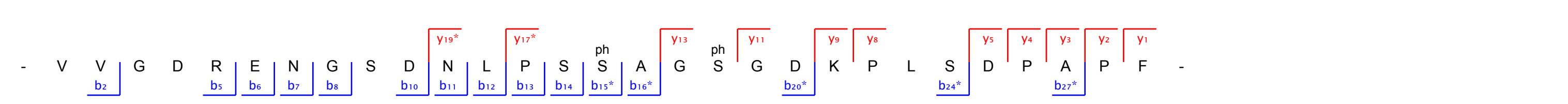
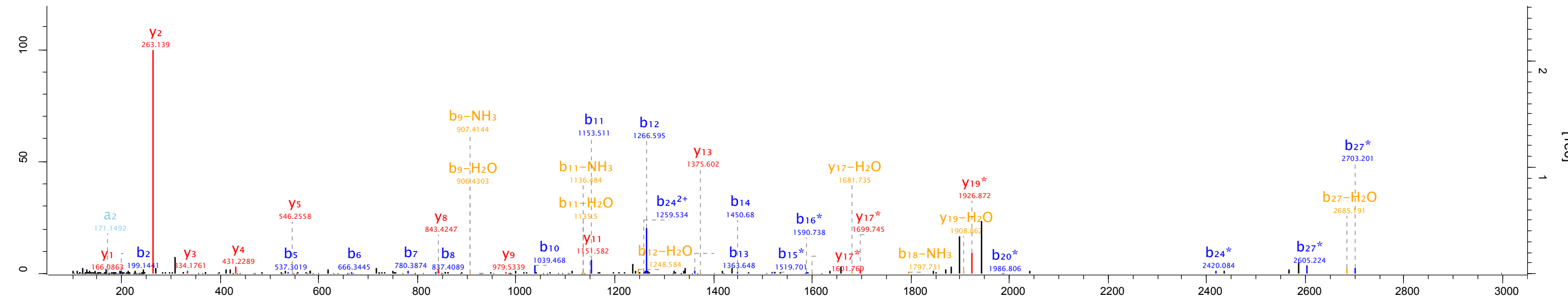


- R y17*
ph S Q y15*
ph T y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 E y2 y1 -

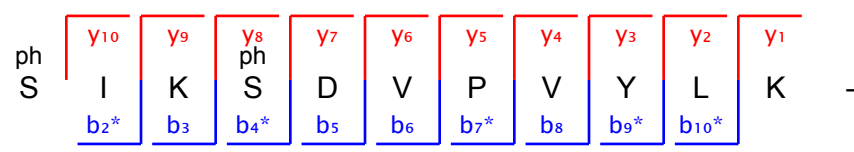
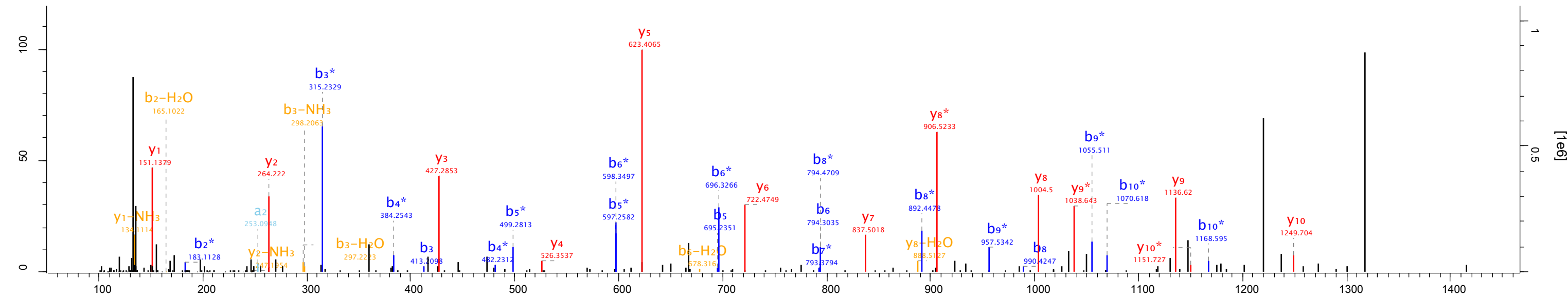
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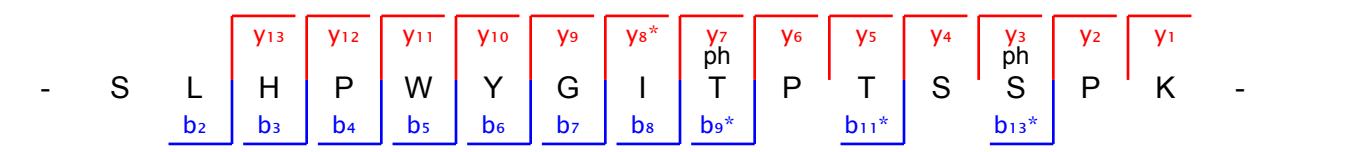
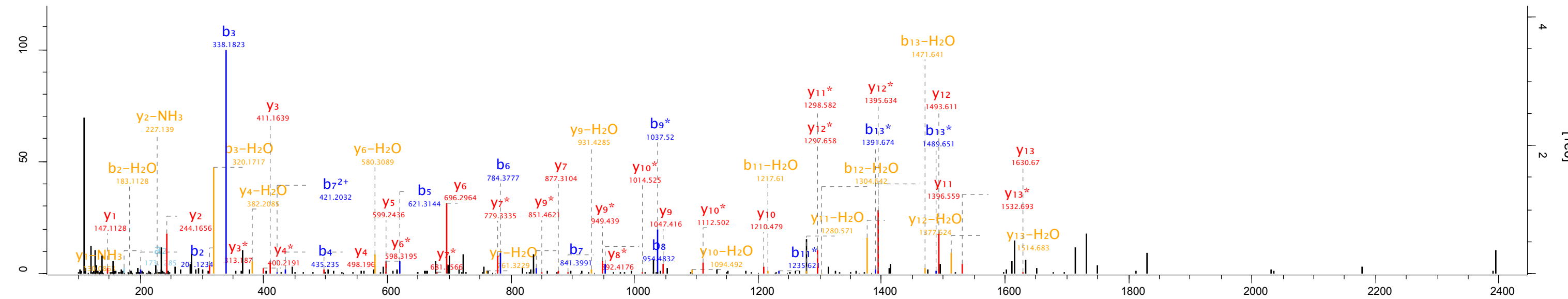
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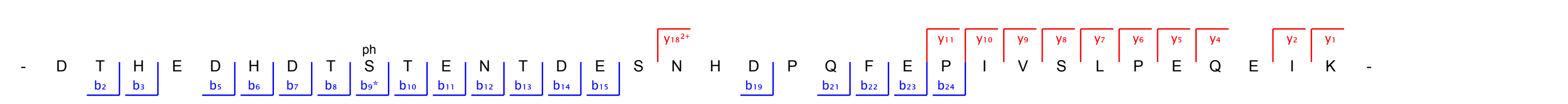
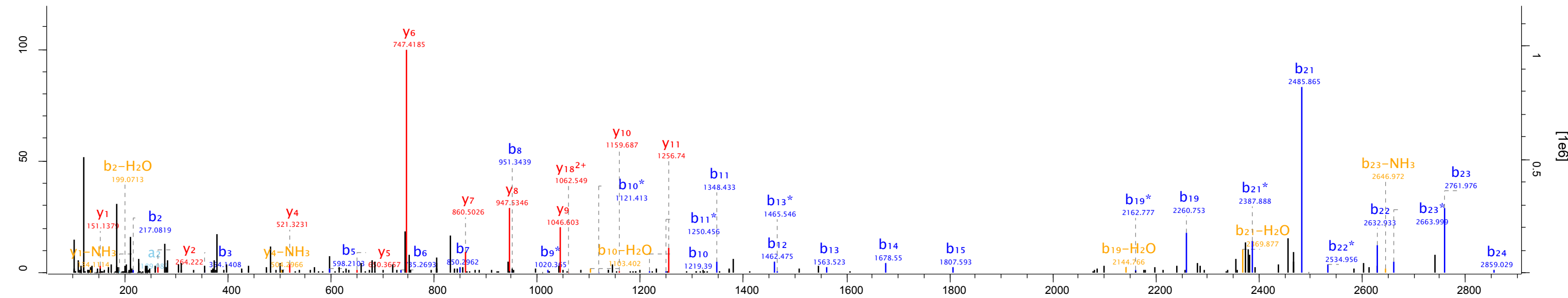
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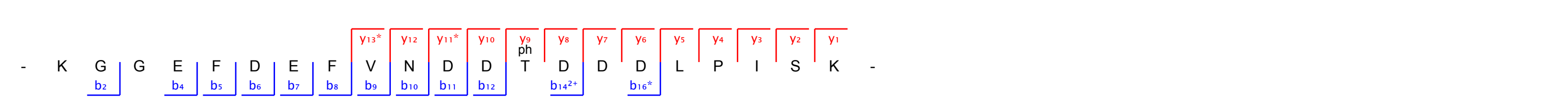
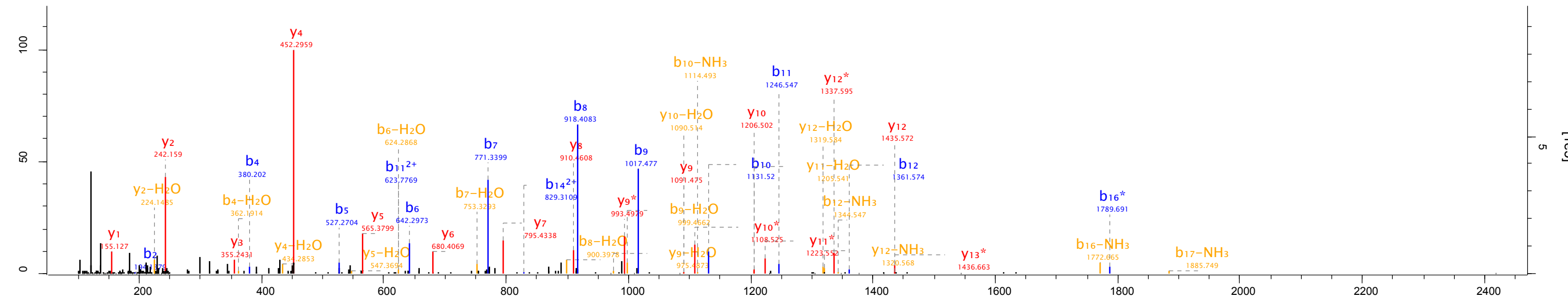
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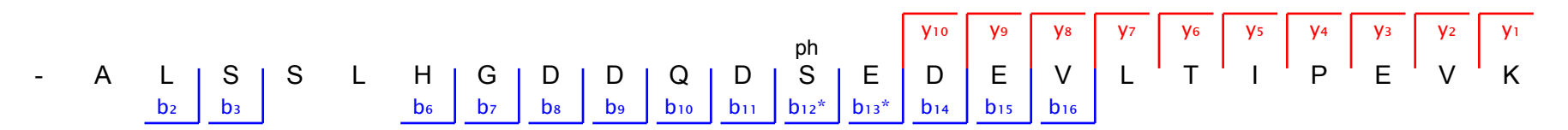
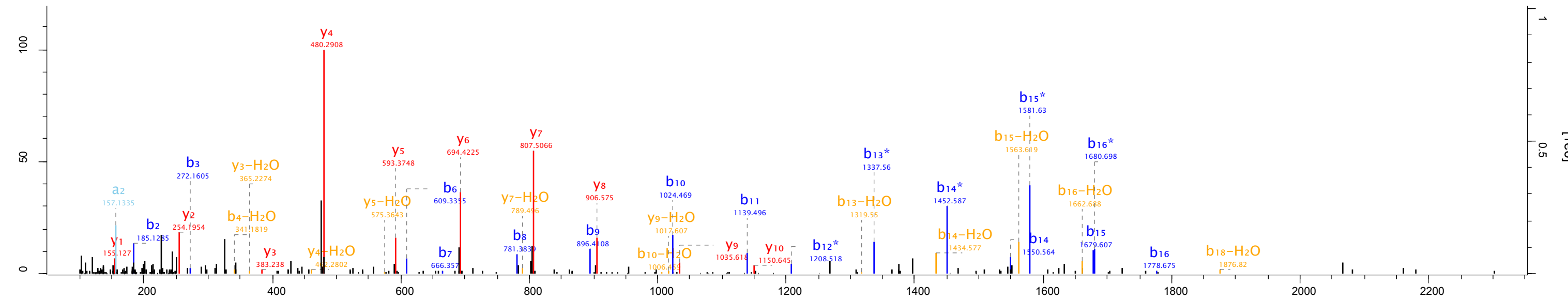


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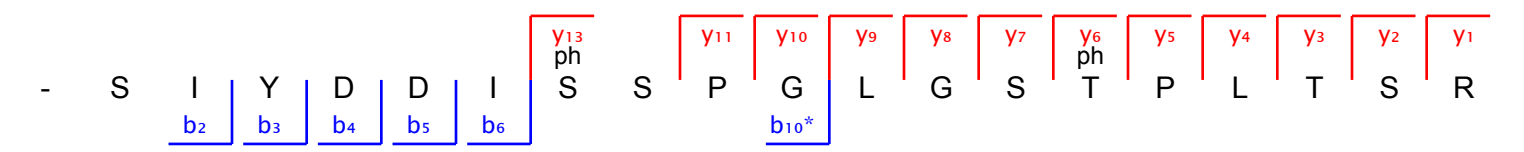
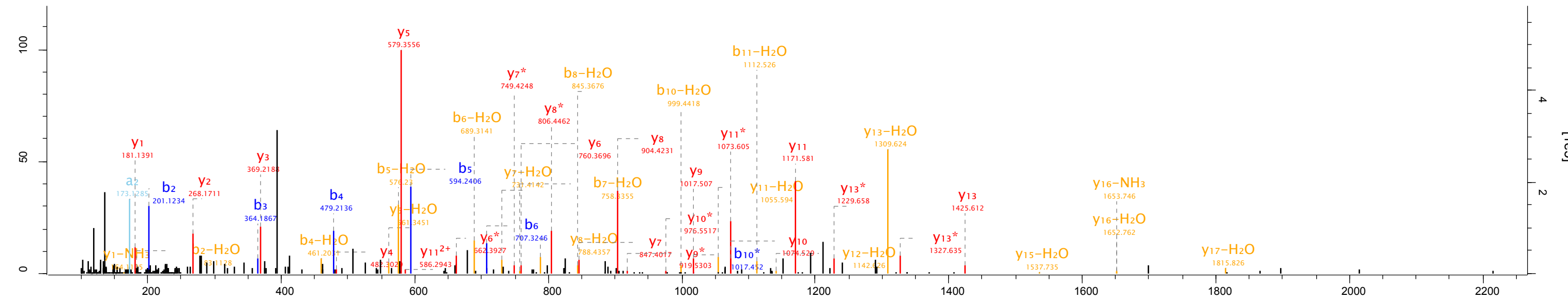
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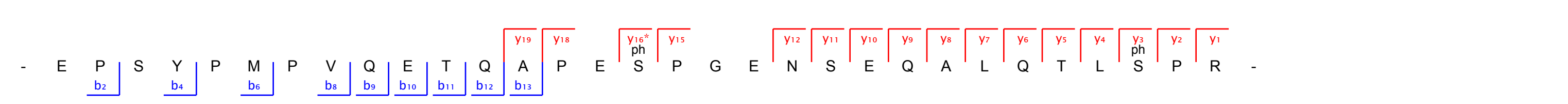
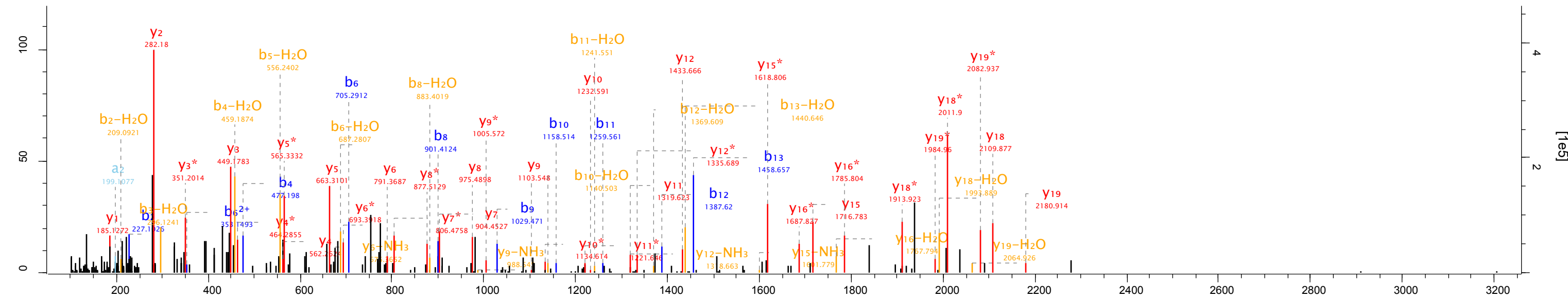


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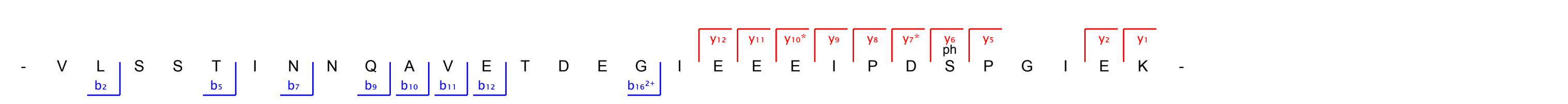
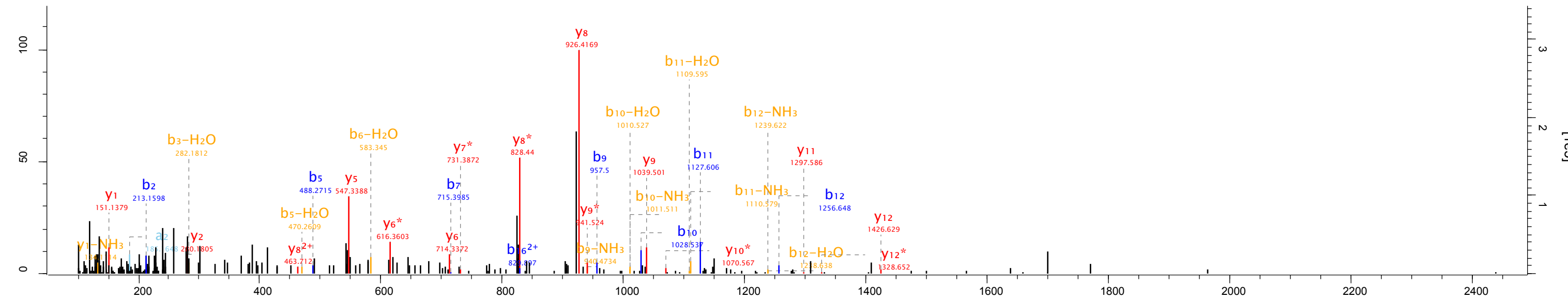
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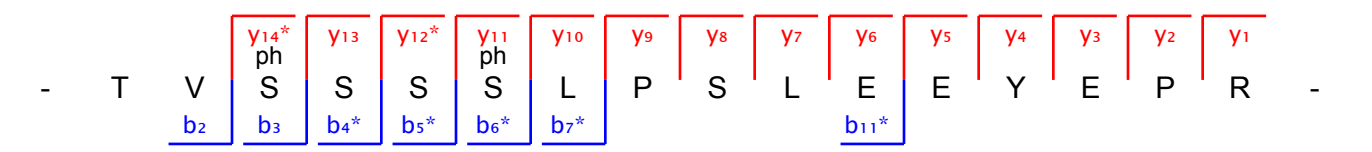
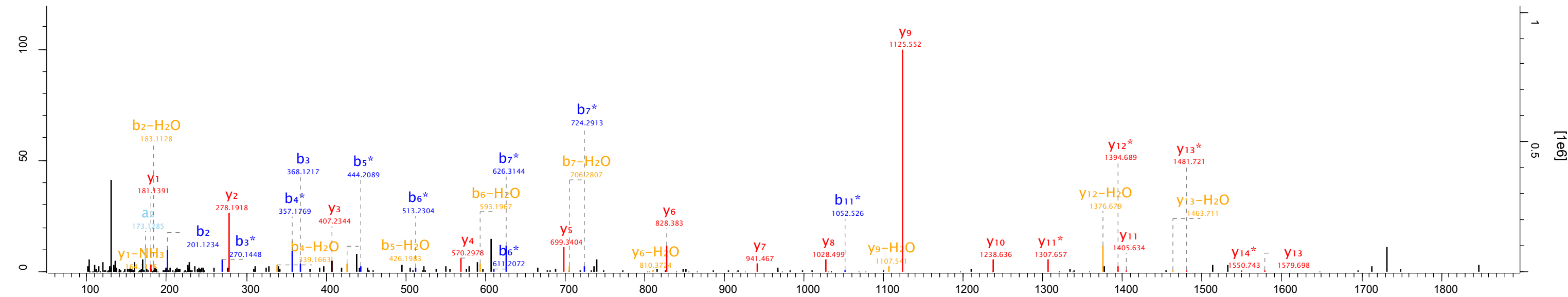
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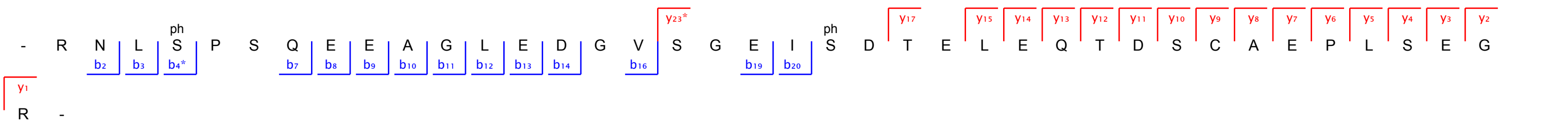
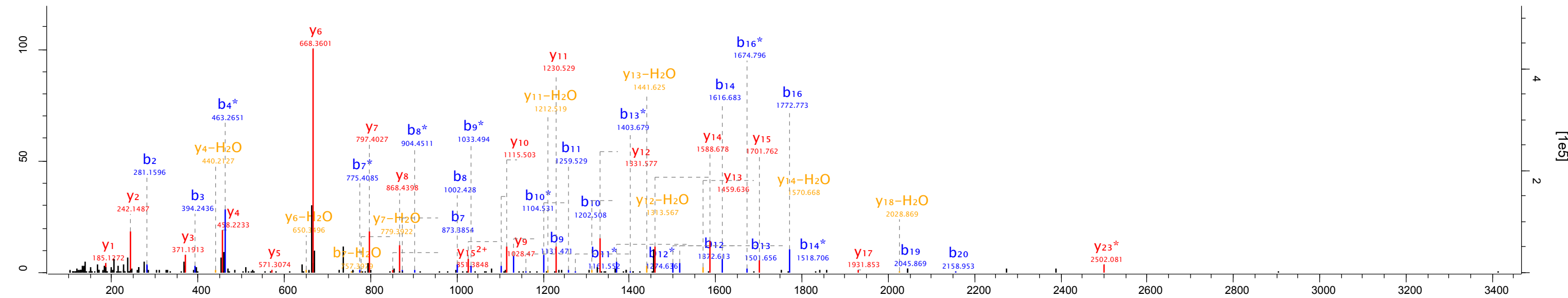
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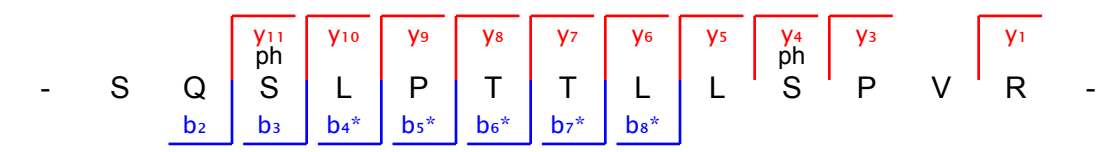
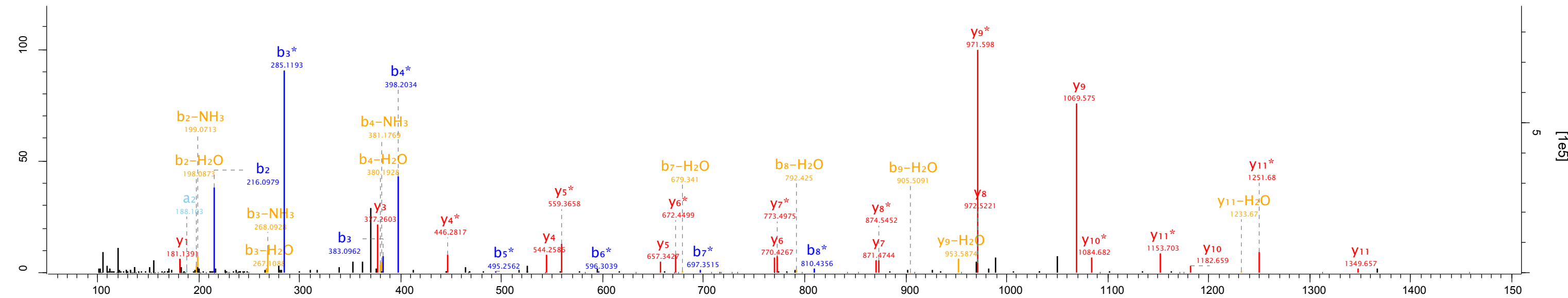
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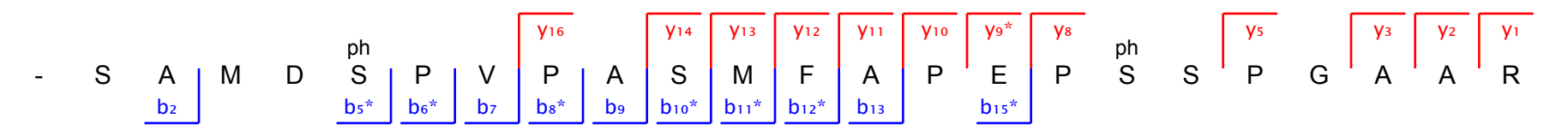
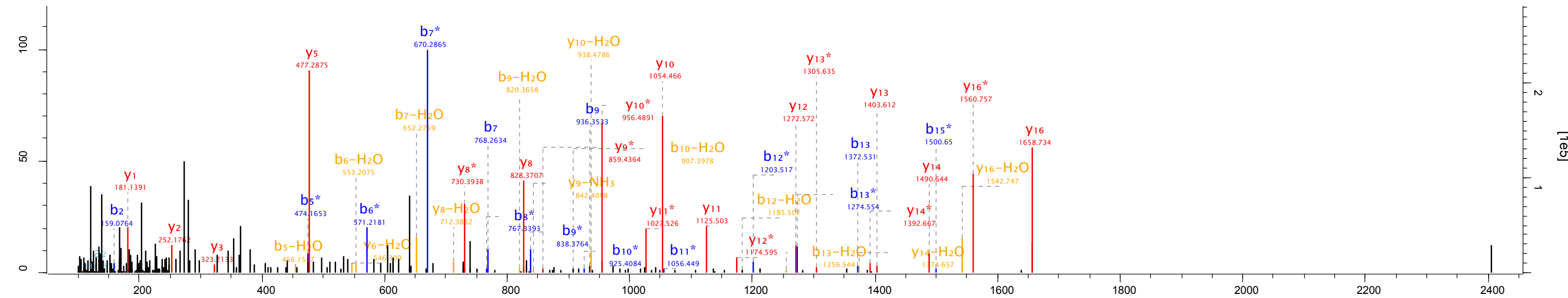
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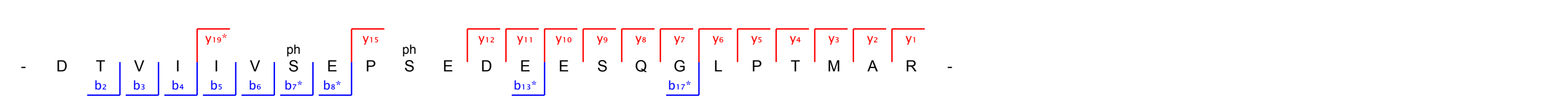
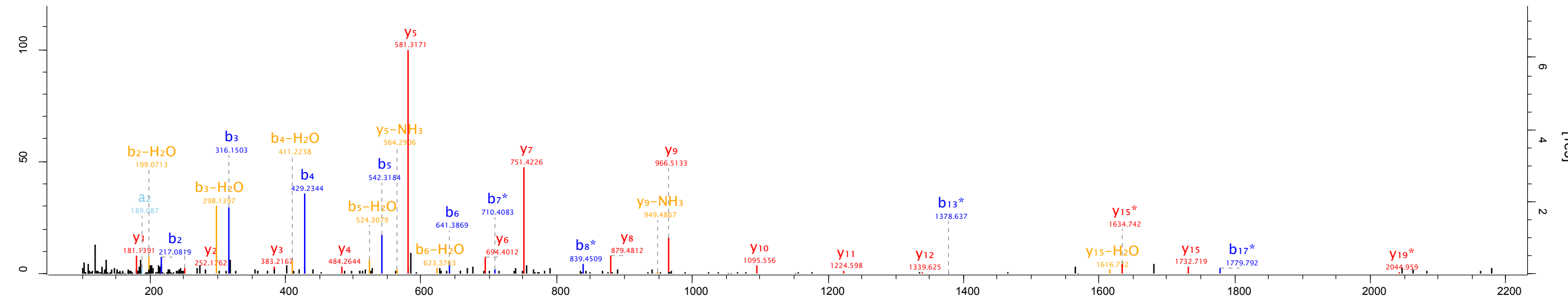
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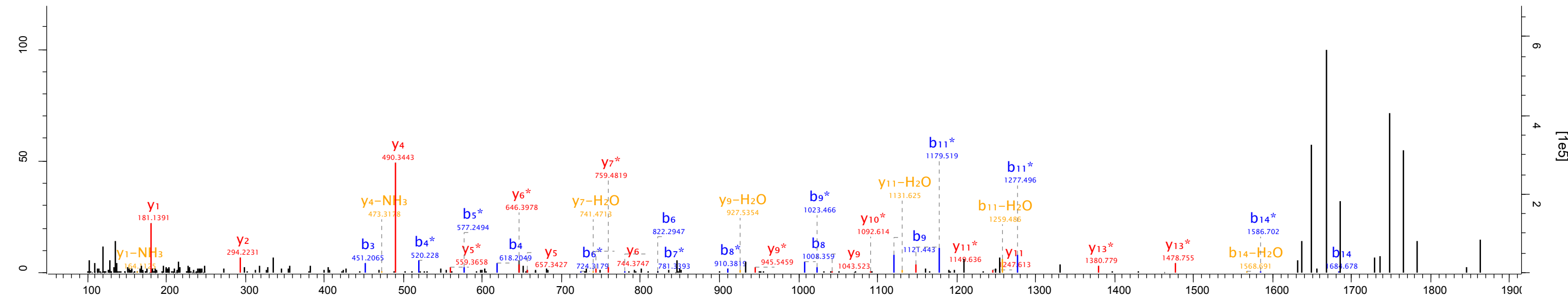
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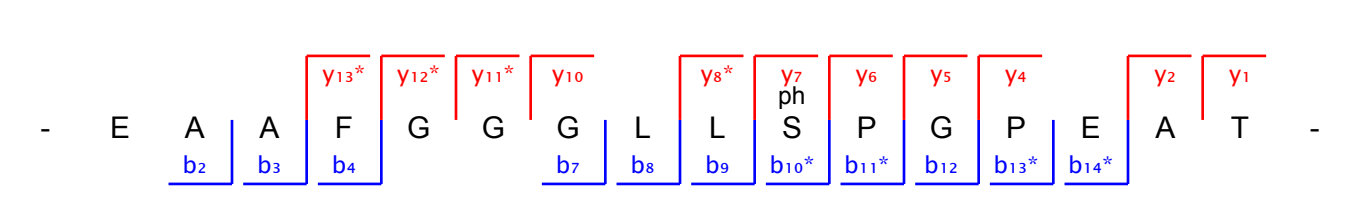
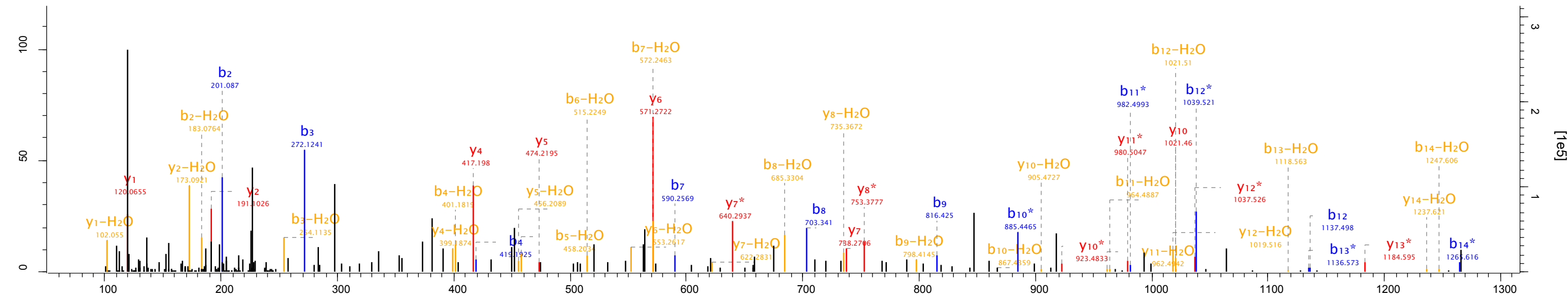


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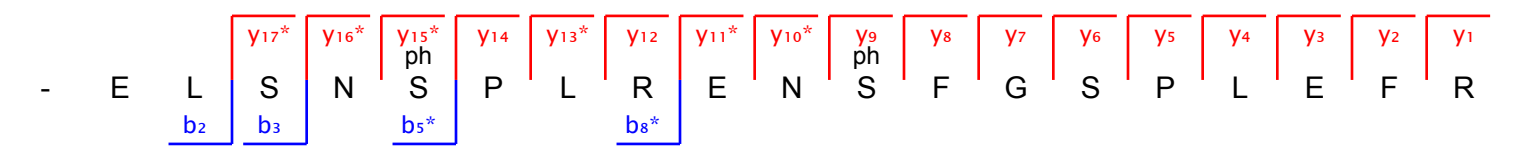
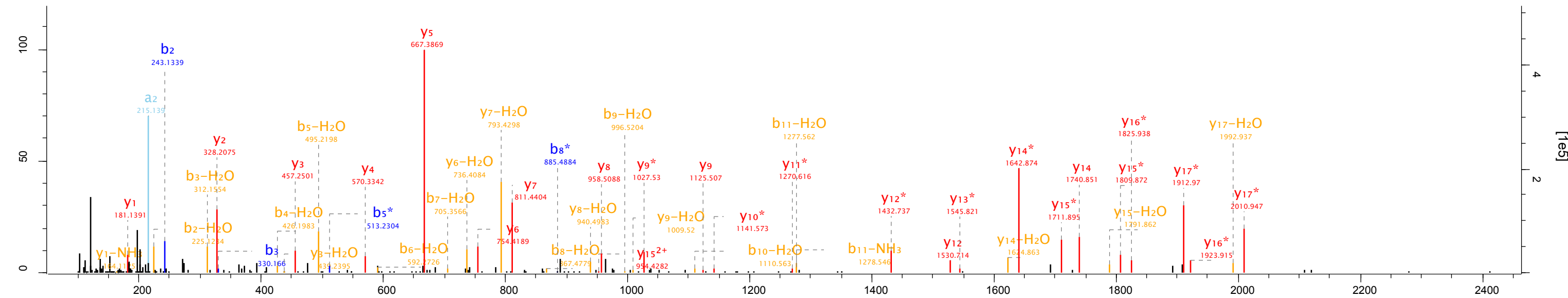
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- b4: S
- b5*: G
- b6: F
- b7*: G
- b8: E
- b9: I
- b11*: S
- b14: V
- y1: R
- y2: I
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- y7*: I
- y9: G
- y10*: F
- y11: G
- y13*: G

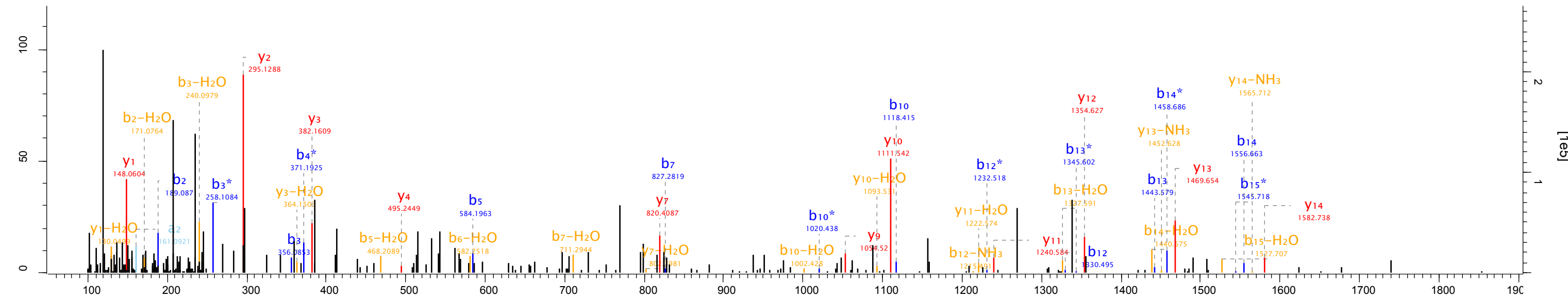
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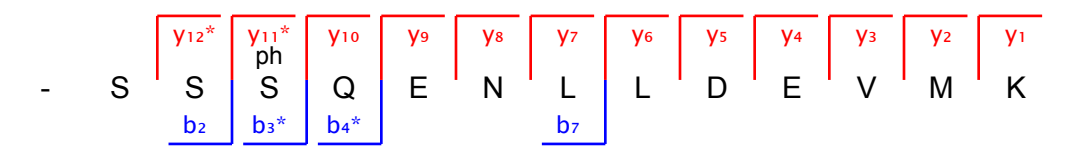
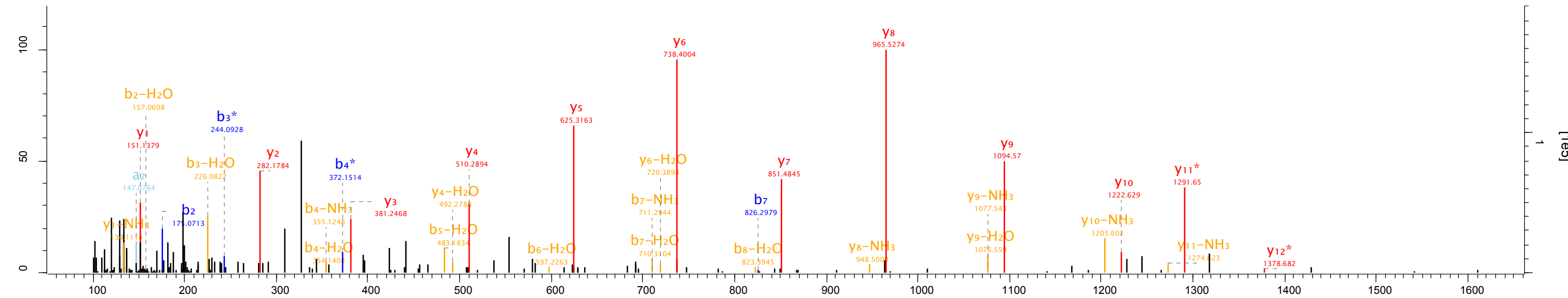
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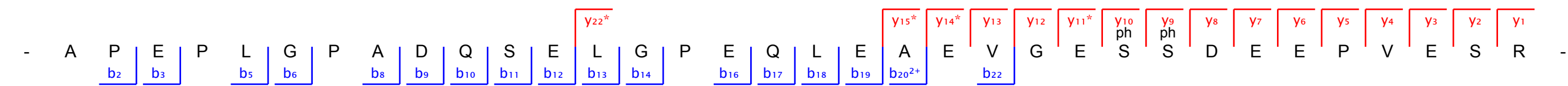
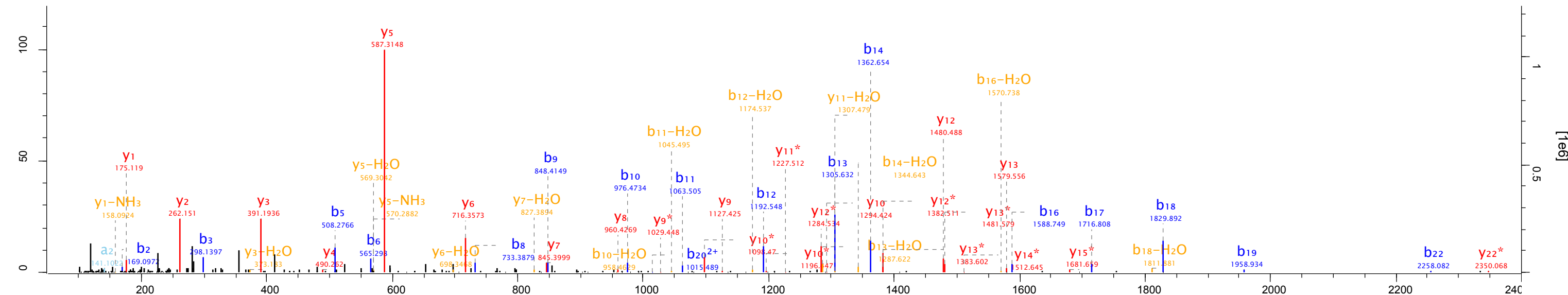
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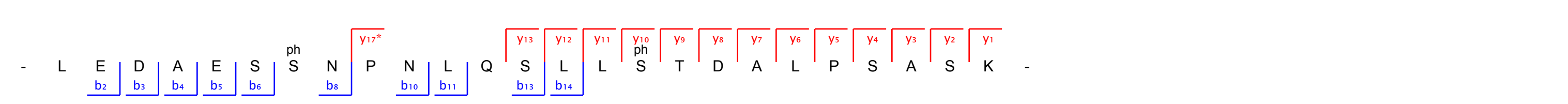
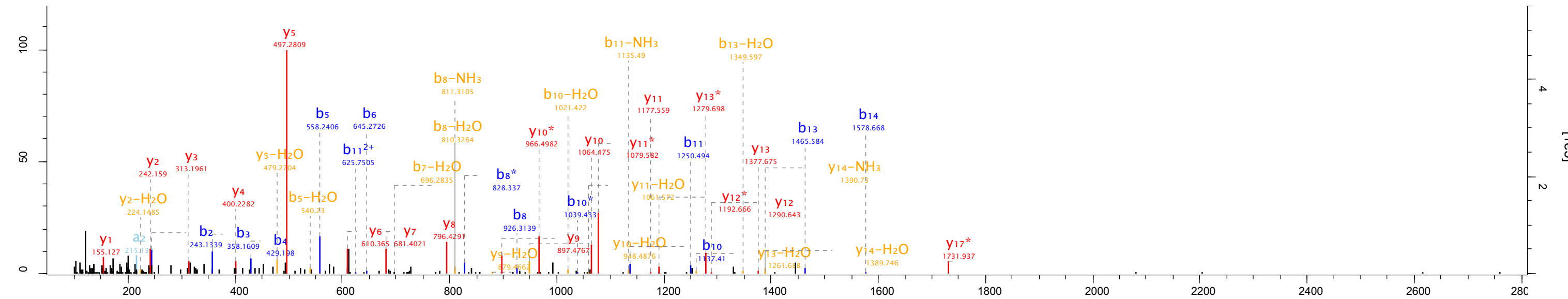
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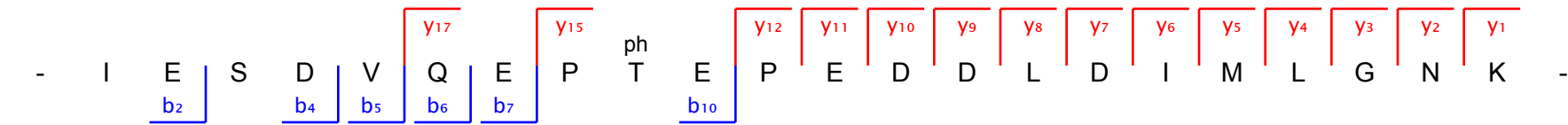
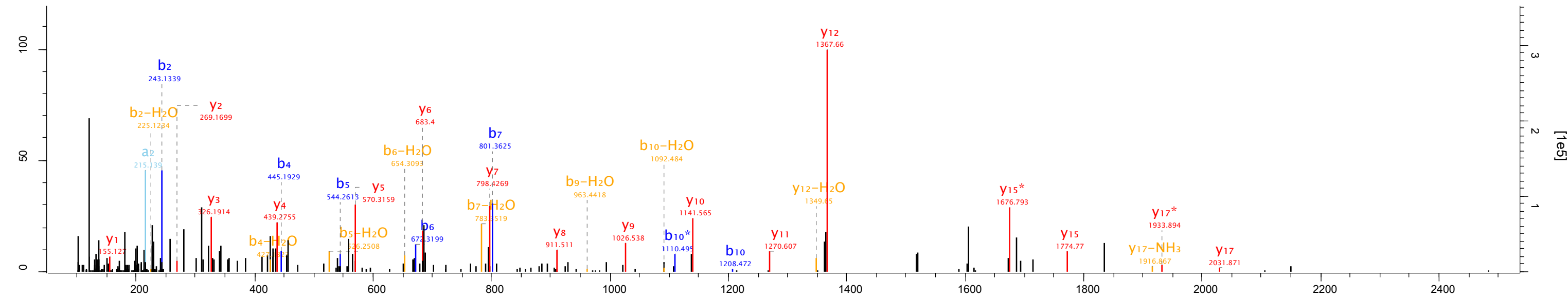


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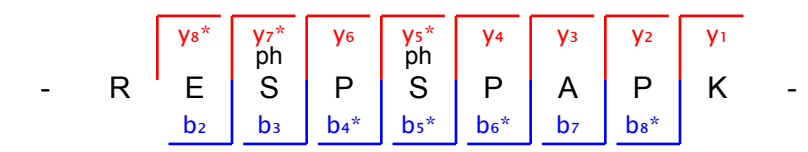
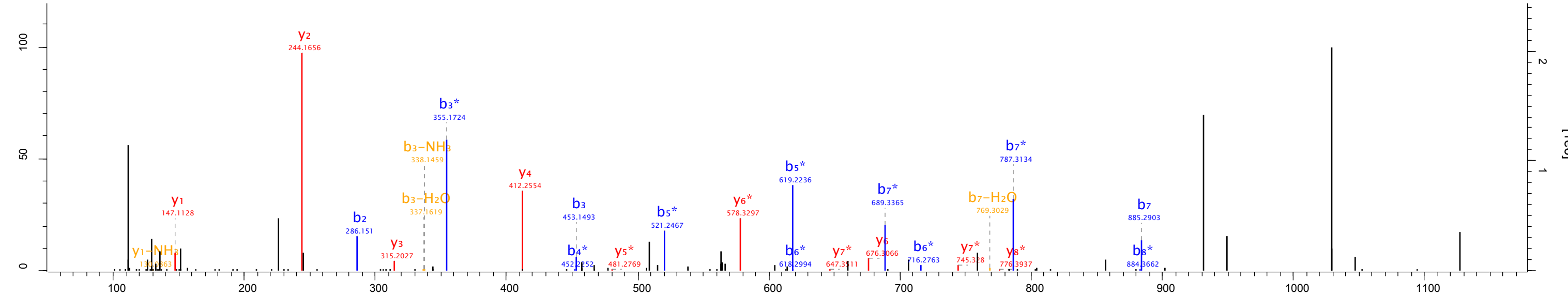


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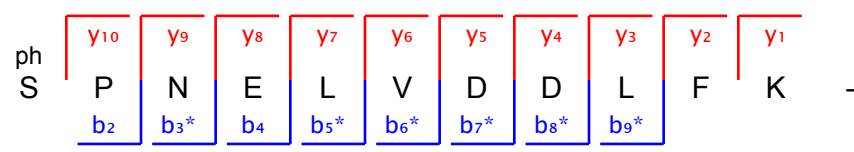
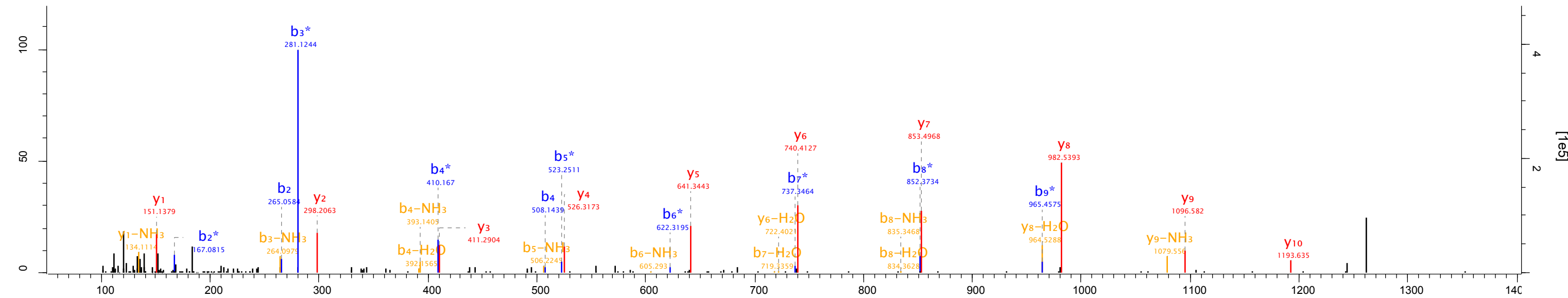




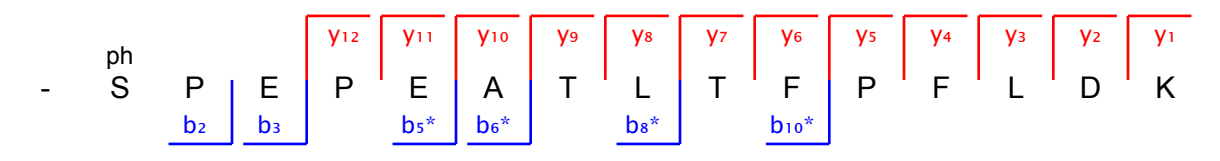
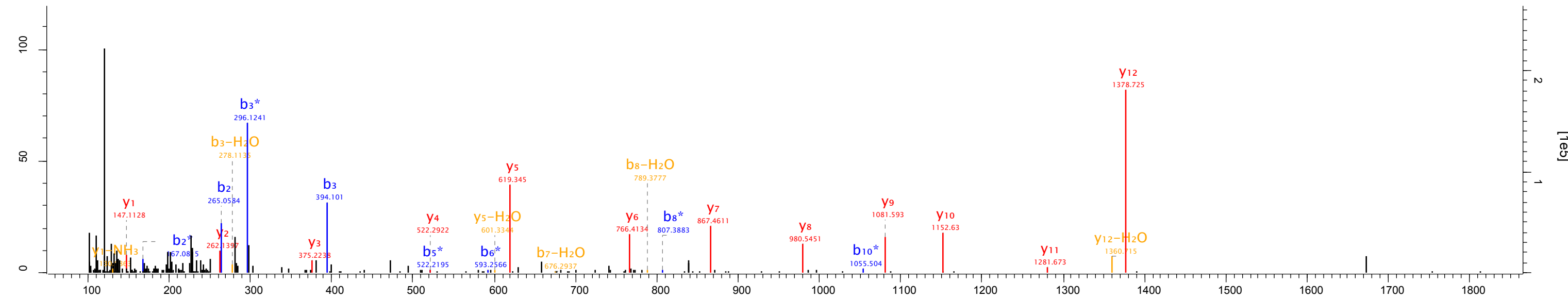
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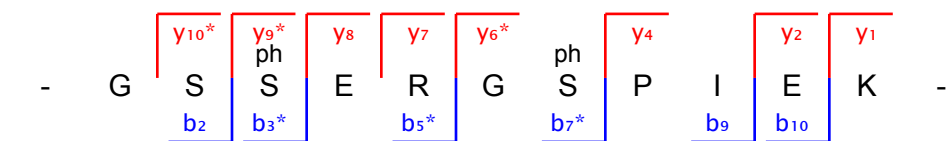
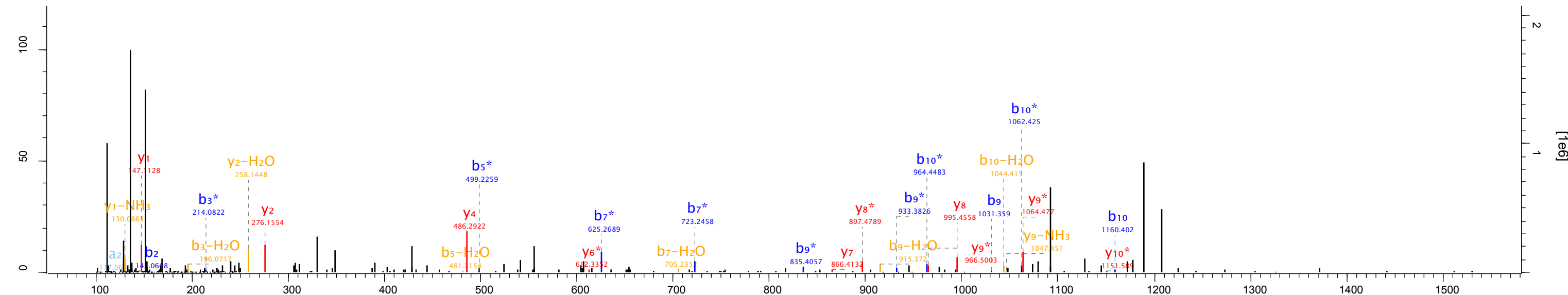


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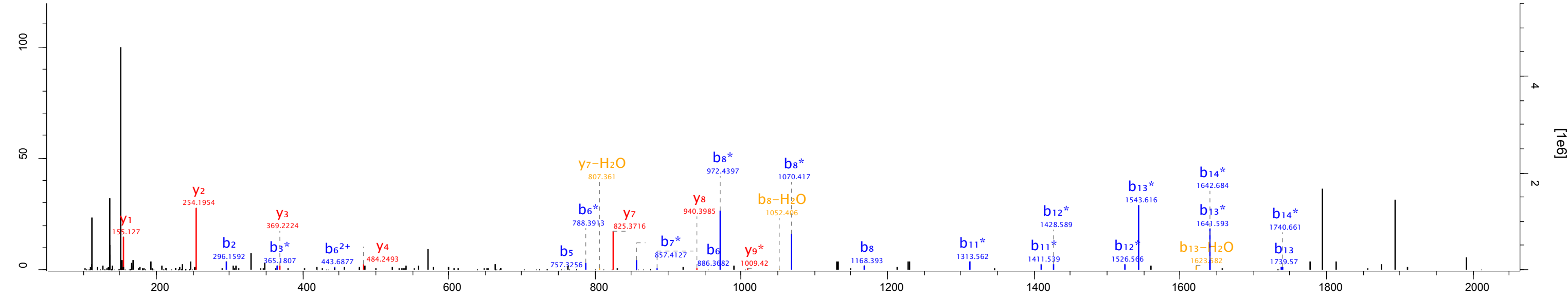
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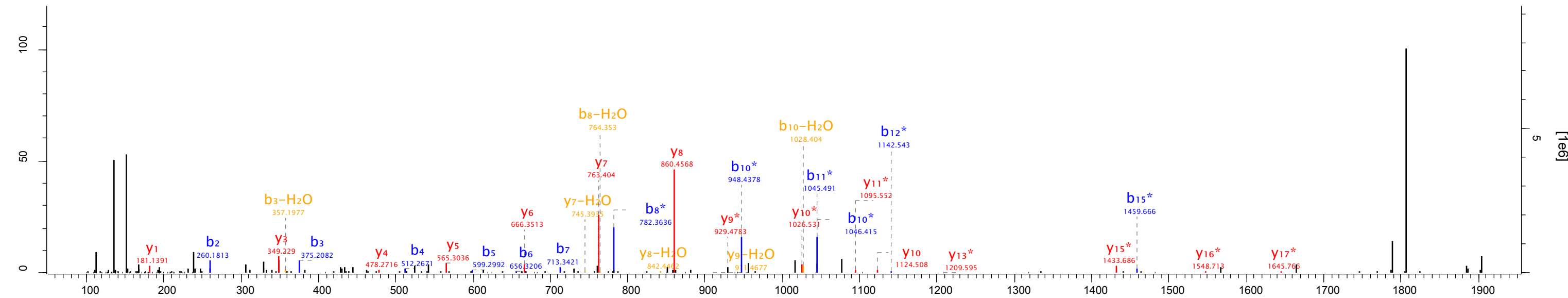




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20171215_MaS_33SR_LMH_phospho2_03

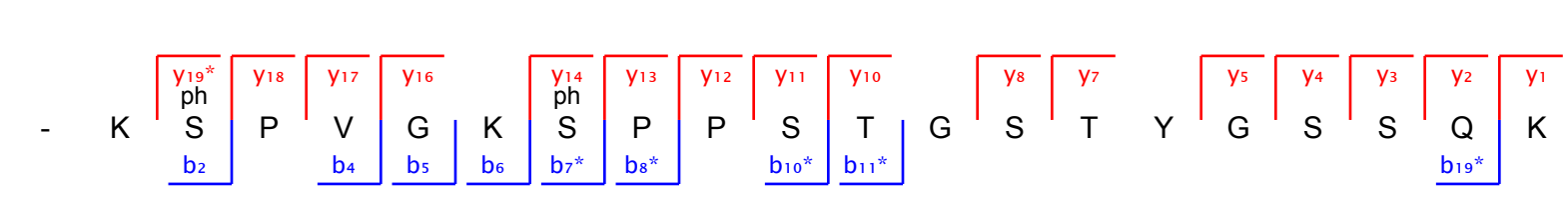
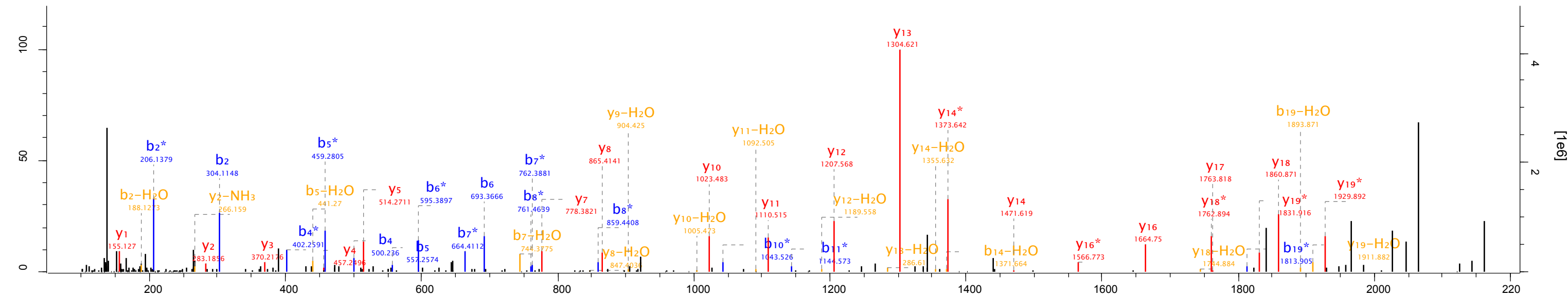




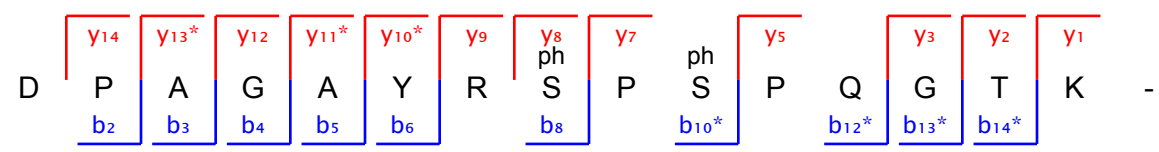
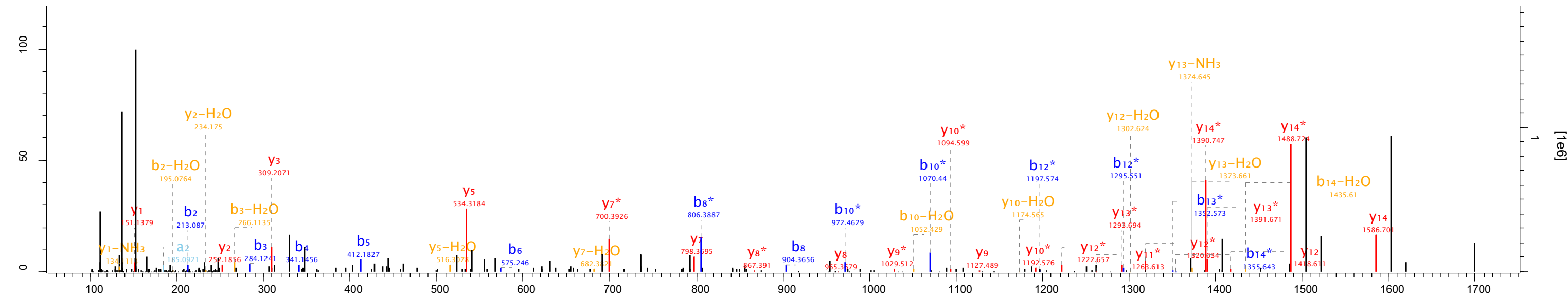
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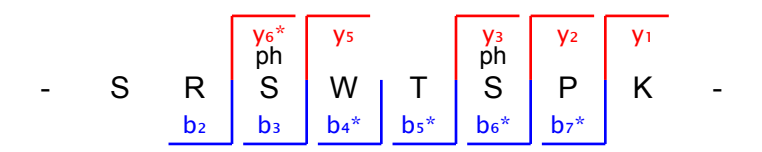
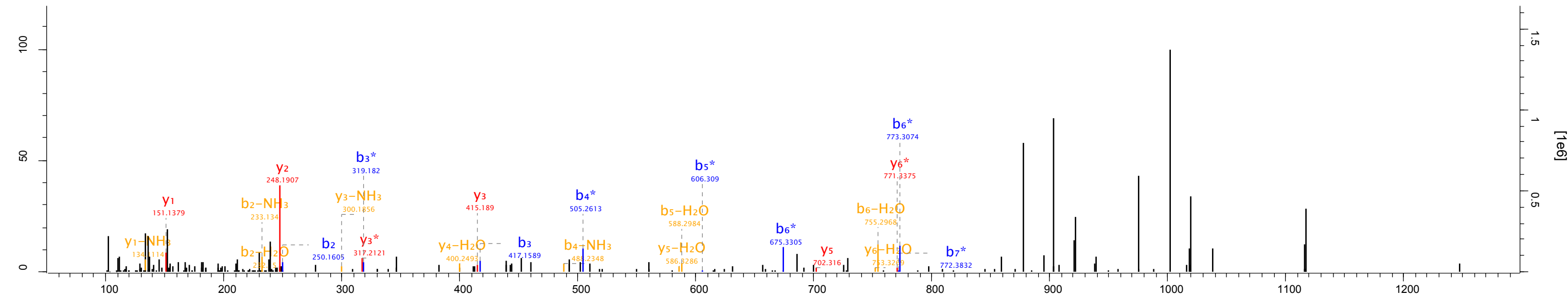
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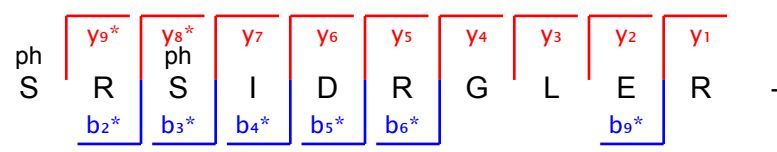
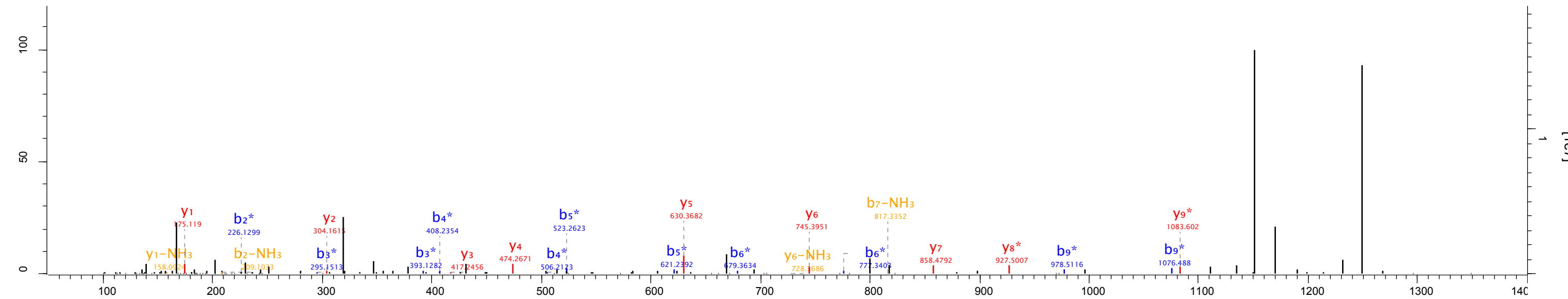
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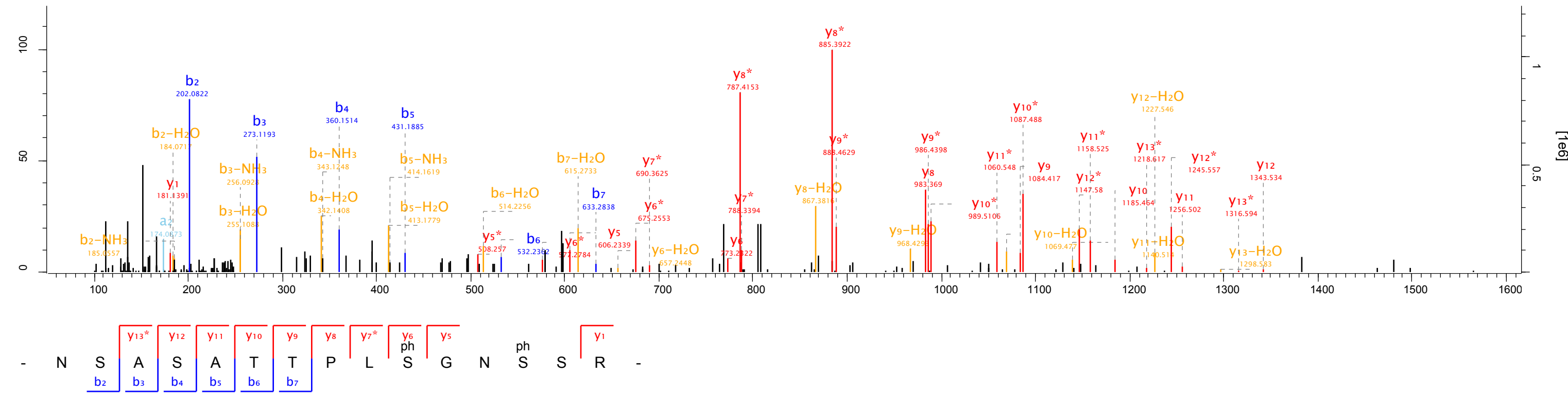


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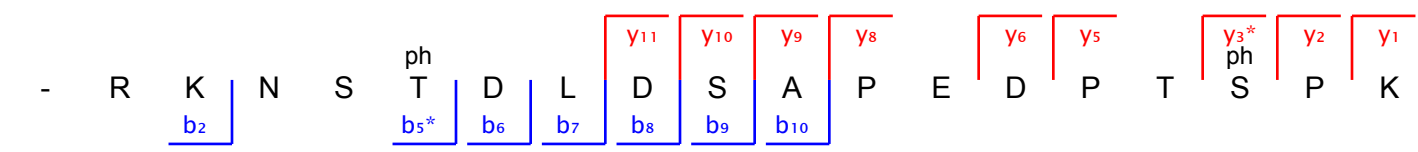
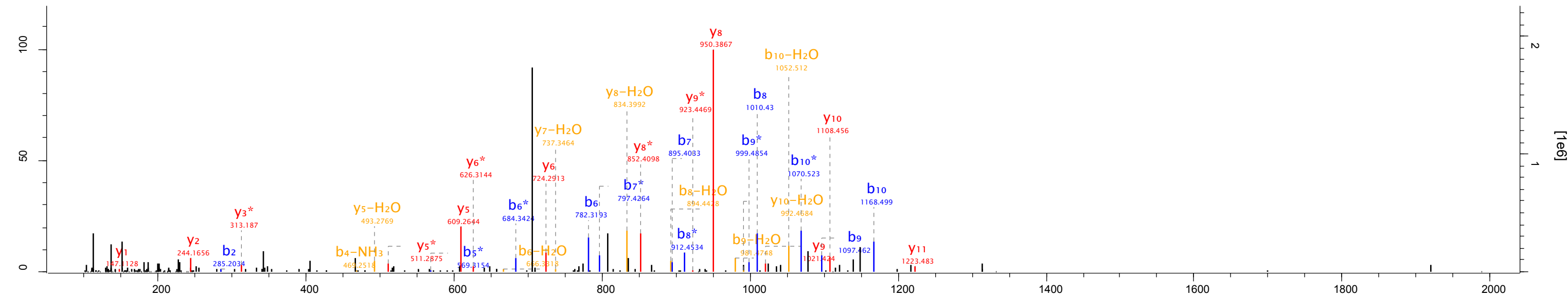


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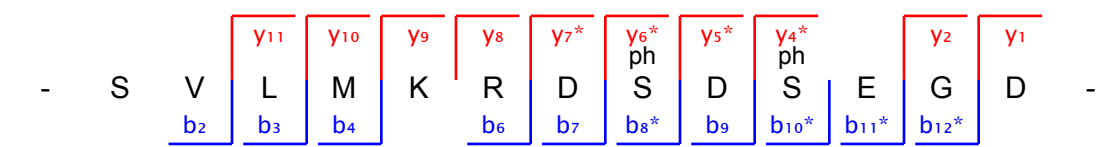
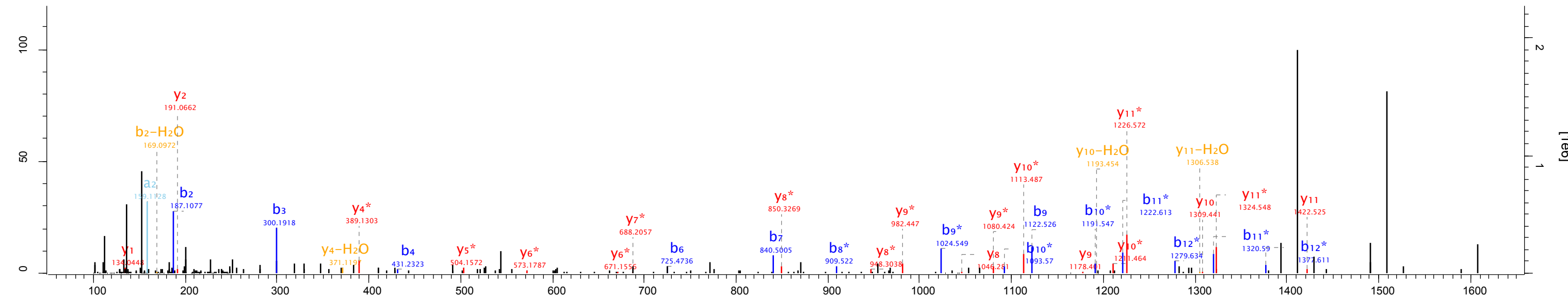


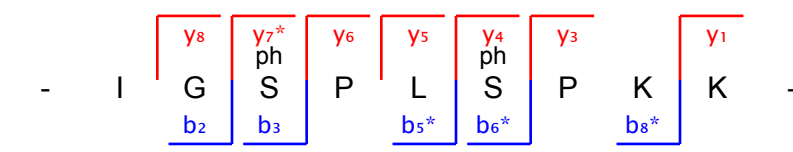
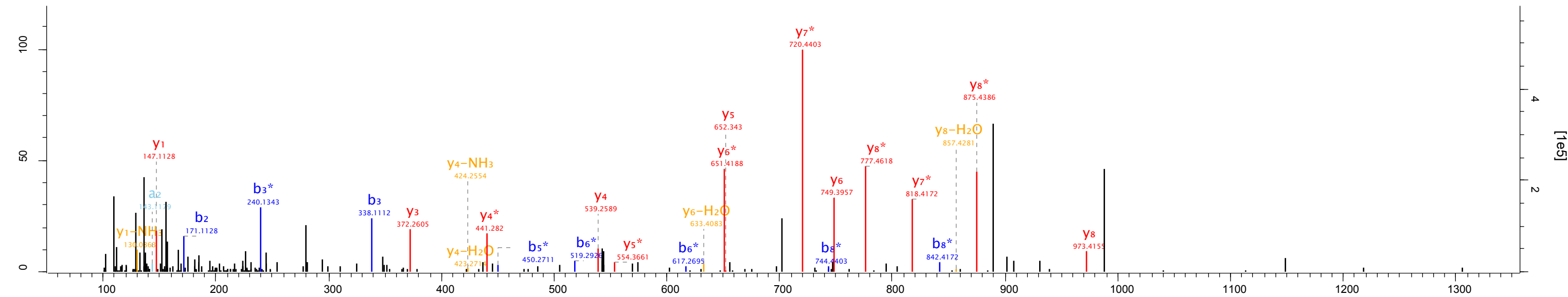


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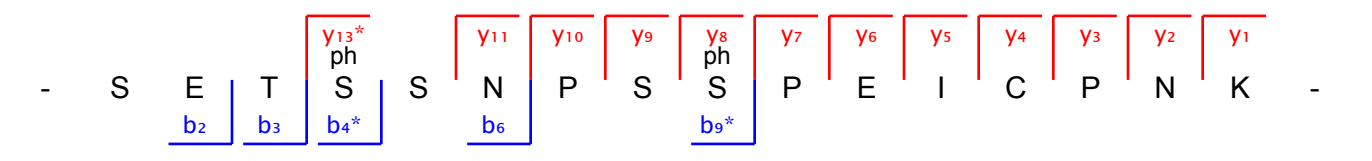
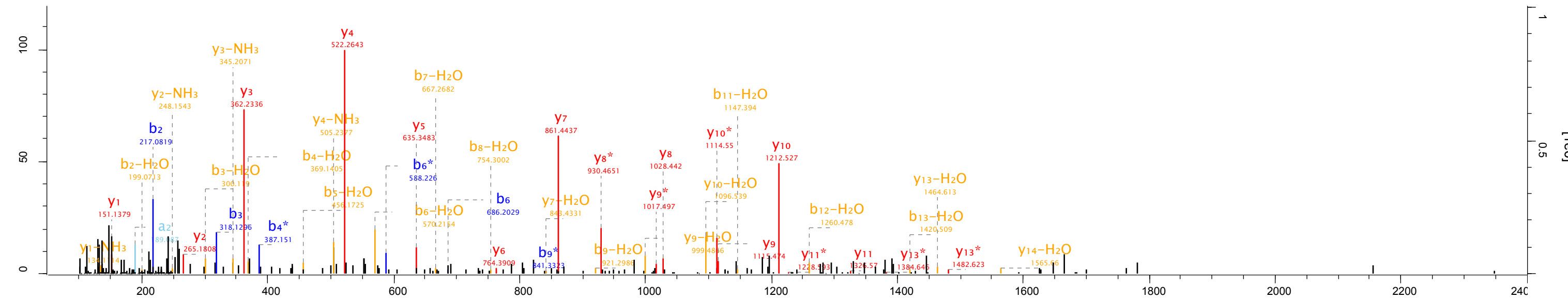


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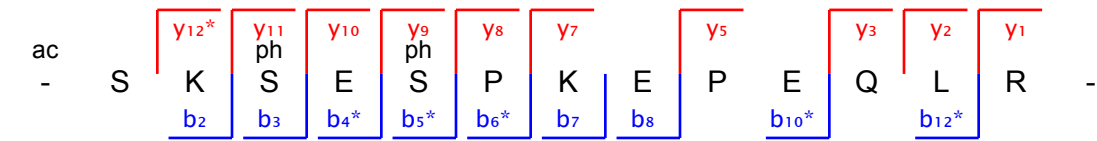
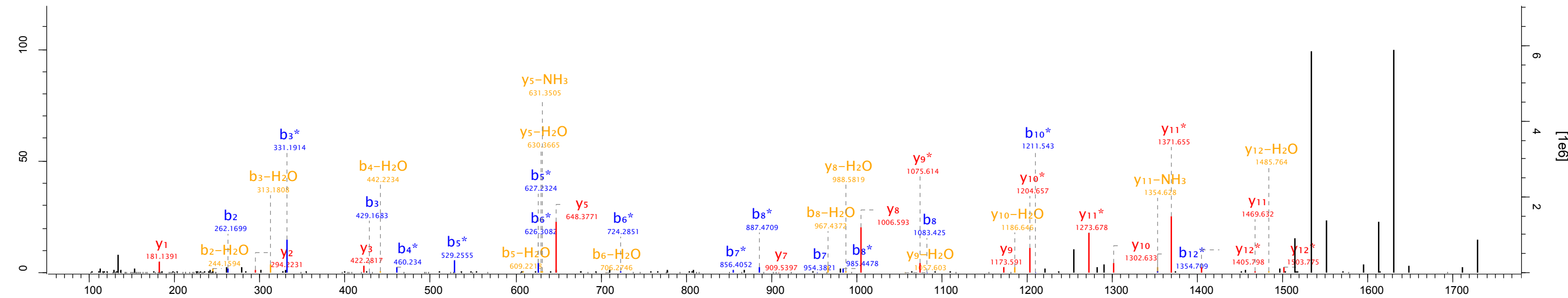




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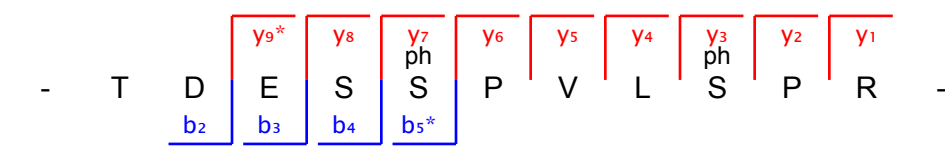
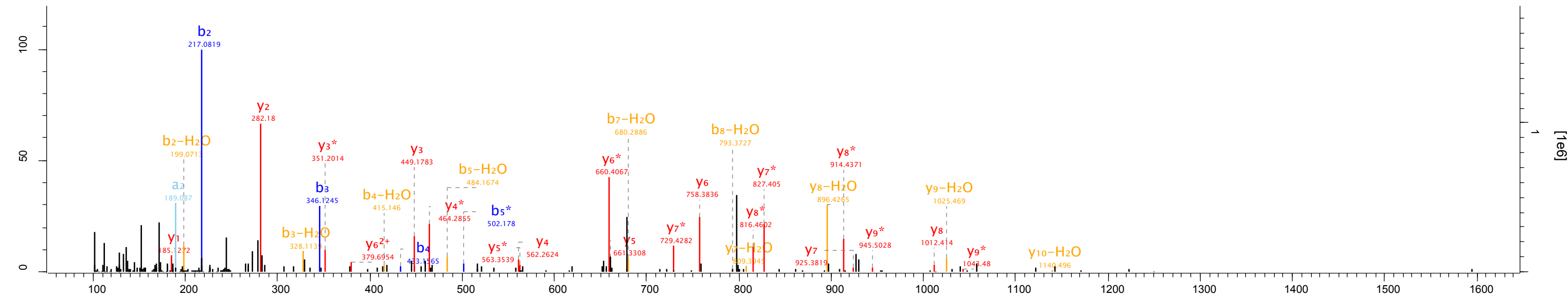


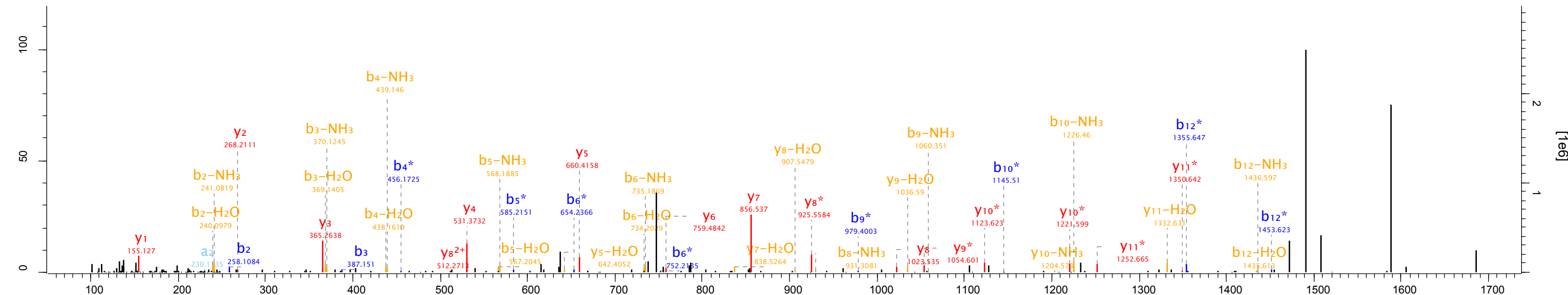
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Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 6190 Method FTMS; HCD Score 130.02 m/z 679.27 Gene names POC5





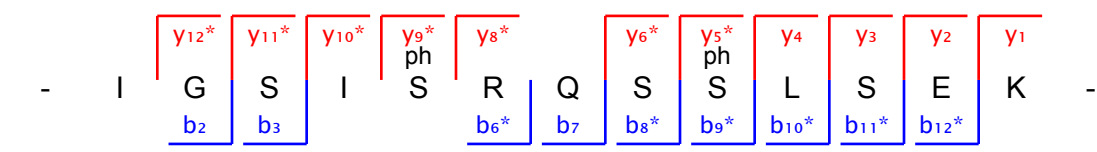
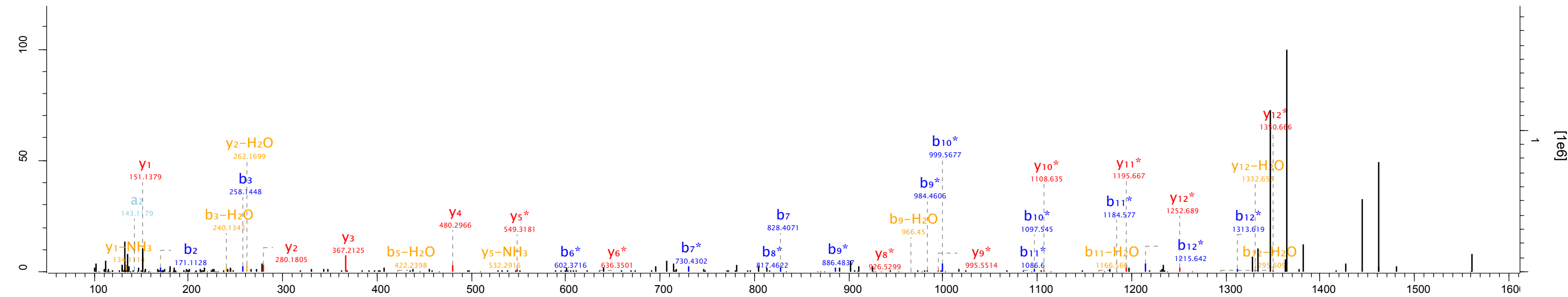
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b₁₀^{*}
b₁₂^{*}

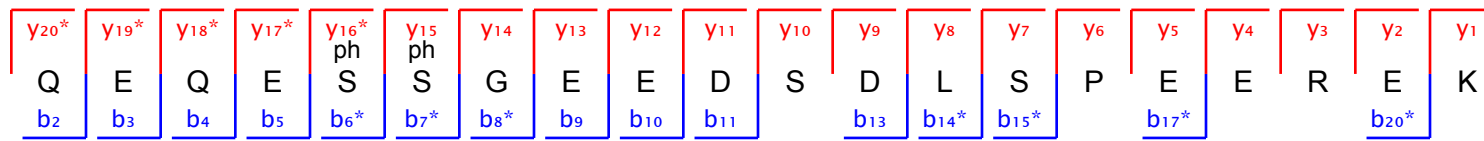
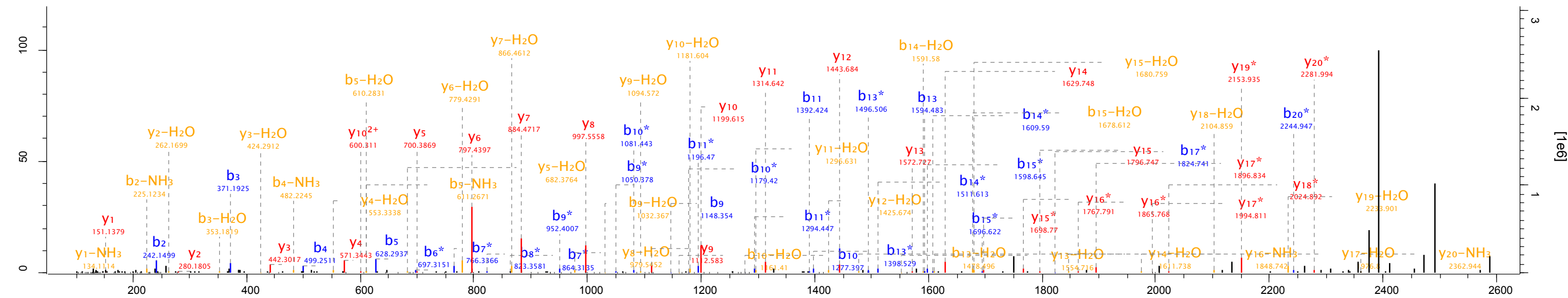
y₁₁^{*}
y₁₀^{*}
y₉^{*}
y₈^{*}
y₇
y₆
y₅
y₄
y₃
y₂
y₁

ph
ph

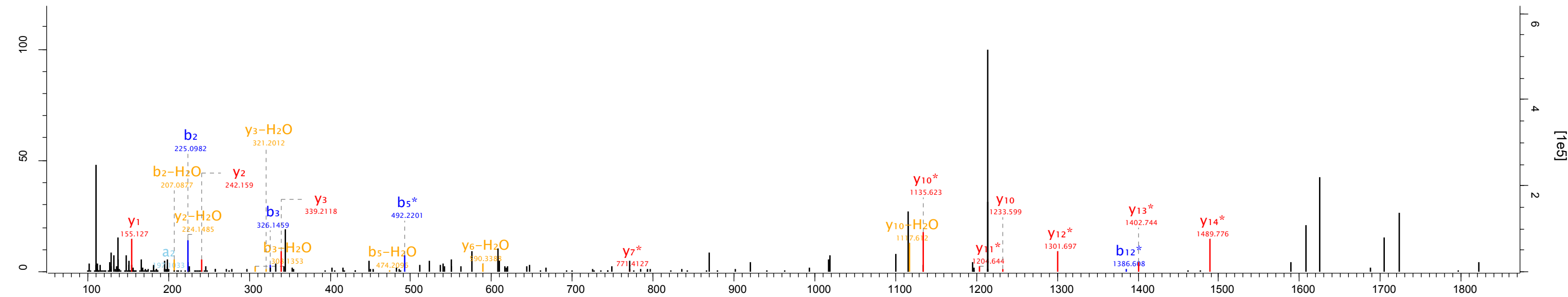
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6300 Method FTMS; HCD Score 90.44 m/z 781.37 Gene names KIF21A



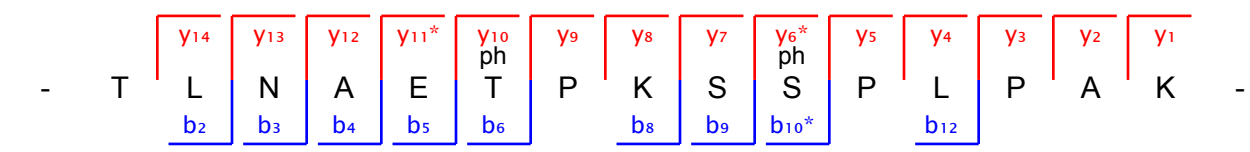
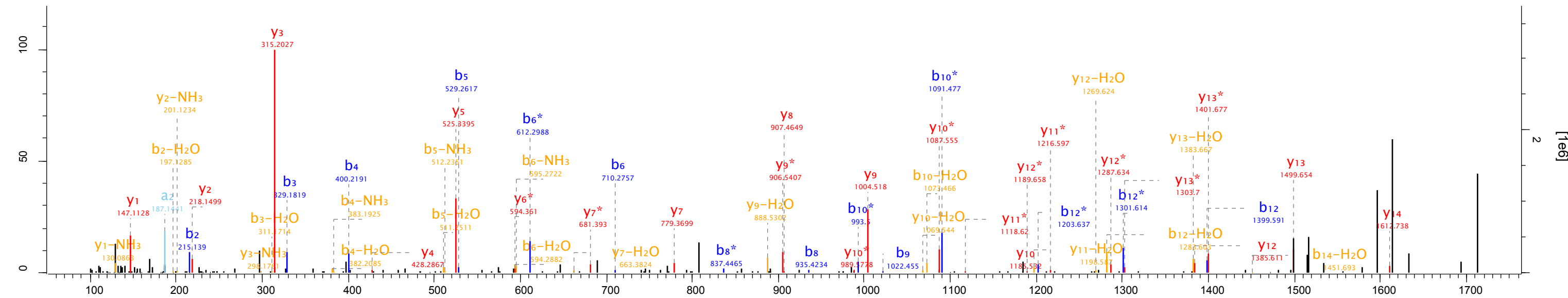
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6540 Method FTMS; HCD Score 286.58 m/z 1296.52 Gene names PPP1R2;PPP1R2P3

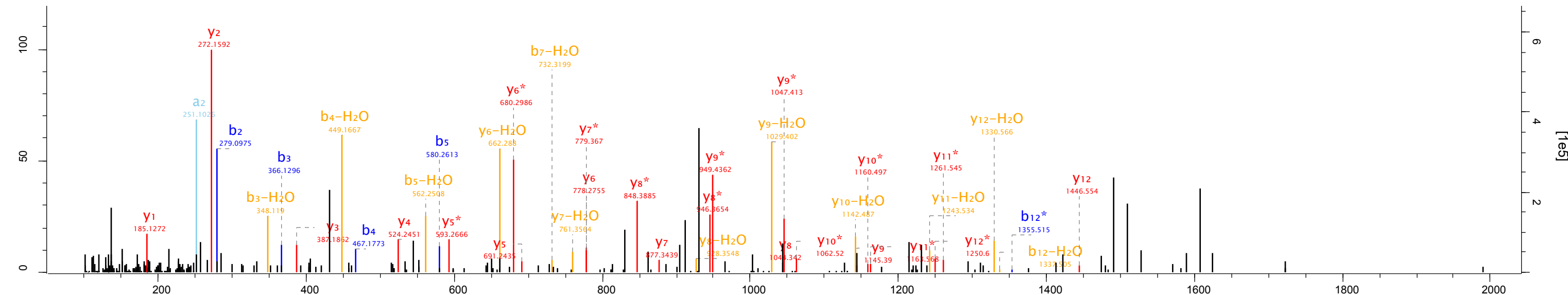


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6670 Method FTMS; HCD Score 44.05 m/z 608.27 Gene names RANBP2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6820 Method FTMS; HCD Score 214.95 m/z 857.4 Gene names MEPCE



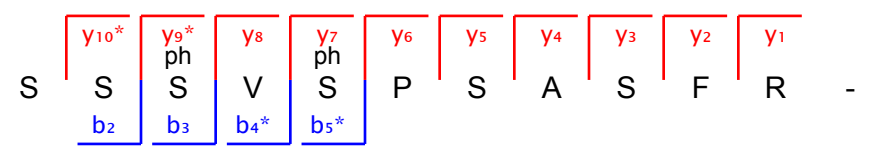
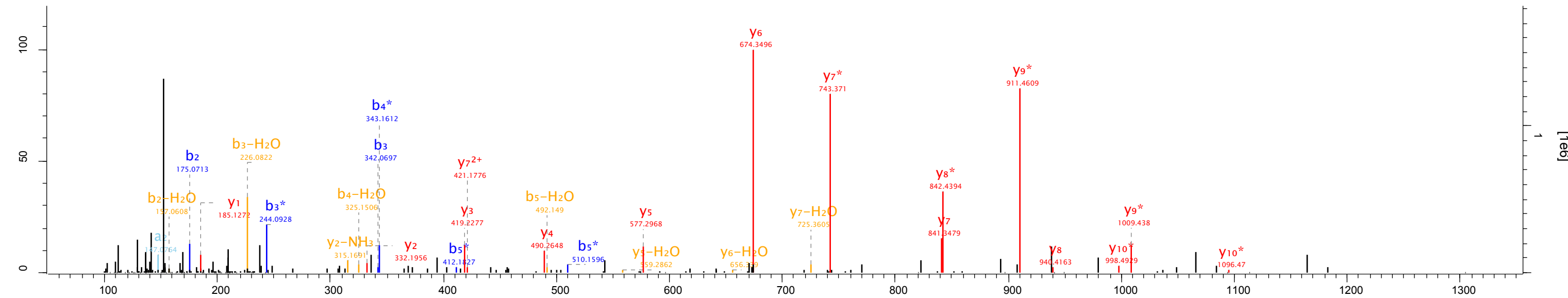


- D Y S T L T S V S S H D S R -

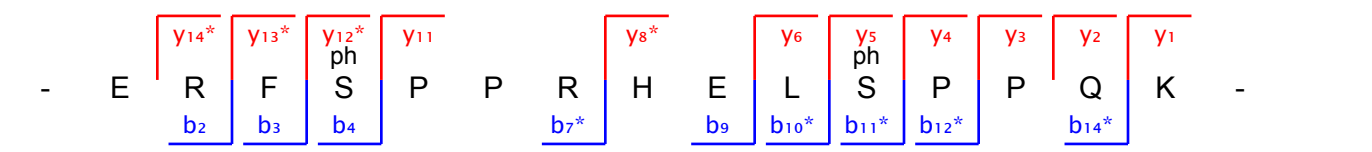
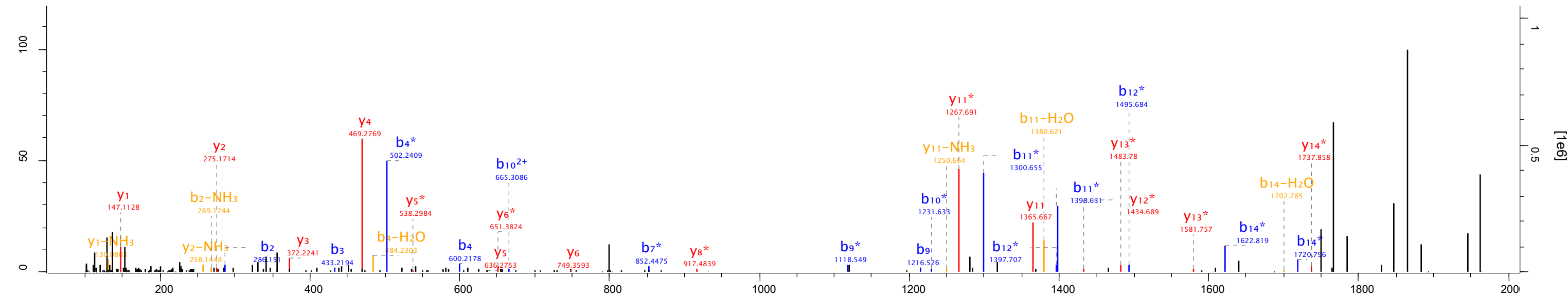
Fragmentation mapping (b and y ions):

- b₂ (under Y)
- b₃ (under S)
- b₄ (under T)
- b₅ (under L)
- b₁₂* (under D)
- y₁ (under R)
- y₂ (under S)
- y₃ (under D)
- y₄ (under H)
- y₅ (under S)
- y₆ (under S)
- y₇ (under V)
- y₈ (under S)
- y₉ (under T)
- y₁₀* (under L)
- y₁₁* (under T)
- y₁₂ (under S)

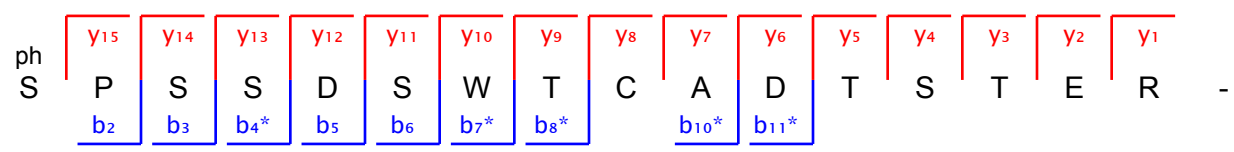
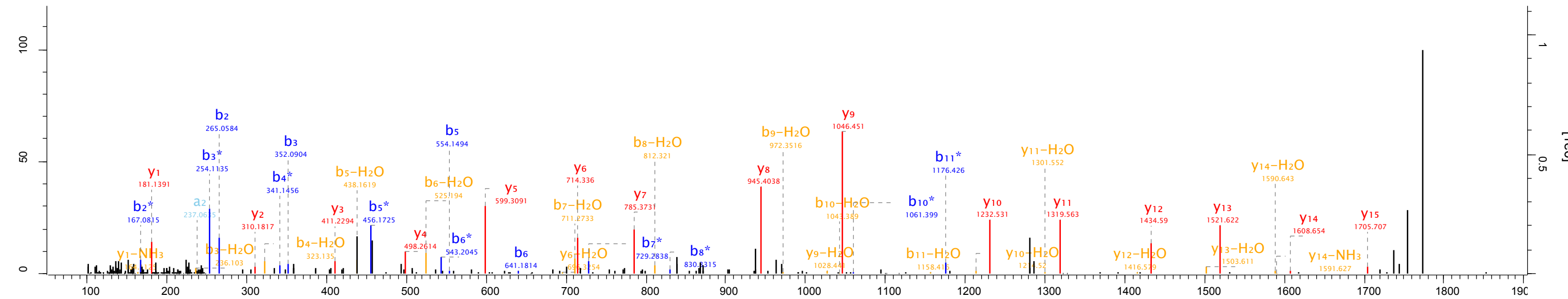
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 7950 Method FTMS; HCD Score 118.2 m/z 641.24 Gene names TLE4

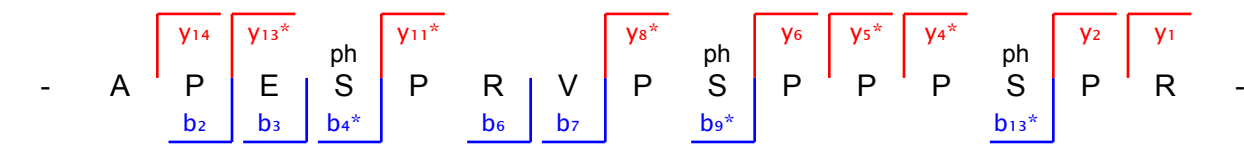
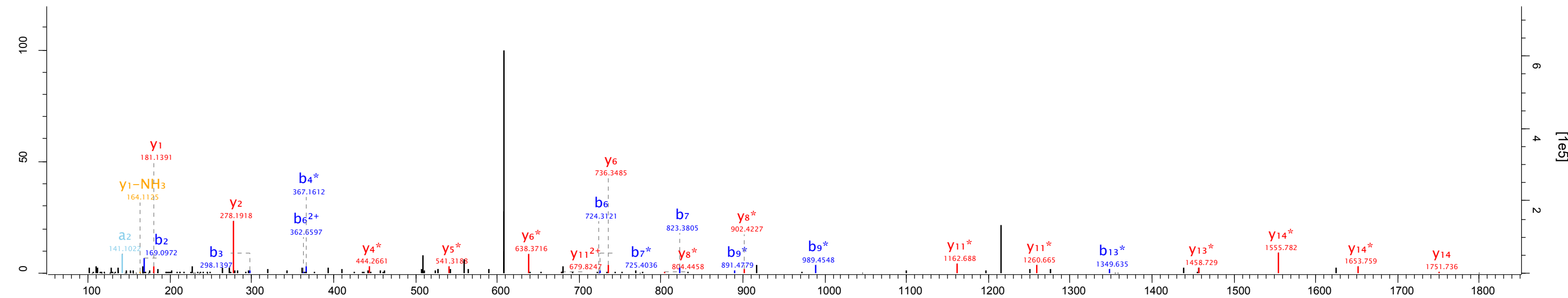


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 8160 Method: FTMS; HCD Score: 143.47 m/z: 655.97 Gene names: SRRT

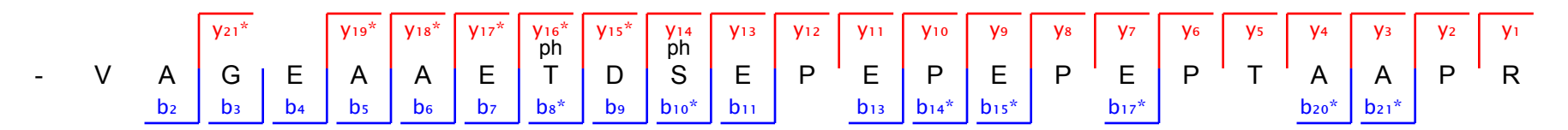
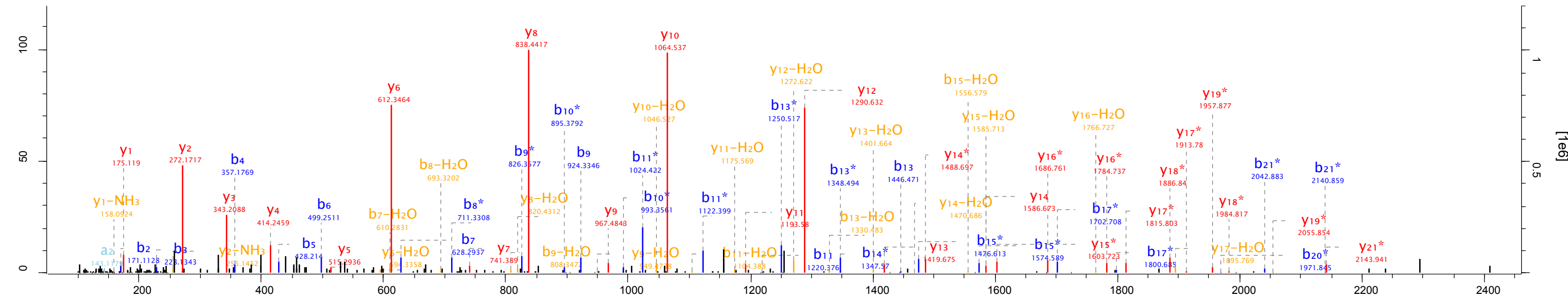


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 8330 Method: FTMS; HCD Score: 204.78 m/z: 937.35 Gene names: ARFGAP1

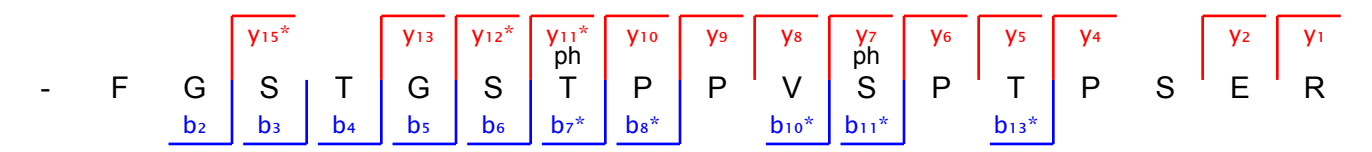
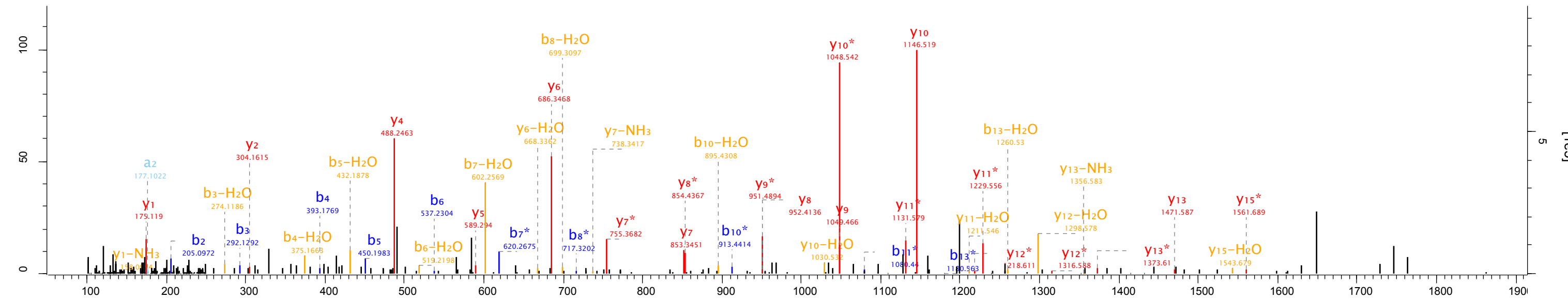




Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8480 Method FTMS; HCD Score 257.77 m/z 1255.51 Gene names BLOC1S3

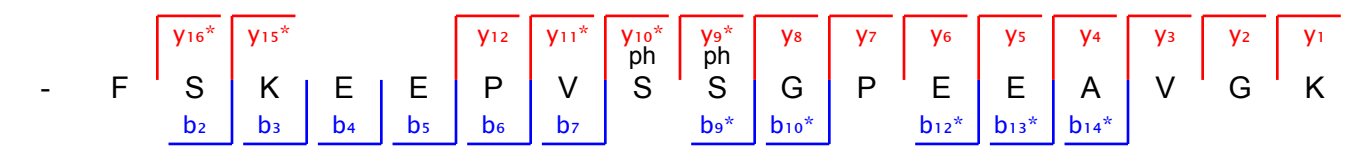
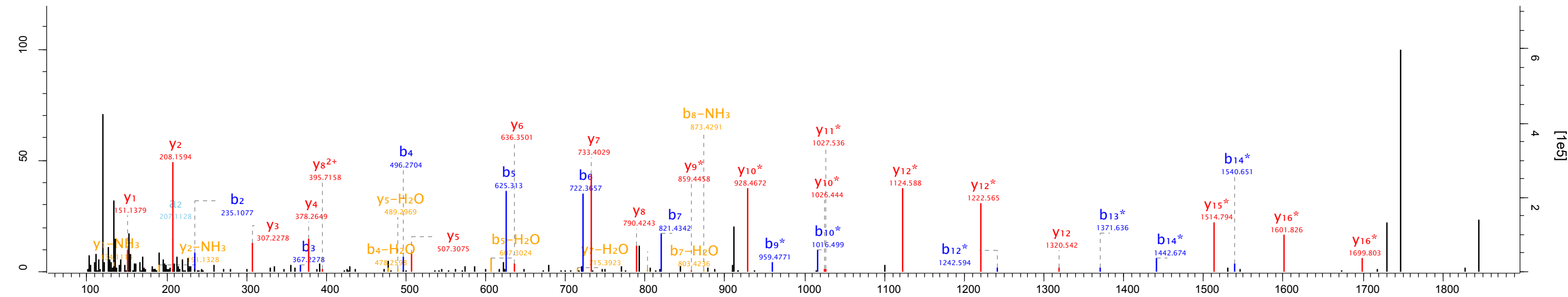


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 8630 Method: FTMS; HCD Score: 149.93 m/z: 932.89 Gene names: MKL1; mkl1



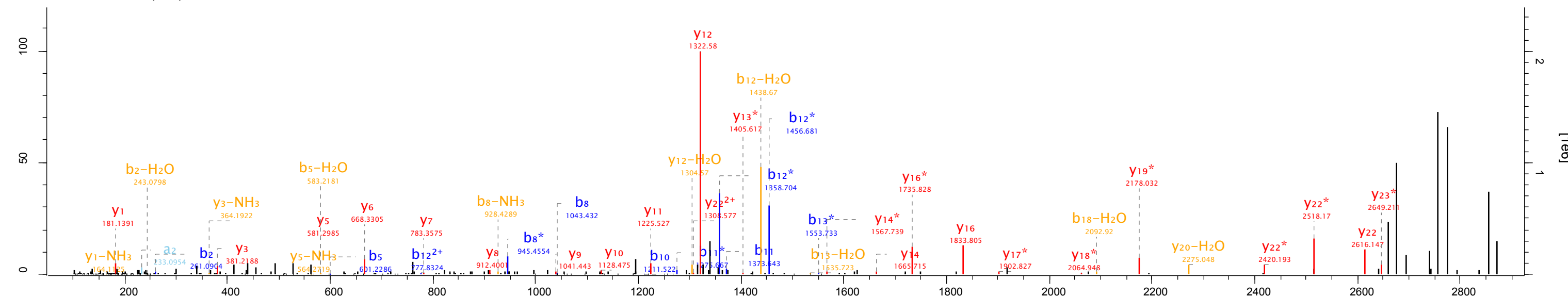
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 8640 Method FTMS; HCD Score 151.42 m/z 649.29 Gene names NOP56



Raw file
20171215_MaS_33SR_LMH_phospho2_03

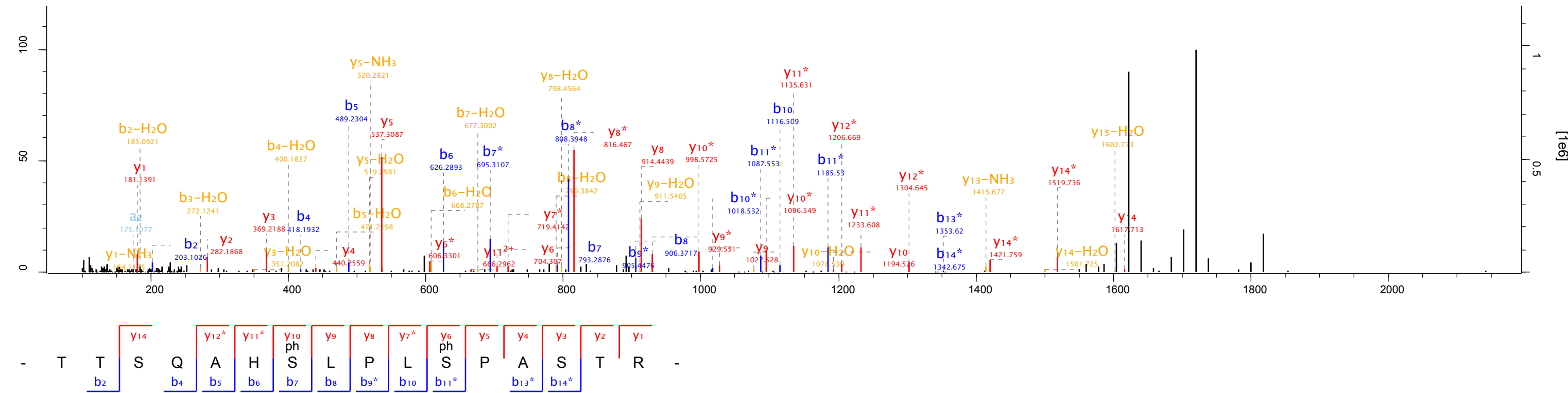
Scan 8740 Method FTMS; HCD Score 80.69 m/z 959.75 Gene names SGTA



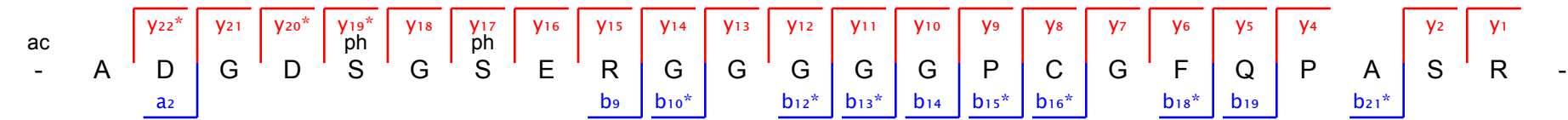
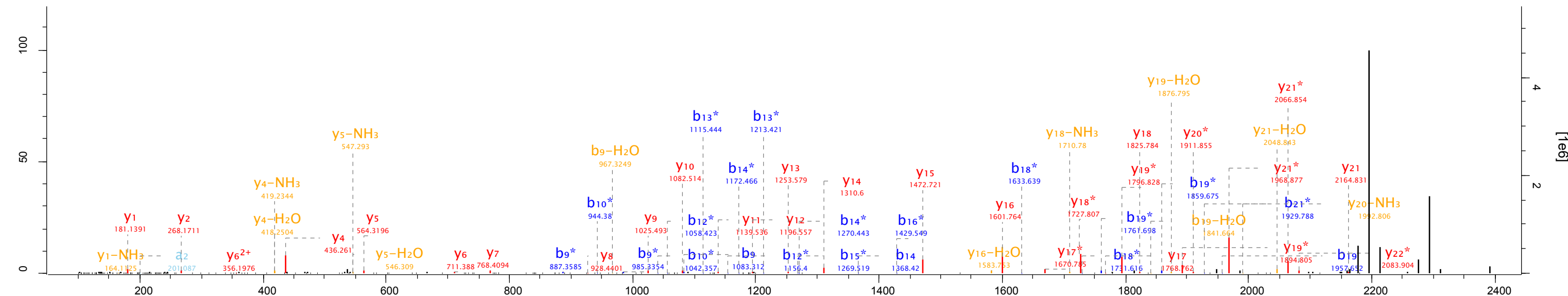
- E M P Q D L R S P A R T P P S E E D S A E A E R -

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

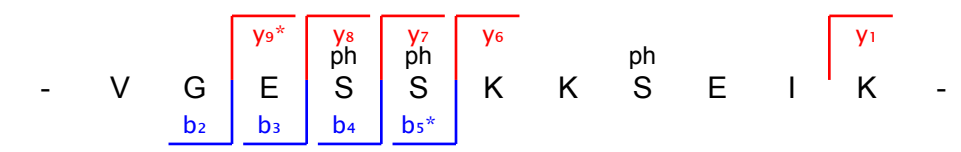
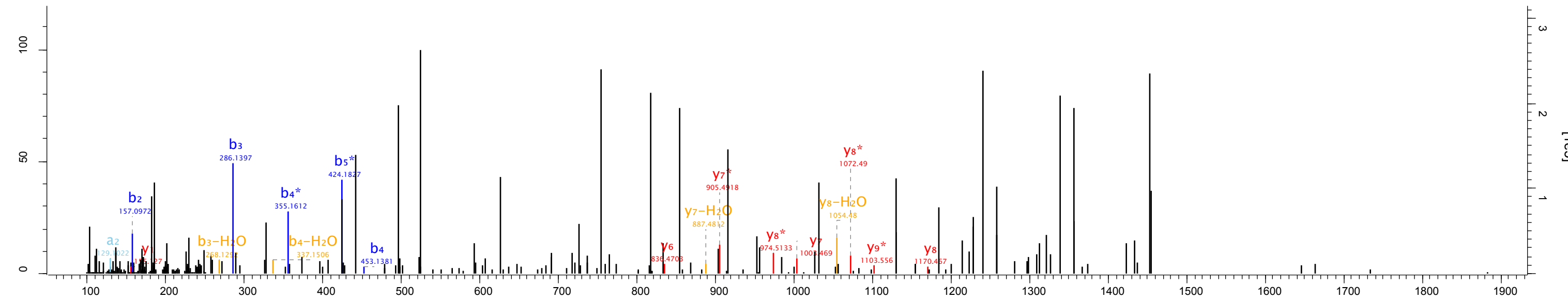
- Red boxes: y23* (M), y22 (P), y19* (L), y18* (R), y17* (S), y16 (P), y14 (R), y13* (T), y12 (P), y11 (P), y10 (S), y9 (E), y8 (E), y7 (D), y6 (S), y5 (A), y3 (A), y1 (R)
- Blue boxes: b2 (M), b5 (D), b8 (S), b10 (A), b11 (R), b12* (T), b13* (P)



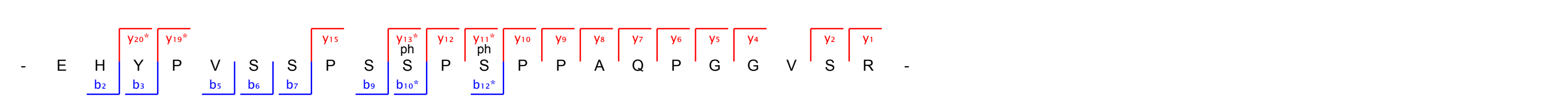
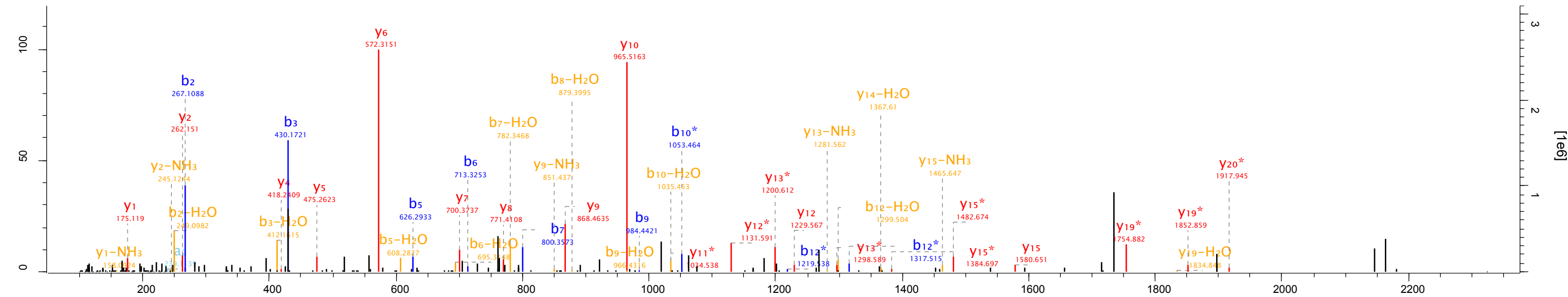
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8840 Method FTMS; HCD Score 164.39 m/z 1197.45 Gene names PURB



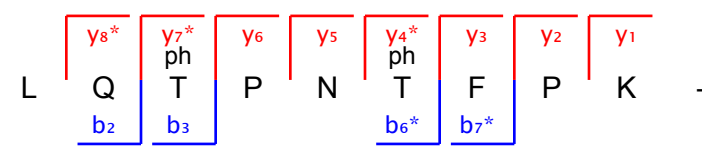
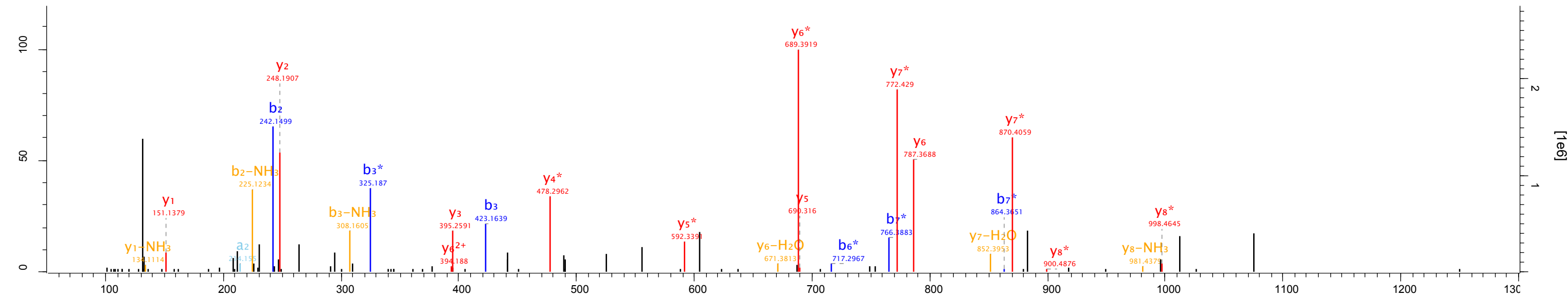
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8860 Method FTMS; HCD Score 47.22 m/z 728.3 Gene names CEP350

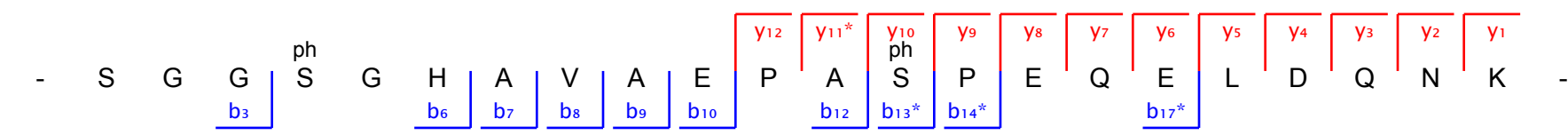
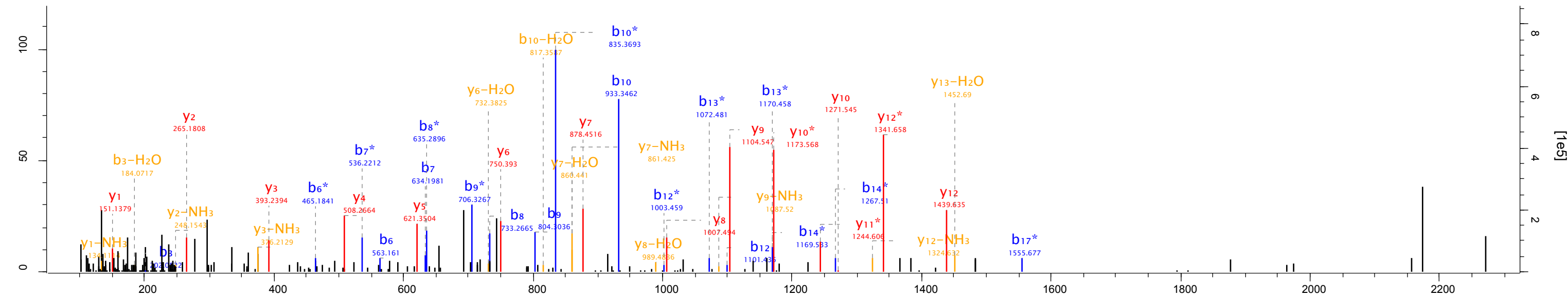


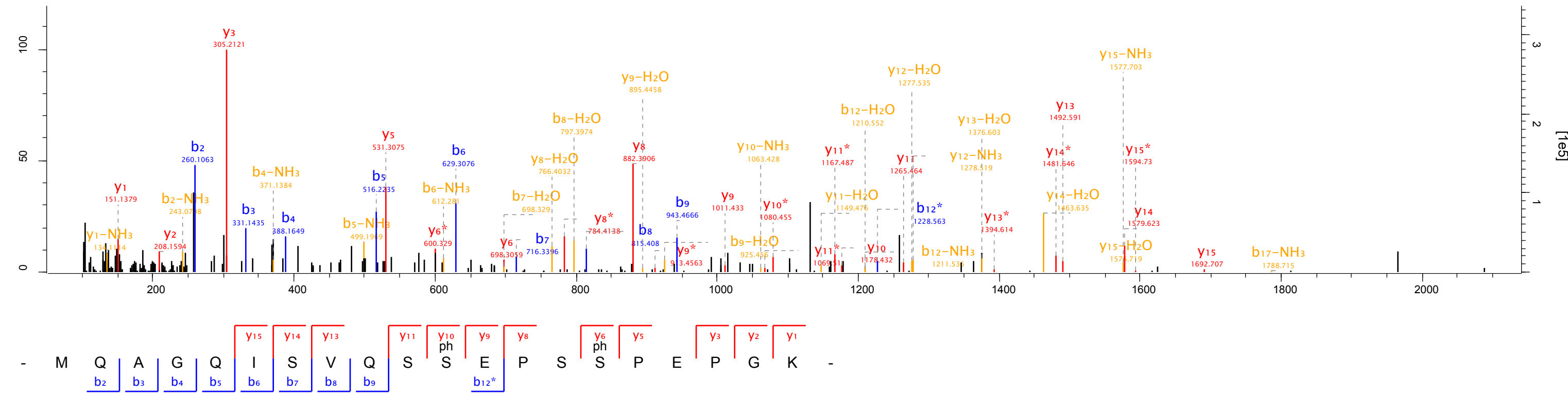
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8960 Method FTMS; HCD Score 118.15 m/z 794 Gene names ANKRD17



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 9020 Method: FTMS; HCD Score: 119.88 m/z: 605.27 Gene names: NOLC1

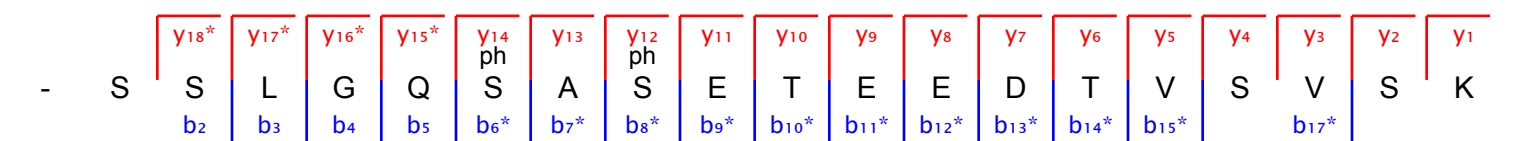
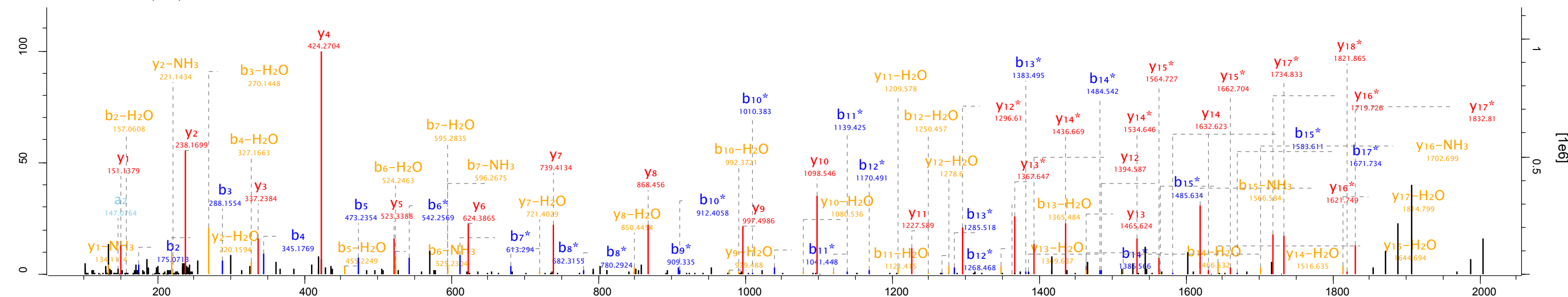




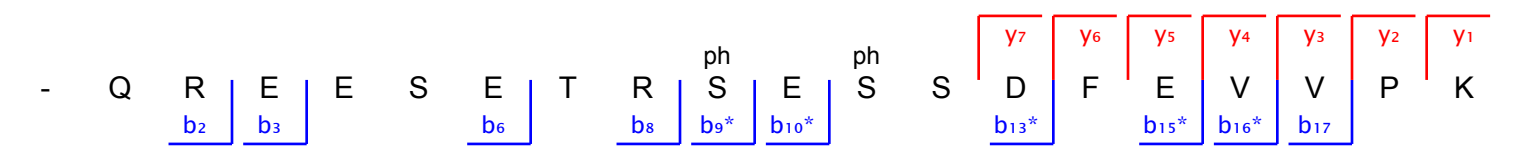
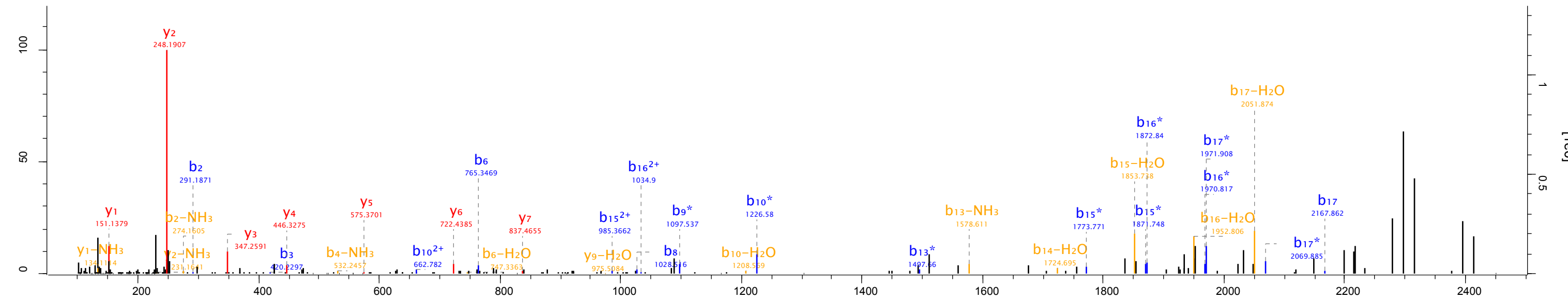


Raw file
20171215_MaS_33SR_LMH_phospho2_03

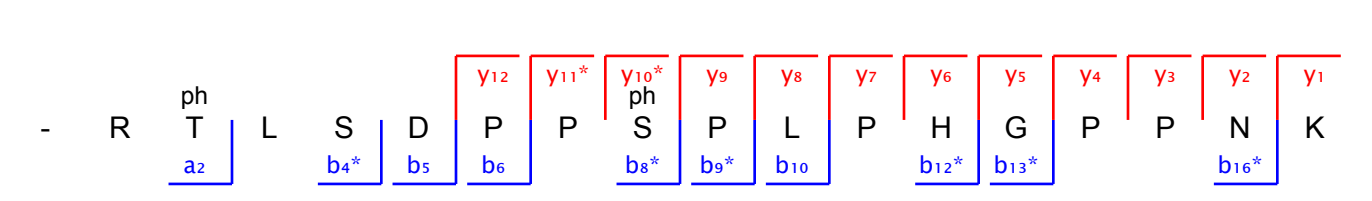
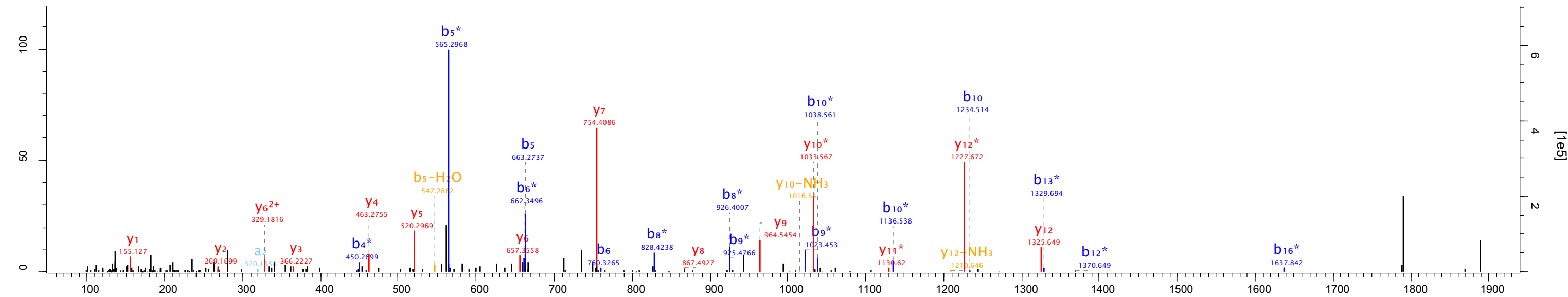
Scan 9400 Method FTMS; HCD Score 285.62 m/z 1052.93 Gene names SF3B2

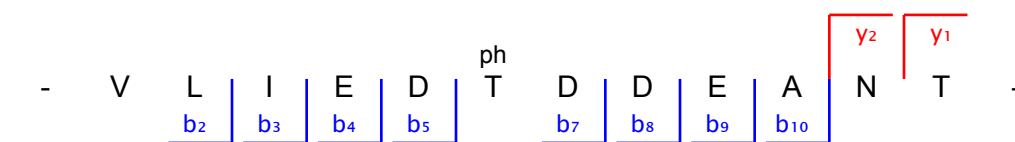
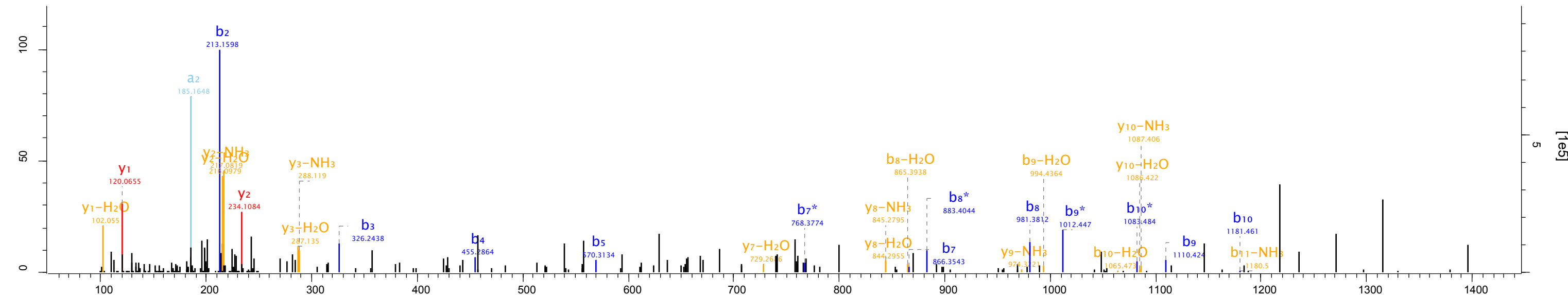


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9480 Method FTMS; HCD Score 73.07 m/z 806.02 Gene names PRRC2C

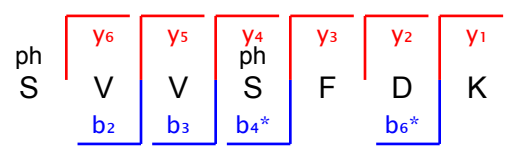
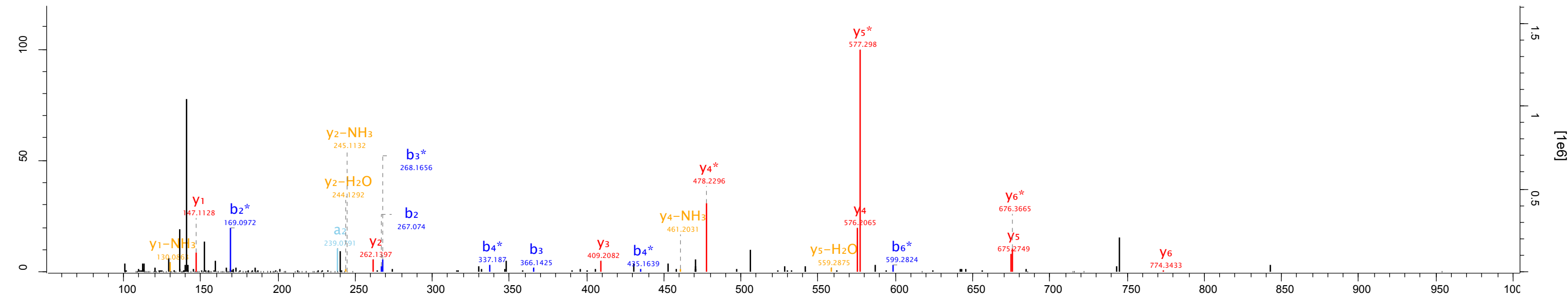


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9650 Method FTMS; HCD Score 116.45 m/z 663.31 Gene names ASAP1

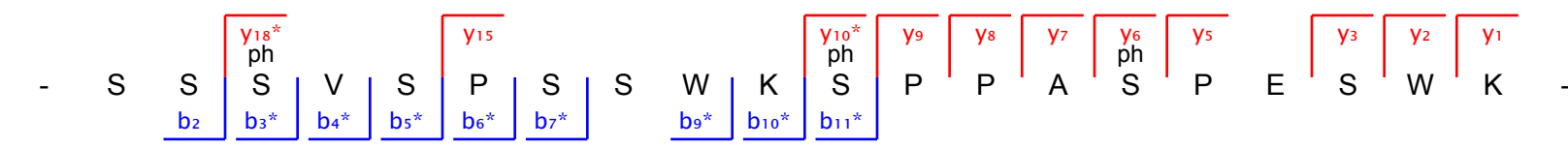
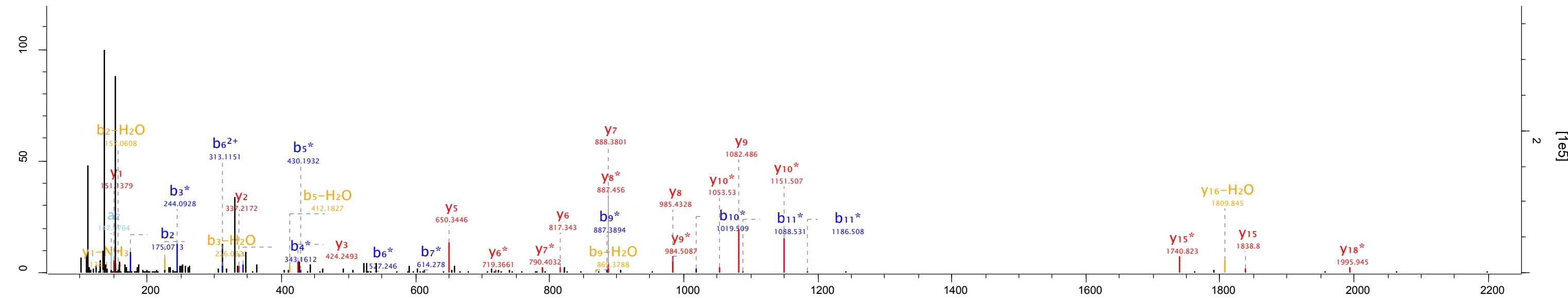




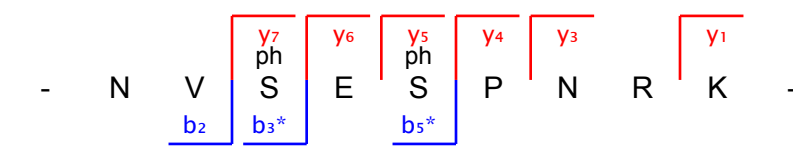
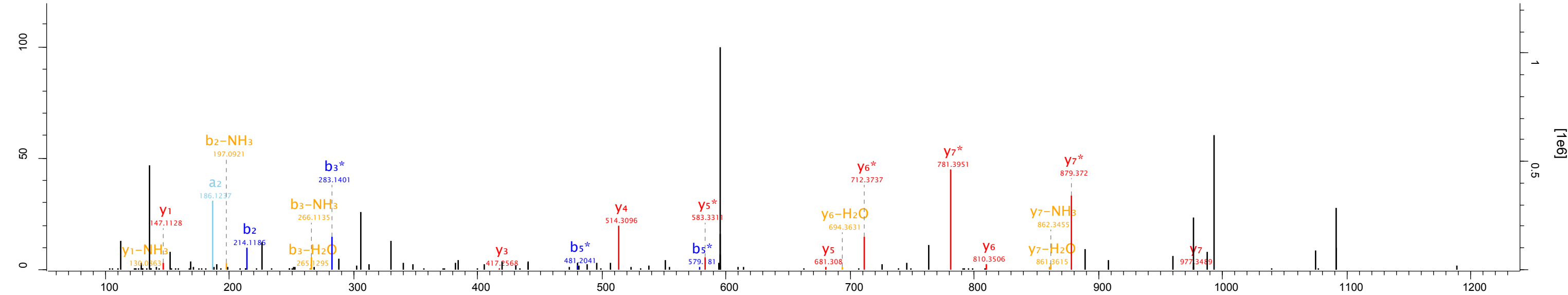
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9840 Method FTMS; HCD Score 98.9 m/z 471.17 Gene names SAFB



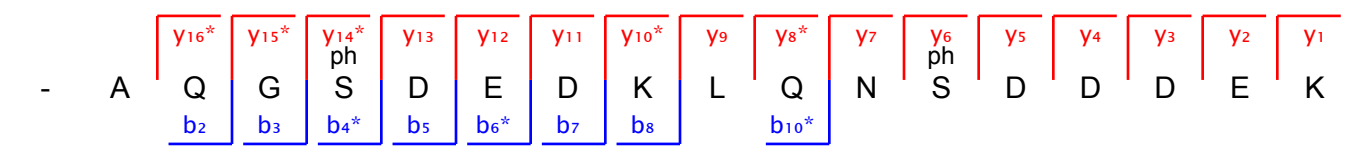
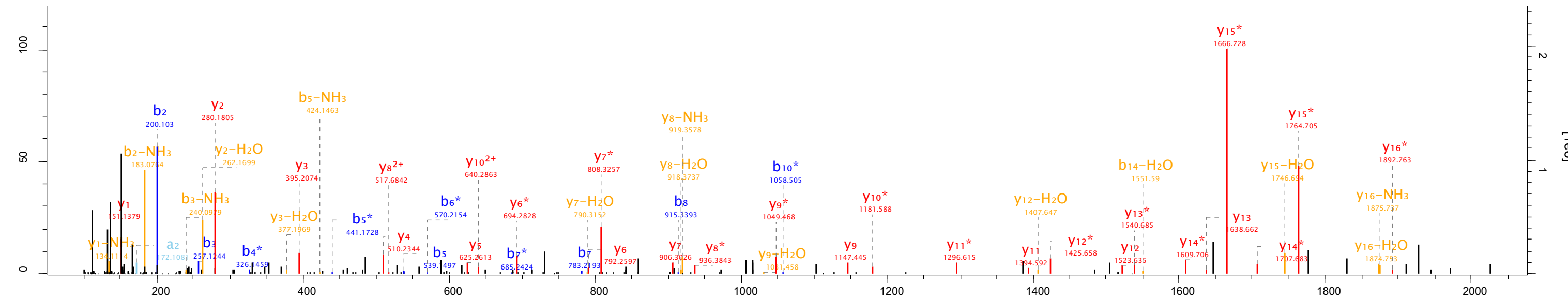
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 12700 Method FTMS; HCD Score 54.53 m/z 789.33 Gene names CHAMP1



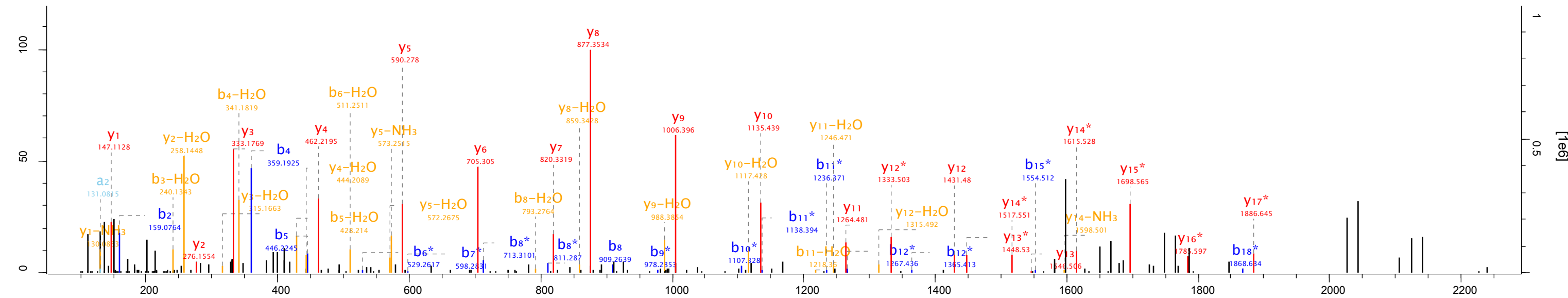
20171215_MaS_33SR_LMH_phospho2_04 2170 FTMS; HCD 73.27 595.73 PPIG



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 3130 Method FTMS; HCD Score 145.65 m/z 688.27 Gene names LEO1



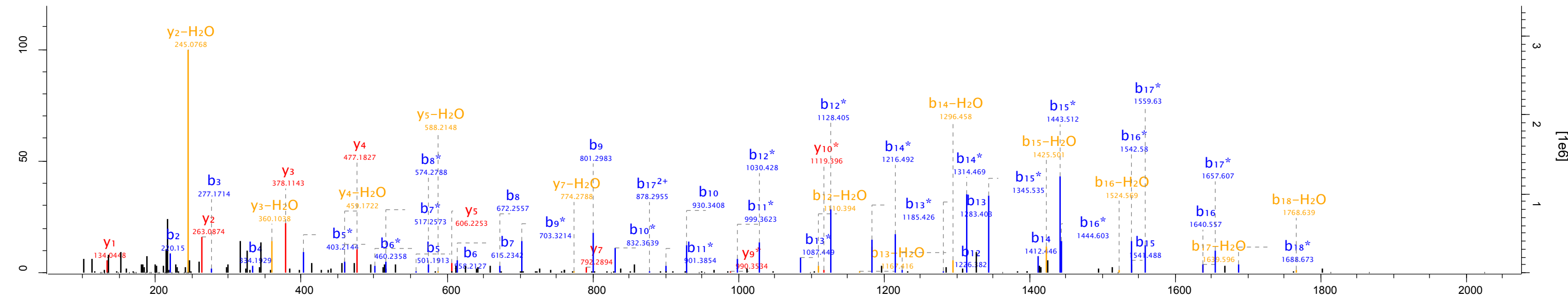
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 3460 Method FTMS; HCD Score 194.19 m/z 1170.37 Gene names PSIP1



- T G V T S T ph S D S E E E G D D Q E G E K -

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

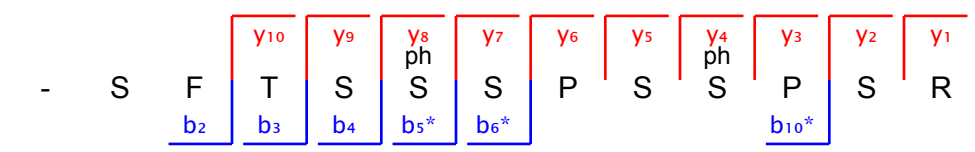
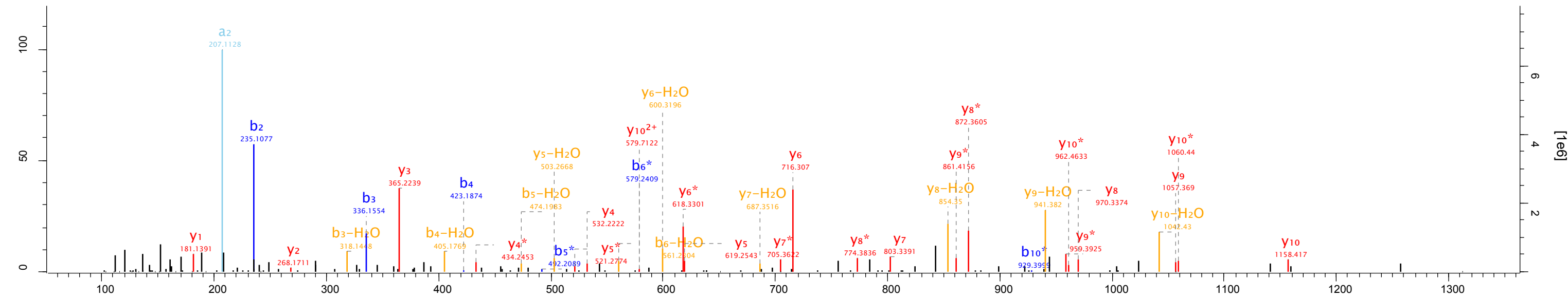
- b₂ (under G)
- b₄ (under T), b₅ (under S), b₆^{*} (under T), b₇^{*} (under ph), b₈ (under S), b₉^{*} (under S), b₁₀^{*} (under E), b₁₁^{*} (under E), b₁₂^{*} (under E), b₁₅^{*} (under D), b₁₈^{*} (under G)
- y₁ (under E), y₂ (under E), y₃ (under G), y₄ (under E), y₅ (under Q), y₆ (under E), y₇ (under D), y₈ (under G), y₉ (under E), y₁₀ (under E), y₁₁ (under S), y₁₂ (under S), y₁₃ (under D), y₁₄^{*} (under ph), y₁₅^{*} (under T), y₁₆^{*} (under S), y₁₇^{*} (under T)



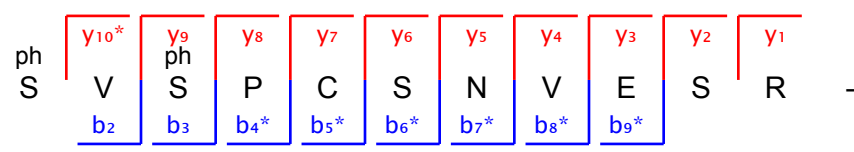
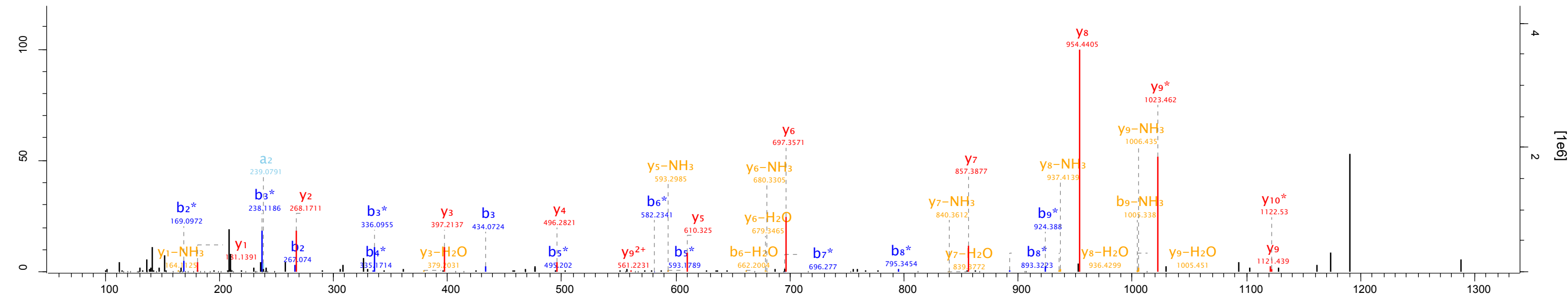
- R G G G ph S G G G E E S E G E E V D E D -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
y₁₀*
y₉^{ph}
y₇
y₅
y₄
y₃
y₂
y₁

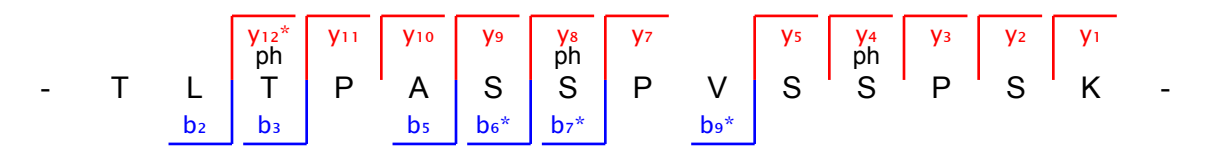
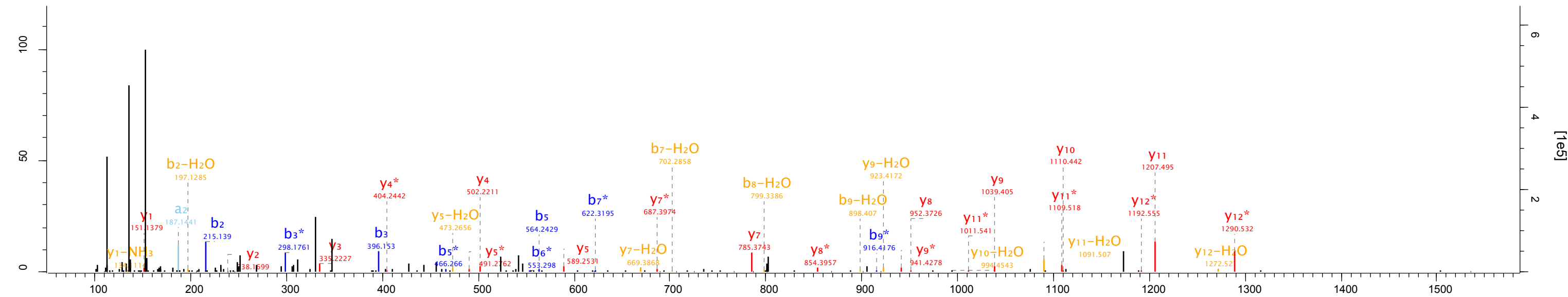
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 4170 Method FTMS; HCD Score 184.22 m/z 696.76 Gene names SORBS2



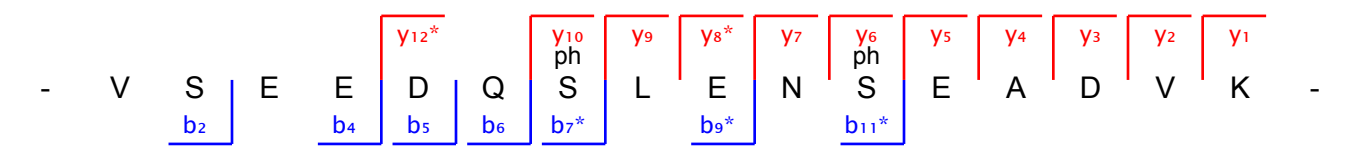
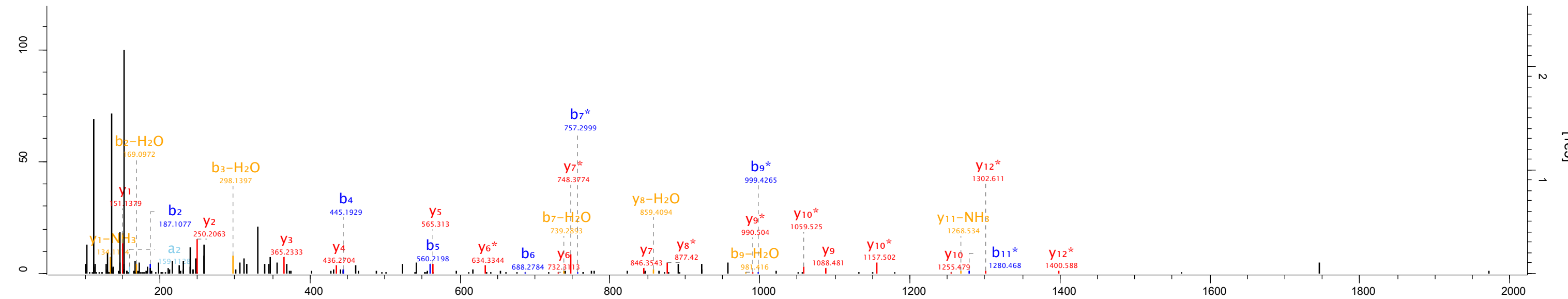
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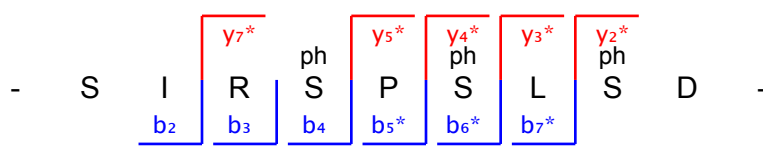
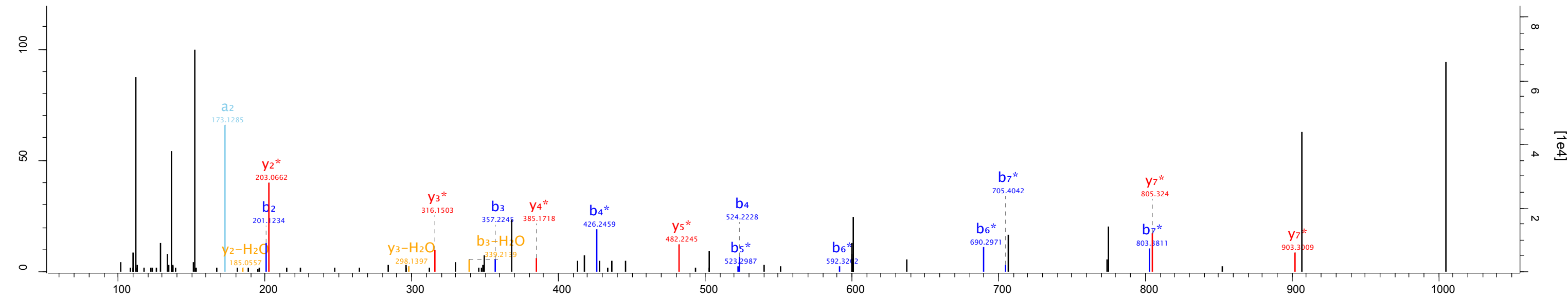
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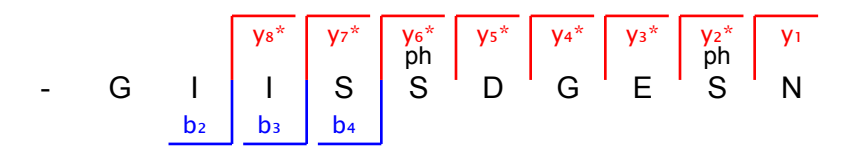
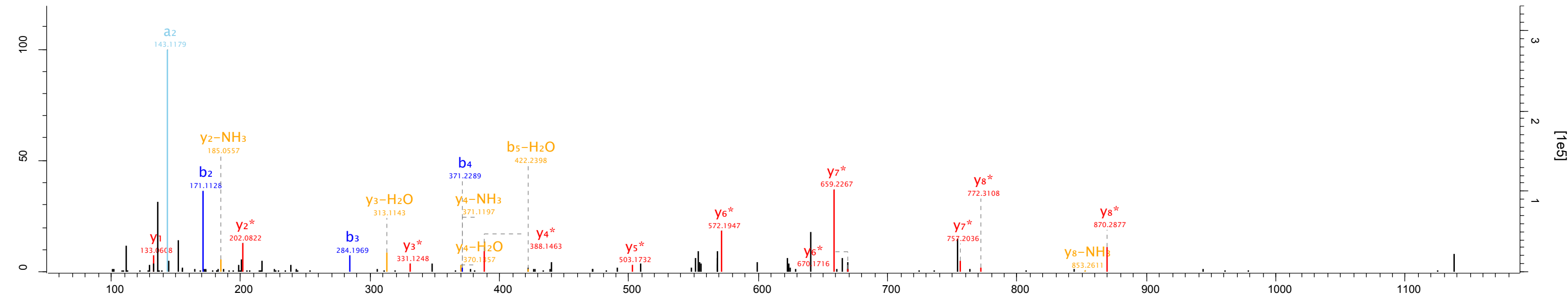
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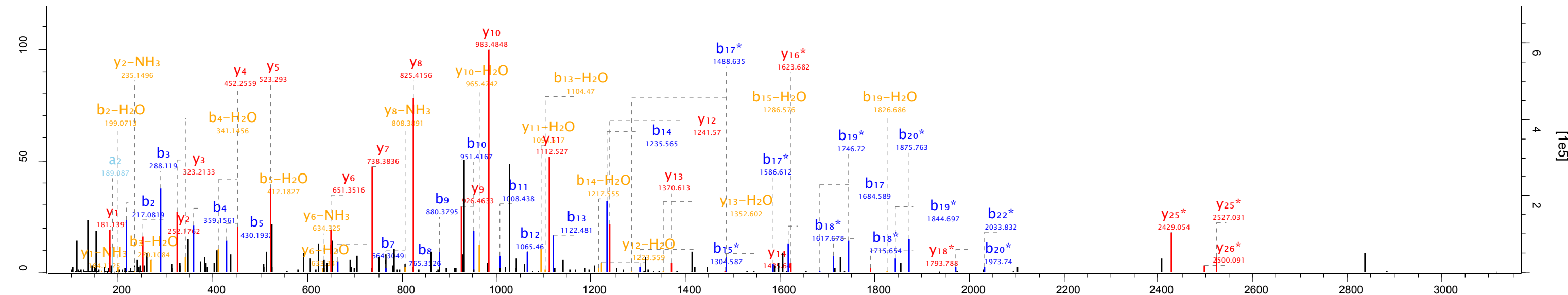


Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5910 Method FTMS; HCD Score 64.31 m/z 601.2 Gene names TAF2



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 6070 Method FTMS; HCD Score 80.91 m/z 569.69 Gene names HIRIP3

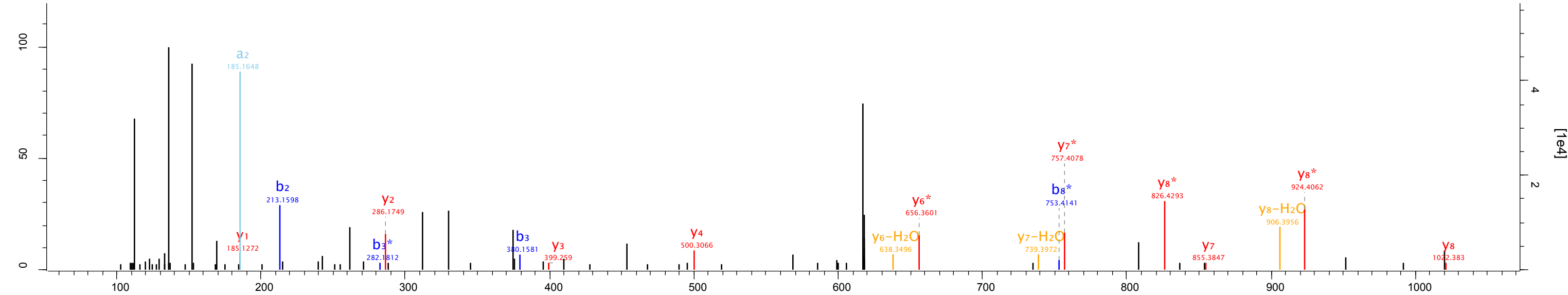


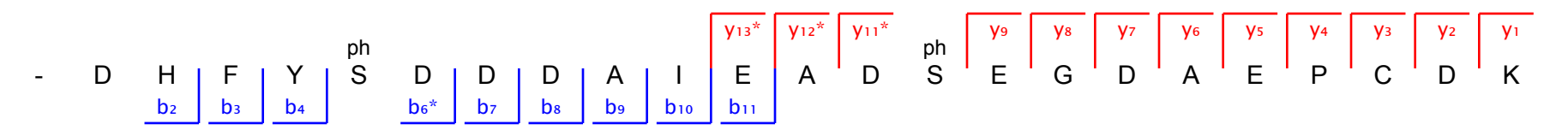
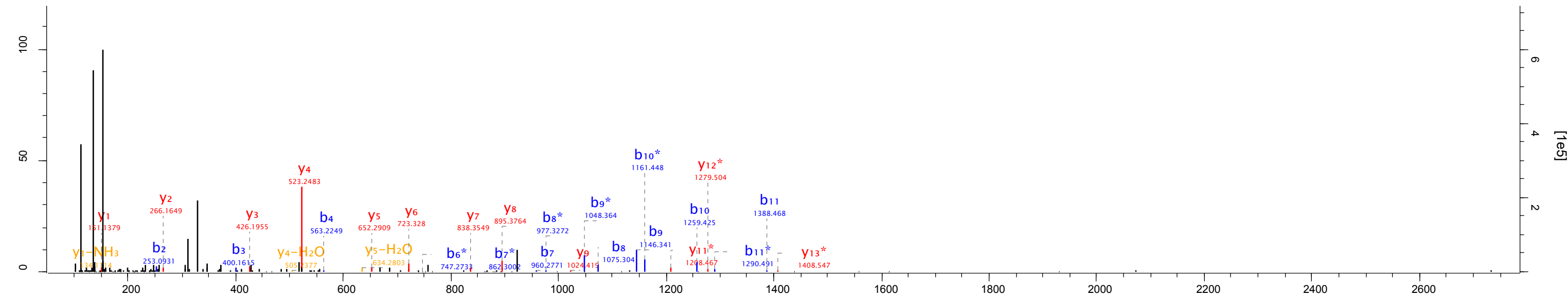


- S E A A A P H T D A G G G L ph S D E E E G T S S Q A E A A R -

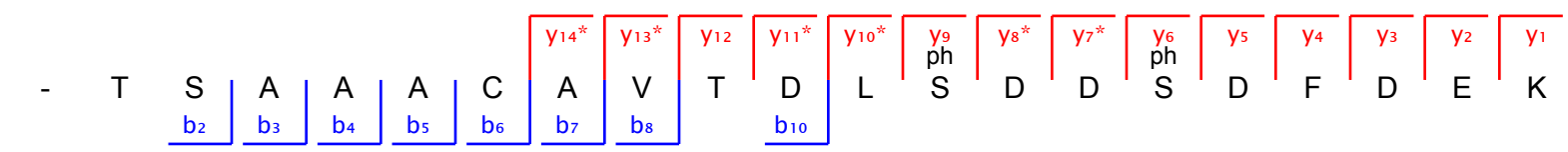
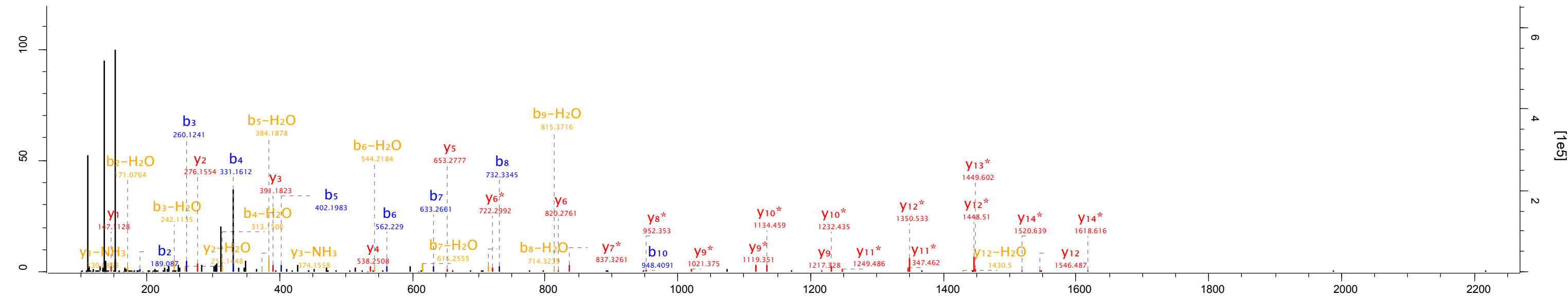
b₂
b₃
b₄
b₅
y₂₆*
y₂₅*
b₇
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃
b₁₄
b₁₅*
y₁₈*
y₁₆*
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

20171215_MaS_33SR_LMH_phospho2_04 8750 FTMS; HCD 56.53 617.77 ITGB4

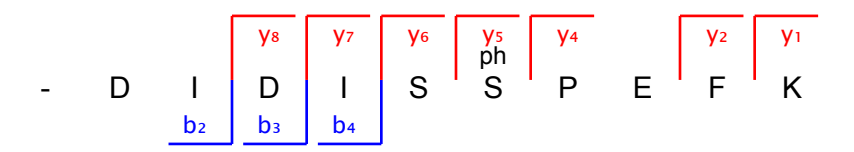
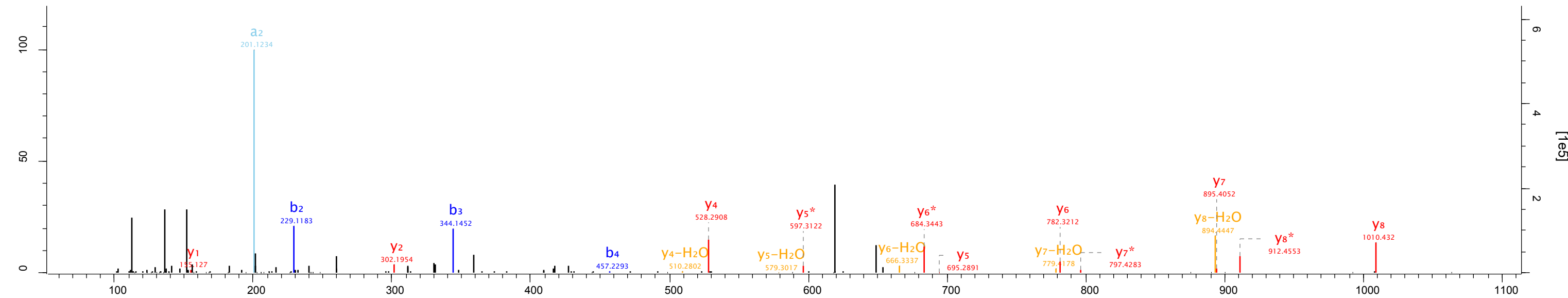




Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 11350 Method FTMS; HCD Score 130.57 m/z 1139.4 Gene names UTP3



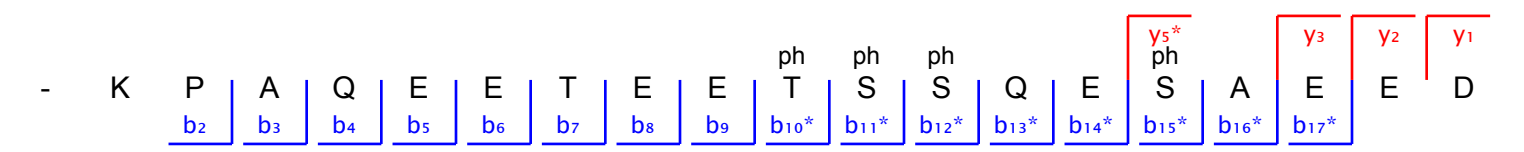
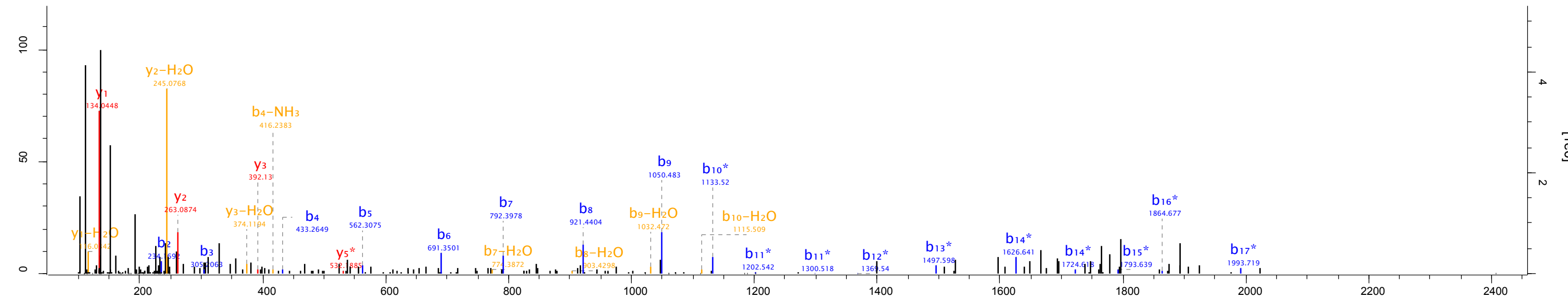
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Raw file

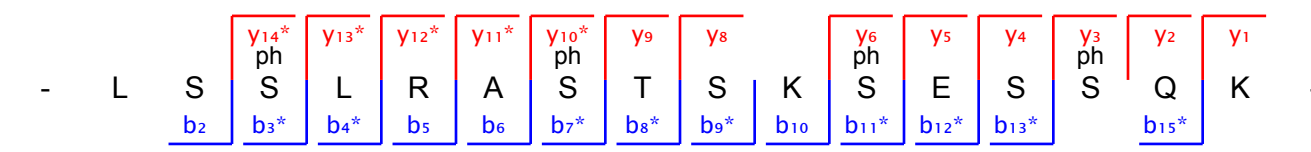
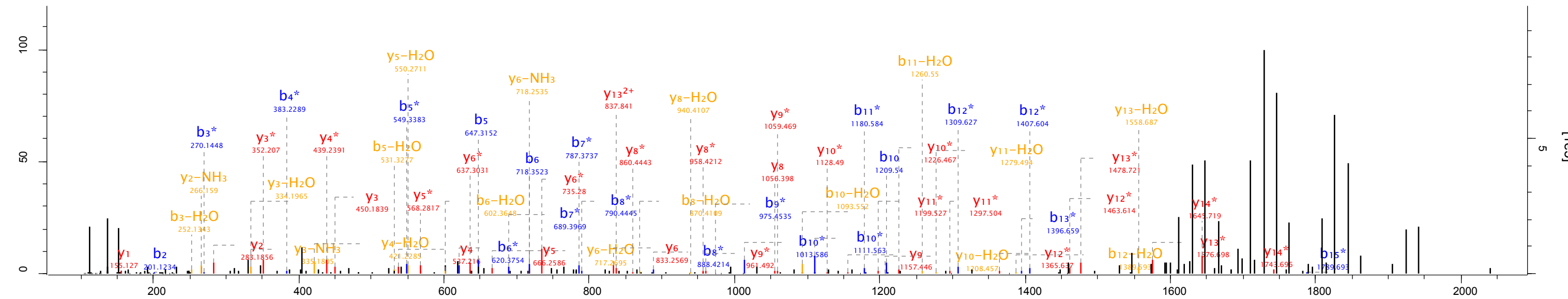
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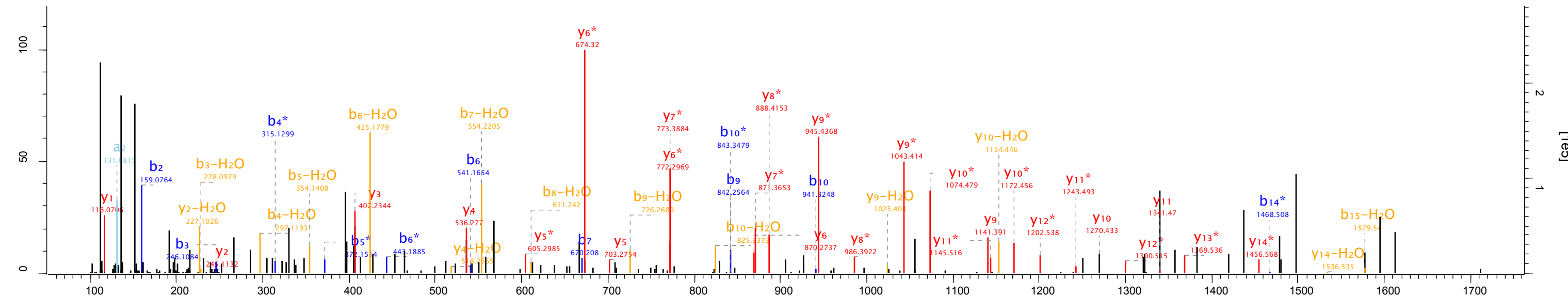
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Raw file
20171215_MaS_33SR_LMH_phospho2_05

Scan 3870 Method FTMS; HCD Score 191.59 m/z 1021.4 Gene names RPS6





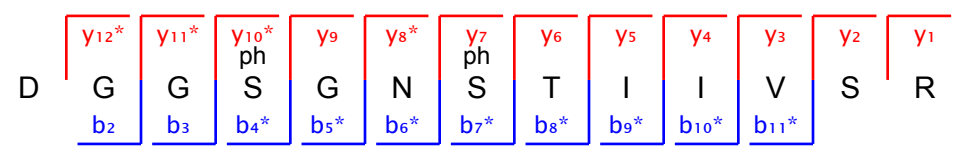
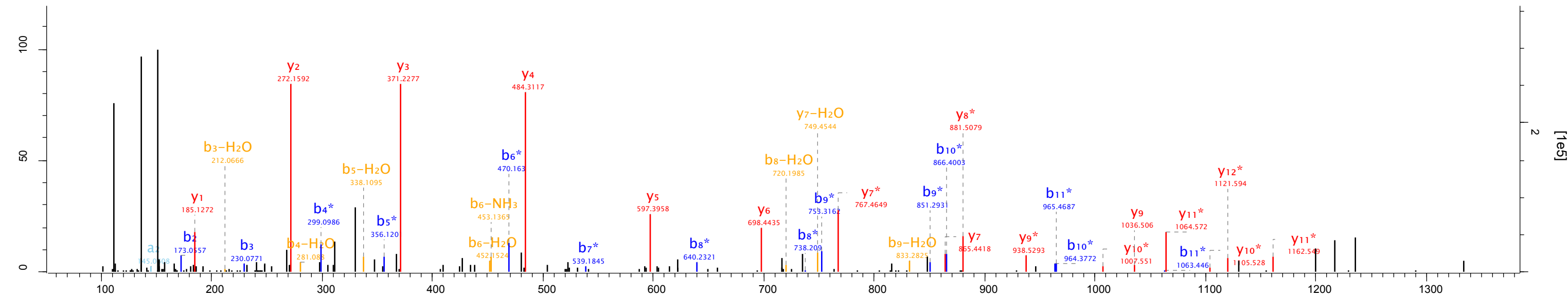
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b₂ b₃ b₄* b₅* b₆ b₇ b₉ b₁₀ b₁₄*

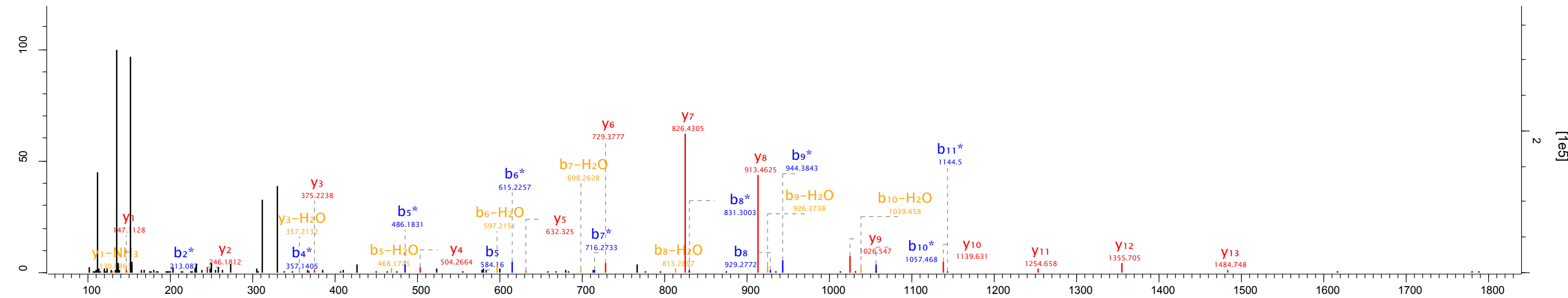
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ph ph

Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 7110 Method FTMS; HCD Score 172.6 m/z 716.79 Gene names HUWE1

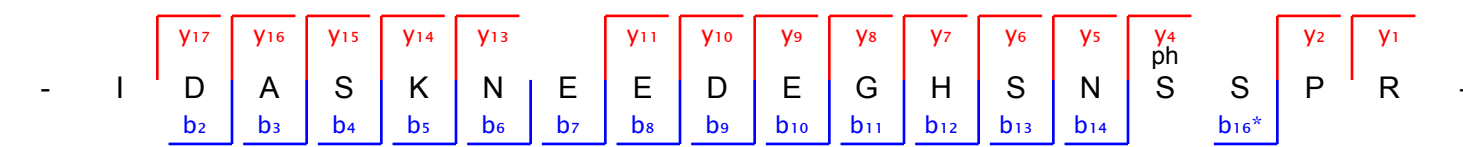
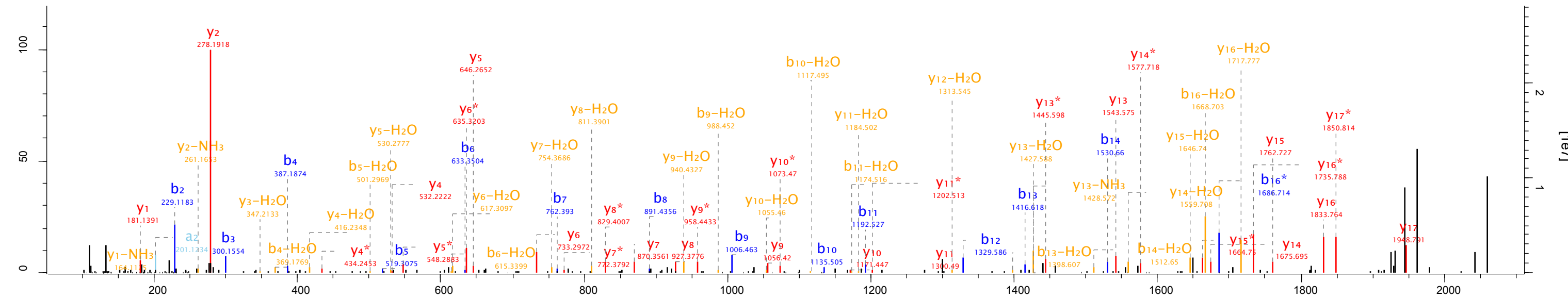


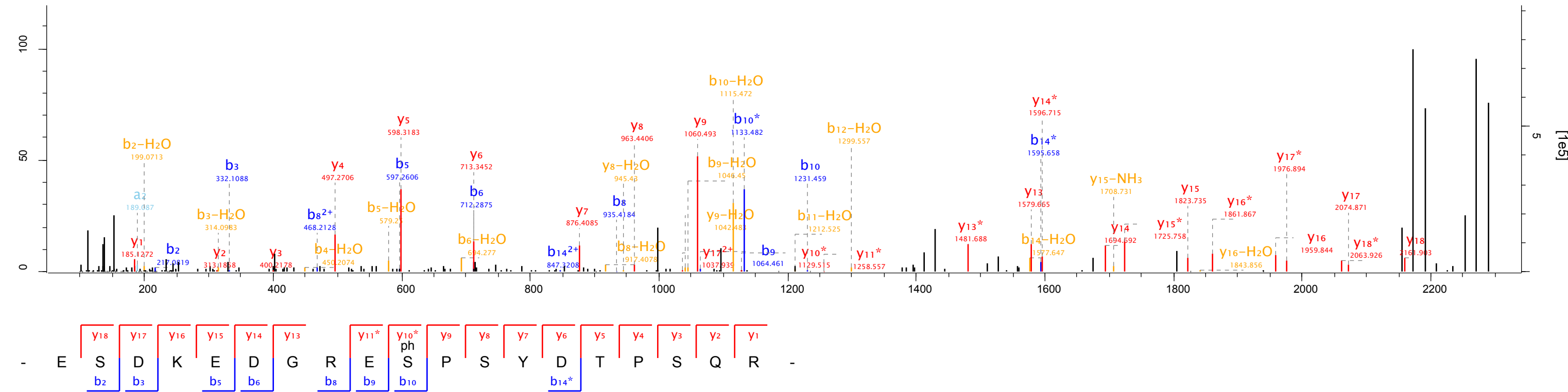
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ph
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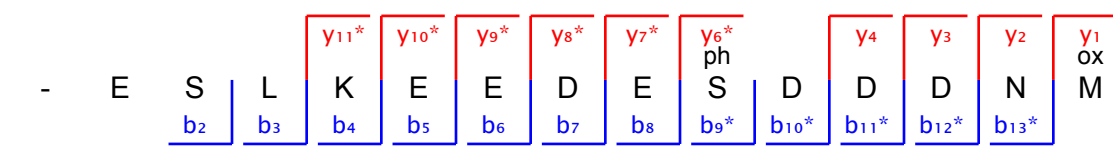
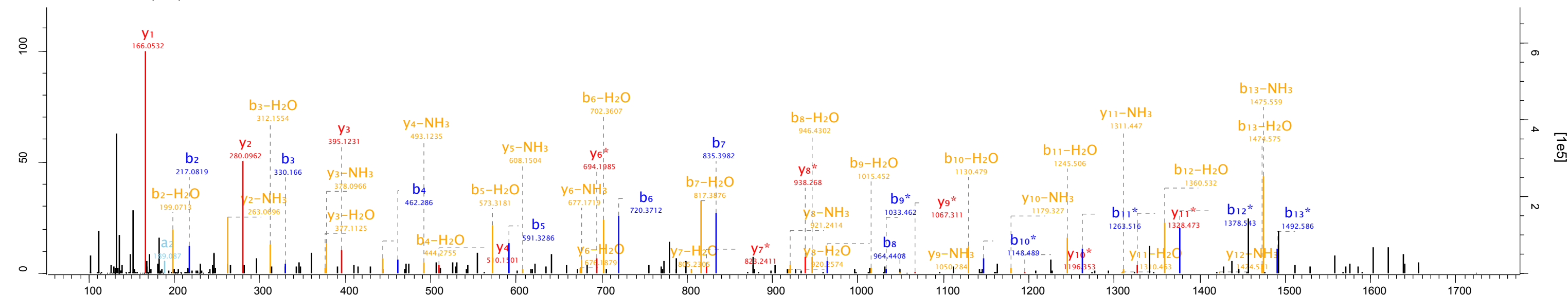
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 - b2* (under E)
 - b4* (under G), b5 (under E), b6* (under E), b7* (under T), b8 (under D), b9* (under L), b10* (under I), b11* (under S)
 - y13 (under E), y12 (under T), y11 (under D), y10 (under L), y9 (under I), y8 (under S), y7 (under P), y6 (under P), y5 (under Q), y4 (under E), y3 (under E), y2 (under V), y1 (under K)



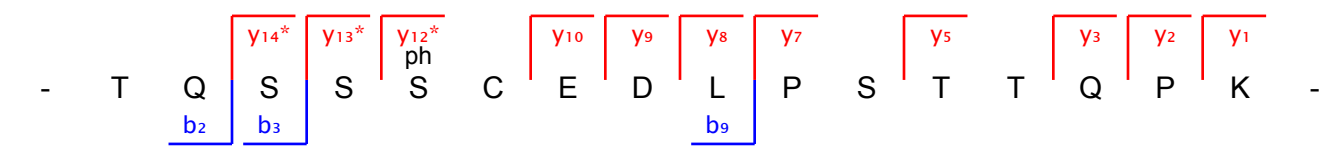
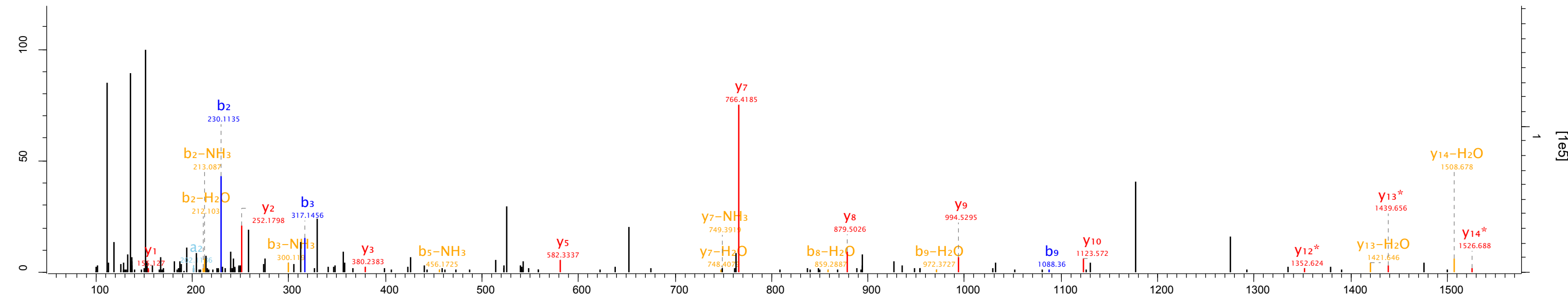


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20171215_MaS_33SR_LMH_phospho2_06

Scan 3020 Method FTMS; HCD Score 214.28 m/z 878.81 Gene names PSMA3



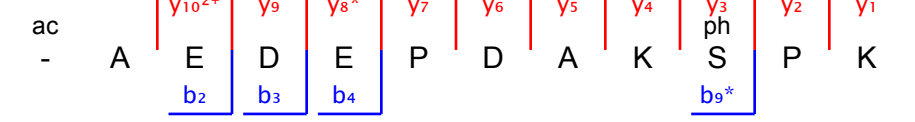
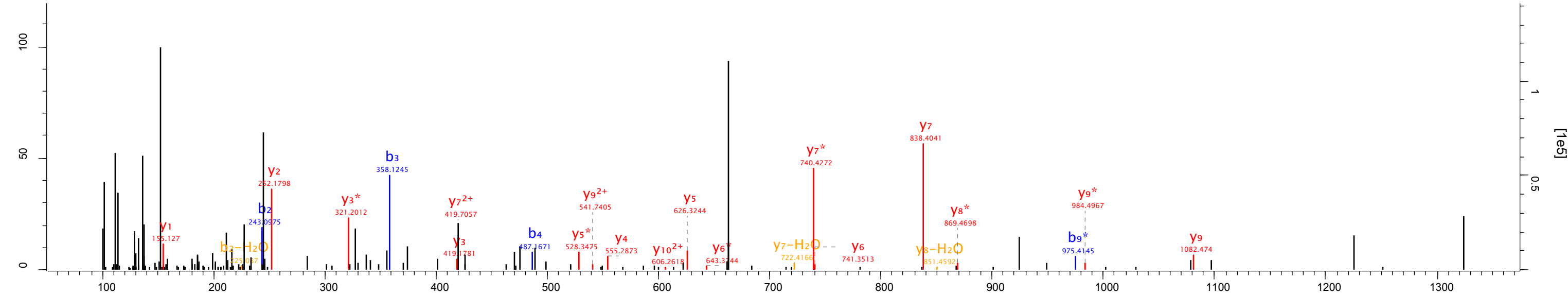
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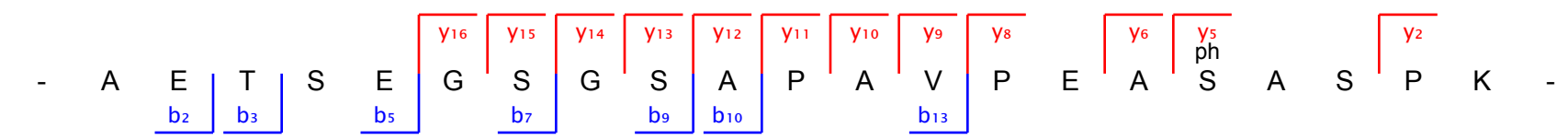
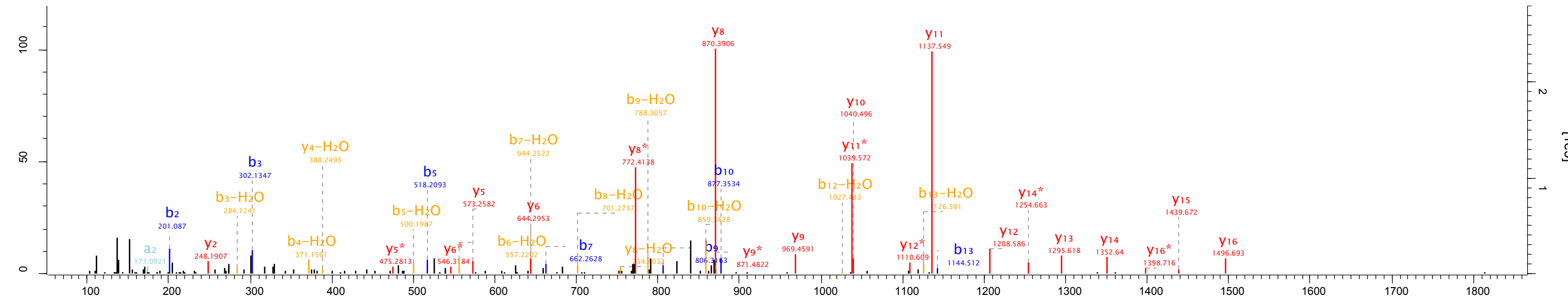
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20171215_MaS_33SR_LMH_phospho2_08

Scan 2910 Method FTMS; HCD Score 75.97 m/z 662.79 Gene names RFX5



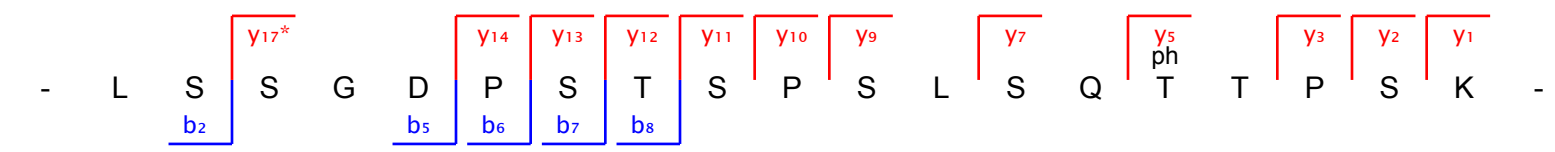
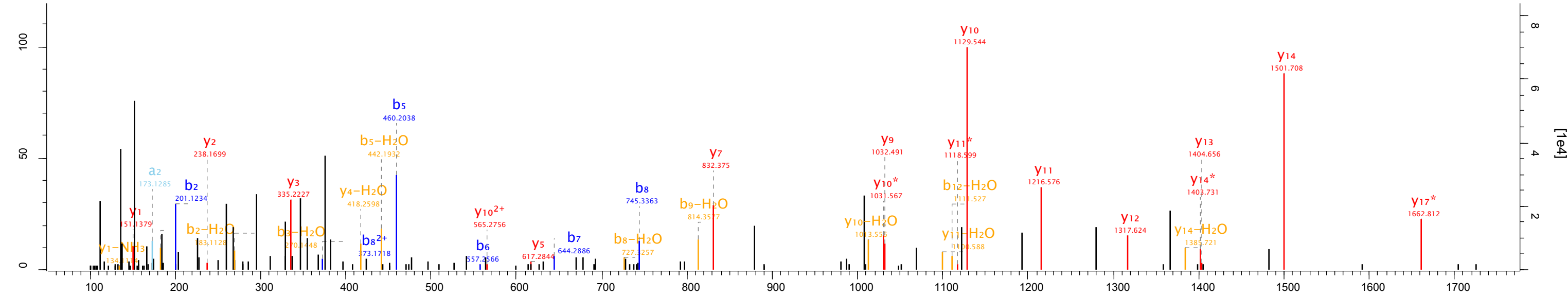
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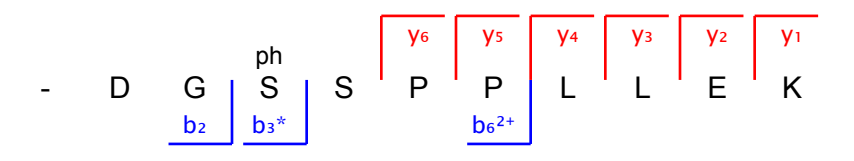
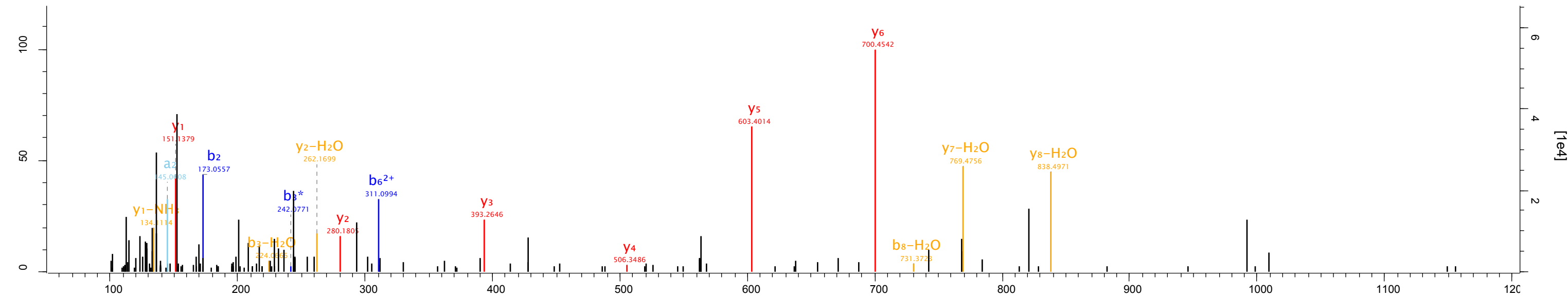
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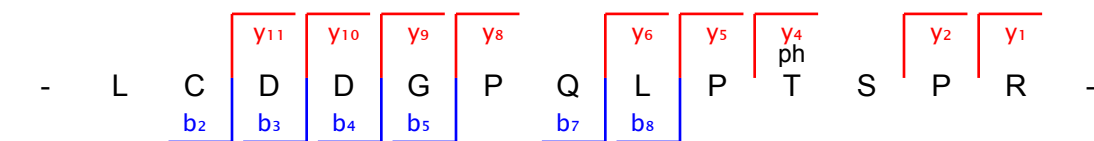
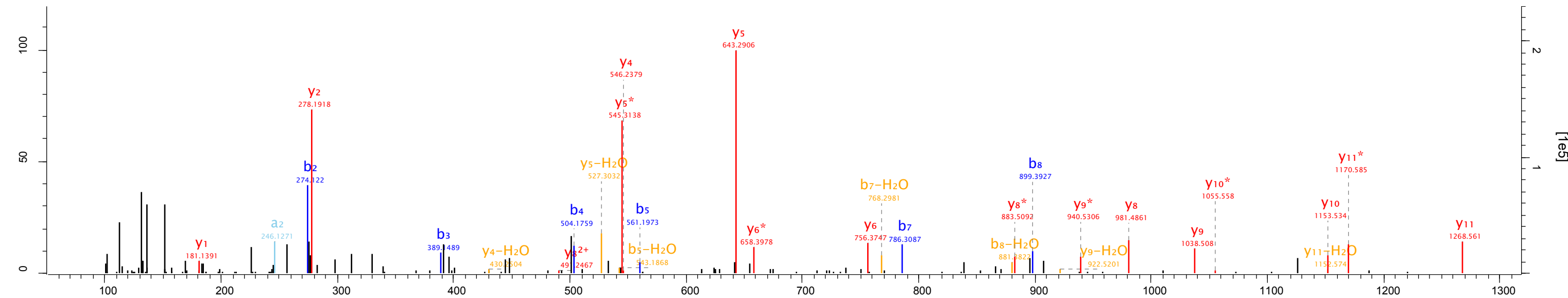
20171215_MaS_33SR_LMH_phospho2_08

Scan	Method	Score	m/z	Gene names
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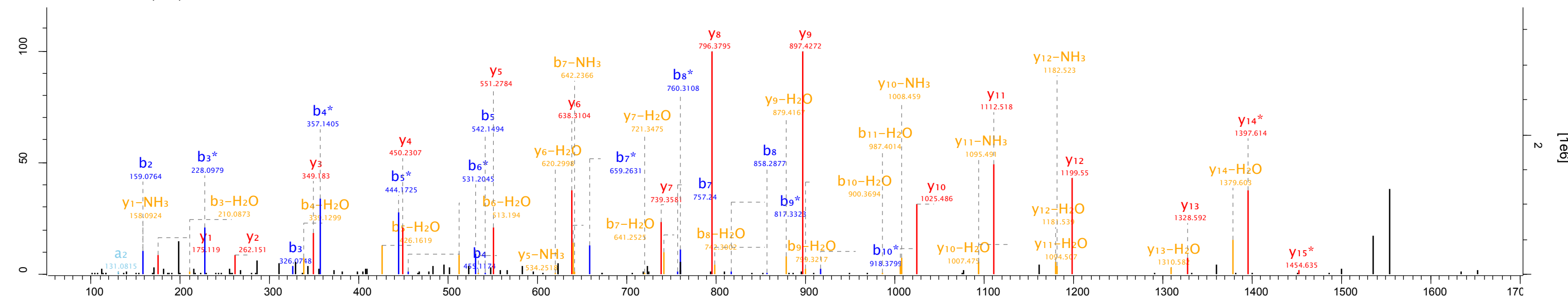
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Raw file
20171215_MaS_33SR_LMH_phospho2_09

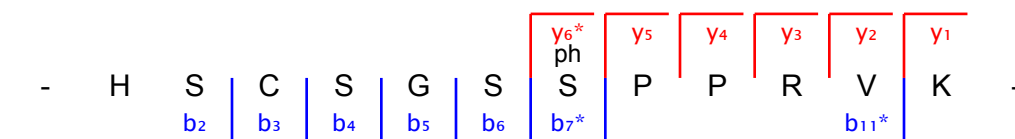
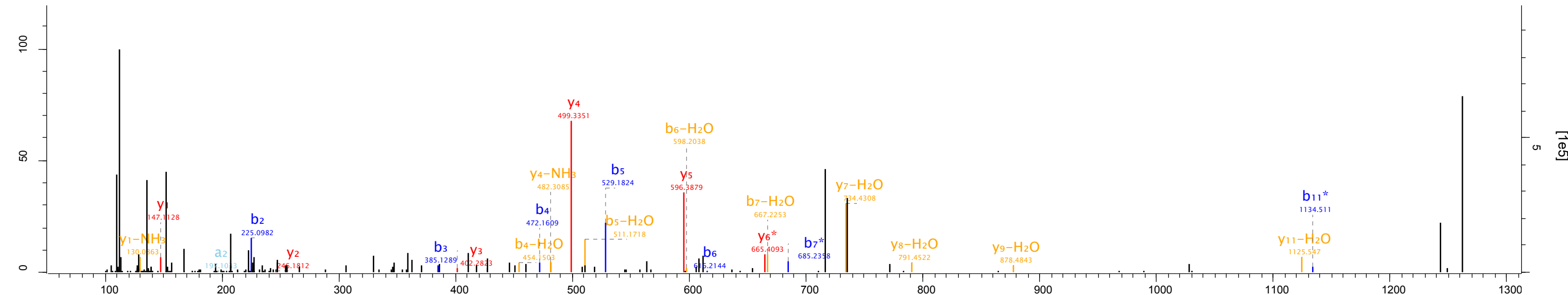
Scan 1960 Method FTMS; HCD Score 236.96 m/z 827.33 Gene names EIF4B



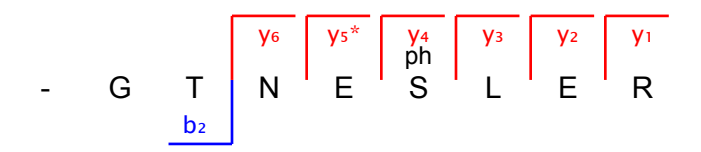
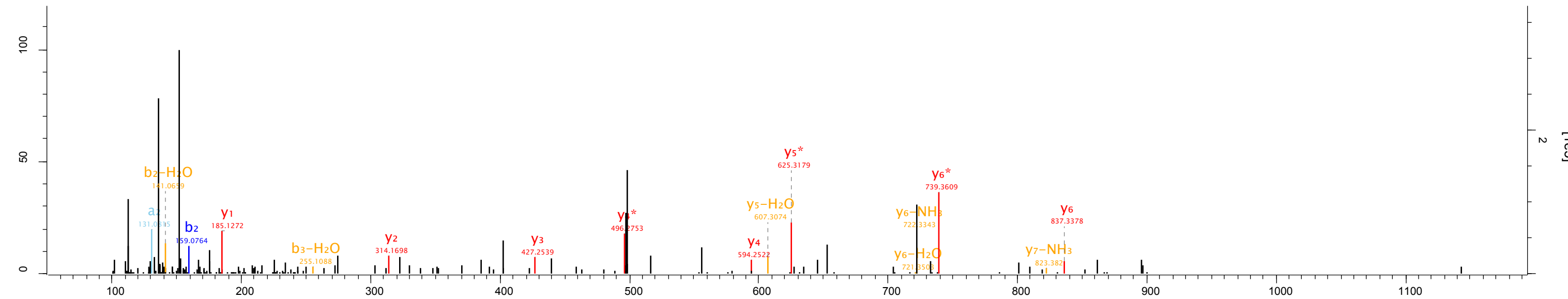
- T G S E S S Q T G T S T T S S R -

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y12
y11
y10
y9
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y6
y5
y4
y3
y2
y1

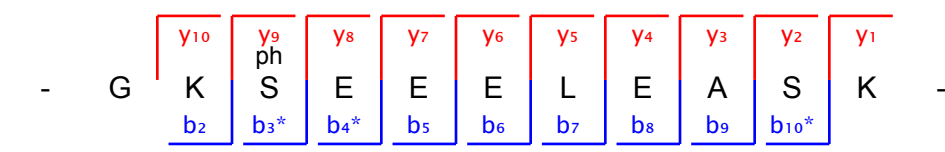
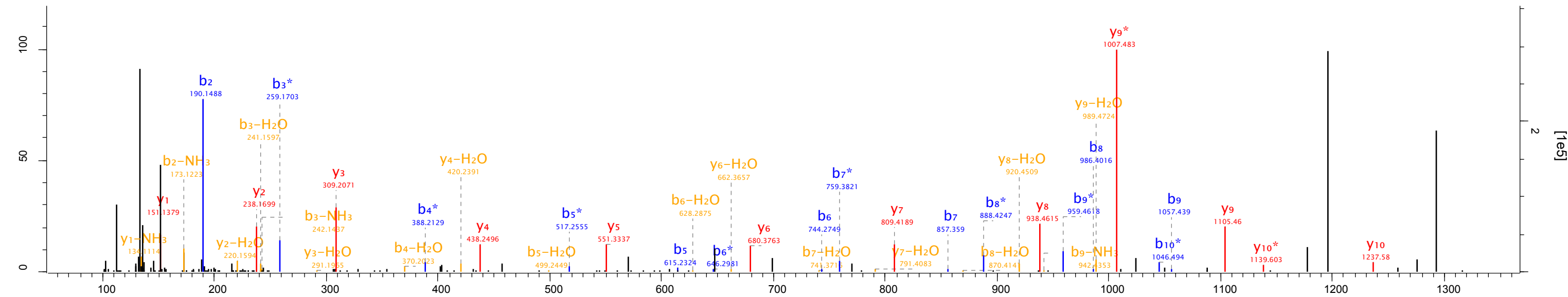
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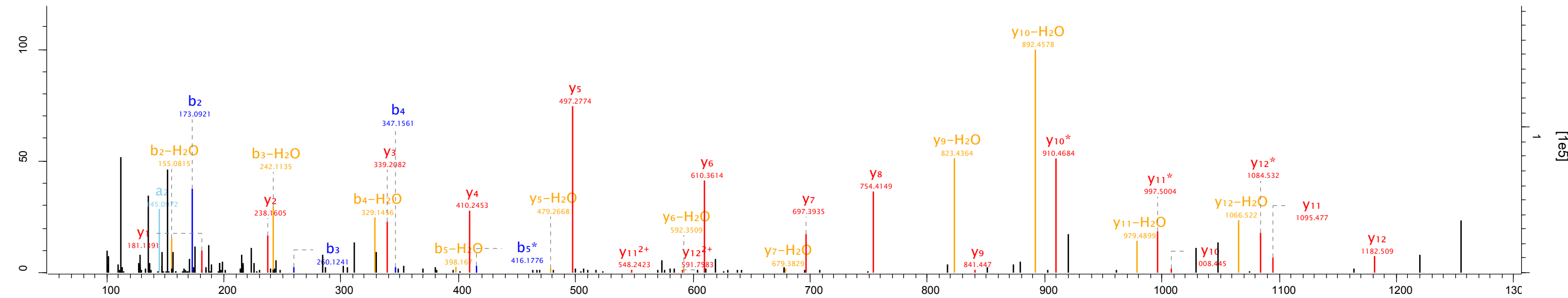


Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 2650 Method FTMS; HCD Score 64.1 m/z 498.21 Gene names VIM;GFAP



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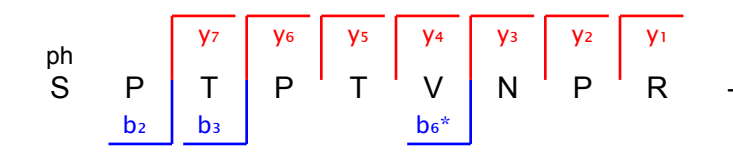
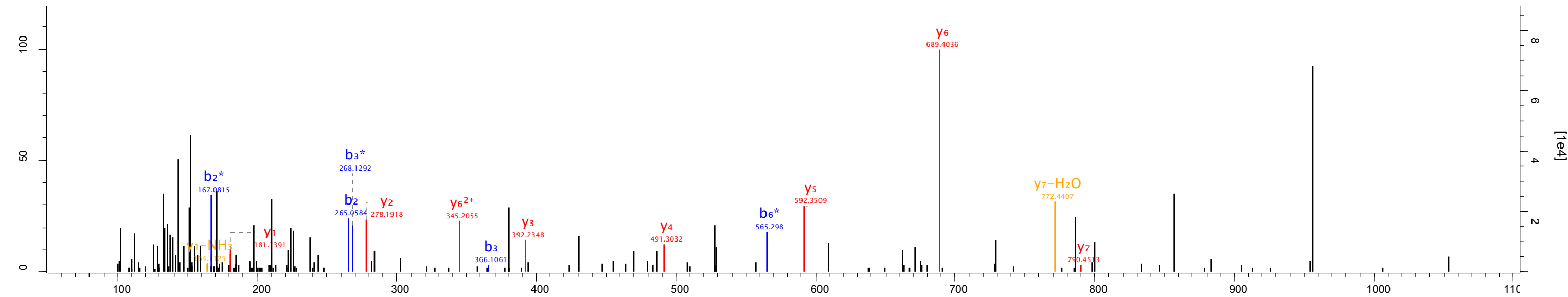


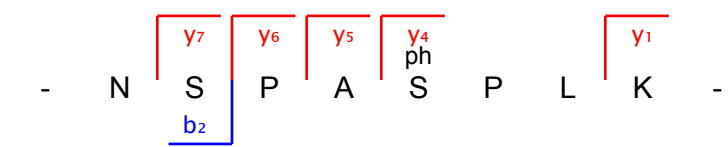
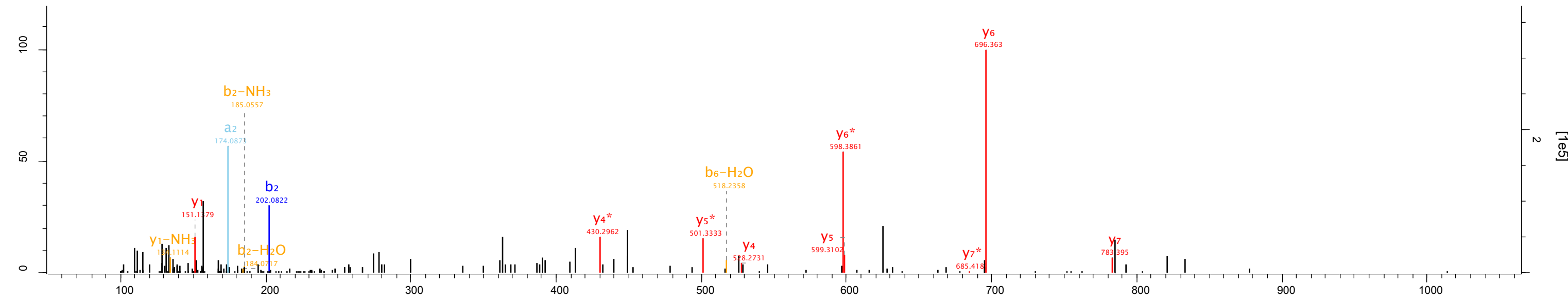


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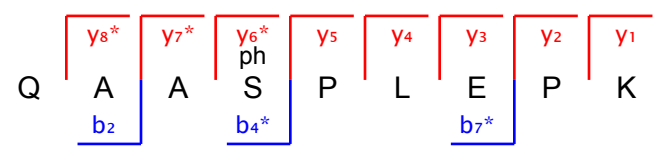
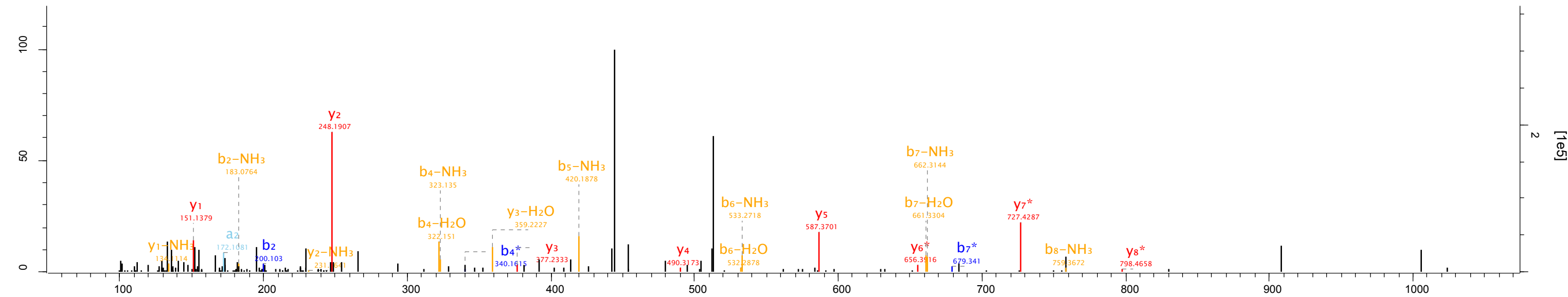
b₂
b₃
b₄
b₅*
y₁₂
y₁₁
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y₂
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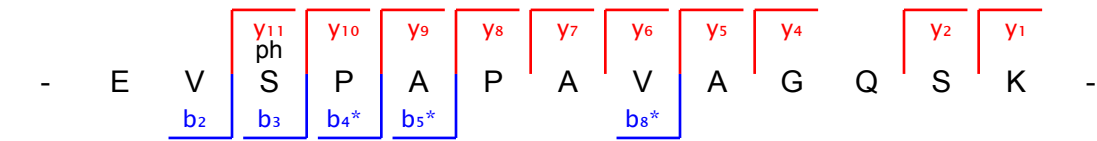
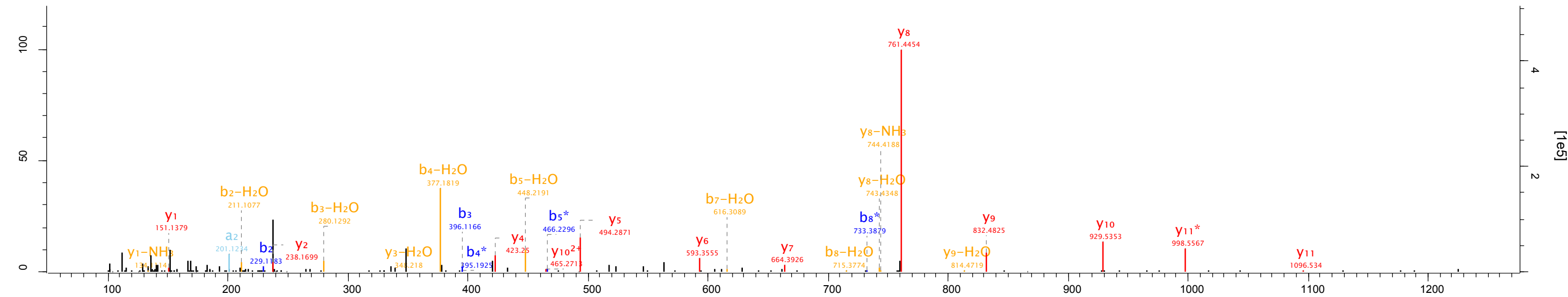
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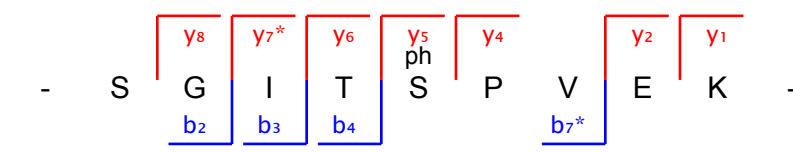
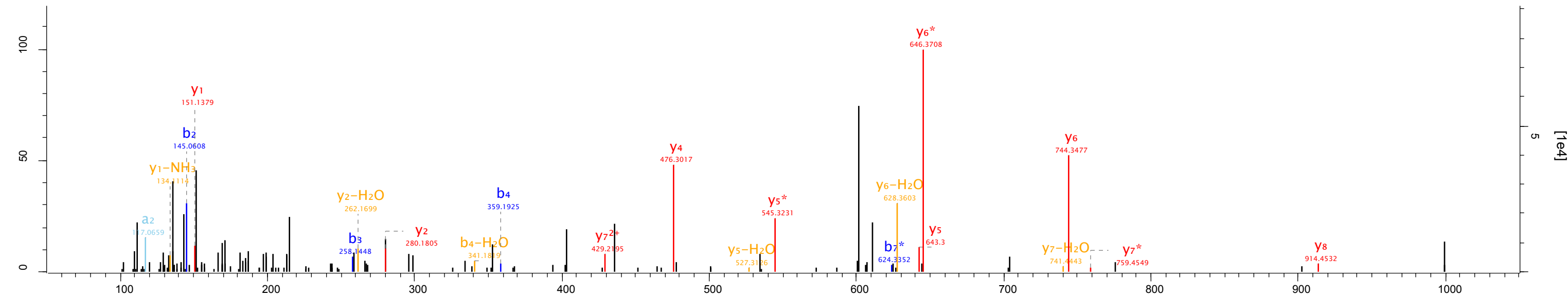


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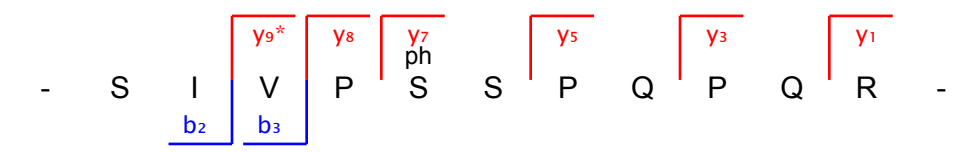
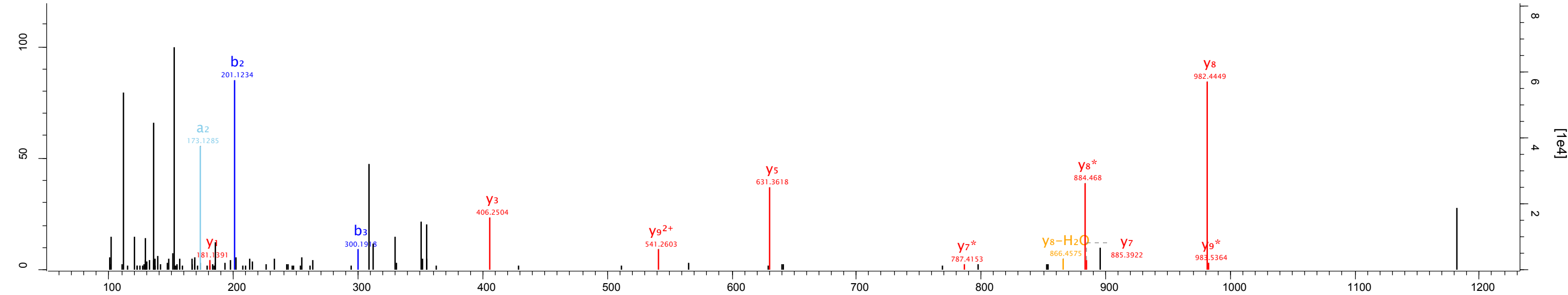


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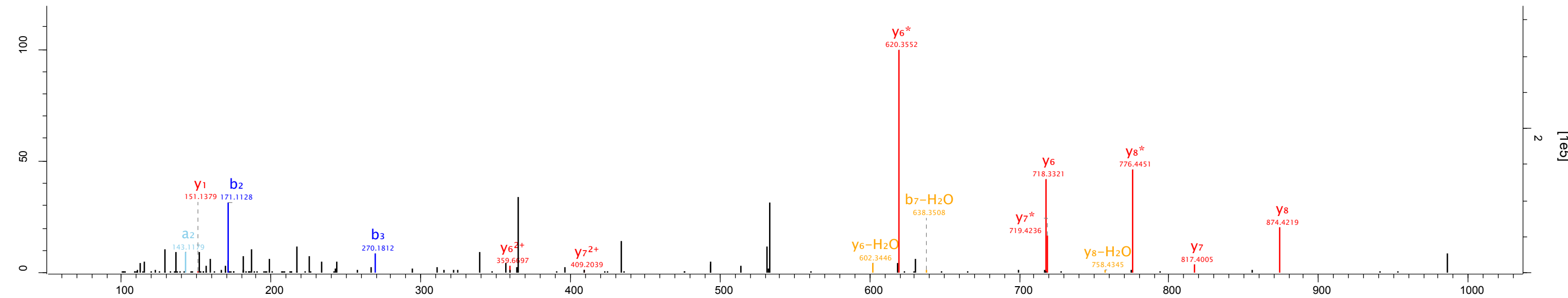
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20171215_MaS_33SR_LMH_phospho2_09

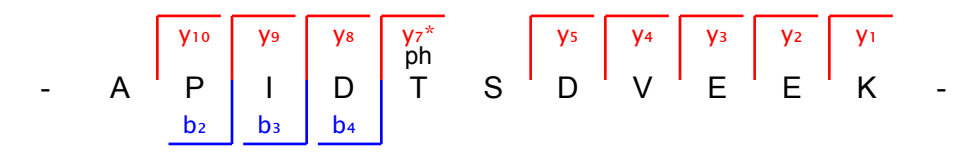
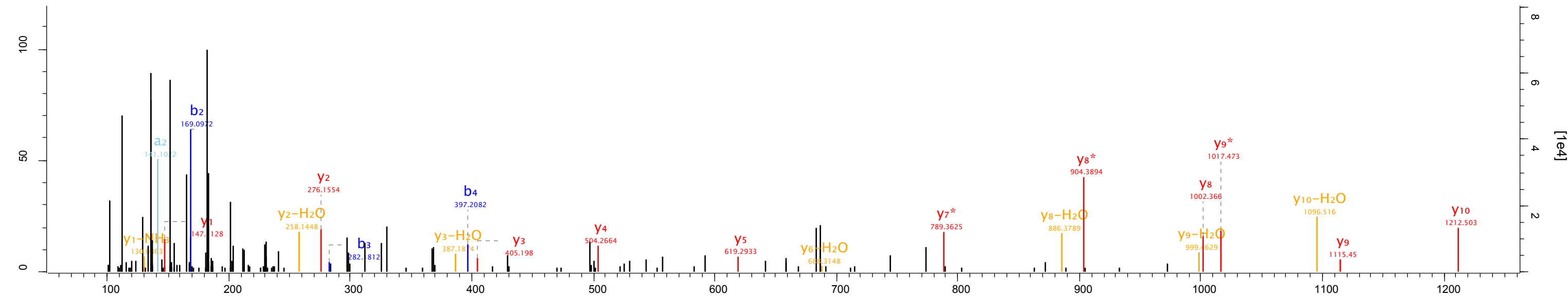
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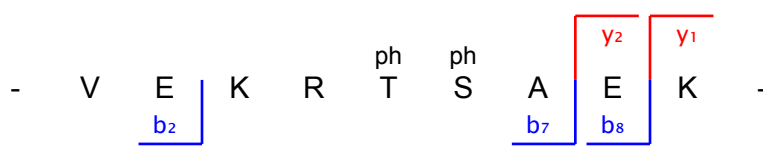
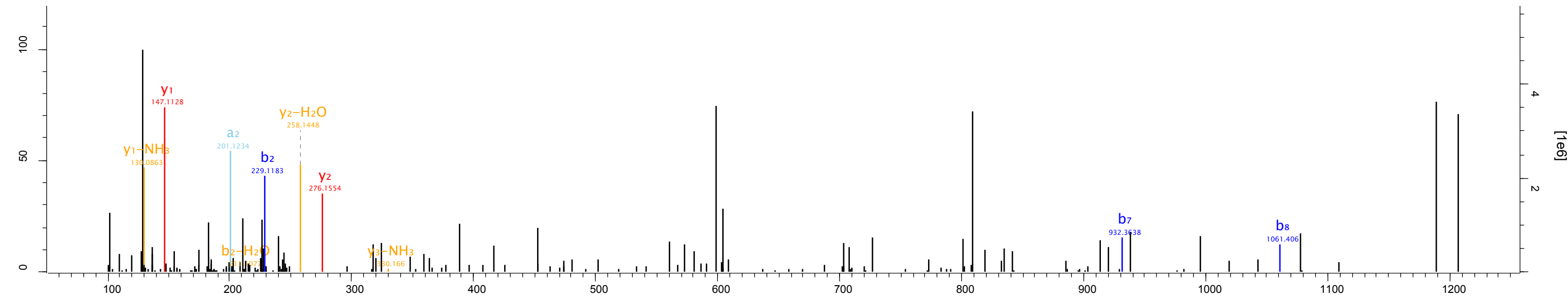
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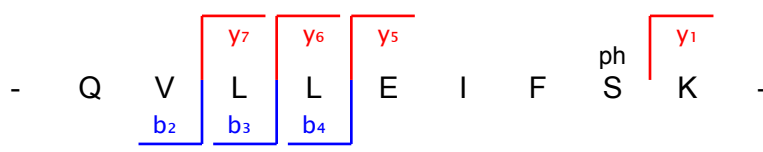
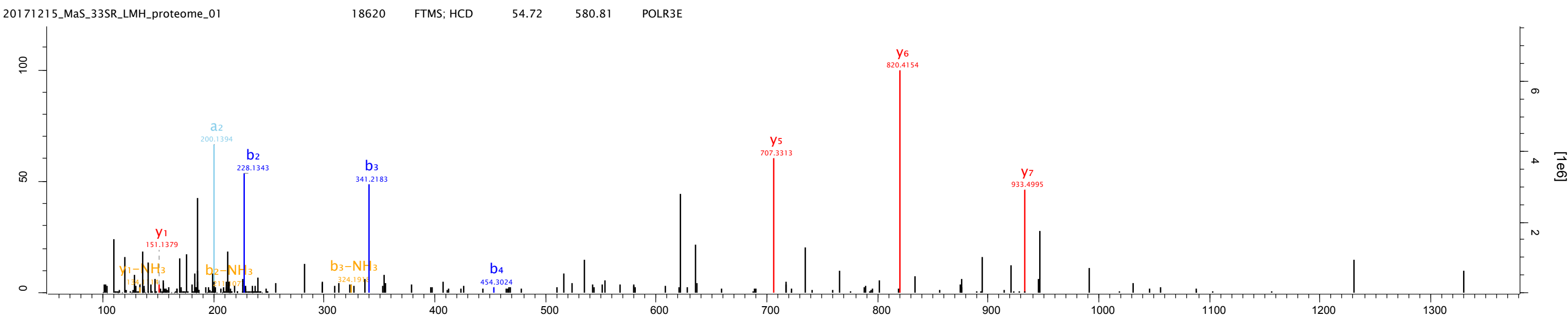
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Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 17020 Method FTMS; HCD Score 68.22 m/z 604.26 Gene names PLCG2

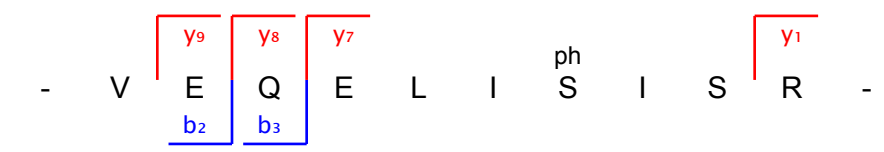
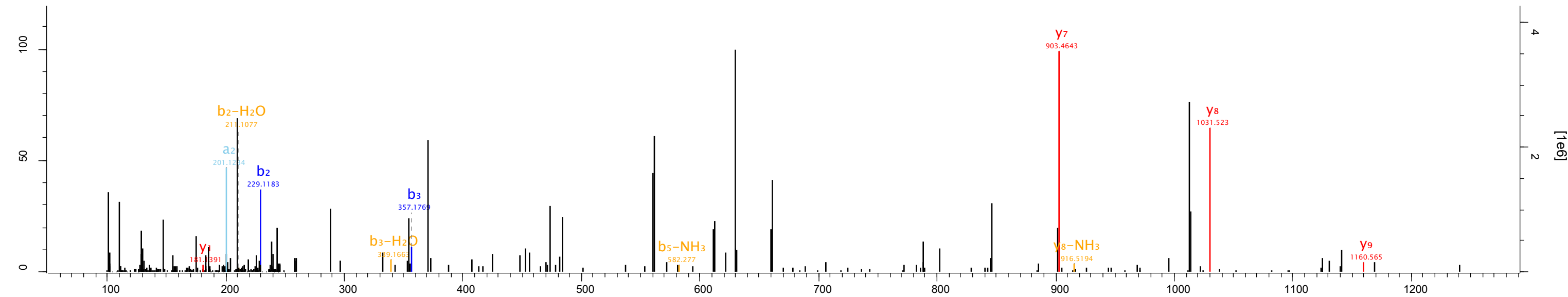


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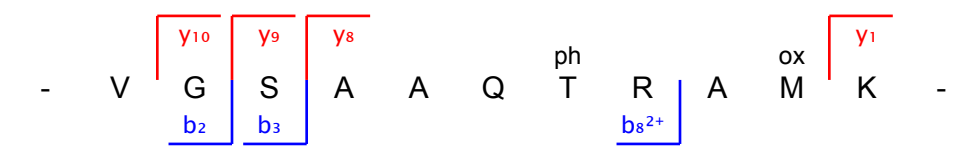
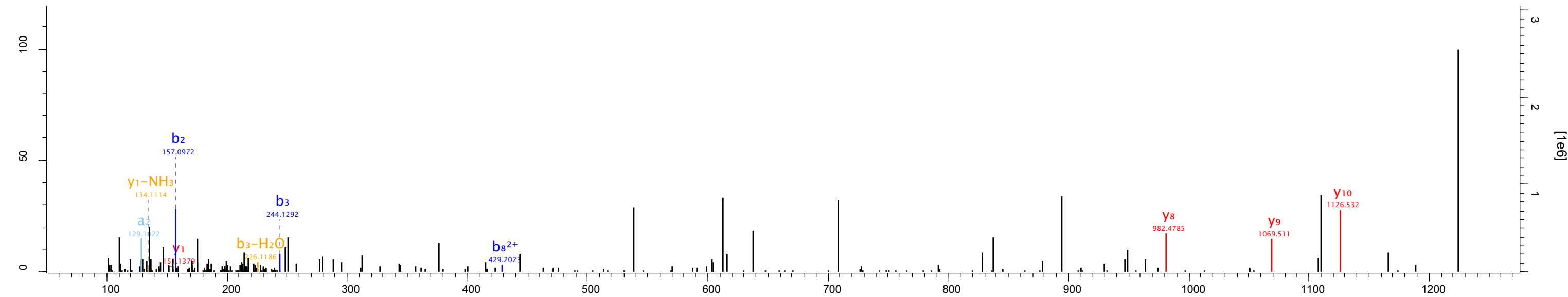


Raw file
20171215_MaS_33SR_LMH_proteome_01

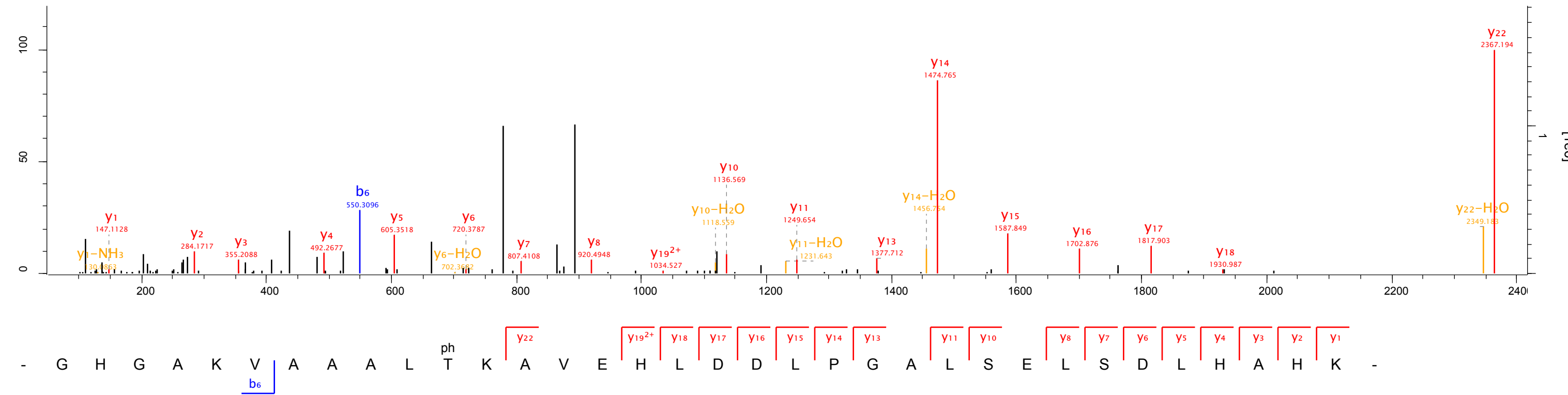
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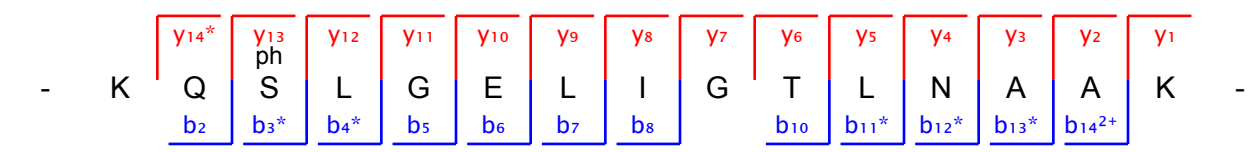
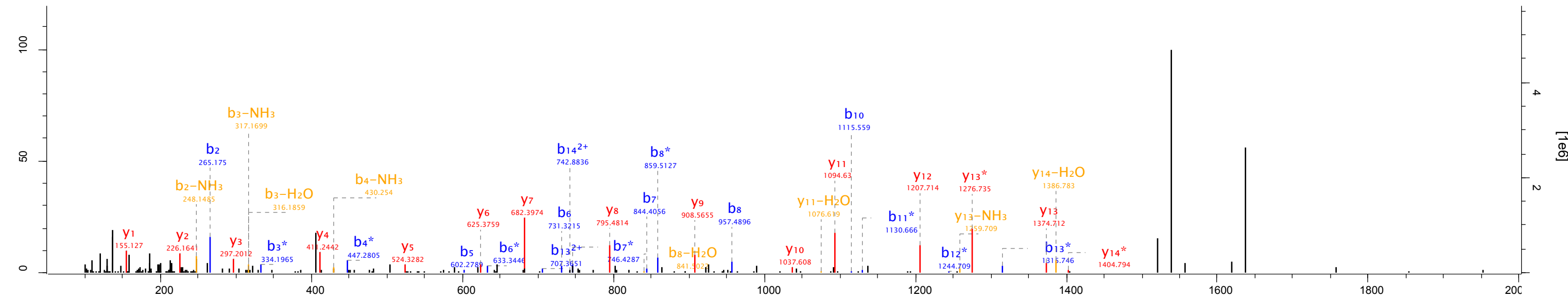
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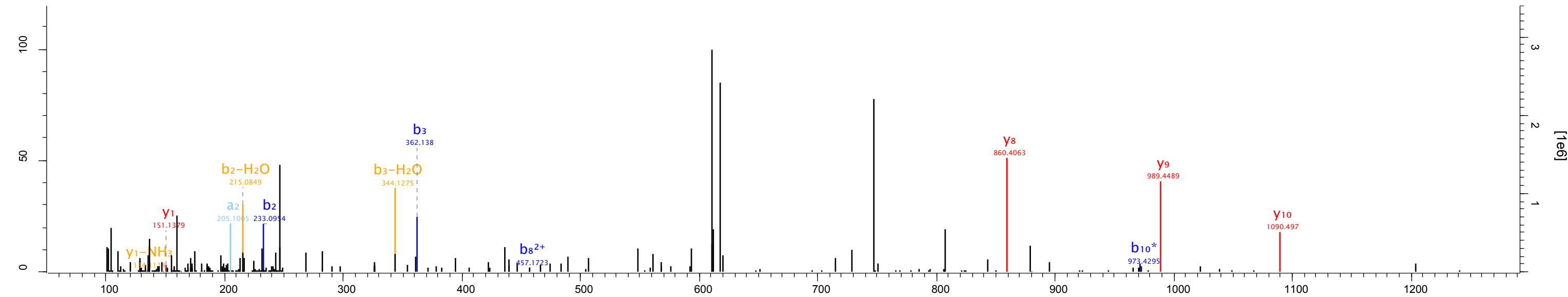
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20171215_MaS_33SR_LMH_proteome_01
Scan 83080 Method FTMS; HCD Score 60.76 m/z 1184.6



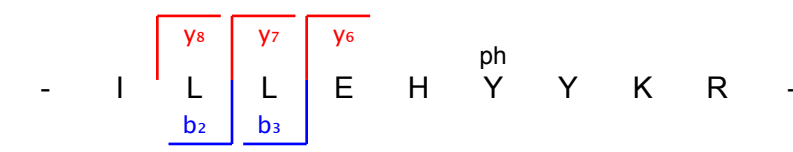
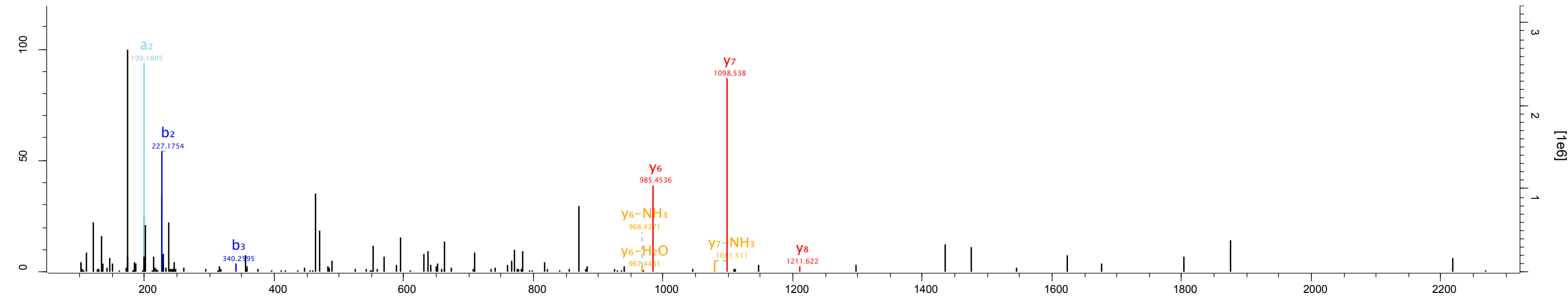
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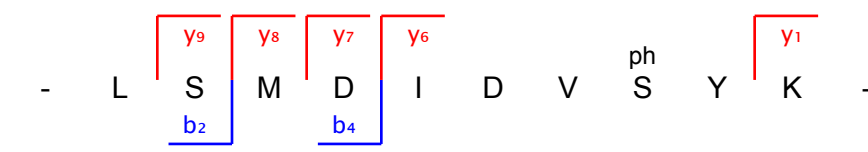
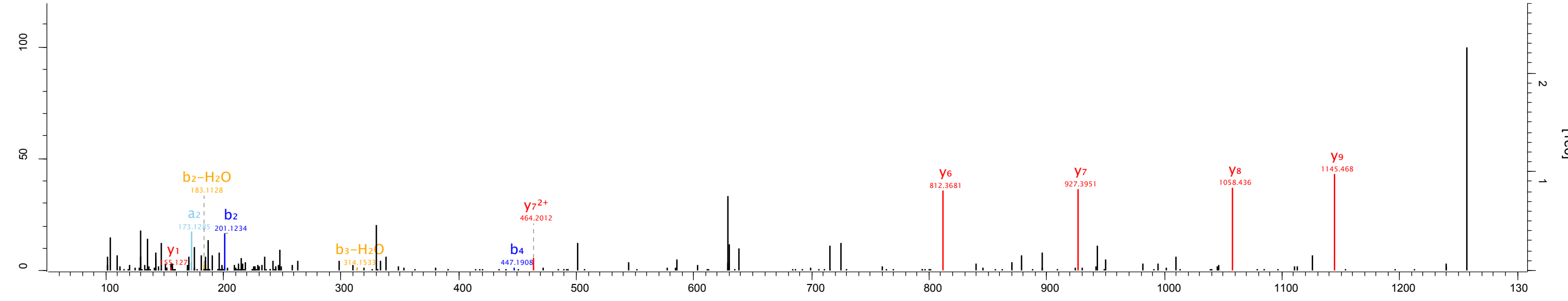
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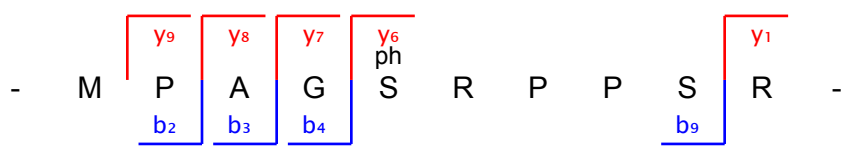
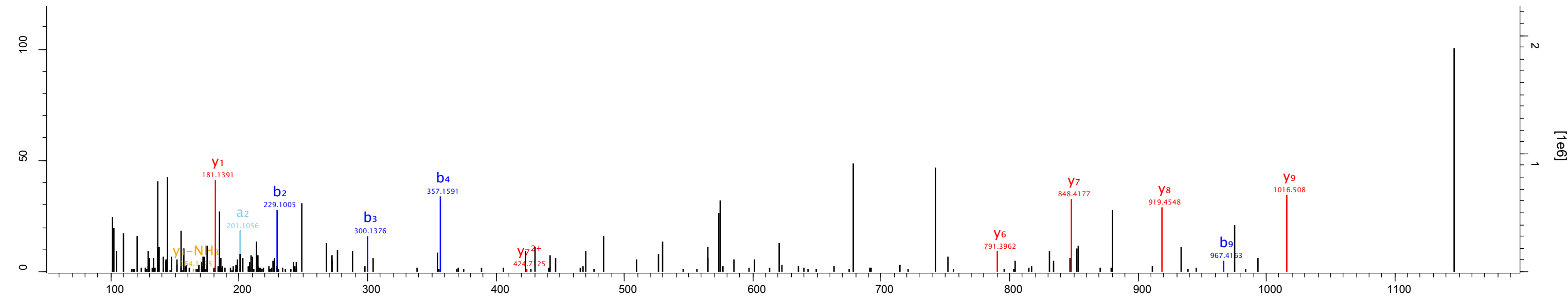
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20171215_MaS_33SR_LMH_proteome_02

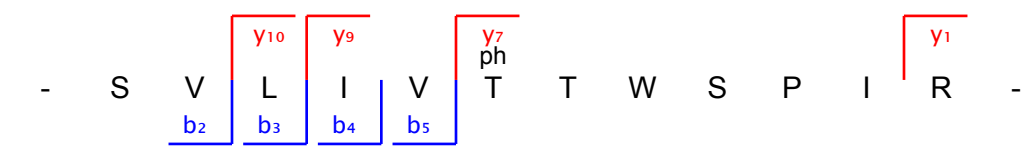
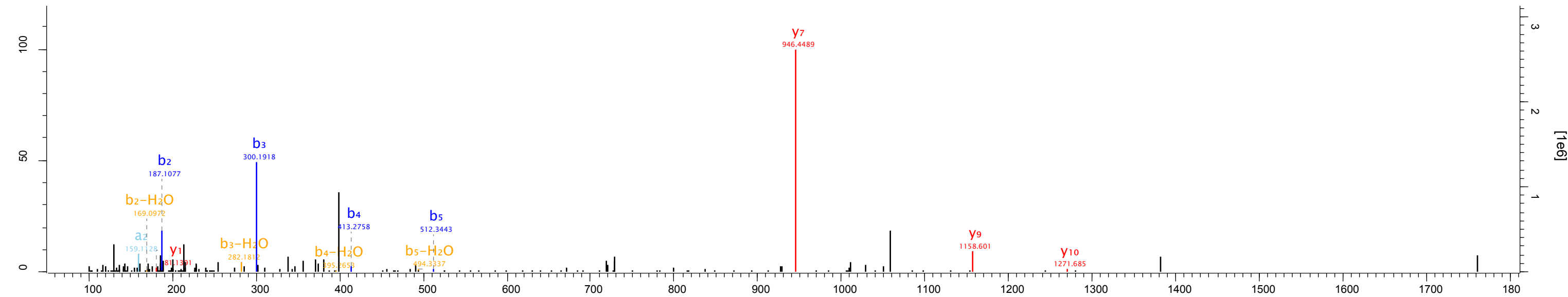
Scan	Method	Score	m/z	Gene names
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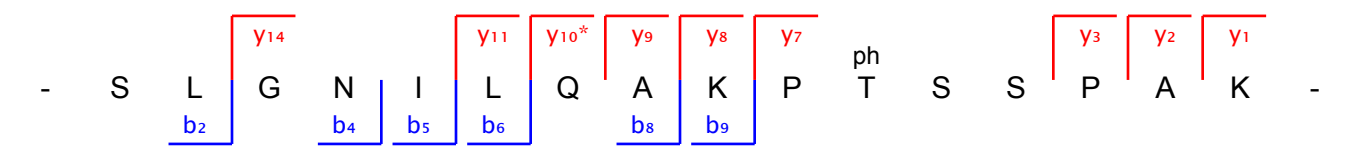
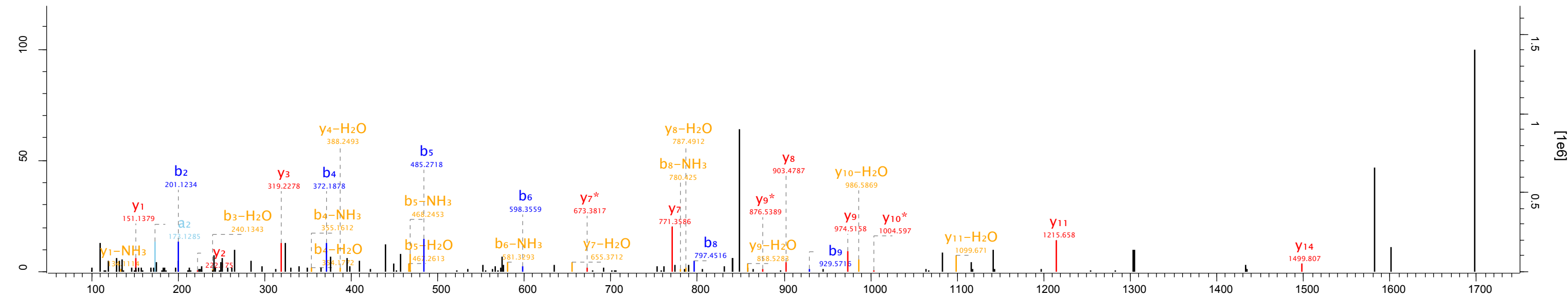
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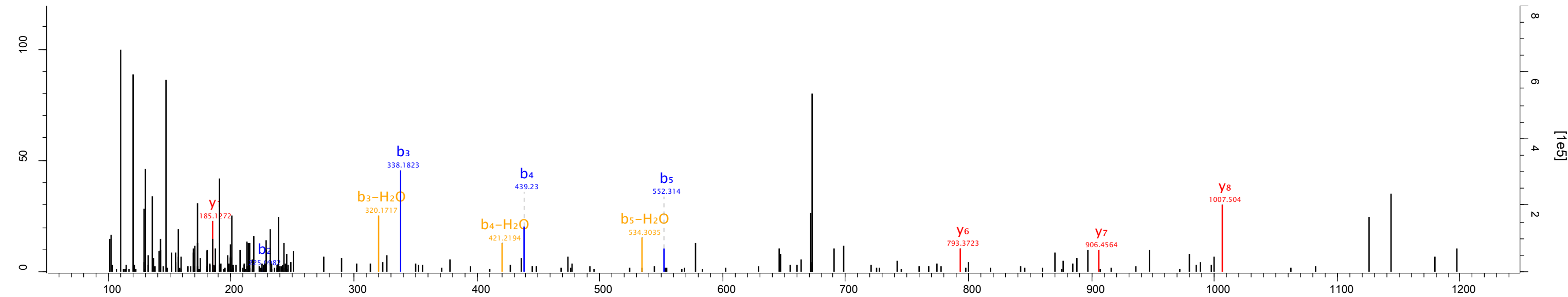
Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 32510 Method FTMS; HCD Score 59.2 m/z 729.39



Raw file: 20171215_MaS_33SR_LMH_proteome_02
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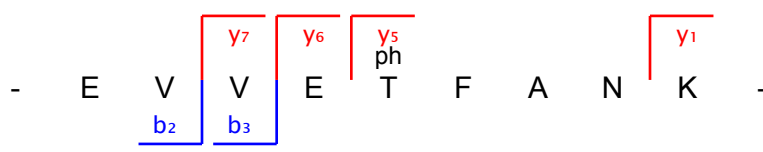
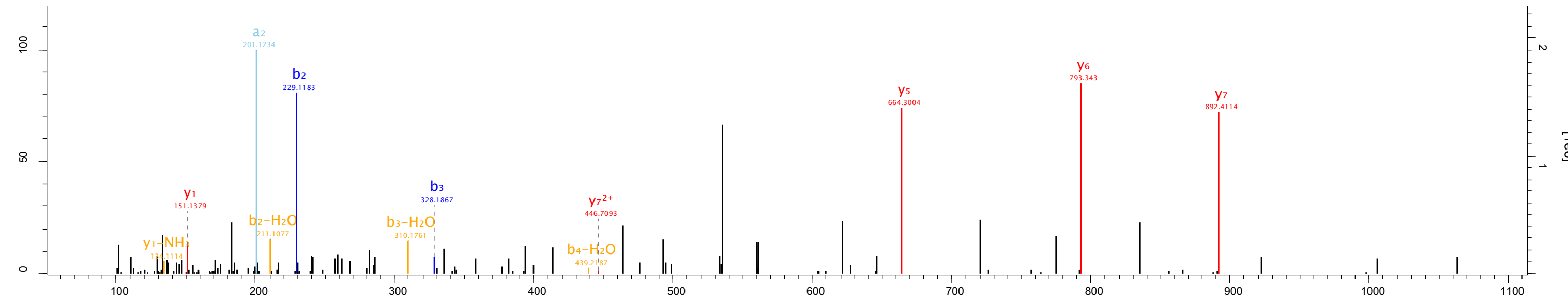
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- S H L T I A ph S K A Y R -

Fragmentation mapping: b₂ (H), b₃ (HL), b₄ (LTI), b₅ (LTI), y₈ (TL), y₇ (TI), y₆ (TIA), y₁ (YR).

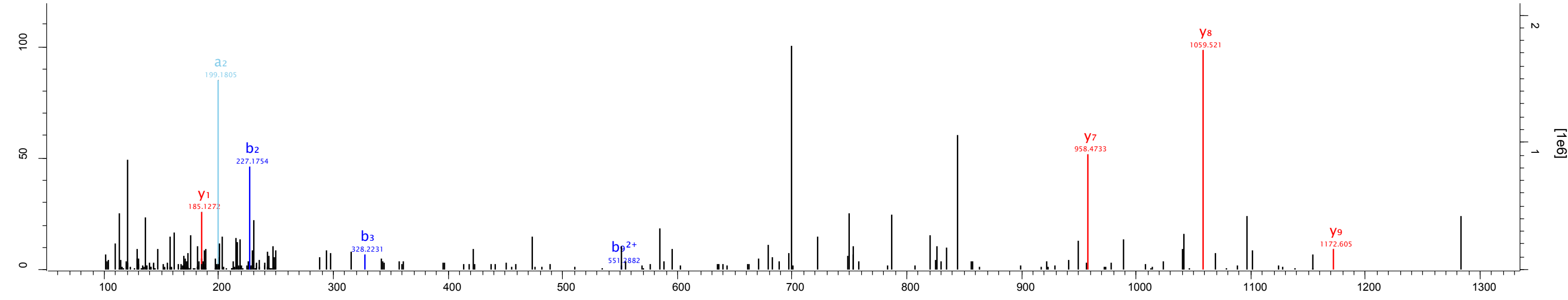
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 Scan: 5170 Method: FTMS; HCD Score: 67.9 m/z: 560.76 Gene names: RGPD5;RGPD8



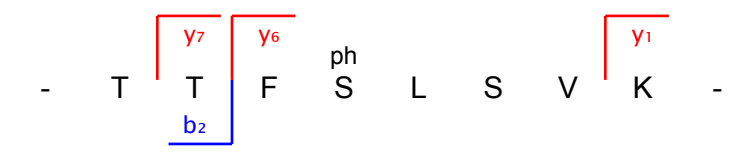
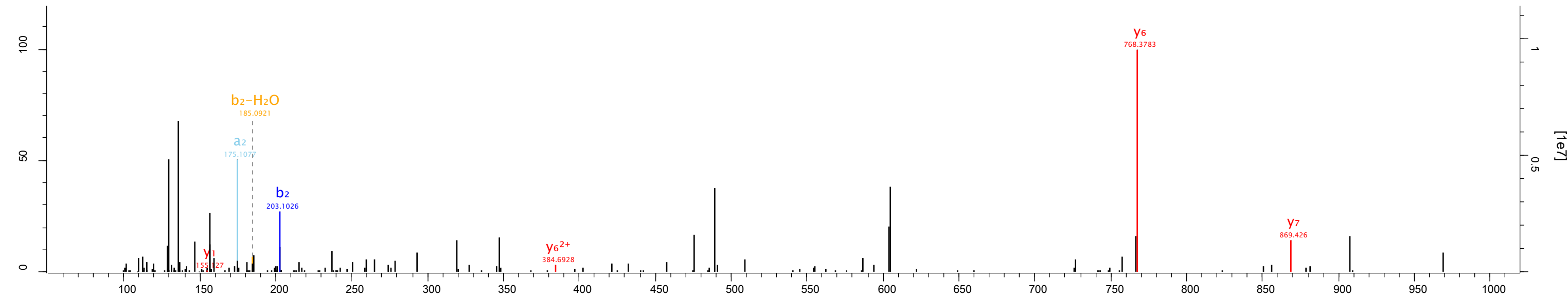
Raw file

20171215_MaS_33SR_LMH_proteome_02

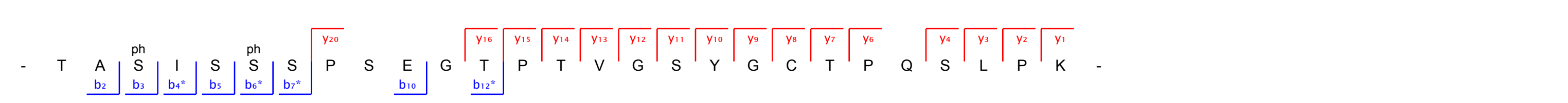
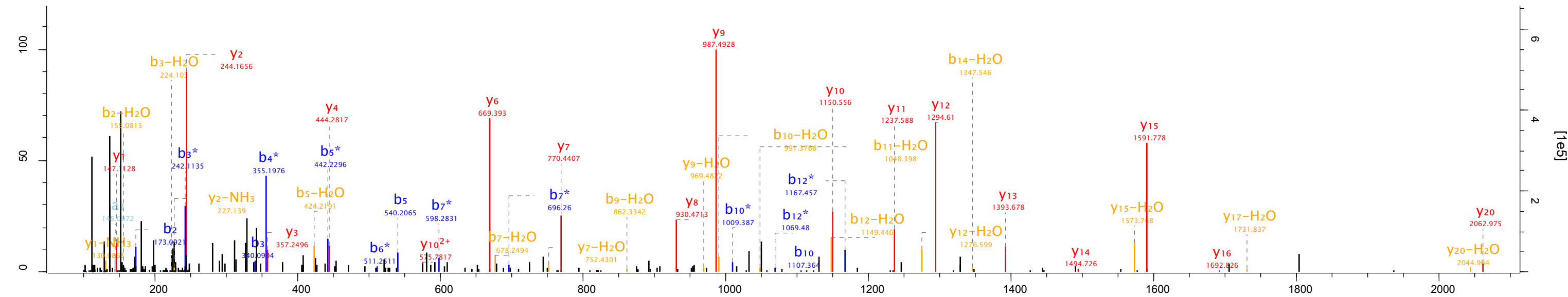
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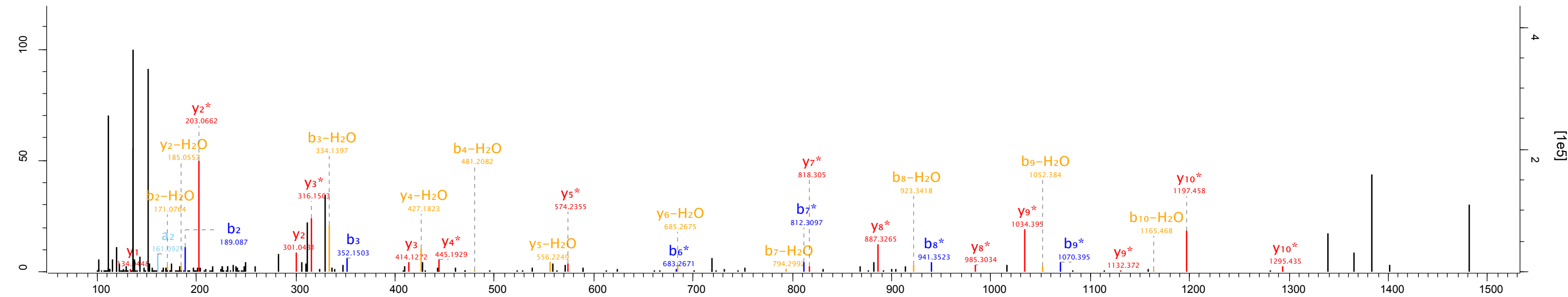
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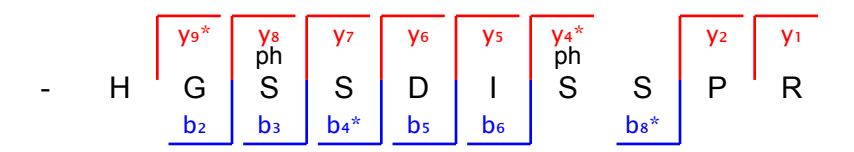
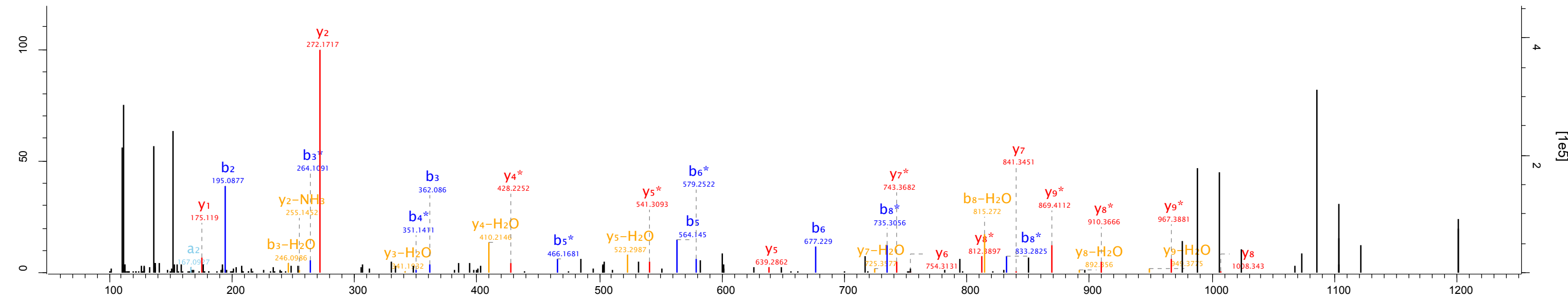
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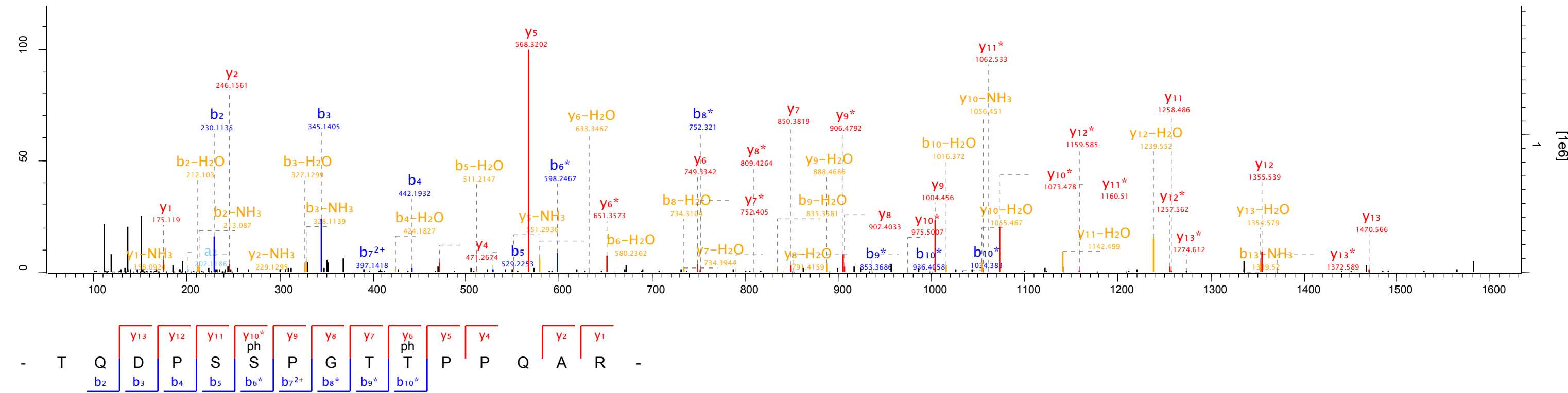


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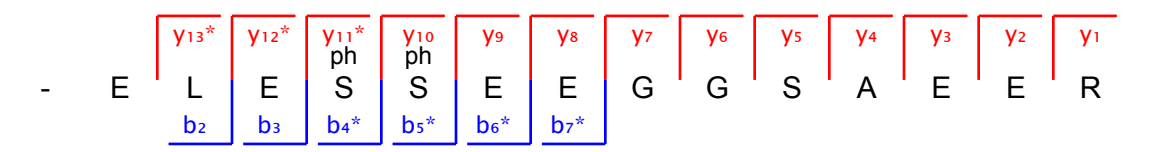
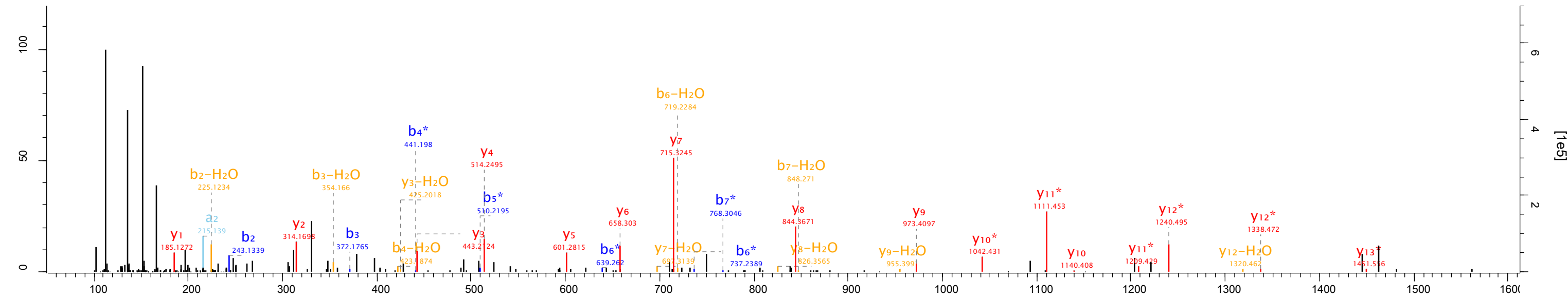


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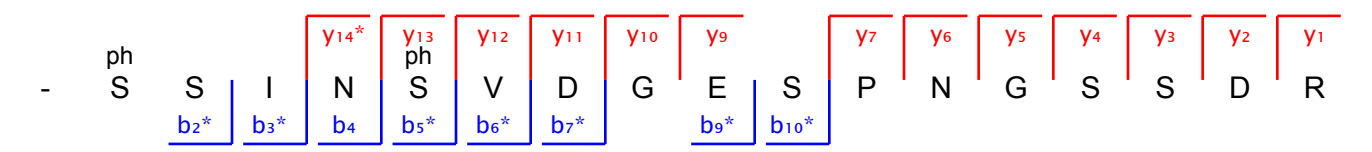
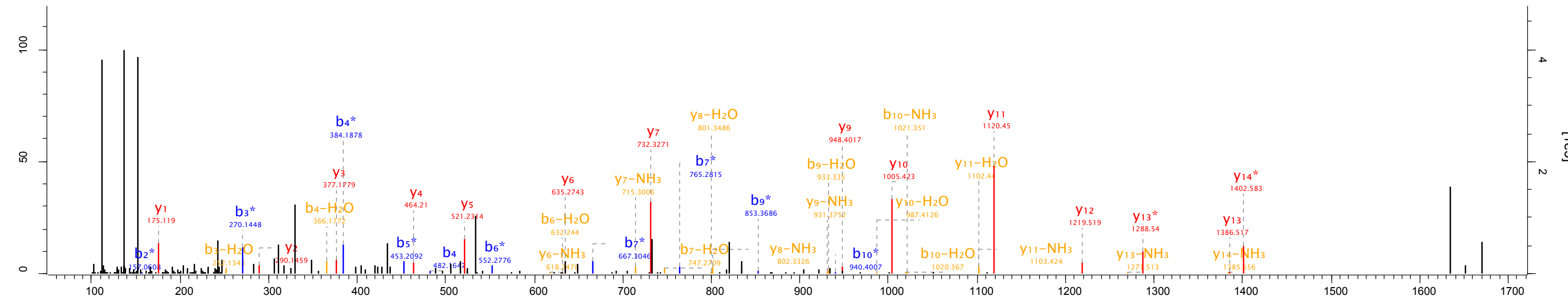


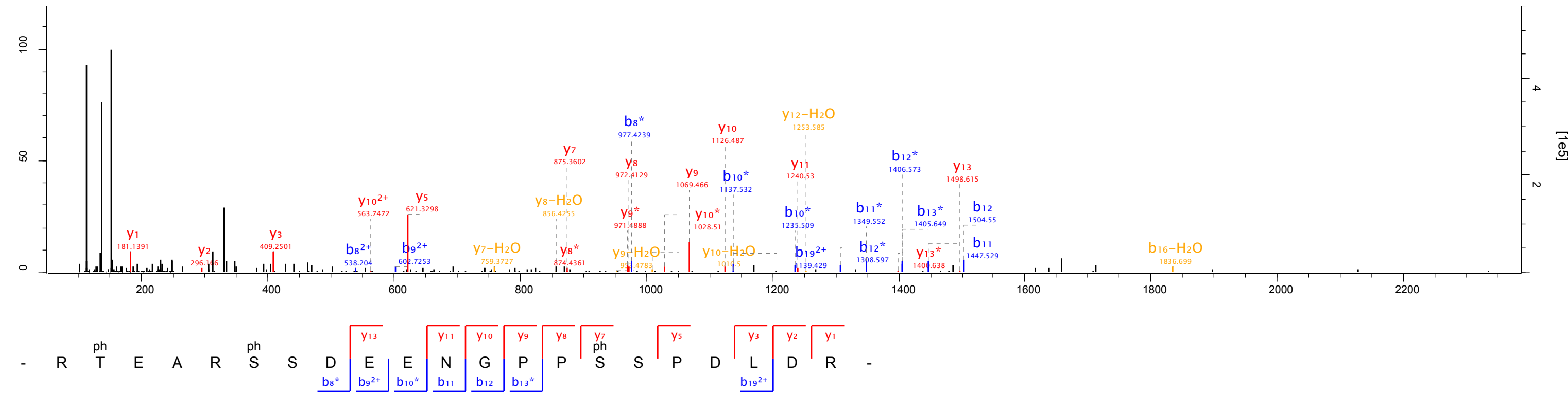


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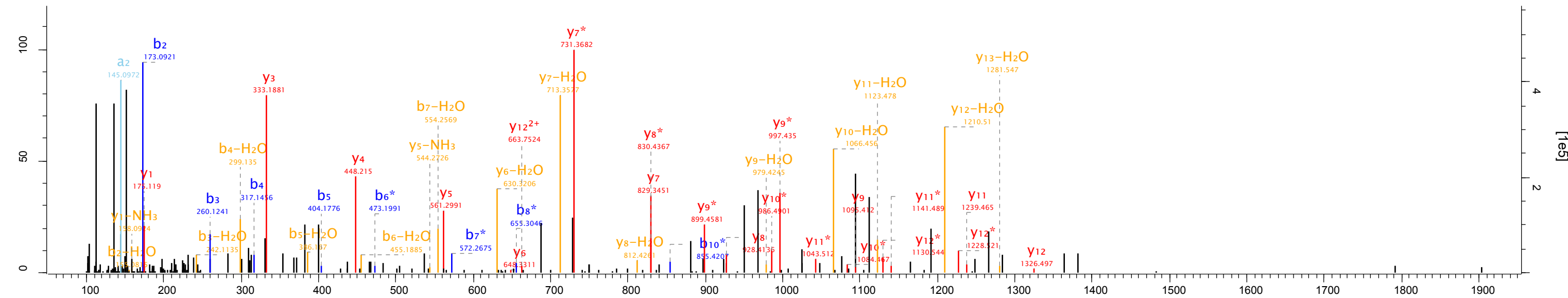


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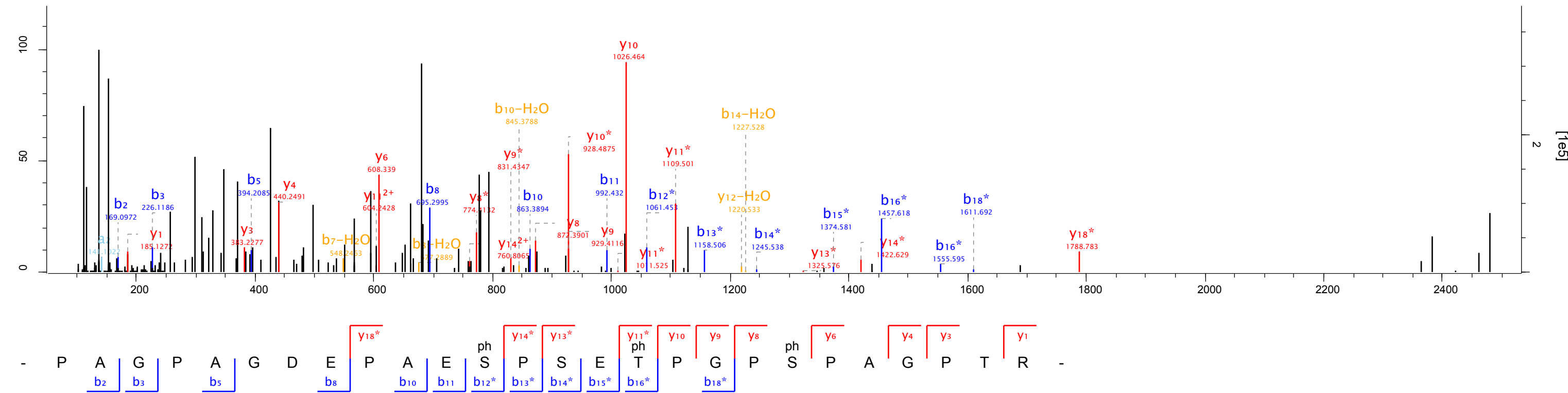
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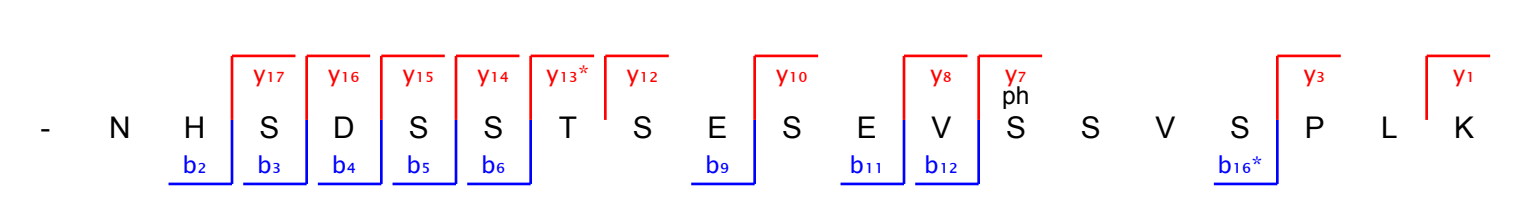
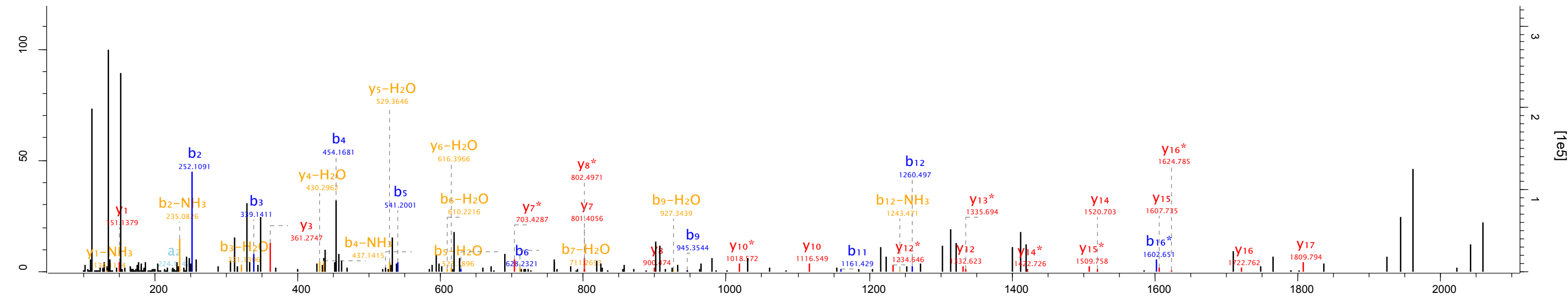
- T A S G S S V T S L D G T R -

b₂
b₃
b₄
b₅
b₆^{*}
b₇^{*}
b₈^{*}
b₁₀^{*}

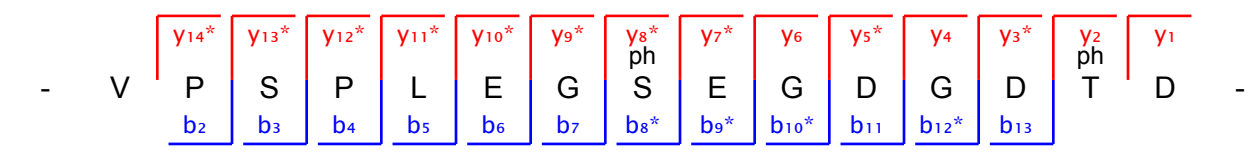
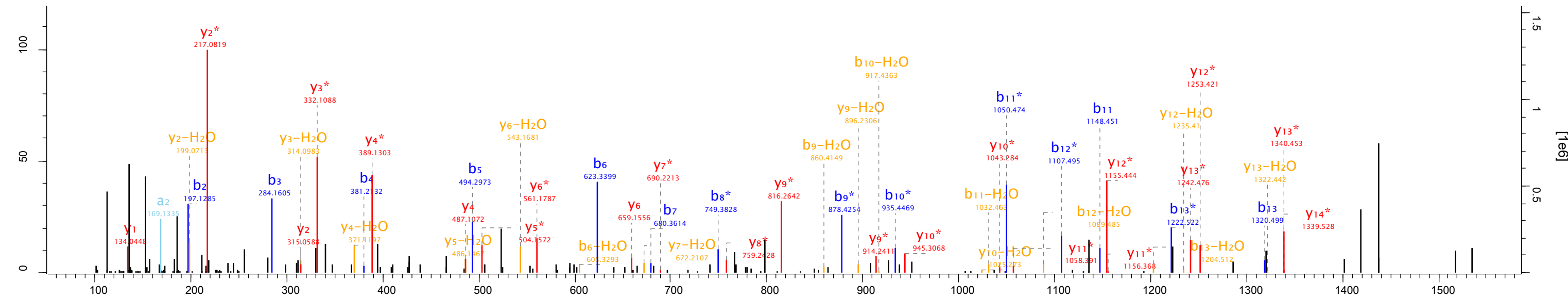
y₁₂
y₁₁
y₁₀^{*}
y₉
ph
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y₇
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y₆
y₅
y₄
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y₁



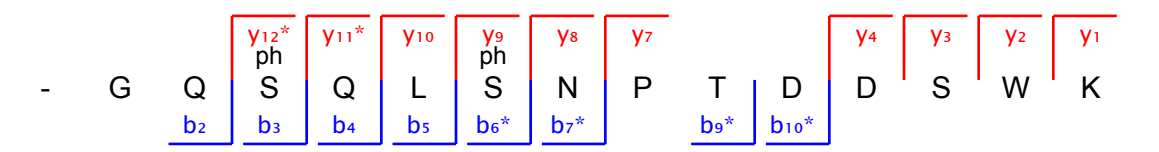
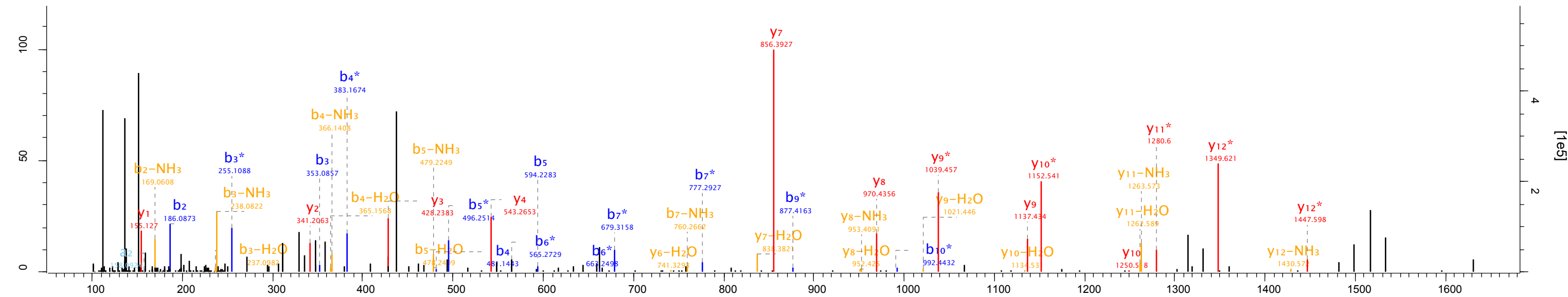
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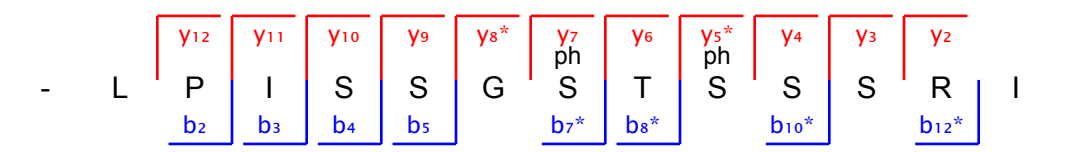
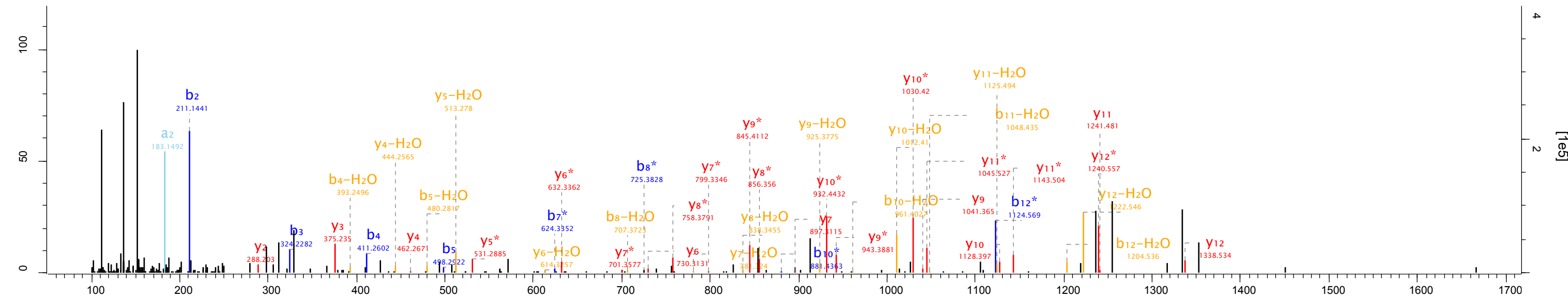
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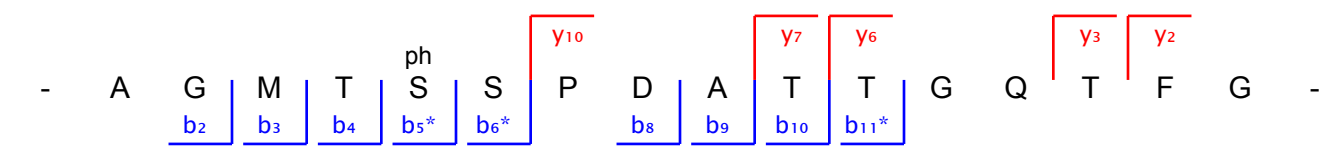
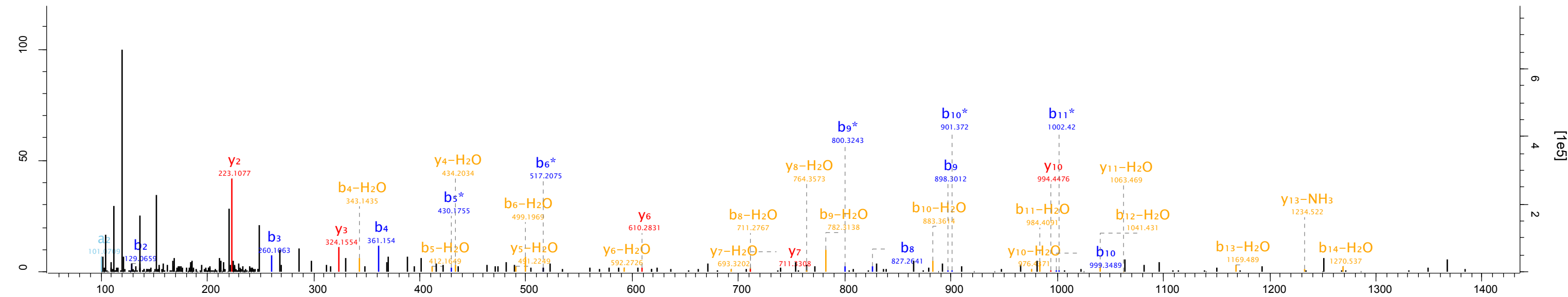
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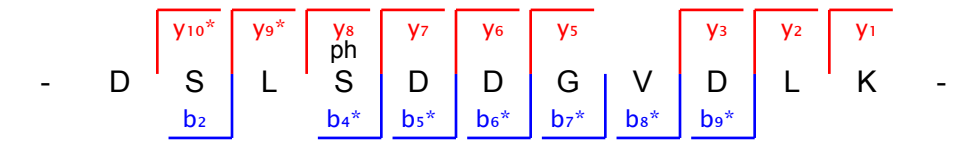
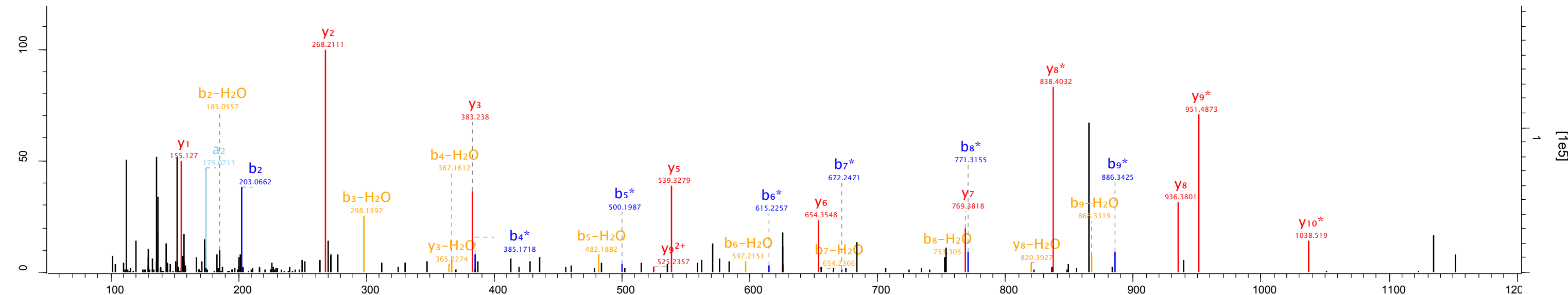
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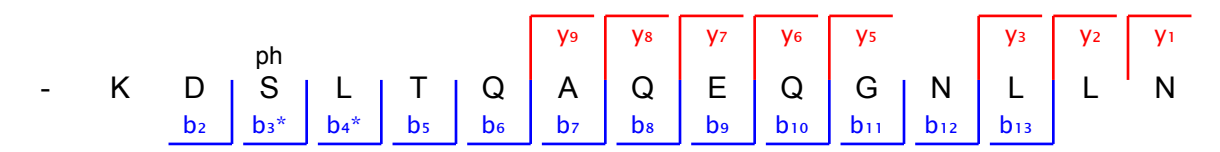
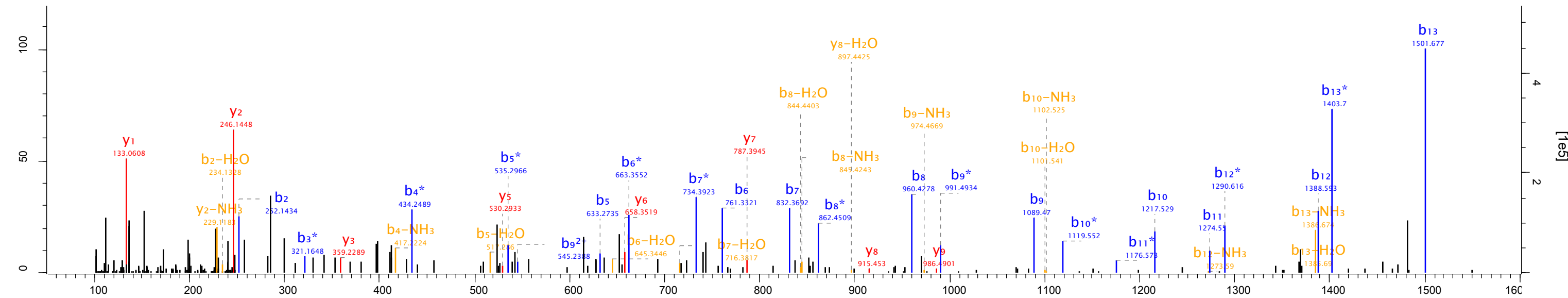
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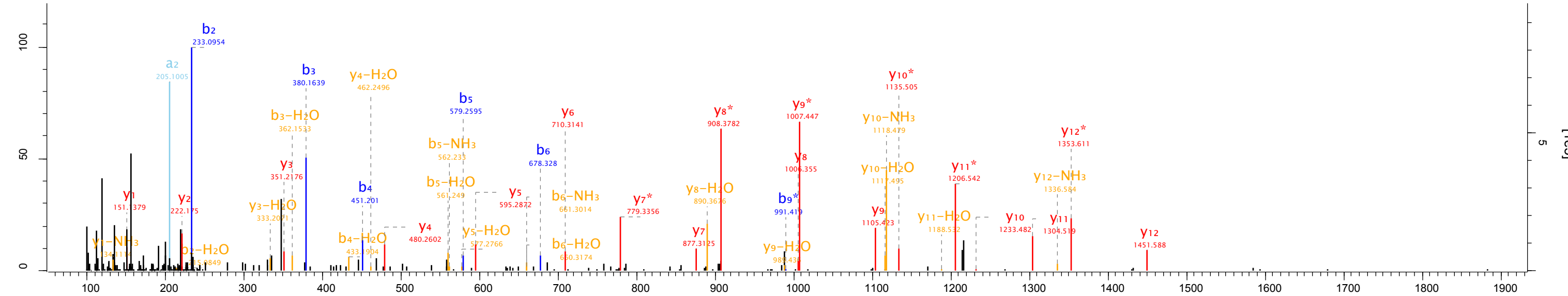
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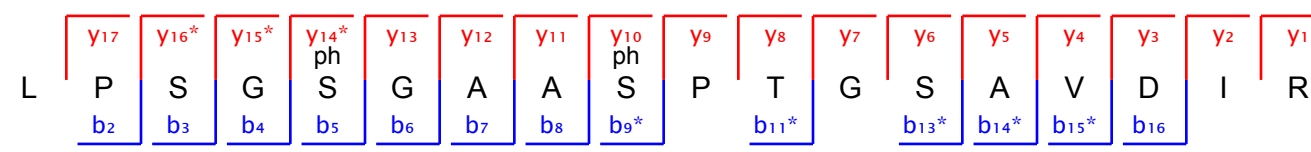
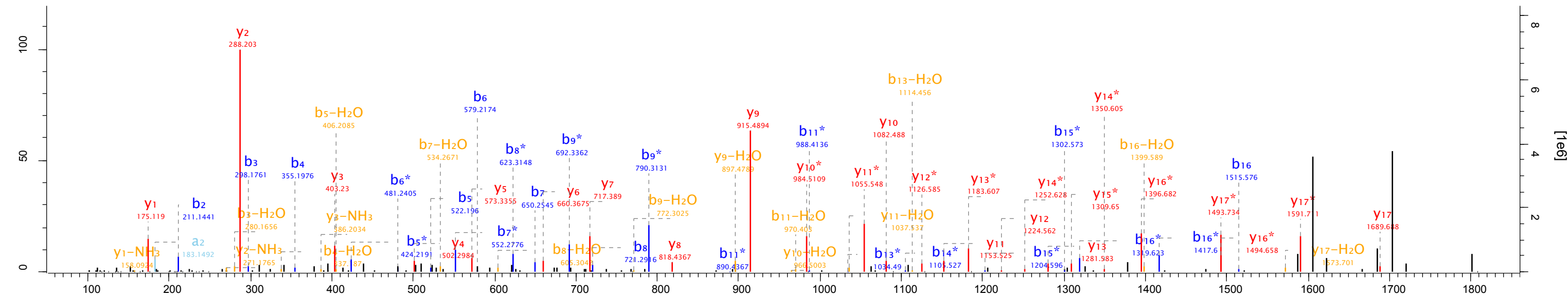
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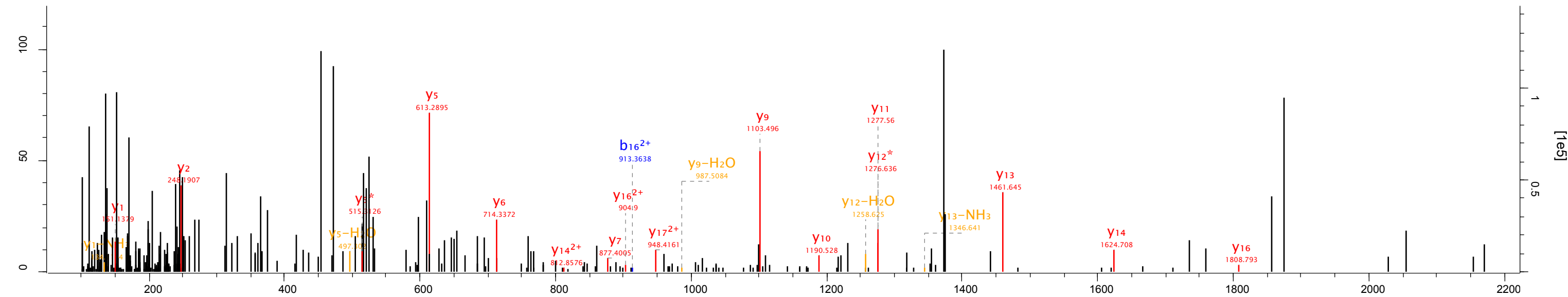
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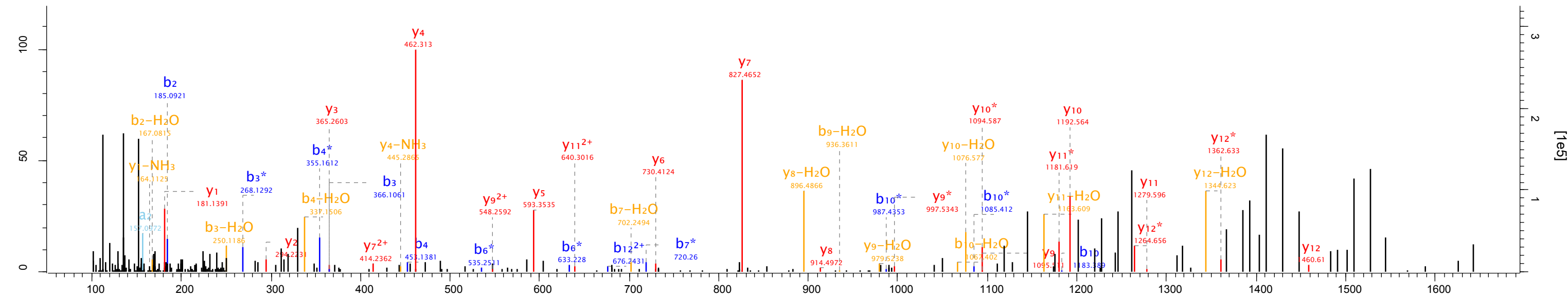
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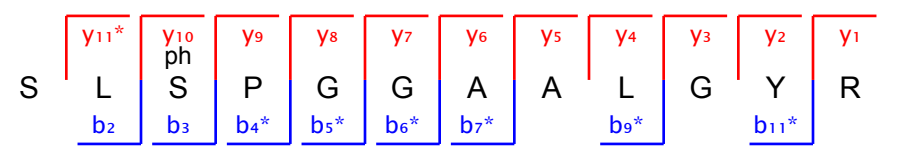
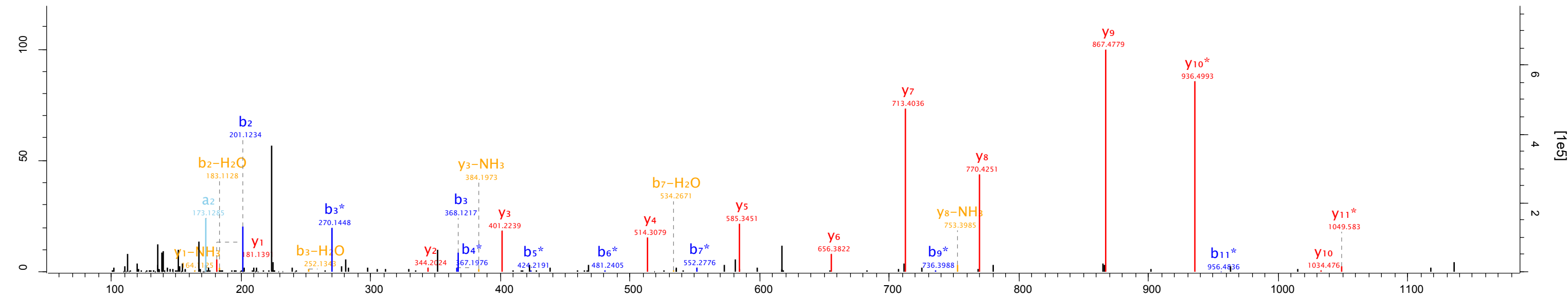
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┌ y17²⁺ └ ┌ y16 └ ┌ y14 └ ┌ y13 └ ┌ y12* └ ┌ y11 └ ┌ y10 └ ┌ y9 └
┌ b16²⁺ └

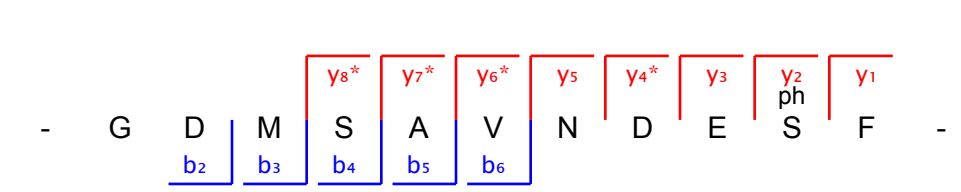
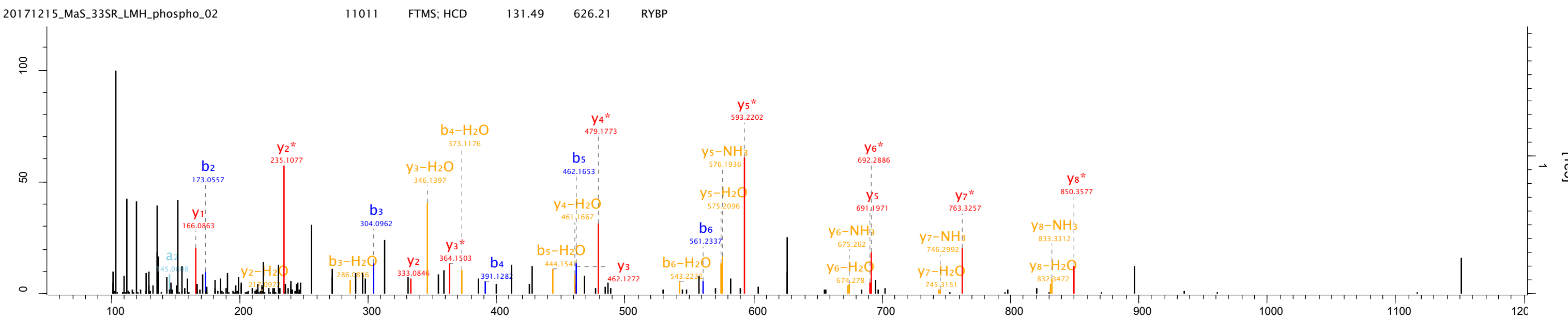
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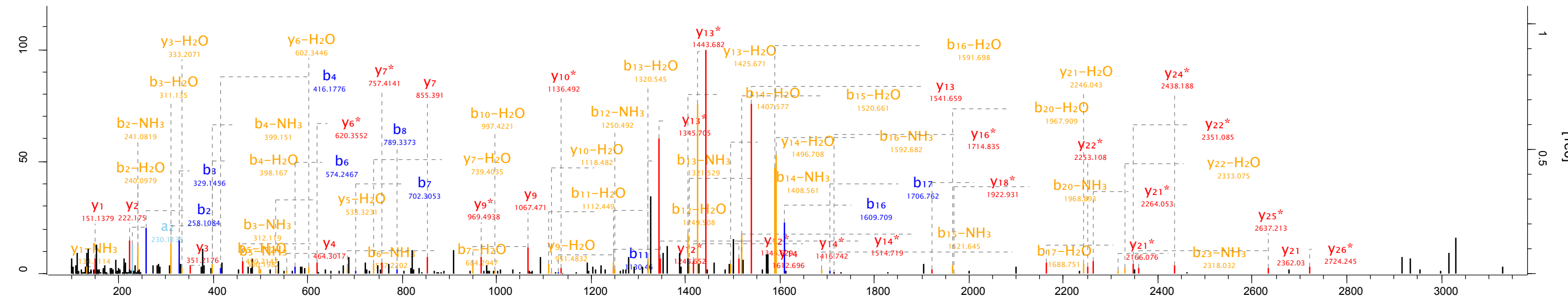
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Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 11011 Method FTMS; HCD Score 131.49 m/z 626.21 Gene names RYBP



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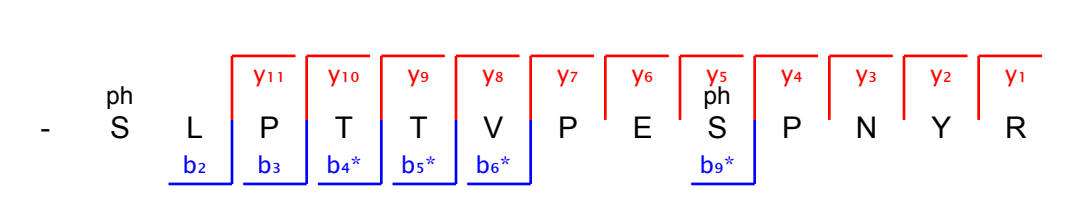
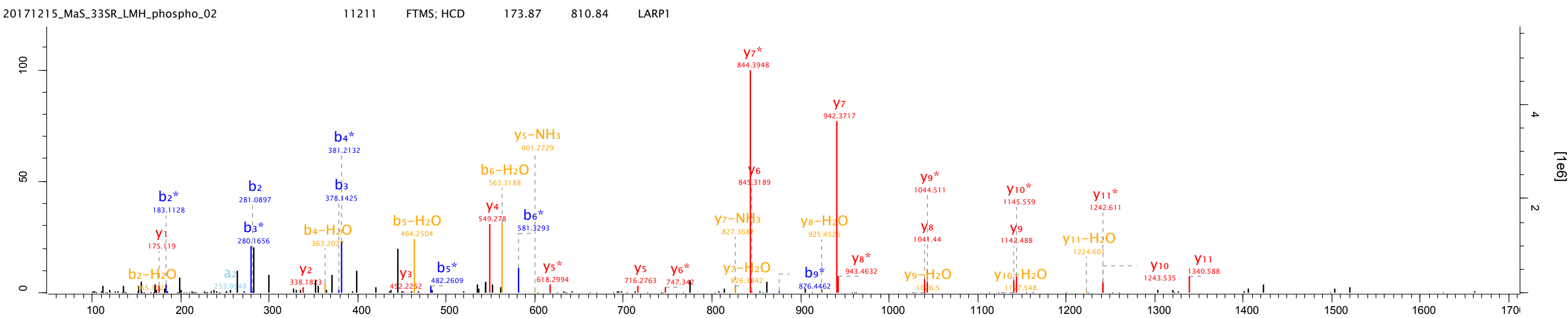


Protein sequence: - Q E A S T G Q S P E D H A S L A P P L S P D H S S L E A K -

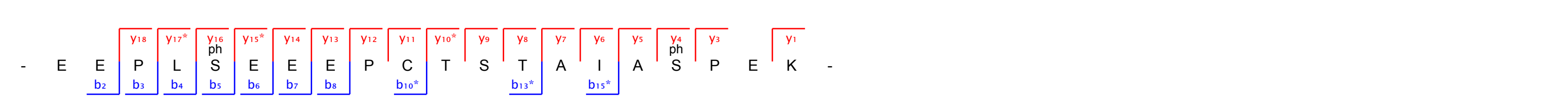
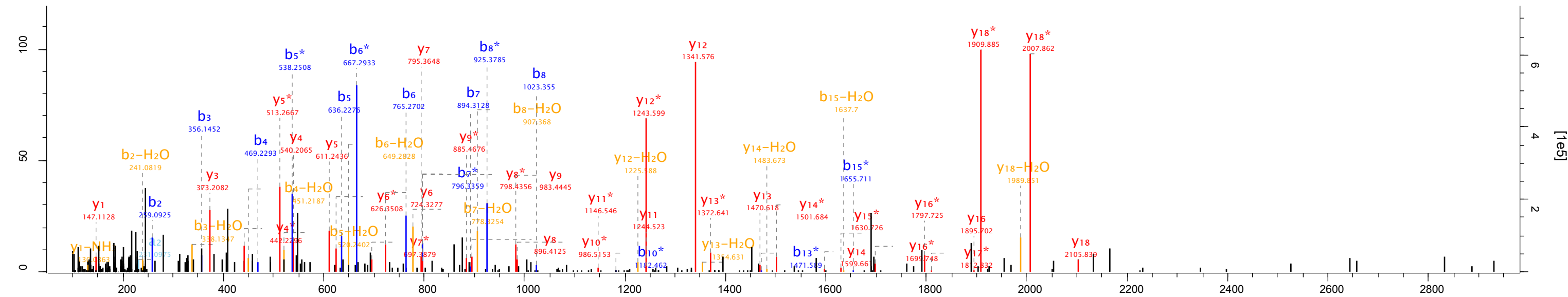
Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets (b ions): b₂ (E), b₃ (EA), b₄ (EAS), b₆ (GQ), b₇ (GQ), b₈ (GQS), b₁₁ (D), b₁₆ (A), b₁₇ (AP)
- Red brackets (y ions): y₂₆^{*} (S), y₂₅^{*} (ST), y₂₄^{*} (STG), y₂₂^{*} (STG), y₂₁ (STGQ), y₁₈^{*} (D), y₁₆^{*} (D), y₁₄ (A), y₁₃ (AP), y₁₂^{*} (APP), y₁₀^{*} (S), y₉ (SP), y₇ (D), y₆^{*} (D), y₄ (S), y₃ (SL), y₂ (SL), y₁ (SL)

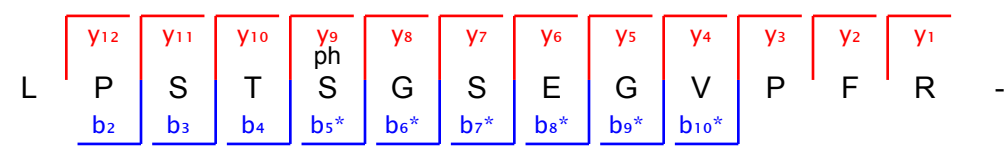
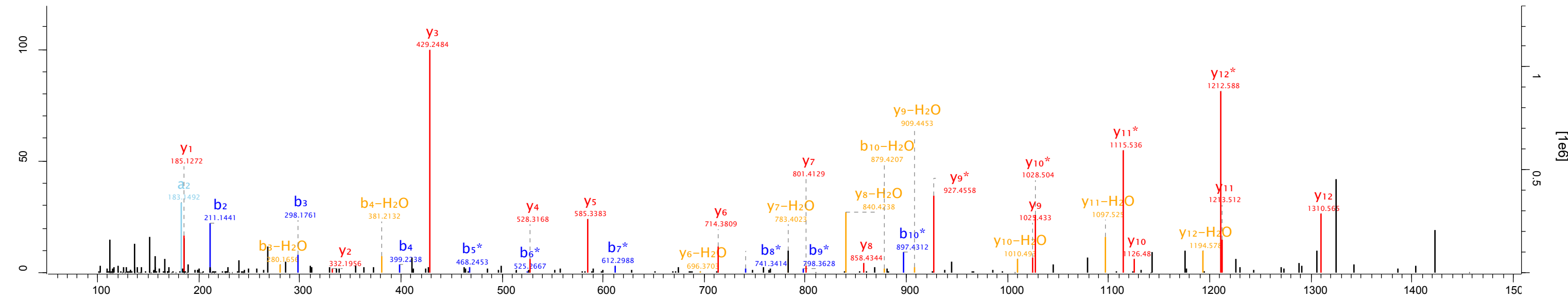
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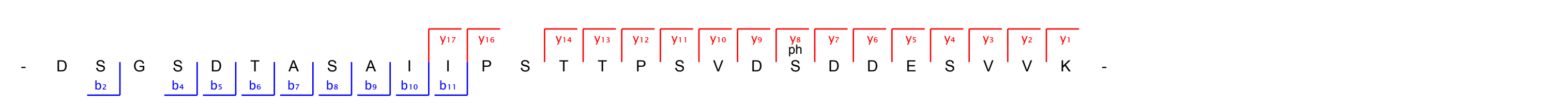
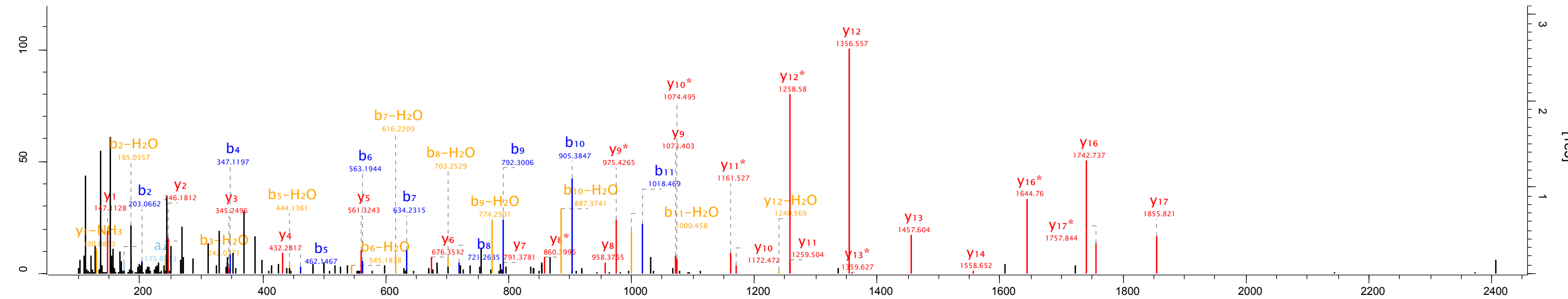
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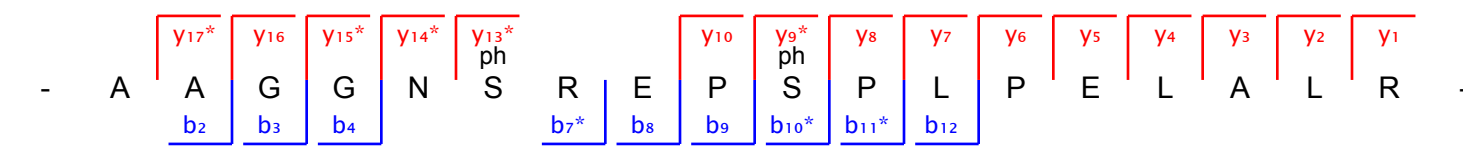
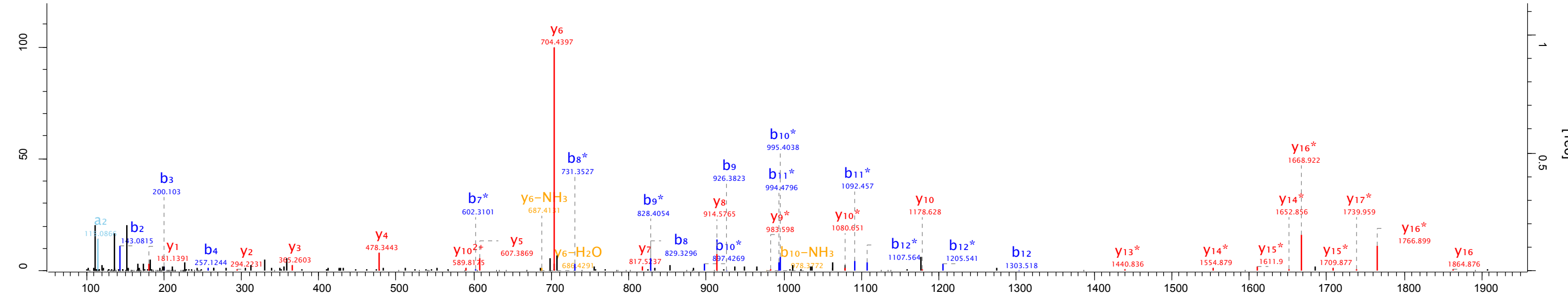
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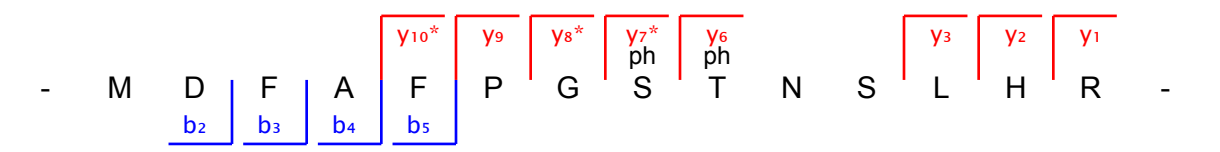
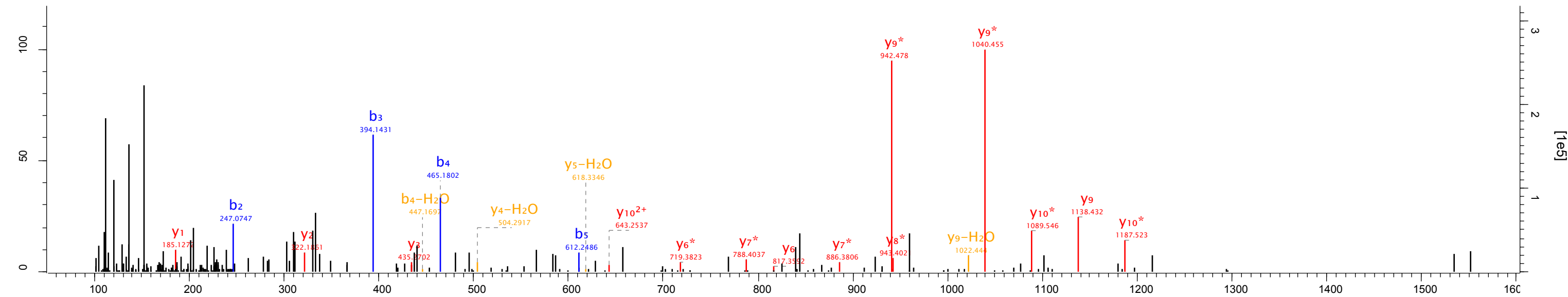
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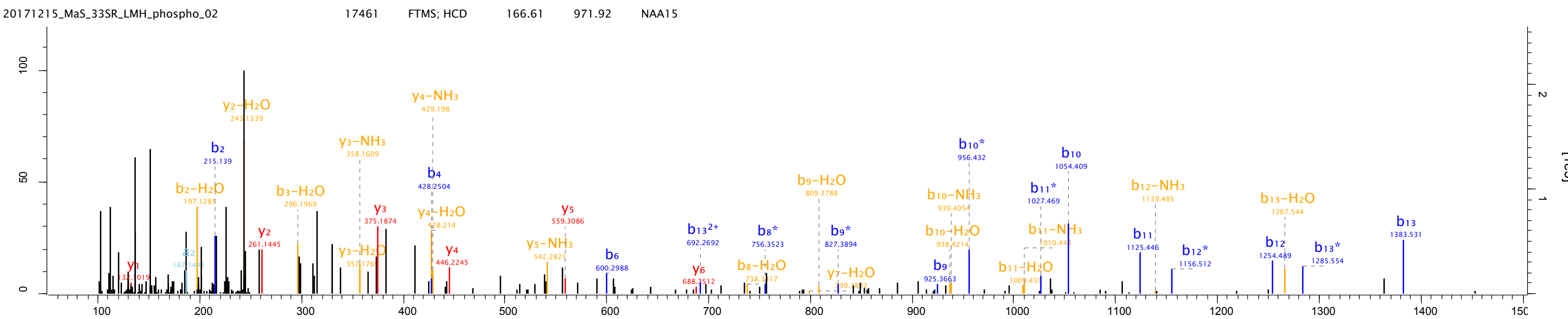


20171215_MaS_33SR_LMH_phospho_02 15151 FTMS; HCD 104.96 669.65 TBX2

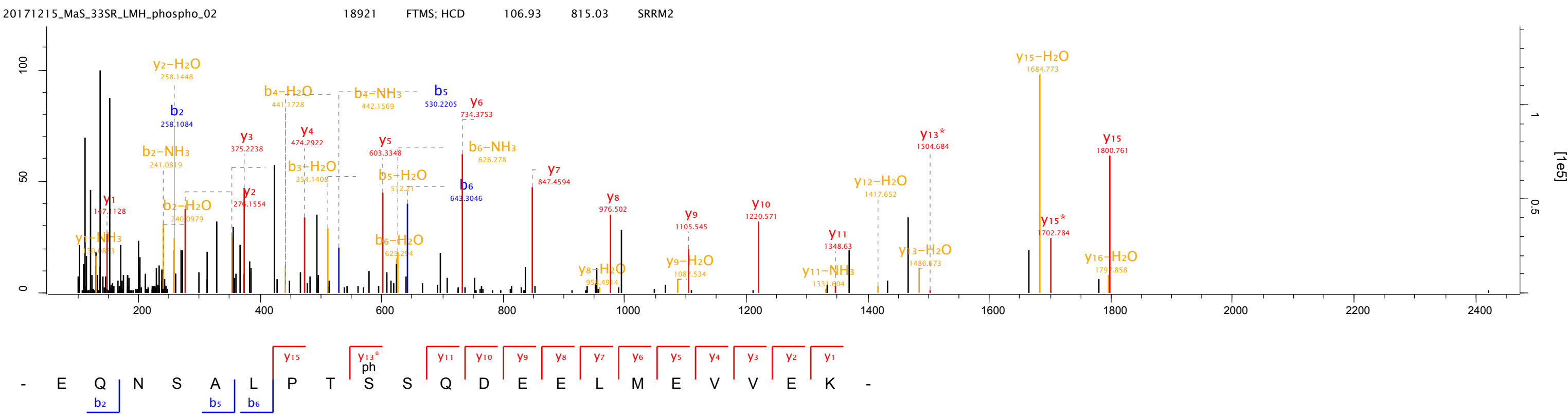


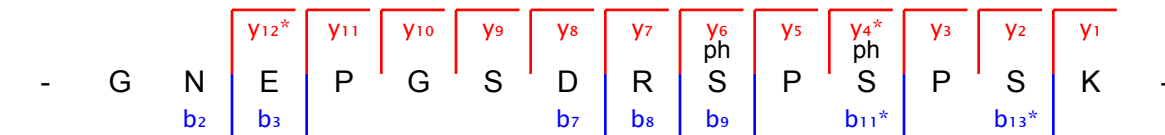
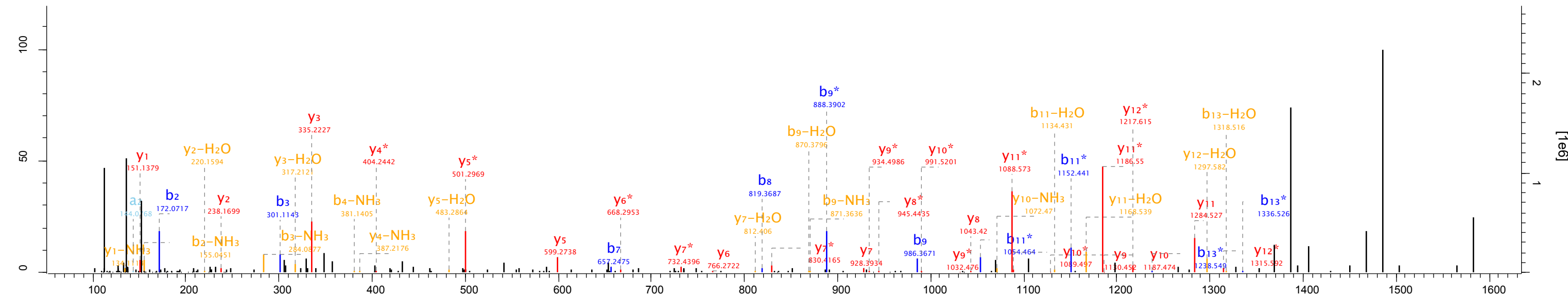
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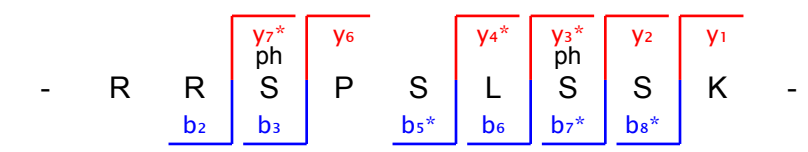
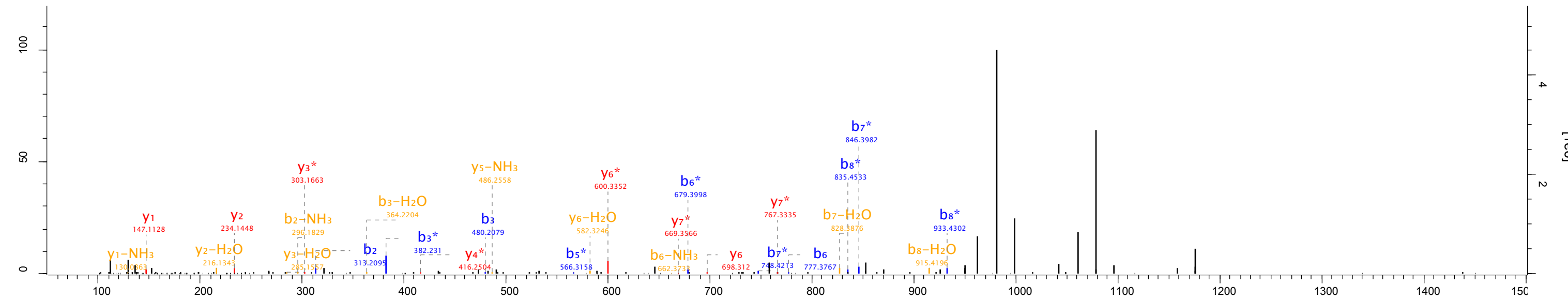
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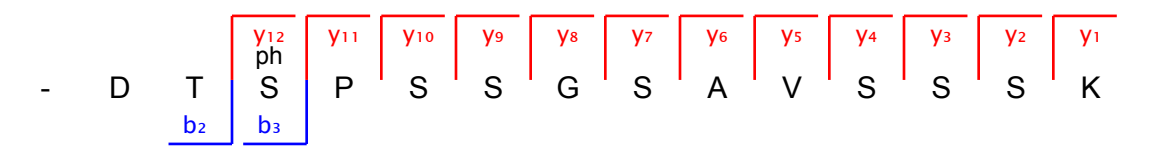
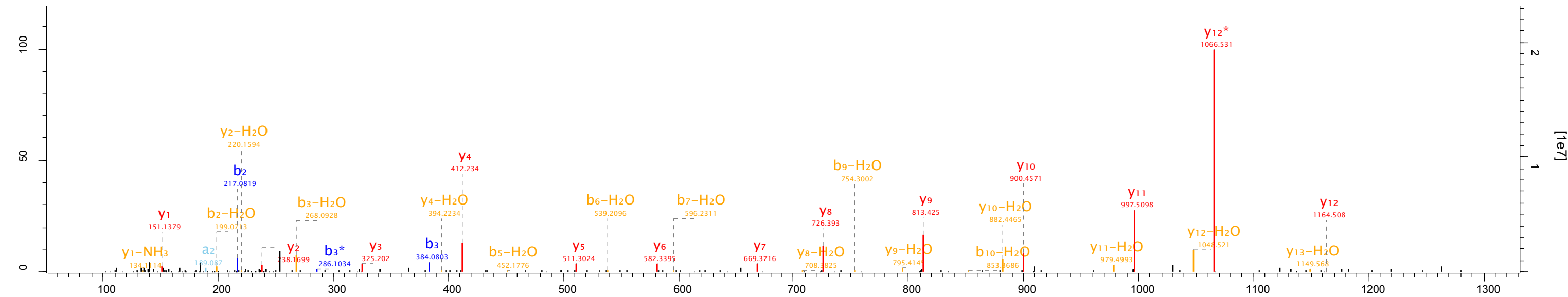


Raw file
20171215_MaS_33SR_LMH_phospho_02

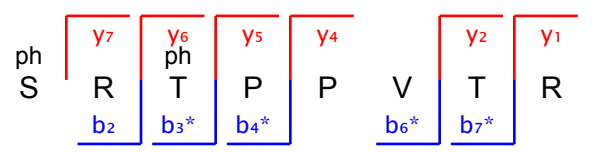
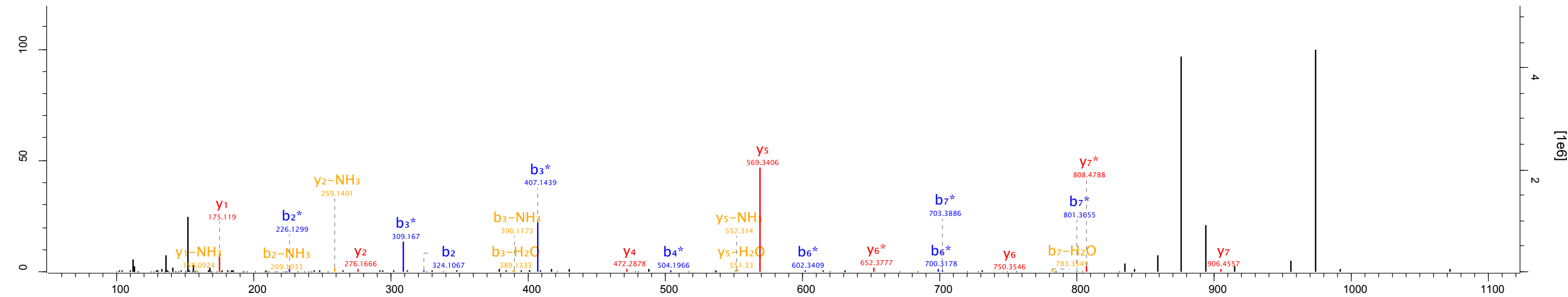
Scan Method Score m/z Gene names
2401 FTMS; HCD 107.46 589.26 SRRM1



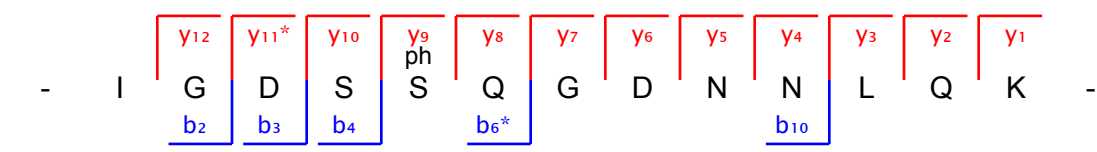
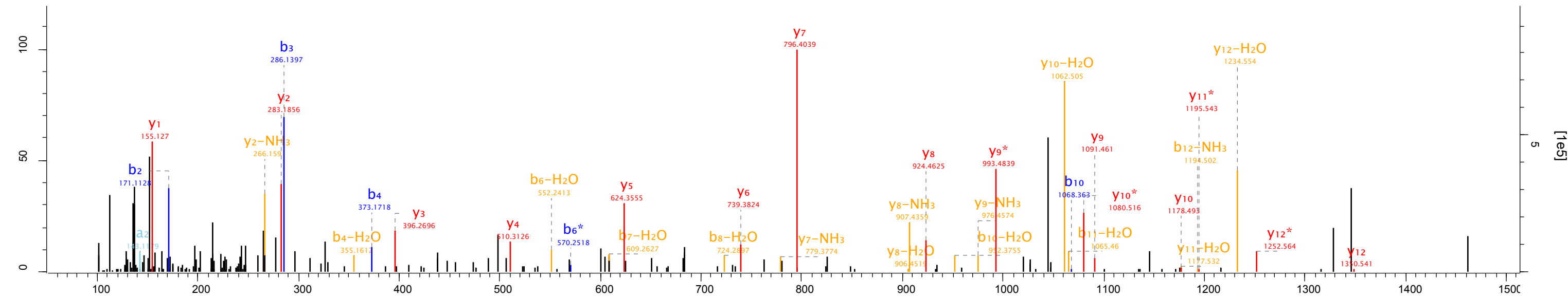
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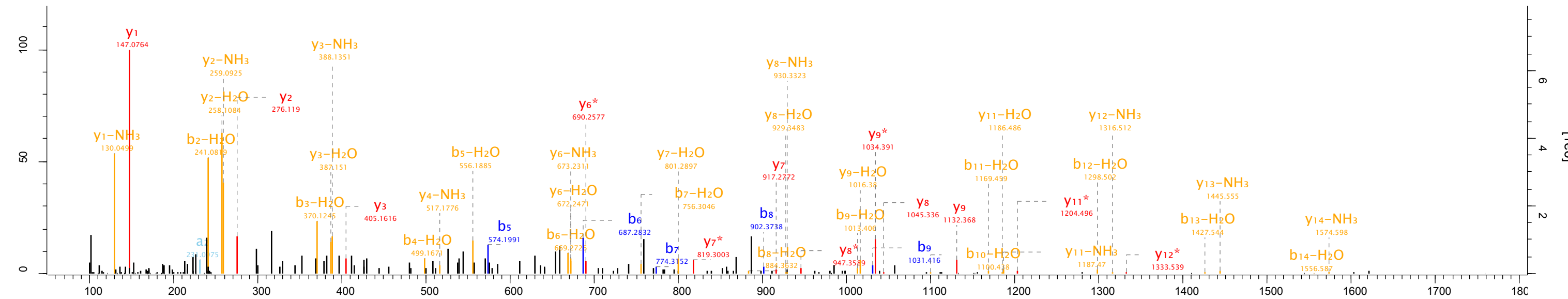


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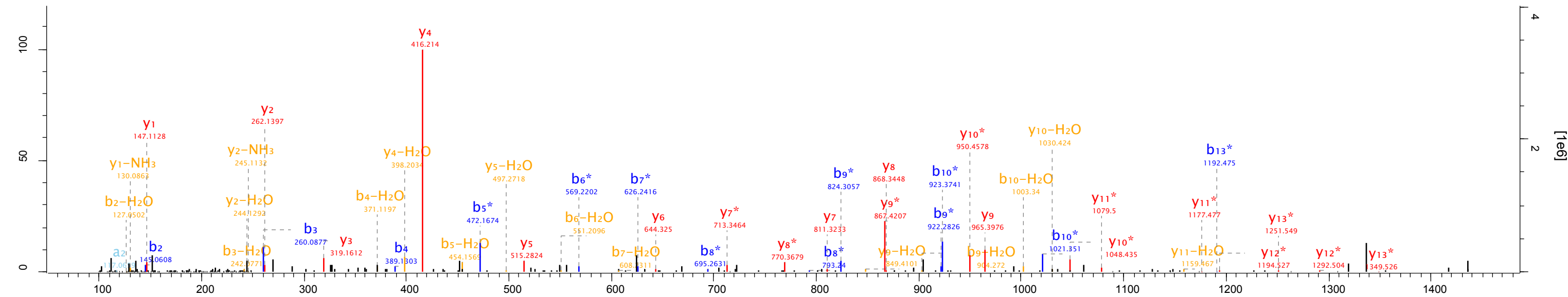


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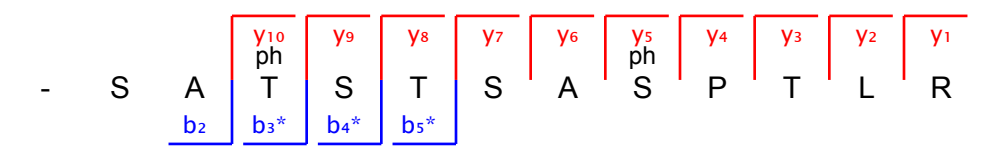
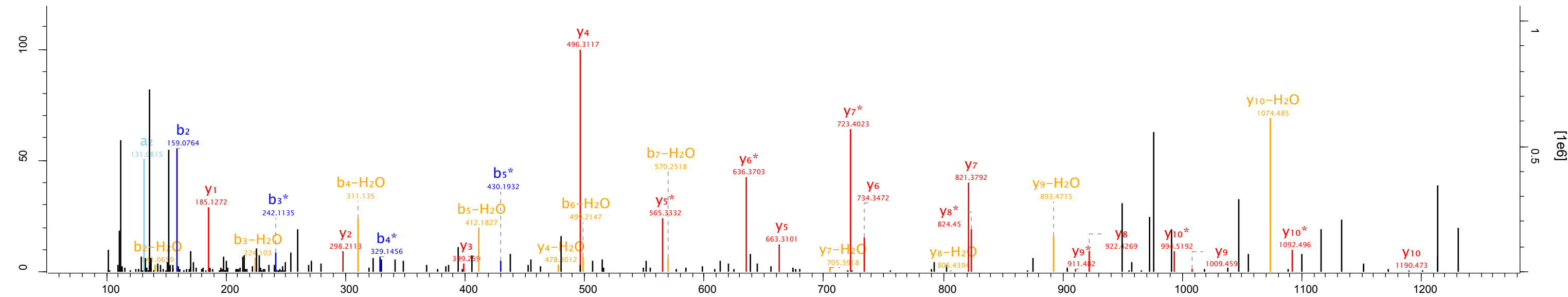
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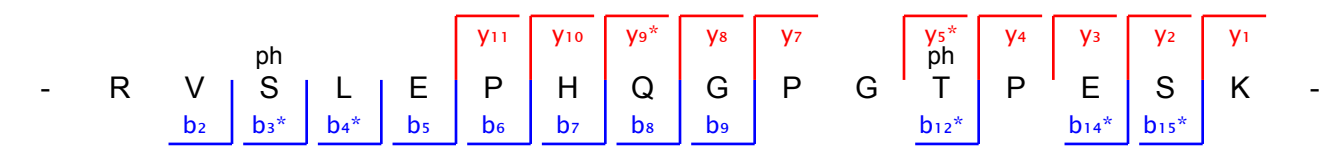
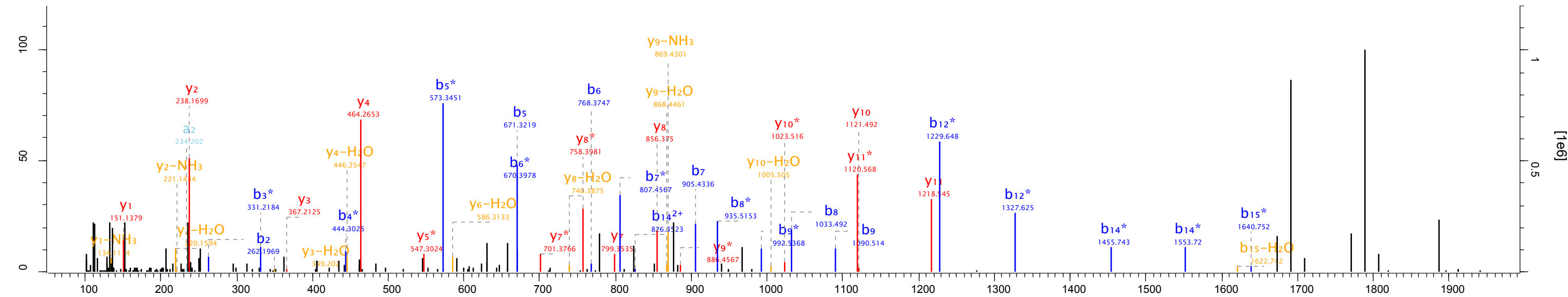
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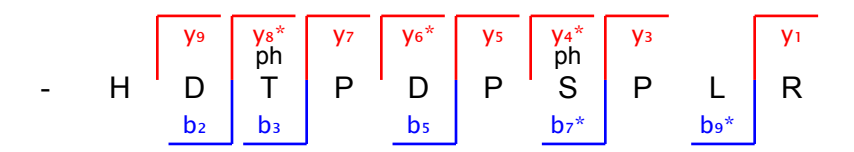
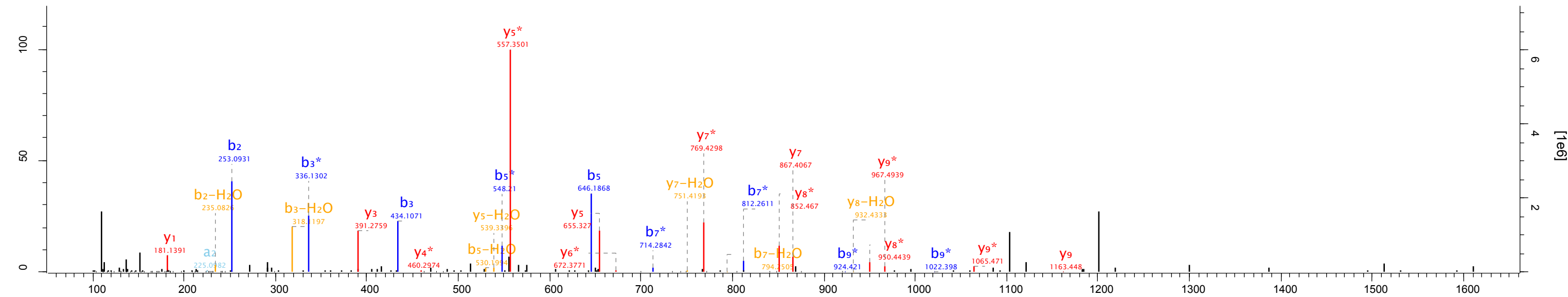
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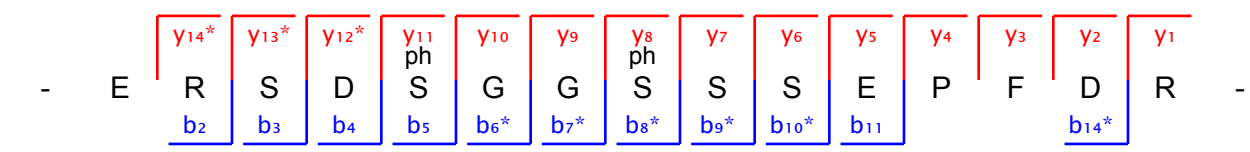
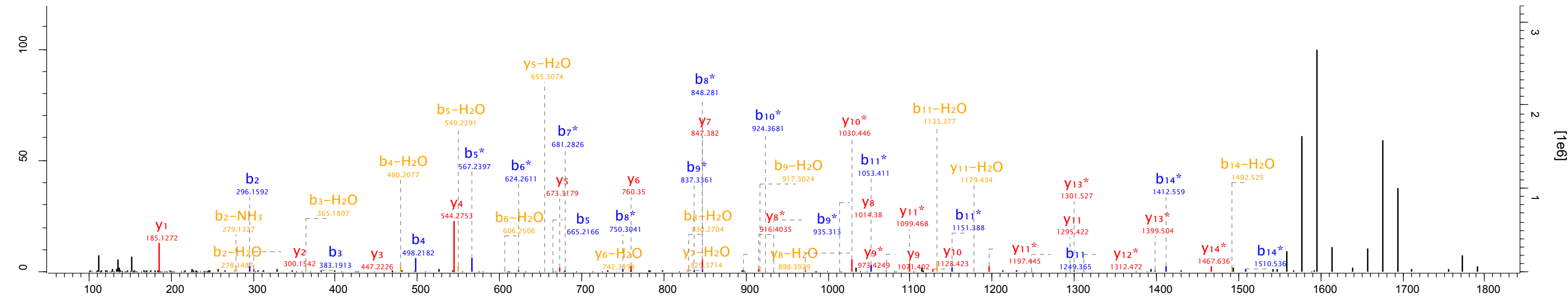


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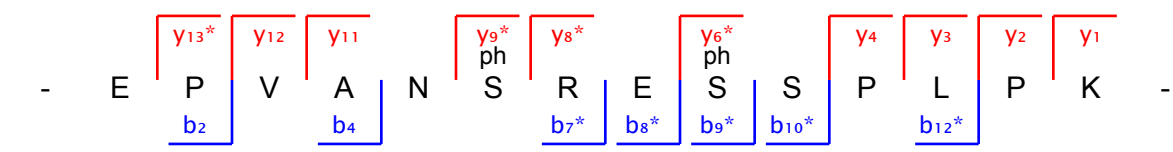
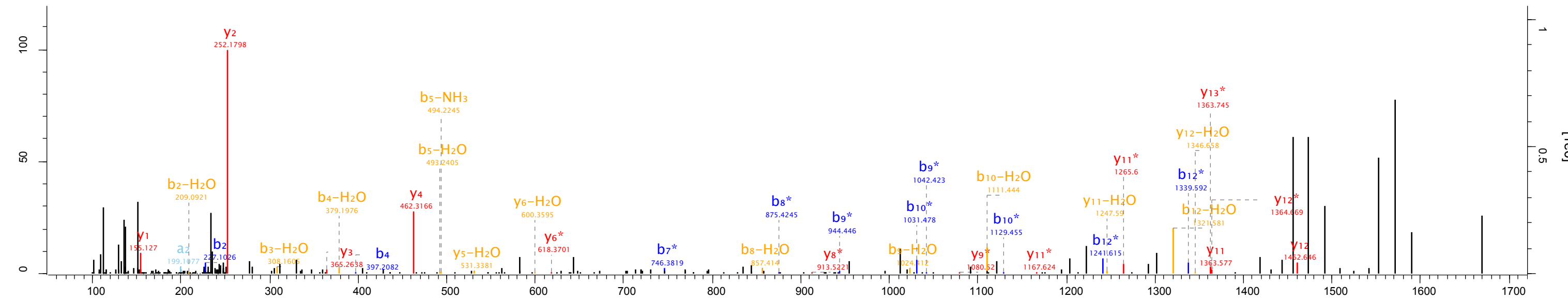


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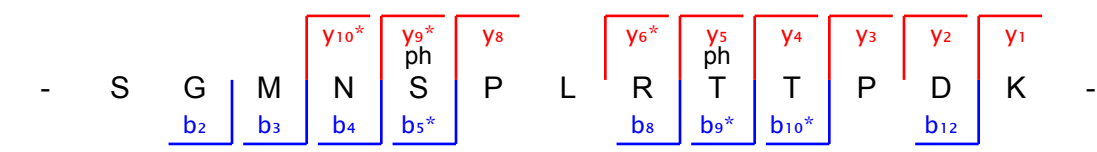
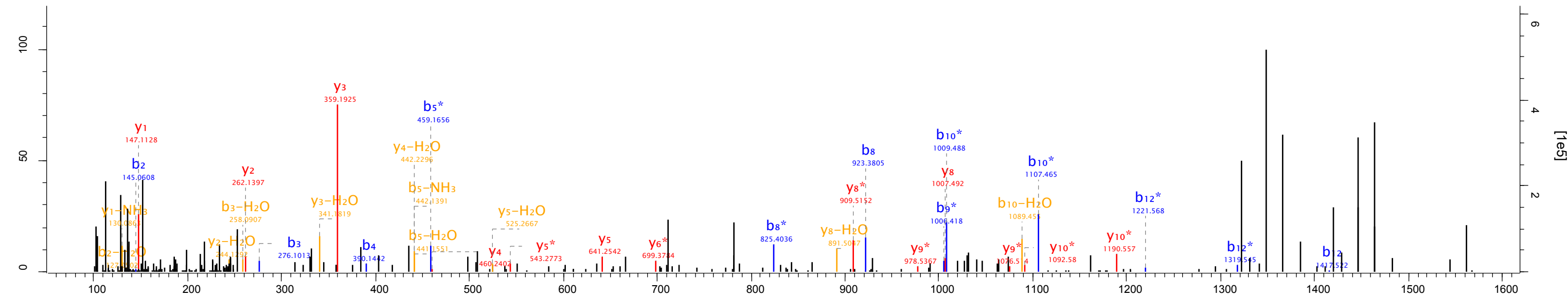




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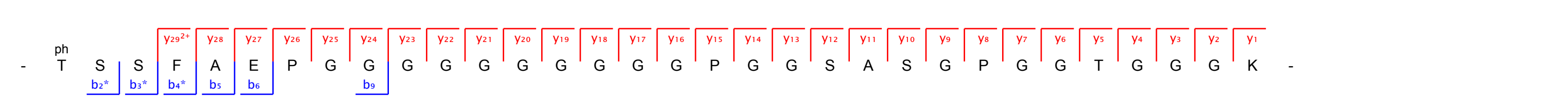
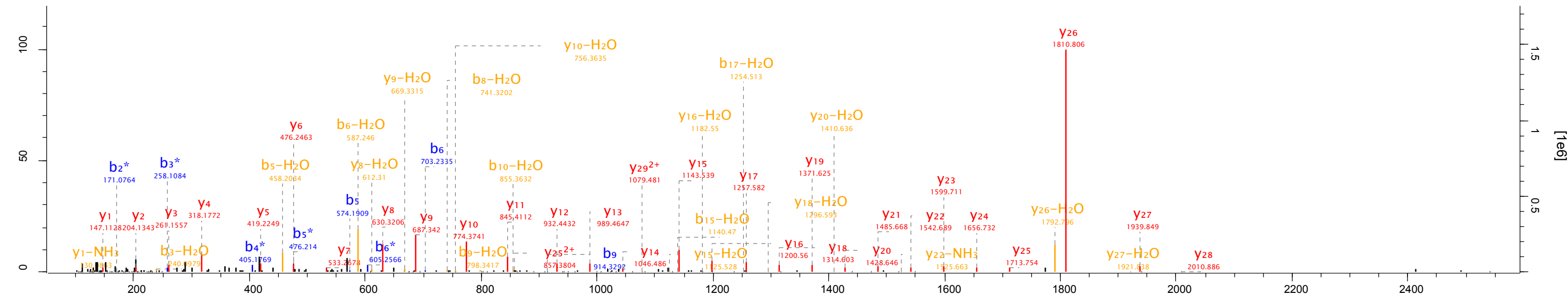


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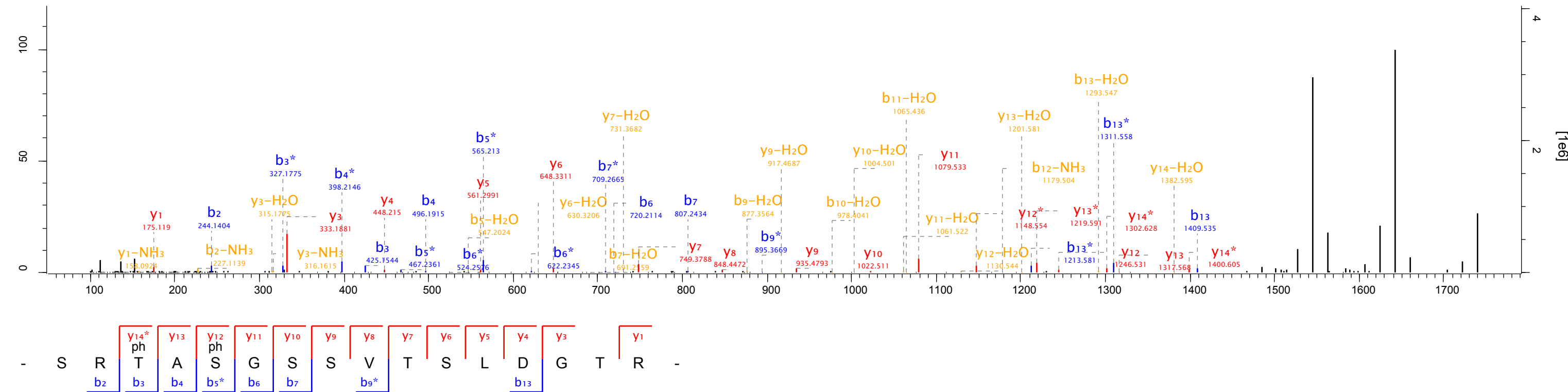


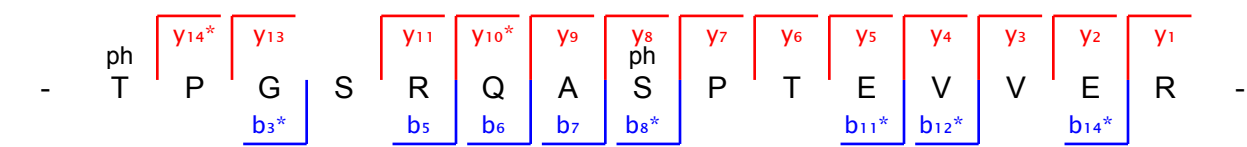
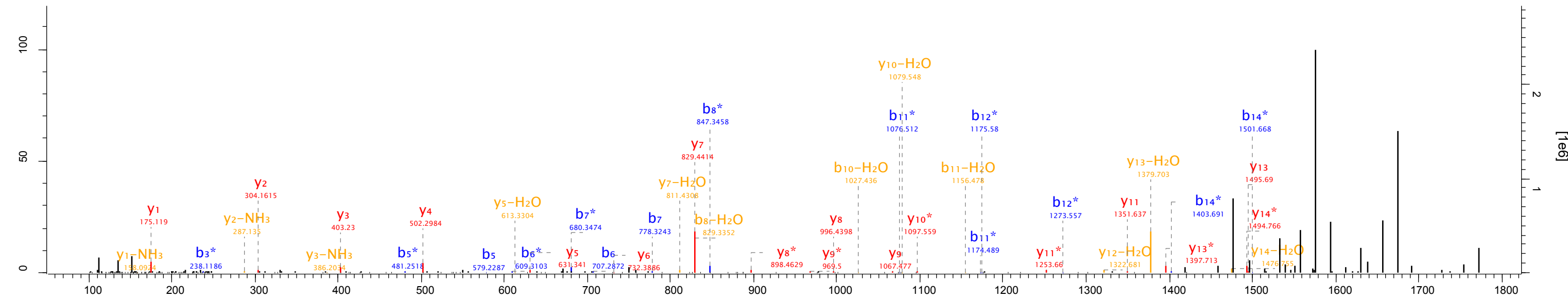
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20171215_MaS_33SR_LMH_phospho_02

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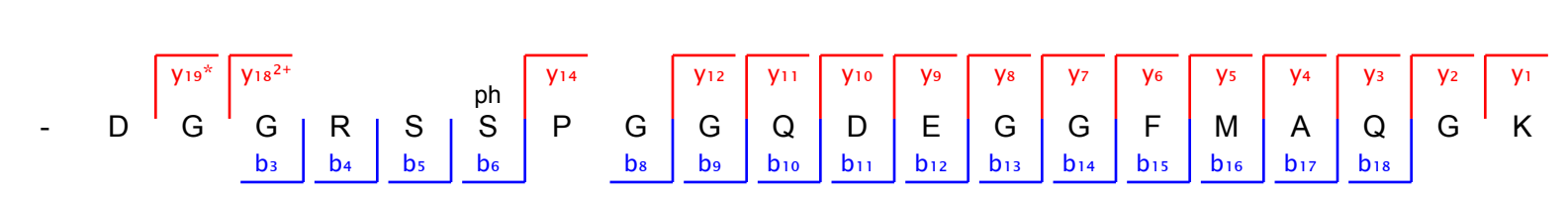
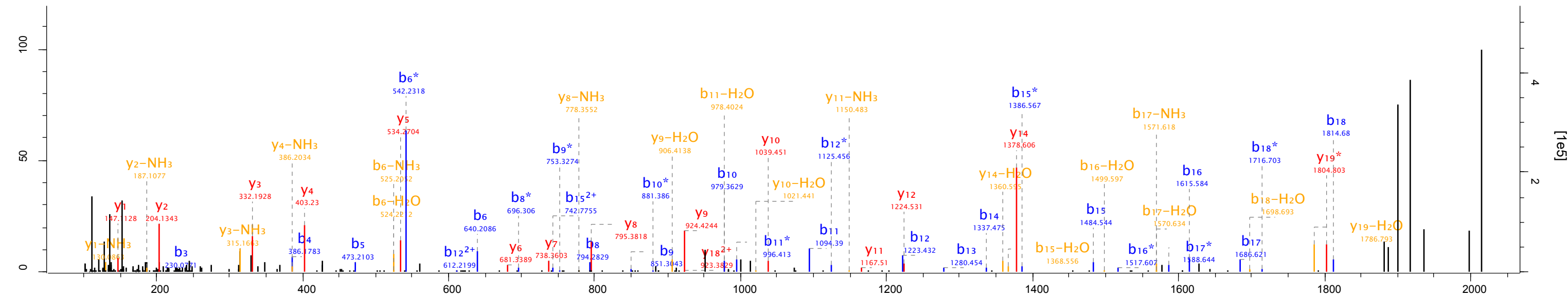


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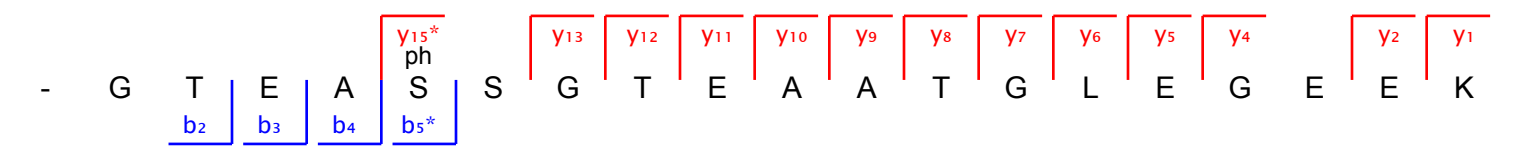
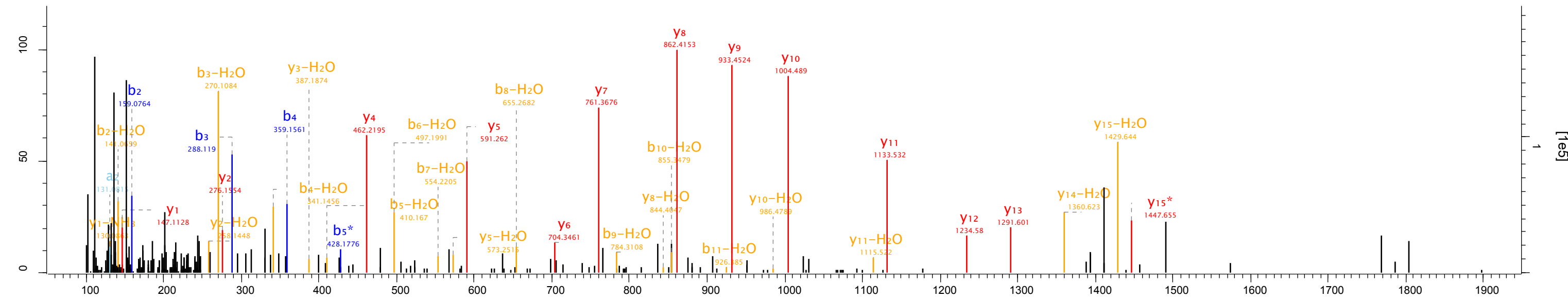




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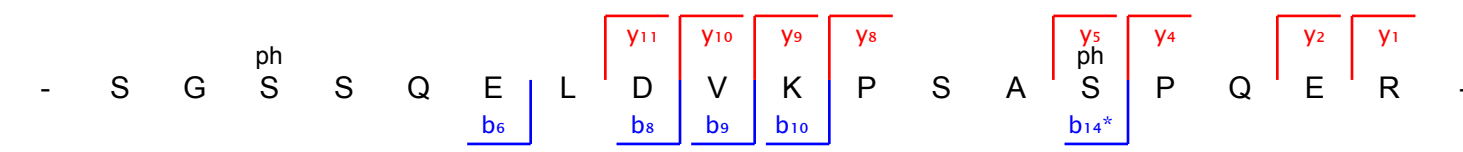
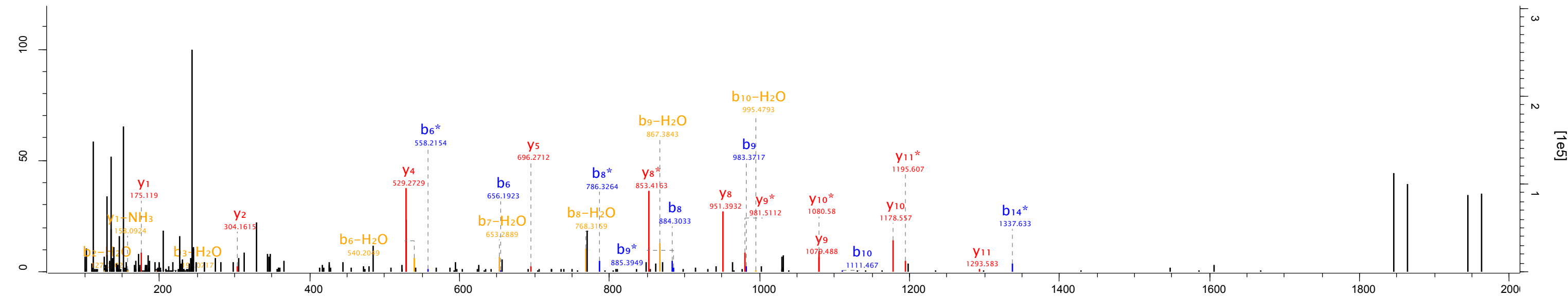
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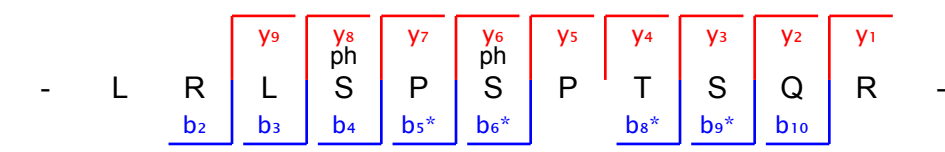
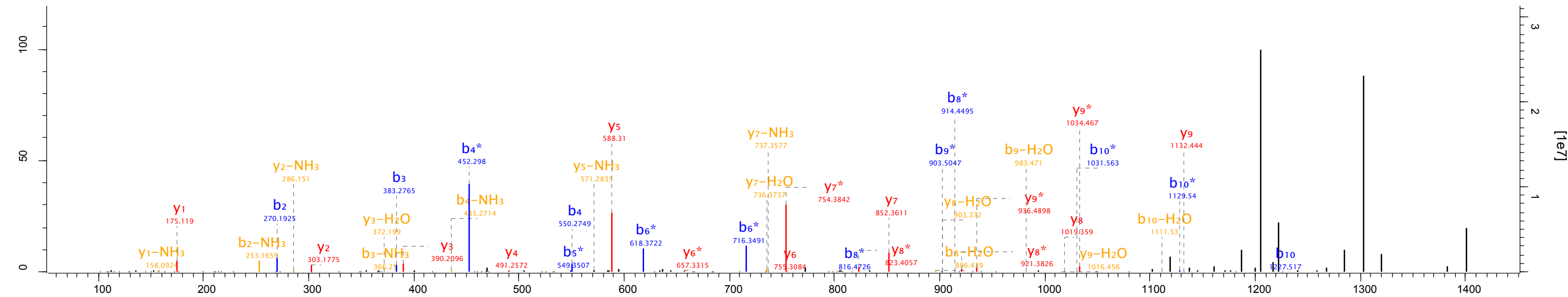
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20171215_MaS_33SR_LMH_phospho_02

Scan 6861 Method FTMS; HCD Score 42.06 m/z 1031.43 Gene names SRRM2

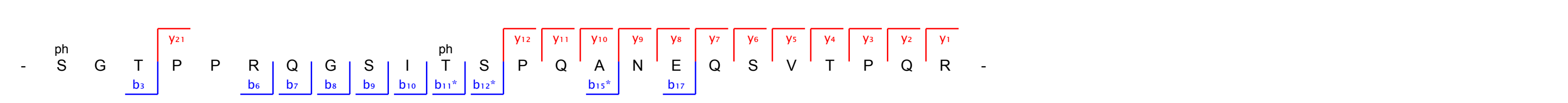
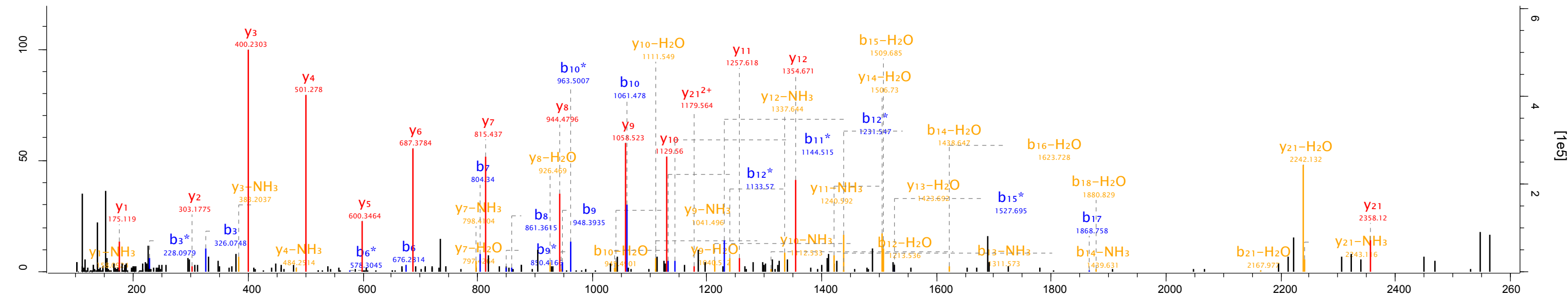


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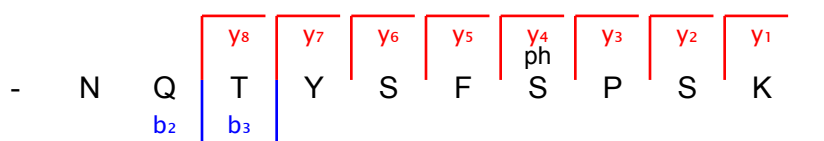
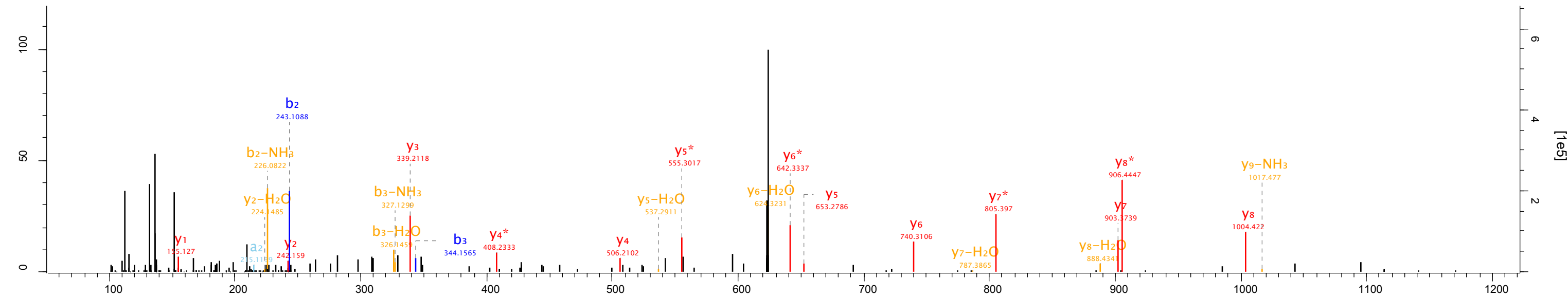


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20171215_MaS_33SR_LMH_phospho_02

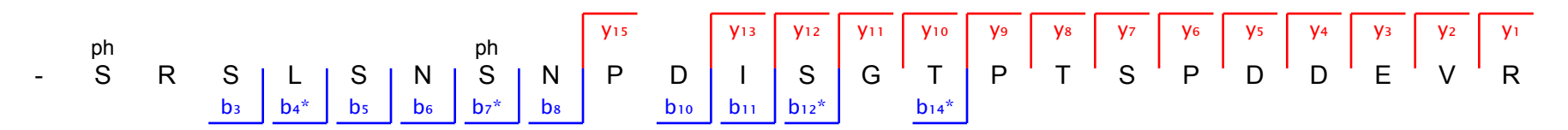
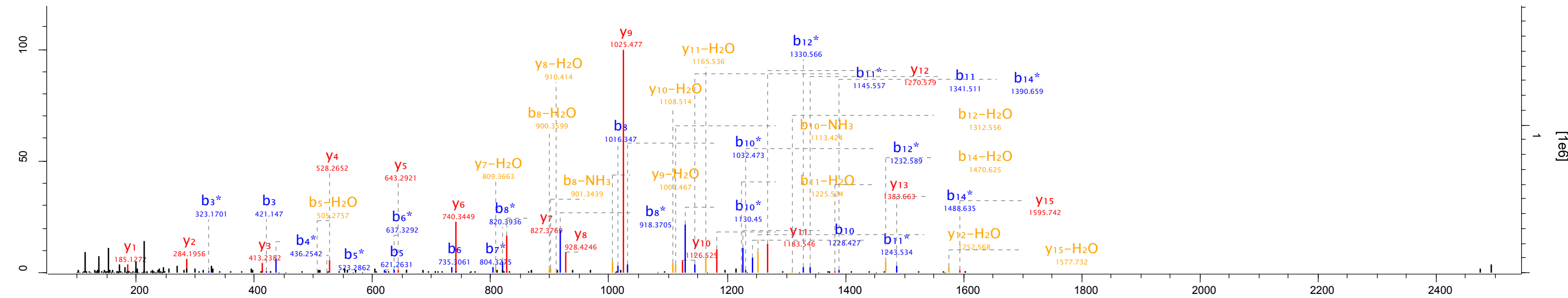
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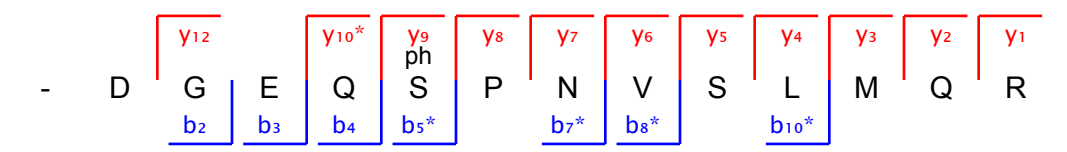
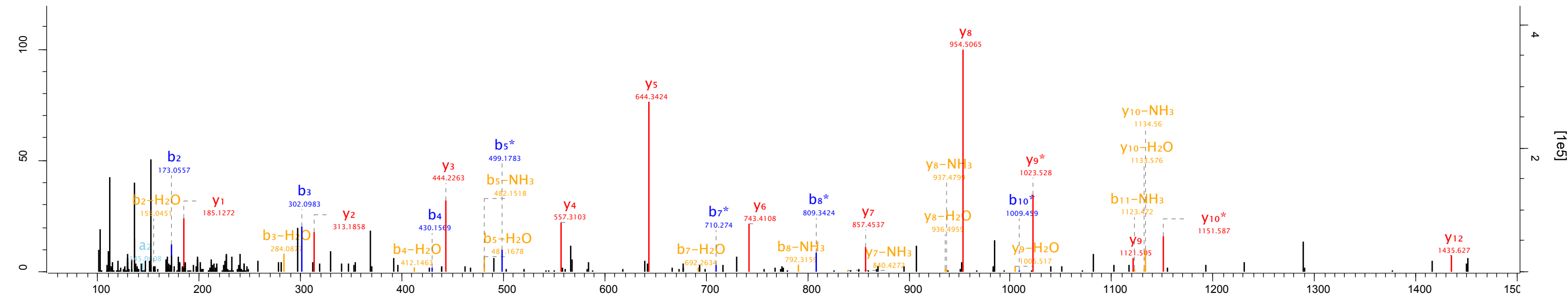
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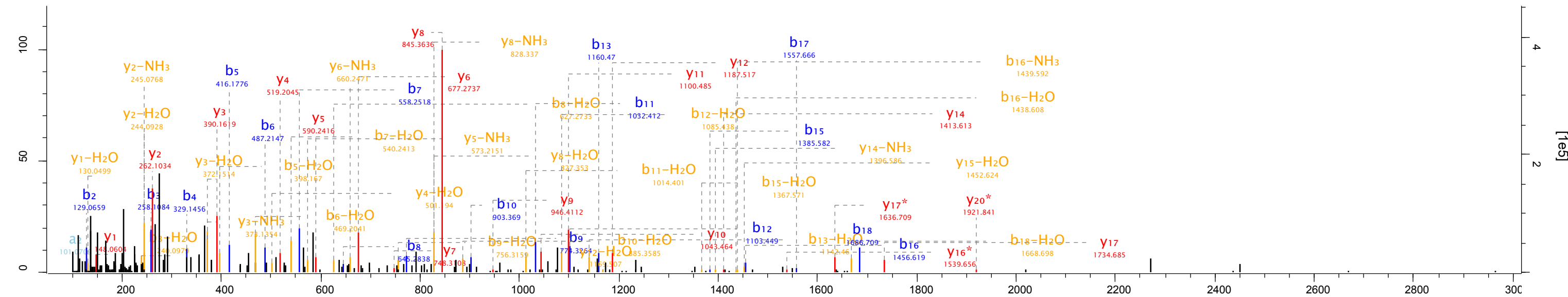


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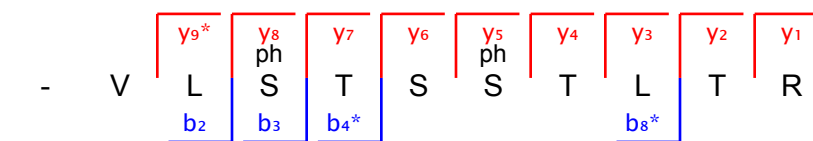
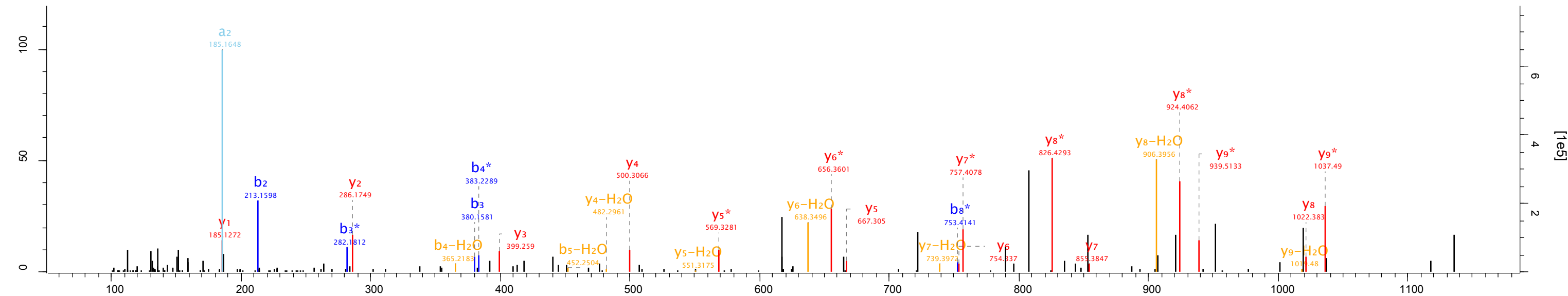


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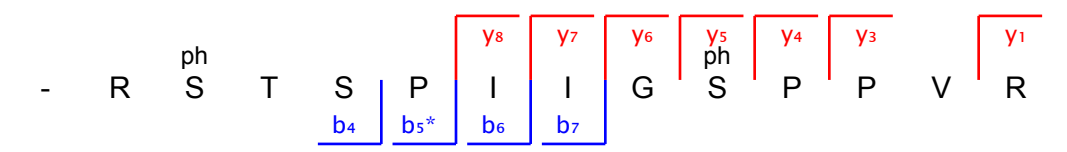
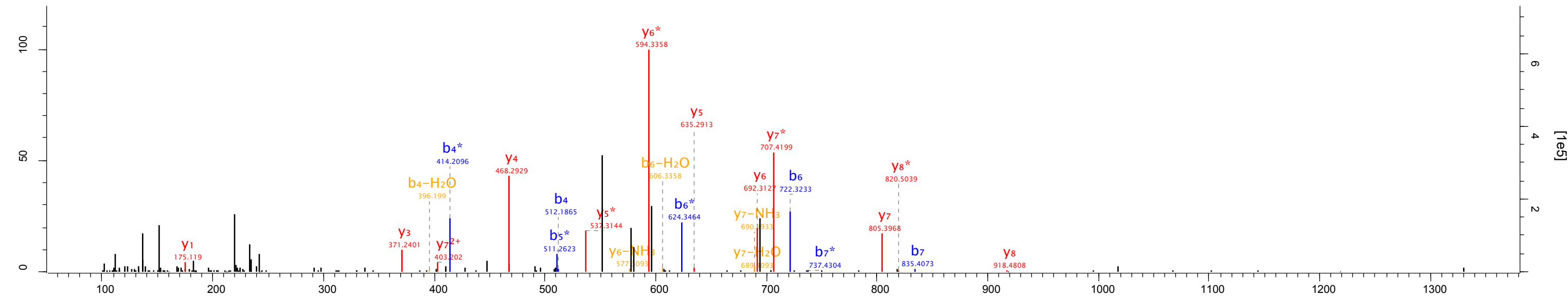
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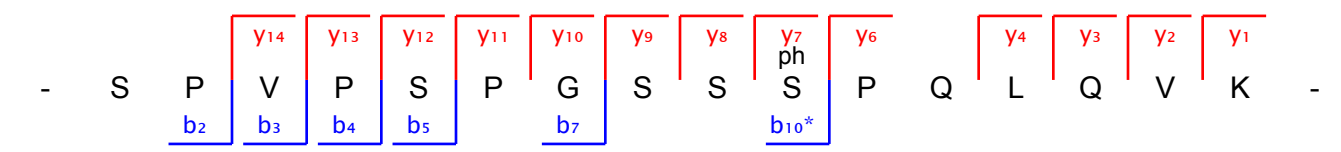
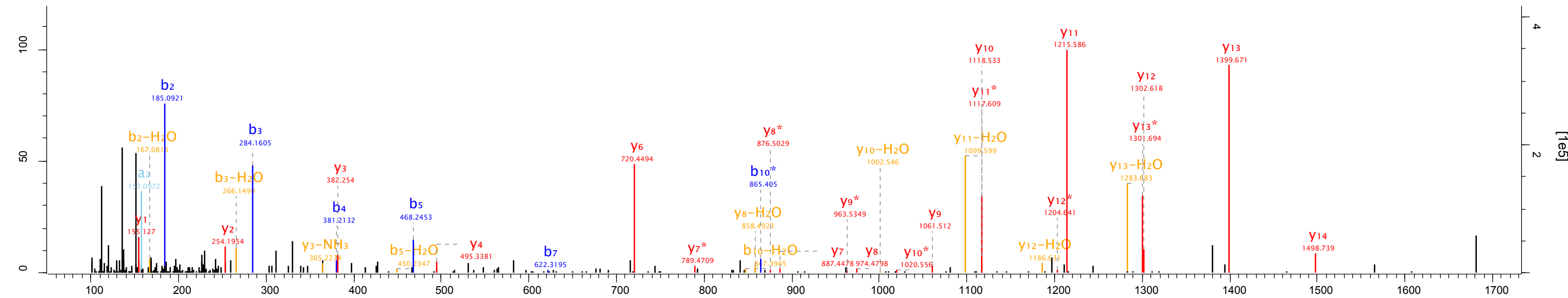
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20171215_MaS_33SR_LMH_phospho_02

Scan	Method	Score	m/z	Gene names
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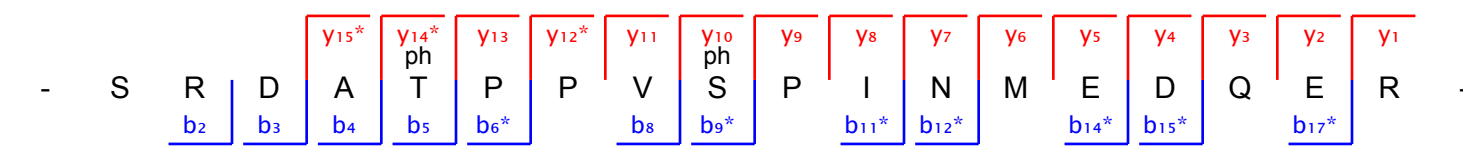
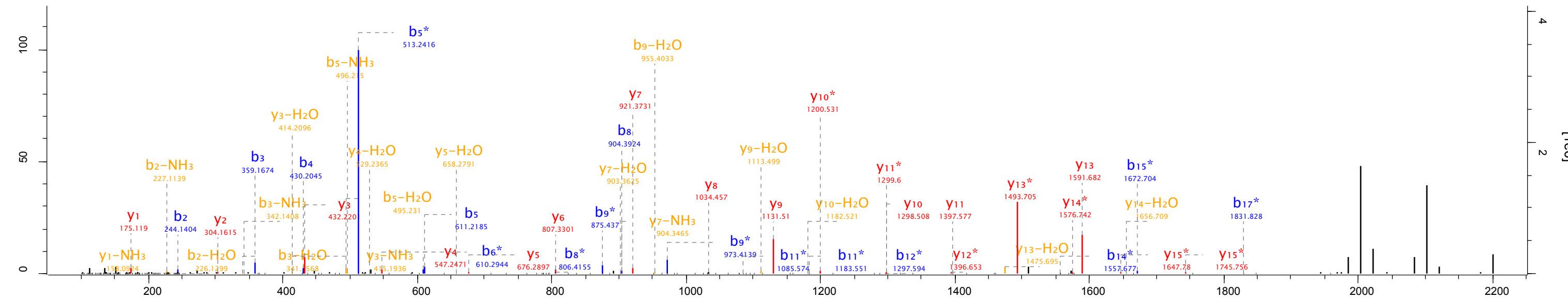


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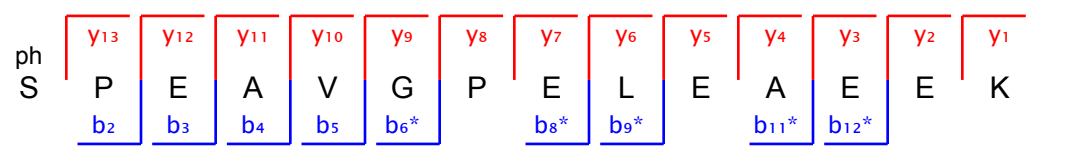
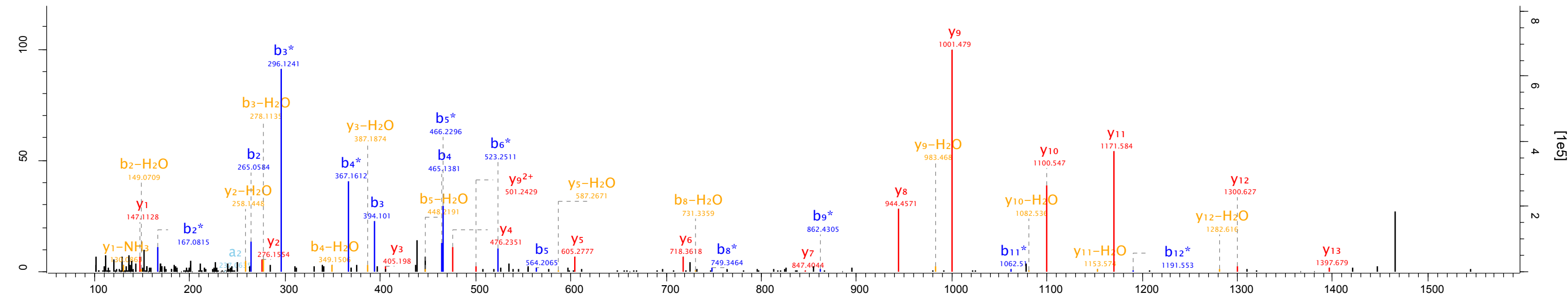


Raw file
20171215_MaS_33SR_LMH_phospho_02

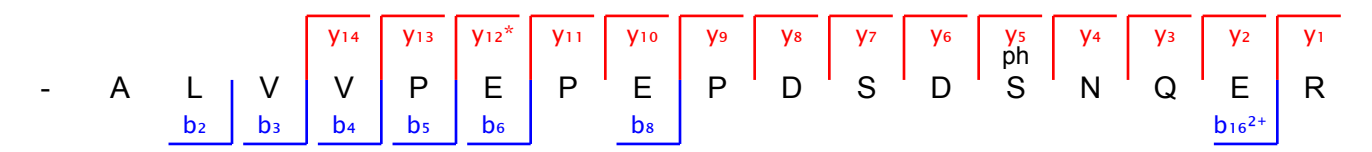
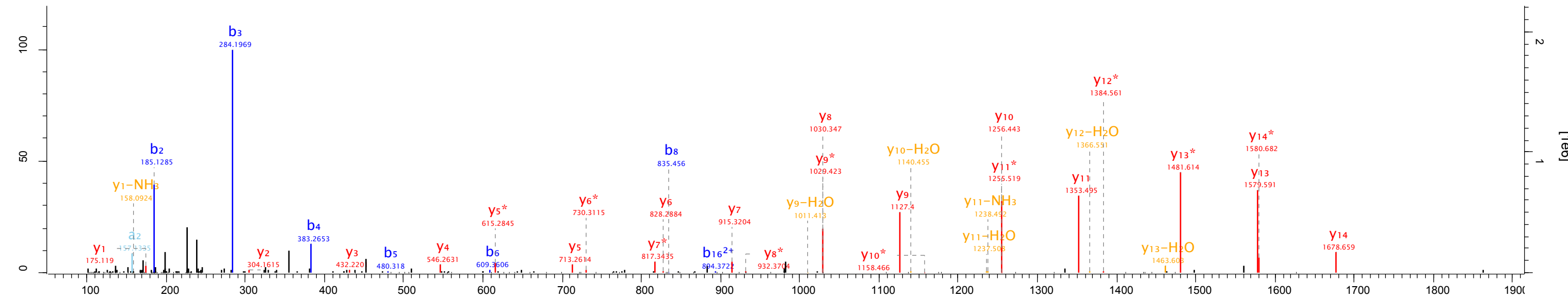
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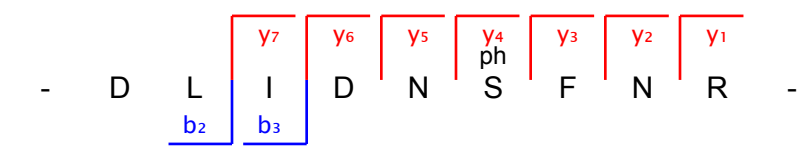
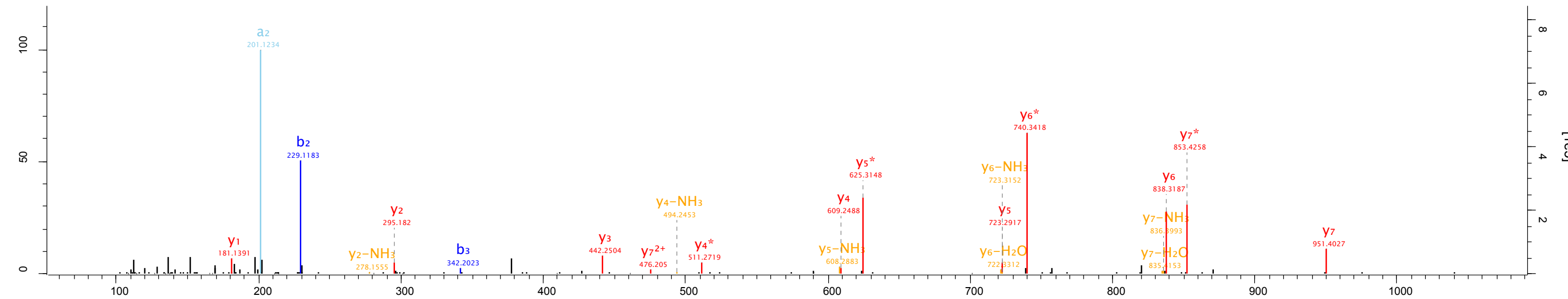
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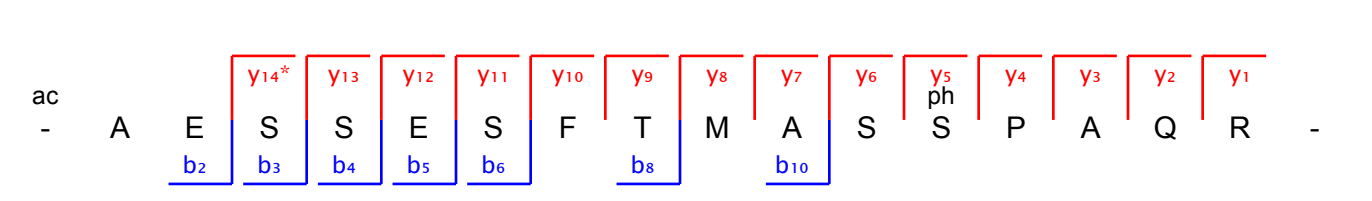
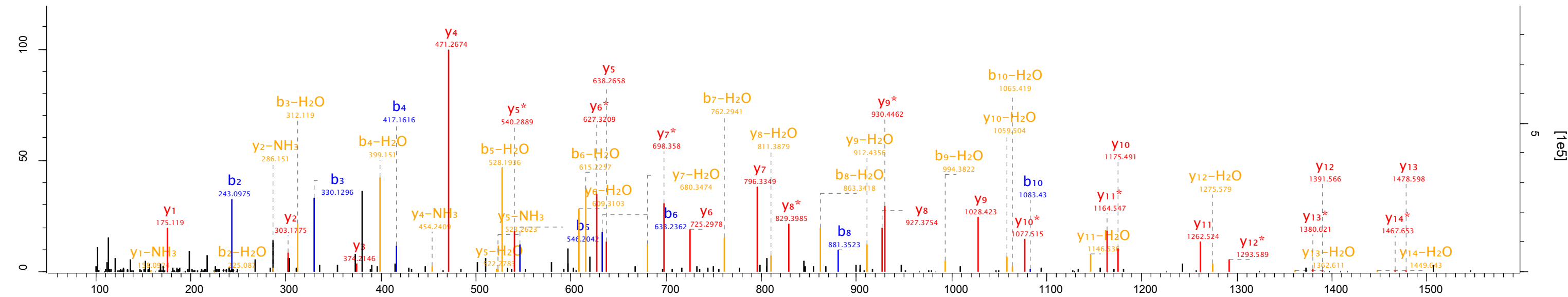
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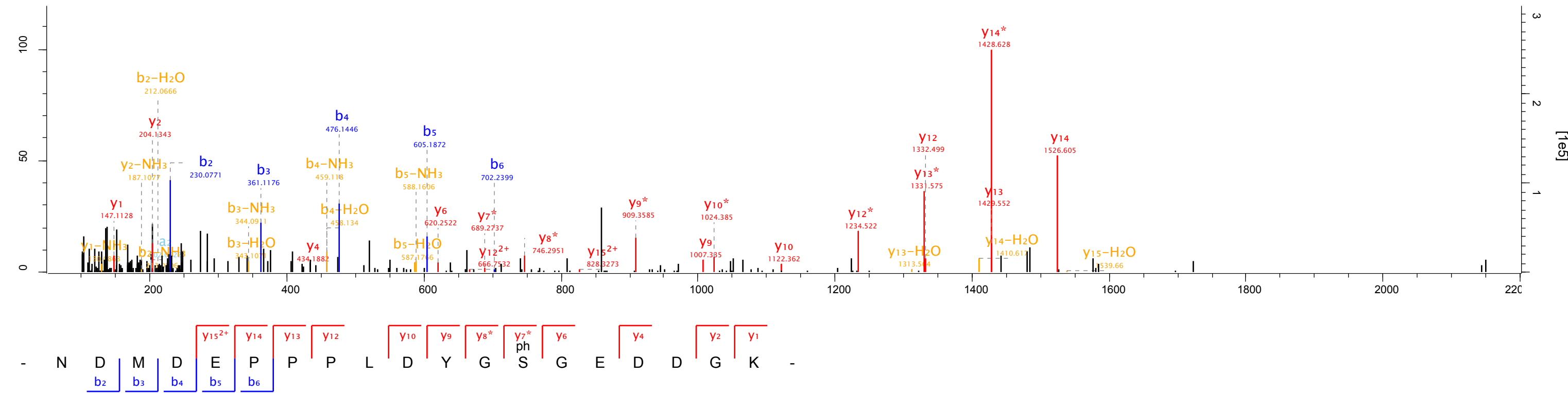
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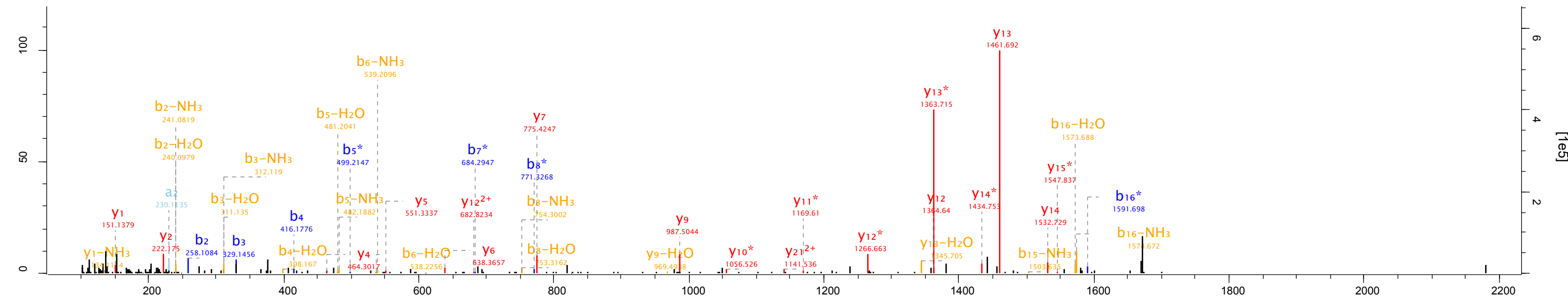
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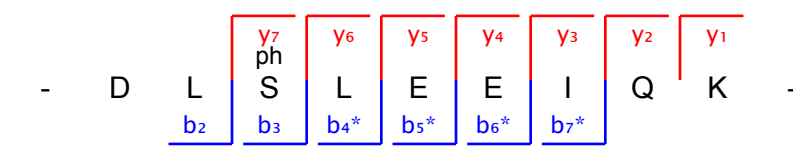
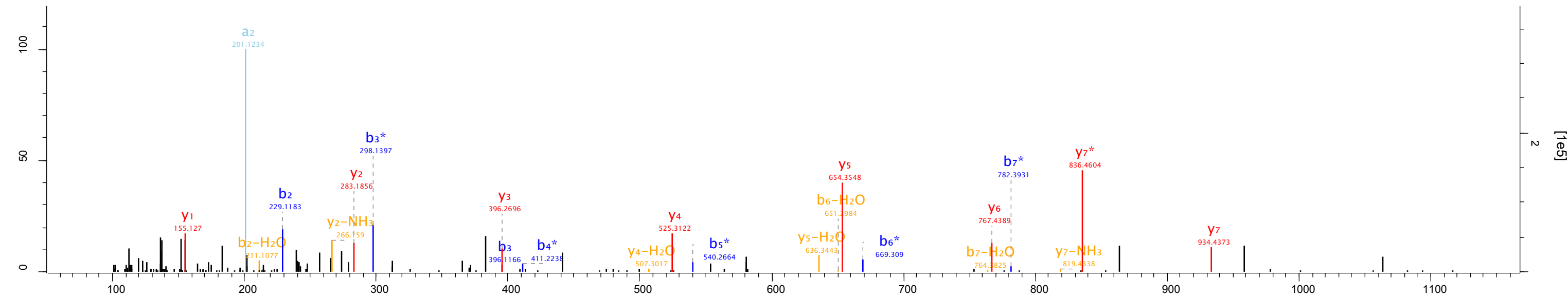


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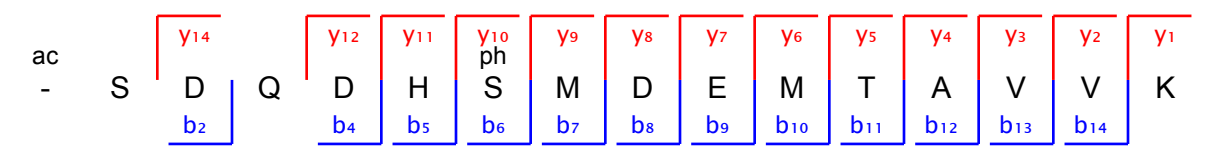
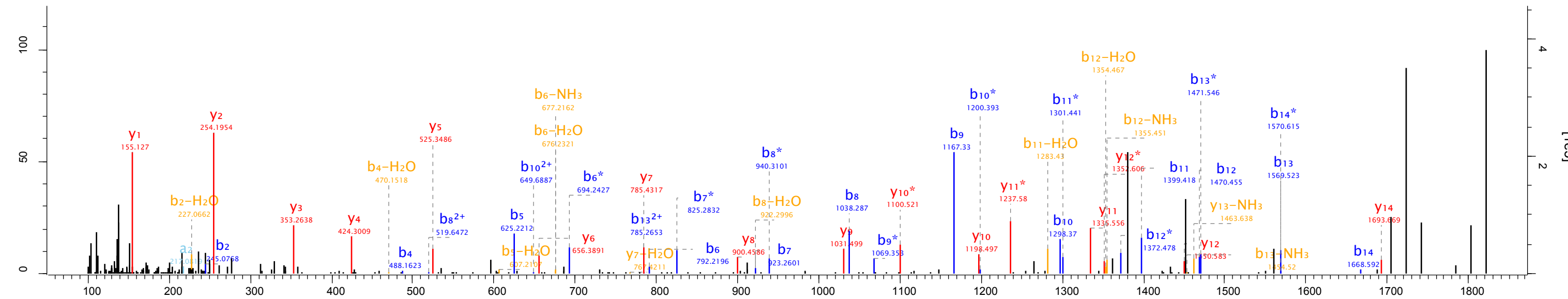
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- b₂ (E), b₃ (A), b₄ (S), b₅* (T), b₇* (Q), b₈* (S), b₁₆* (A)
- y₁ (K), y₂ (E), y₄ (L), y₅ (S), y₆ (S), y₇ (D), y₉ (P), y₁₀* (S), y₁₁* (L), y₁₂ (P), y₁₃ (A), y₁₄ (L), y₁₅* (S), y₂₁²⁺ (P)

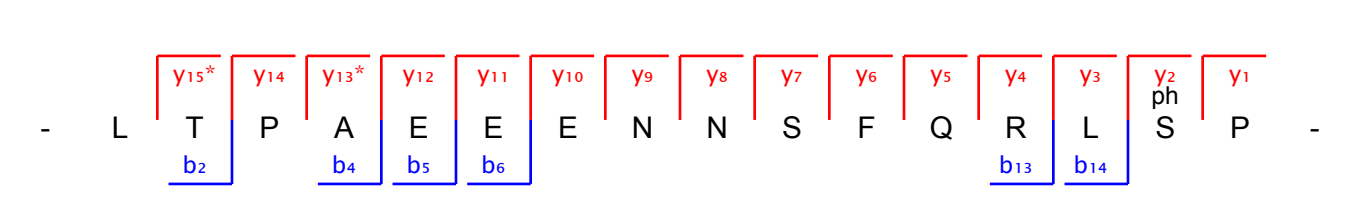
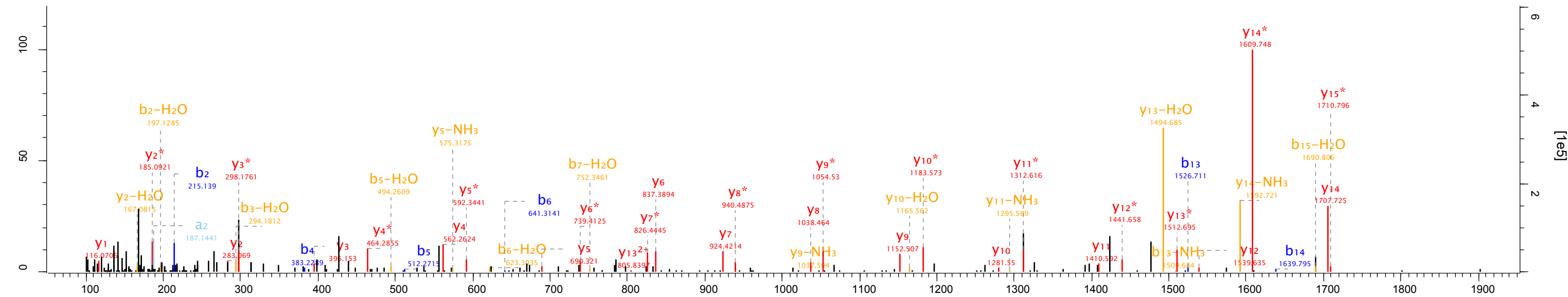
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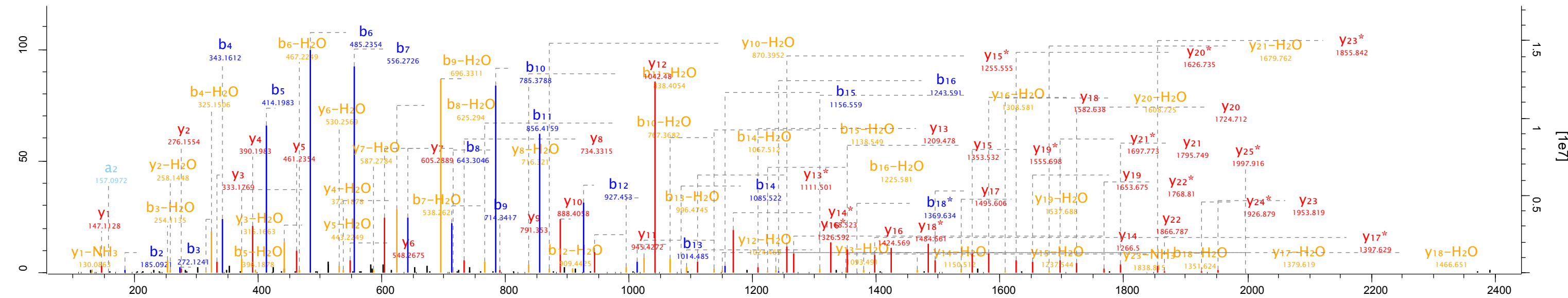
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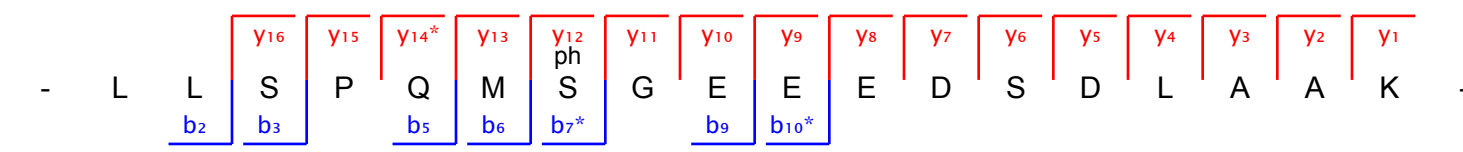
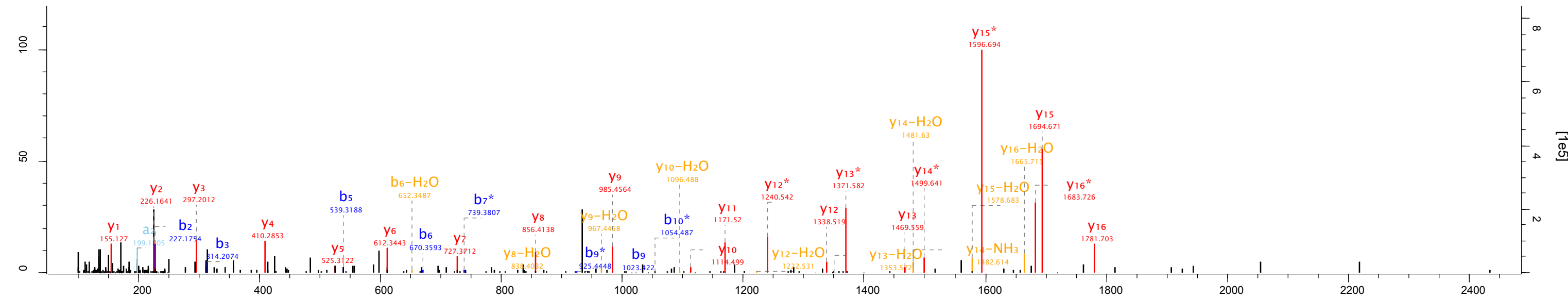
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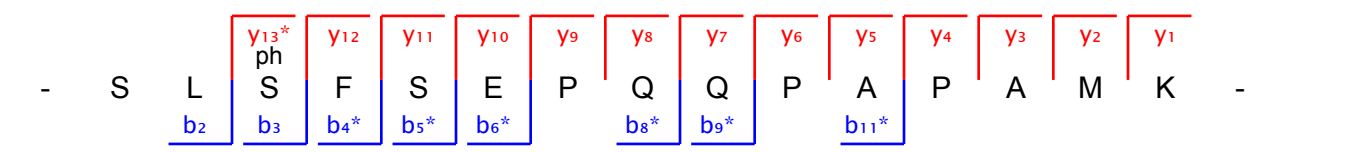
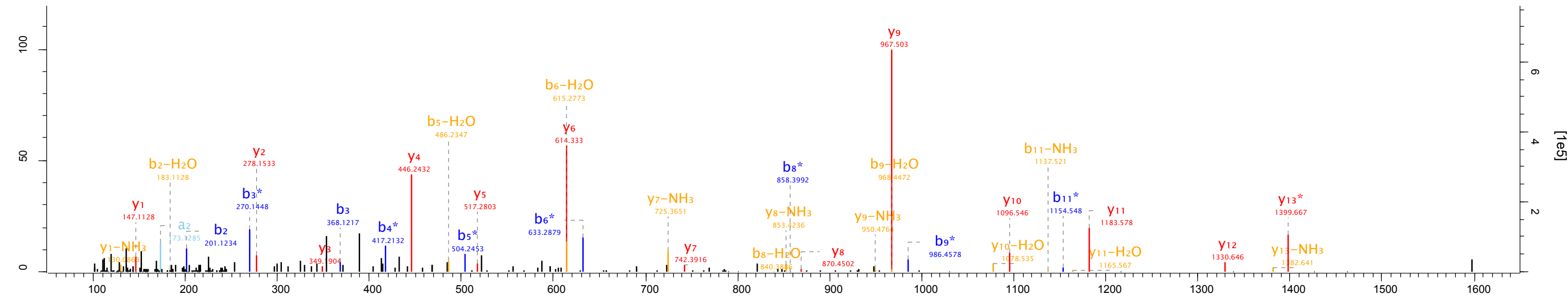
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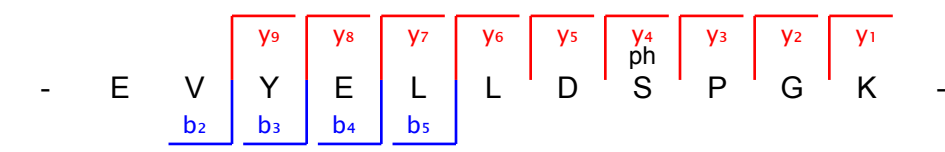
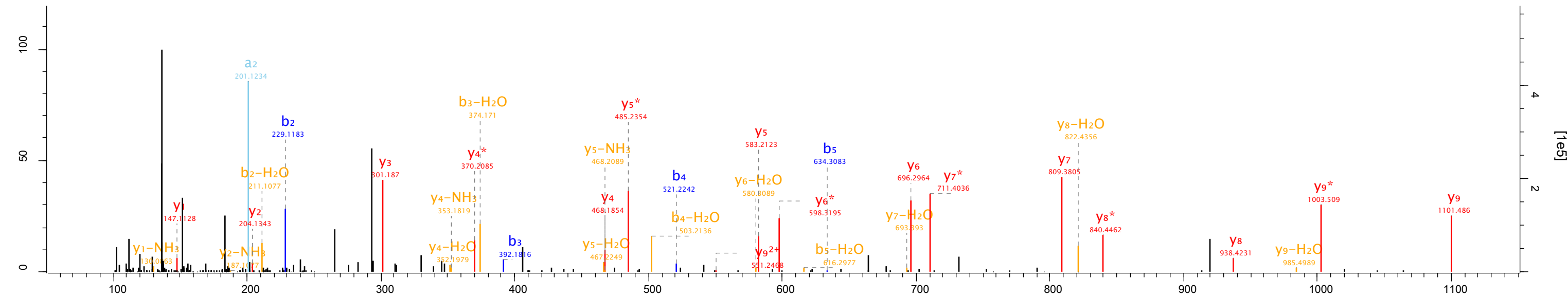
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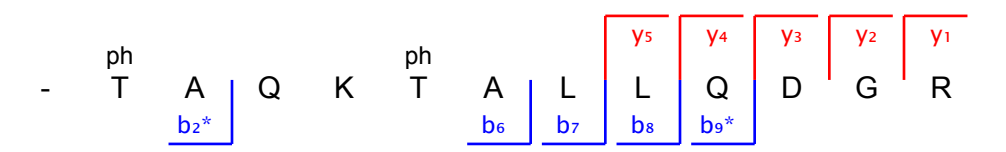
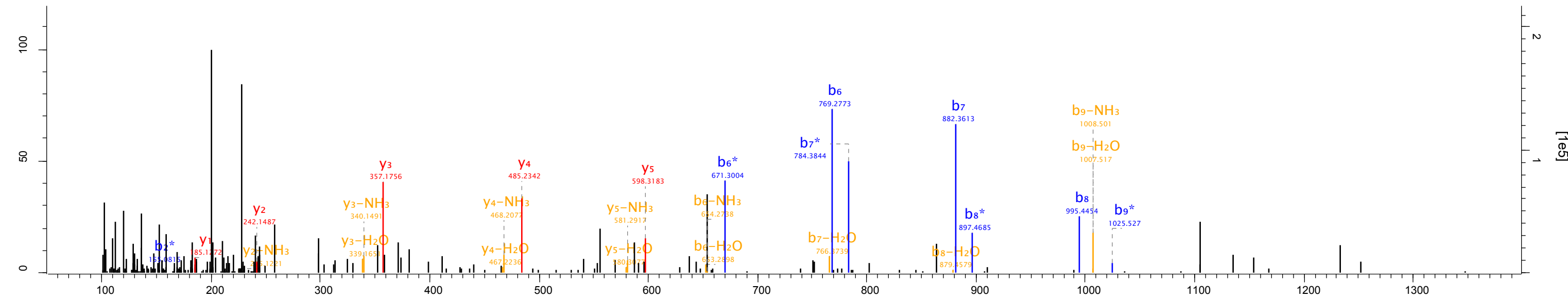
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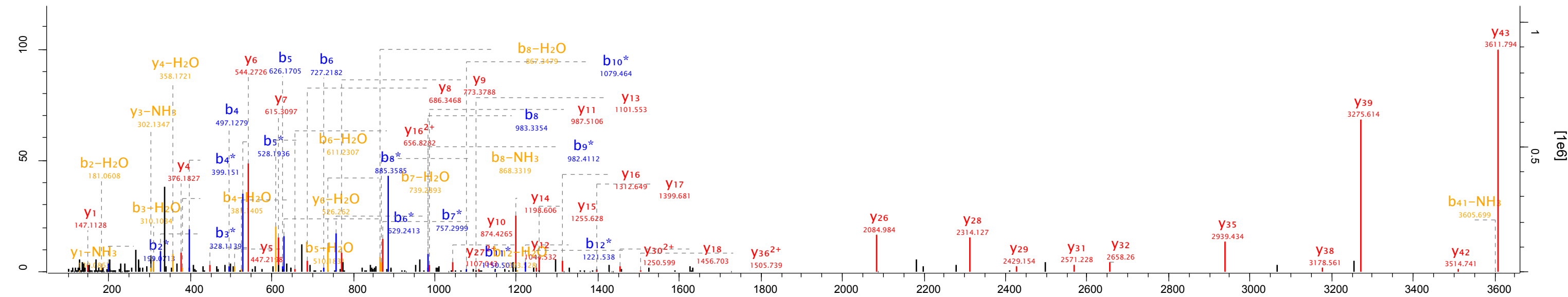
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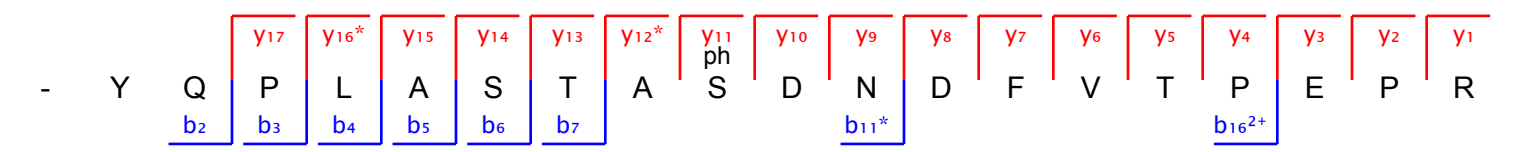
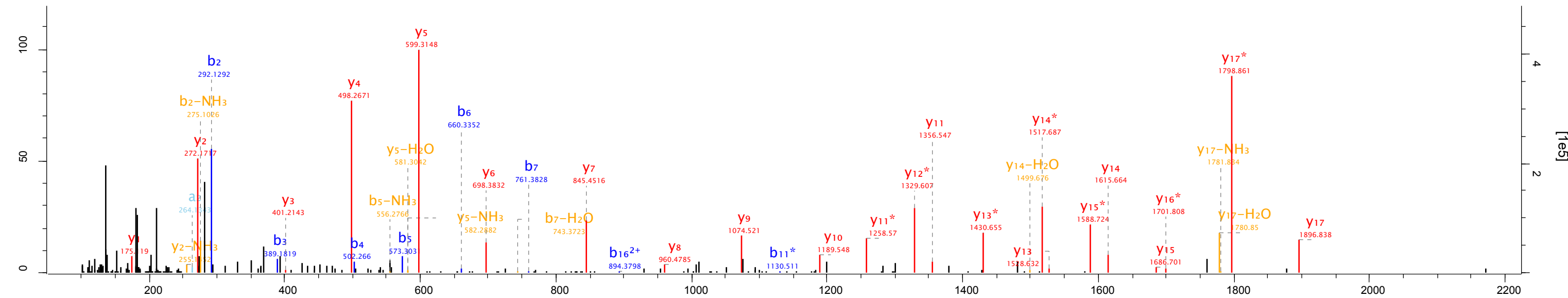
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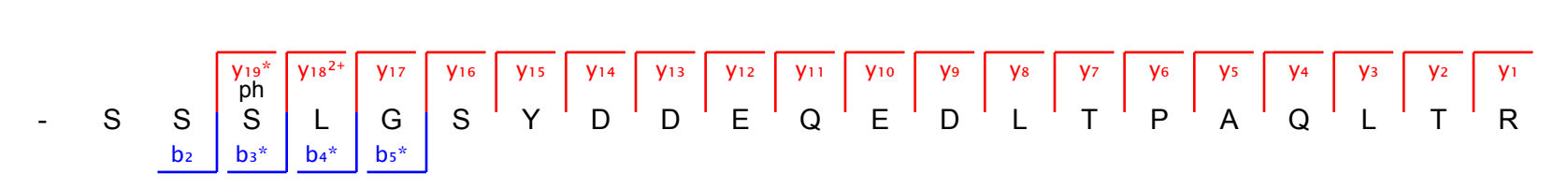
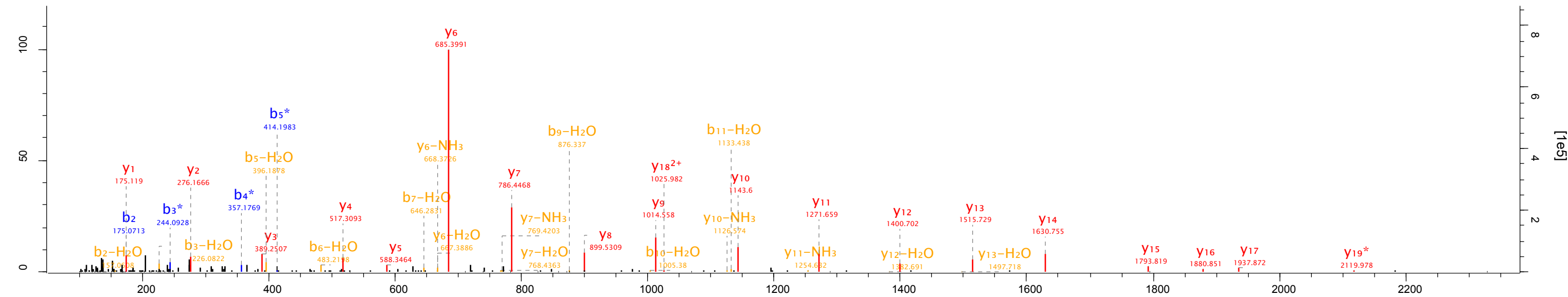
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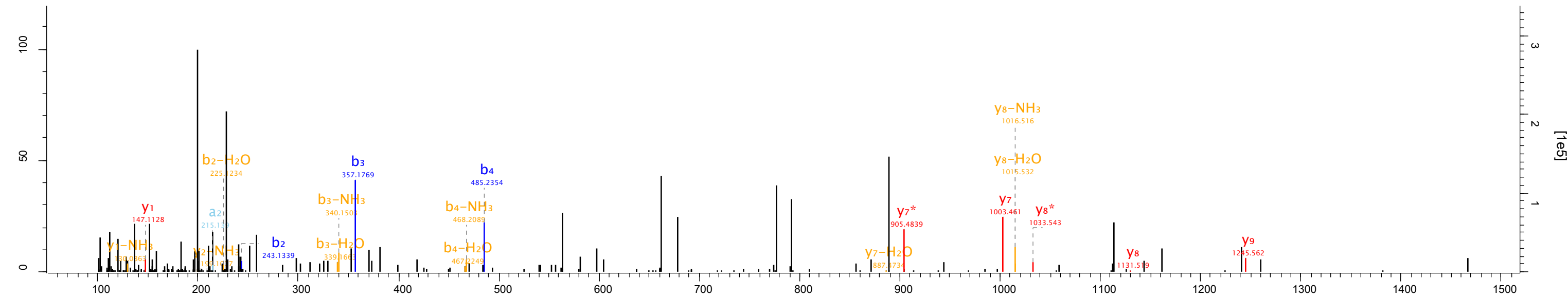
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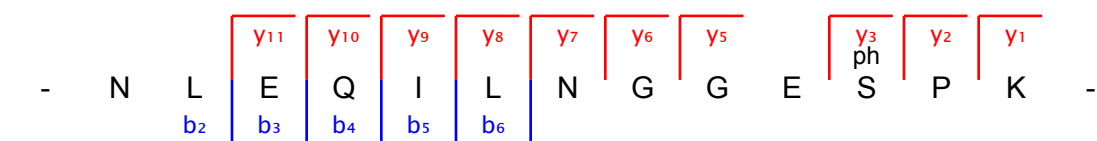
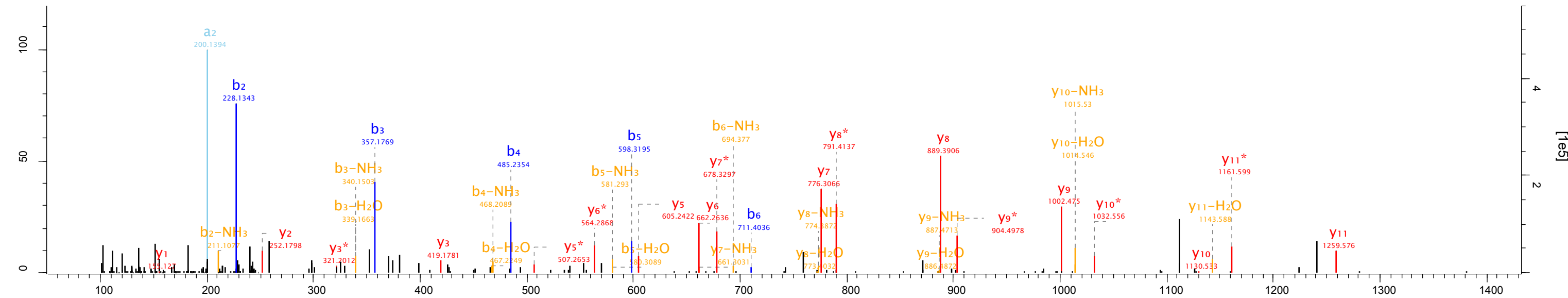


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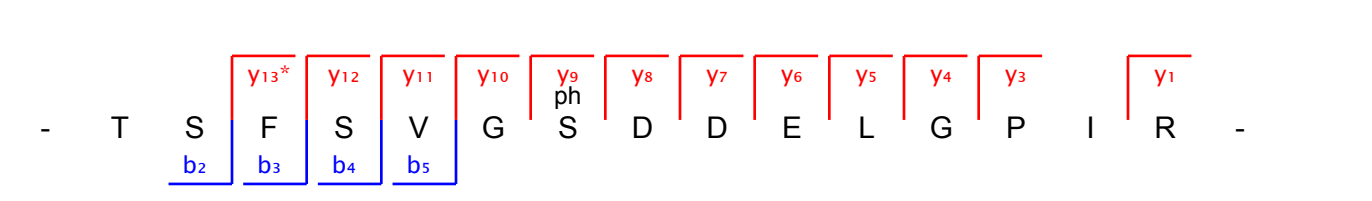
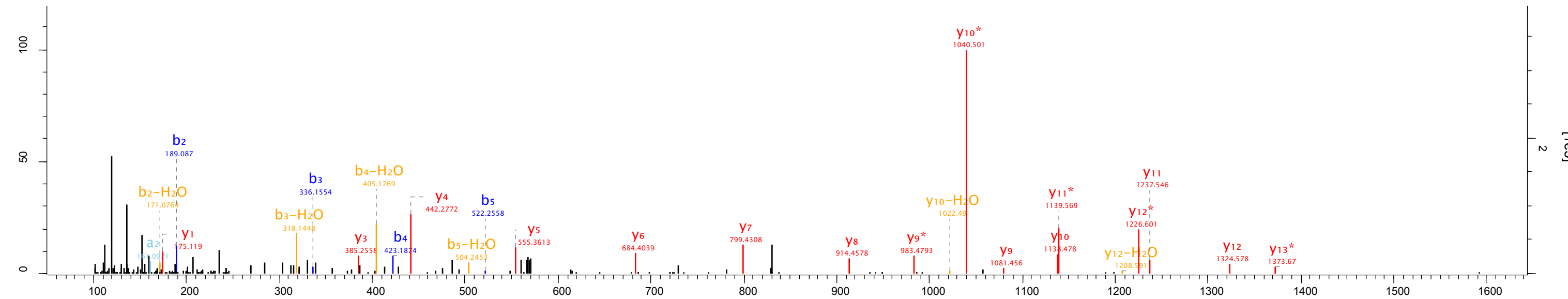


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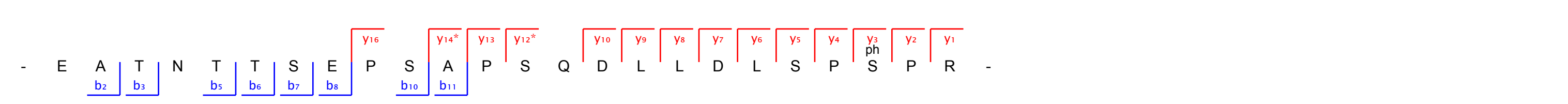
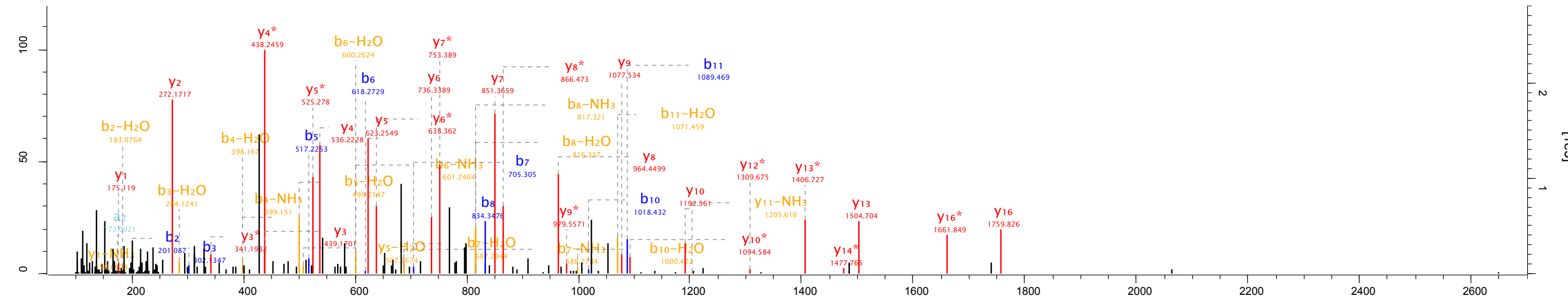
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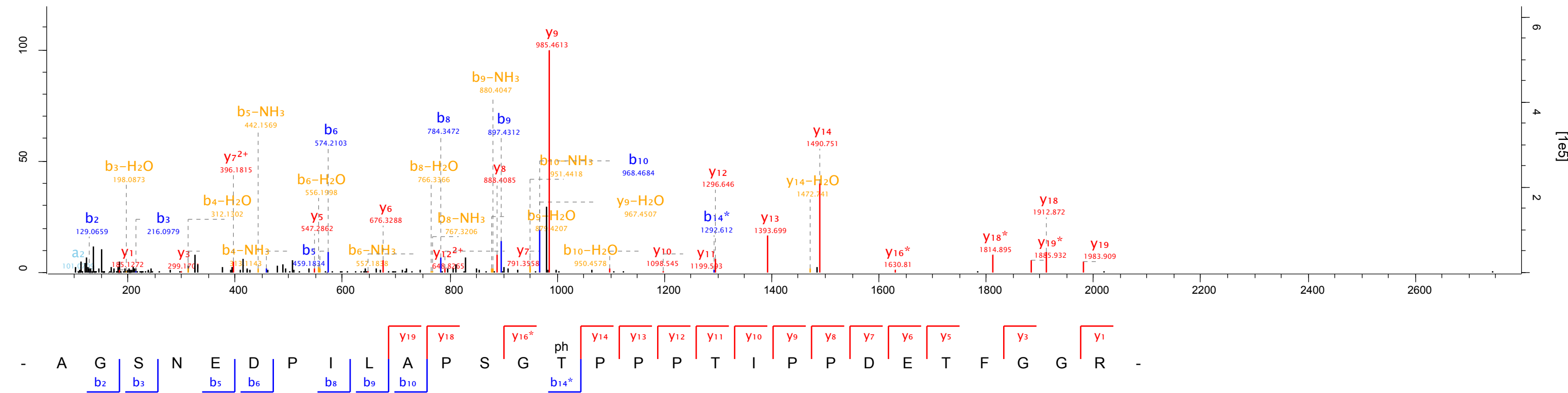


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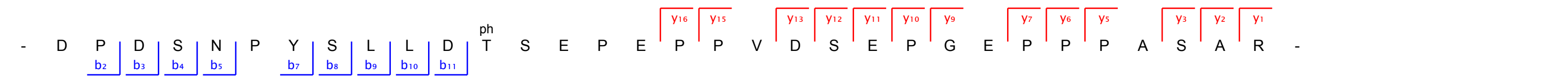
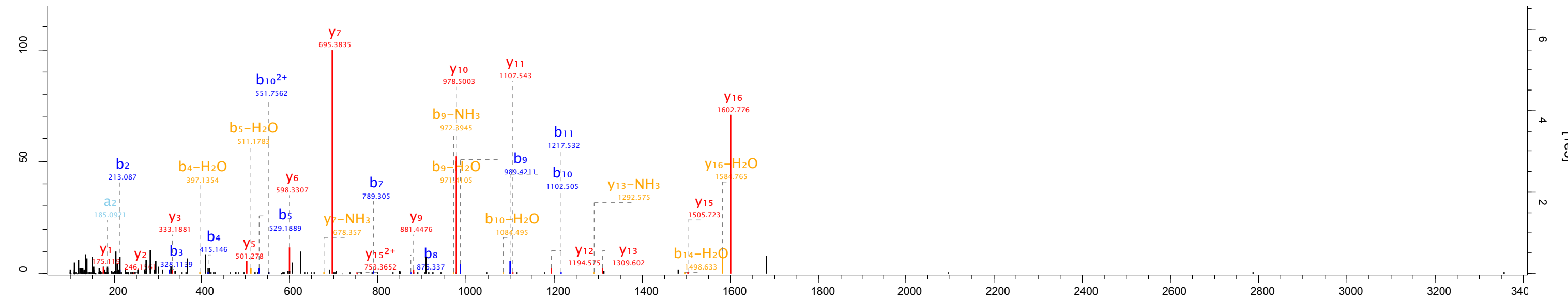


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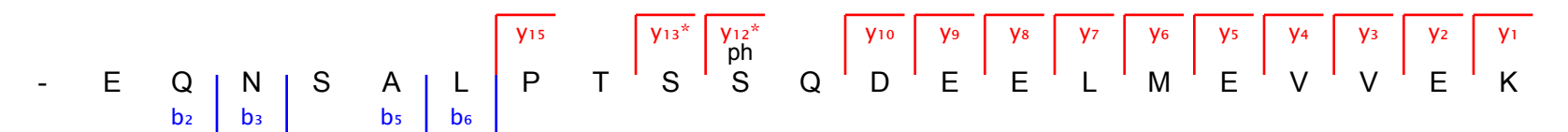
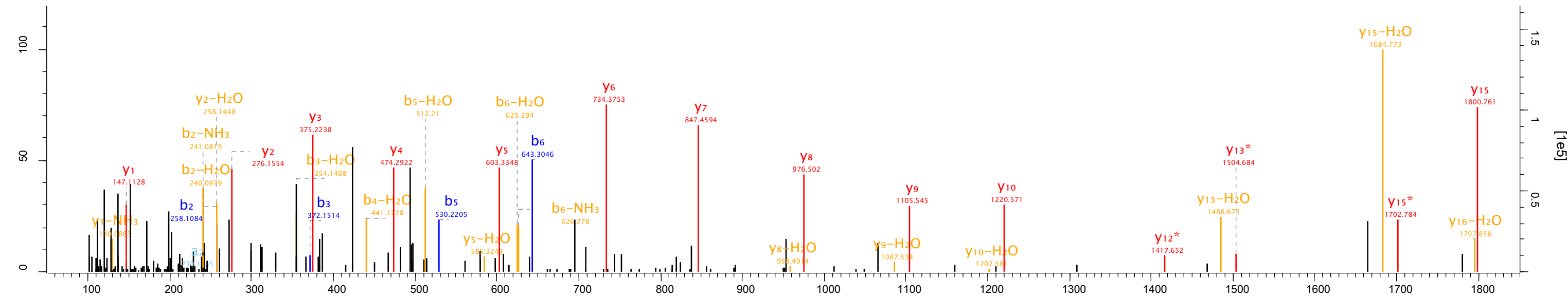
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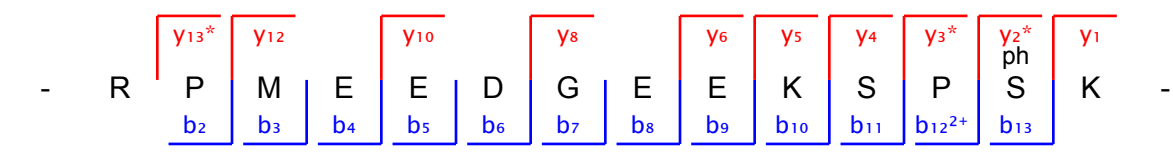
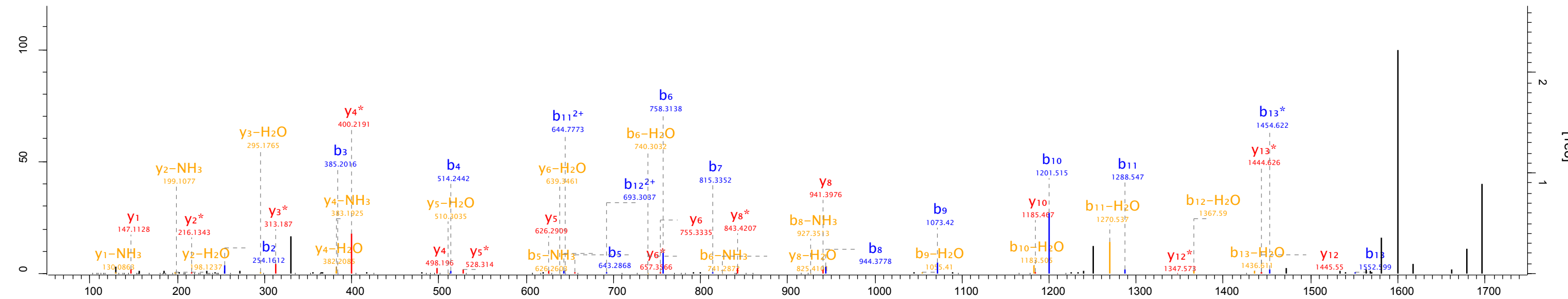
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20171215_MaS_33SR_LMH_phospho_03

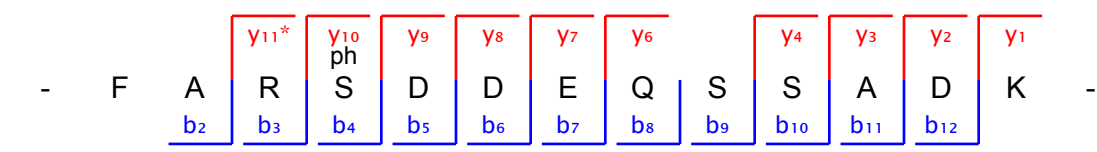
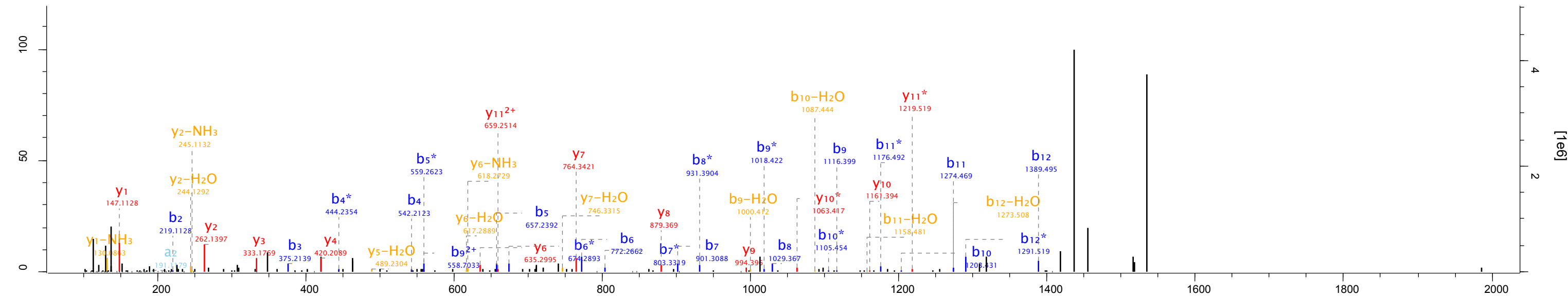
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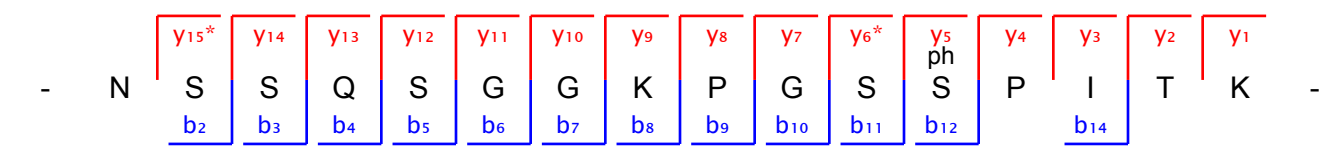
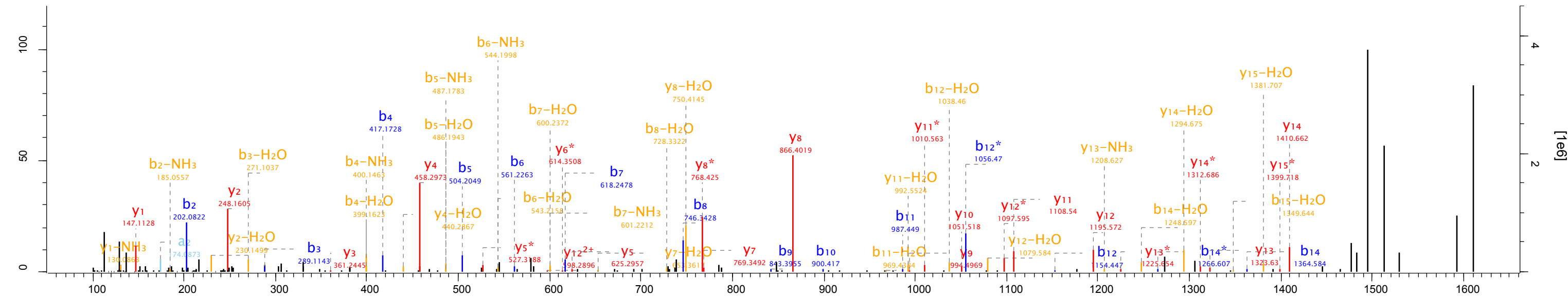
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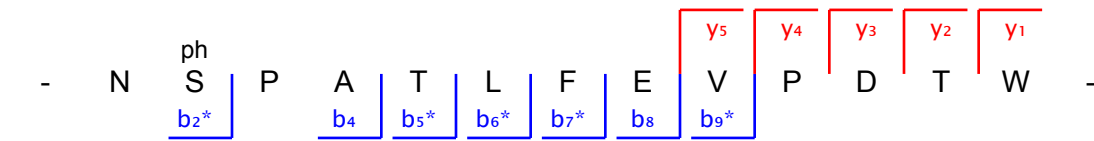
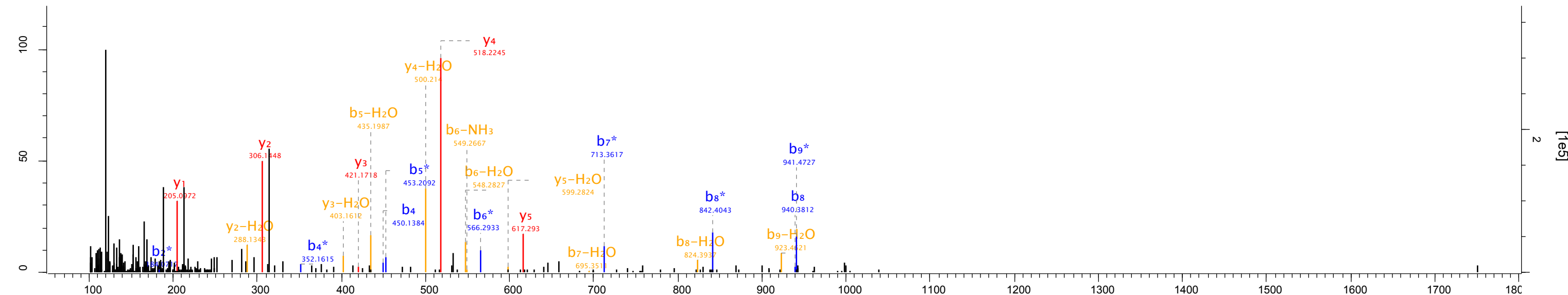
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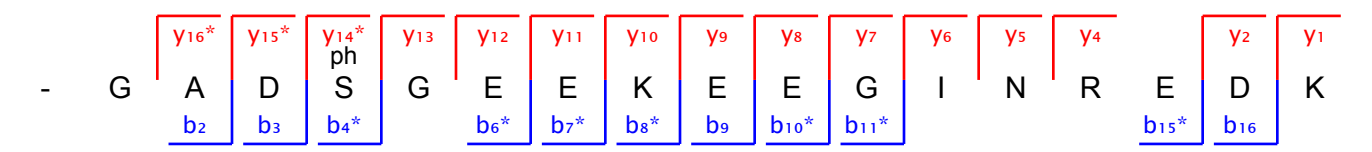
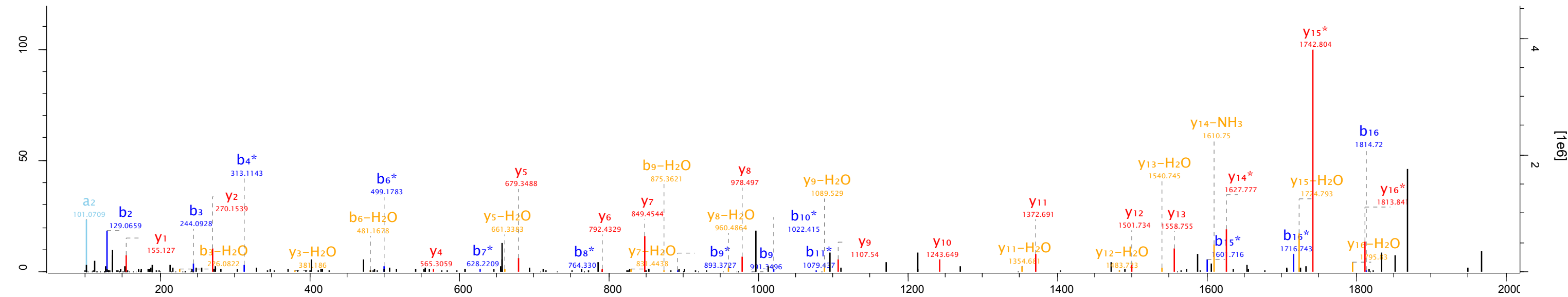
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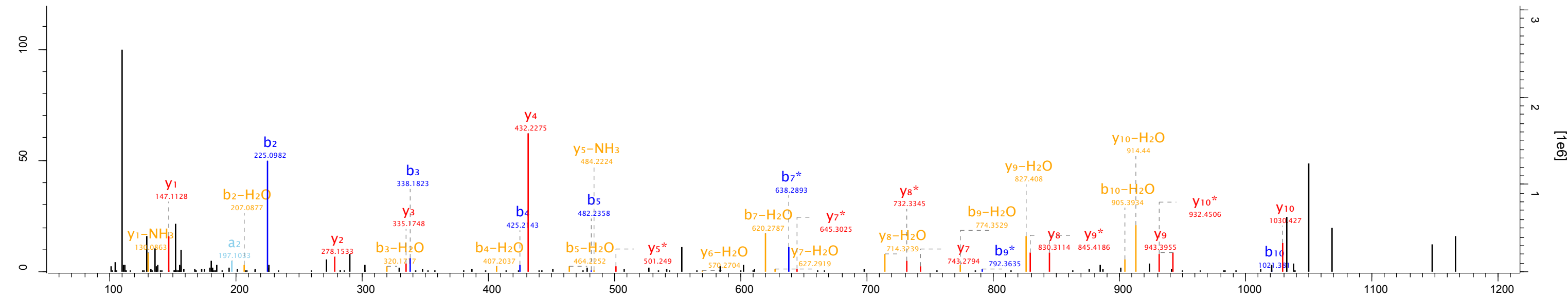
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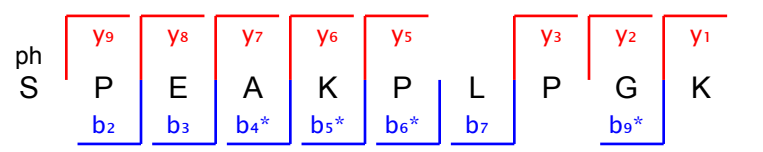
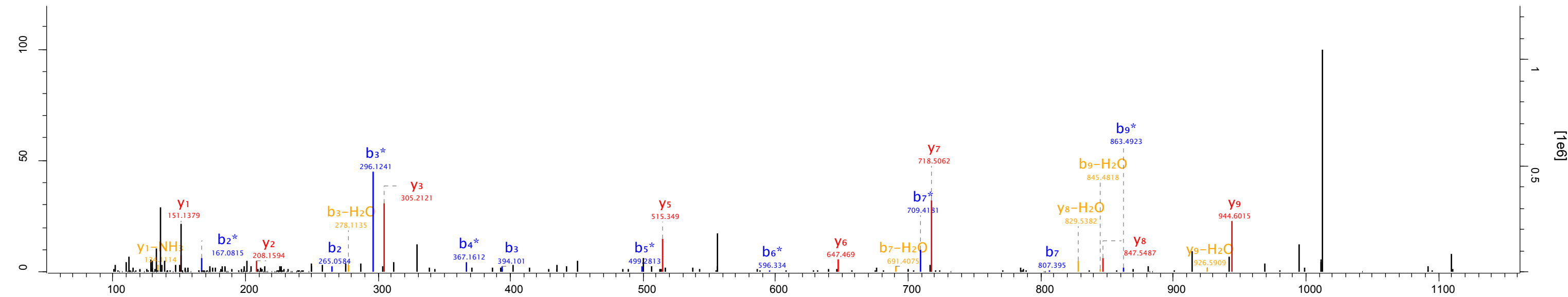
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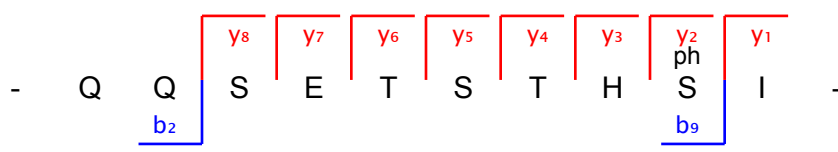
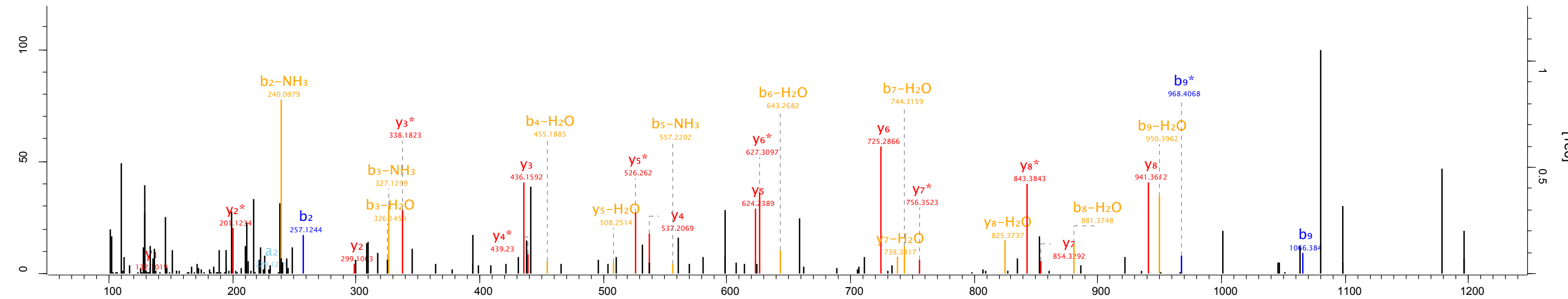
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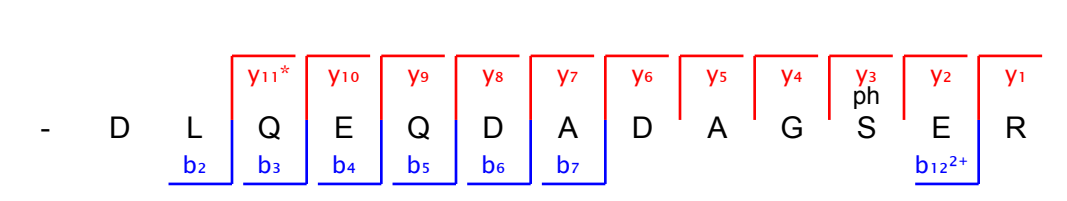
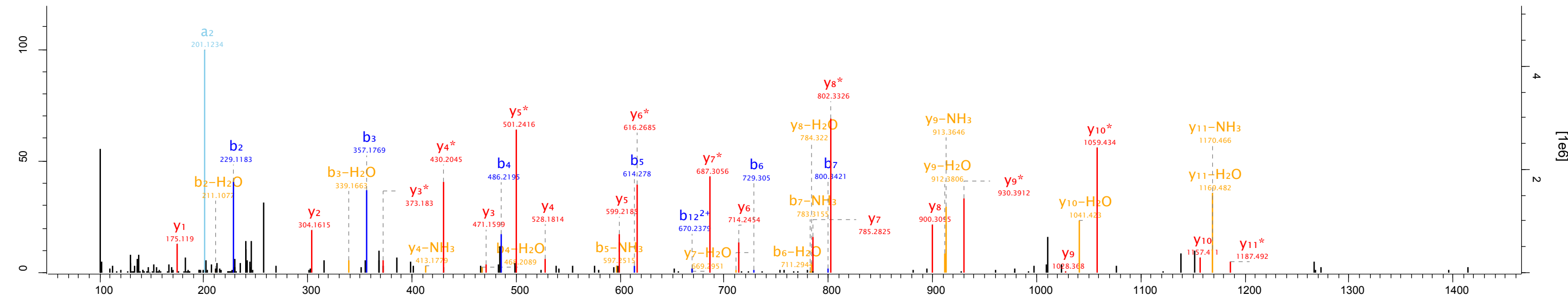
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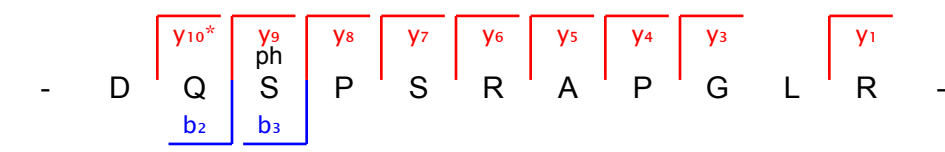
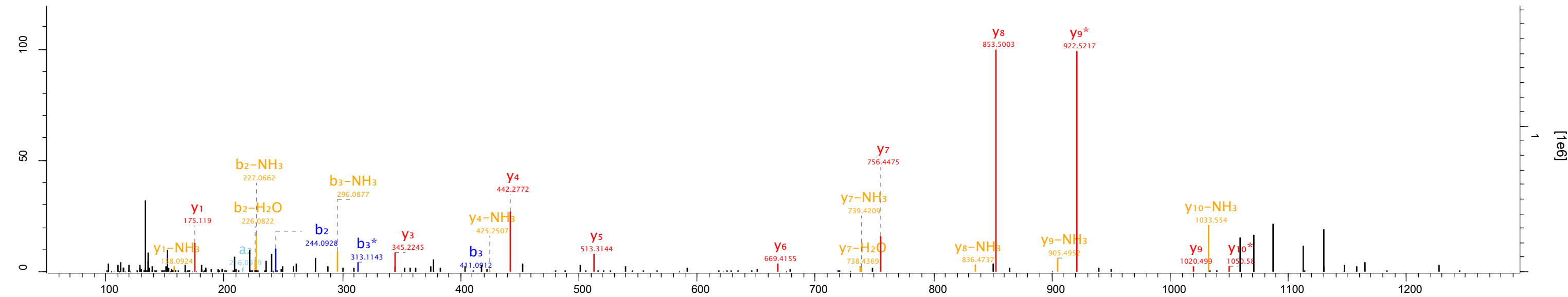
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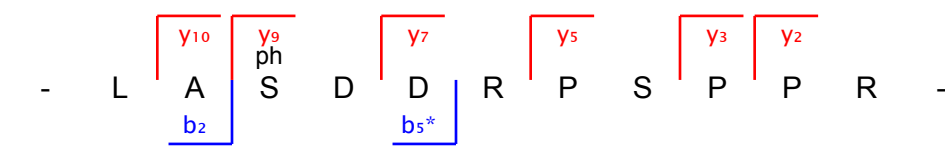
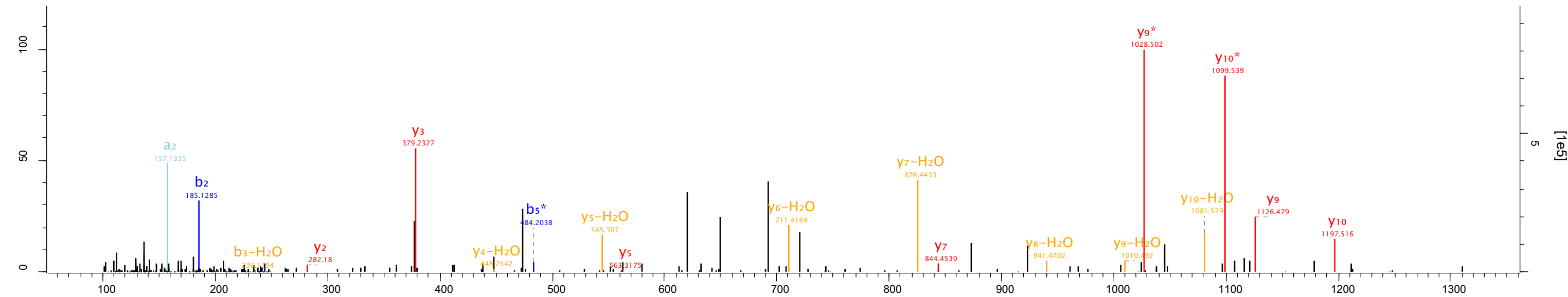
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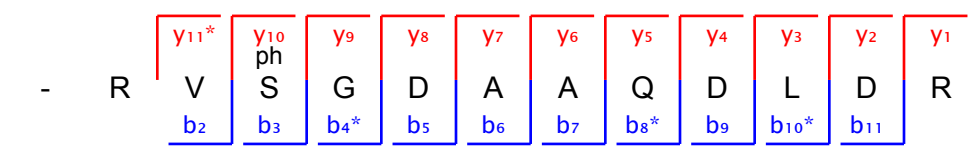
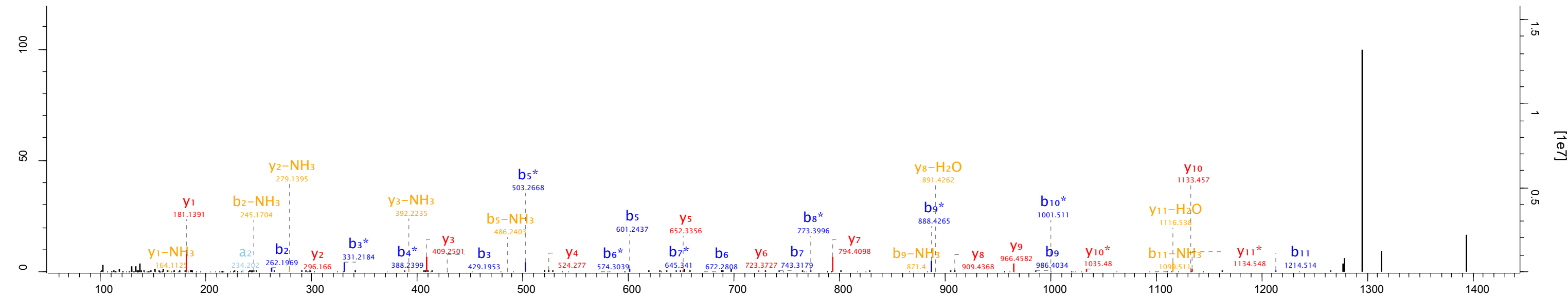
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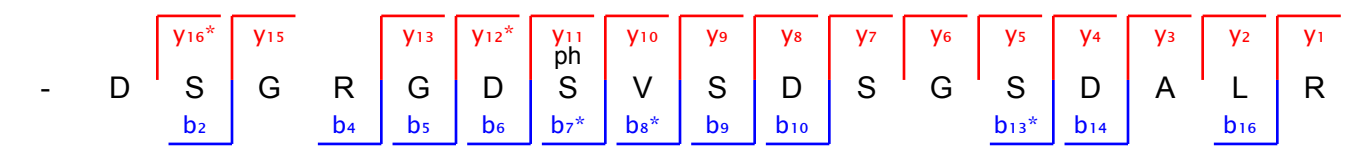
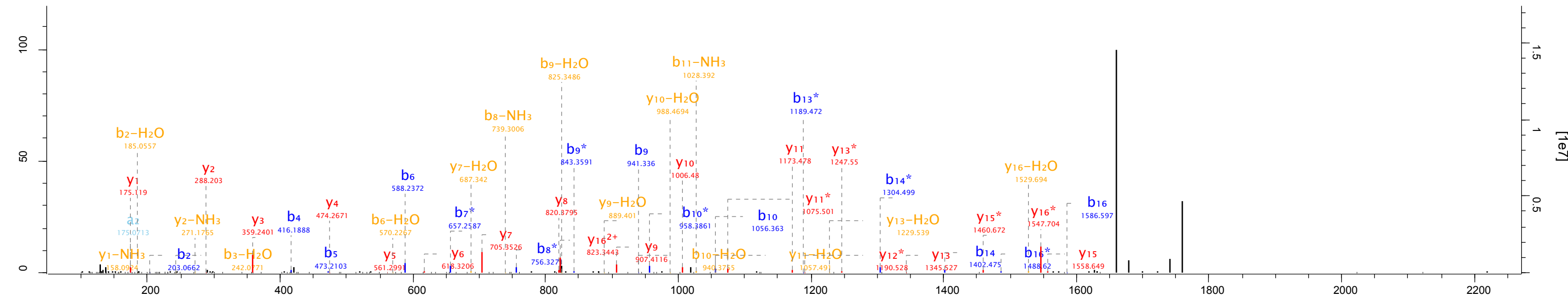
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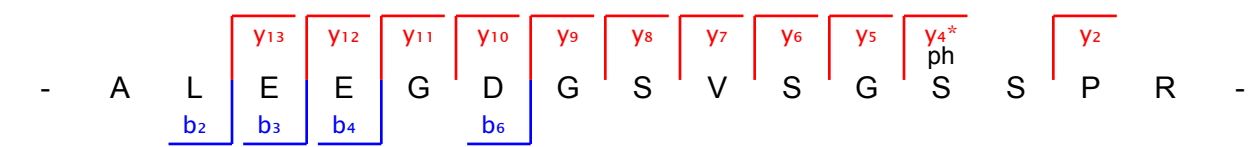
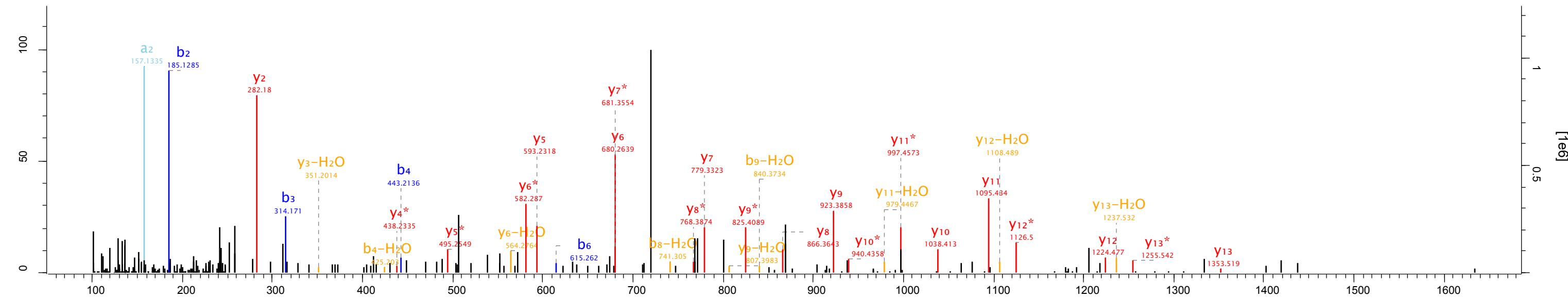


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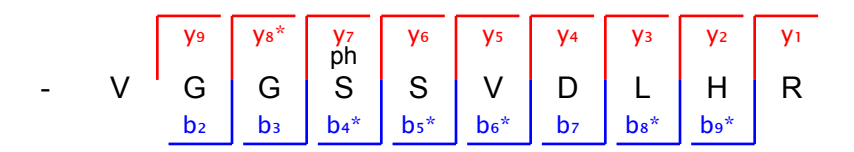
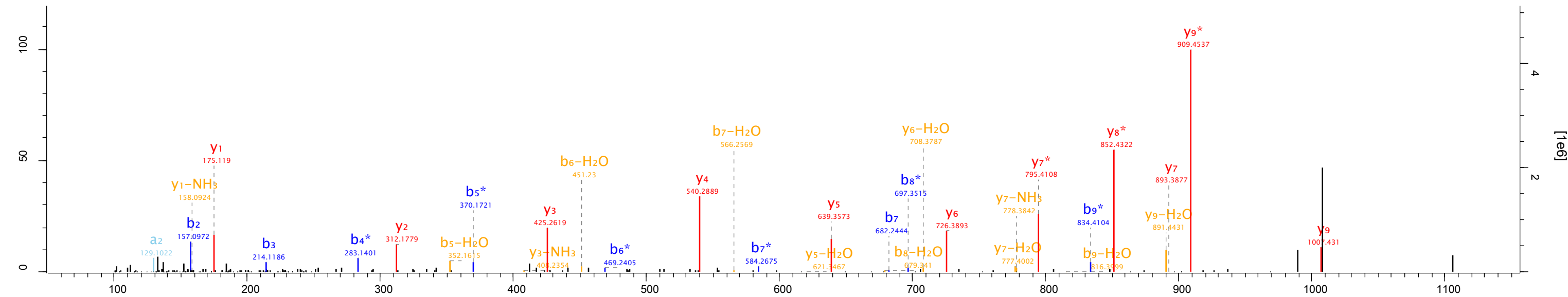


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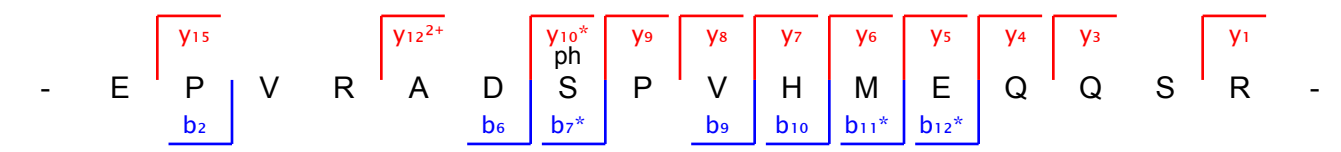
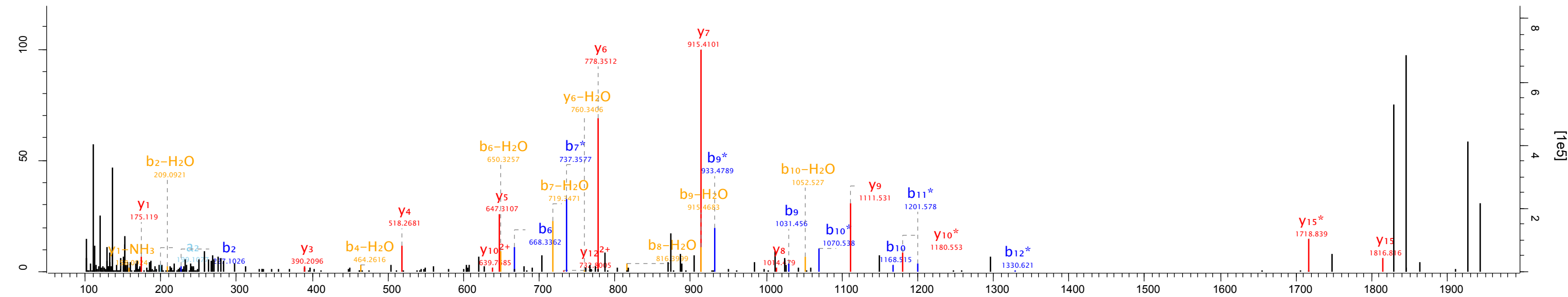




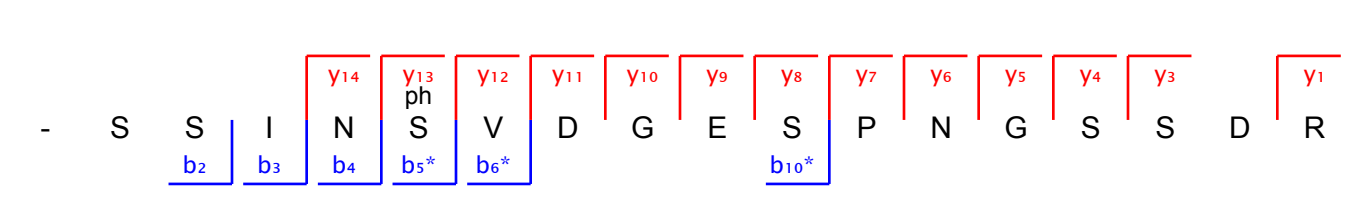
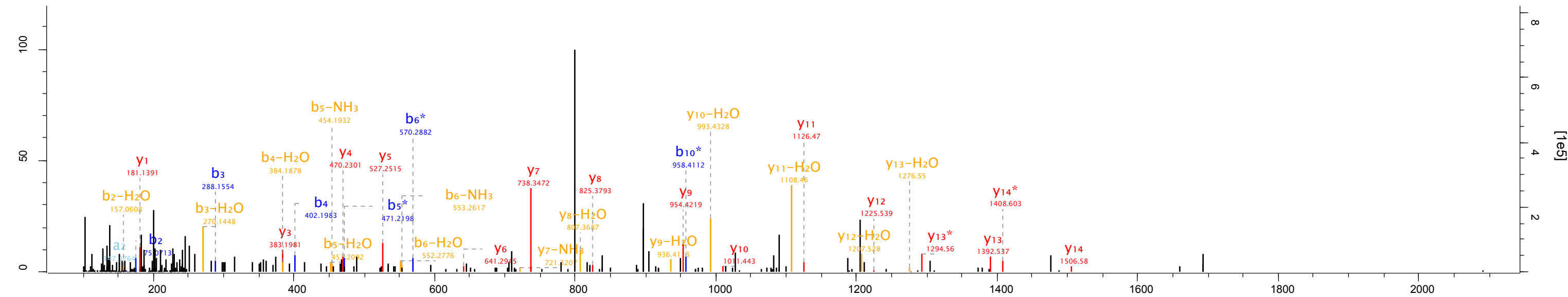
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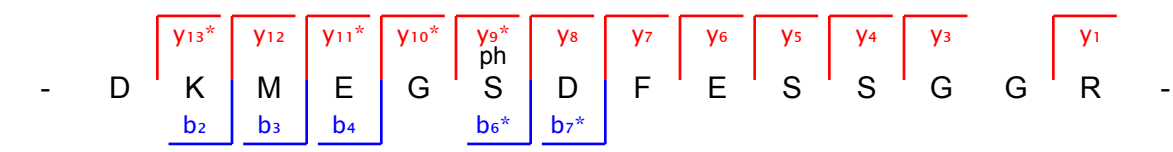
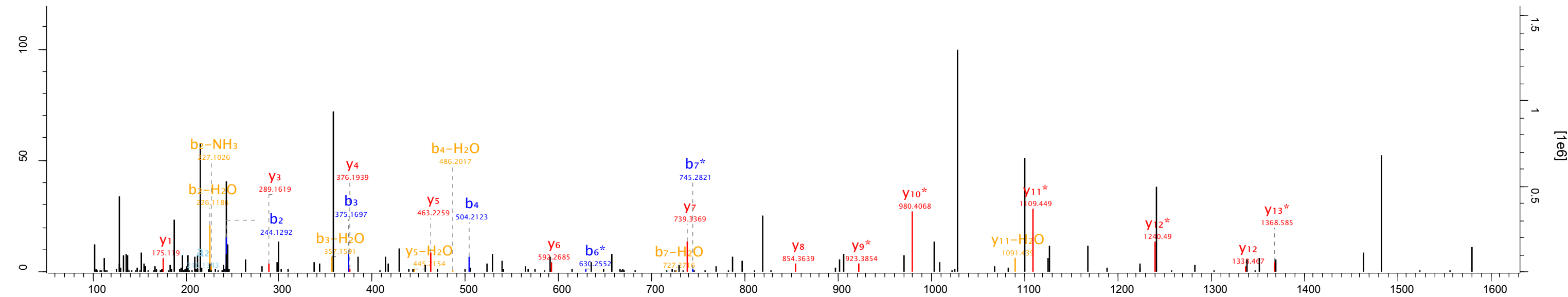
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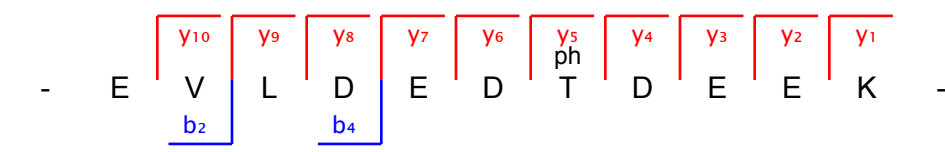
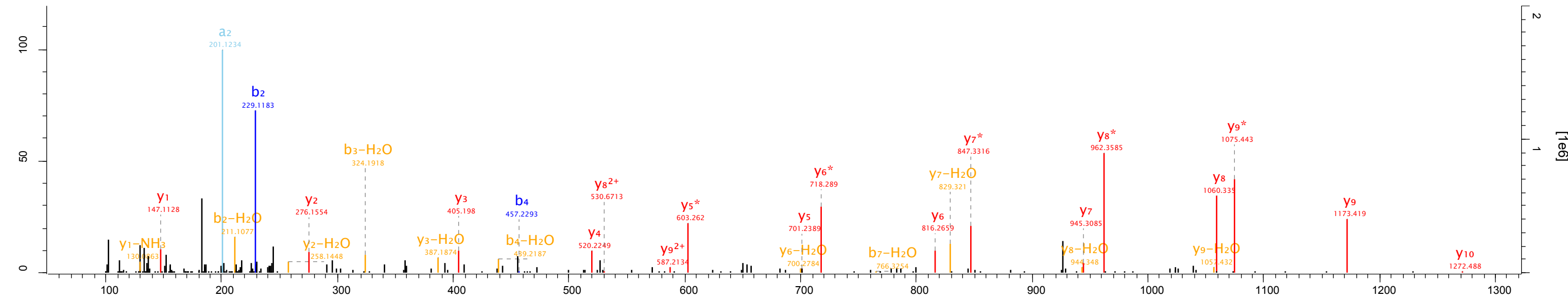
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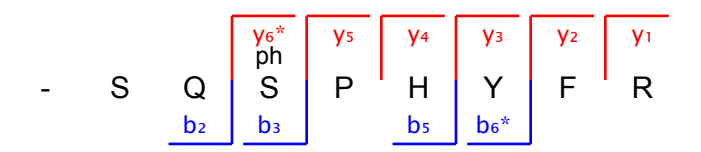
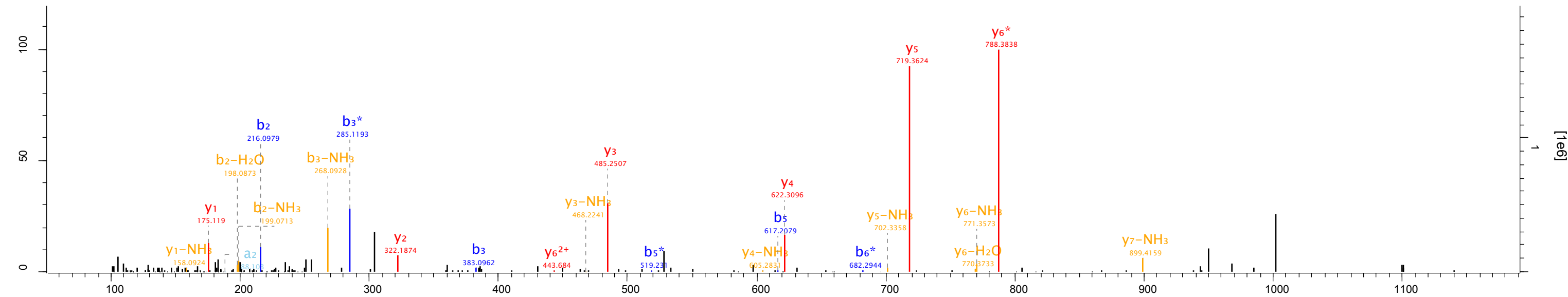
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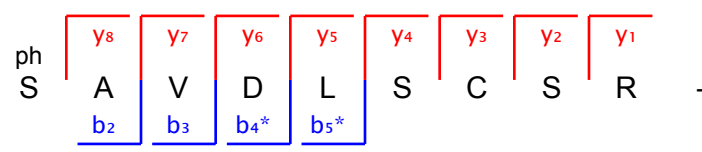
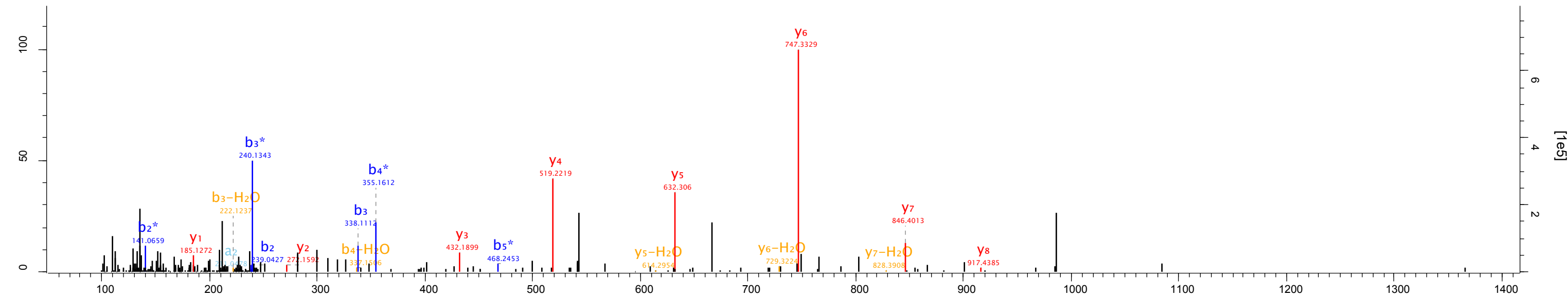
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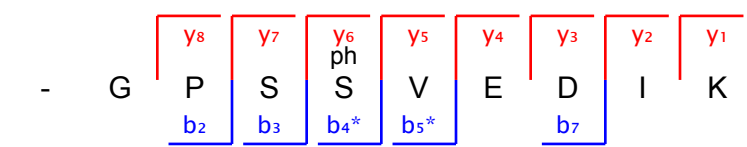
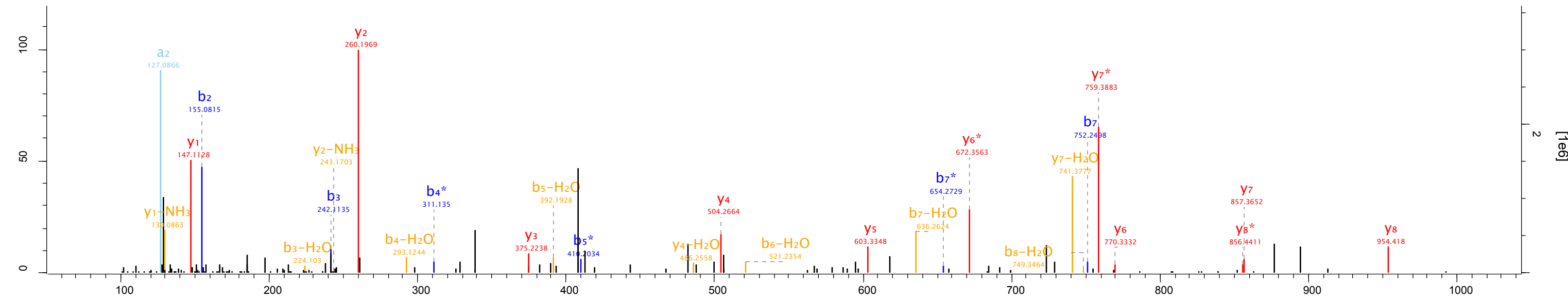
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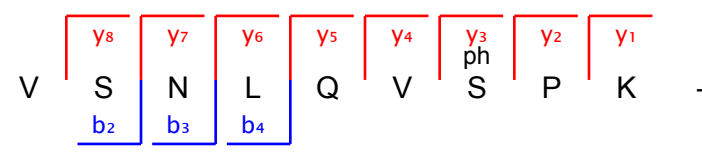
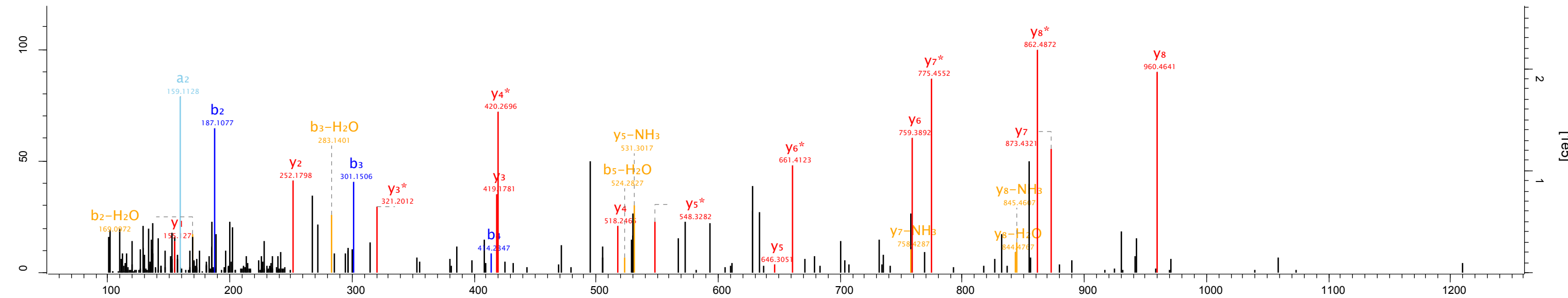
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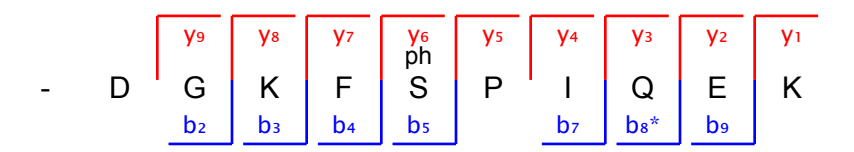
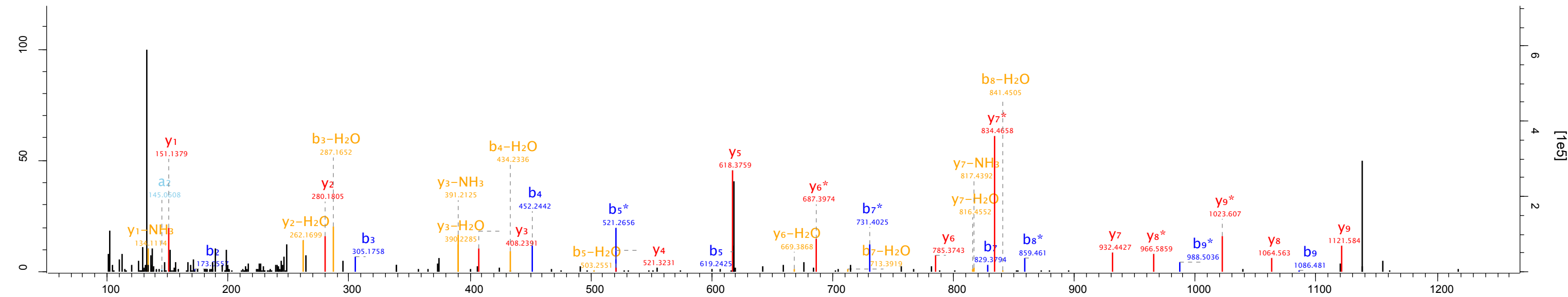
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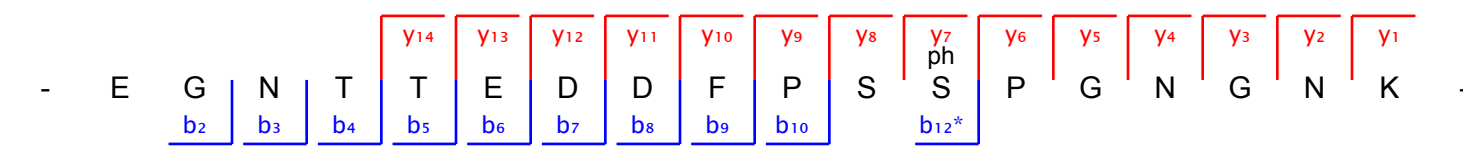
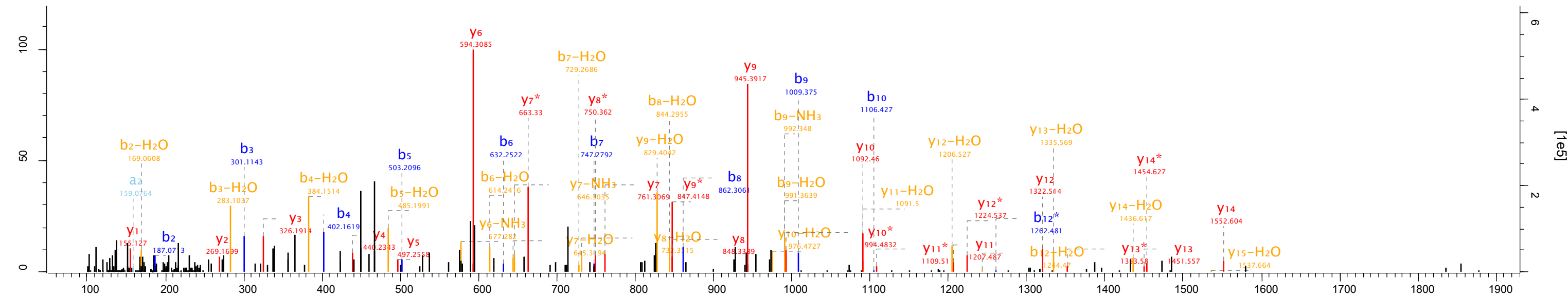
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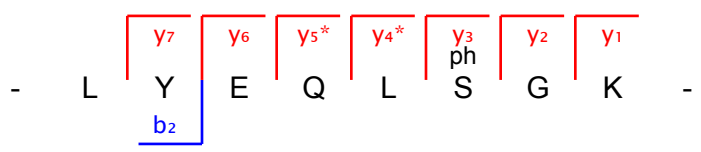
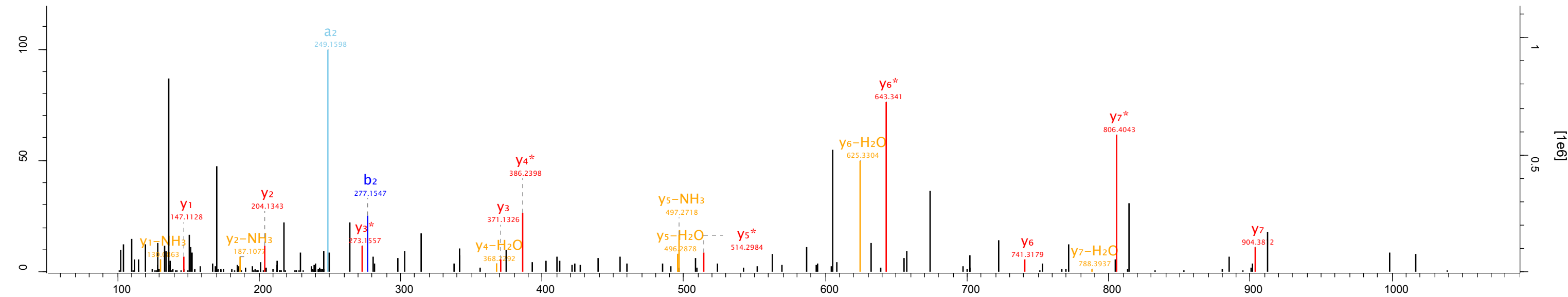
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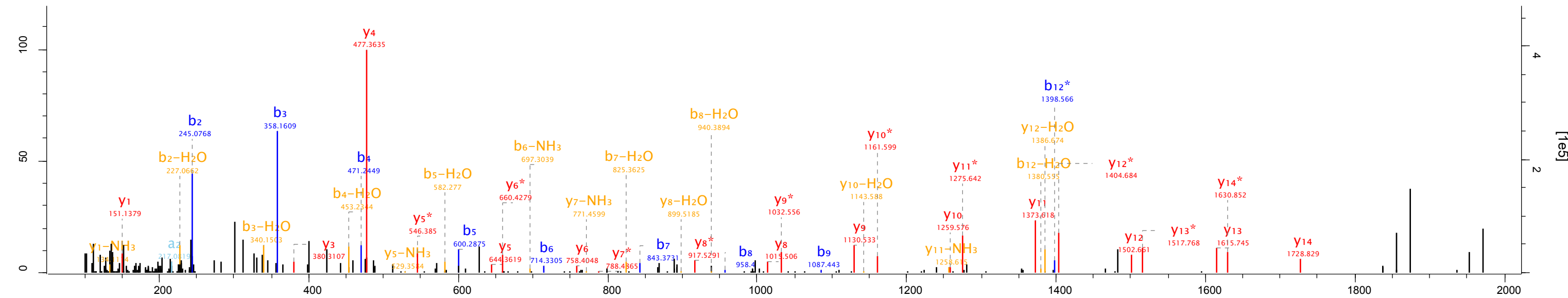


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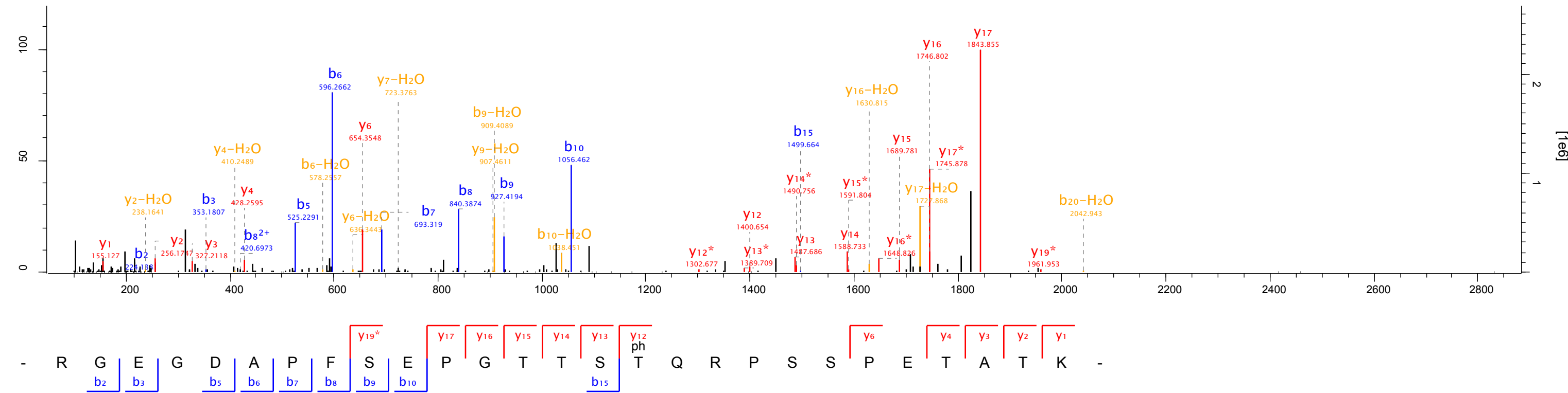




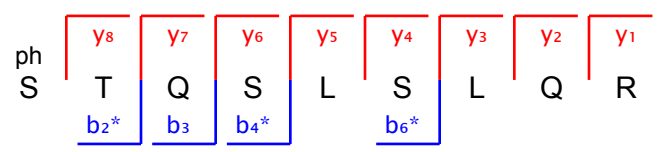
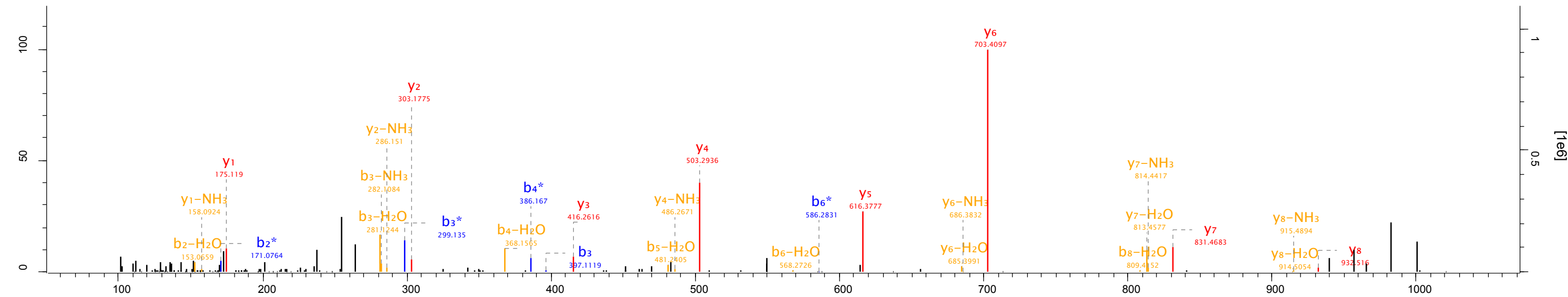
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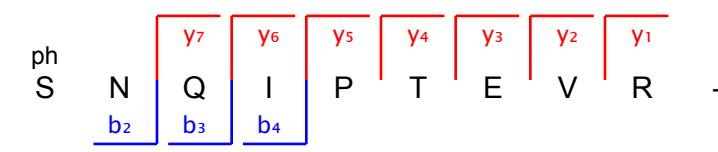
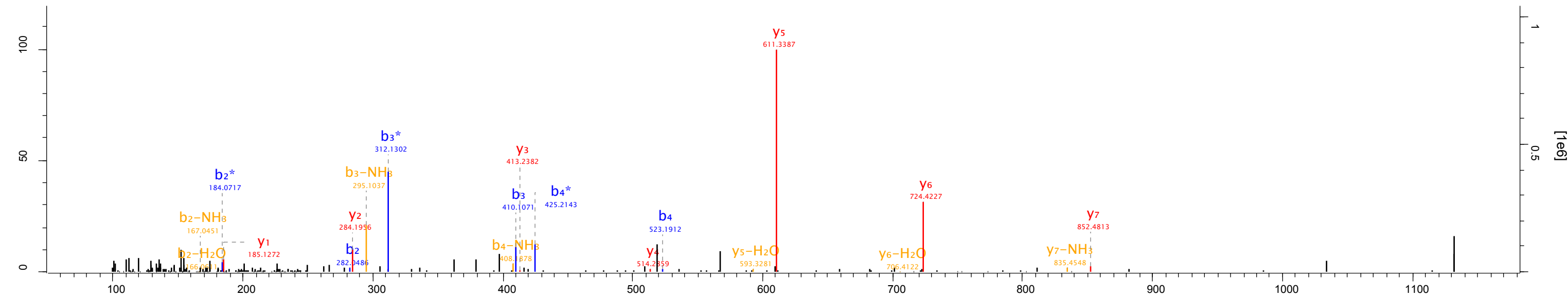
- Red boxes: y14, y13, y12, y11, y10, y9, y8, y7*, y6, y5^{ph}, y4, y3, y1
- Blue boxes: b2, b3, b4, b5, b6, b7, b8, b9, b12*



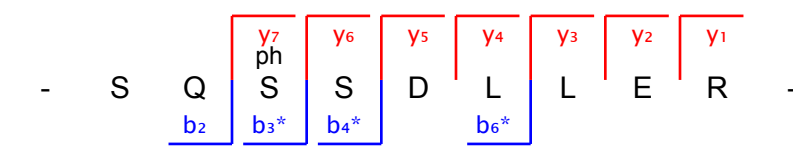
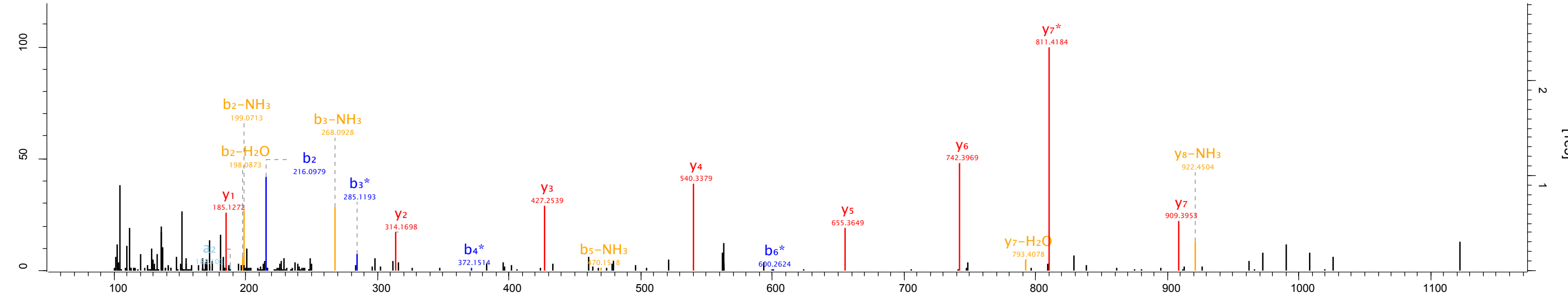
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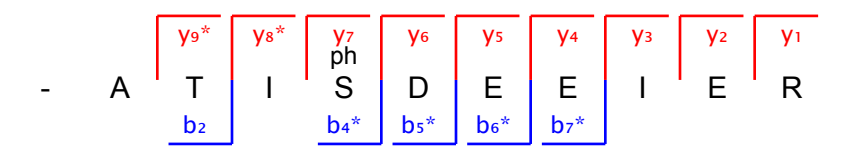
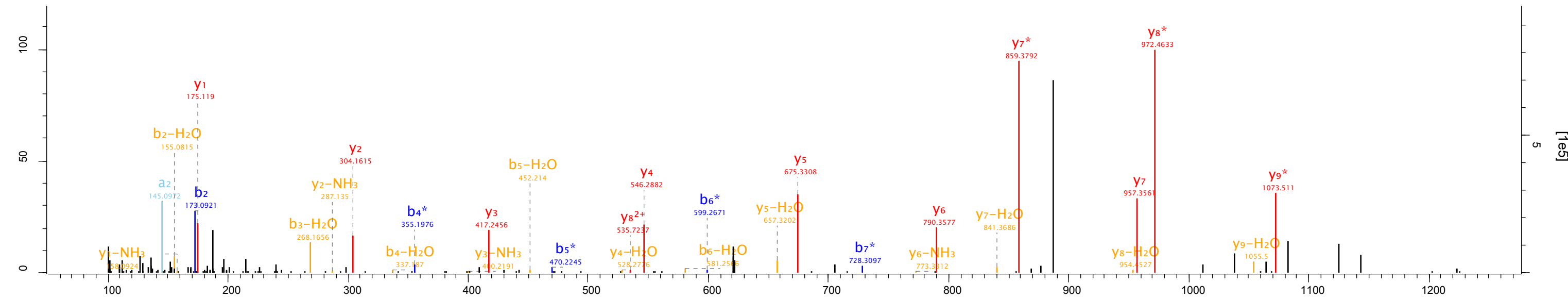
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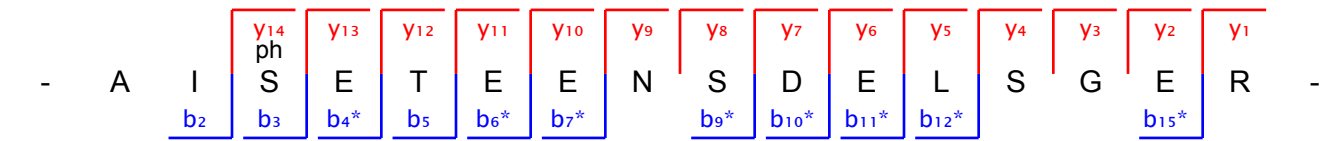
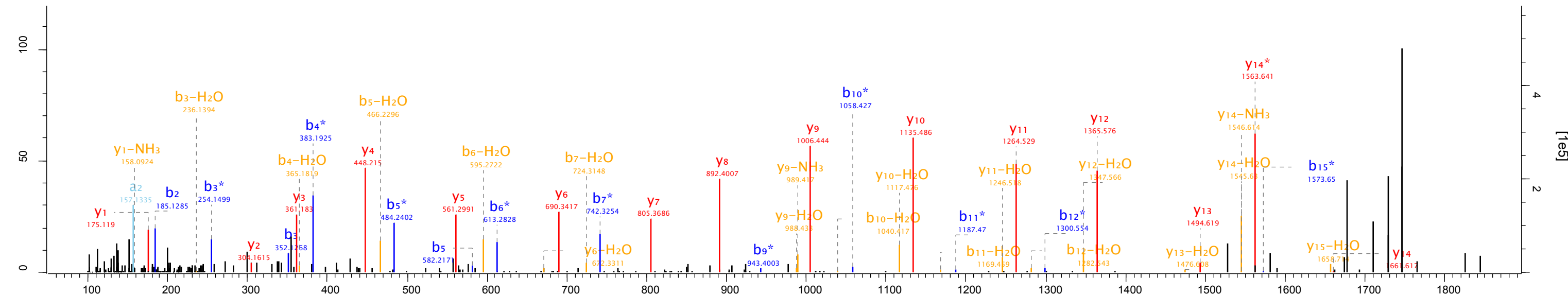
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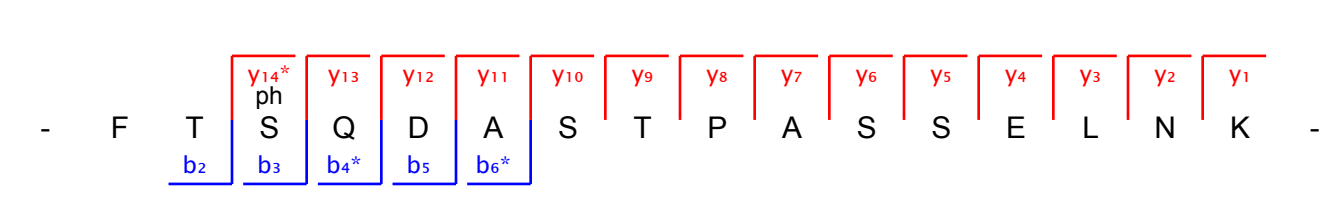
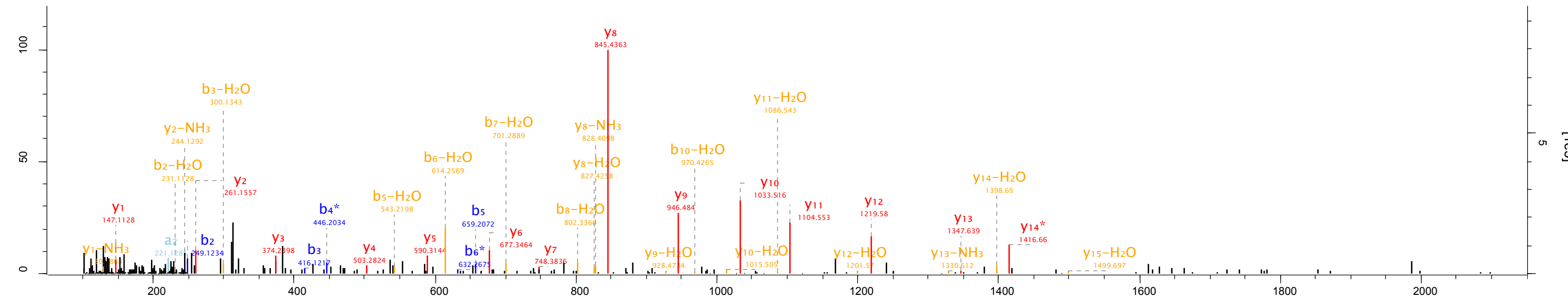
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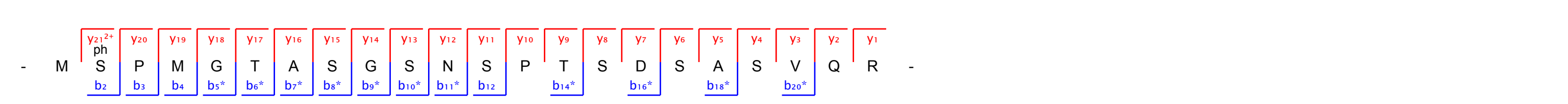
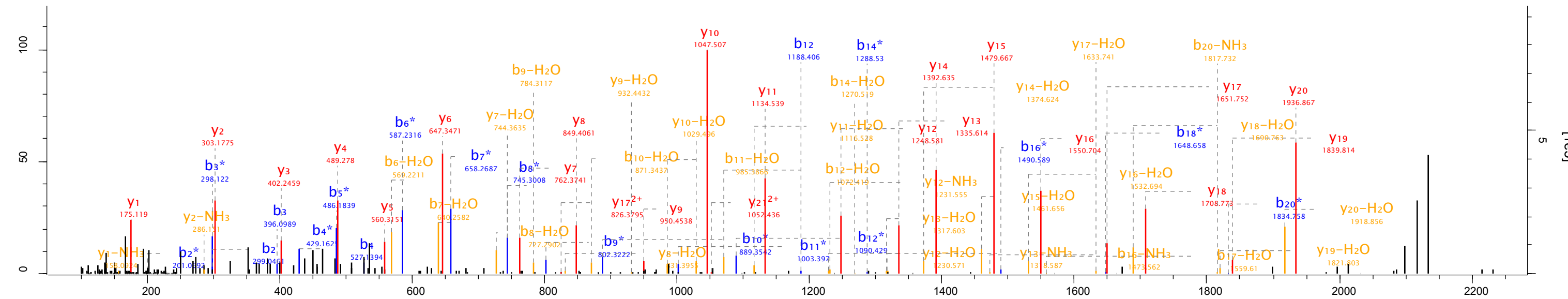
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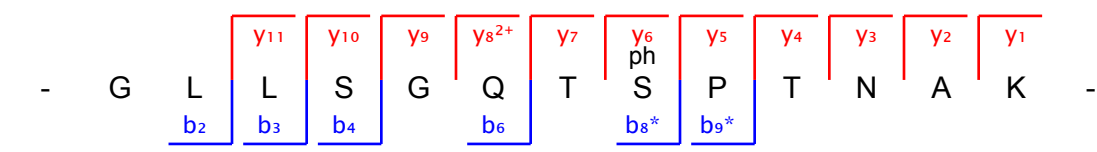
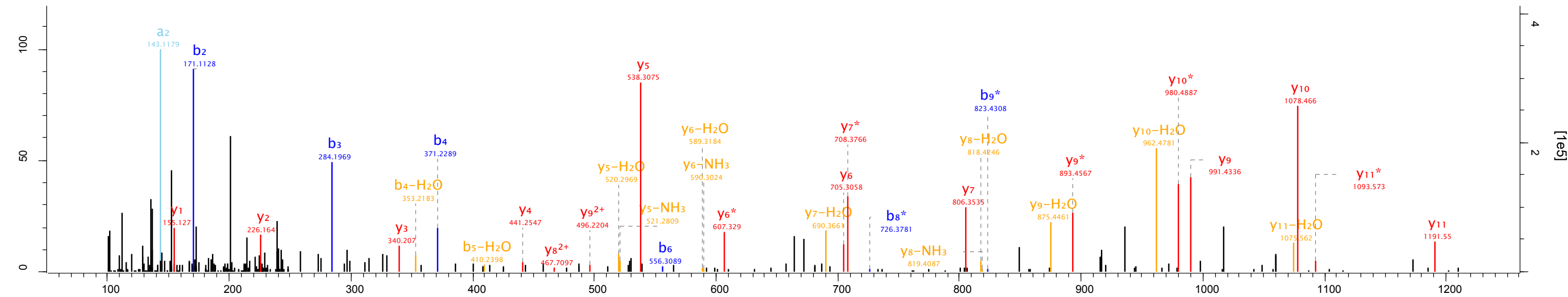
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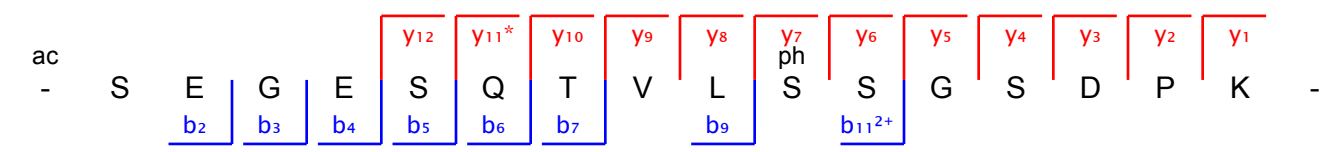
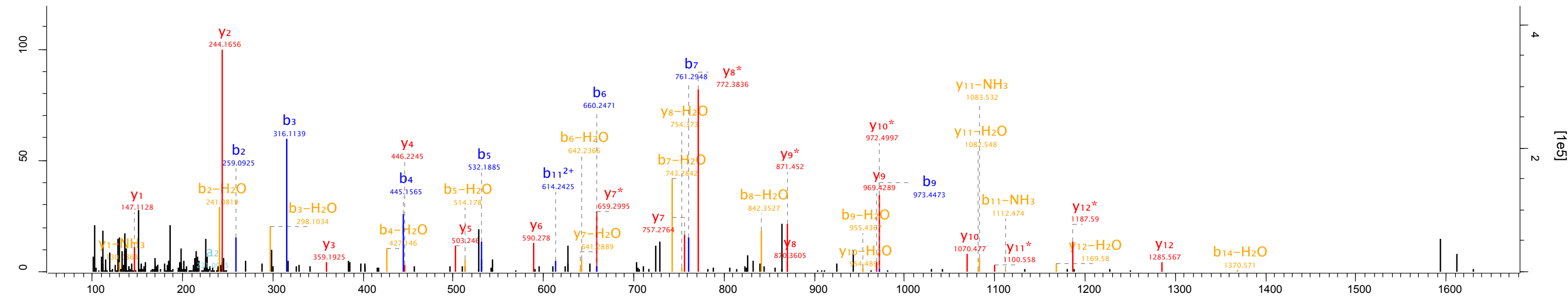
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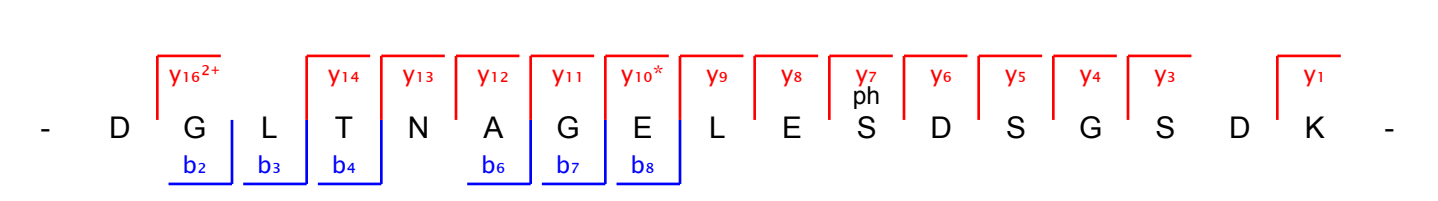
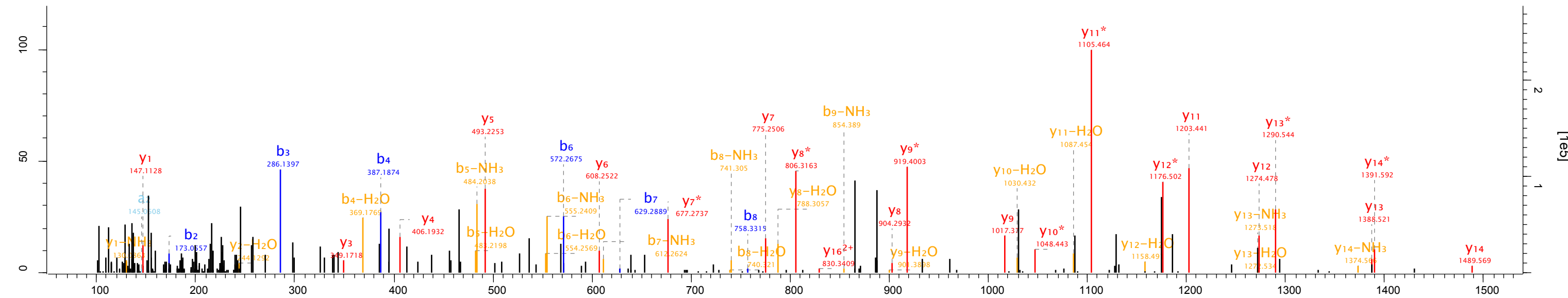
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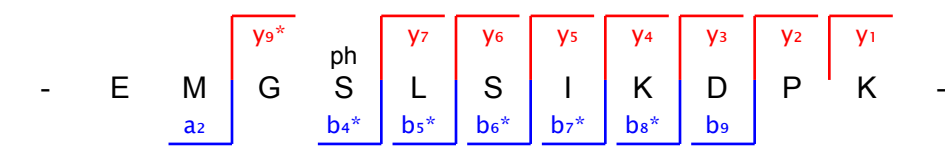
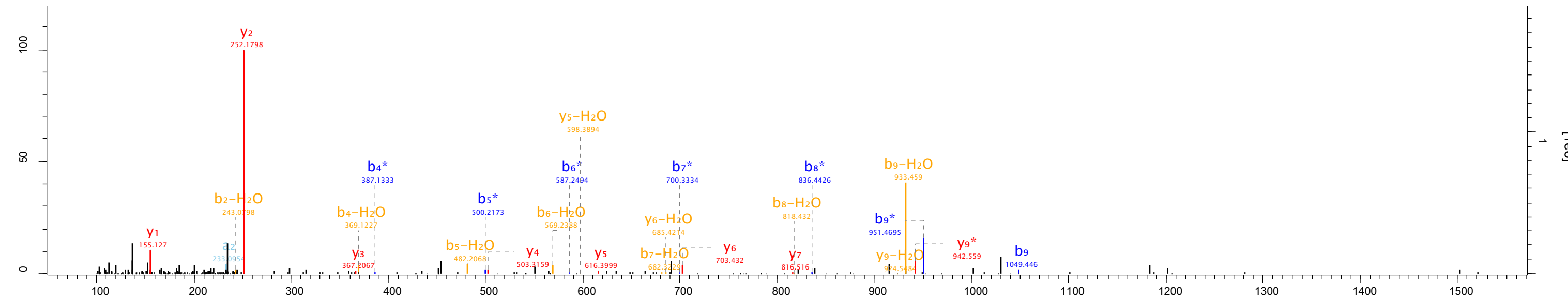
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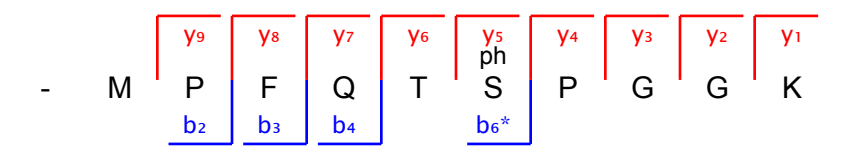
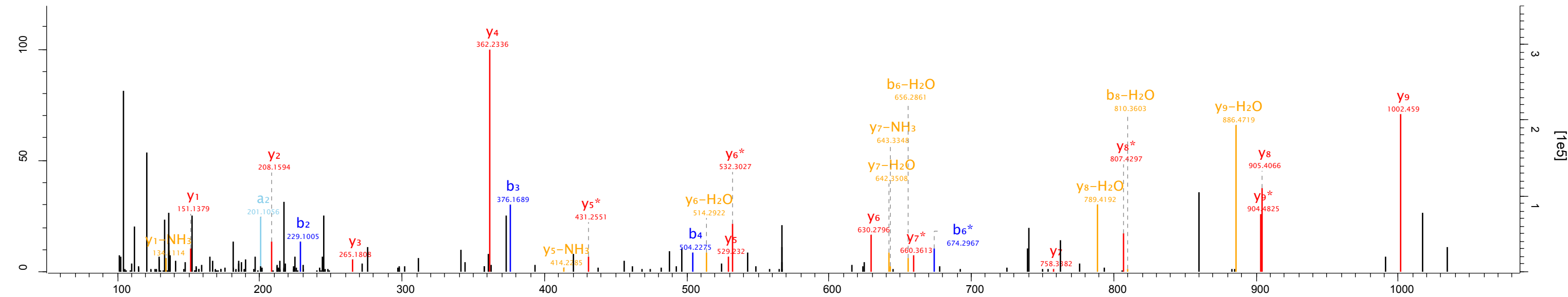
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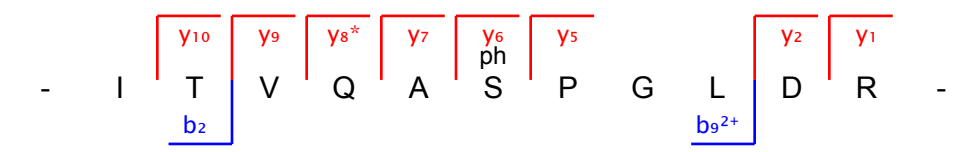
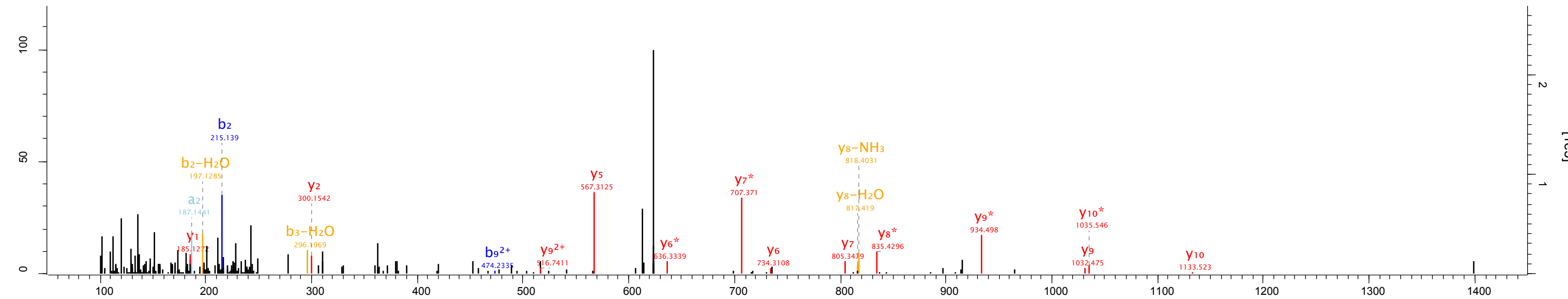
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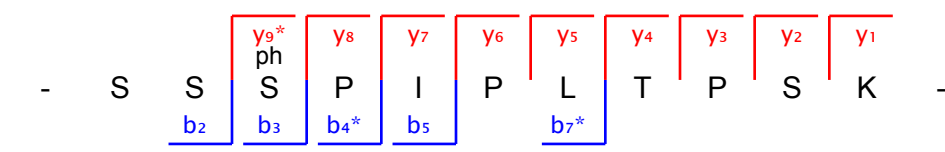
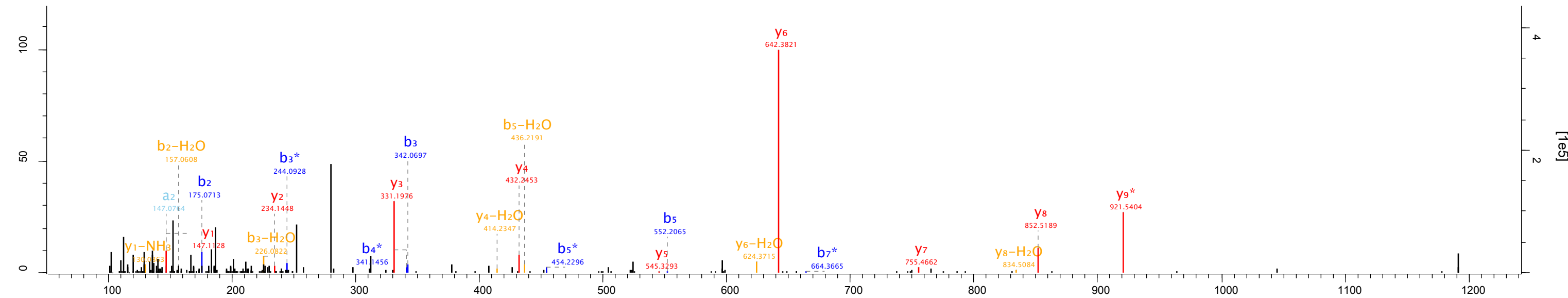
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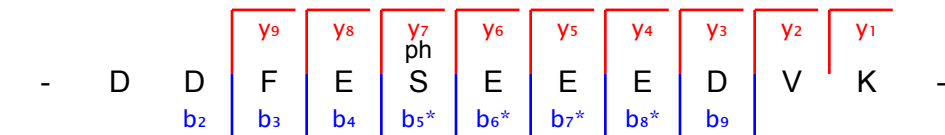
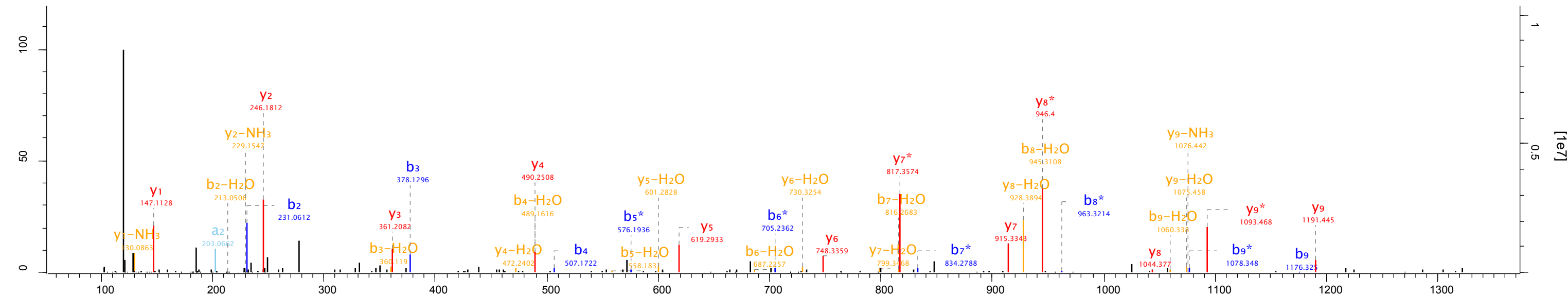


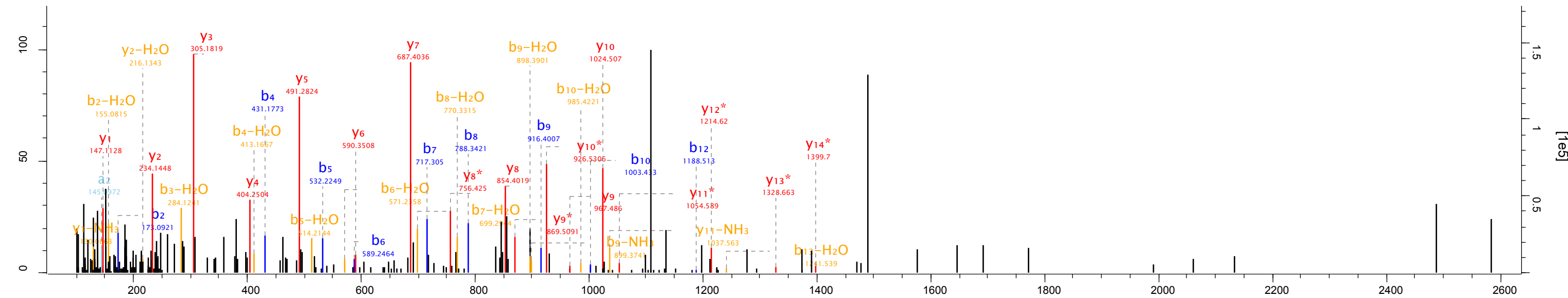
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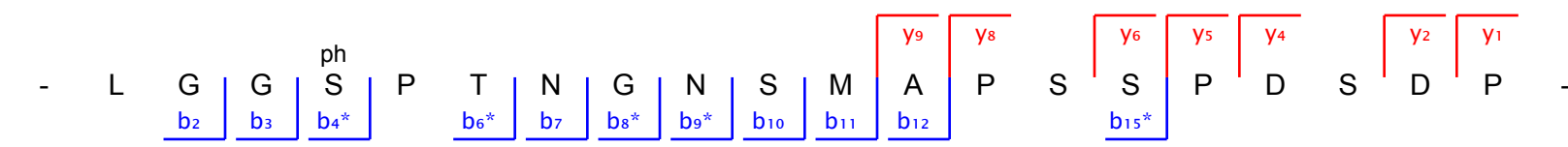
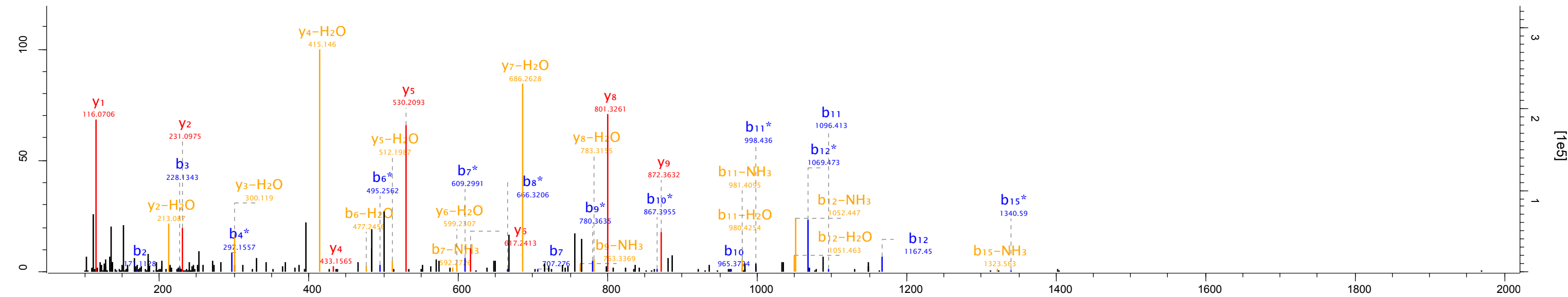




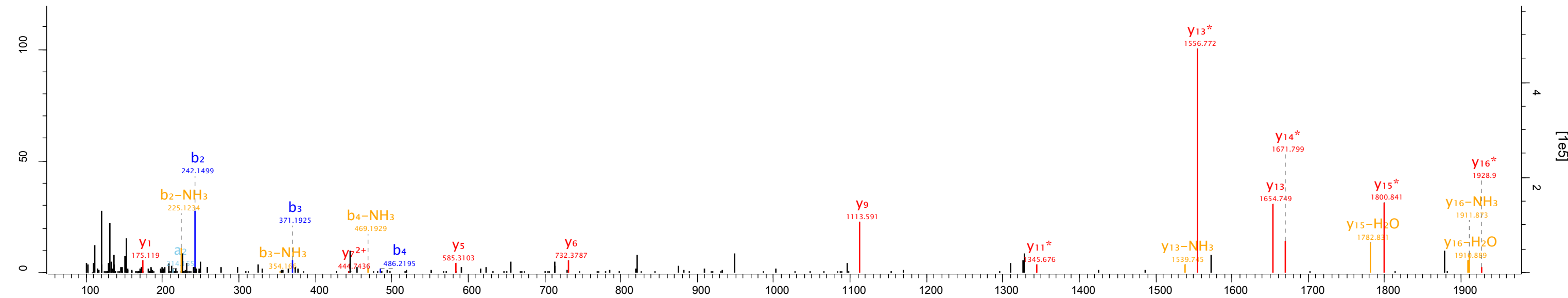


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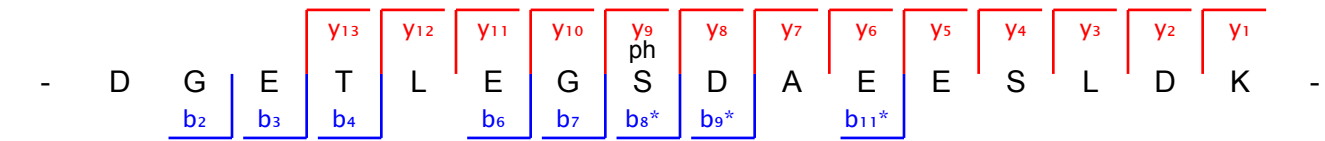
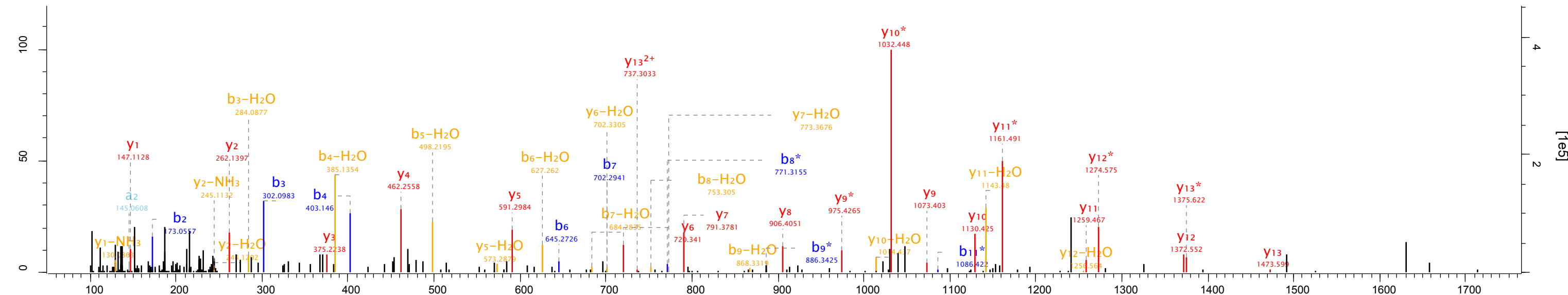
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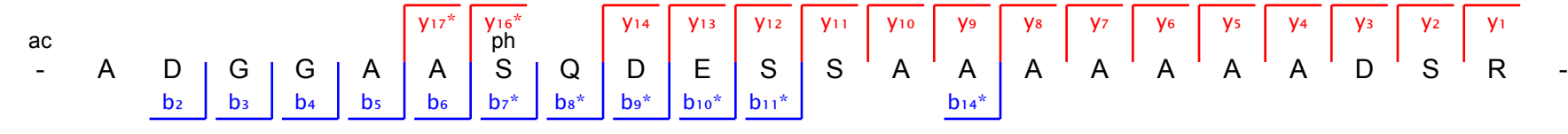
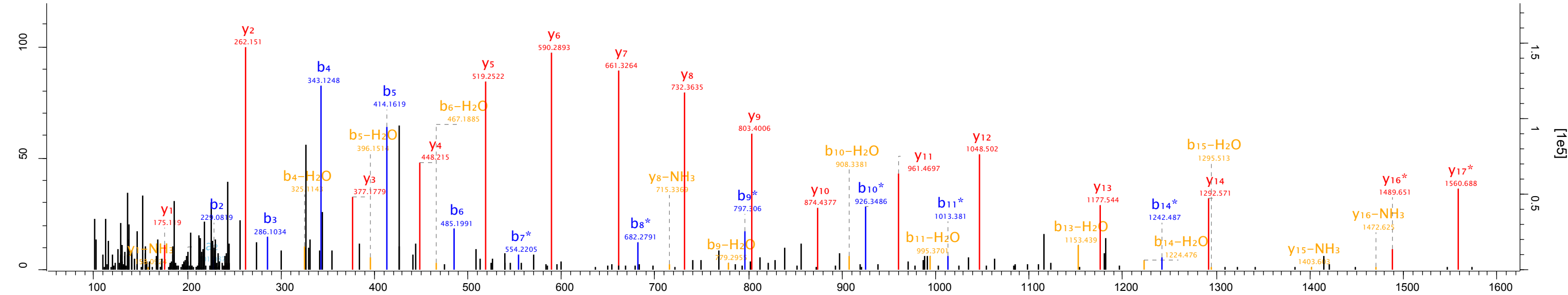
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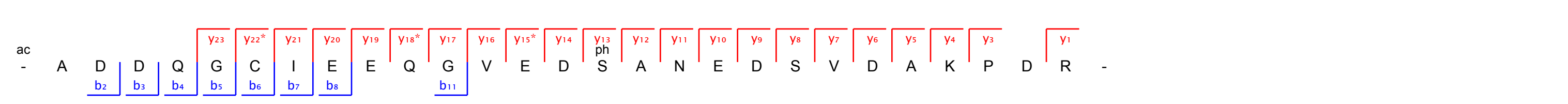
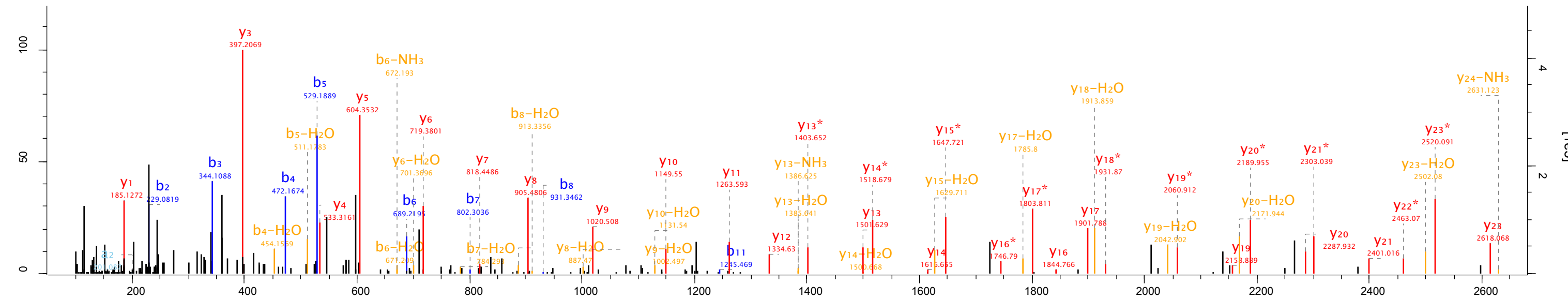
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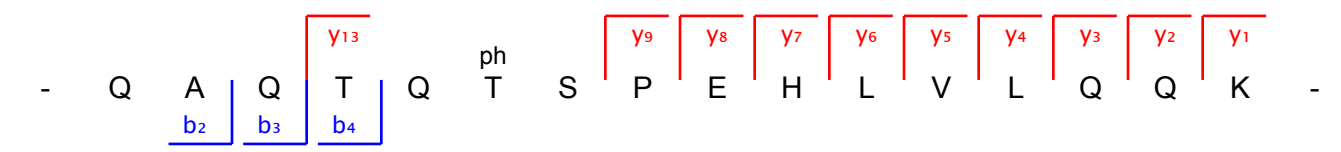
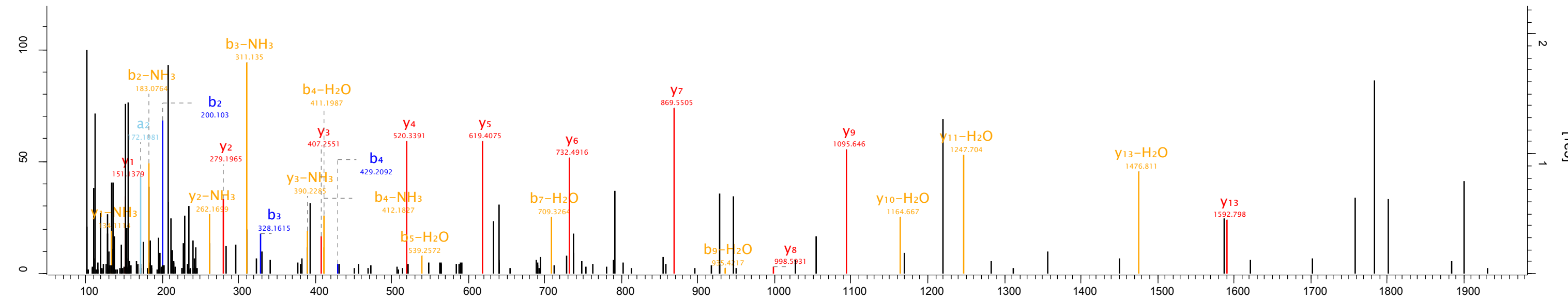
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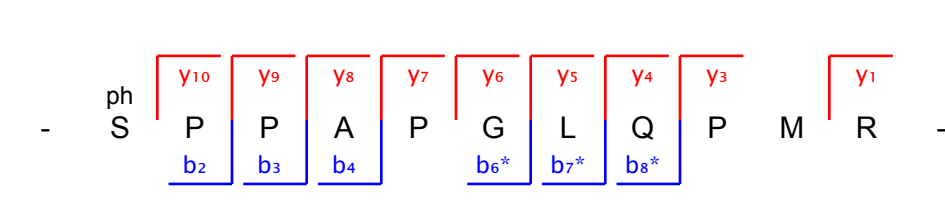
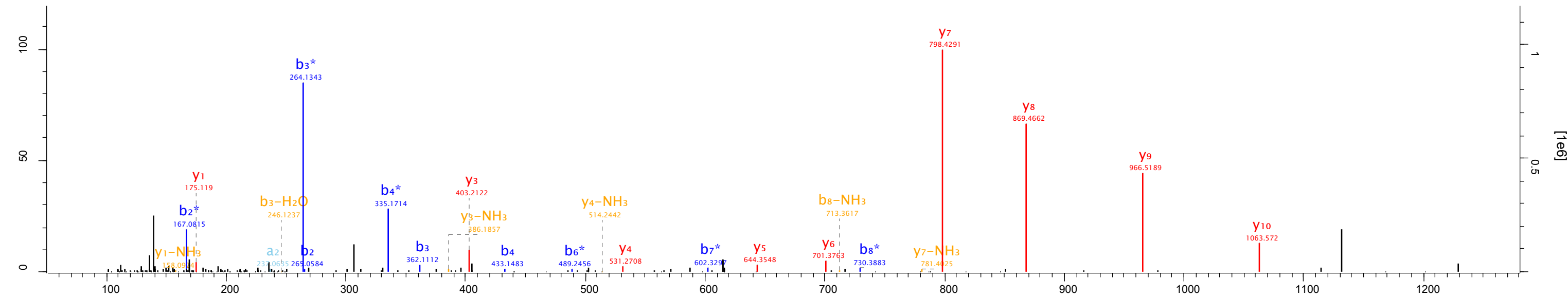


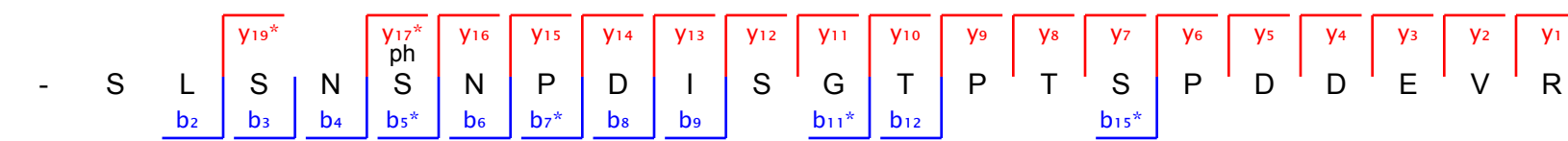
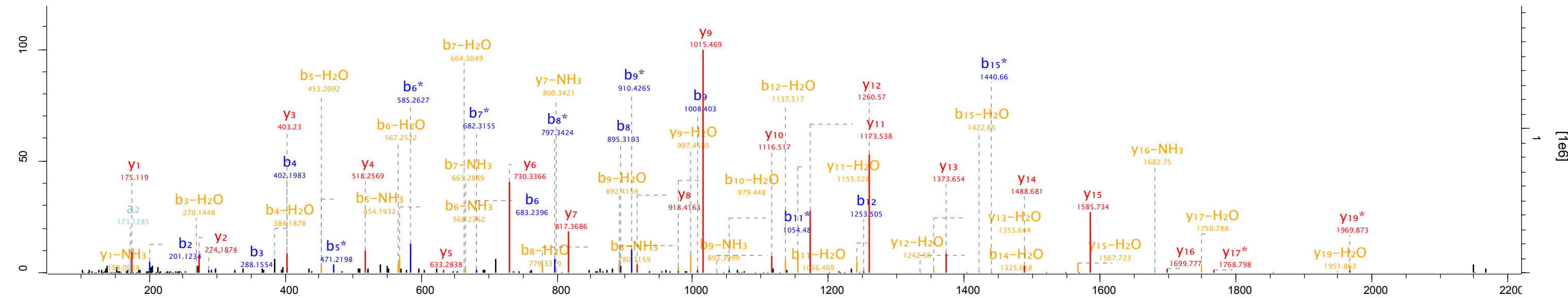
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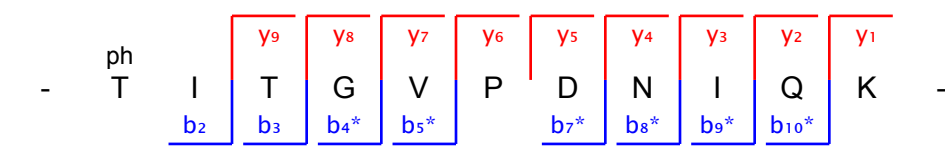
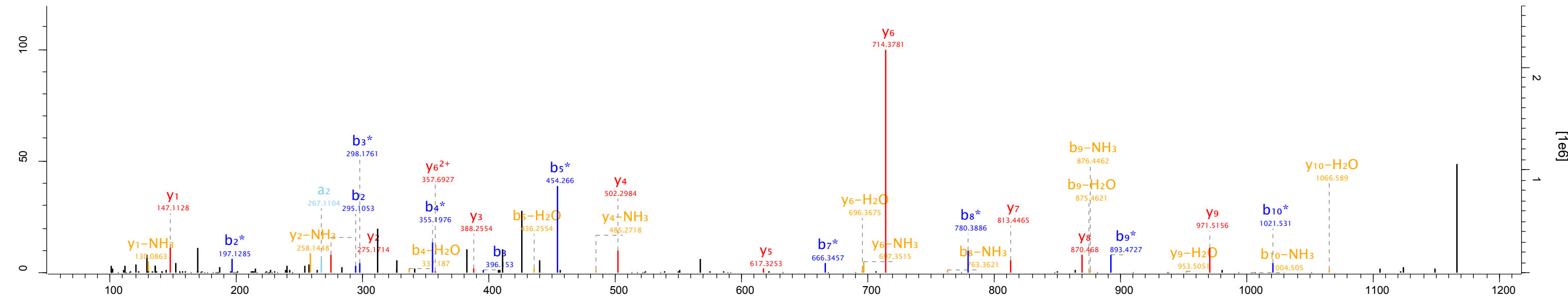
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20171215_MaS_33SR_LMH_phospho_03

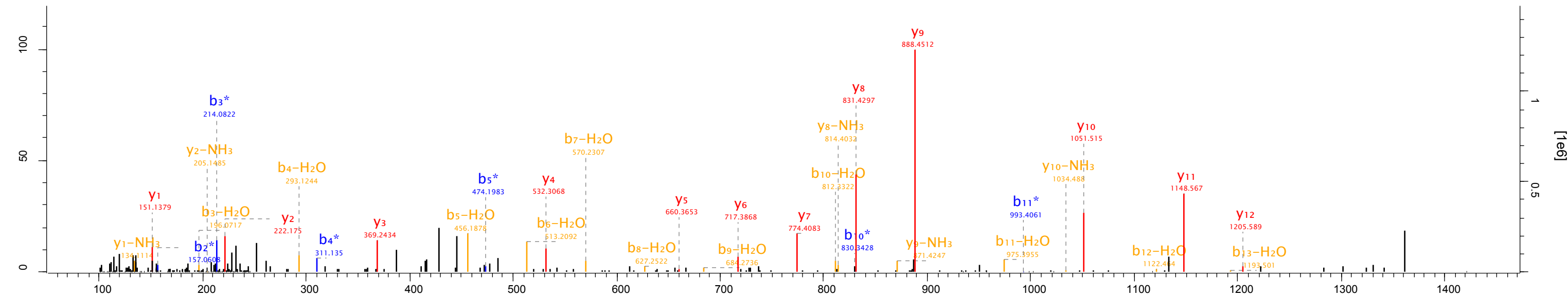




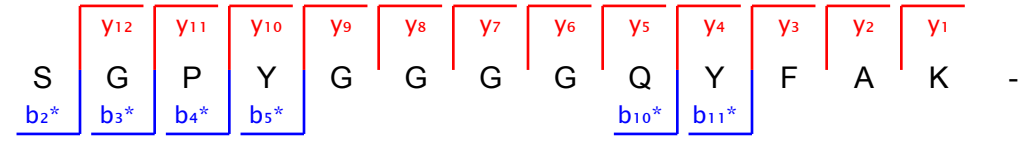
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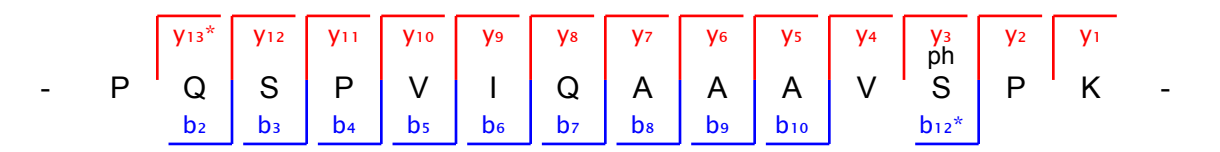
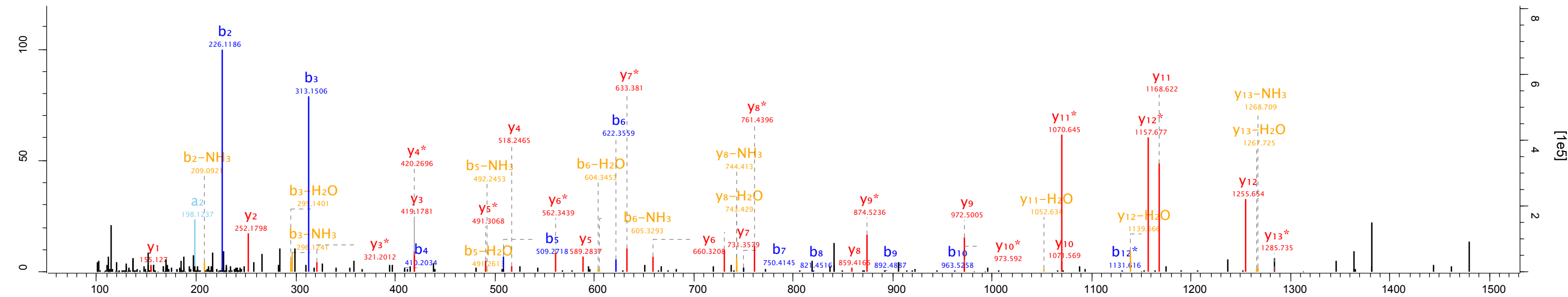
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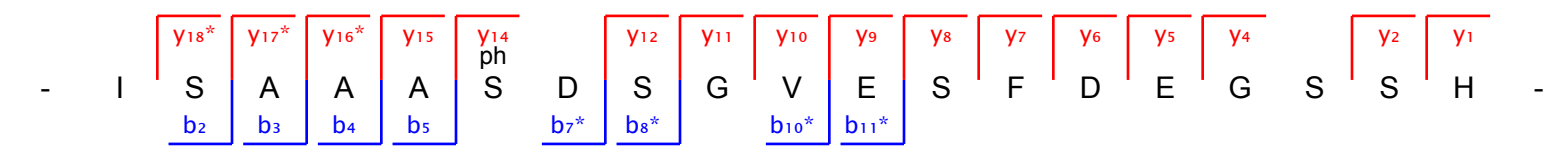
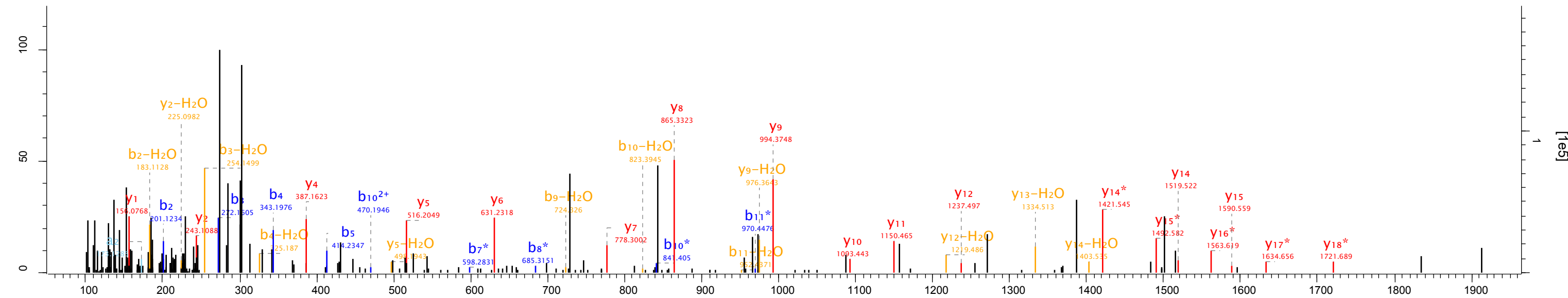
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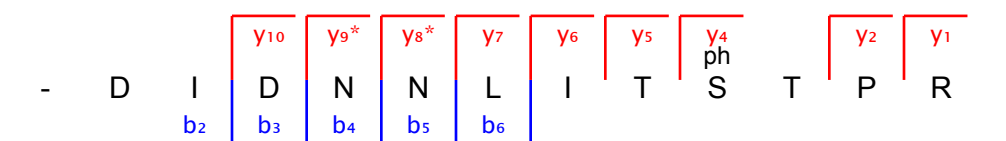
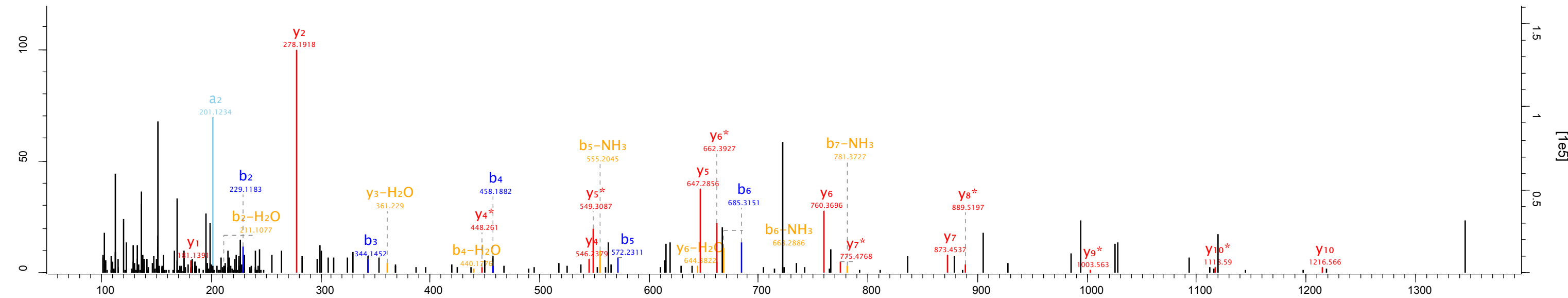
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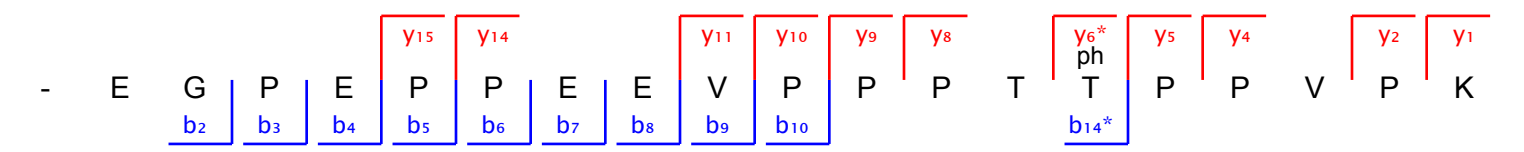
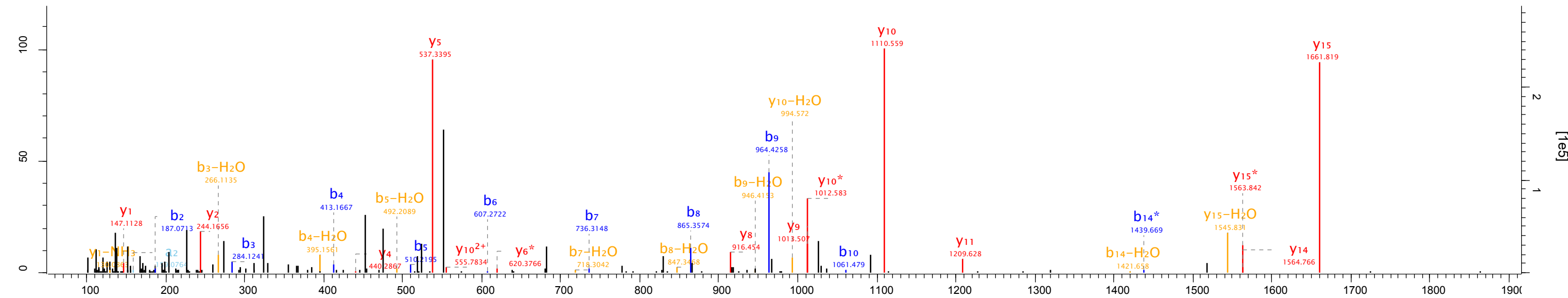
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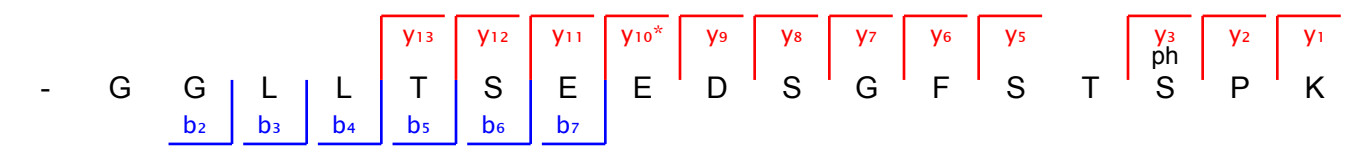
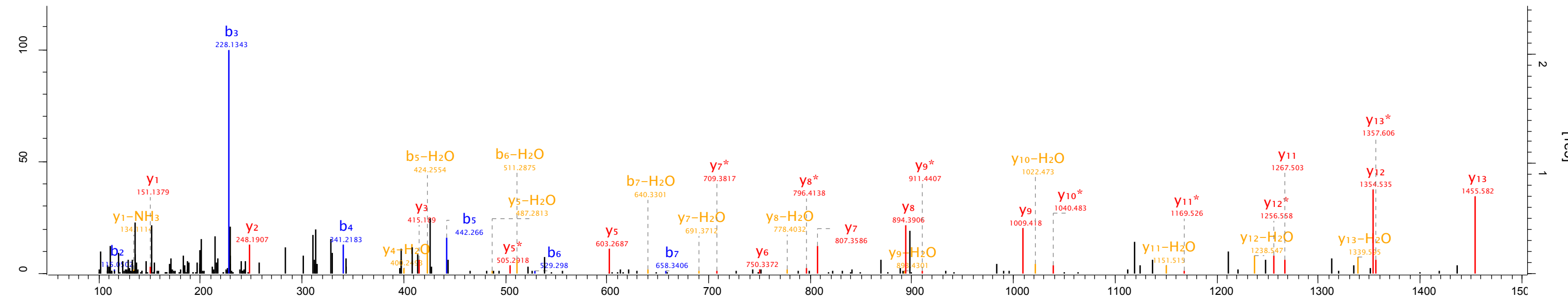
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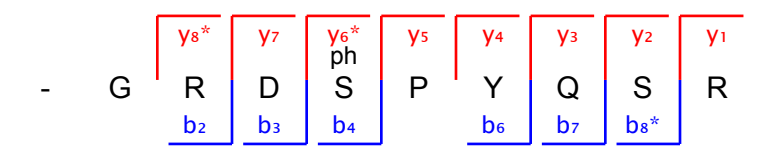
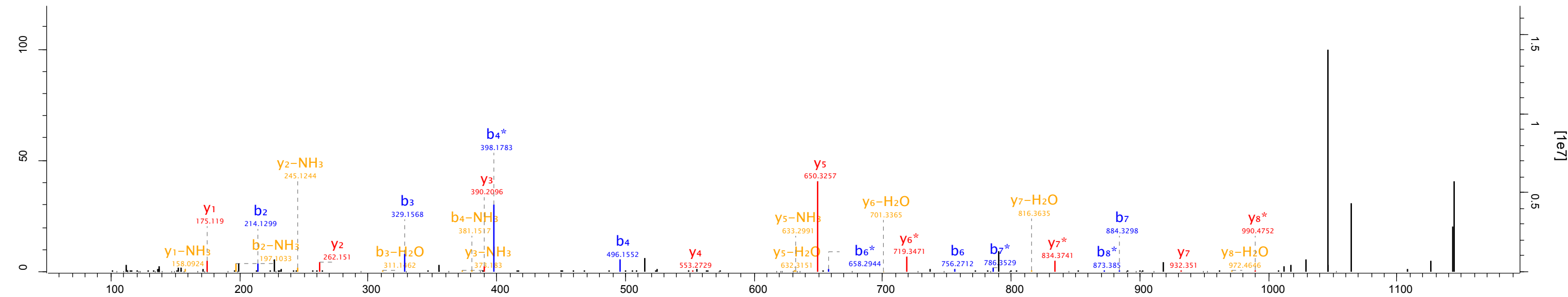
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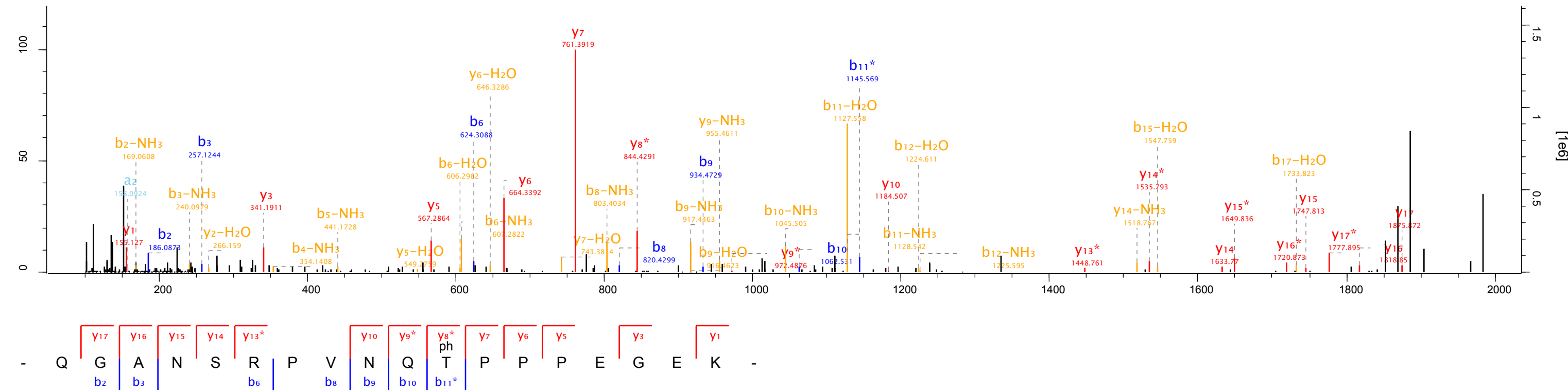


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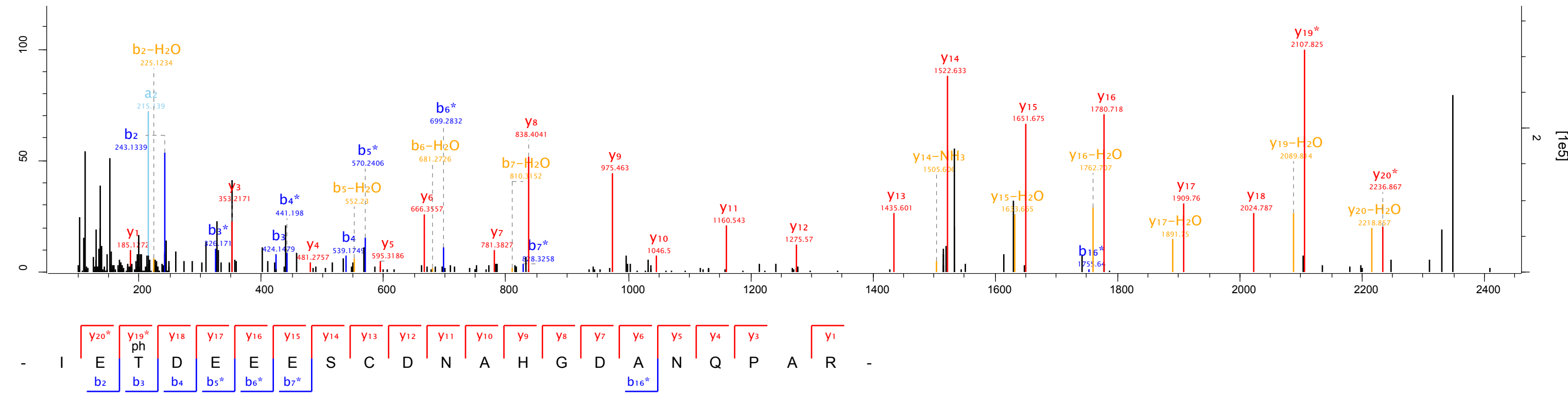


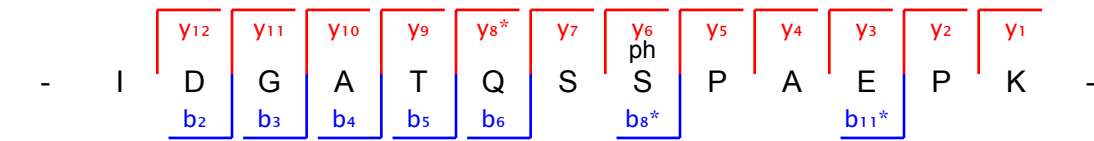
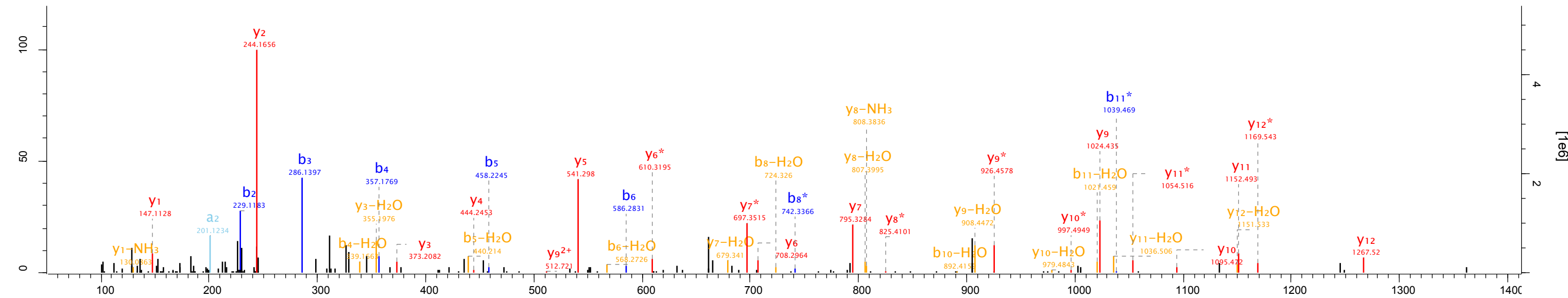
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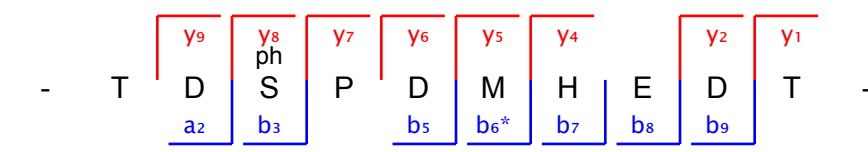
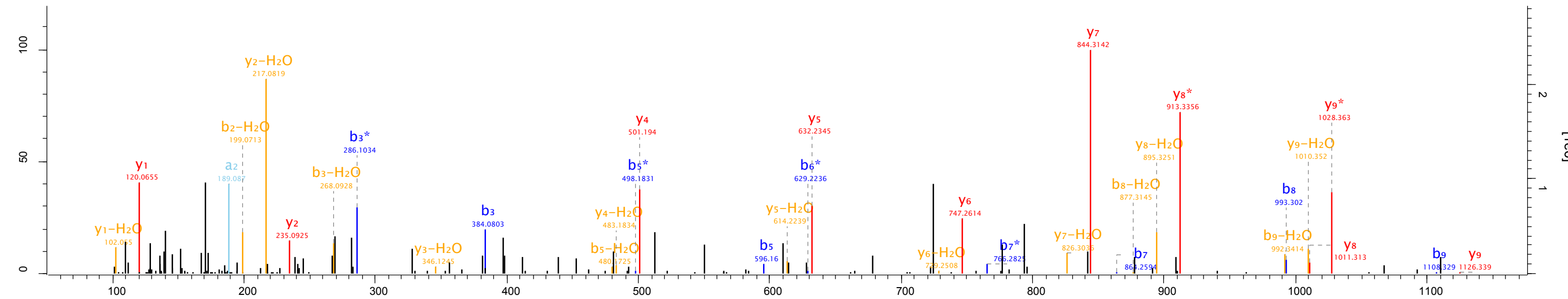


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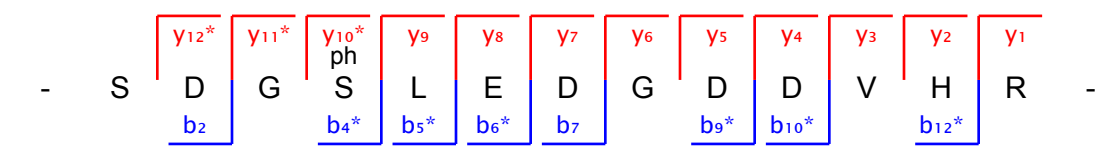
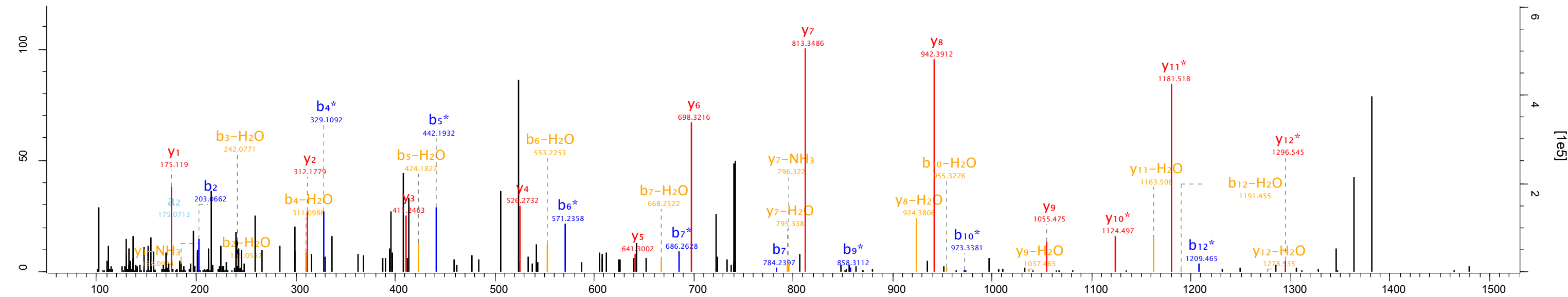




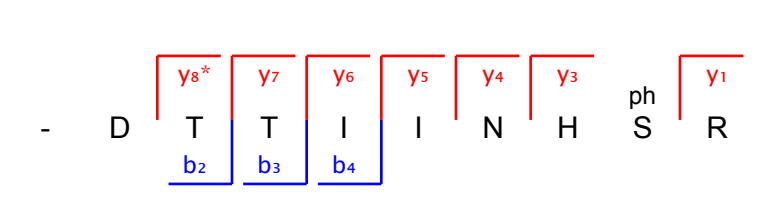
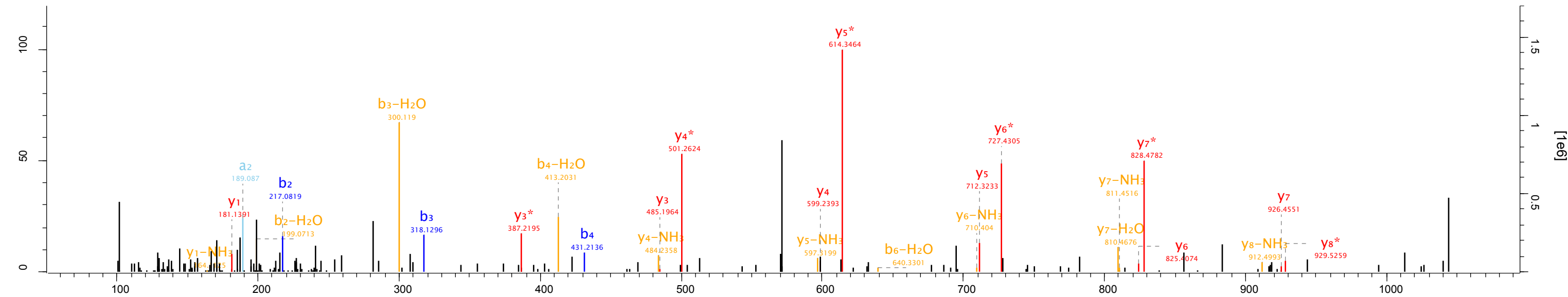
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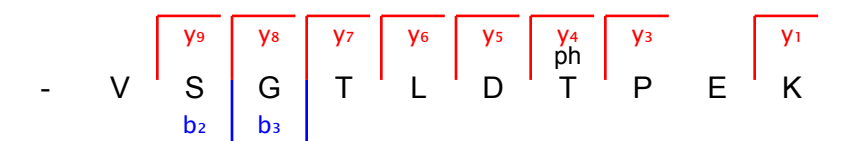
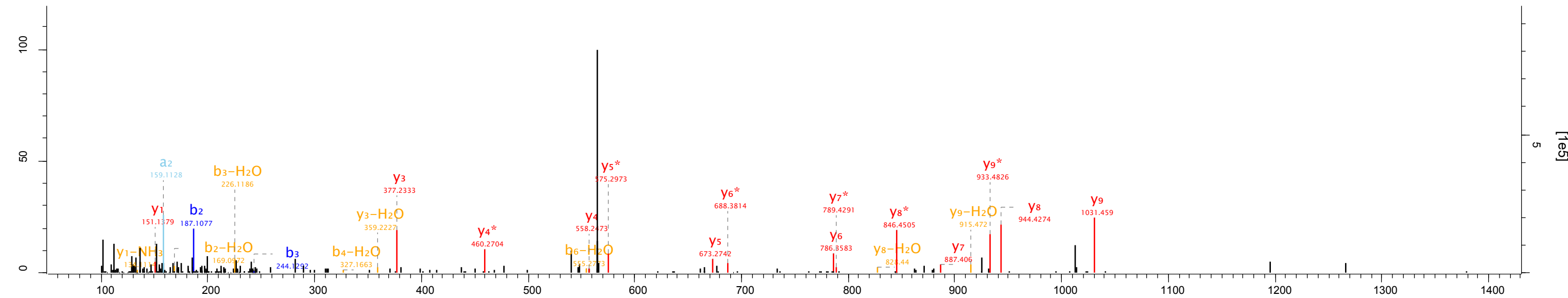
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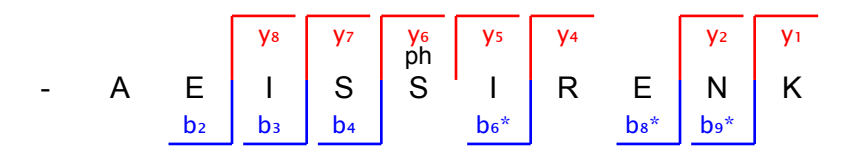
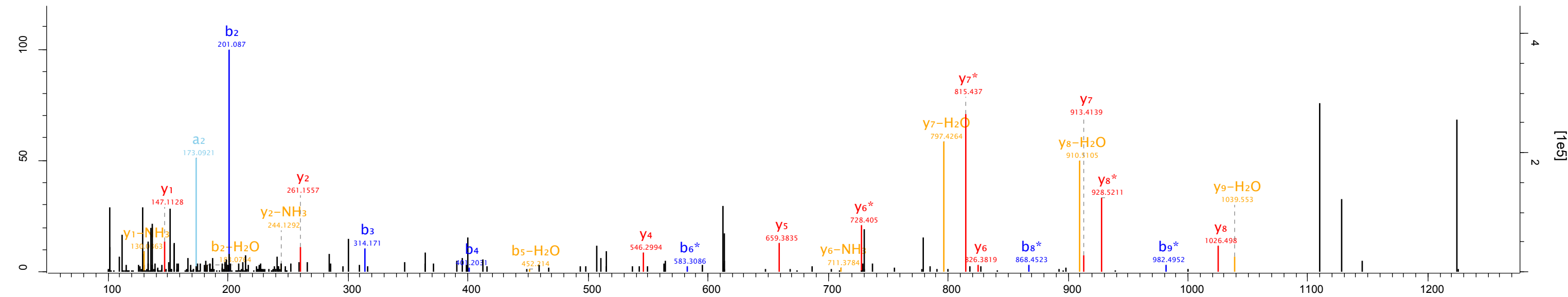
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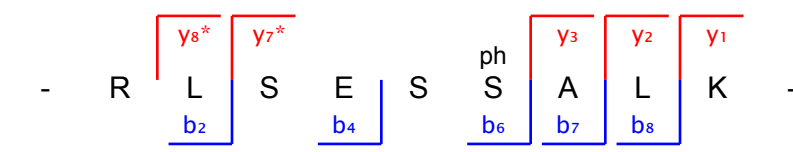
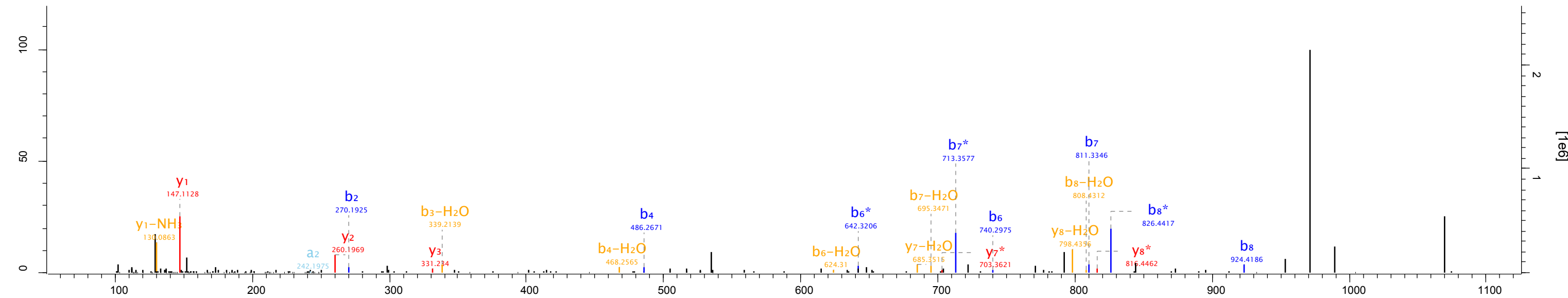
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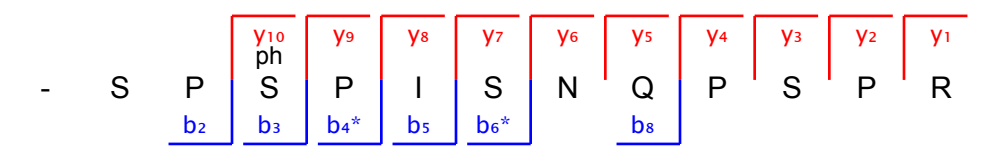
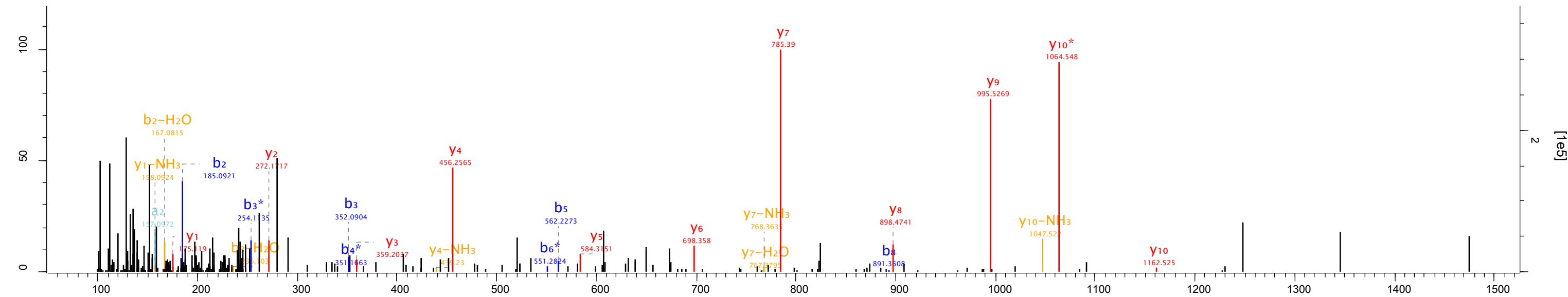
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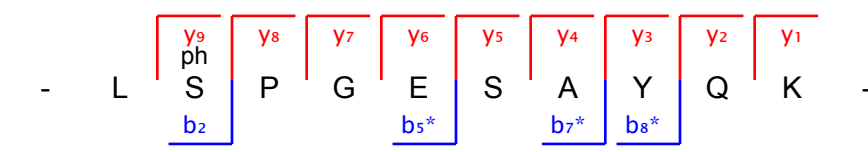
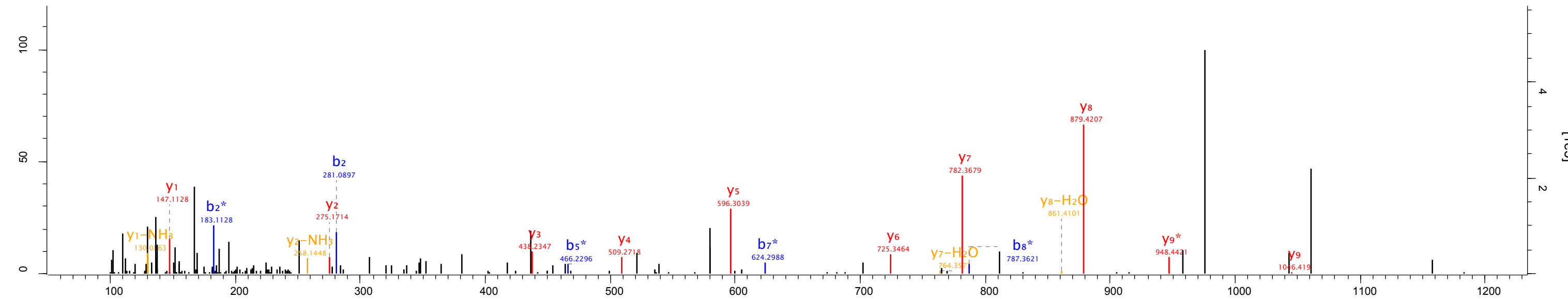
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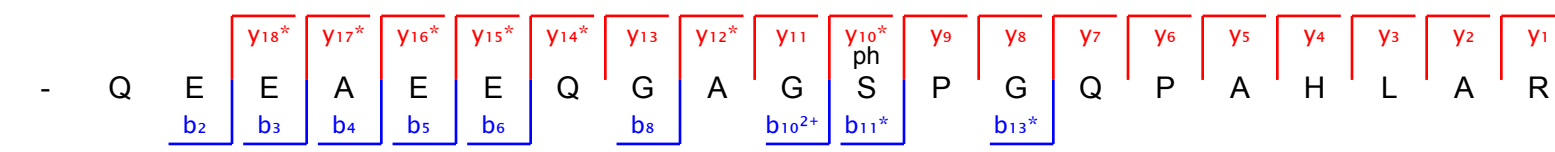
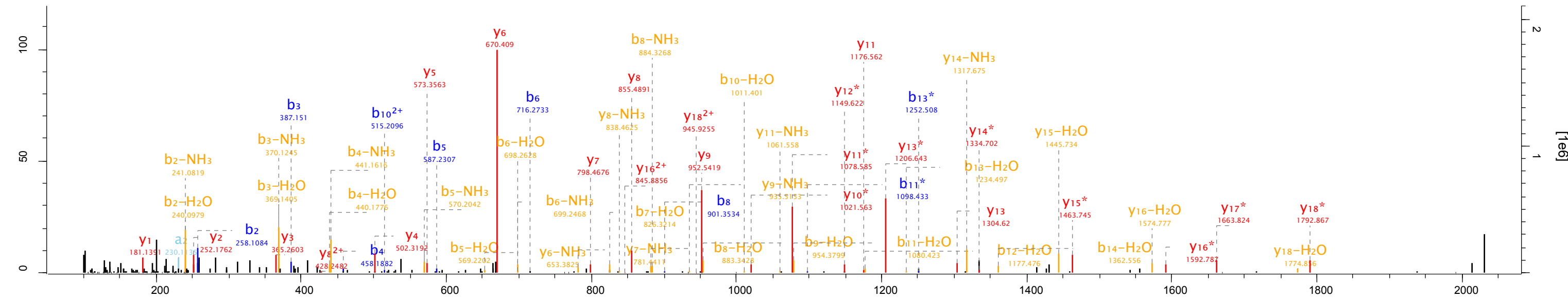
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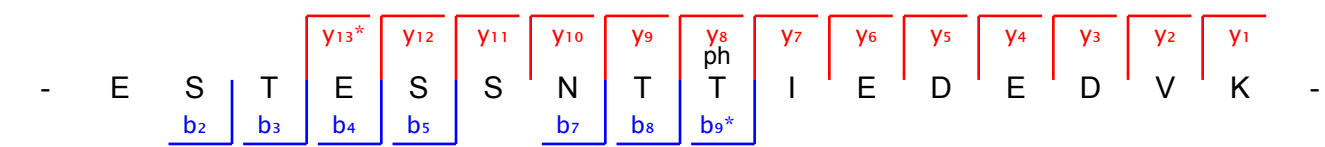
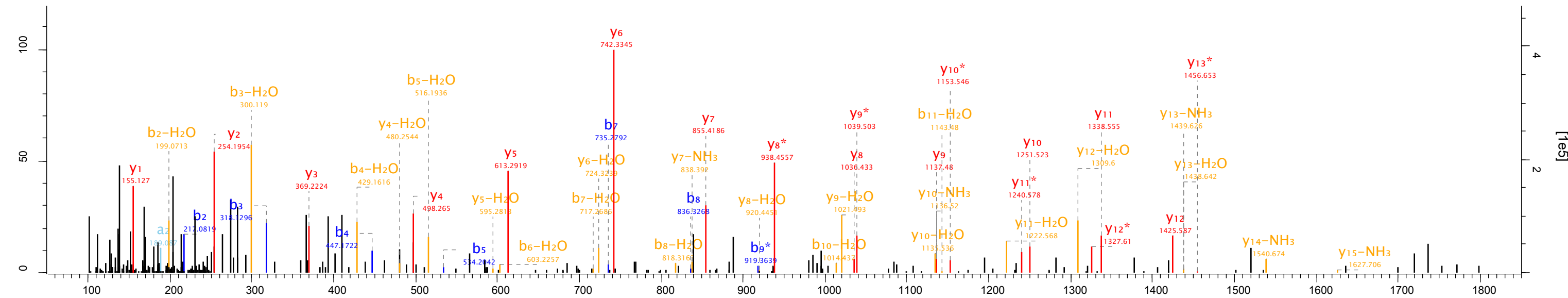
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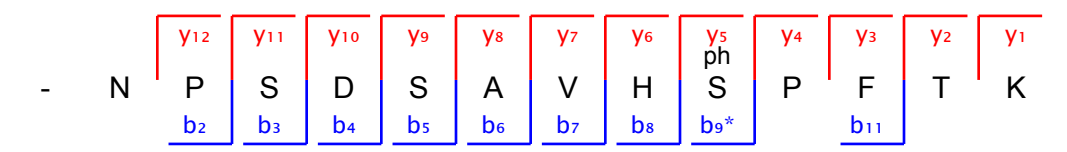
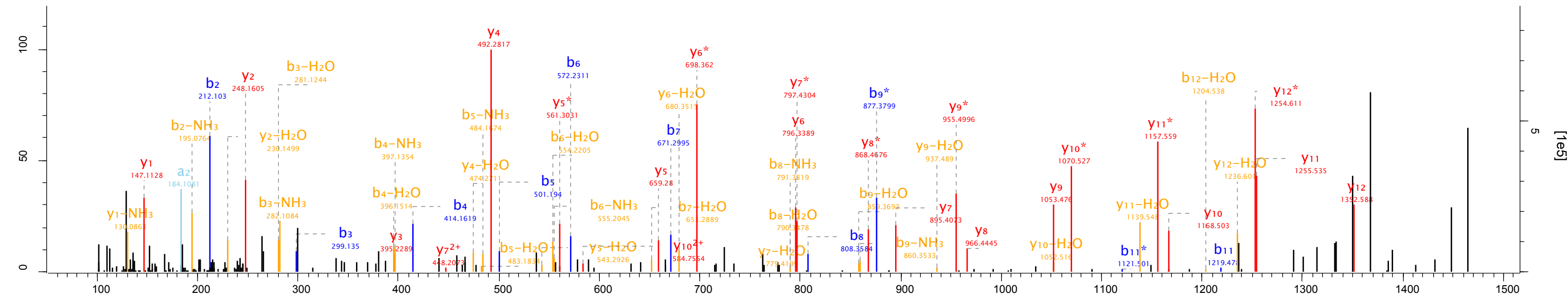
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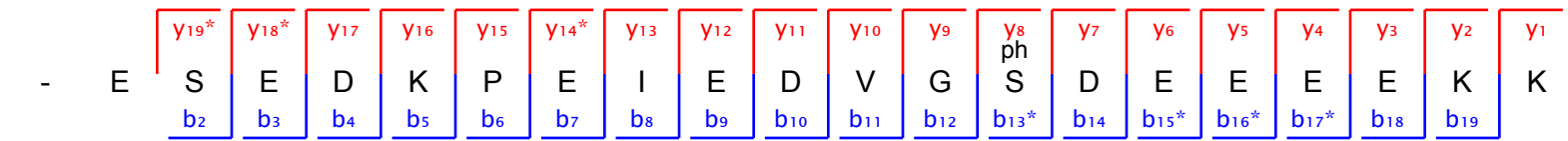
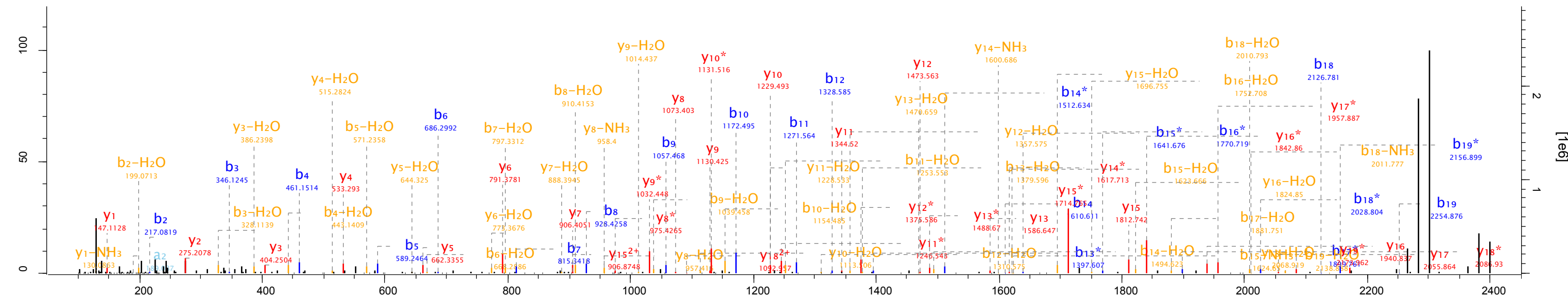
Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 5231 Method FTMS; HCD Score 185.21 m/z 936.88 Gene names CAMK2D



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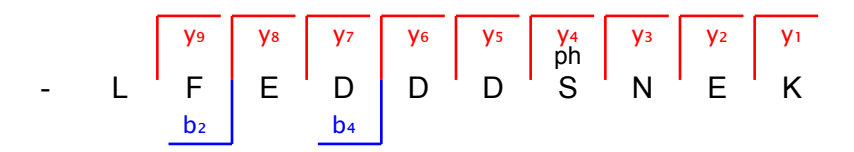
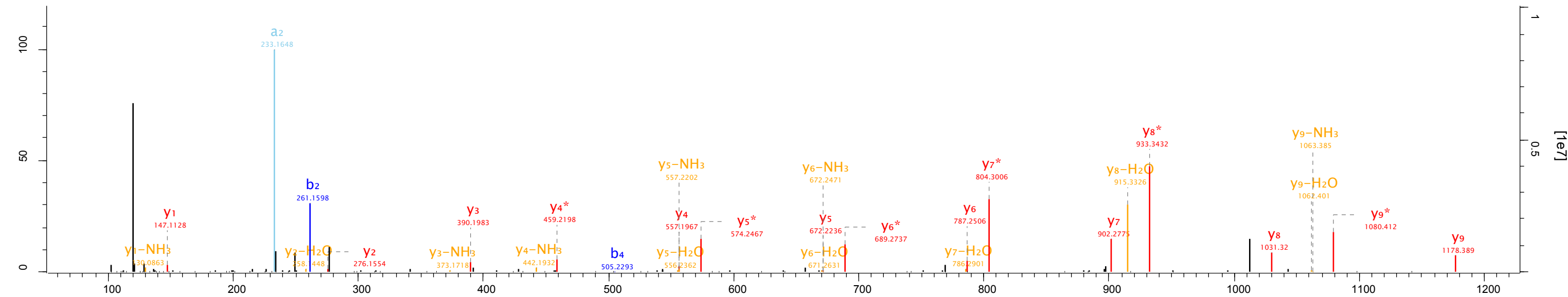


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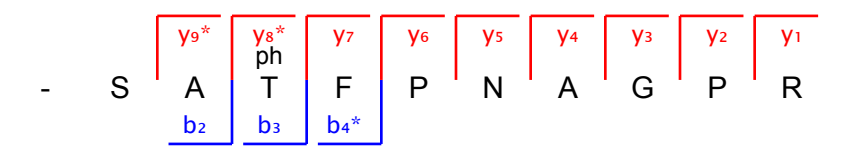
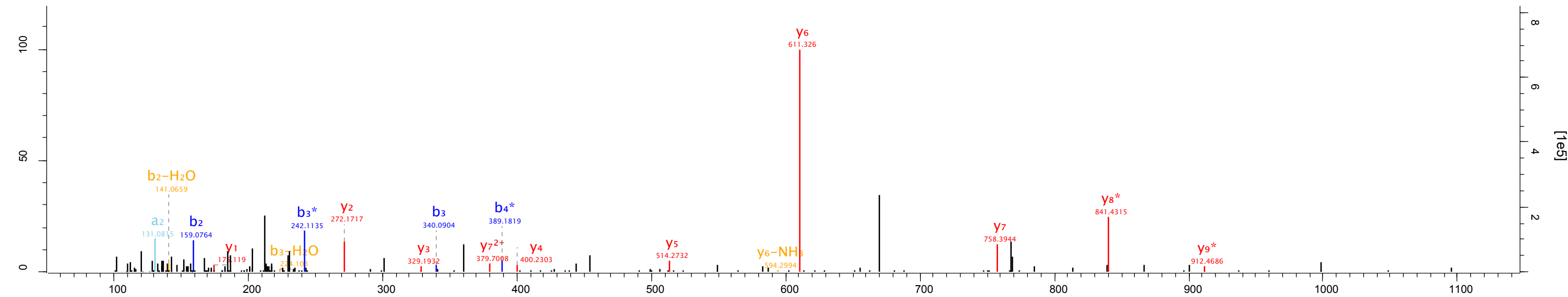


Raw file
20171215_MaS_33SR_LMH_phospho_05

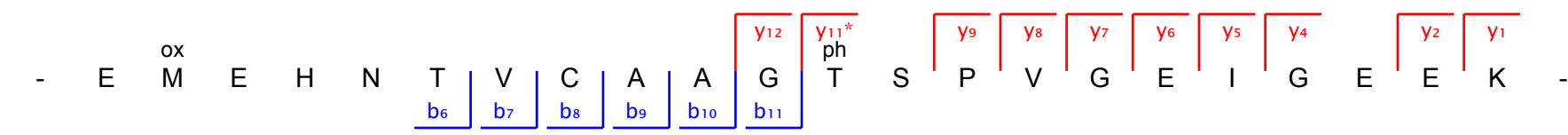
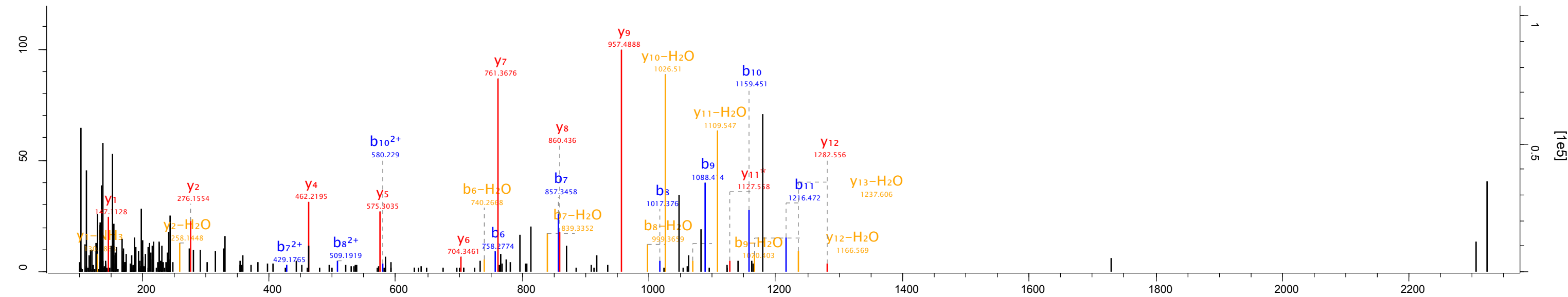
Scan Method Score m/z Gene names
6001 FTMS; HCD 186.51 646.24 HTATSFI



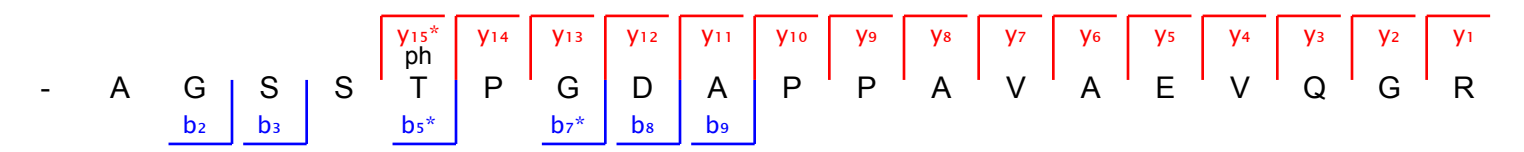
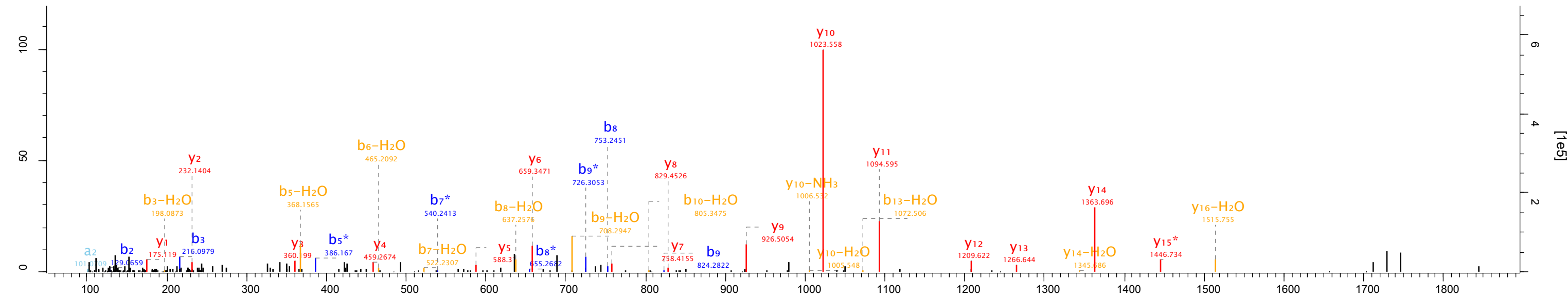
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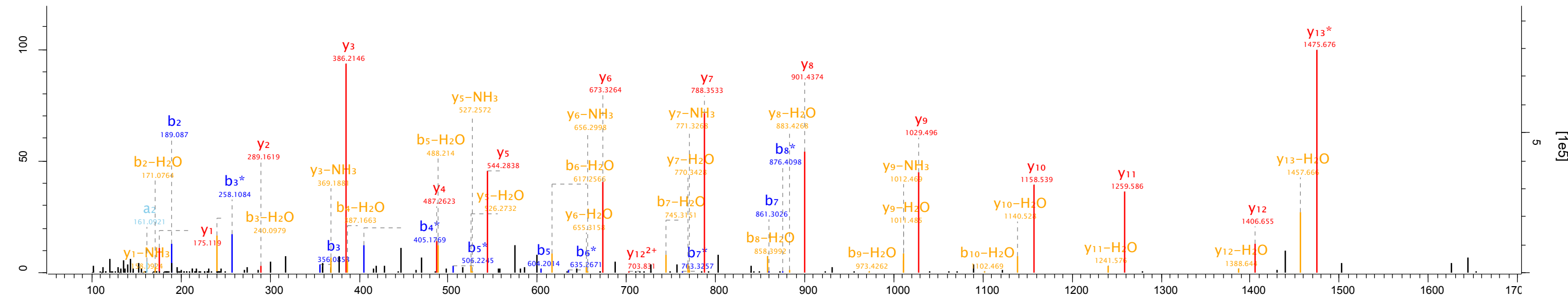
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Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 8951 Method FTMS; HCD Score 102.66 m/z 923.92 Gene names HUWE1



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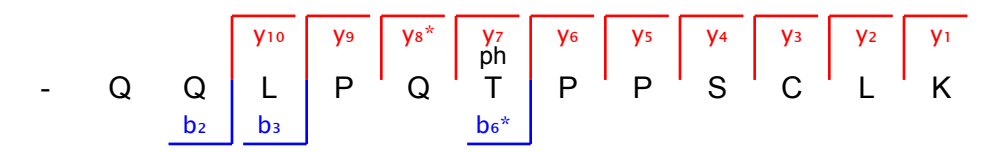
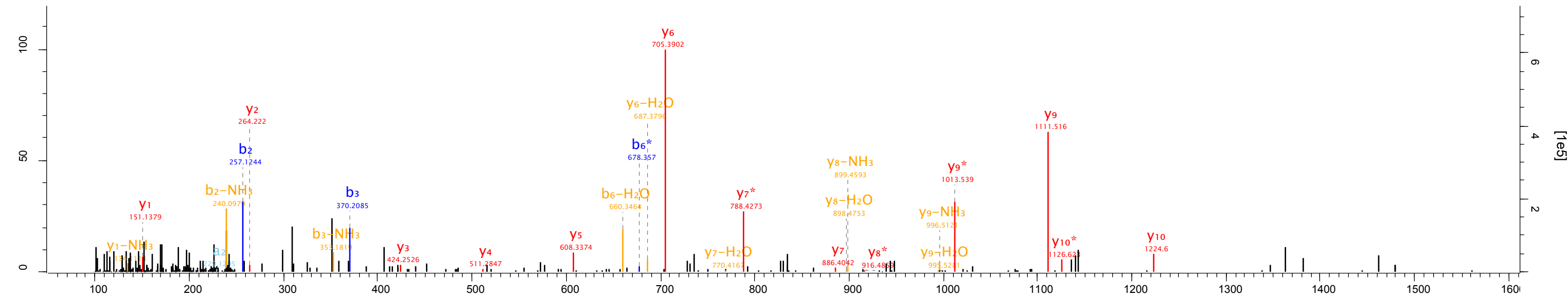


- T S S F T E Q L D E G T P N R -

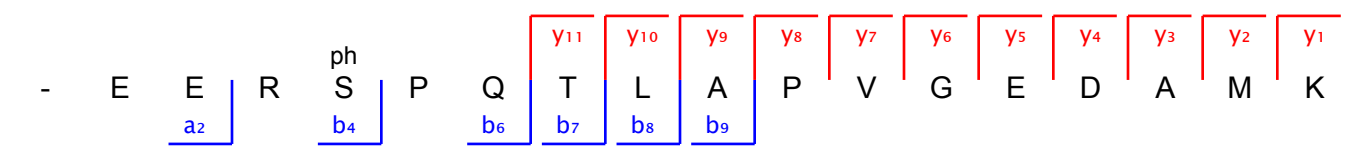
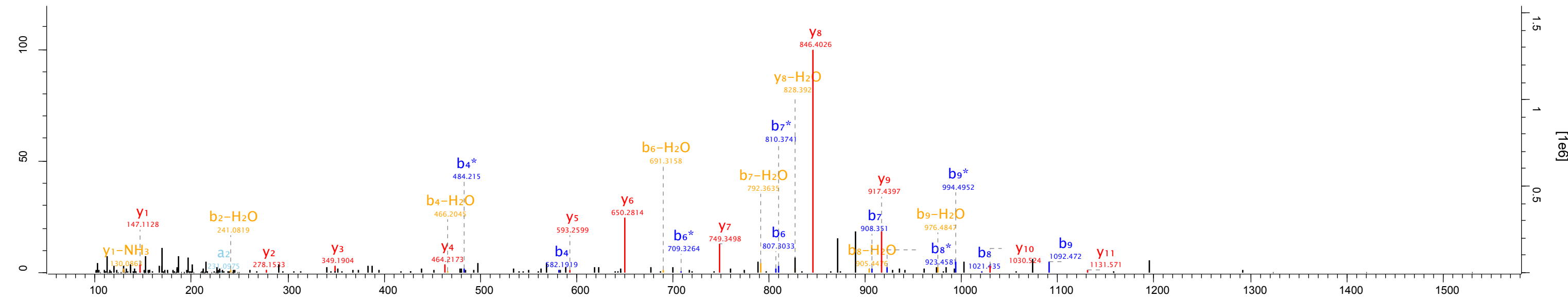
Fragmentation mapping:

- b₂ (blue box) under S
- b₃ (blue box) under S
- b₄* (blue box) under F
- b₅ (blue box) under T
- b₆* (blue box) under E
- b₇ (blue box) under Q
- b₈* (blue box) under L
- y₁ (red box) under R
- y₂ (red box) under N
- y₃ (red box) under P
- y₄ (red box) under T
- y₅ (red box) under G
- y₆ (red box) under E
- y₇ (red box) under D
- y₈ (red box) under L
- y₉ (red box) under Q
- y₁₀ (red box) under E
- y₁₁ (red box) under T
- y₁₂ (red box) under F
- y₁₃* (red box) under S

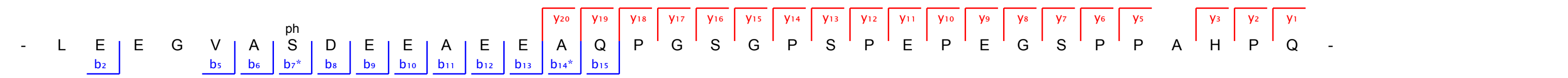
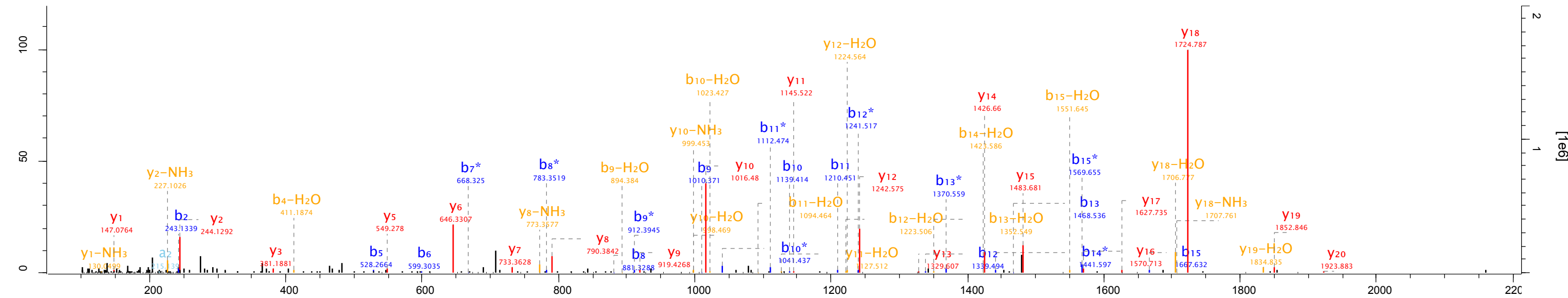
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 10001 Method FTMS; HCD Score 79.35 m/z 741.36 Gene names FTSJ3



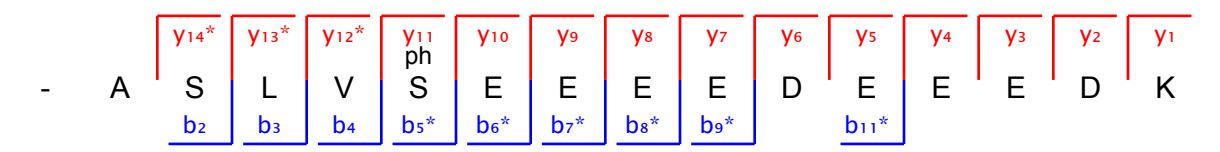
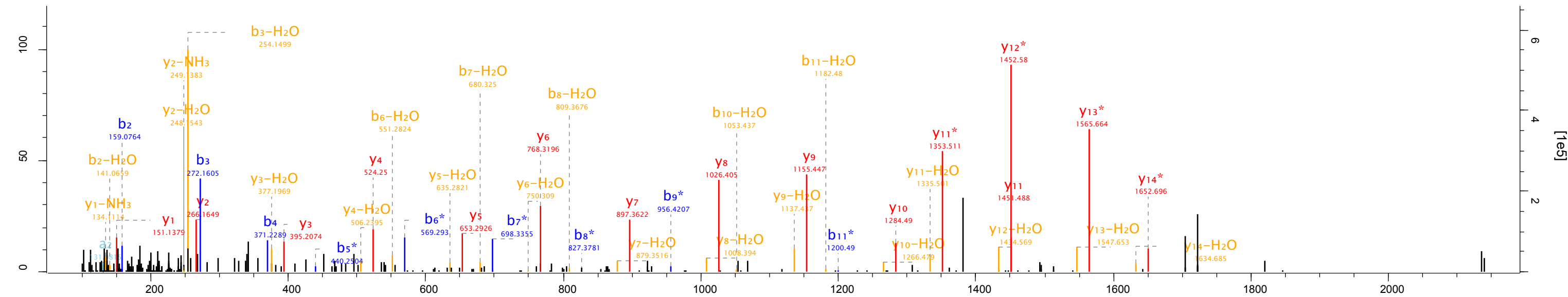
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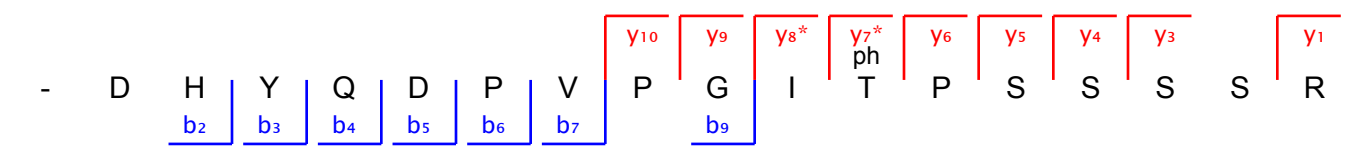
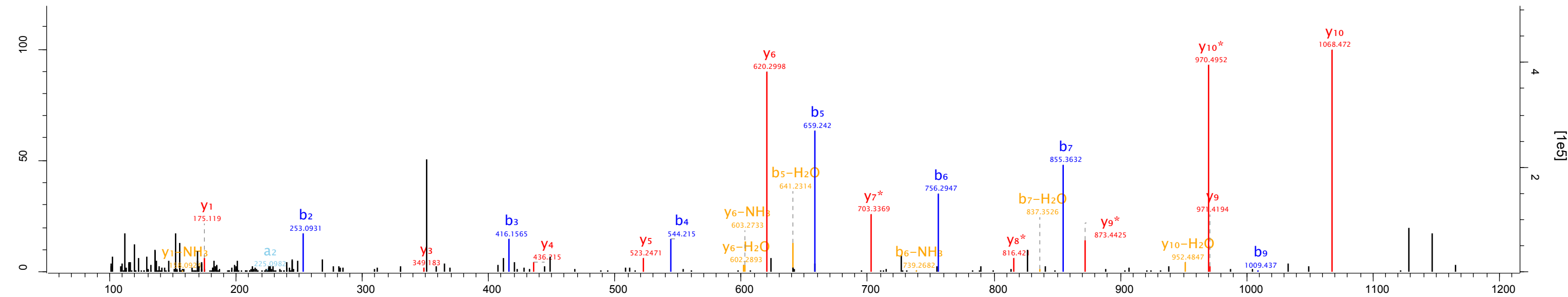
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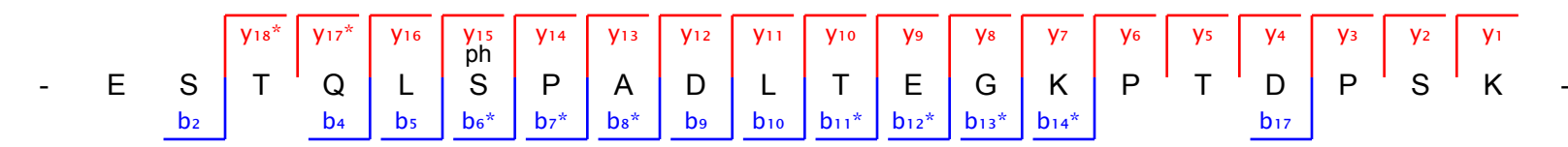
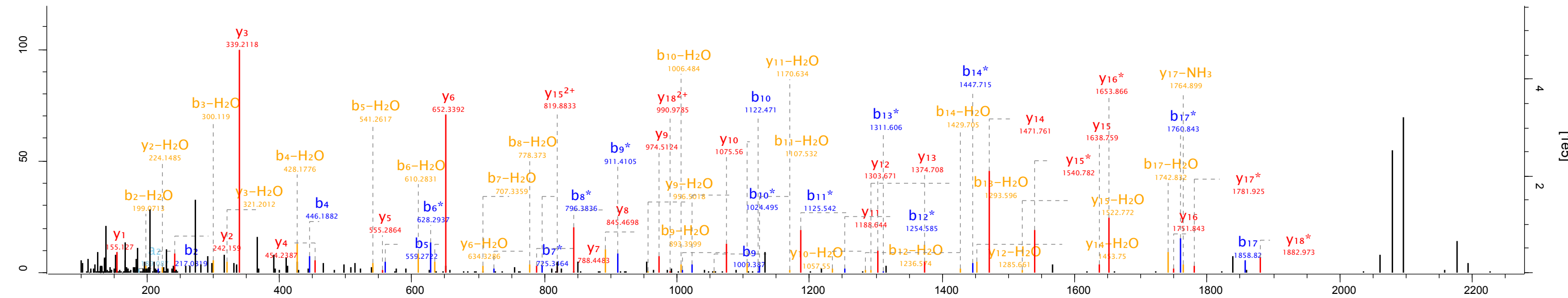
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 Scan: 10351 Method: FTMS; HCD Score: 233.49 m/z: 911.86 Gene names: CDCA7L



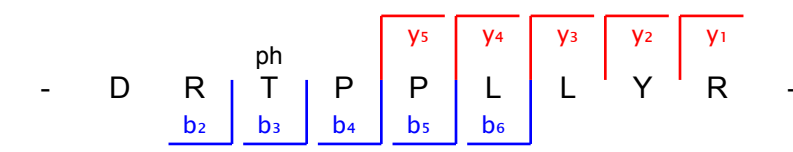
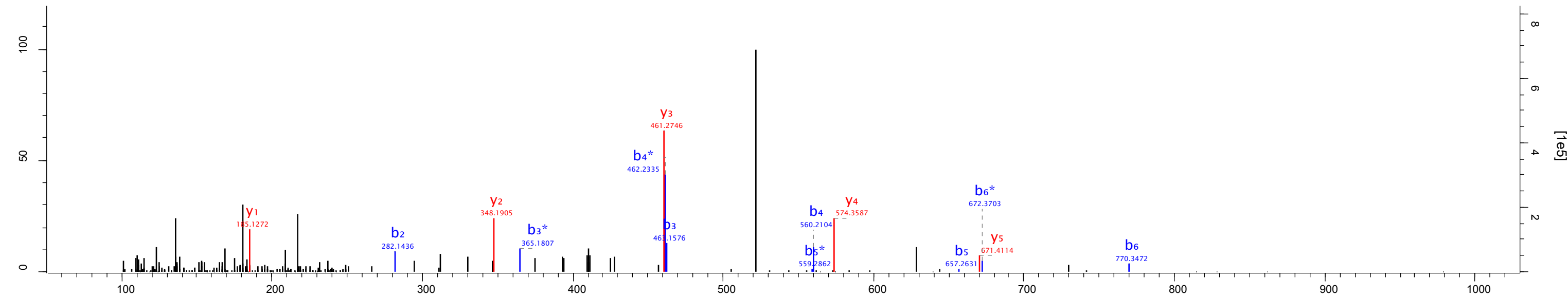
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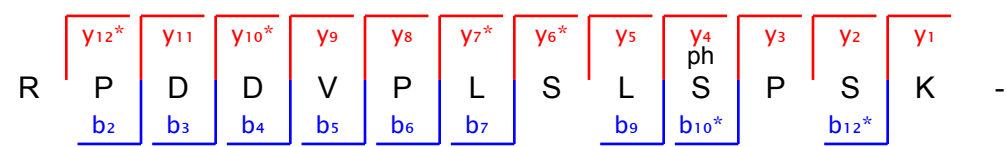
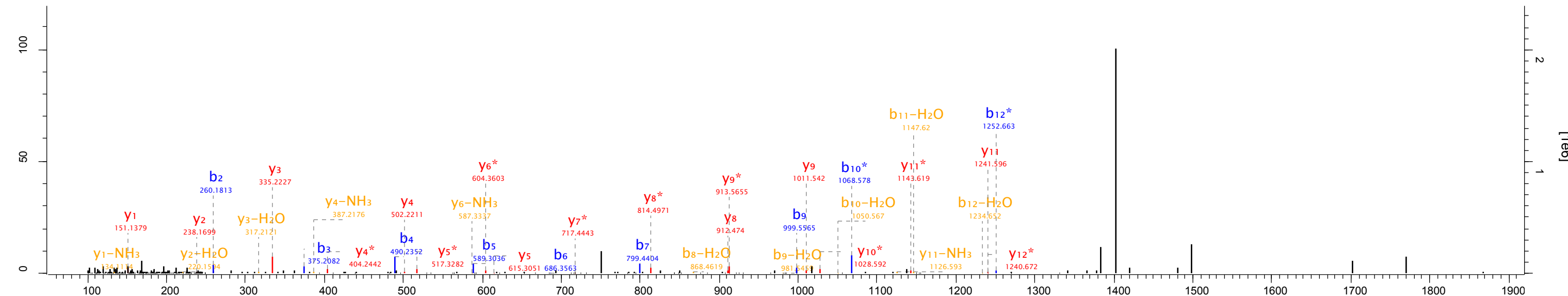
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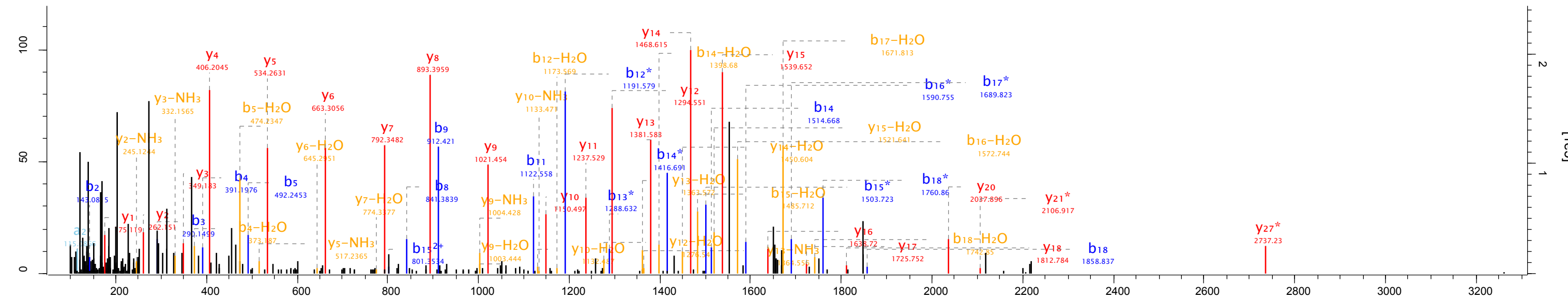
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 10851 Method FTMS; HCD Score 66.39 m/z 410.87 Gene names RBM15



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11131 Method FTMS; HCD Score 83.07 m/z 750.89 Gene names LRWD1



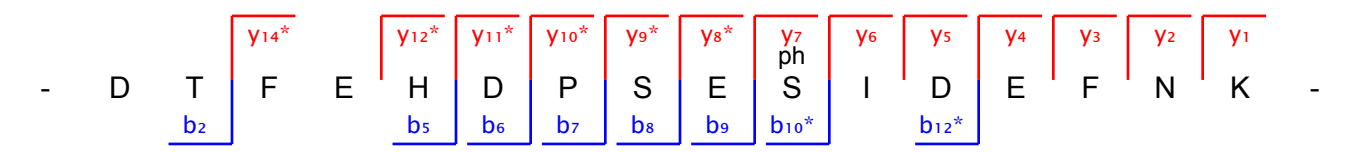
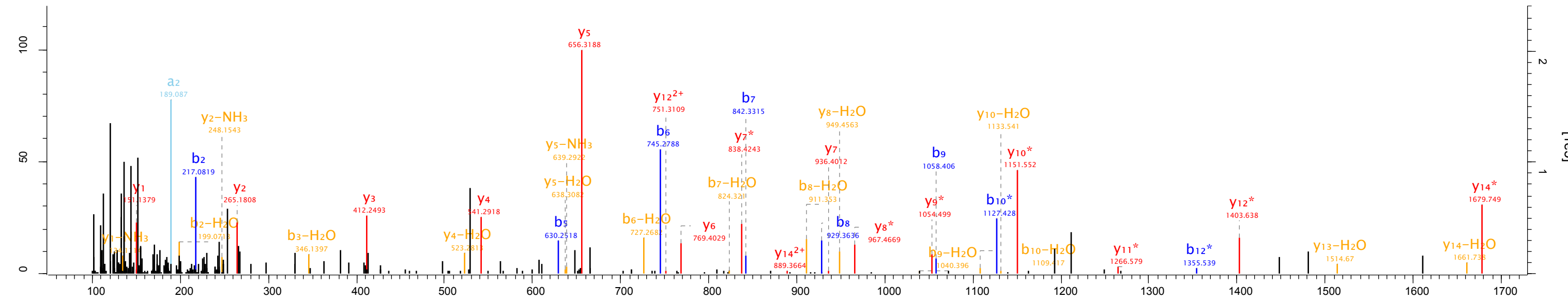
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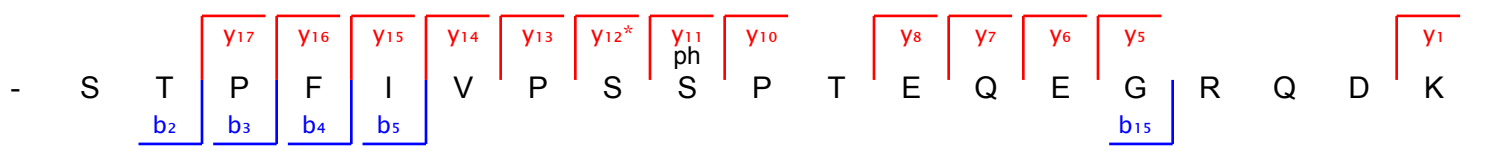
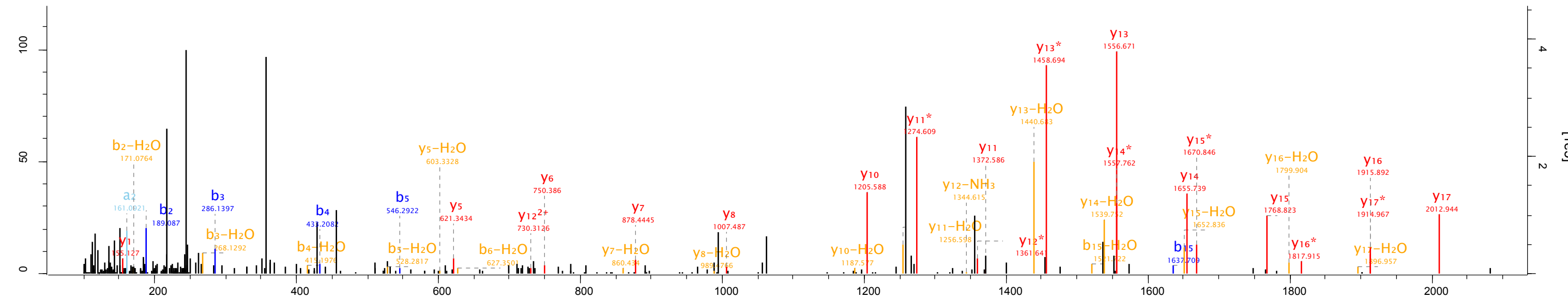
- A A F T T P D H A P L S P Q S S V A S S G S E Q T E E Q G S S R -

b₂
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b₄
b₅
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y₂₇^{*}

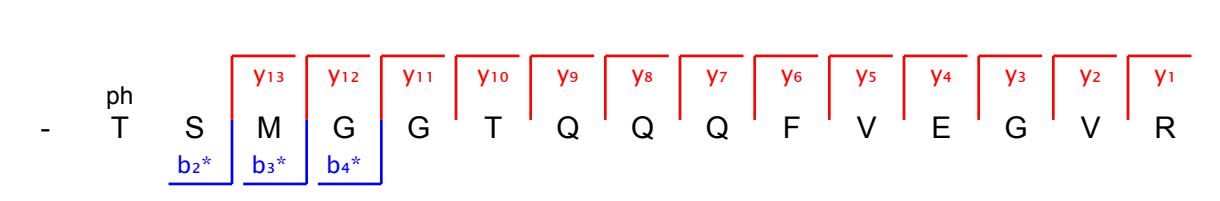
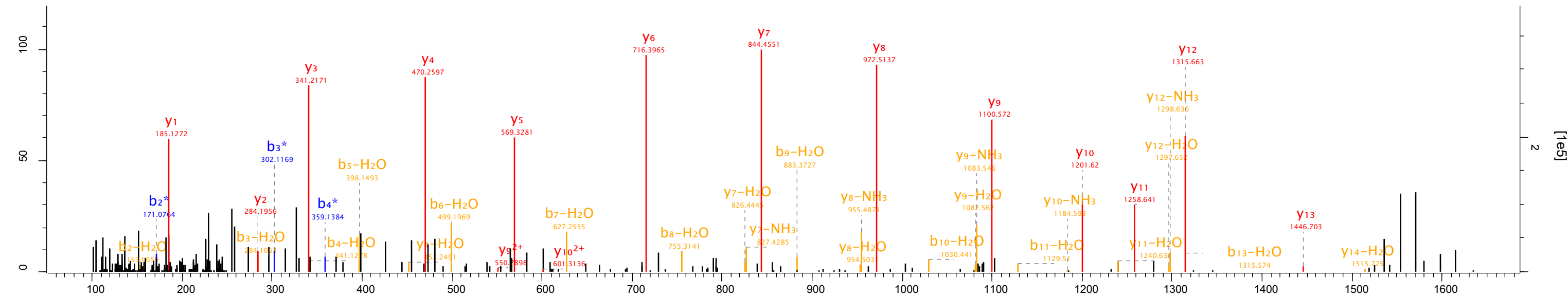
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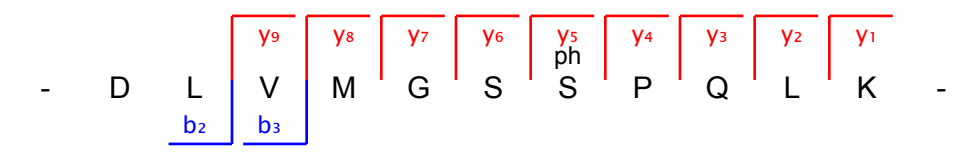
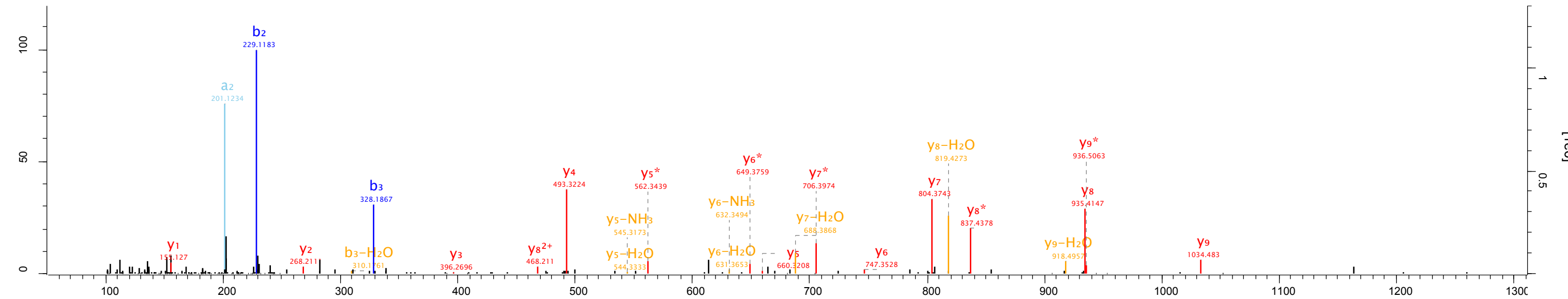
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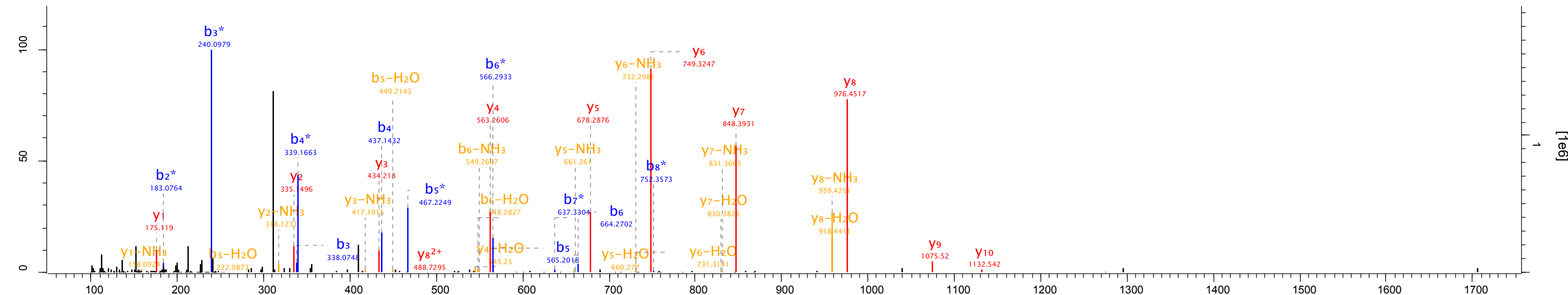


Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11811 Method FTMS; HCD Score 97.8 m/z 858.38 Gene names CTNNB1



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11941 Method FTMS; HCD Score 116.9 m/z 631.8 Gene names SOWAHC





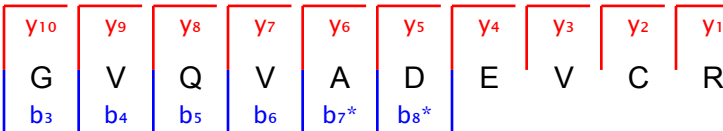
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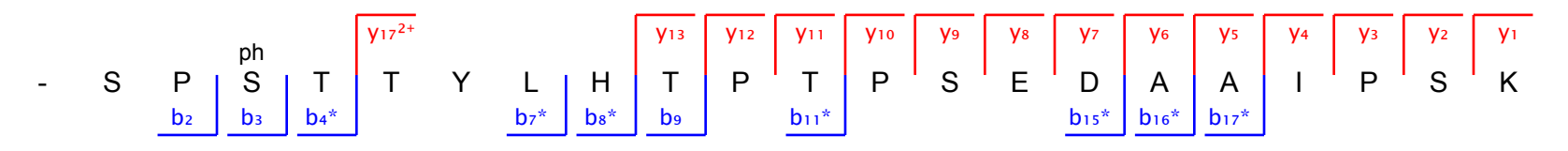
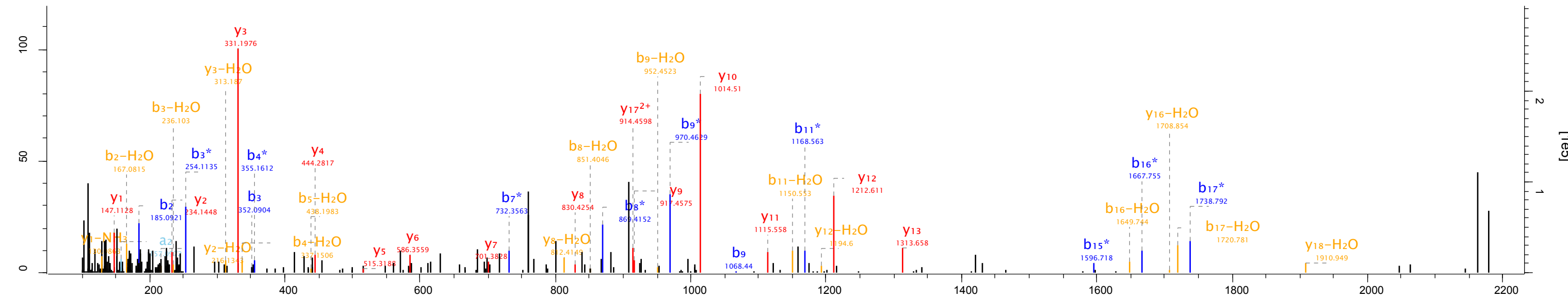
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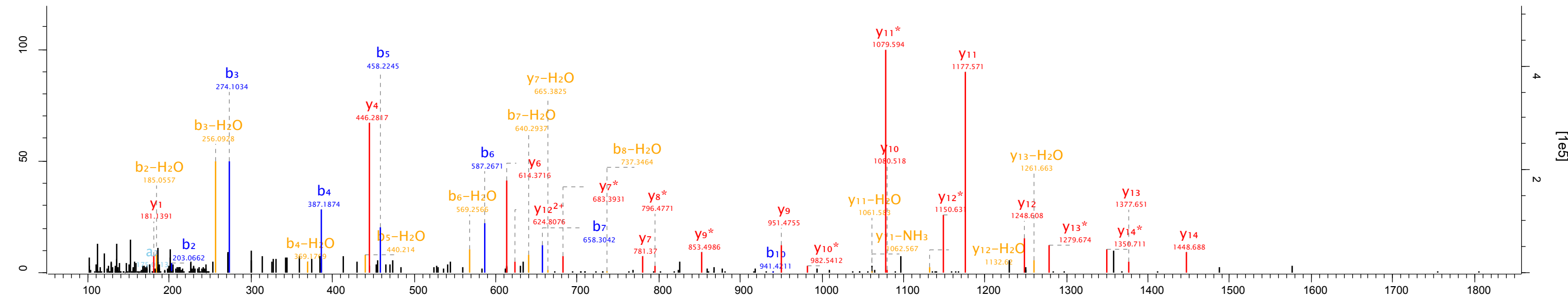
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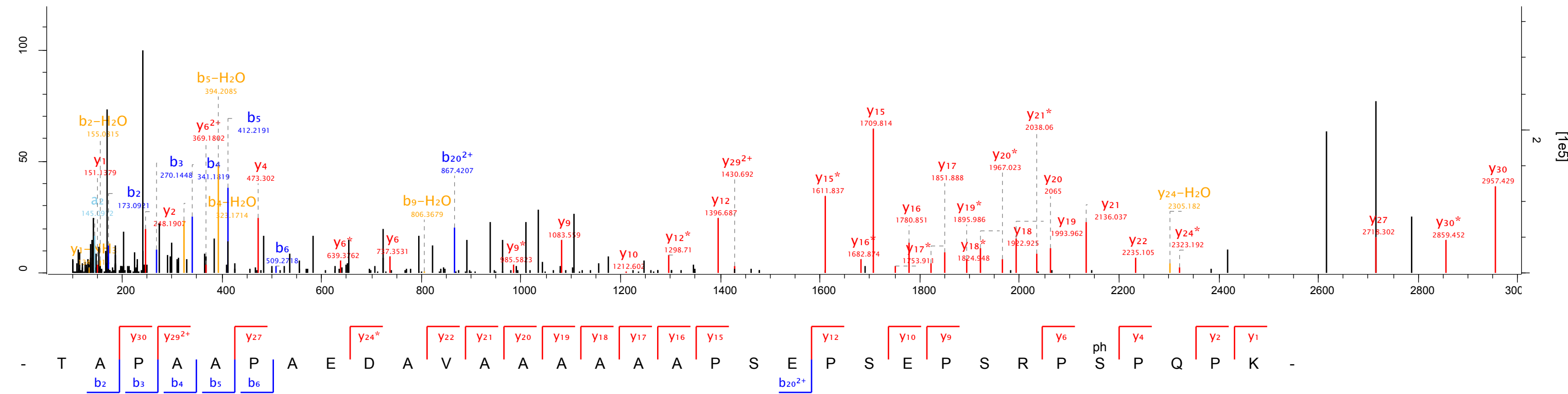
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 Scan: 12191 Method: FTMS; HCD Score: 87.42 m/z: 761.02 Gene names: CHAF1A



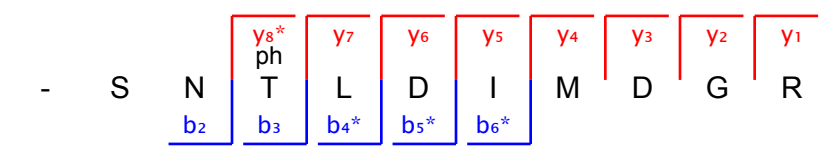
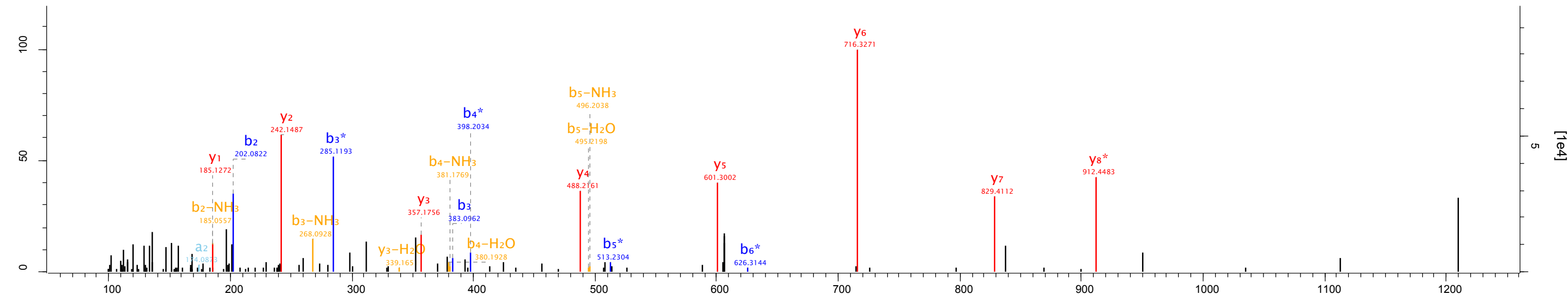
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12301 Method FTMS; HCD Score 158 m/z 917.94 Gene names USP42



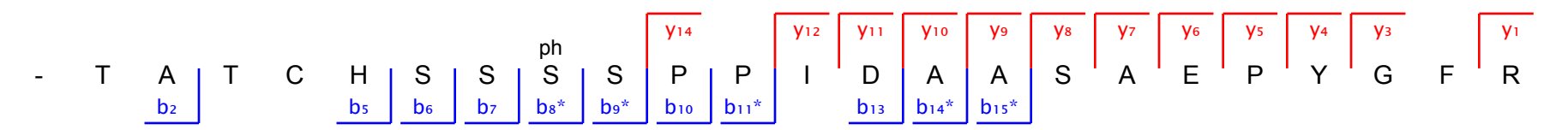
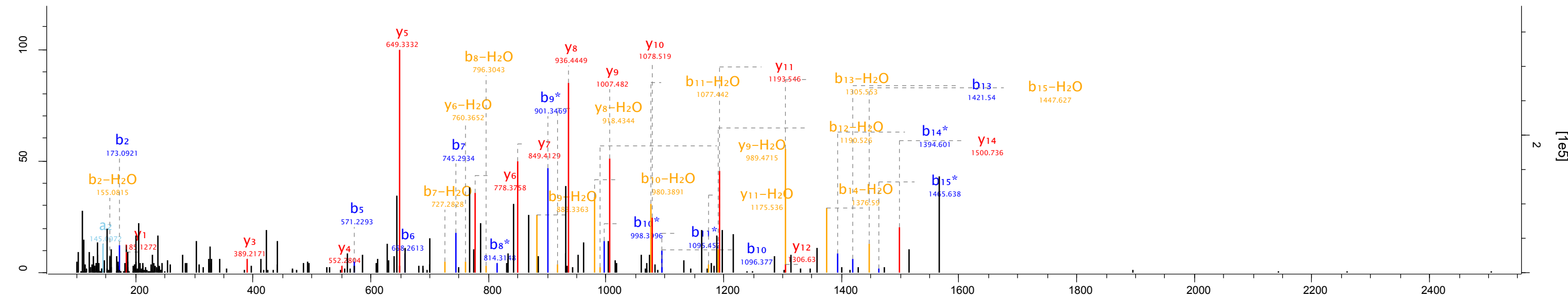
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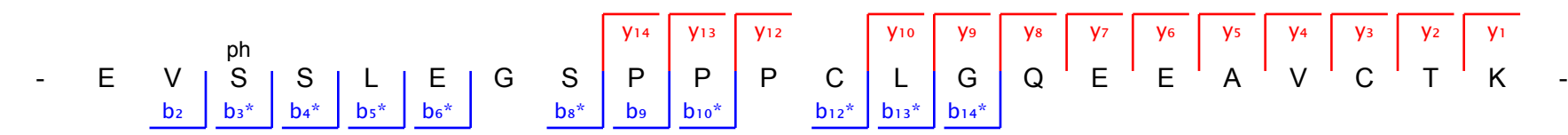
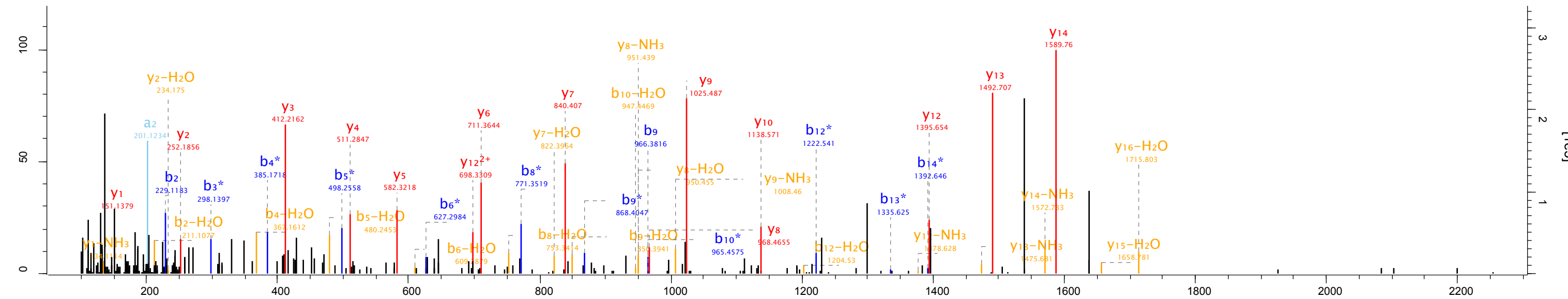
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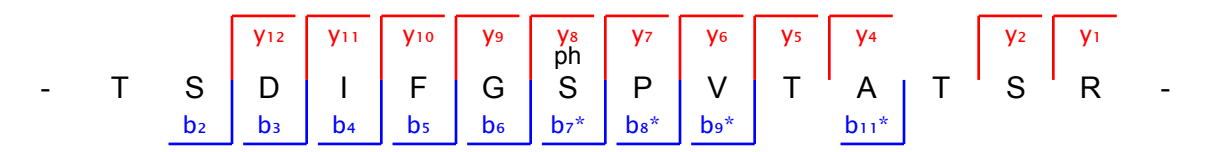
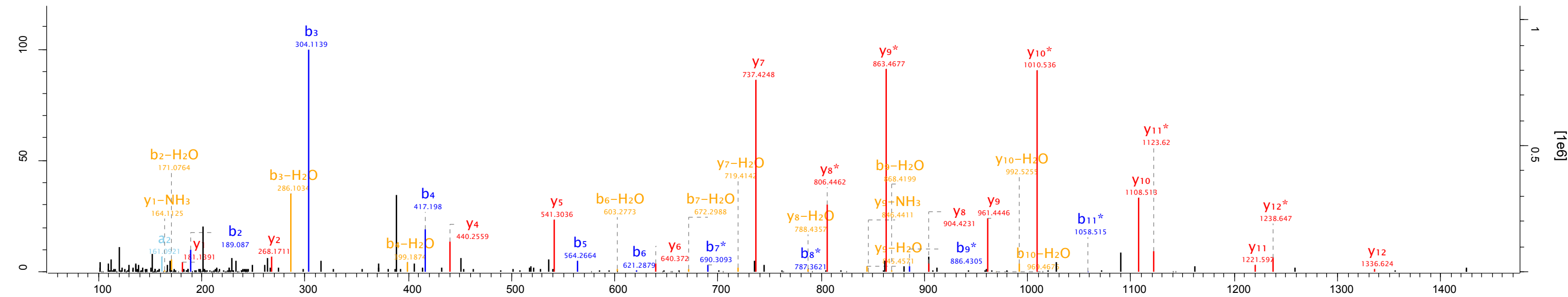


[1e4]

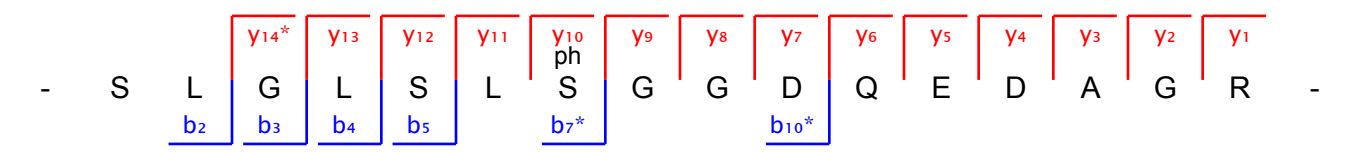
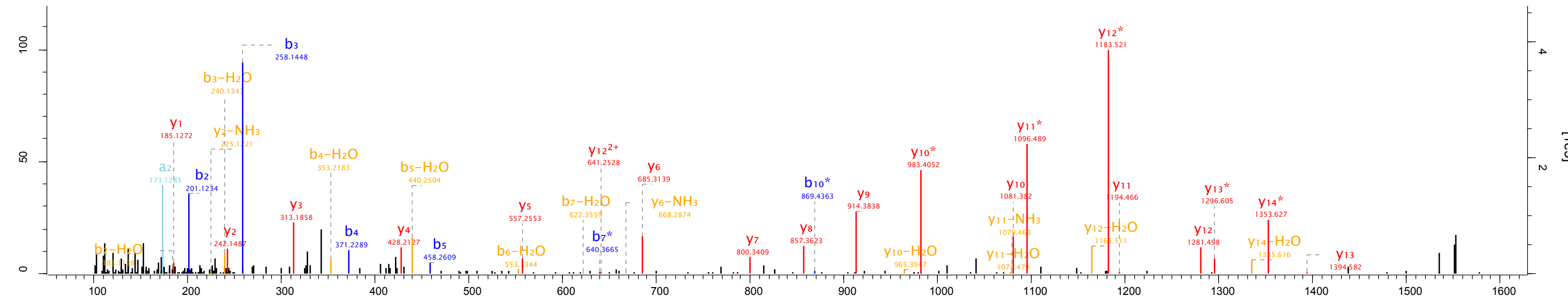


Raw file: 20171215_MaS_33SR_LMH_phospho_06
 Scan: 12931 Method: FTMS; HCD Score: 155.91 m/z: 820.37 Gene names: AKAP12

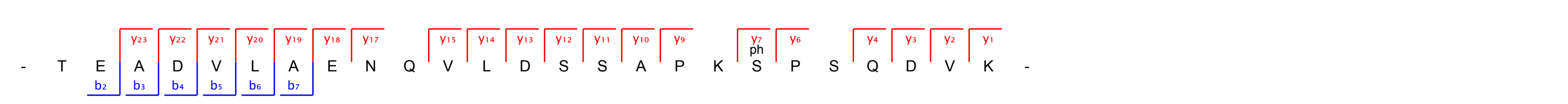
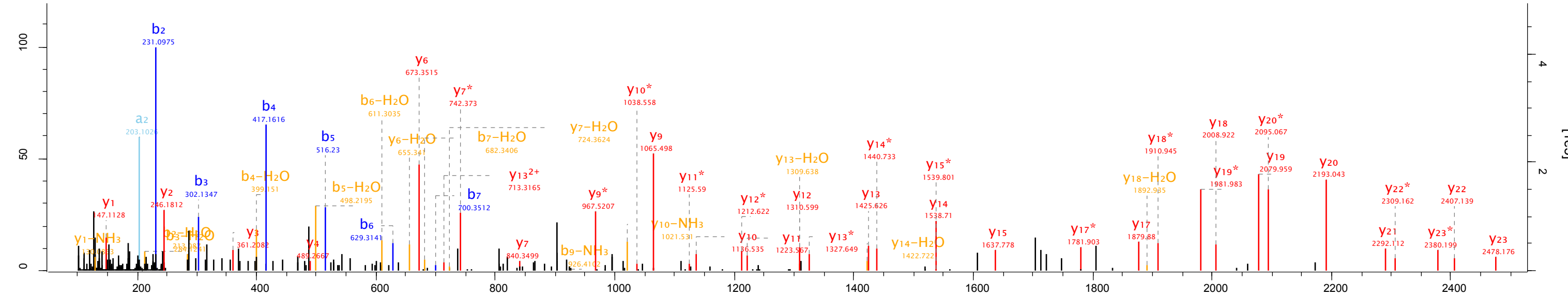




Raw file: 20171215_MaS_33SR_LMH_phospho_06
 Scan: 13141 Method: FTMS; HCD Score: 154.55 m/z: 826.36 Gene names: NAGK

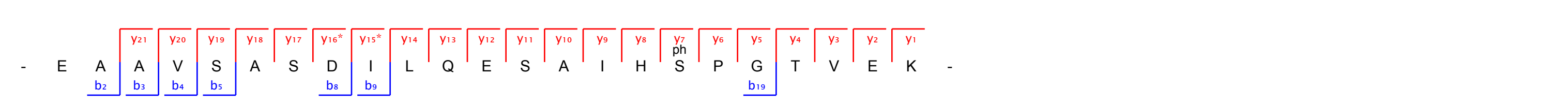
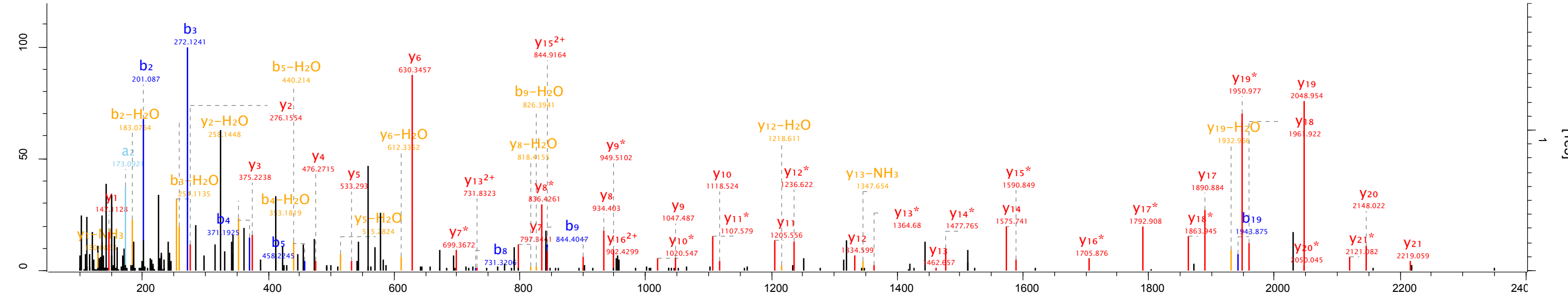


20171215_MaS_33SR_LMH_phospho_06 13251 FTMS; HCD 235.07 903.76 NUFIP1

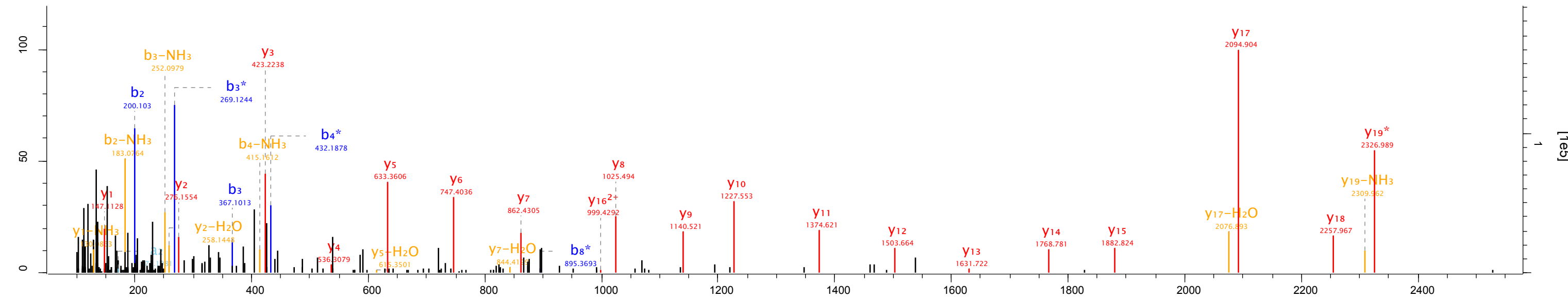


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho_06 14991 FTMS; HCD 217.37 807.38 C12orf43



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 15191 Method FTMS; HCD Score 91.08 m/z 875.69 Gene names MAP3K2

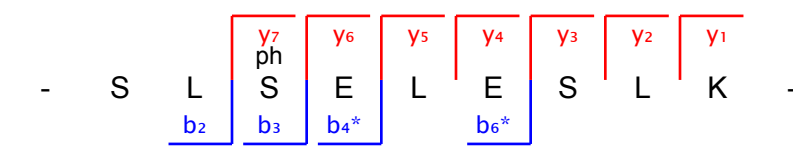
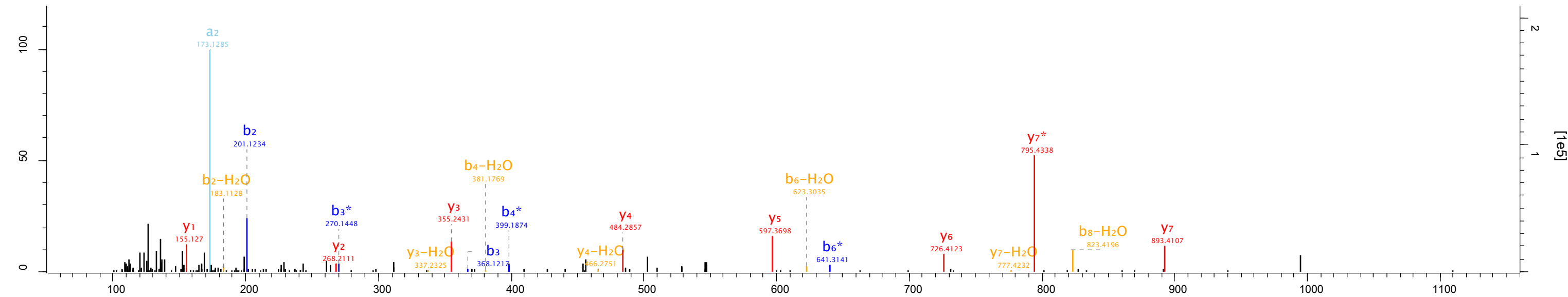


- A Q S Y P D N H Q E F S D Y D N P I F E K -

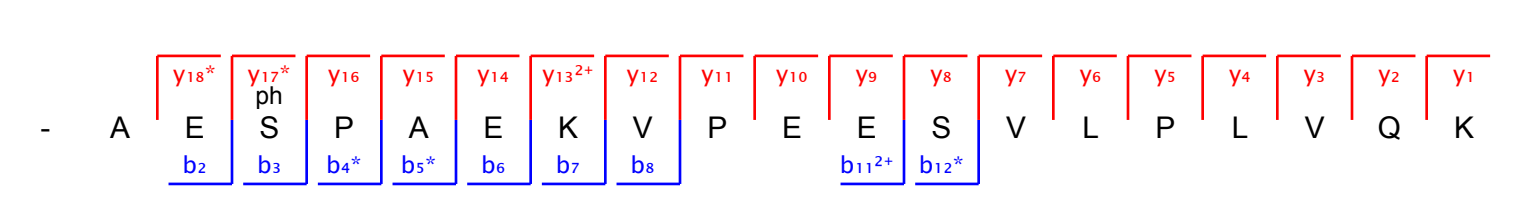
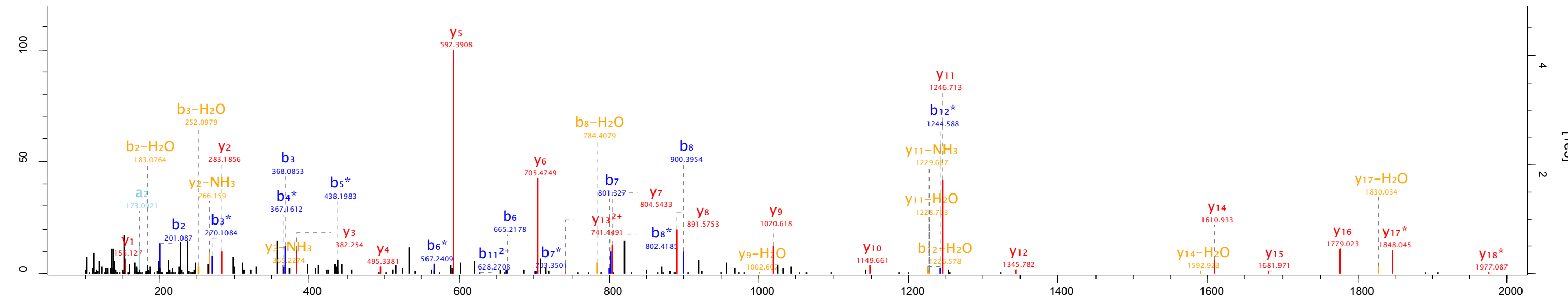
Fragmentation mapping (b and y ions) is shown below the sequence:

- b2: A-Q
- b3: Q-S
- b4*: S-Y
- b8*: N-H
- y1: E-K
- y2: F-E
- y3: D-F
- y4: N-D
- y5: P-N
- y6: S-P
- y7: D-S
- y8: Y-D
- y9: D-Y
- y10: S-D
- y11: F-S
- y12: E-F
- y13: Q-E
- y14: H-Q
- y15: N-H
- y16²⁺: D-N
- y17: P-D
- y18: Y-P
- y19*: S-Y

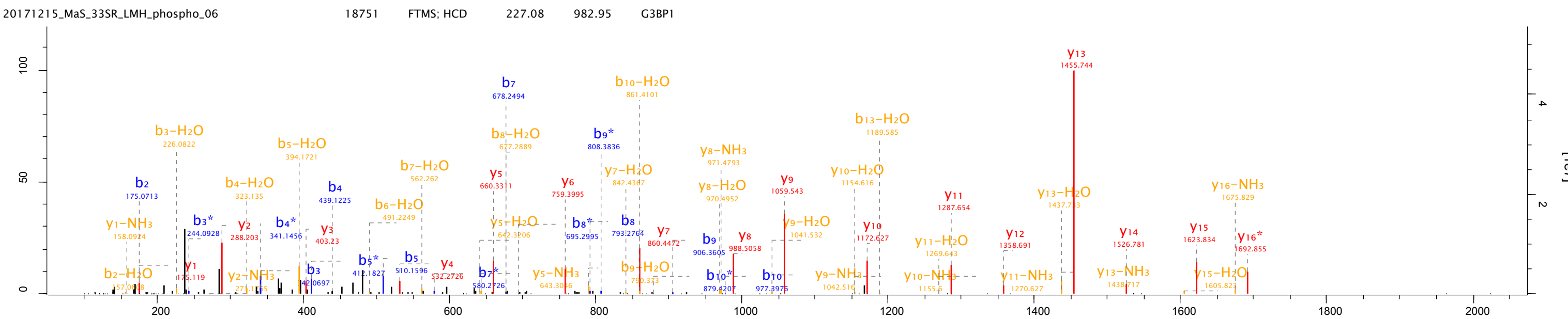
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 15411 Method FTMS; HCD Score 71.08 m/z 547.27 Gene names OSBP



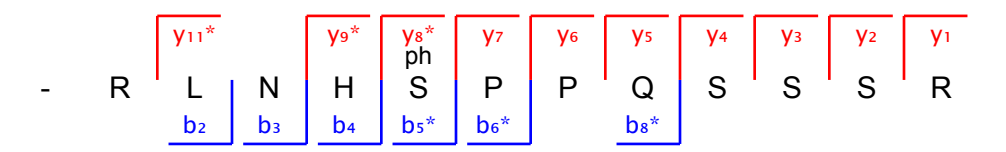
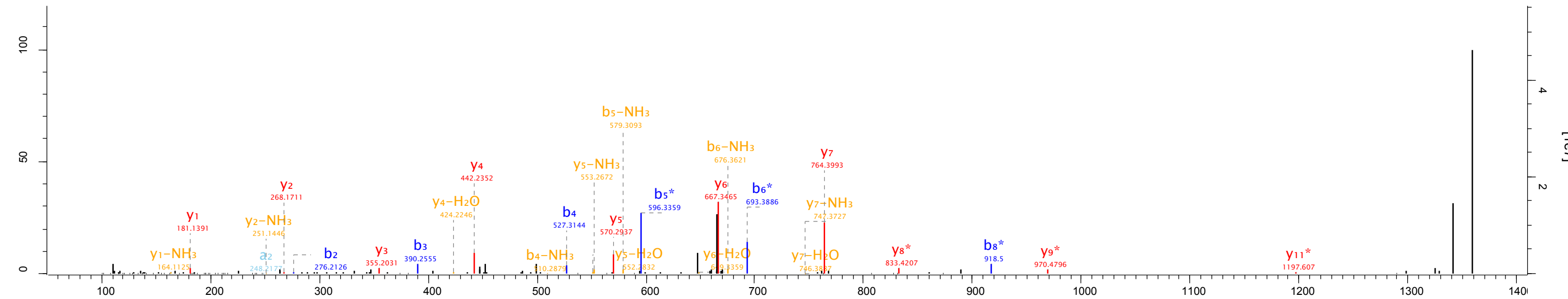
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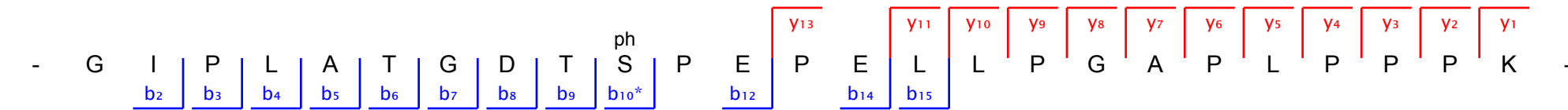
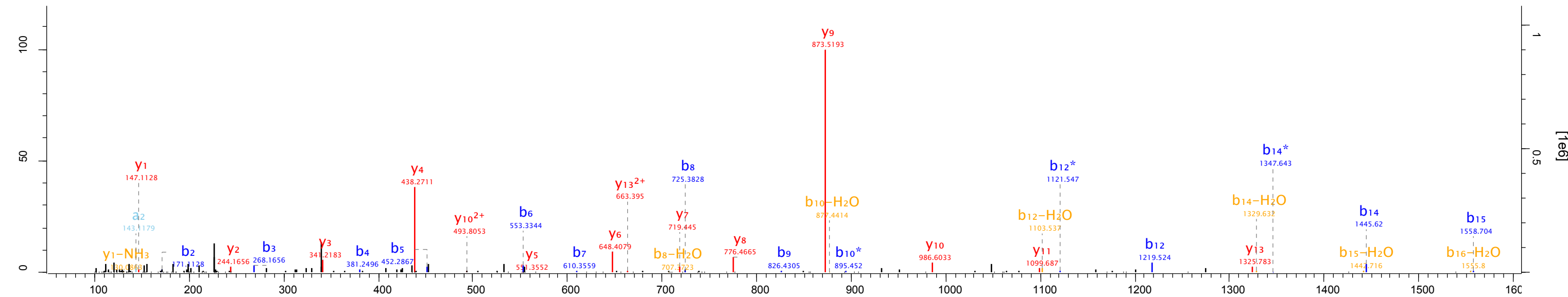


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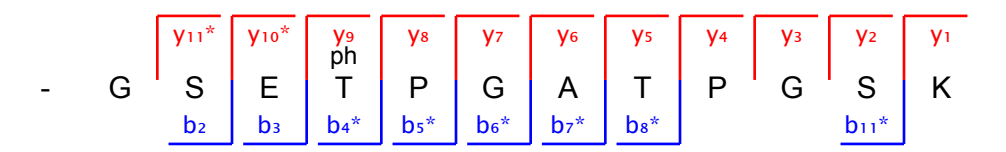
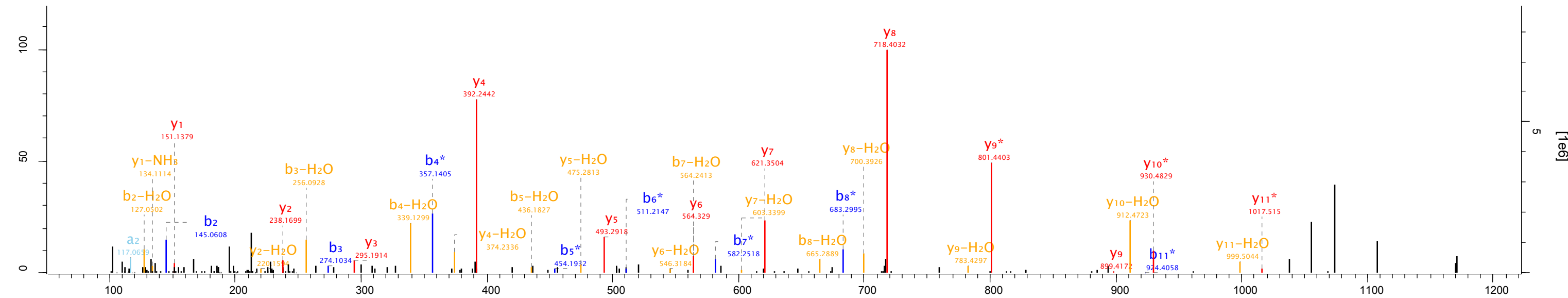


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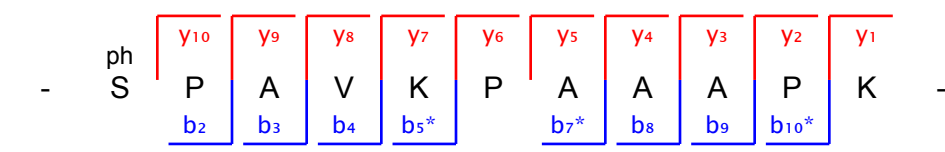
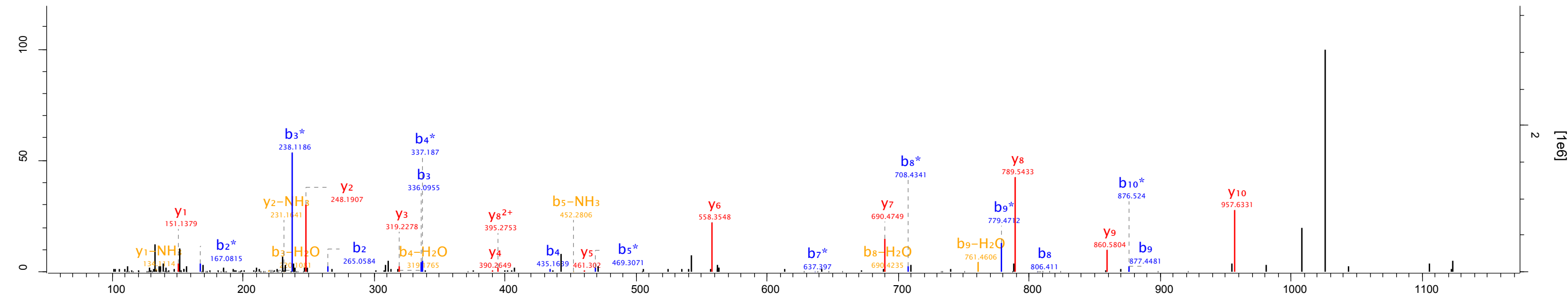




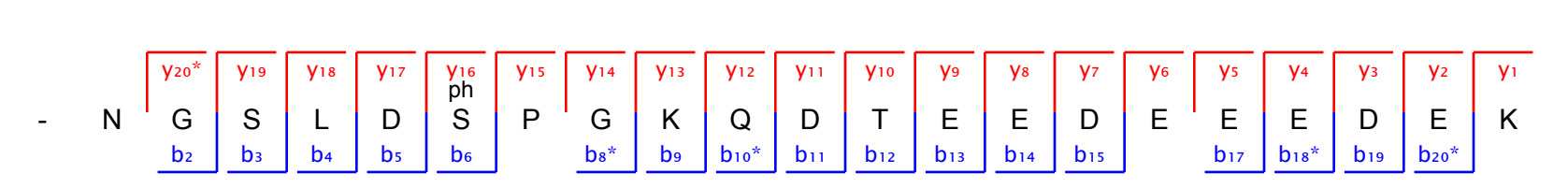
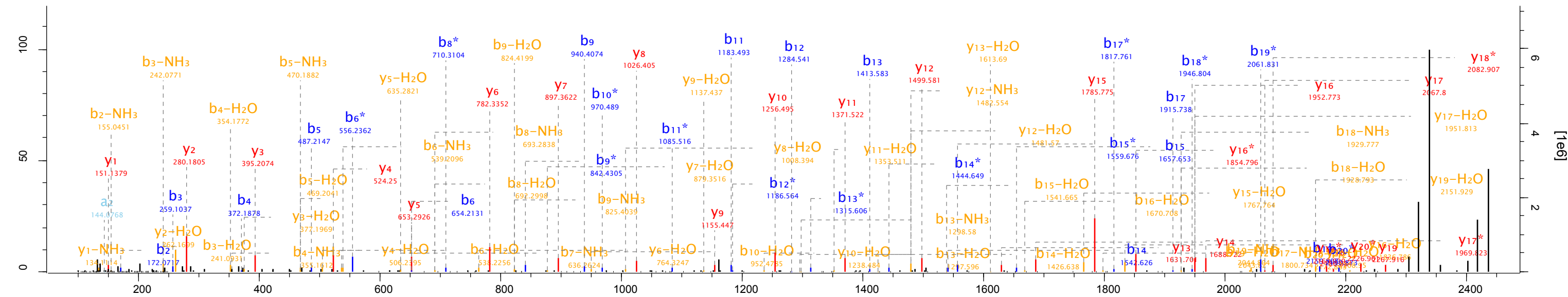
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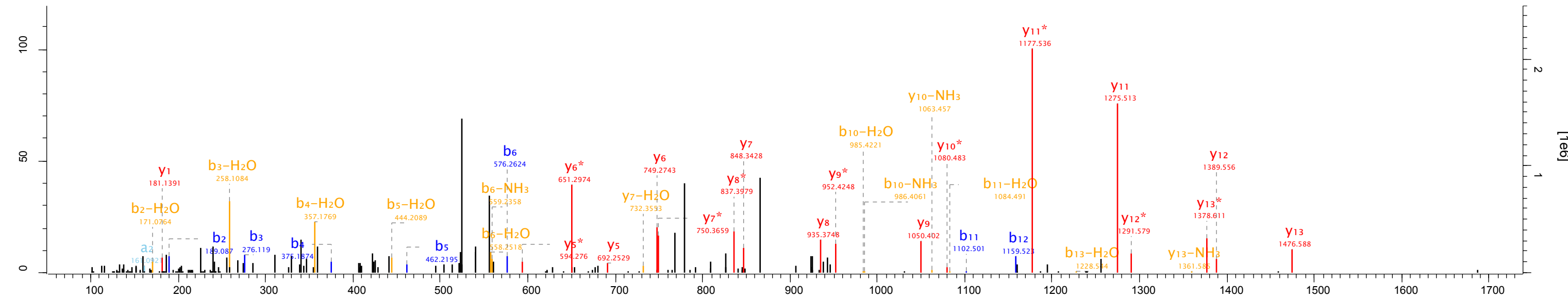
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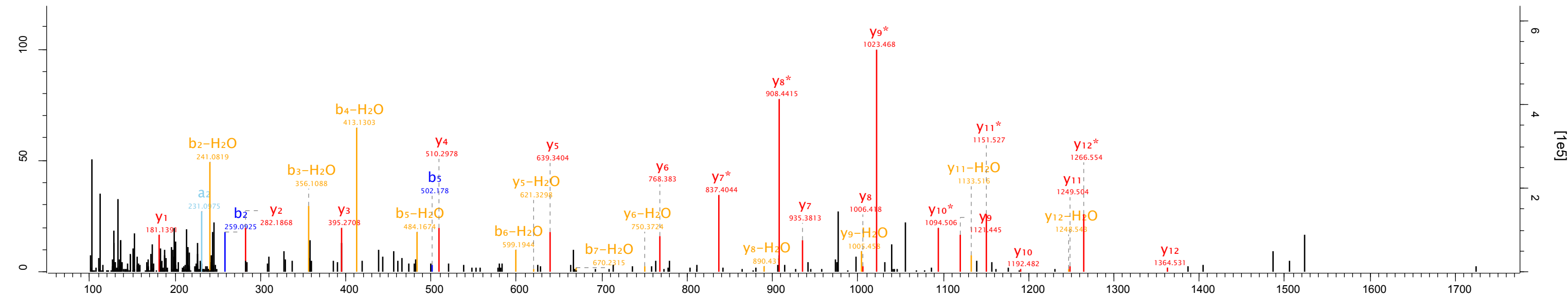
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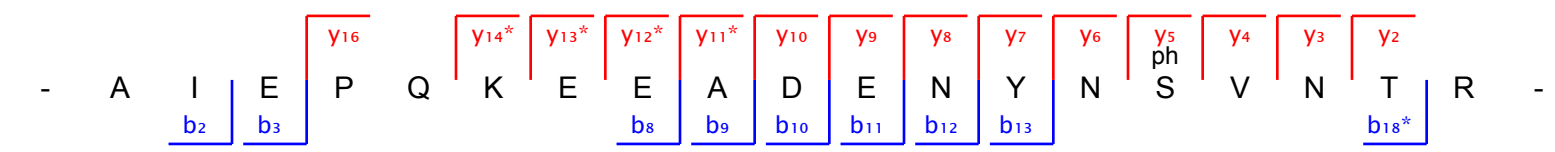
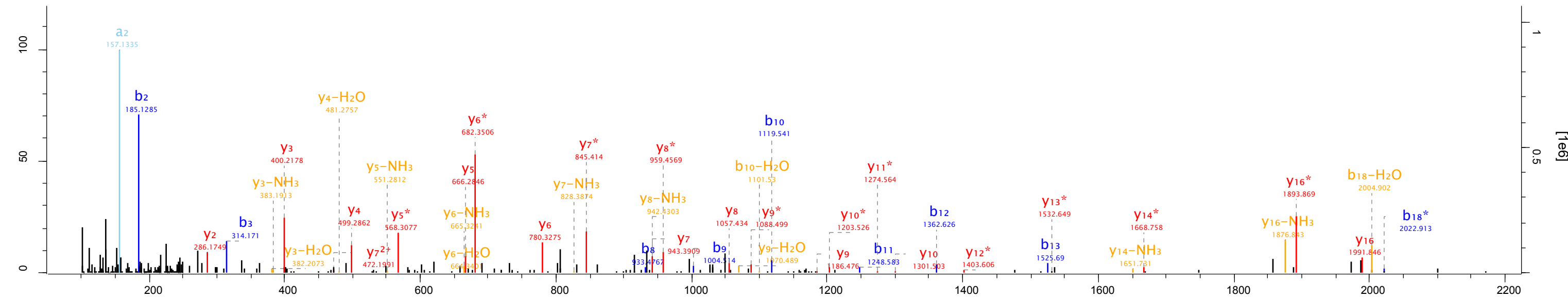
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Fragmentation mapping: b2 (S), b3 (S), b4 (V), b5 (S), b6 (N), b11 (V), b12 (G), y1 (R), y5 (S), y6 (G), y7 (V), y8 (S), y9 (D), y10* (Q), y11 (P), y12 (N), y13 (S).

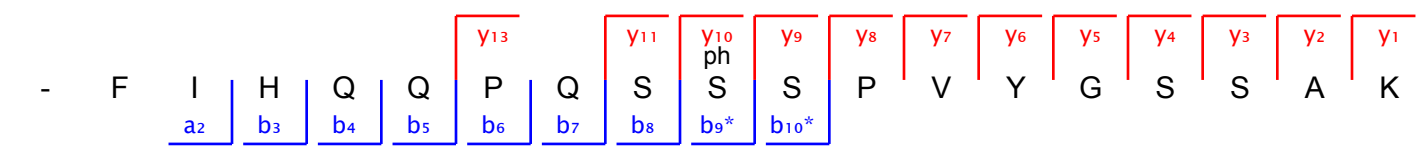
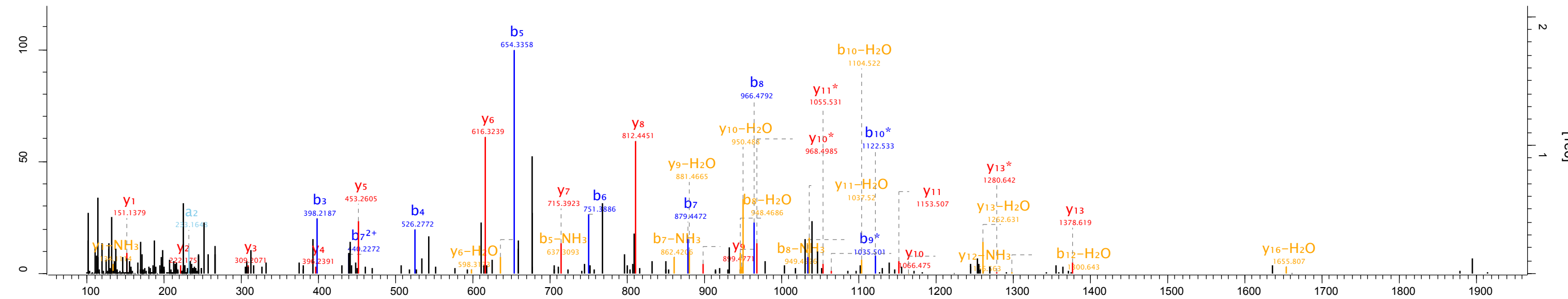
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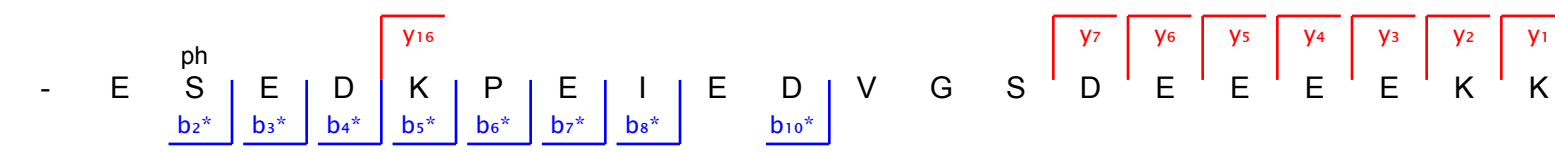
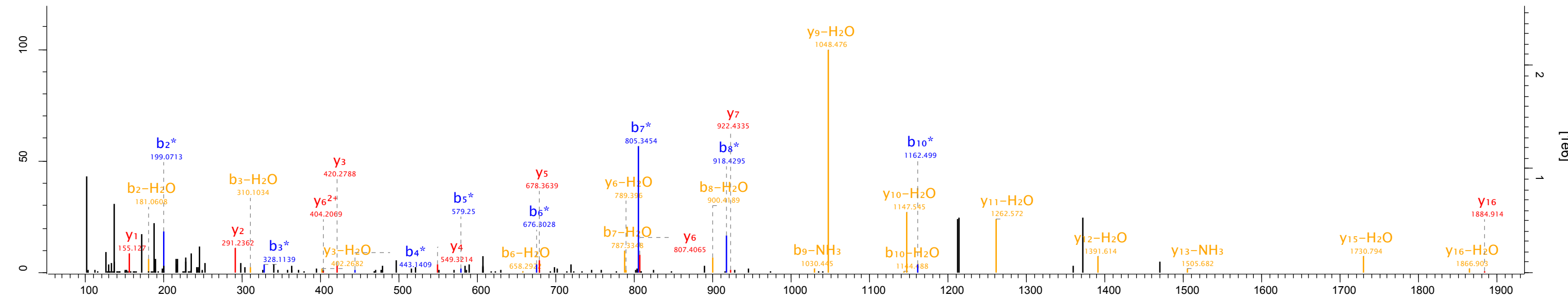
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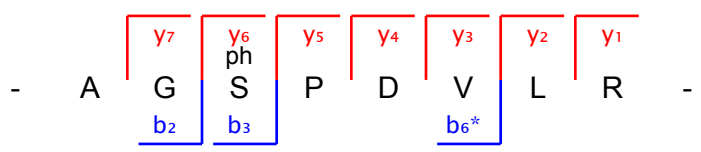
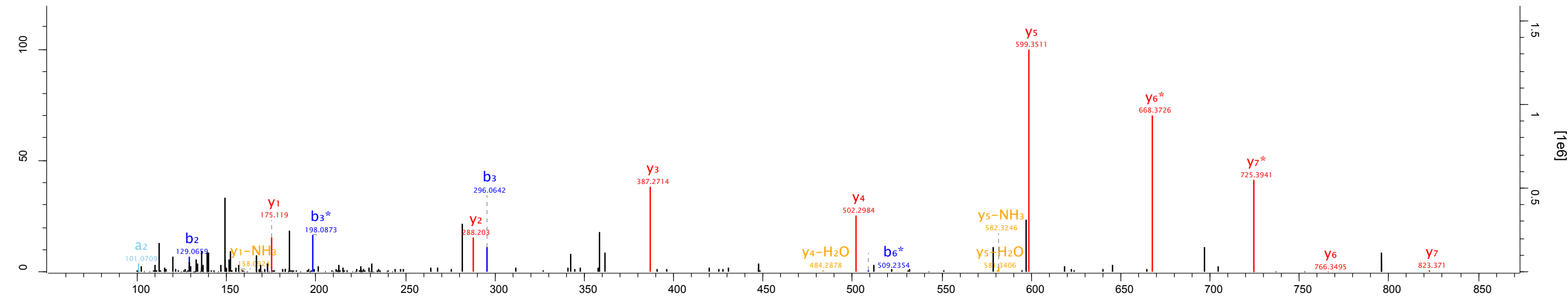
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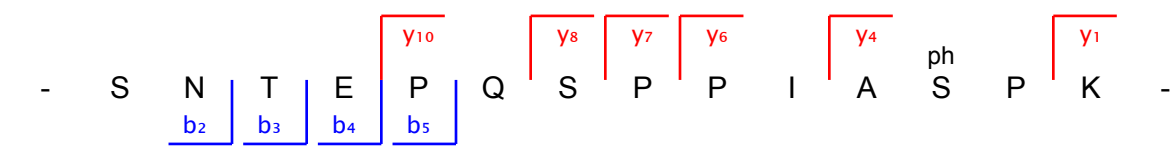
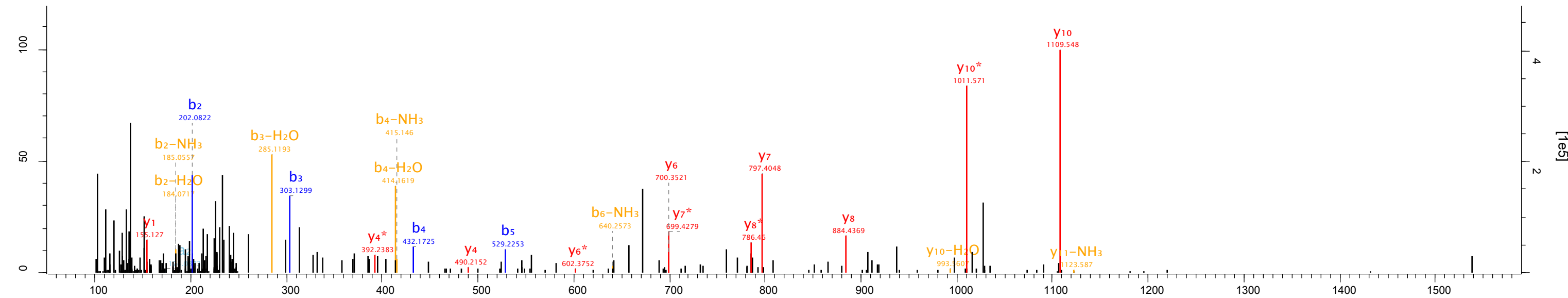


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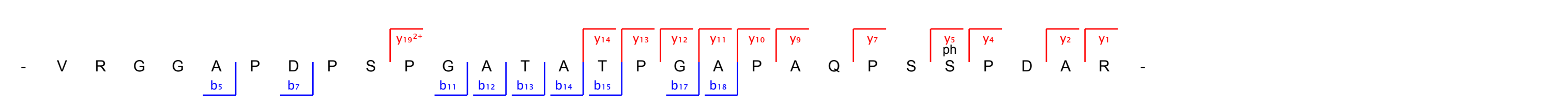
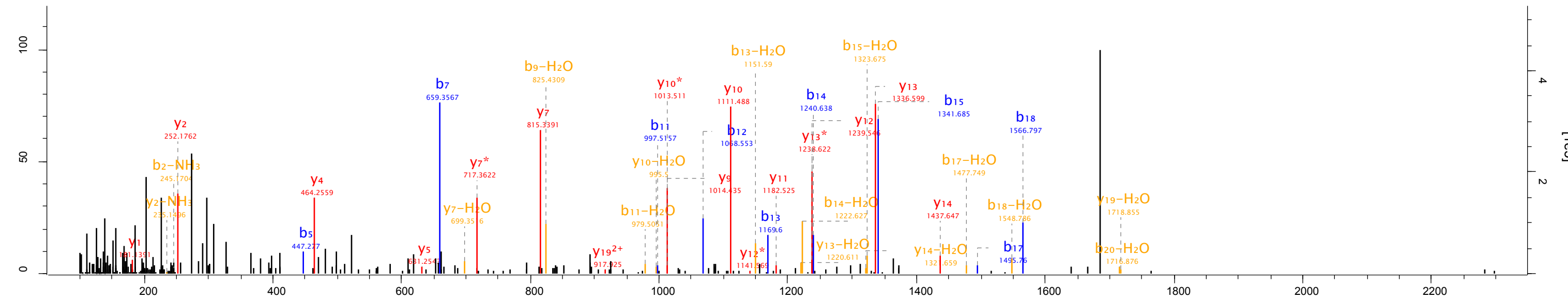


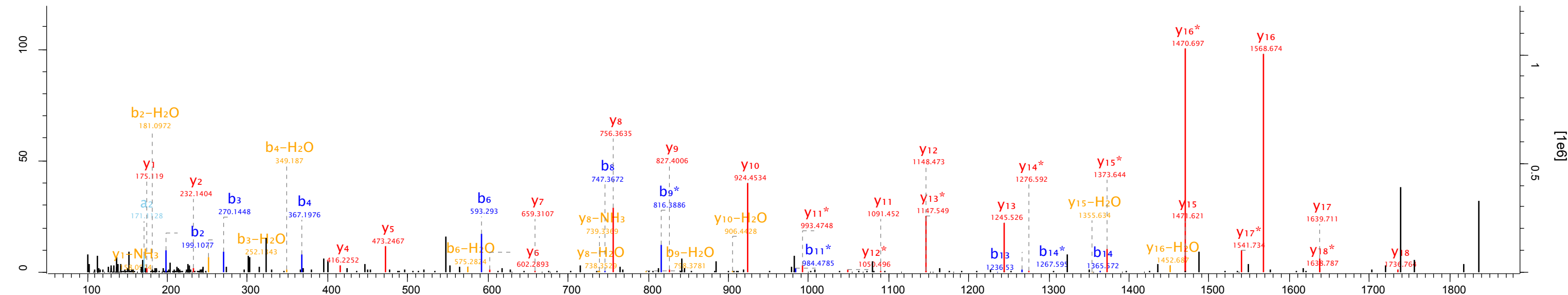
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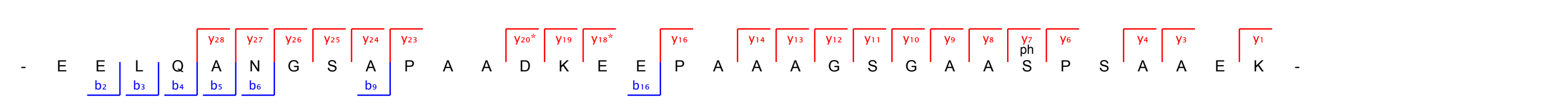
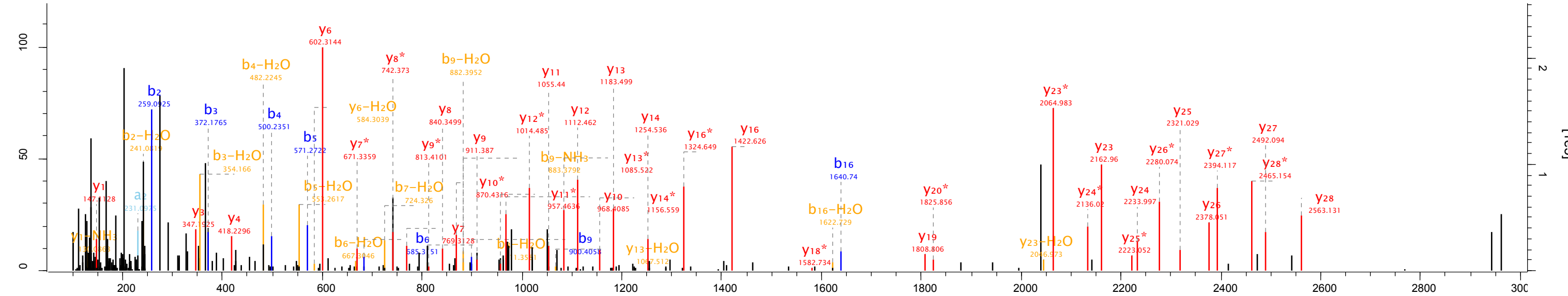


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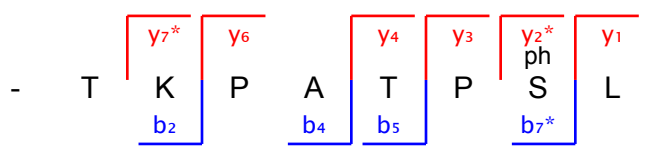
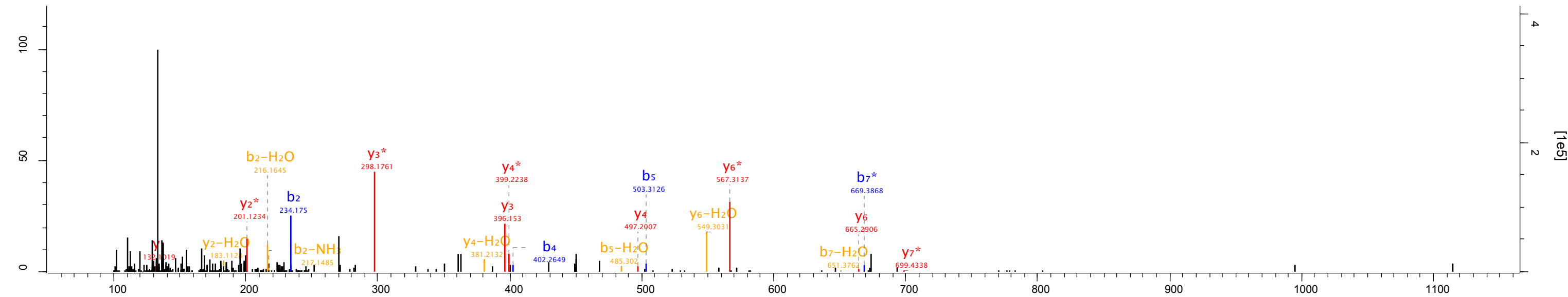
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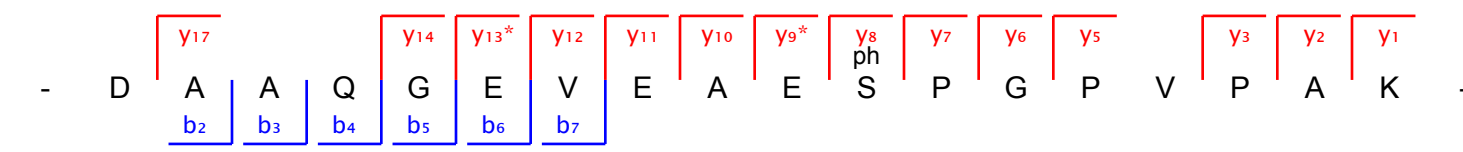
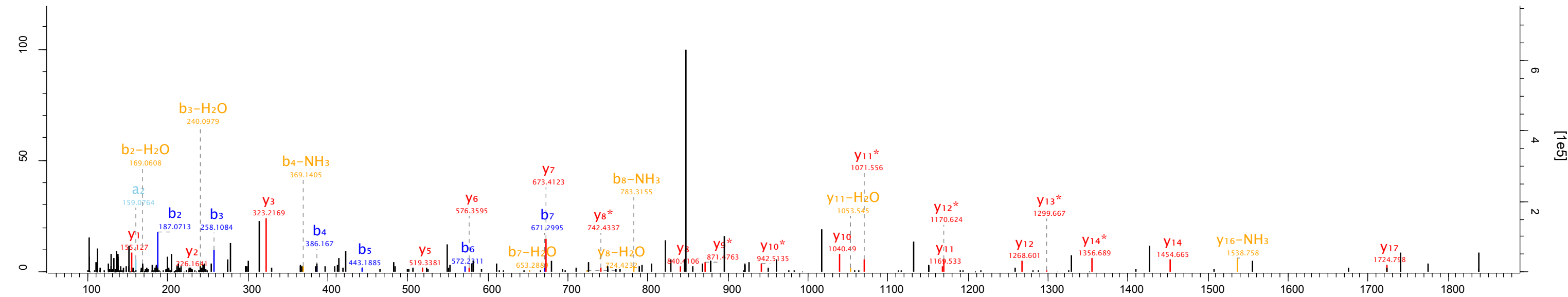
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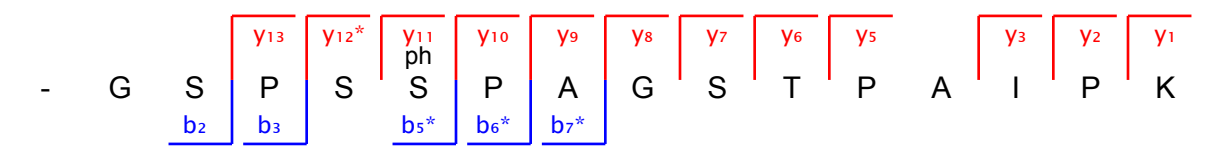
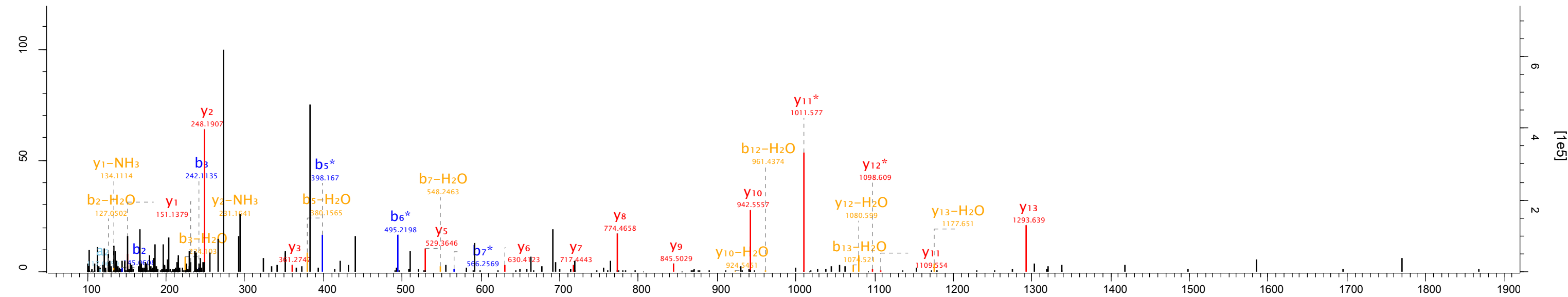
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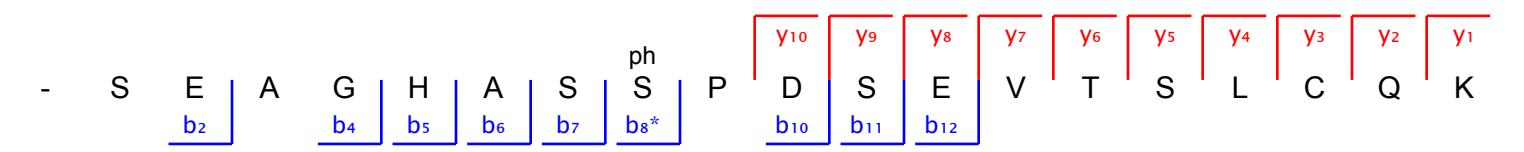
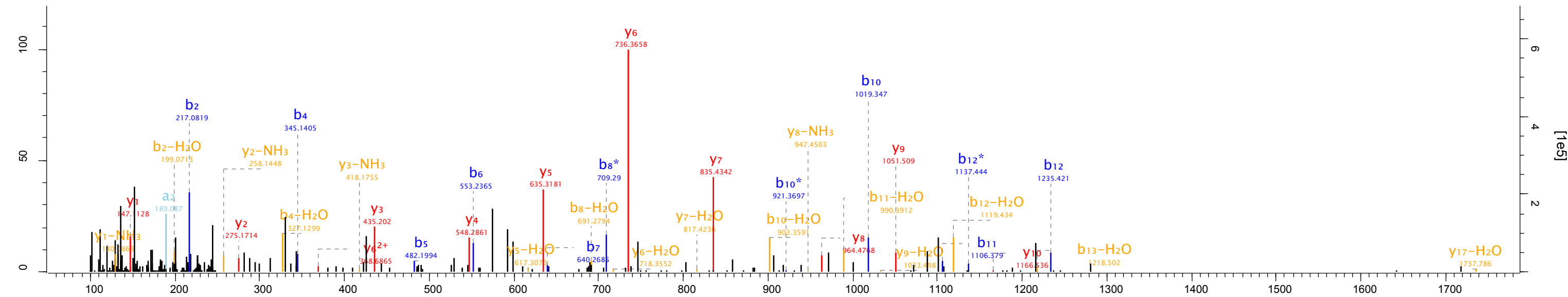
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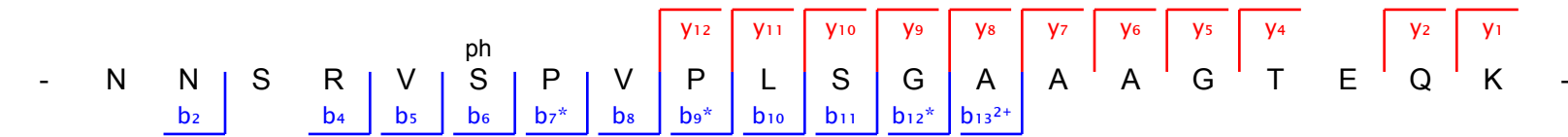
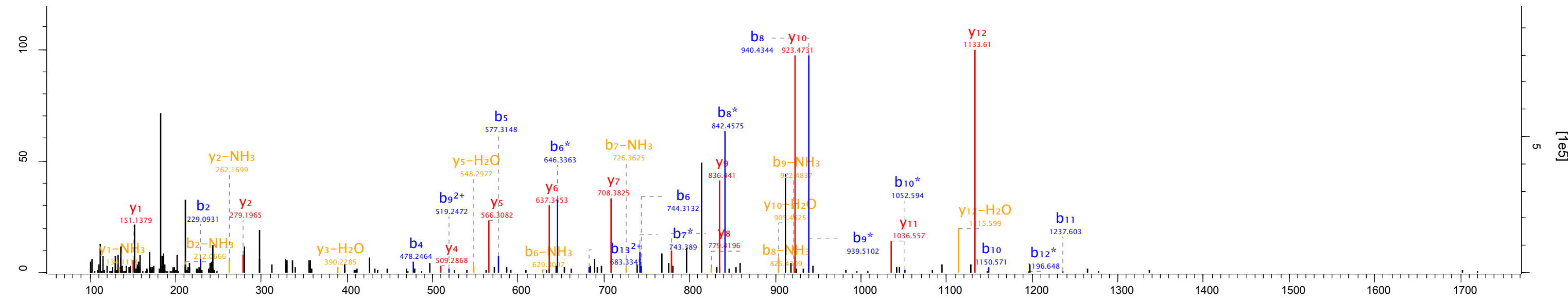


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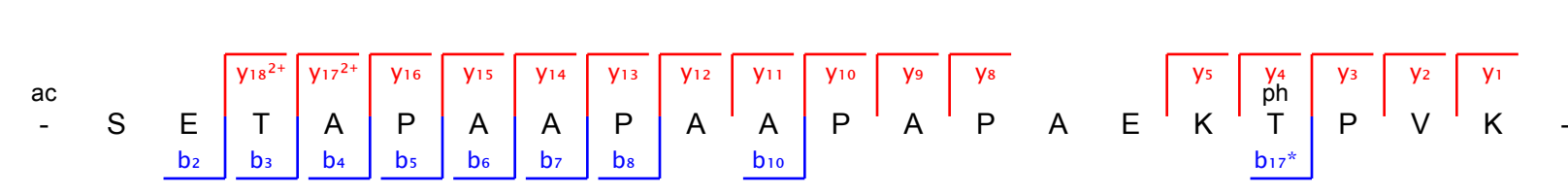
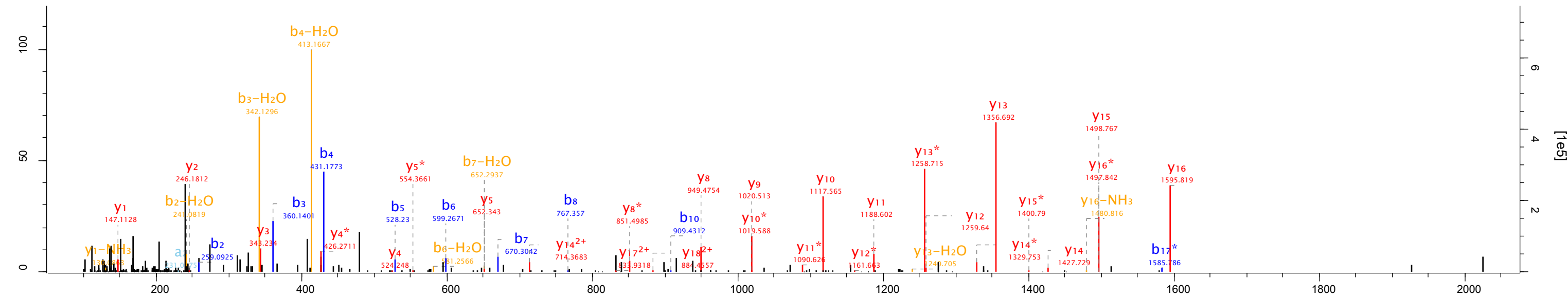


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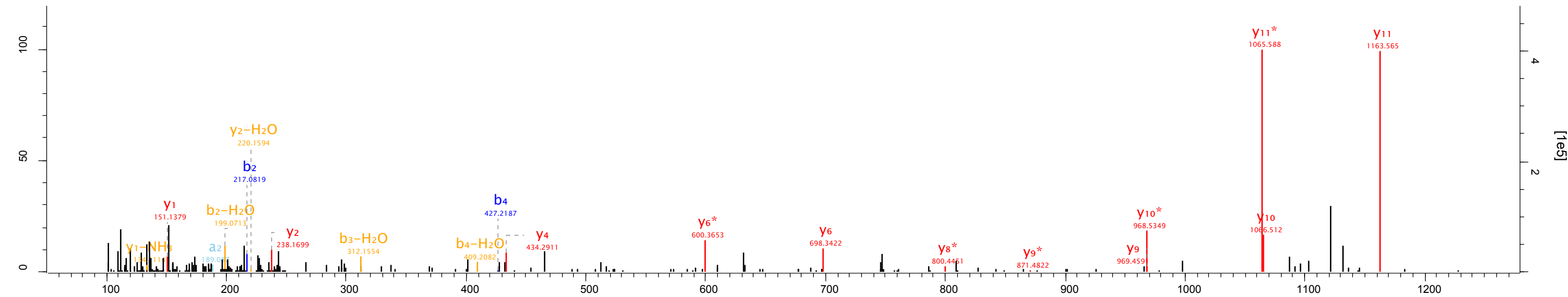




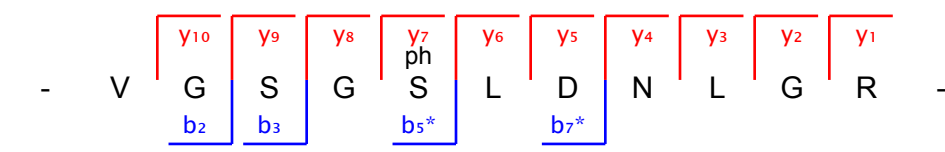
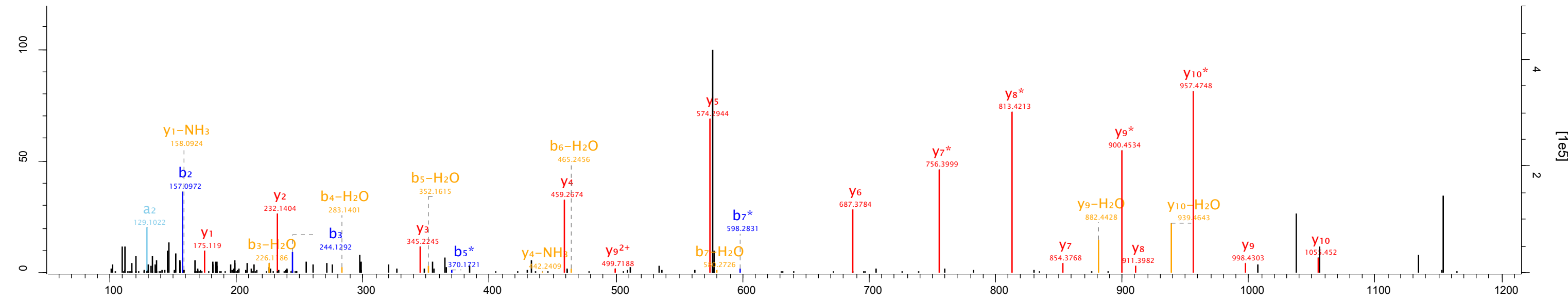
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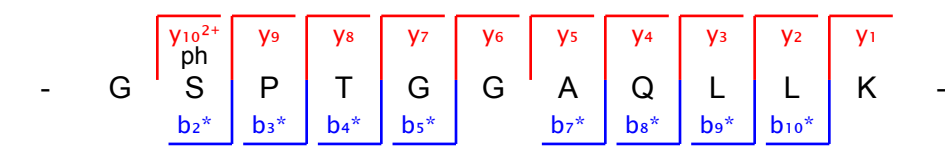
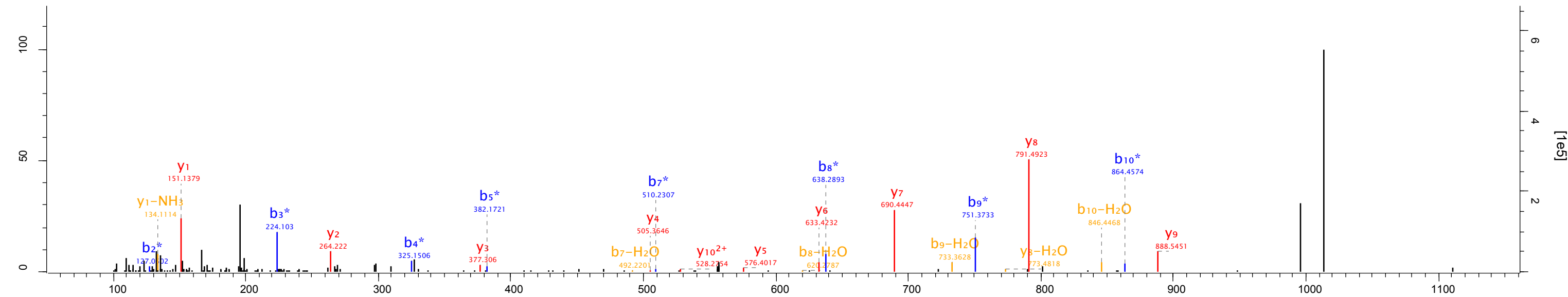
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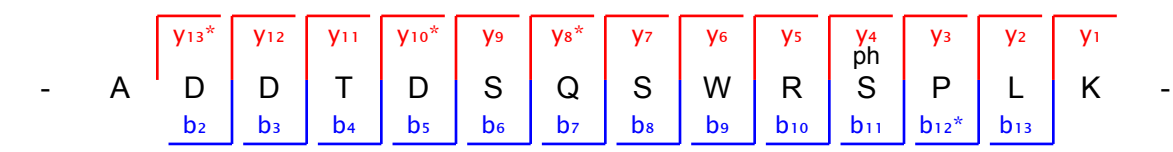
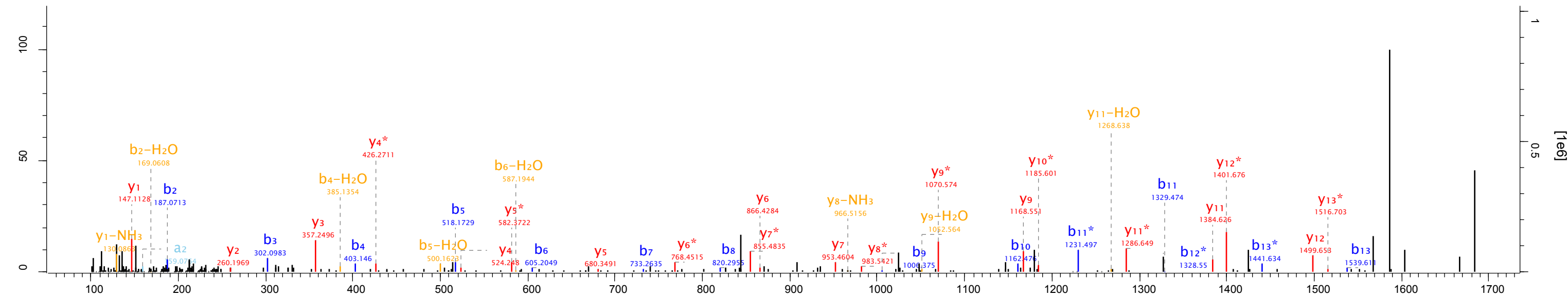
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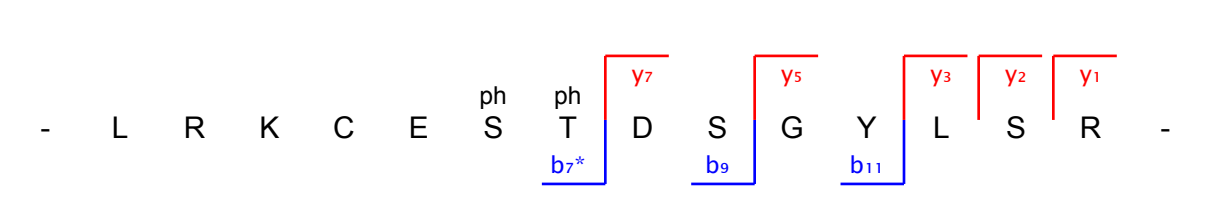
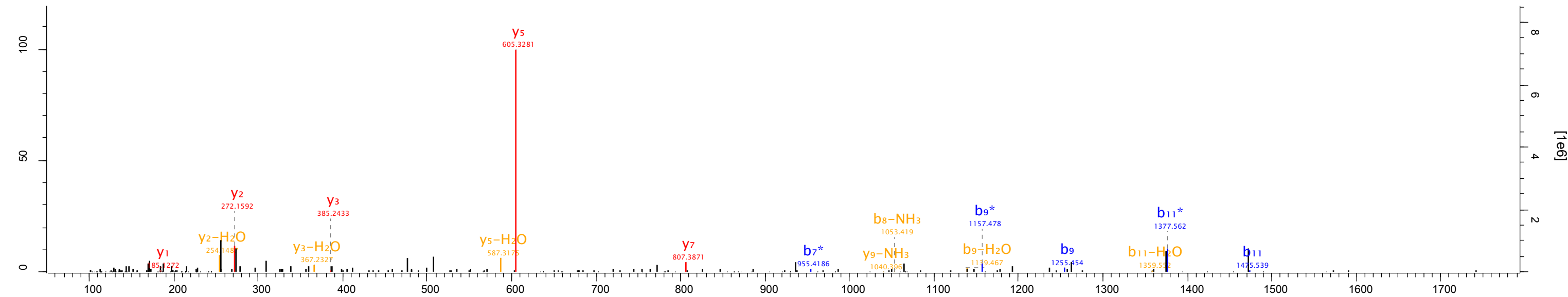
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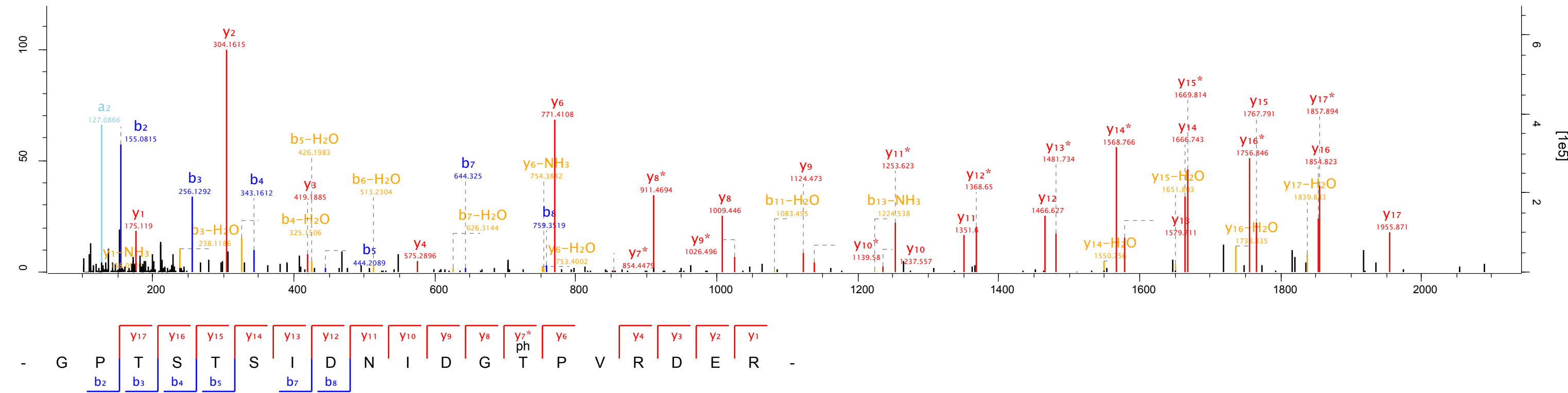


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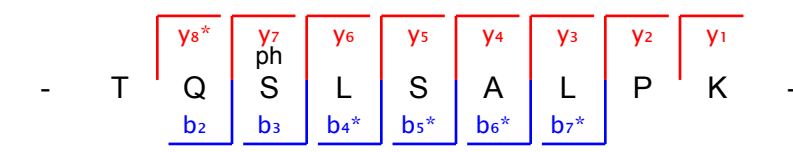
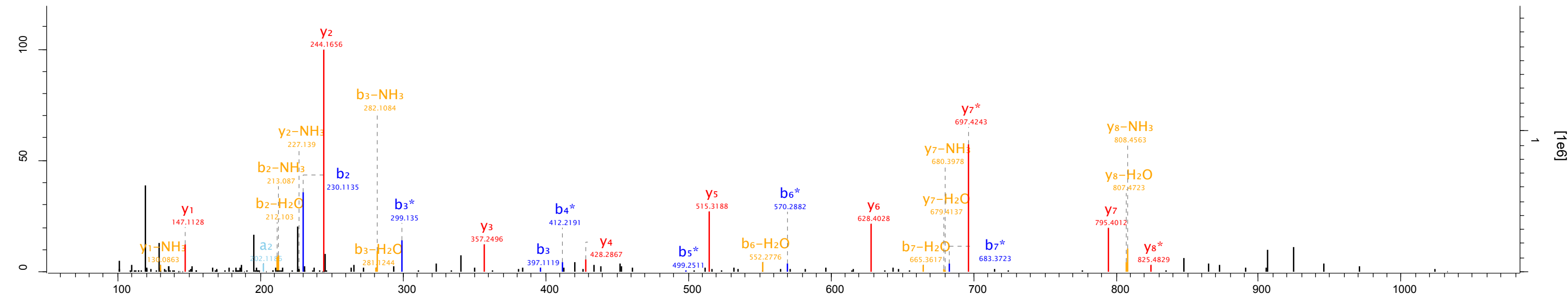


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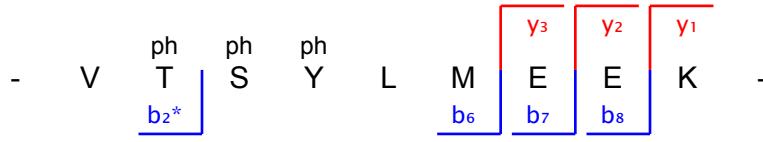
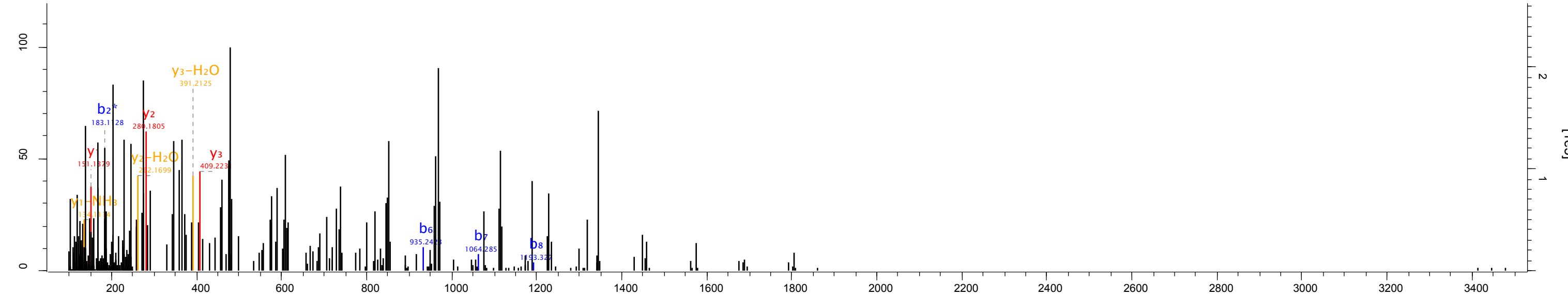




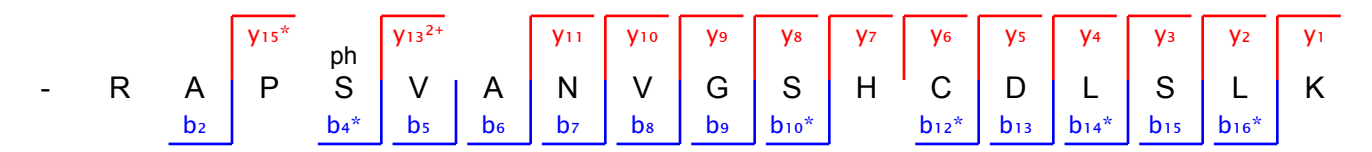
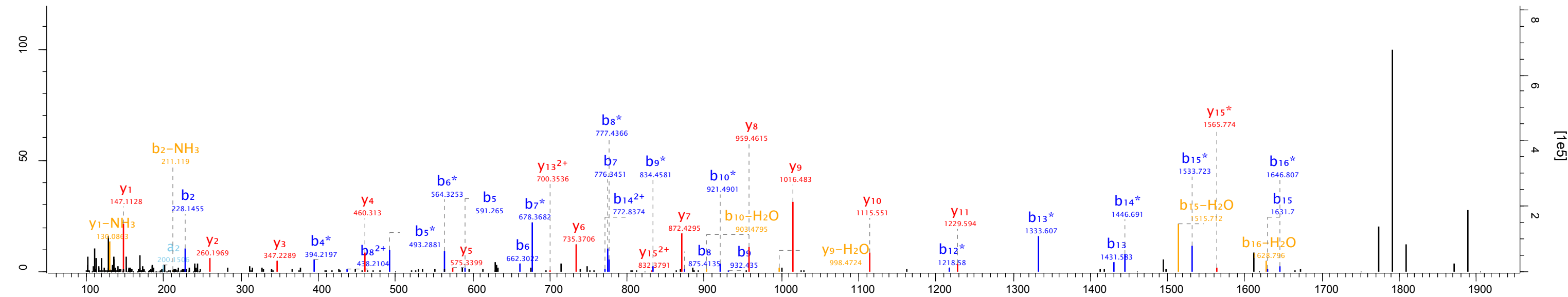
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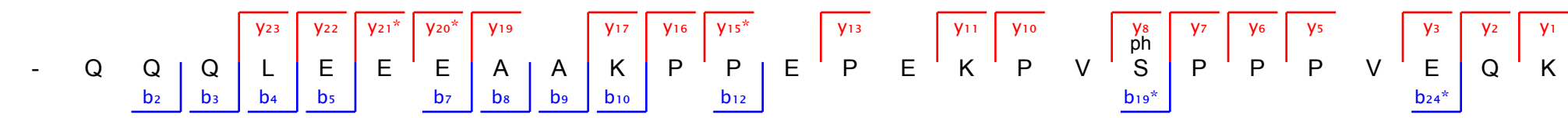
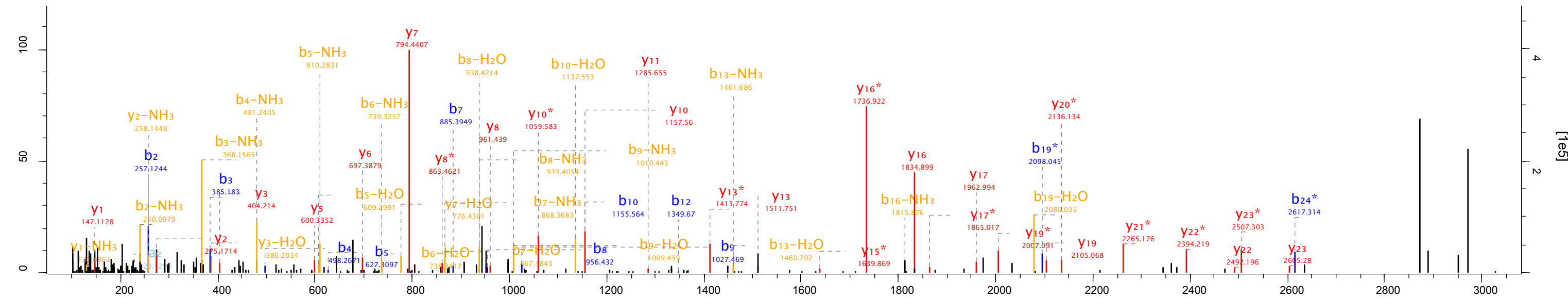
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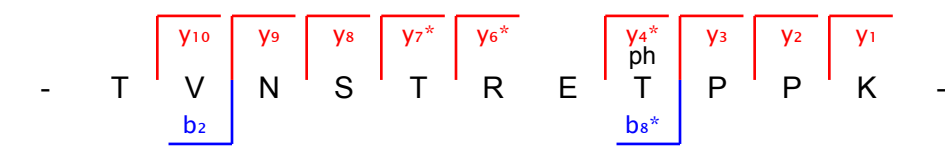
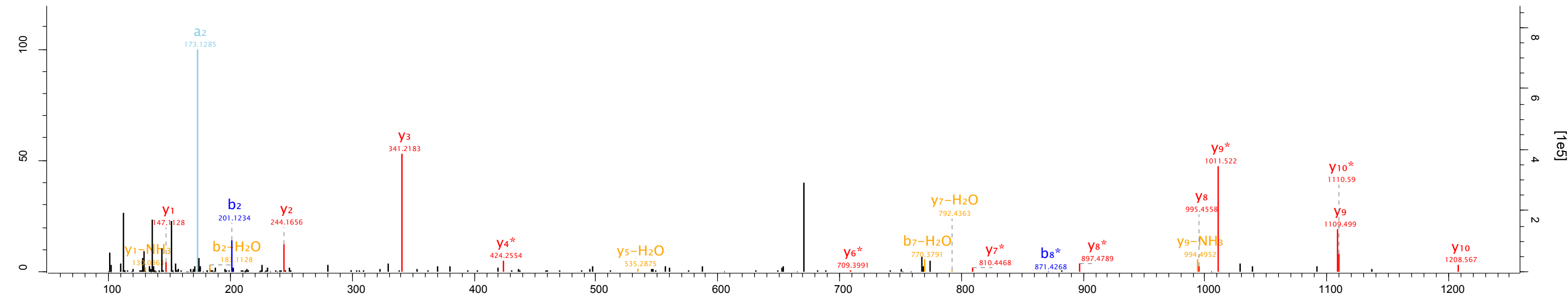
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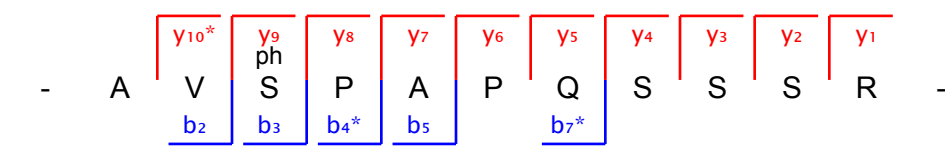
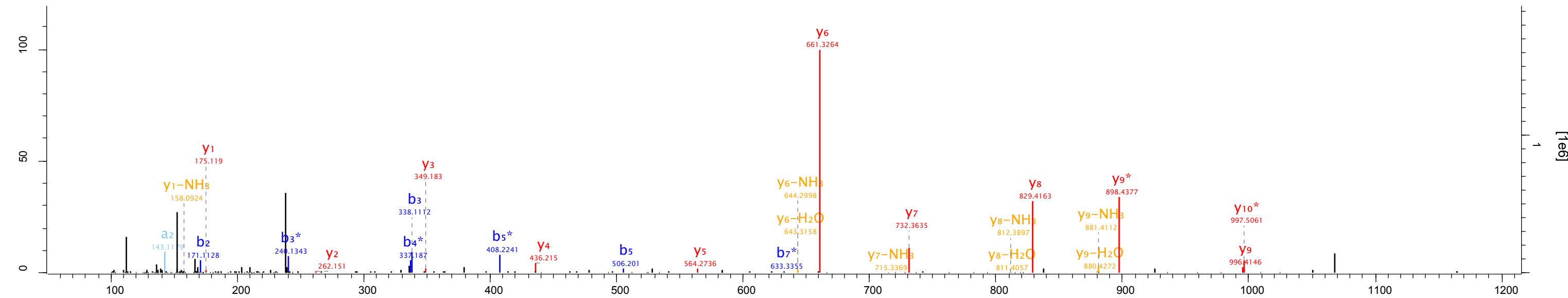
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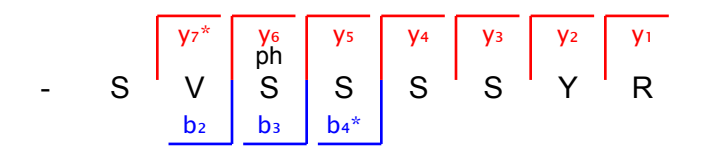
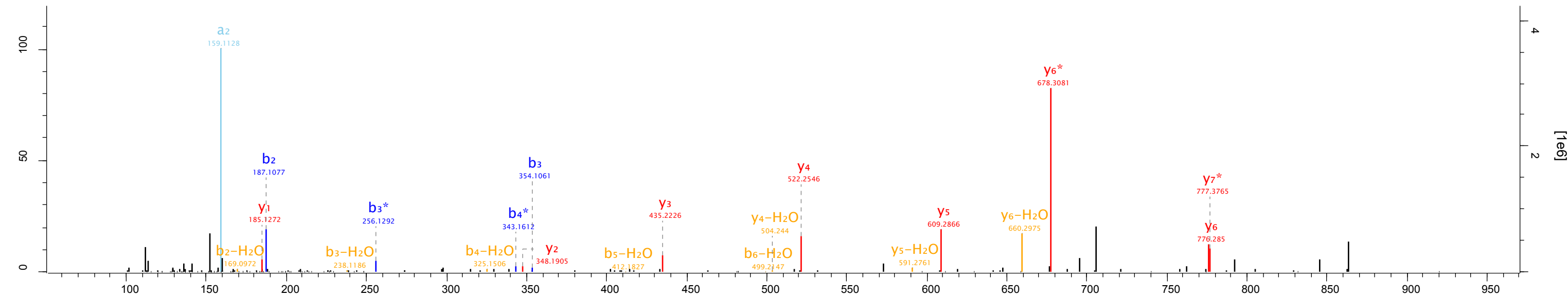
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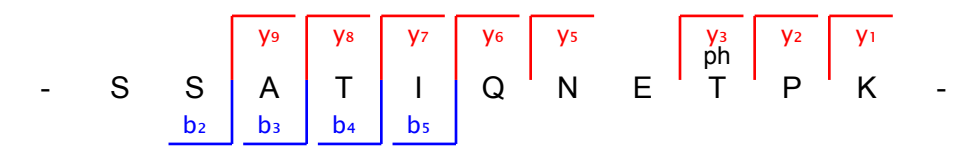
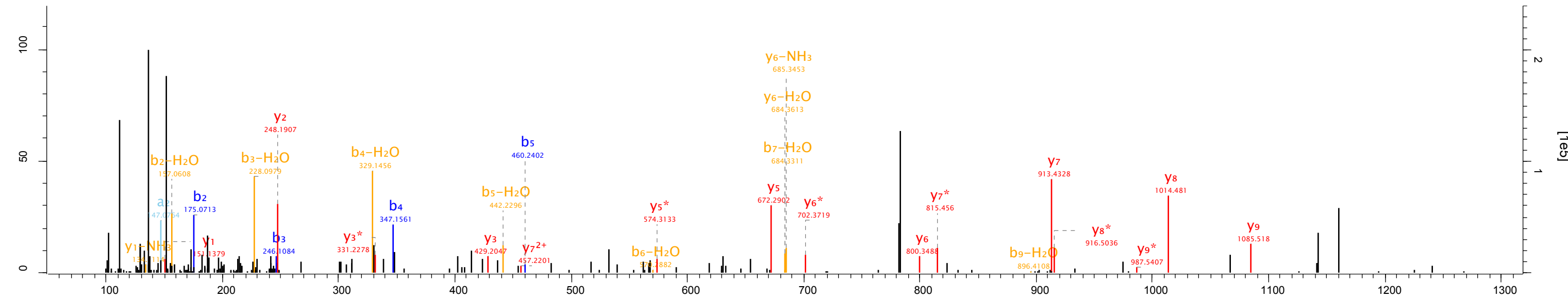
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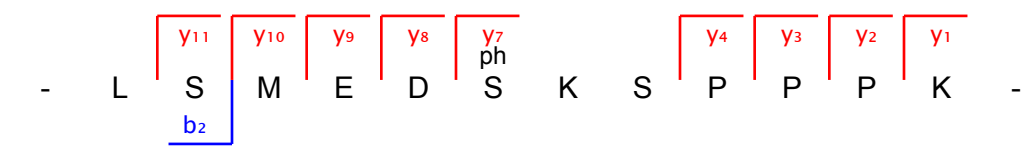
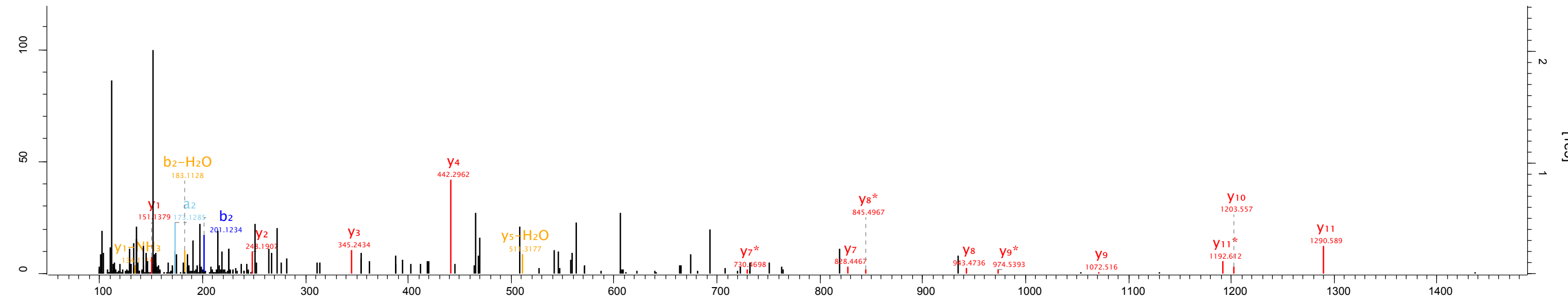
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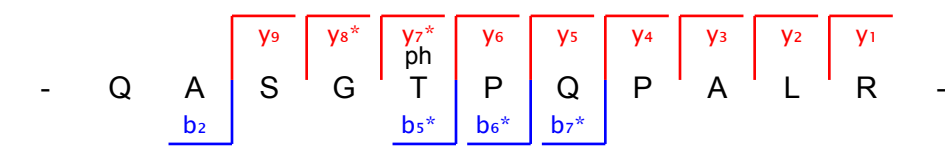
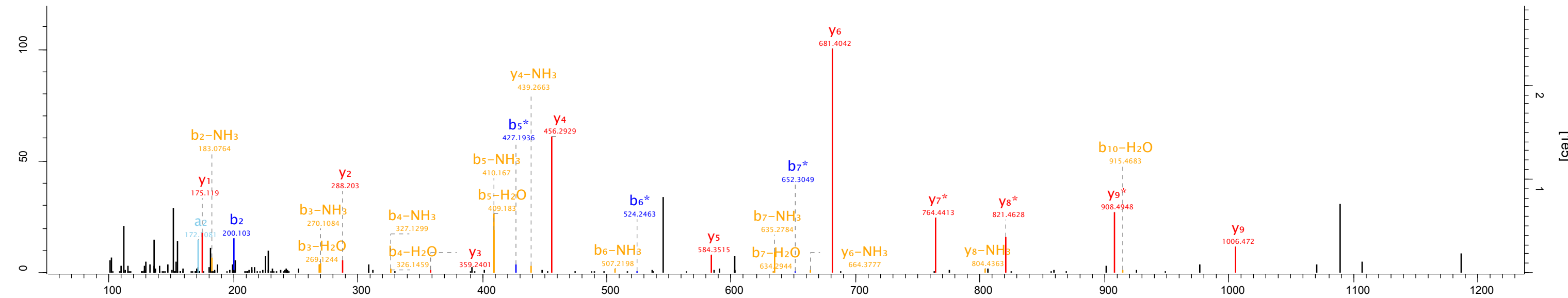
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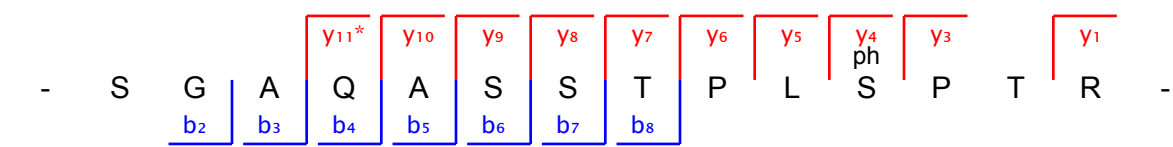
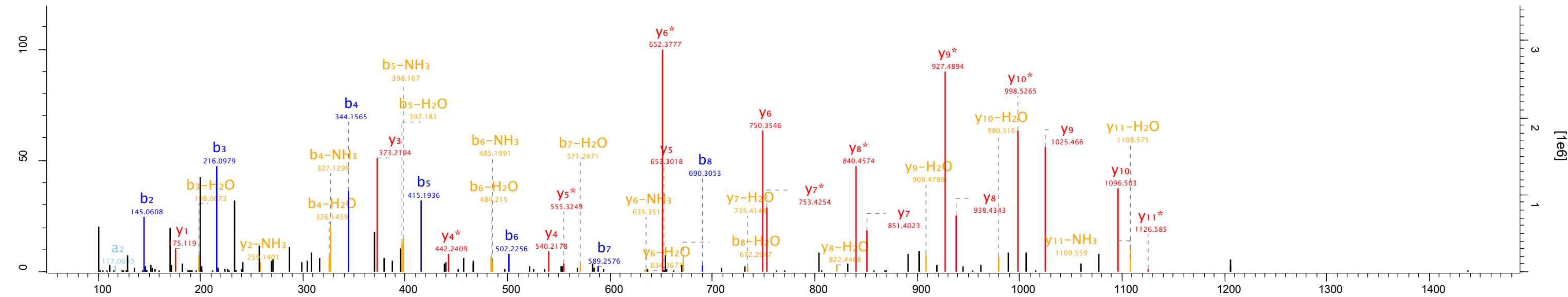
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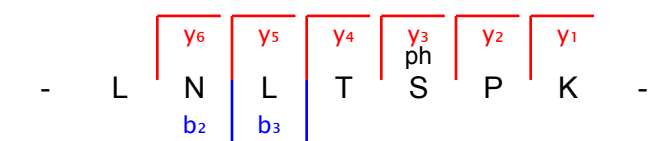
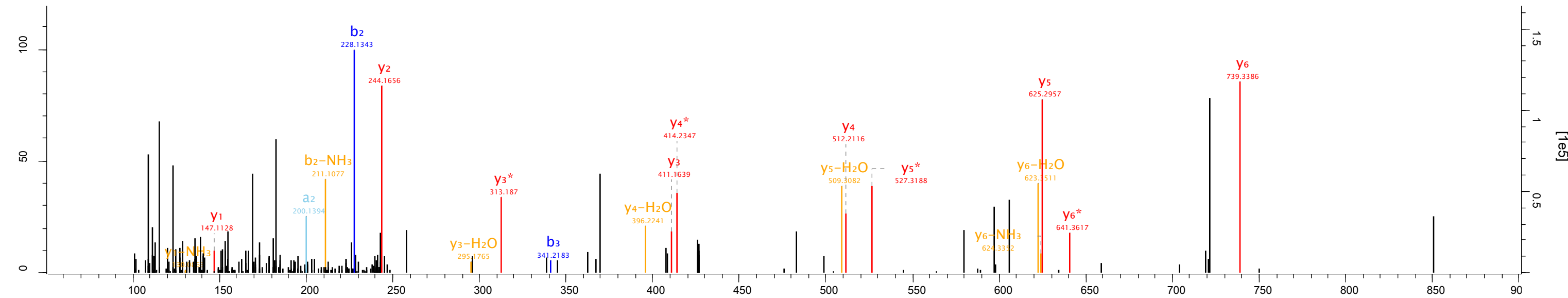


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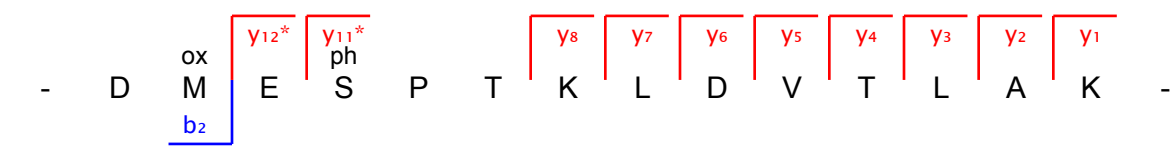
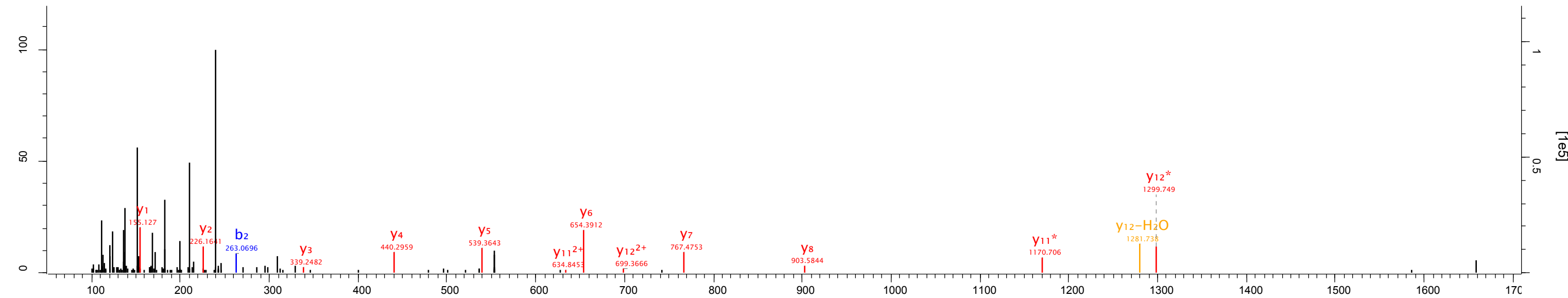


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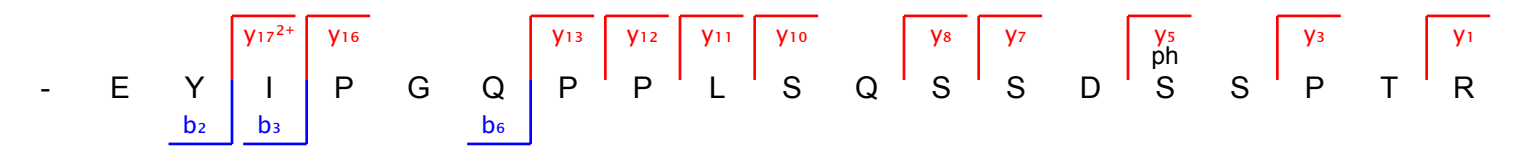
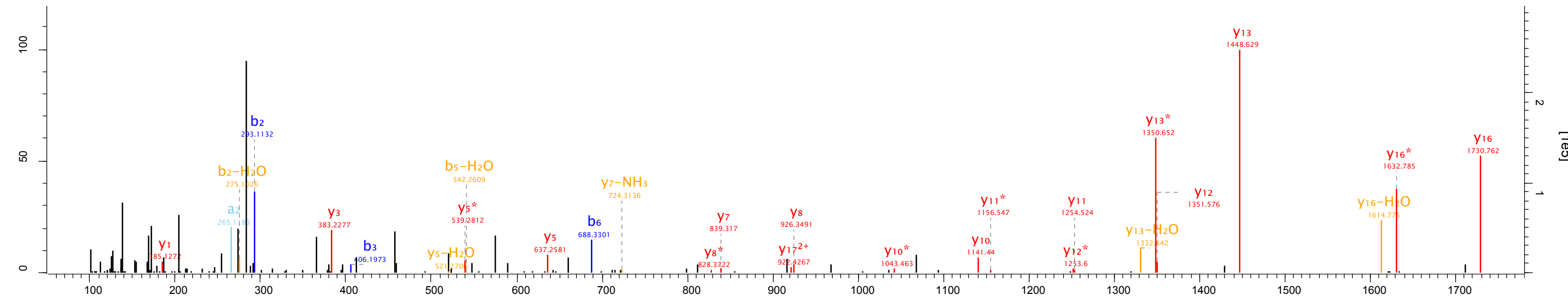


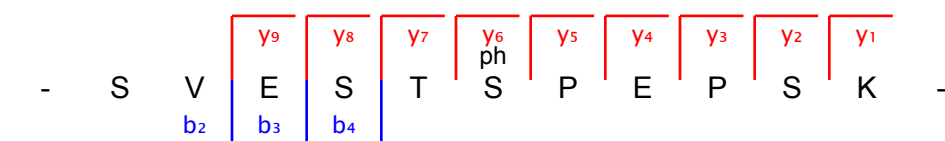
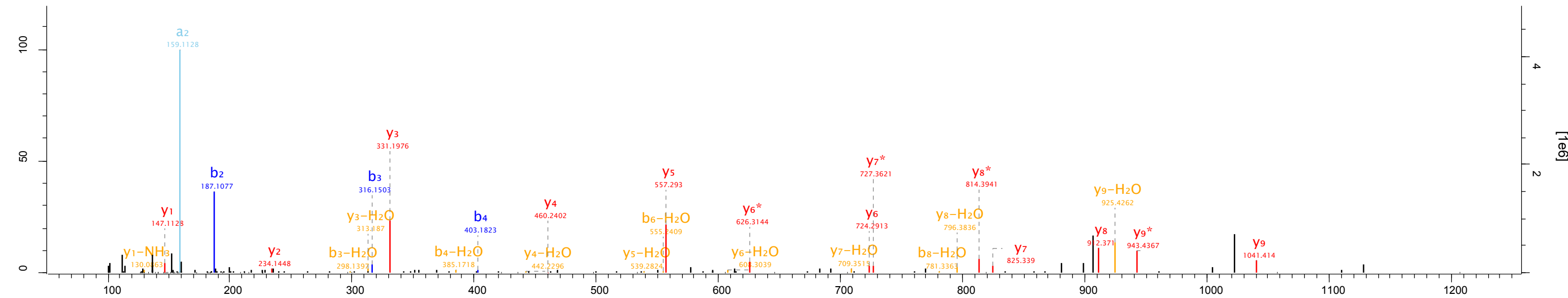


Raw file 20171215_MaS_33SR_LMH_phospho_08 Scan 10021 Method FTMS; HCD Score 52.17 m/z 554.27 Gene names MAP4

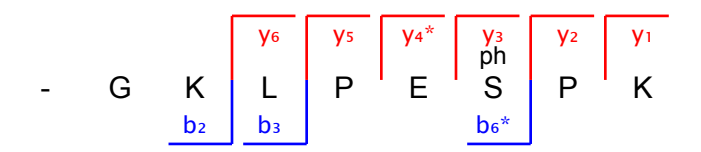
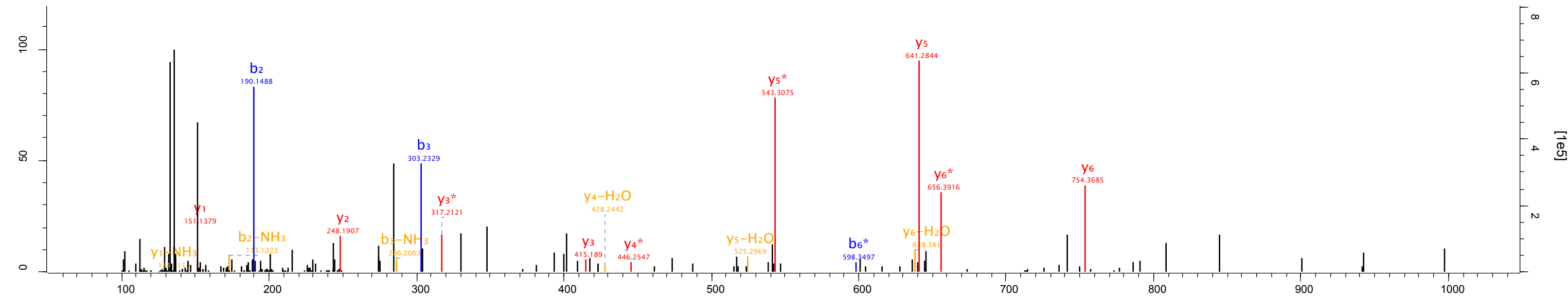


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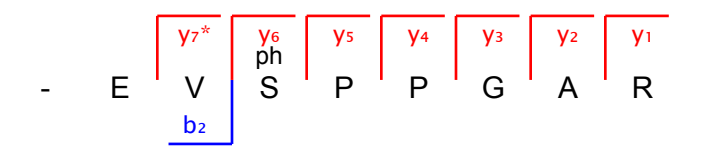
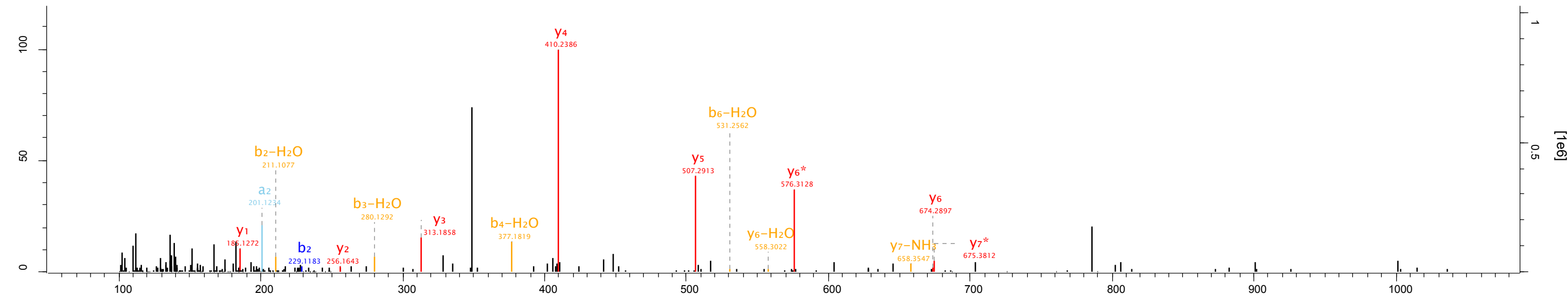




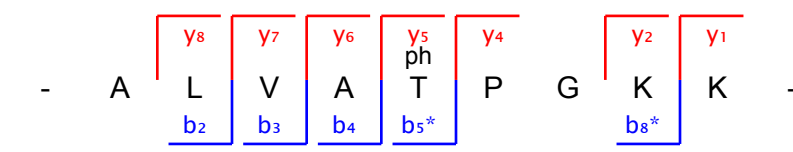
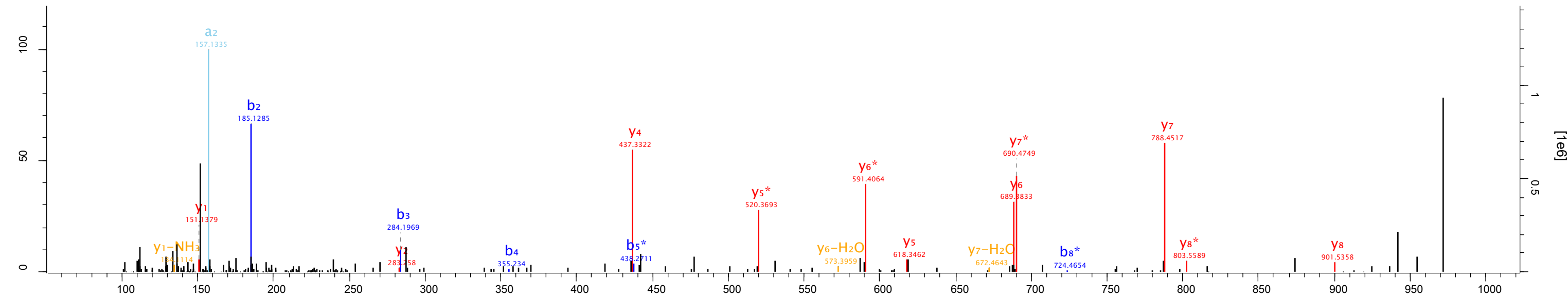
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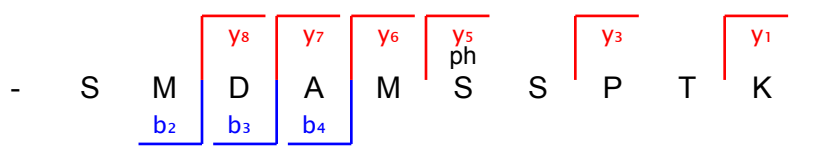
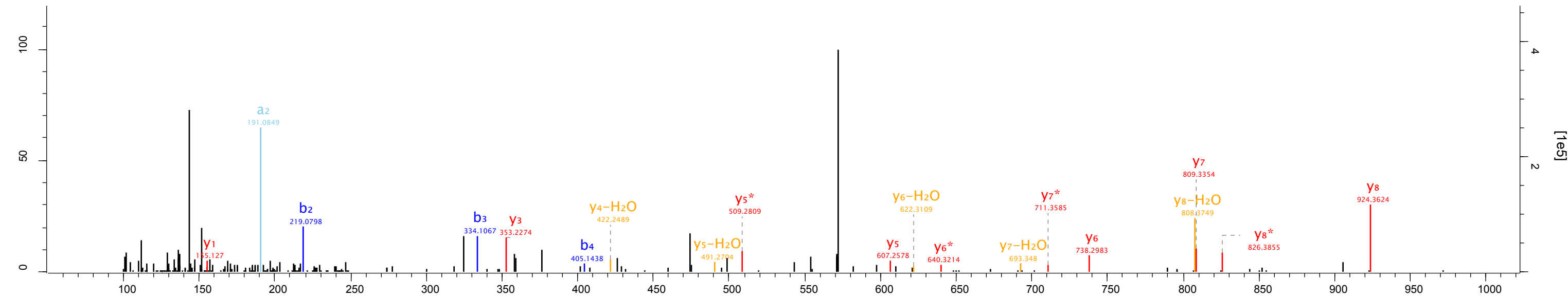
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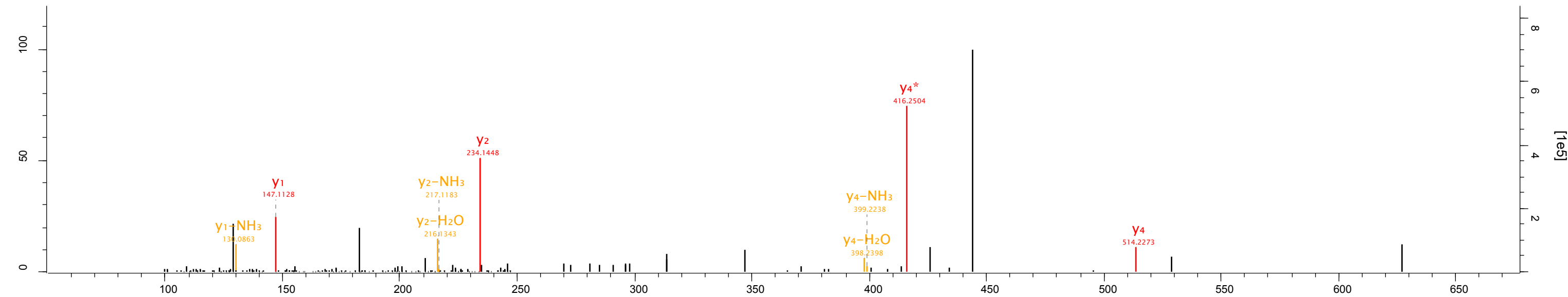
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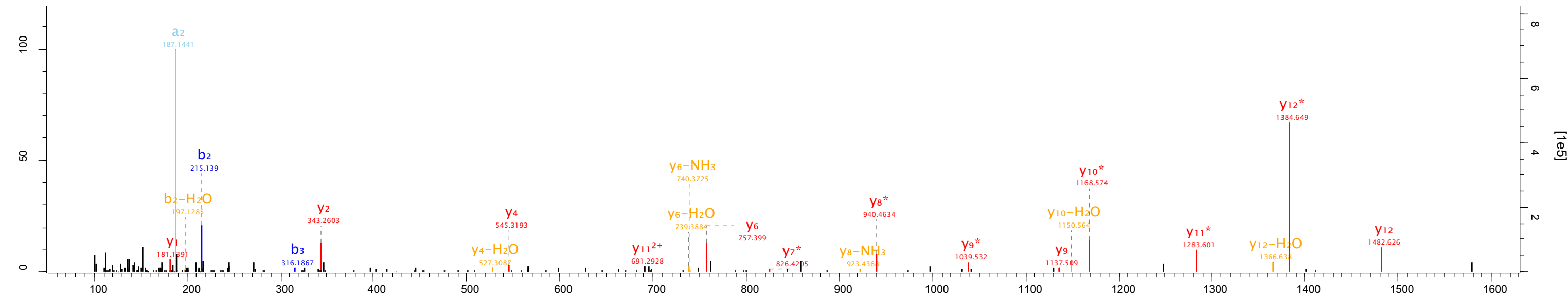
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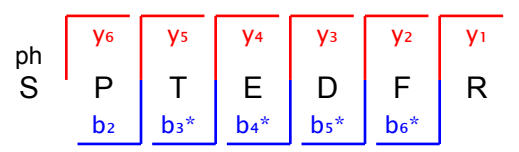
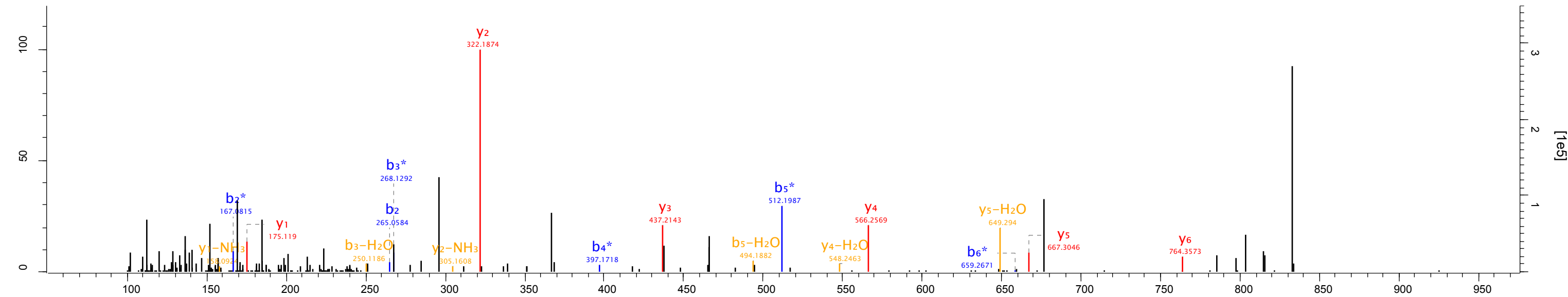
- A Q A R I S S K -

Fragmentation mapping: y4 covers I and S; y2 covers S; y1 covers K.

Raw file 20171215_MaS_33SR_LMH_phospho_08 Scan 4601 Method FTMS; HCD Score 87.43 m/z 566.26 Gene names SMARCC2



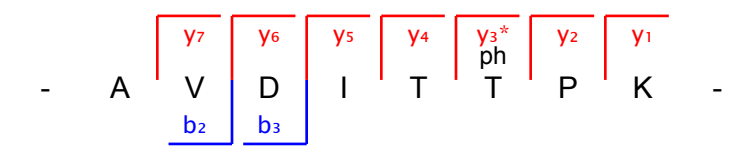
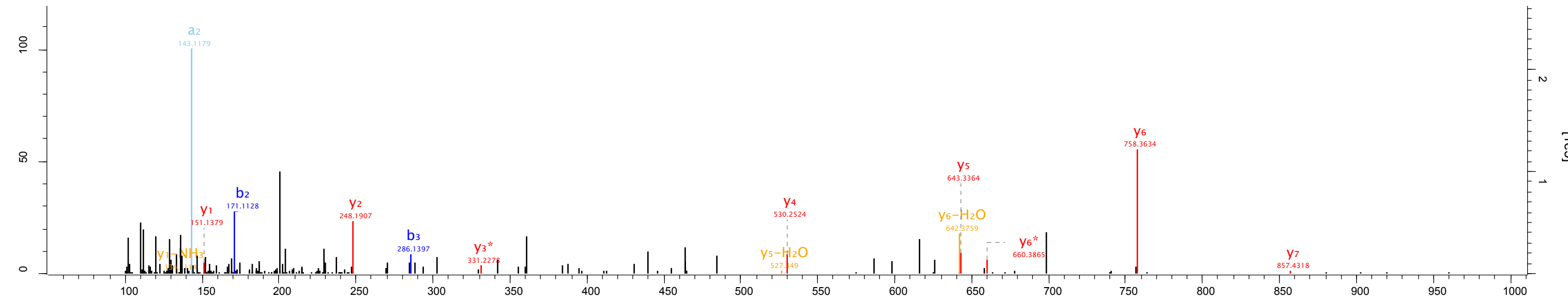
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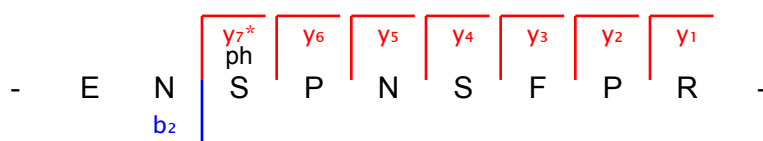
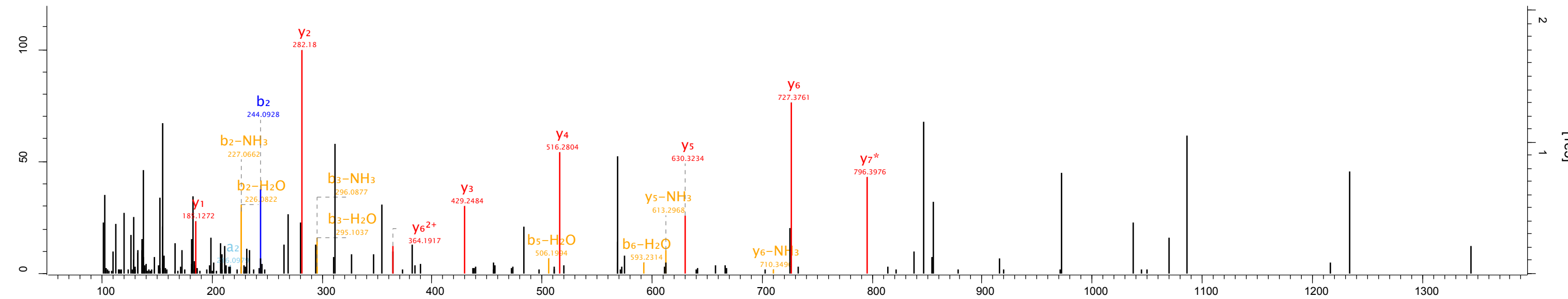
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20171215_MaS_33SR_LMH_phospho_08

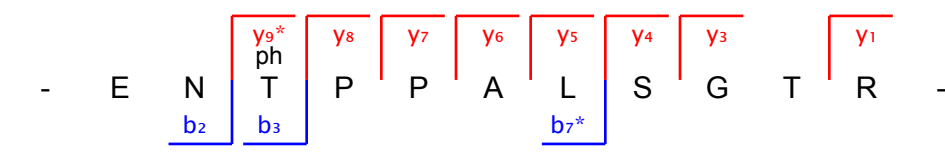
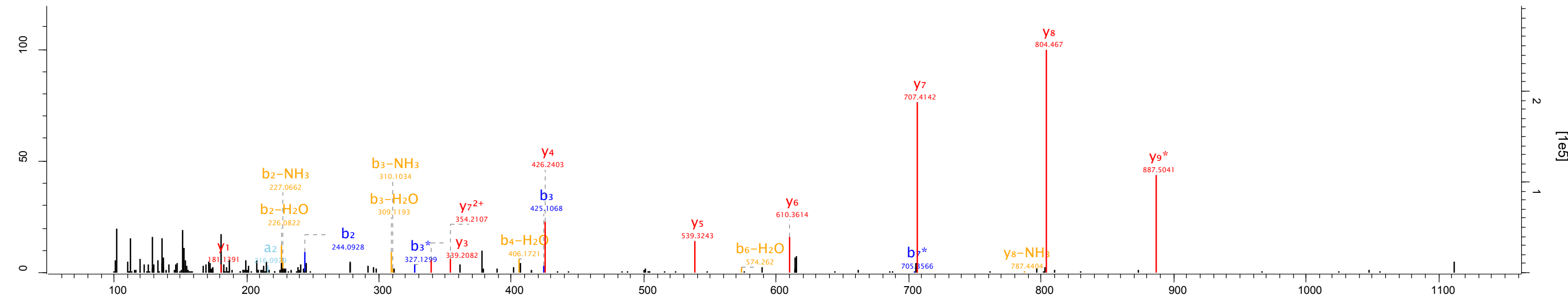
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5411	FTMS; HCD	64.73	464.74	PSIP1



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 Scan: 5461 Method: FTMS; HCD Score: 56.92 m/z: 569.23 Gene names: KIAA1468

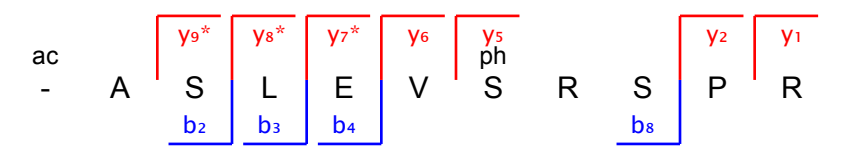
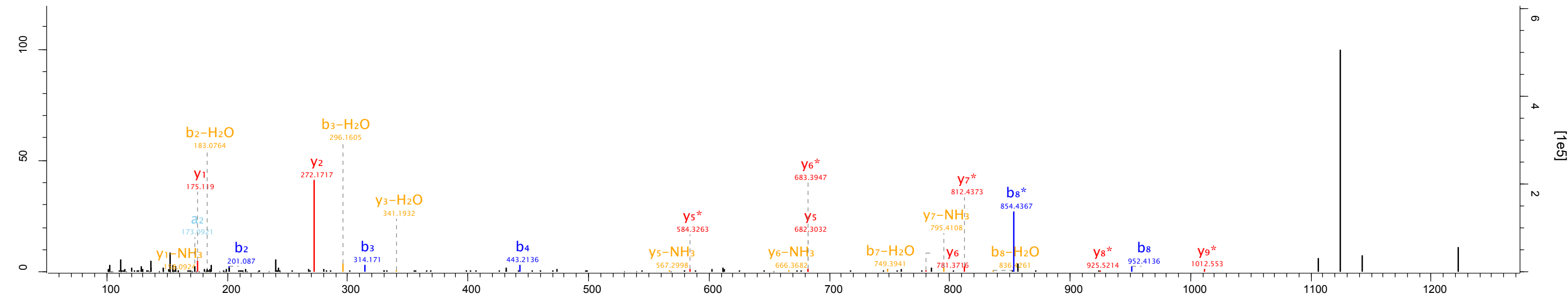


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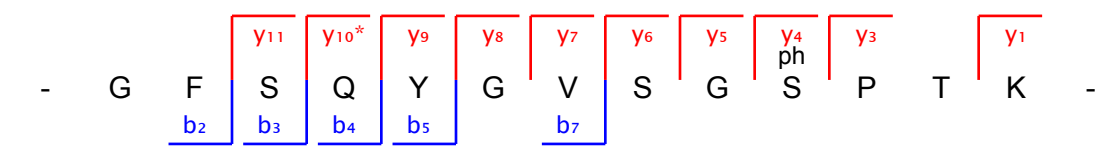
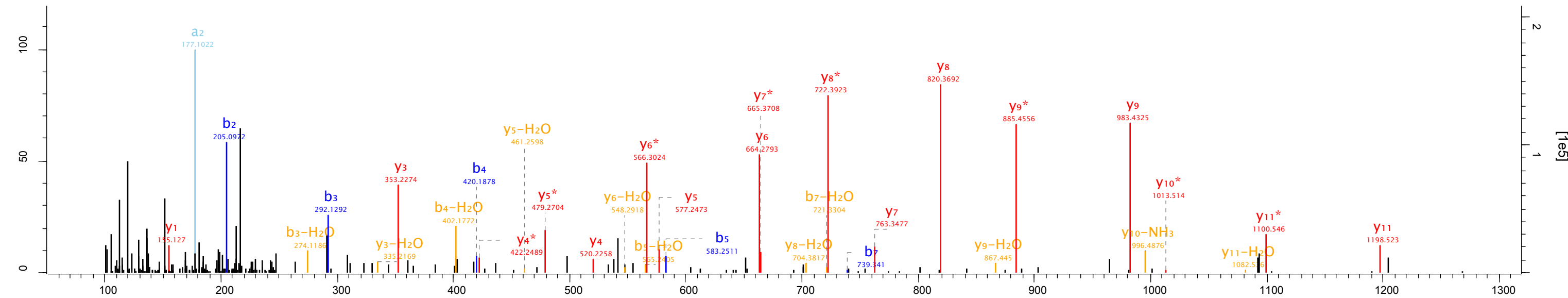


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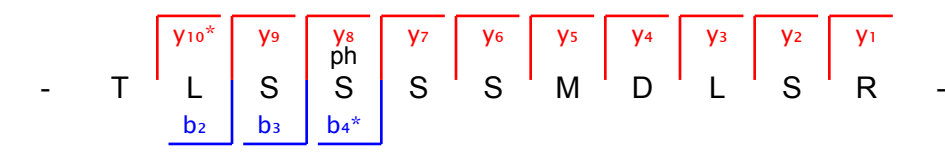
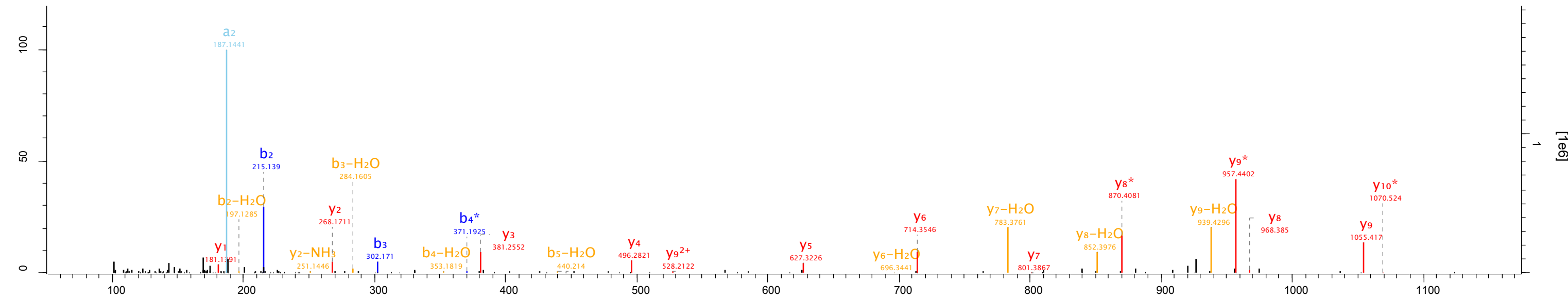
20171215_MaS_33SR_LMH_phospho_08



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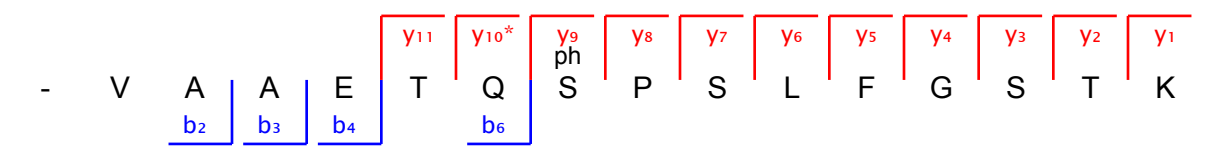
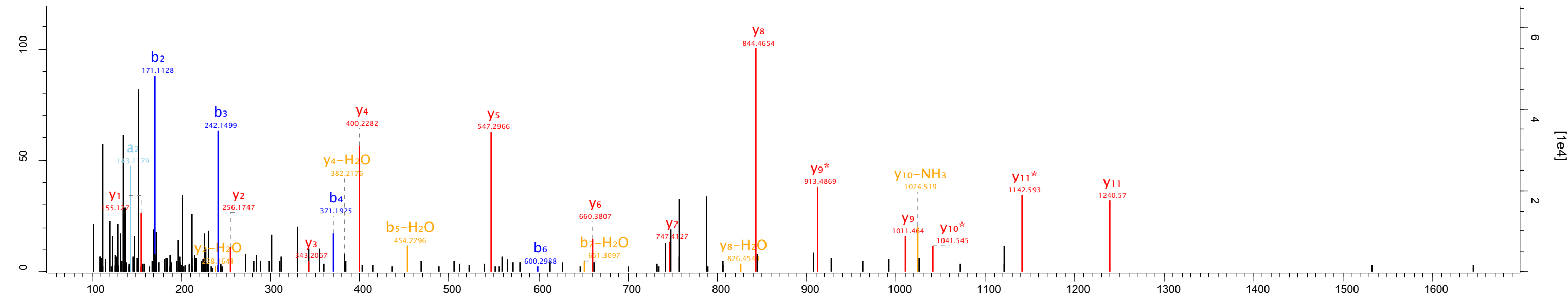


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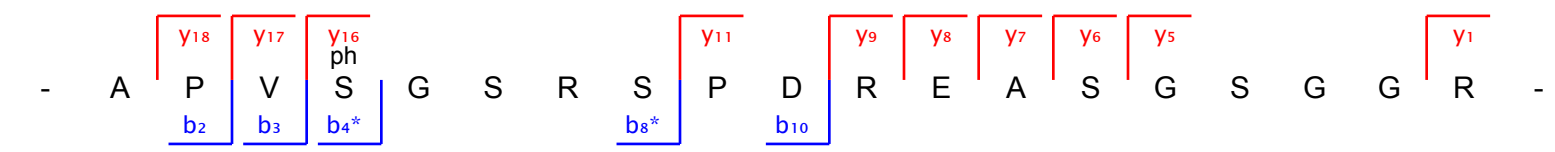
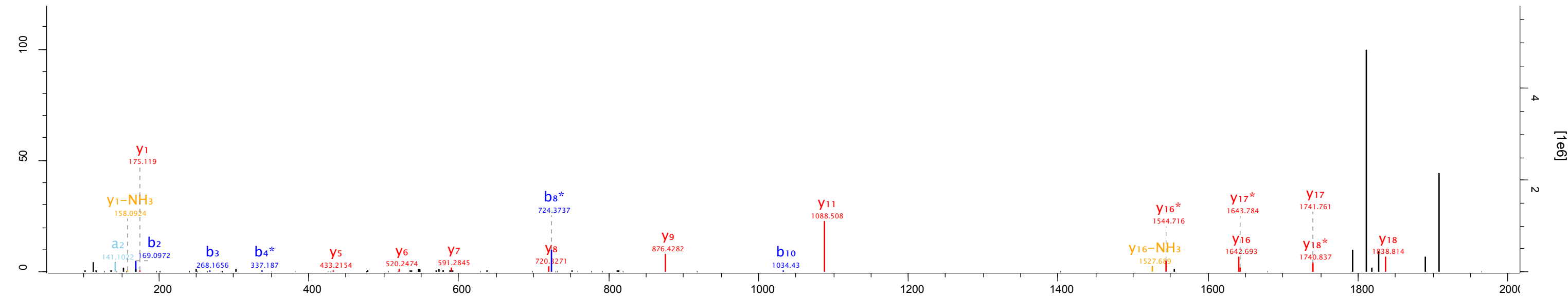


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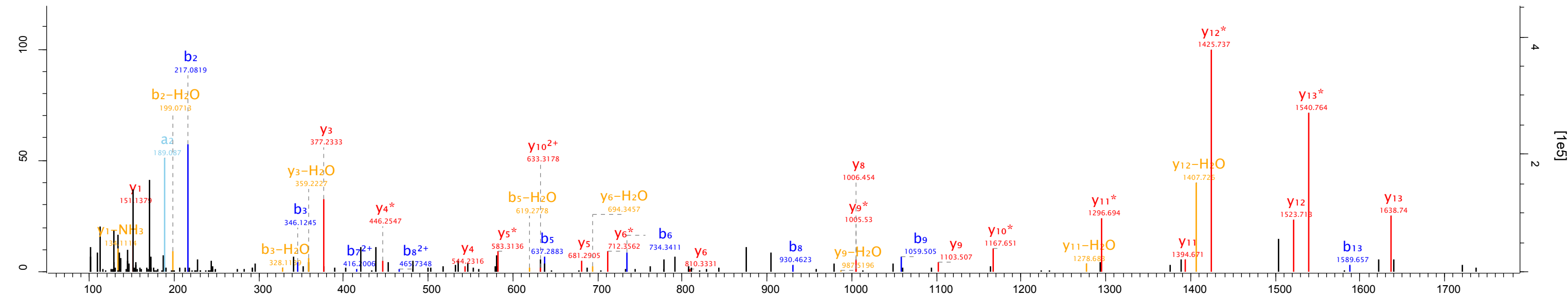
20171215_MaS_33SR_LMH_phospho_08



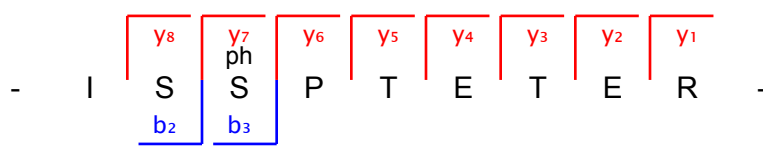
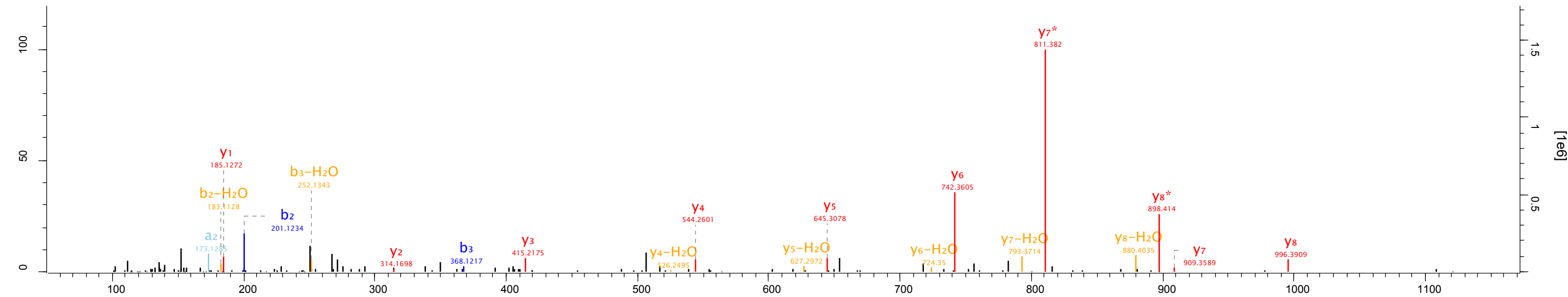
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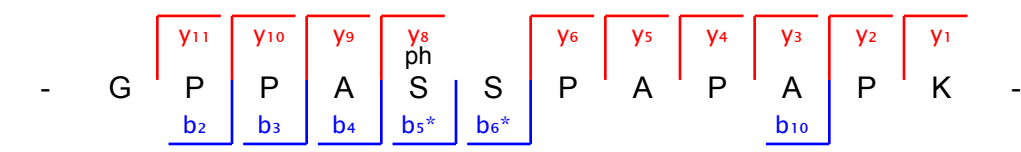
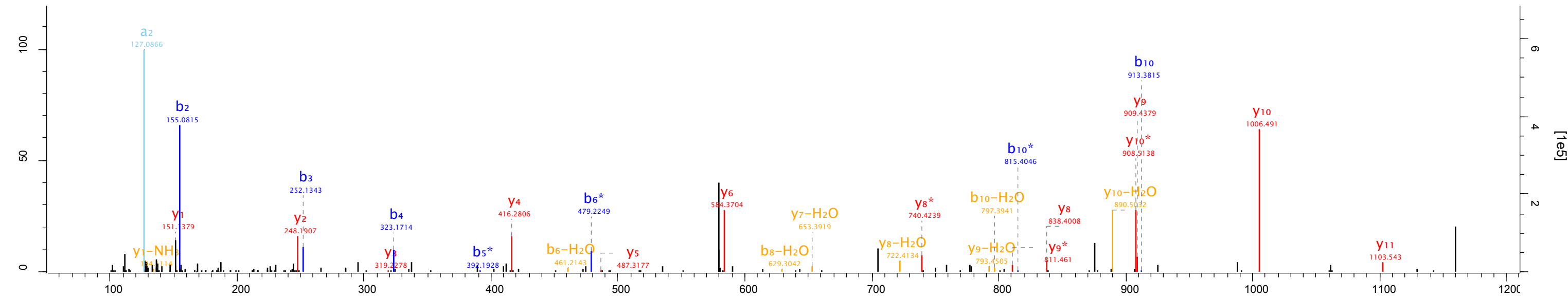


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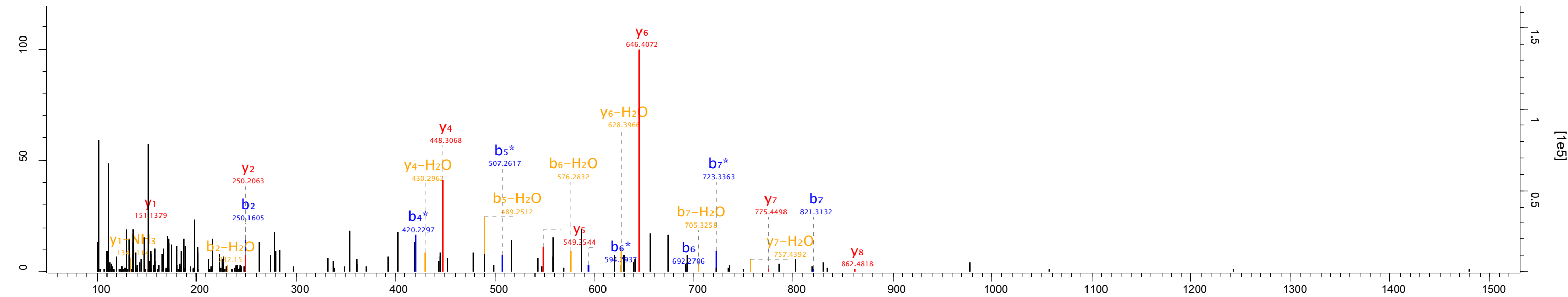


20171215_MaS_33SR_LMH_phospho_09

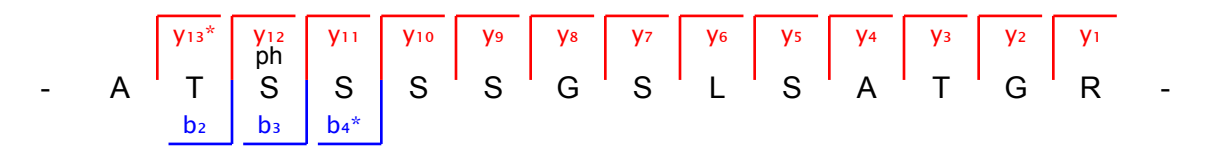
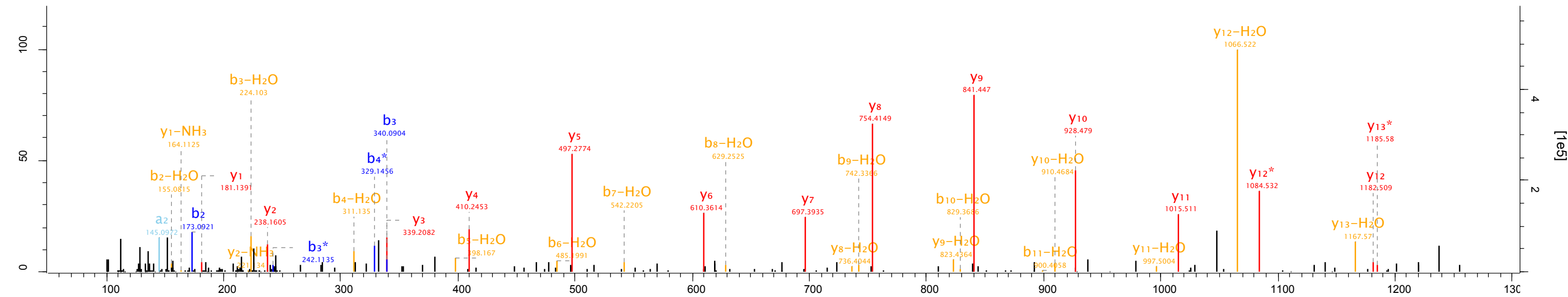
2801 FTMS; HCD 97.8 580.79 ZYX



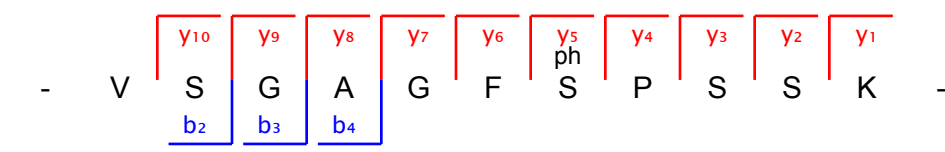
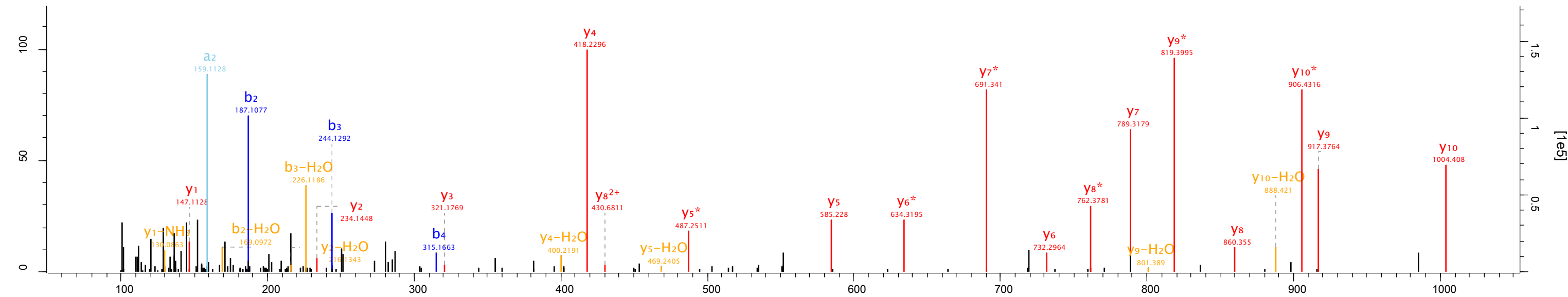
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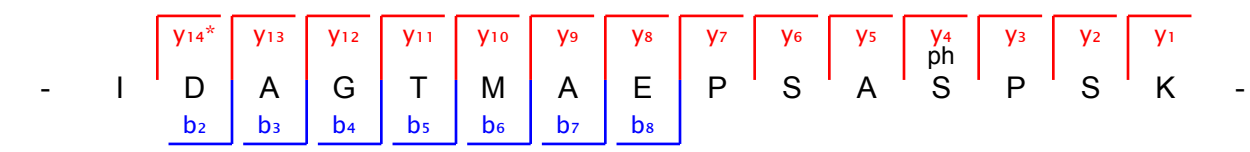
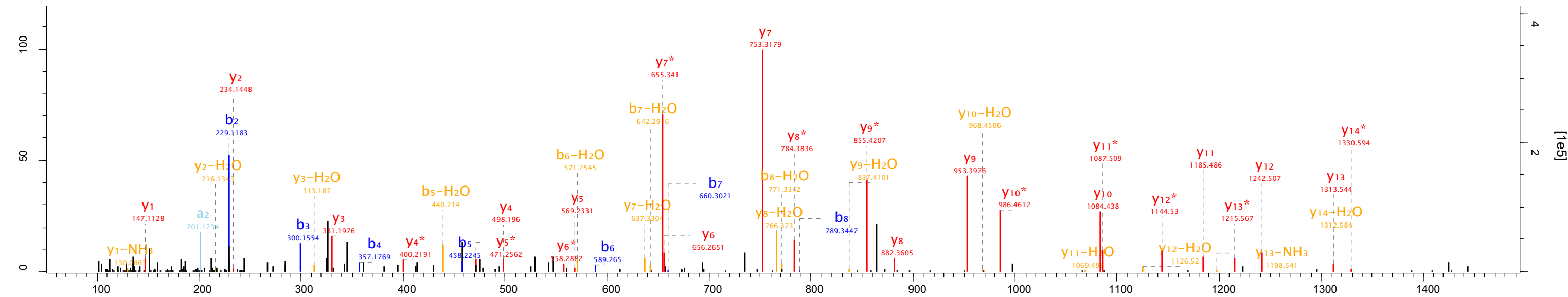
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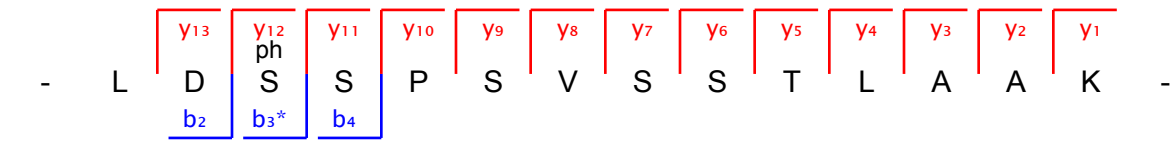
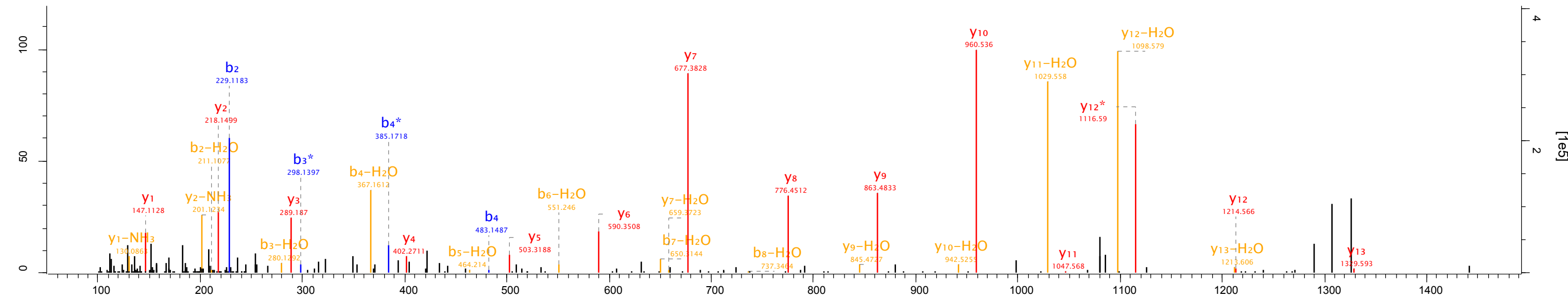


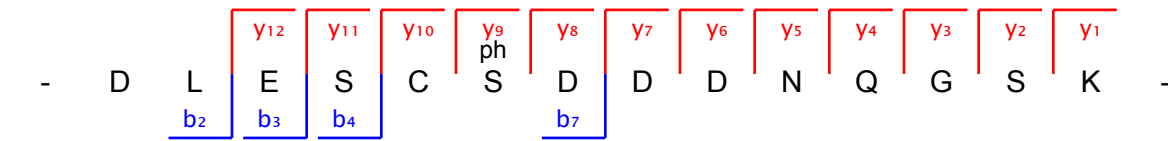
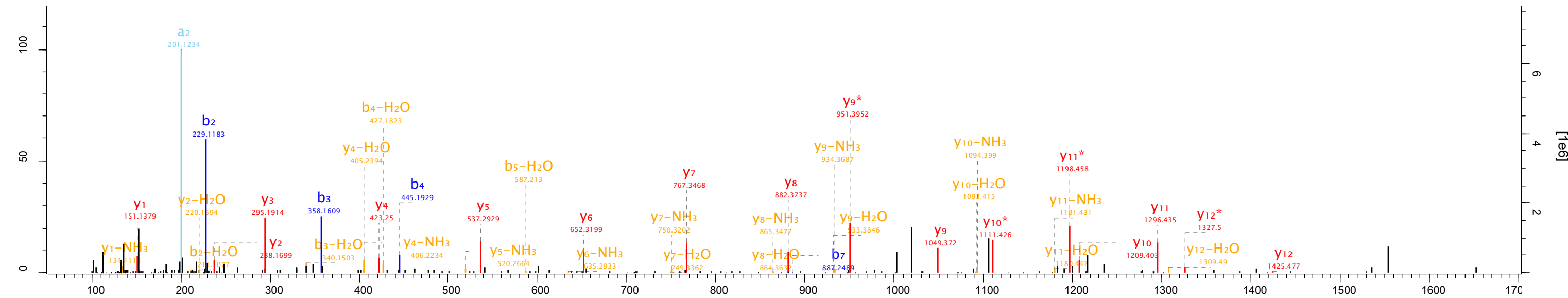
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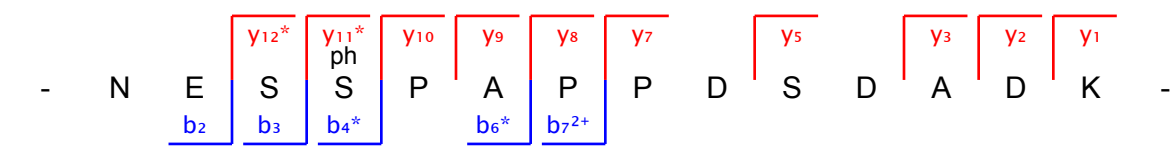
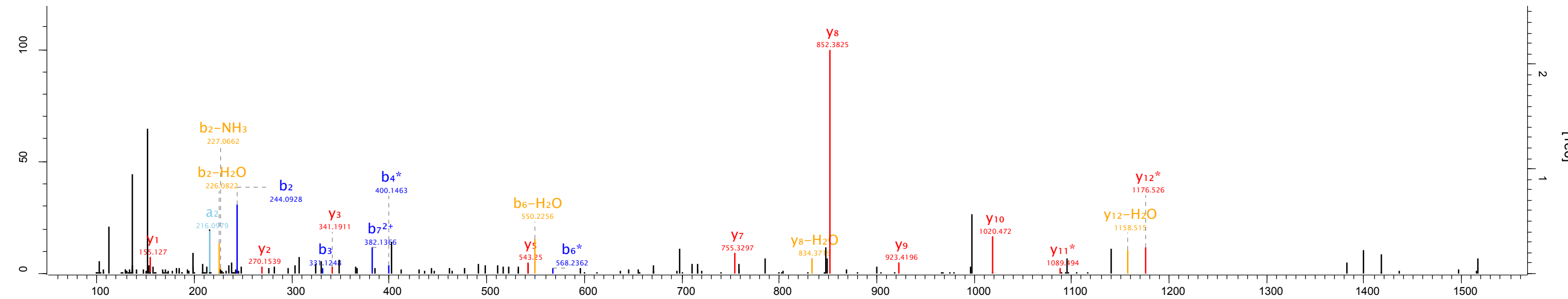




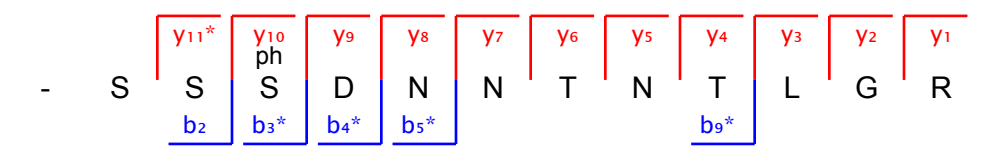
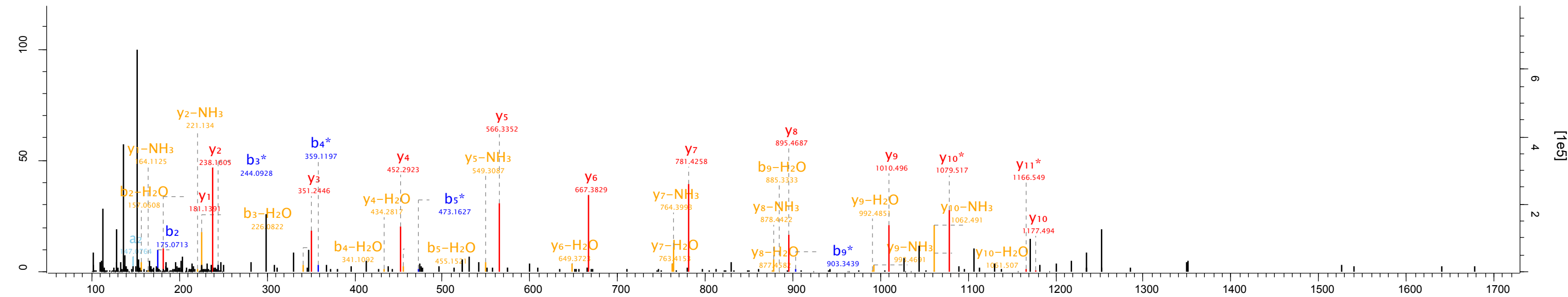
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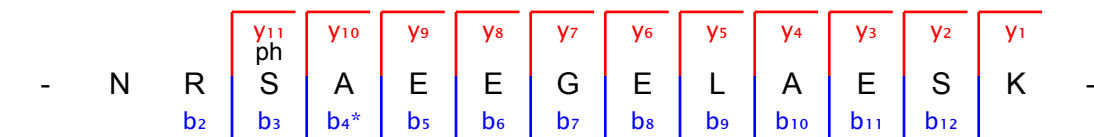
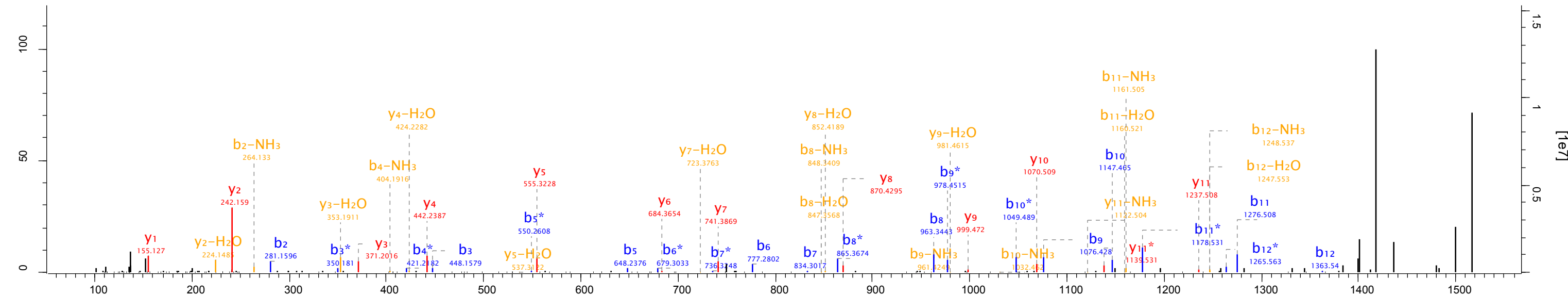
20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
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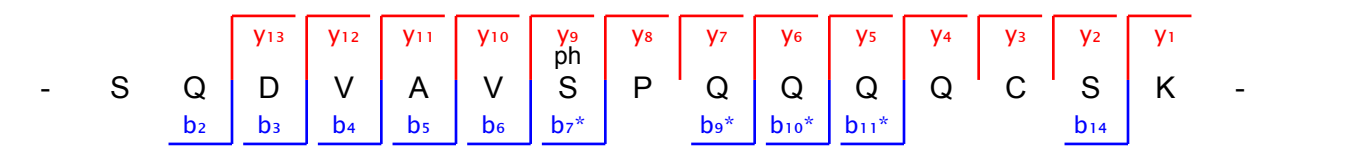
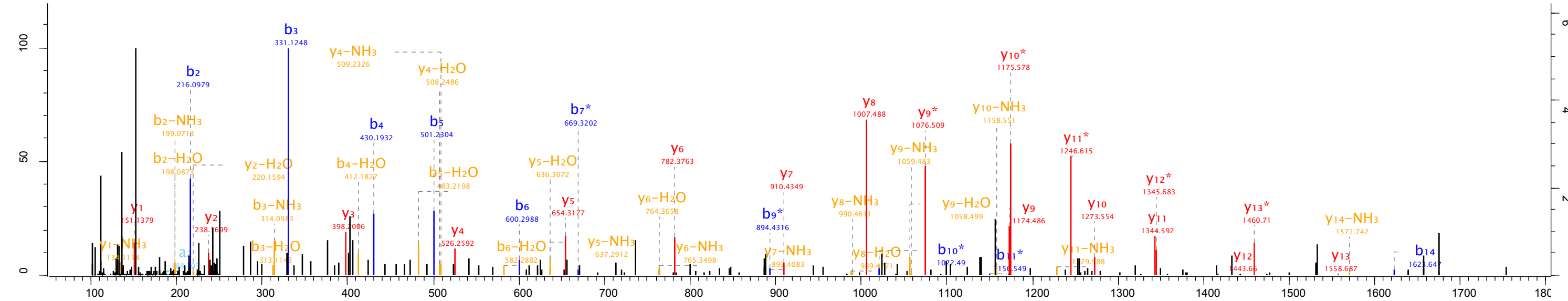
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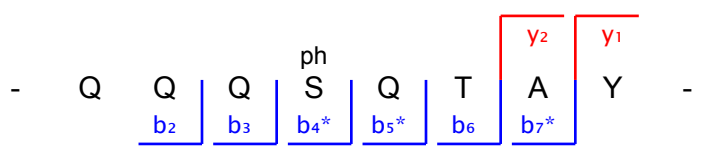
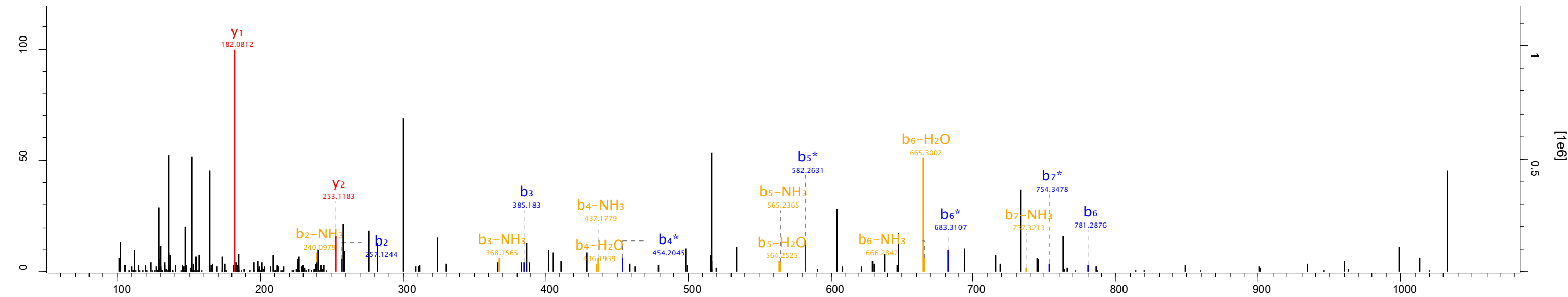


20171215_MaS_33SR_LMH_phospho2_01

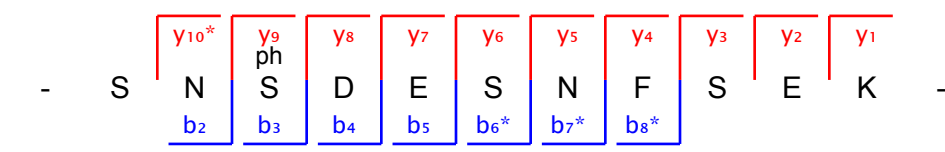
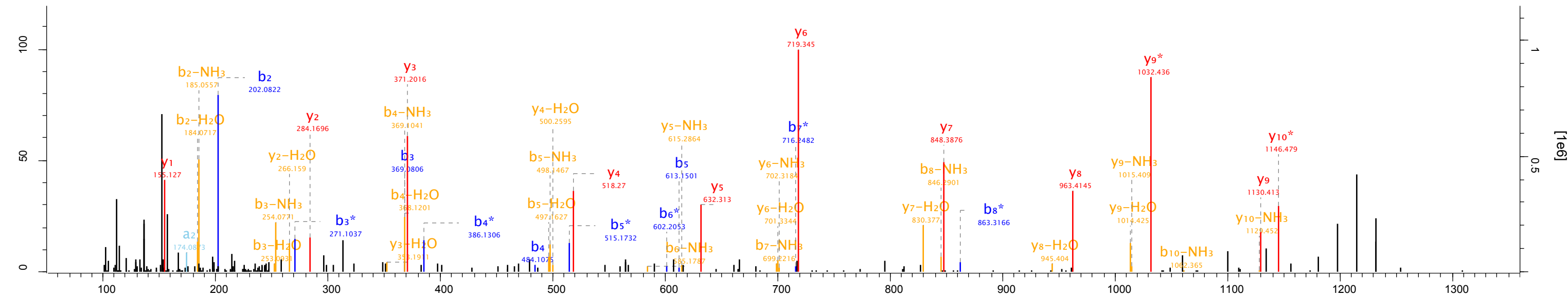
3541 FTMS; HCD 138.04 887.89 EDC3



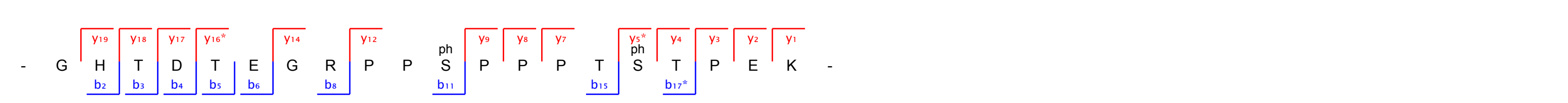
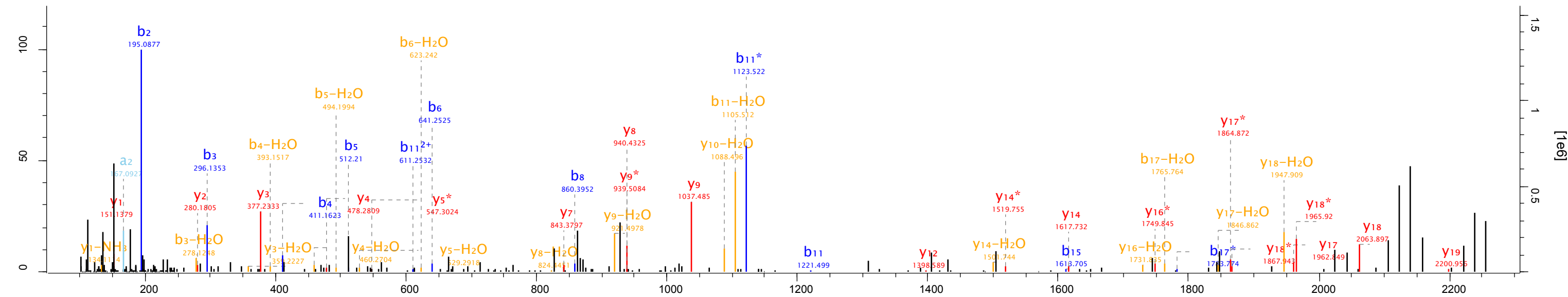
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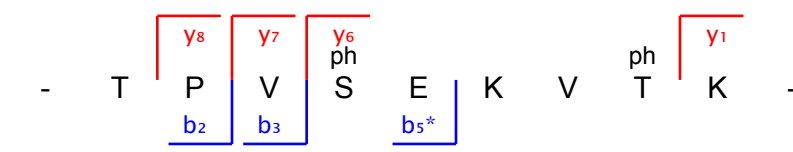
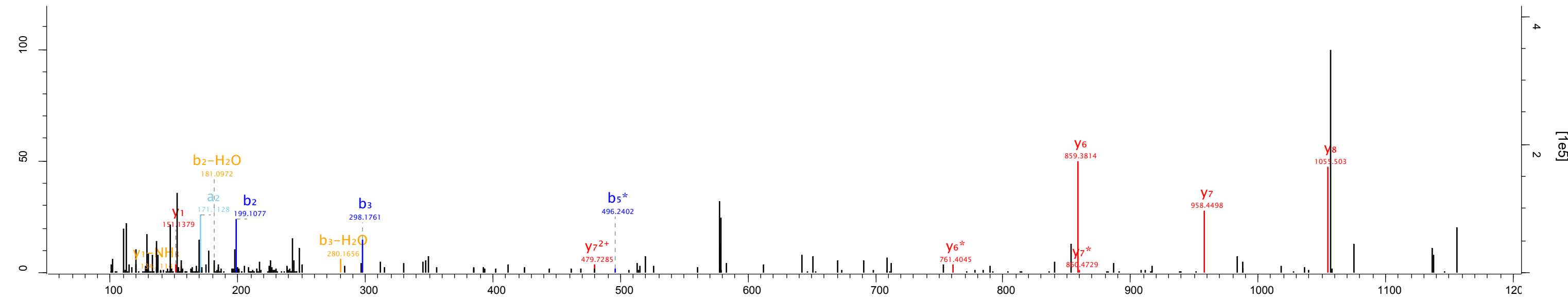
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 Scan: 3591 Method: FTMS; HCD Score: 193.19 m/z: 666.25 Gene names: BCL10



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 Scan: 3881 Method: FTMS; HCD Score: 134 m/z: 753.66 Gene names: HSF1



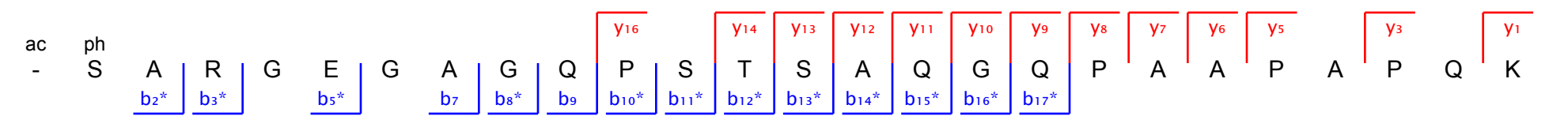
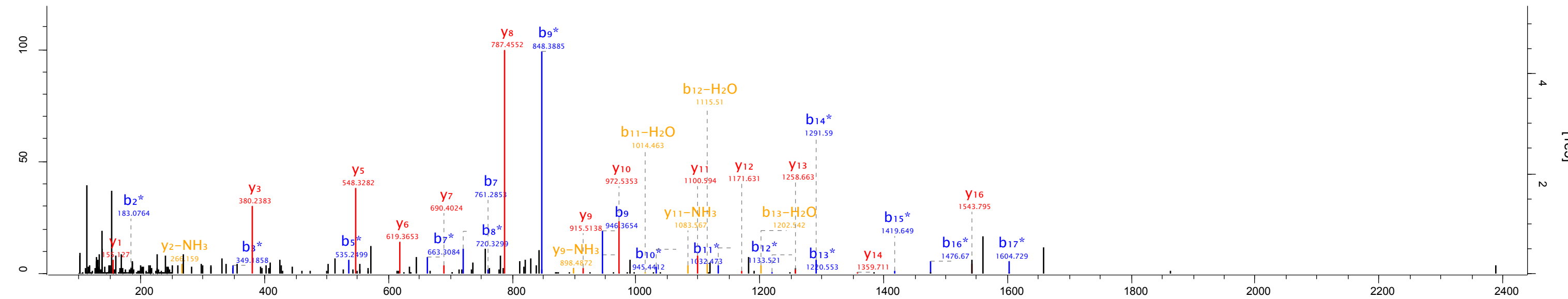
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Raw file

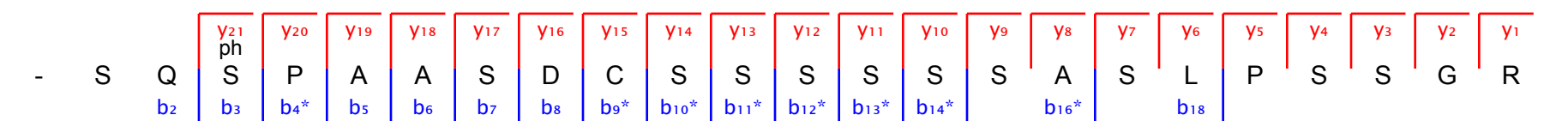
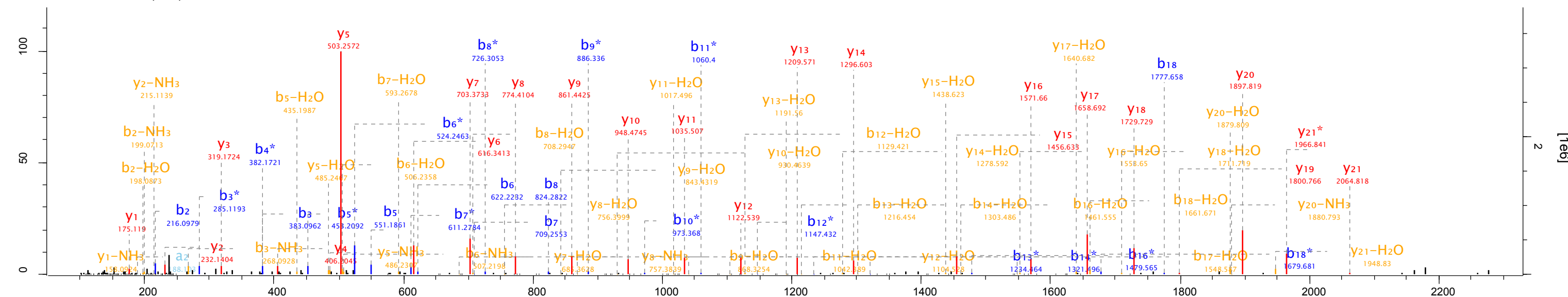
20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
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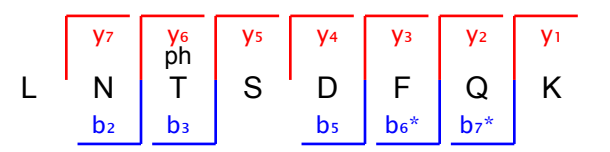
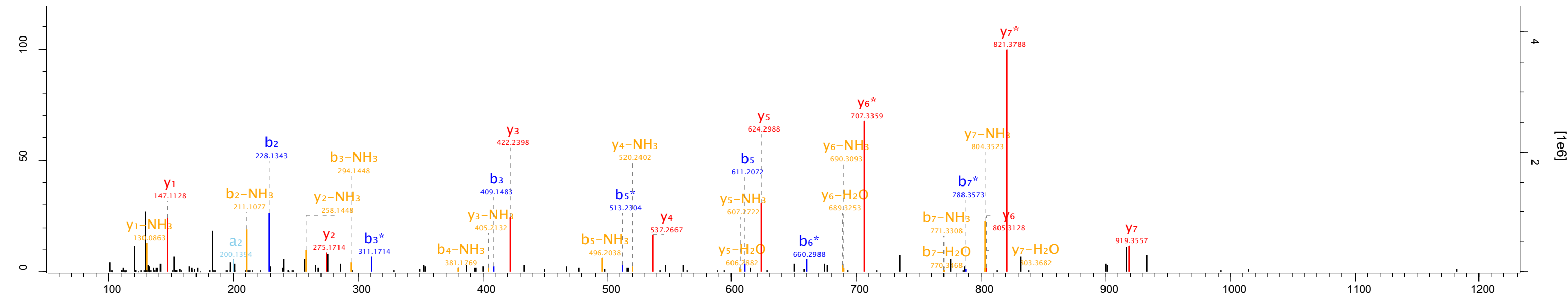


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20171215_MaS_33SR_LMH_phospho2_01

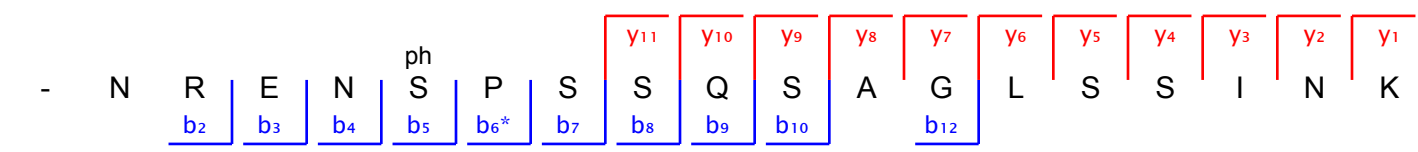
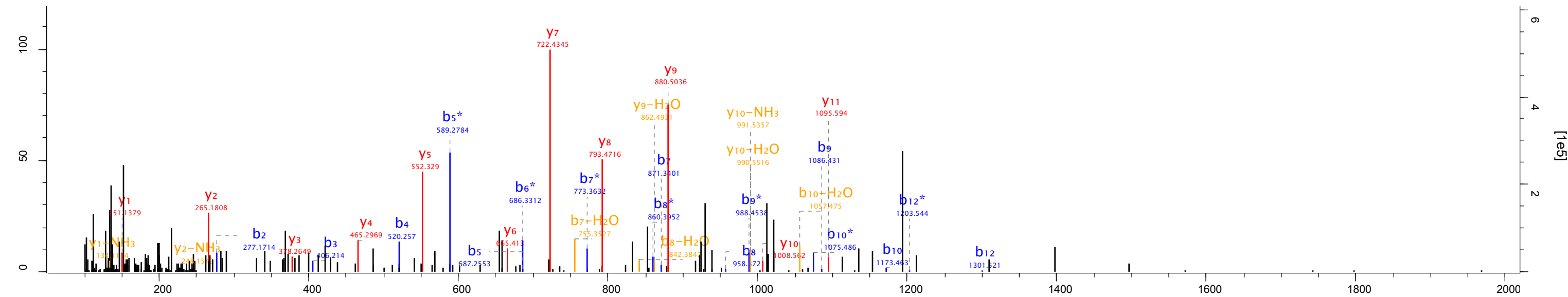
Scan Method Score m/z Gene names
4831 FTMS; HCD 255.88 1140.96 BAG3



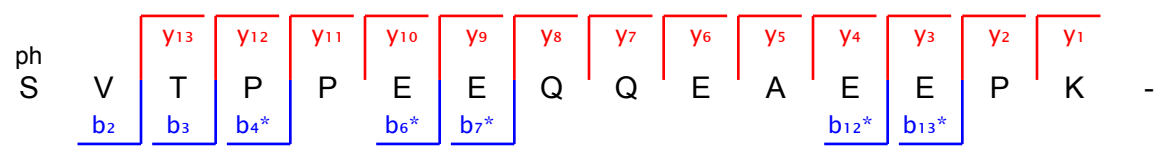
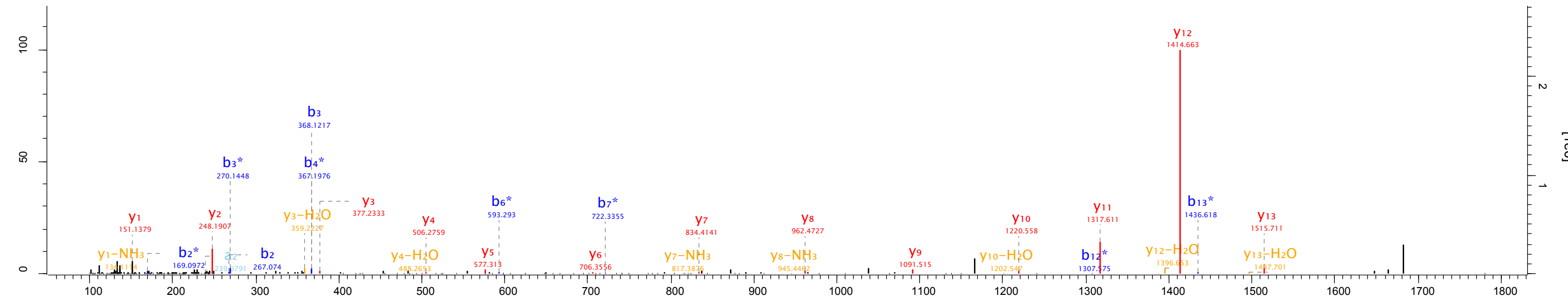
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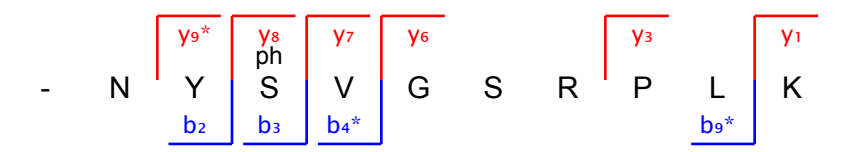
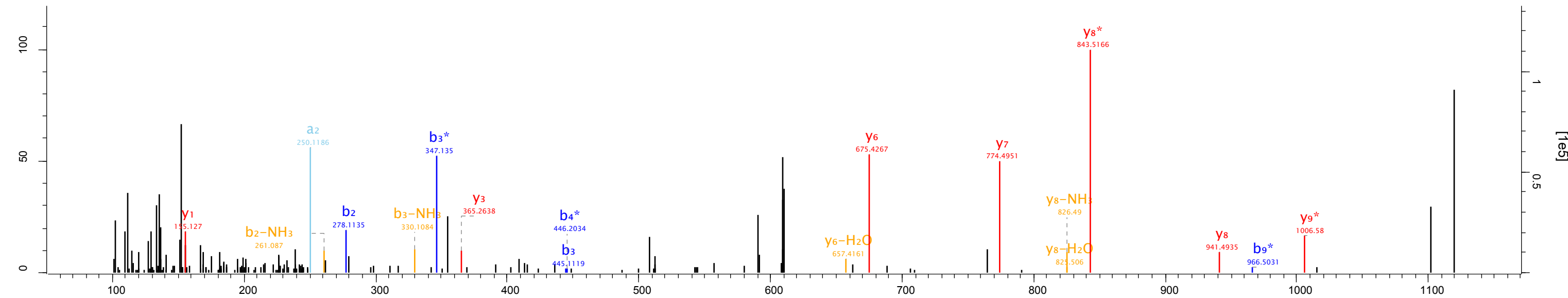
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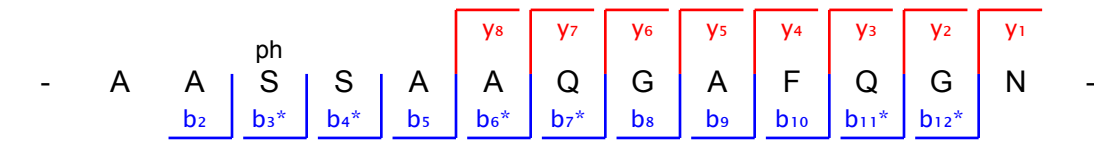
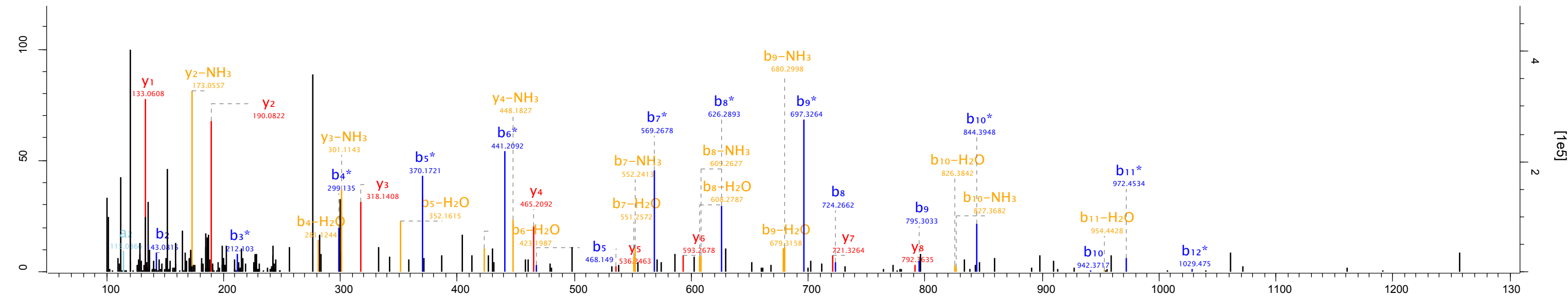


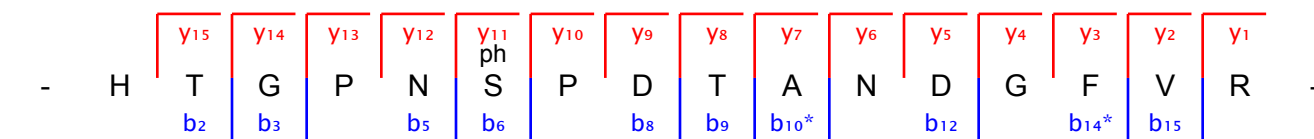
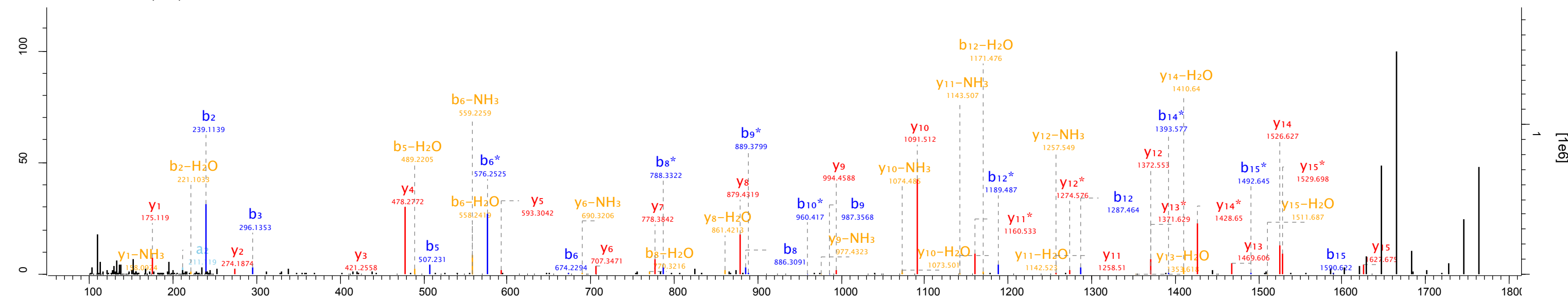
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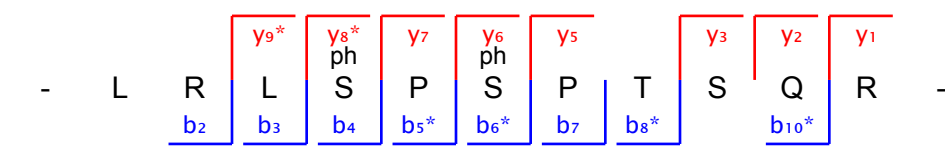
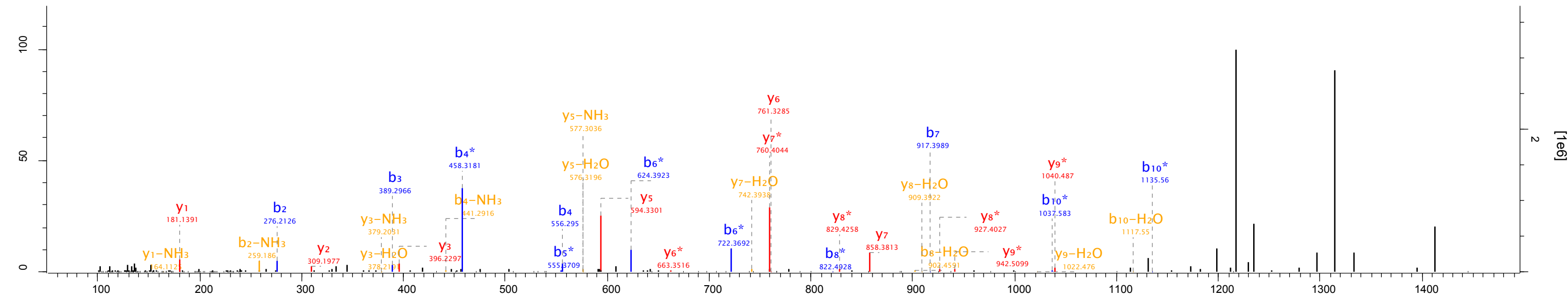
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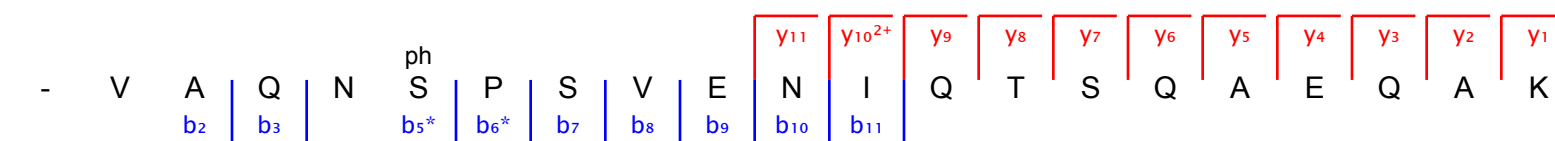
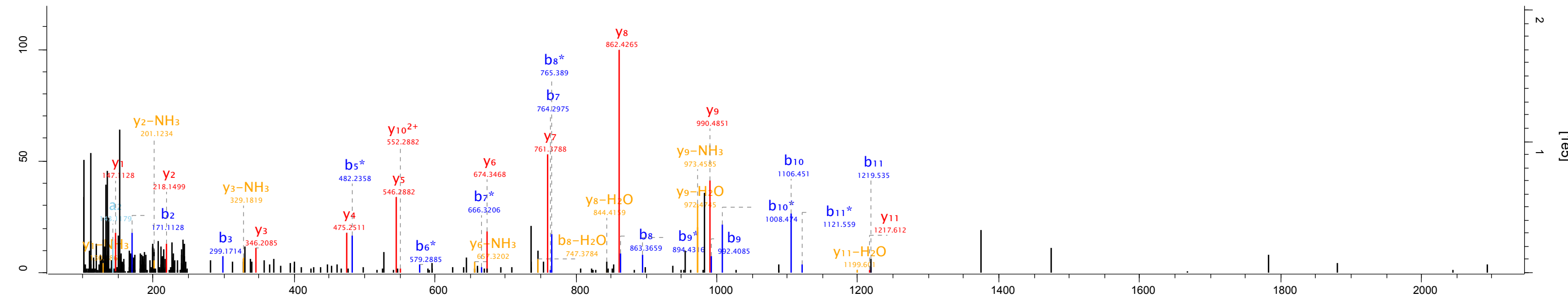




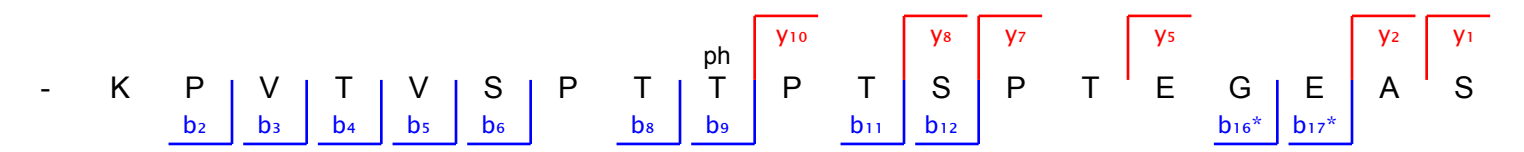
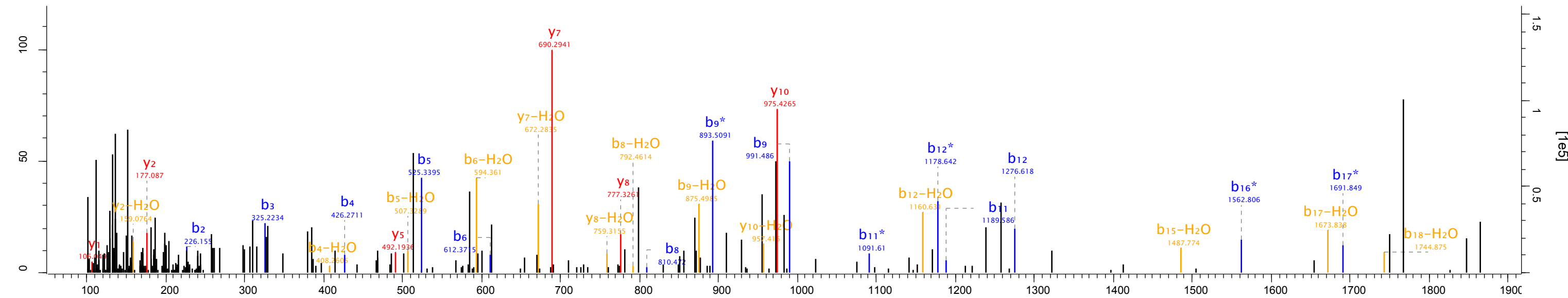


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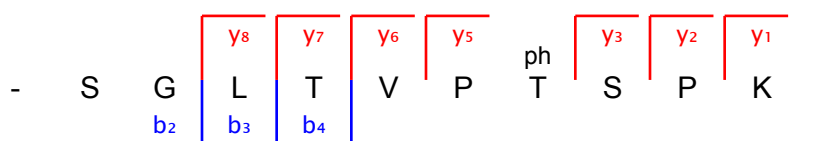
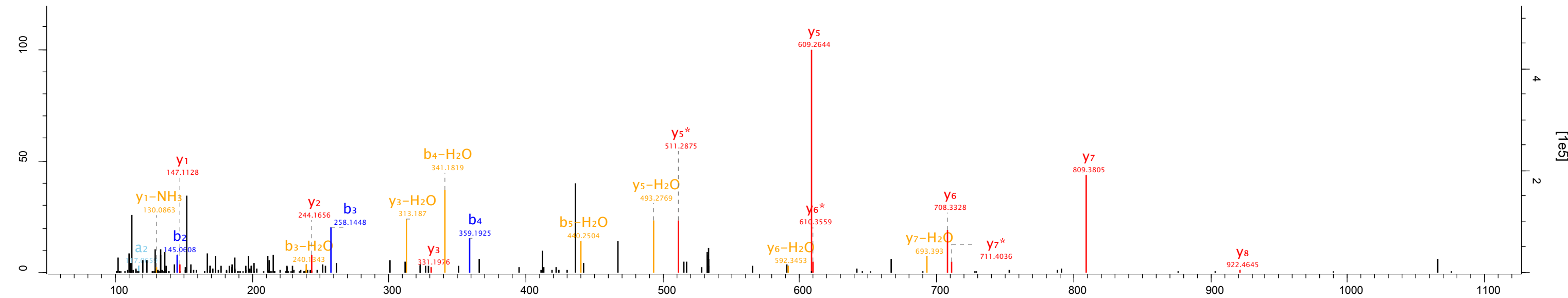




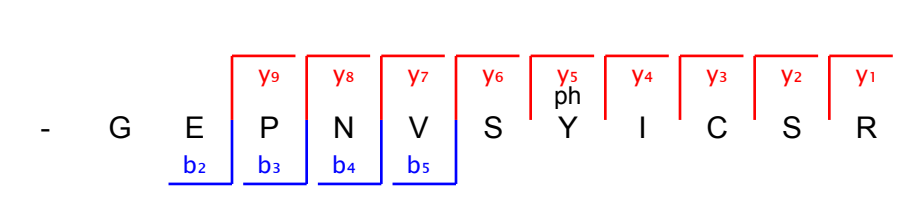
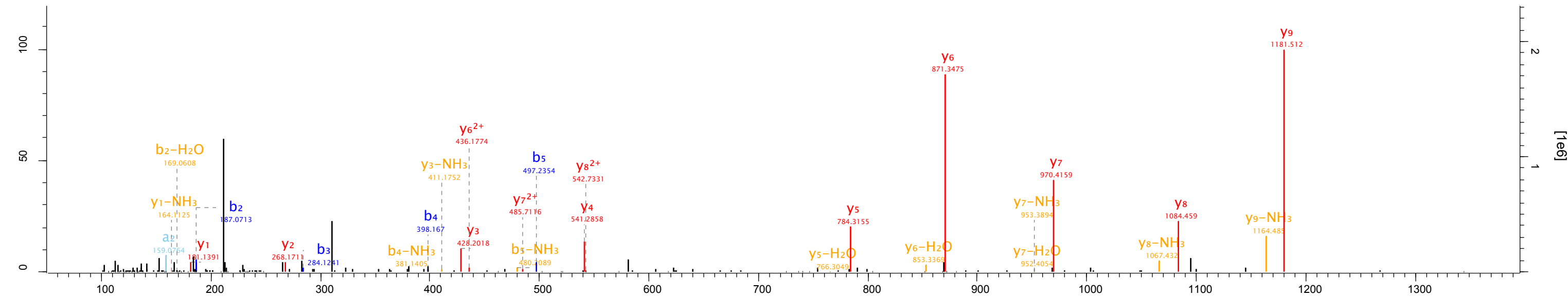
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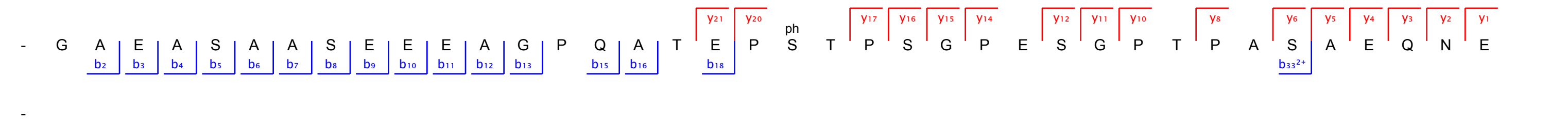
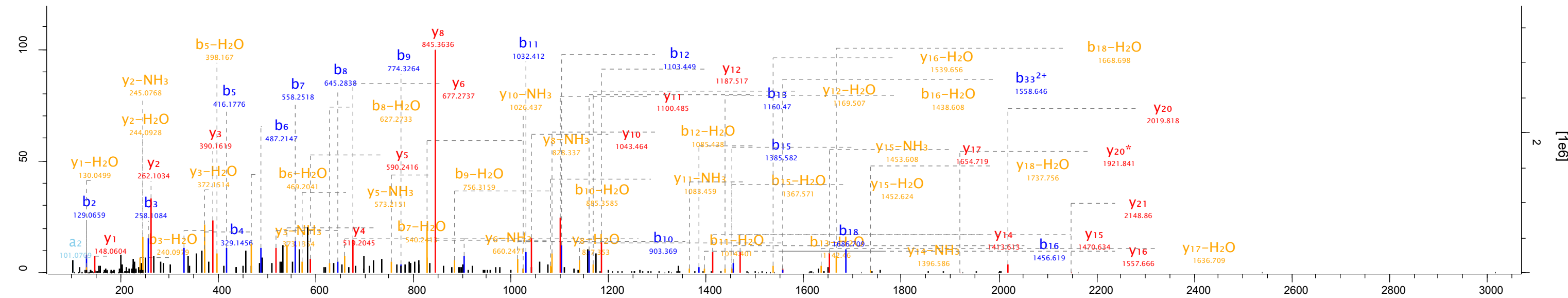
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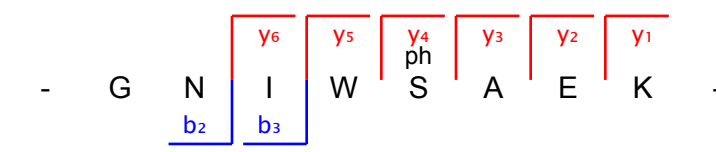
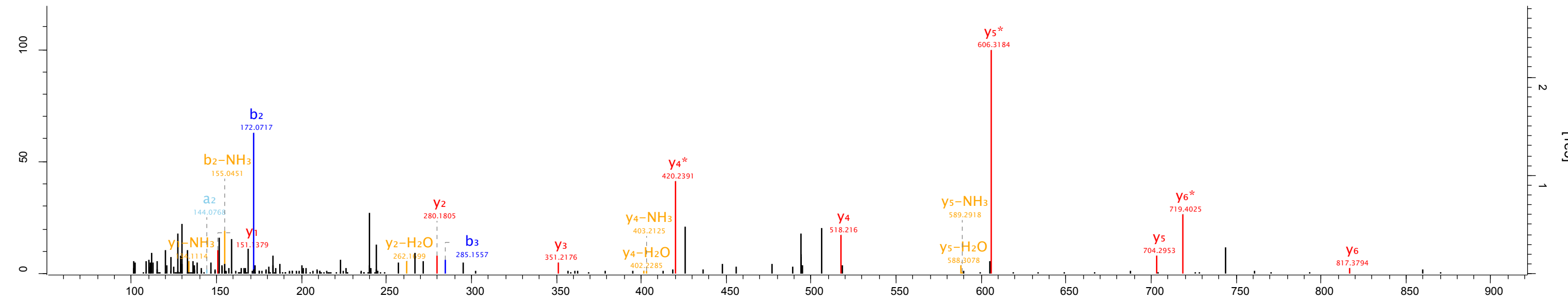
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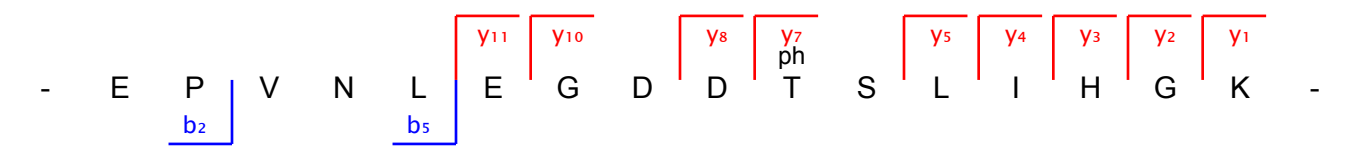
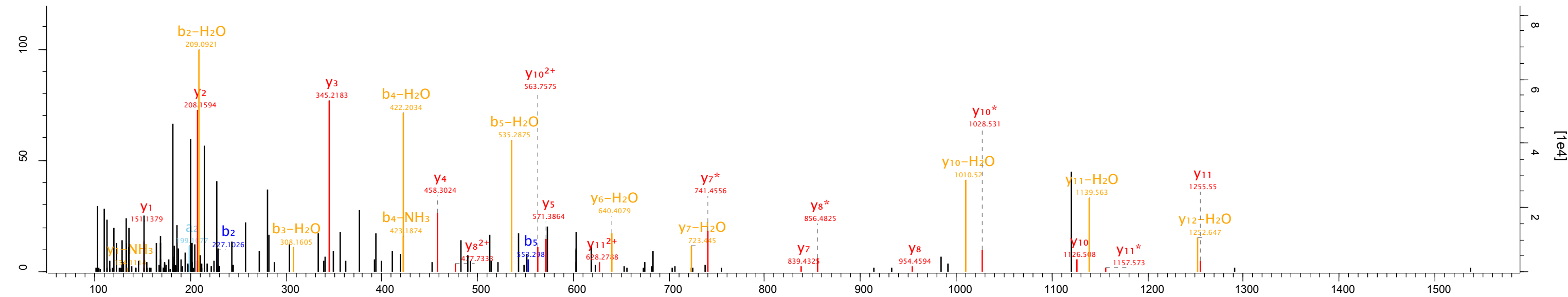
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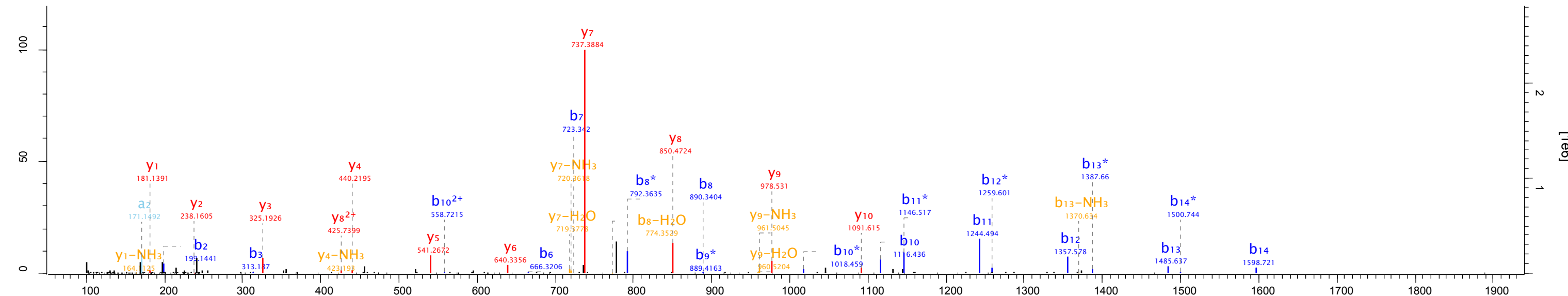


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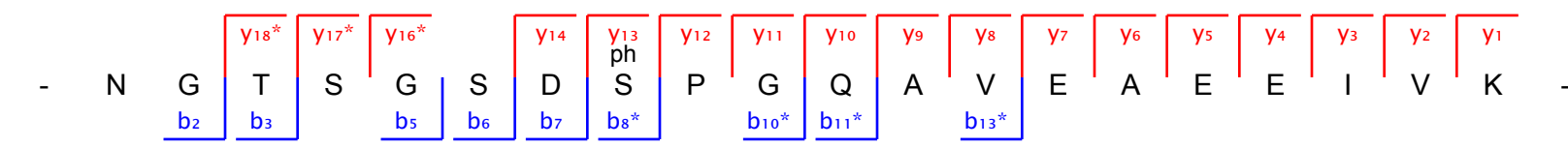
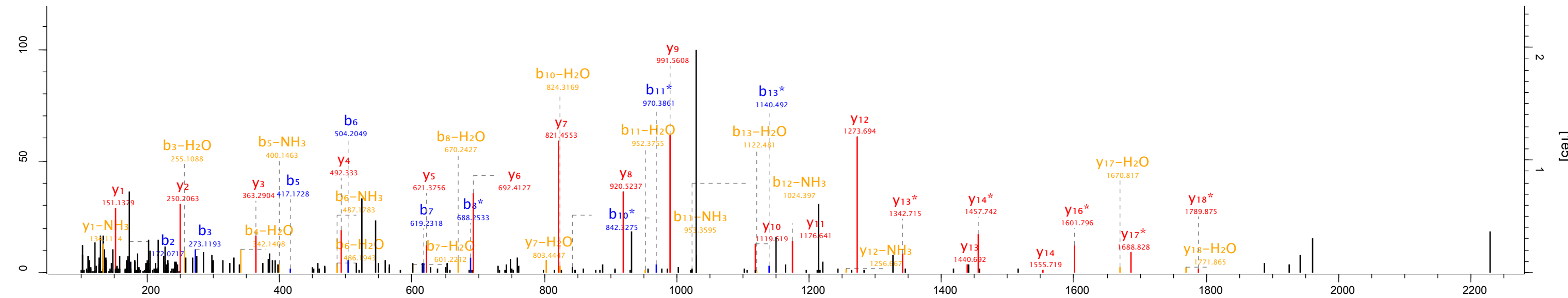


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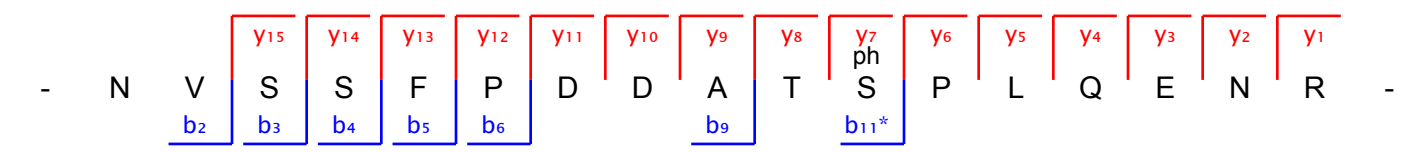
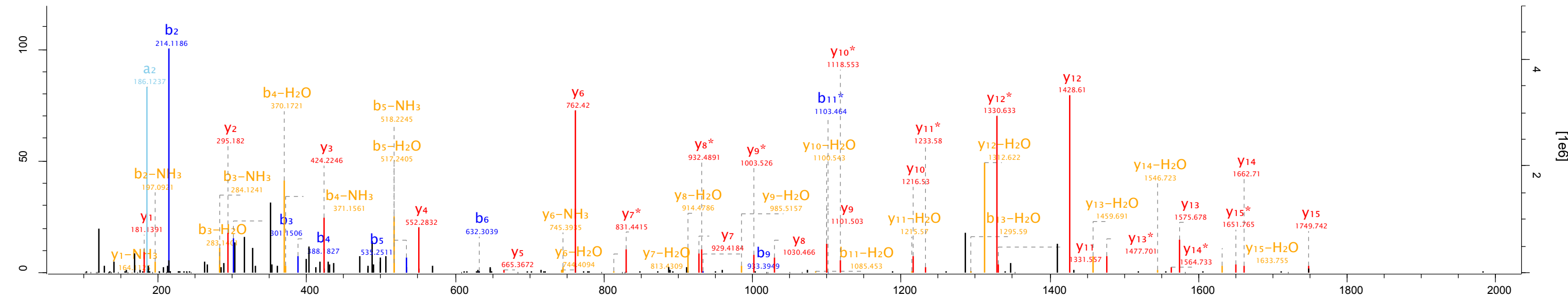
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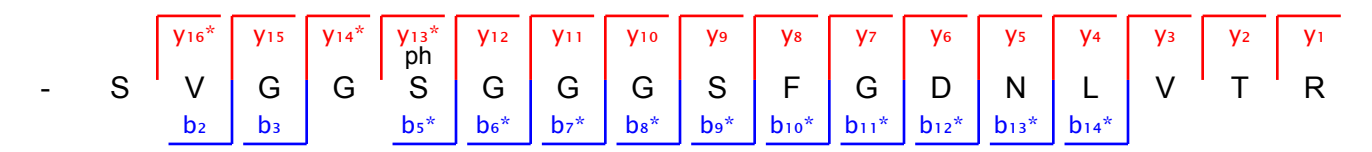
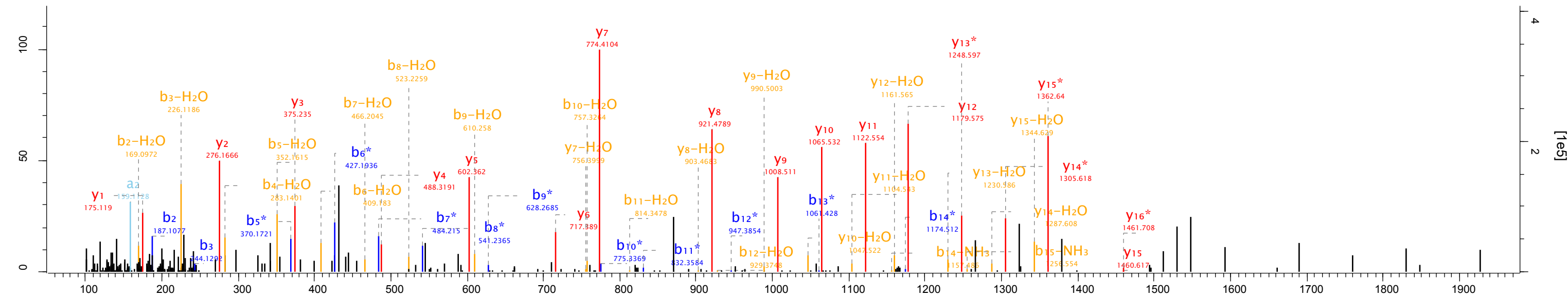
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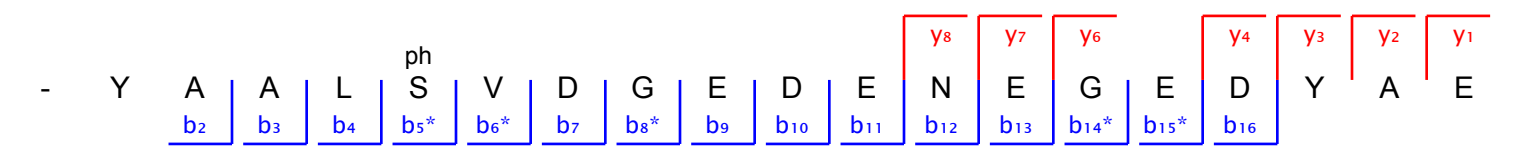
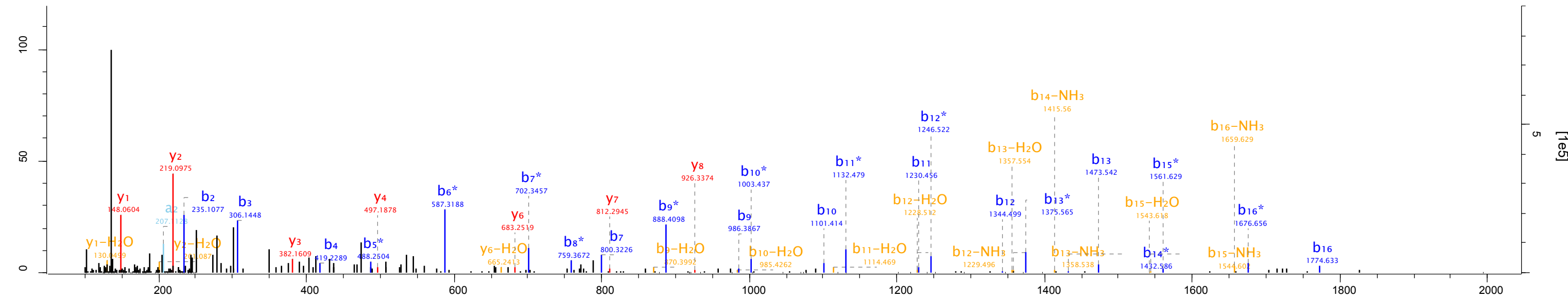
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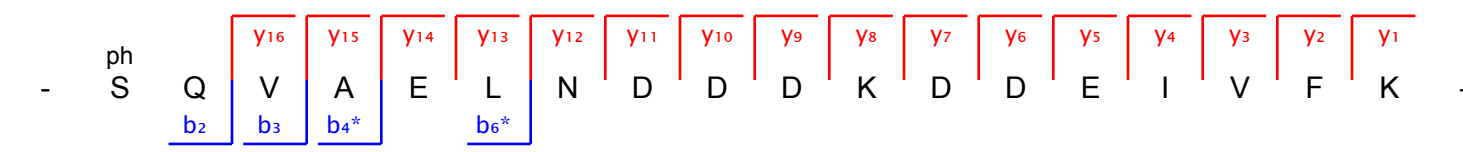
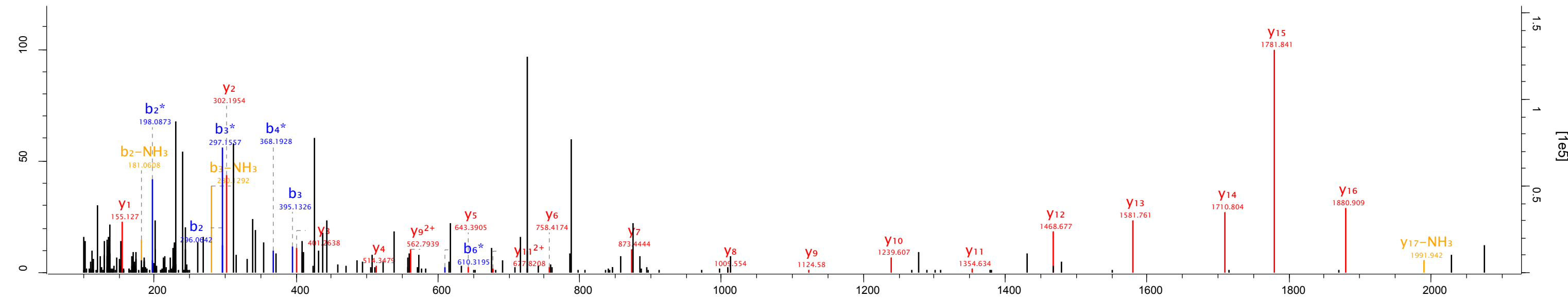
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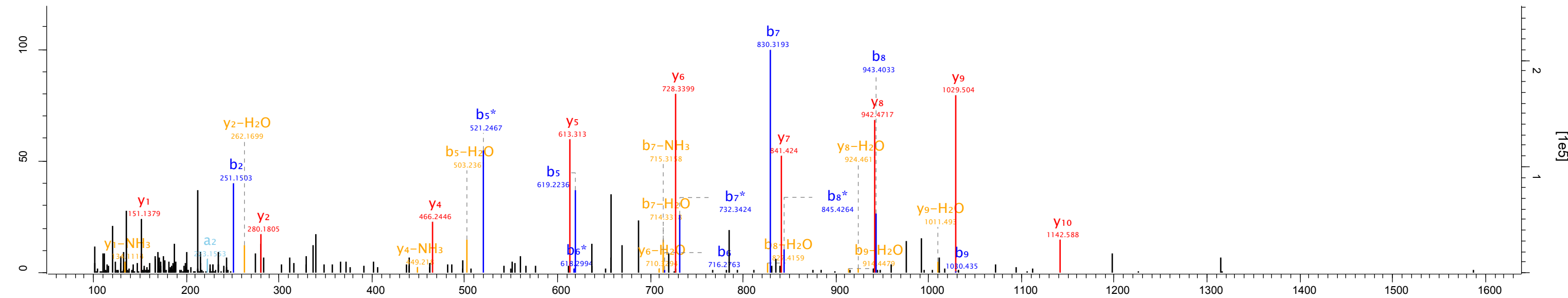


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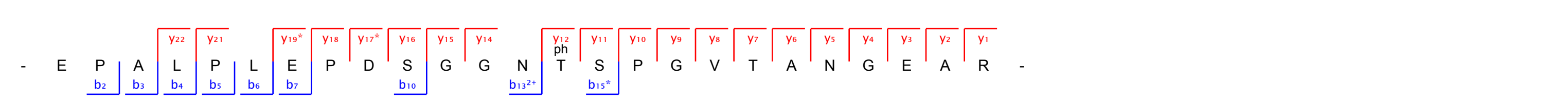
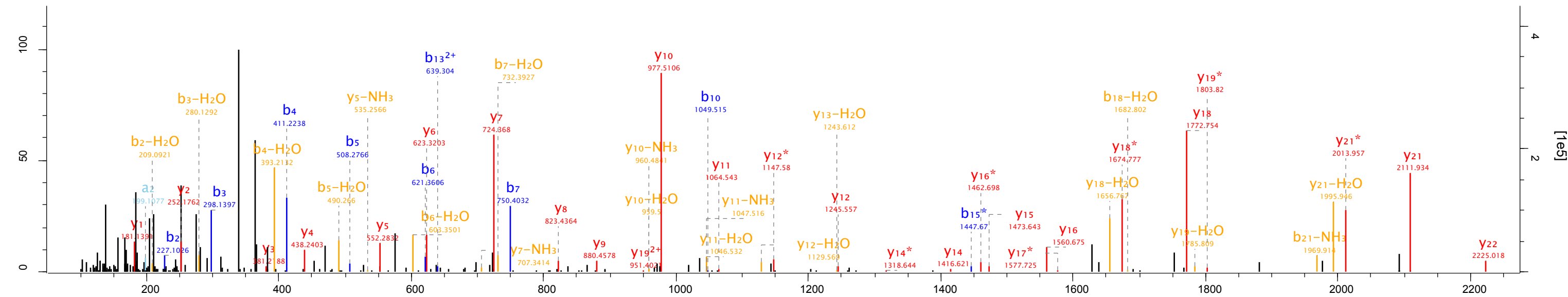


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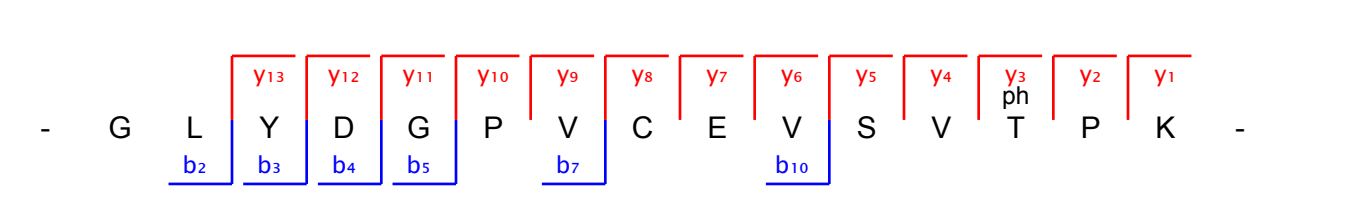
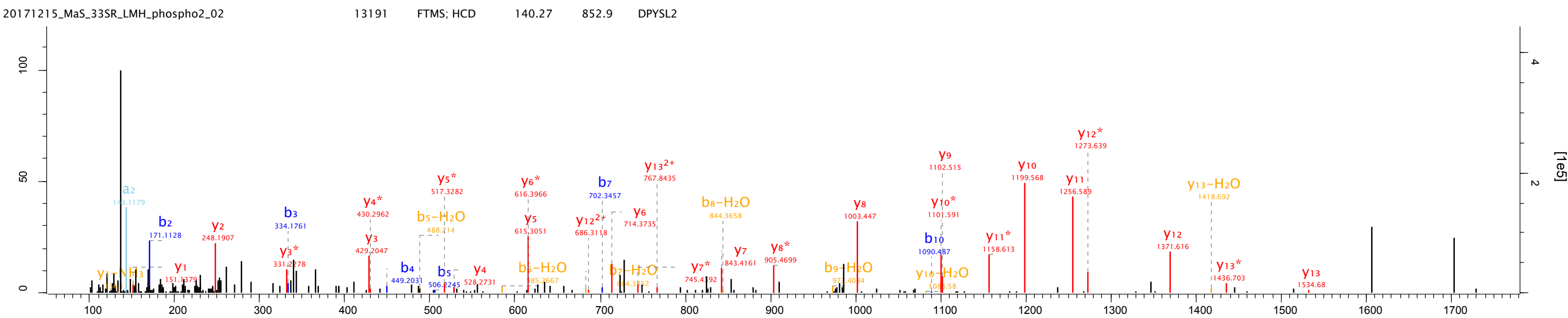




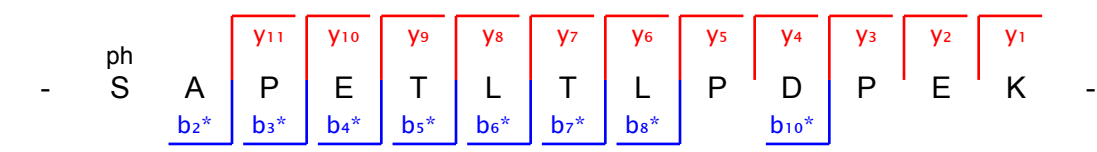
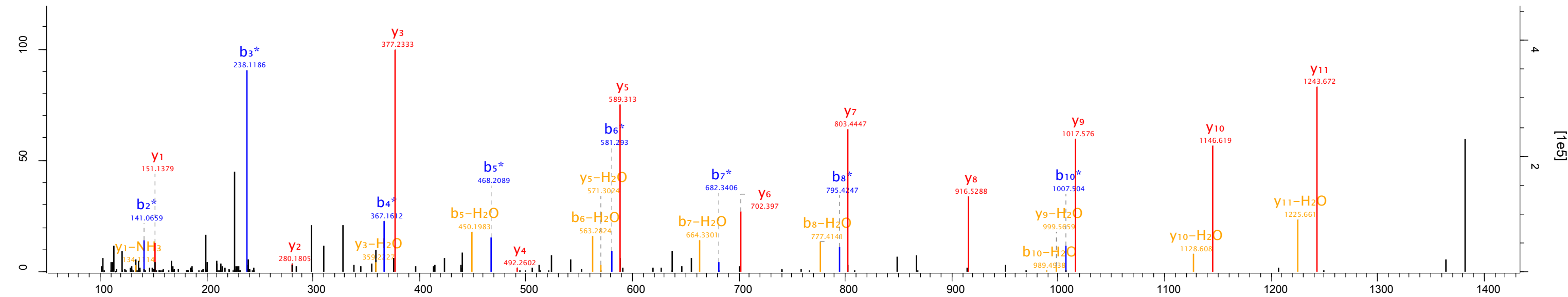
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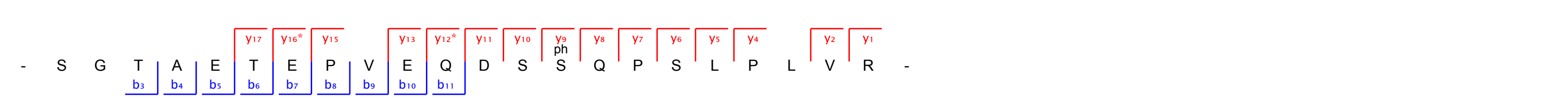
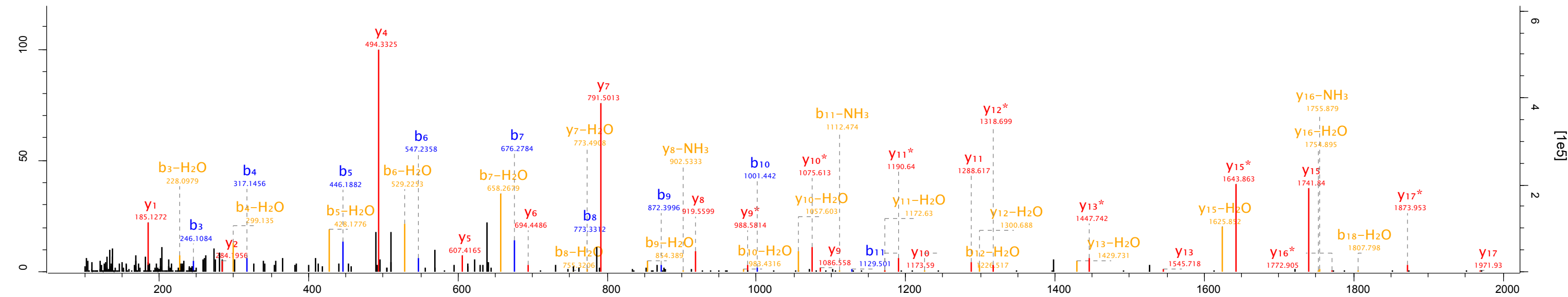
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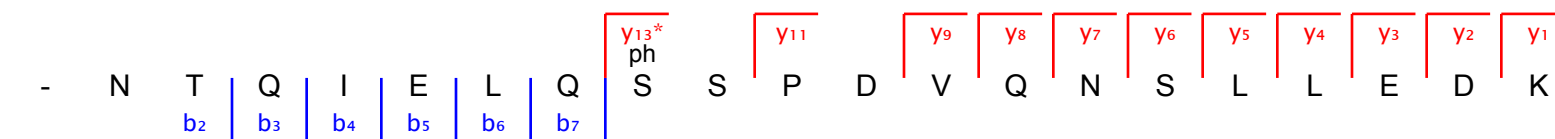
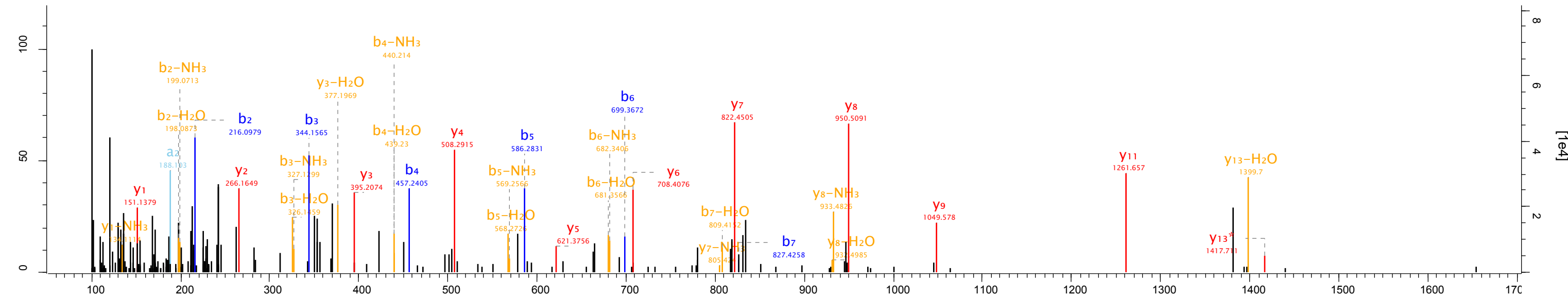
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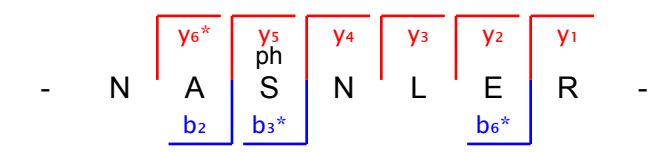
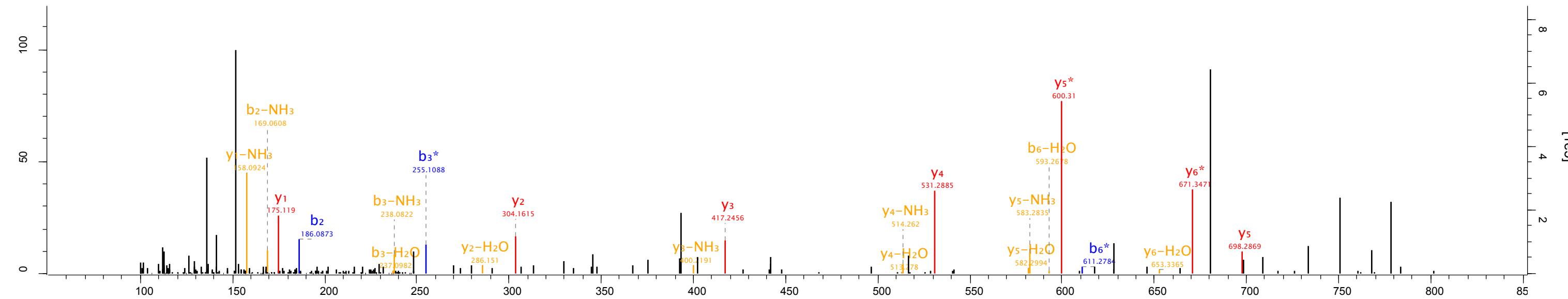
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20171215_MaS_33SR_LMH_phospho2_02

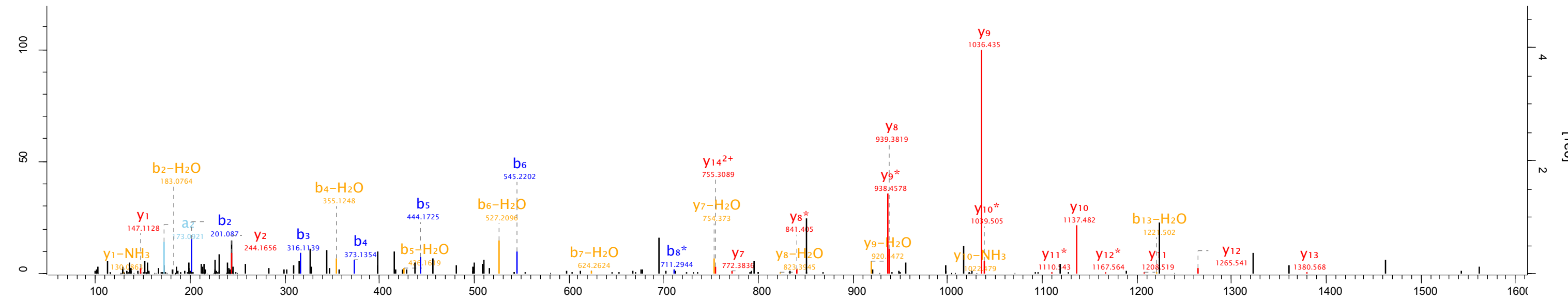
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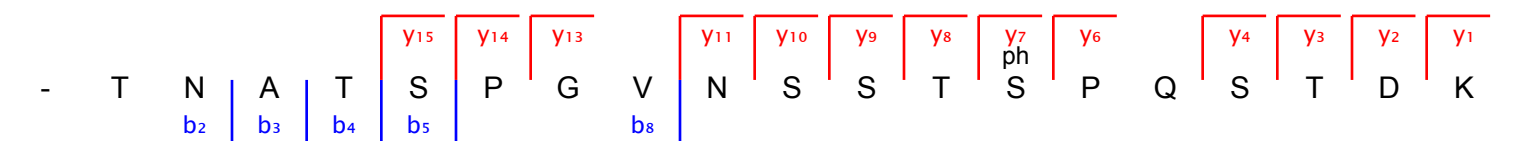
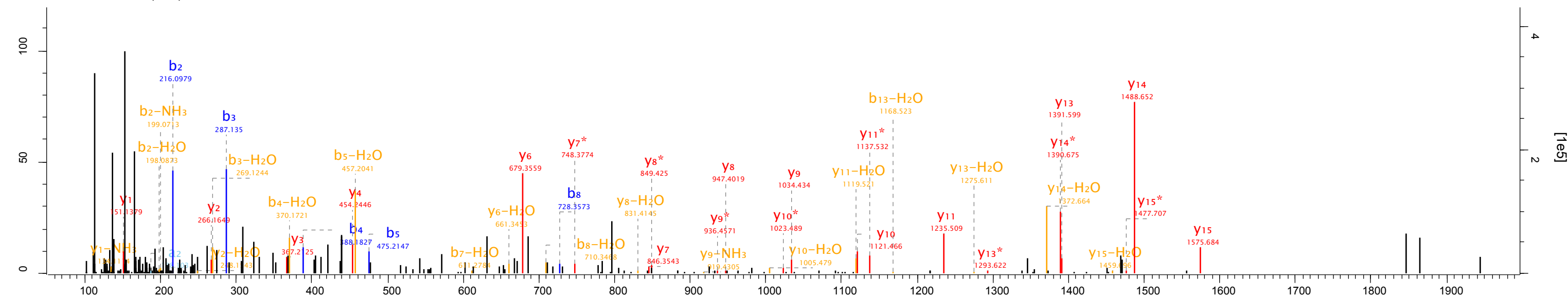


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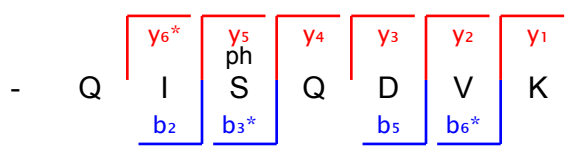
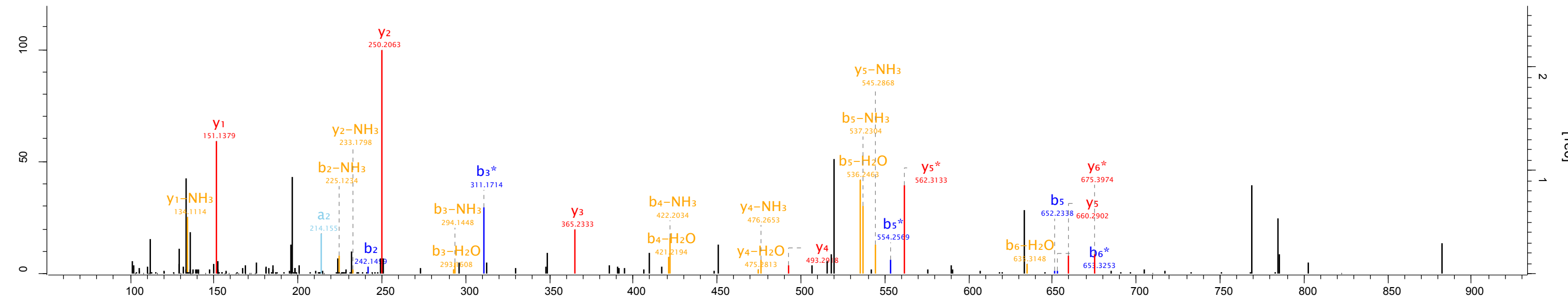


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20171215_MaS_33SR_LMH_phospho2_02

Scan 3391 Method FTMS; HCD Score 129.06 m/z 982.44 Gene names SRGAP2

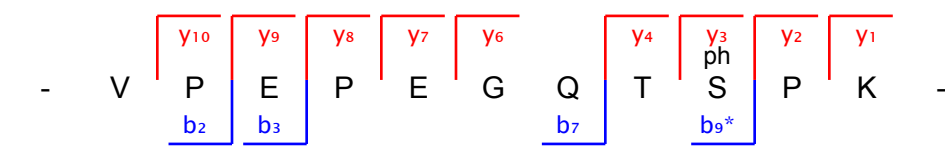
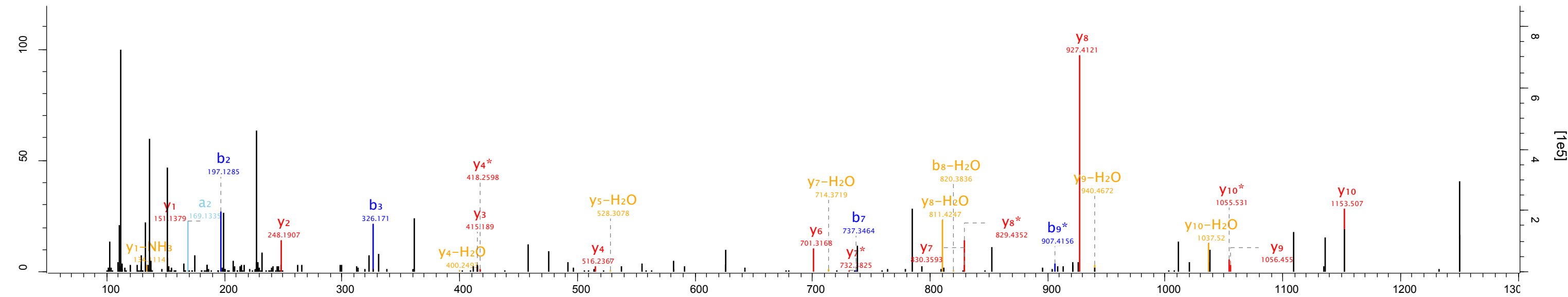


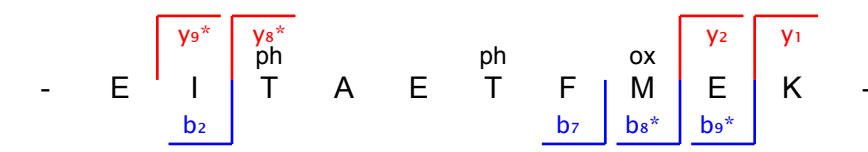
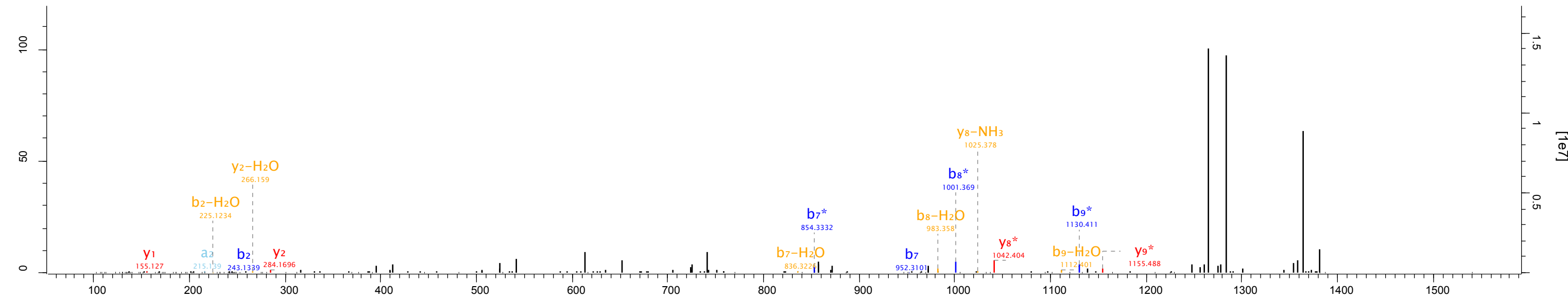
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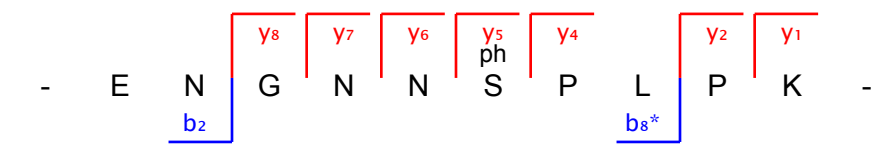
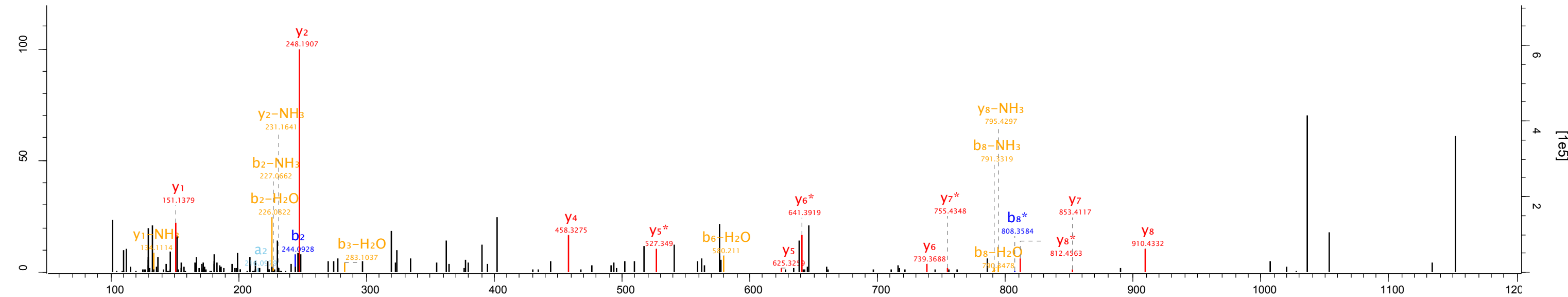


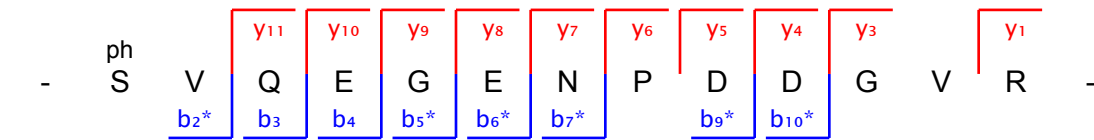
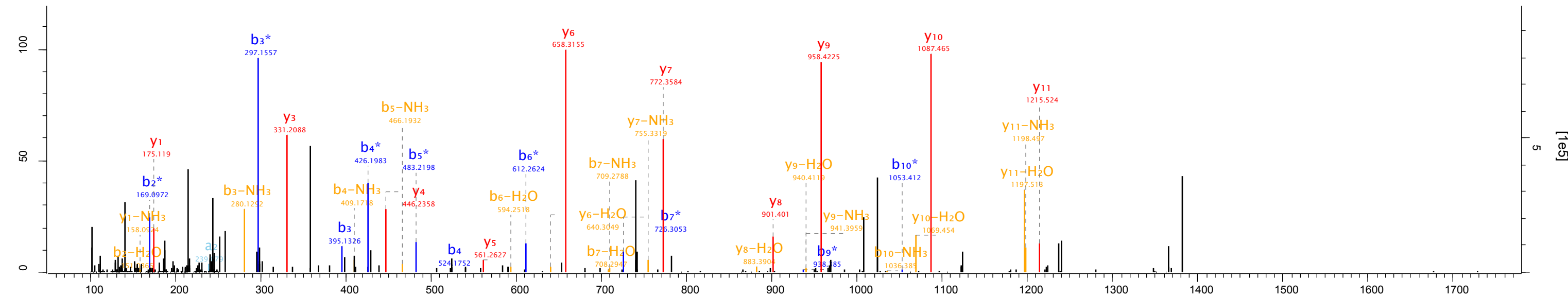
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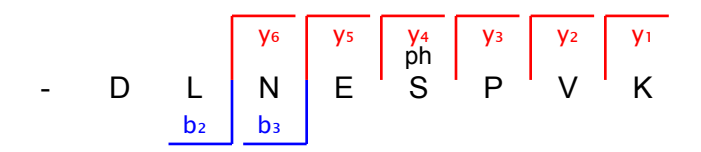
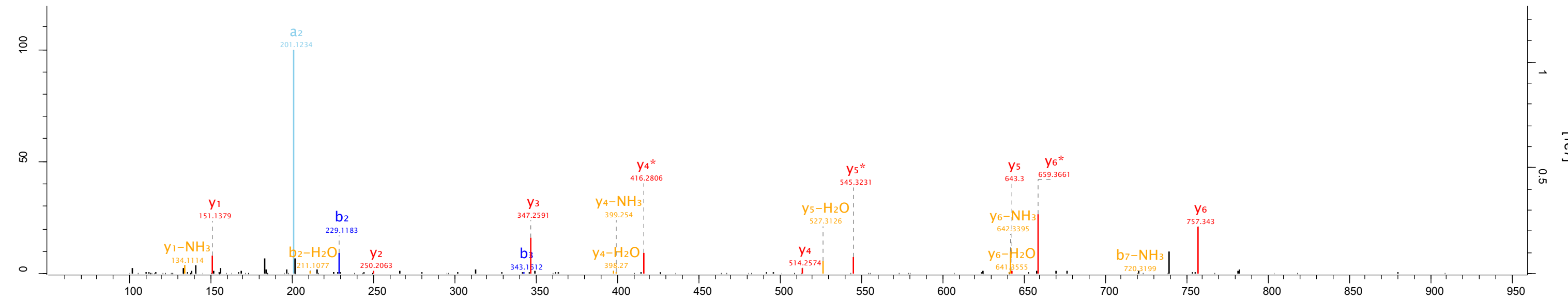






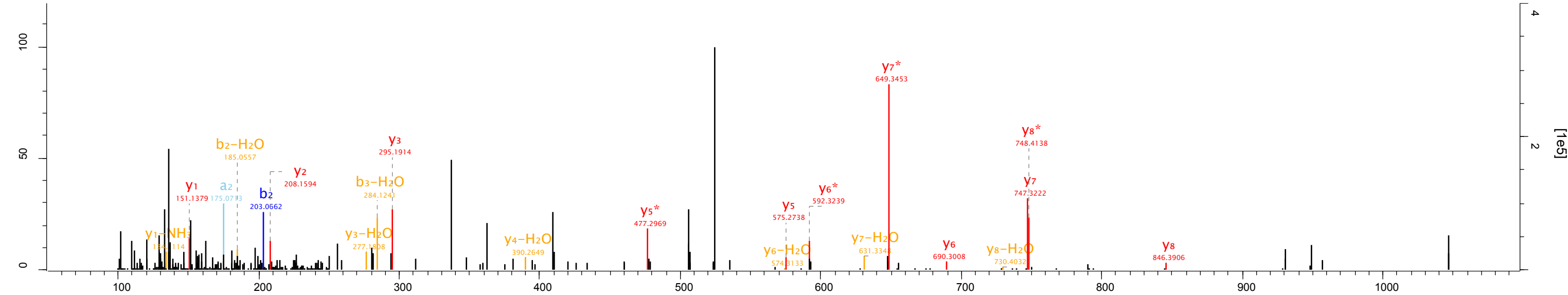


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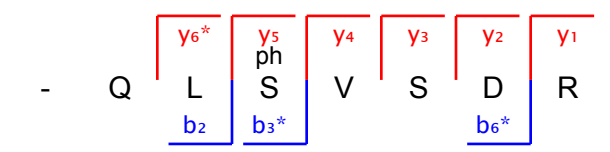
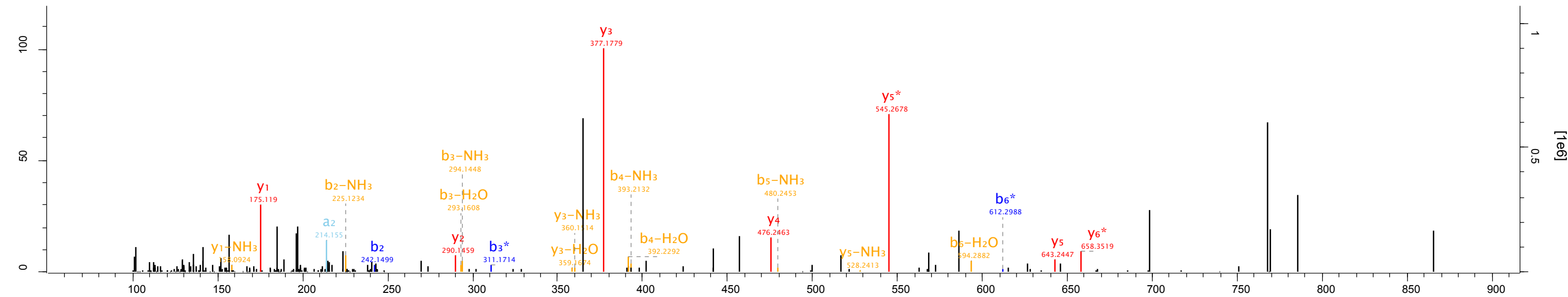


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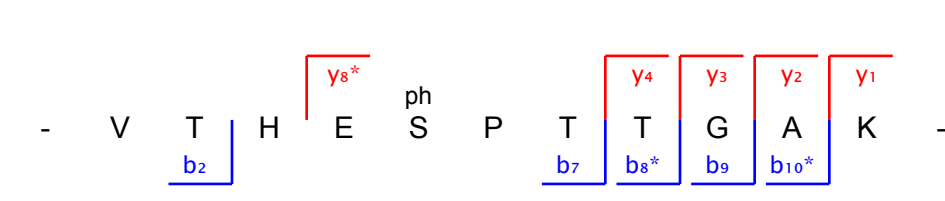
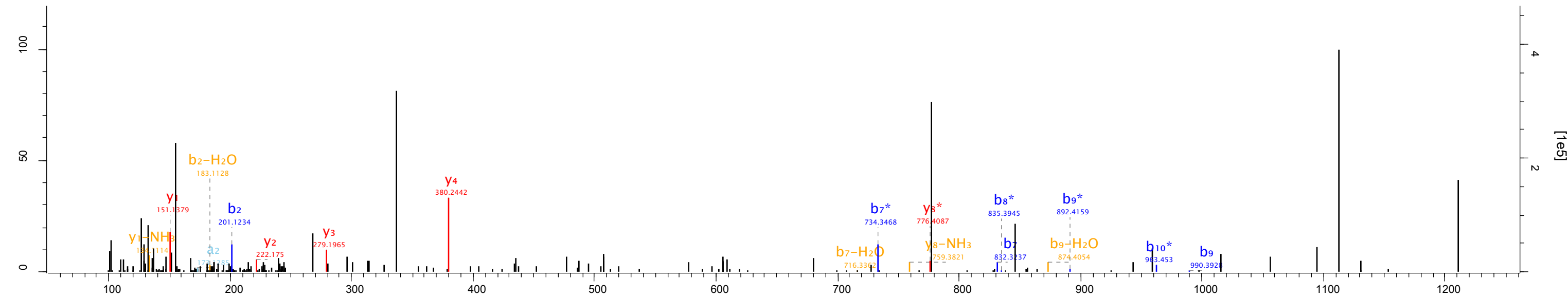
20171215_MaS_33SR_LMH_phospho2_02



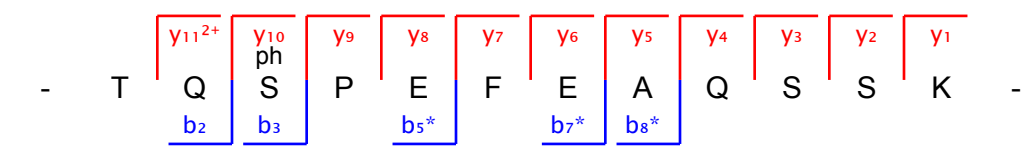
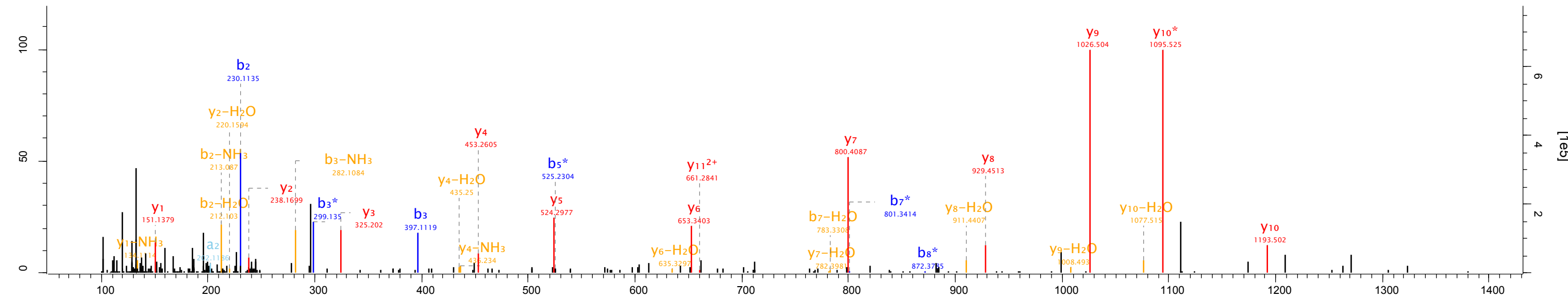
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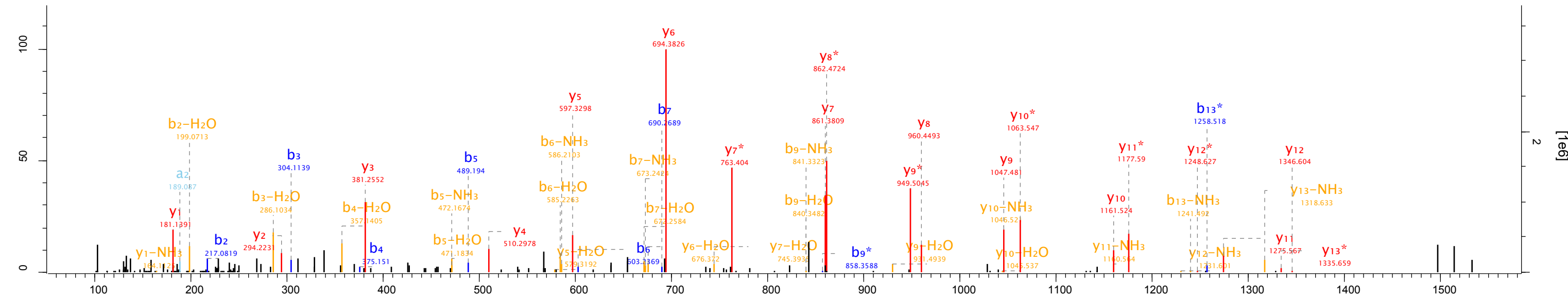


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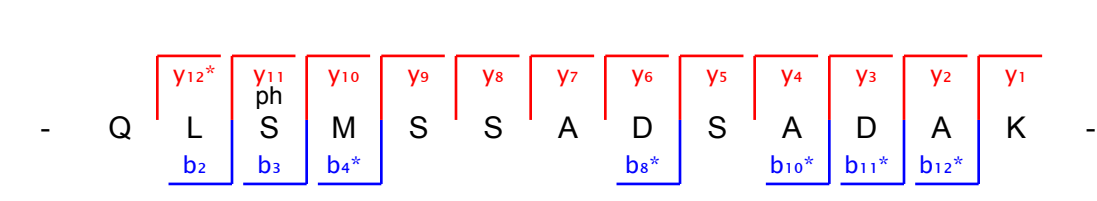
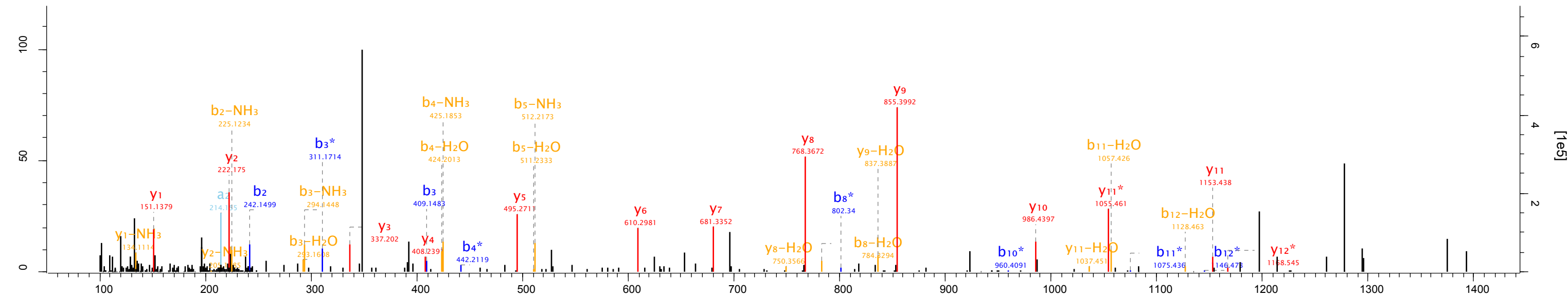


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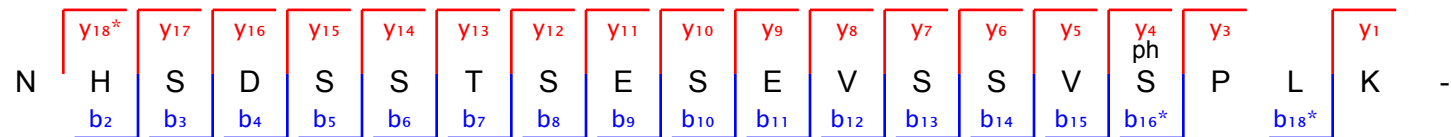
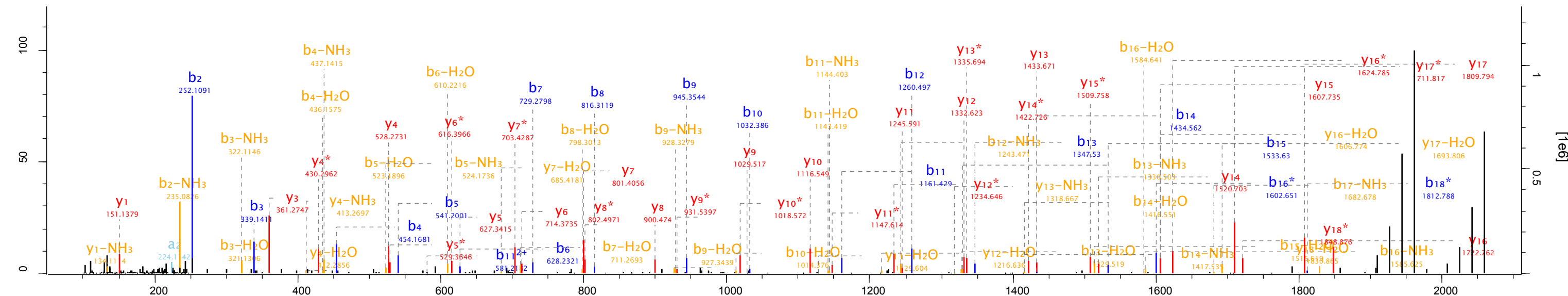
b₂
b₃
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b₆
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b₉*
b₁₃*

y₁₃*
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y₇
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Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6231 Method FTMS; HCD Score 147.36 m/z 697.79 Gene names PRRC2B

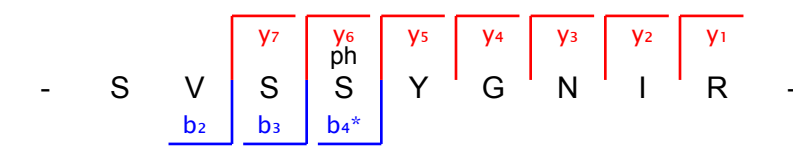
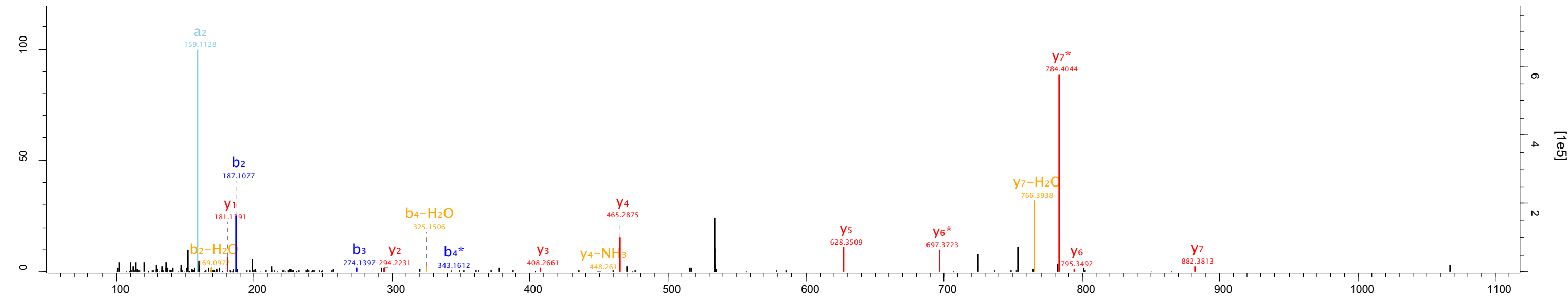


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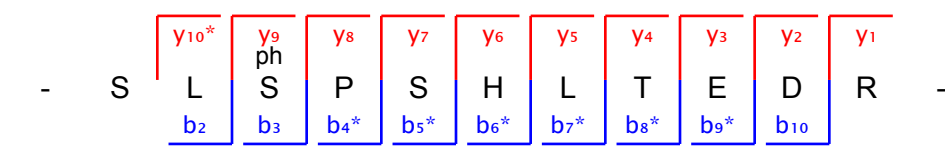
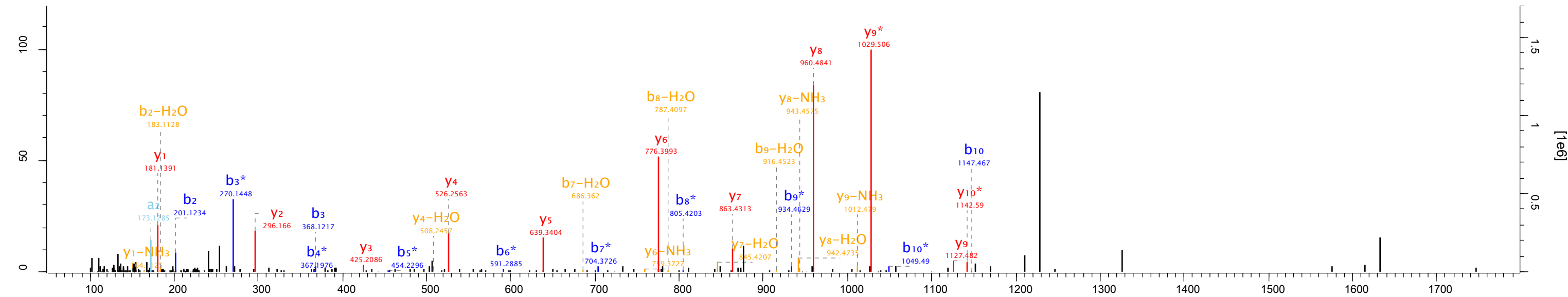
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20171215_MaS_33SR_LMH_phospho2_02

Scan 6871 Method FTMS; HCD Score 77.06 m/z 534.74 Gene names RPTOR

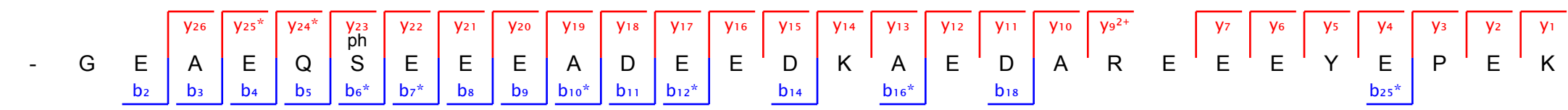
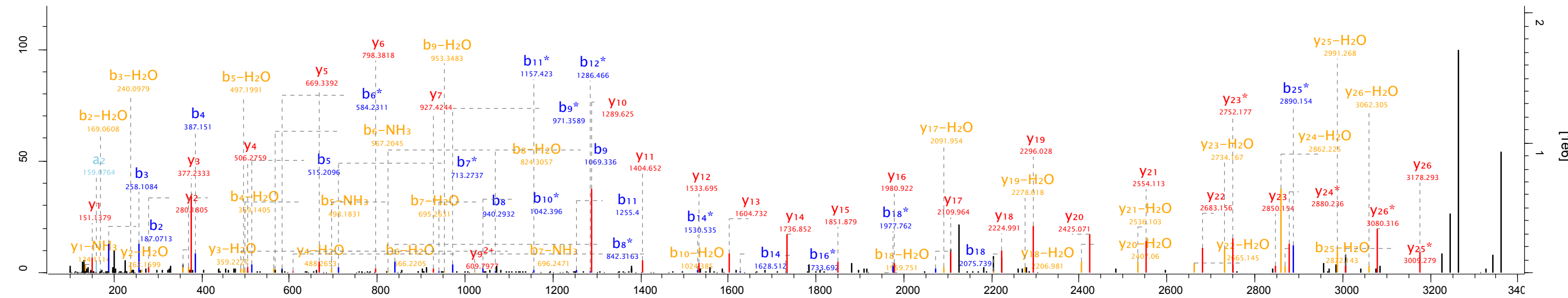


Raw file
20171215_MaS_33SR_LMH_phospho2_02

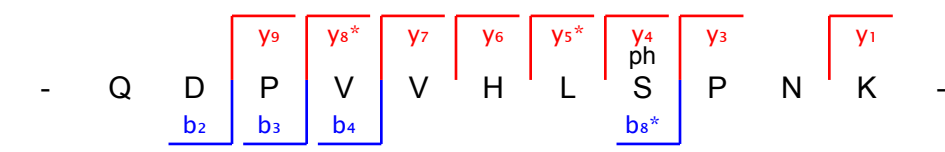
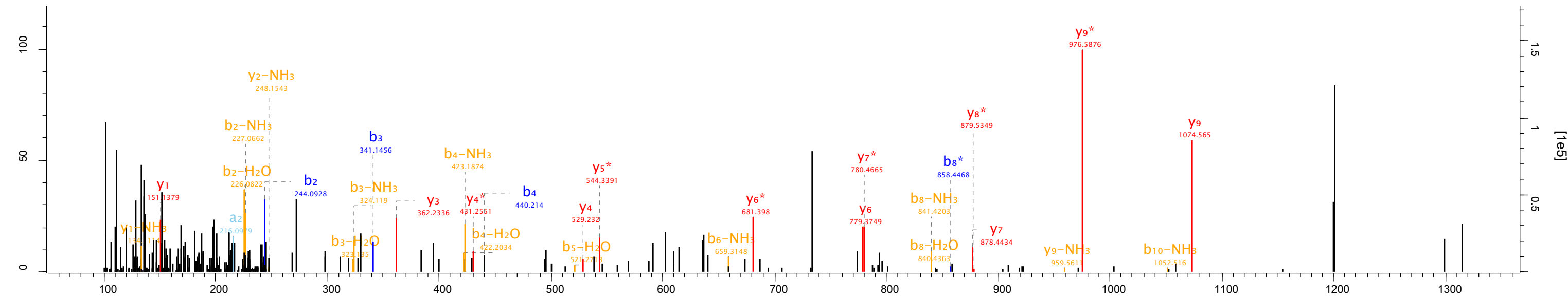
Scan 7091 Method FTMS; HCD Score 133.47 m/z 664.3 Gene names ZC3H13



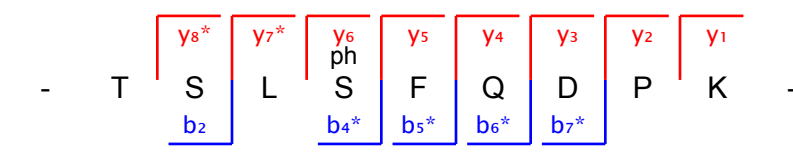
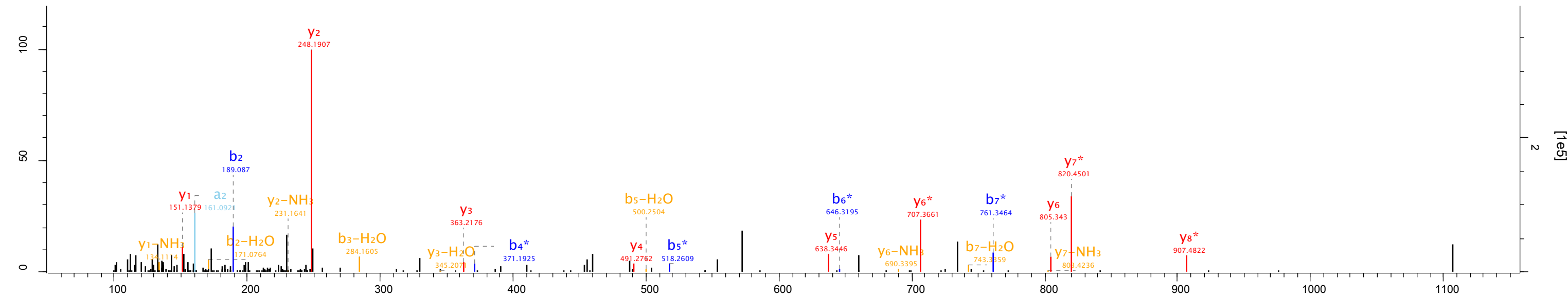
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 7171 Method: FTMS; HCD Score: 251.71 m/z: 1122.46 Gene names: MAP1B



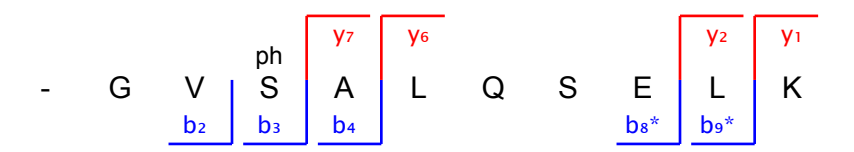
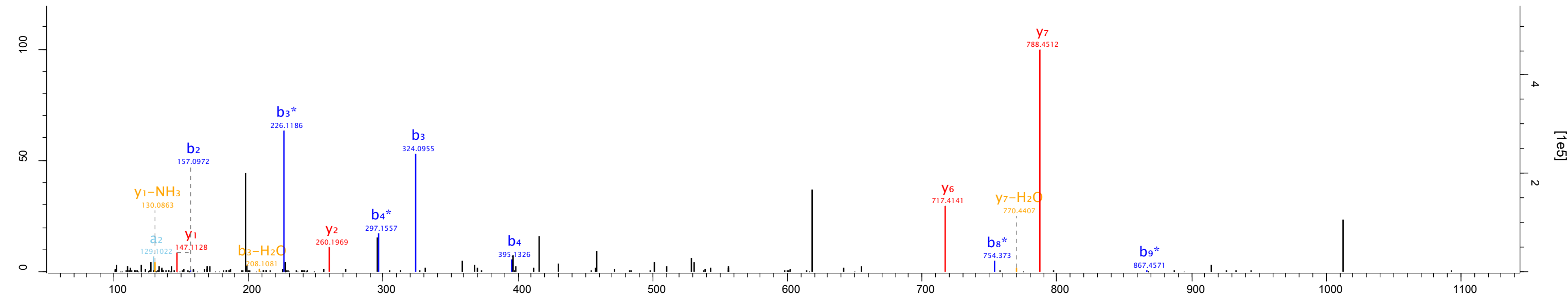
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 7261 Method FTMS; HCD Score 78.69 m/z 659.33 Gene names SIPA1L1



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 8711 Method FTMS; HCD Score 90.7 m/z 554.26 Gene names NES

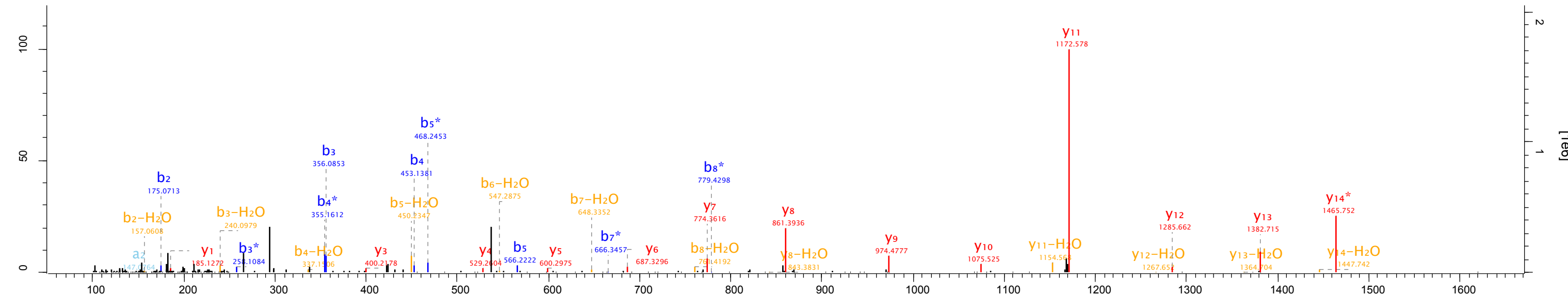


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 9071 Method FTMS; HCD Score 64.12 m/z 556.27



Raw file
20171215_MaS_33SR_LMH_phospho2_02

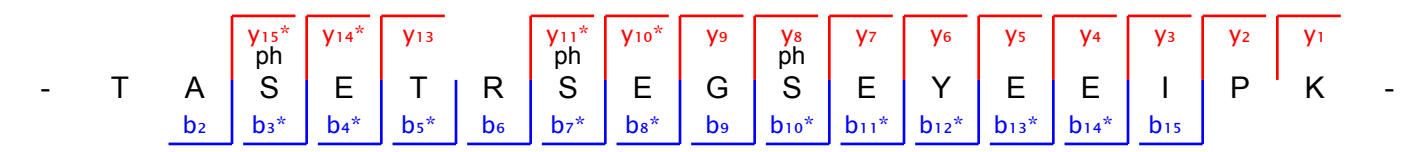
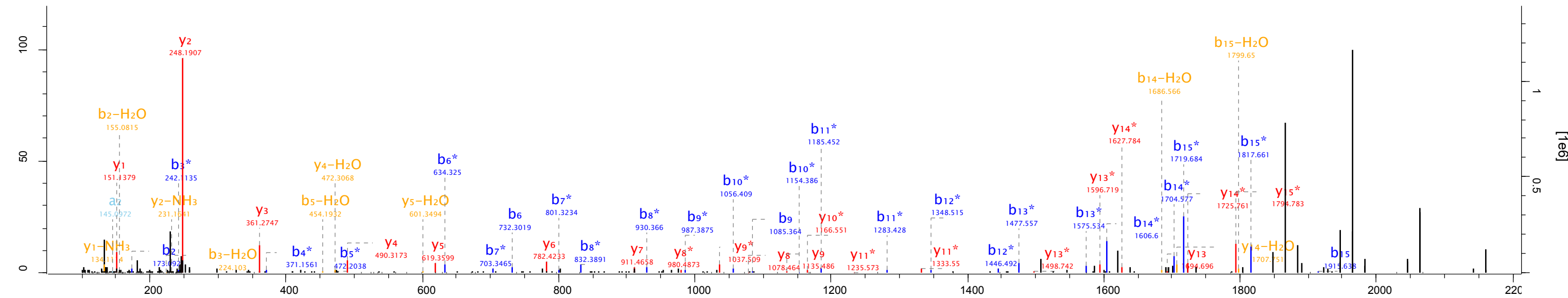
Scan 9461 Method FTMS; HCD Score 125.23 m/z 869.4 Gene names TMPO

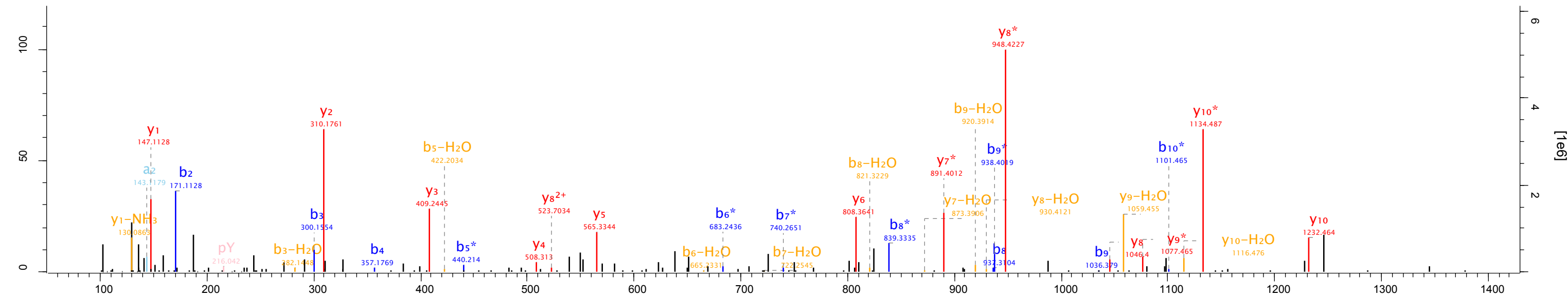


- S S S T P L P T I S S S A E N T R -

Fragmentation mapping:
- b2 (S) b3 (S) b4 (P) b5 (L) b7* (T) b8* (I) y1 (R) -

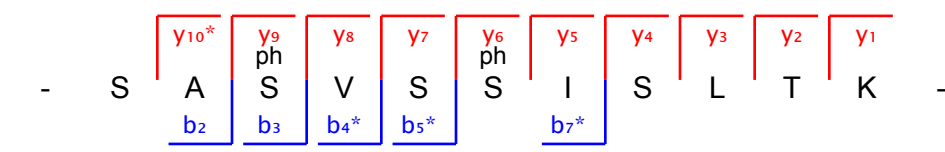
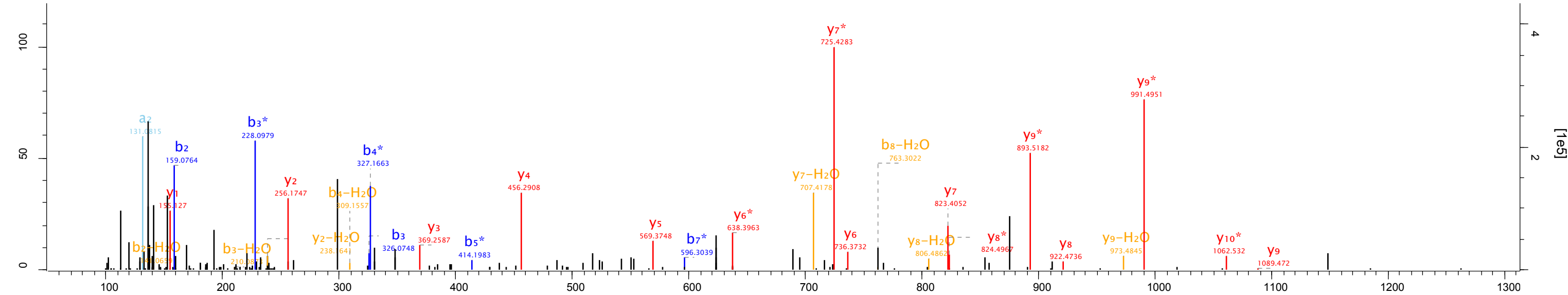
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10031 Method FTMS; HCD Score 181.92 m/z 1081.91 Gene names PRRC2A

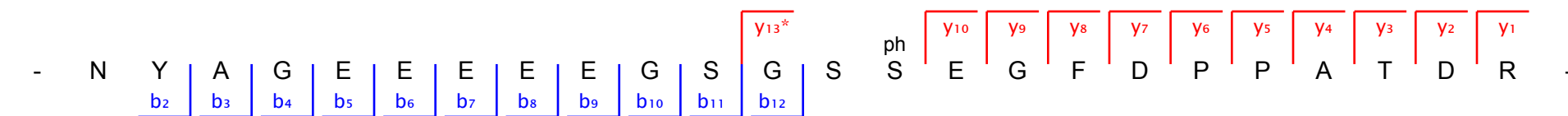
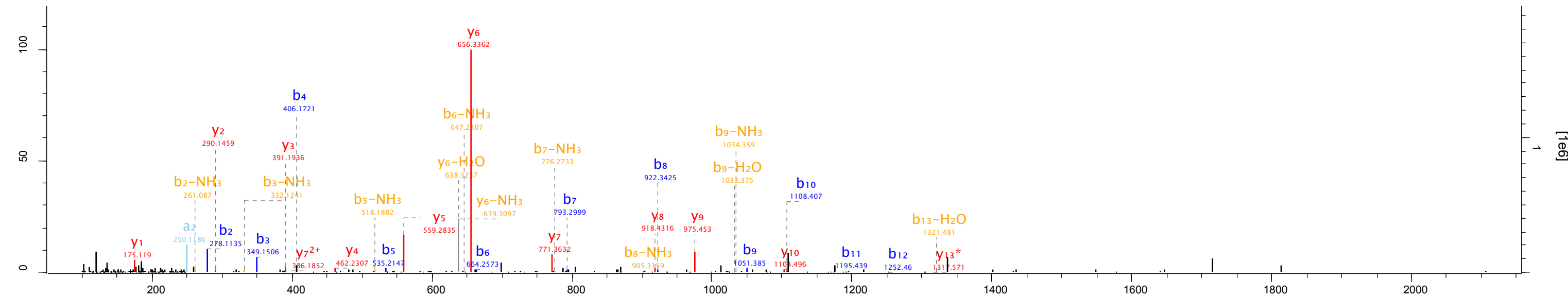




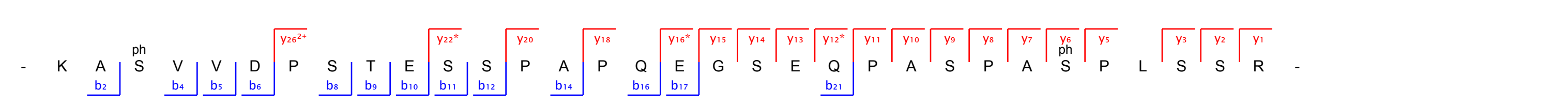
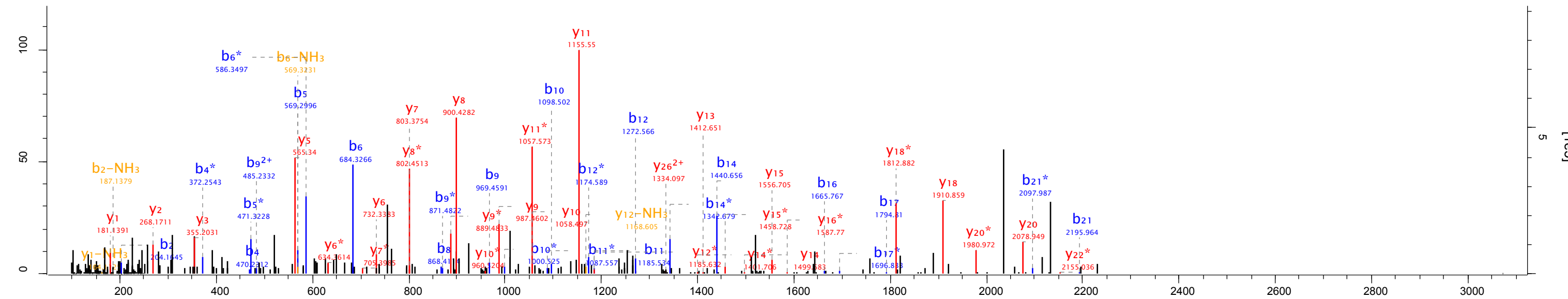
- I y10 y9* y8 y7^{ph} y6^{ph} y5 y4 y3 y2 y1 -
G E G T Y G V V Y K -
b2 b3 b4 b5* b6* b7* b8 b9 b10*

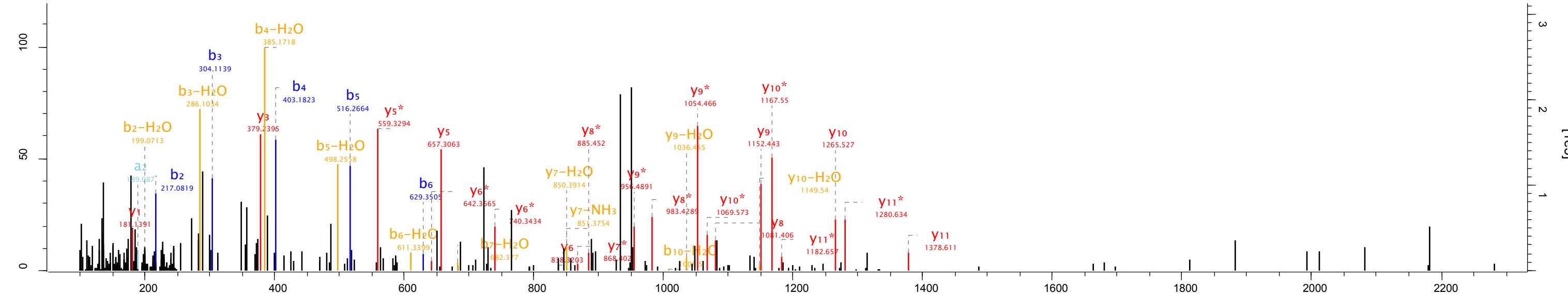
20171215_MaS_33SR_LMH_phospho2_03 10221 FTMS; HCD 103.01 624.27 SOS1



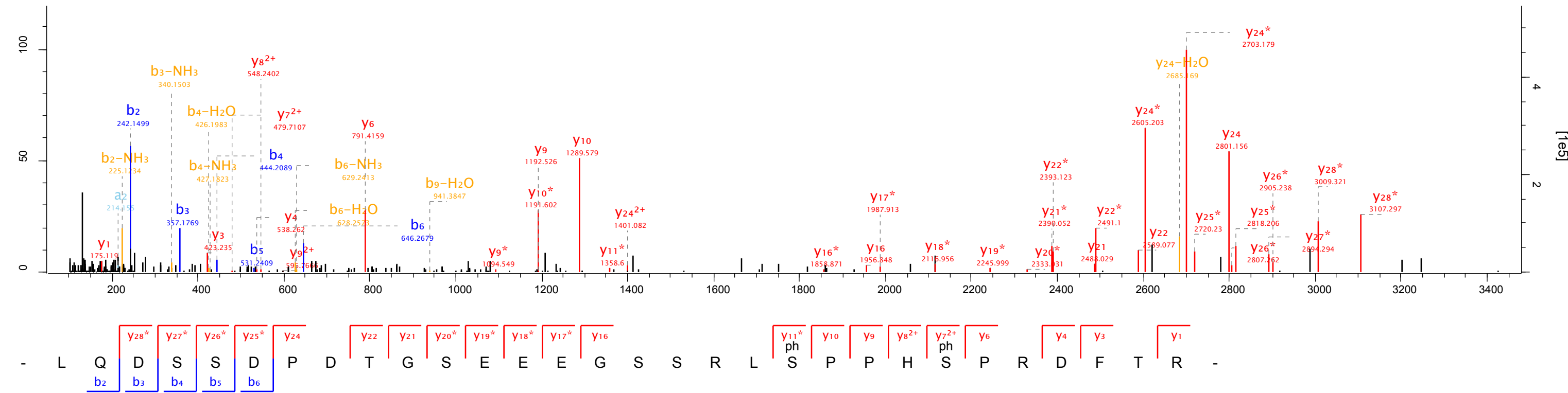


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10371 Method FTMS; HCD Score 64.45 m/z 1117.84 Gene names TBC1D9B

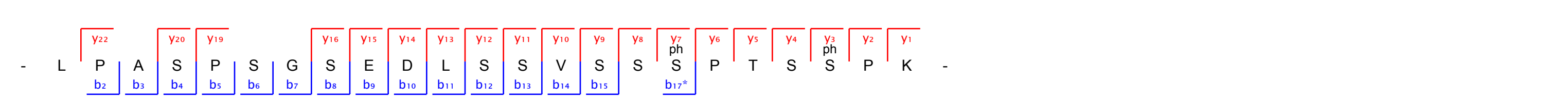
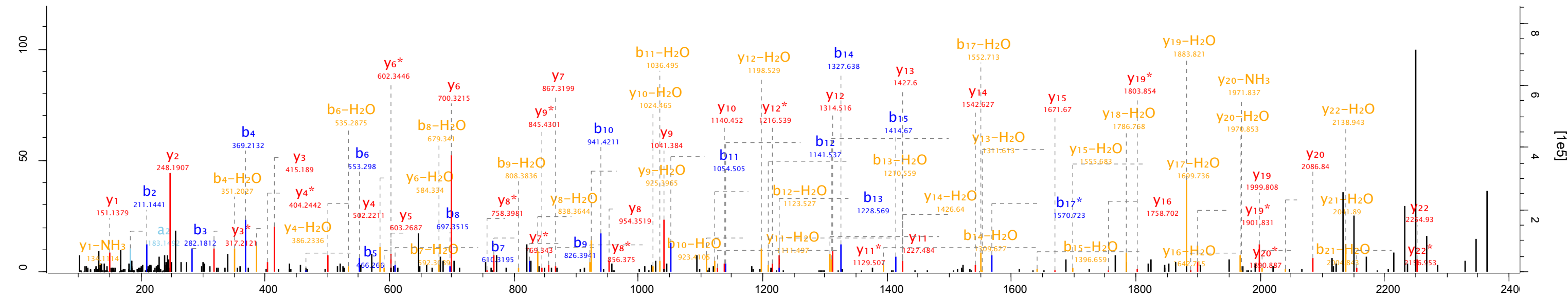




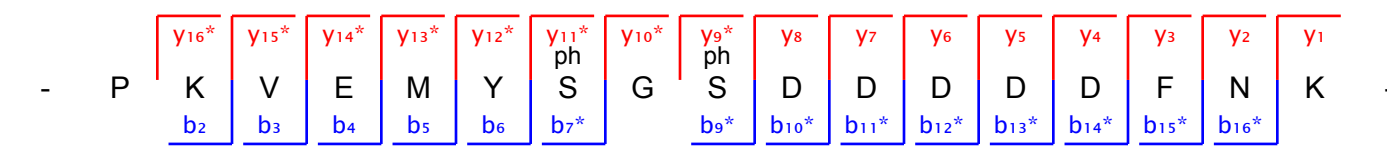
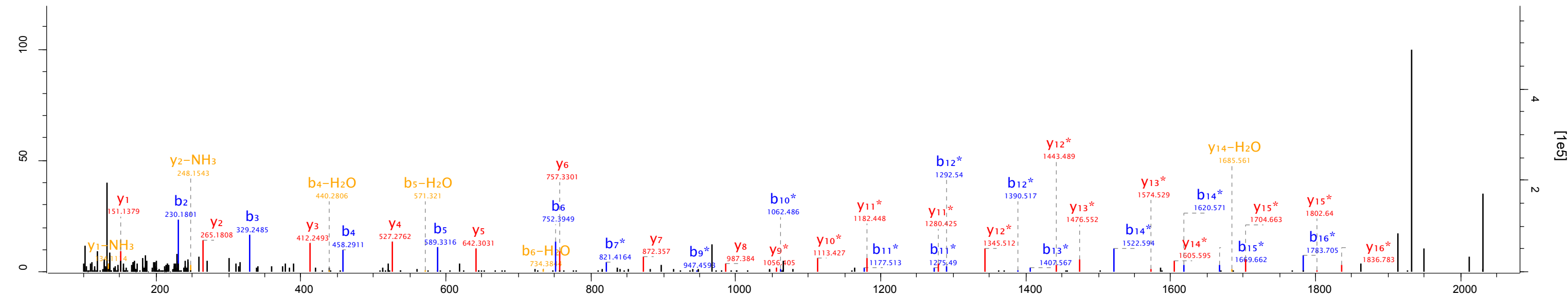
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10631 Method: FTMS; HCD Score: 94.43 m/z: 862.61 Gene names: ARHGEF2



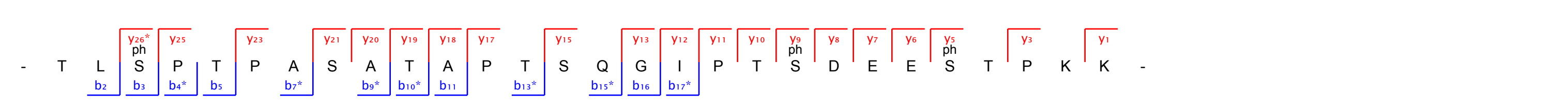
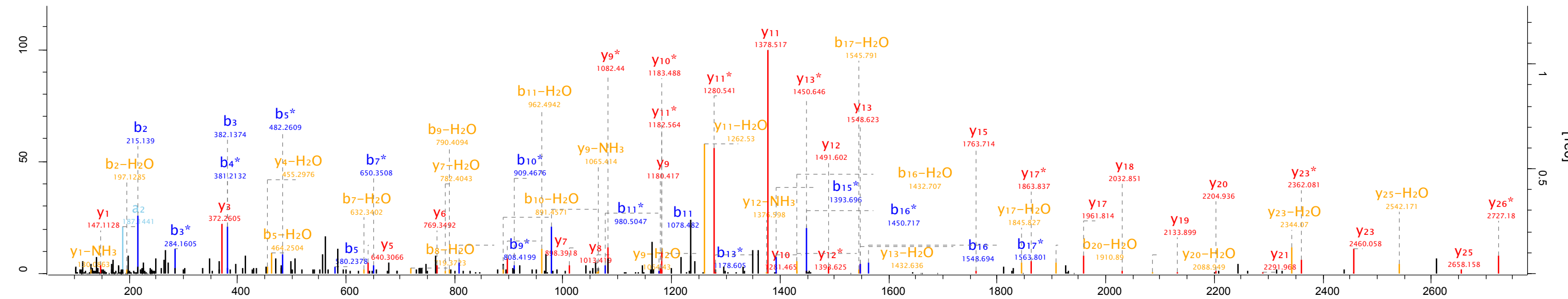
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10691 Method FTMS; HCD Score 236.35 m/z 1185.01 Gene names KANSL3



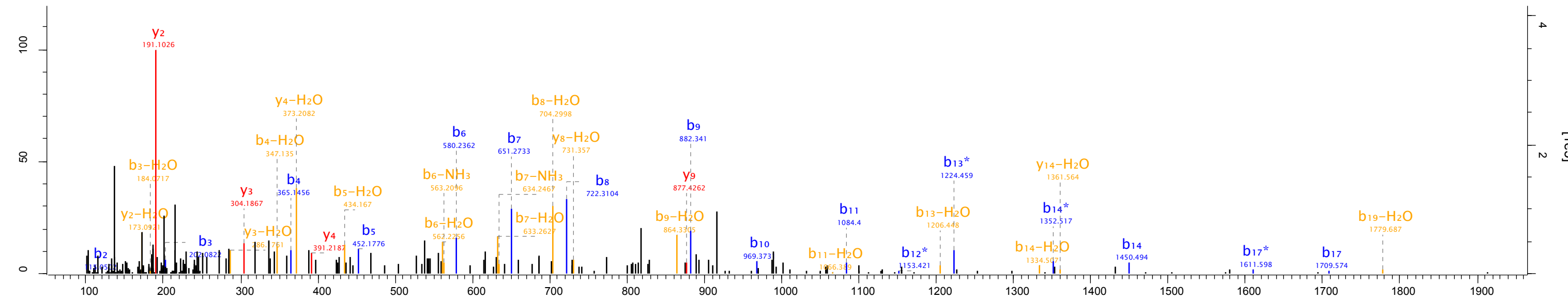
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10721 Method FTMS; HCD Score 179.17 m/z 1065.9 Gene names EIF5B



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10791 Method: FTMS; HCD Score: 163.95 m/z: 1014.1 Gene names: INCENP



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10861 Method FTMS; HCD Score 96.05 m/z 1100.43 Gene names HLA-B

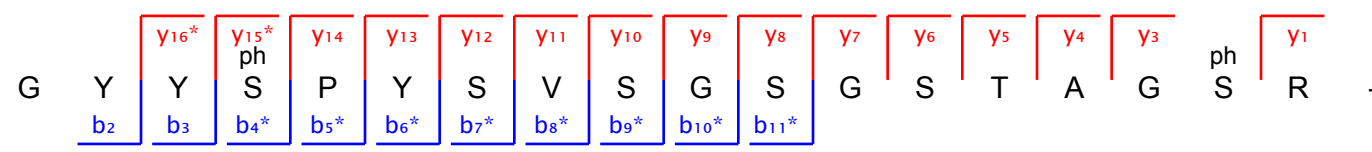
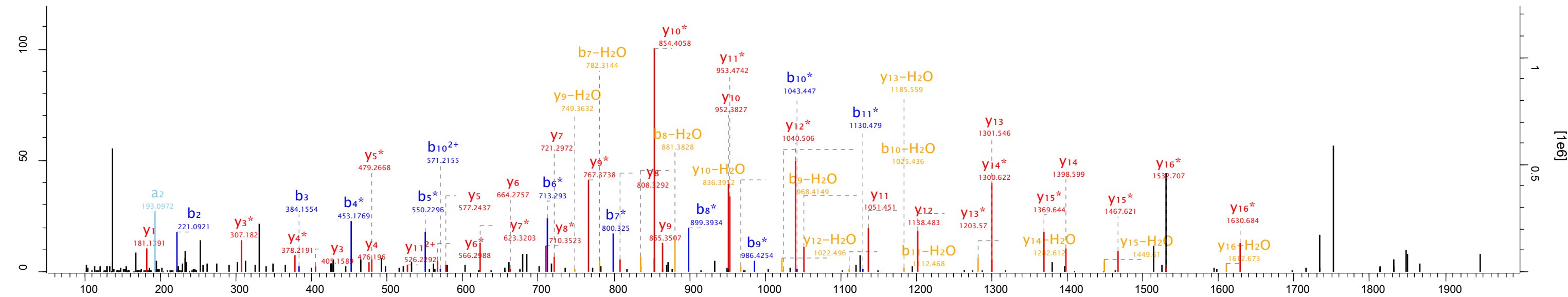


- G G S Y S Q A A C S D S A Q G S D V S L T A -

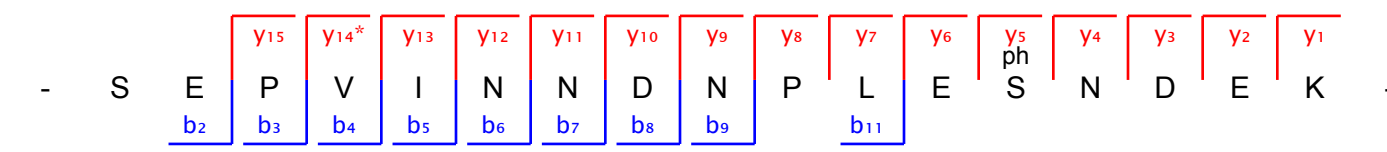
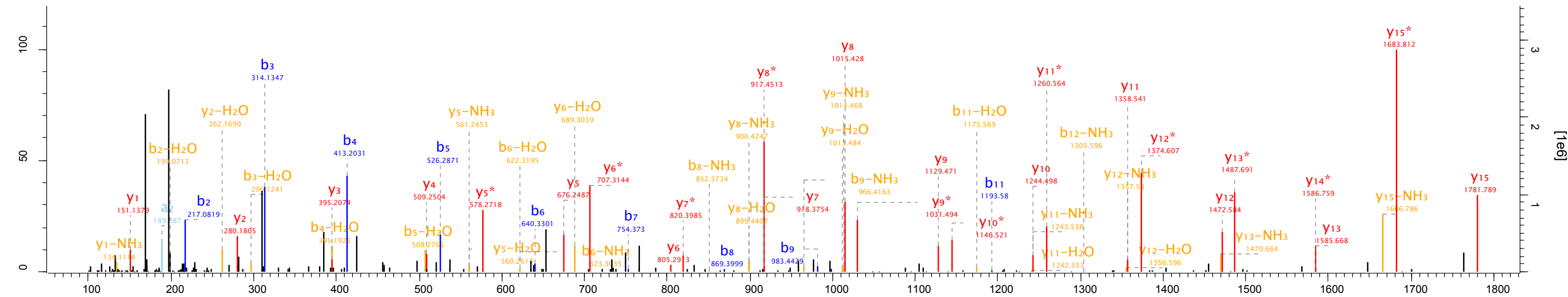
b2
b3
b4
b5
b6
b7
b8
b9
b10
b11
b12*
b13*
b14
b17

y9
y4
y3
y2

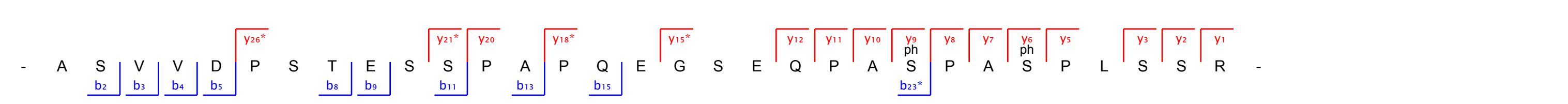
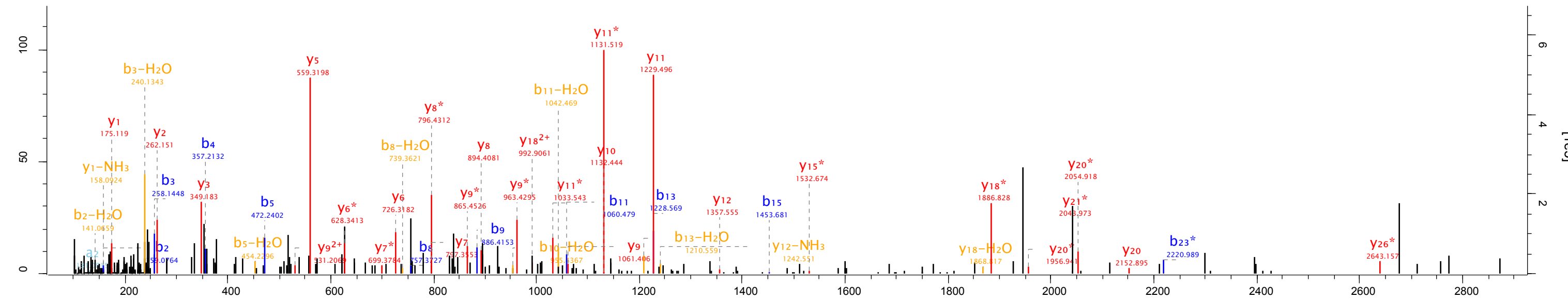
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10911 Method: FTMS; HCD Score: 209.17 m/z: 974.88 Gene names: PLEC



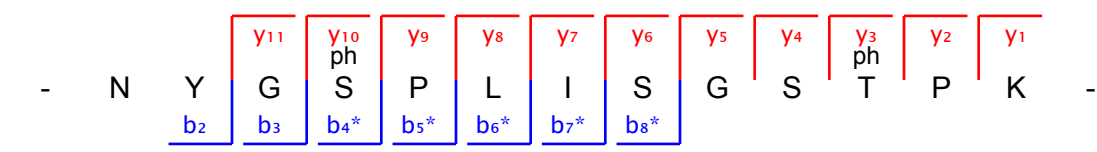
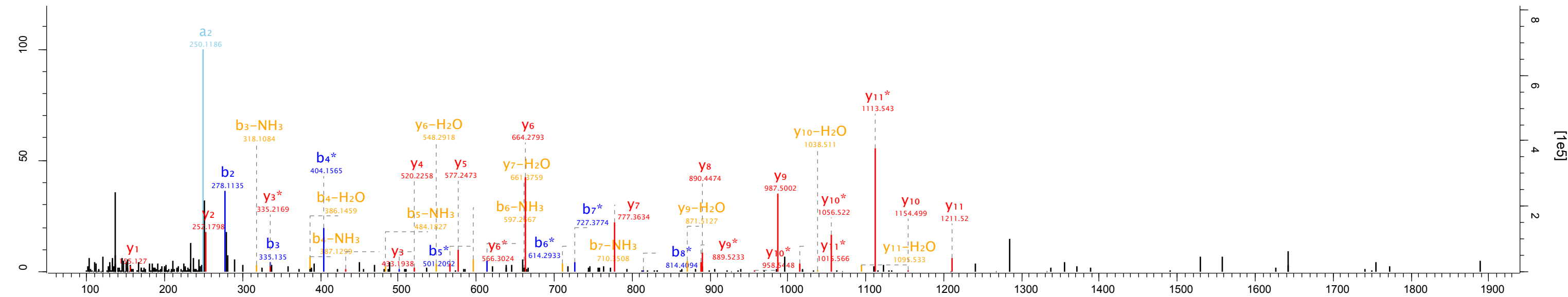
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 11041 Method: FTMS; HCD Score: 319.18 m/z: 999.94 Gene names: SP100



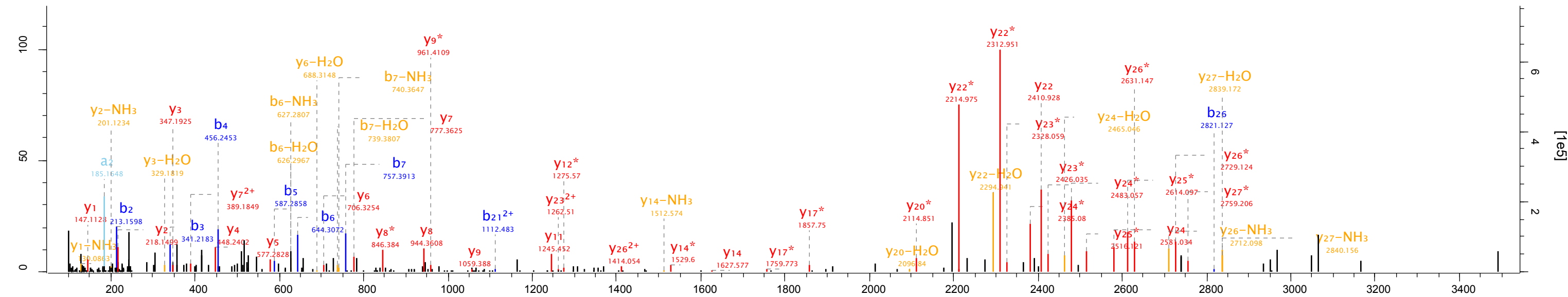
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11441 Method FTMS; HCD Score 81.83 m/z 1071.8 Gene names TBC1D9B



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11501 Method FTMS; HCD Score 108.12 m/z 744.82 Gene names MED1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11621 Method FTMS; HCD Score 165.97 m/z 1056.78 Gene names ILF3

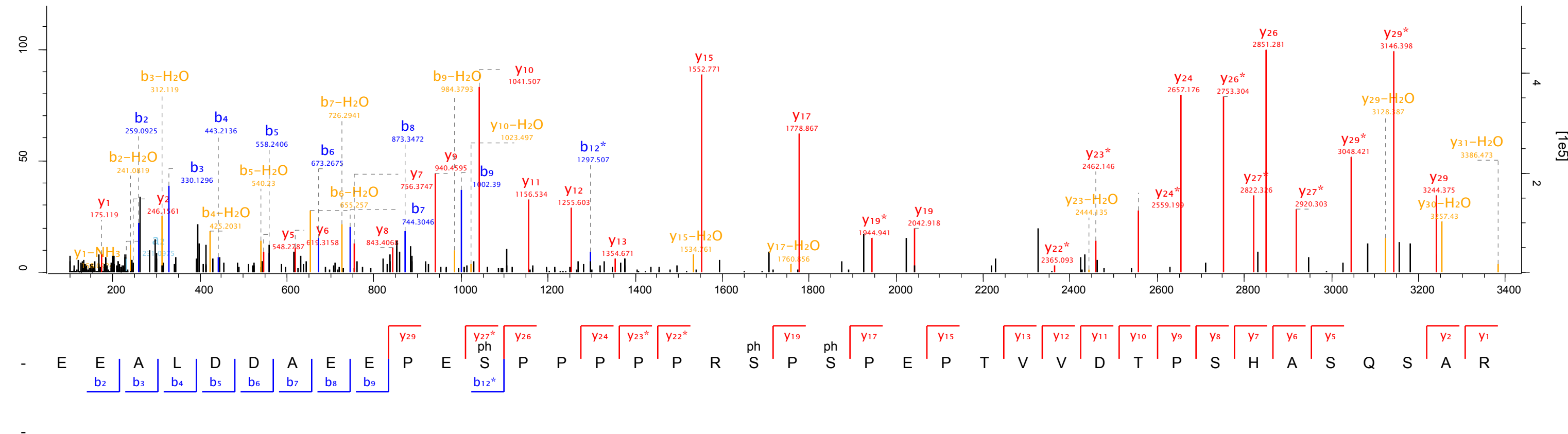


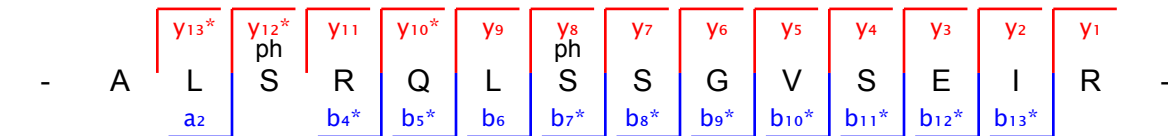
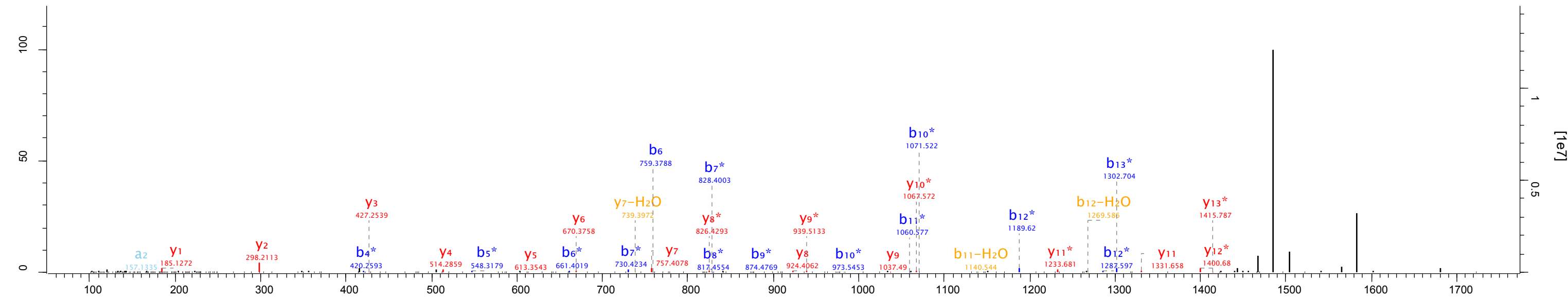
- V L Q D M G L P T G A E G R D S S K G E D S A E E T E A K -

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

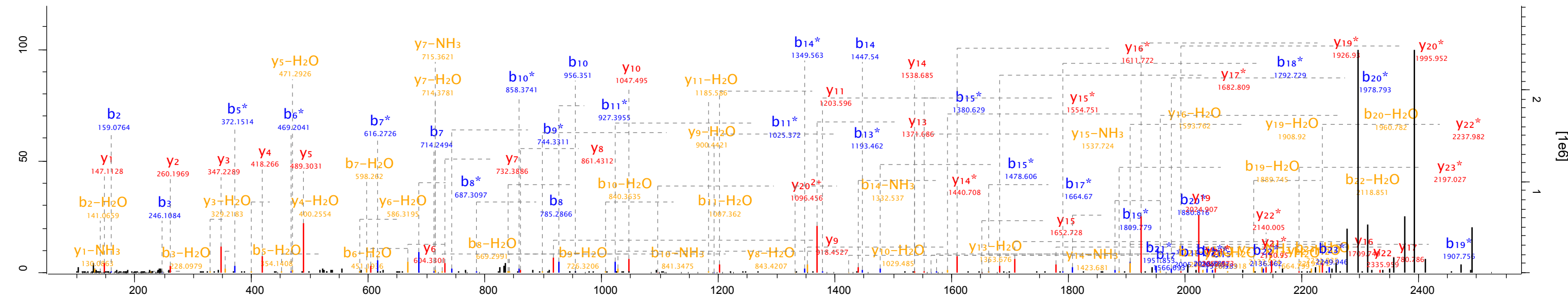
- Red boxes (y ions): y27* (Q), y26* (D), y25* (M), y24 (G), y23* (L), y22 (P), y20* (G), y17* (G), y14 (S), y12* (K), y11 (G), y9 (D), y8 ph (S), y7 (A), y6 (E), y5 (E), y4 (T), y3 (E), y2 (A), y1 (K).
- Blue boxes (b ions): b2 (L), b3 (Q), b4 (D), b5 (M), b6 (G), b7 (L), b21²⁺ (D), b26 (T).

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11911 Method FTMS; HCD Score 143.24 m/z 1062.45 Gene names RERE





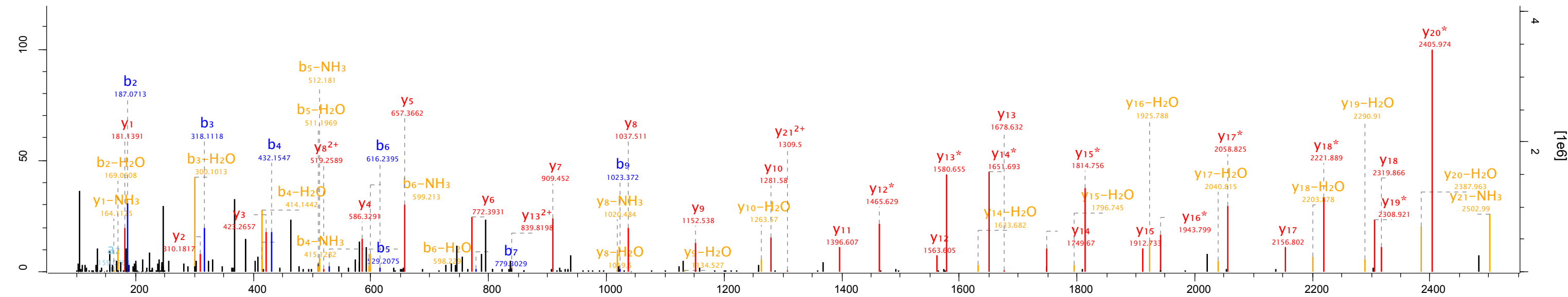
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11971 Method FTMS; HCD Score 340.34 m/z 1248.02 Gene names ZC3H4



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

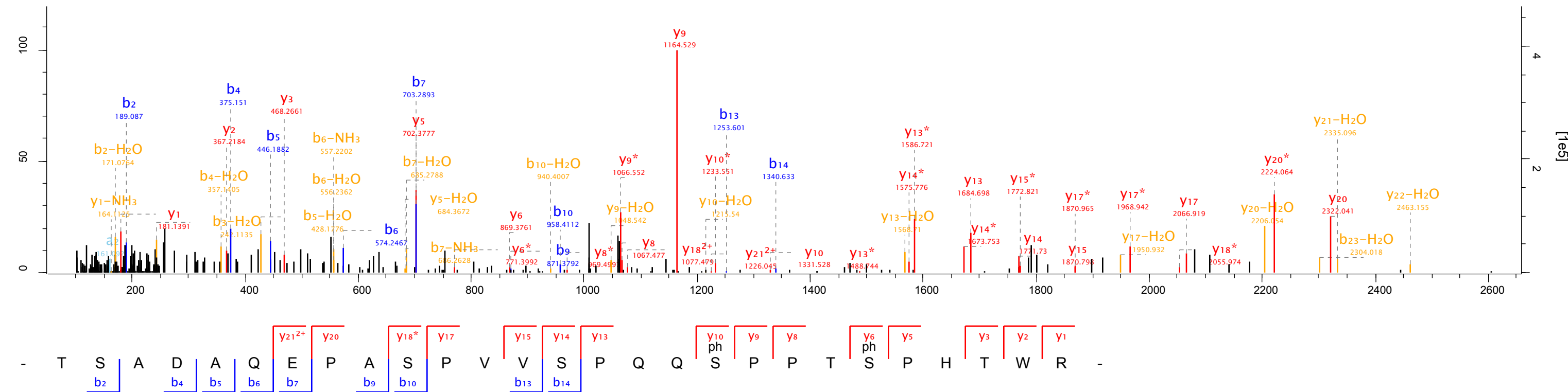
b₂ b₃ b₅* b₆* b₇ b₈ b₉* b₁₀ b₁₁* b₁₃* b₁₄ b₁₅ b₁₇* b₁₈* b₁₉ b₂₀* b₂₁* b₂₂* b₂₃*

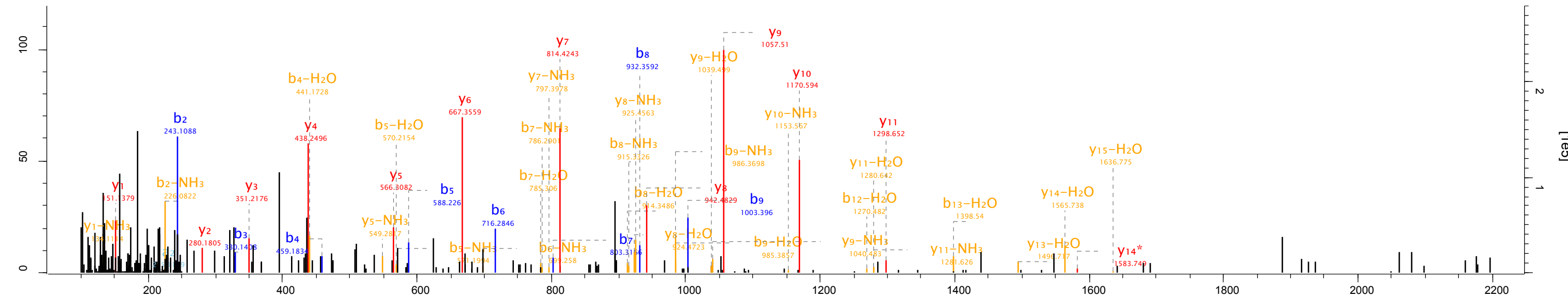
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 12171 Method: FTMS; HCD Score: 228.55 m/z: 979.04 Gene names: SSRP1



- E G M N P S Y D E Y A D S D E D Q H D A Y L E R -
 (b2) (b3) (b4) (b5) (b6) (b7) (b9)

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12451 Method FTMS; HCD Score 131.76 m/z 1009.11 Gene names REPS1



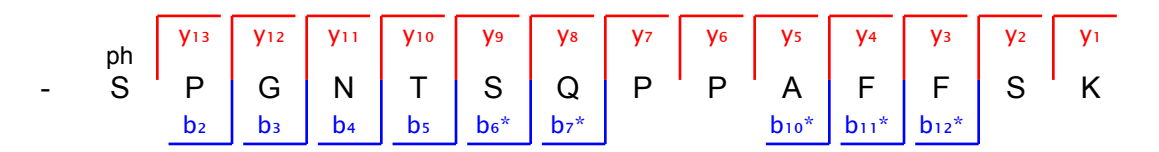
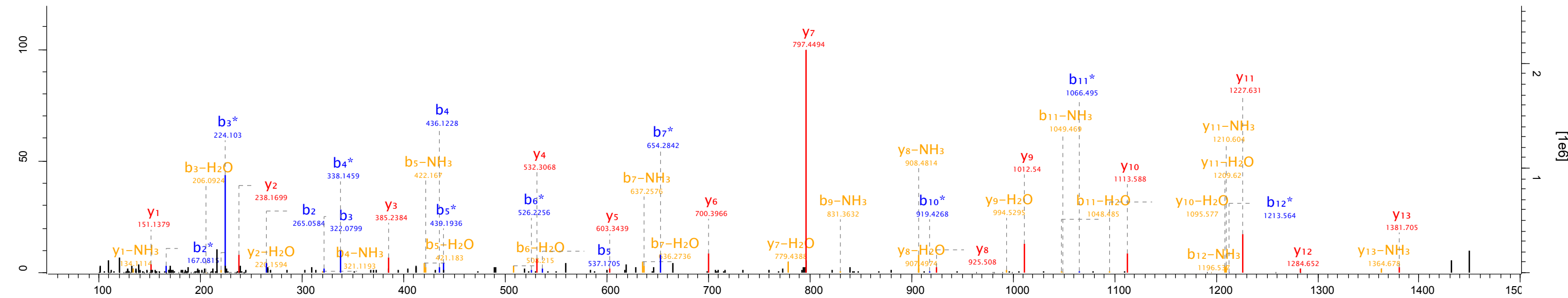


- N Q S E E Q S E A S S E Q L D Q F T Q S A E K -

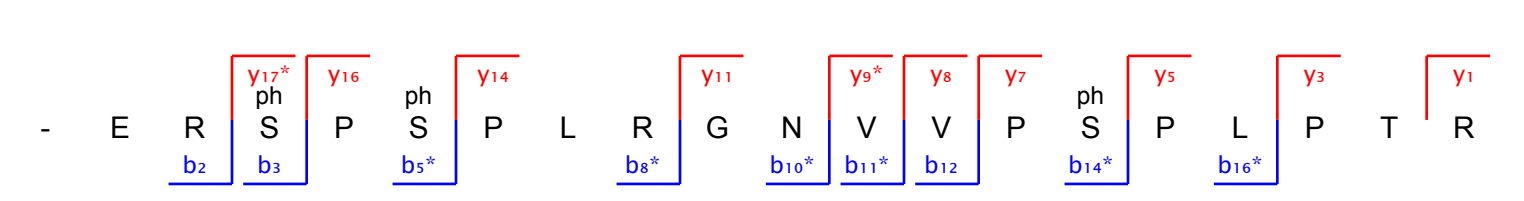
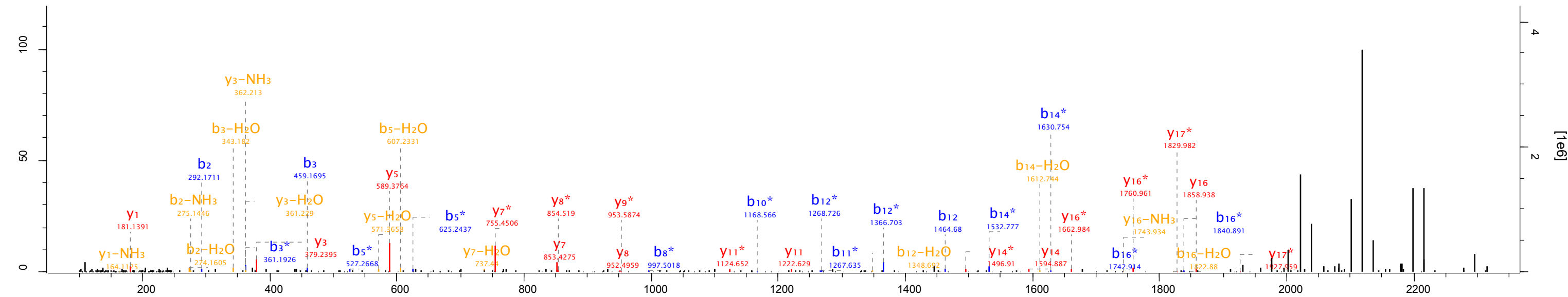
Fragmentation sites are indicated by brackets below the amino acid sequence:

- b2: N-Q
- b3: Q-S
- b4: S-E
- b5: E-E
- b6: E-Q
- b7: Q-S
- b8: S-E
- b9: E-A
- y14*ph: A-S
- y11: Q-L
- y10: L-D
- y9: D-Q
- y8: Q-F
- y7: F-T
- y6: T-Q
- y5: Q-S
- y4: S-A
- y3: A-E
- y2: E-K

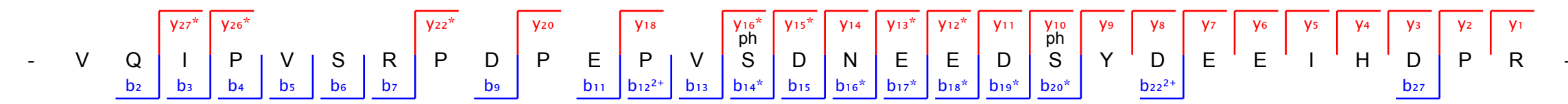
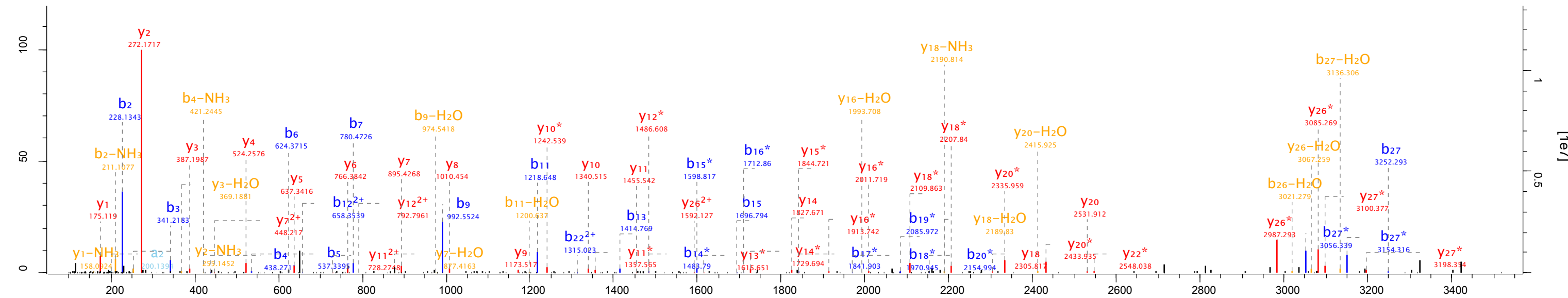
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13031 Method: FTMS; HCD Score: 199.41 m/z: 774.85 Gene names: NCOR2



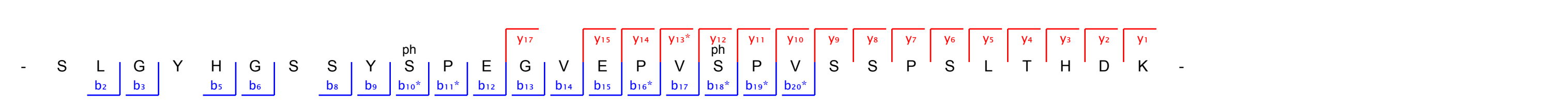
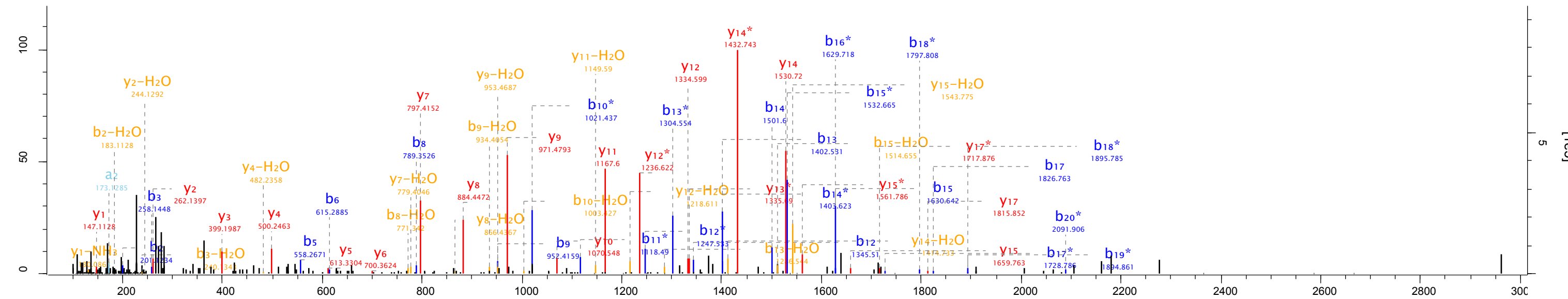
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13221 Method FTMS; HCD Score 151.19 m/z 1159.05 Gene names CARHSP1



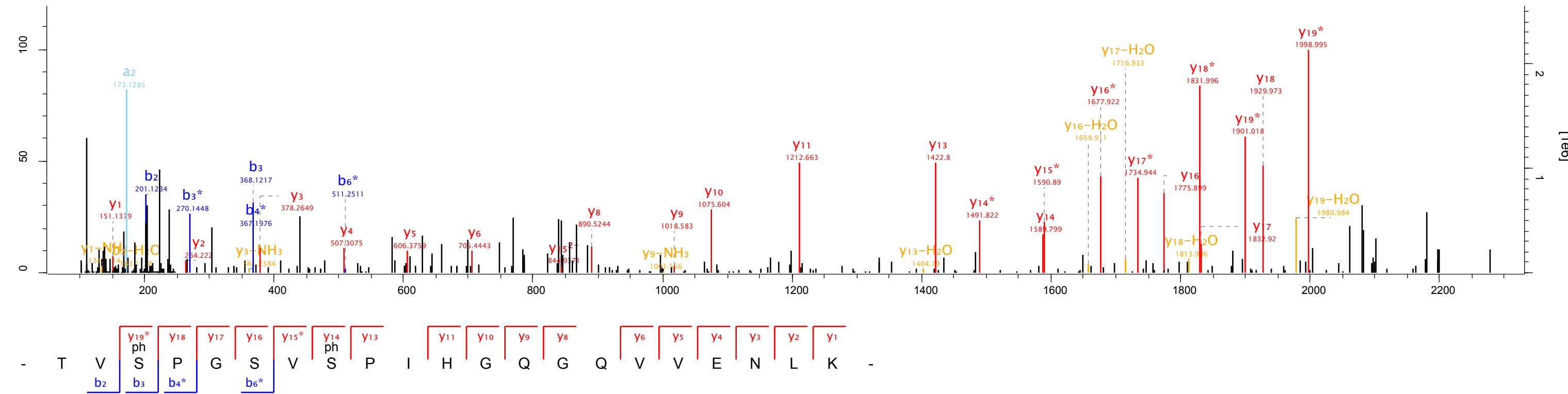
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13351 Method FTMS; HCD Score 180.69 m/z 1175.49 Gene names TJP1



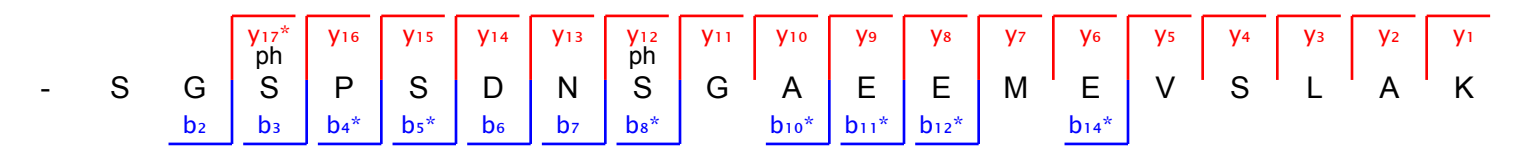
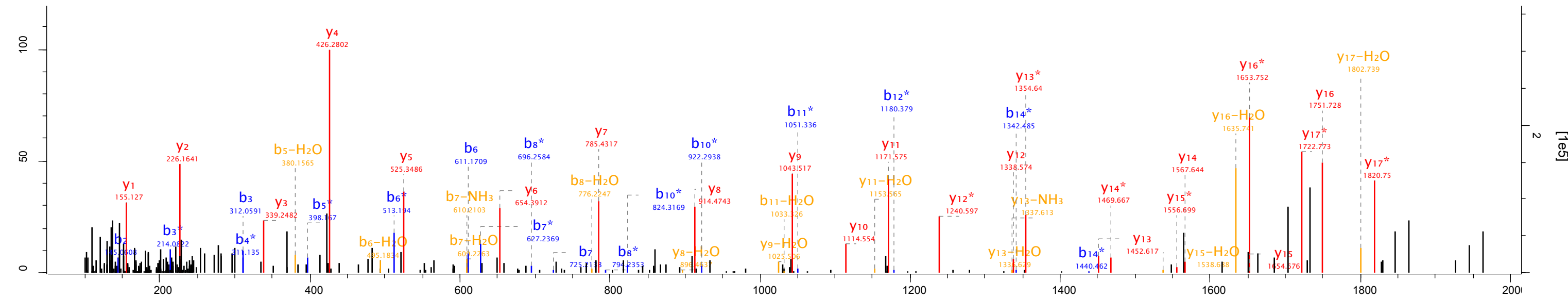
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13381 Method: FTMS; HCD Score: 169.22 m/z: 1054.46 Gene names: NCOR2



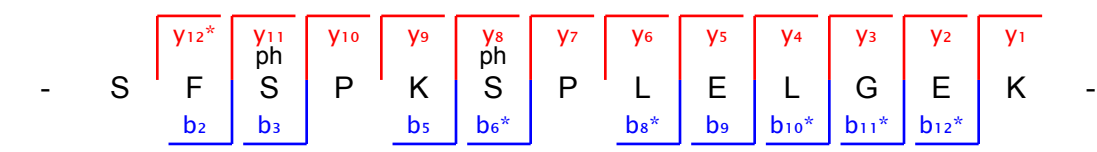
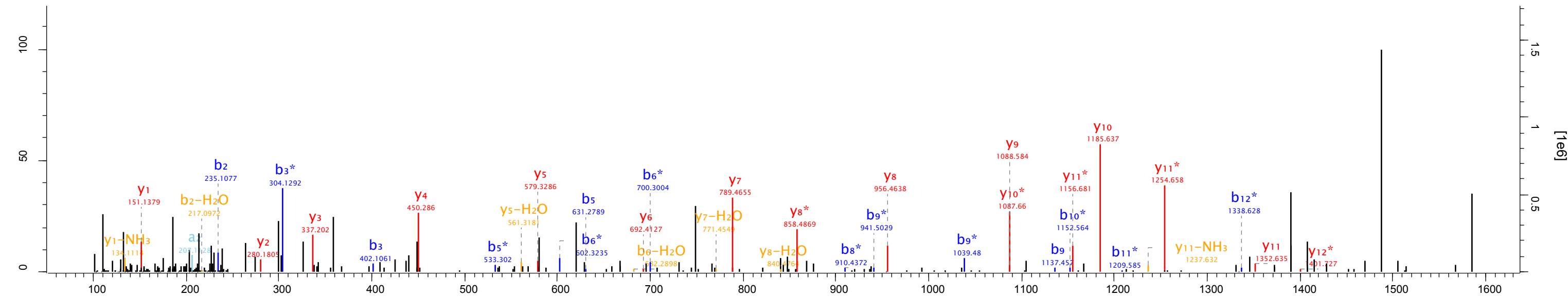
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13501 Method FTMS; HCD Score 88.71 m/z 766.7 Gene names ITSN2



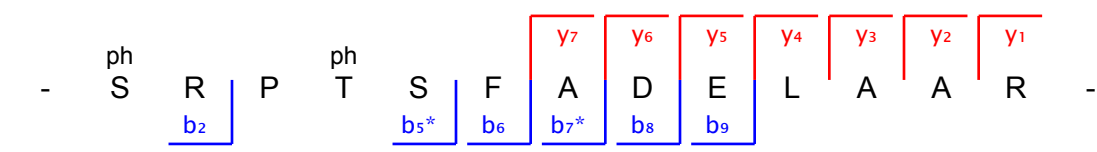
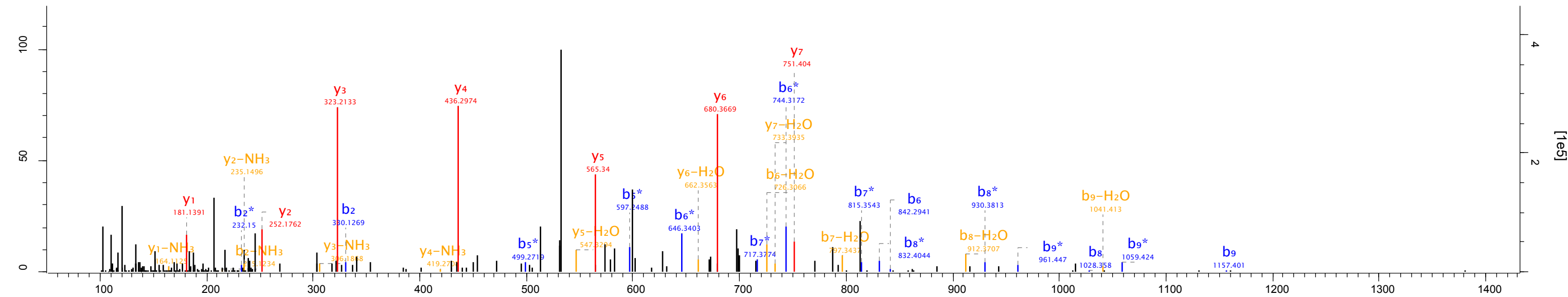
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13521 Method FTMS; HCD Score 140.55 m/z 1031.89 Gene names AKT1

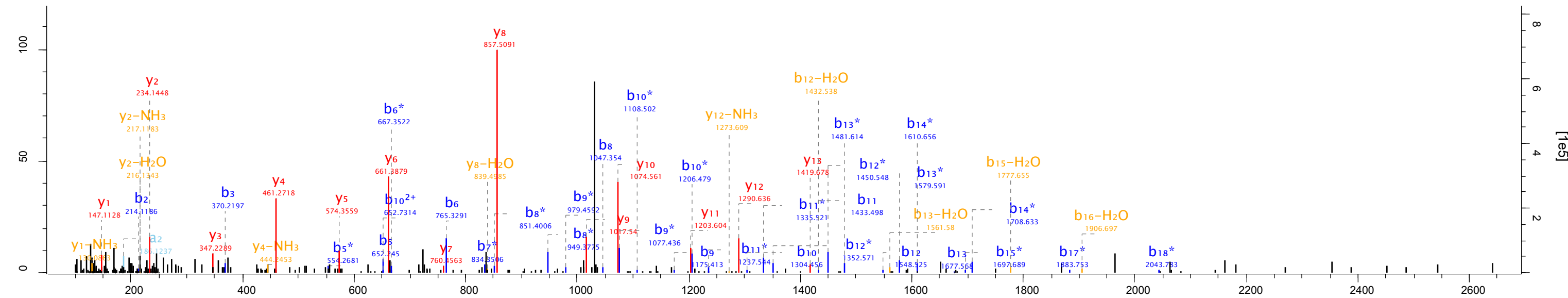


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13911 Method FTMS; HCD Score 96 m/z 793.87 Gene names NAB2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13941 Method FTMS; HCD Score 84.21 m/z 531.57 Gene names FAM21A;FAM21C

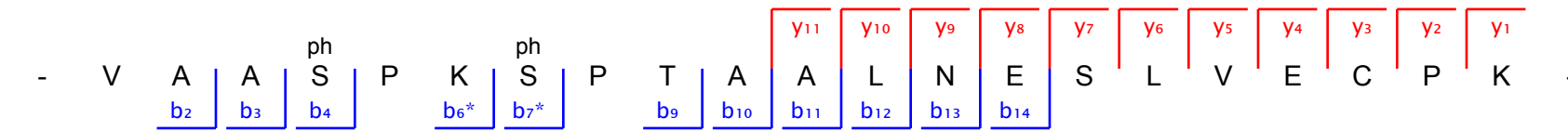
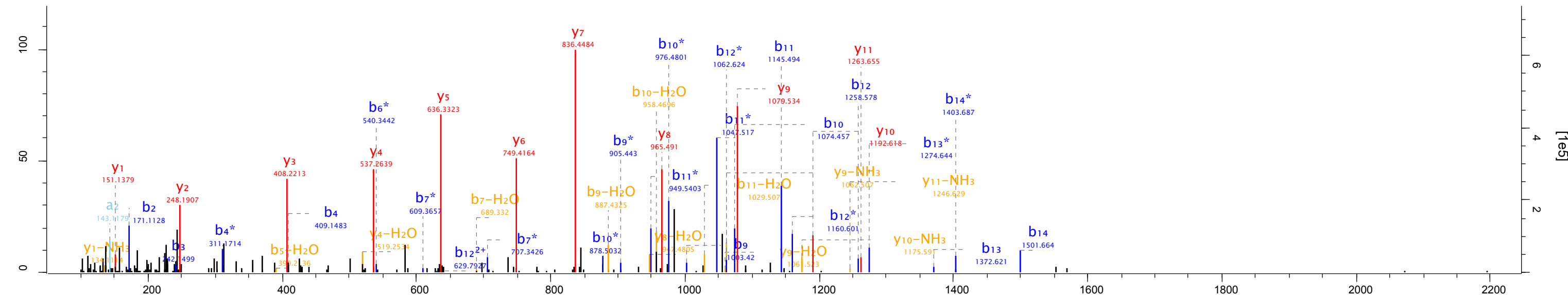




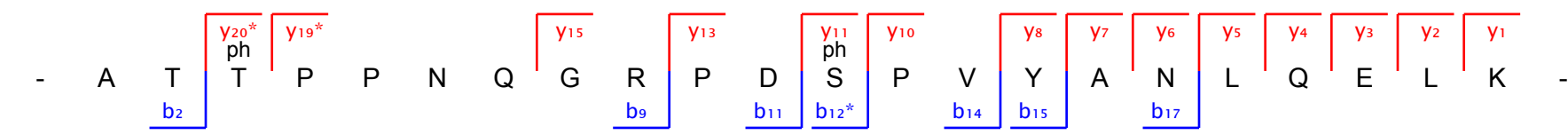
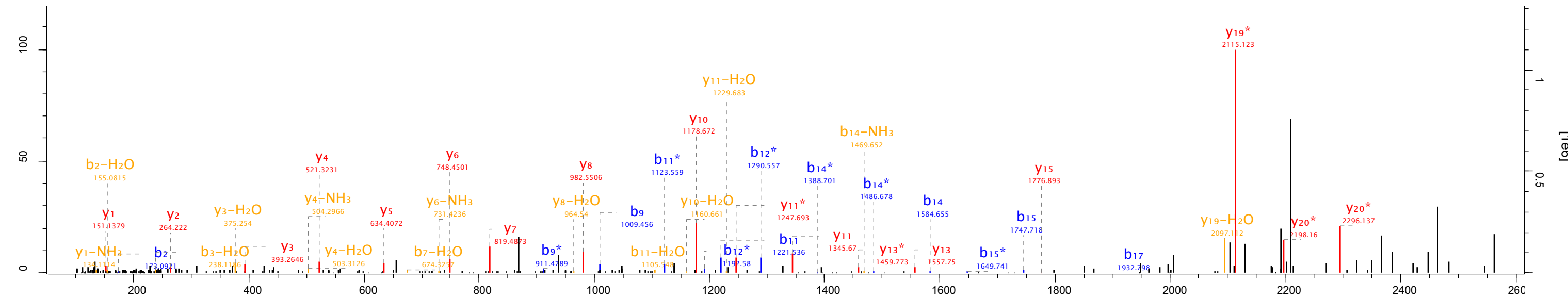
- N V R S D I S D Q E E D E E S E G C P V S I N L S K -

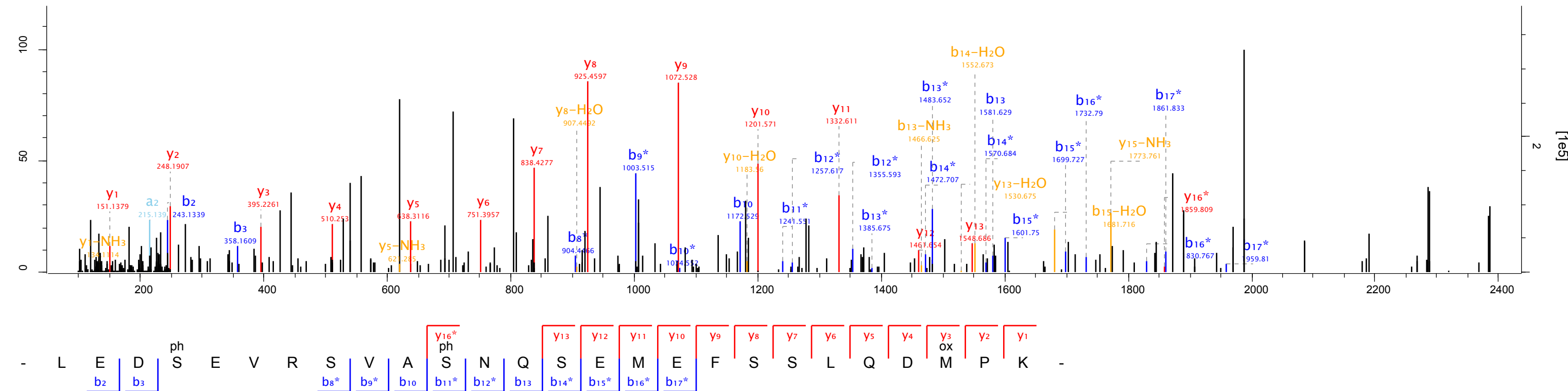
ph ph

b₂ b₃ b₅ b₆ b₇^{*} b₈ b₉ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄^{*} b₁₅^{*} b₁₇^{*} b₁₈^{*} y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

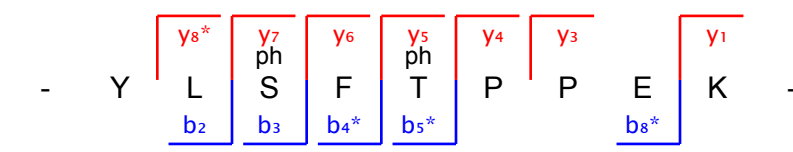
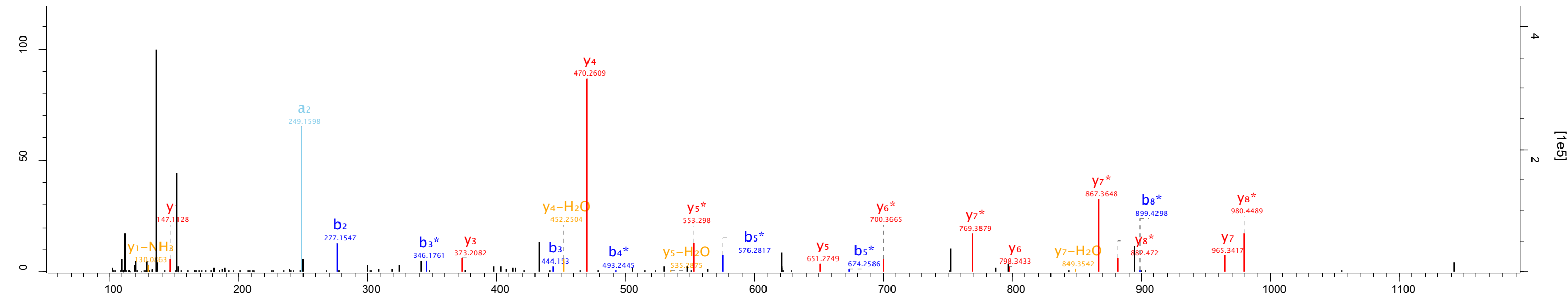


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15031 Method FTMS; HCD Score 128.71 m/z 1283.6 Gene names ARHGAP12

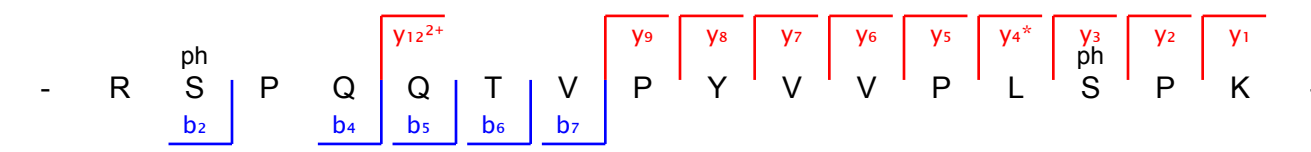
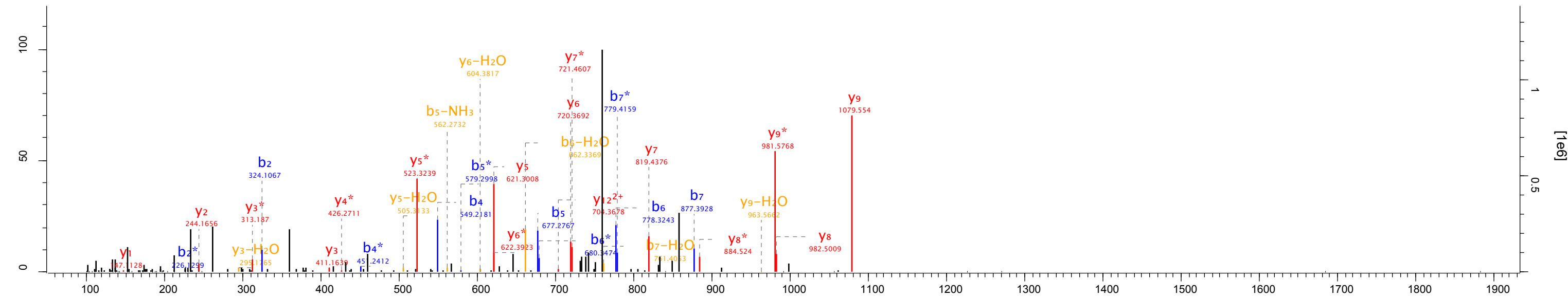




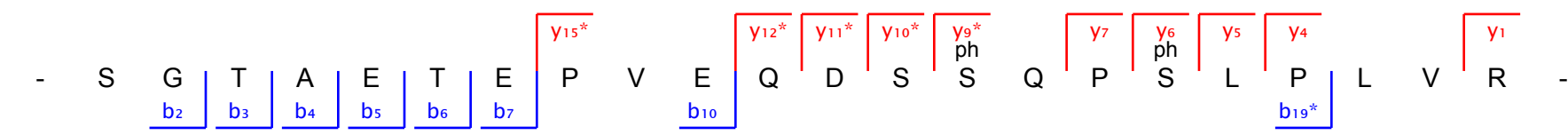
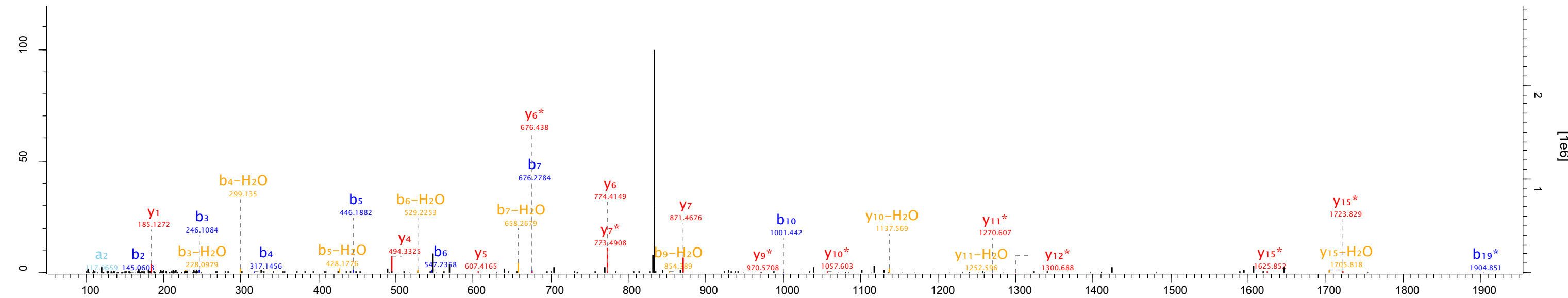
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15201 Method FTMS; HCD Score 102.33 m/z 621.25 Gene names PAK2



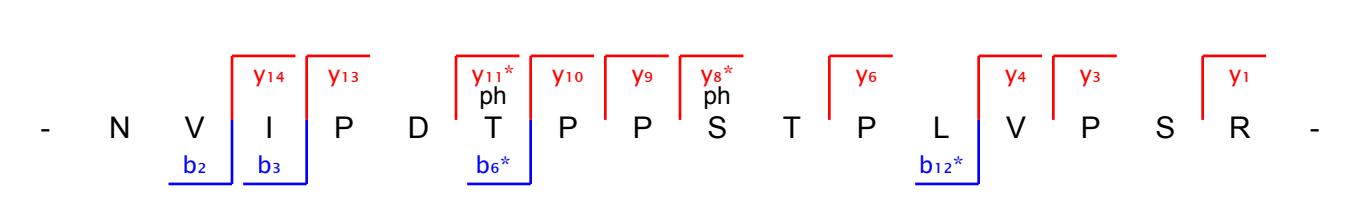
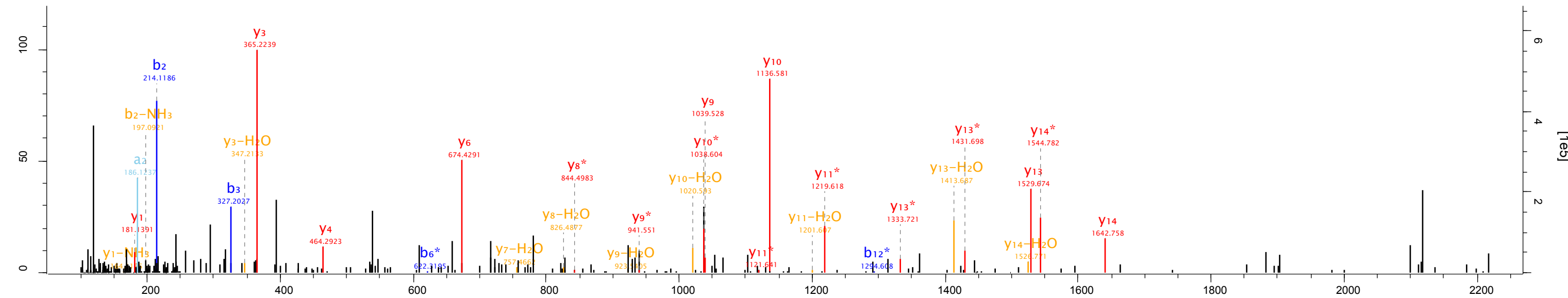
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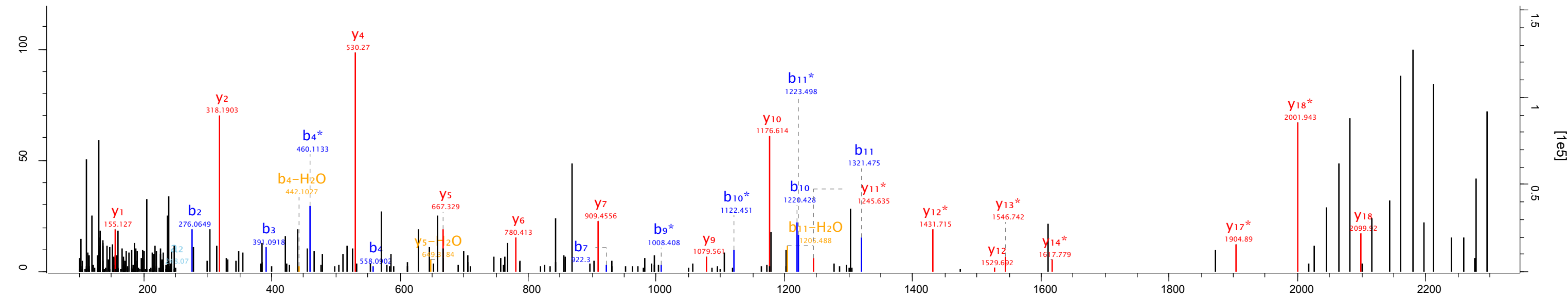
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15601 Method FTMS; HCD Score 70.12 m/z 928.44 Gene names AKAP11

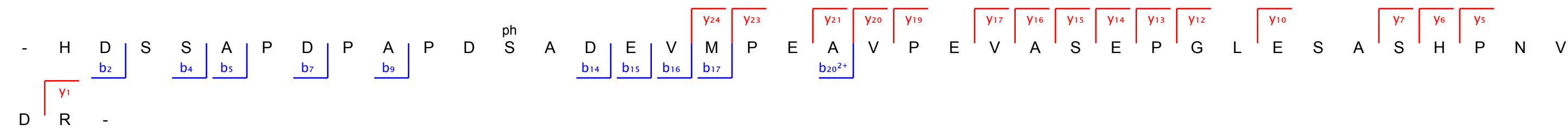
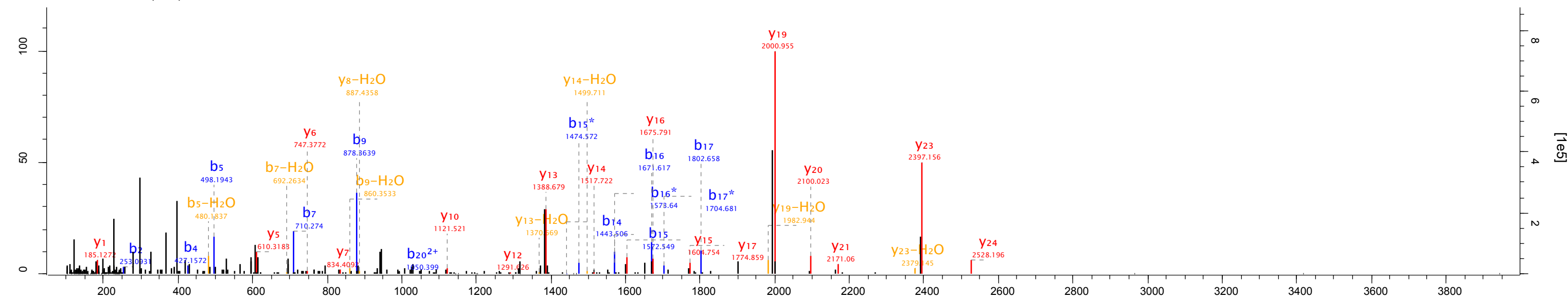


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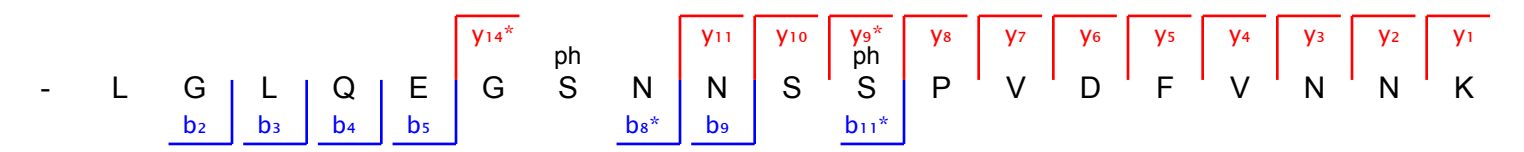
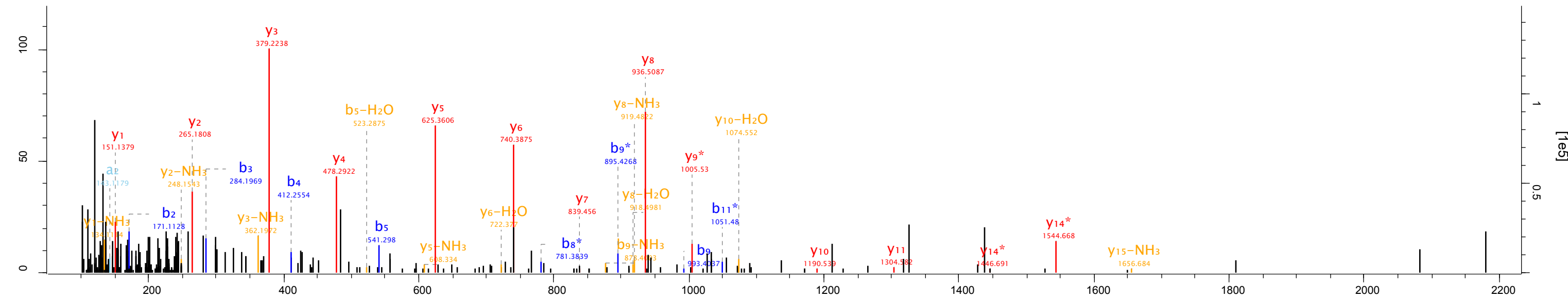


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20171215_MaS_33SR_LMH_phospho2_03

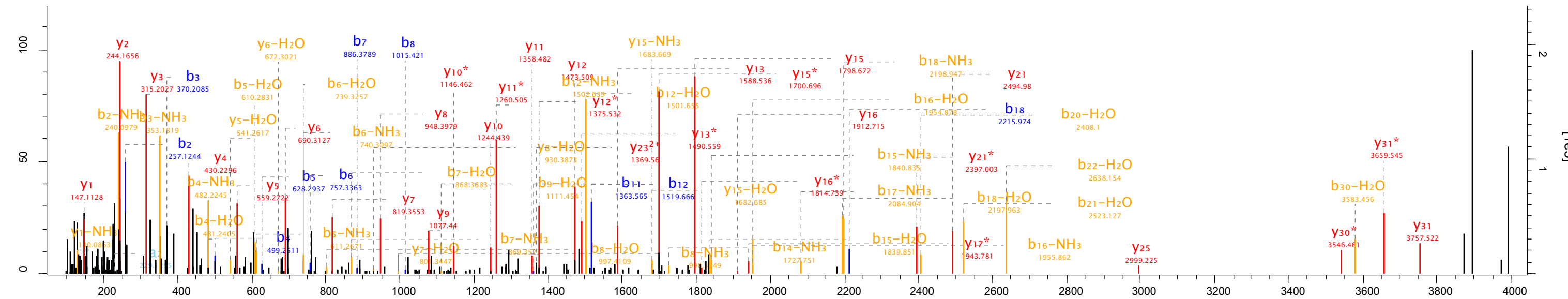
Scan 15921 Method FTMS; HCD Score 61.4 m/z 1050.96 Gene names DIDO1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16021 Method FTMS; HCD Score 55.18 m/z 1092.47 Gene names SPAG5



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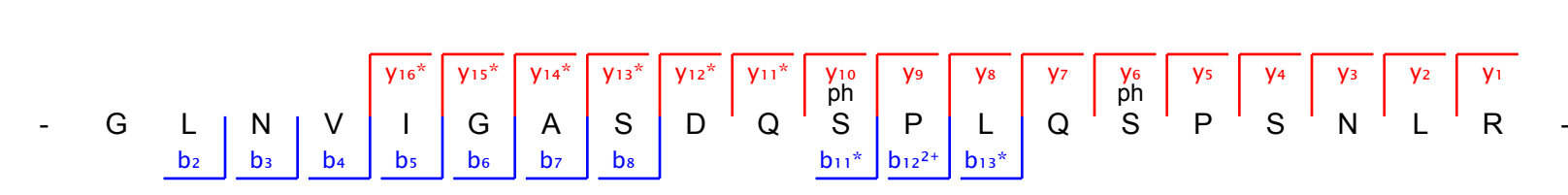
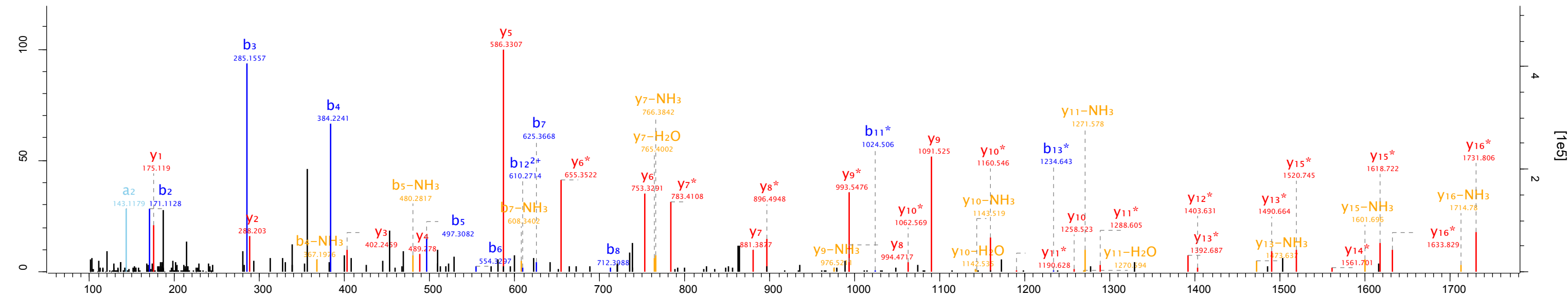


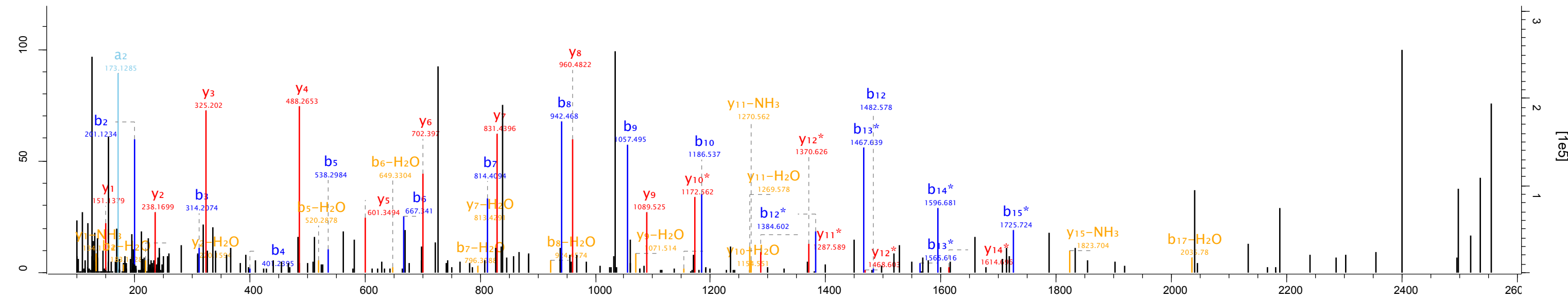
Protein sequence: - Q Q L E E E E N F S R P Q I D E N P L D D N S E E E M E D A P K -

Fragmentation sites are indicated by brackets below the sequence:

- Red brackets (y ions): y₃₁, y₃₀*, y₂₅, y₂₃²⁺, y₂₁, y₁₇*, y₁₆, y₁₅, y₁₃, y₁₂, y₁₁, y₁₀ph, y₉, y₈, y₇, y₆, y₅, y₄, y₃, y₂, y₁
- Blue brackets (b ions): b₂, b₃, b₄, b₅, b₆, b₇, b₈, b₁₁, b₁₂, b₁₈

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16161 Method FTMS; HCD Score 202.47 m/z 738.34 Gene names PLEKHA5

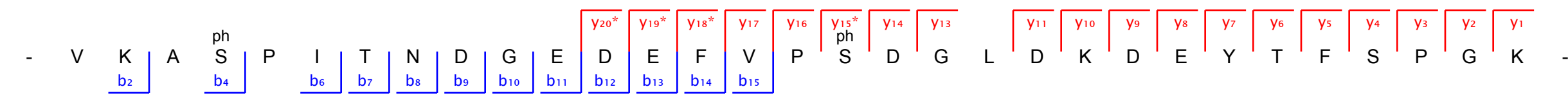
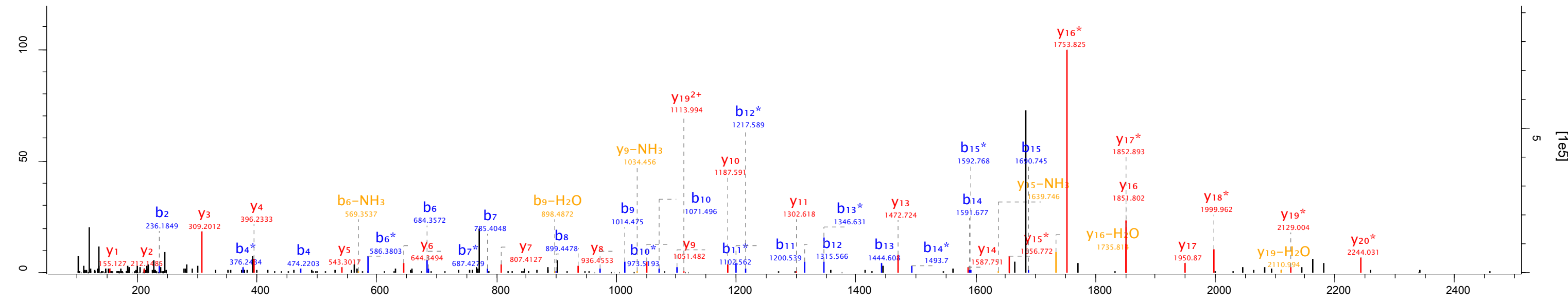




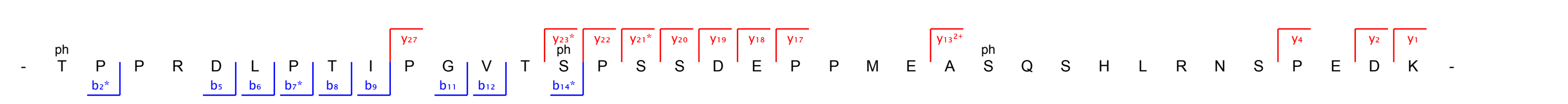
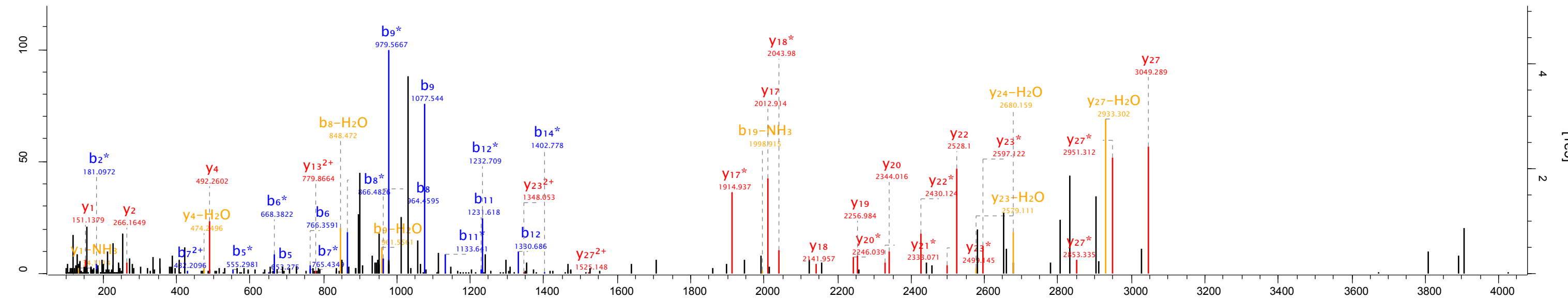
- S L L S H E F Q D E T D D T E E E T L Y S S K -

b₂
b₃
b₄
b₅
b₆
b₇
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b₉
b₁₀
y₁₄*
y₁₂*
ph
y₁₁*
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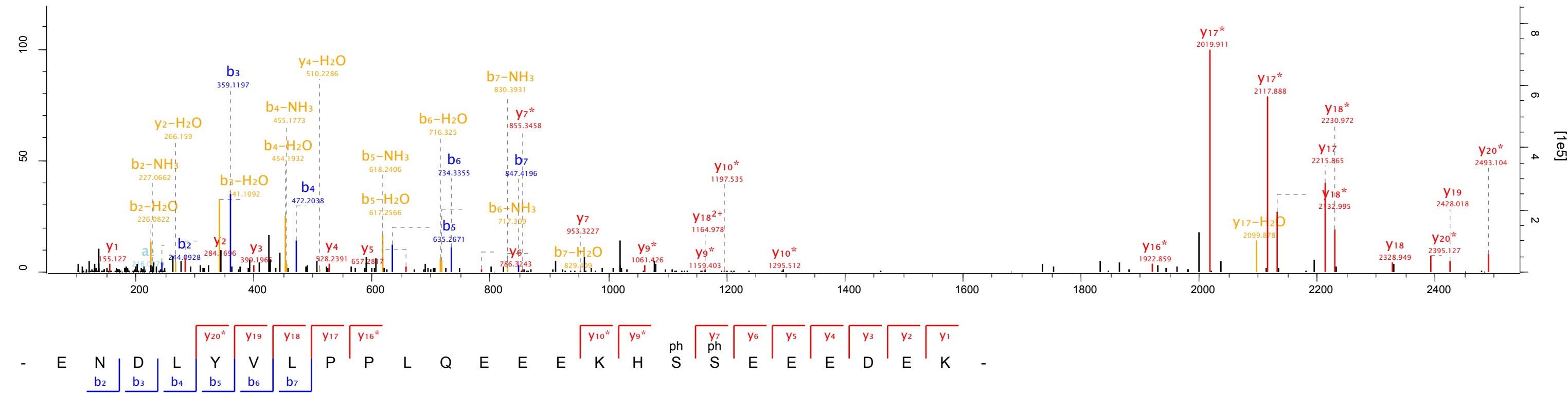
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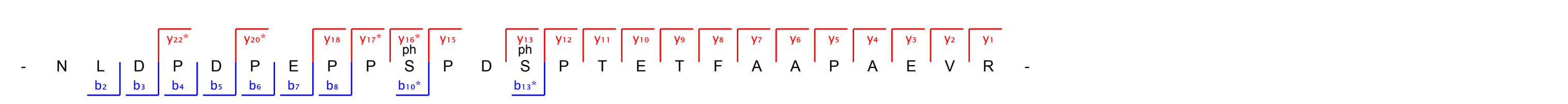
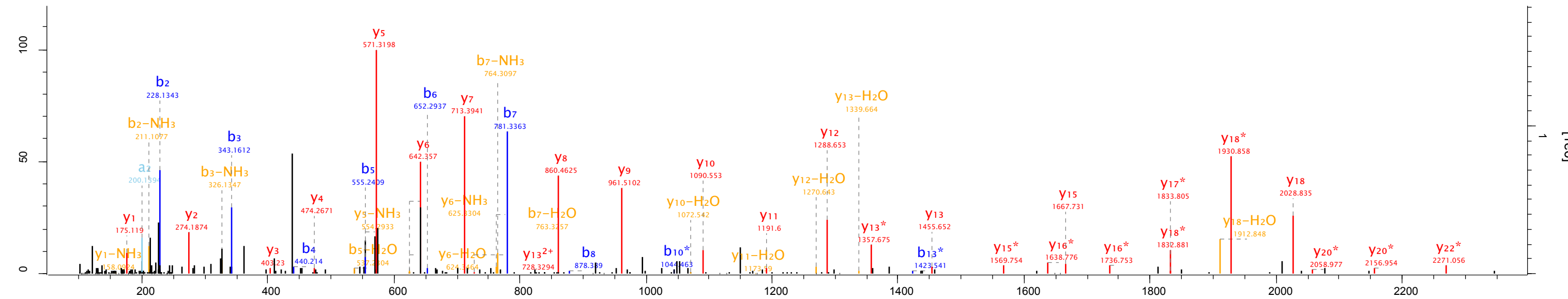
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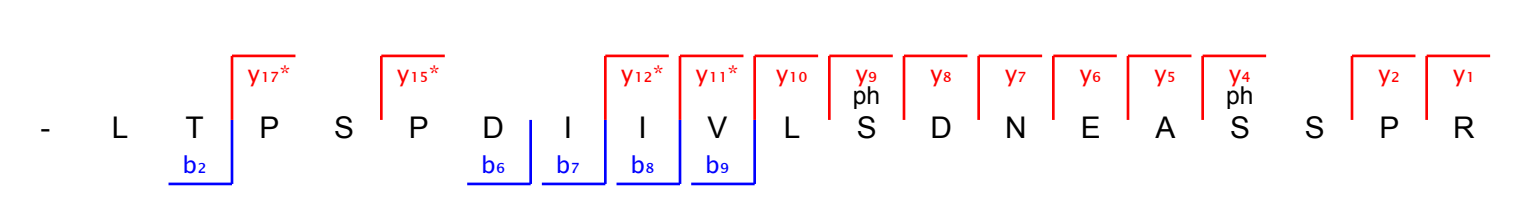
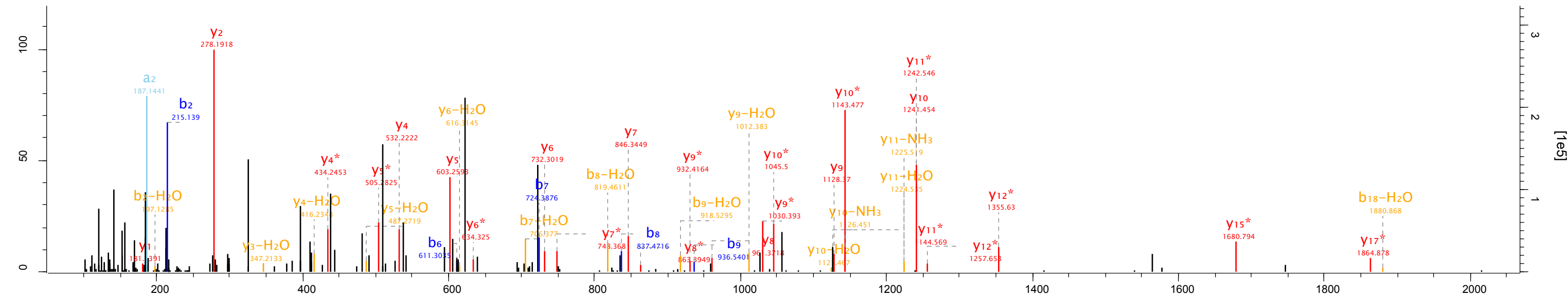
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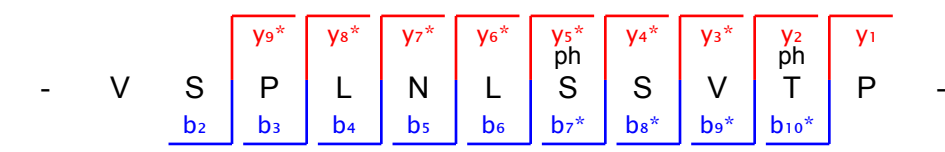
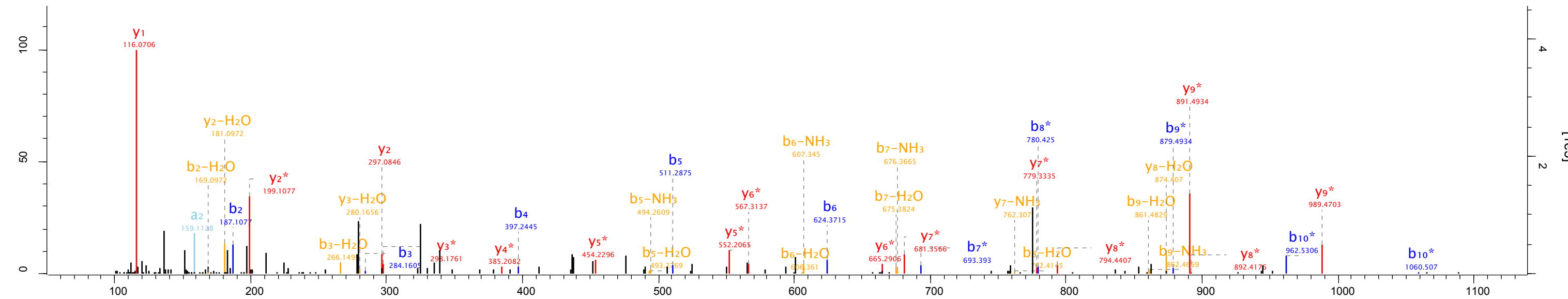
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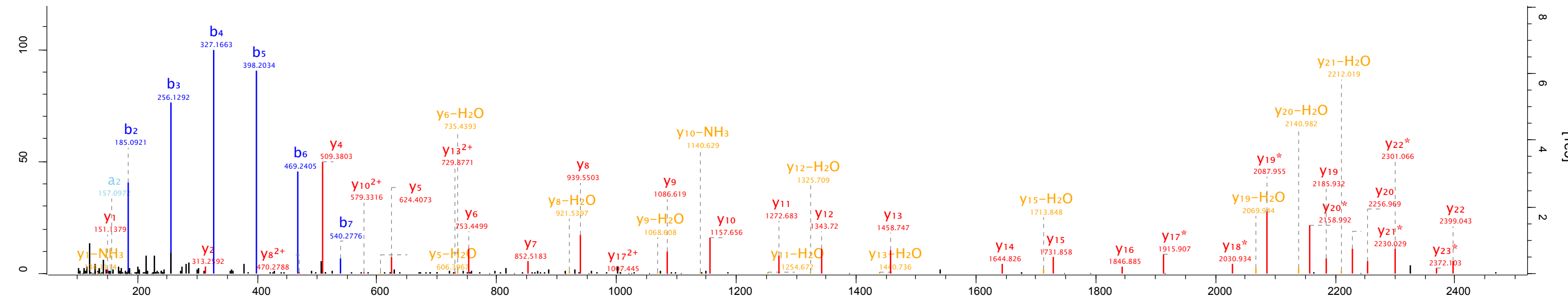
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18081 Method FTMS; HCD Score 159.41 m/z 637.28 Gene names CDC23



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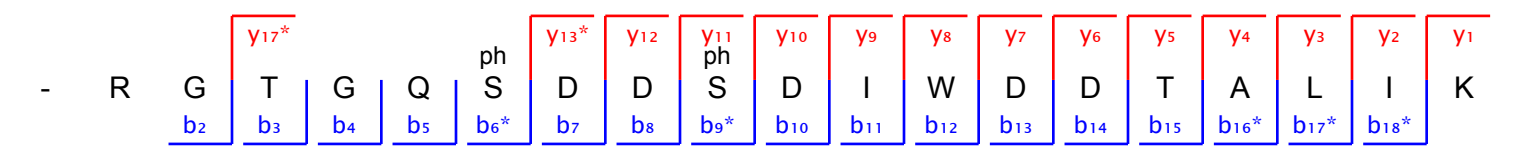
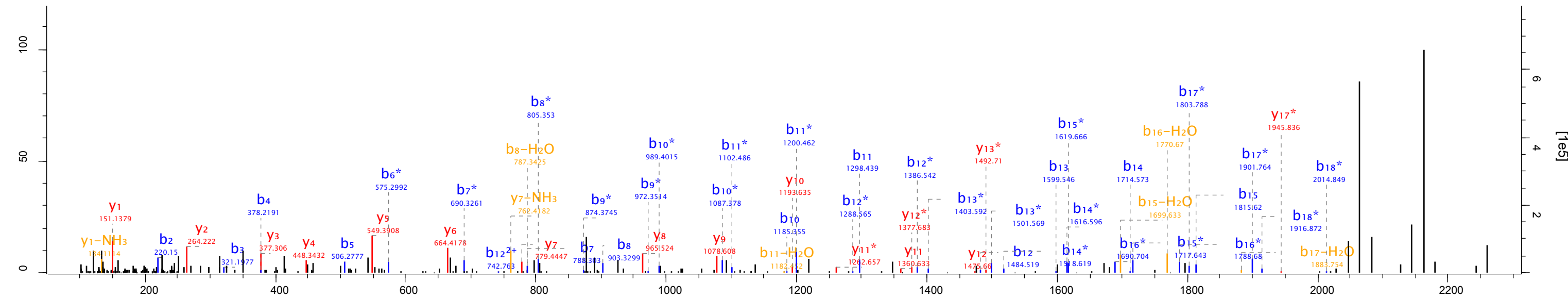


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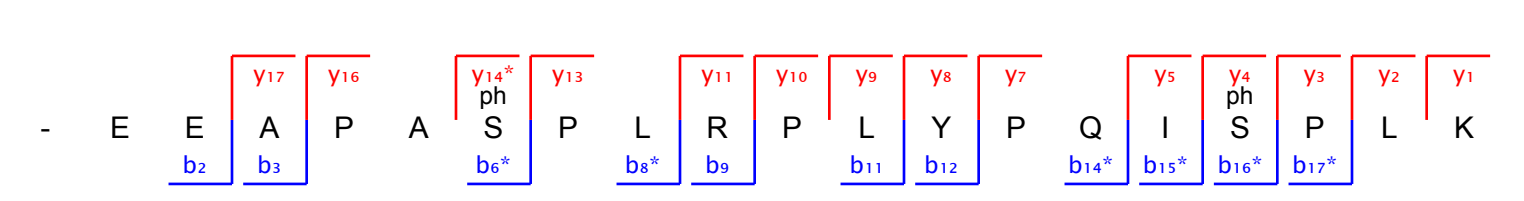
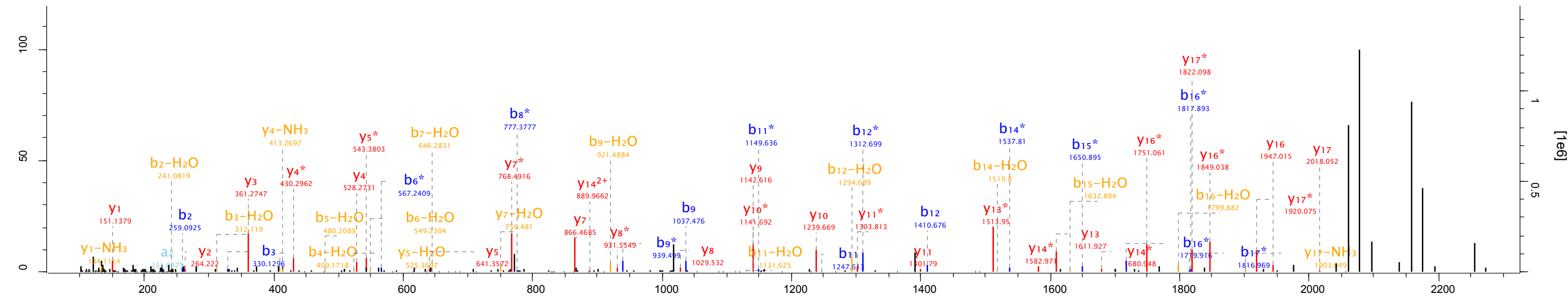
Fragmentation mapping (b-ions in blue, y-ions in red):

- b₂ (A), b₃ (A), b₄ (A), b₅ (A), b₆ (A), b₇ (A)
- y₂₃* (A), y₂₂ (A), y₂₁* (A), y₂₀ (A), y₁₉ (G), y₁₈* (D), y₁₇* (S), y₁₆ (D), y₁₅ (S), y₁₄ (W), y₁₃ (D), y₁₂ (A), y₁₁ (D), y₁₀ (A), y₉ (F), y₈ (S), y₇ (V), y₆ (E), y₅ (D), y₄ (P), y₂ (V), y₁ (R), y₁ (K)

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 Scan: 18851 Method: FTMS; HCD Score: 208.93 m/z: 1131.98 Gene names: SMN1



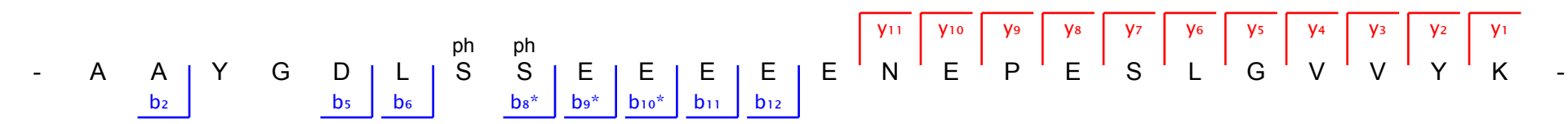
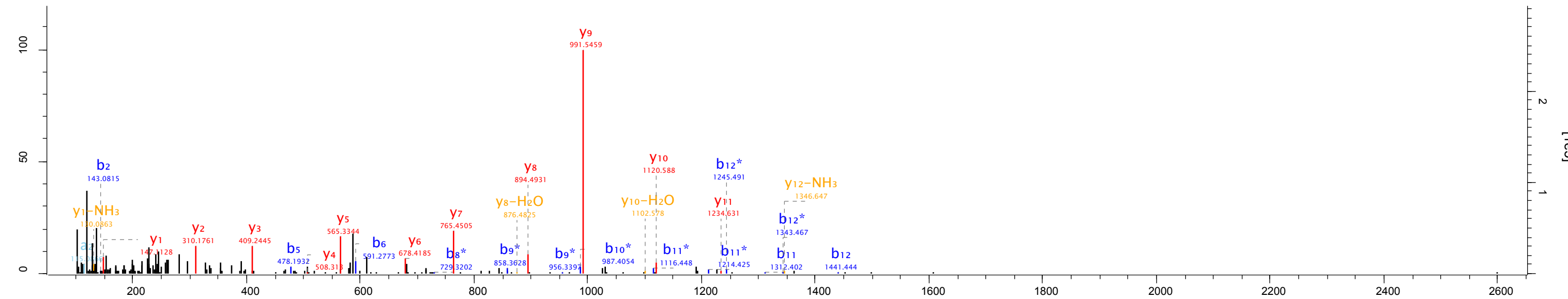
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Raw file

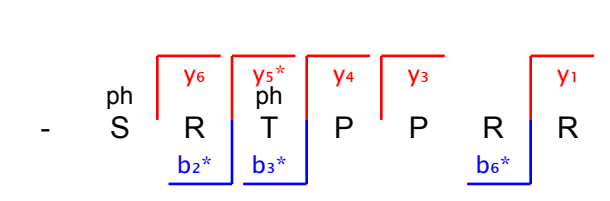
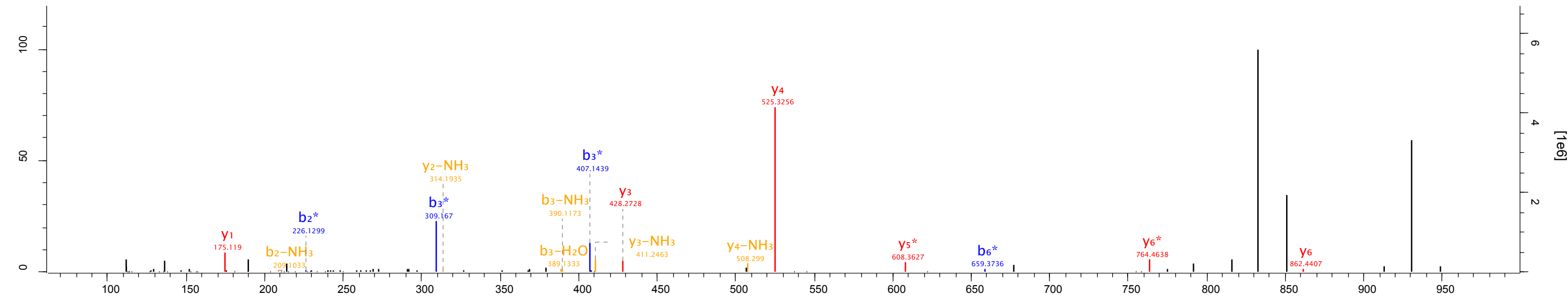
20171215_MaS_33SR_LMH_phospho2_03

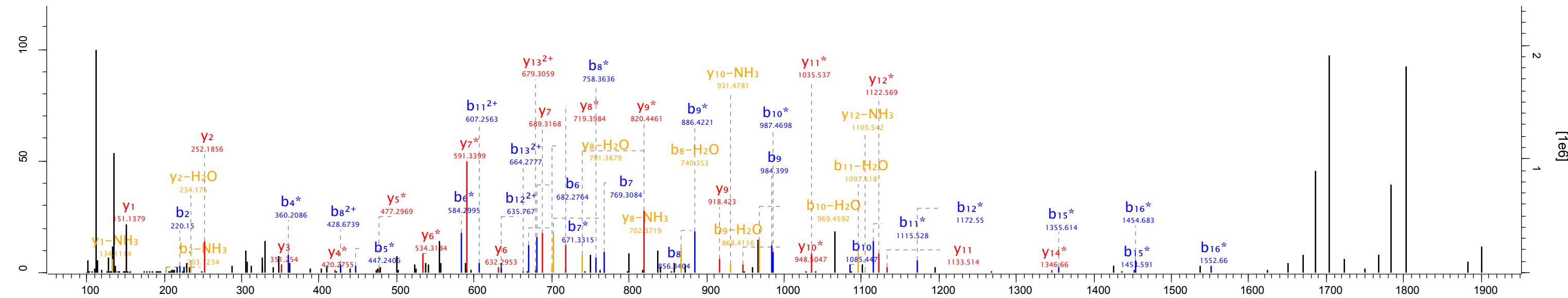
Scan	Method	Score	m/z	Gene names
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 1991 Method FTMS; HCD Score 58.59 m/z 343.82 Gene names SRRM2

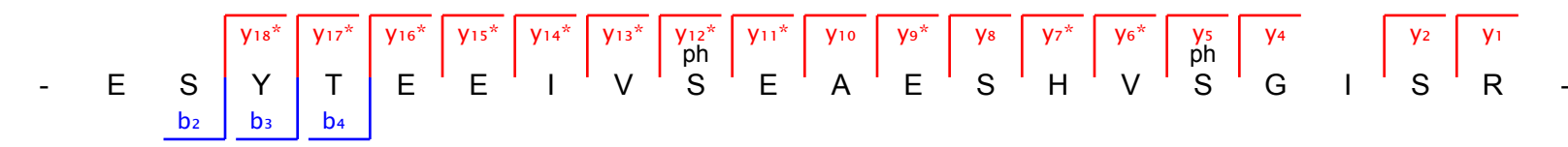
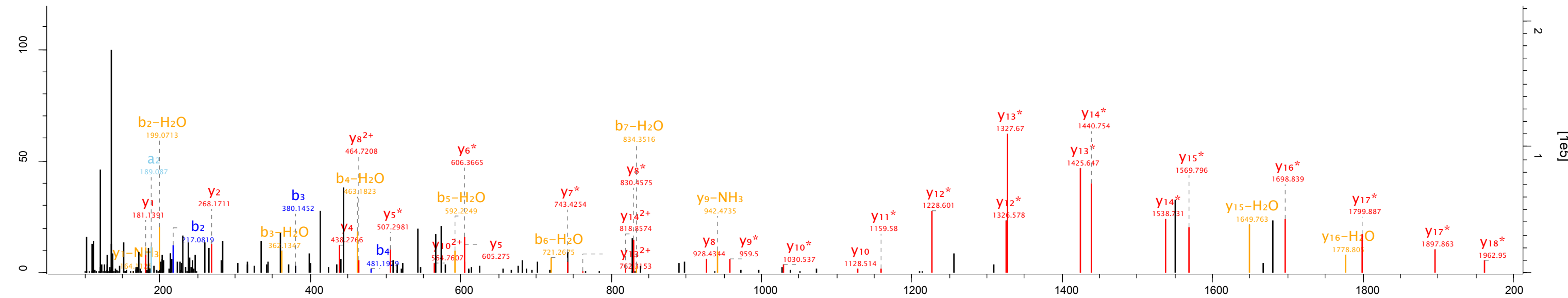
20171215_MaS_33SR_LMH_phospho2_03



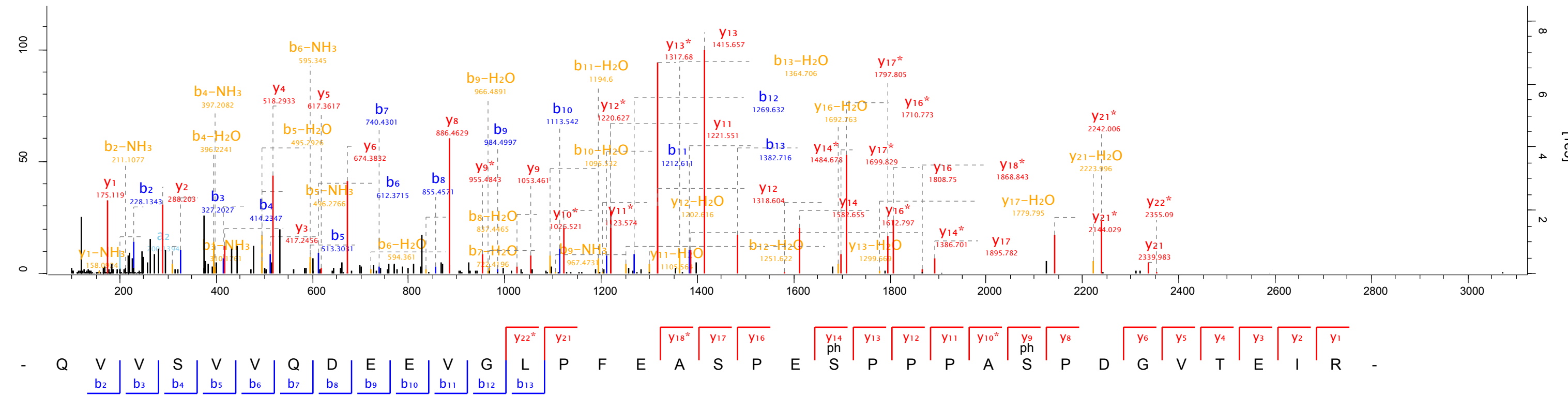


- G R A ph S S H S S Q T Q G G G S ph S V T K -
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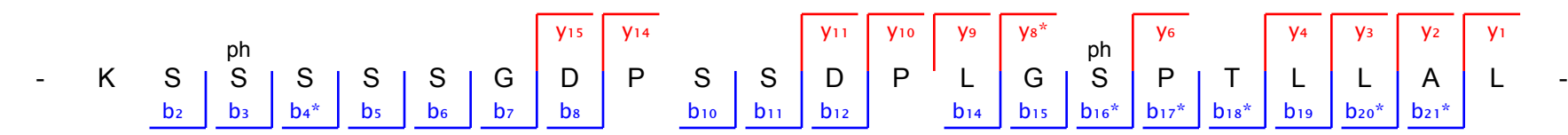
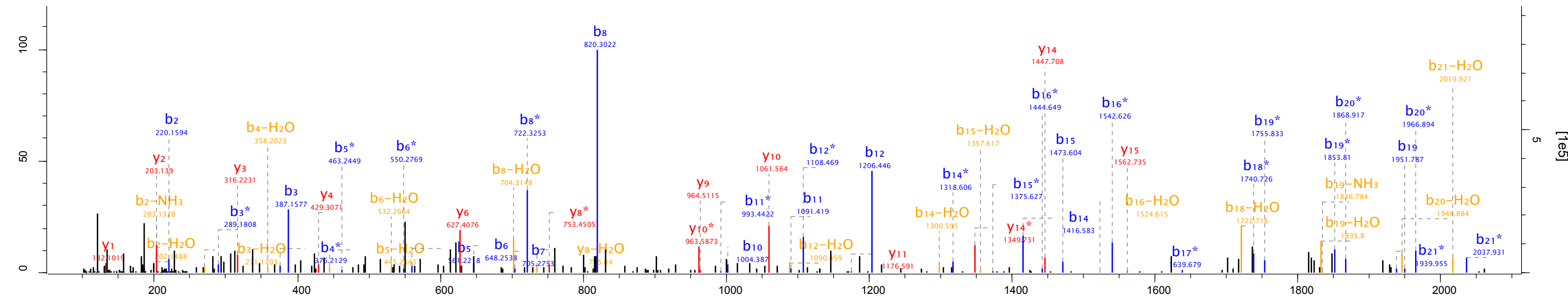
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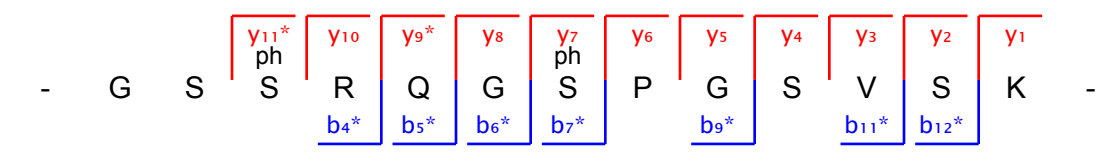
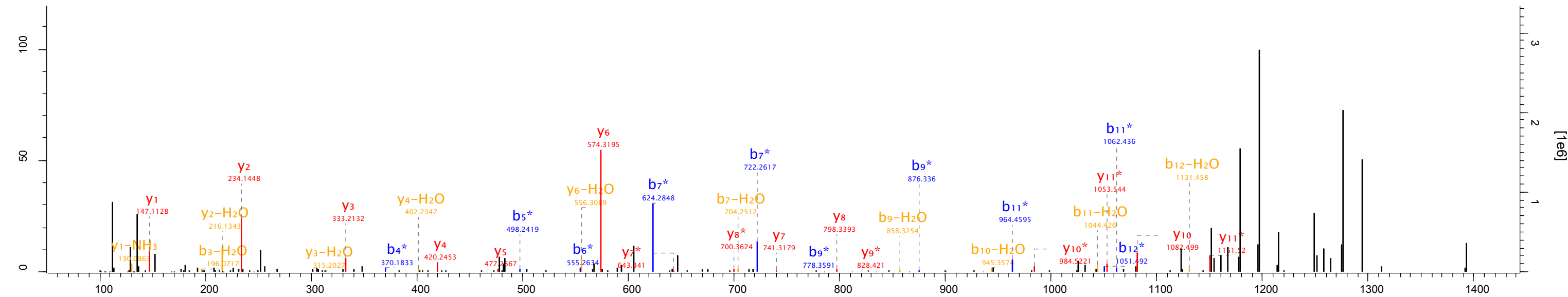
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 22201 Method FTMS; HCD Score 157.09 m/z 1241.57 Gene names FAM129B



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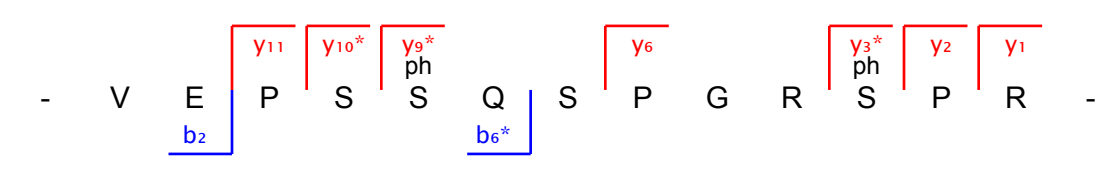
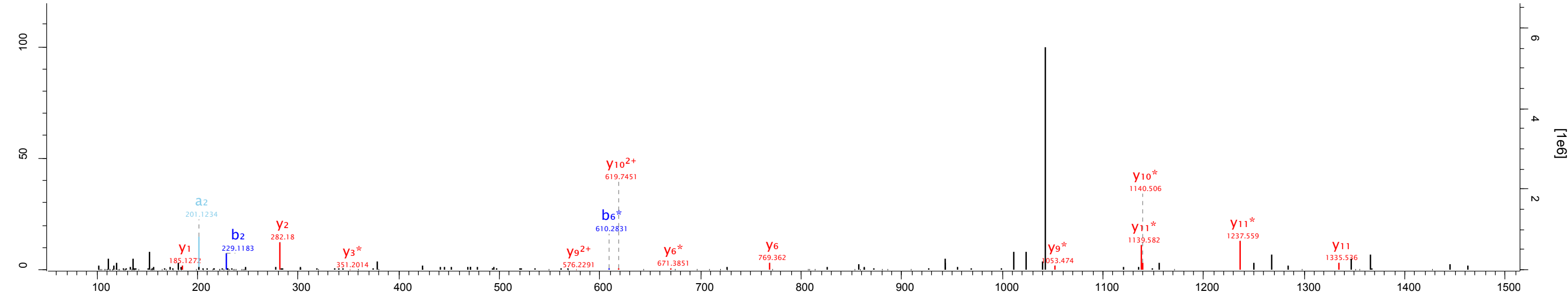
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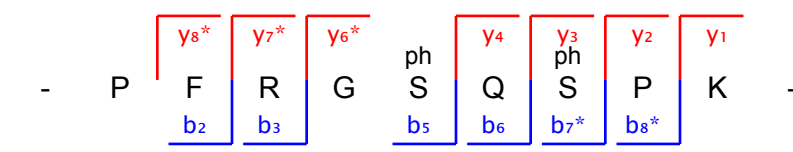
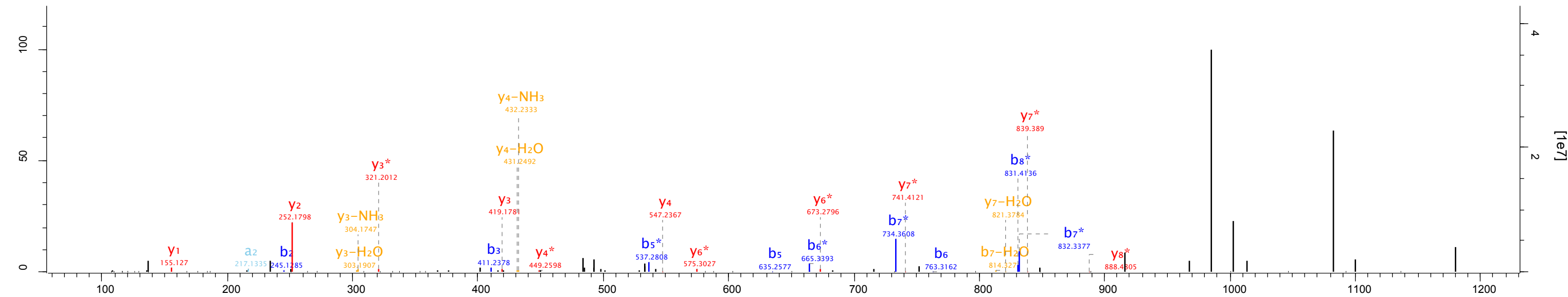
Raw file

20171215_MaS_33SR_LMH_phospho2_03

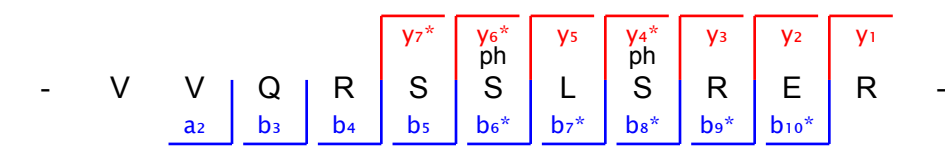
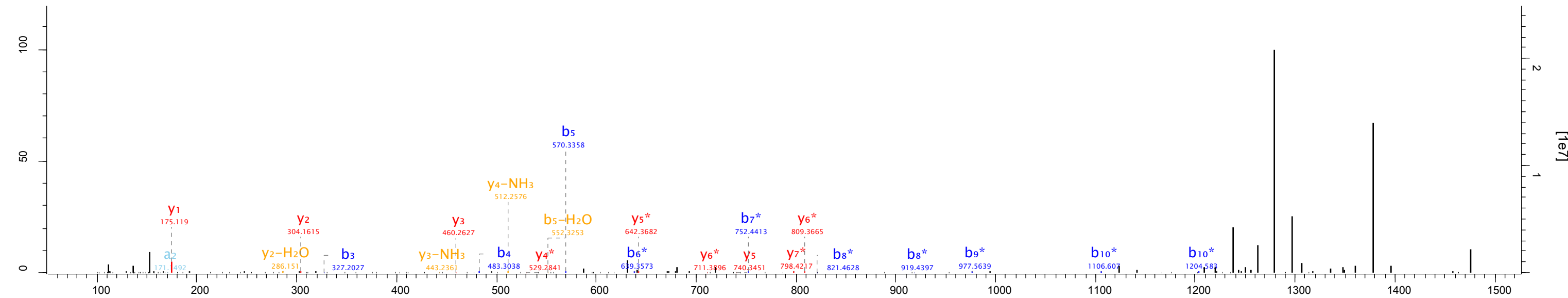
Scan	Method	Score	m/z	Gene names
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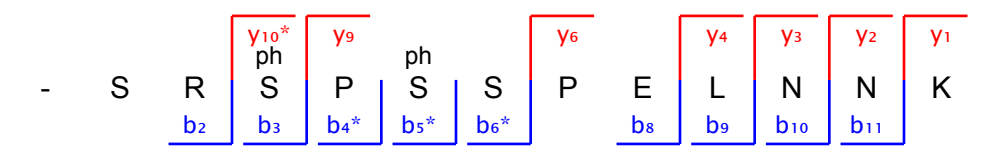
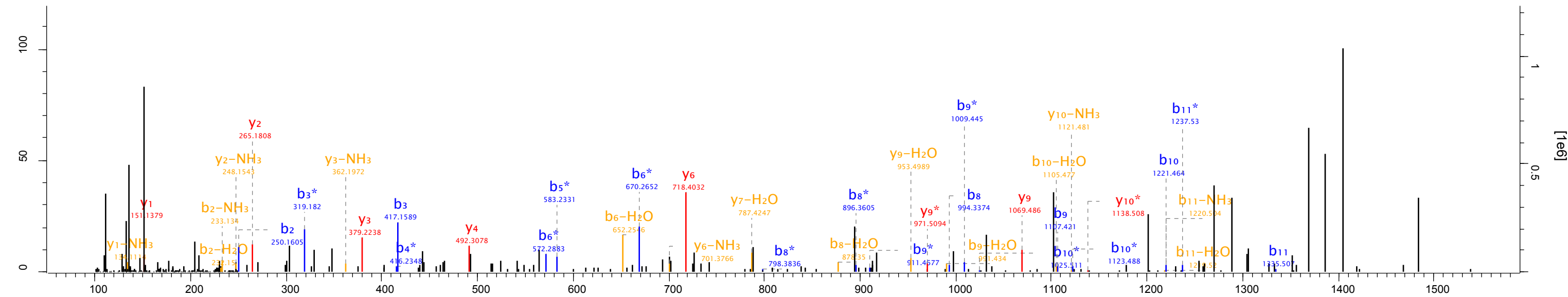
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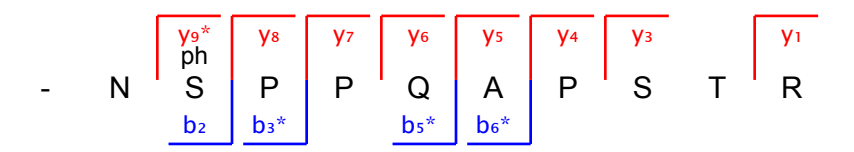
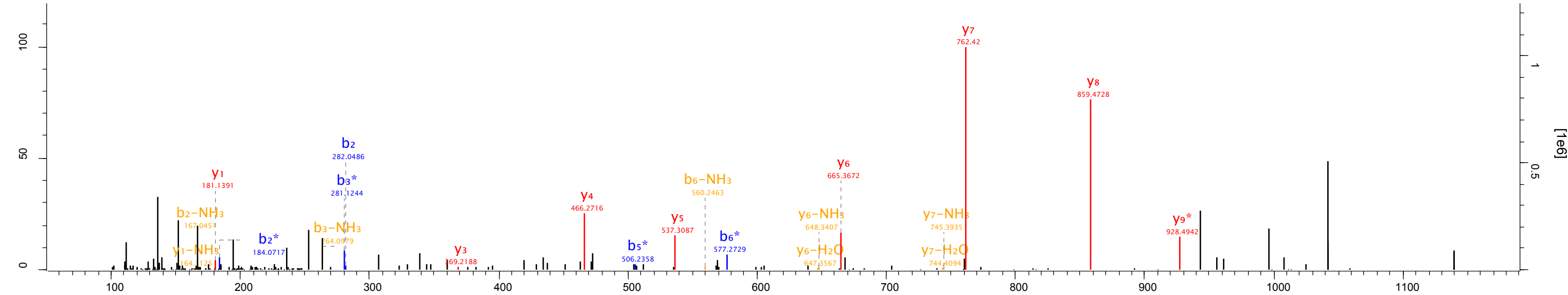
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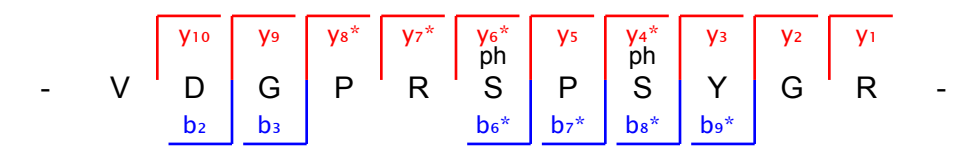
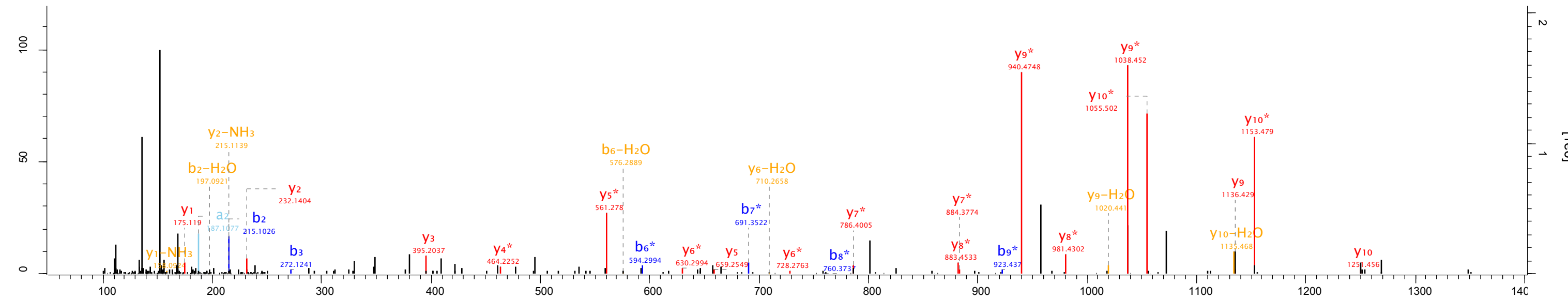
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20171215_MaS_33SR_LMH_phospho2_03

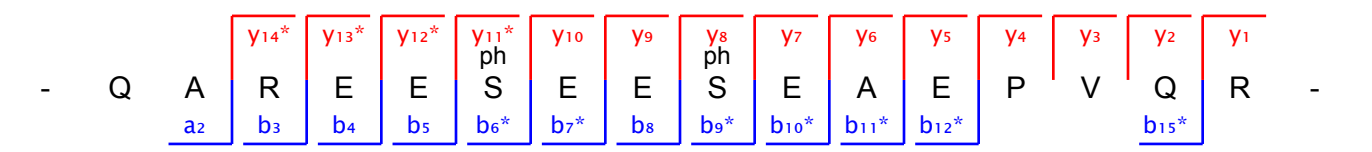
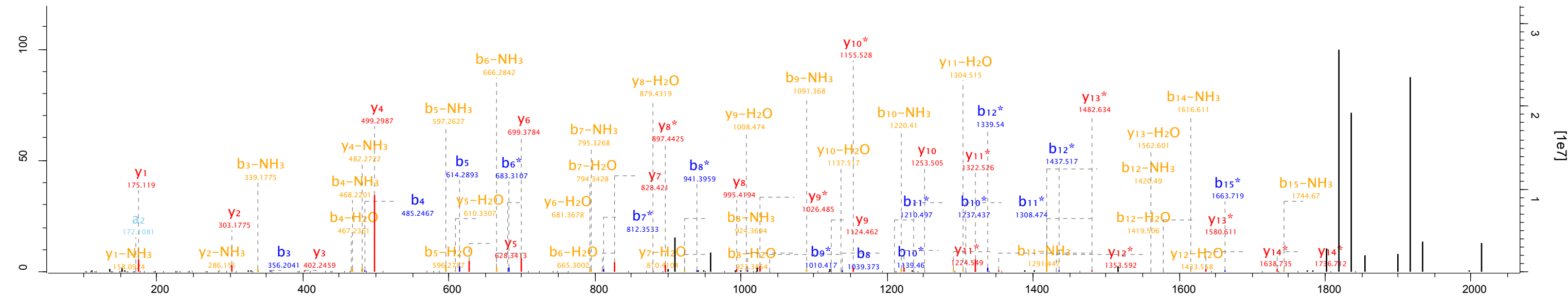
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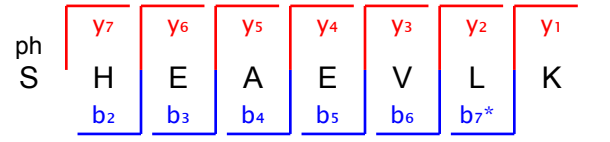
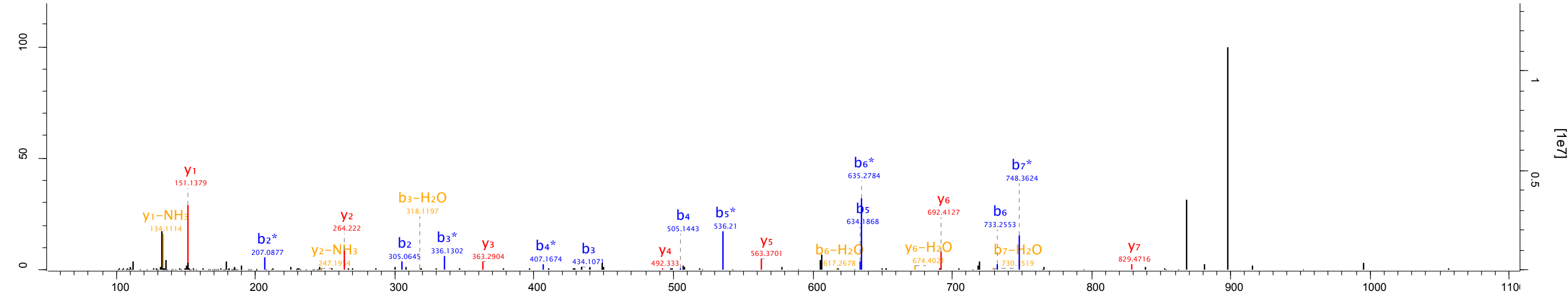
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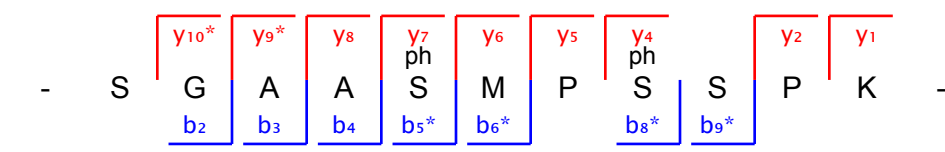
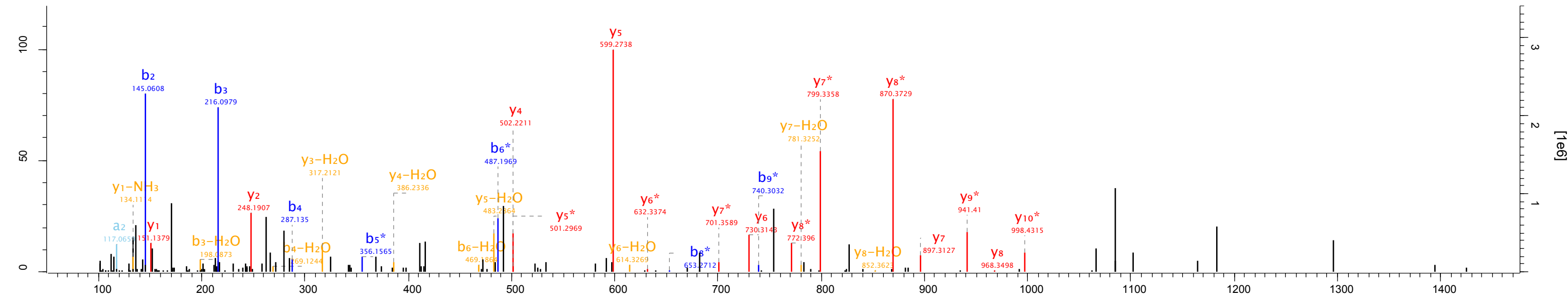
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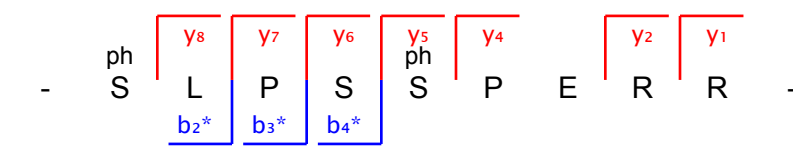
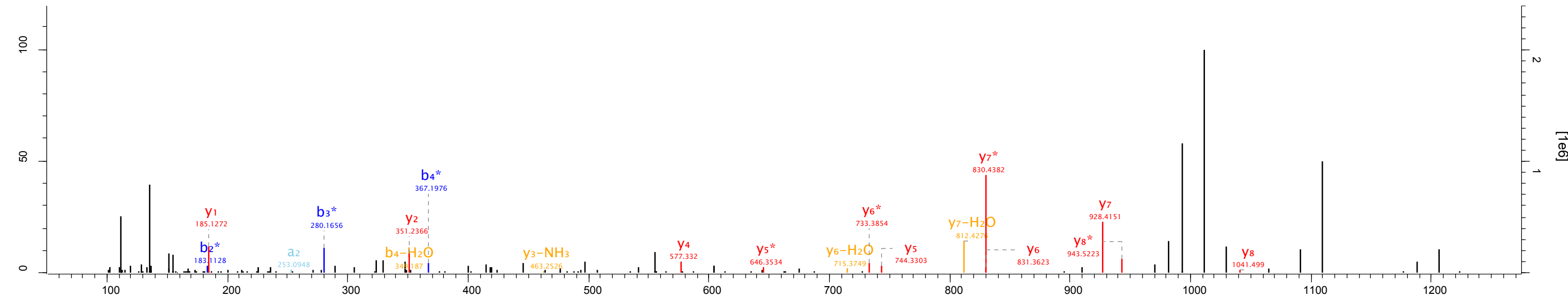
20171215_MaS_33SR_LMH_phospho2_03 3901 FTMS; HCD 119.34 498.74 STMN1



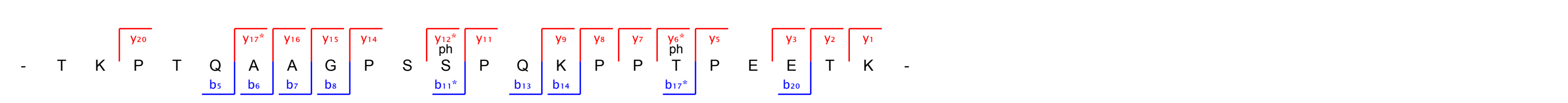
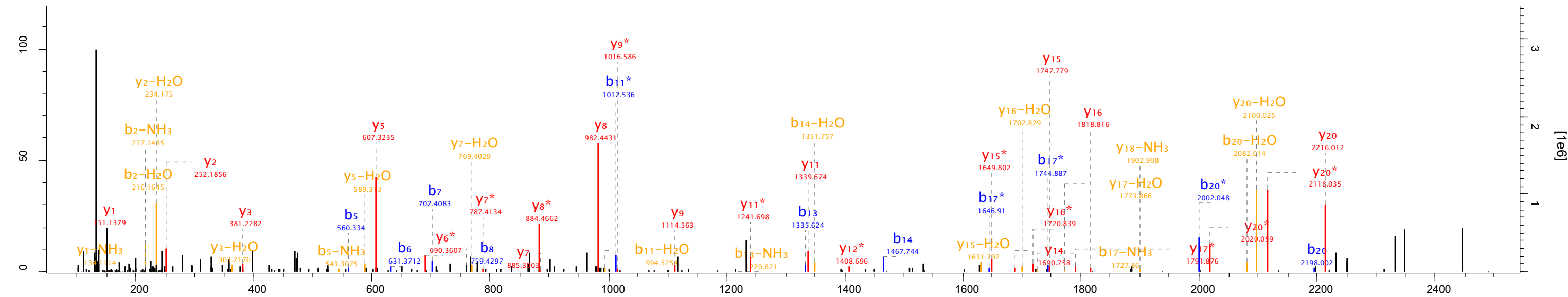
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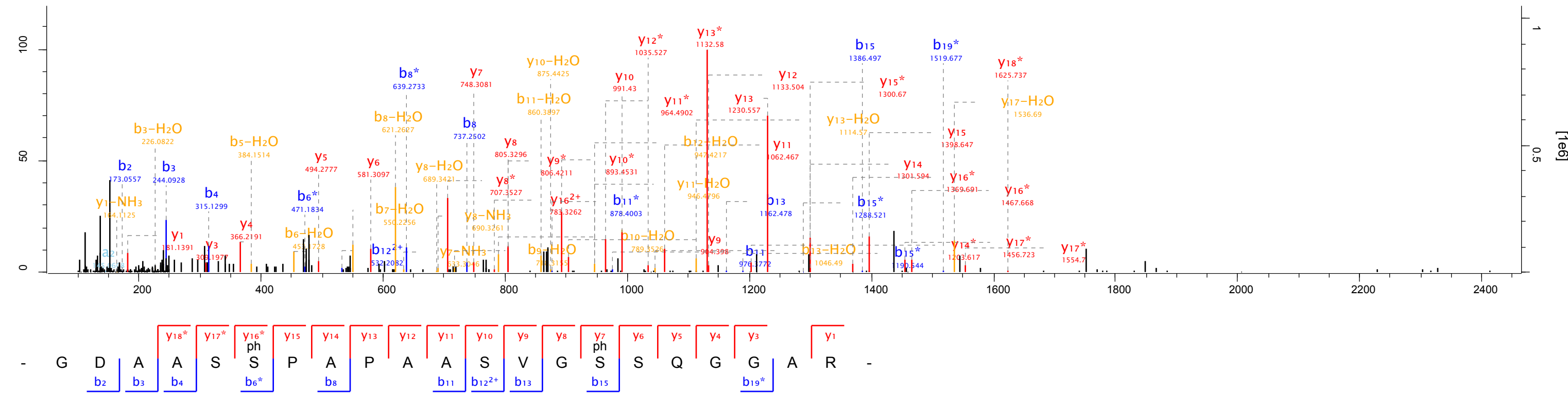


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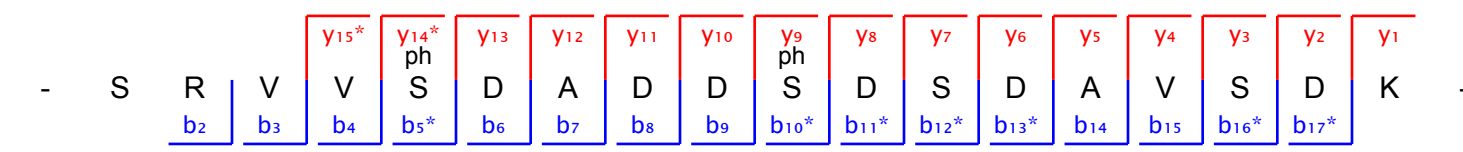
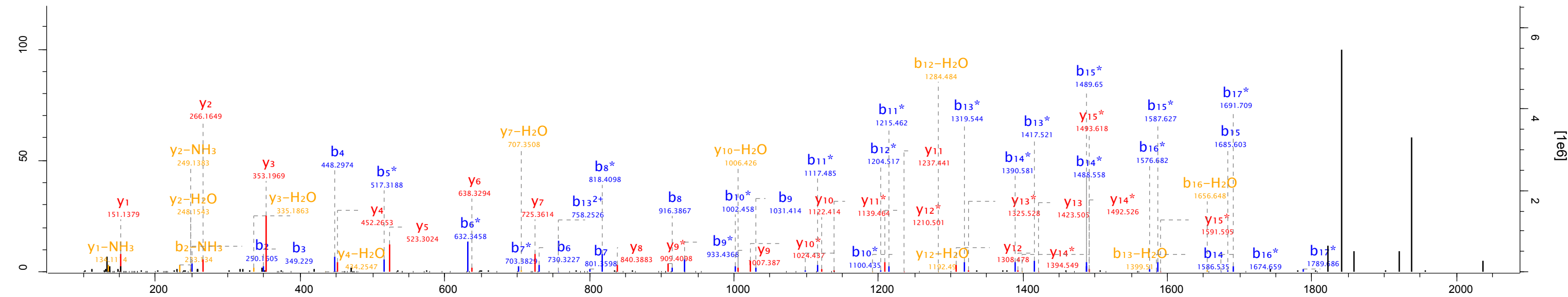
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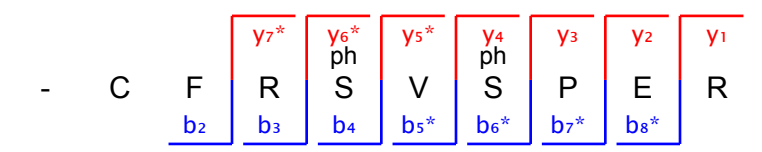
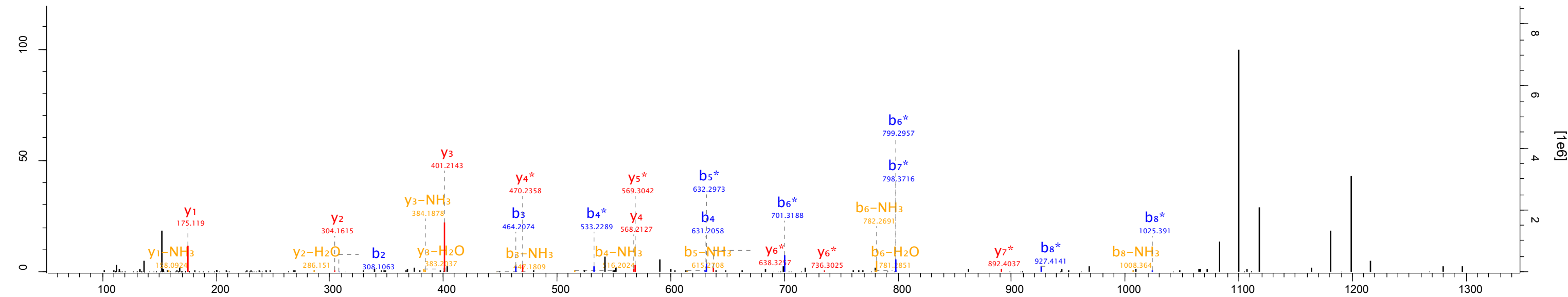


Raw file
20171215_MaS_33SR_LMH_phospho2_03

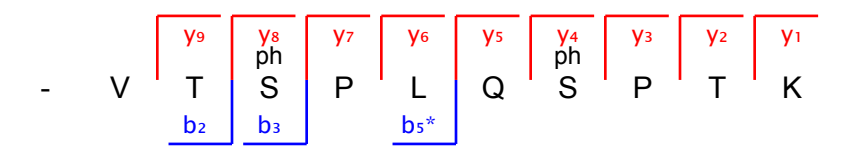
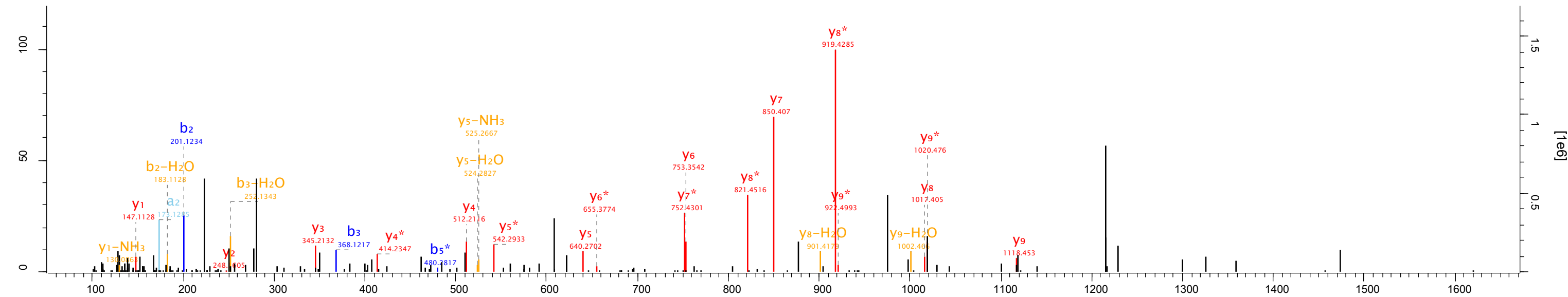
Scan 4811 Method FTMS; HCD Score 246.31 m/z 1019.9 Gene names IWS1



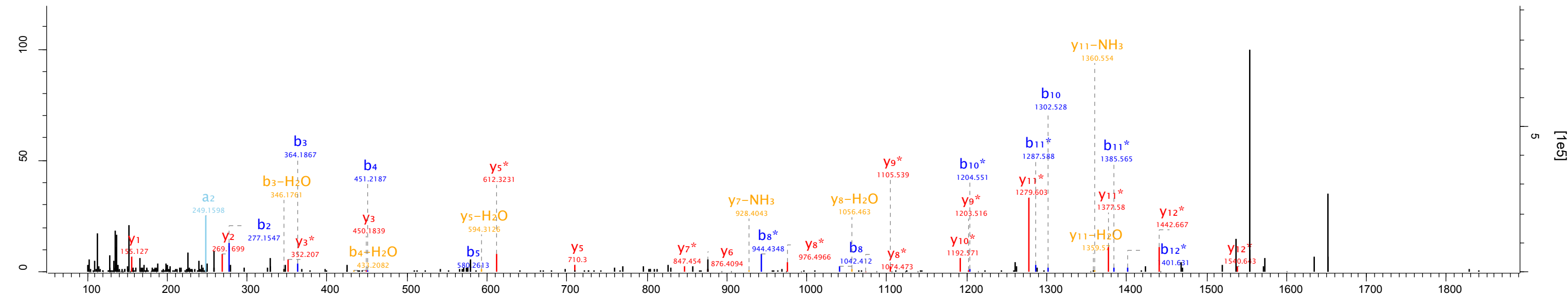
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 Scan: 4981 Method: FTMS; HCD Score: 89.86 m/z: 649.24 Gene names: ZNF638



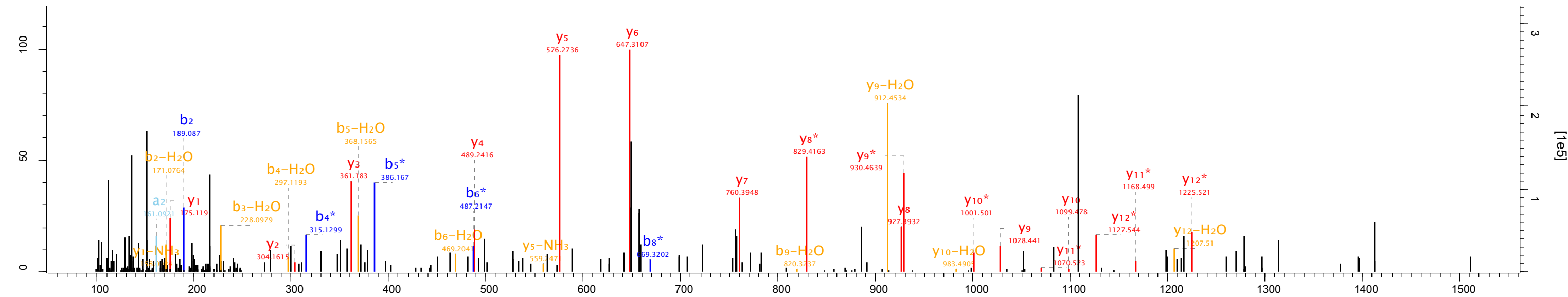
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 Scan: 5071 Method: FTMS; HCD Score: 138.01 m/z: 609.26 Gene names: PLEKHA7



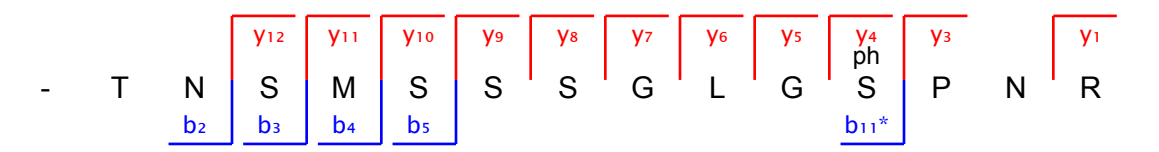
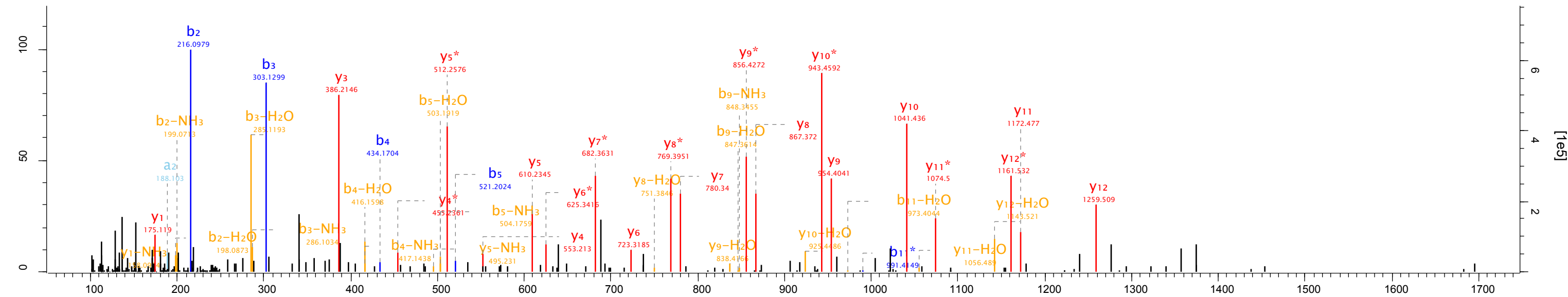
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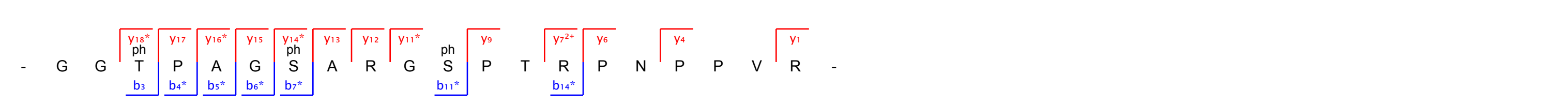
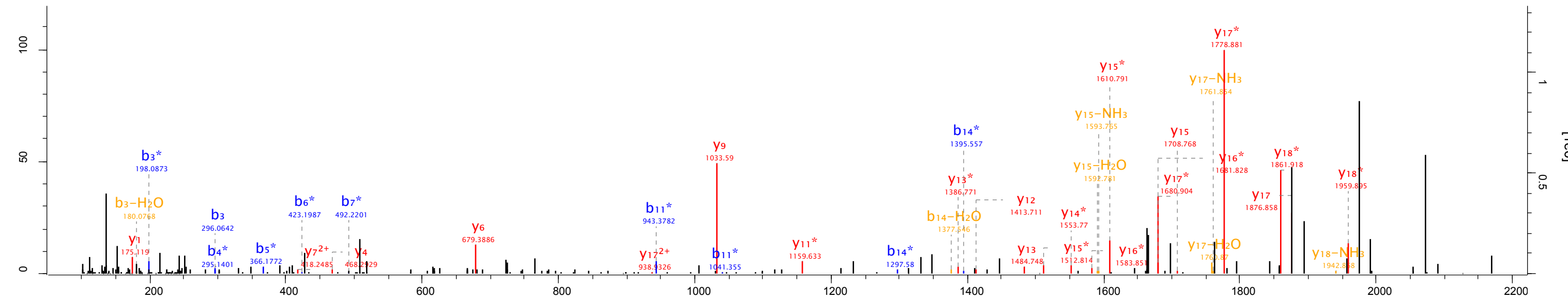
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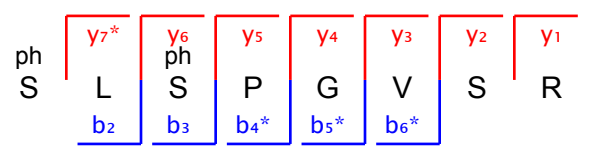
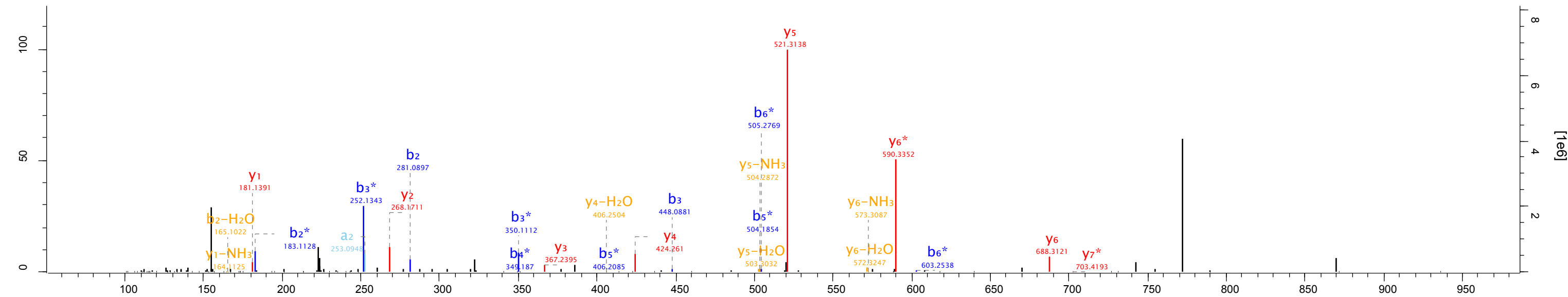
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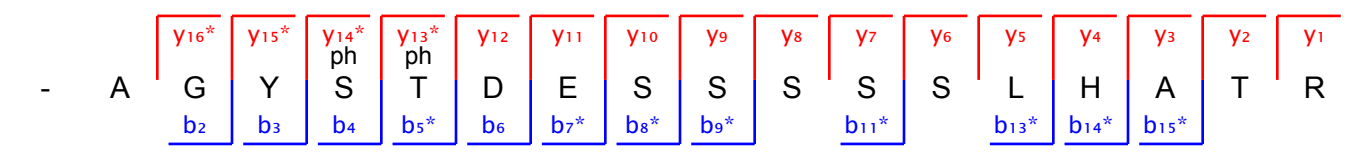
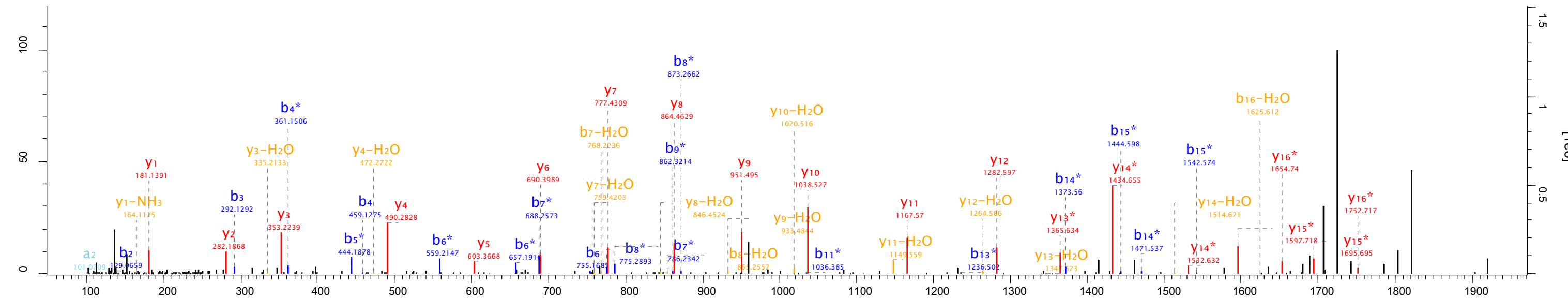
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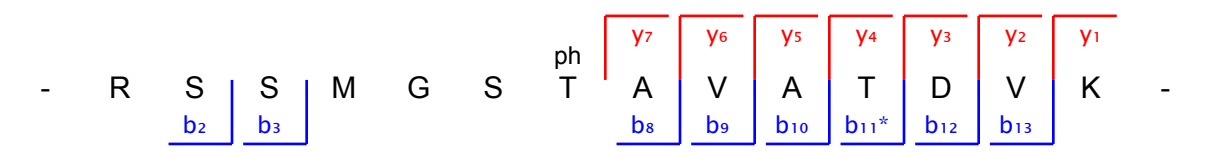
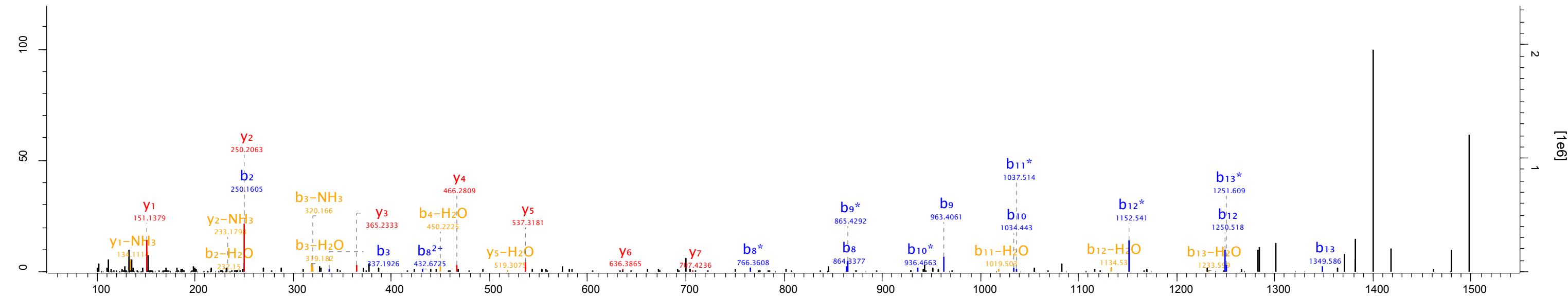
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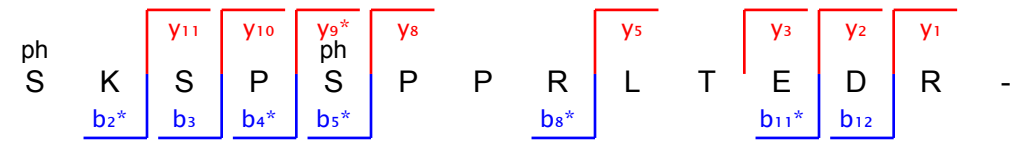
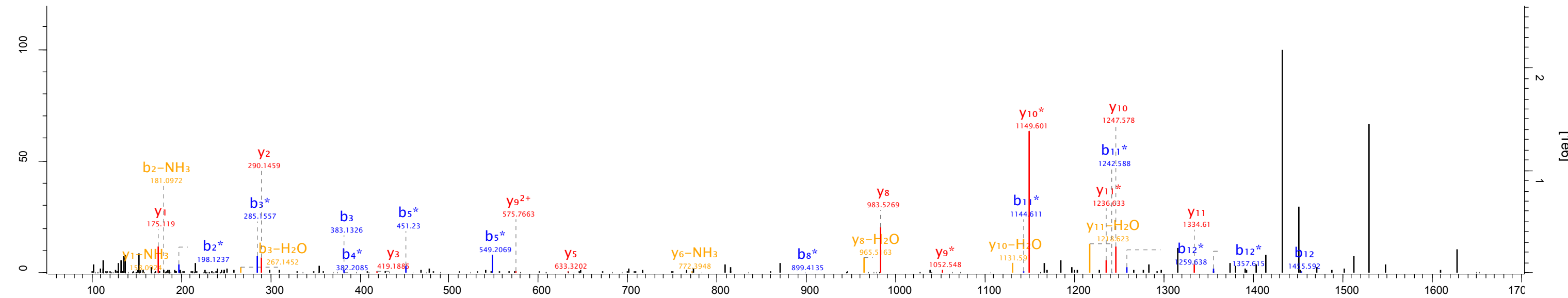
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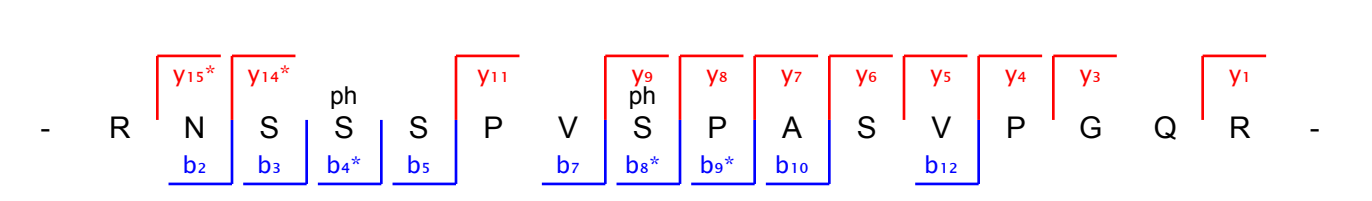
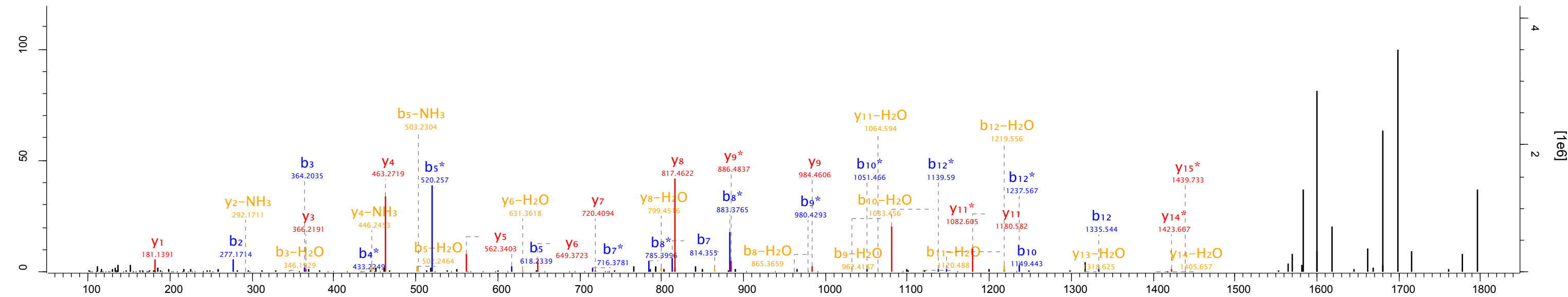
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 Scan: 5551 Method: FTMS; HCD Score: 114.03 m/z: 750.36 Gene names: BAIAP2L2



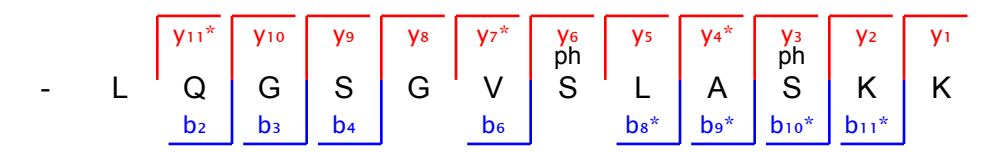
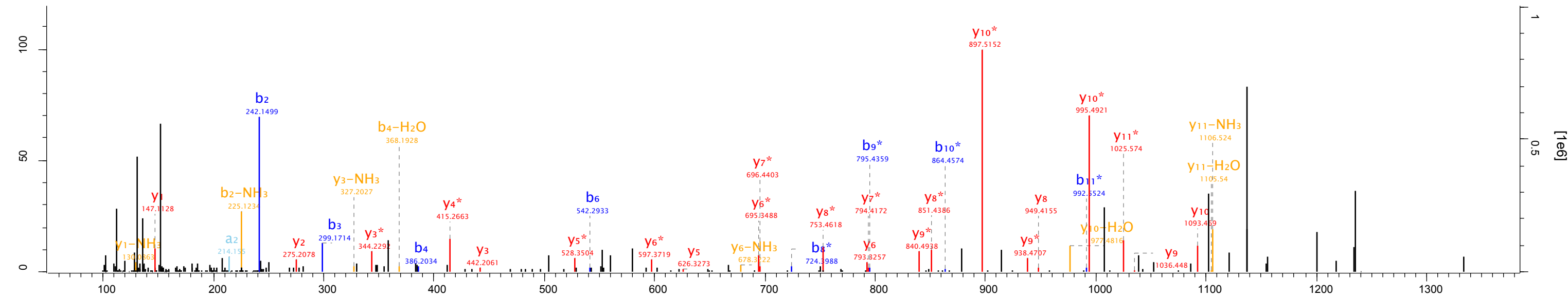
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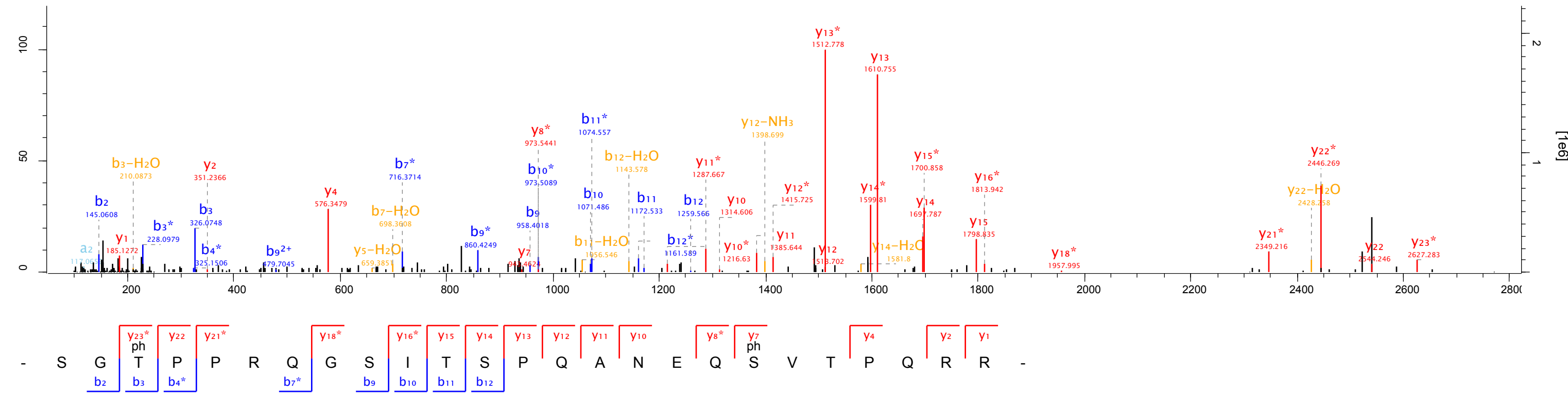


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 Scan: 5711 Method: FTMS; HCD Score: 181.75 m/z: 899.41 Gene names: IRF2BPL

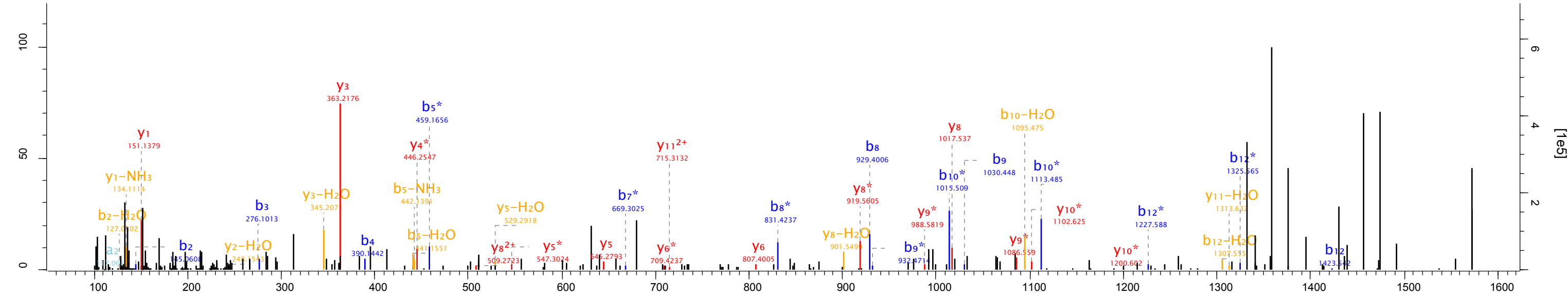


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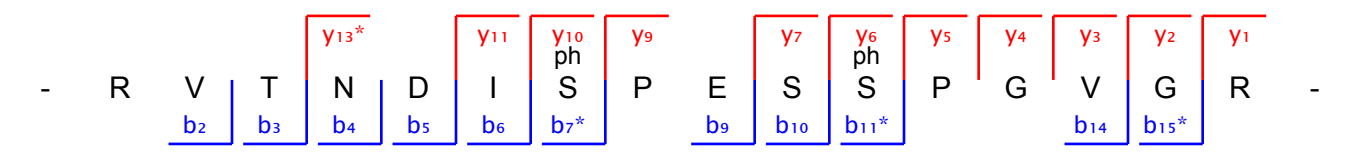
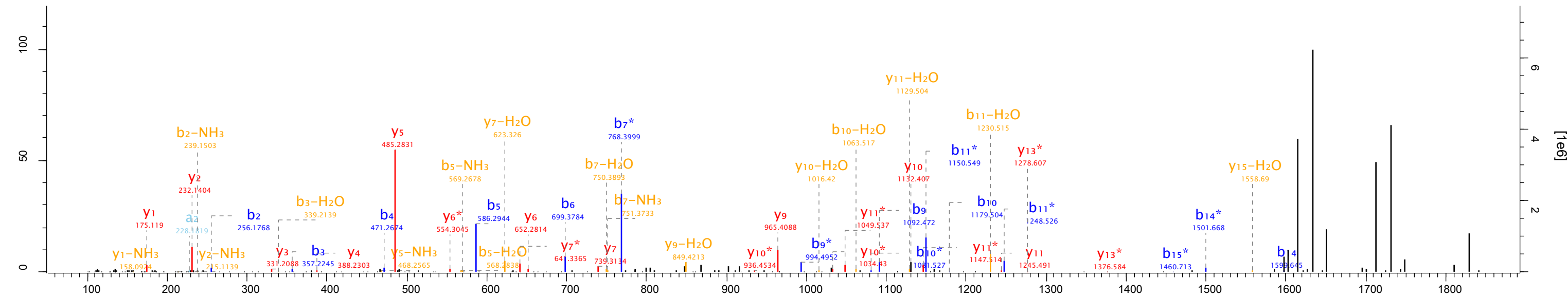




20171215_MaS_33SR_LMH_phospho2_03 6111 FTMS; HCD 78.4 787.34 ZNF148

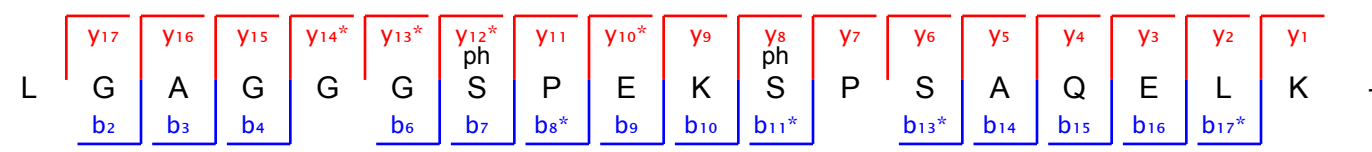
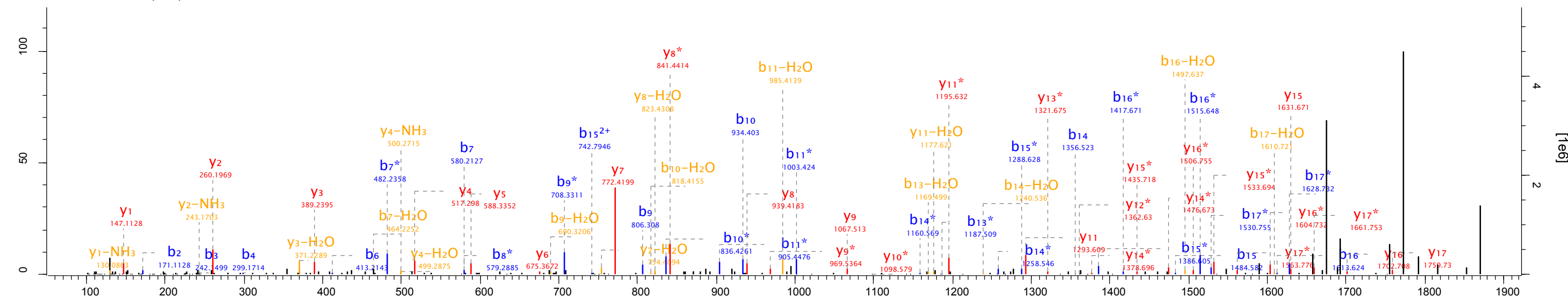


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 Scan: 6371 Method: FTMS; HCD Score: 183.75 m/z: 916.39 Gene names: PCM1

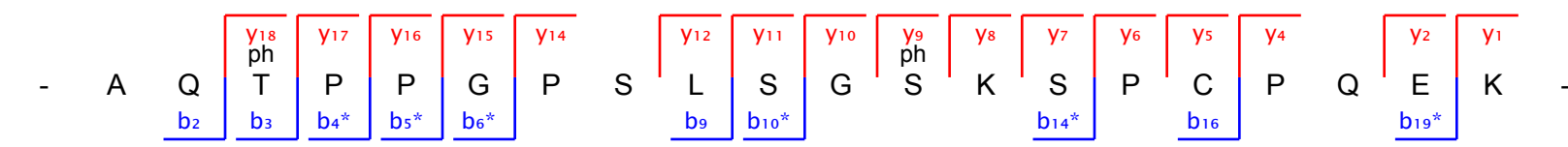
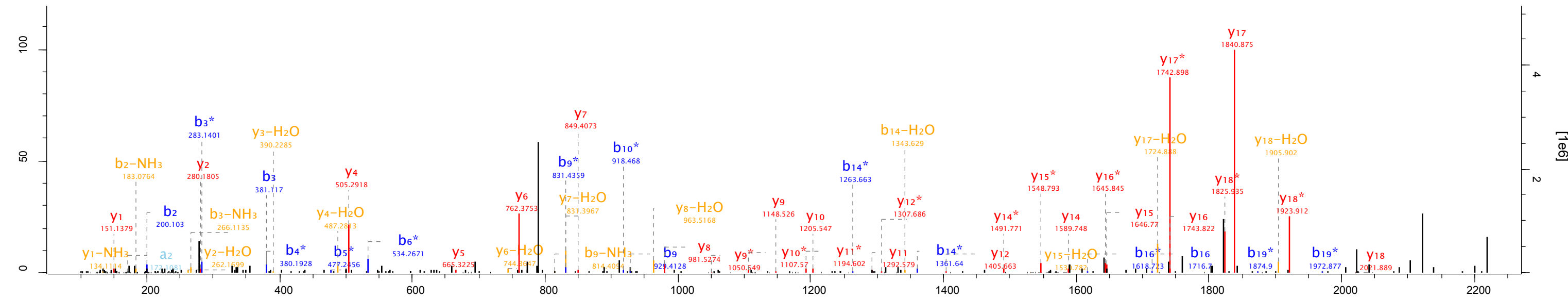


Raw file
20171215_MaS_33SR_LMH_phospho2_03

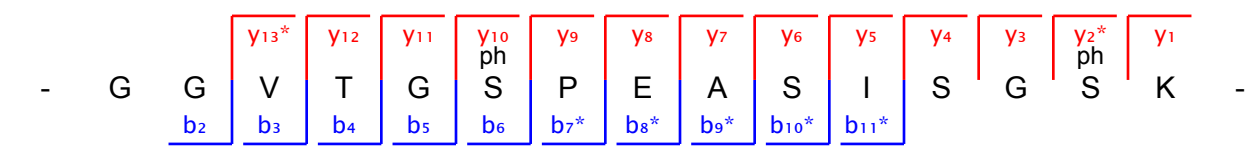
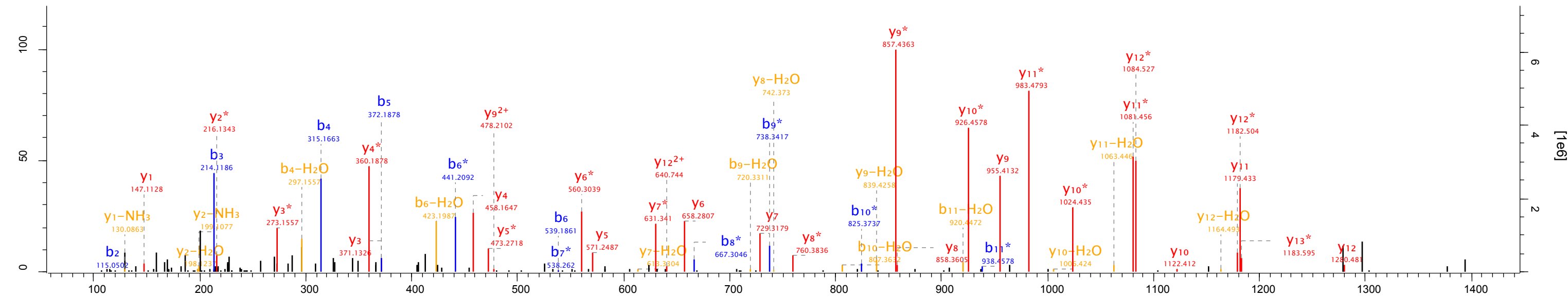
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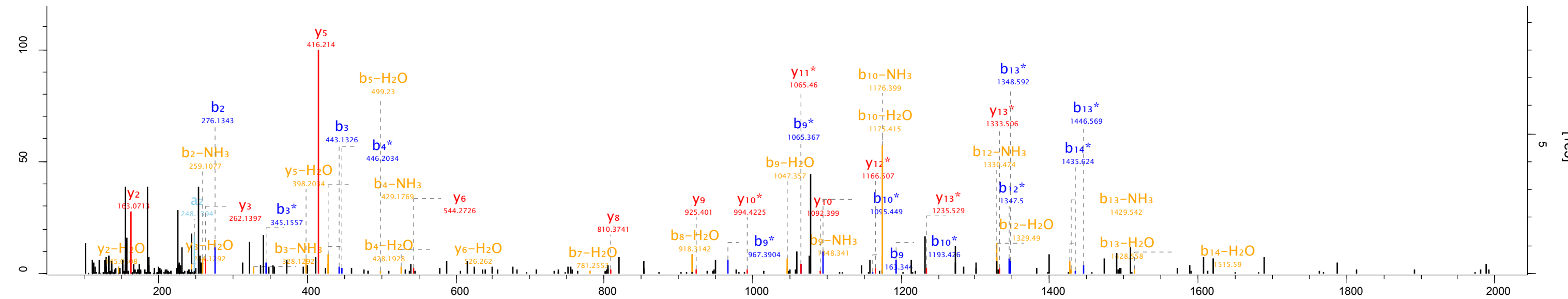
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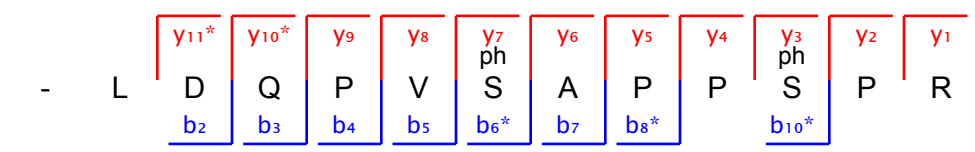
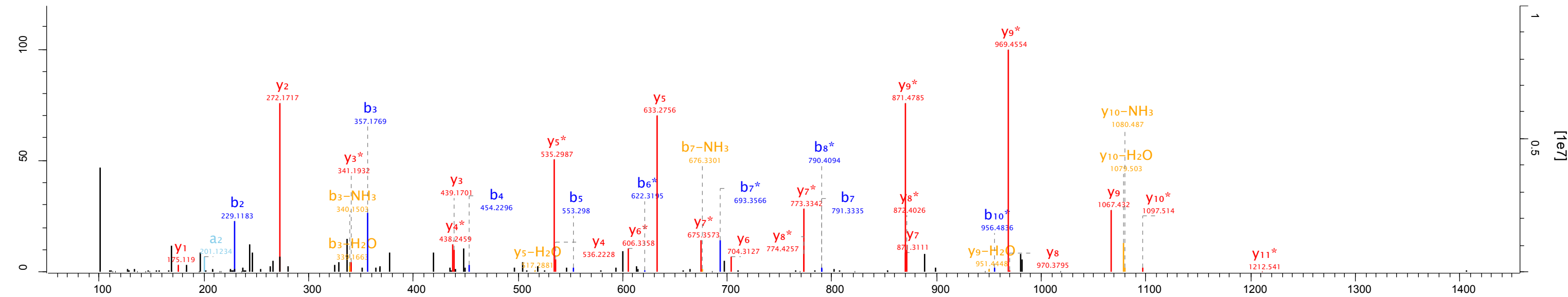
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 6891 Method: FTMS; HCD Score: 199.28 m/z: 747.3 Gene names: AHNAK



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 Scan: 7141 Method: FTMS; HCD Score: 101.1 m/z: 854.31 Gene names: TBC1D9B

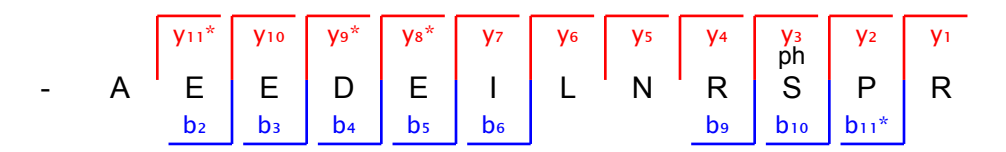
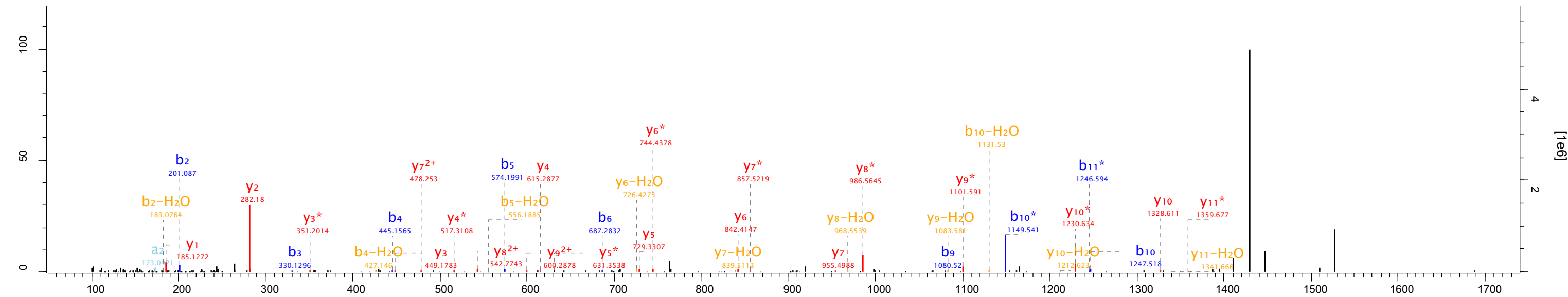


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 7241 Method FTMS; HCD Score 144.23 m/z 712.3 Gene names CCDC6

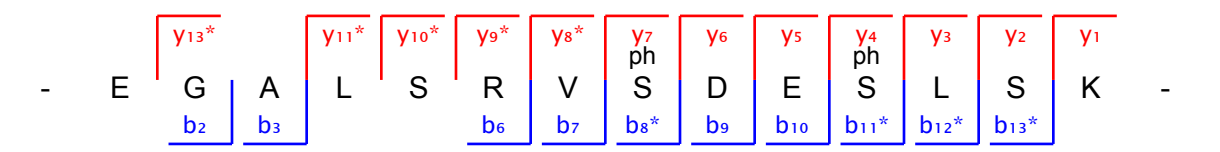
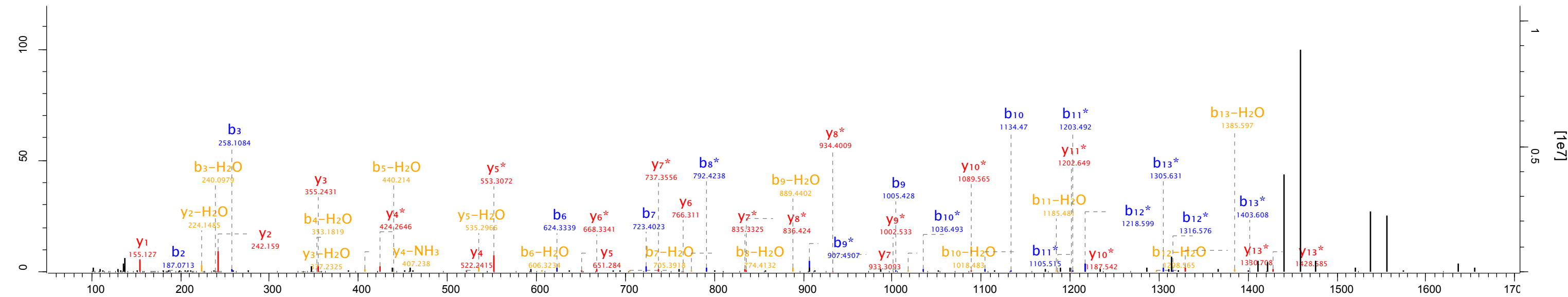


Raw file
20171215_MaS_33SR_LMH_phospho2_03

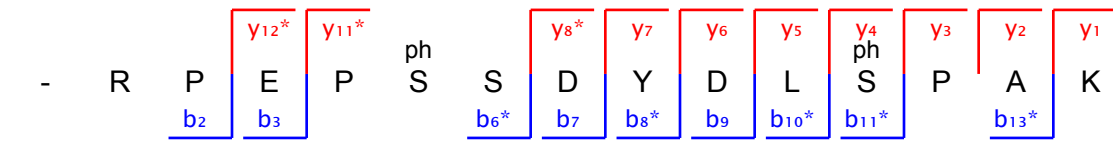
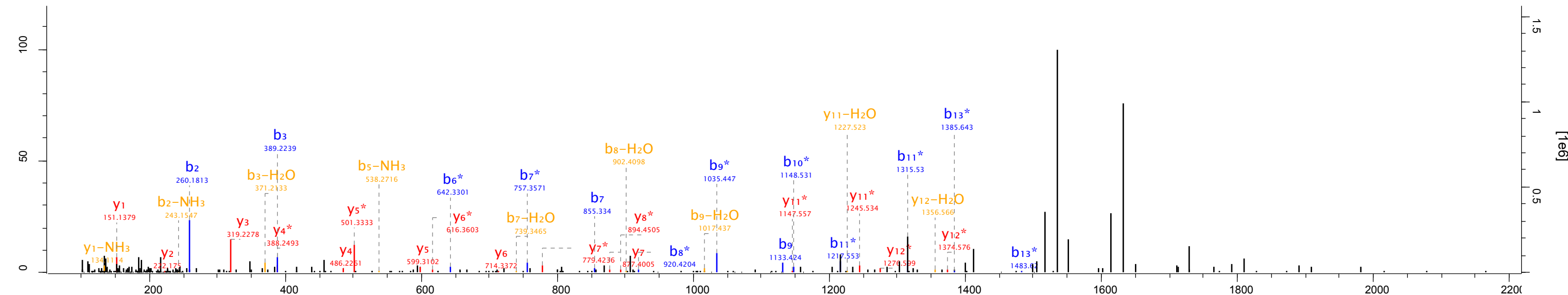
Scan 7251 Method FTMS; HCD Score 199.33 m/z 764.85 Gene names CANX



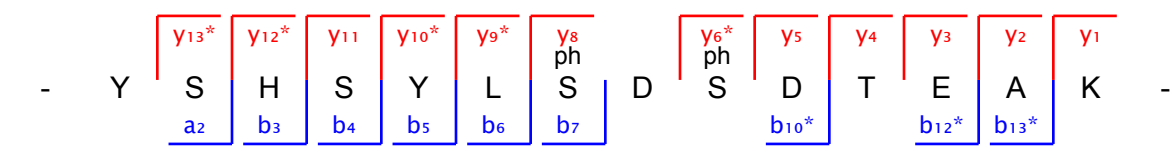
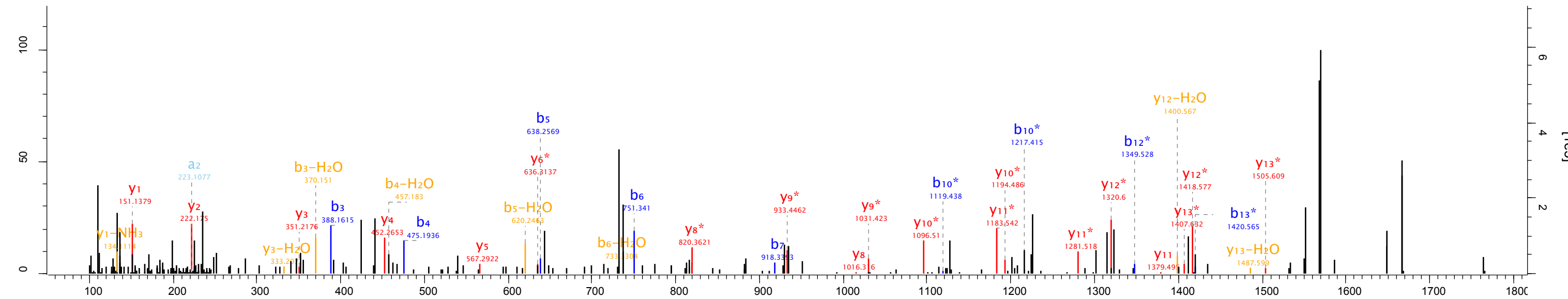
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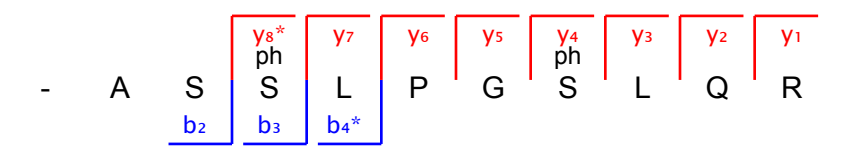
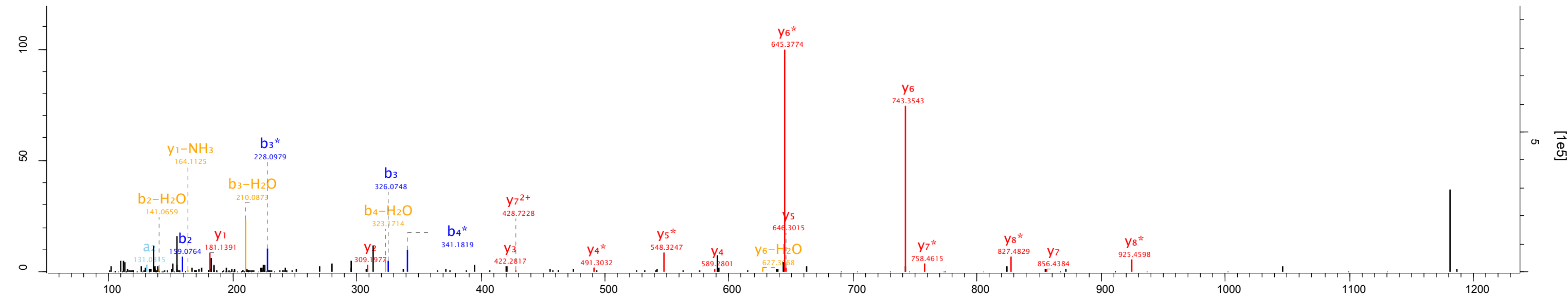
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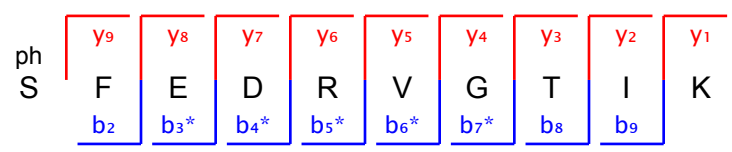
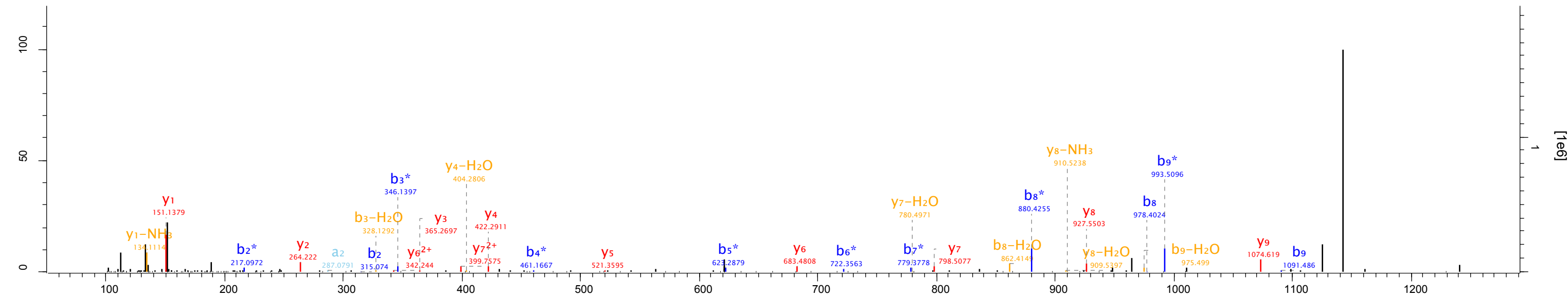
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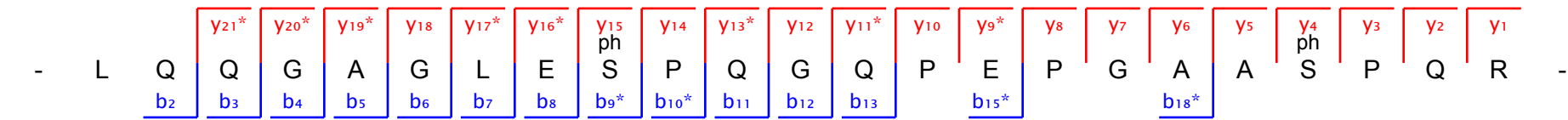
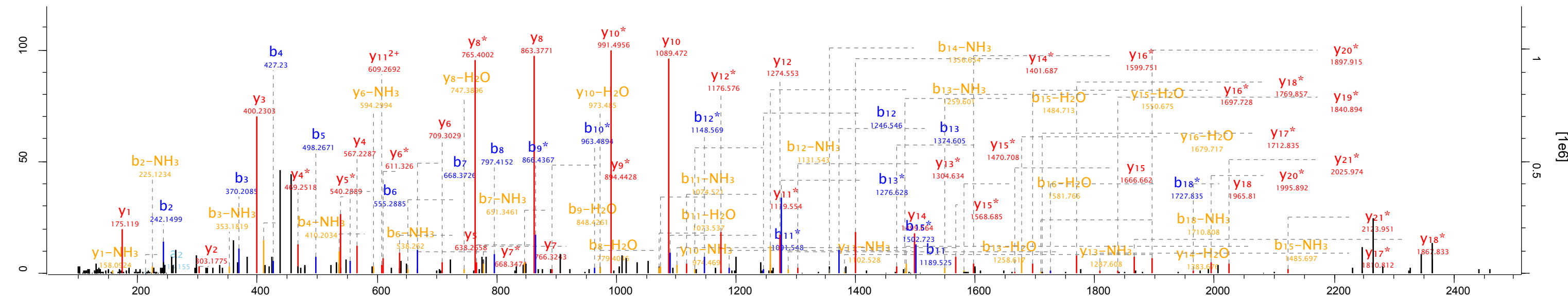
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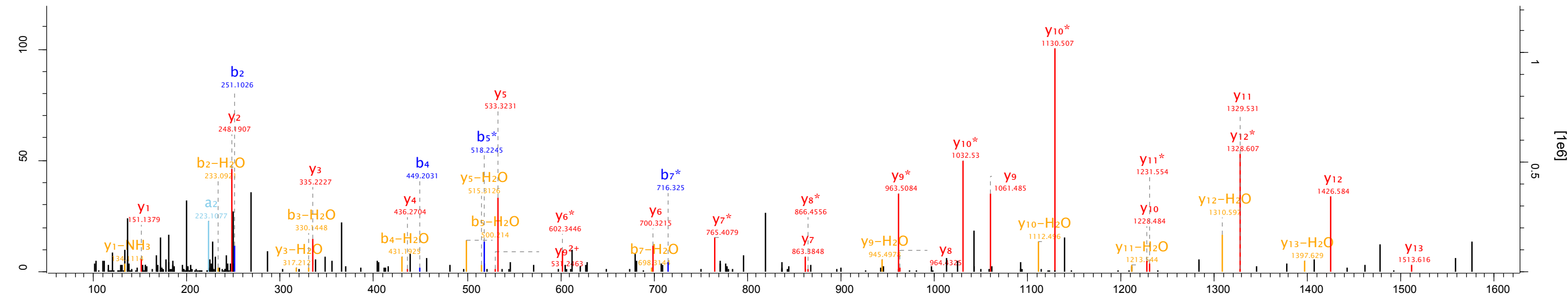
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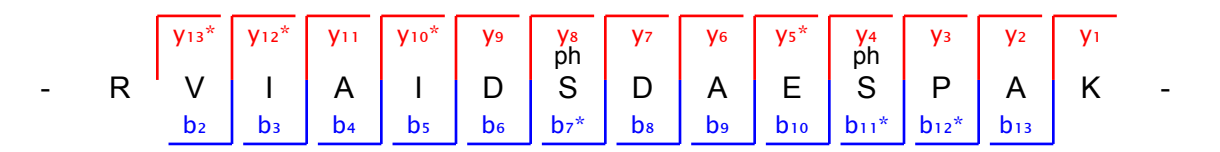
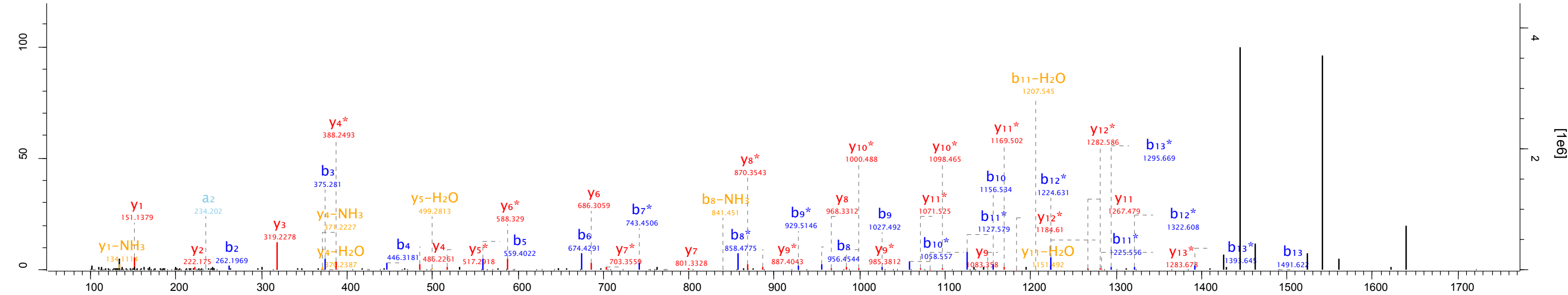
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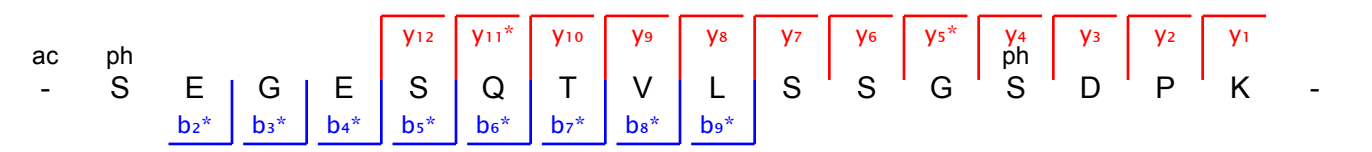
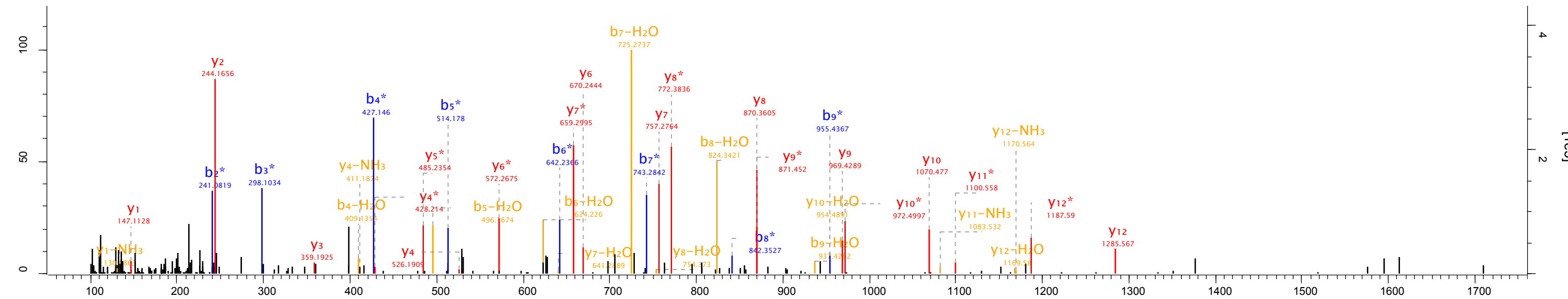
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 Scan: 8321 Method: FTMS; HCD Score: 143.69 m/z: 838.84 Gene names: POLR2A



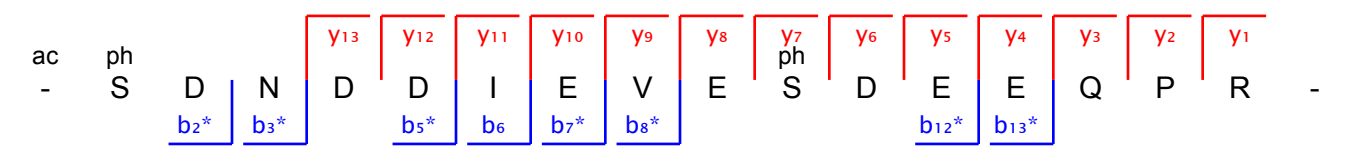
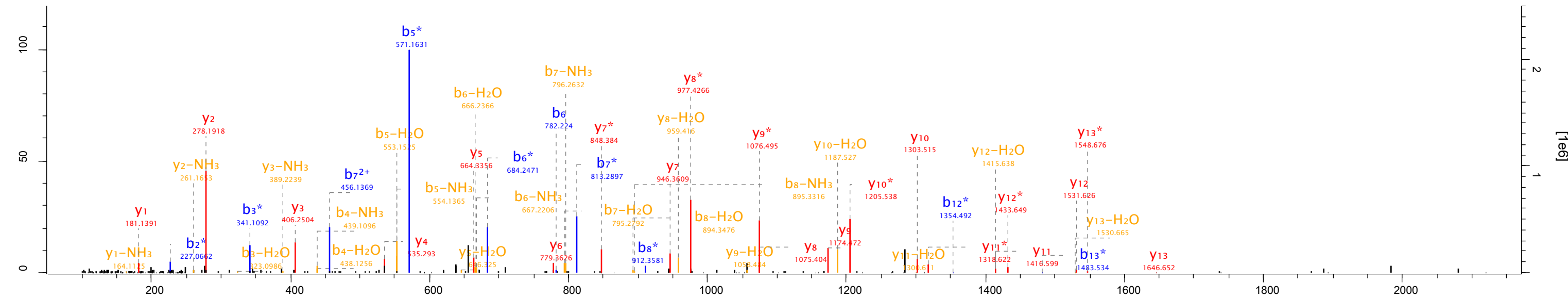
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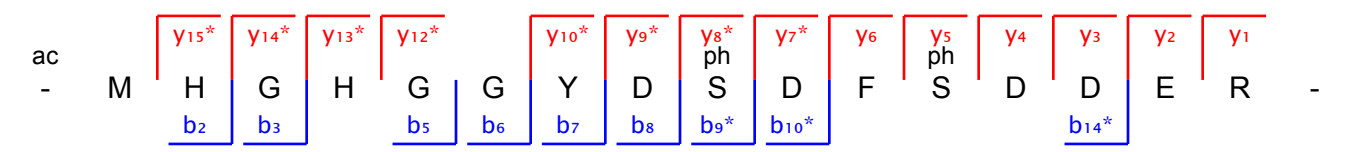
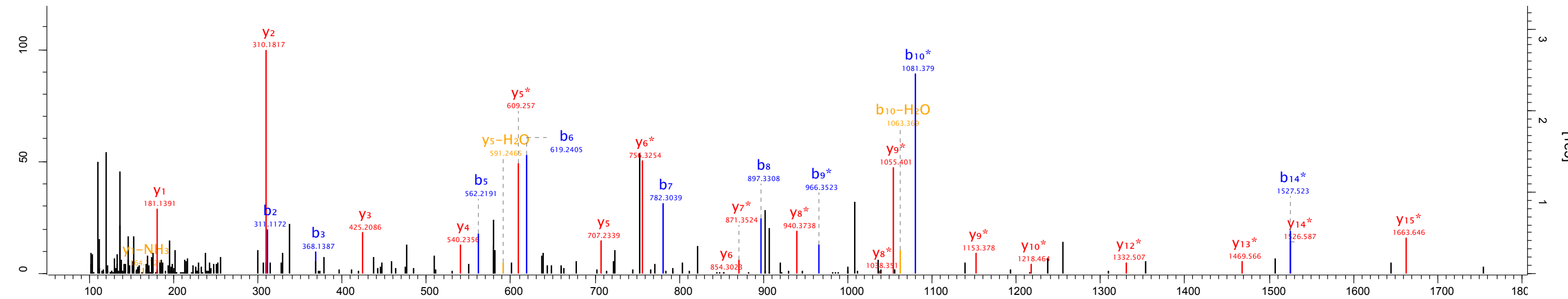
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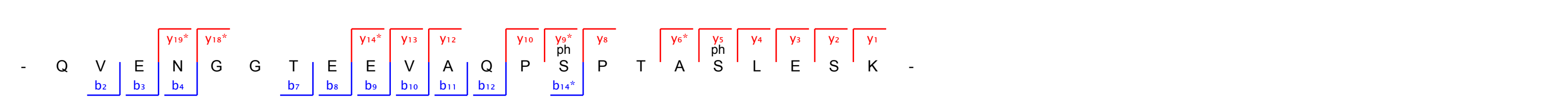
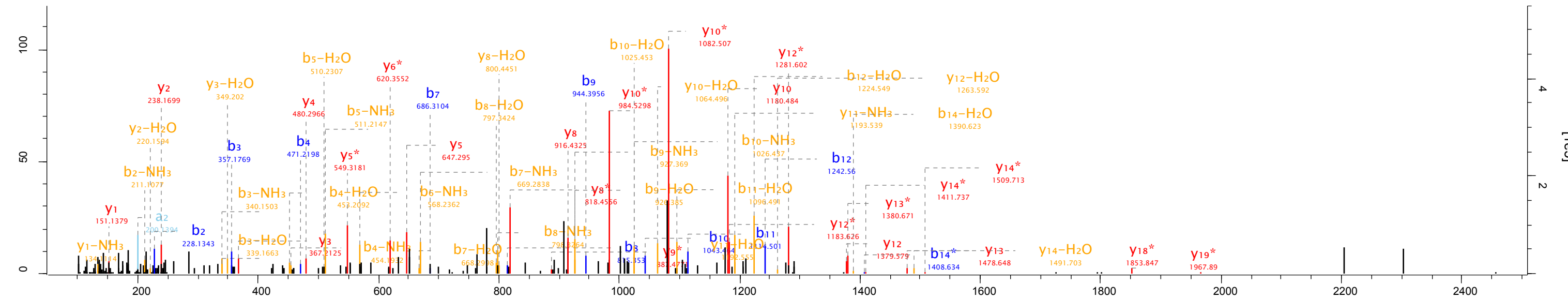
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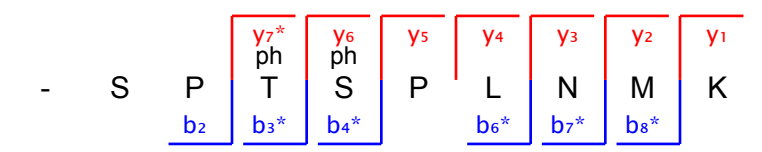
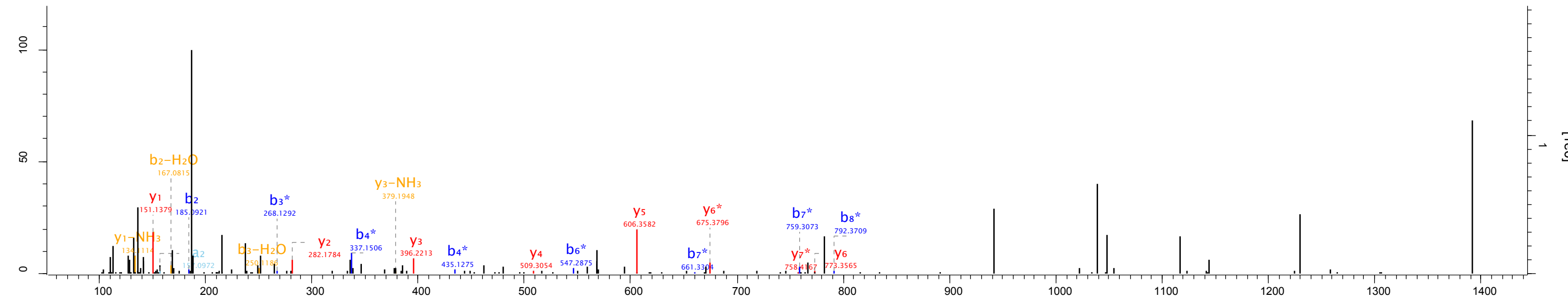
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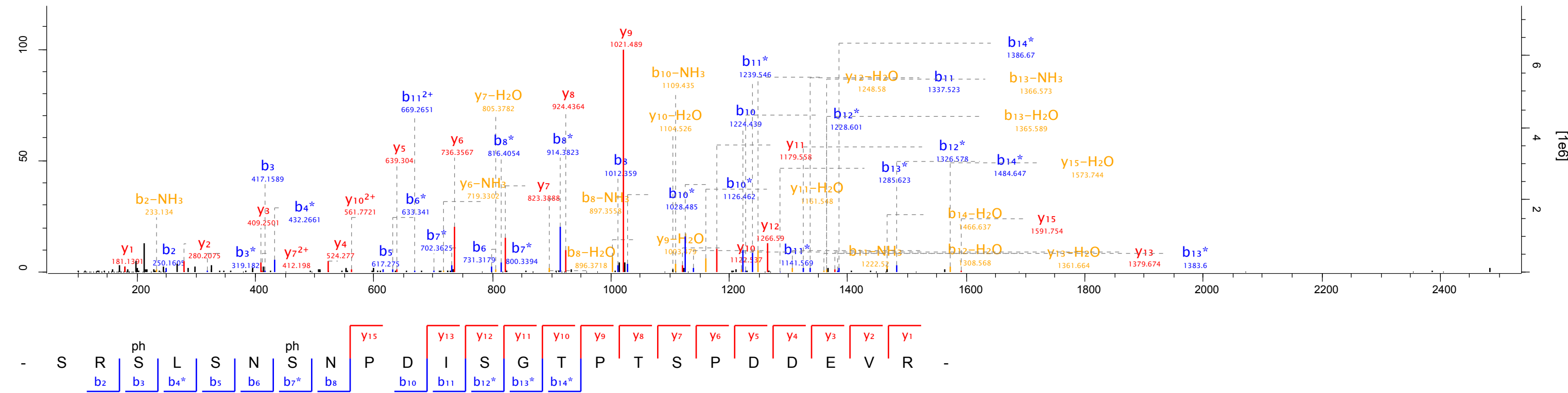


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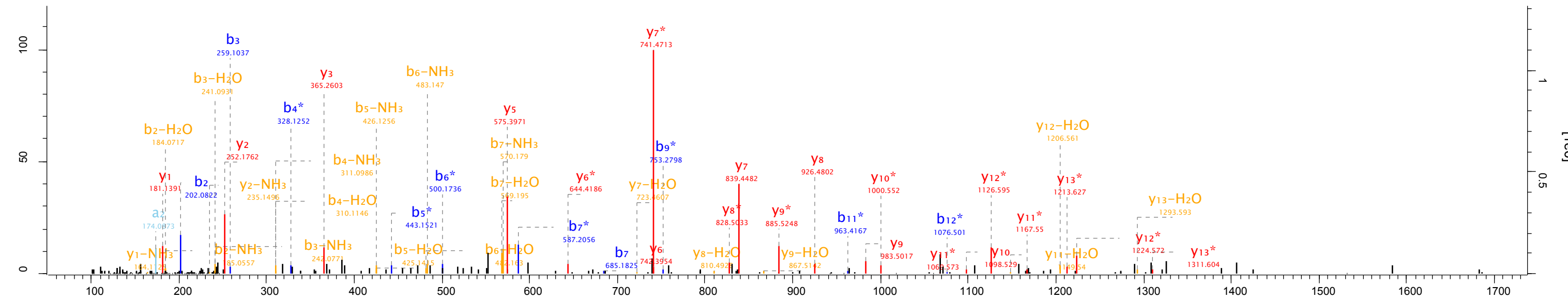


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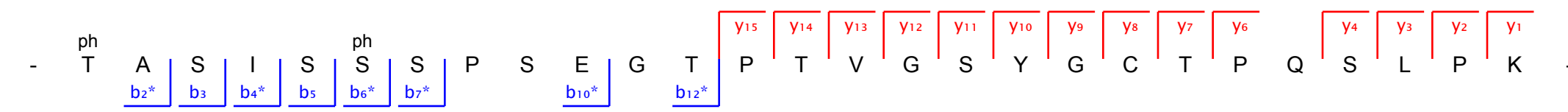
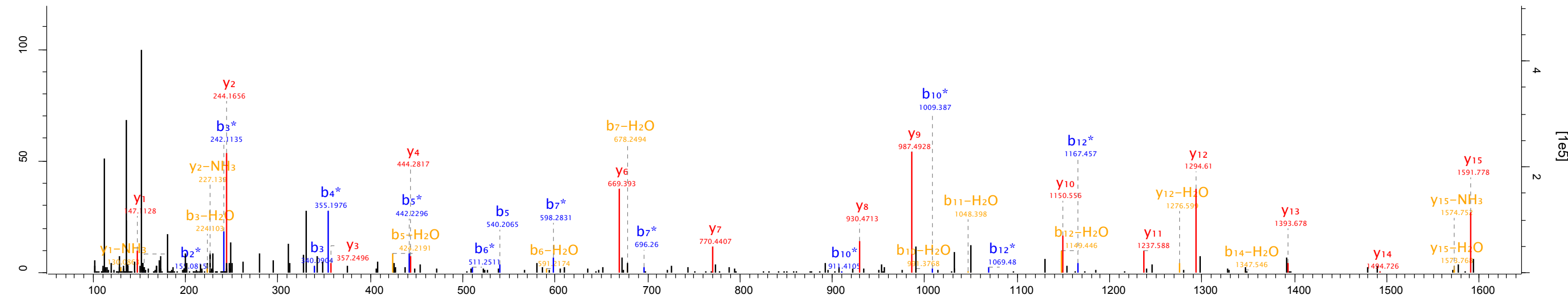




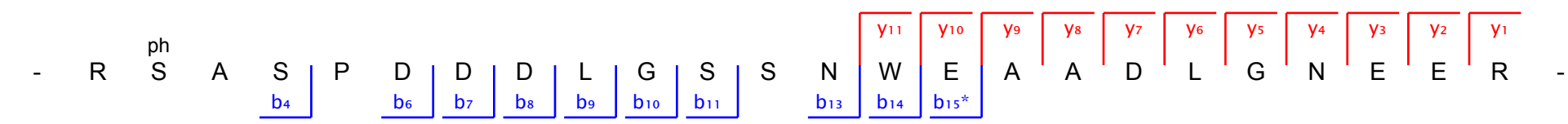
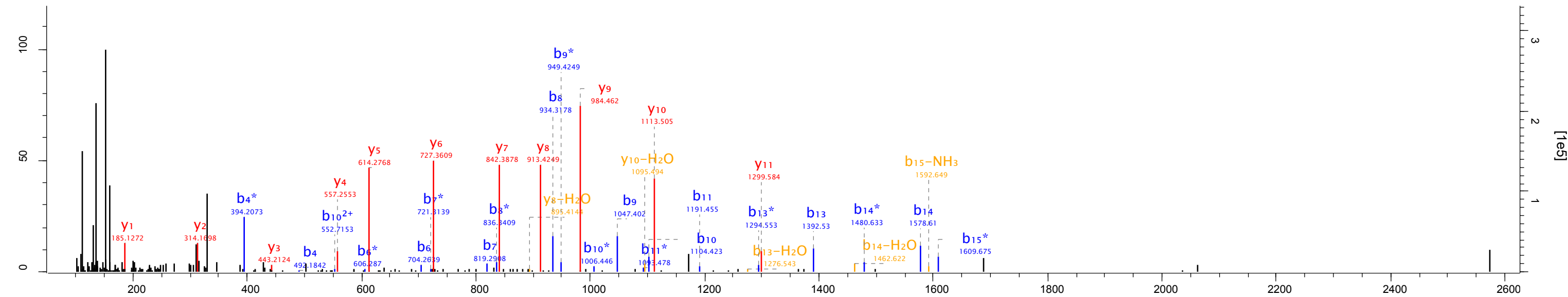
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 Scan: 9691 Method: FTMS; HCD Score: 205 m/z: 762.31 Gene names: NCKAP5L



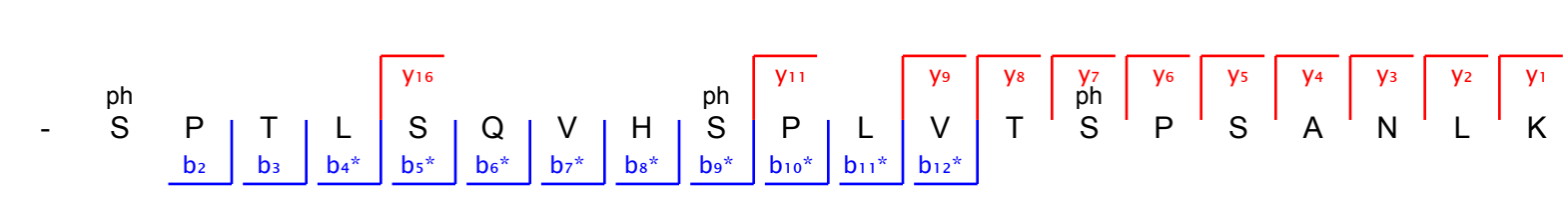
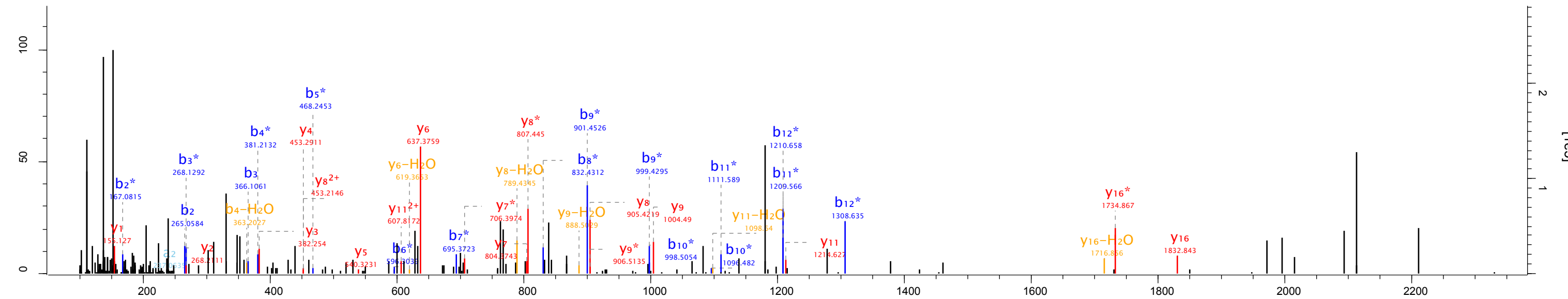
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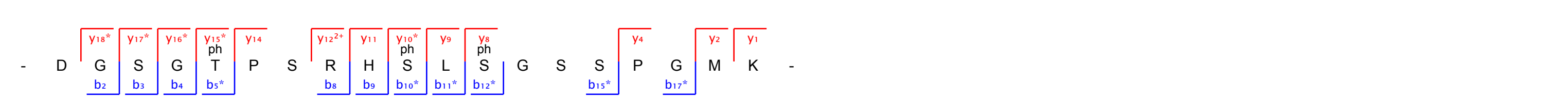
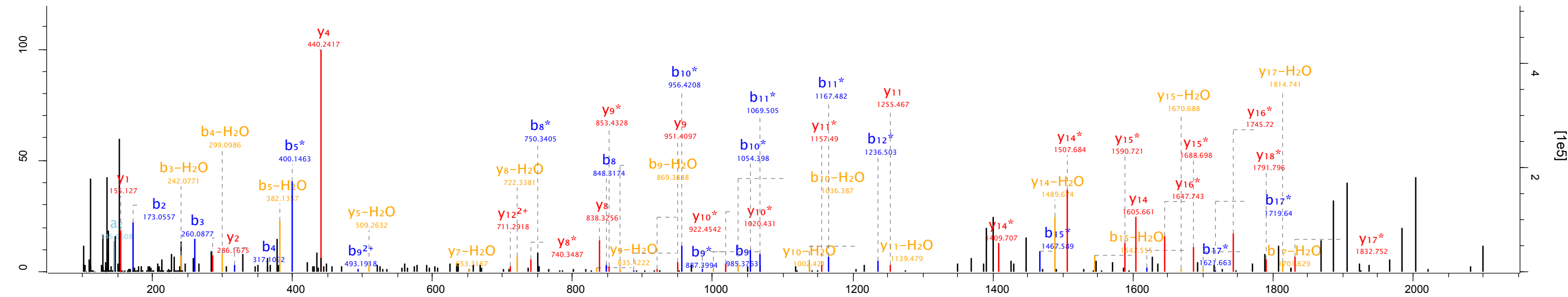


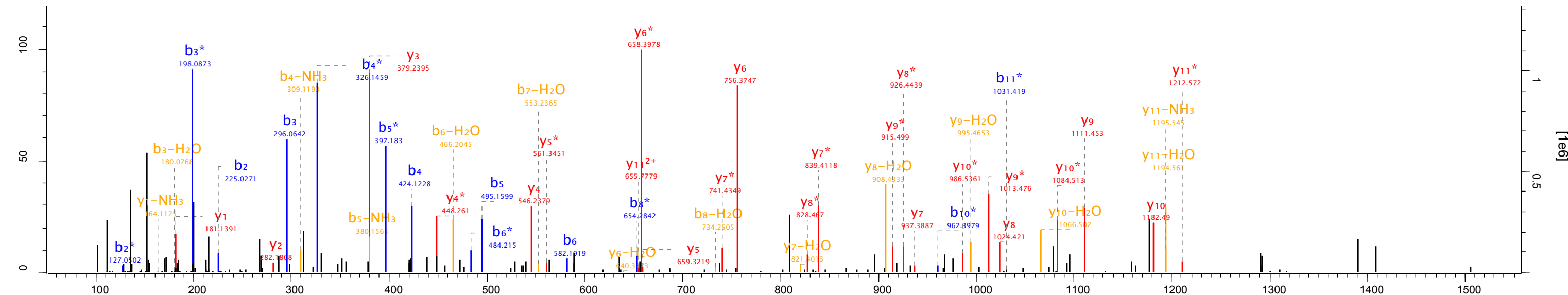
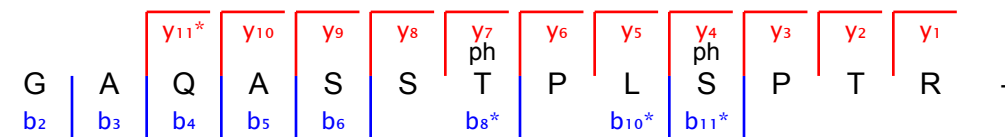
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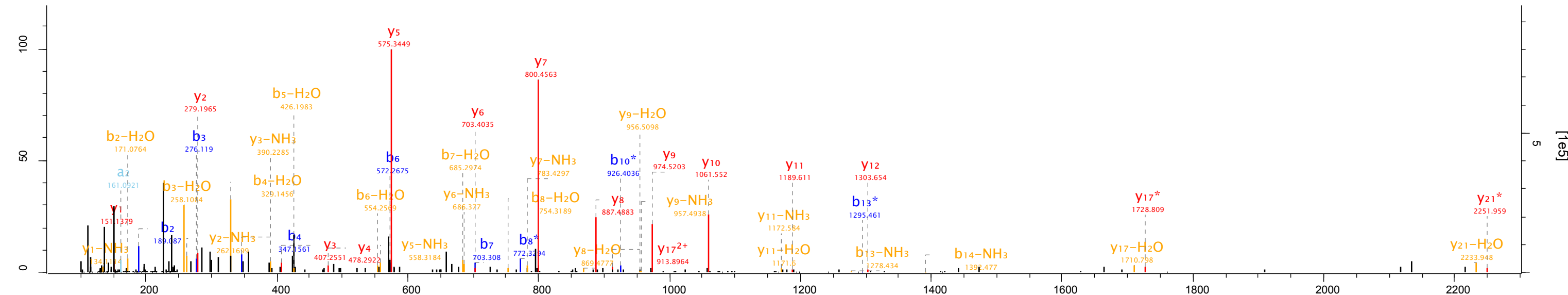


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_04 4081 FTMS; HCD 174.55 701.59 SRRM2



ph
S

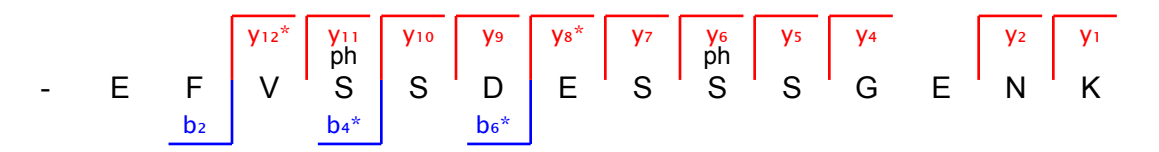
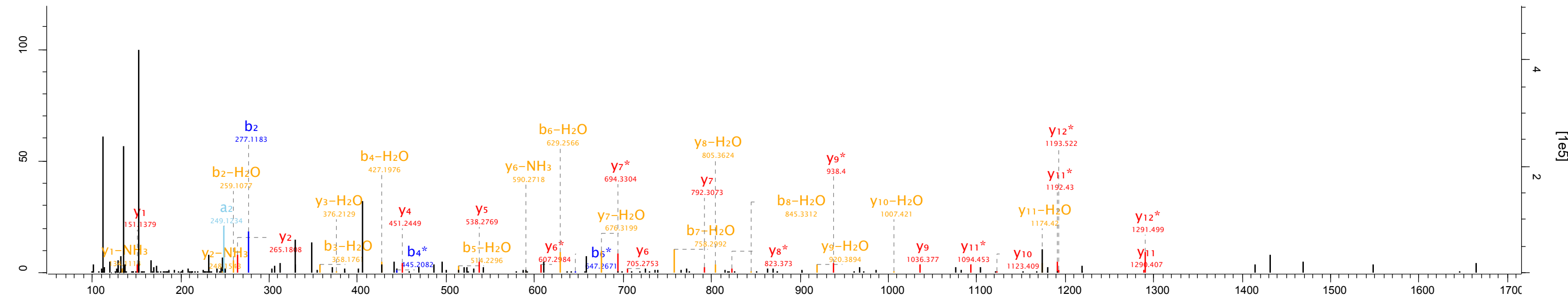


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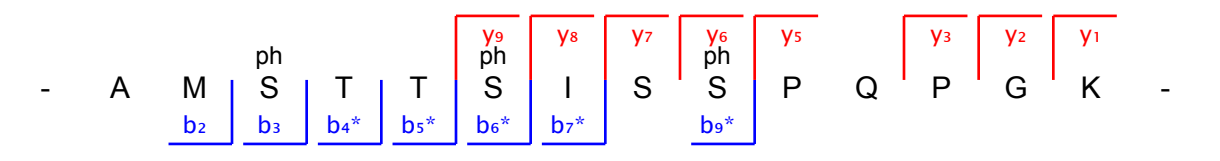
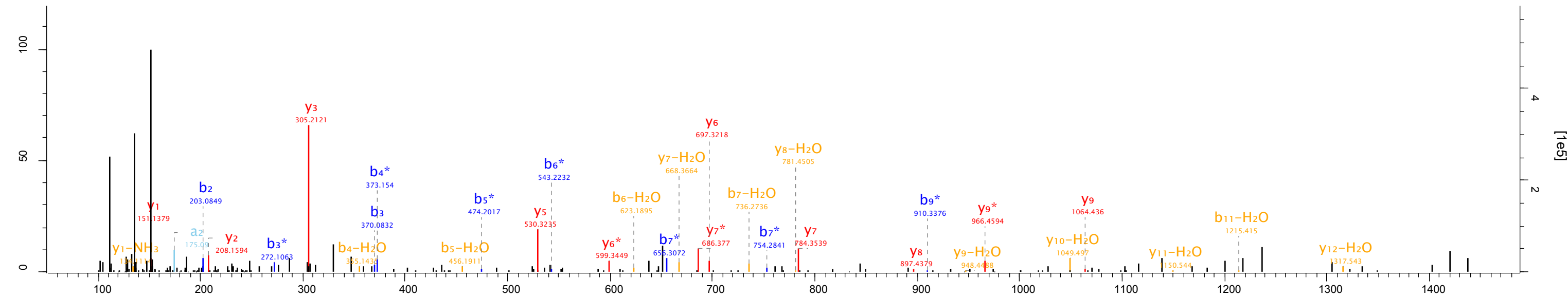
Fragmentation mapping (b and y ions):

- b2: T
- b3: S
- b4: A
- b6: Q
- b7: M
- b8*: S
- b10*: G
- b13*: D
- y1: K
- y2: Q
- y3: A
- y4: P
- y5: Q
- y6: P
- y7: S
- y8: S
- y9: S
- y10: S
- y11: N
- y12: D
- y17*: P
- y21*: P

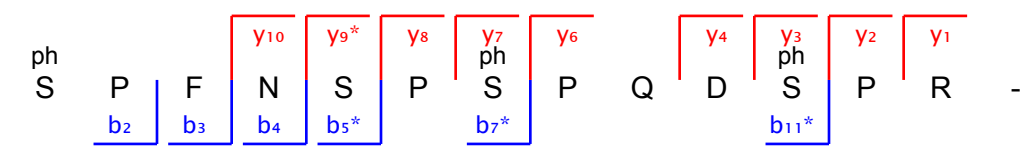
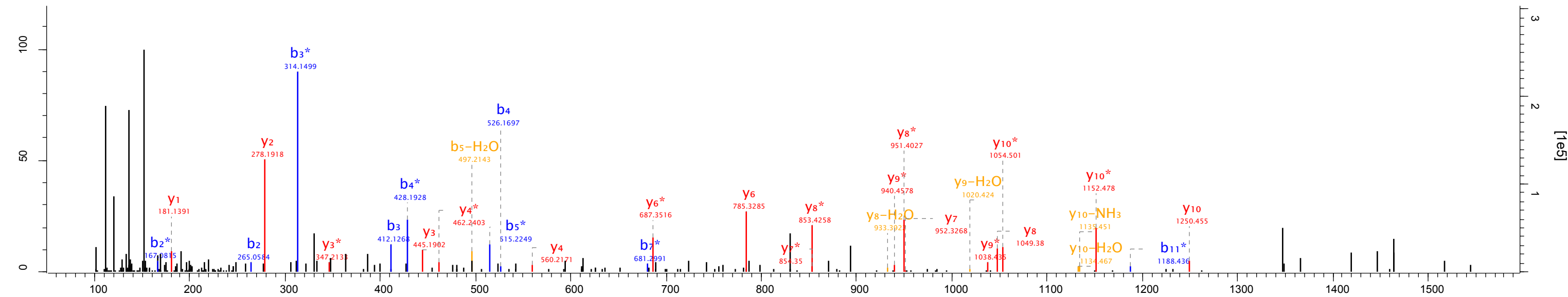
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 4821 Method FTMS; HCD Score 86.54 m/z 833.3 Gene names SSRP1



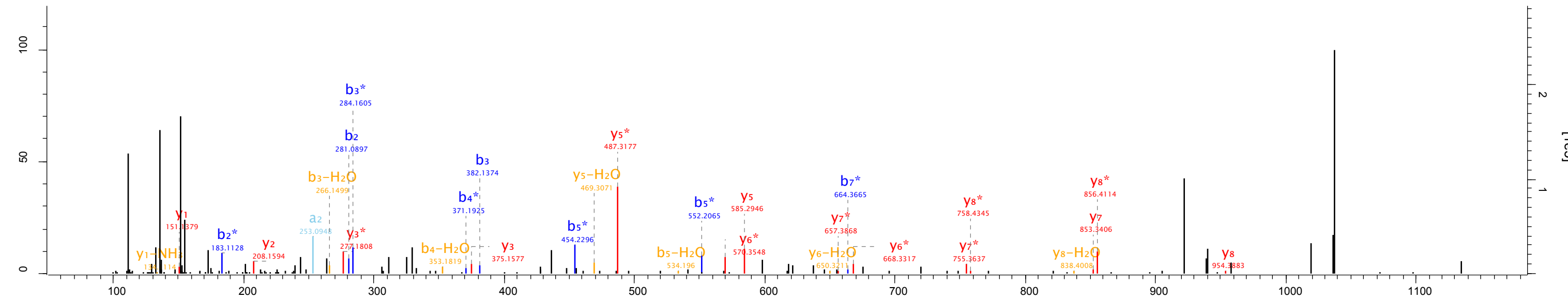
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5501 Method FTMS; HCD Score 63.44 m/z 818.31 Gene names DBNL



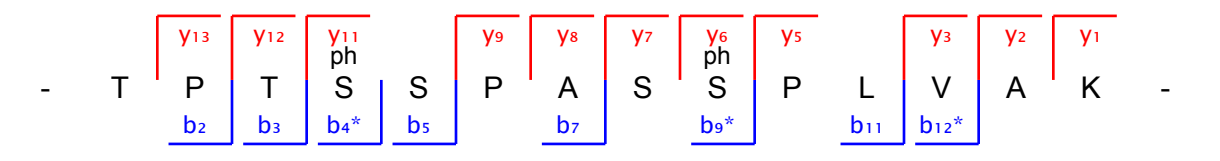
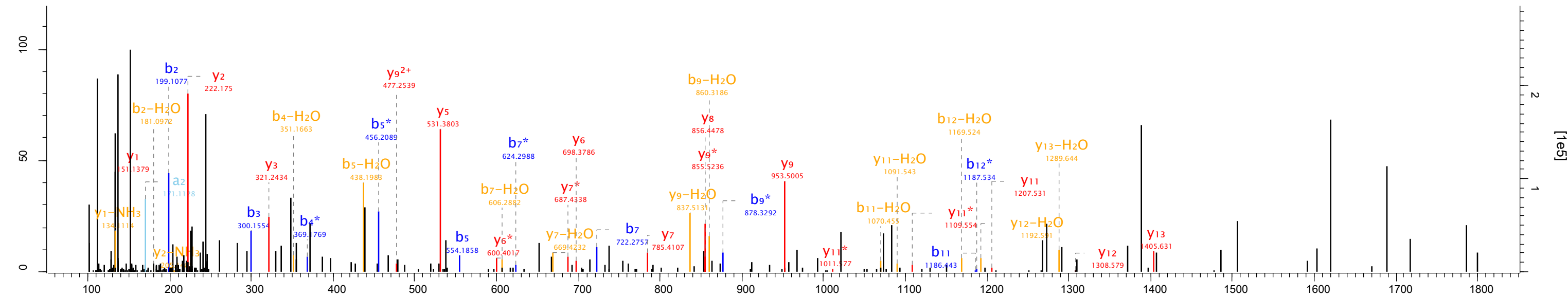
Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5911 Method FTMS; HCD Score 101.6 m/z 831.29 Gene names NFIC

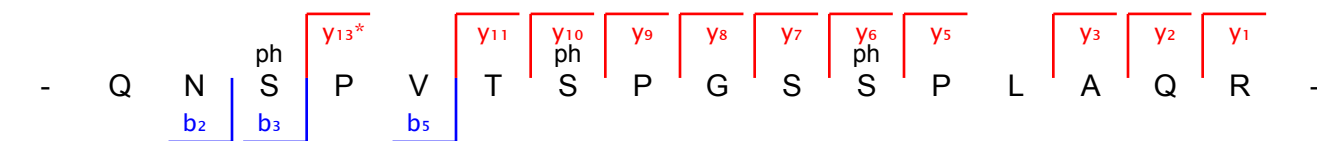
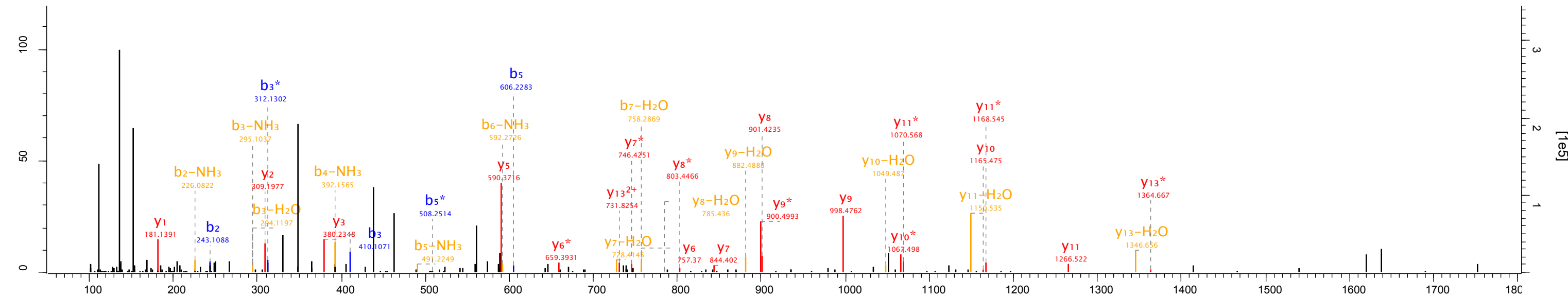


Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5951 Method FTMS; HCD Score 91.59 m/z 617.74 Gene names RAI14

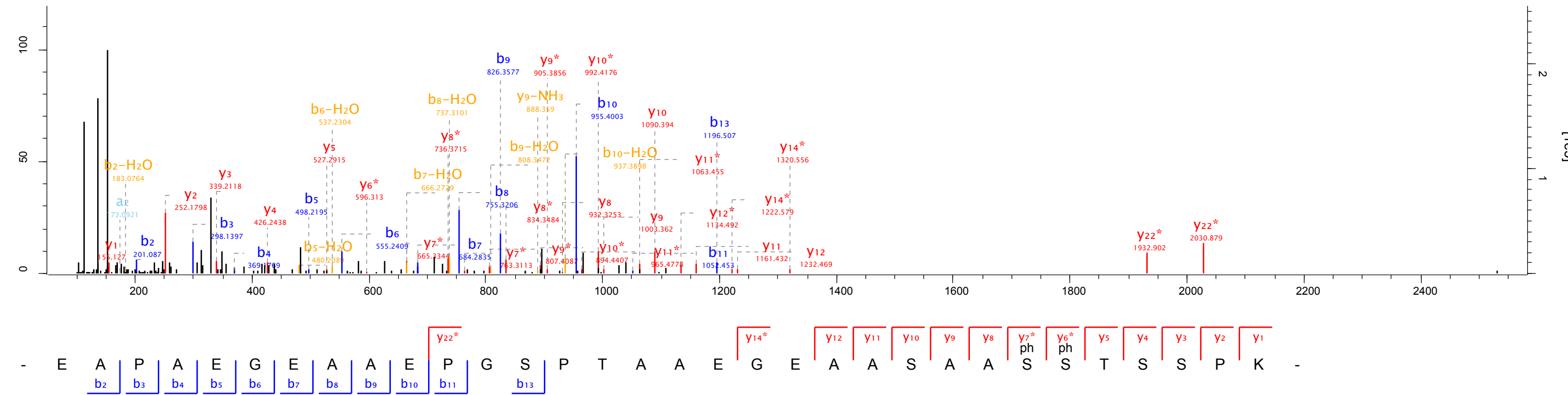


Raw file: 20171215_MaS_33SR_LMH_phospho2_04
 Scan: 6201 Method: FTMS; HCD Score: 134.4 m/z: 753.84 Gene names: RRP1B

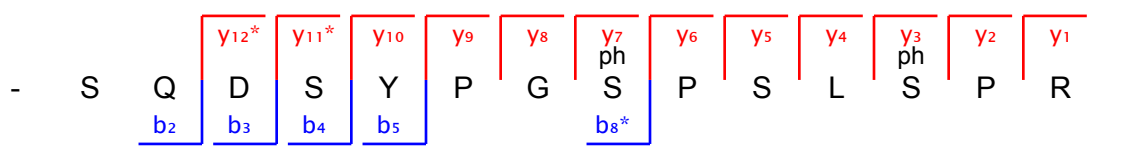
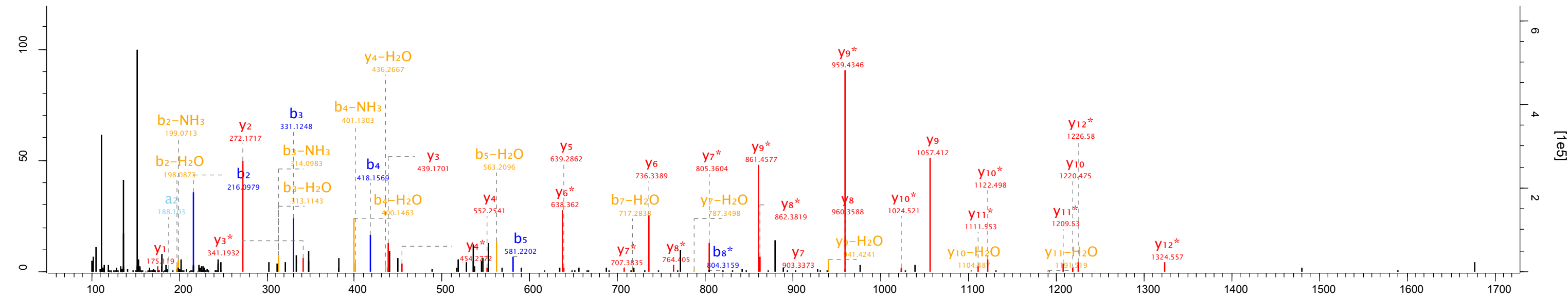




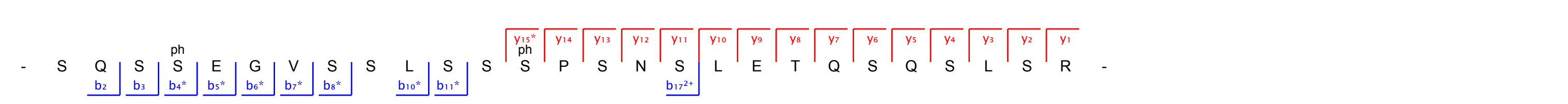
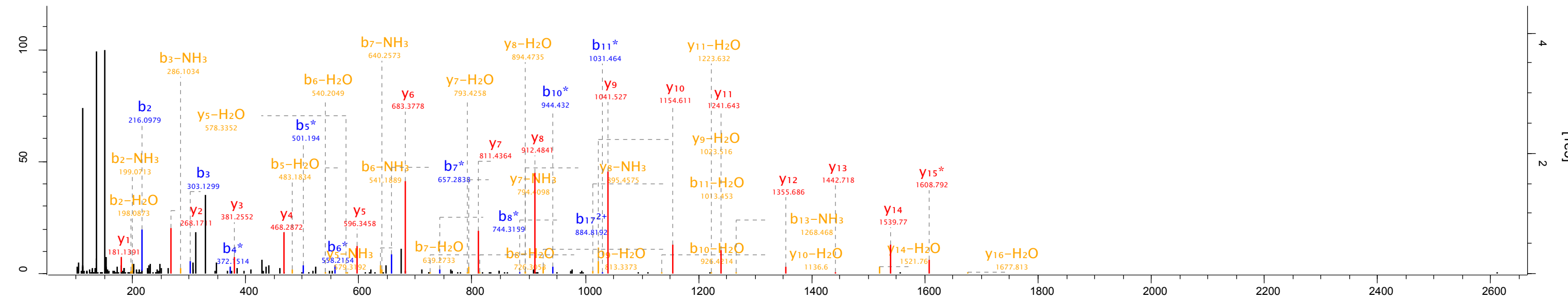
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 Scan: 7651 Method: FTMS; HCD Score: 62.21 m/z: 1028.76 Gene names: MARCKS



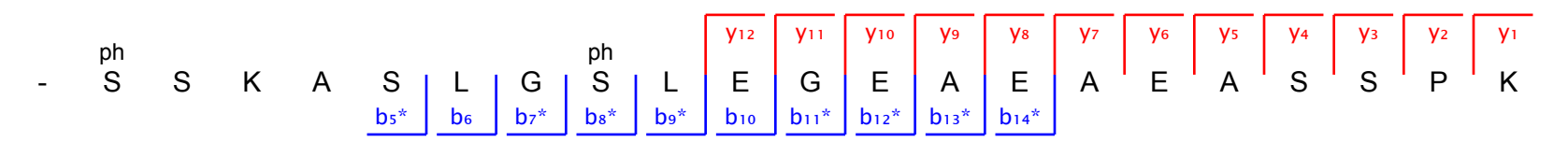
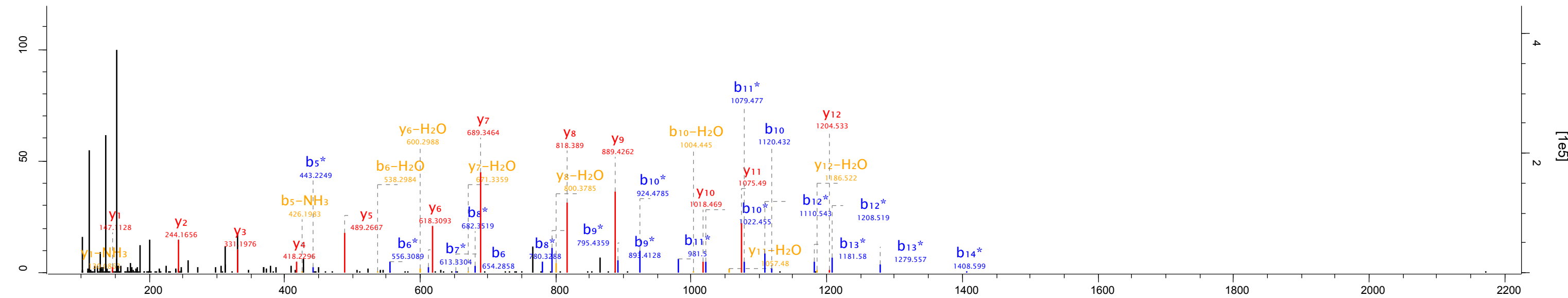
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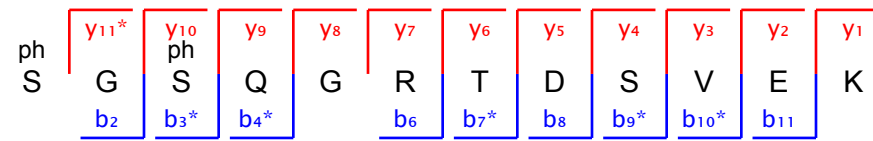
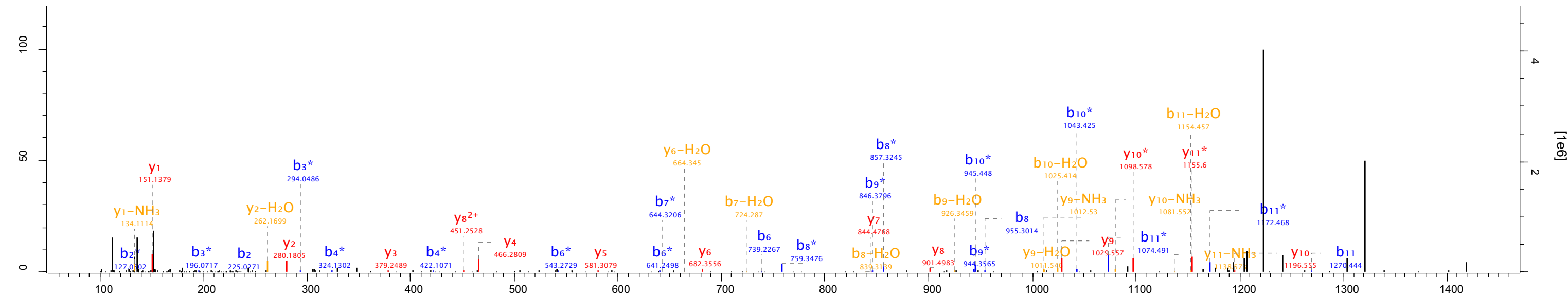


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 Scan: 10881 Method: FTMS; HCD Score: 106.3 m/z: 975.08 Gene names: UBE4B

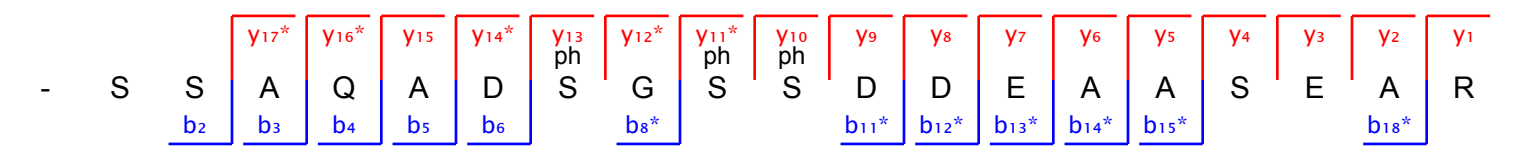
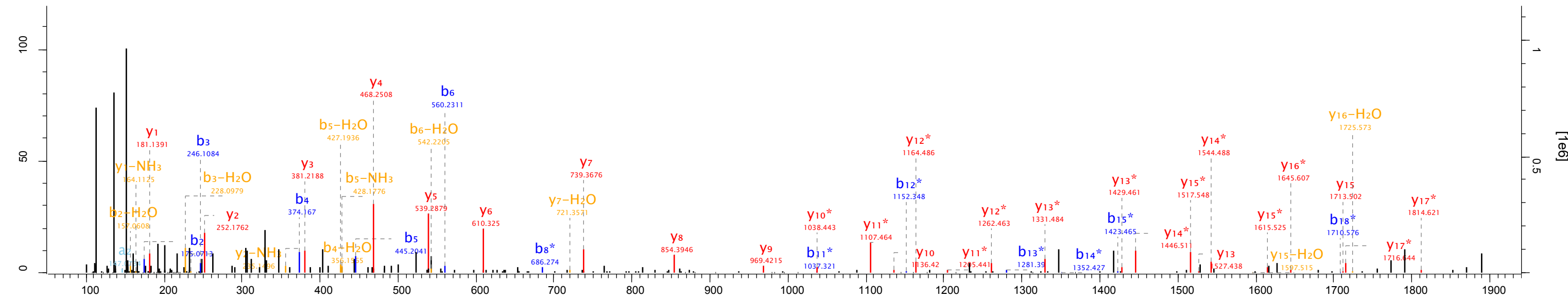


Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 12971 Method FTMS; HCD Score 96.6 m/z 732.65 Gene names AHNAK

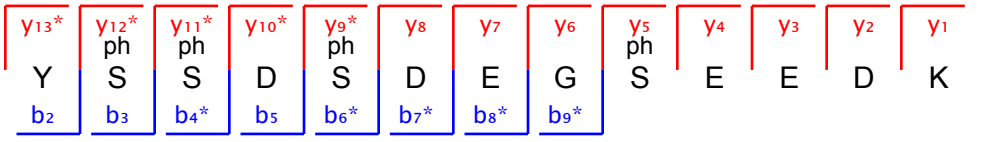
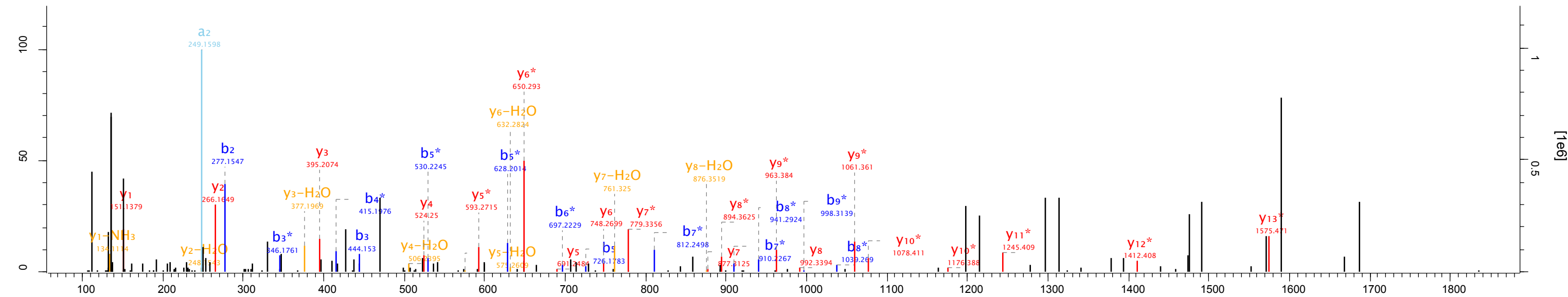




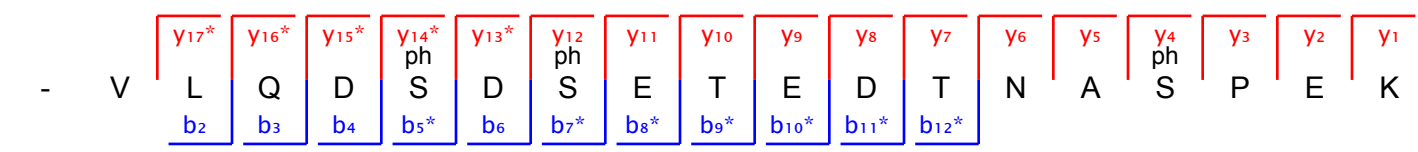
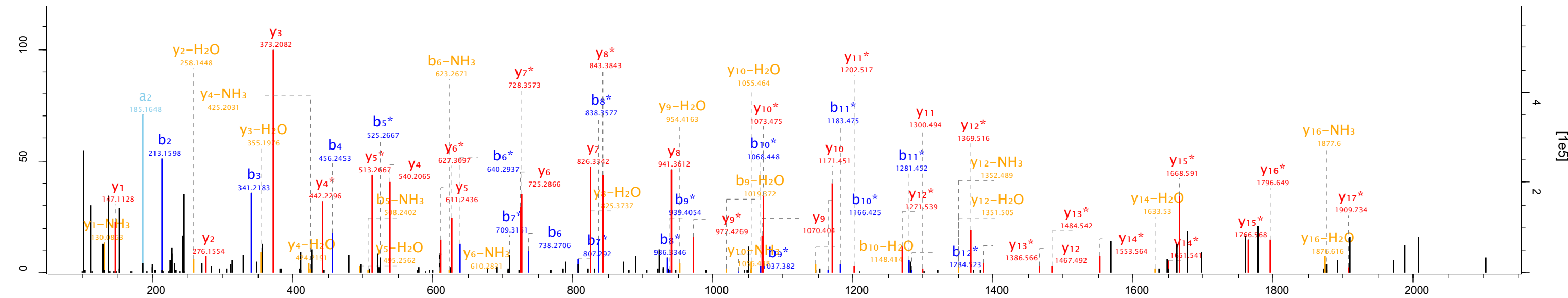
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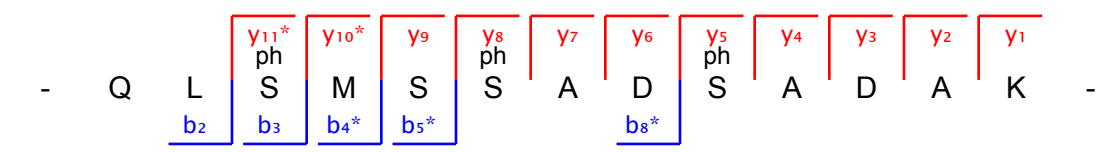
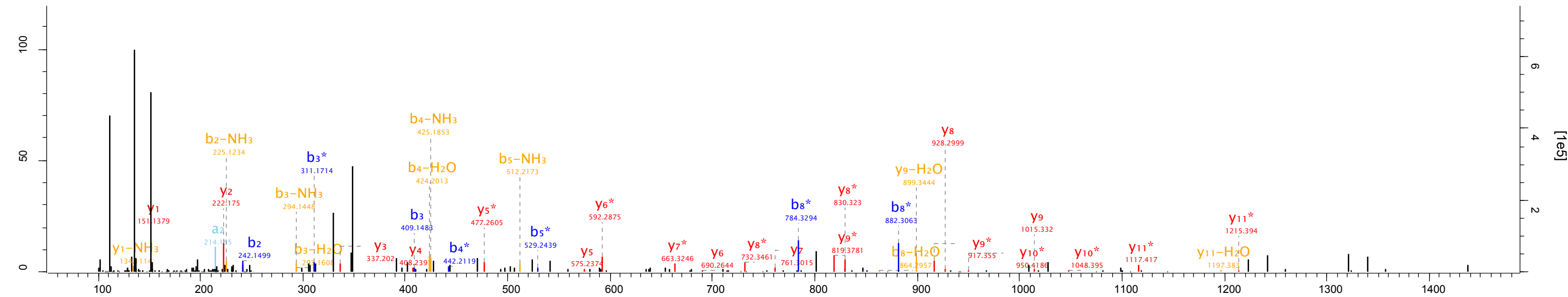
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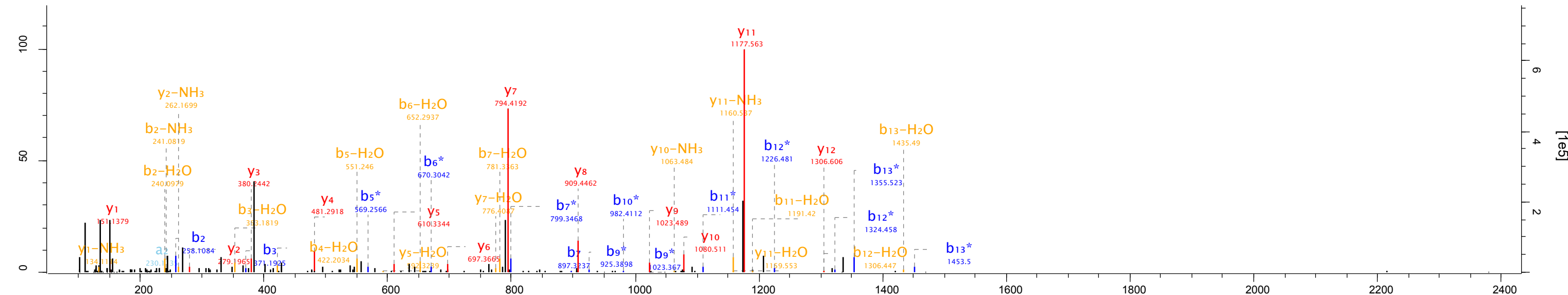


Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 4621 Method FTMS; HCD Score 271.53 m/z 1102.88 Gene names CLSPN



Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 5181 Method FTMS; HCD Score 109.09 m/z 777.76 Gene names PRRC2B



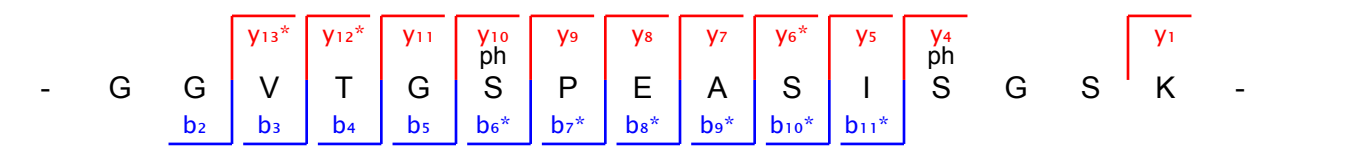
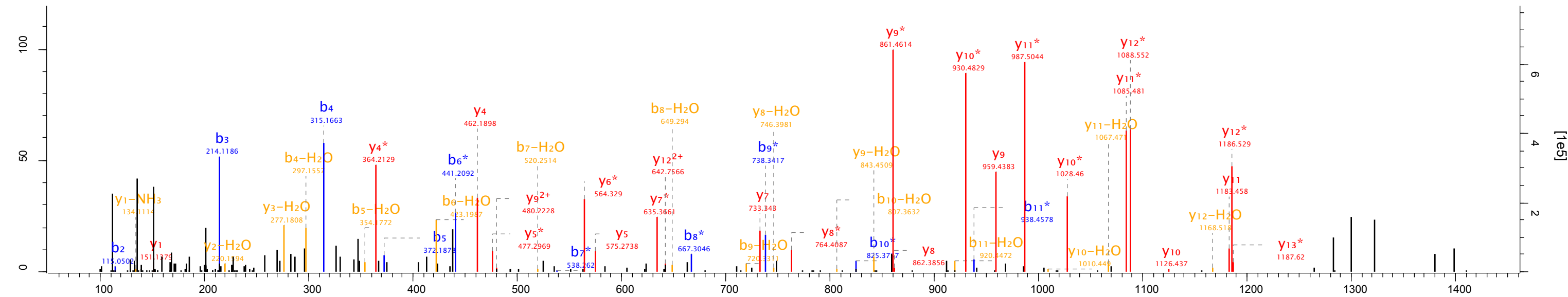


- E Q L S E T E G S G E D E P G N D P S E T T Q K -

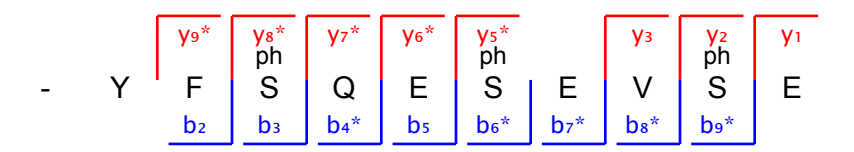
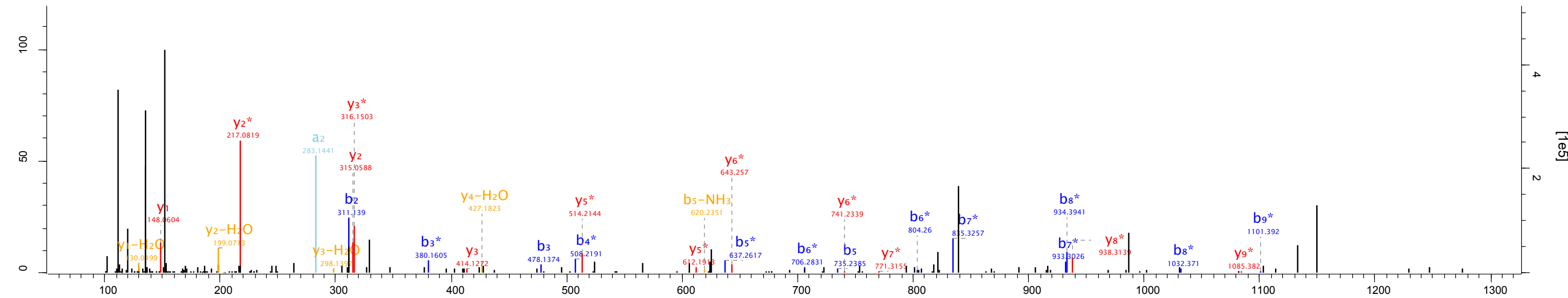
ph ph

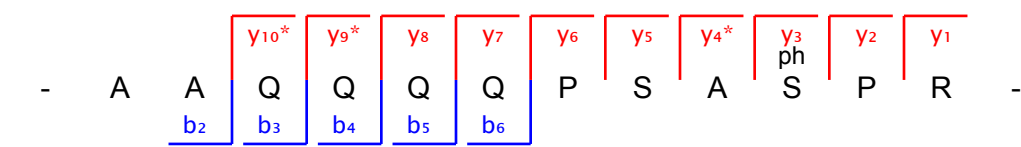
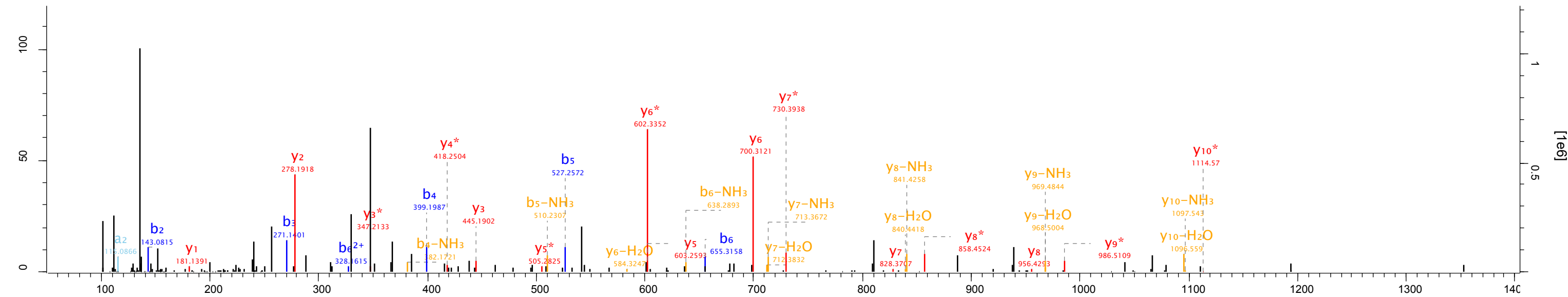
b₂ b₃ b₅* b₆* b₇ b₉* b₁₀* b₁₁* b₁₂* b₁₃* y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

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 Scan: 5931 Method: FTMS; HCD Score: 165.88 m/z: 749.31 Gene names: AHNAK

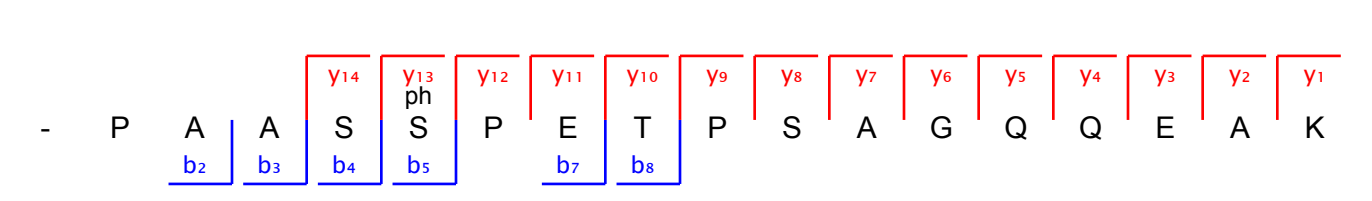
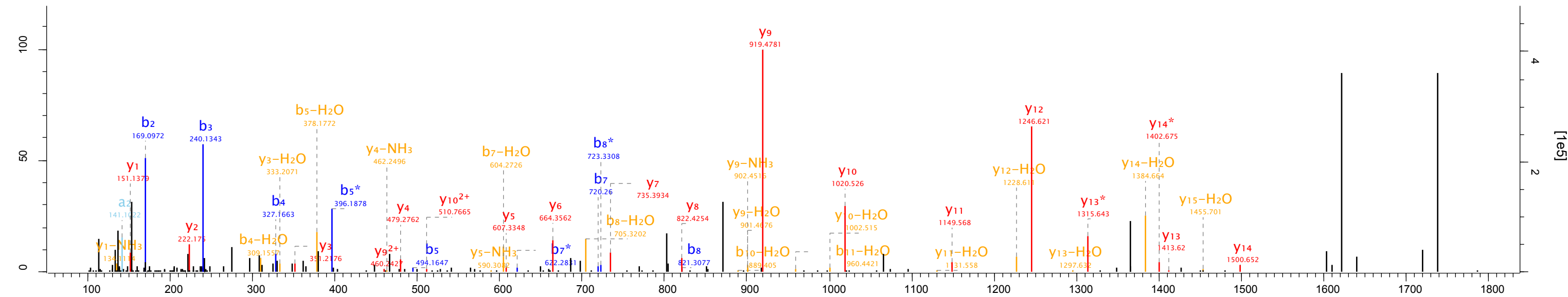


Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 9481 Method FTMS; HCD Score 104.97 m/z 722.7 Gene names KRT80

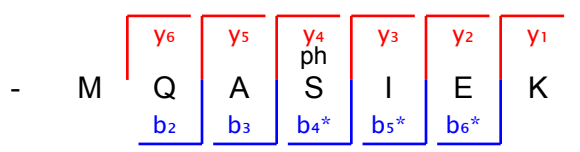
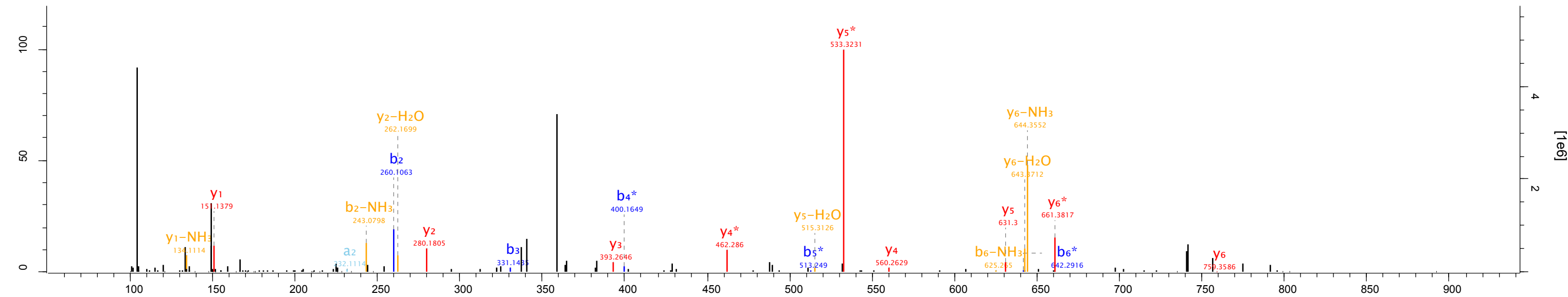


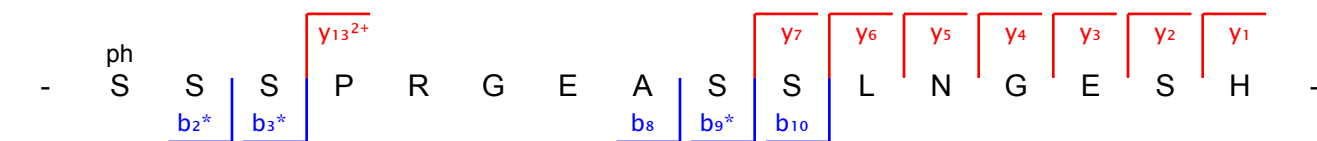
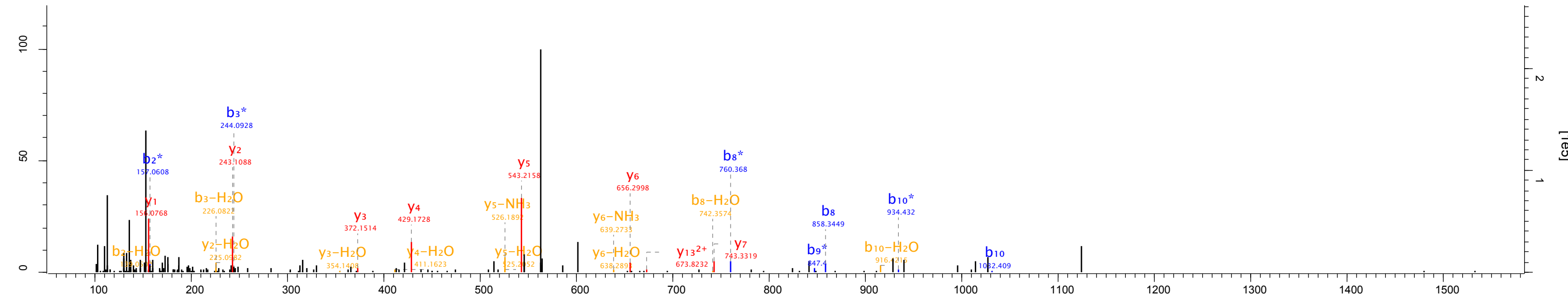


Raw file 20171215_MaS_33SR_LMH_phospho2_06 Scan 3171 Method FTMS; HCD Score 164.9 m/z 870.89 Gene names INCENP



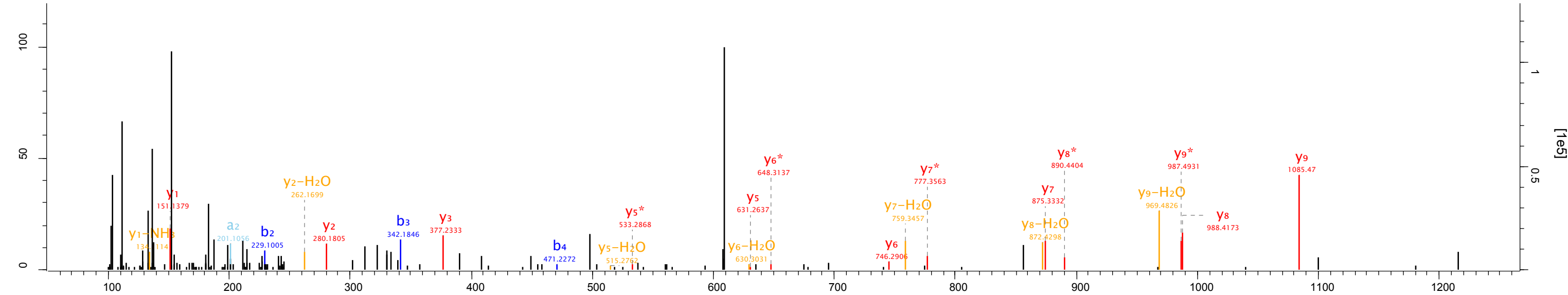
Raw file 20171215_MaS_33SR_LMH_phospho2_06 Scan 3611 Method FTMS; HCD Score 106.37 m/z 445.7 Gene names NPM1



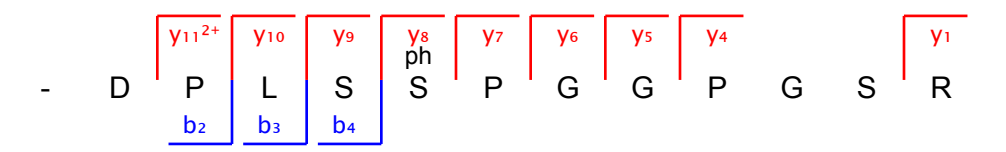
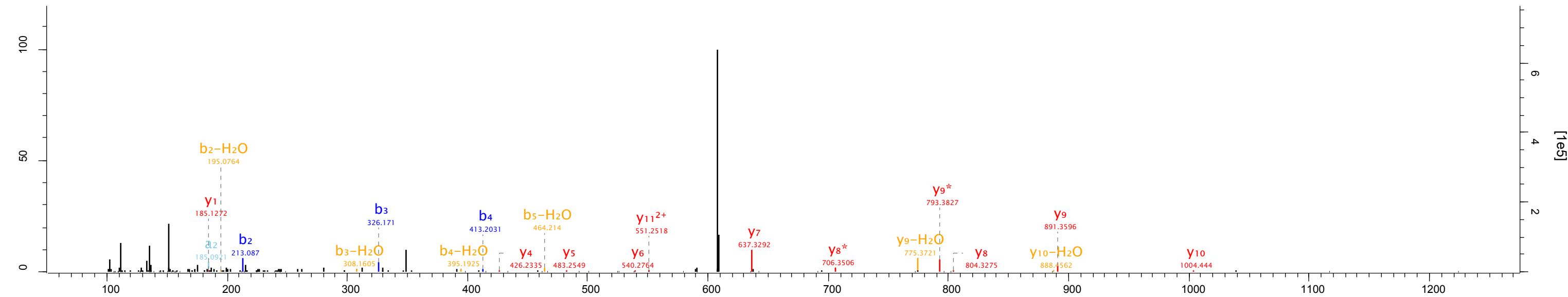


Raw file 20171215_MaS_33SR_LMH_phospho2_06 Scan 5141 Method FTMS; HCD Score 93.65 m/z 608.76 Gene names NCOR1

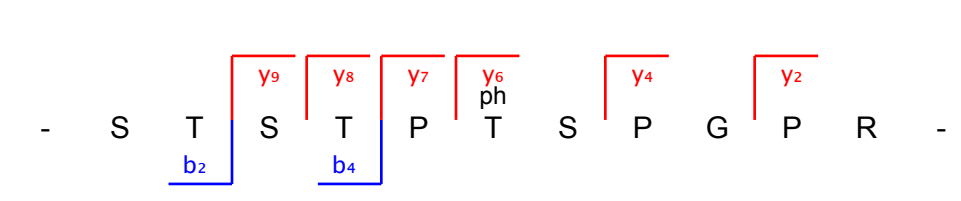
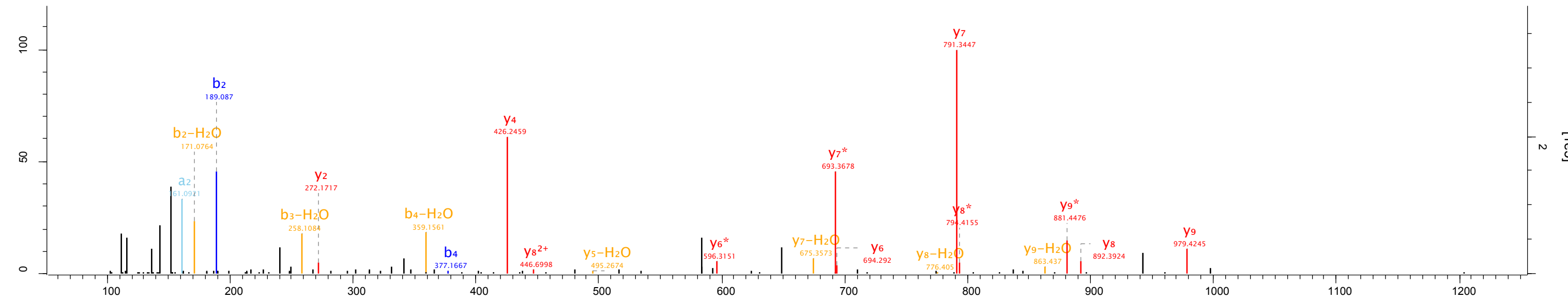
20171215_MaS_33SR_LMH_phospho2_06



Raw file 20171215_MaS_33SR_LMH_phospho2_06 Scan 5191 Method FTMS; HCD Score 44.31 m/z 608.77 Gene names EML3

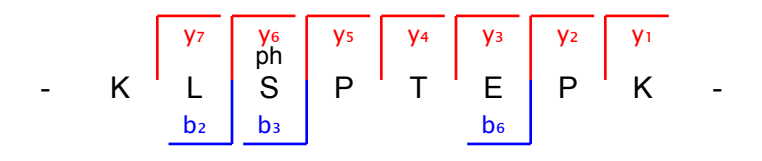
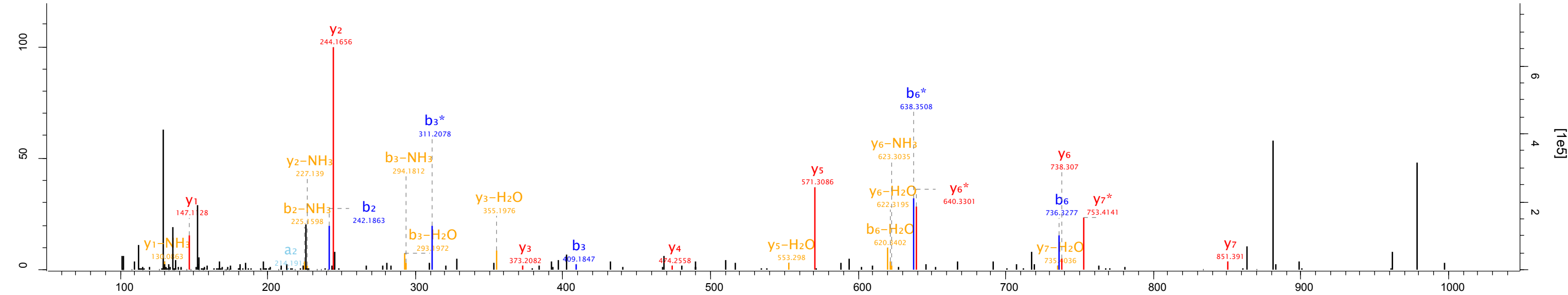


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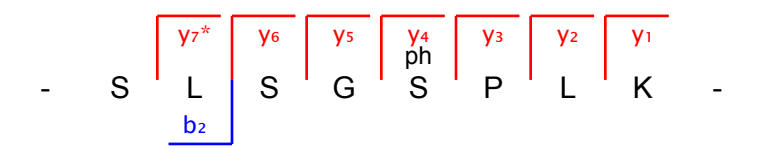
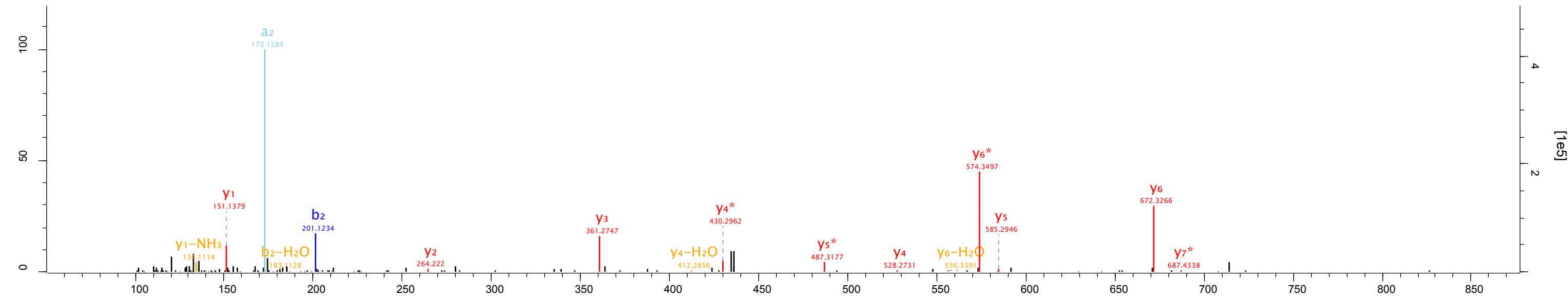


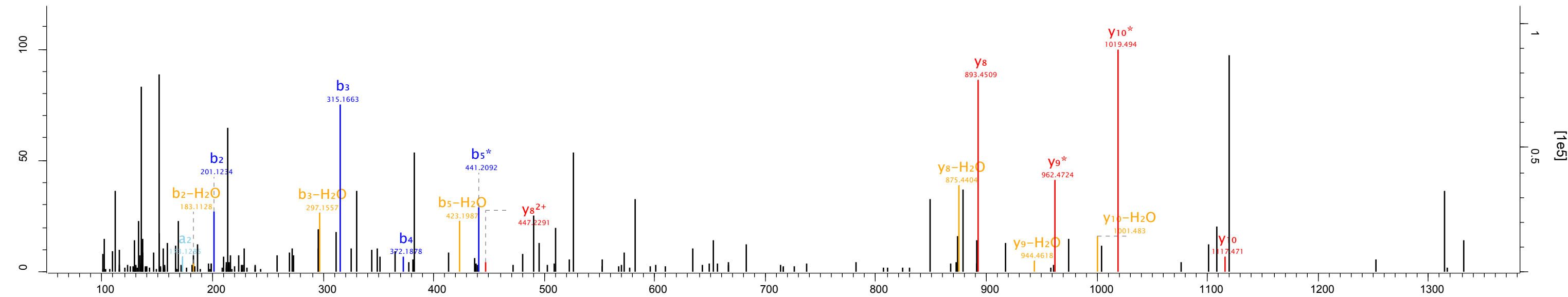
Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_08 2801 FTMS; HCD 124.18 490.25 SCAMP3



Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 4861 Method FTMS; HCD Score 64.91 m/z 436.72 Gene names BAZ1B





- S L N G S L S V Q M S G R -

Fragmentation sites are indicated by brackets below the sequence:

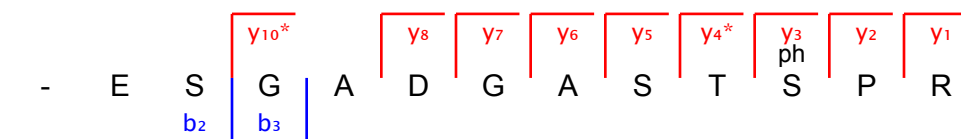
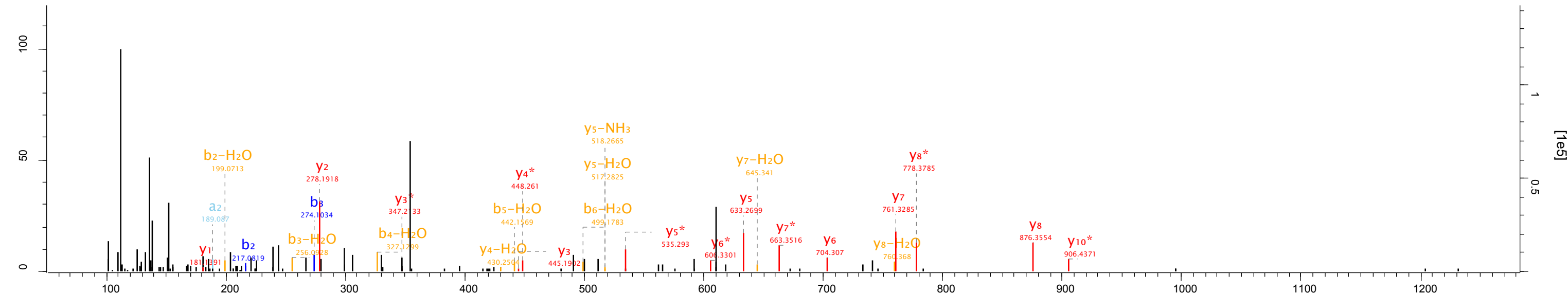
- Blue brackets: b₂ (L), b₃ (N), b₄ (G), b₅* (S)
- Red brackets: y₁₀ (G), y₉* (S), y₈ (L)

Other labels: ox (M)

Raw file

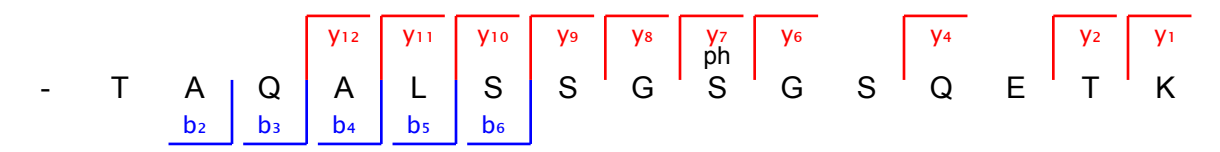
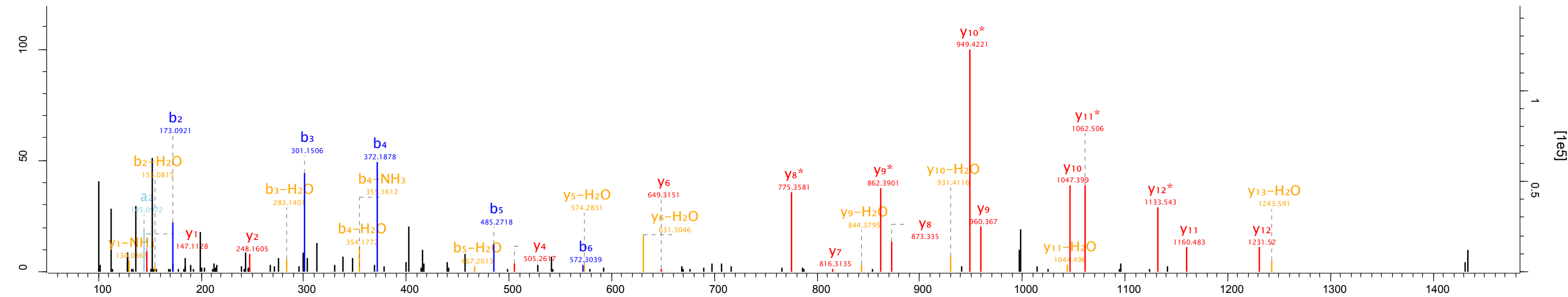
20171215_MaS_33SR_LMH_phospho2_09

Scan	Method	Score	m/z	Gene names
2021	FTMS; HCD	41.94	610.75	TADA3



Raw file
20171215_MaS_33SR_LMH_phospho2_09

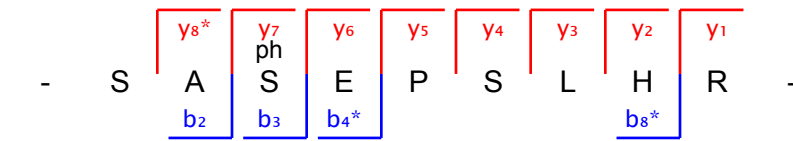
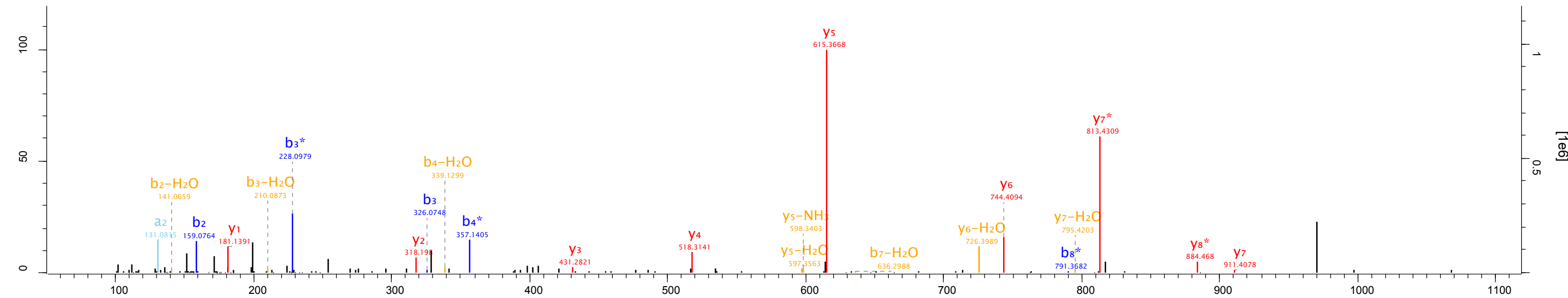
Scan 2781 Method FTMS; HCD Score 101.23 m/z 766.33 Gene names OXSR1

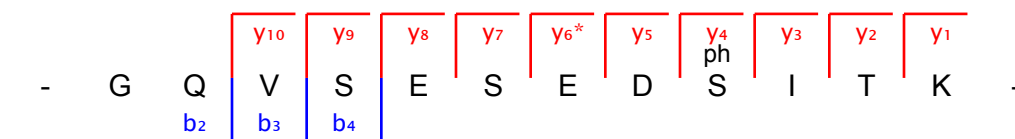
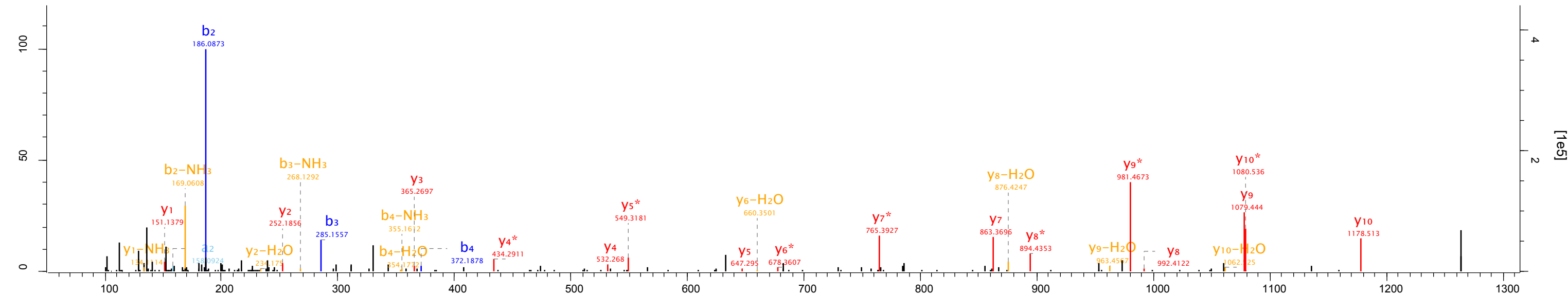


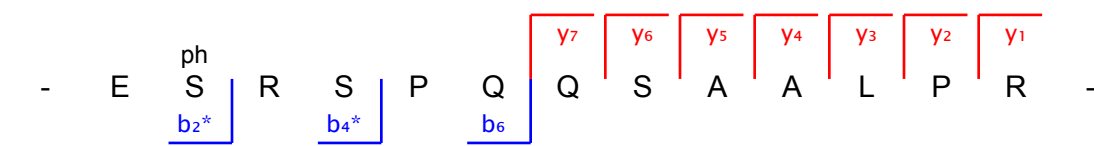
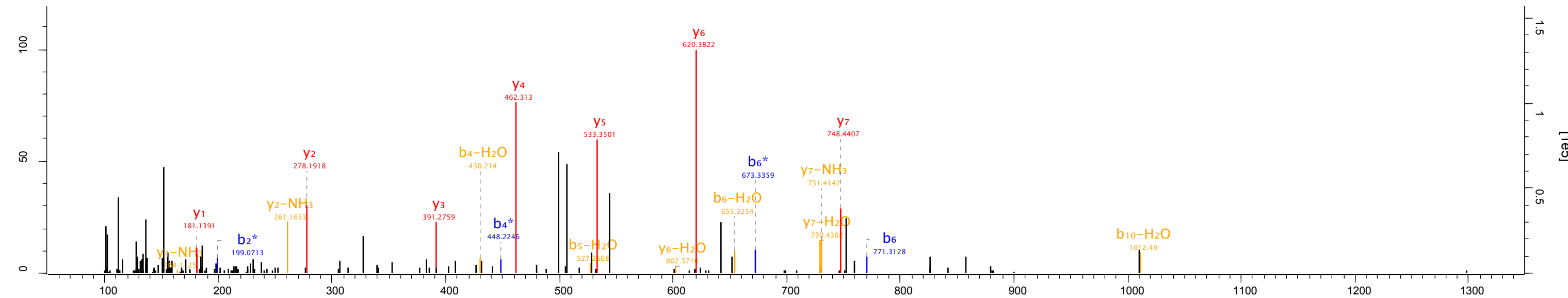
Raw file

20171215_MaS_33SR_LMH_phospho2_09

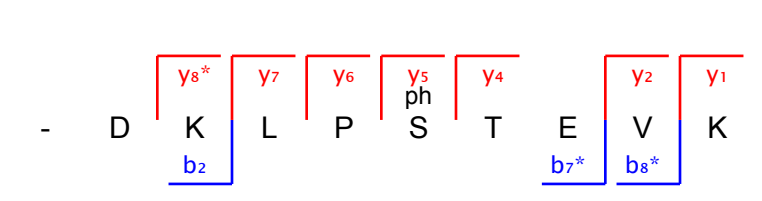
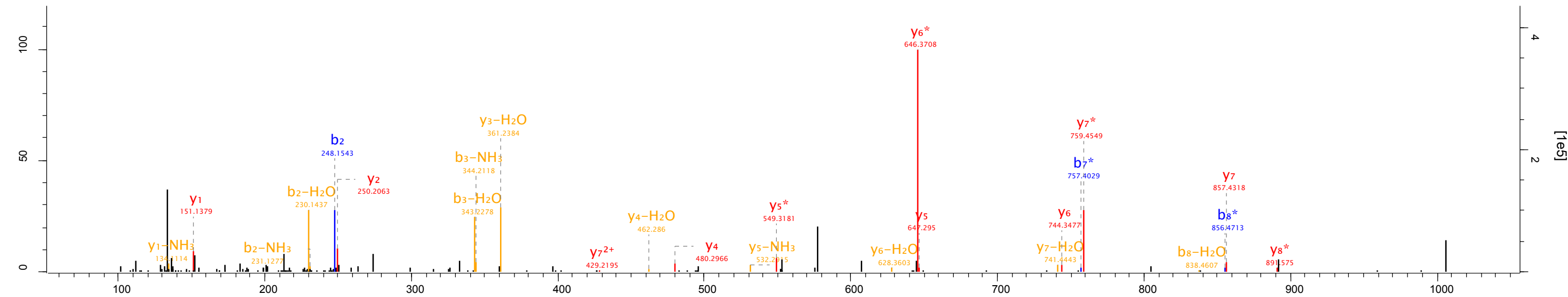
Scan	Method	Score	m/z	Gene names
2901	FTMS; HCD	113.22	535.24	RAF1;ARAF



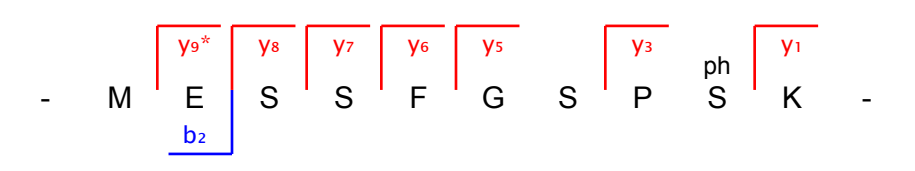
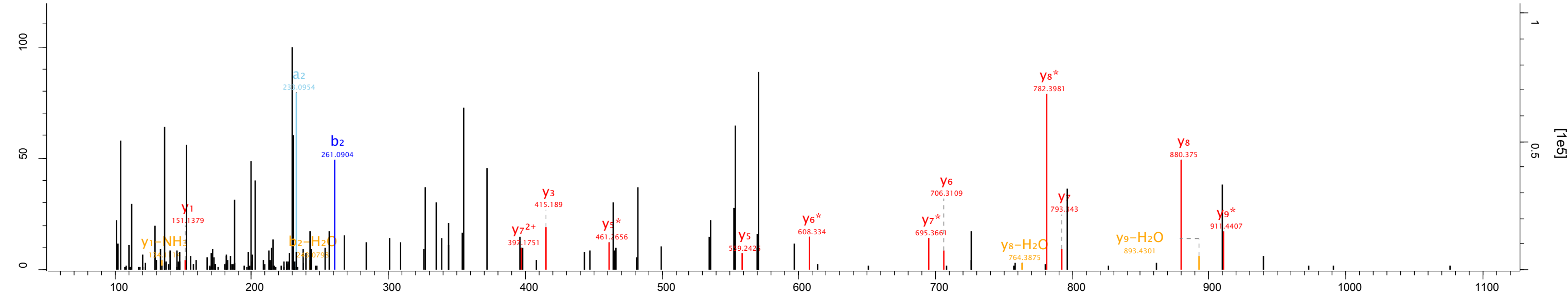




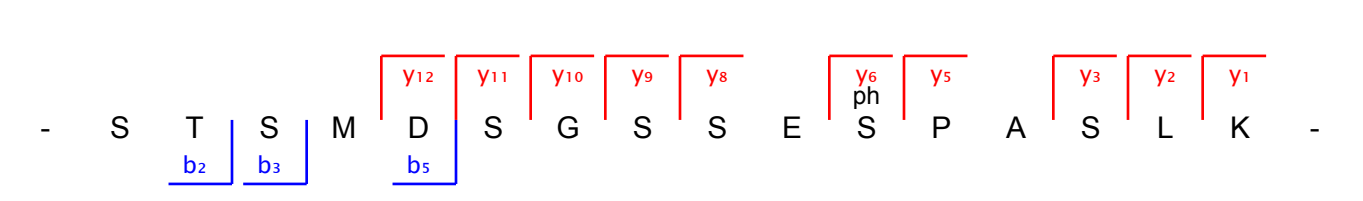
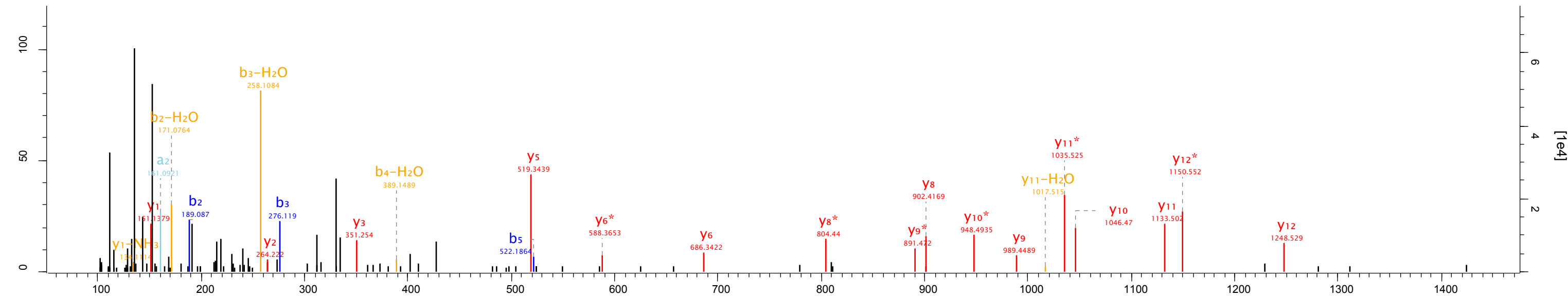
Raw file: 20171215_MaS_33SR_LMH_phospho2_09
 Scan: 4031 Method: FTMS; HCD Score: 132.86 m/z: 552.79 Gene names: NFKB2



20171215_MaS_33SR_LMH_phospho2_09 4541 FTMS; HCD 45.35 570.73 ATF7IP



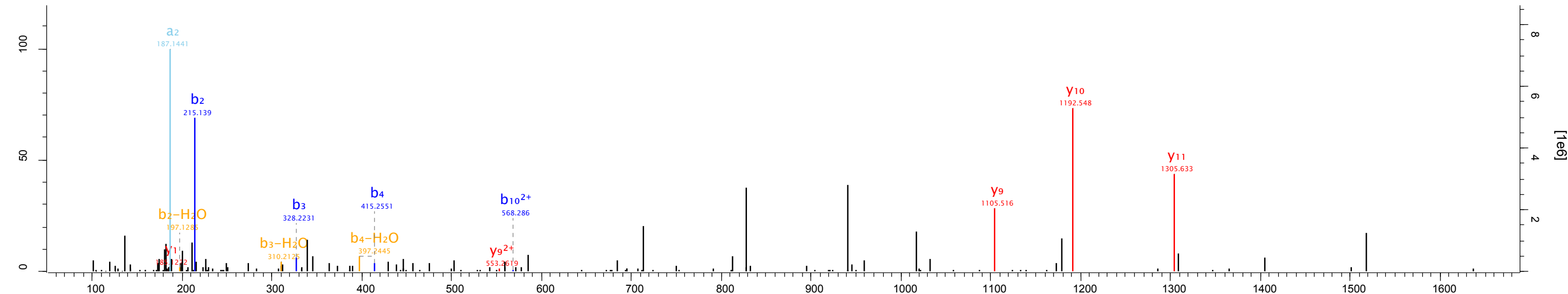
Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 5031 Method FTMS; HCD Score 79.47 m/z 828.34 Gene names ITSN1



Raw file

20171215_MaS_33SR_LMH_proteome_01

Scan 101441 Method FTMS; HCD Score 47.43 m/z 760.39

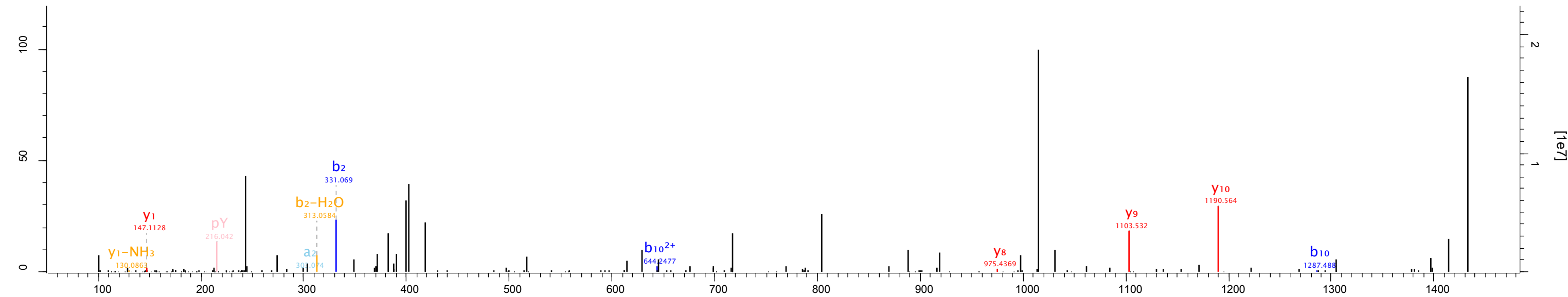


- L T I S L S P L T E A E R -

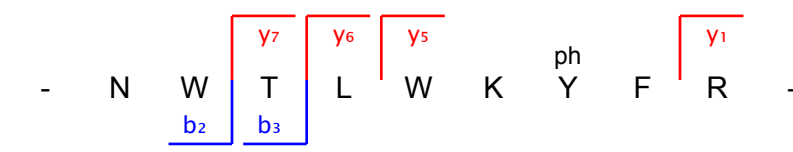
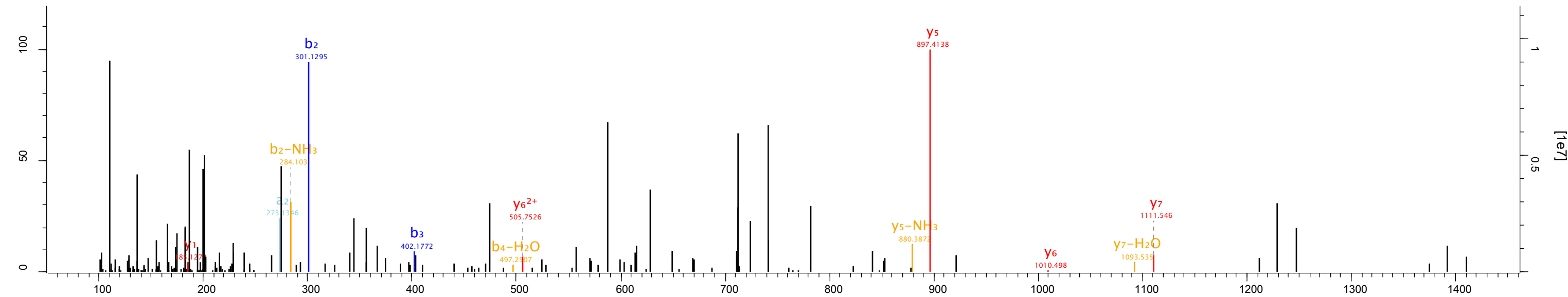
Fragmentation mapping:

- Red boxes: y11 (I), y10 (S), y9 (L)
- Blue boxes: b2 (L), b3 (I), b4 (S), b10²⁺ (E)

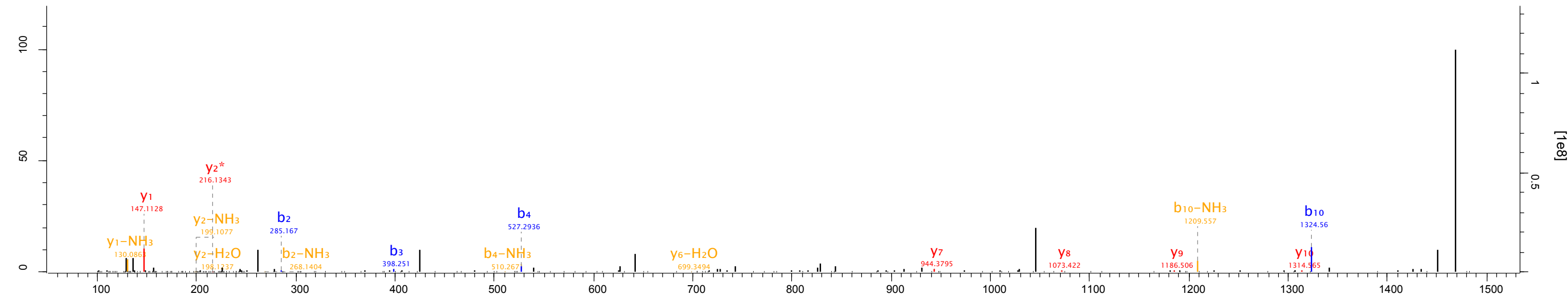
Raw file: 20171215_MaS_33SR_LMH_proteome_01
 Scan: 2661 Method: FTMS; HCD Score: 54.26 m/z: 717.3 Gene names: TNFSF10



Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 3731 Method FTMS; HCD Score 48.42 m/z 471.23 Gene names DGAT2L6



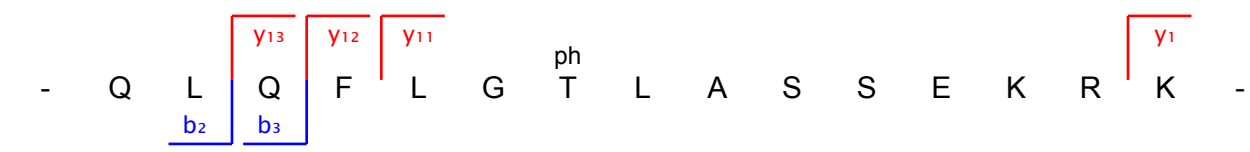
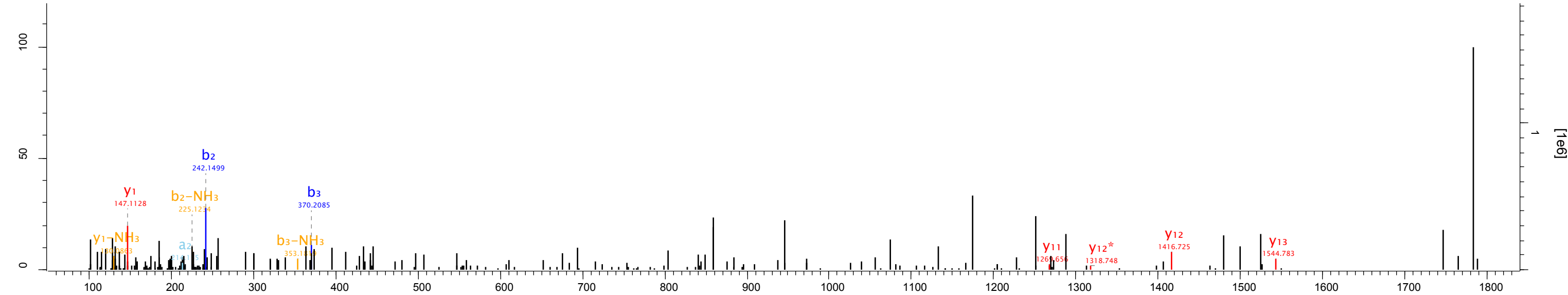
Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 3791 Method FTMS; HCD Score 67.21 m/z 735.84



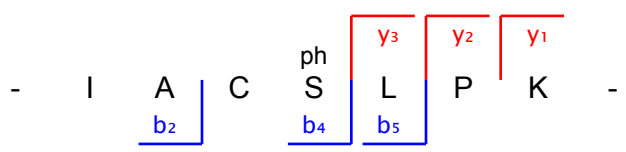
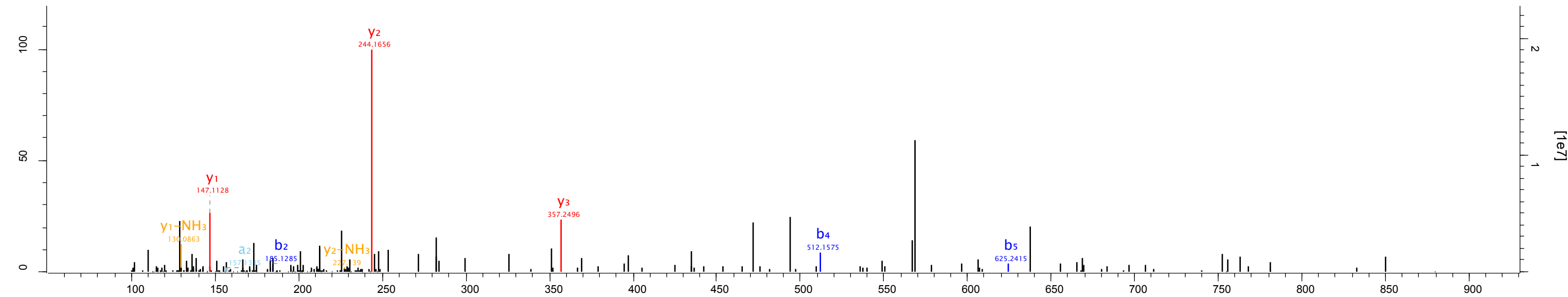
Raw file

20171215_MaS_33SR_LMH_proteome_01

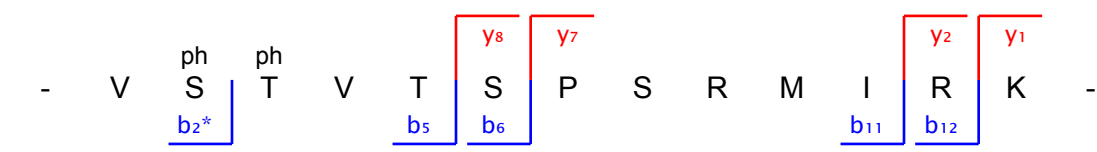
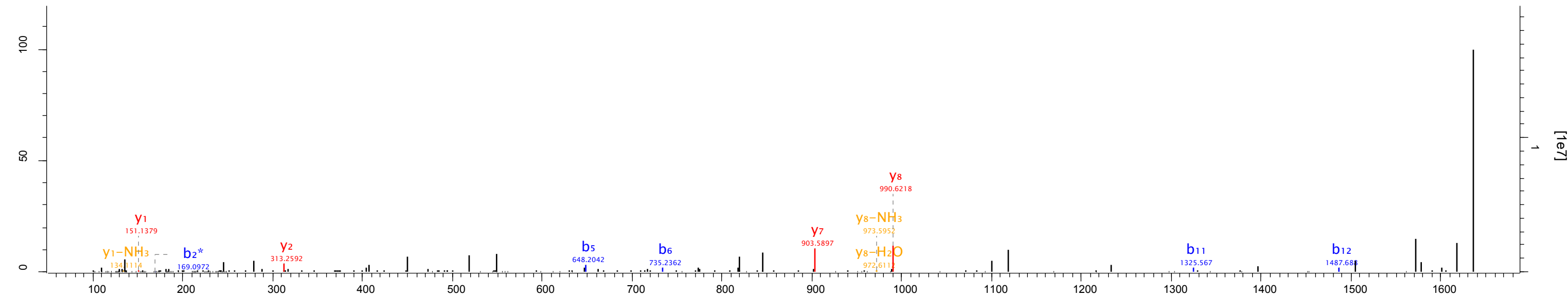
Scan	Method	Score	m/z	Gene names
62491	FTMS; HCD	48.47	893.47	FAM81B



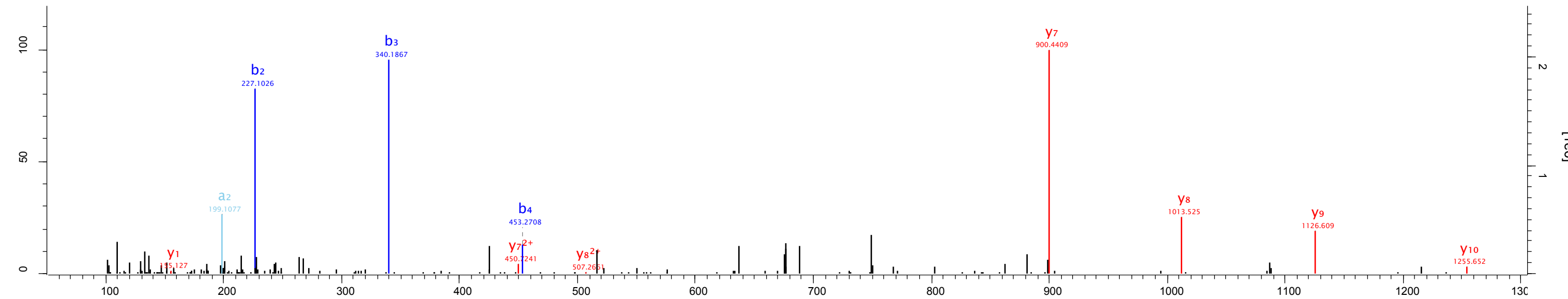
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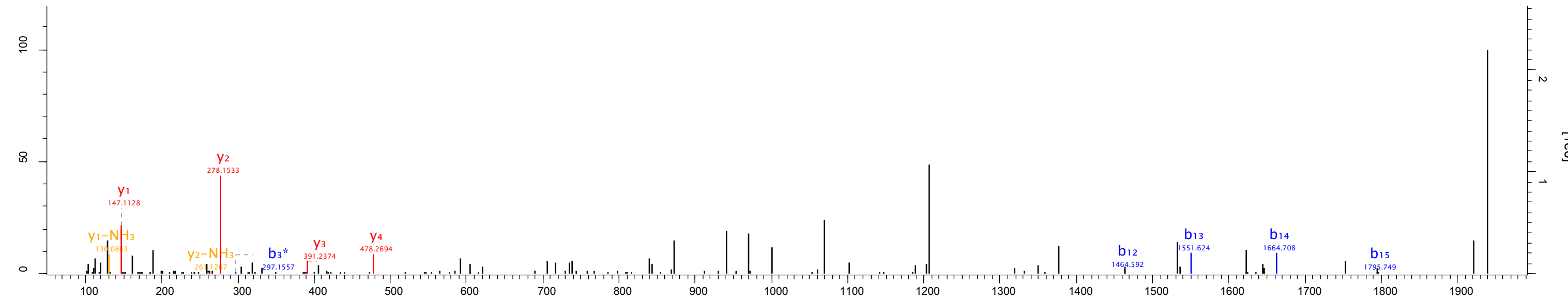
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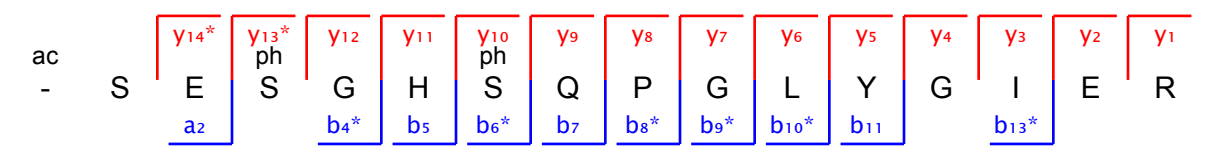
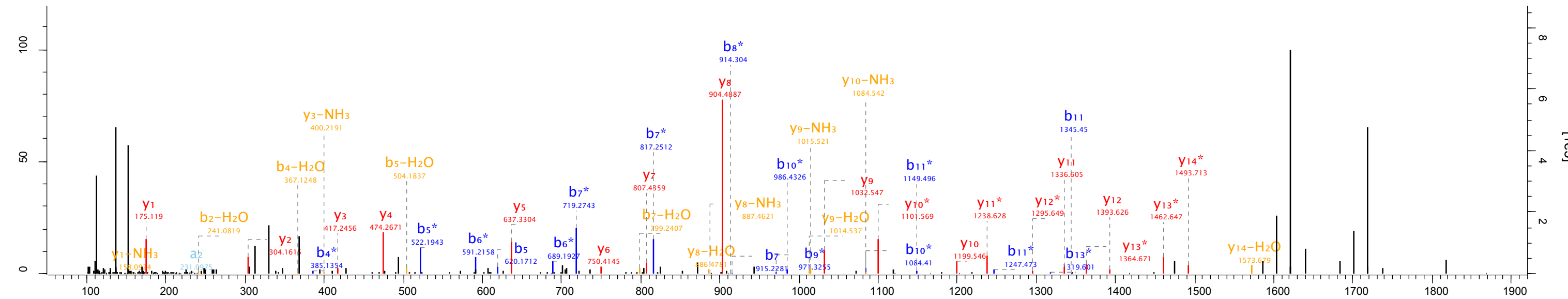
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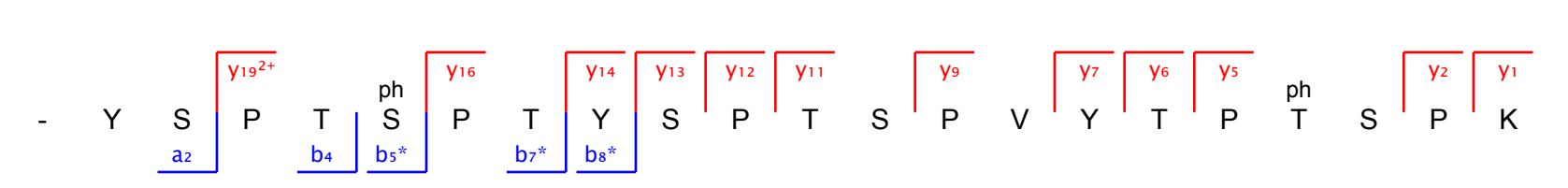
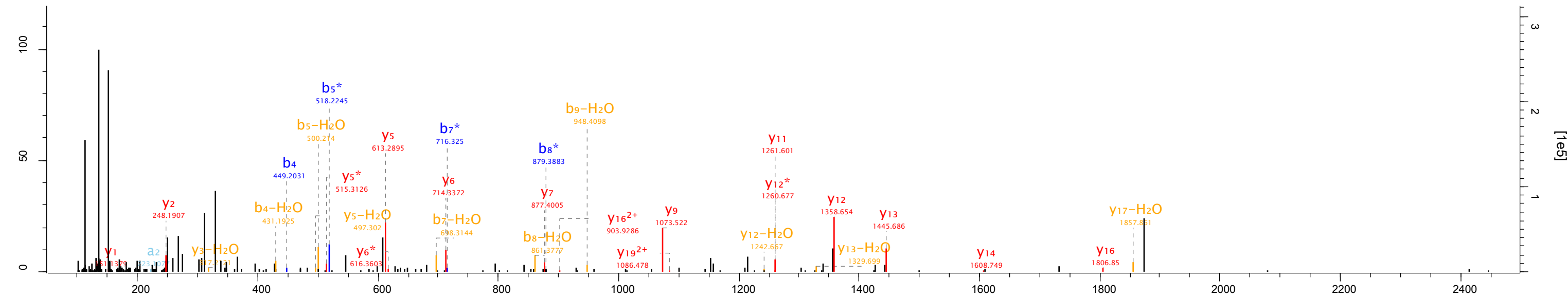
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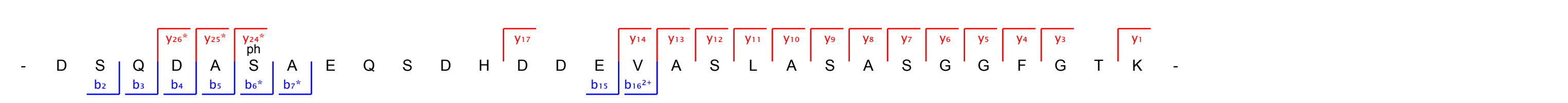
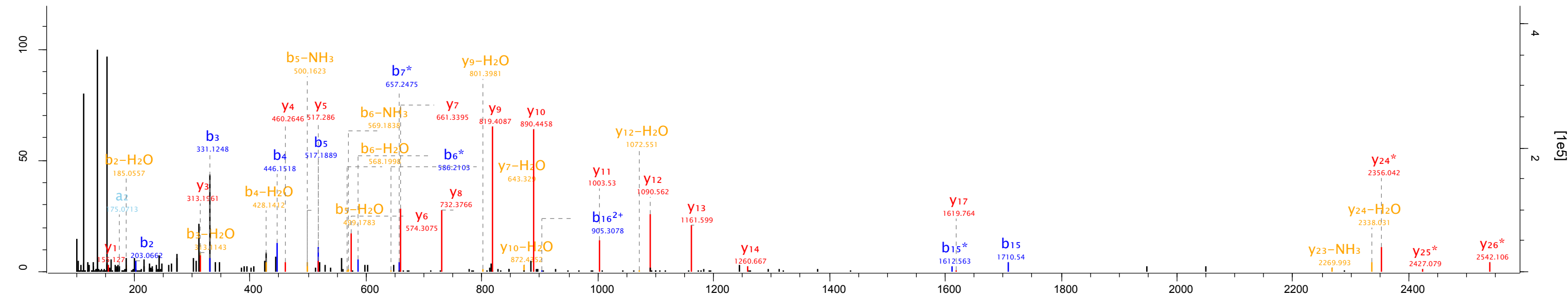
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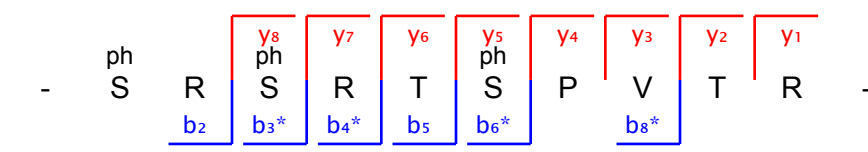
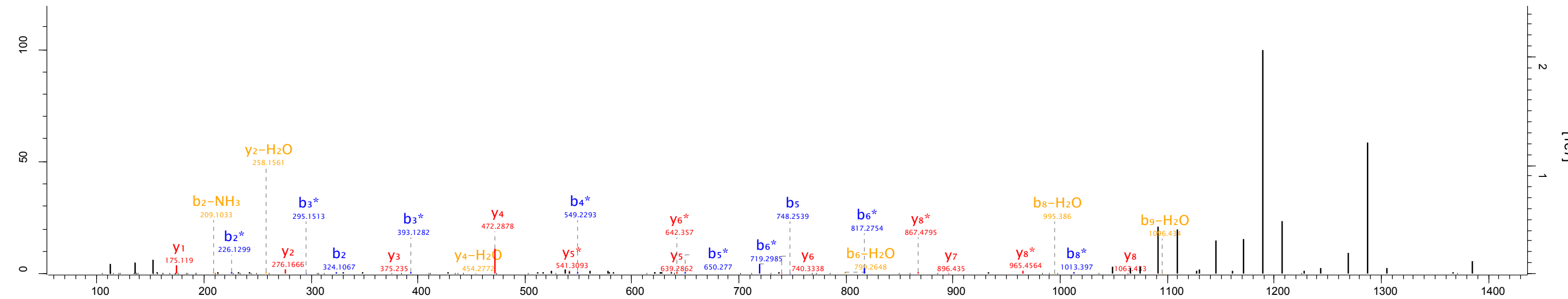
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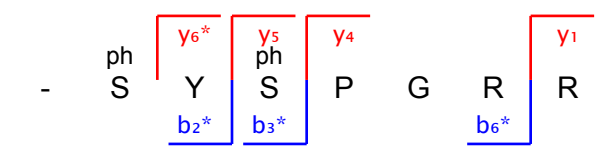
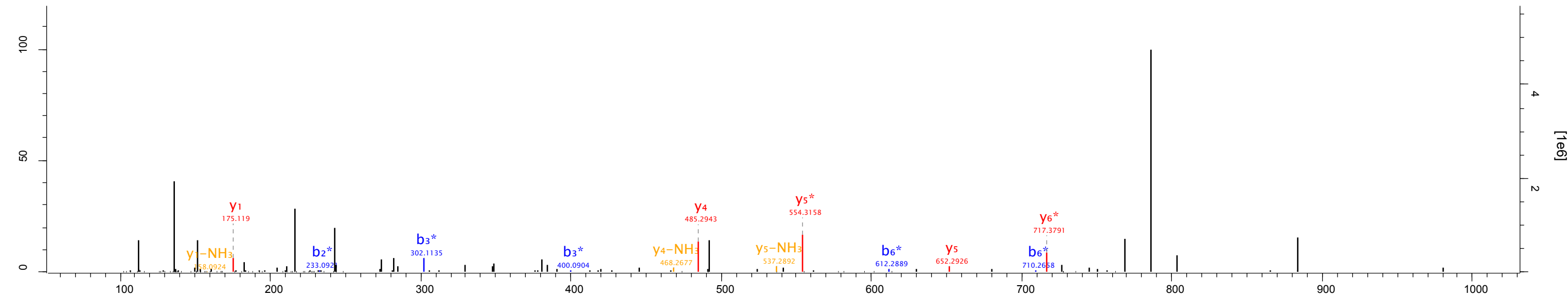
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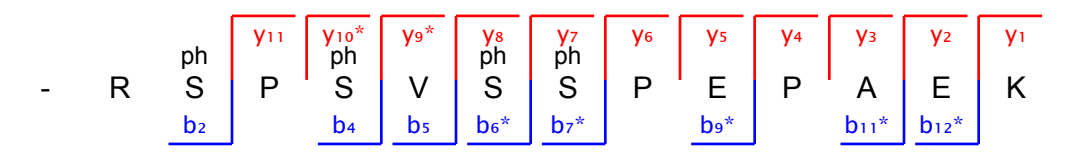
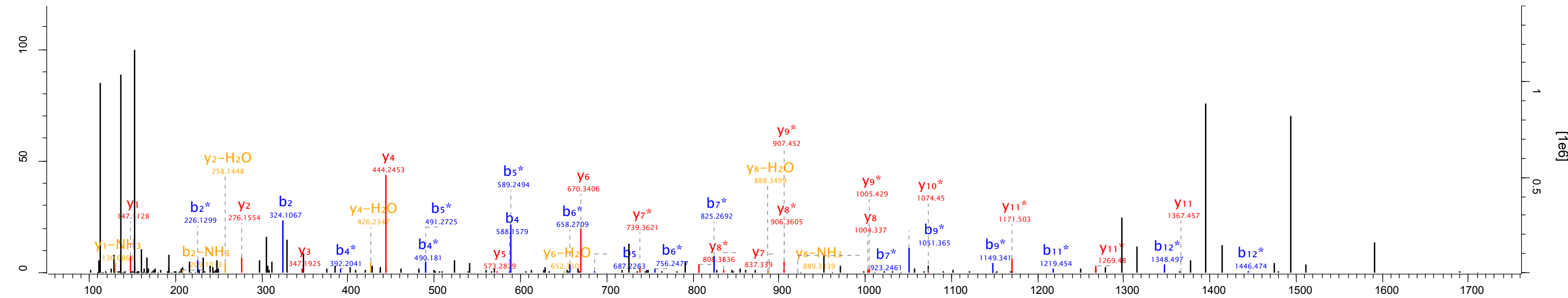
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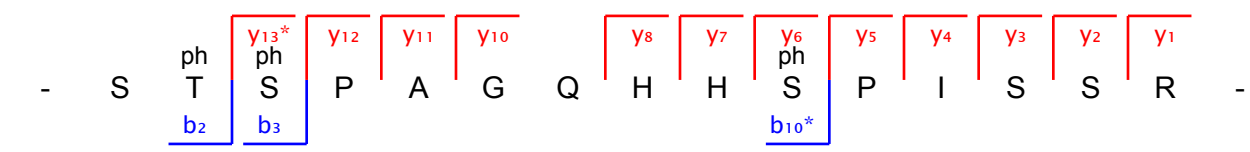
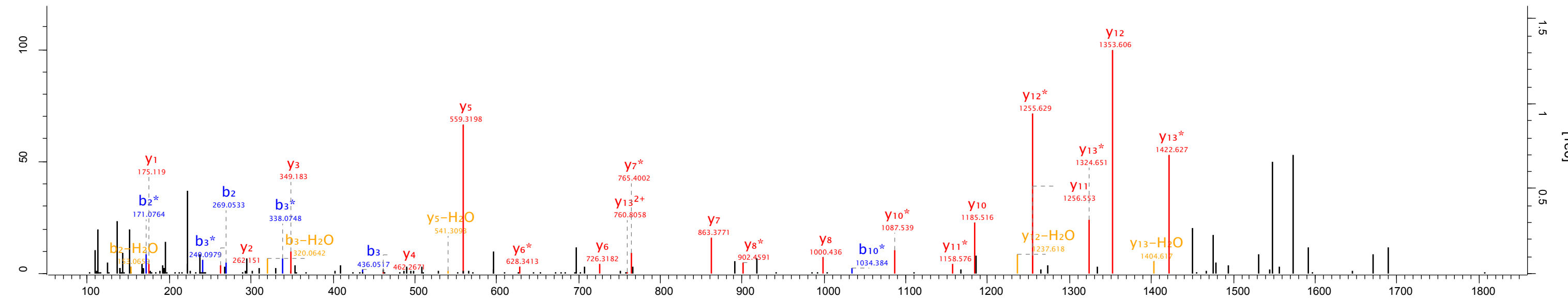
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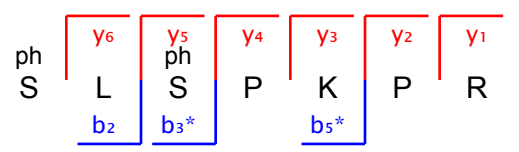
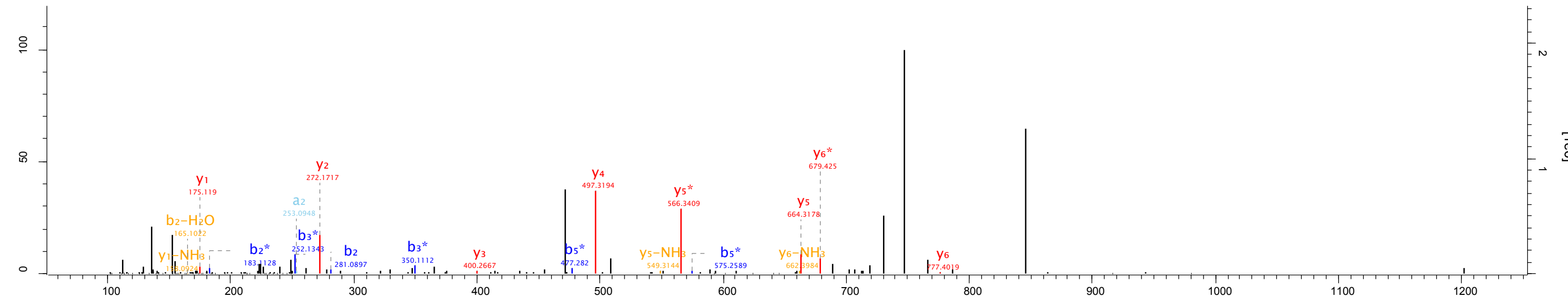
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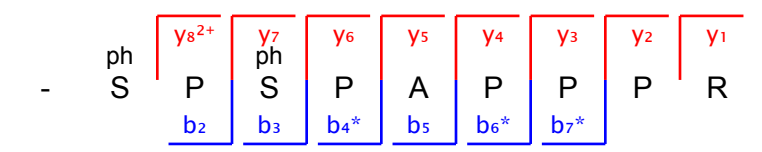
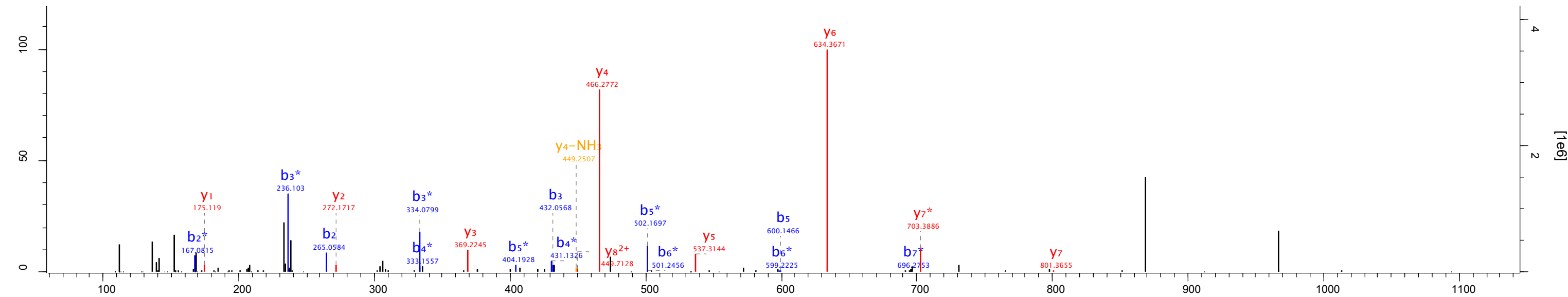
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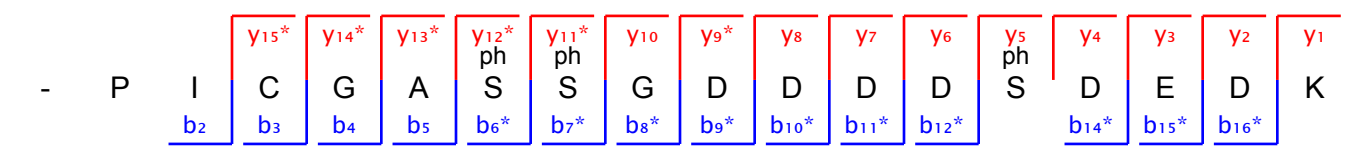
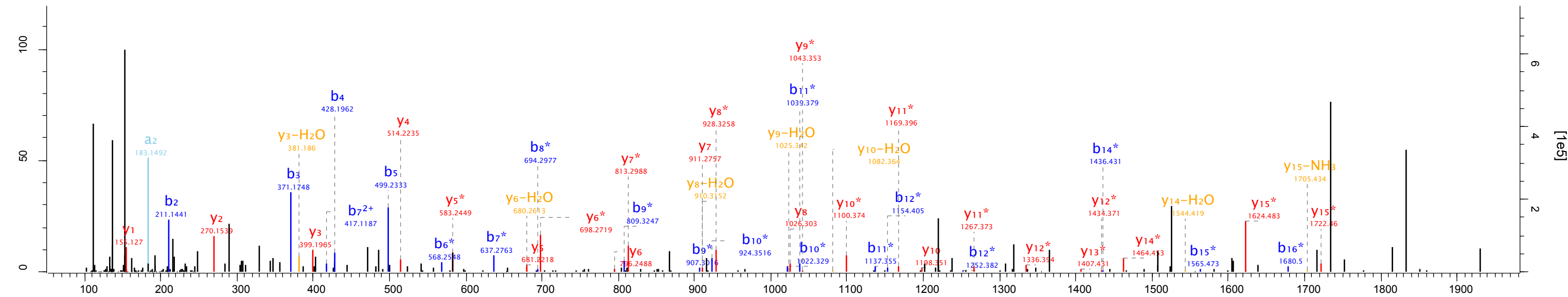
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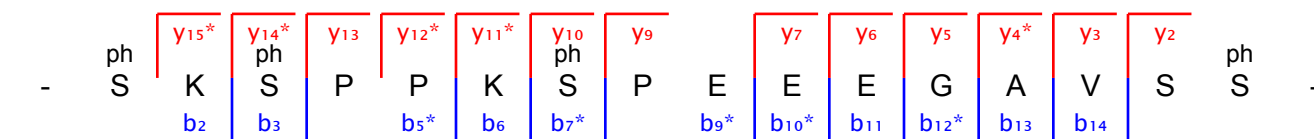
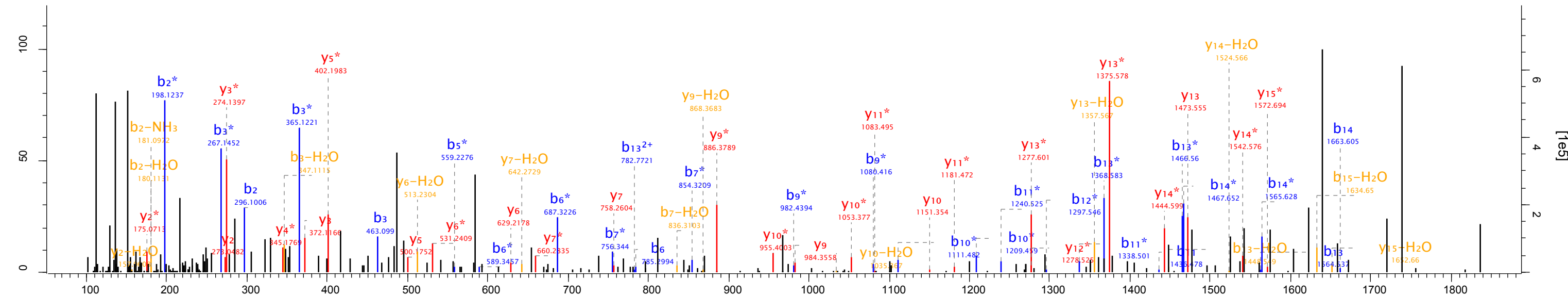


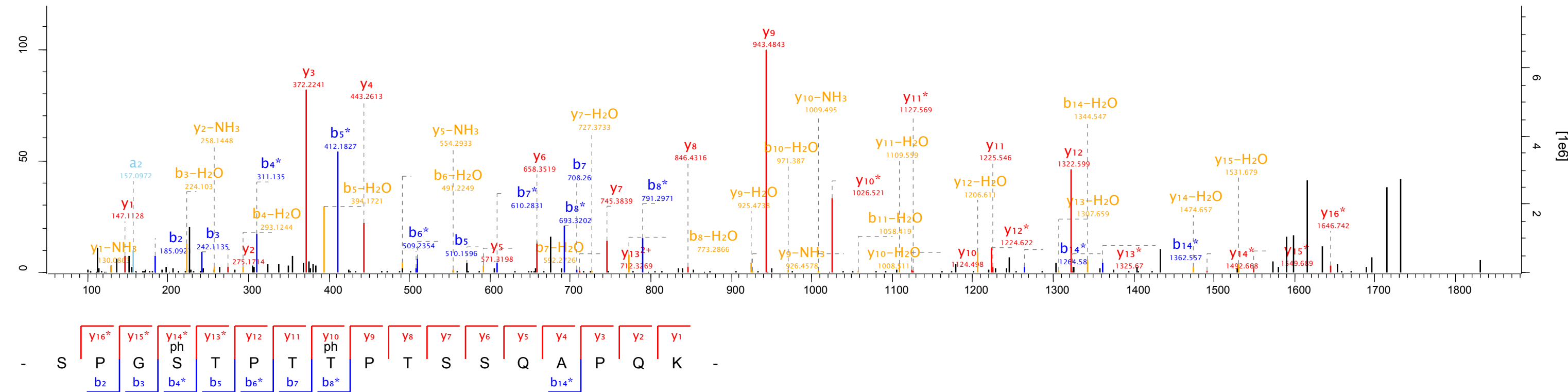
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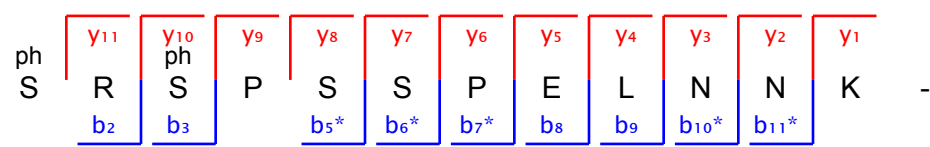
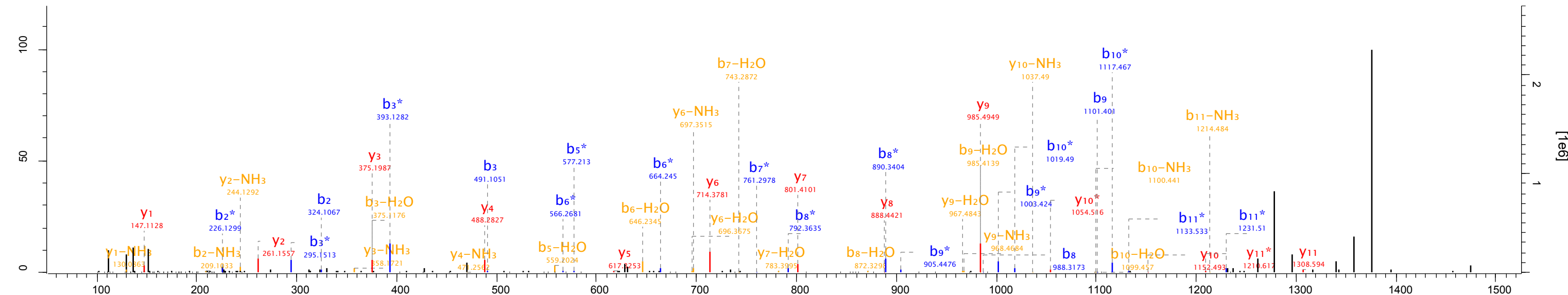
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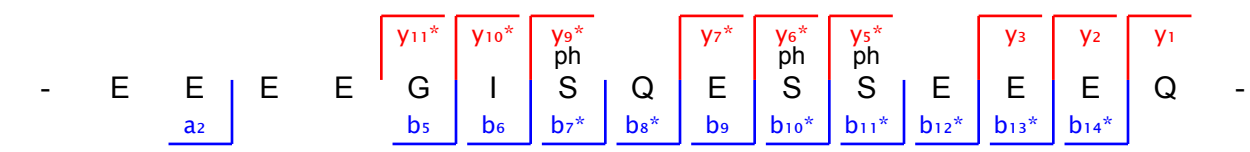
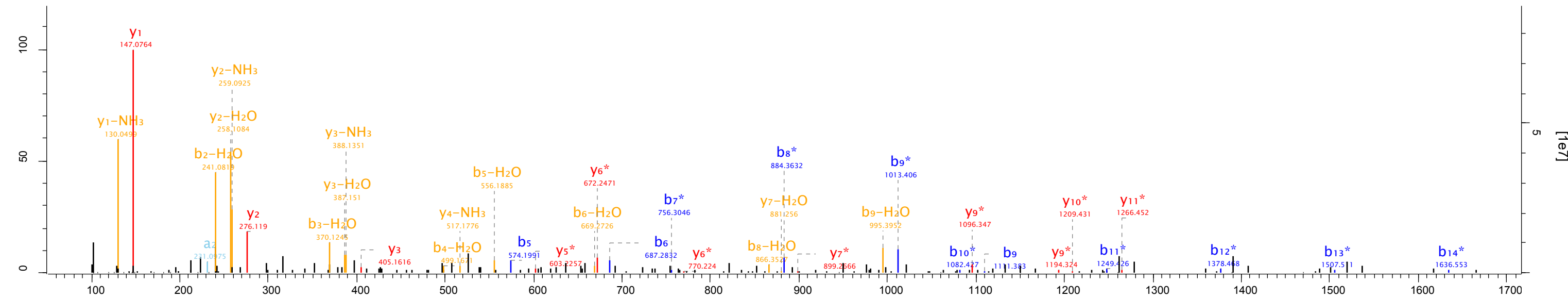




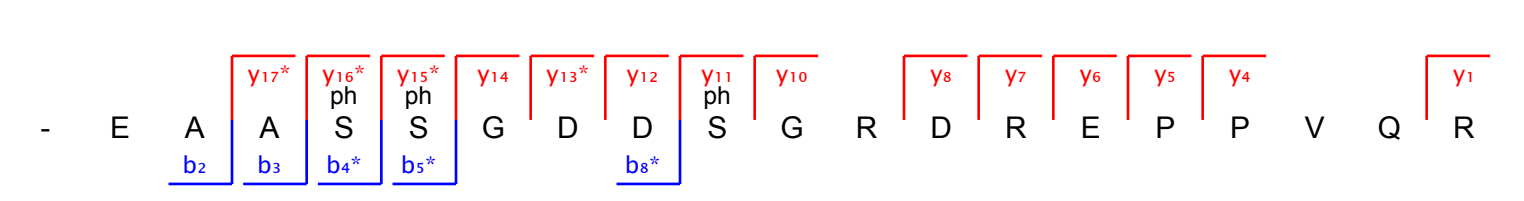
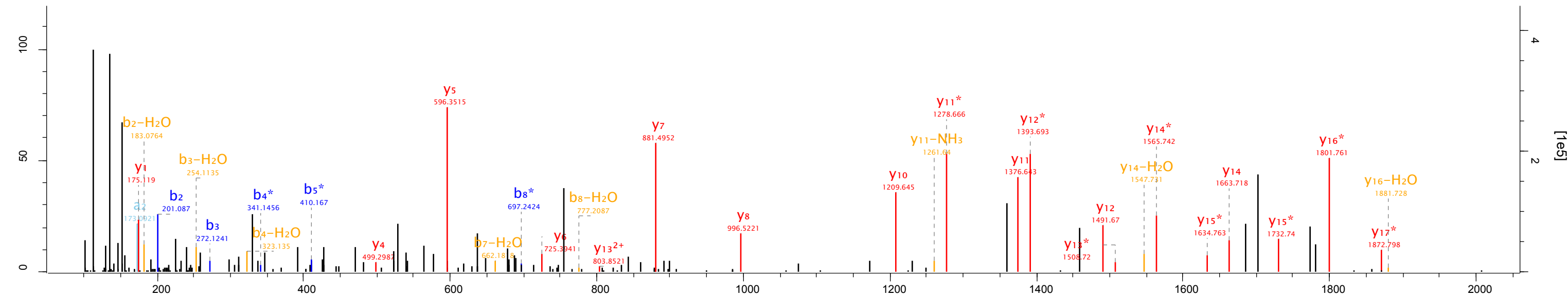
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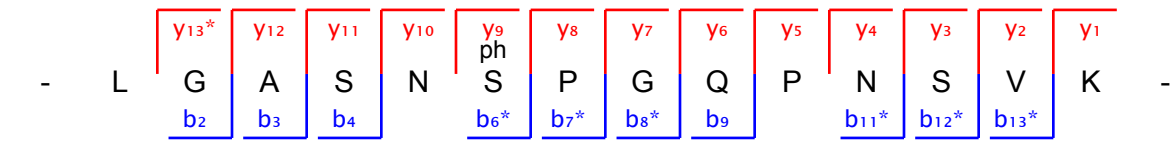
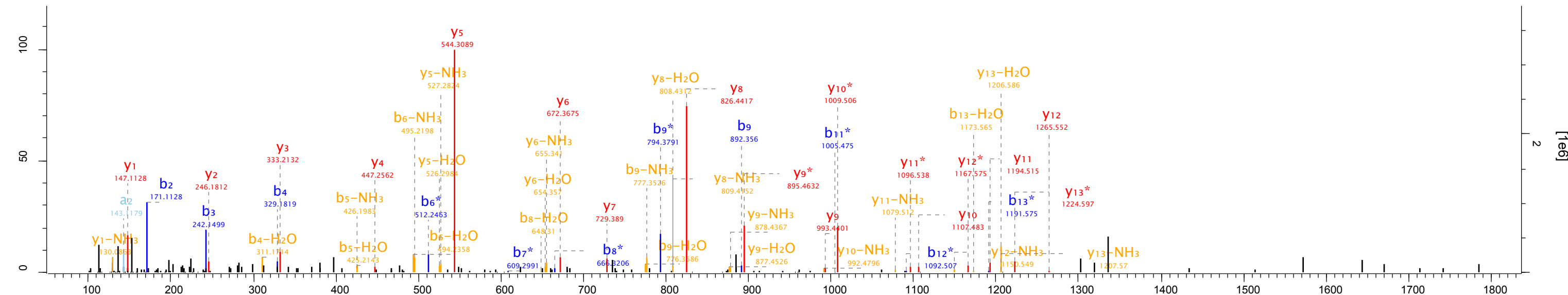
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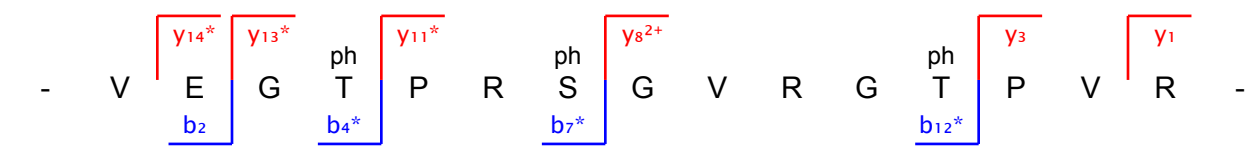
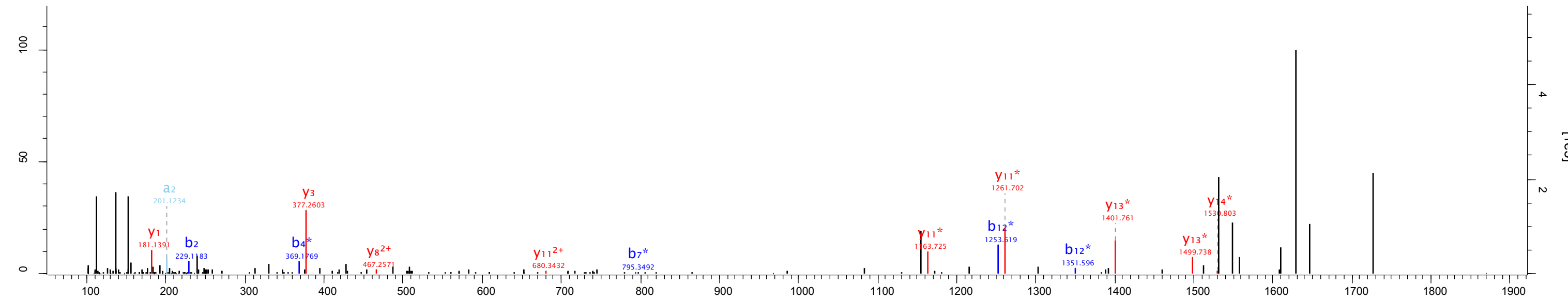
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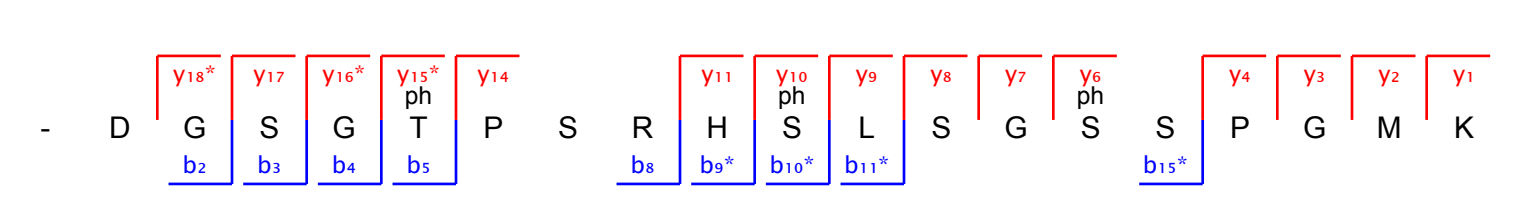
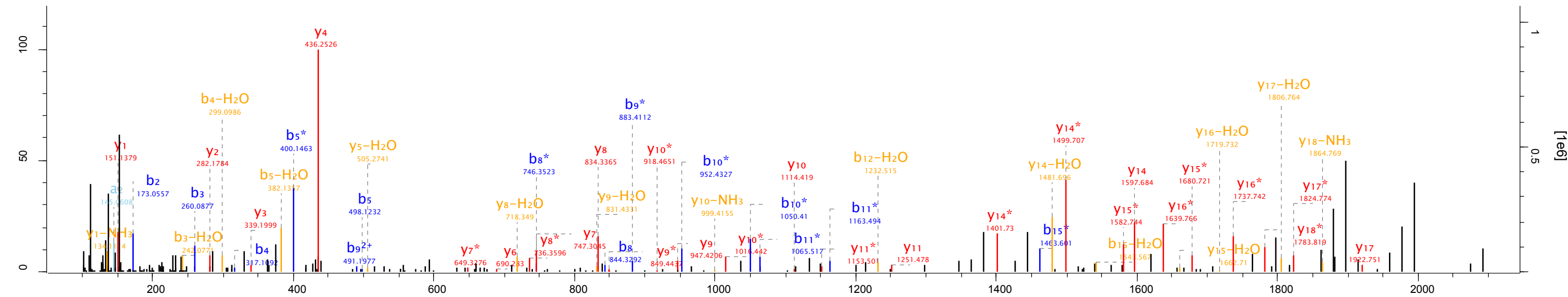
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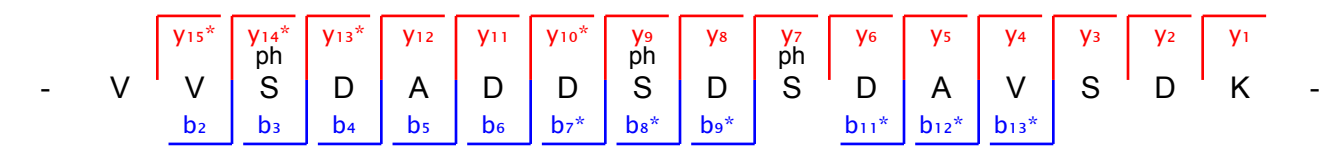
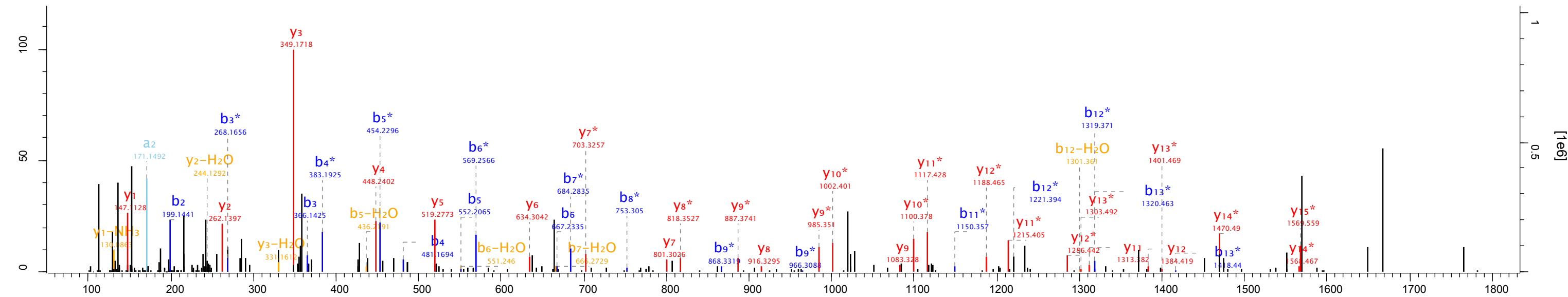
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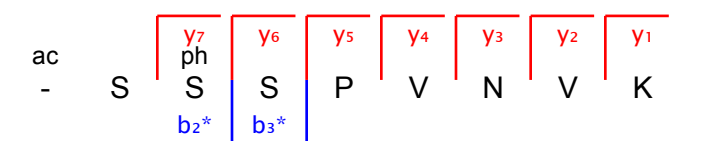
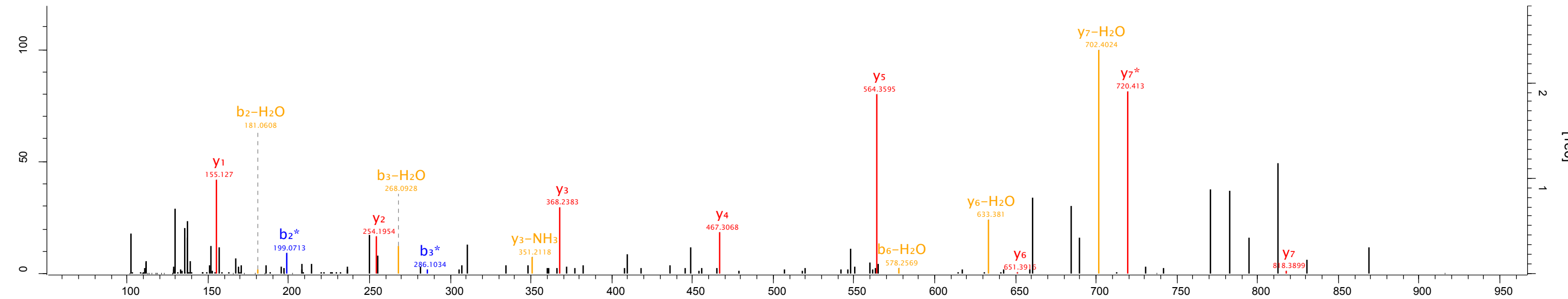
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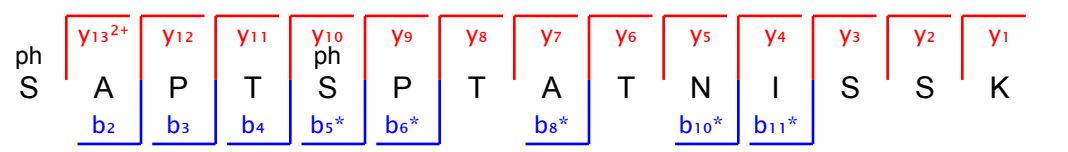
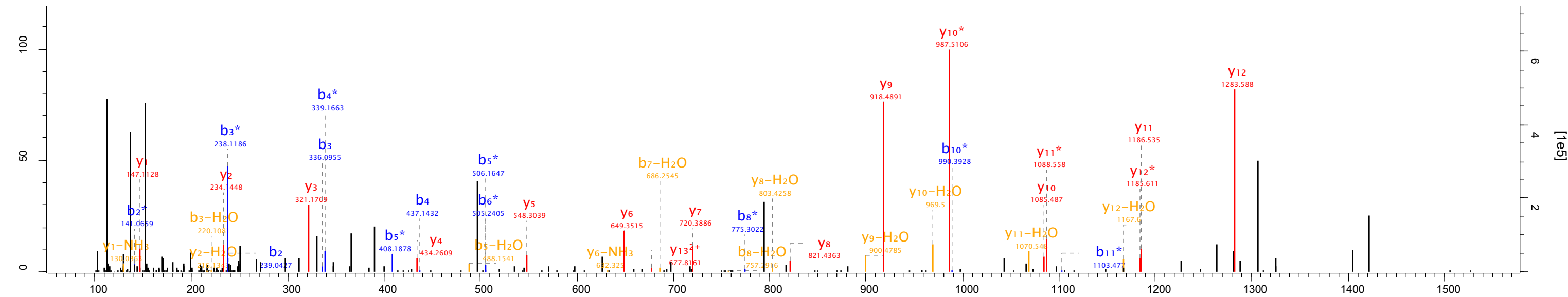
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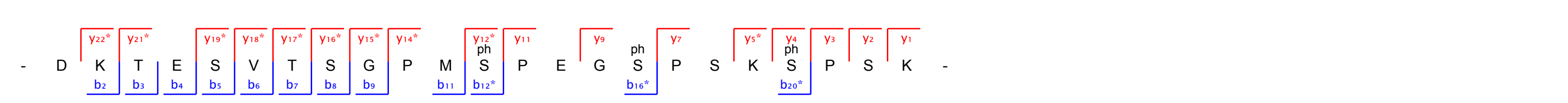
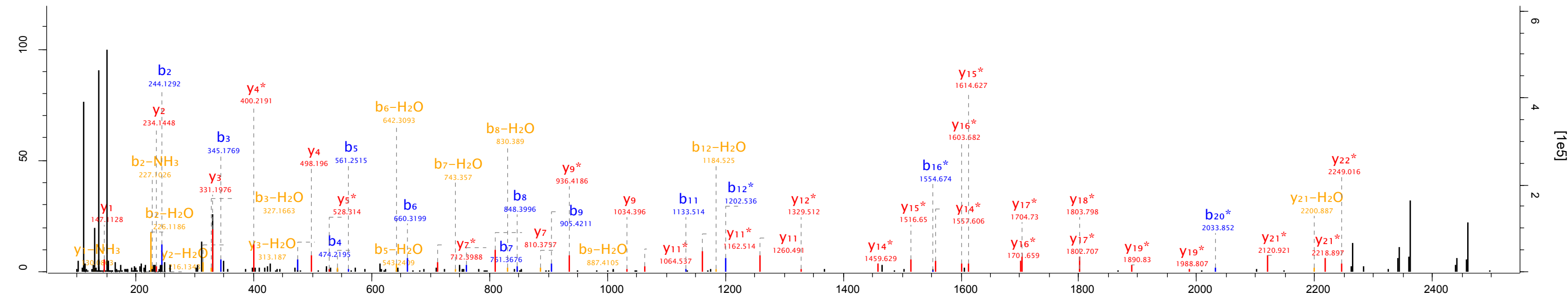
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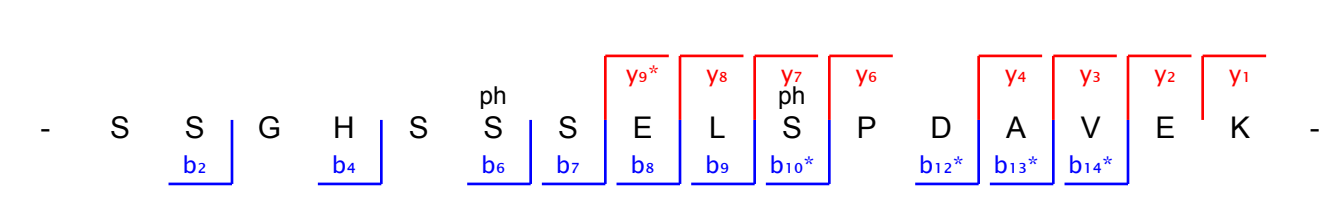
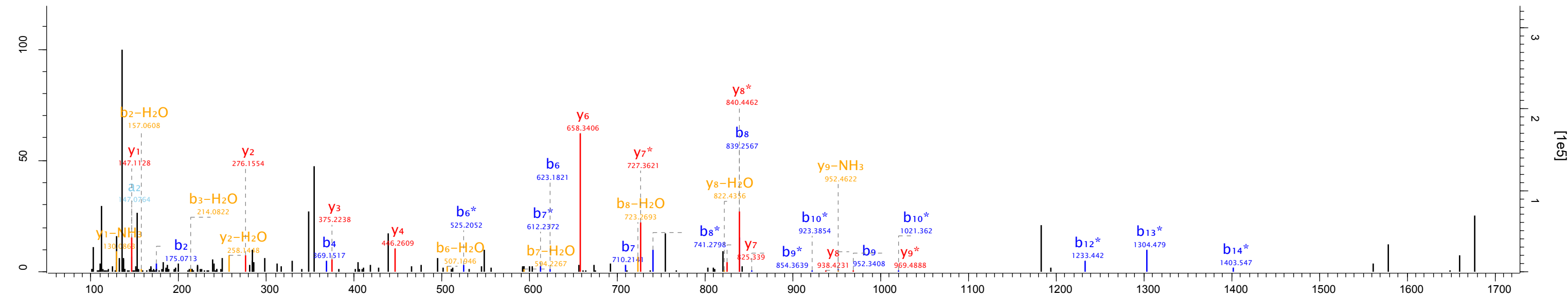
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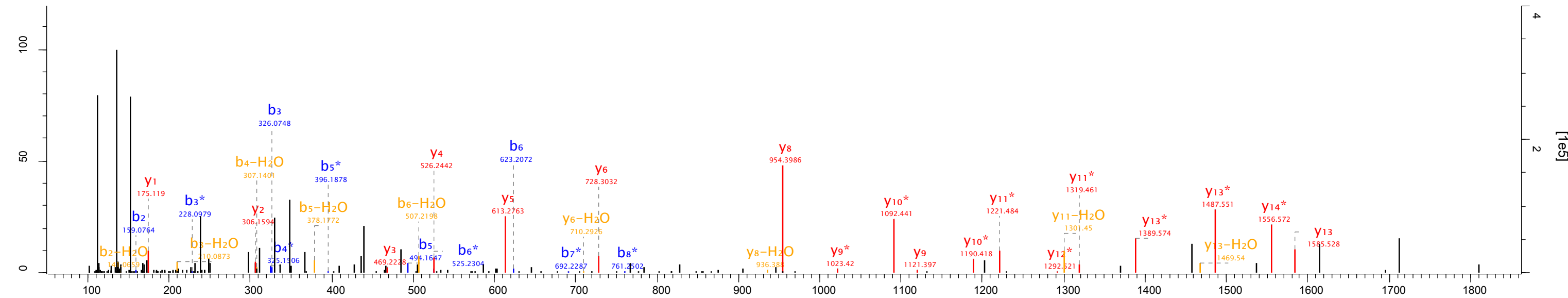
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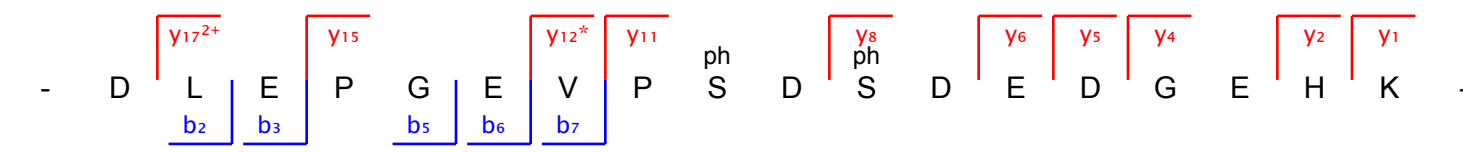
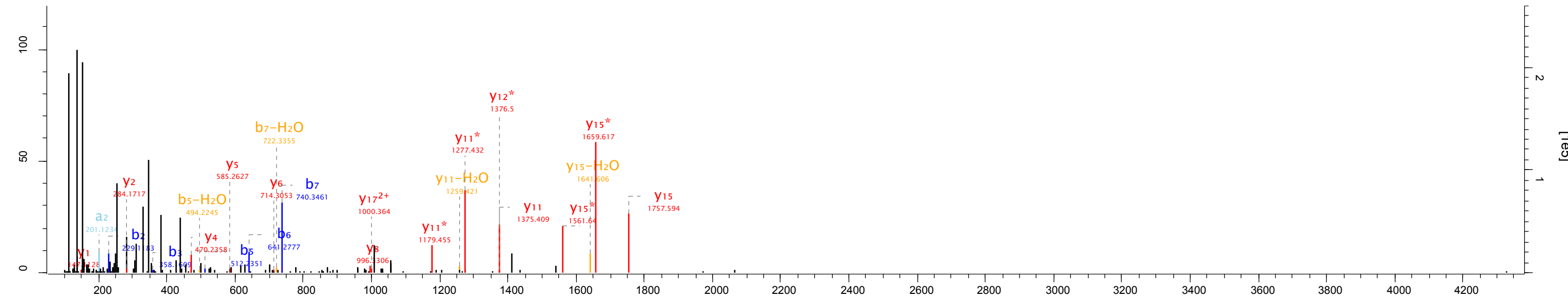
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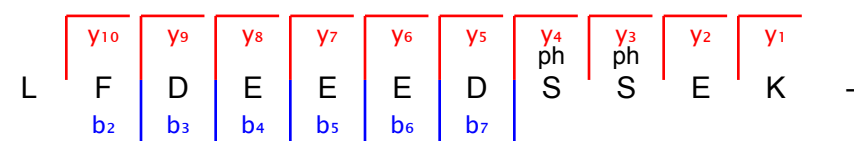
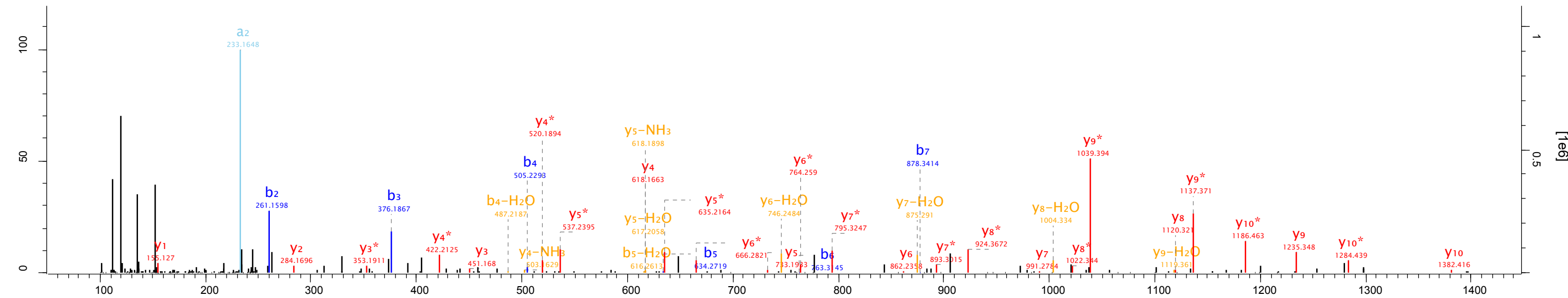
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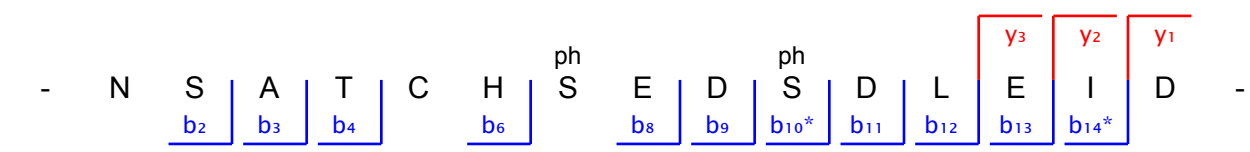
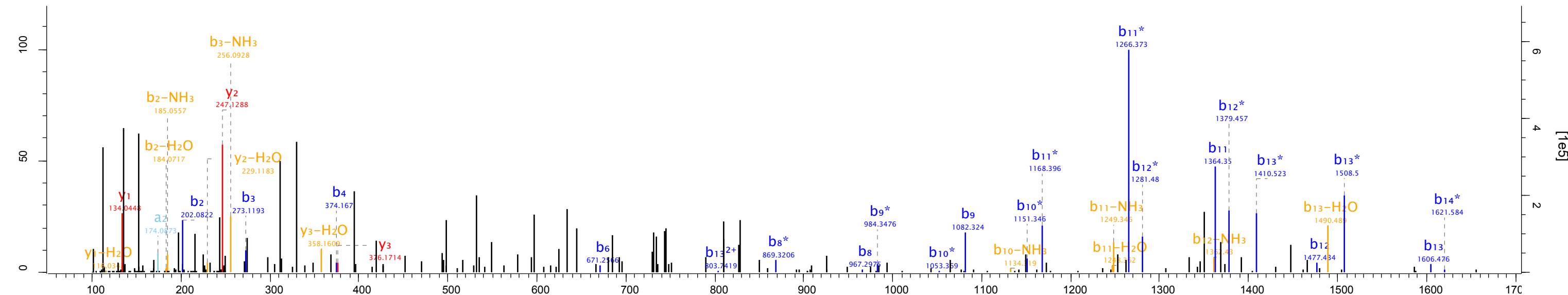
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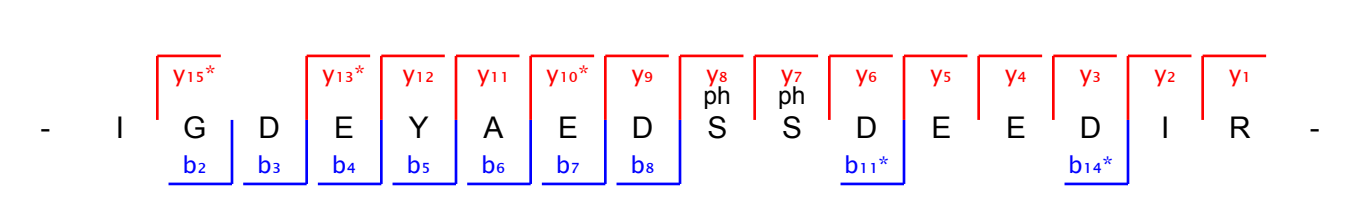
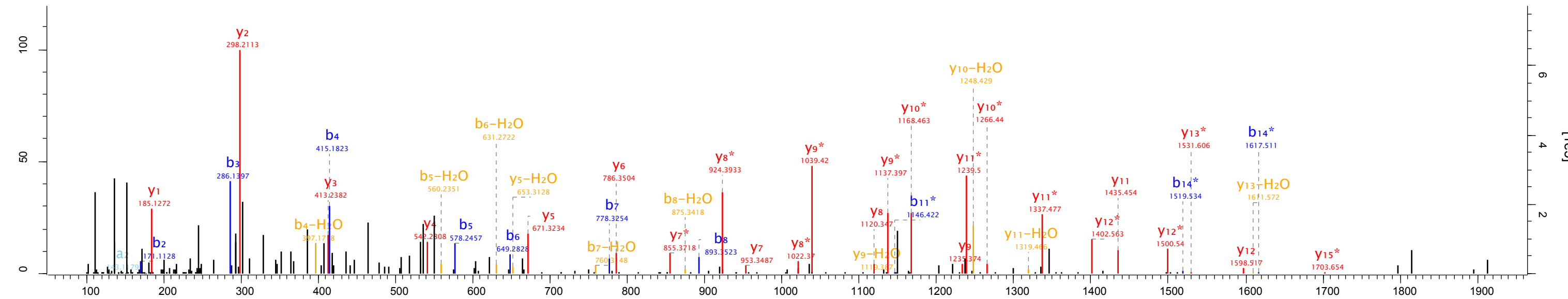
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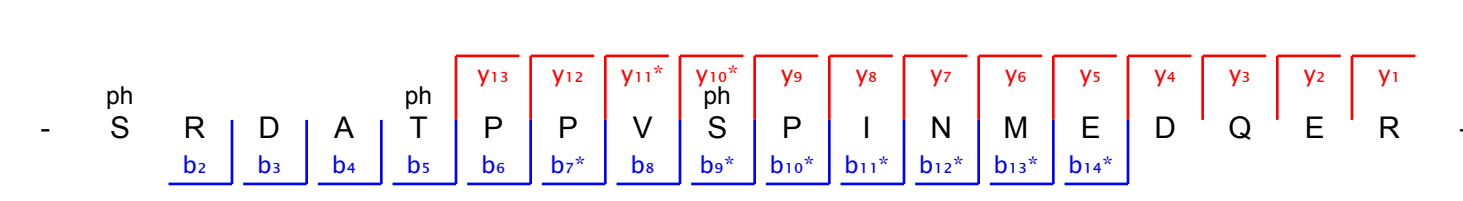
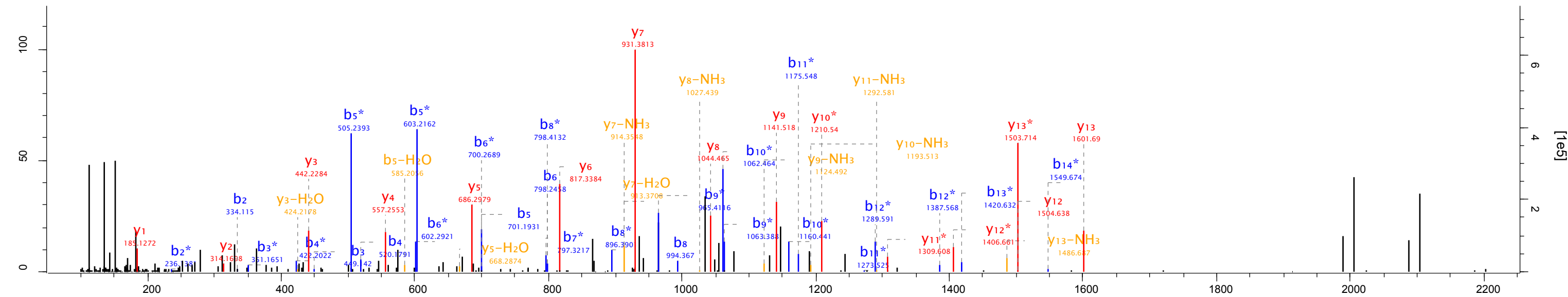
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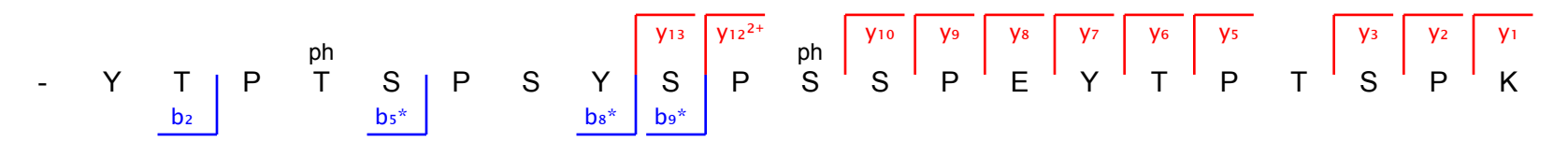
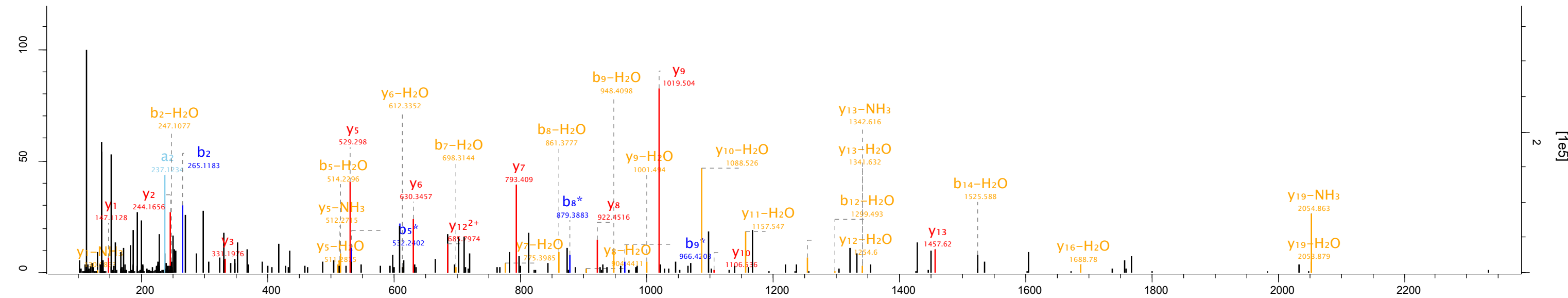
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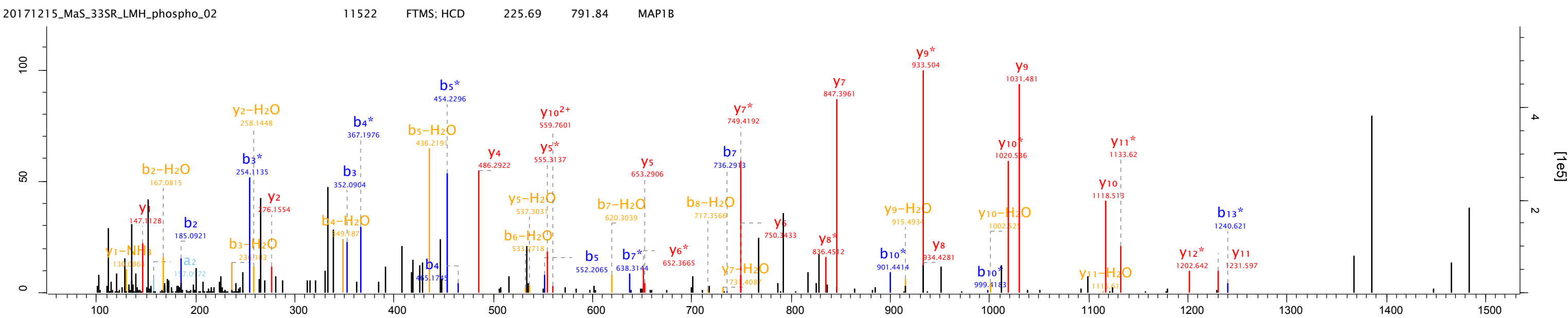
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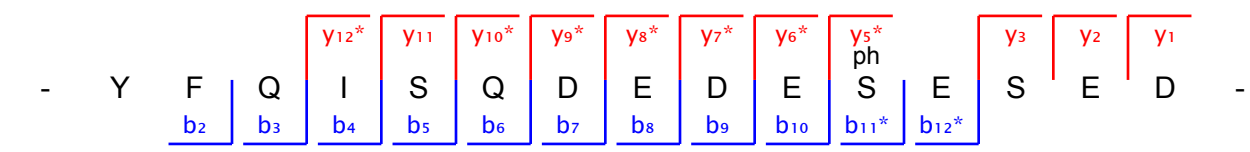
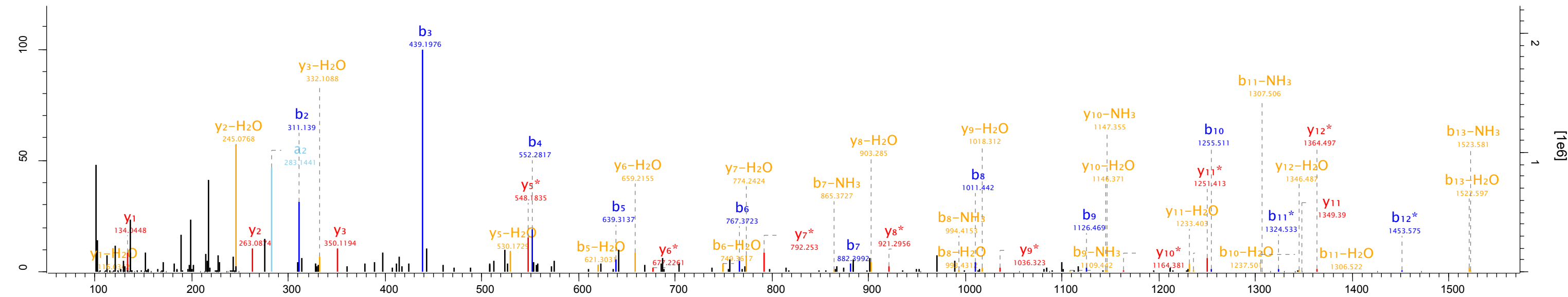
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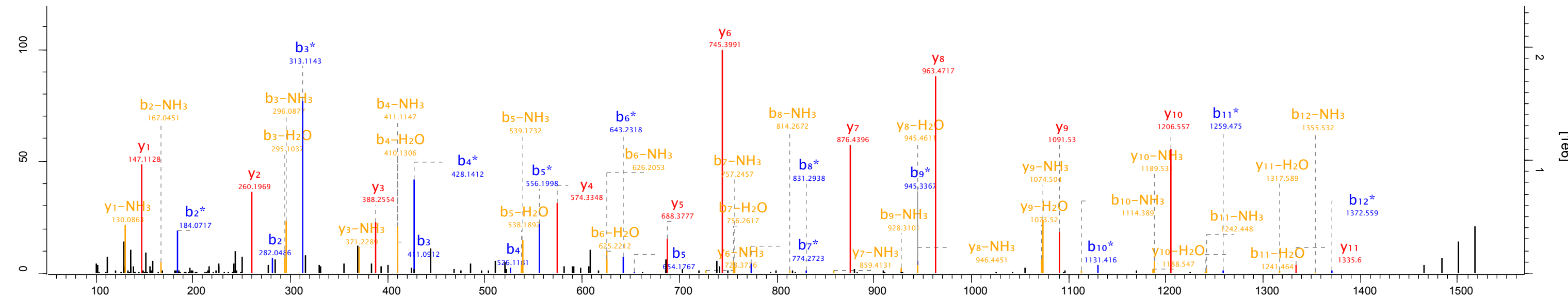
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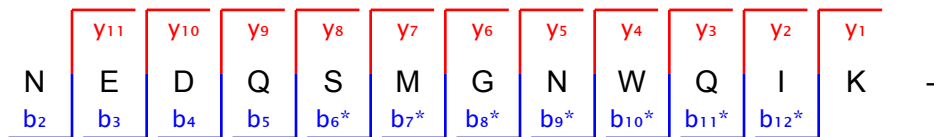
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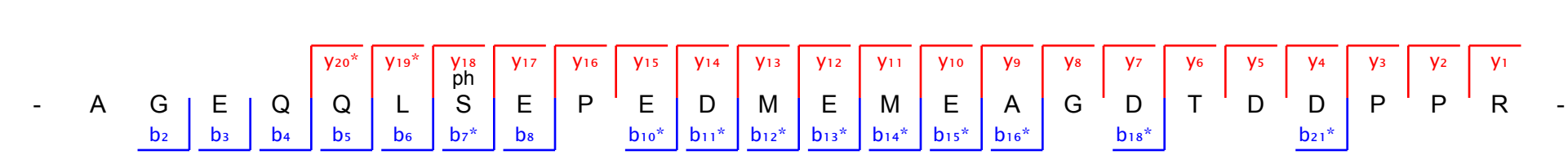
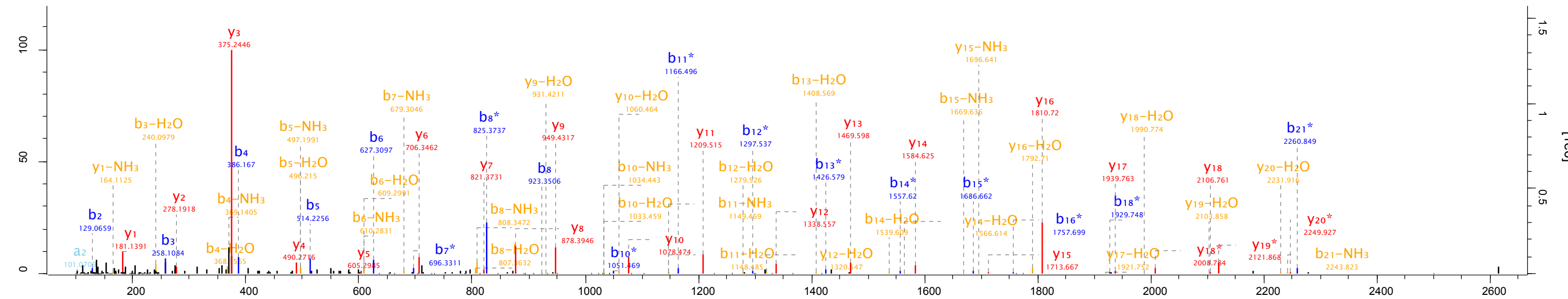
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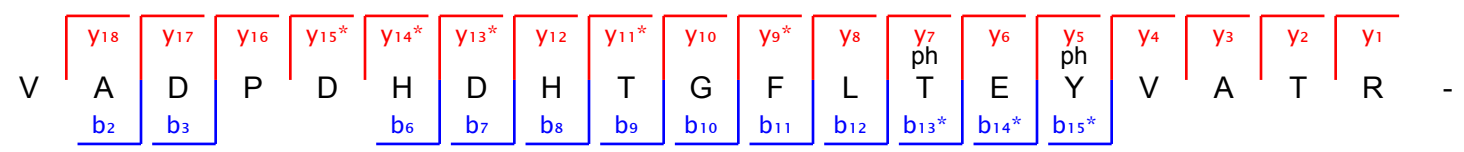
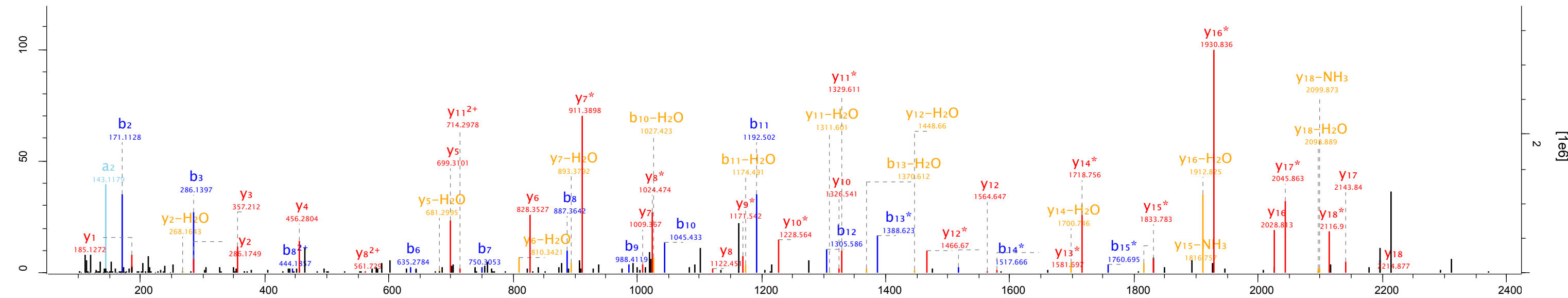
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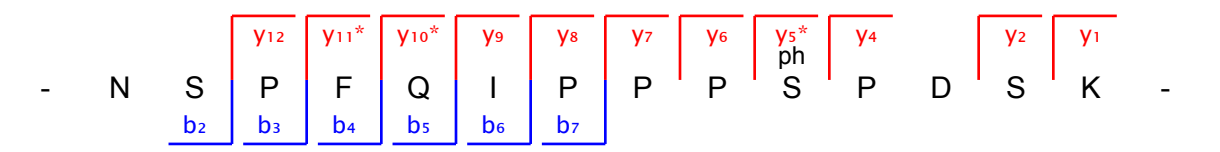
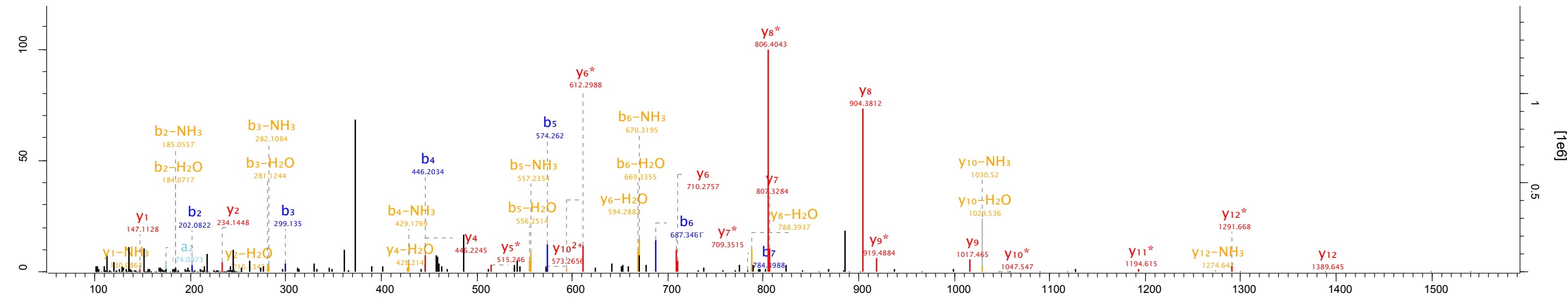
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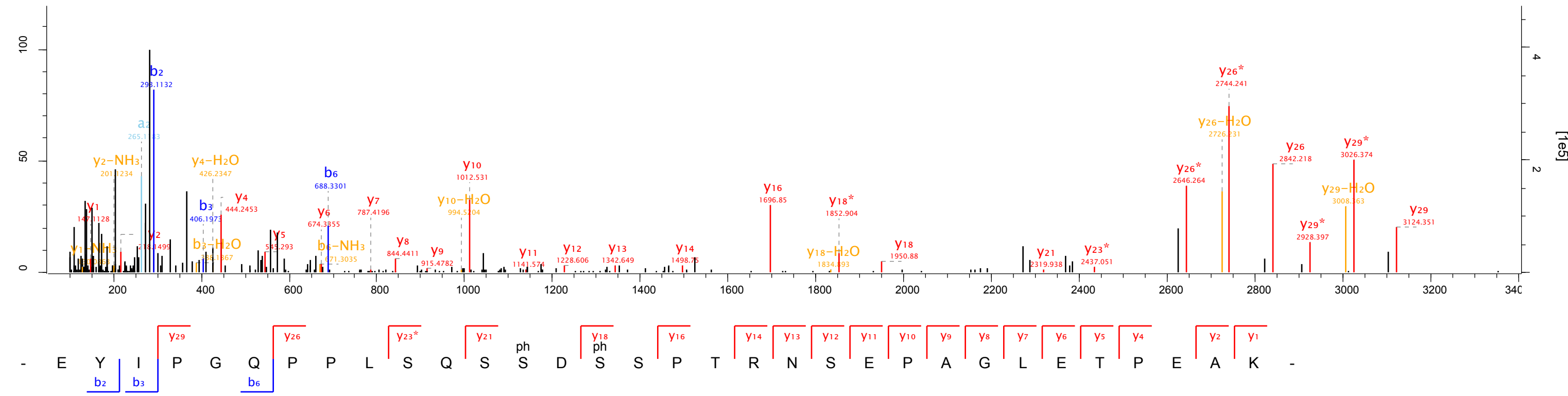
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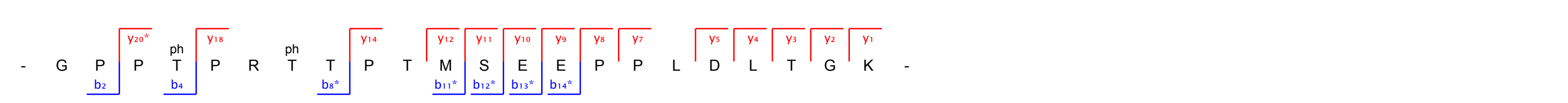
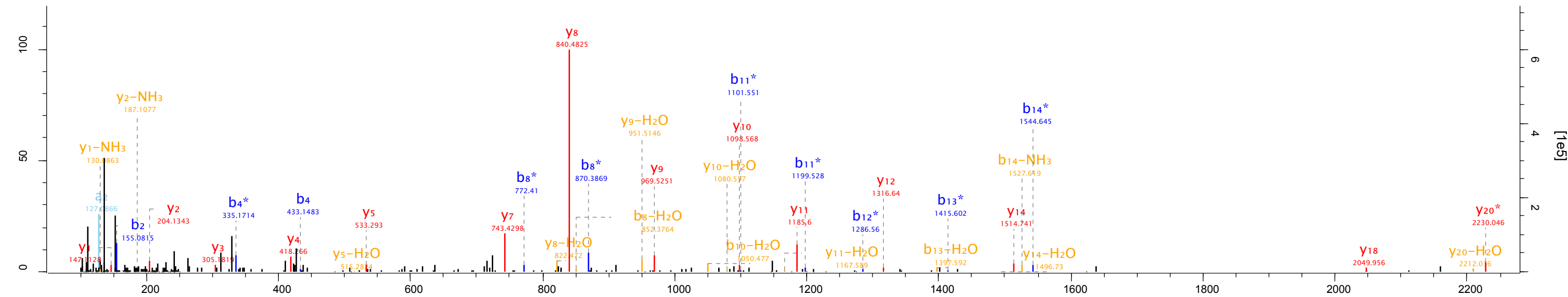
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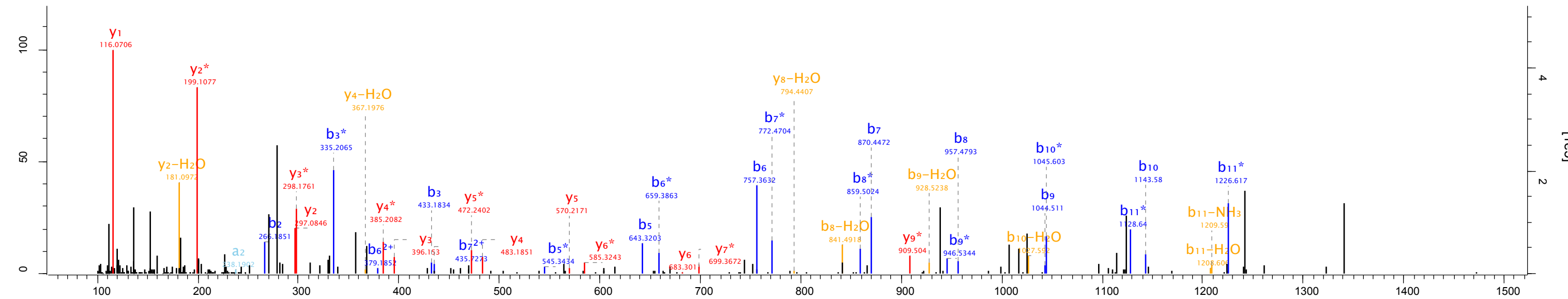


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 Scan: 14372 Method: FTMS; HCD Score: 82.6 m/z: 828.7 Gene names: SIPA1L3

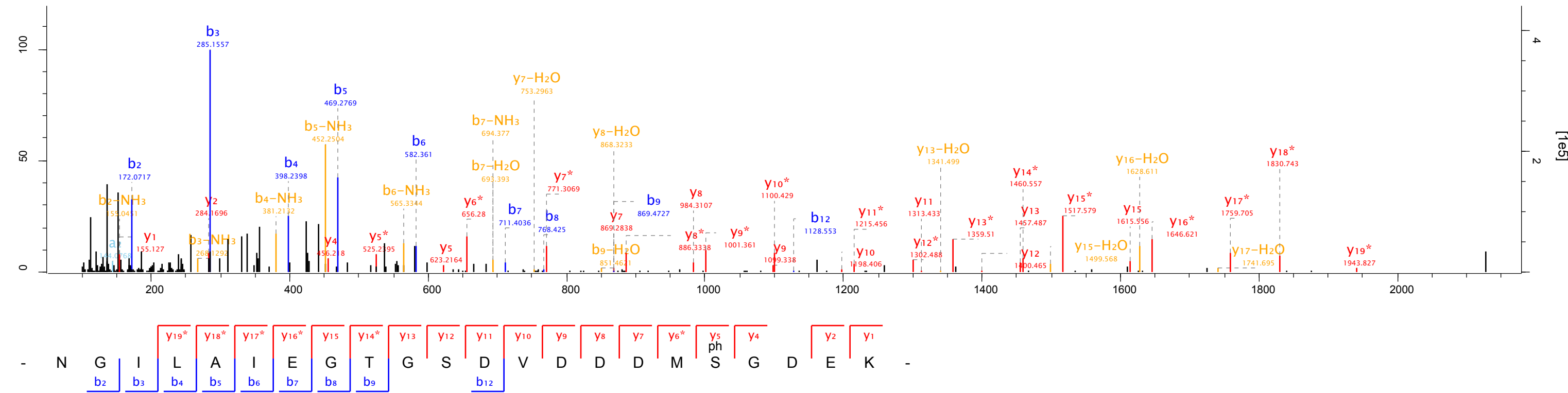


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 14552 Method FTMS; HCD Score 197.38 m/z 720.33 Gene names CDC23

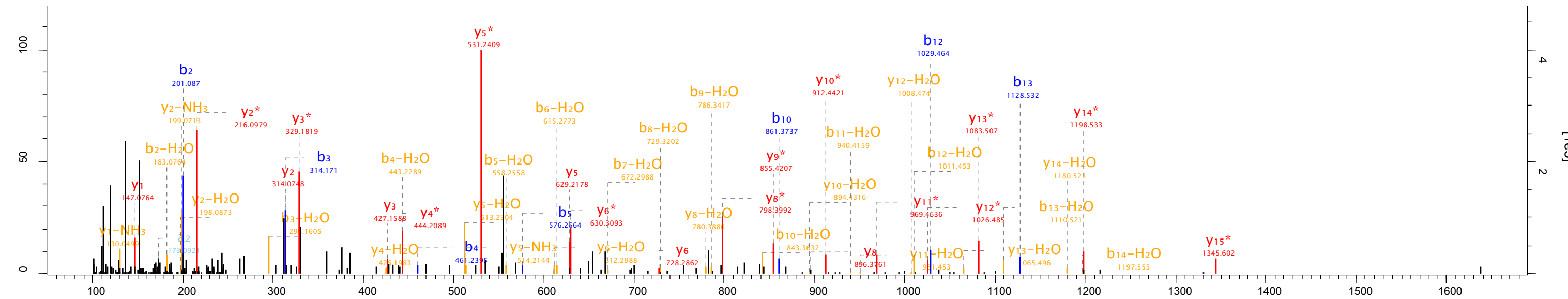
20171215_MaS_33SR_LMH_phospho_02



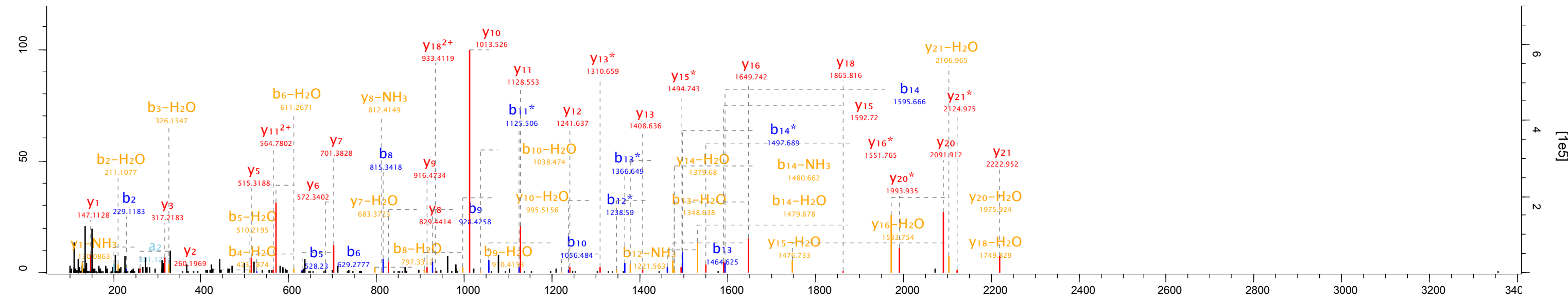
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 14562 Method FTMS; HCD Score 156.03 m/z 1163.48 Gene names USP9X



Raw file: 20171215_MaS_33SR_LMH_phospho_02
 Scan: 15172 Method: FTMS; HCD Score: 123.55 m/z: 879.37 Gene names: CRAMP1L



Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 16702 Method FTMS; HCD Score 126.74 m/z 1229.86 Gene names SQSTM1

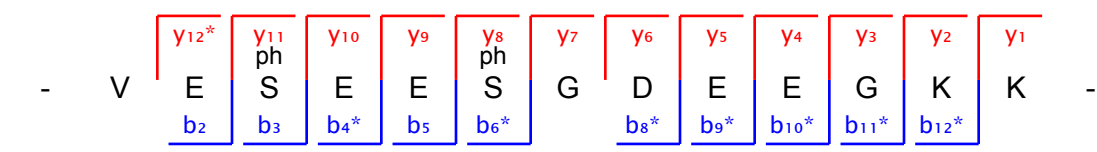
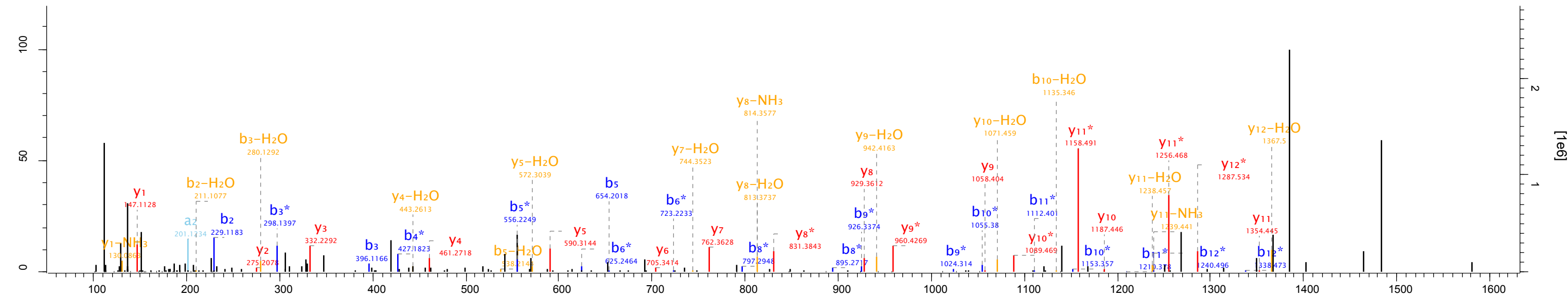


- E V D P S T G E L Q S L Q M P E S E G P S S L D P S Q E G P T G L K -

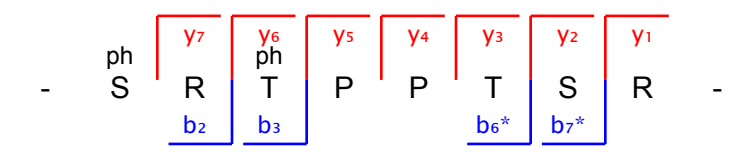
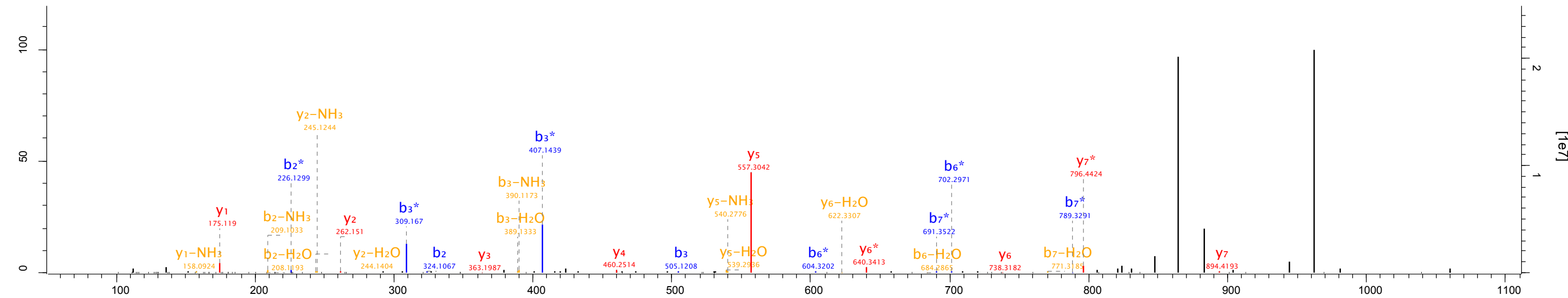
Annotations below the sequence indicate the fragmentation sites for b and y ions:

- Blue boxes under V, S, T, E, L, Q, S, L, Q, M, P indicate b-ion cleavage sites (b₂ to b₁₄).
- Red boxes above S, L, D, P, S, Q, E, G, P, T, G, L, K indicate y-ion cleavage sites (y₁ to y₂₁).
- A red box above S indicates a phospho site (ph).

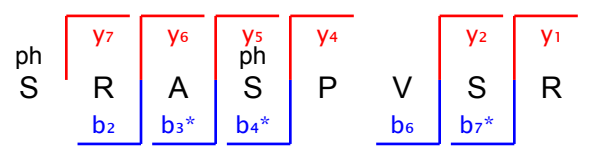
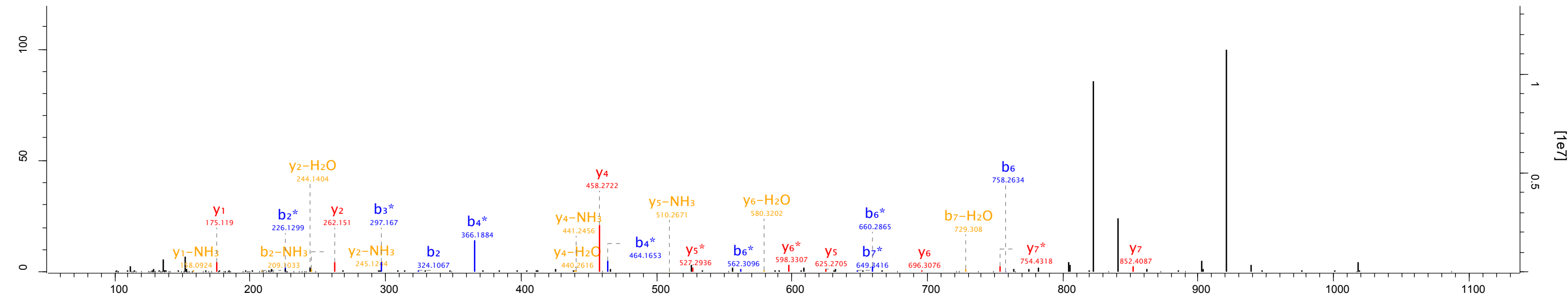
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 1952 Method FTMS; HCD Score 227.34 m/z 791.78 Gene names PPP1R7



Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 2082 Method FTMS; HCD Score 140.01 m/z 531.21 Gene names SRRM2

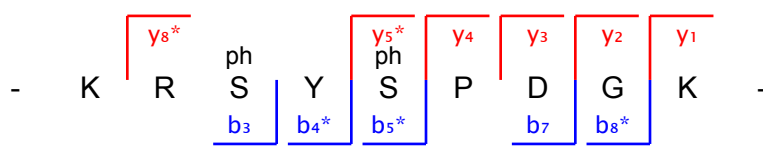
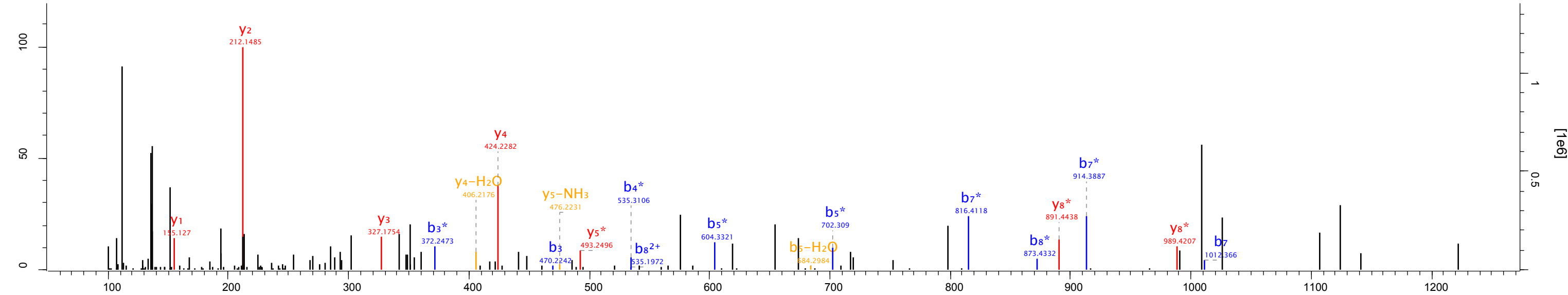


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 Scan: 2092 Method: FTMS; HCD Score: 87.62 m/z: 510.21 Gene names: SRRM2

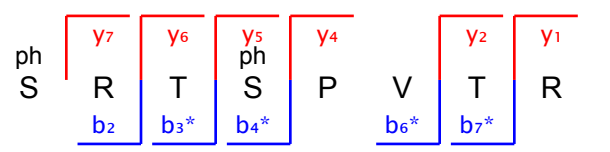
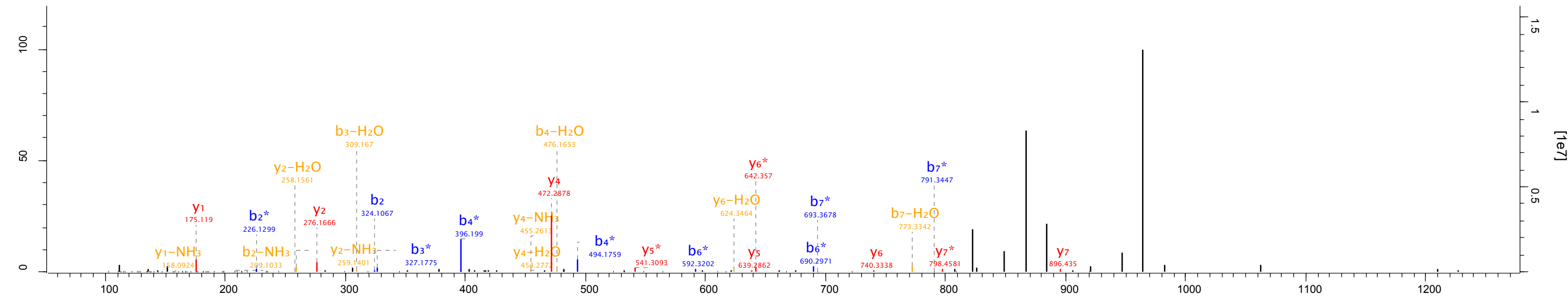


Raw file Scan Method Score m/z Gene names

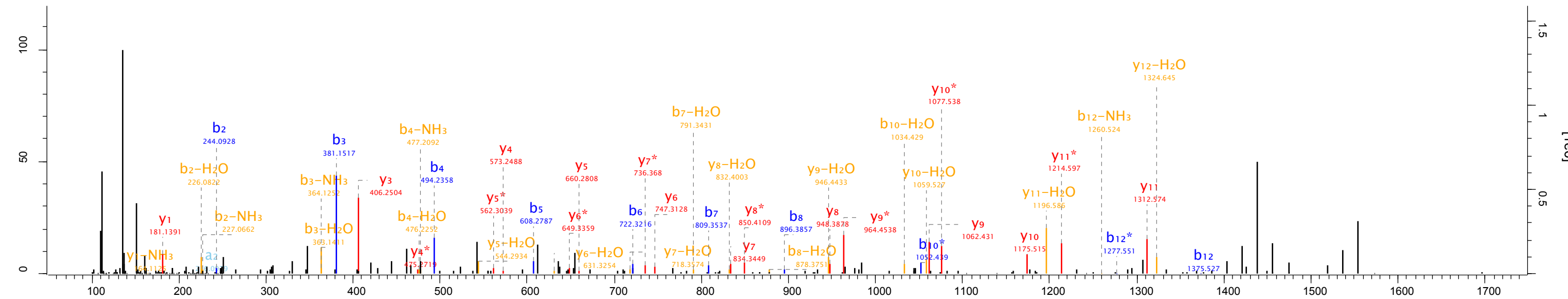
20171215_MaS_33SR_LMH_phospho_02 2142 FTMS; HCD 72.68 408.51 MATR3



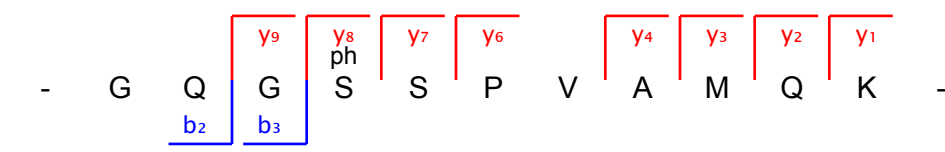
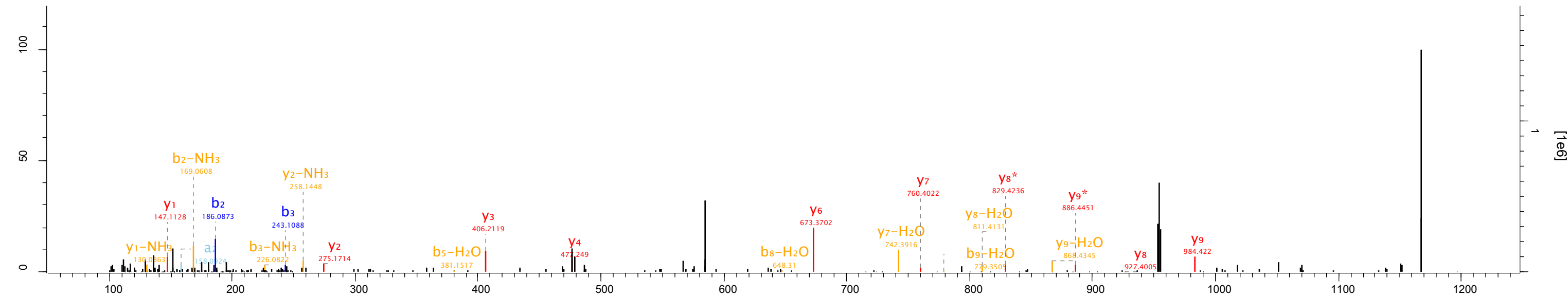
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 2292 Method FTMS; HCD Score 140.01 m/z 532.22 Gene names SRRM2



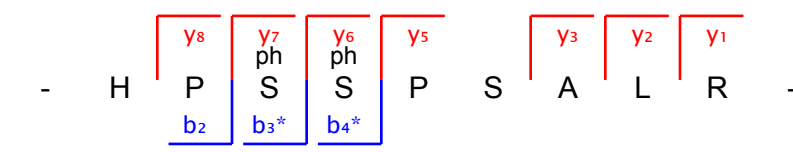
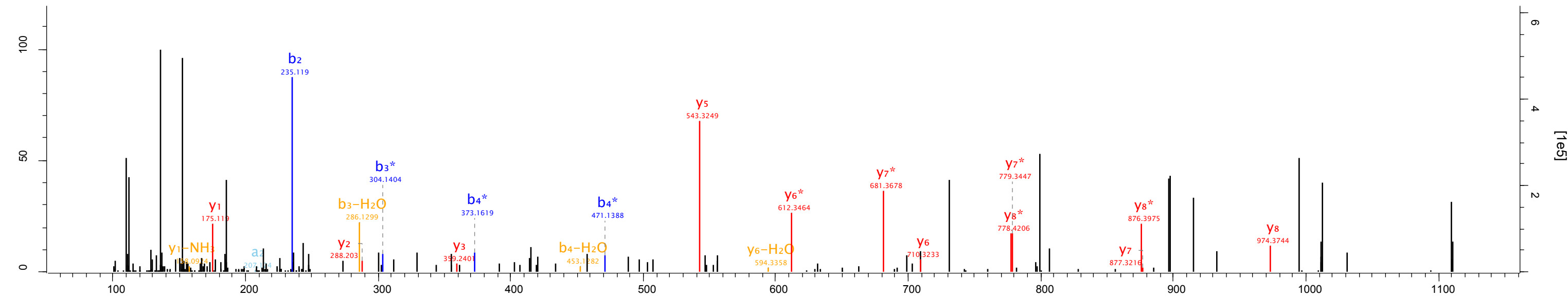
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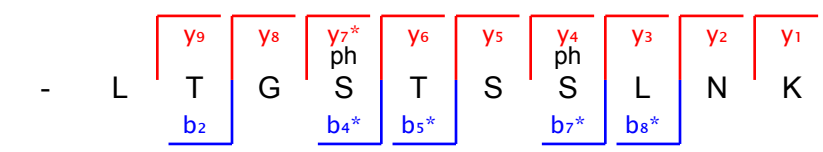
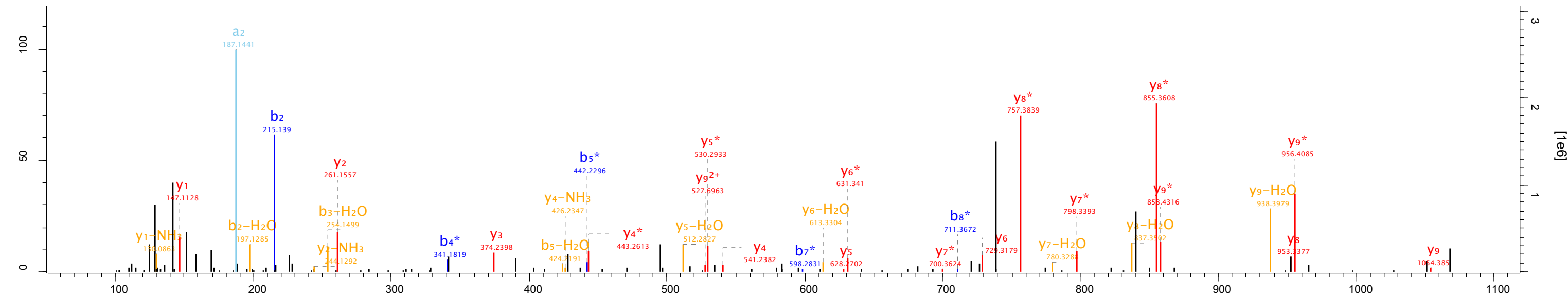
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 3542 Method FTMS; HCD Score 92.86 m/z 585.26 Gene names VCL

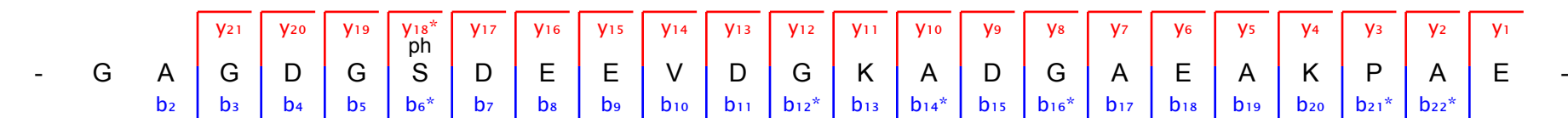
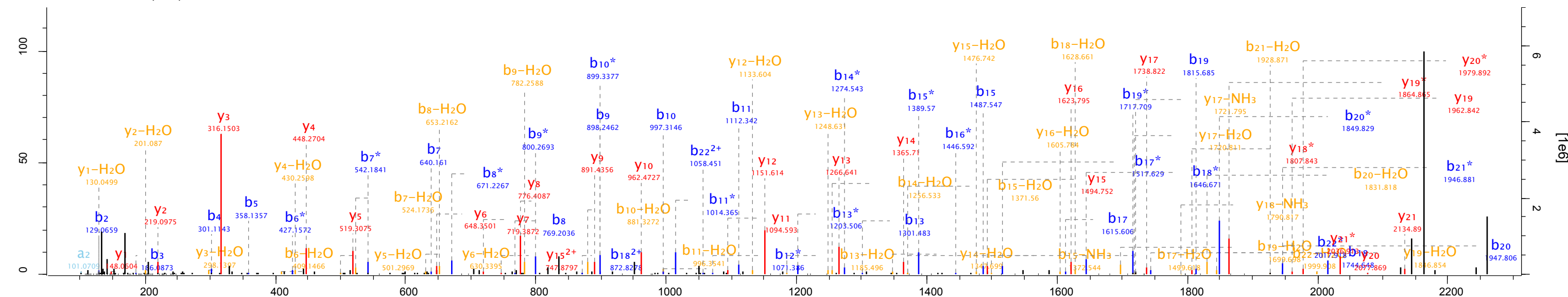


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 3712 Method FTMS; HCD Score 54.28 m/z 556.22 Gene names SORBS3

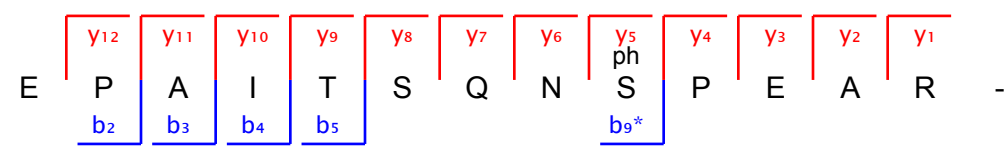
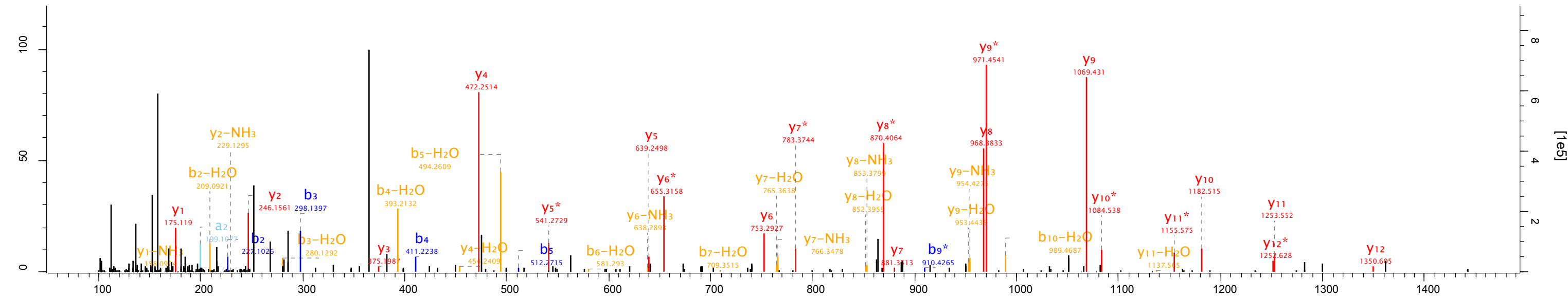


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 3802 Method FTMS; HCD Score 147.39 m/z 584.24 Gene names EXOC1

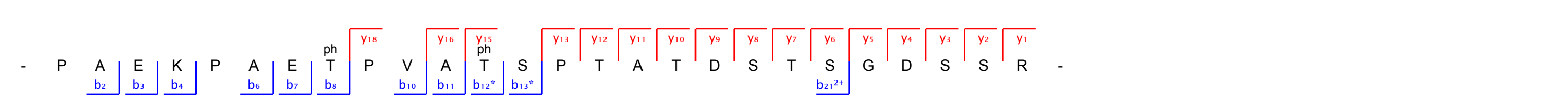
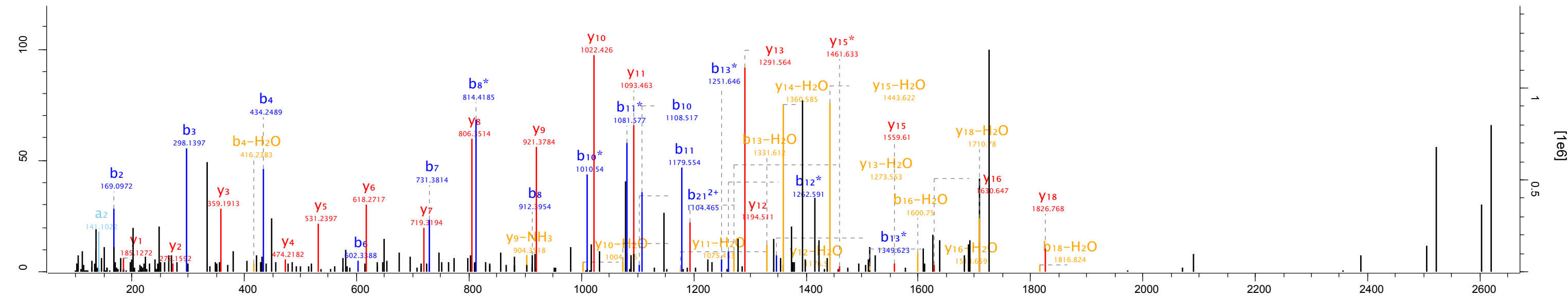




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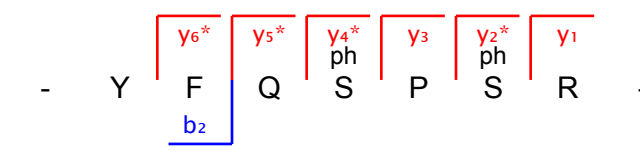
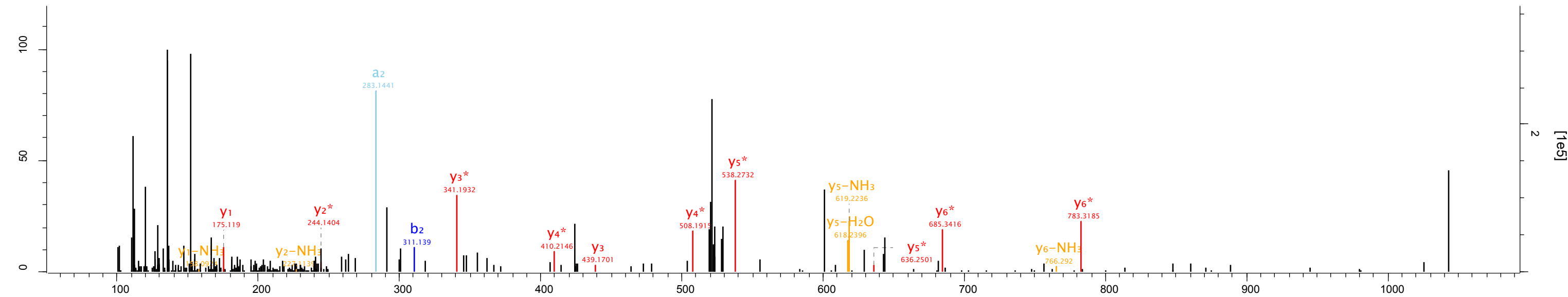
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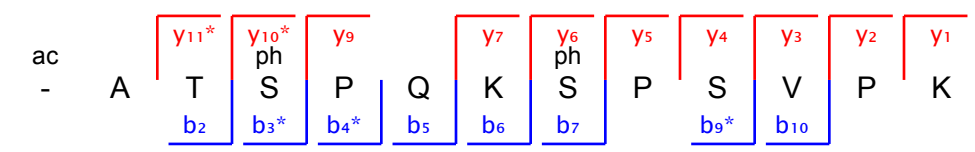
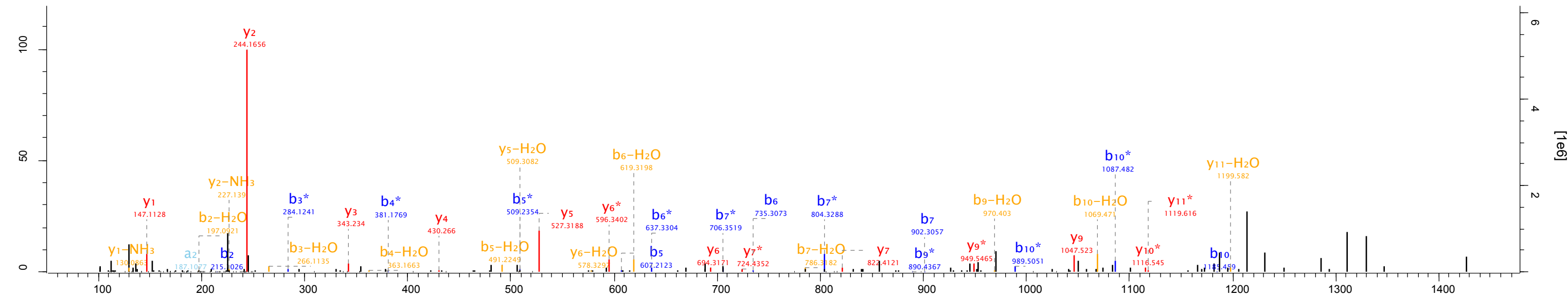
Raw file

20171215_MaS_33SR_LMH_phospho_02

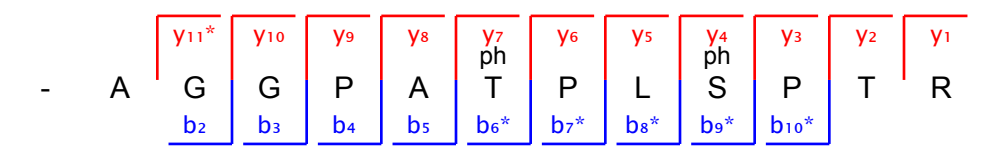
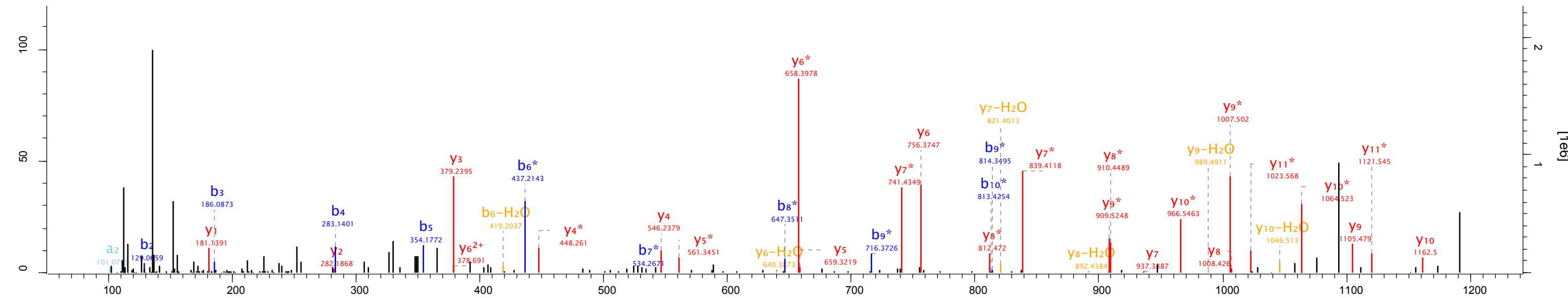
Scan Method Score m/z Gene names
5012 FTMS; HCD 65.72 522.68 SRSF7



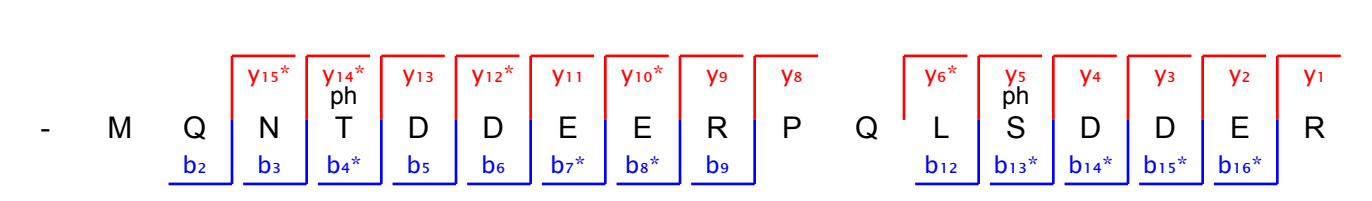
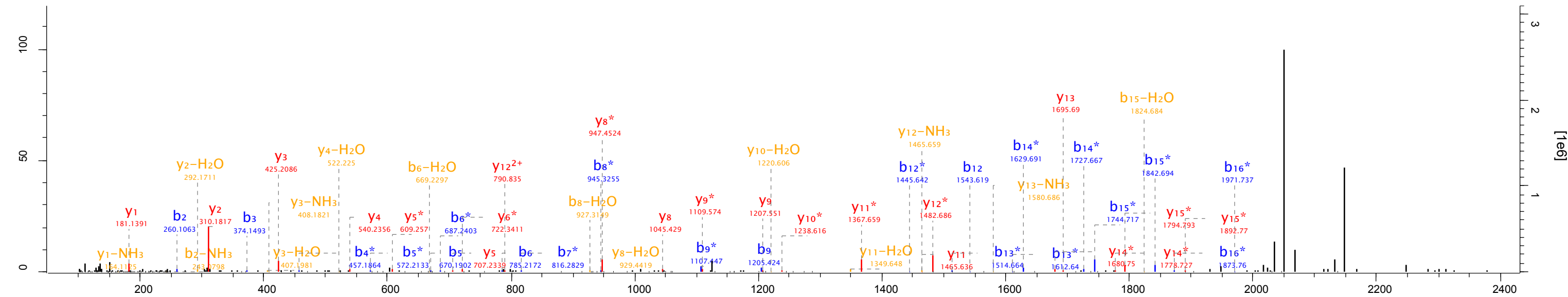
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 Scan: 5082 Method: FTMS; HCD Score: 98.68 m/z: 714.81 Gene names: PARVA



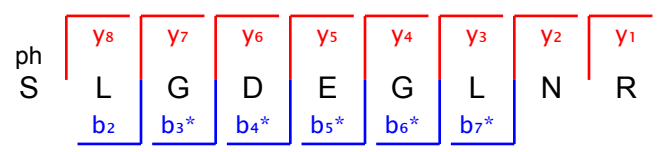
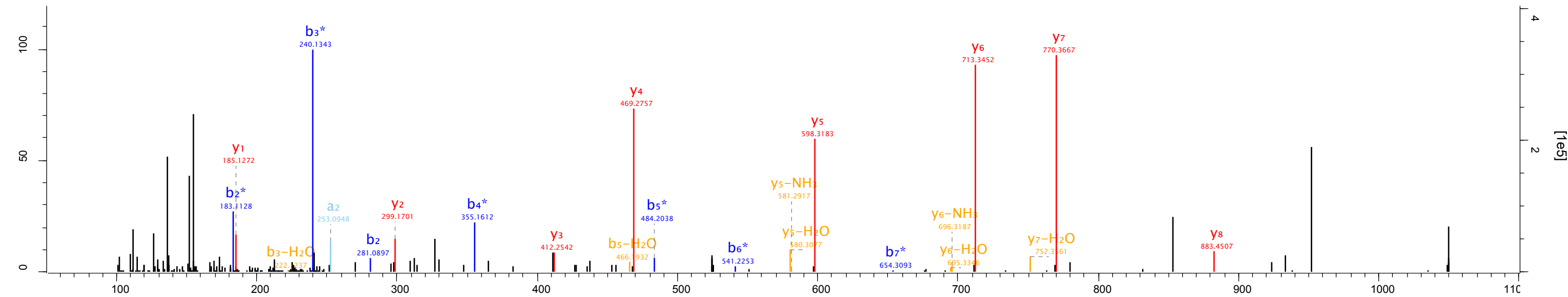
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 5802 Method FTMS; HCD Score 140.51 m/z 645.78 Gene names LMNB2



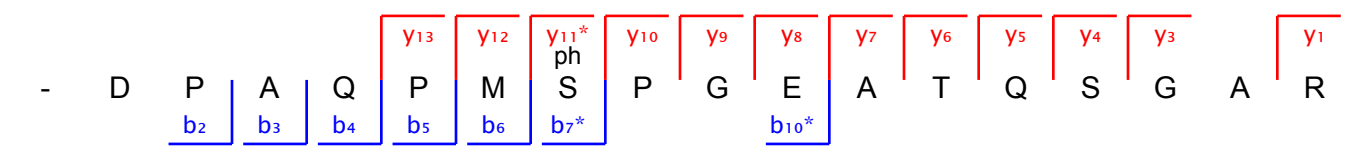
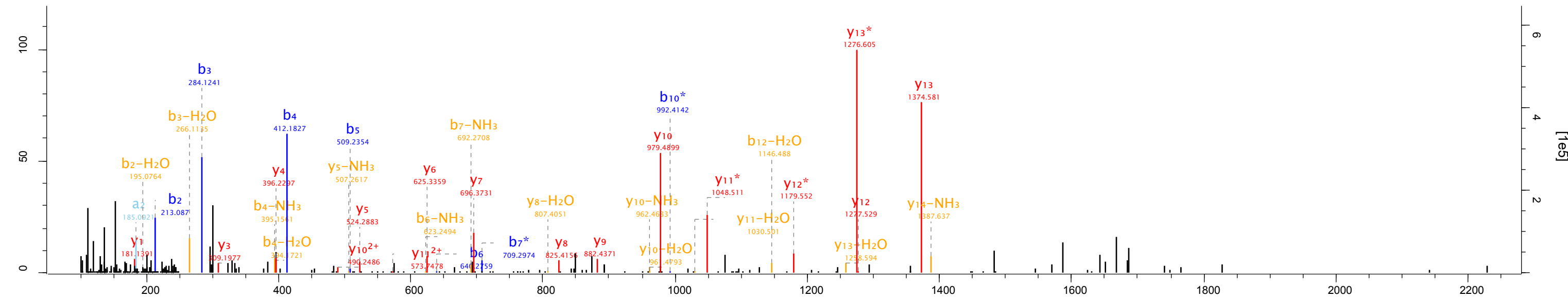
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 Scan: 5892 Method: FTMS; HCD Score: 172.32 m/z: 1125.43 Gene names: LEO1



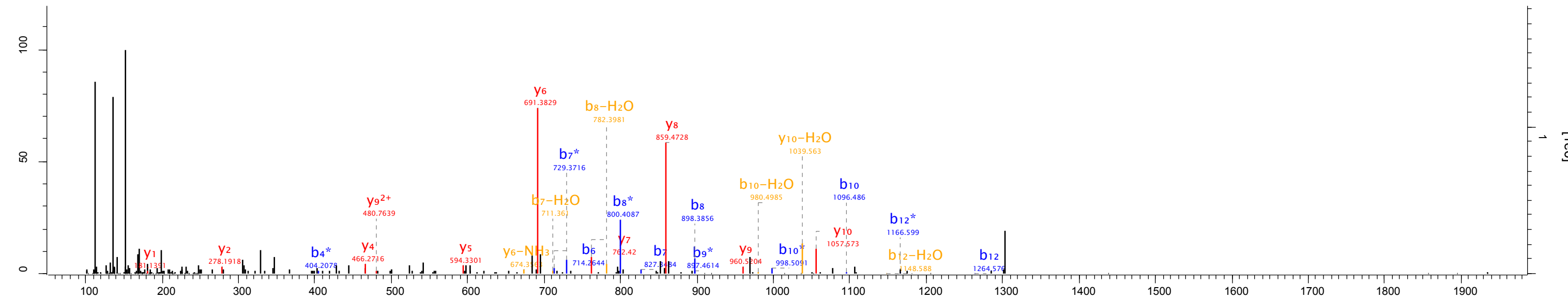
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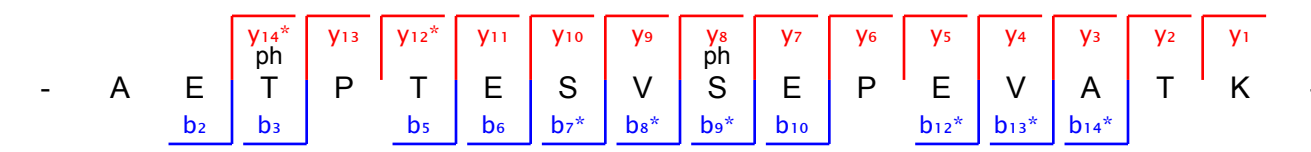
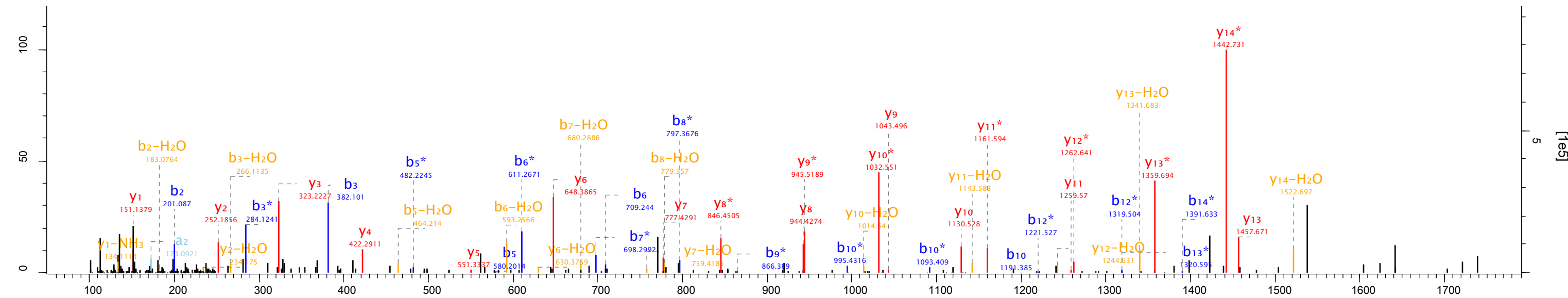
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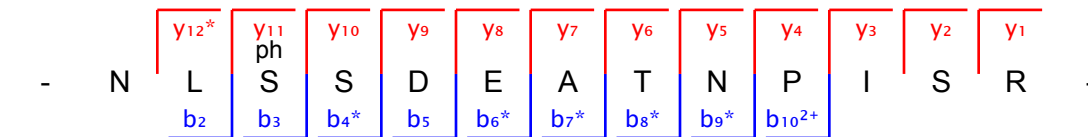
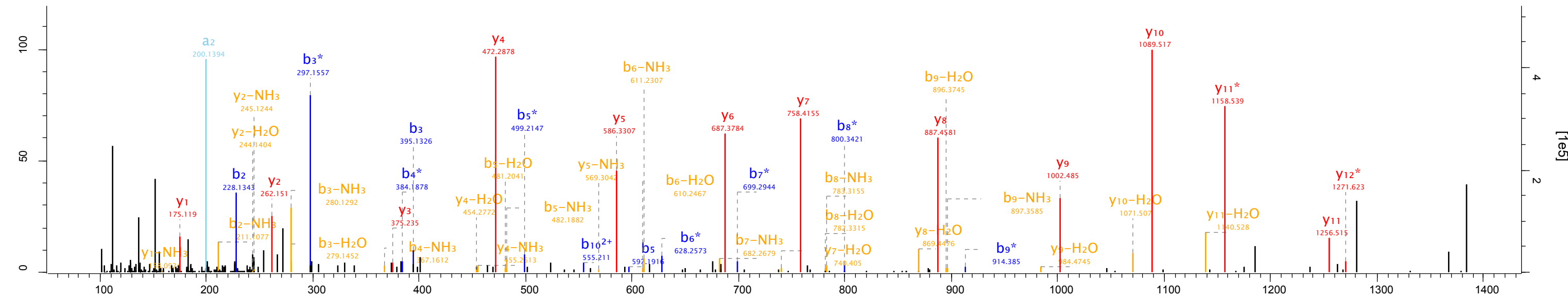


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 6812 Method FTMS; HCD Score 49.59 m/z 652.32 Gene names EIF2A

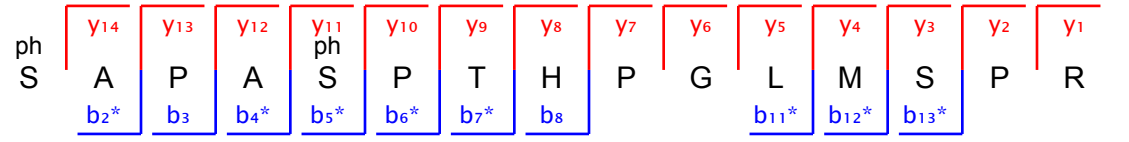
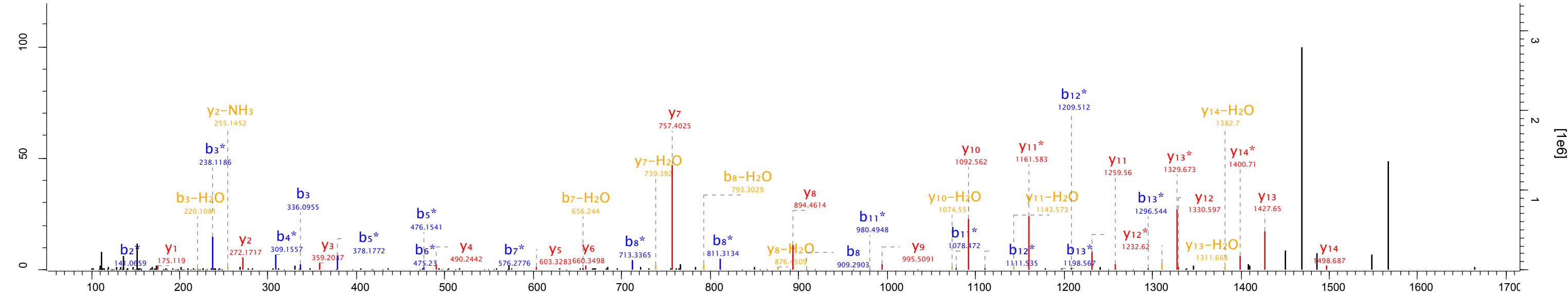


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 7692 Method FTMS; HCD Score 197.69 m/z 919.89 Gene names LIG1

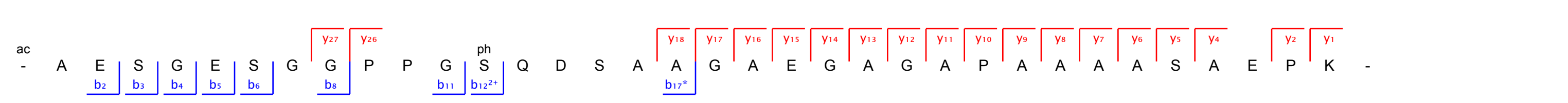
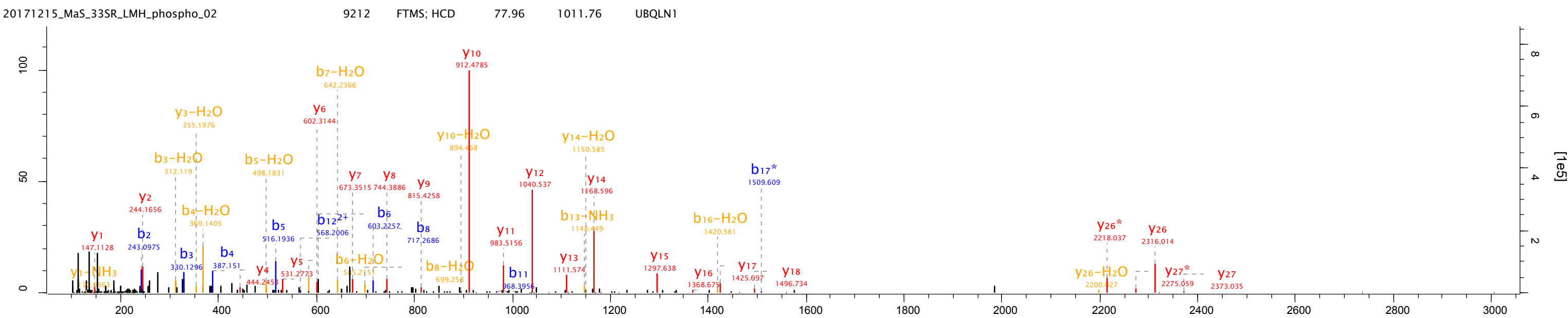




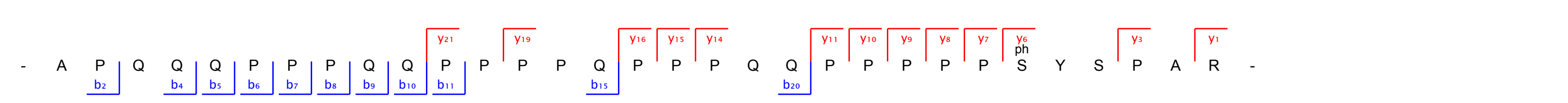
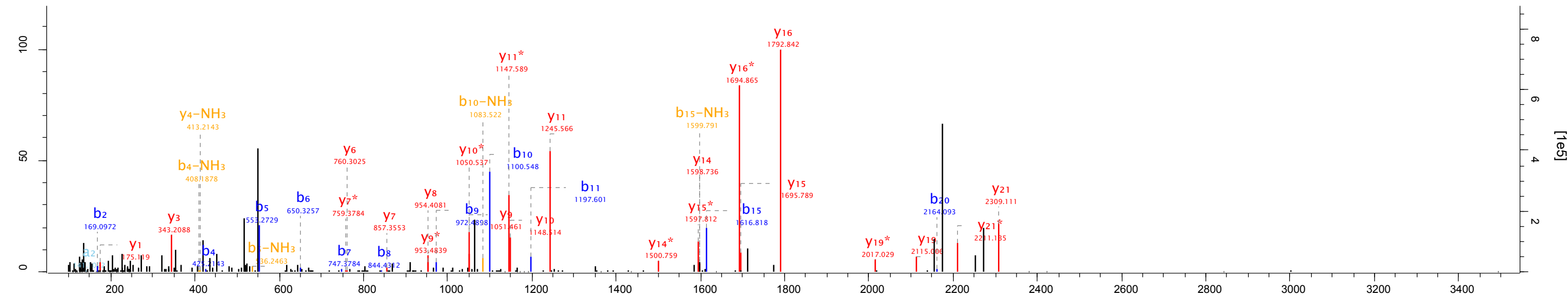
20171215_MaS_33SR_LMH_phospho_02 8702 FTMS; HCD 194.7 833.35 FOXK1



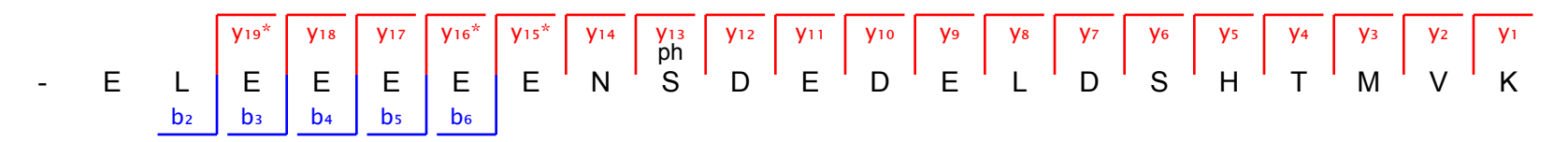
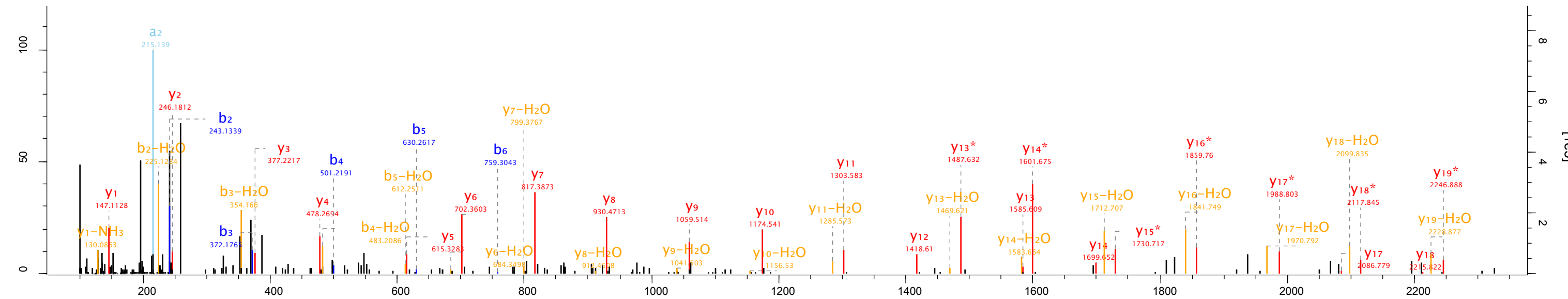
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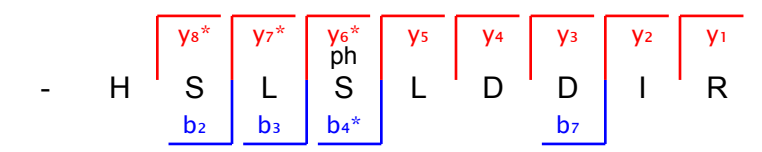
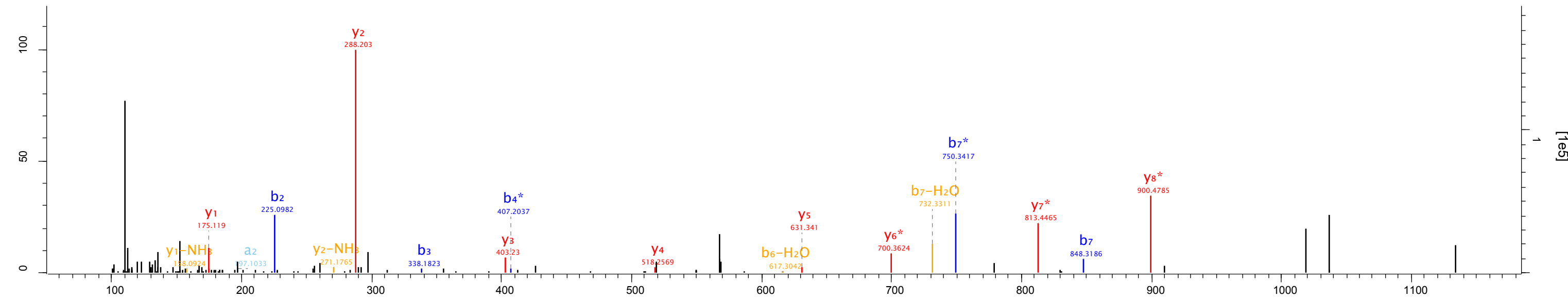
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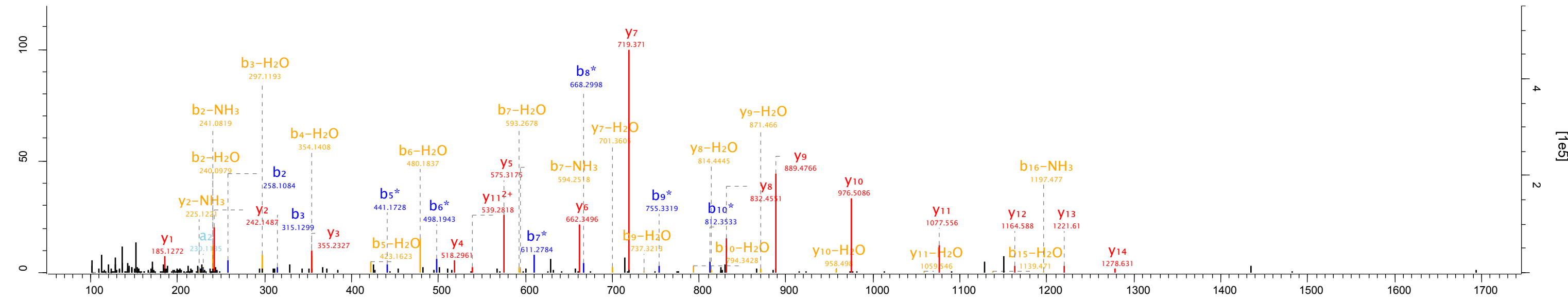
20171215_MaS_33SR_LMH_phospho_03 10442 FTMS; HCD 189.84 863.67 STK3



Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 10462 Method FTMS; HCD Score 73.44 m/z 568.26 Gene names FRMD6



Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 11282 Method FTMS; HCD Score 92.96 m/z 826.36 Gene names AAK1

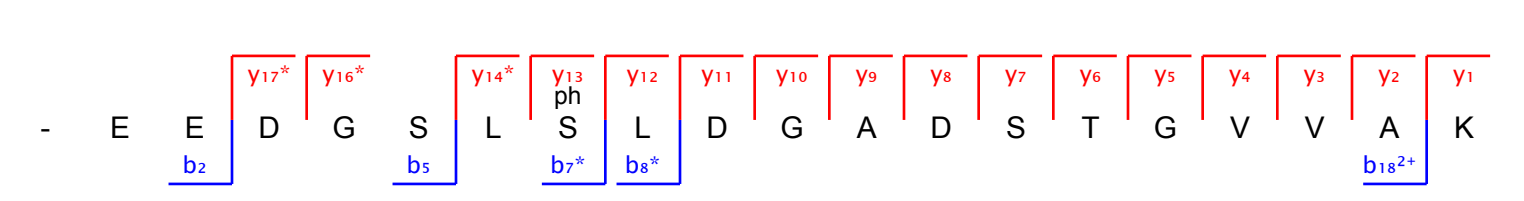
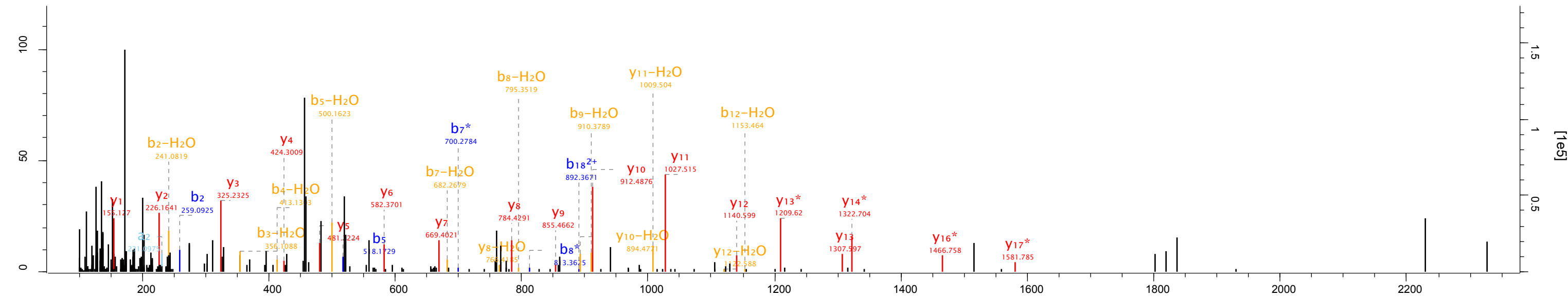


- E Q G G ph S G L G S G S S G G G G G S G L G S G Y I G R -

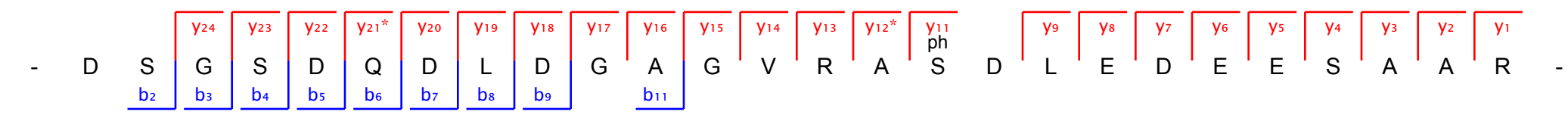
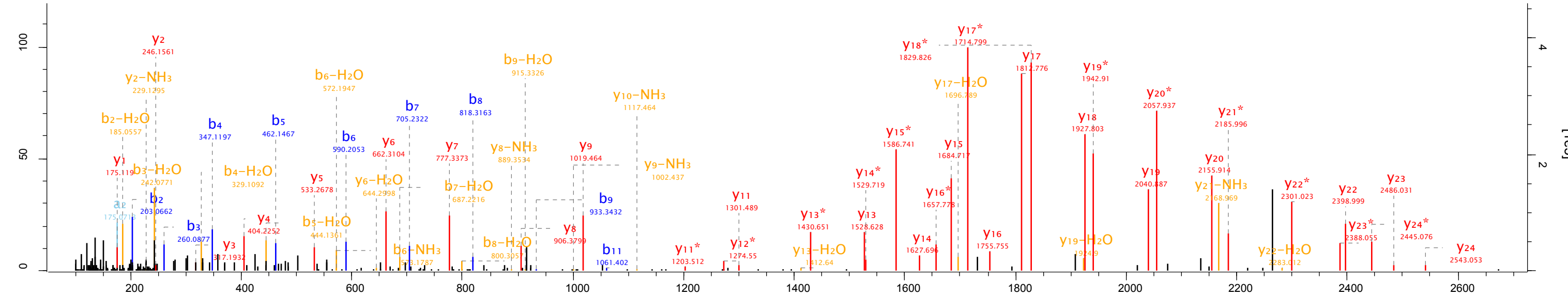
Fragmentation mapping (b and y ions):

- b2: Q
- b3: G
- b5*: S
- b6*: G
- b7*: L
- b8*: G
- b9*: S
- b10*: G
- y1: R
- y2: G
- y3: I
- y4: Y
- y5: S
- y6: S
- y7: G
- y8: L
- y9: G
- y10: S
- y11: T
- y12: S
- y13: G
- y14: G

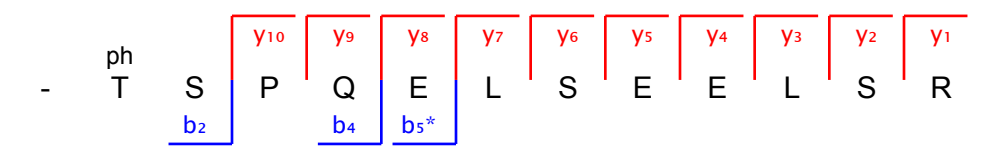
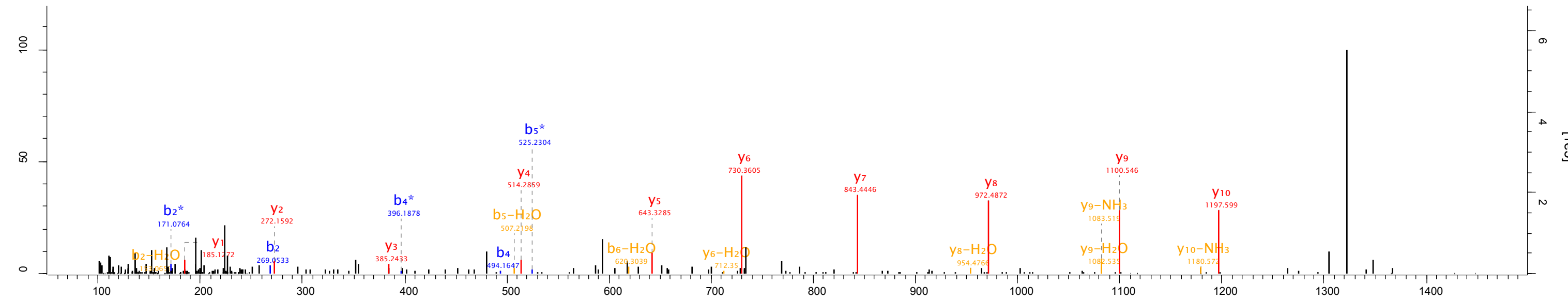
Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 11652 Method FTMS; HCD Score 63.19 m/z 969.43 Gene names TRIM28



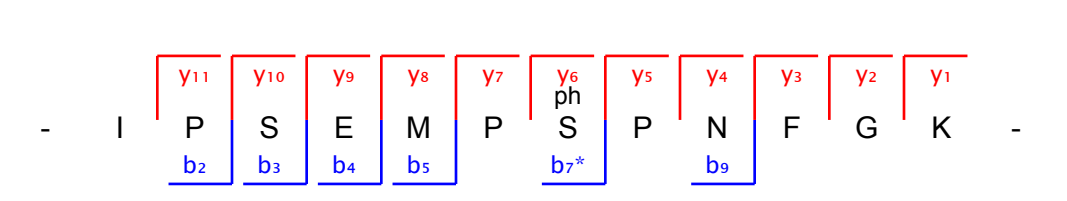
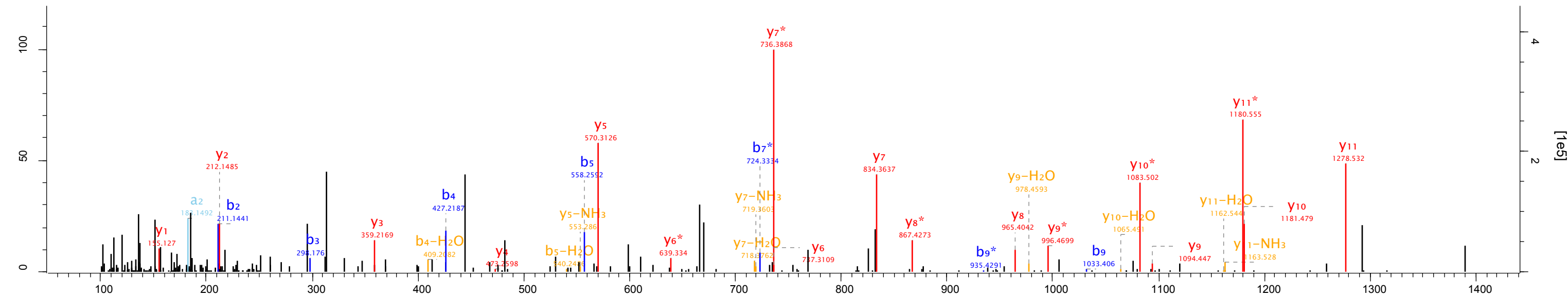
20171215_MaS_33SR_LMH_phospho_03 11852 FTMS; HCD 290.45 916.37 ZC3H18



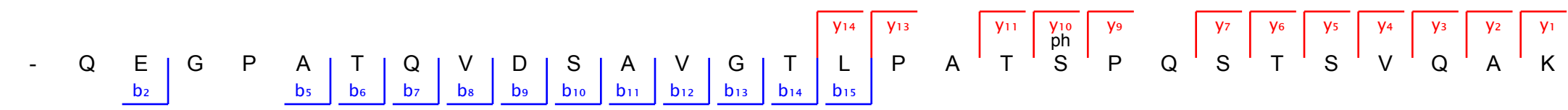
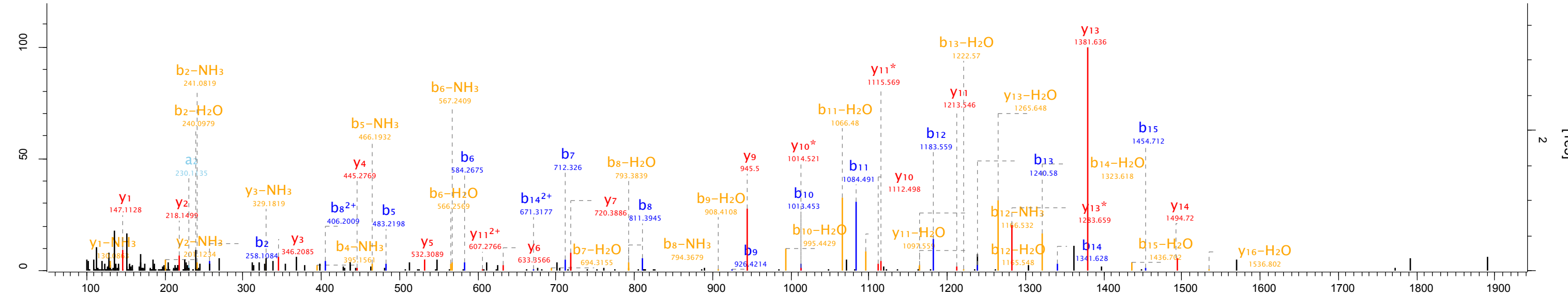
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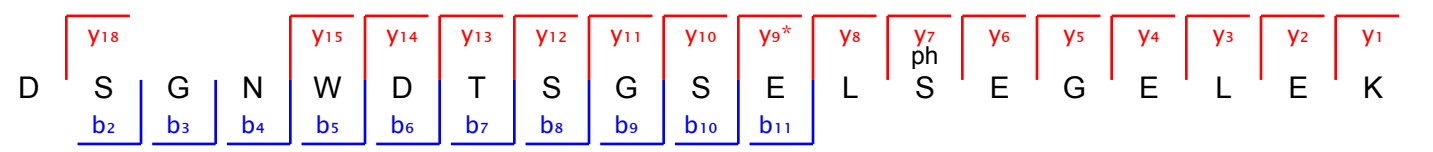
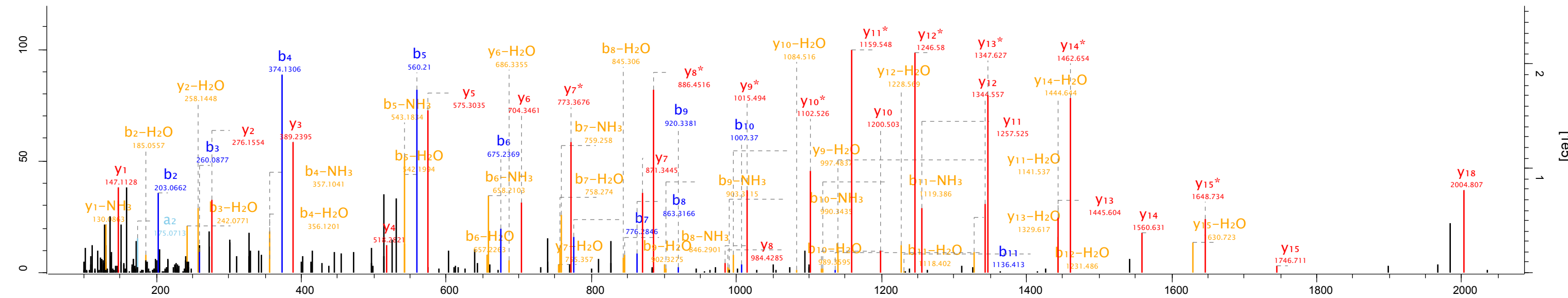
Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 12172 Method FTMS; HCD Score 159.14 m/z 696.31 Gene names SLC6A15



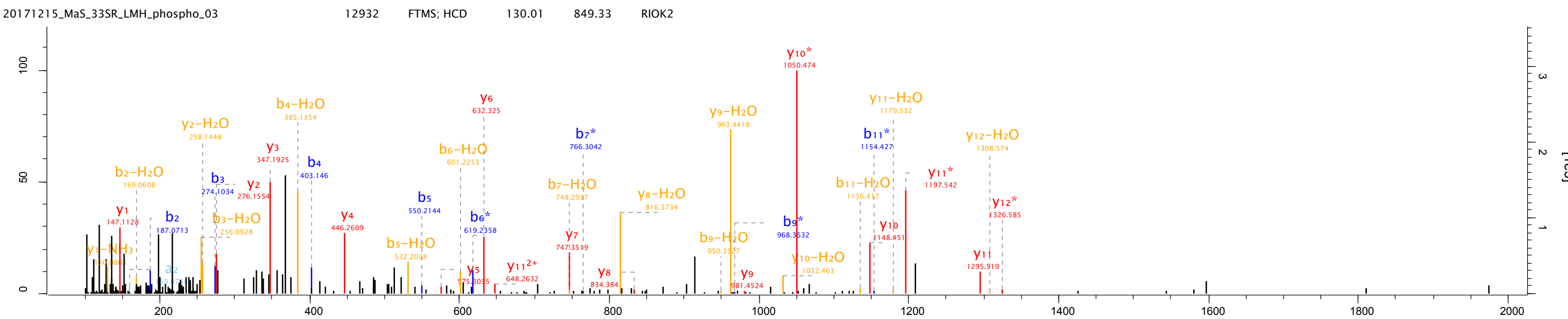
20171215_MaS_33SR_LMH_phospho_03 12422 FTMS; HCD 138.02 946.12 TCOF1



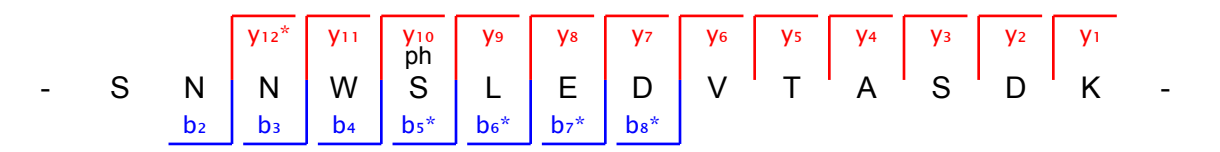
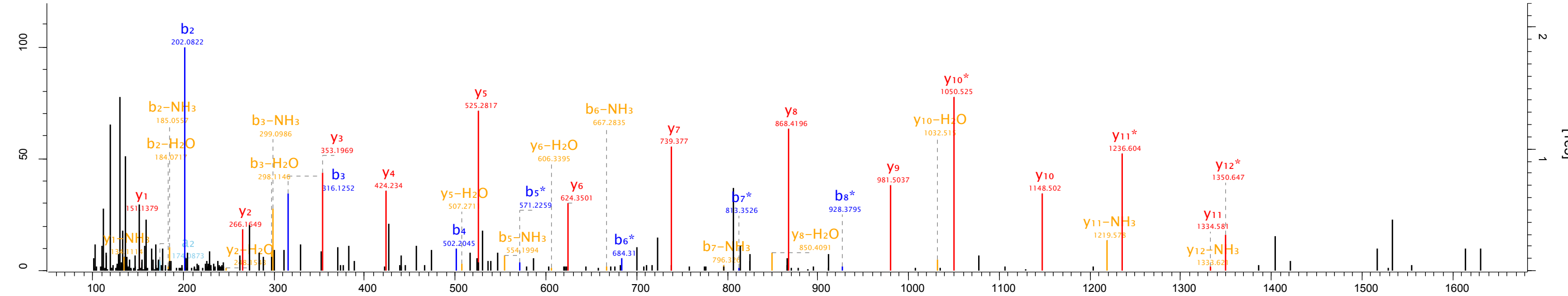
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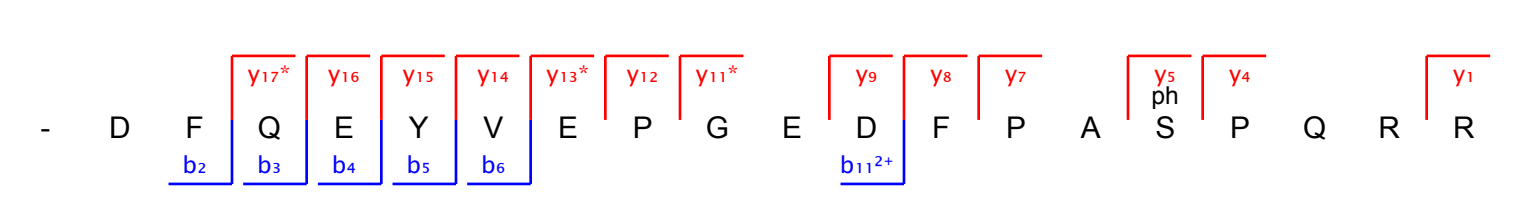
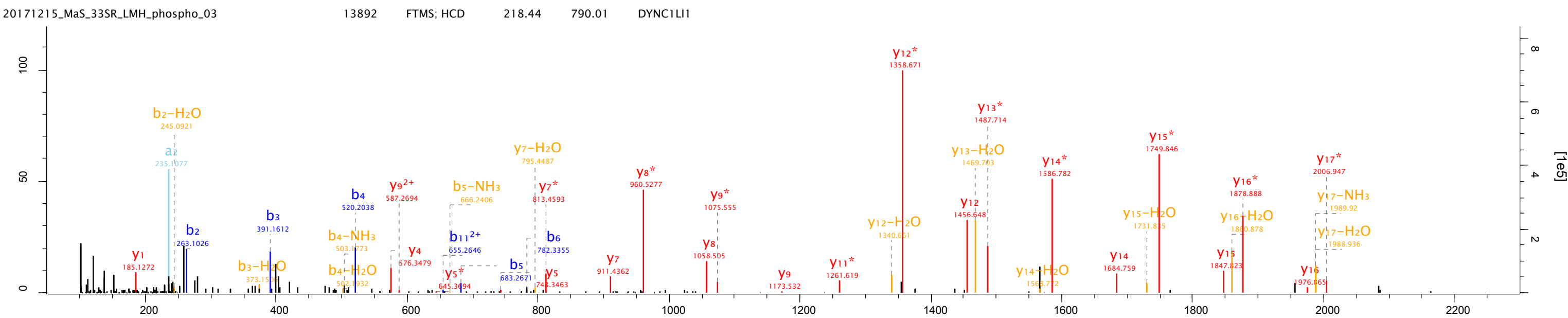
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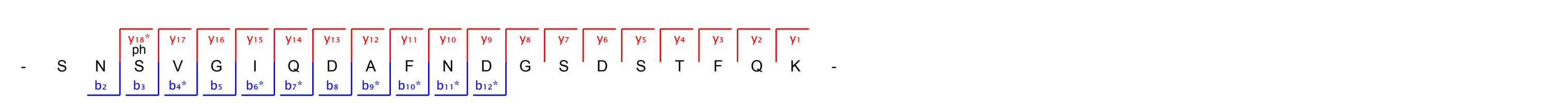
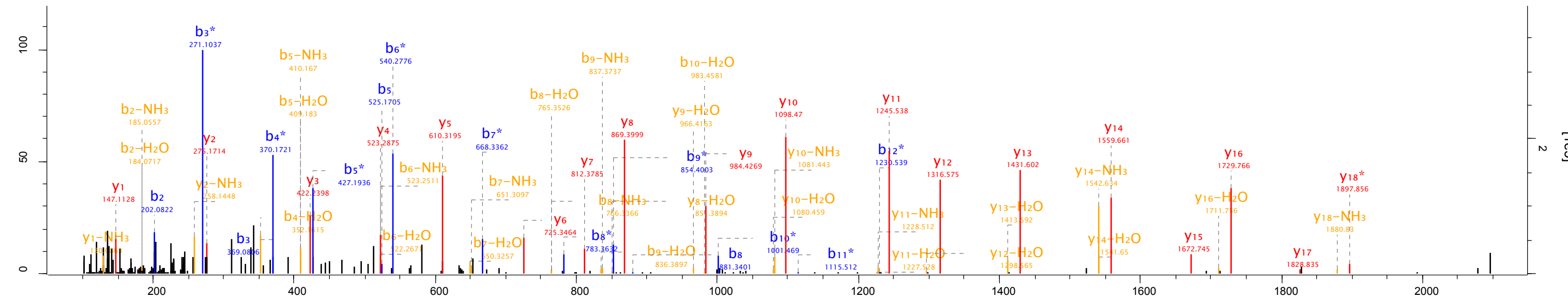
20171215_MaS_33SR_LMH_phospho_03 13202 FTMS; HCD 105.79 825.35 MELK



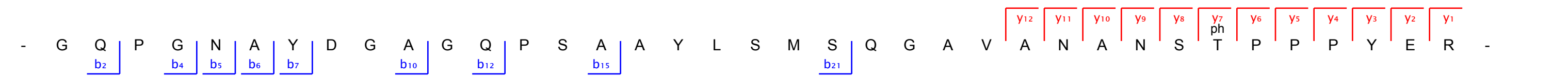
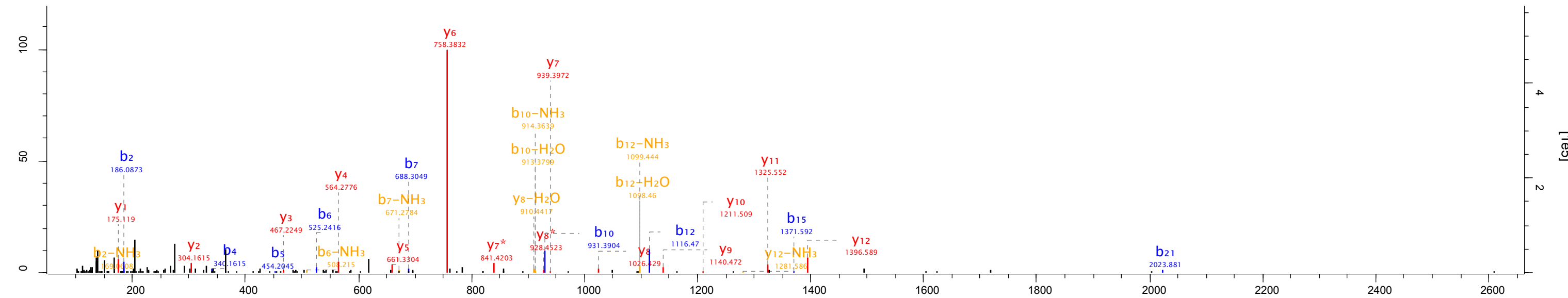
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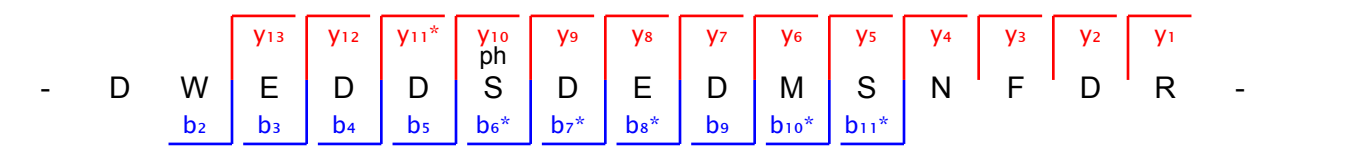
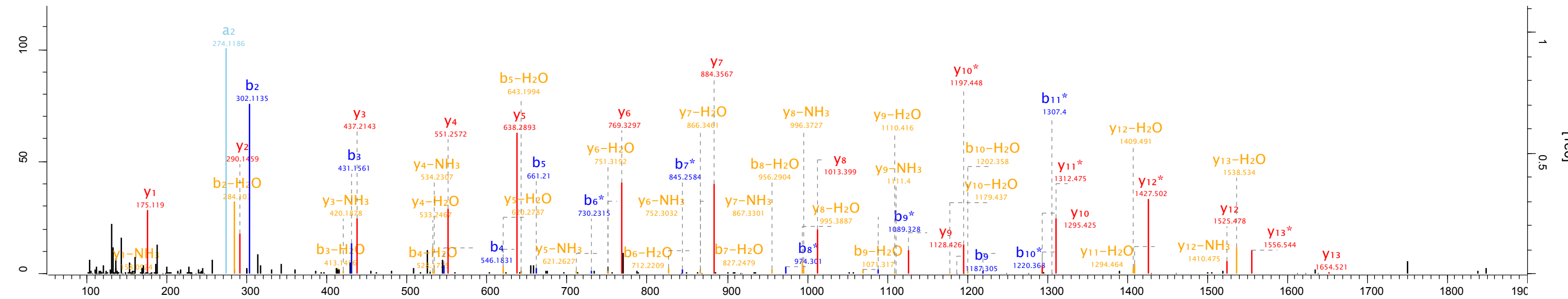
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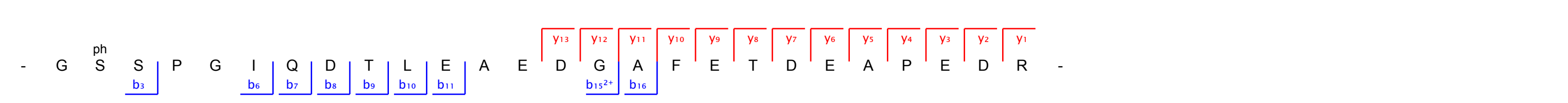
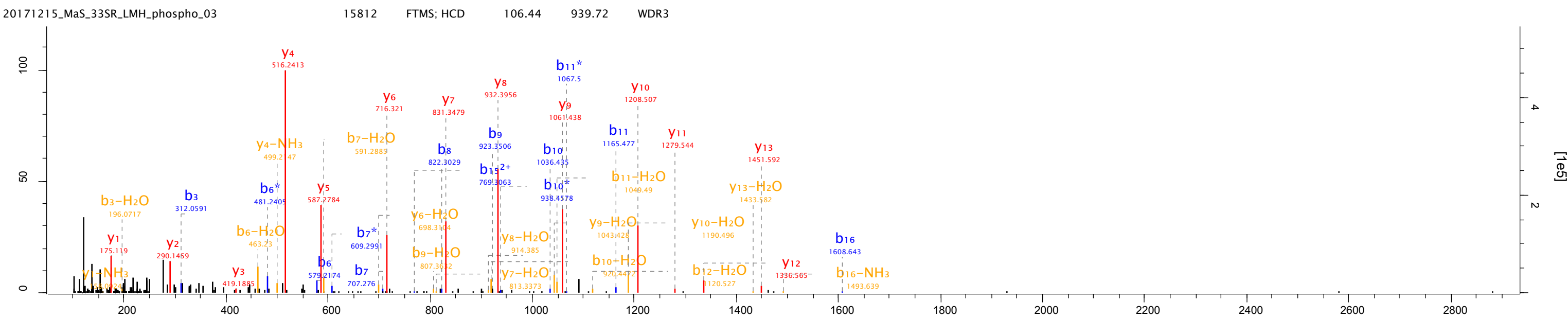


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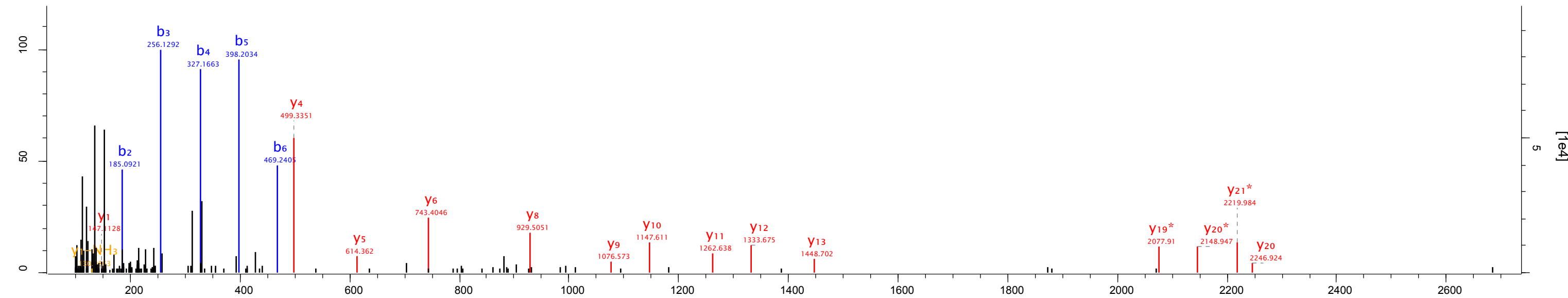


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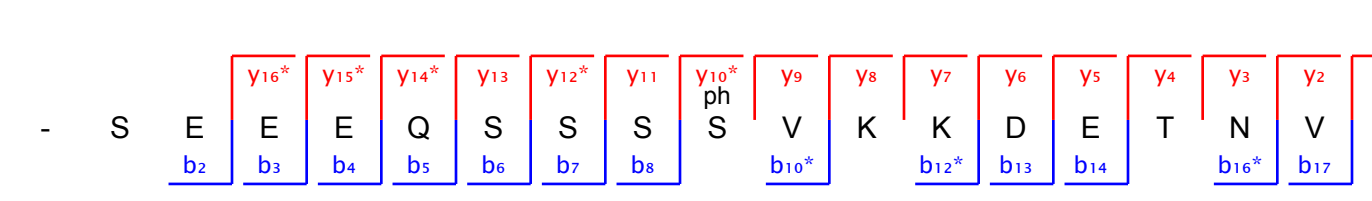
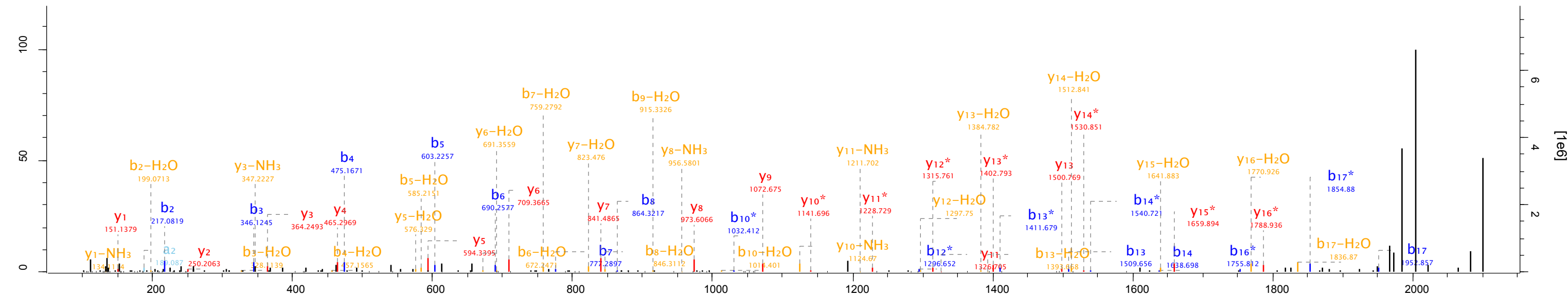


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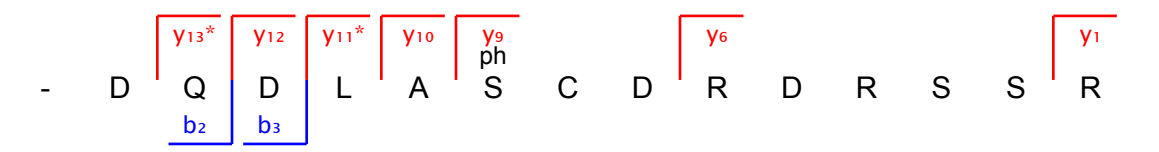
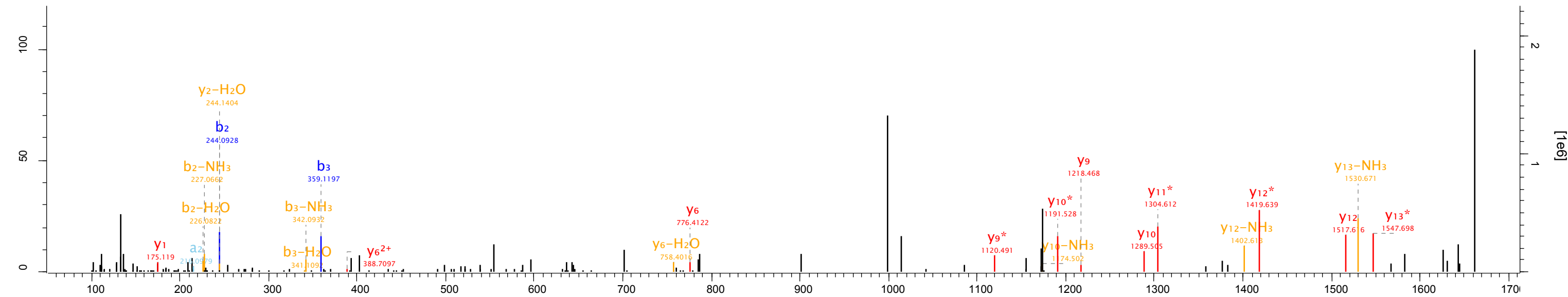
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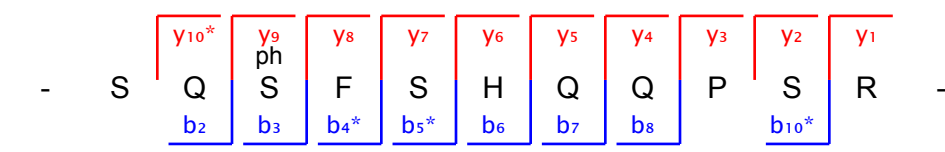
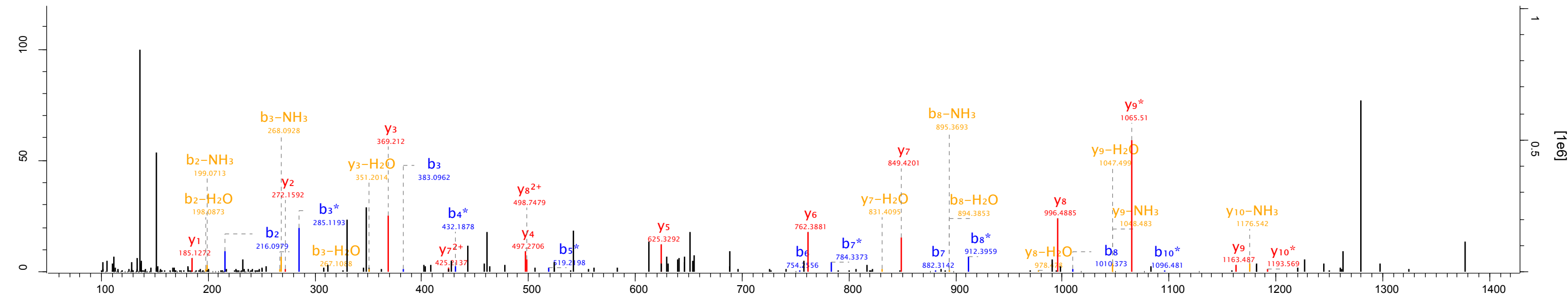
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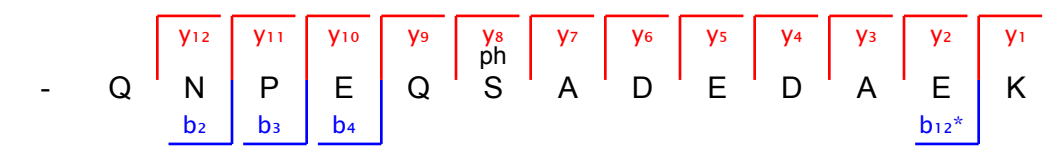
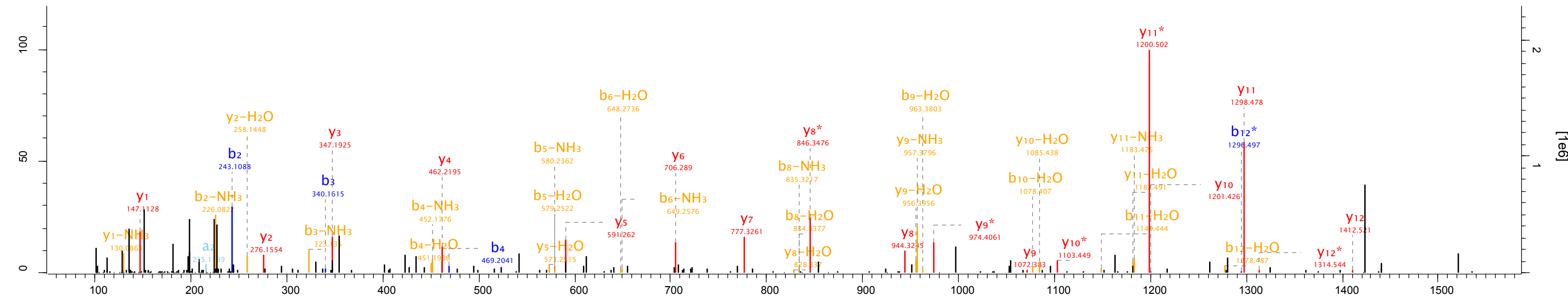
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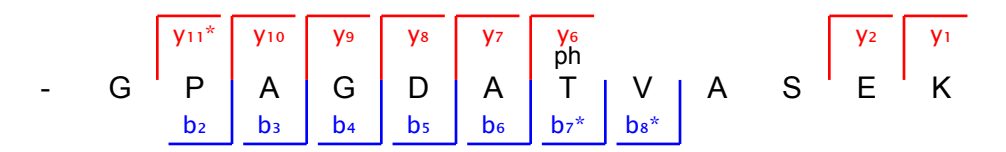
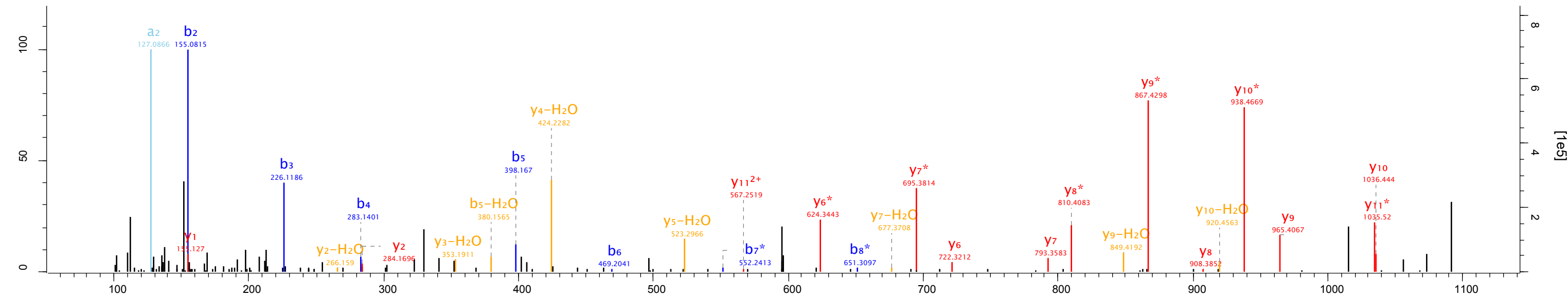
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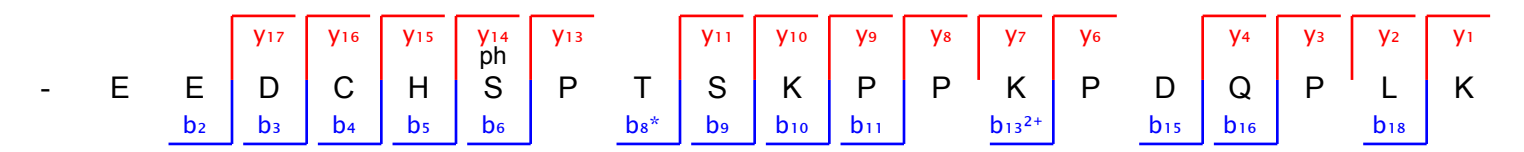
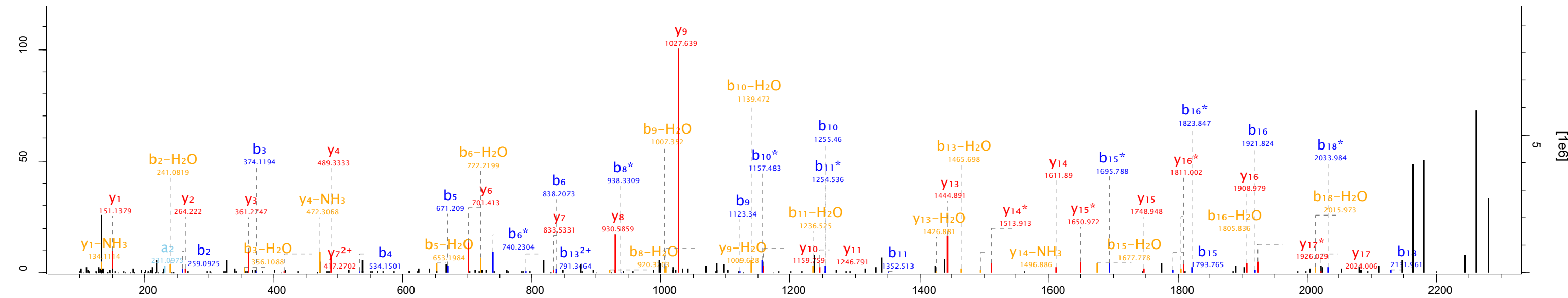
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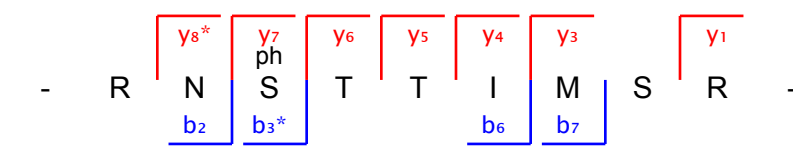
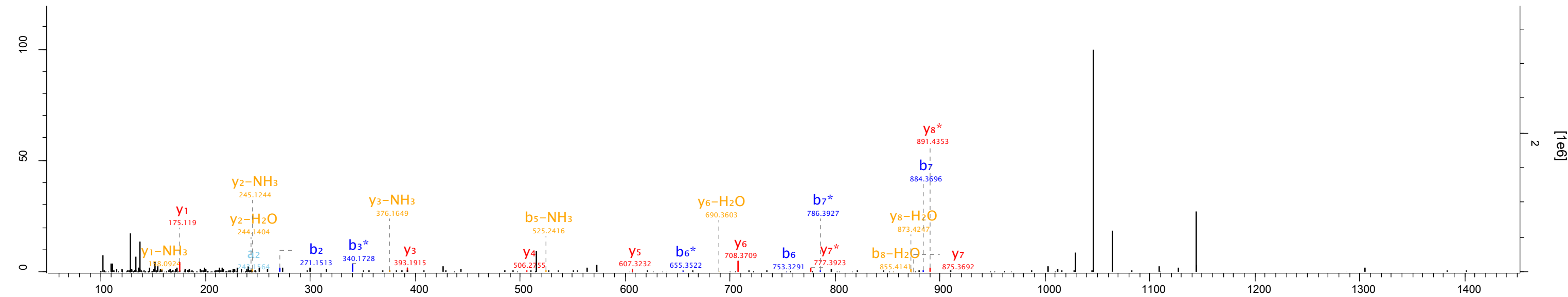
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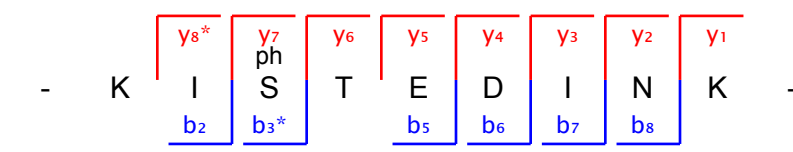
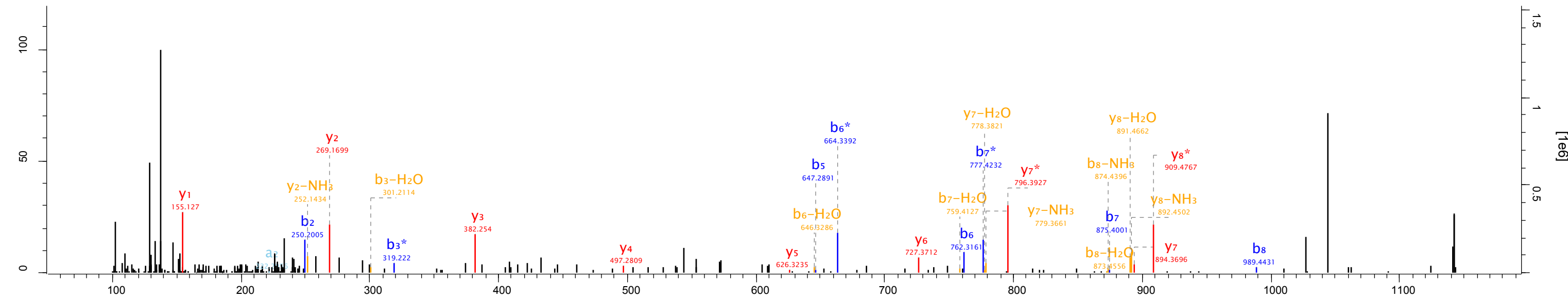
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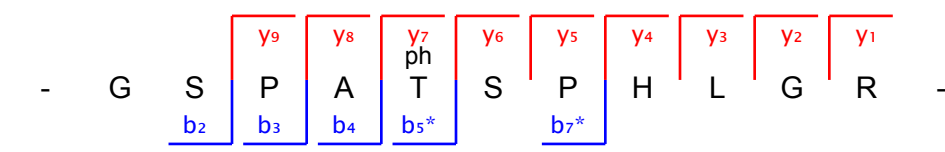
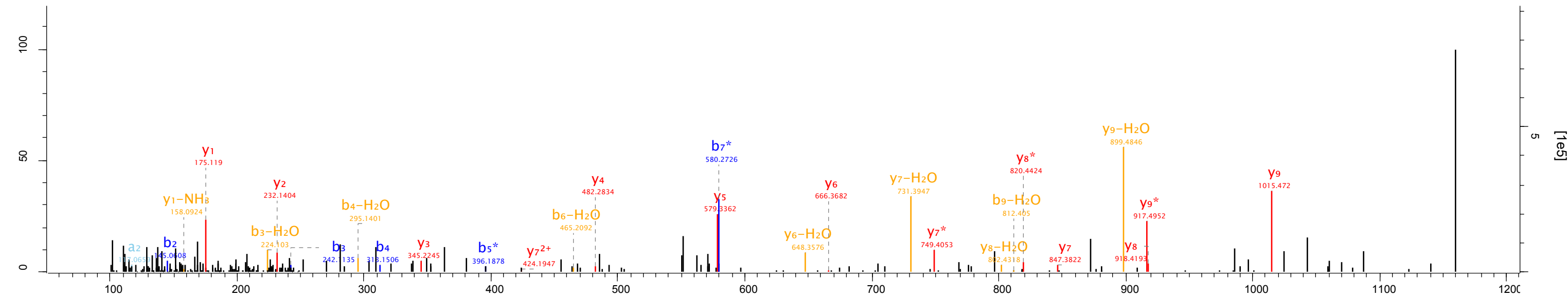
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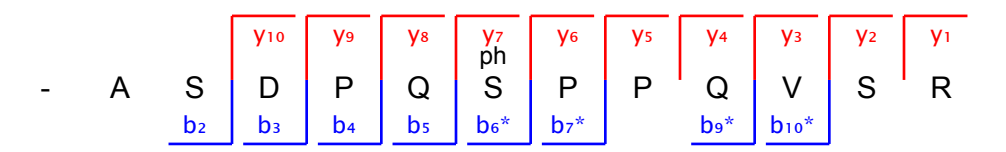
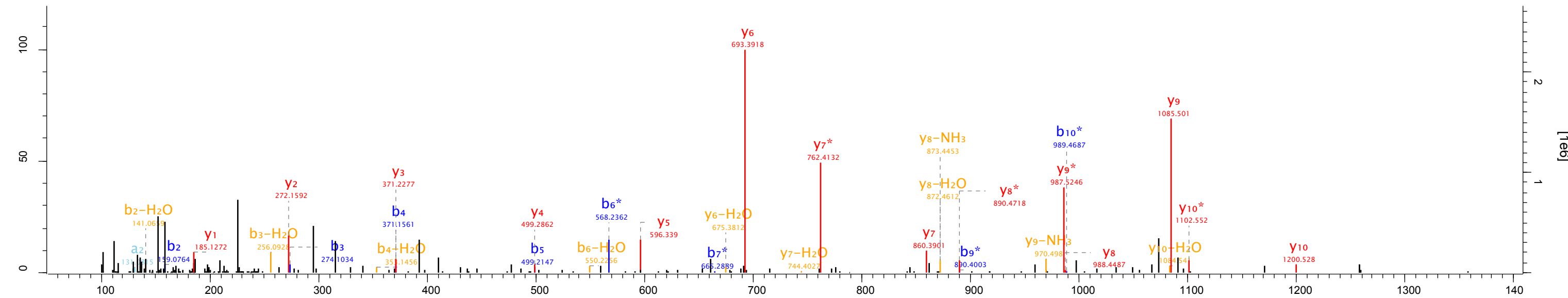
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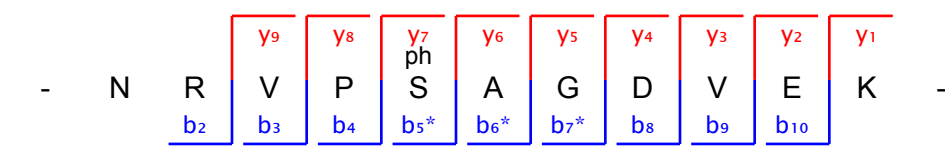
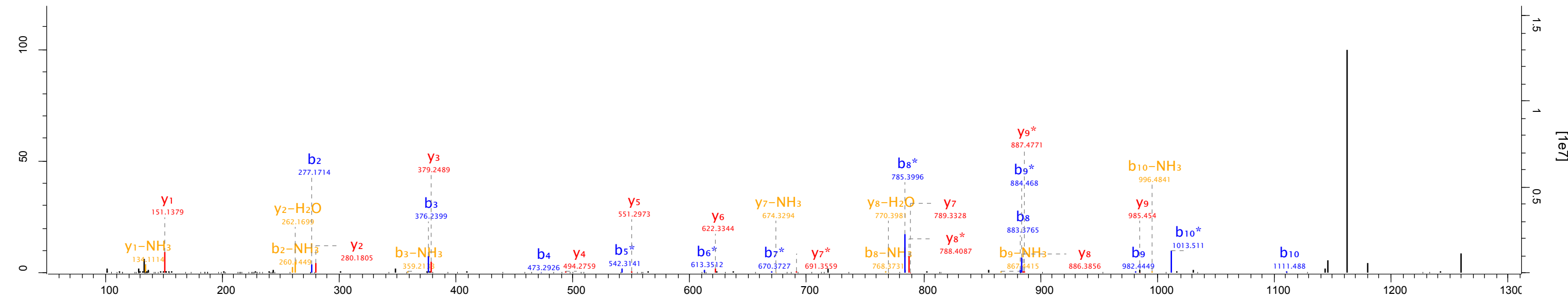
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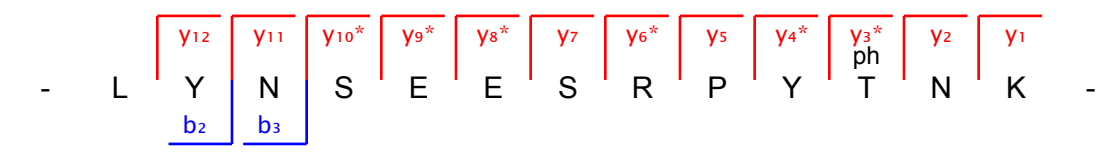
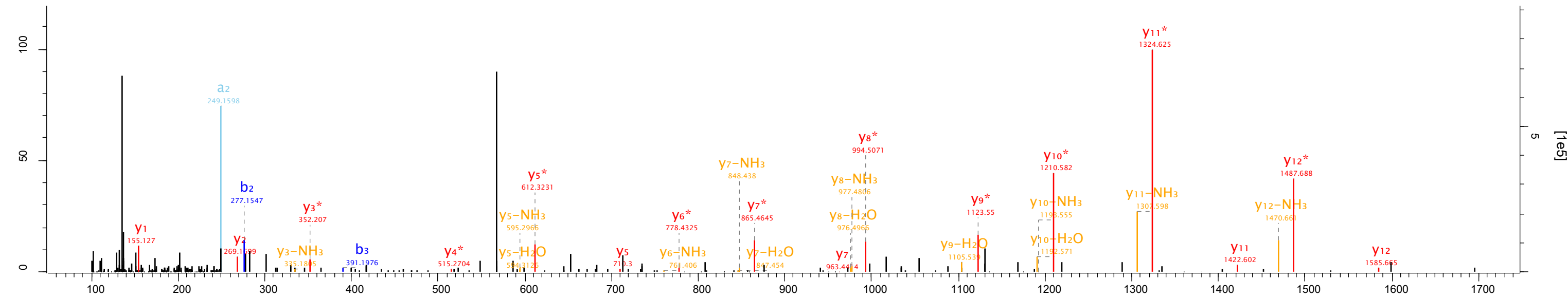
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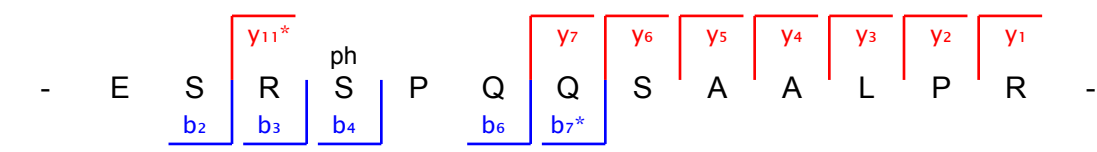
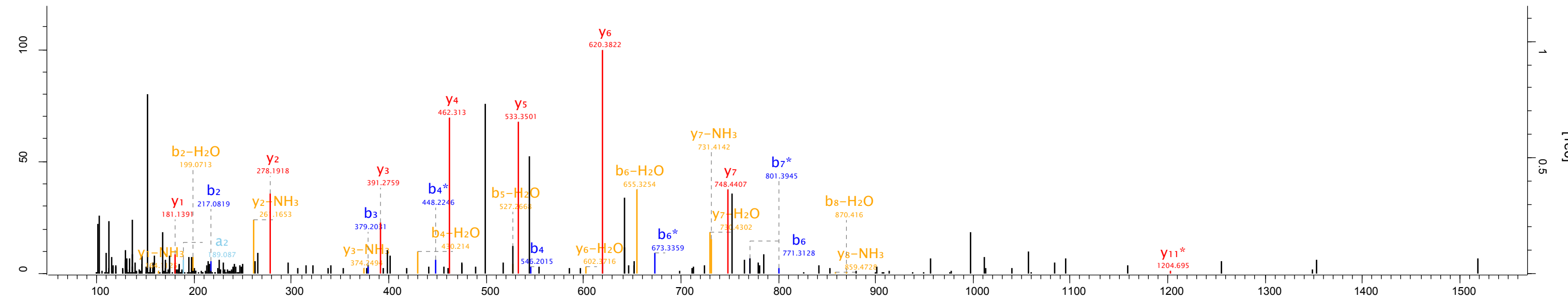
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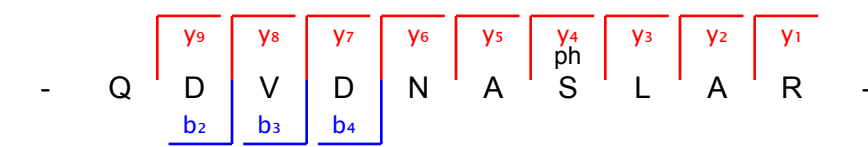
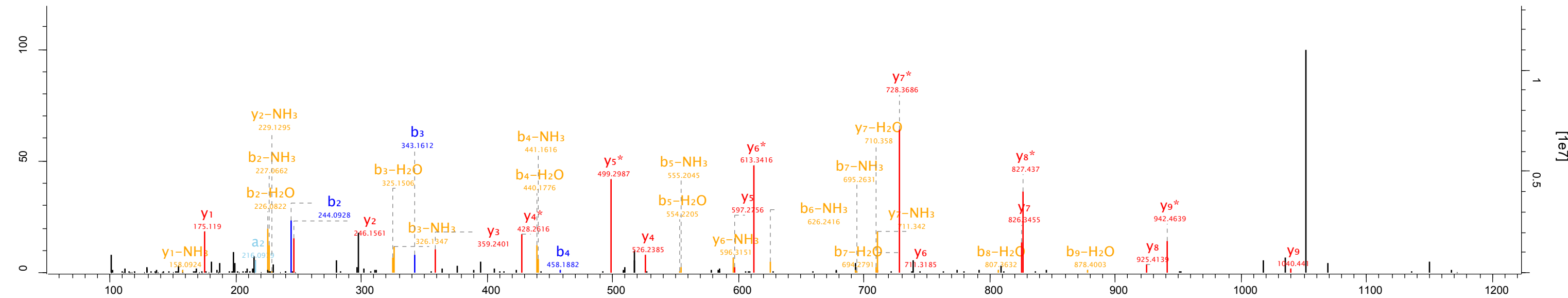


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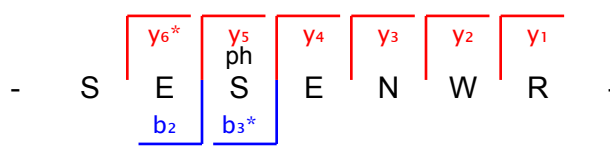
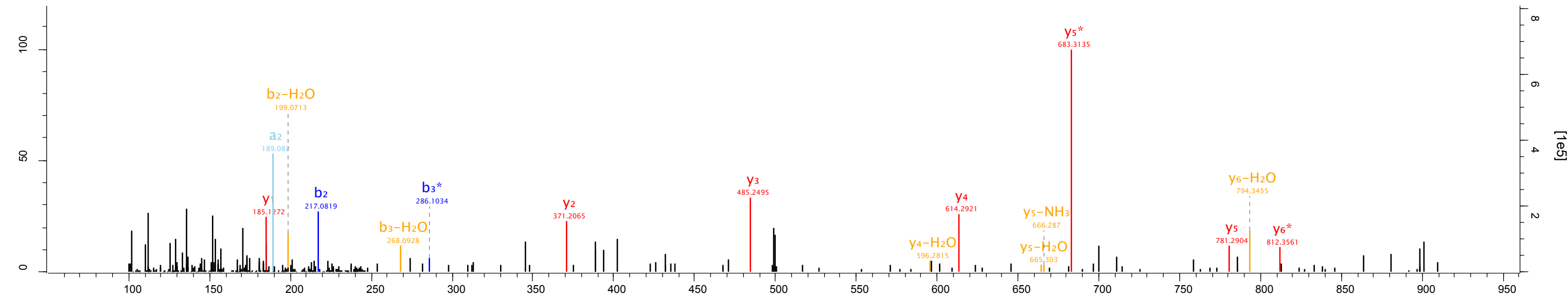


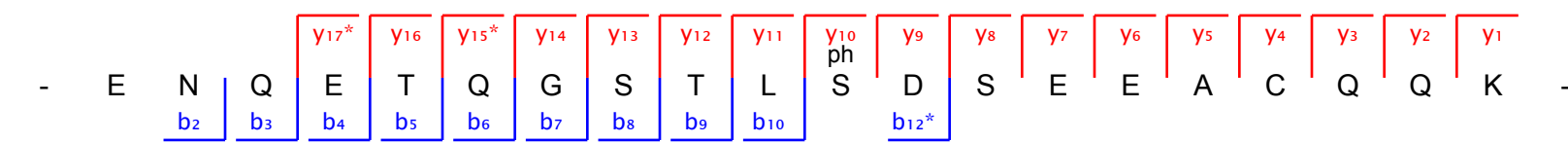
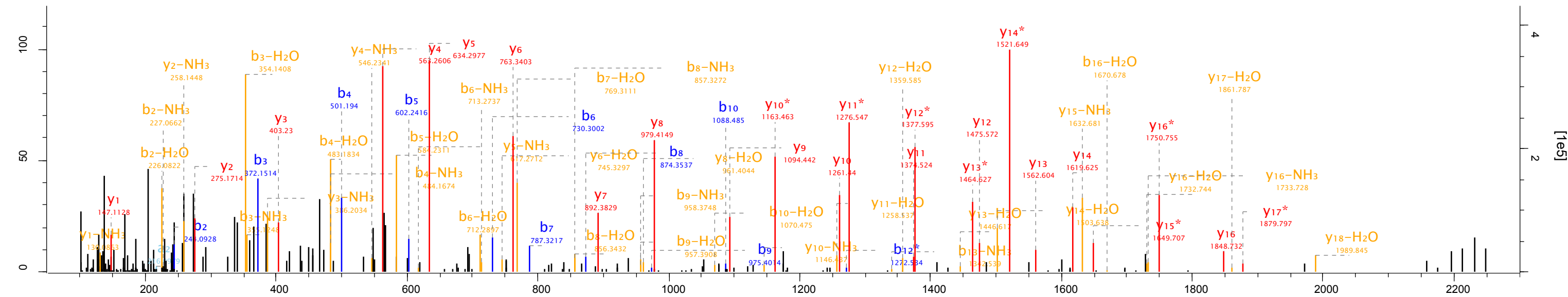
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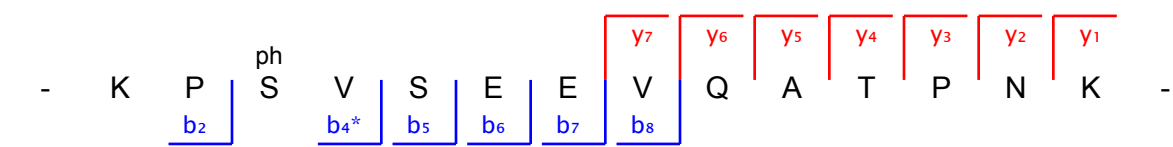
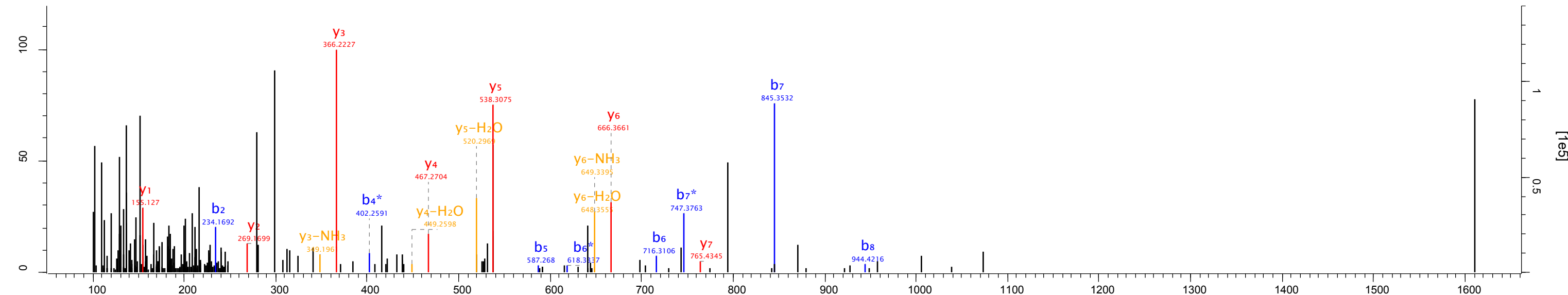


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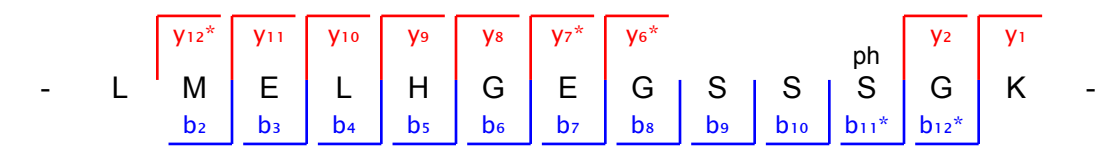
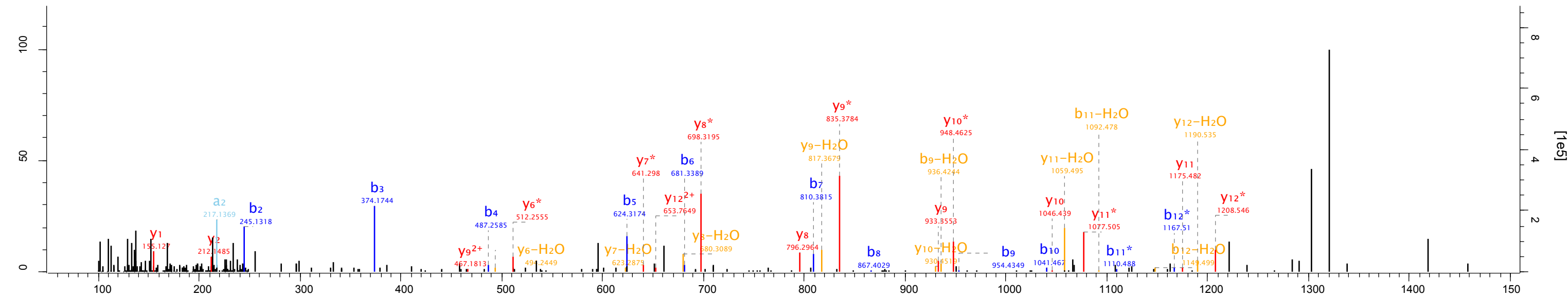




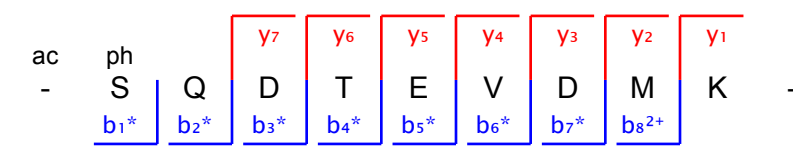
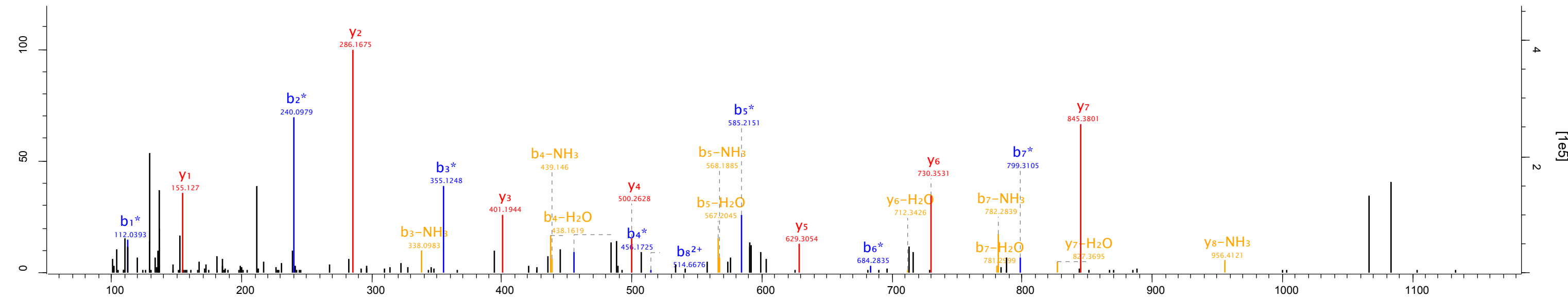
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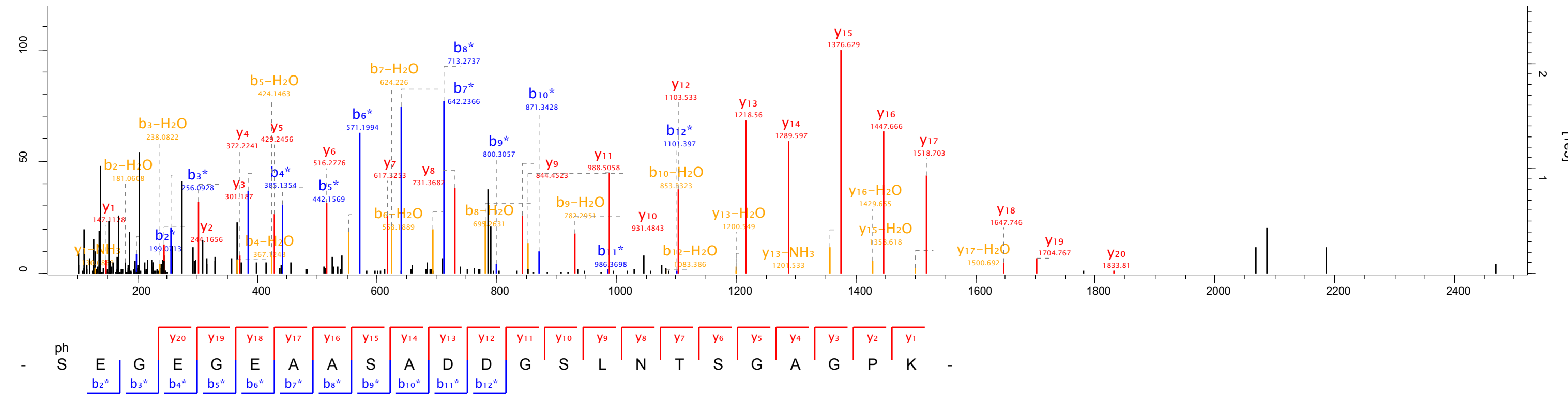
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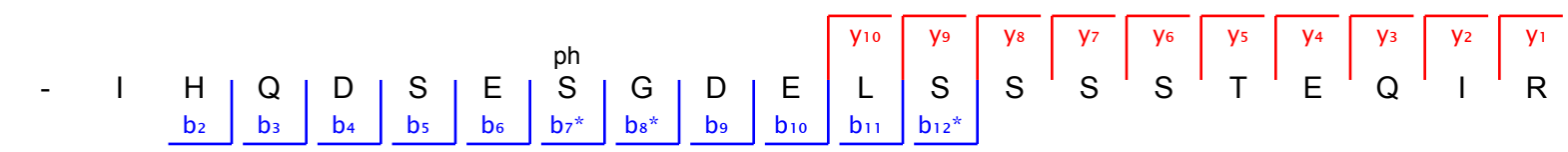
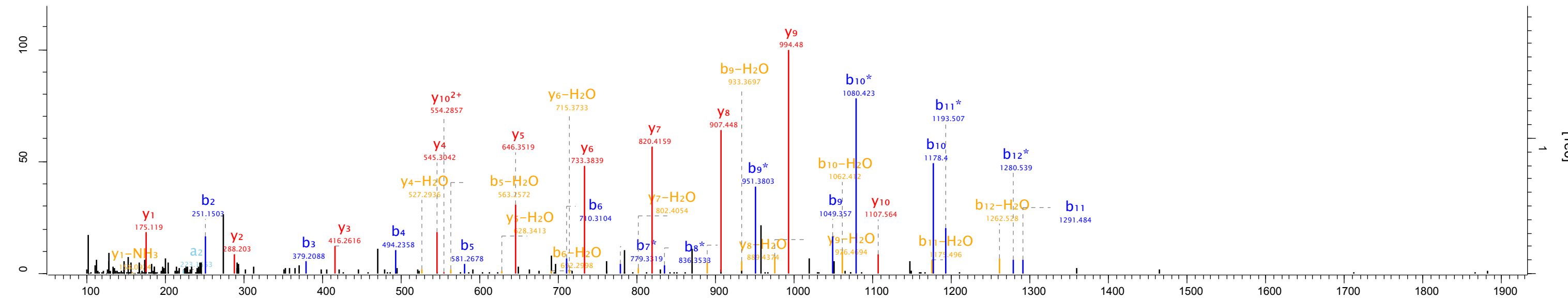
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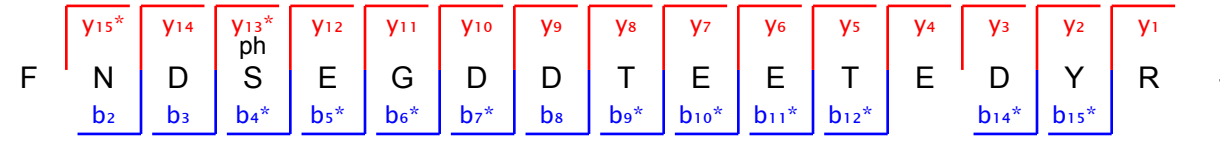
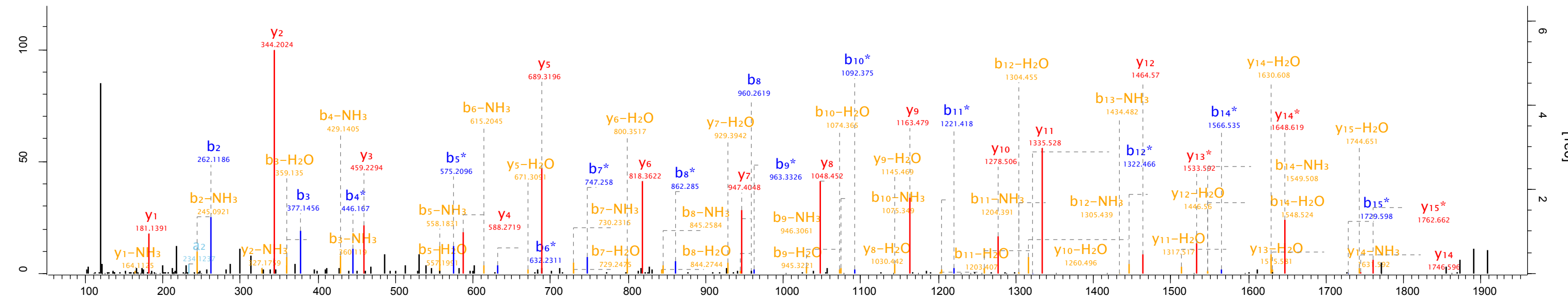
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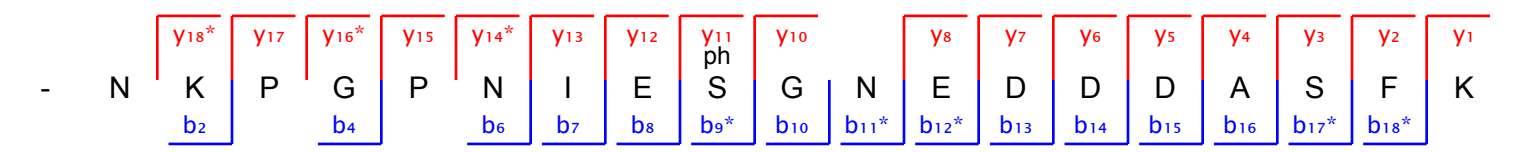
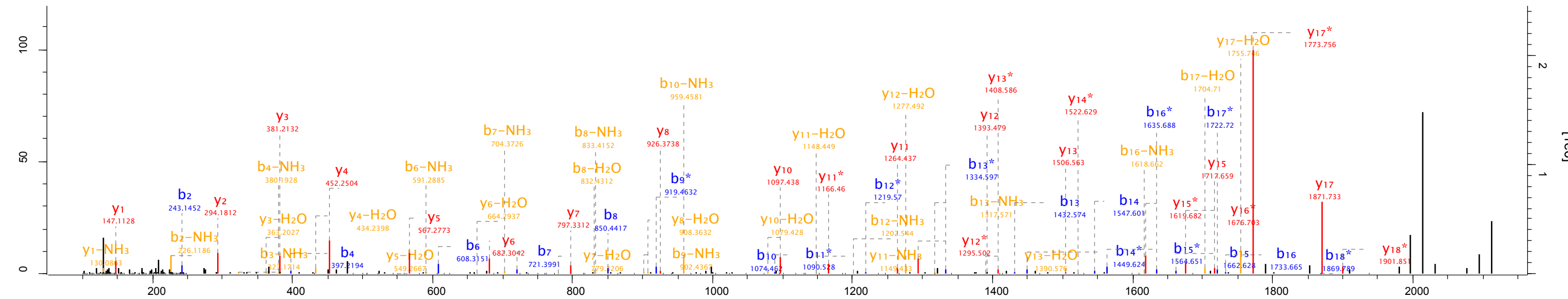
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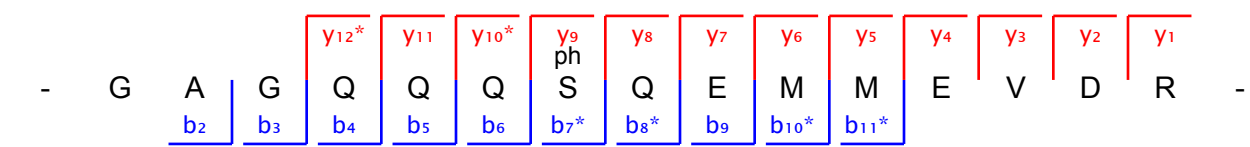
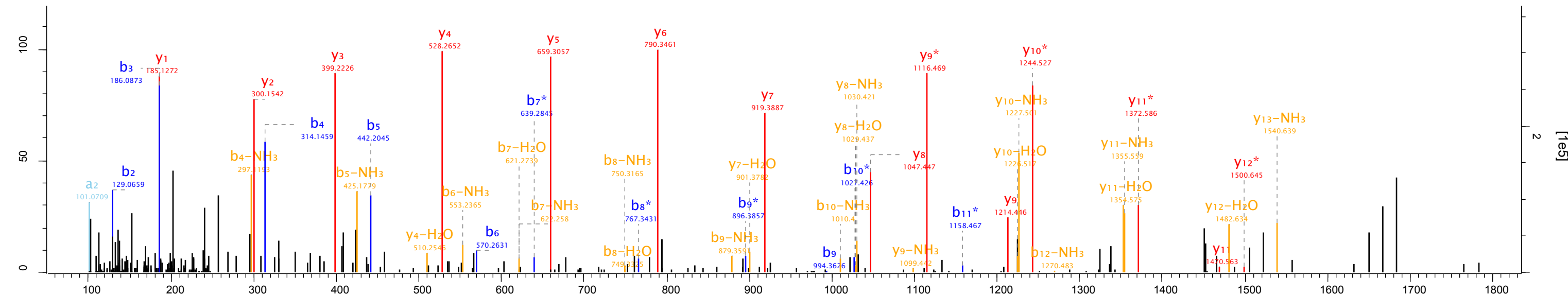
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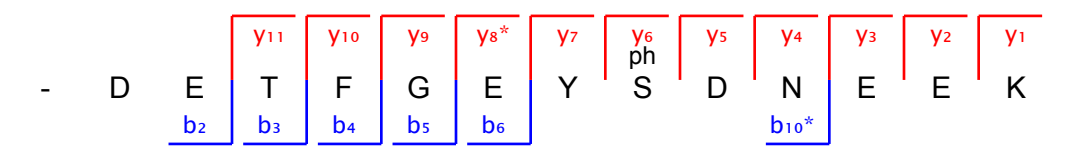
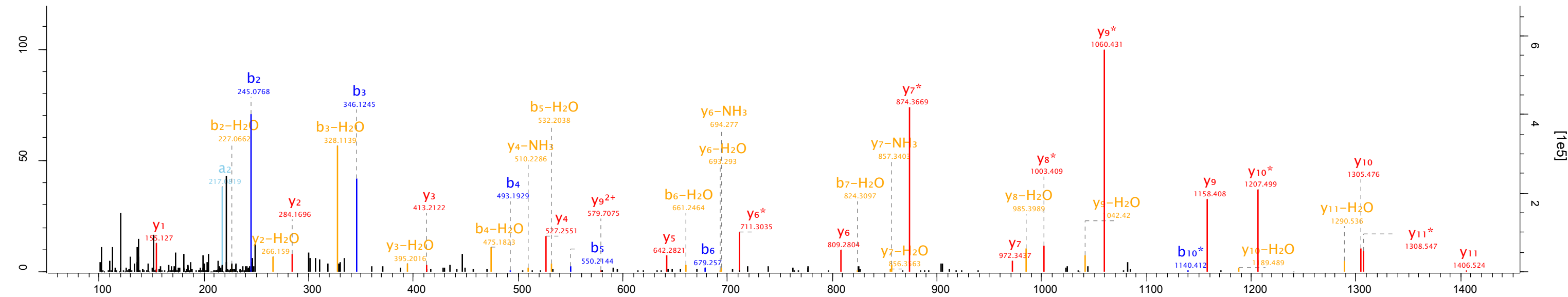
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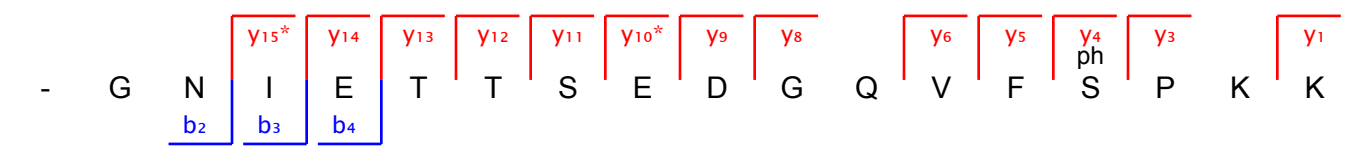
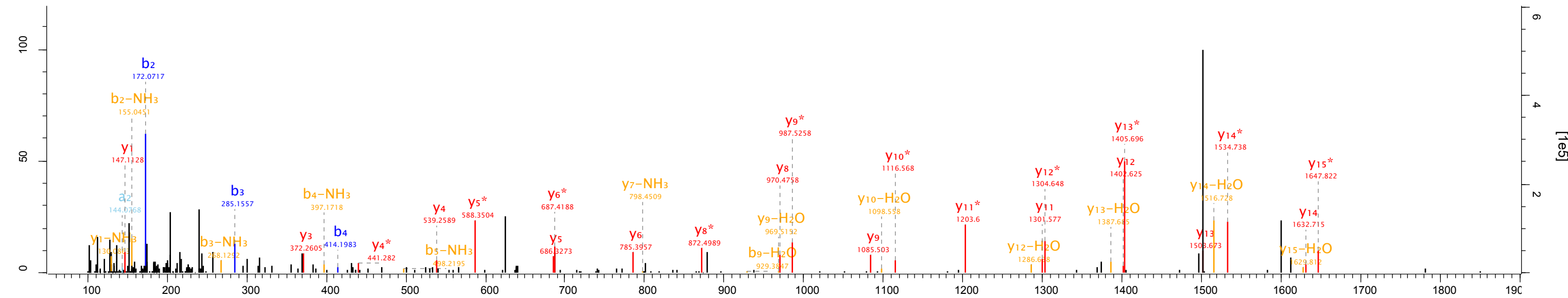
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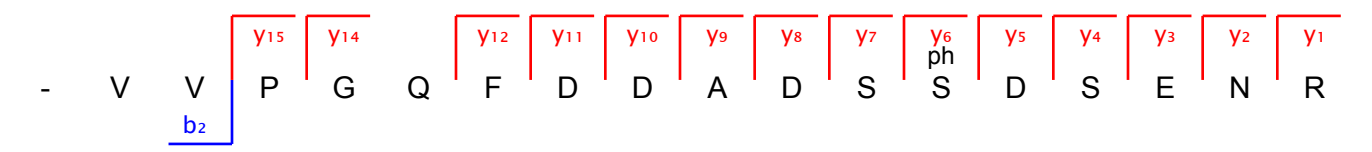
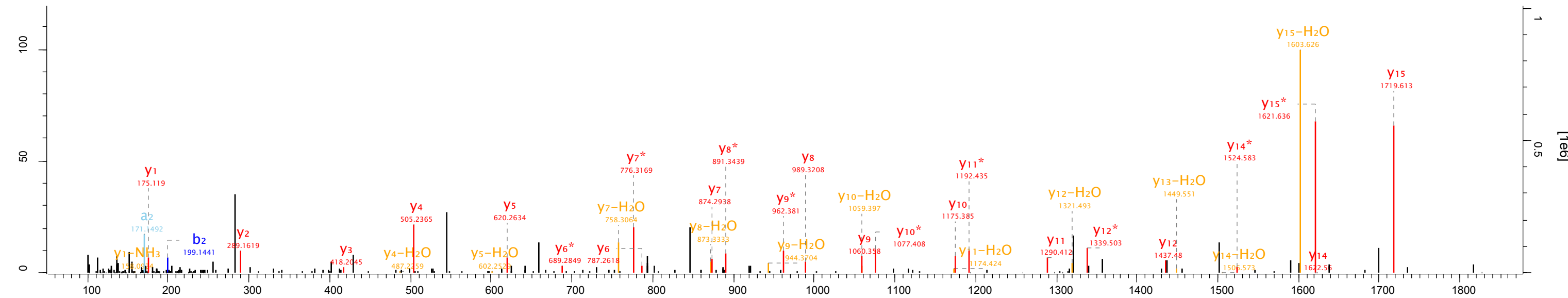
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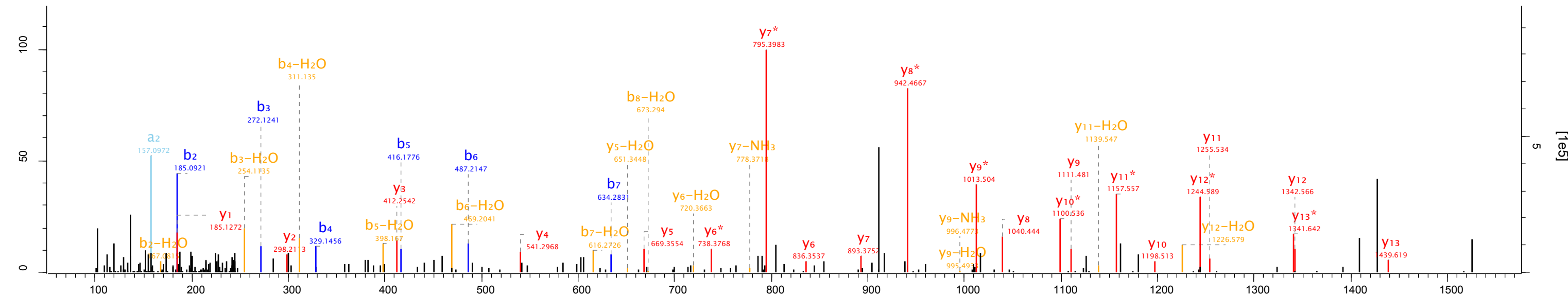


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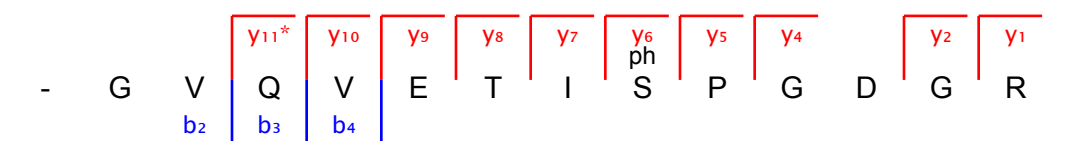
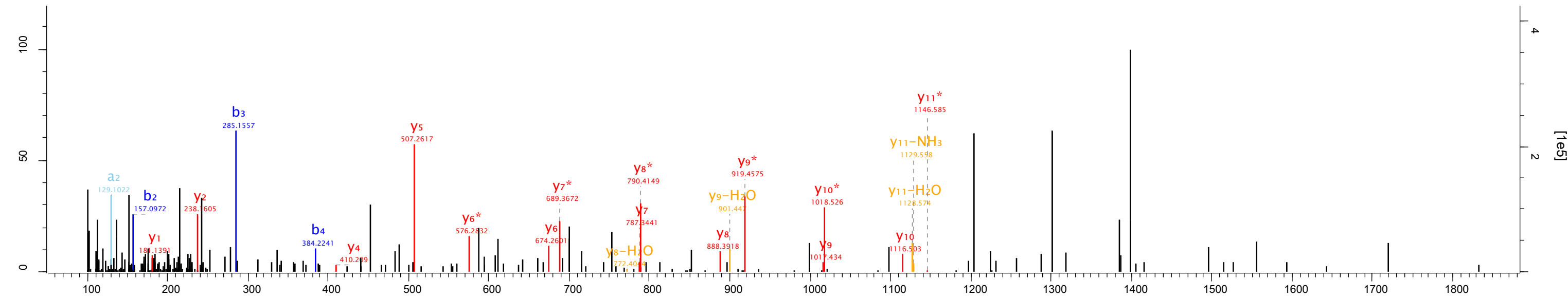
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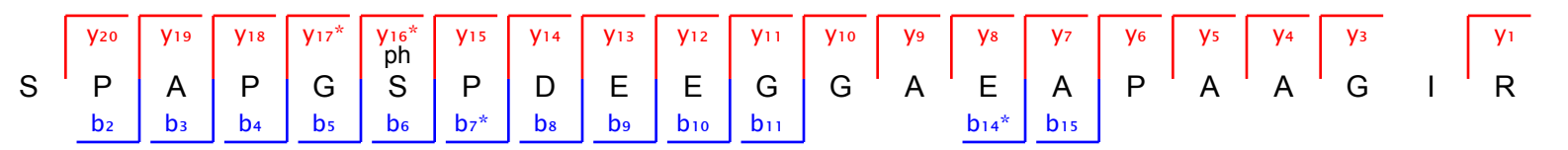
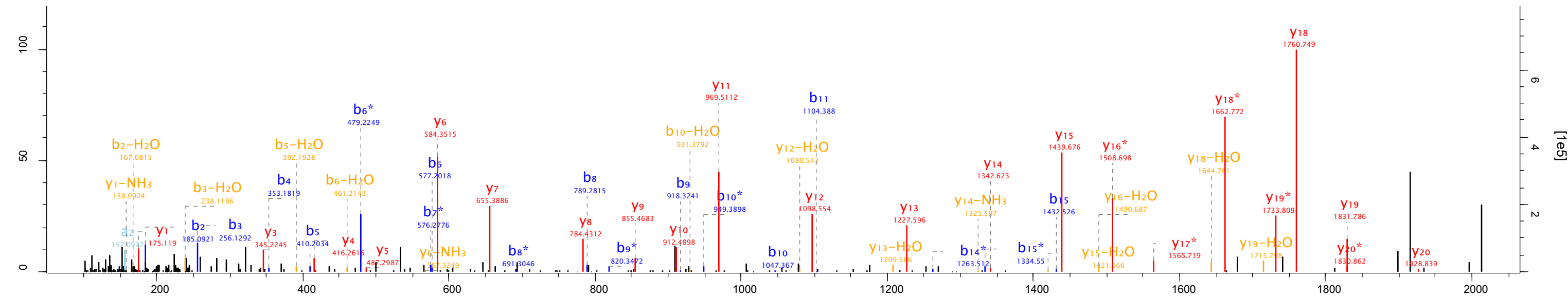


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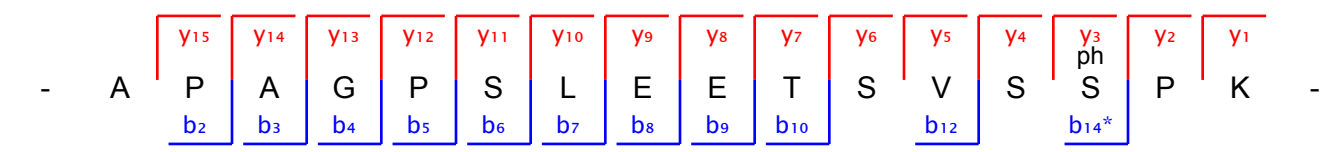
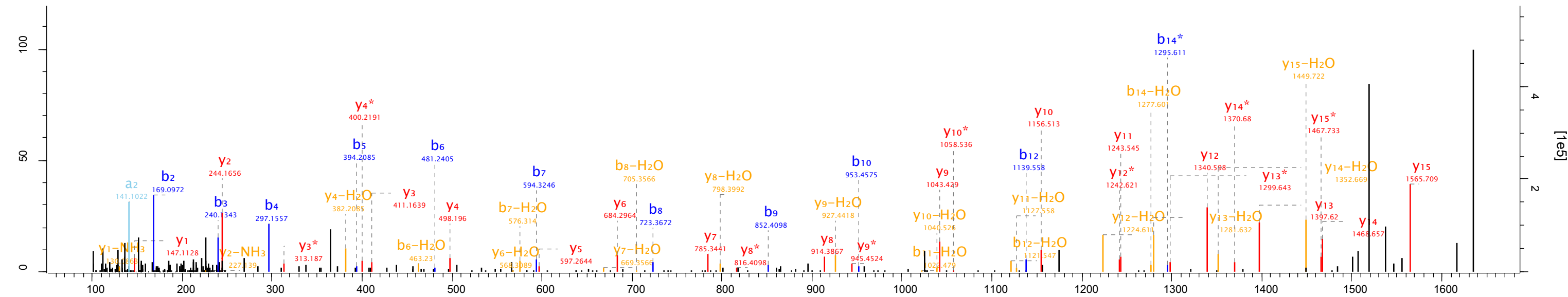
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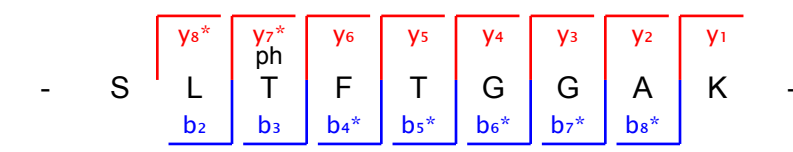
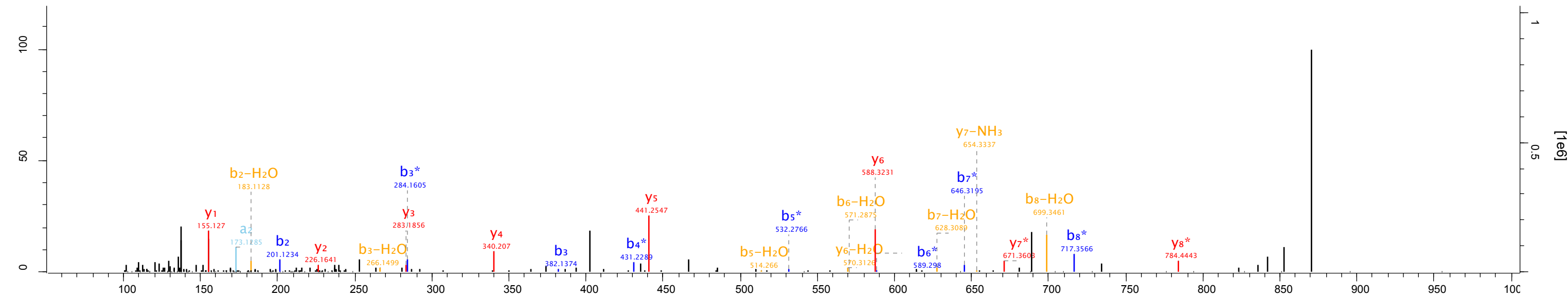
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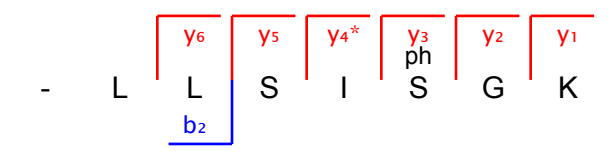
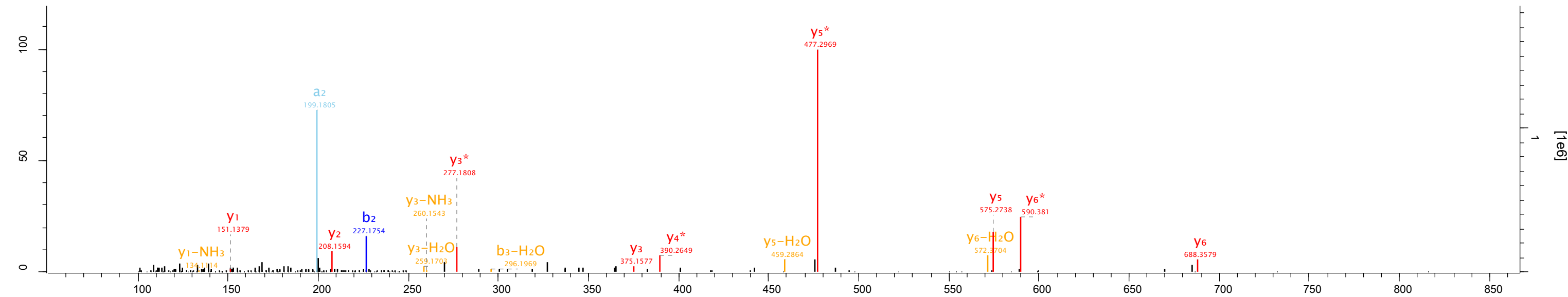
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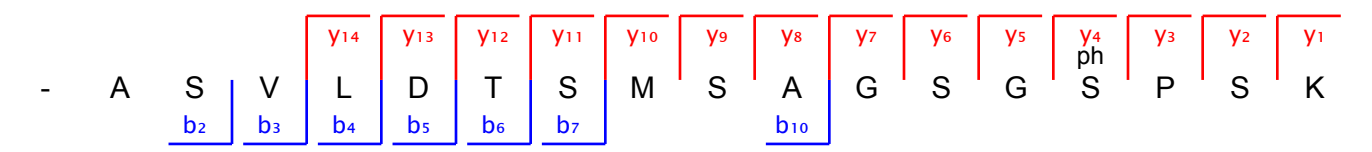
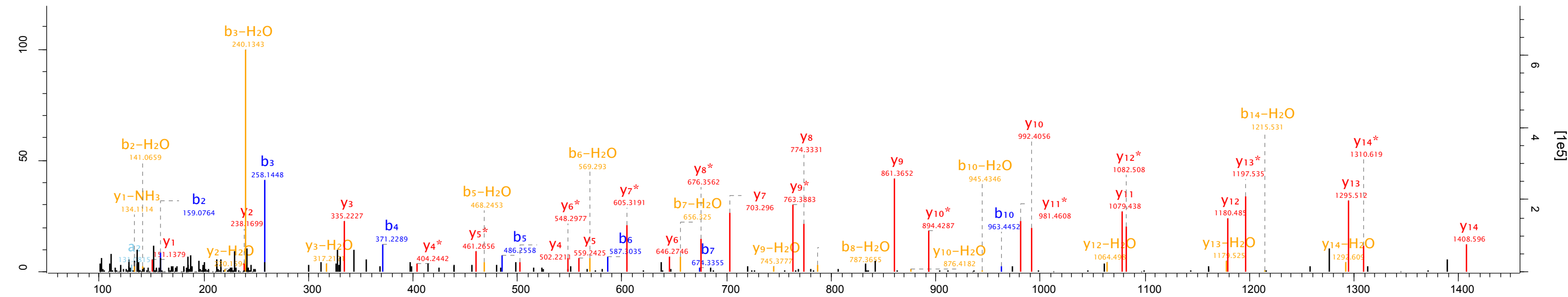
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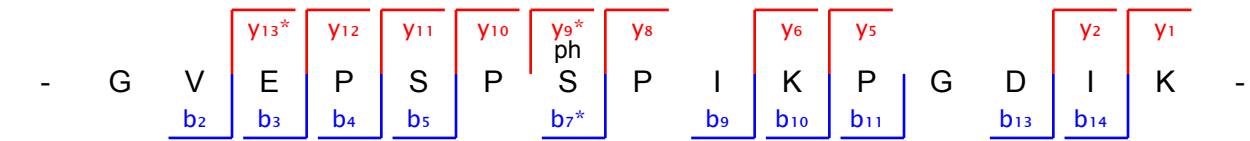
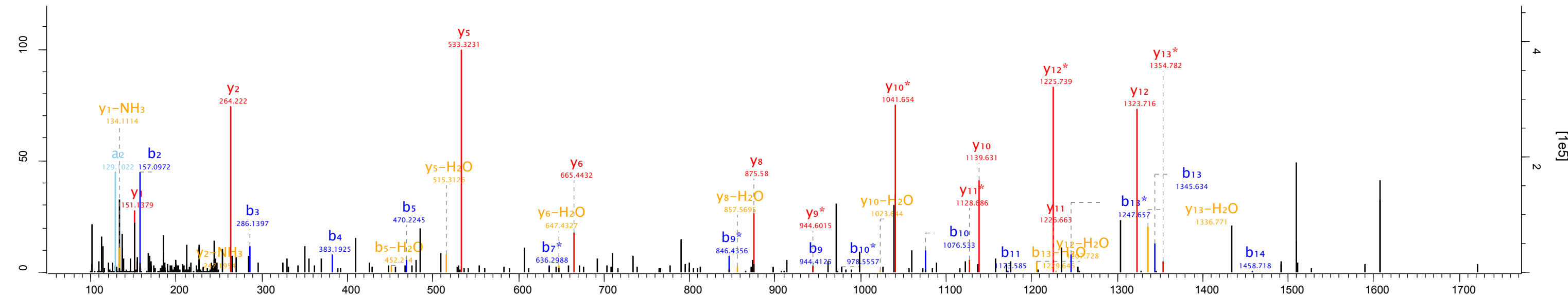
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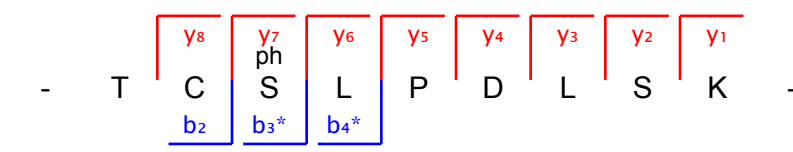
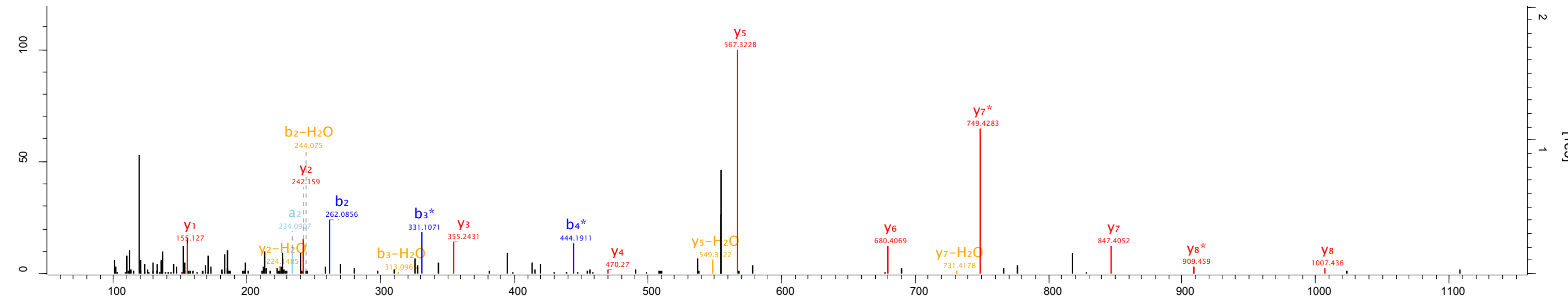
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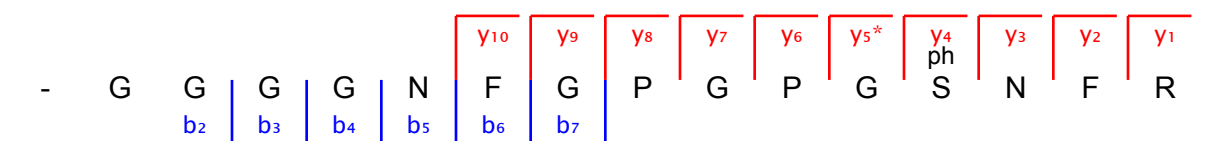
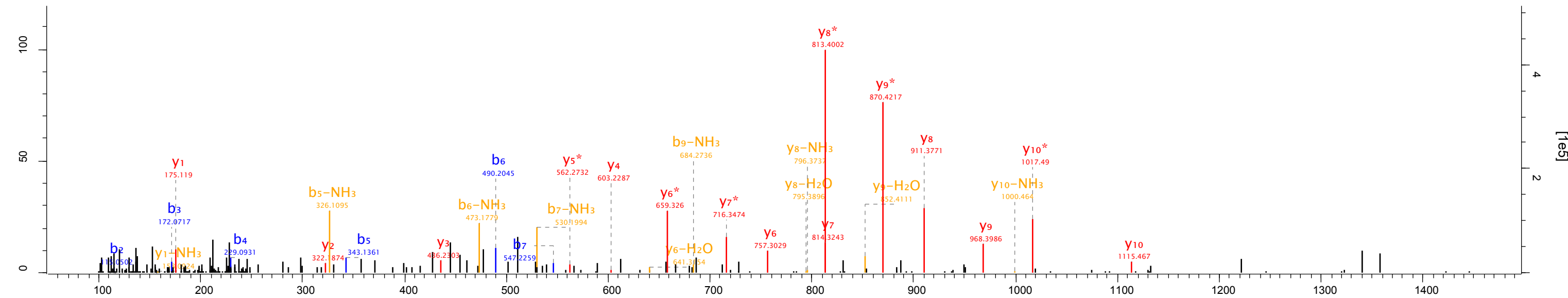
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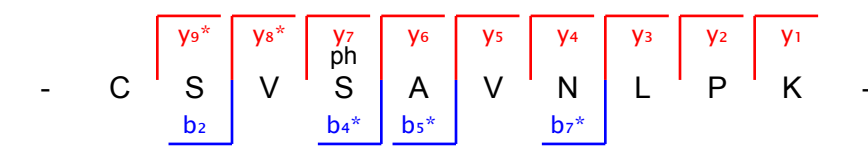
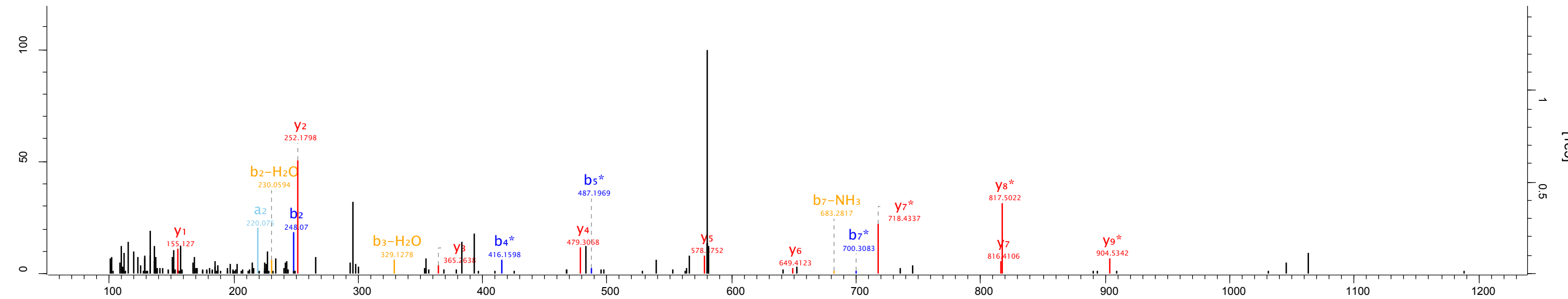
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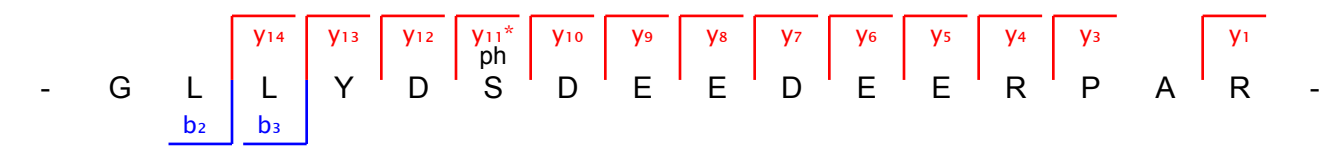
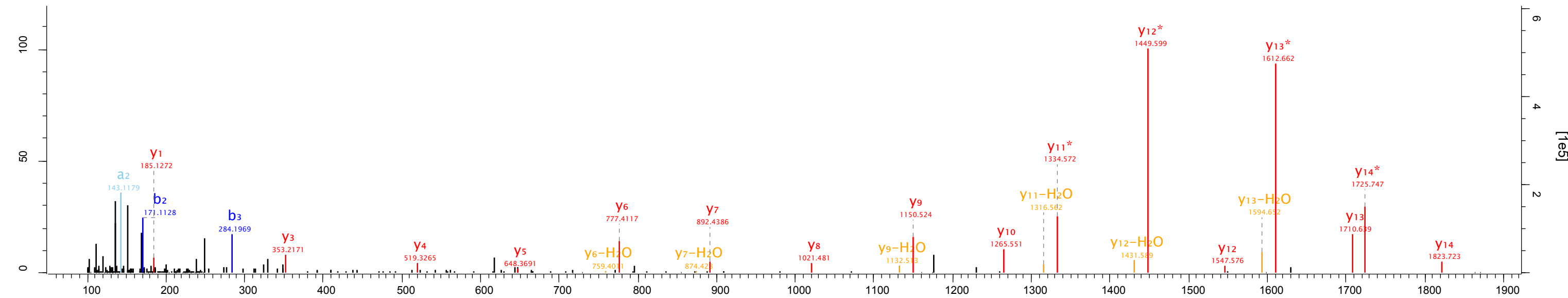
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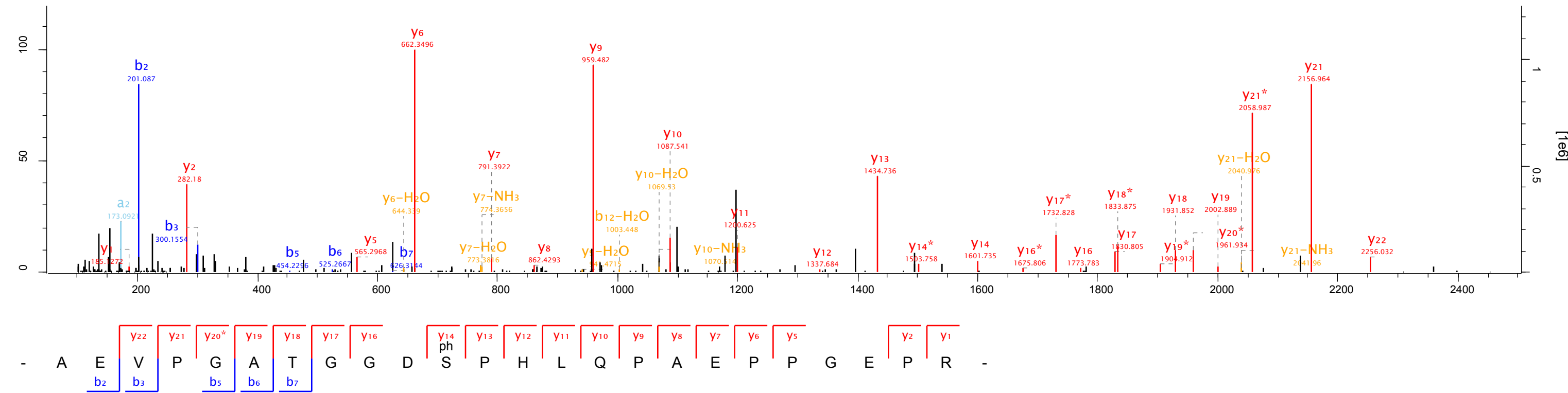
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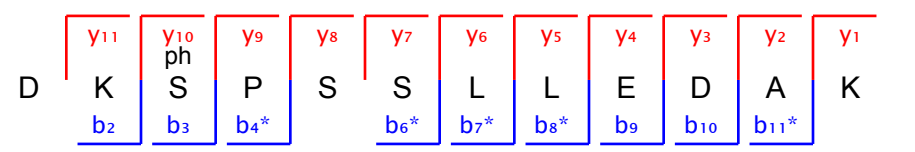
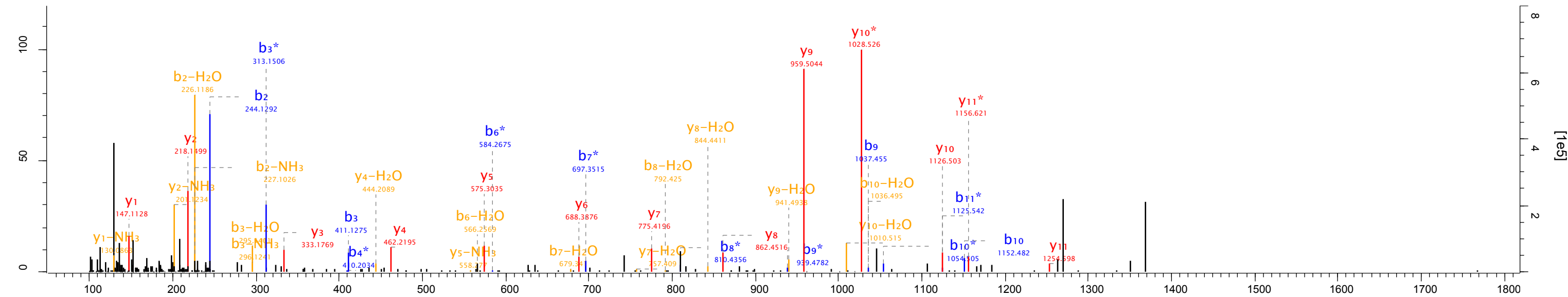
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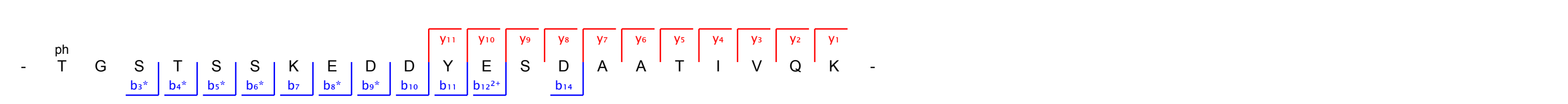
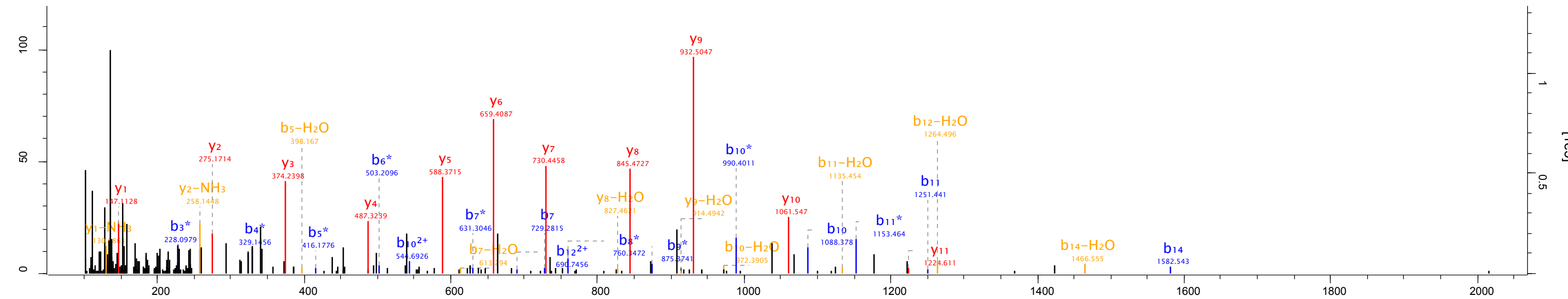
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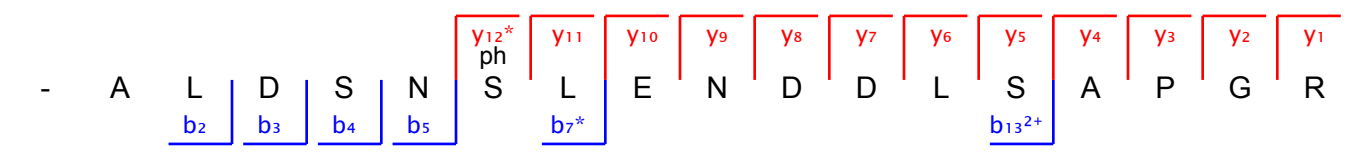
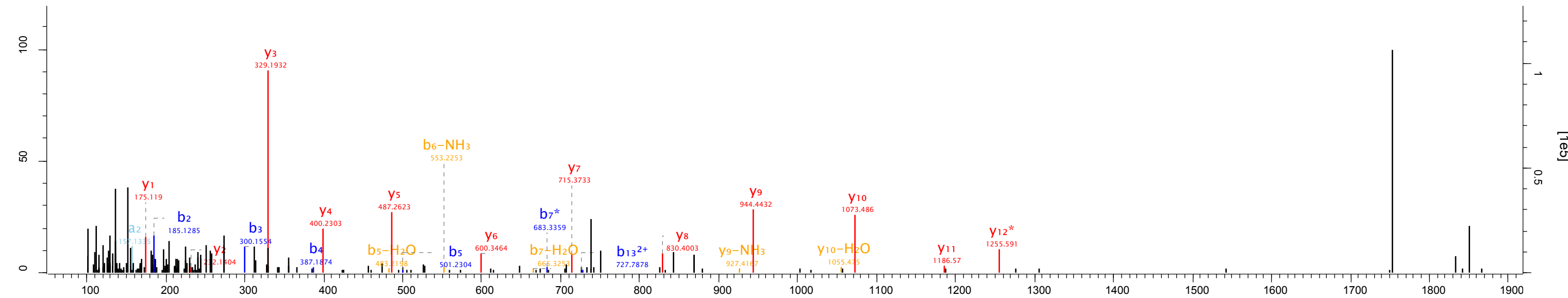
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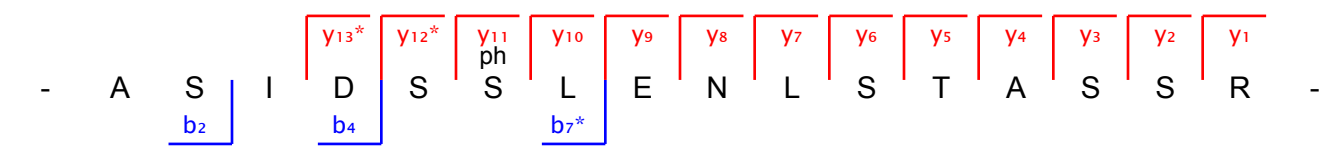
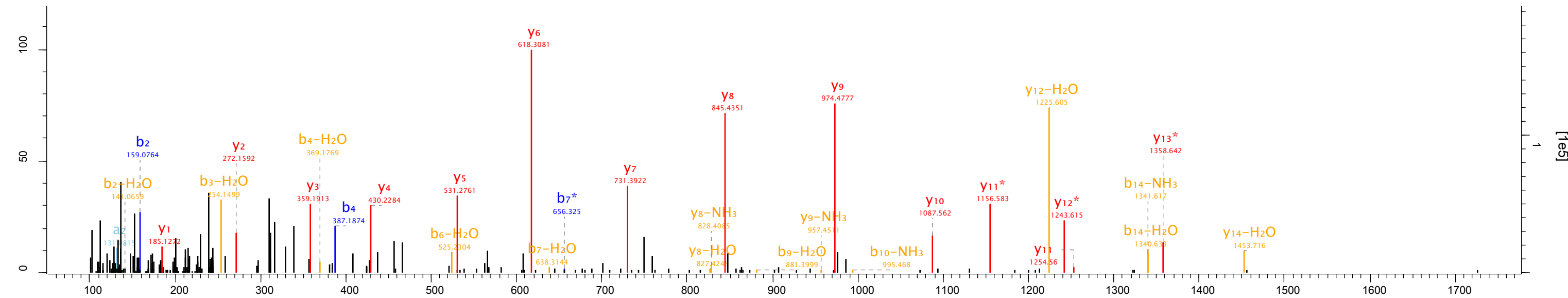
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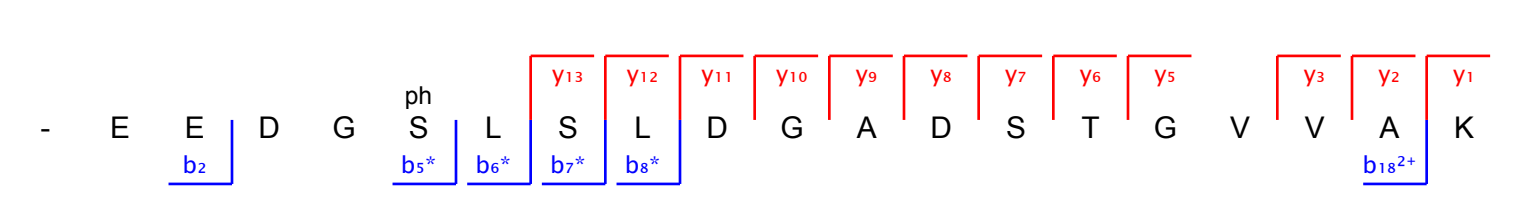
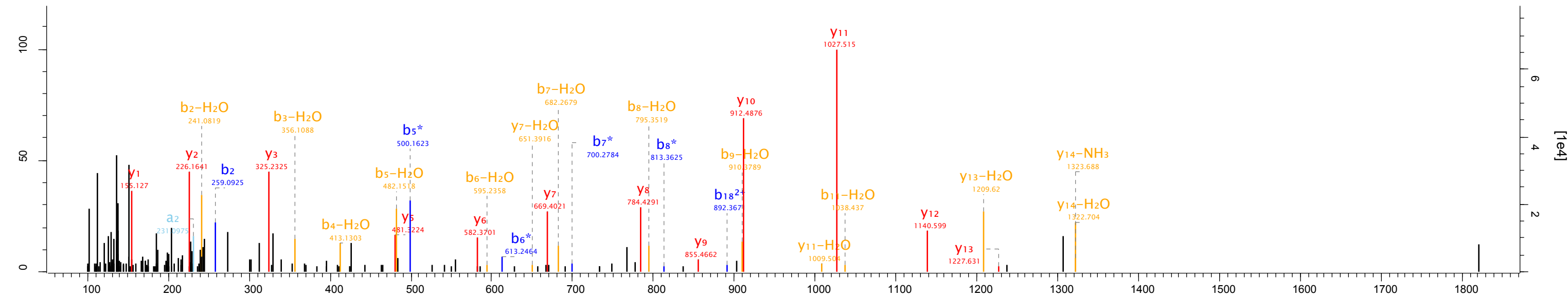
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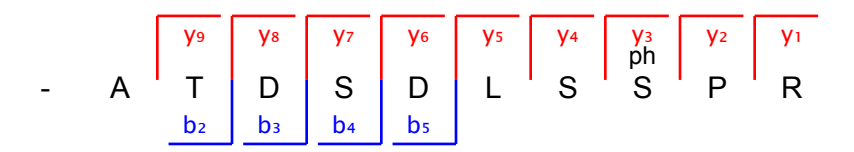
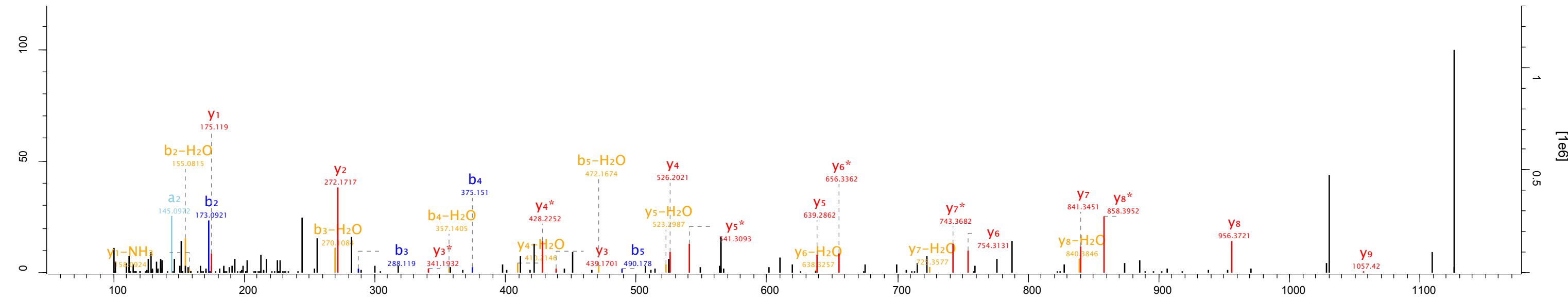
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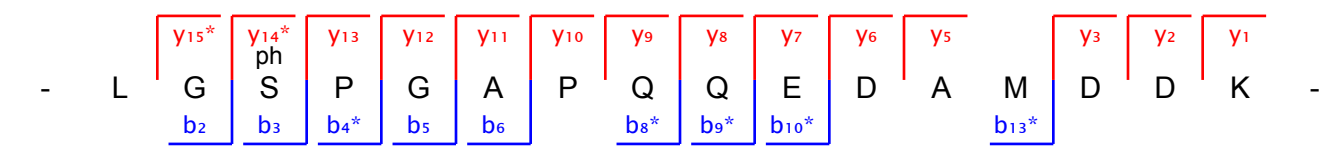
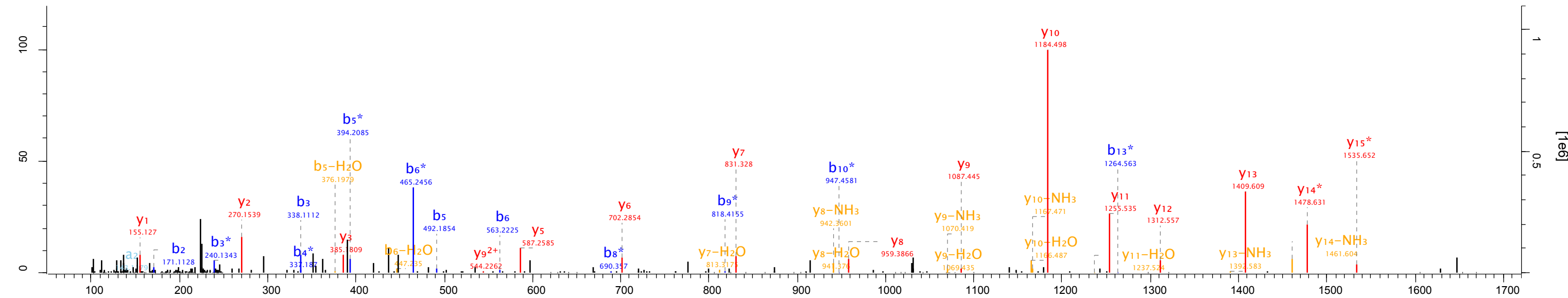
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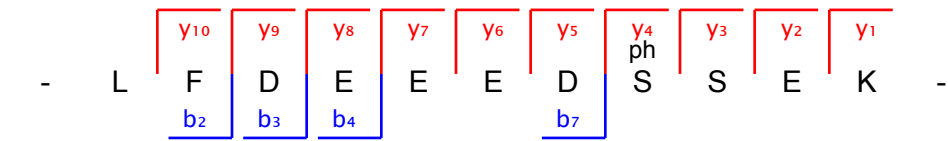
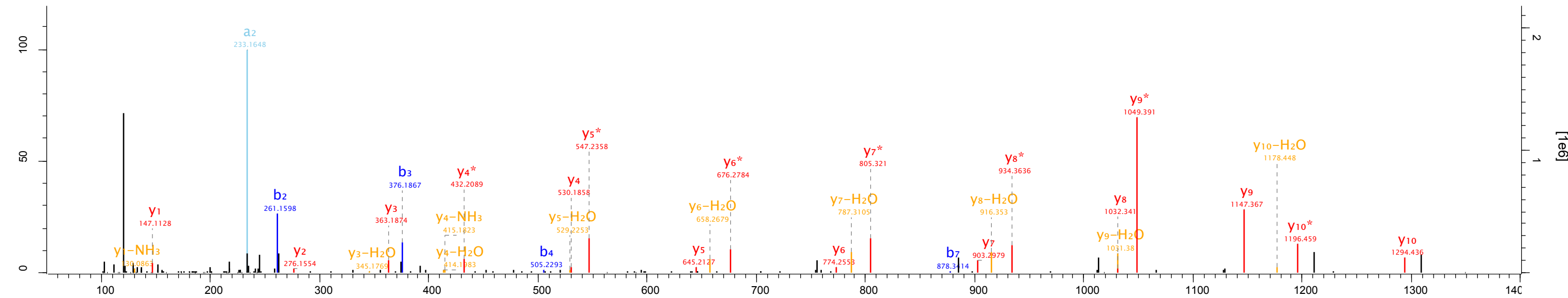


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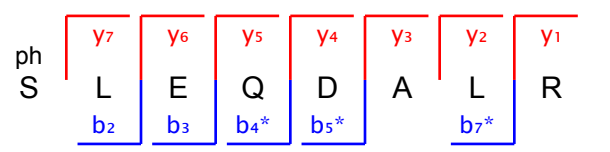
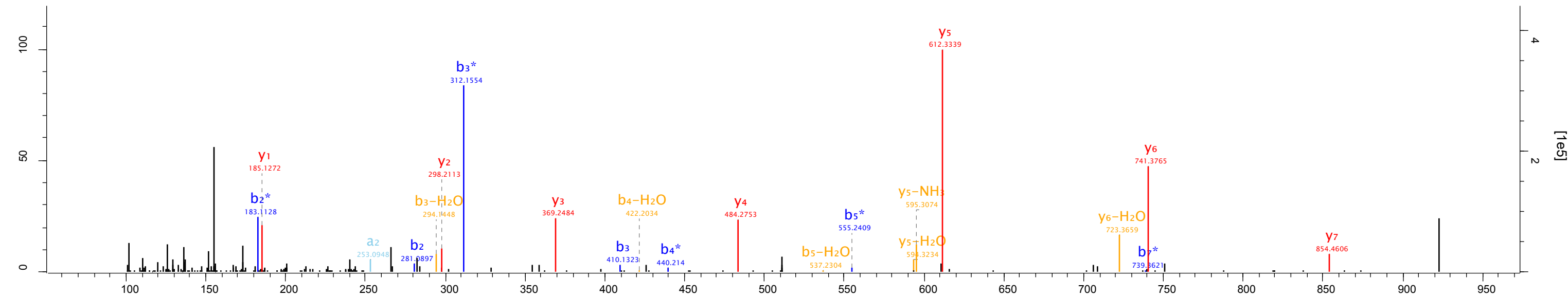


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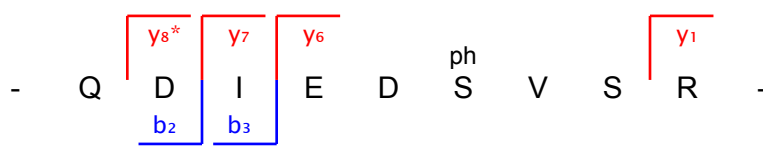
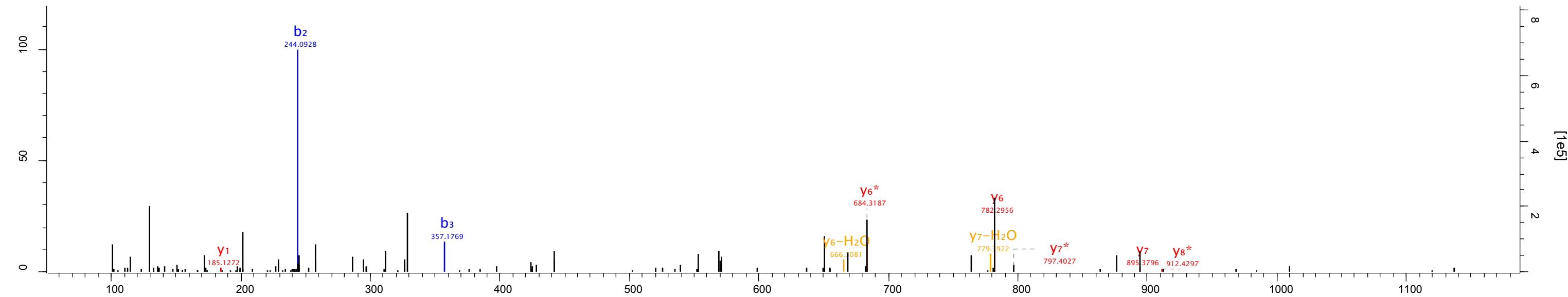
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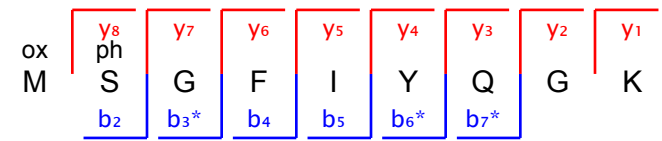
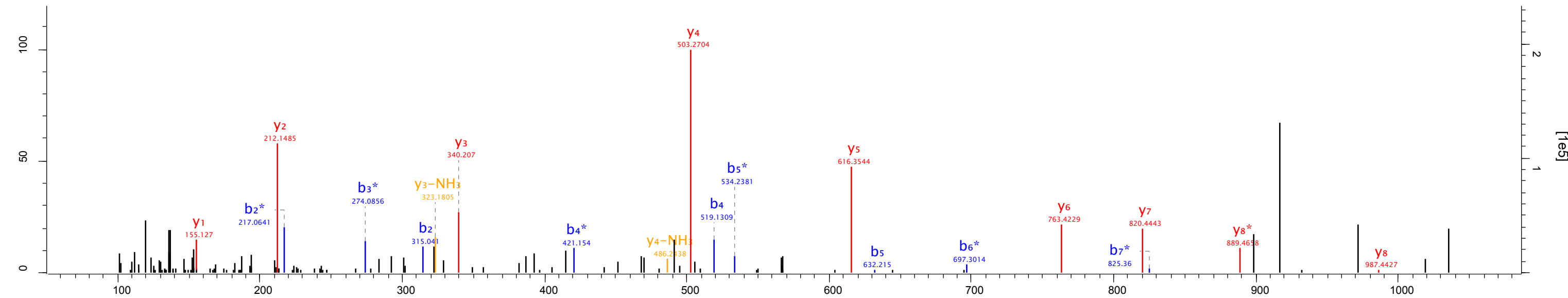
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20171215_MaS_33SR_LMH_phospho_05

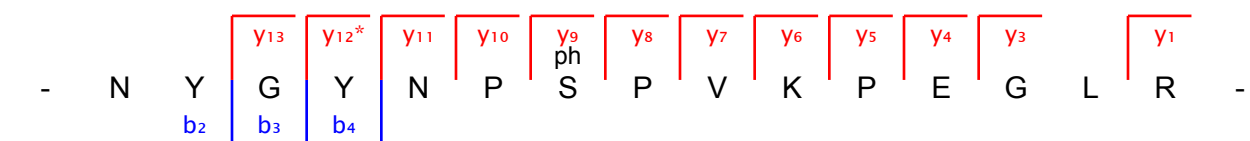
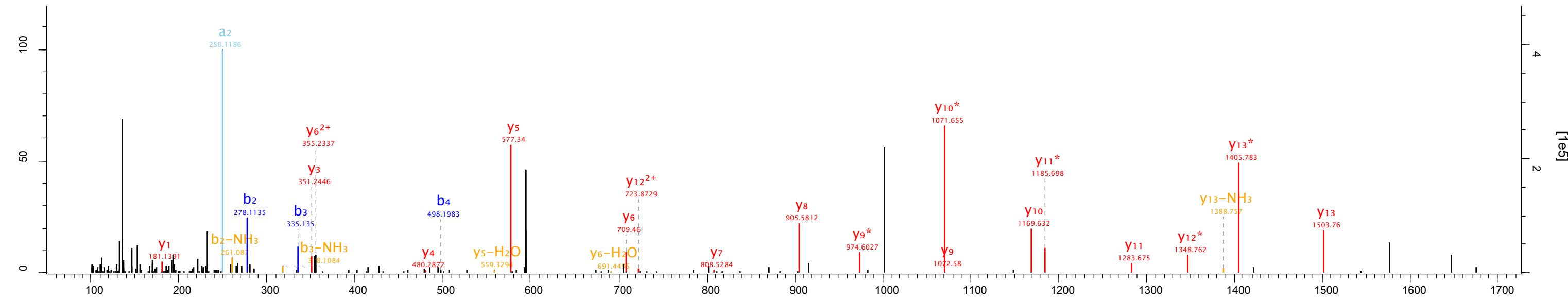
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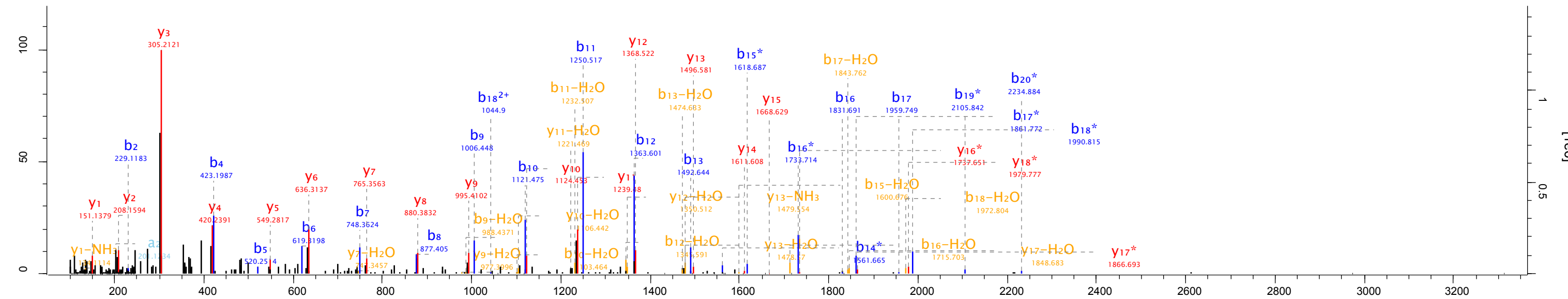
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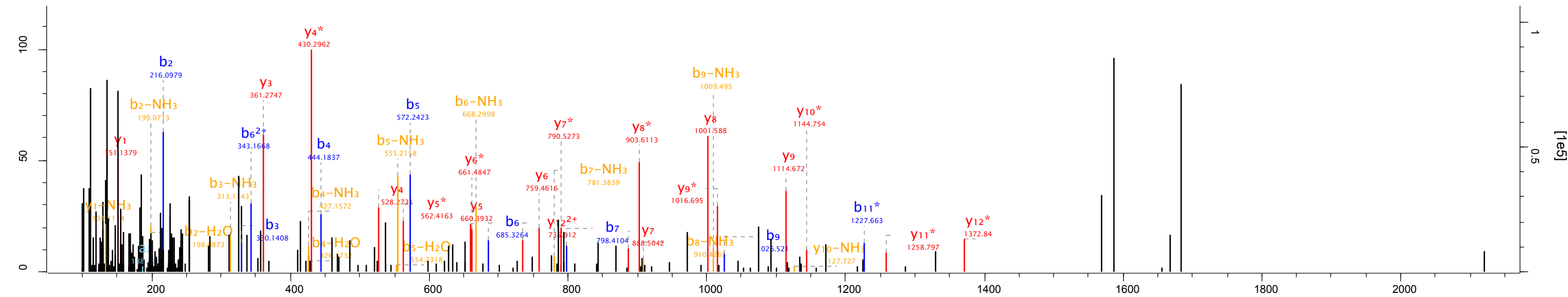
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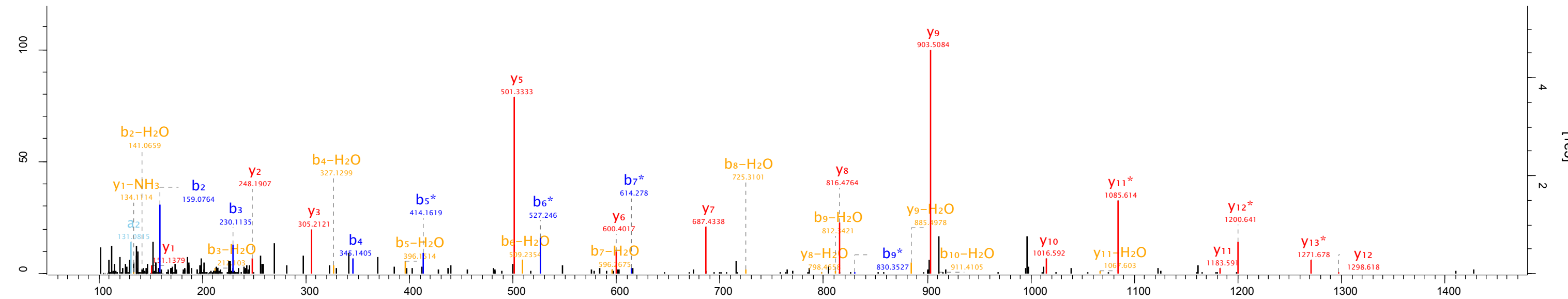
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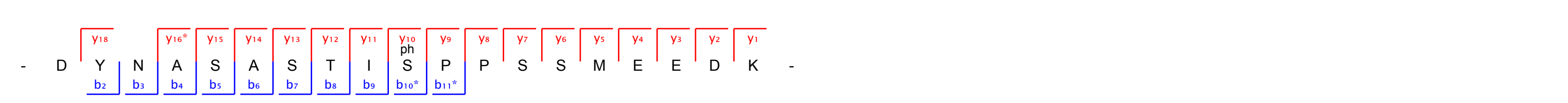
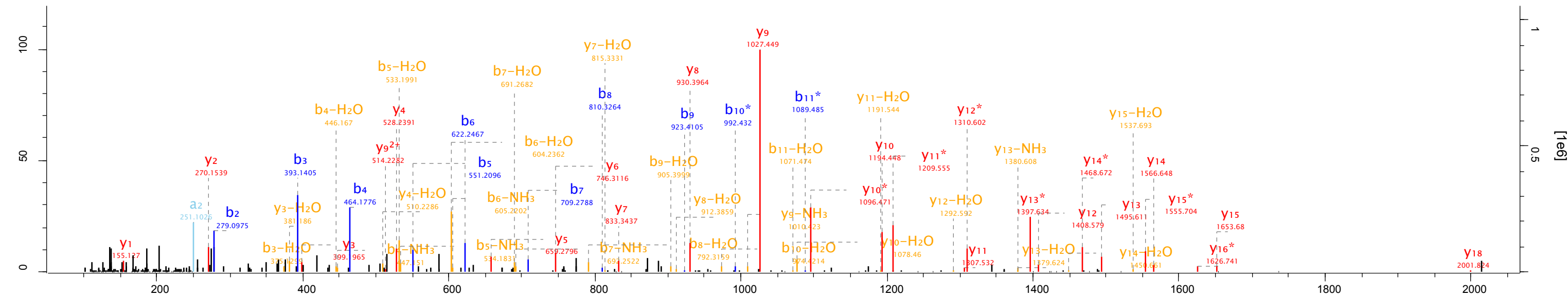
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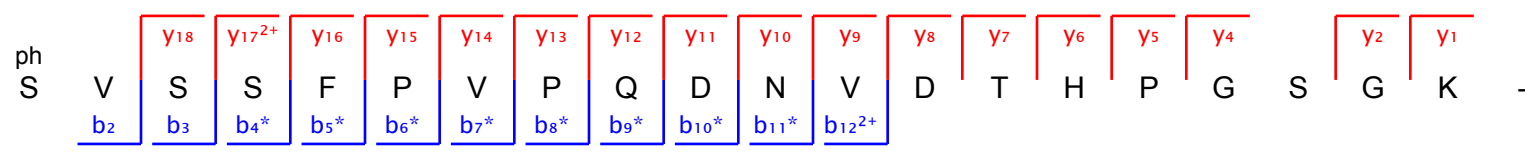
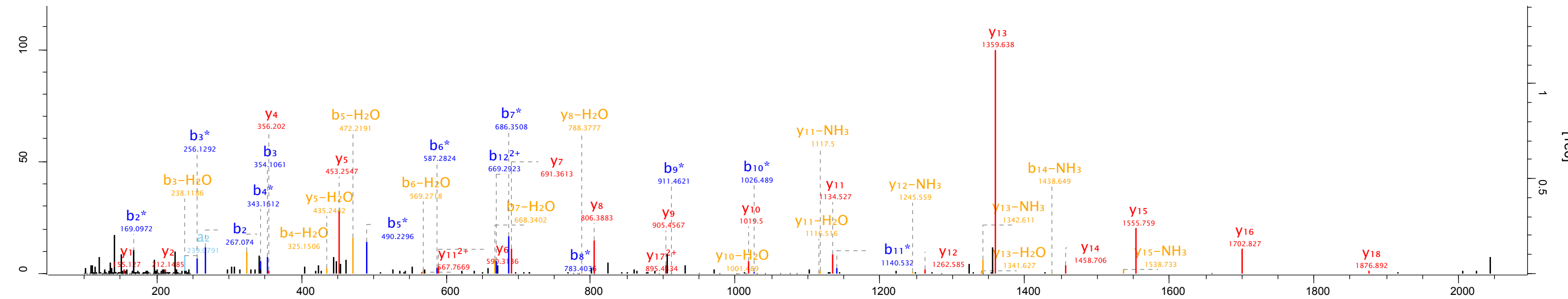
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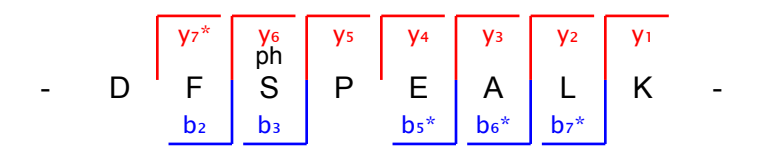
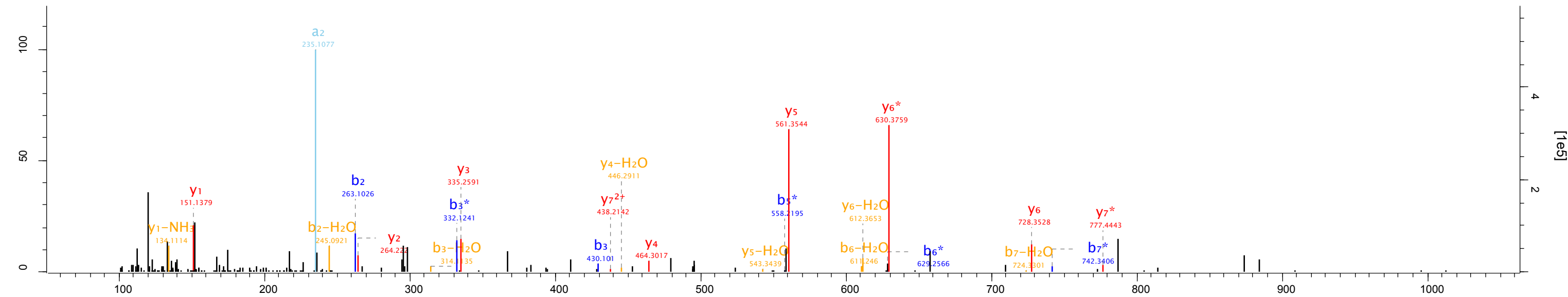
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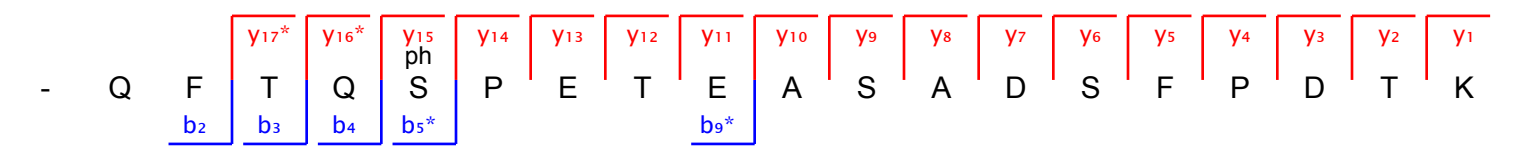
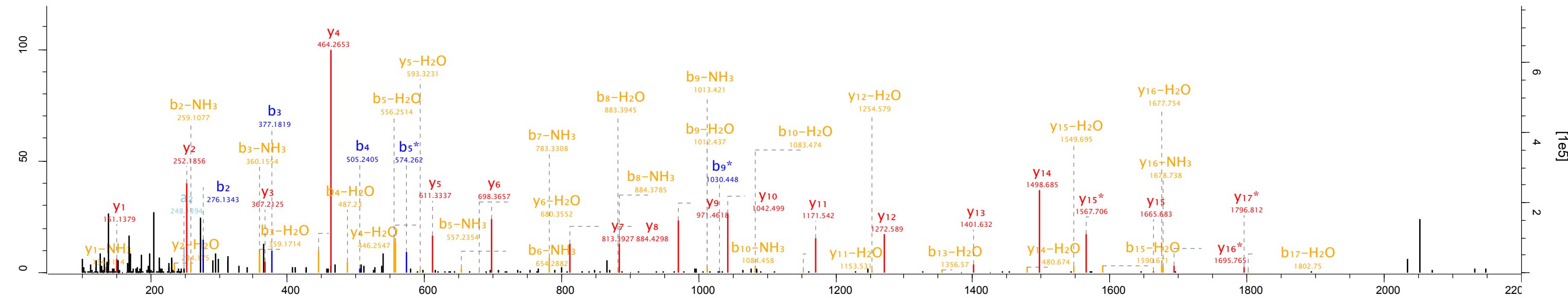
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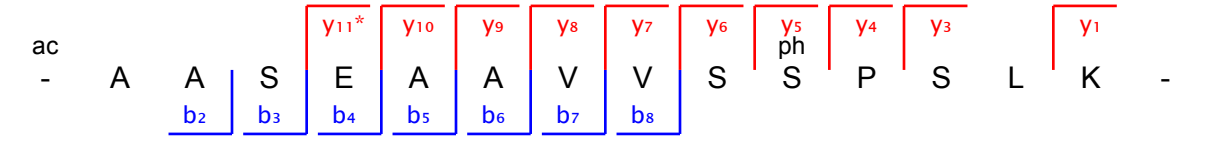
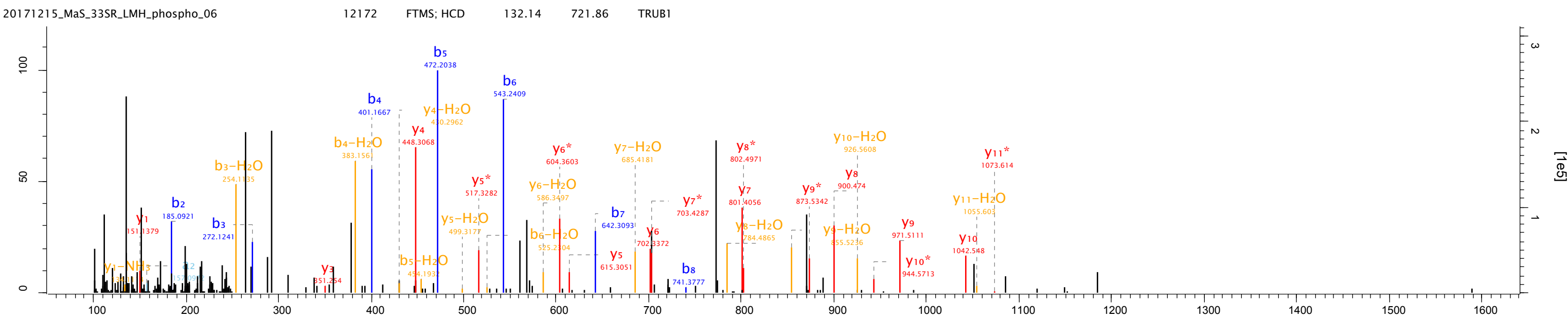
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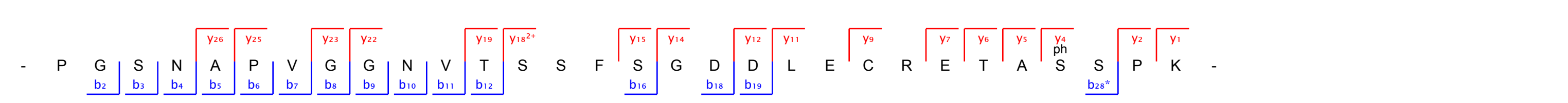
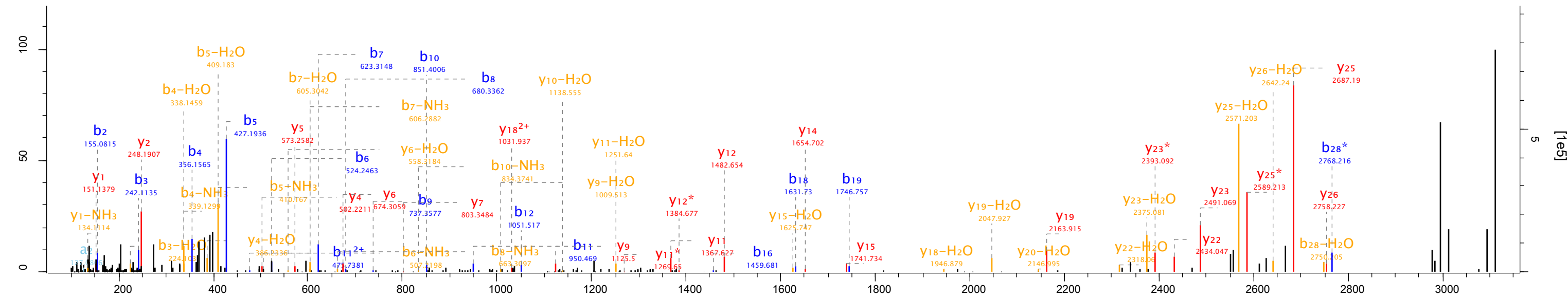
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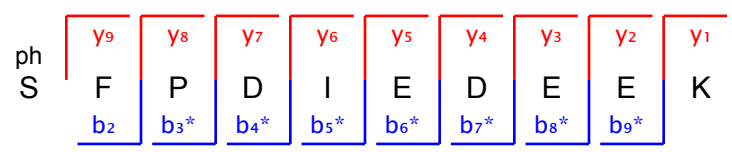
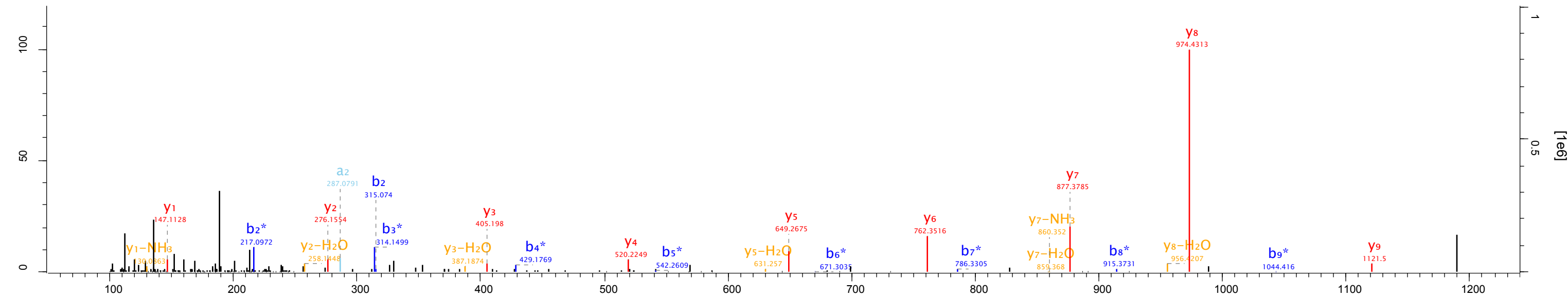
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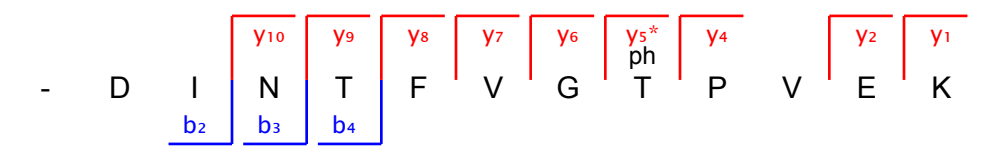
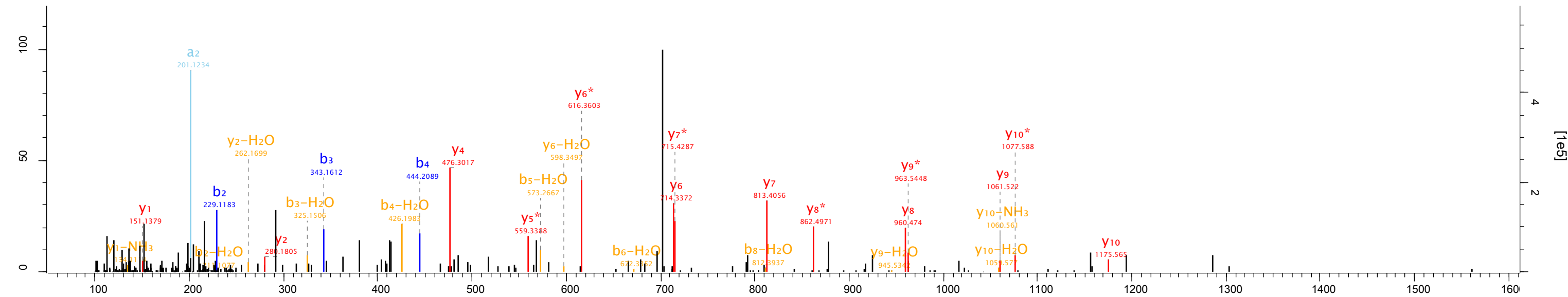
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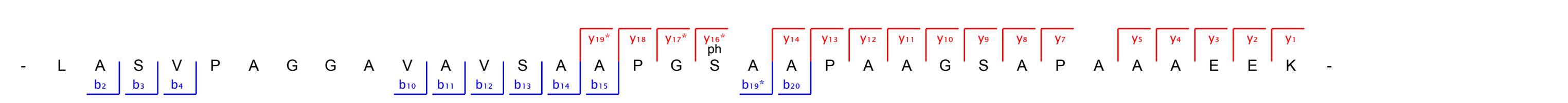
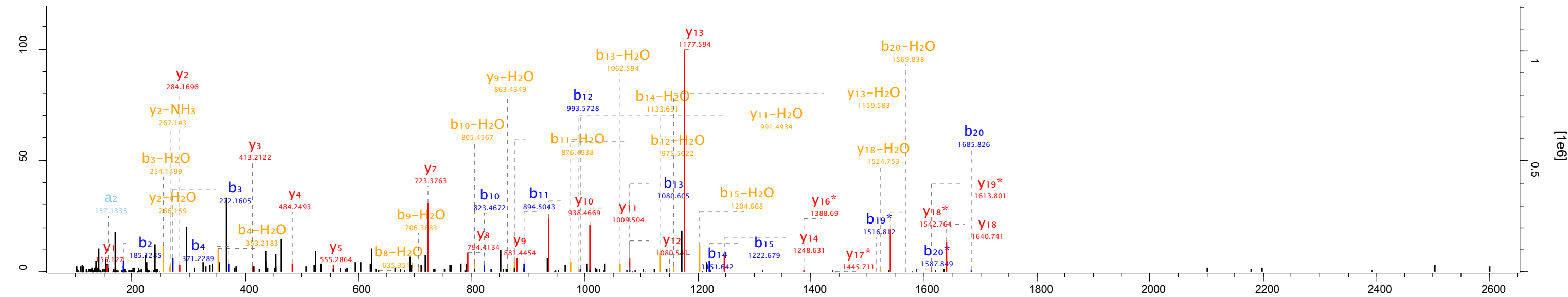
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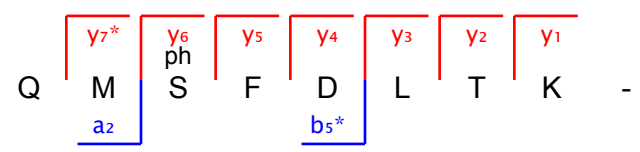
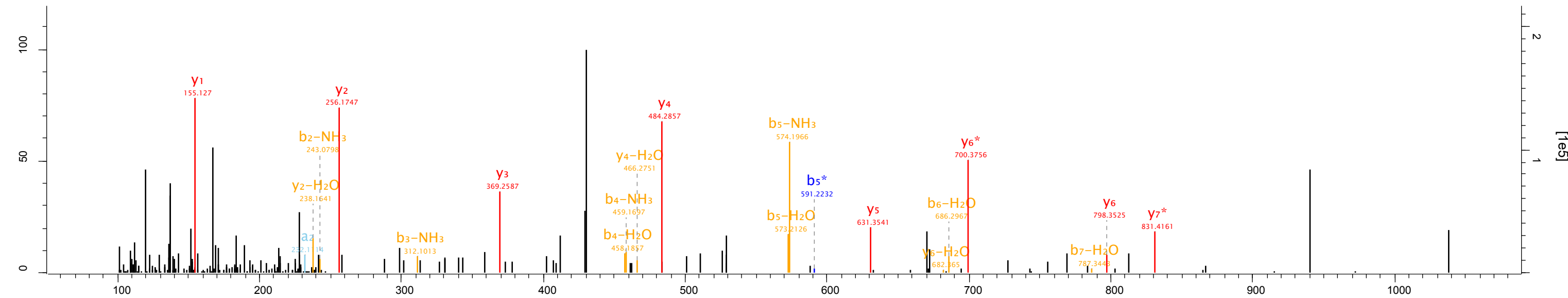
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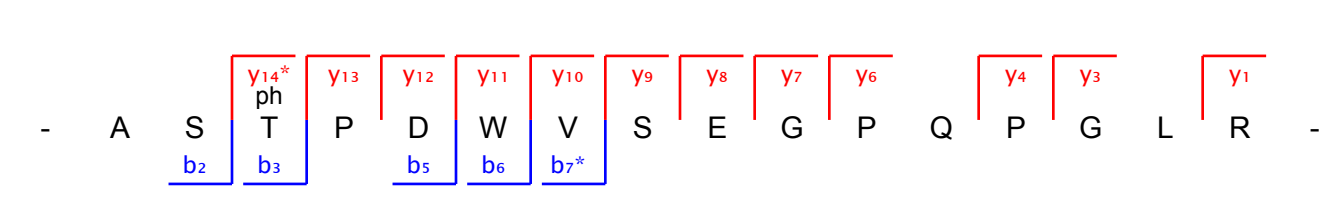
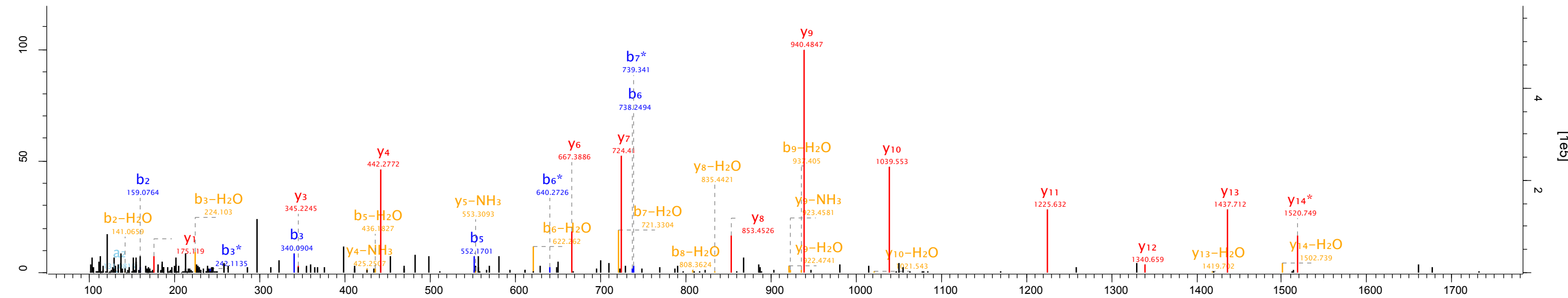
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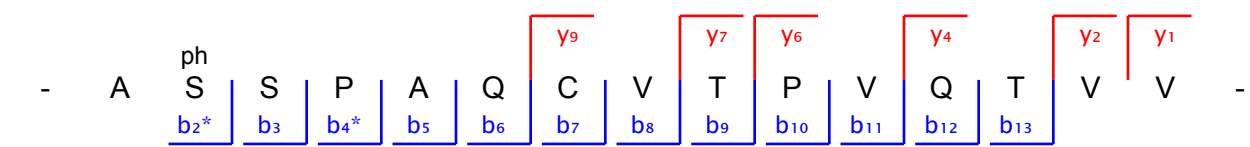
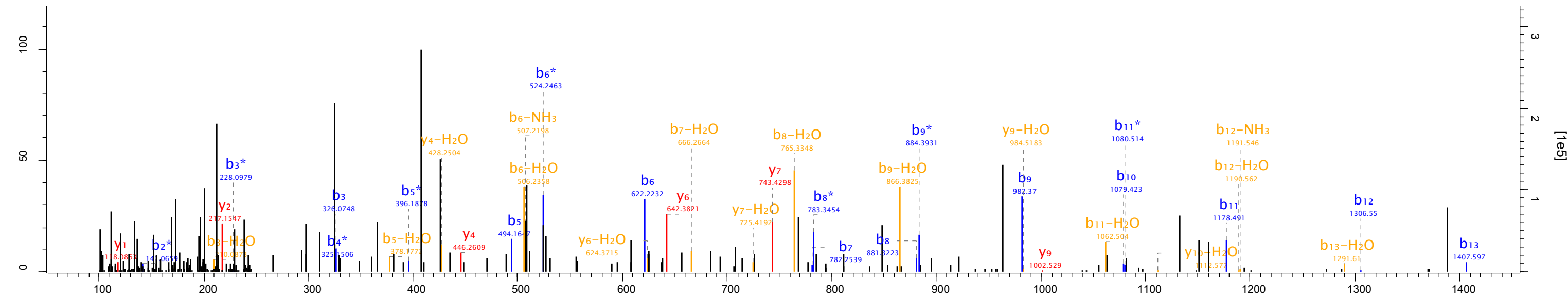


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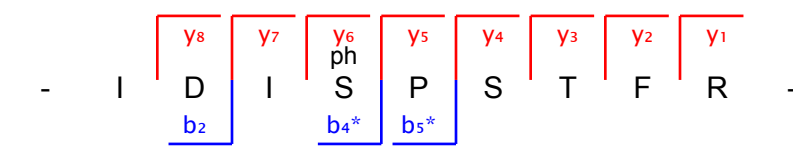
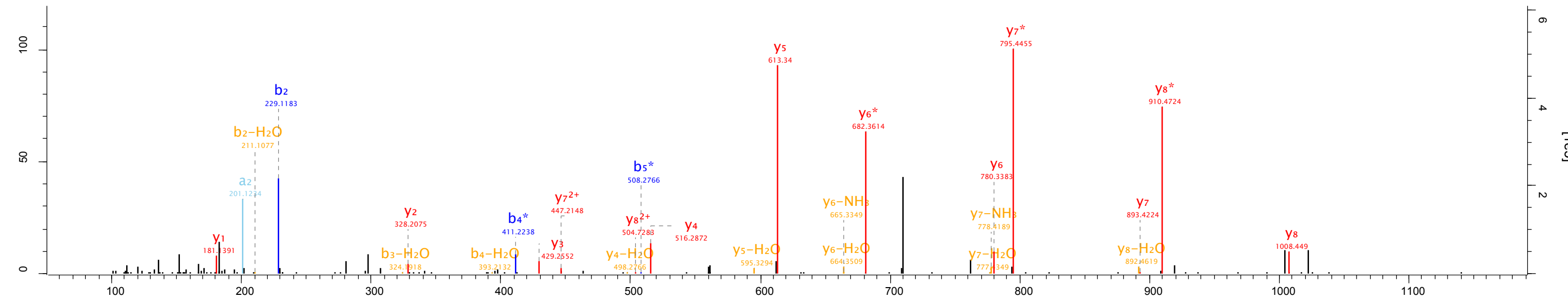


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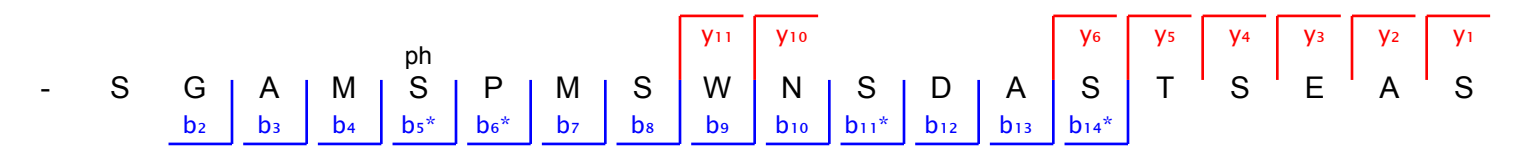
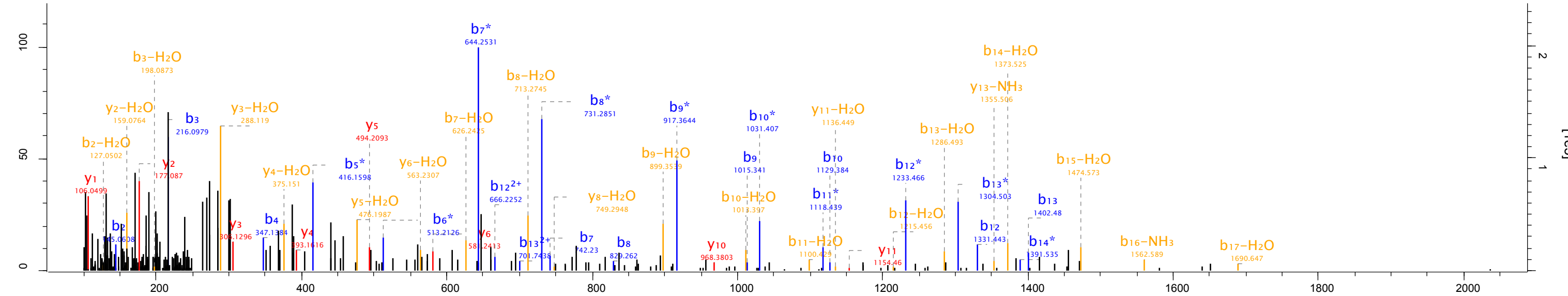




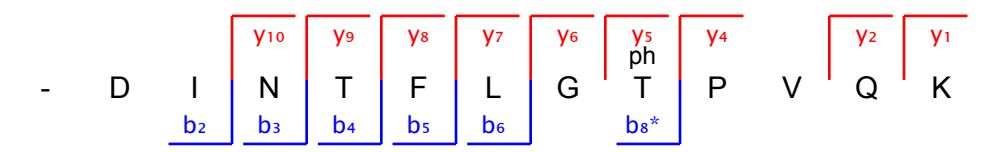
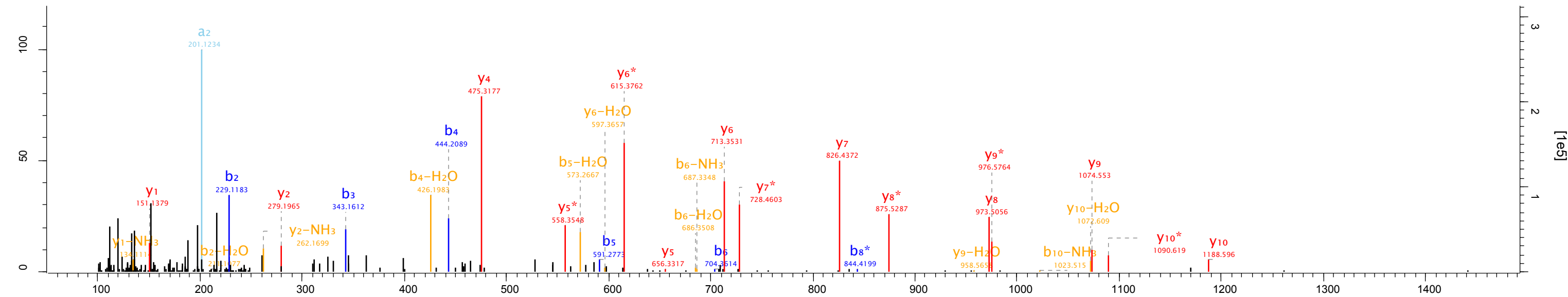
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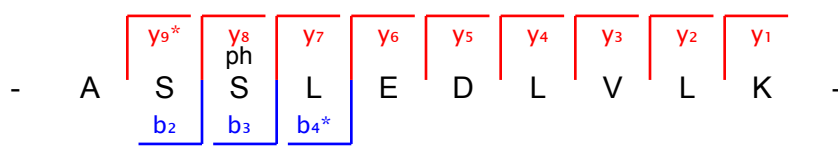
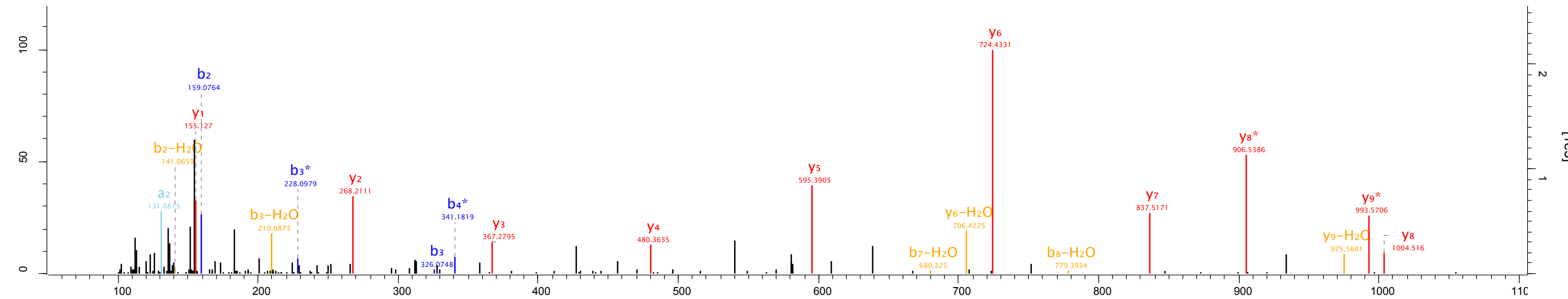
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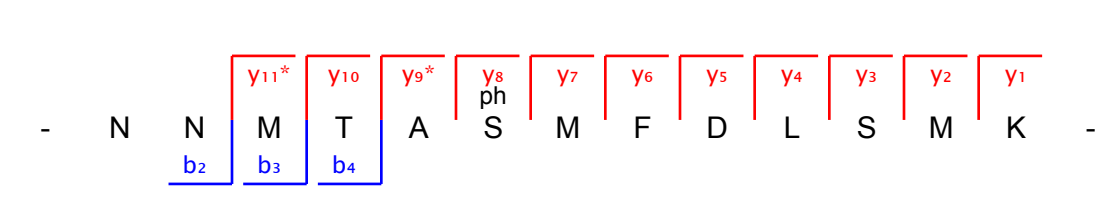
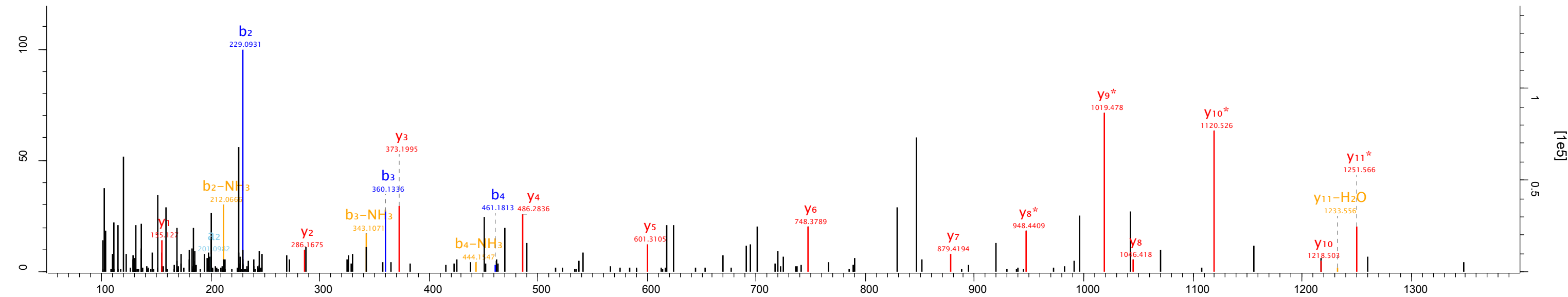
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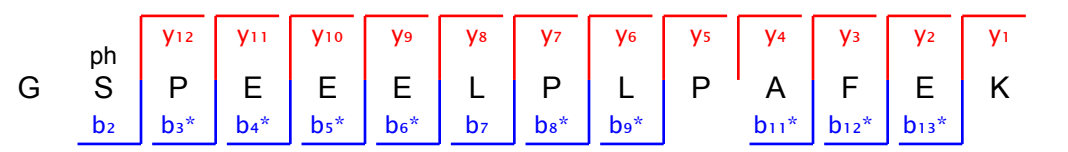
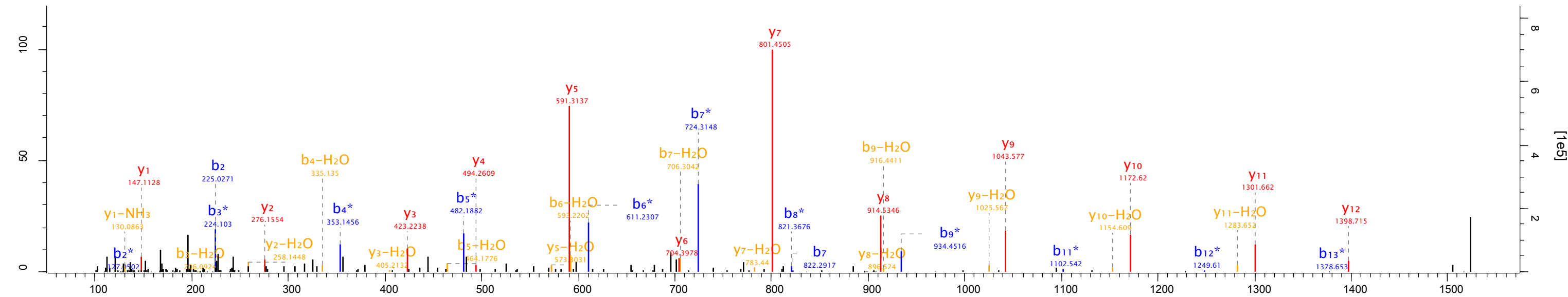
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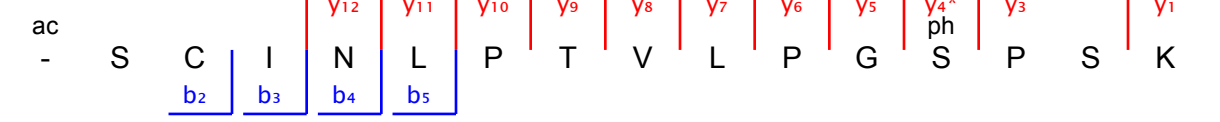
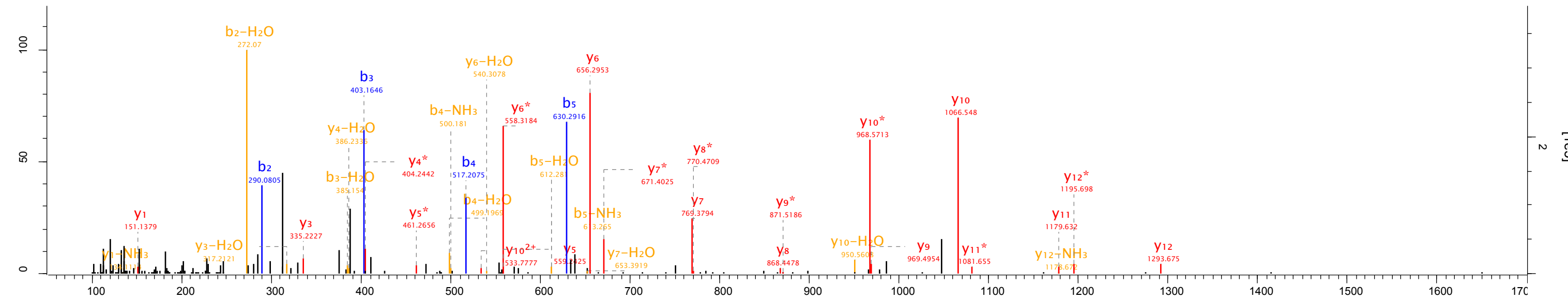


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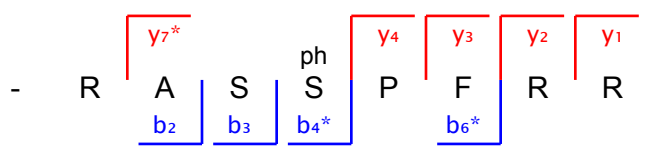
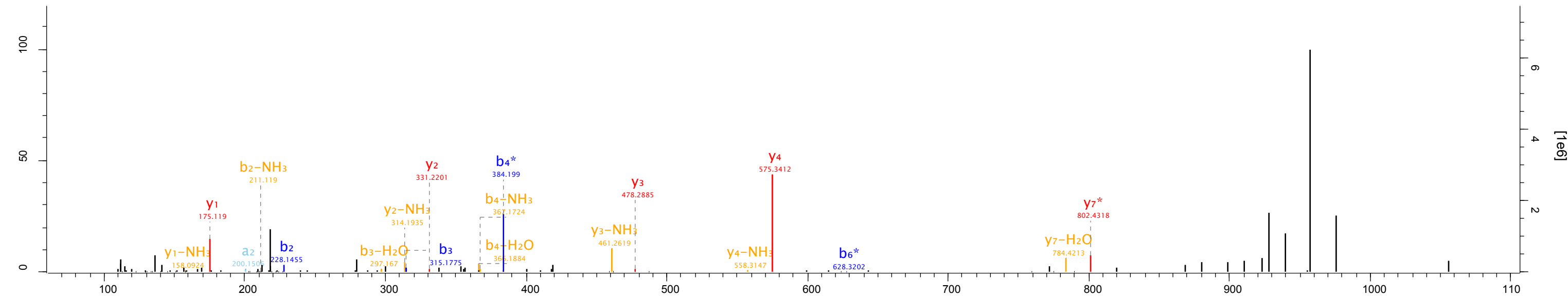
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20171215_MaS_33SR_LMH_phospho_06

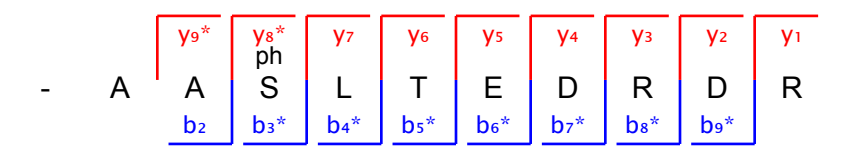
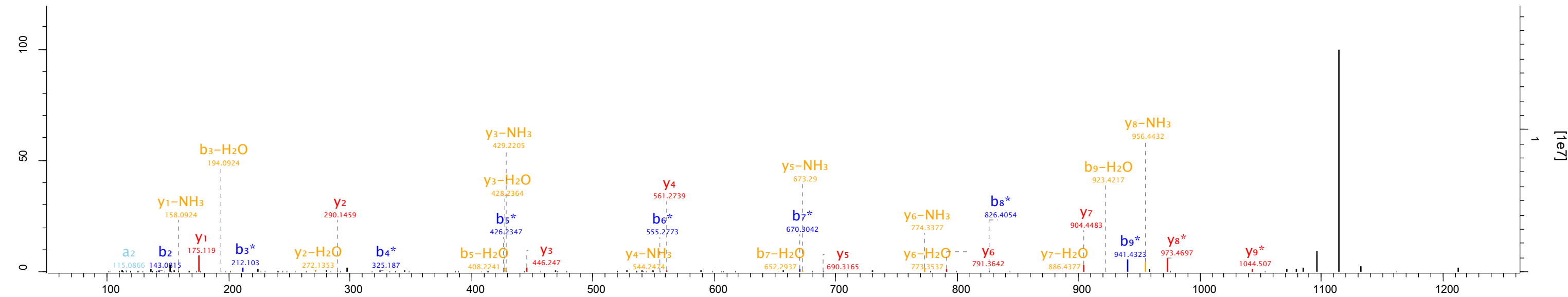


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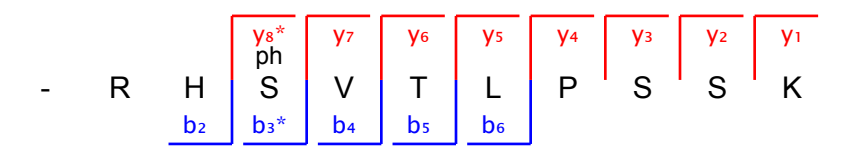
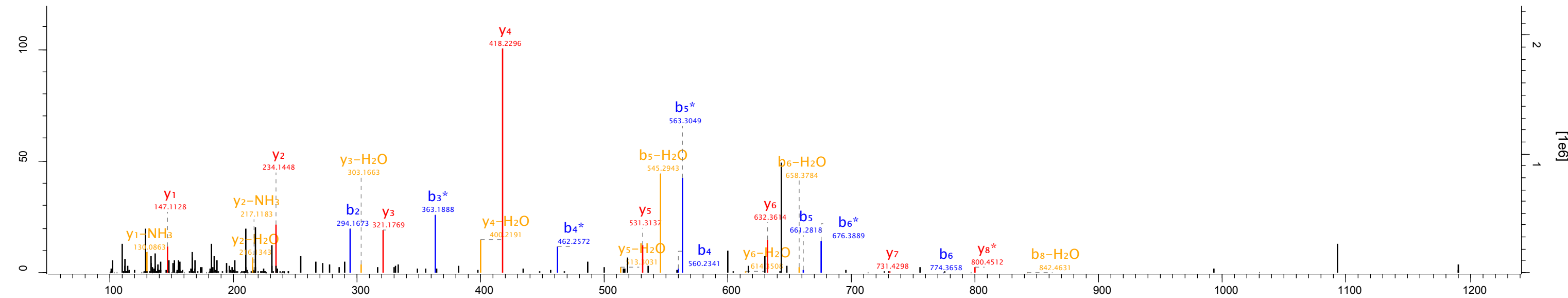
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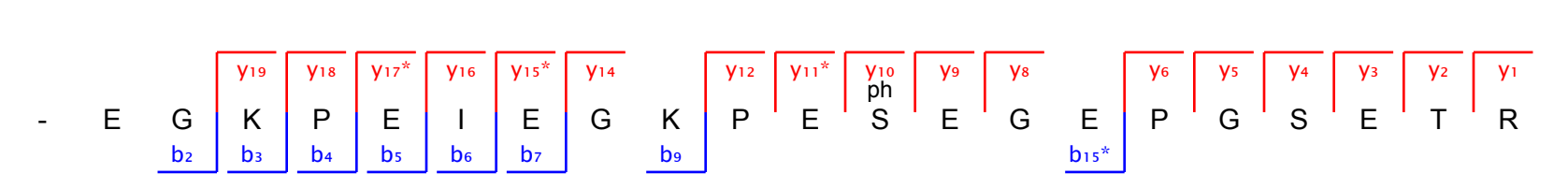
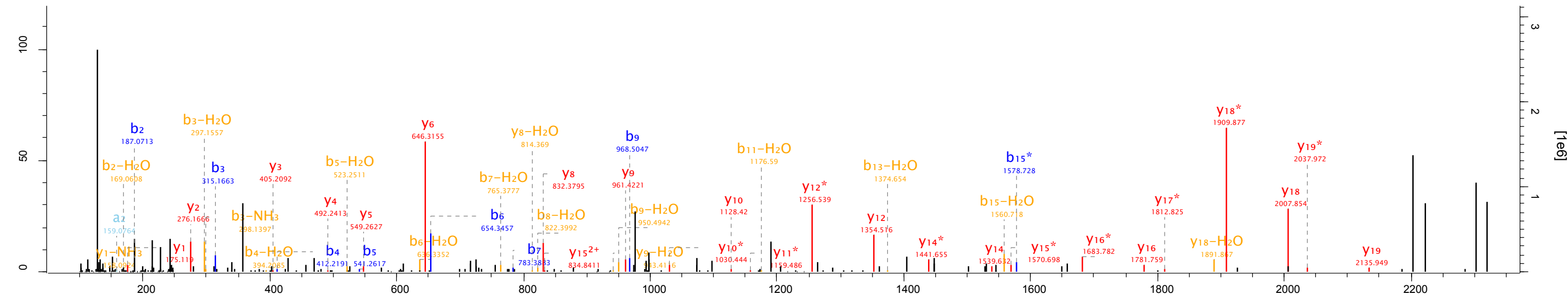
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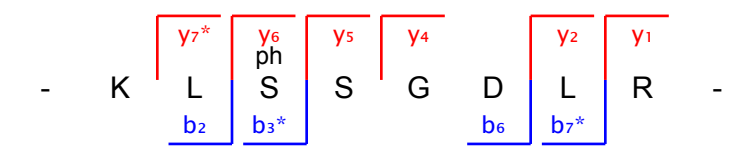
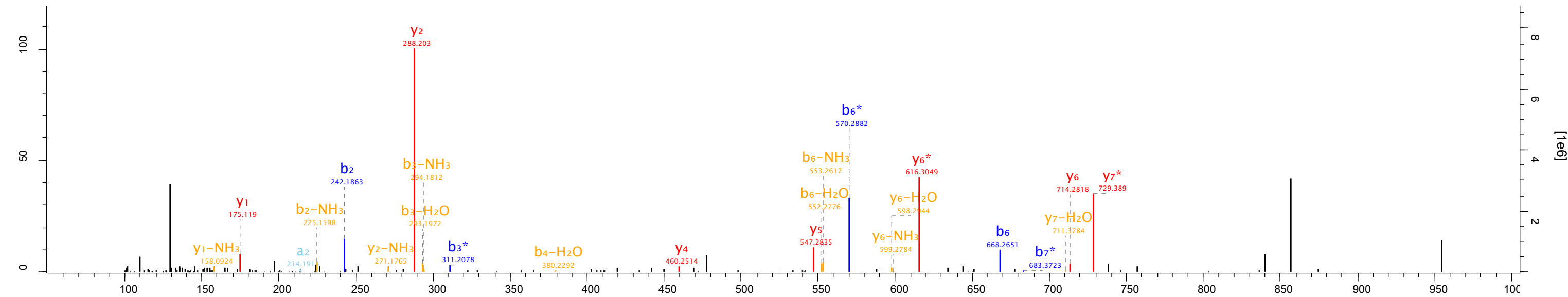
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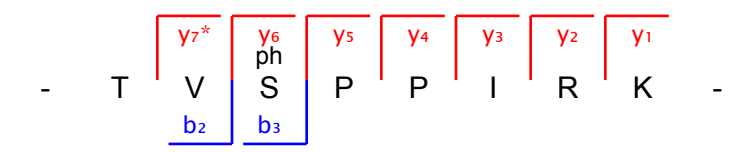
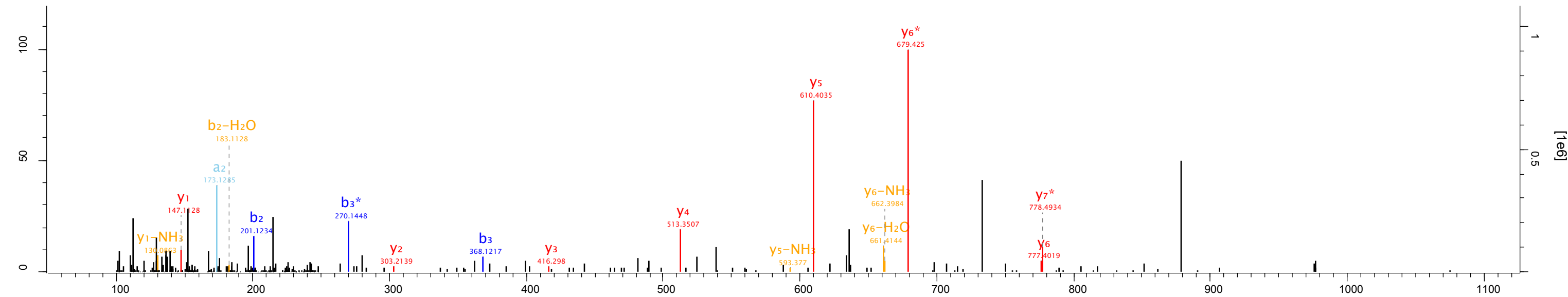
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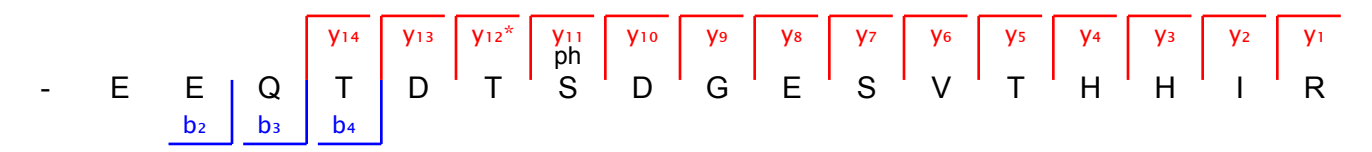
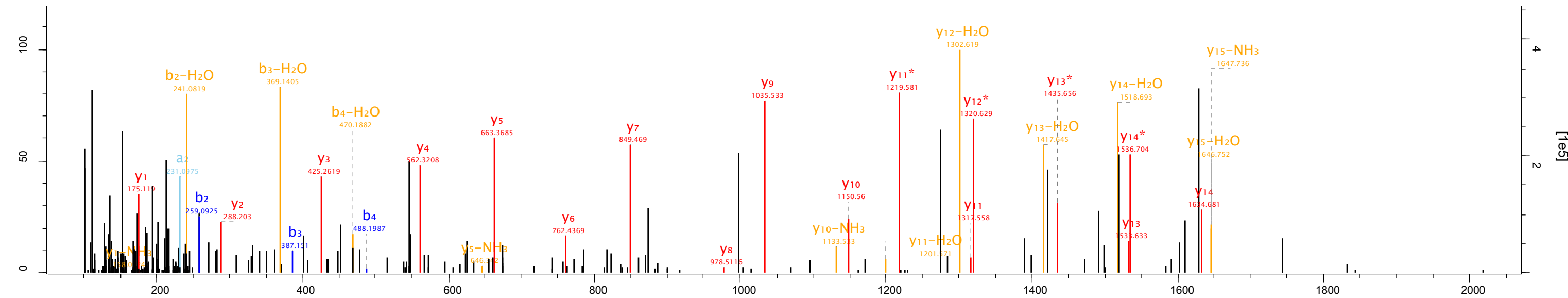
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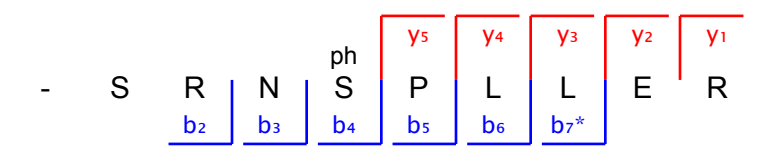
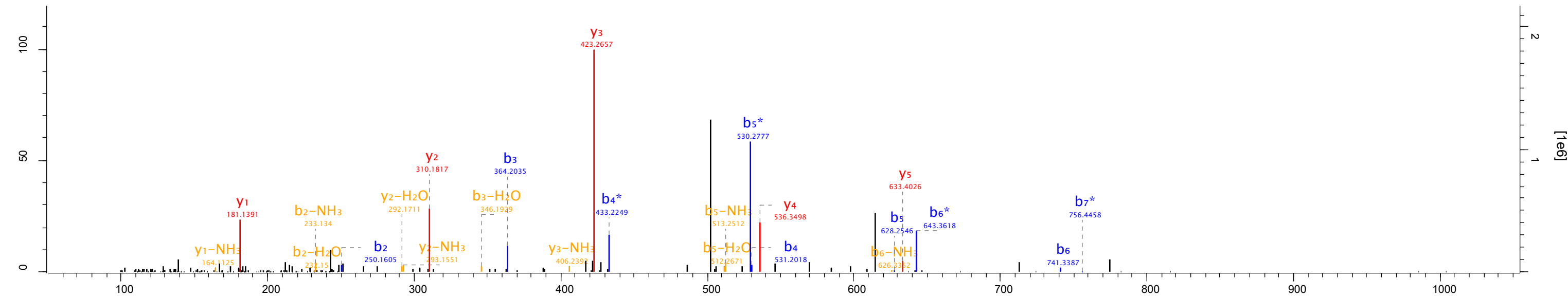
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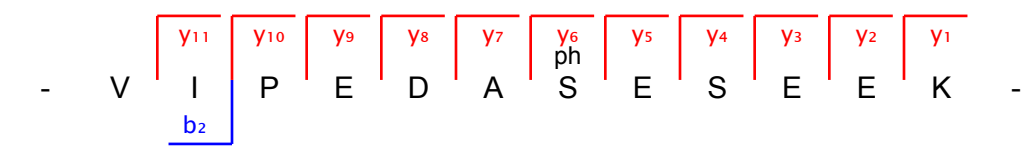
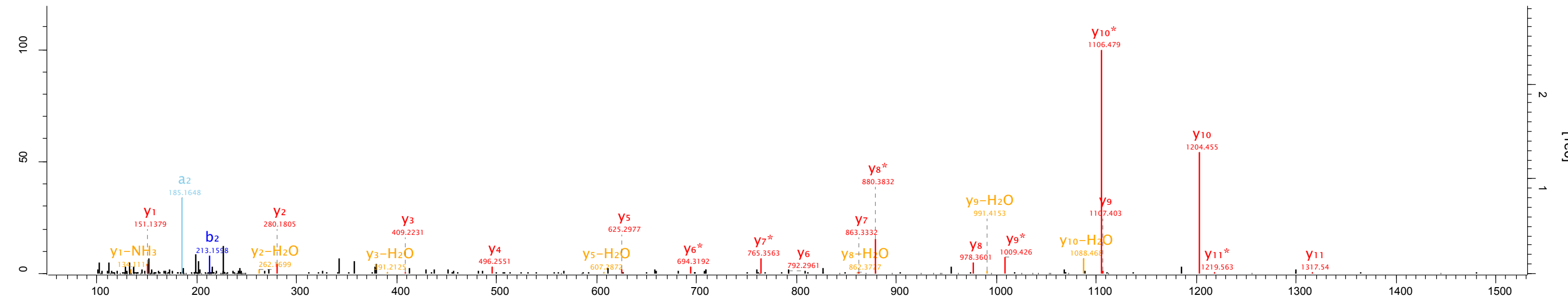
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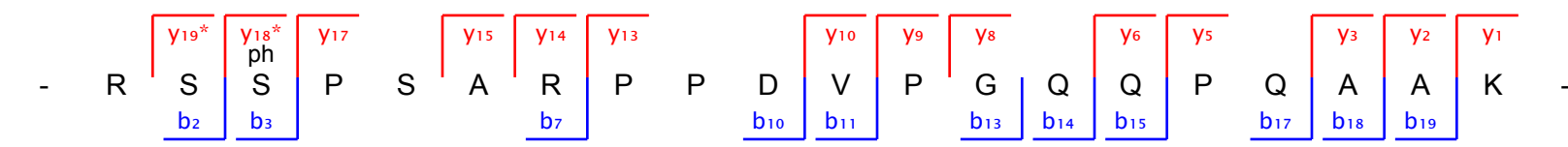
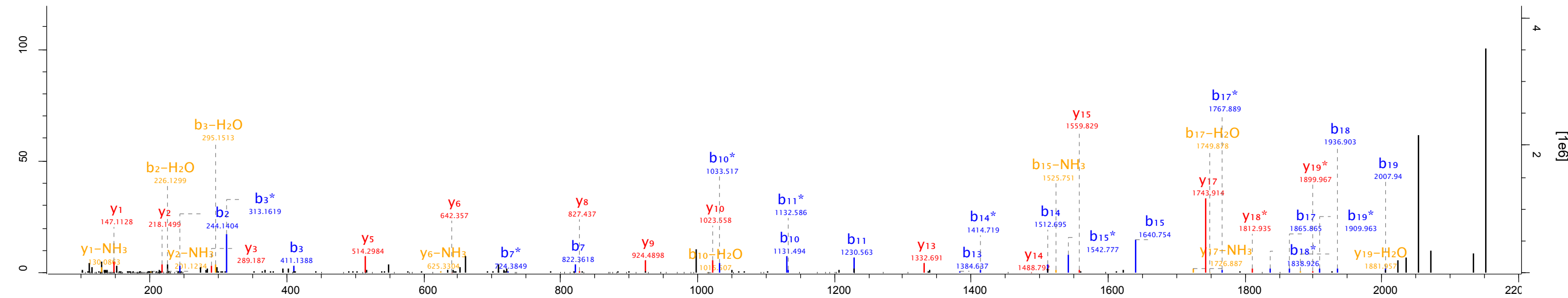
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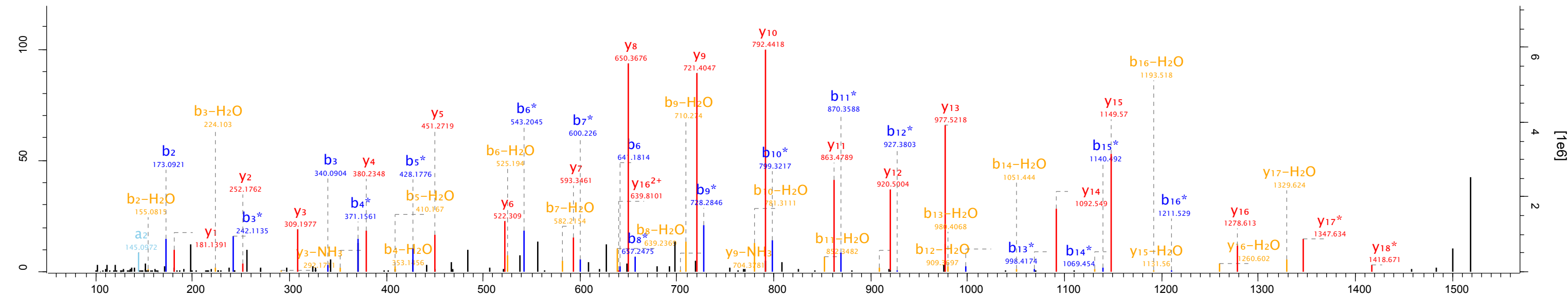
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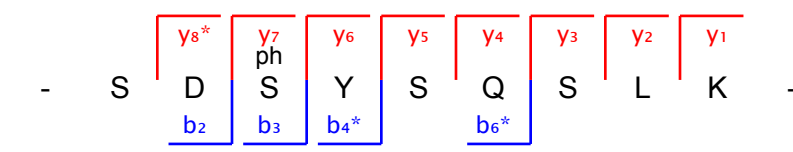
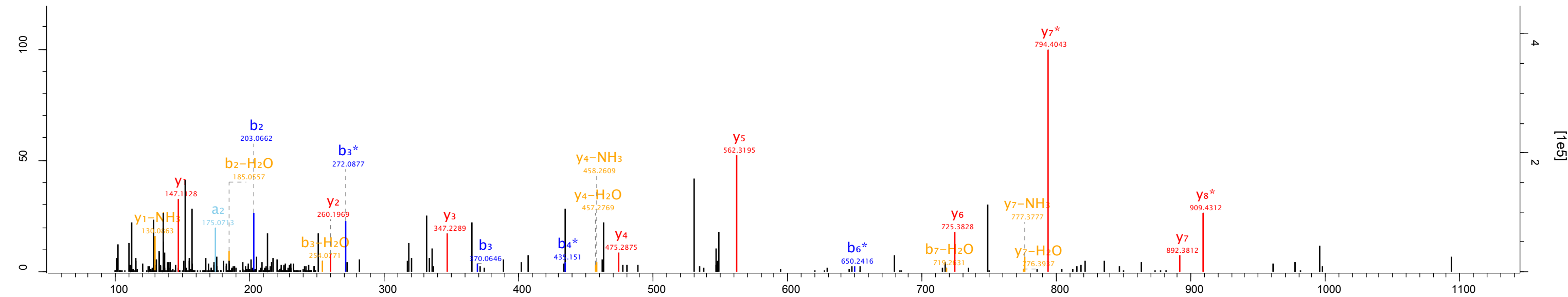


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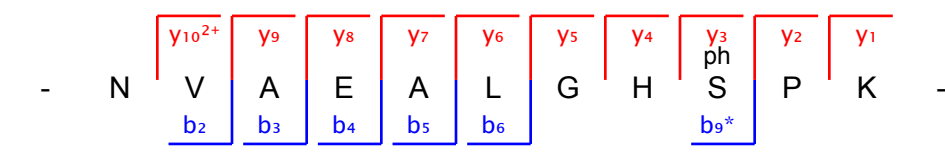
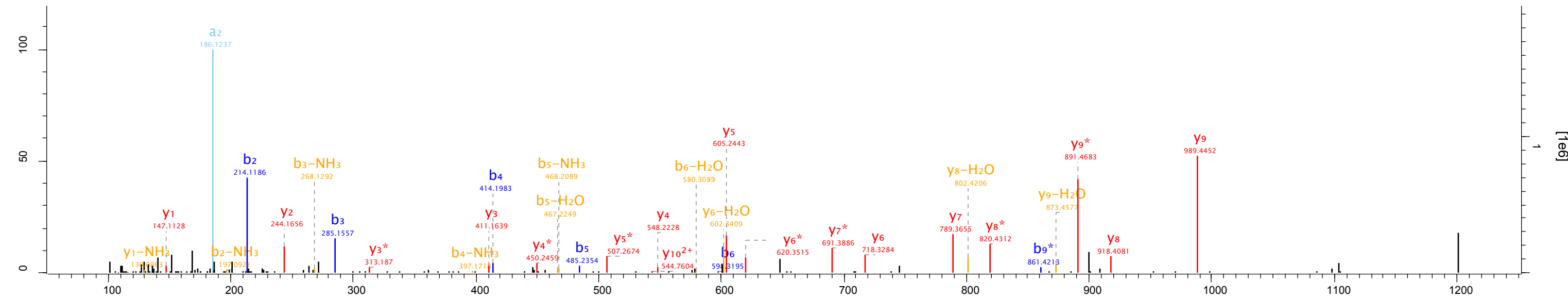


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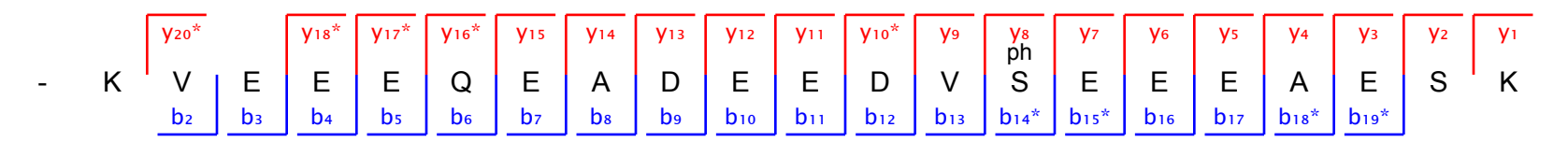
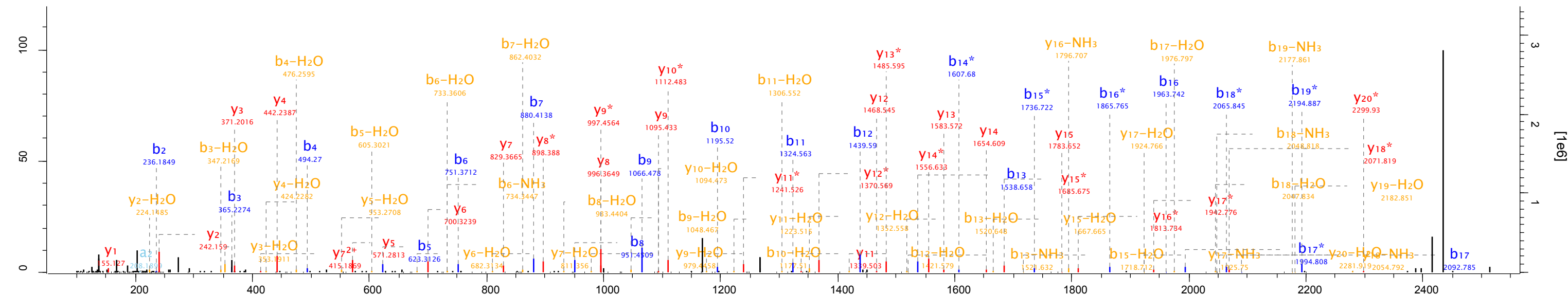
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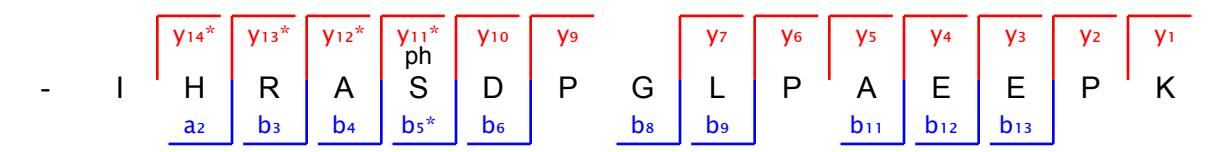
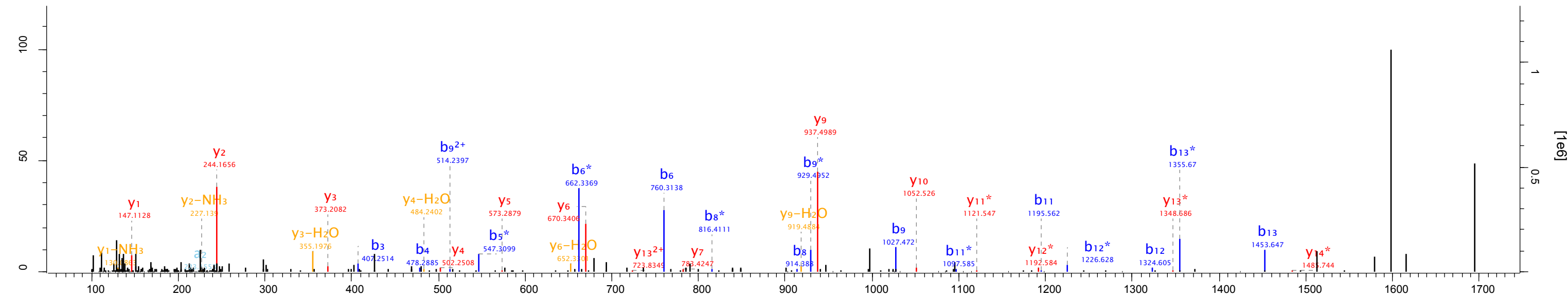
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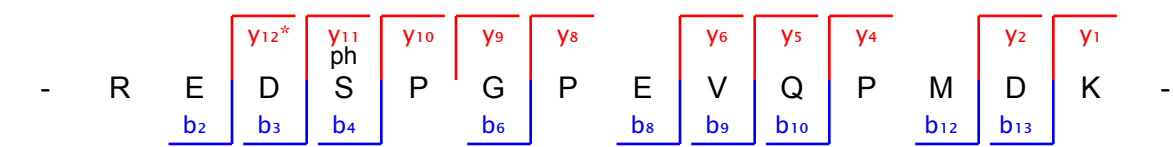
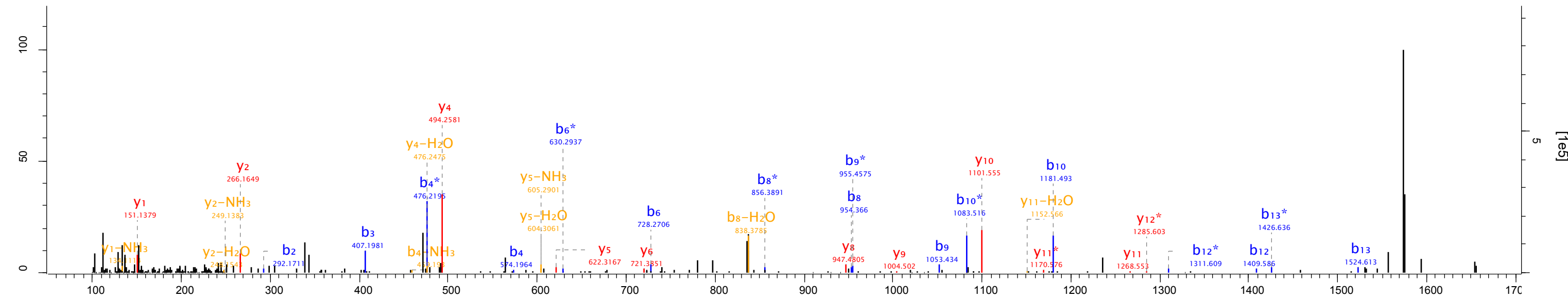
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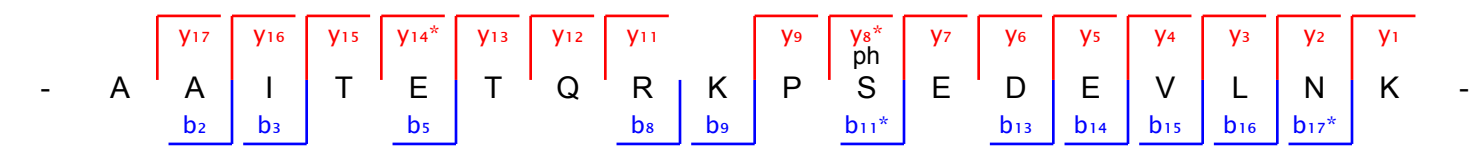
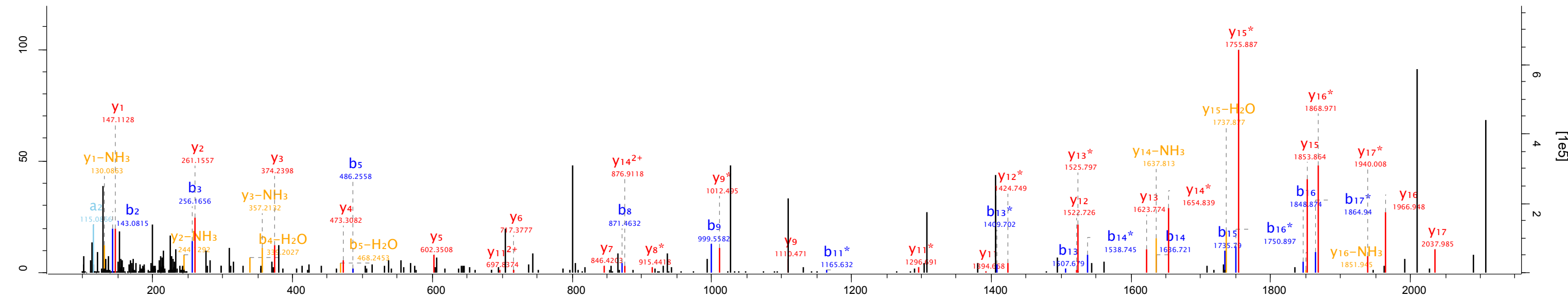
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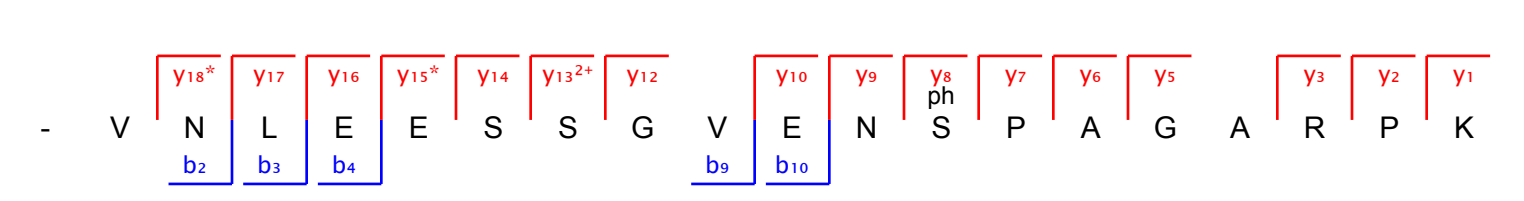
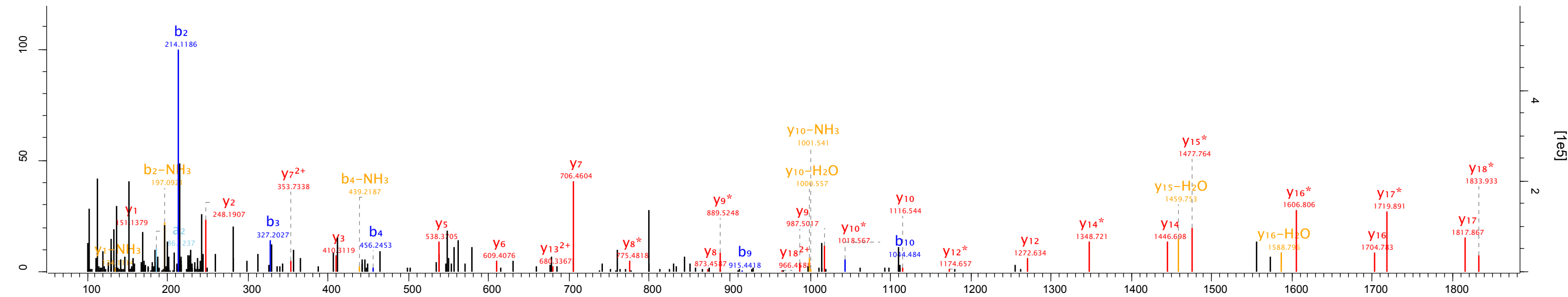
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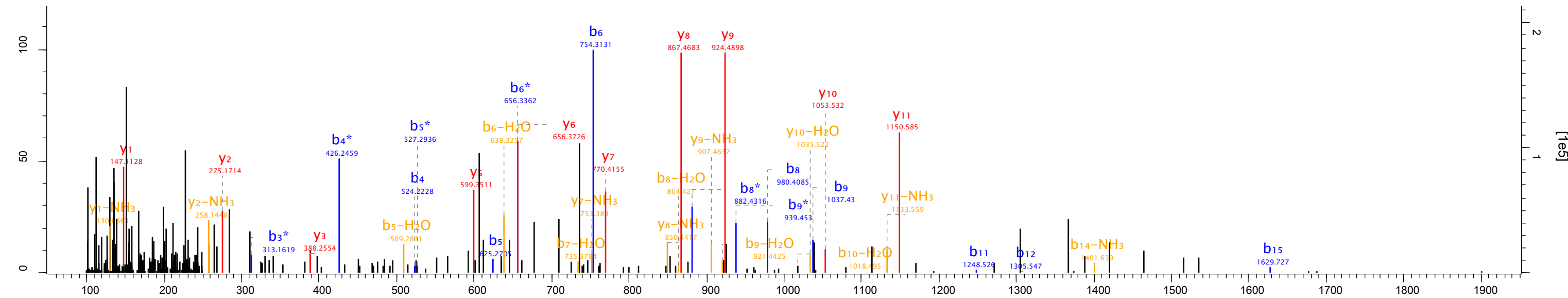
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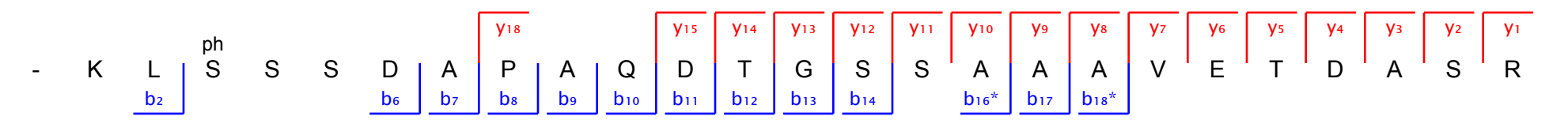
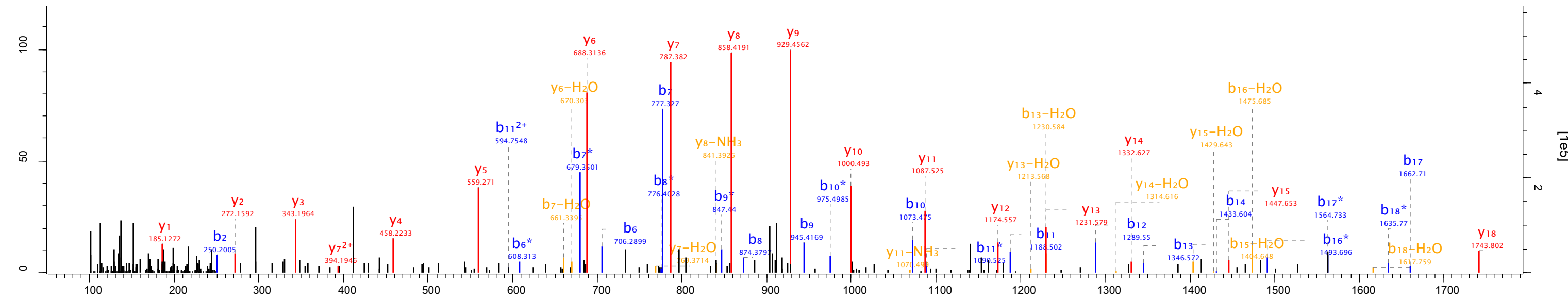
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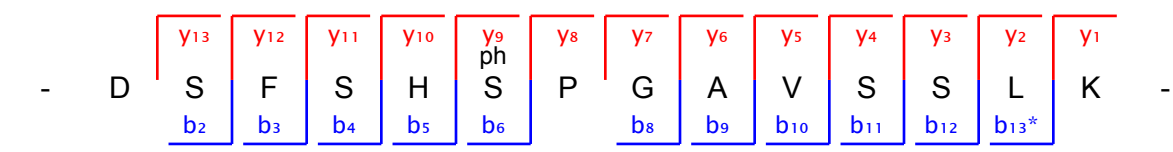
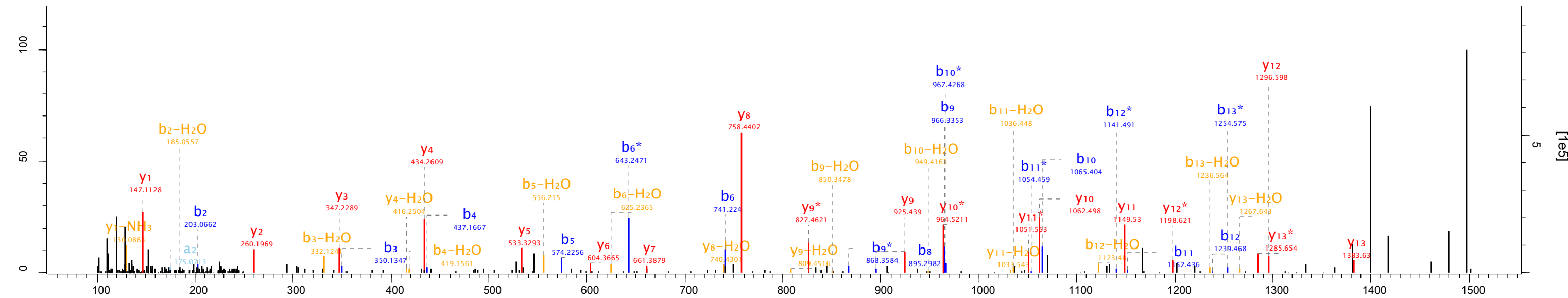
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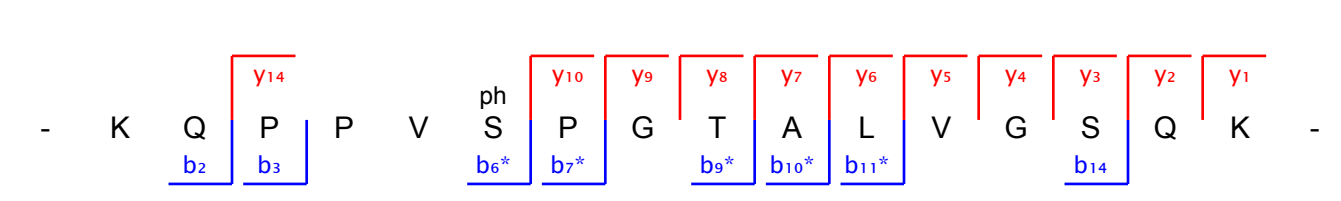
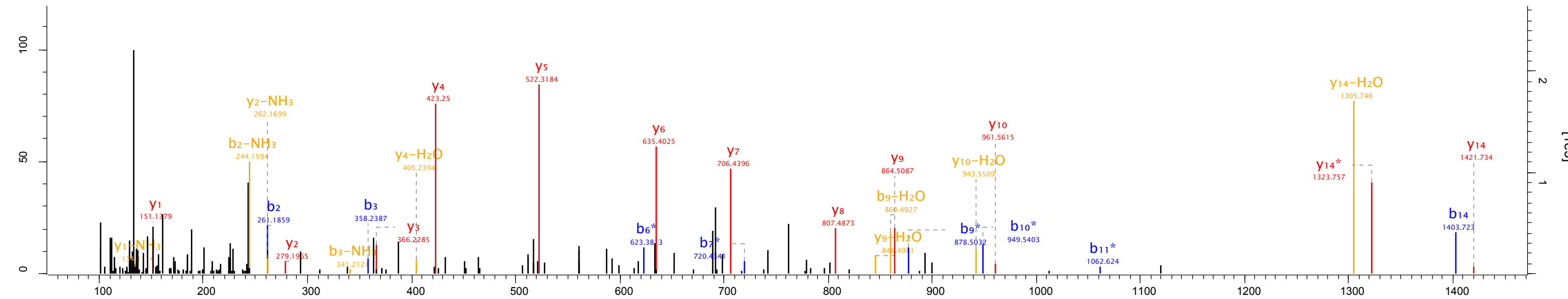
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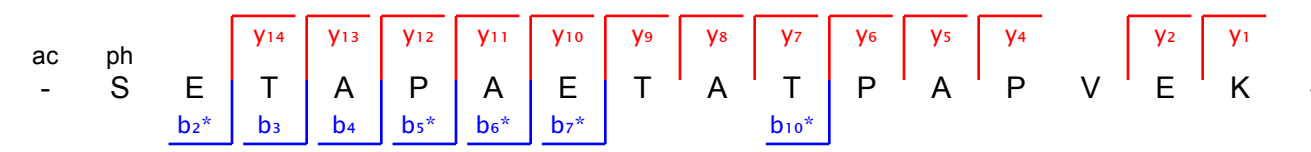
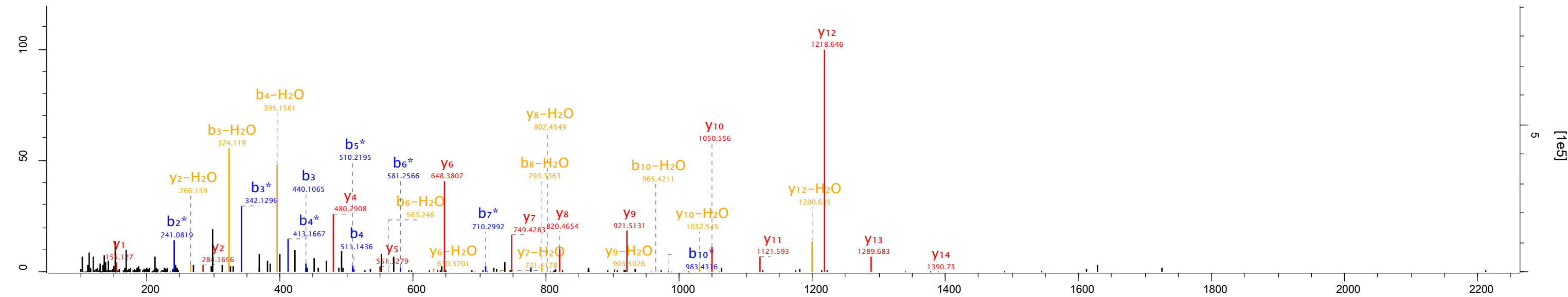
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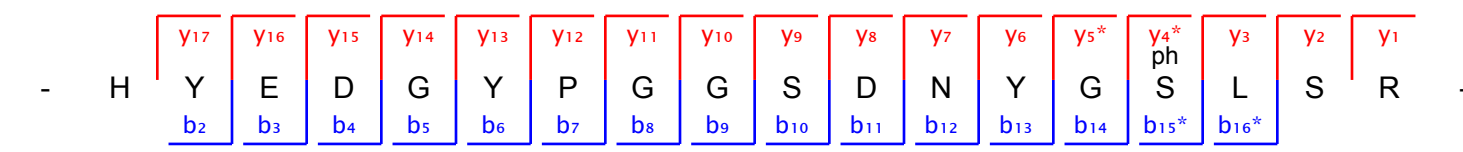
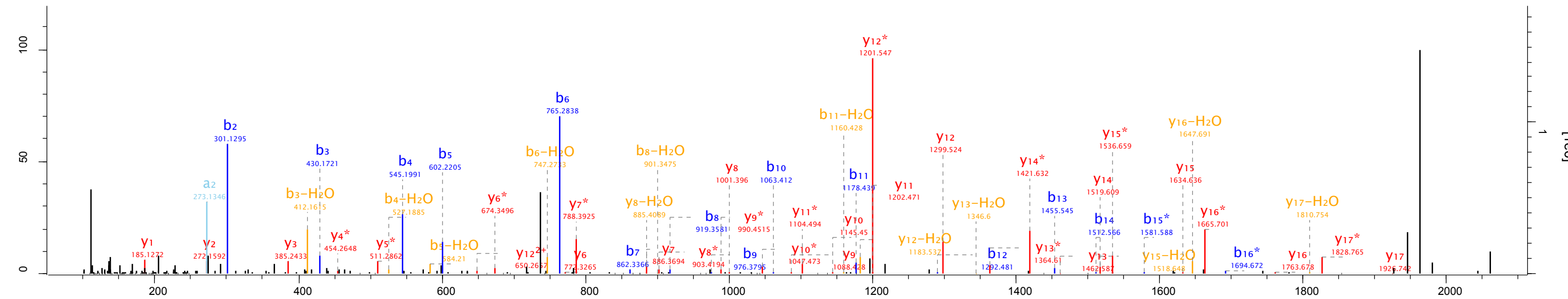
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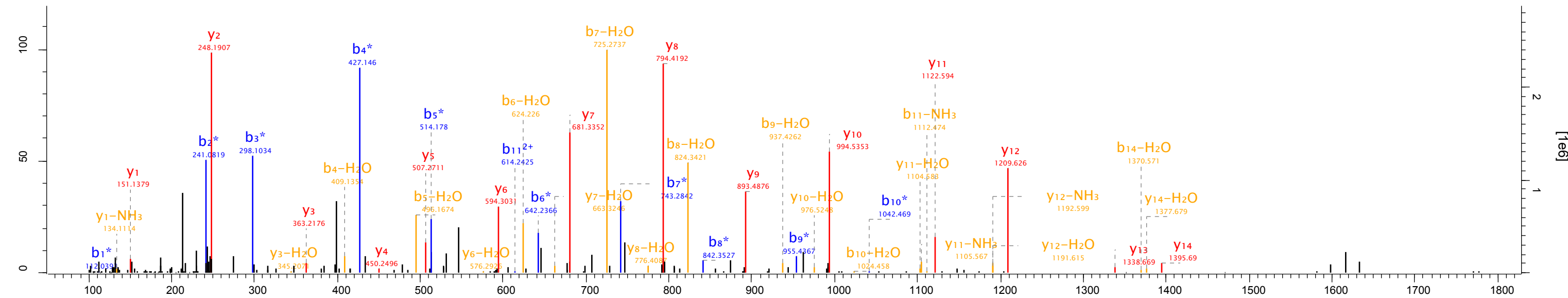


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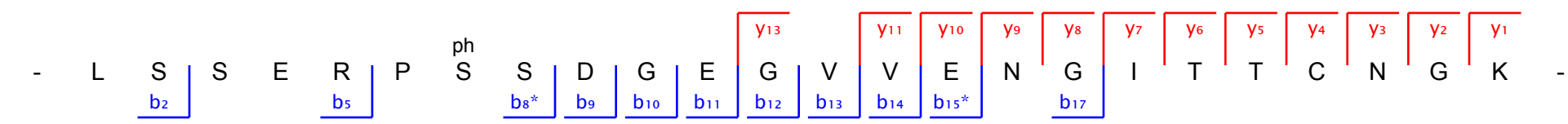
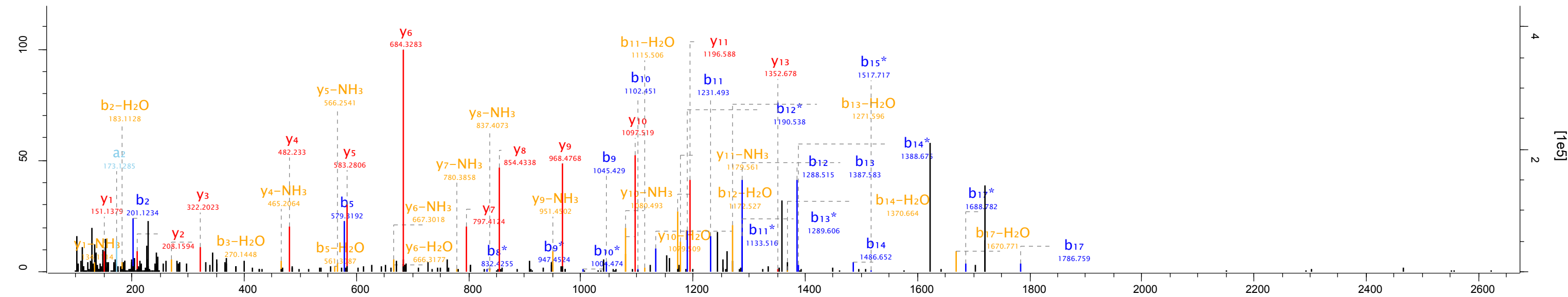




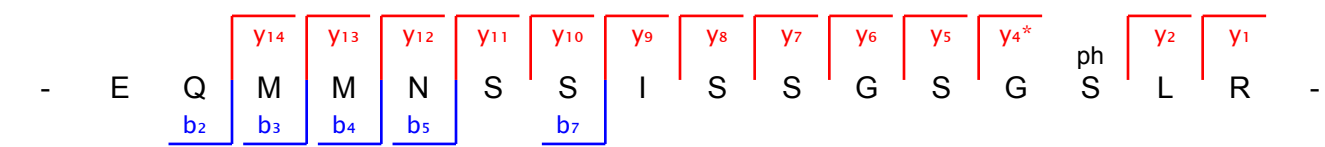
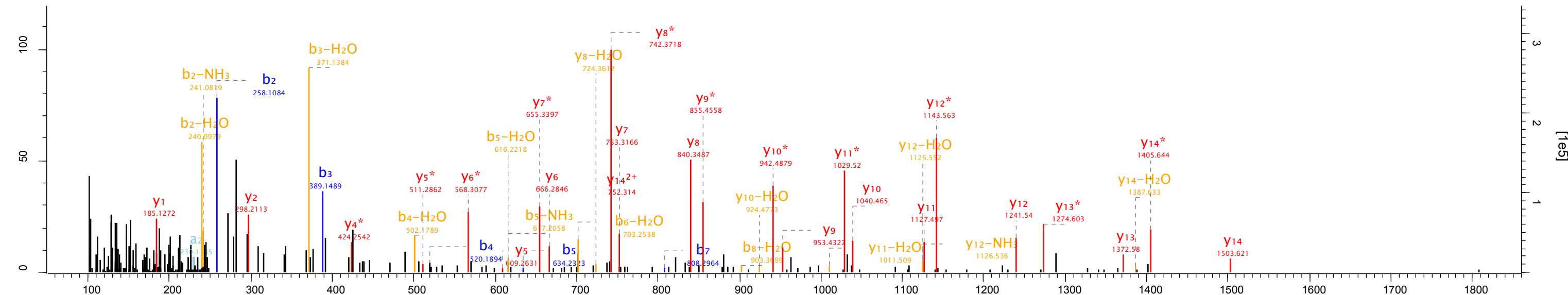
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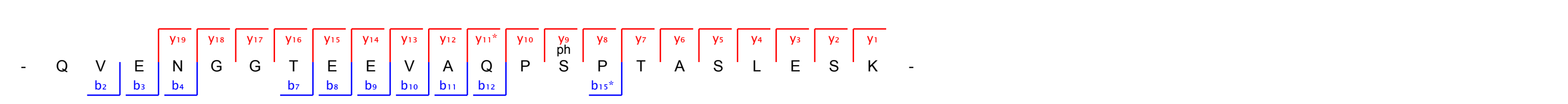
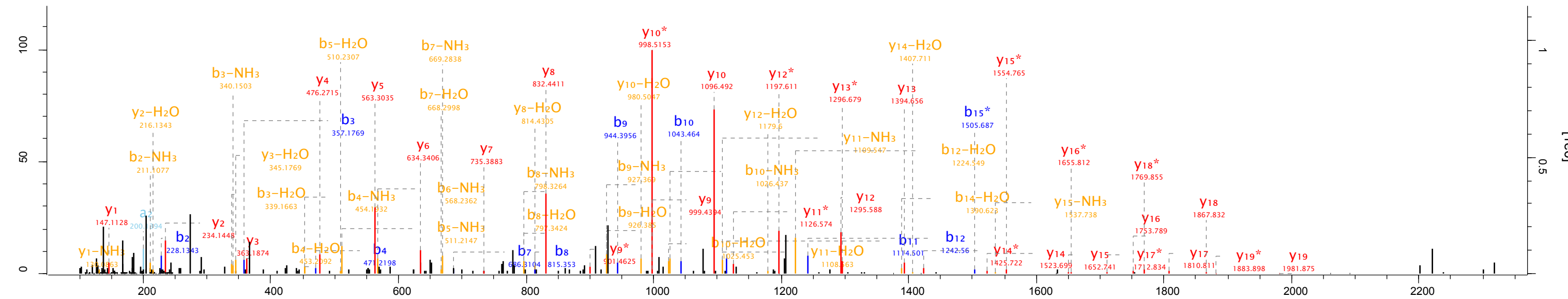
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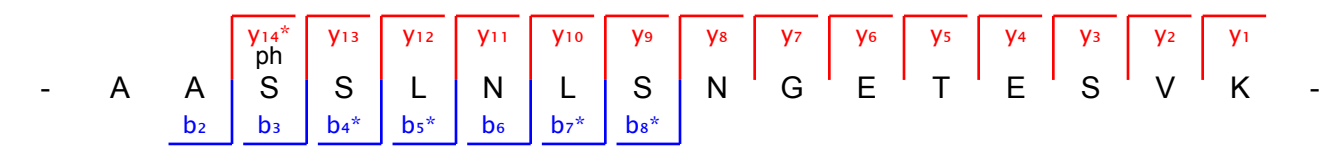
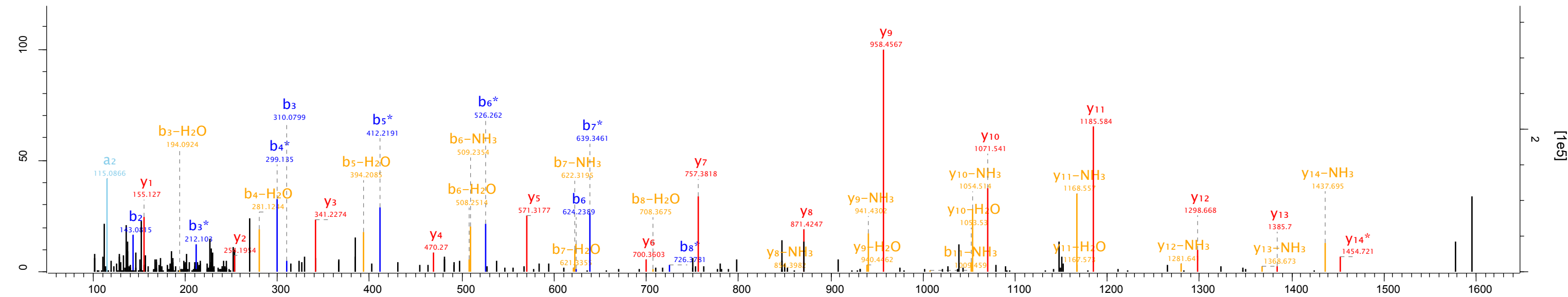
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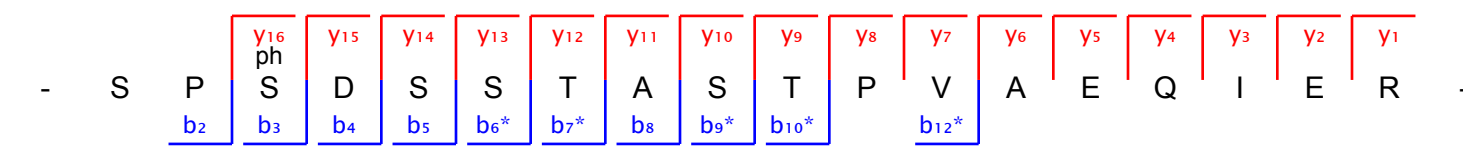
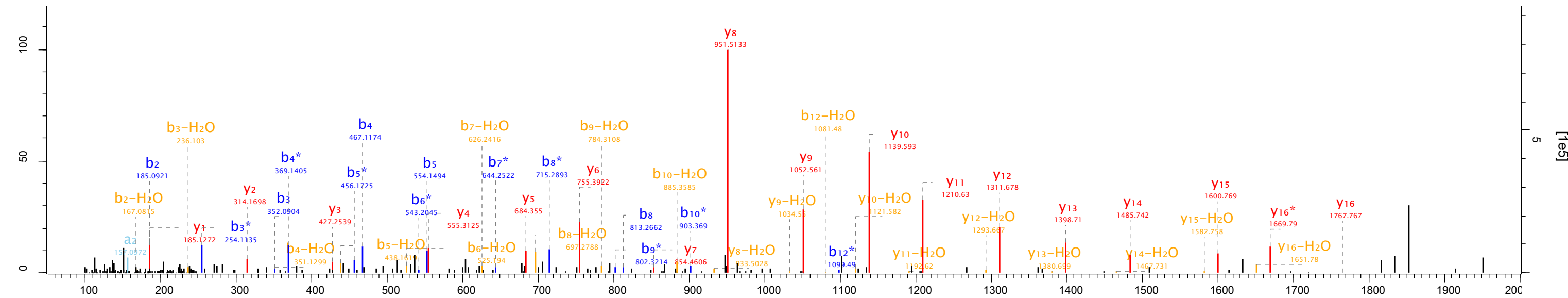
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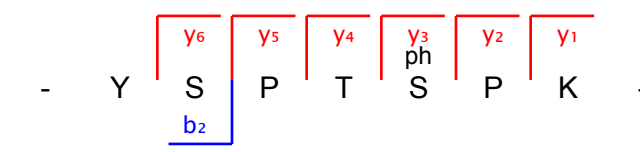
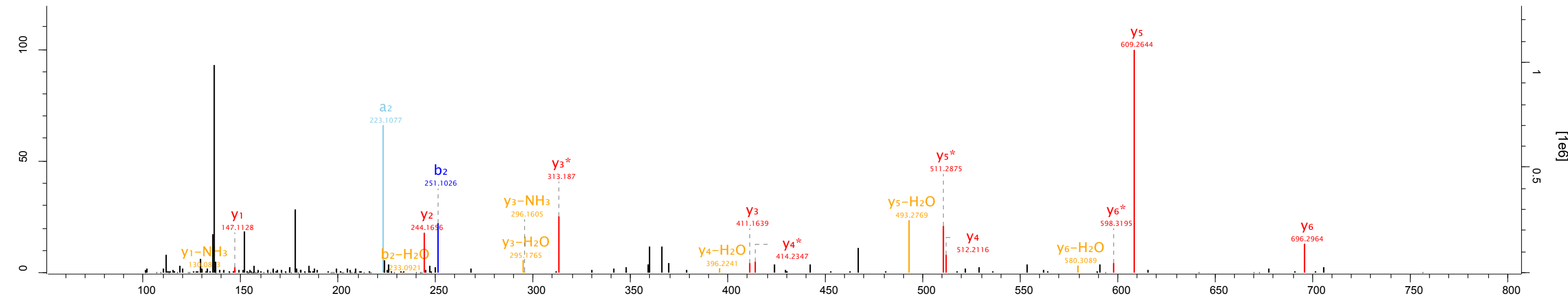
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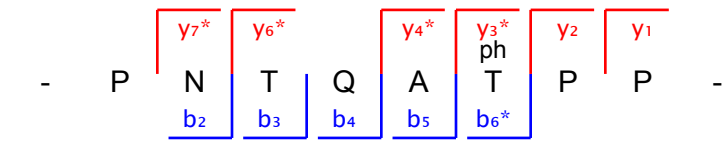
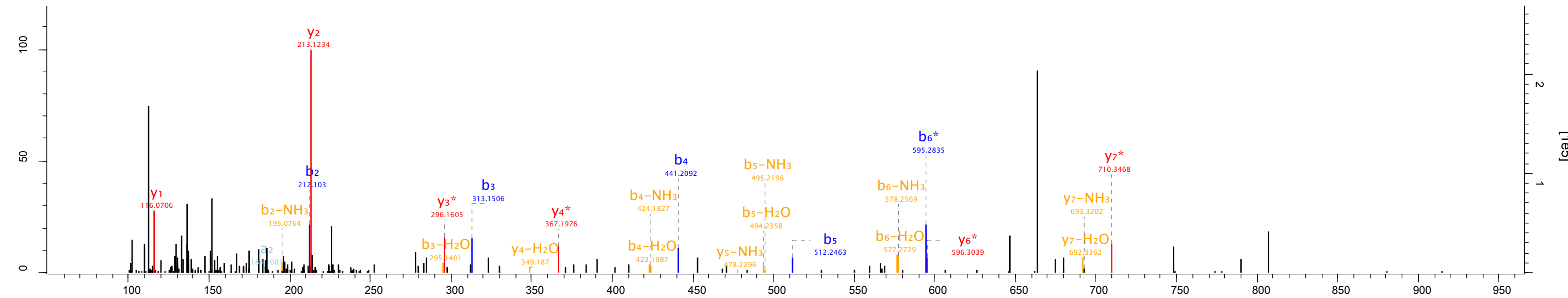


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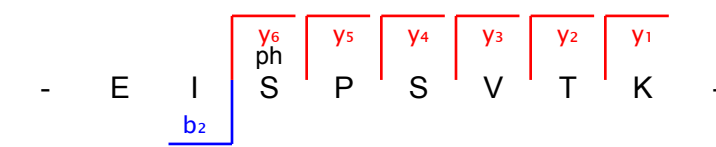
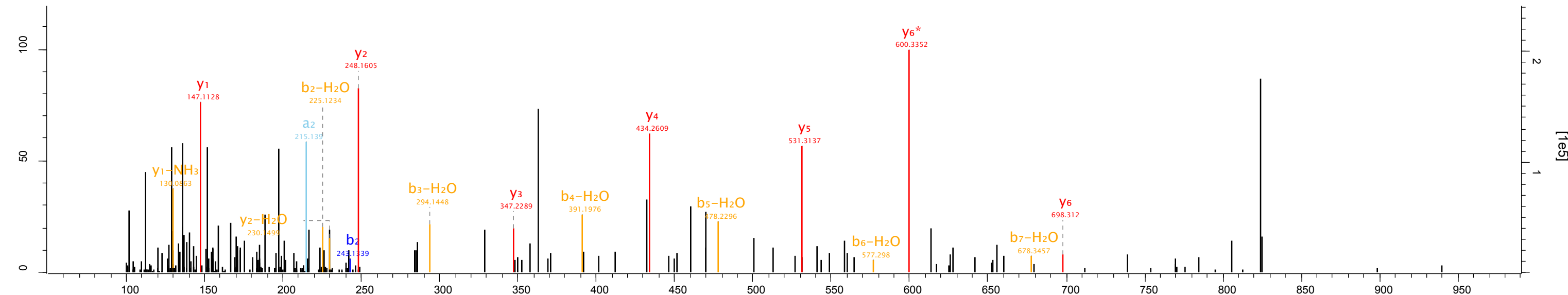


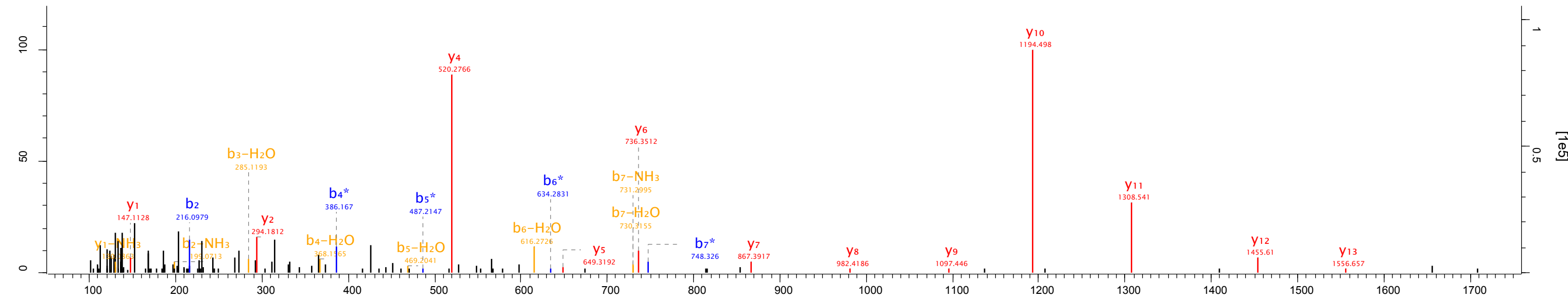
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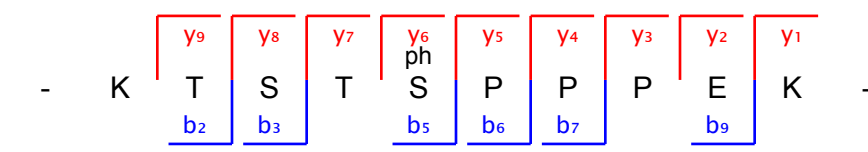
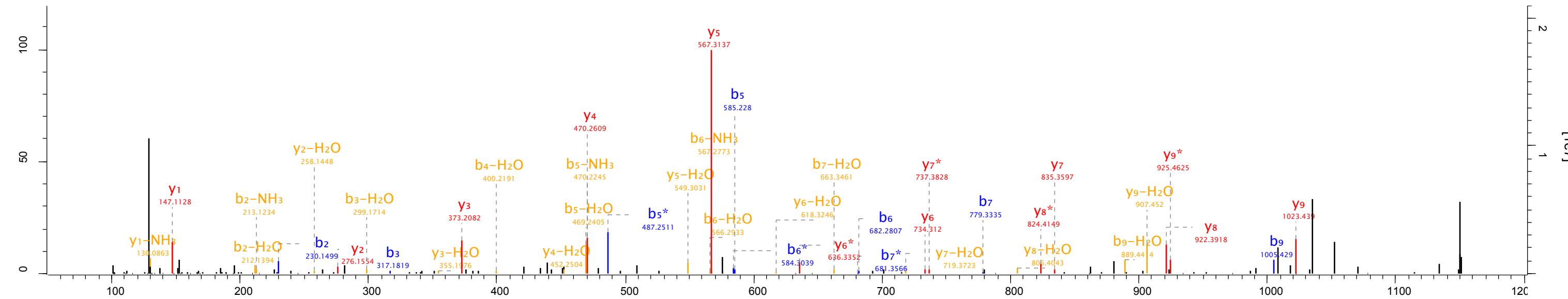




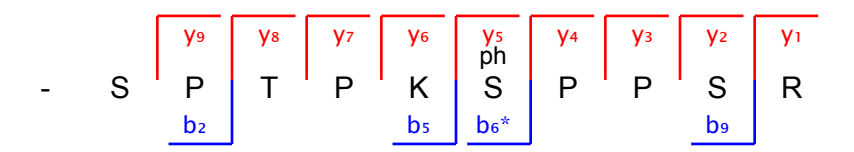
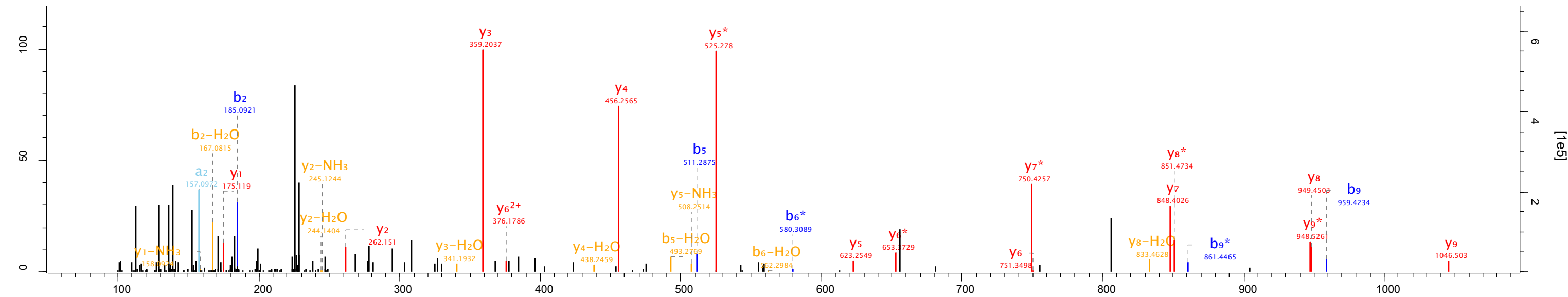
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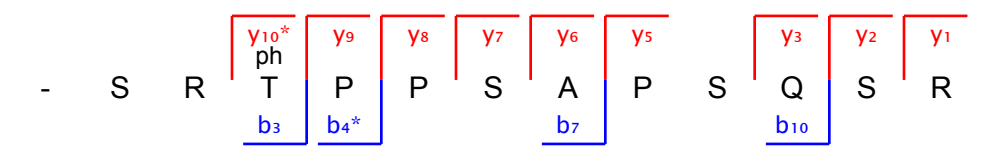
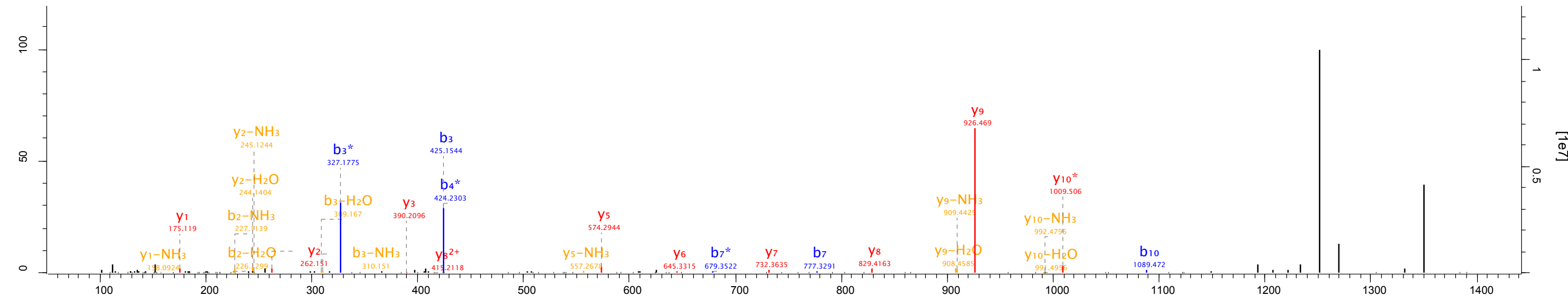
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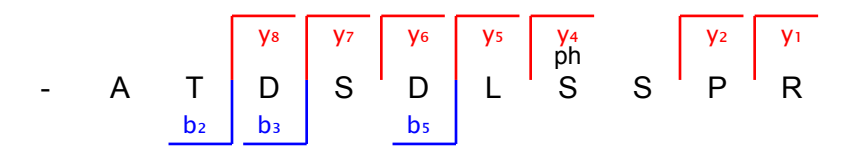
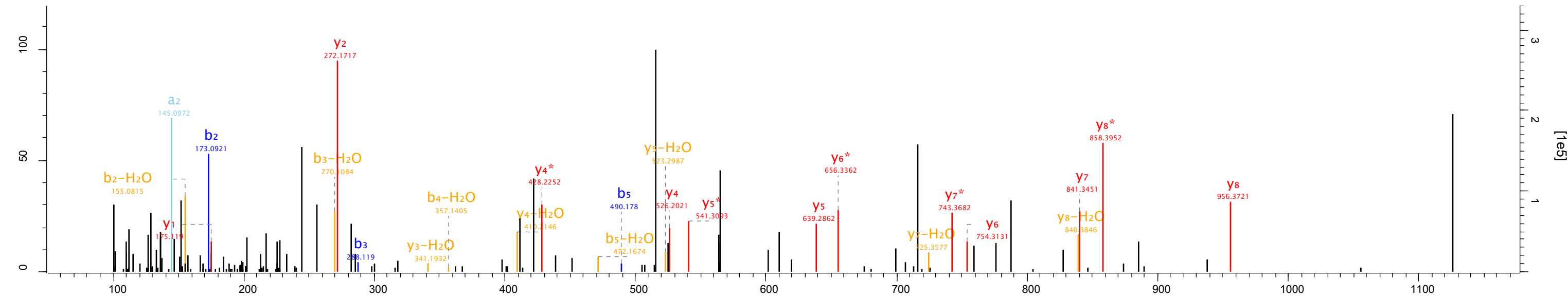
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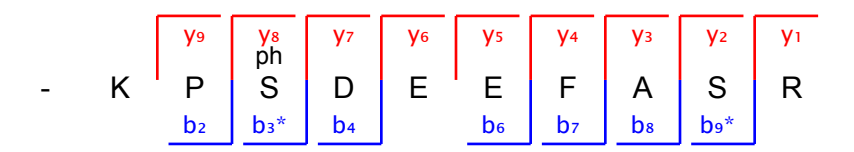
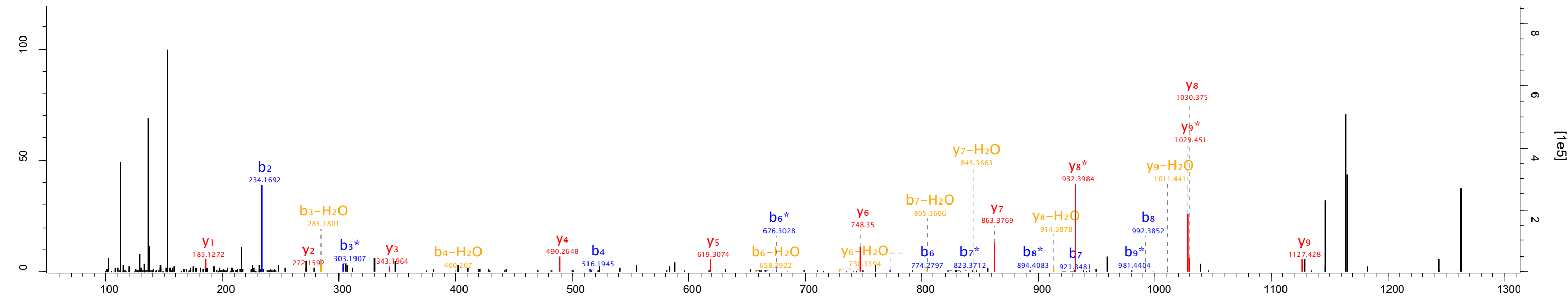
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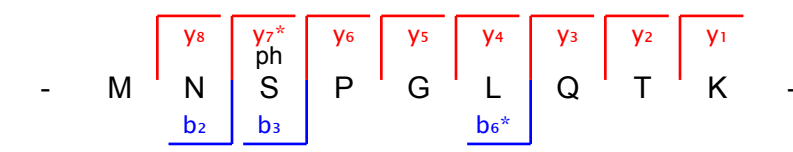
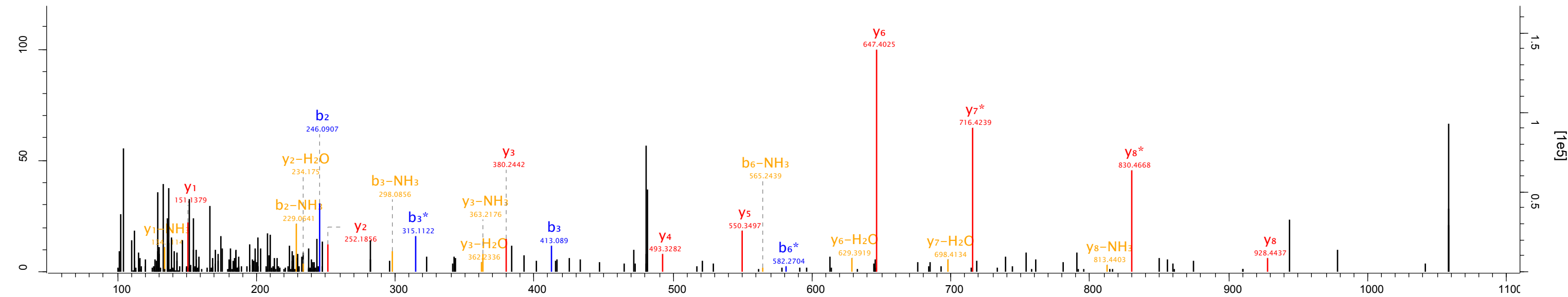
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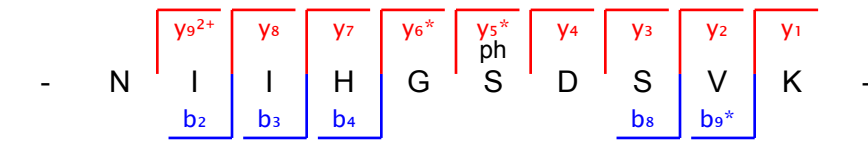
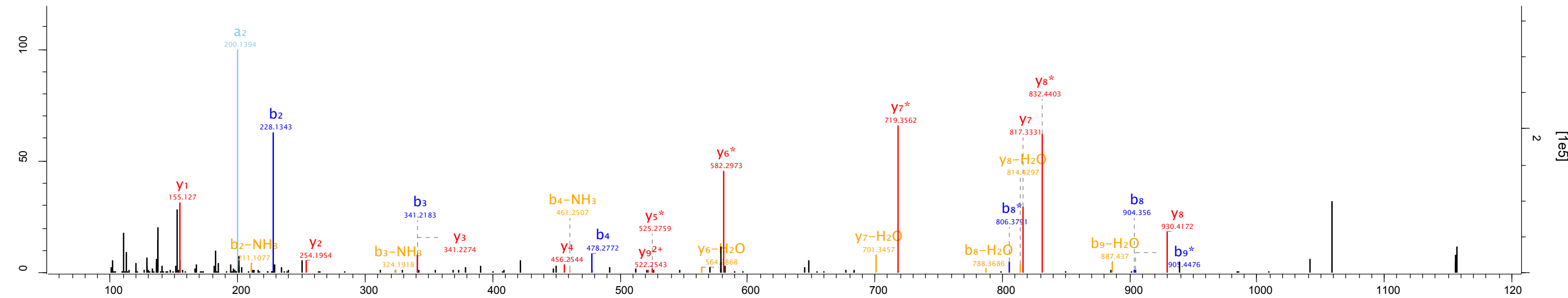


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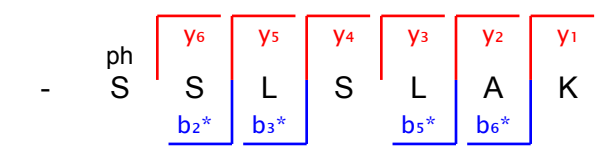
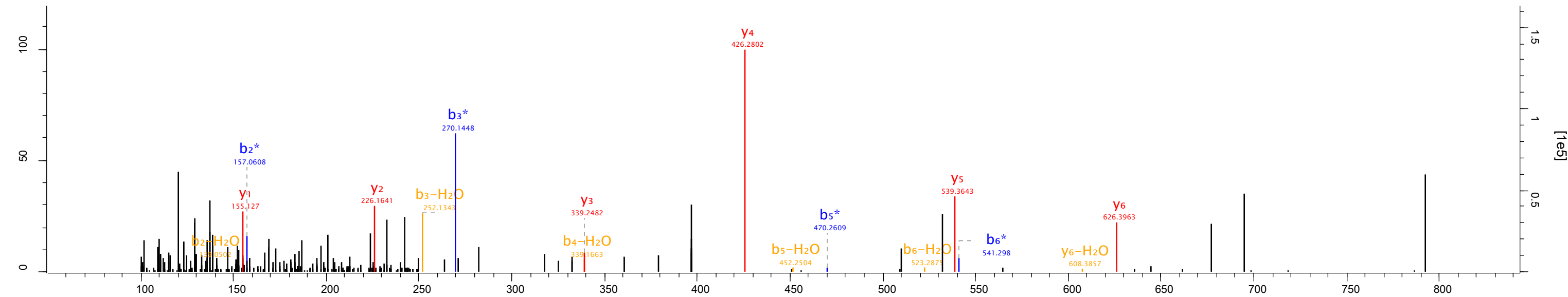


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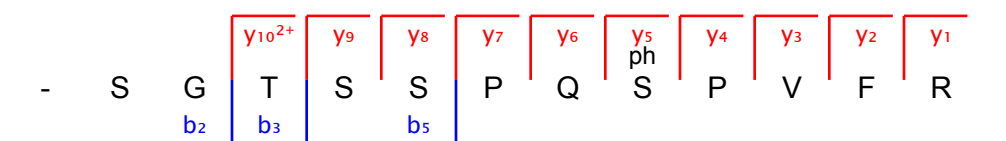
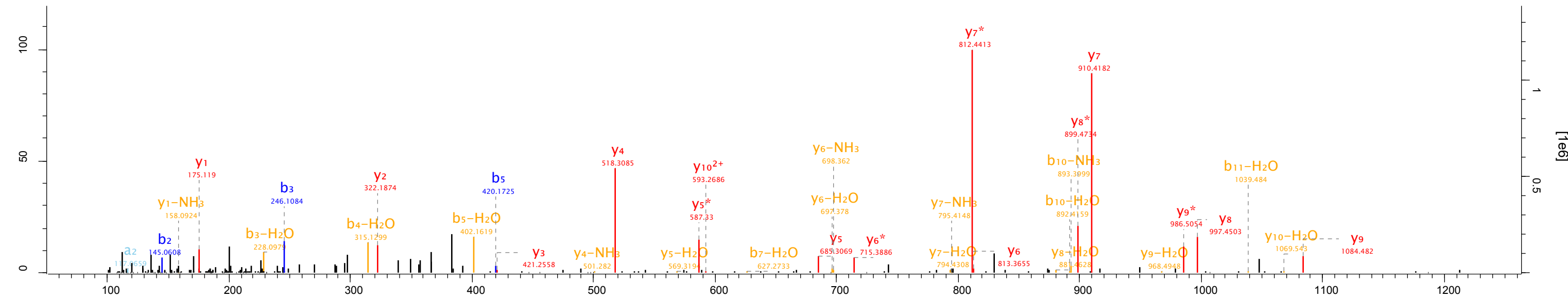




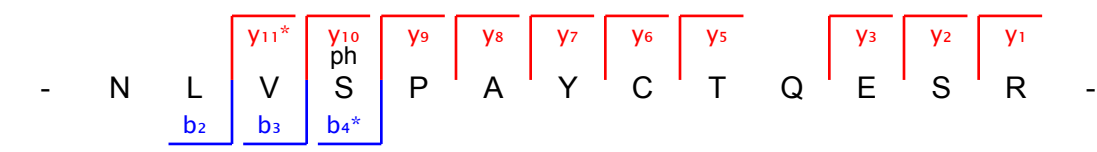
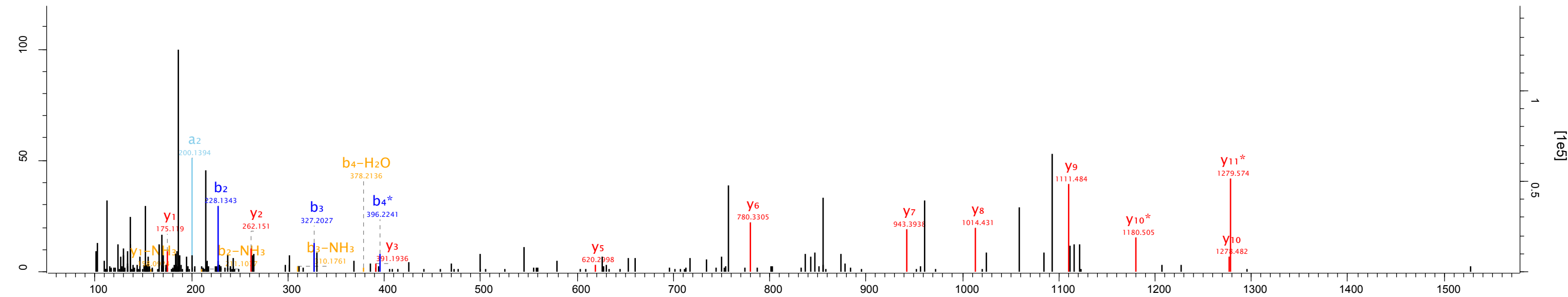
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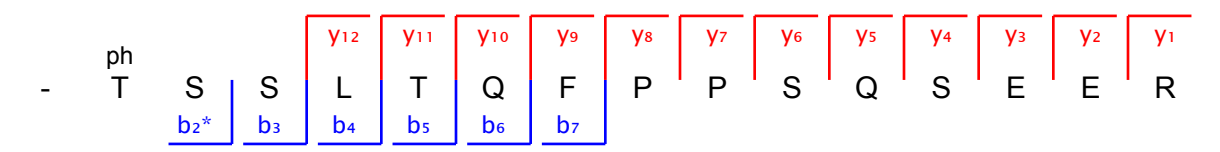
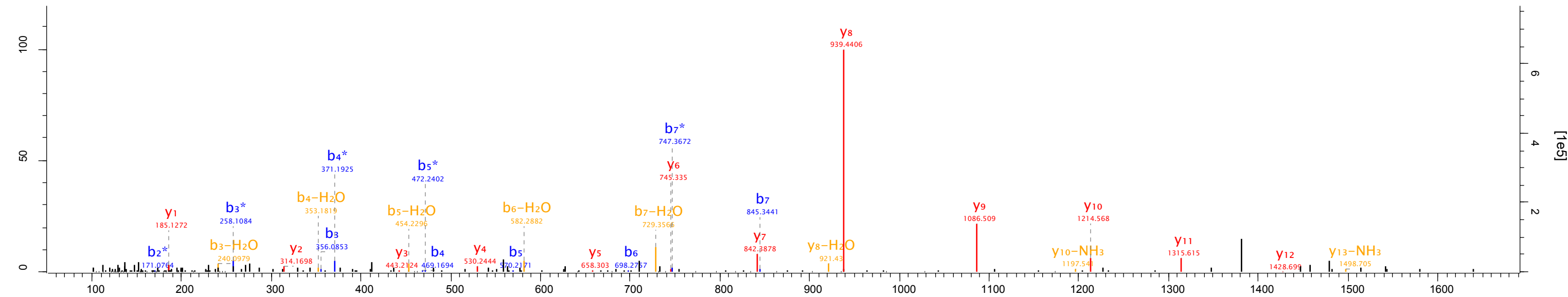
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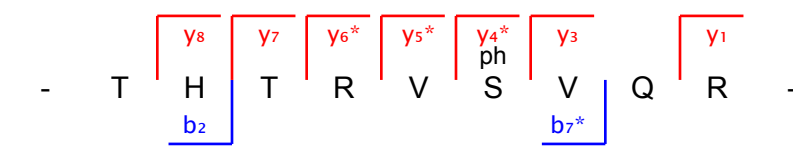
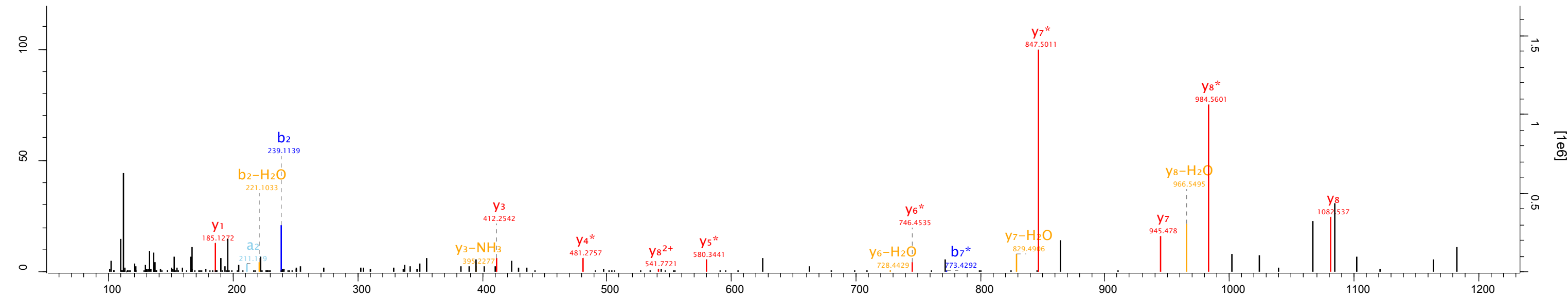
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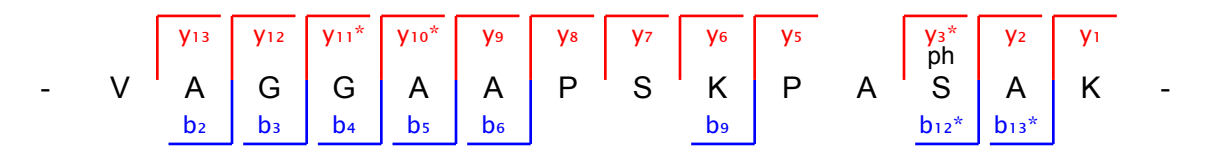
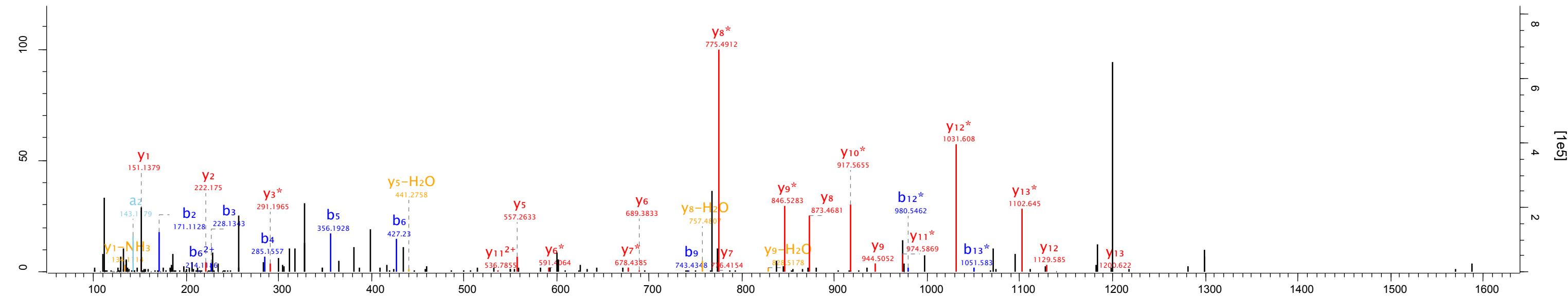
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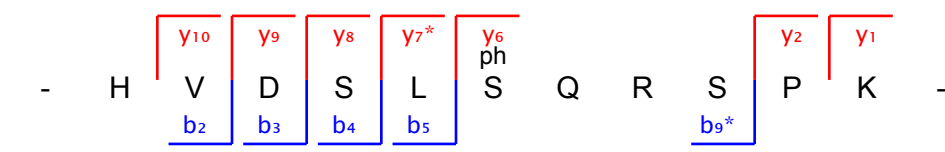
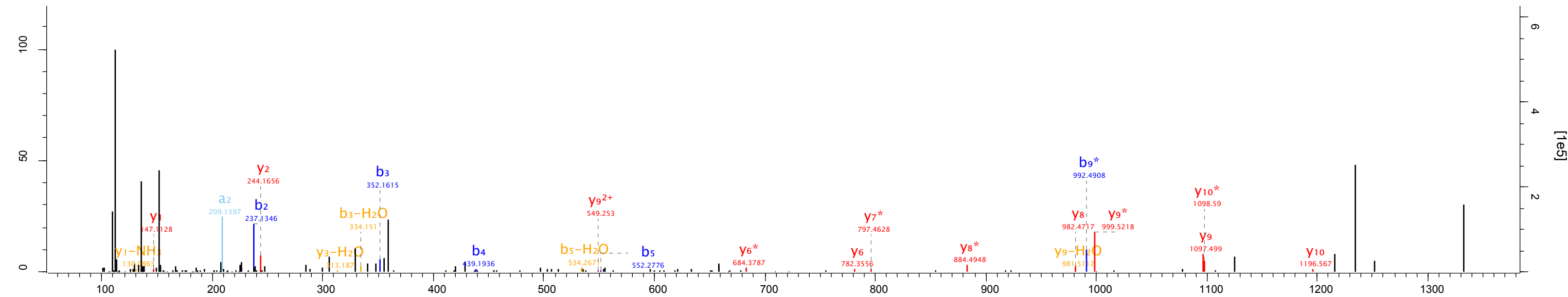
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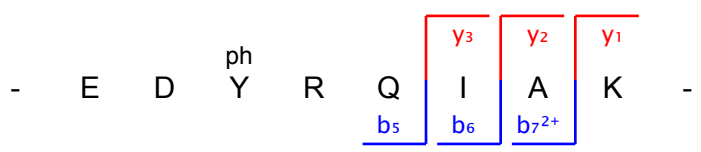
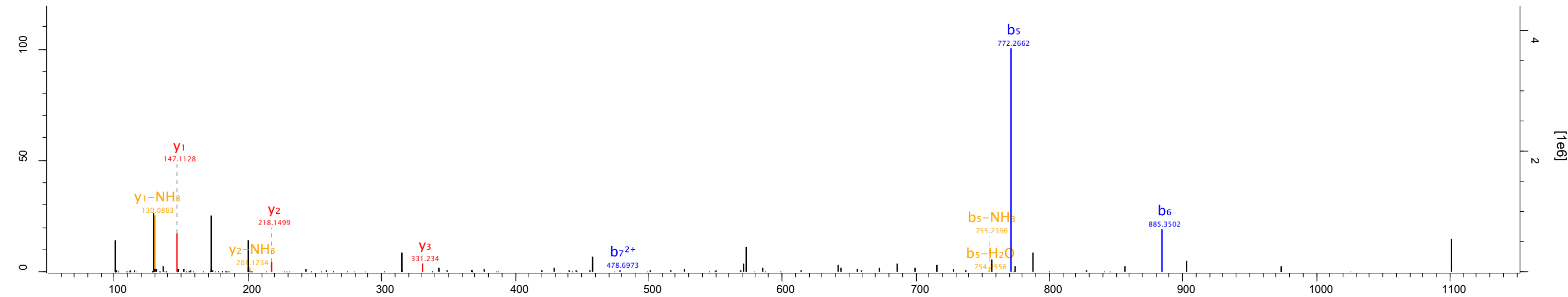
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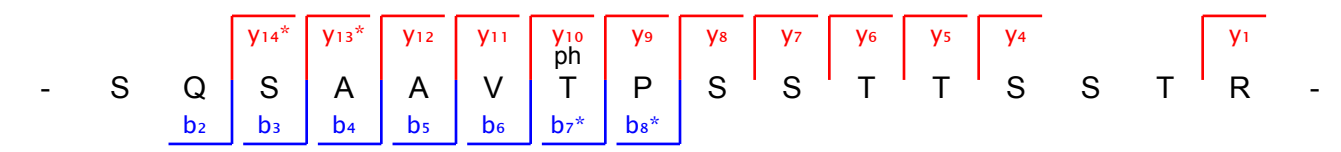
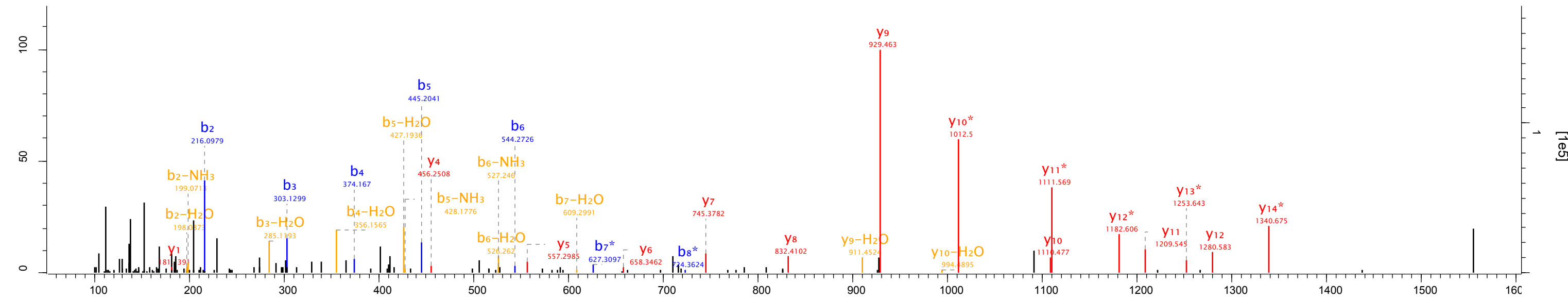
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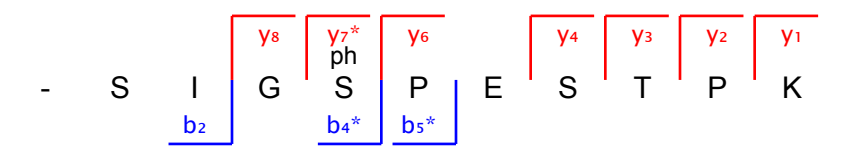
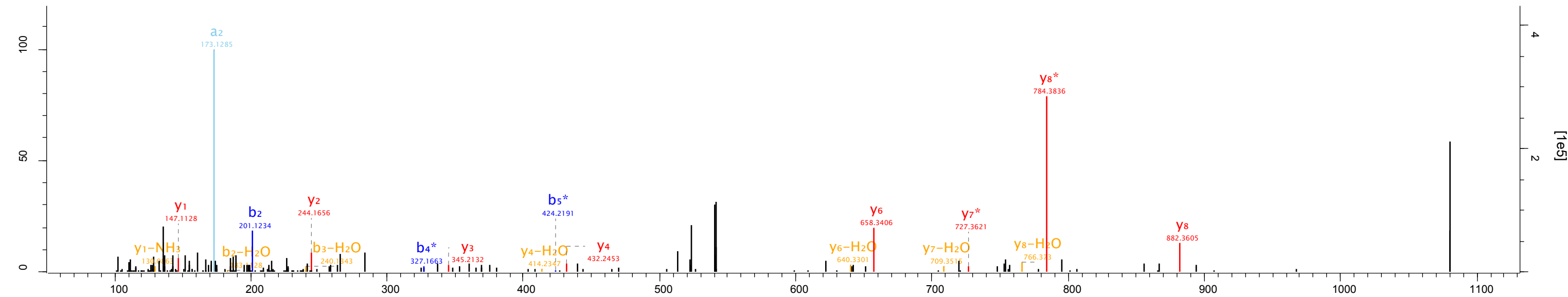
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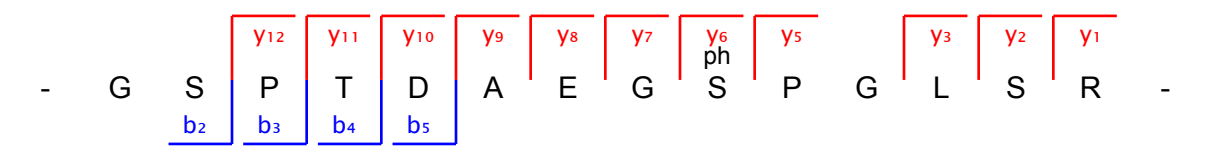
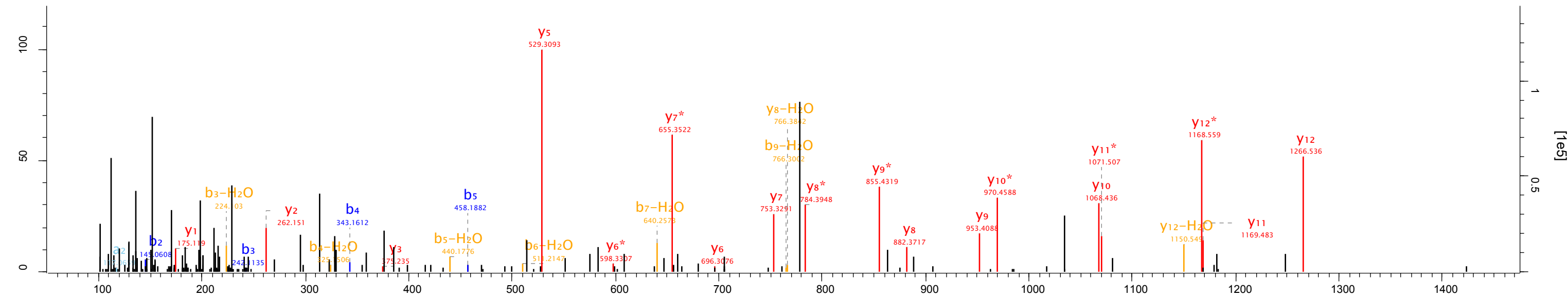
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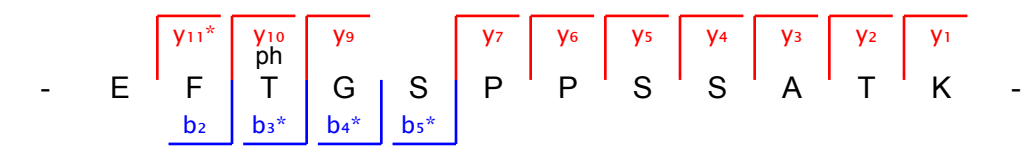
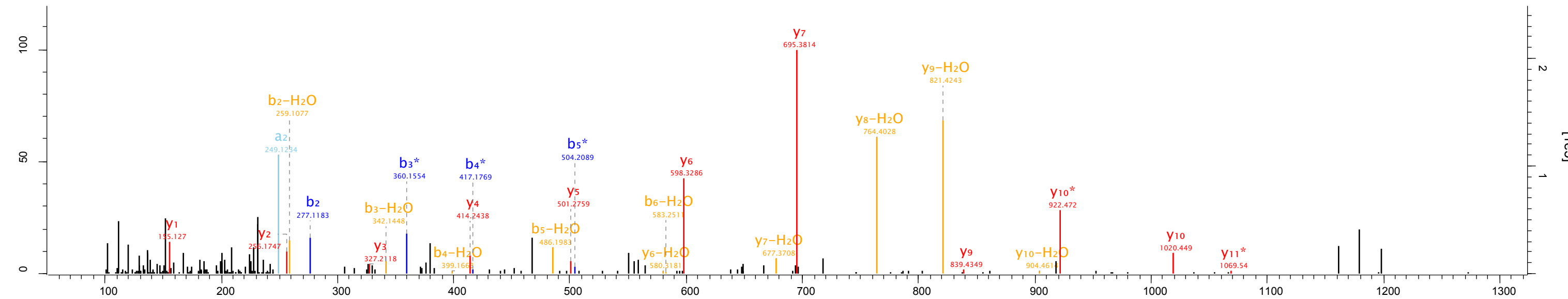
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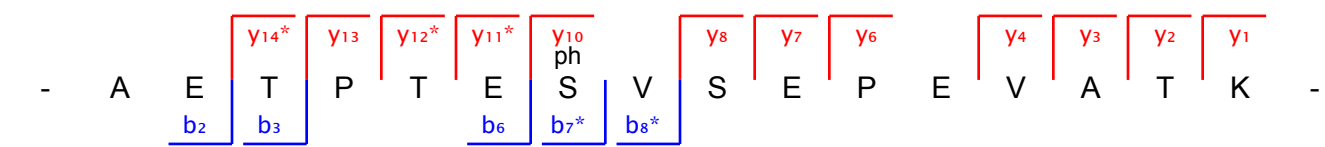
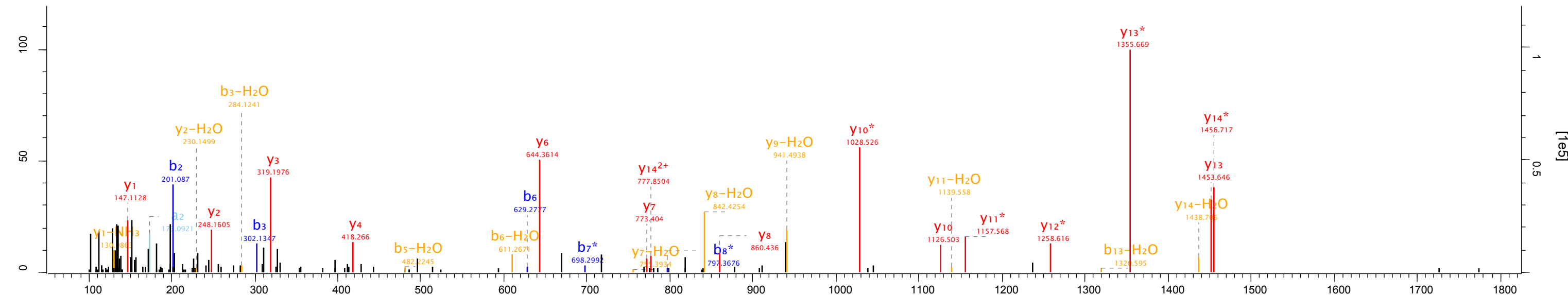
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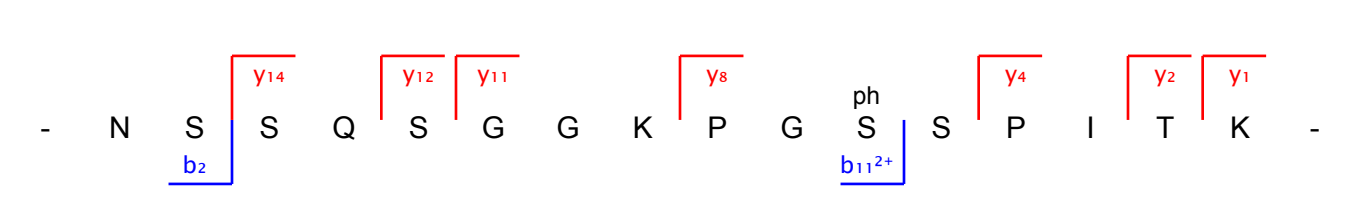
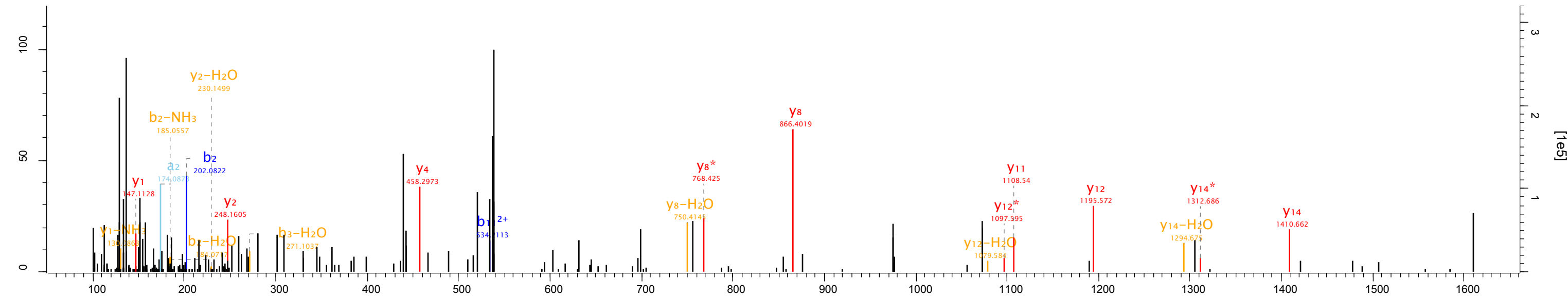
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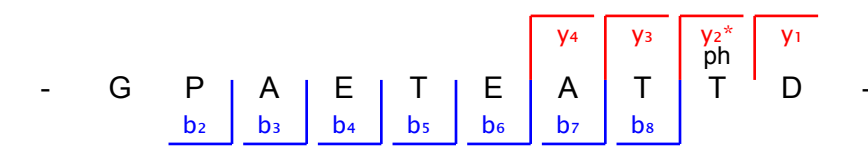
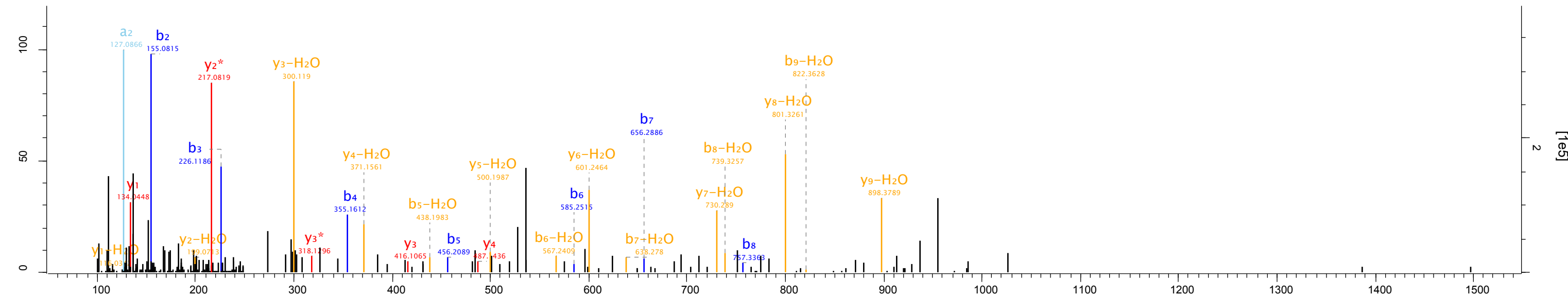


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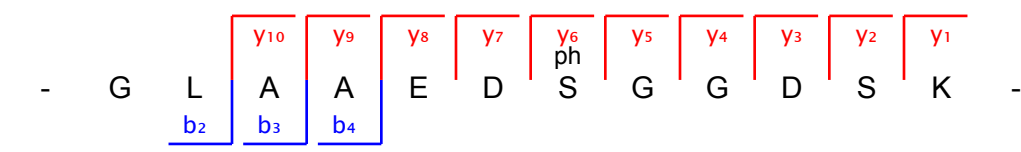
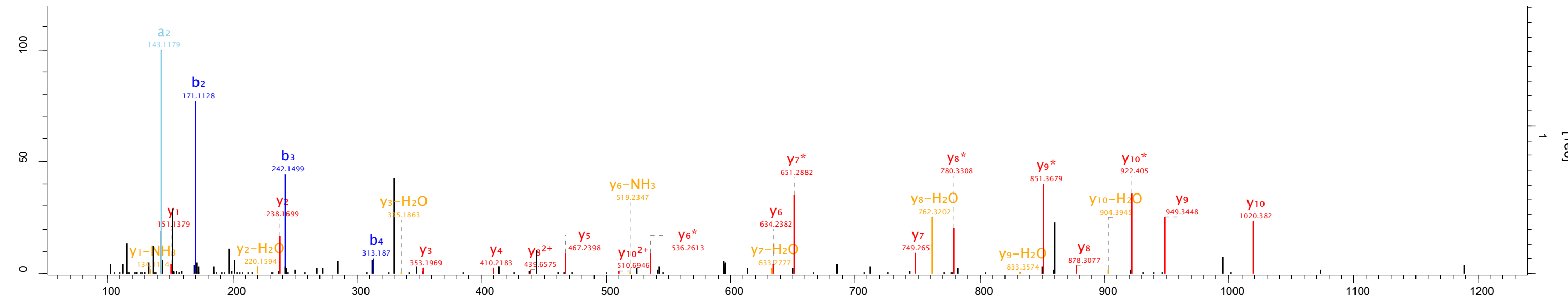


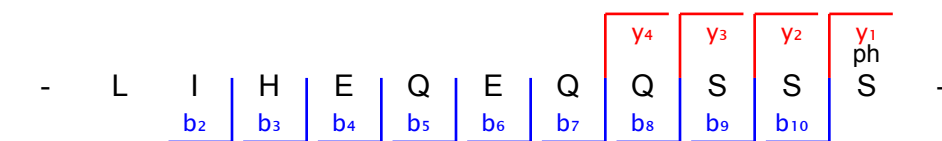
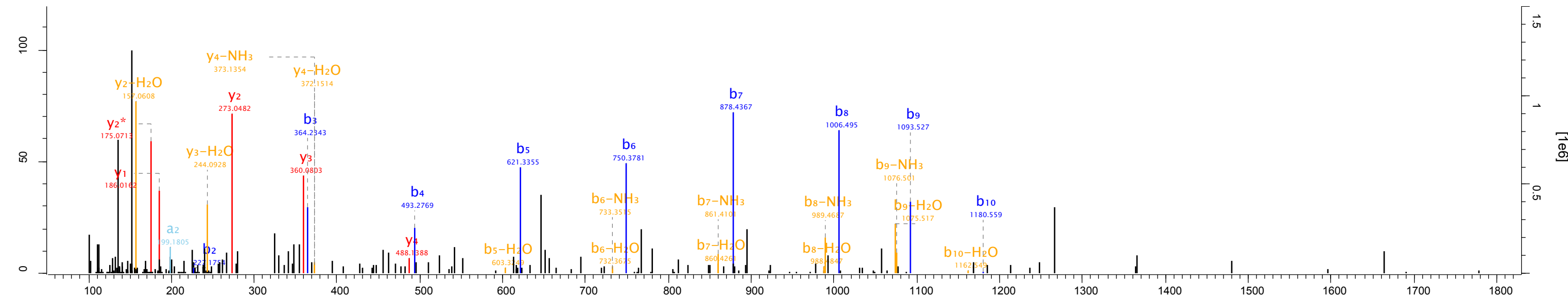
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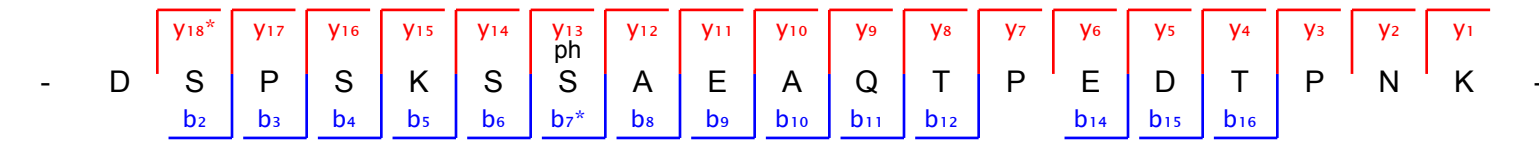
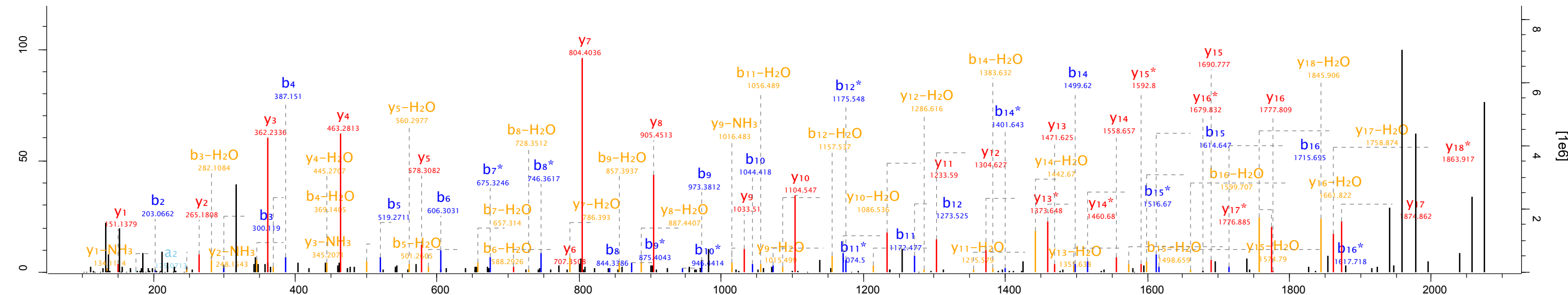


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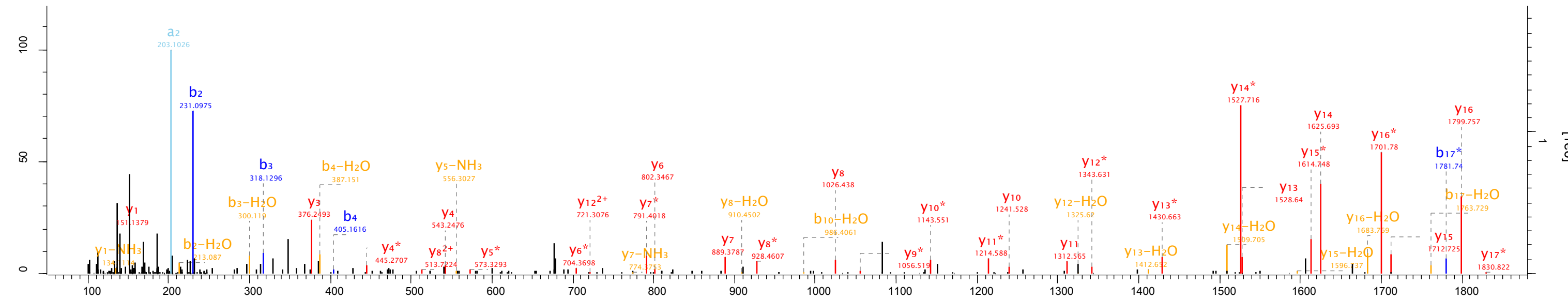




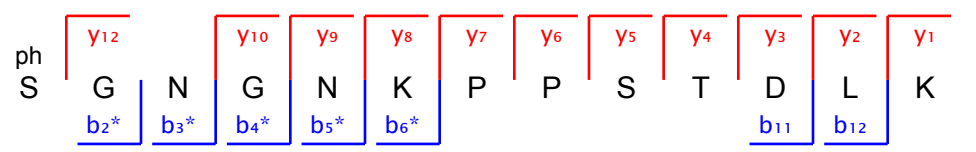
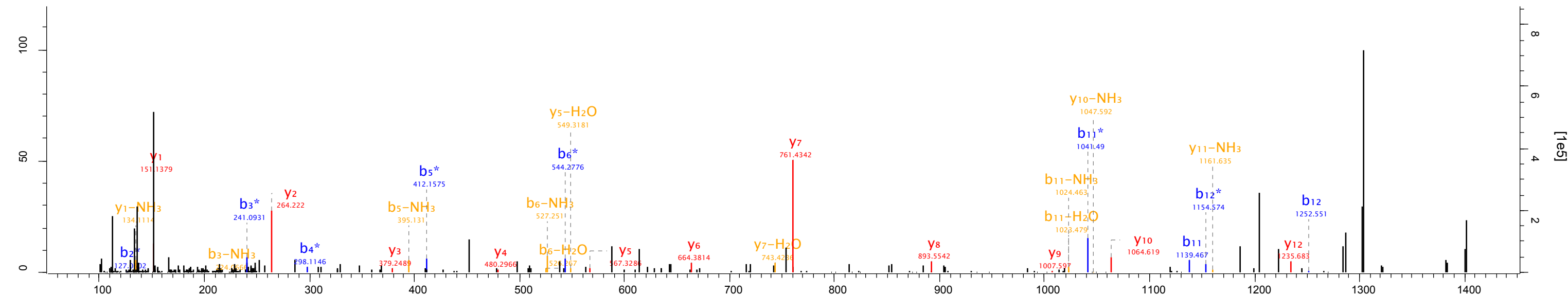
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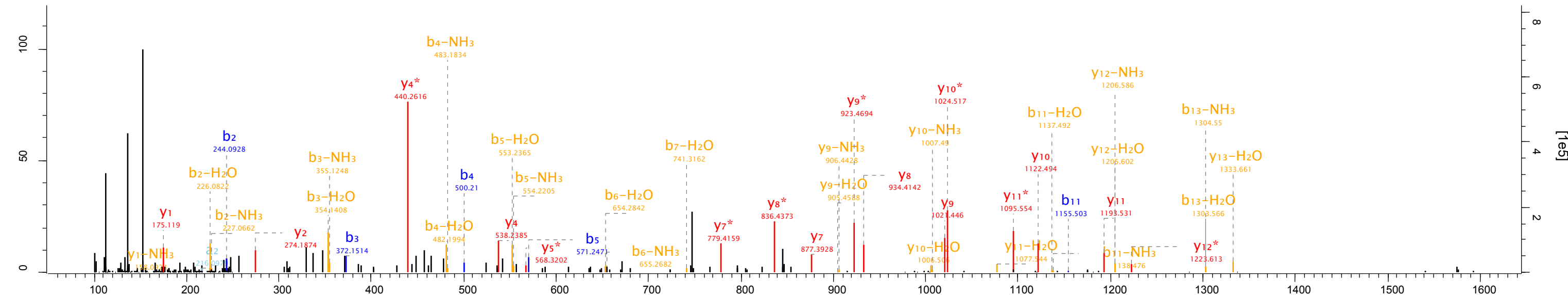


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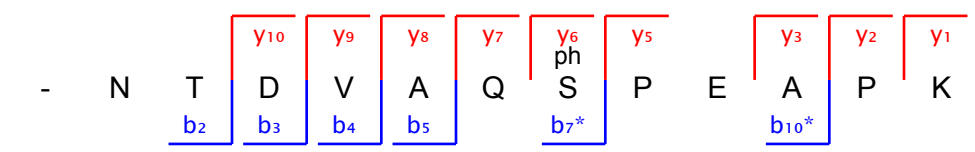
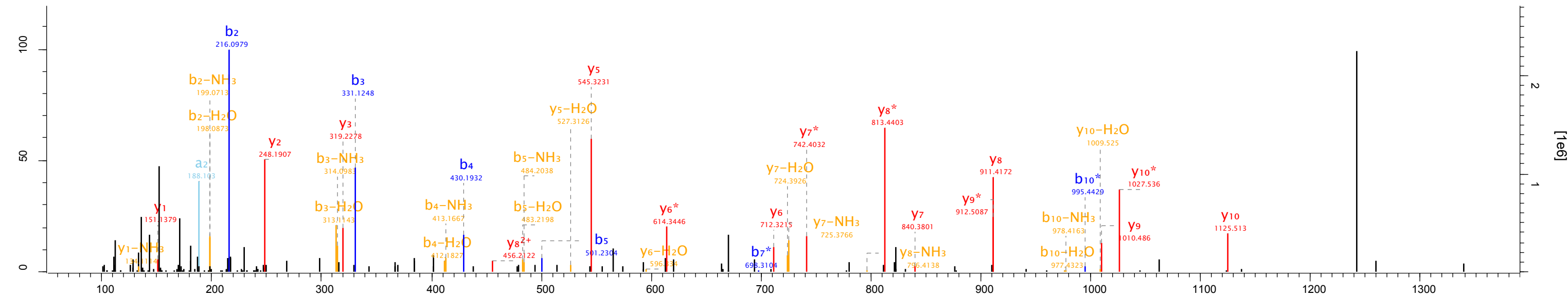


- E N Q Q A T S G P N Q P ph S V R -

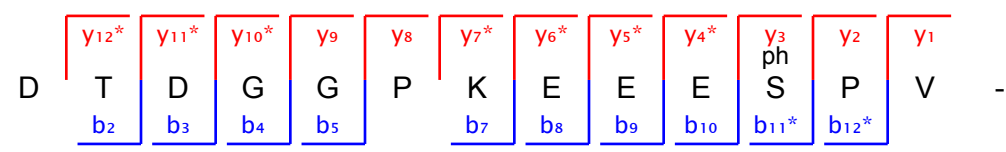
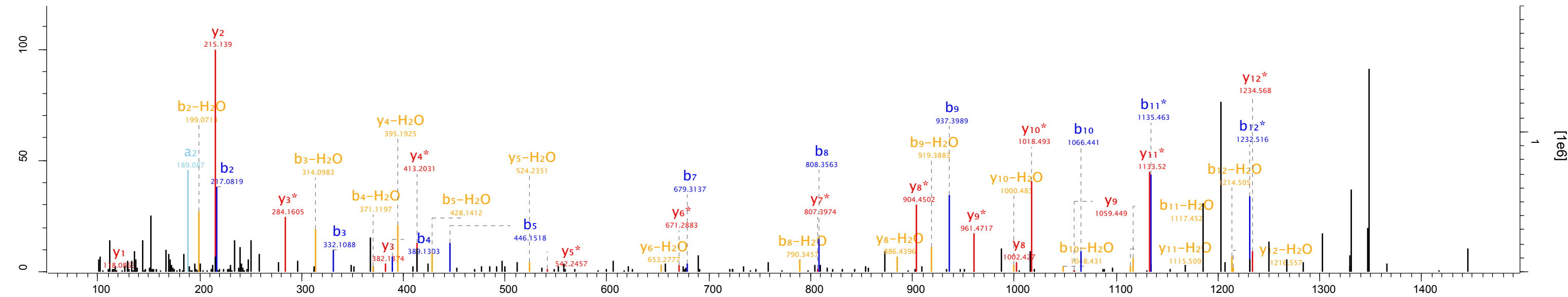
Fragmentation mapping (b and y ions):

- b2: N
- b3: Q
- b4: Q
- b5: A
- b11: Q
- y12*: Q
- y11: A
- y10: T
- y9: S
- y8: G
- y7: P
- y5*: Q
- y4: P
- y2: V
- y1: R

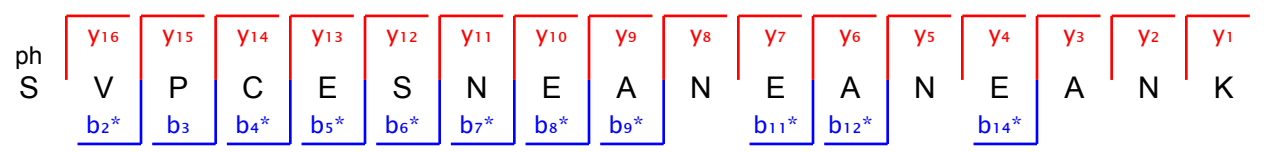
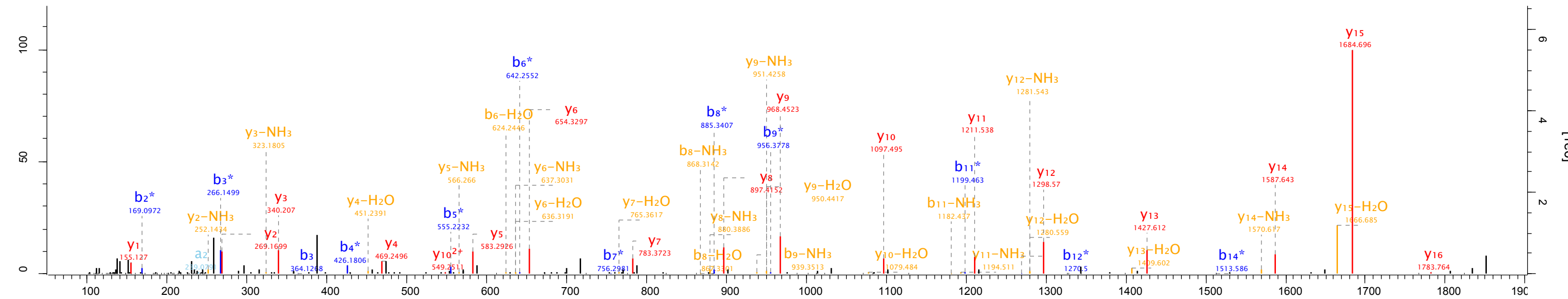
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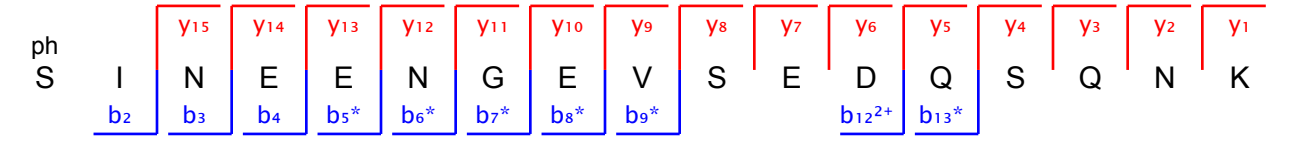
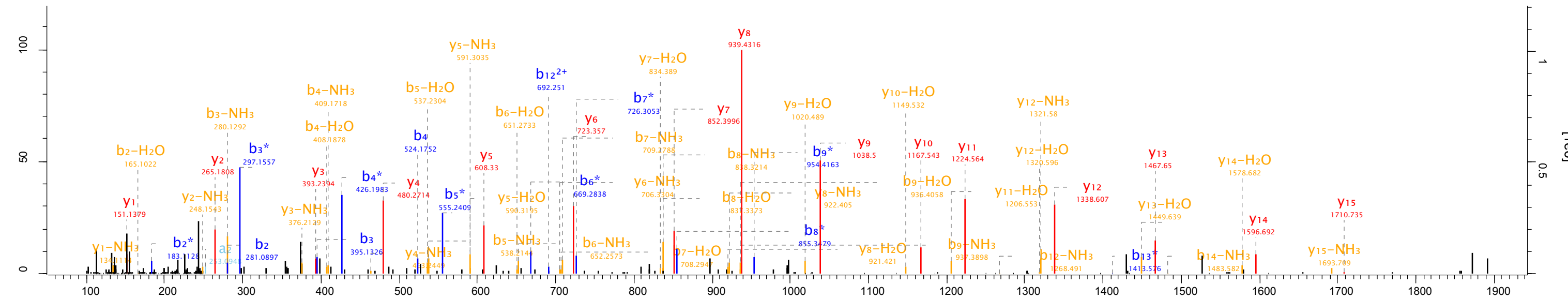
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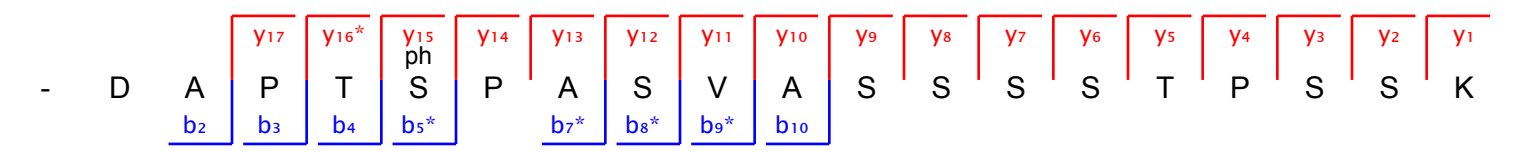
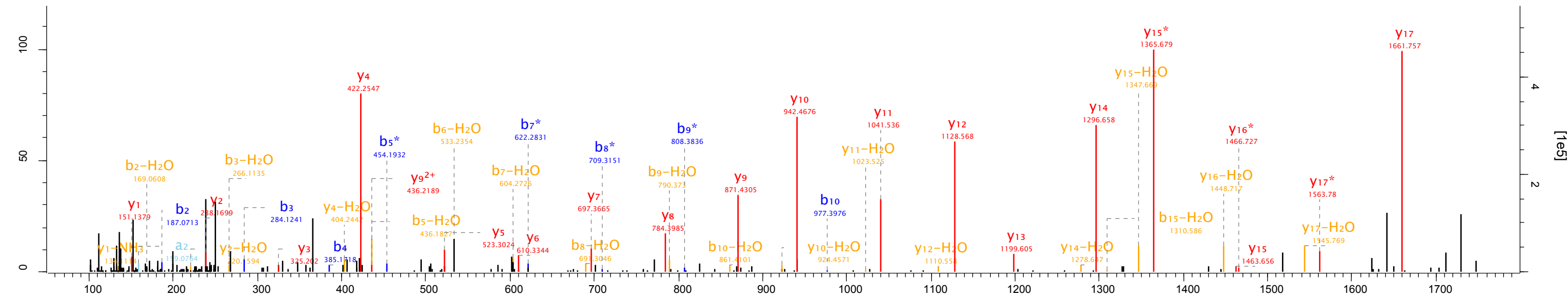
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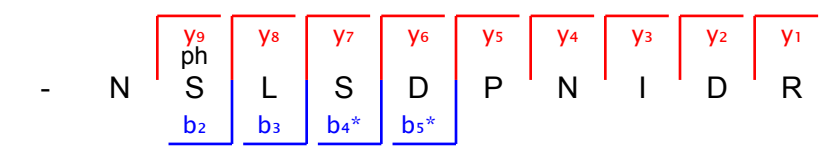
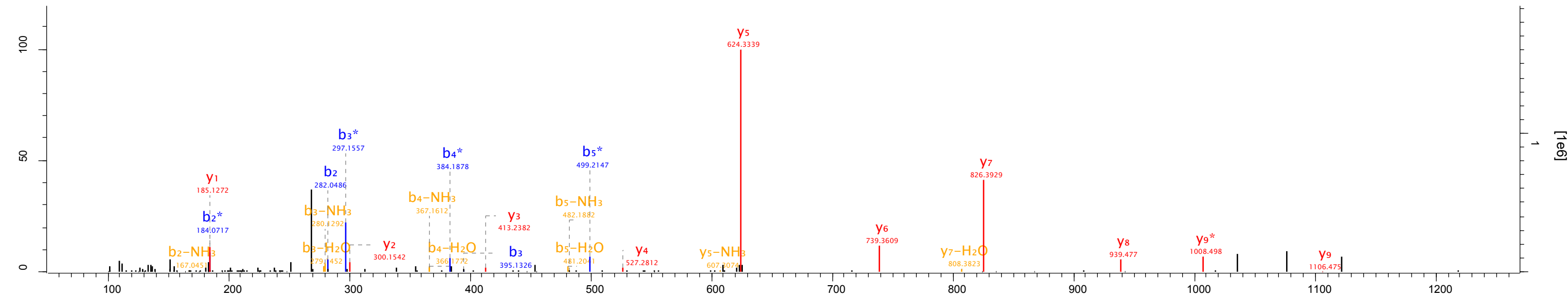
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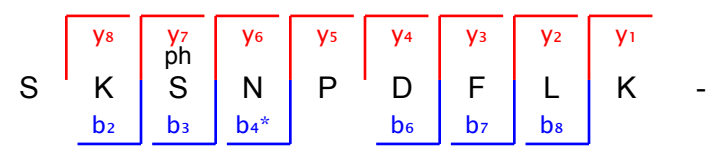
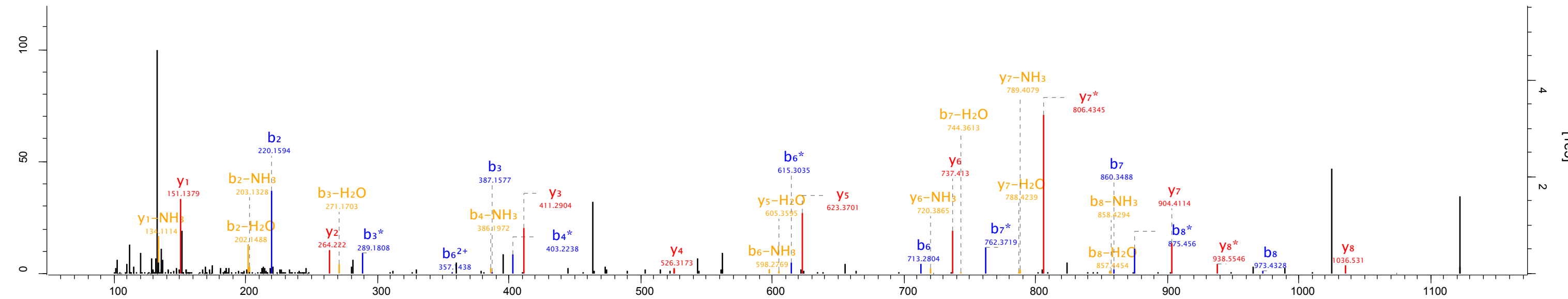
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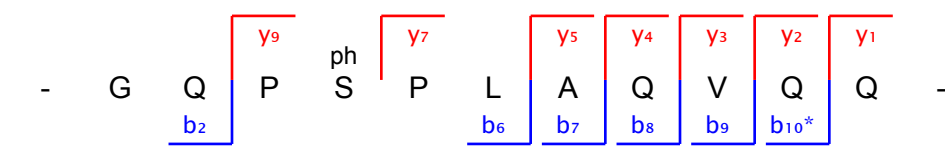
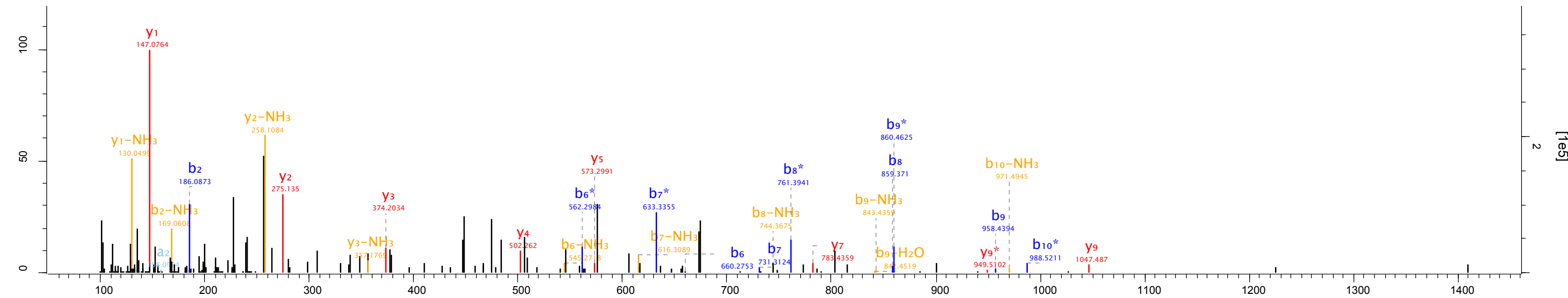
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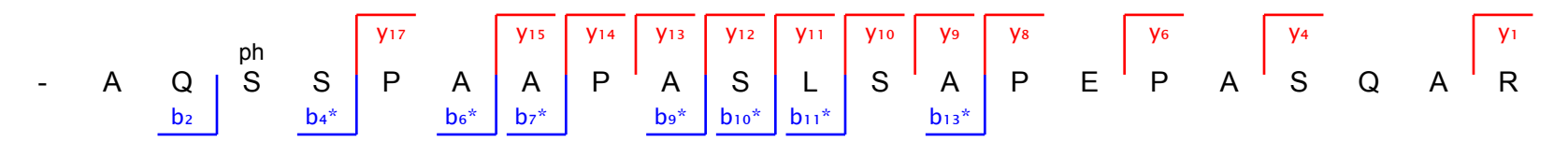
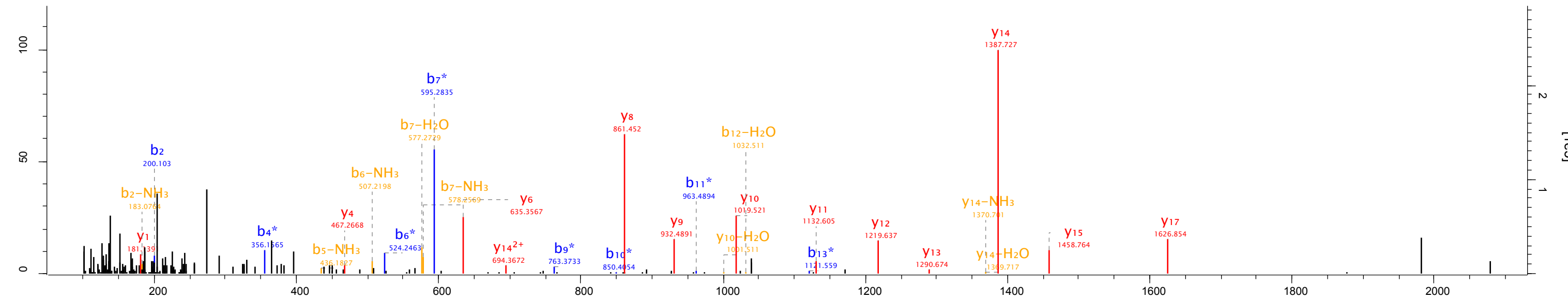
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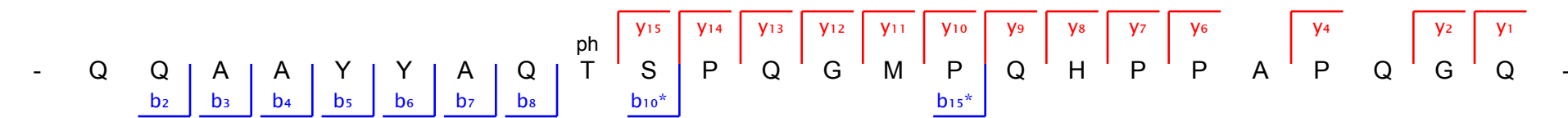
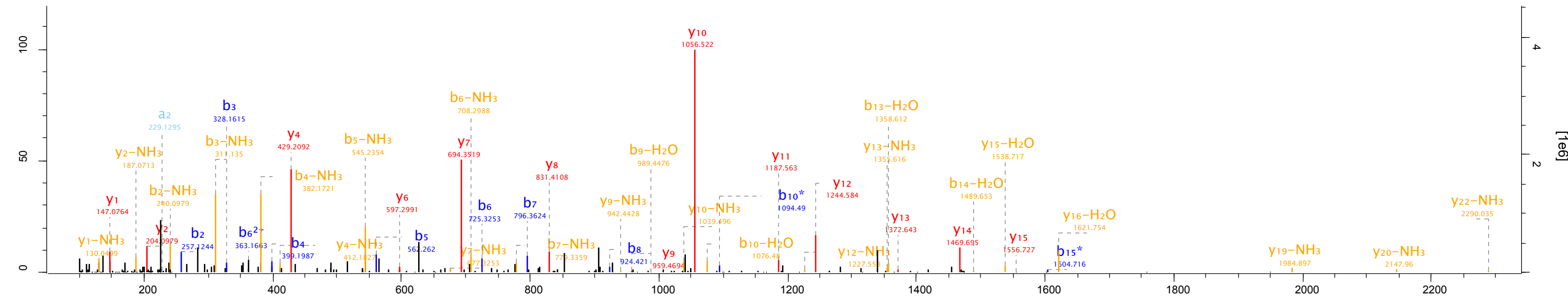


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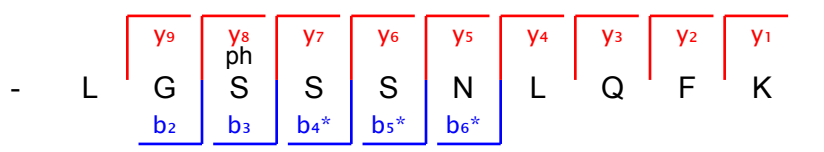
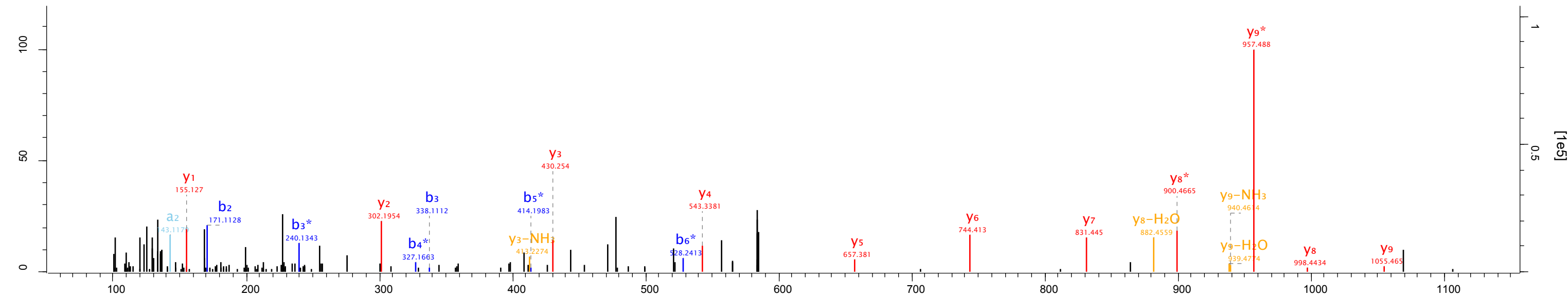


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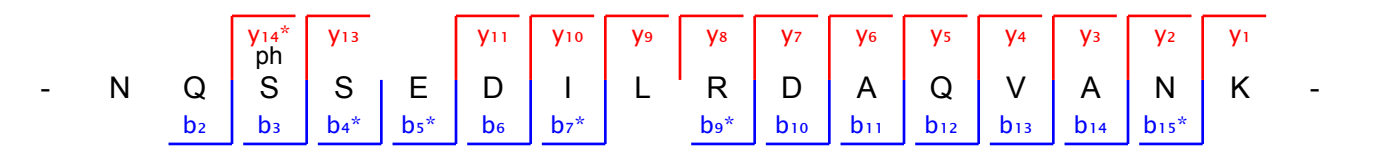
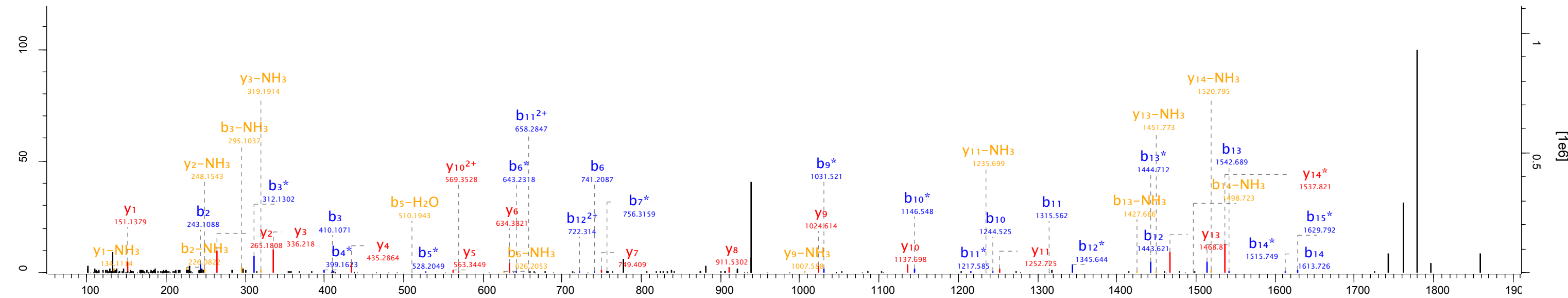




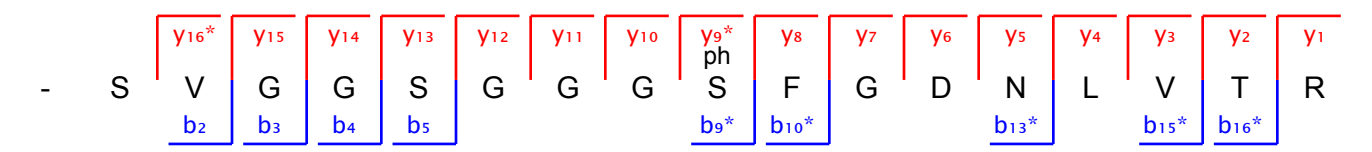
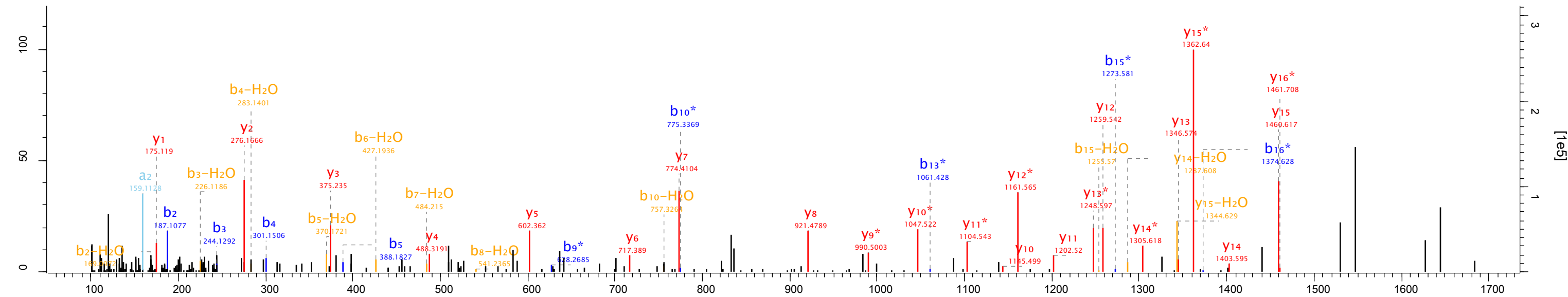
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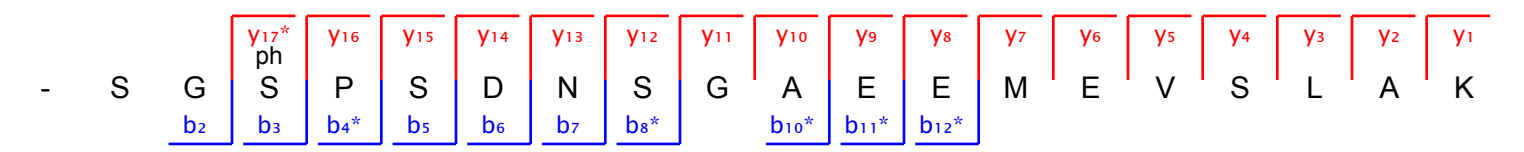
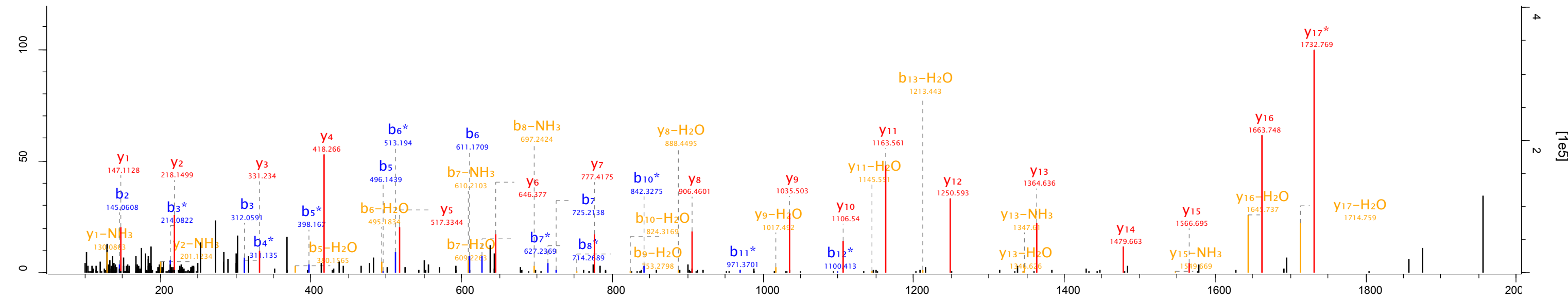
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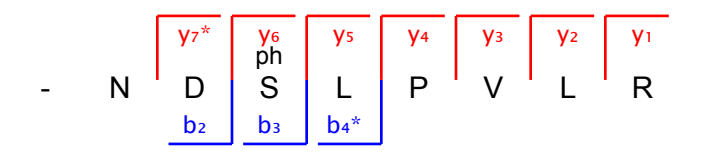
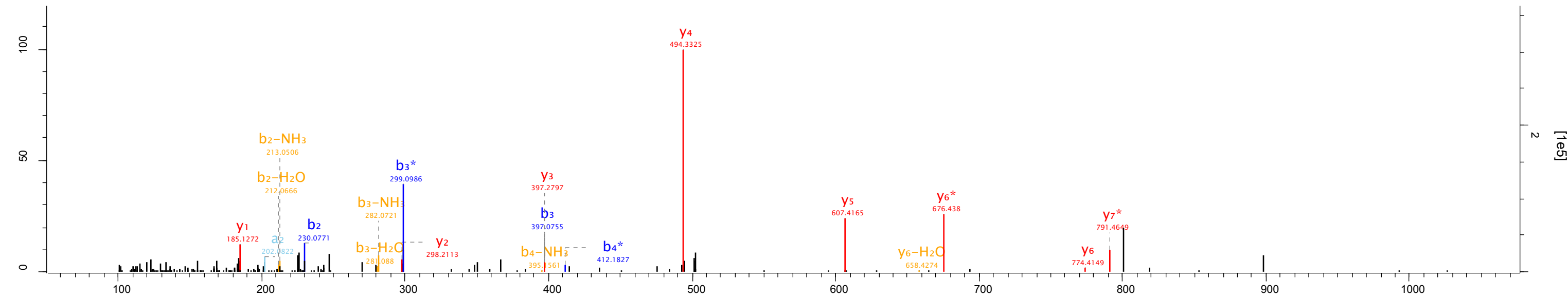
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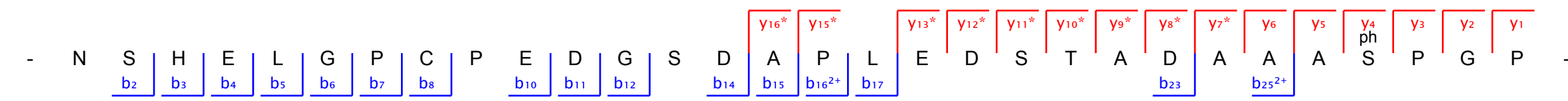
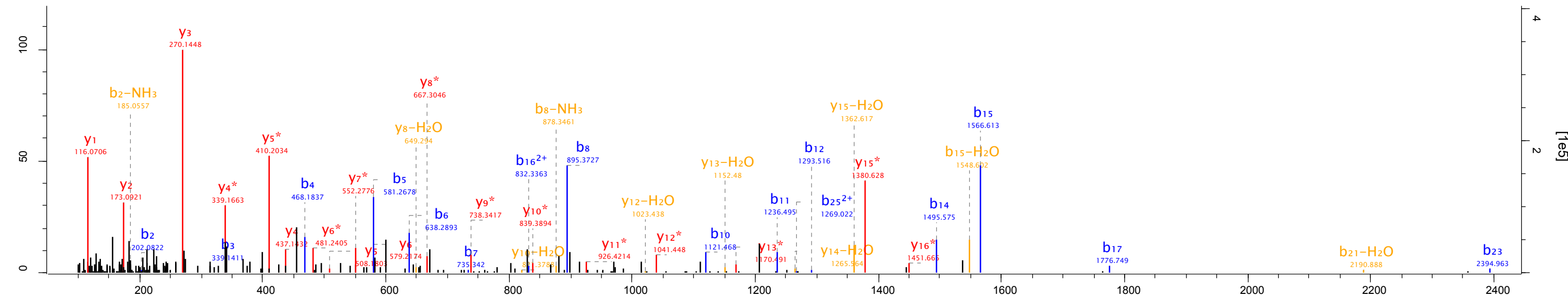
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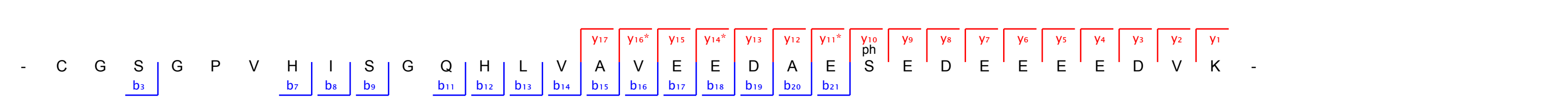
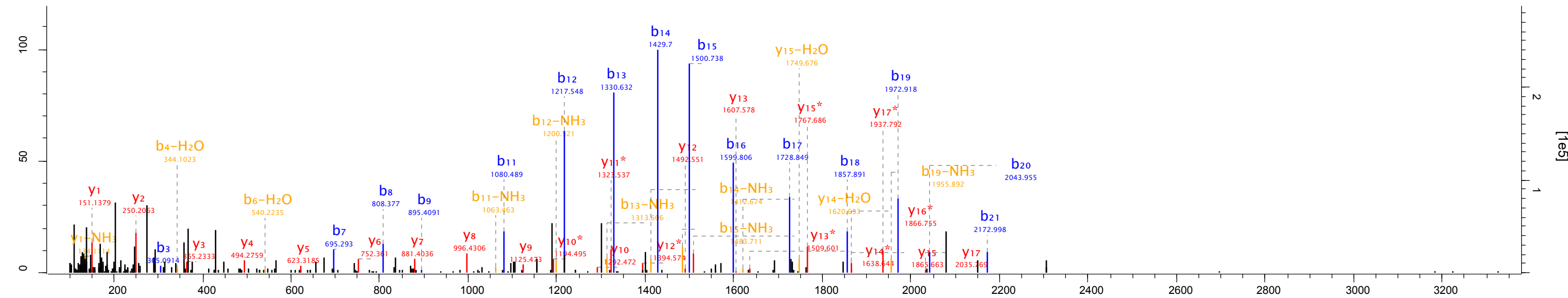
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11712 Method FTMS; HCD Score 54.29 m/z 502.25 Gene names MFF



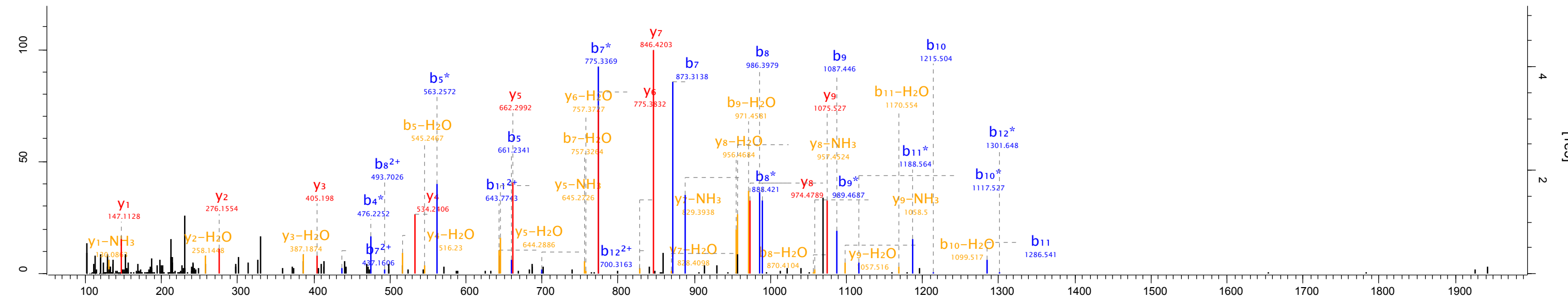
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11722 Method FTMS; HCD Score 91.44 m/z 1016.08 Gene names ARHGEF11



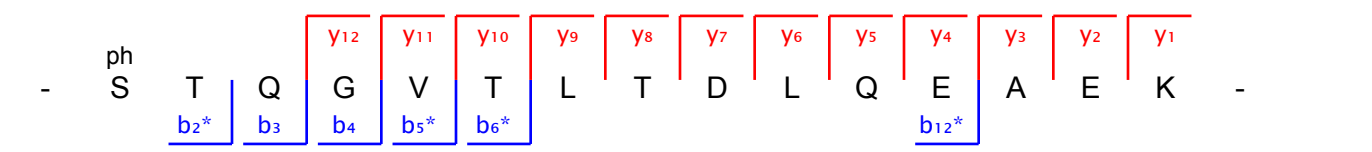
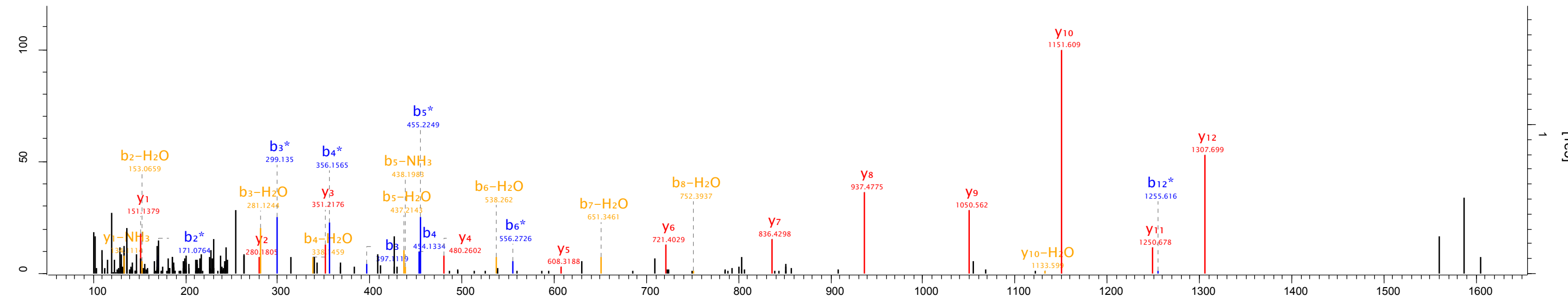
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11872 Method FTMS; HCD Score 126.11 m/z 1155.49 Gene names NPM1



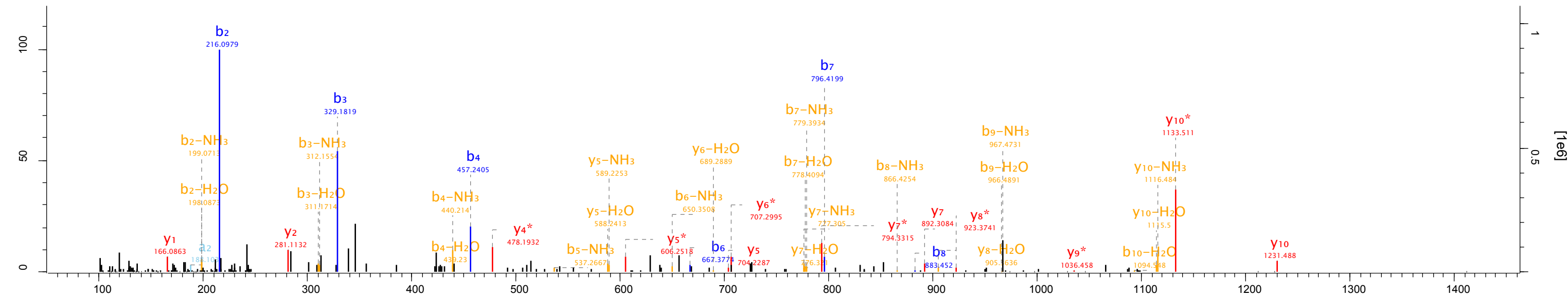
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 12252 Method FTMS; HCD Score 205.21 m/z 687.64 Gene names USP8



Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 13022 Method: FTMS; HCD Score: 79.47 m/z: 852.41 Gene names: PPP1R12A



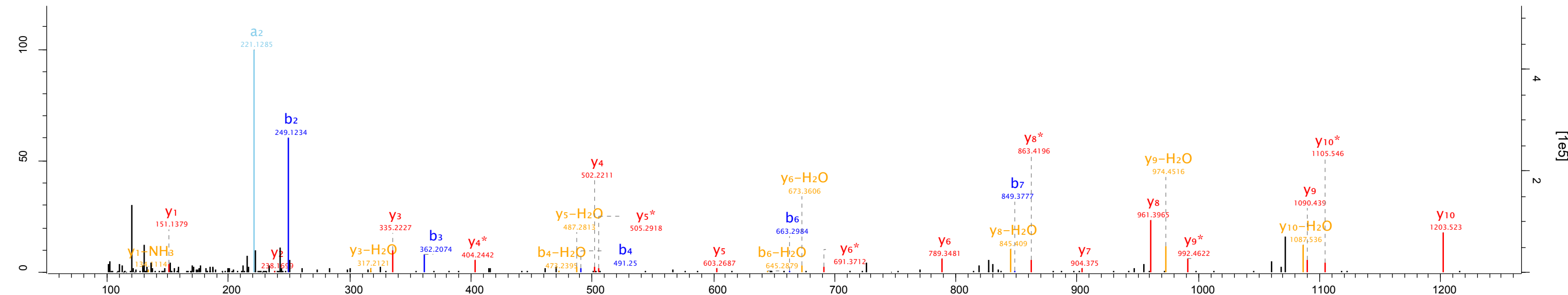
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 14292 Method FTMS; HCD Score 140.81 m/z 844.87 Gene names GINS2



Raw file

20171215_MaS_33SR_LMH_phospho2_02

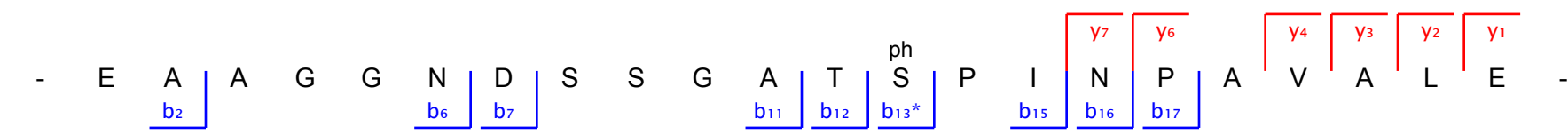
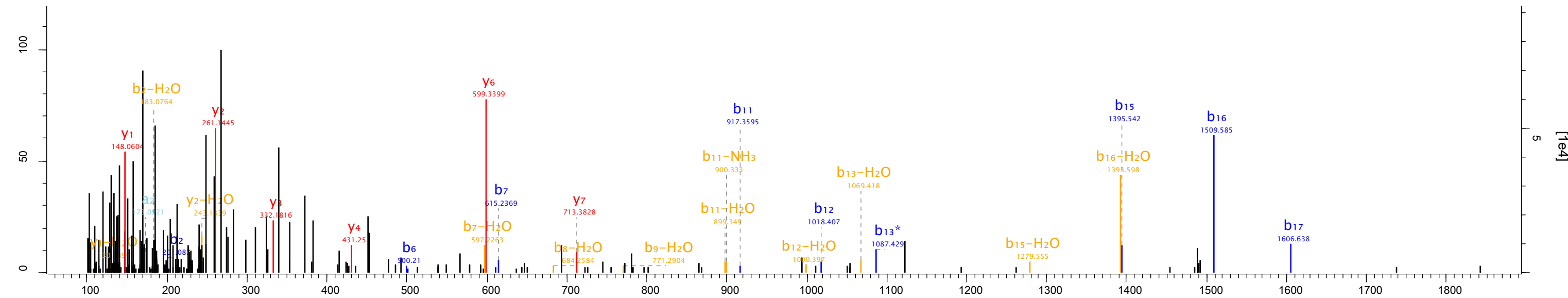
Scan	Method	Score	m/z	Gene names
14522	FTMS; HCD	137.79	726.32	RBM15B

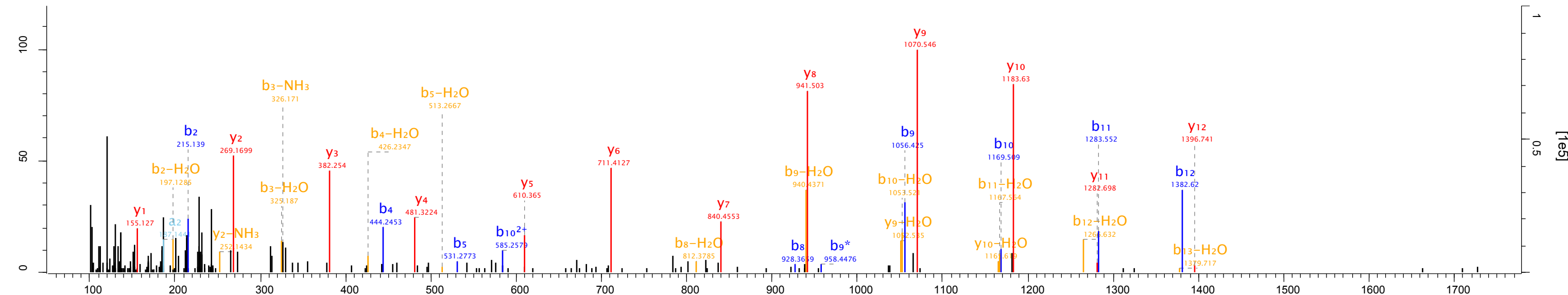


- T F L E G D W T S P S K -

Fragmentation sites are indicated by brackets below the sequence:

- b2: F
- b3: L
- b4: E
- b6: D
- b7: W
- y1: K
- y2: S
- y3: P
- y4-ph: S
- y5: T
- y6: W
- y7: D
- y8: G
- y9: E
- y10: L





- L T Q T S ph S T E Q L N V L E T E T E V L N K -

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

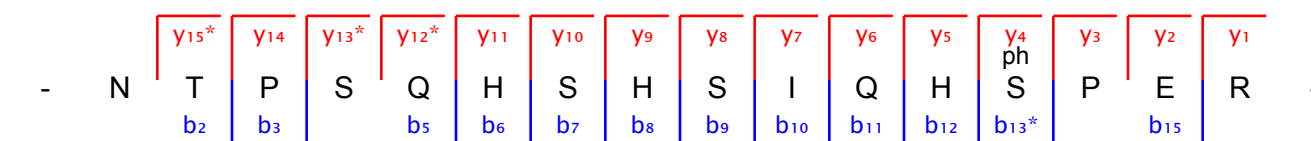
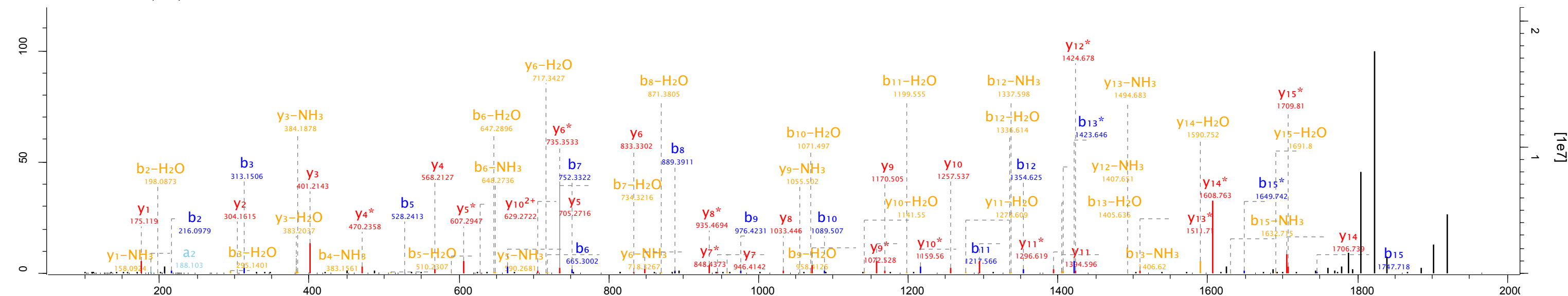
- b2: L T
- b4: T T
- b5: T S
- b8: E E
- b9: E Q
- b10: E Q L
- b11: E Q L N
- b12: E Q L N V

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

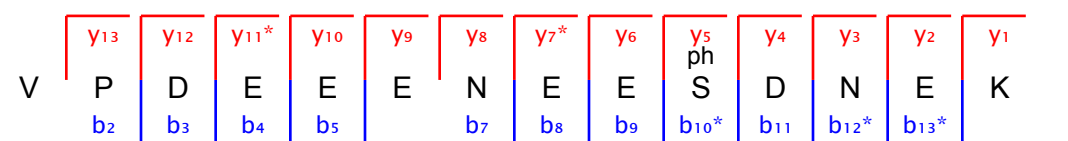
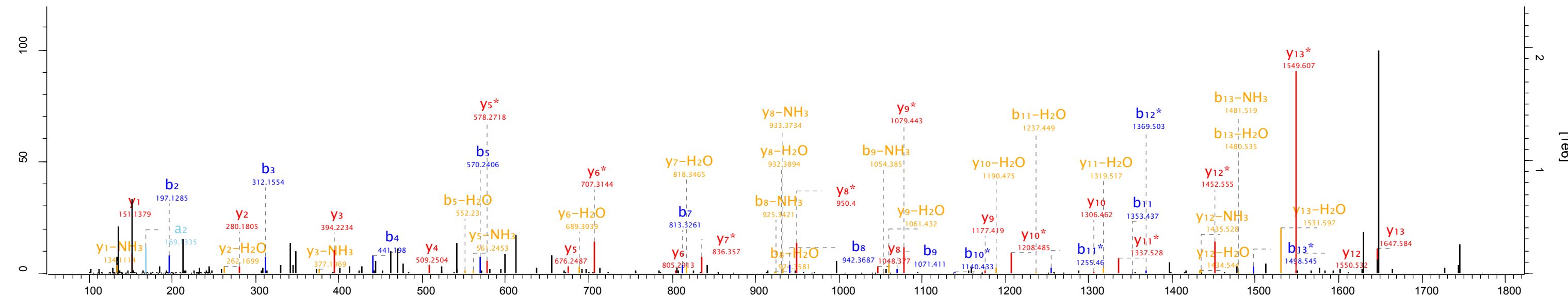
- y1: K
- y2: N
- y3: L
- y4: V
- y5: E
- y6: T
- y7: E
- y8: T
- y9: E
- y10: L
- y11: V
- y12: N

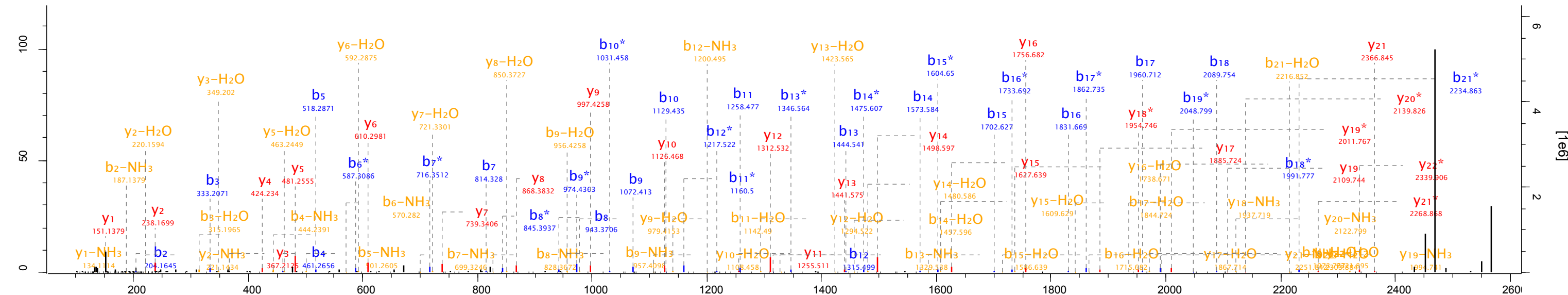
Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 1972 Method FTMS; HCD Score 326.2 m/z 961.92 Gene names BCLAF1



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 2812 Method FTMS; HCD Score 246.9 m/z 873.83 Gene names TOP2A

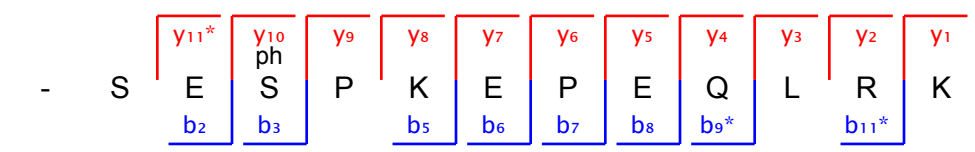
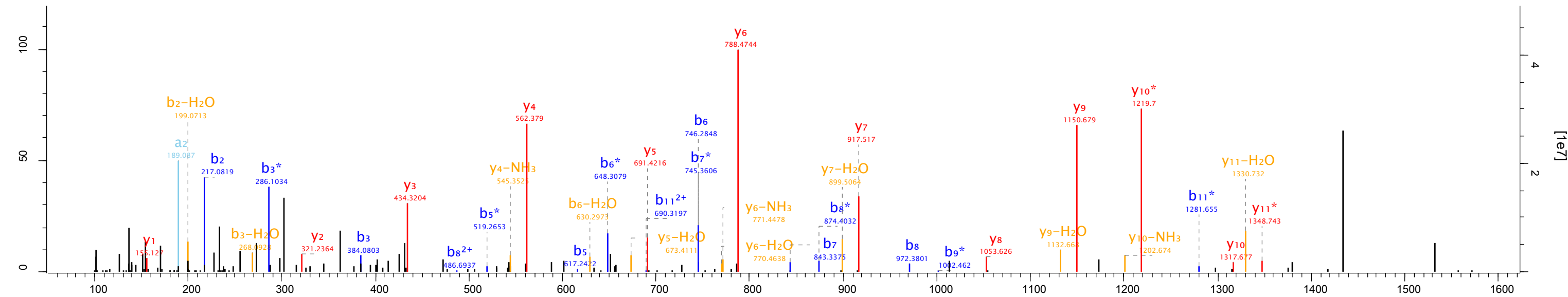


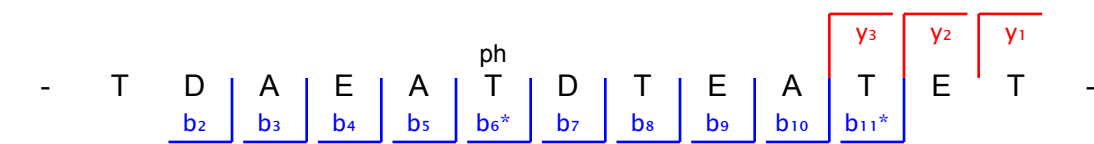
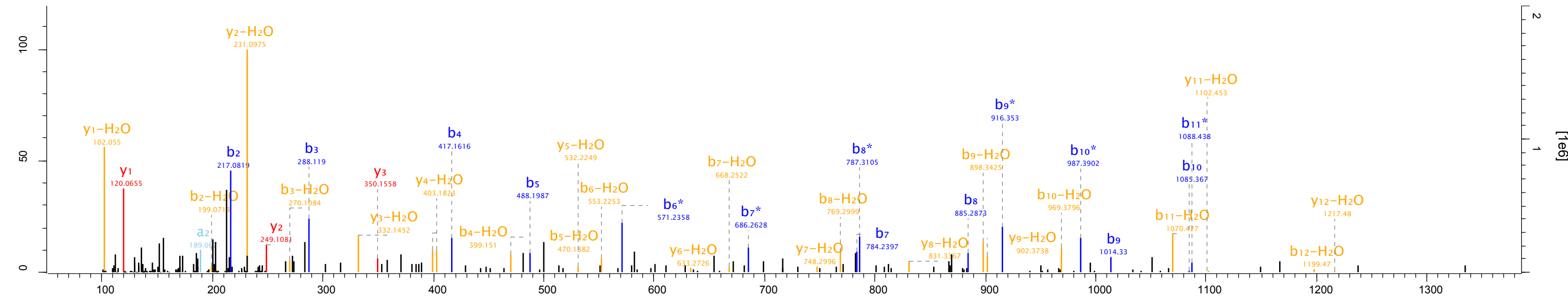


- K y₂₂* y₂₁ y₂₀* y₁₉ y₁₈* y₁₇ y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁ -

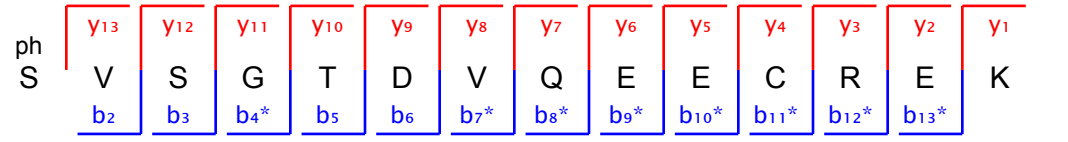
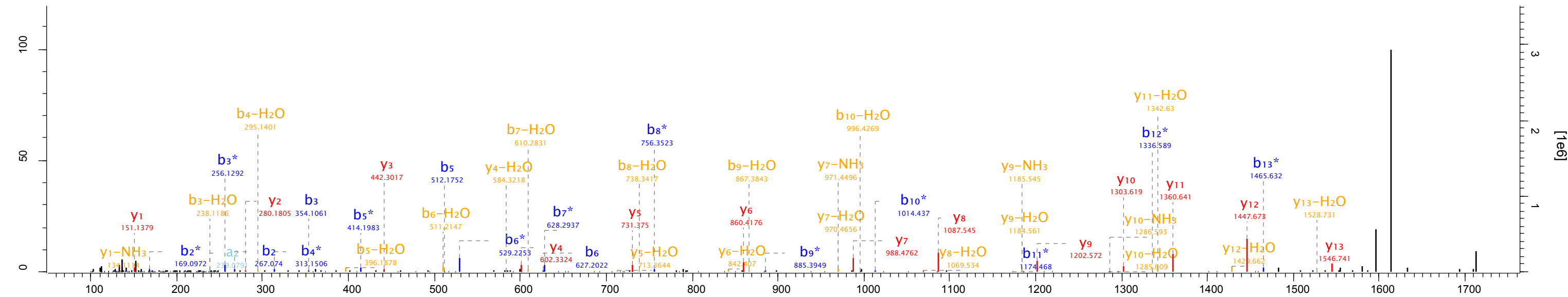
b₂ b₃ b₄ b₅ b₆* b₇ b₈ b₉ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄ b₁₅ b₁₆ b₁₇ b₁₈ b₁₉* G b₂₁* S K -

Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3232 Method FTMS; HCD Score 209.66 m/z 511.92 Gene names HNRNPA1

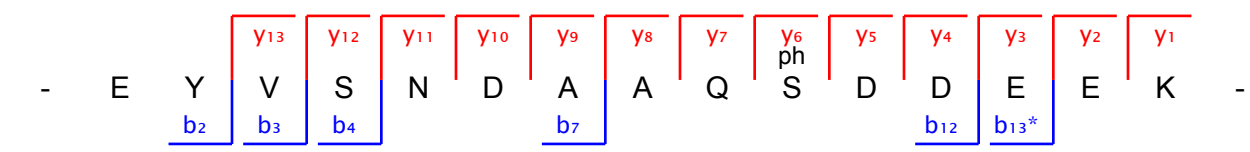
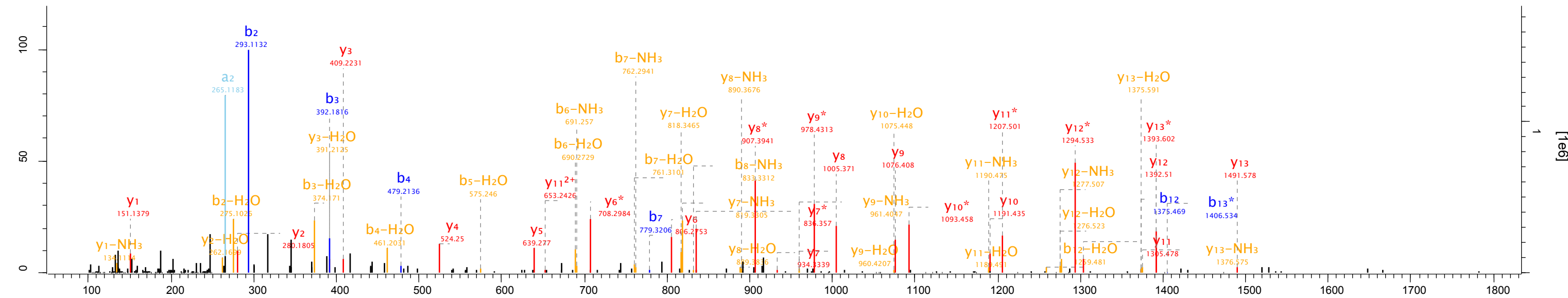




Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 3472 Method: FTMS; HCD Score: 237.86 m/z: 857.37 Gene names: NASP

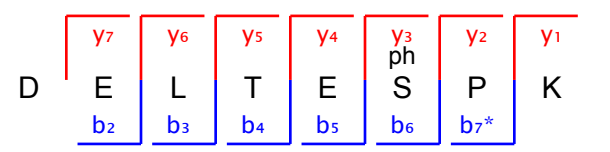
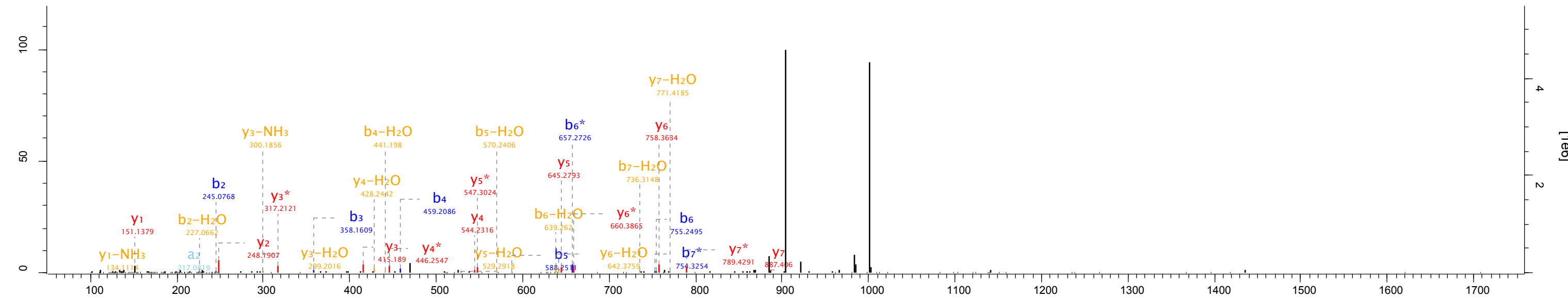


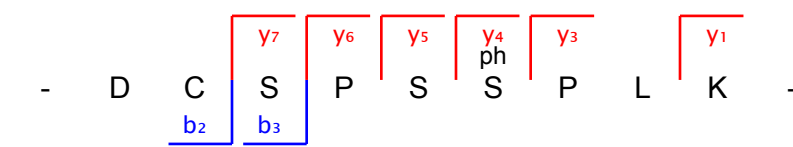
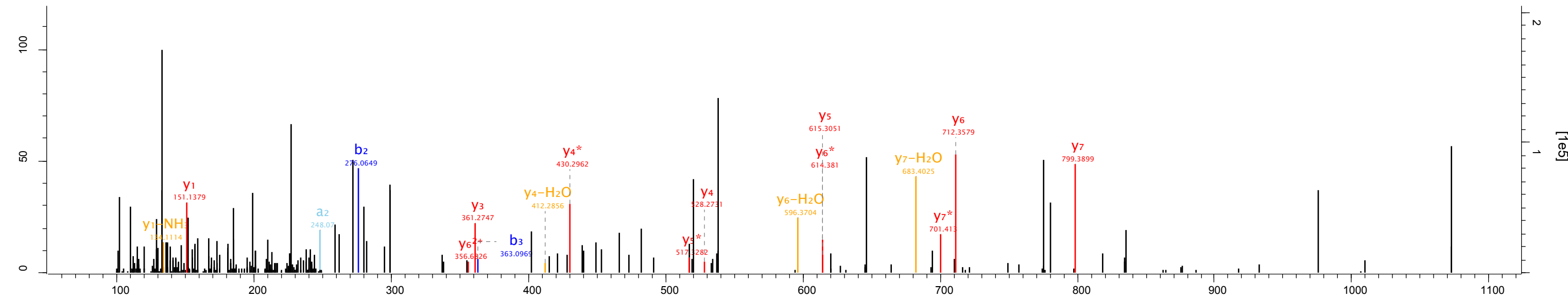
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3772 Method FTMS; HCD Score 277.1 m/z 892.35 Gene names WDR44



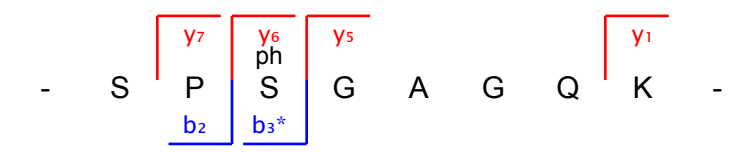
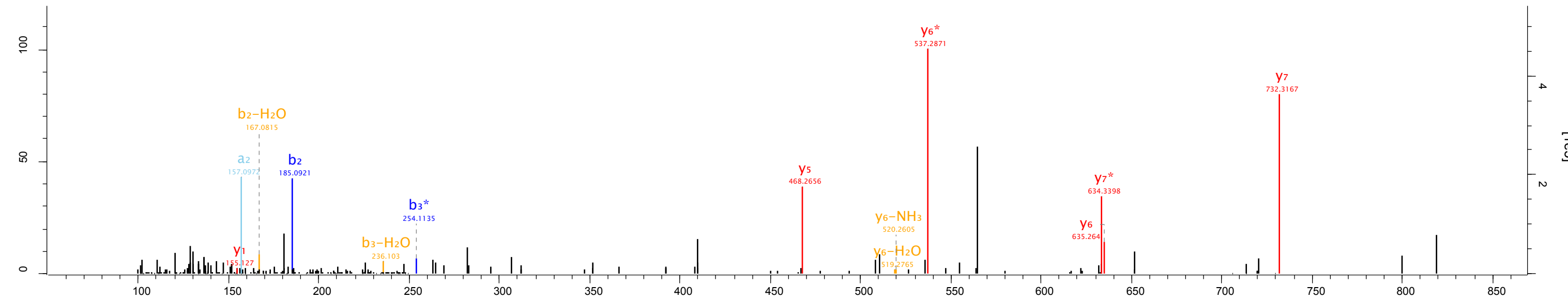
Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 3792 Method FTMS; HCD Score 221.91 m/z 1002.43 Gene names SERBP1

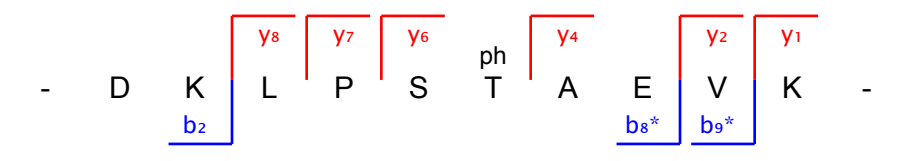
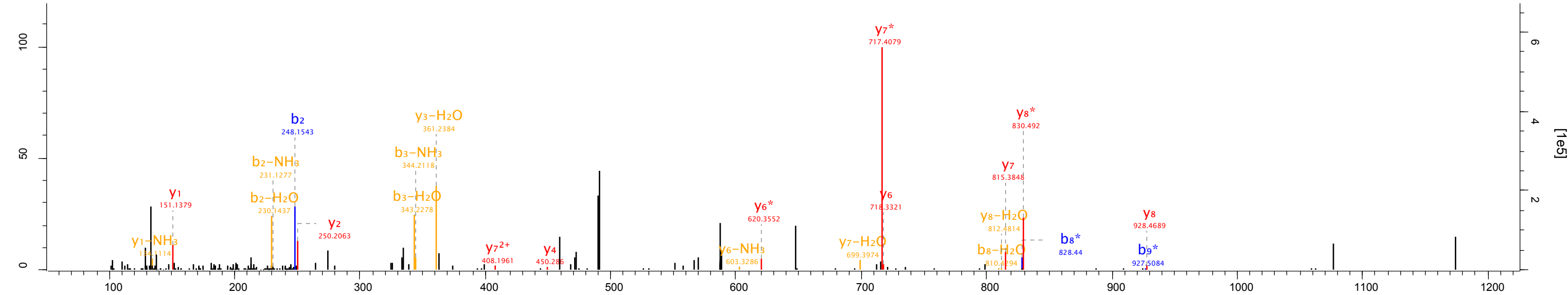




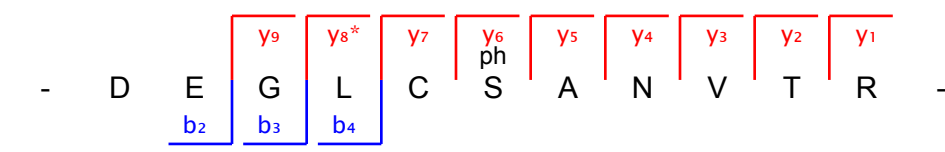
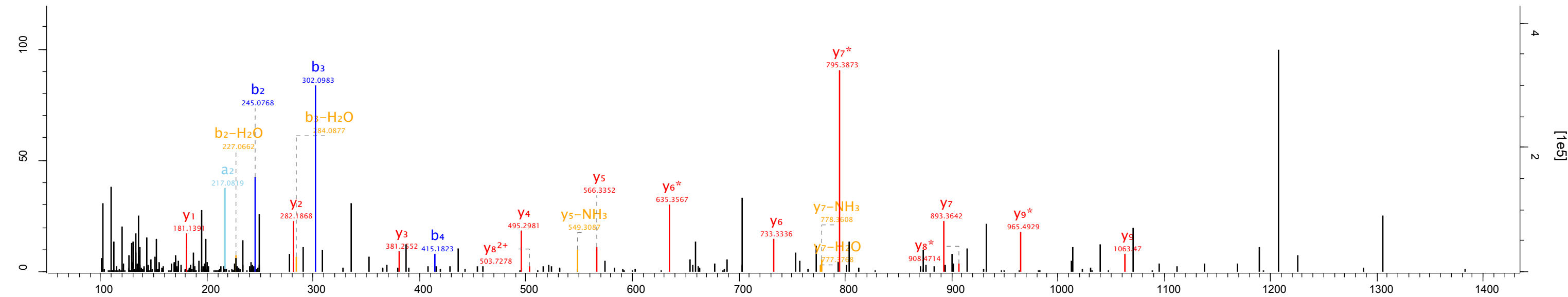
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 5172 Method FTMS; HCD Score 50.11 m/z 410.18



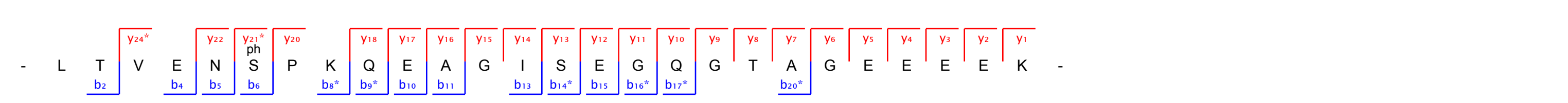
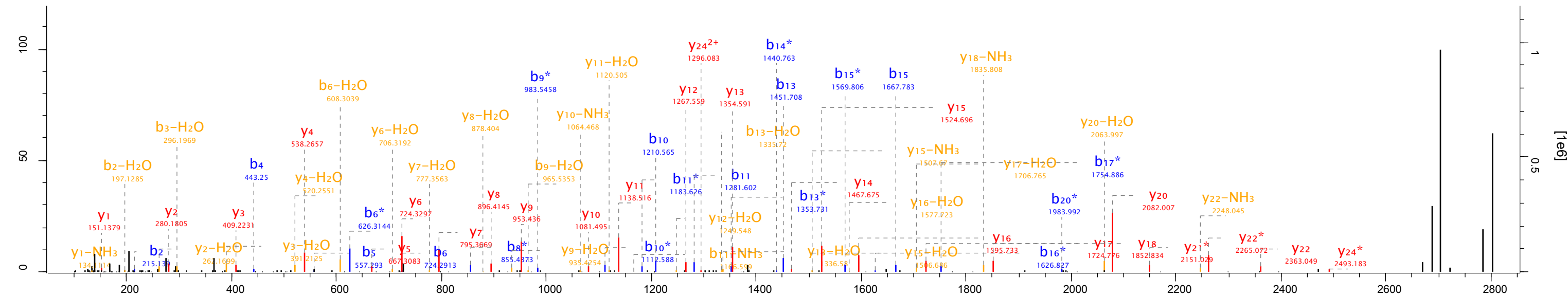
20171215_MaS_33SR_LMH_phospho2_02 5452 FTMS; HCD 101.32 588.31 NFKB2

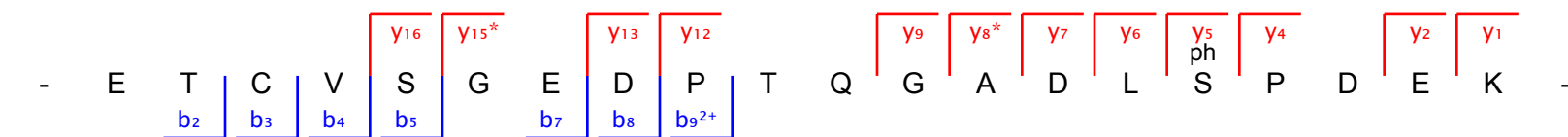
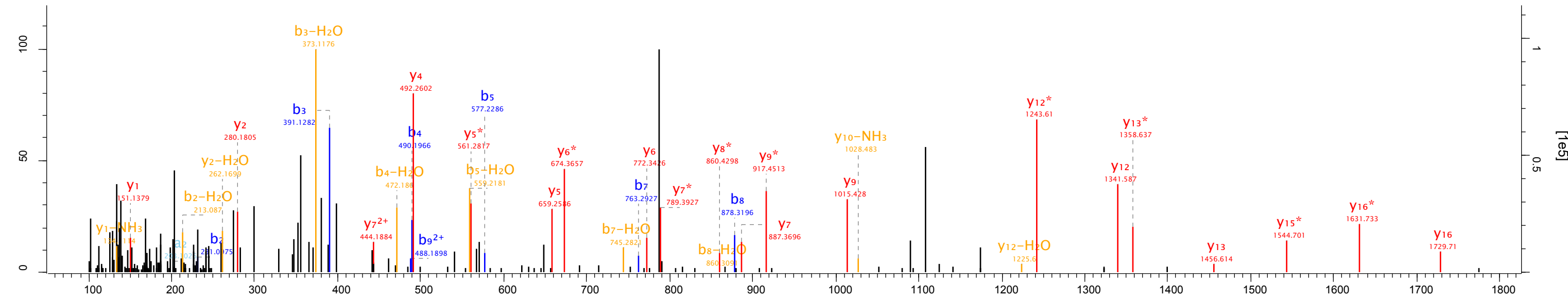


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 6112 Method: FTMS; HCD Score: 78.61 m/z: 654.28 Gene names: TFPI2

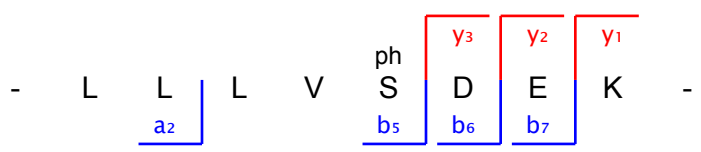
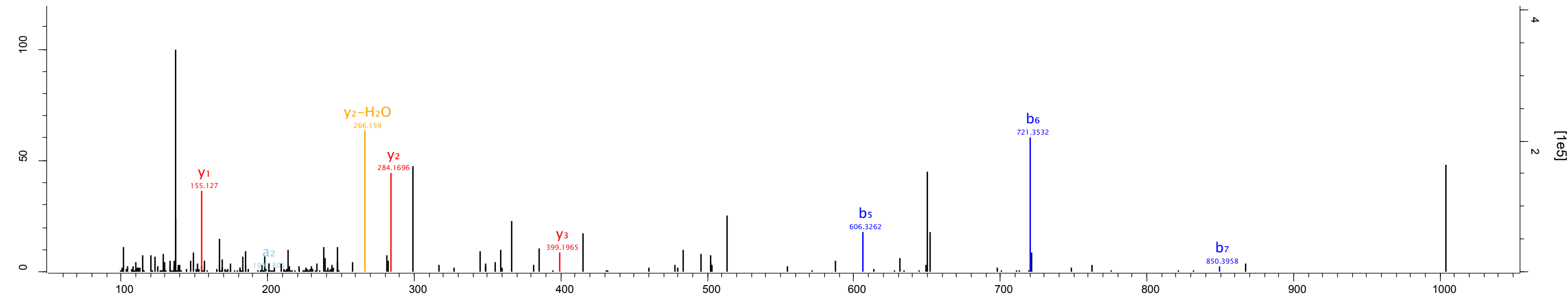


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 7482 Method: FTMS; HCD Score: 278.57 m/z: 1403.66 Gene names: DENR

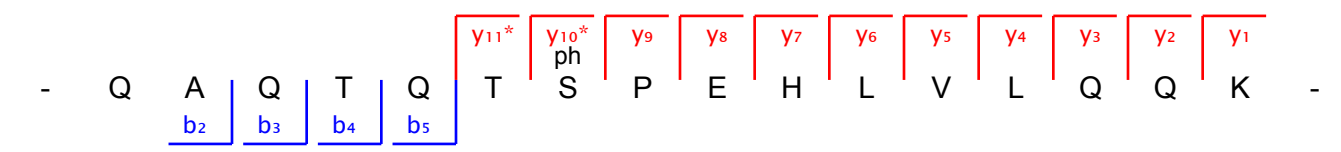
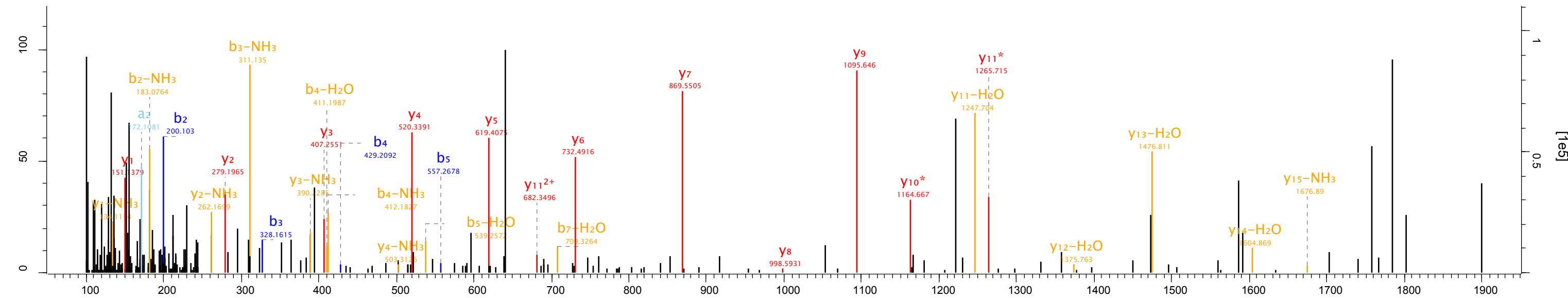




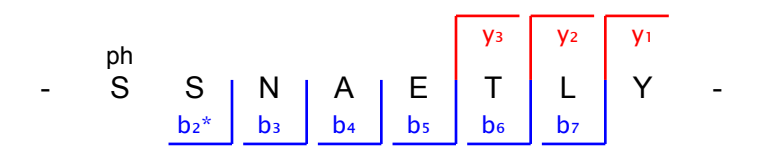
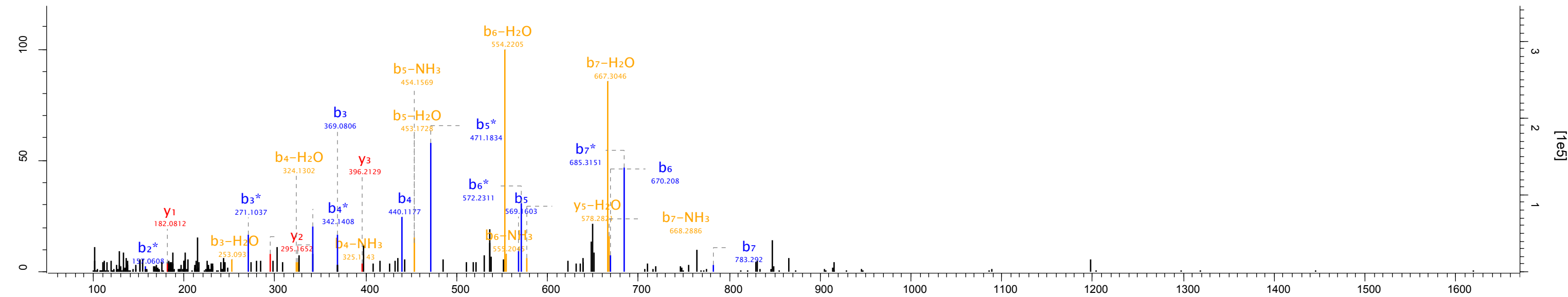
Raw file
20171215_MaS_33SR_LMH_phospho2_02
Scan 8262 Method FTMS; HCD Score 49.1 m/z 502.76



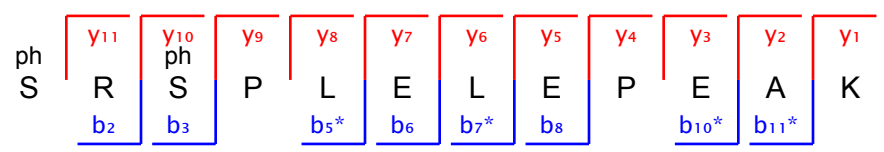
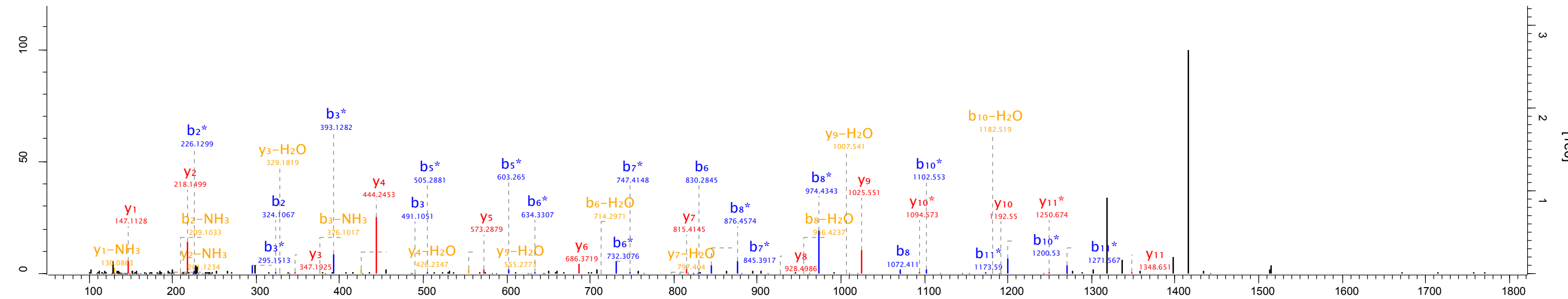
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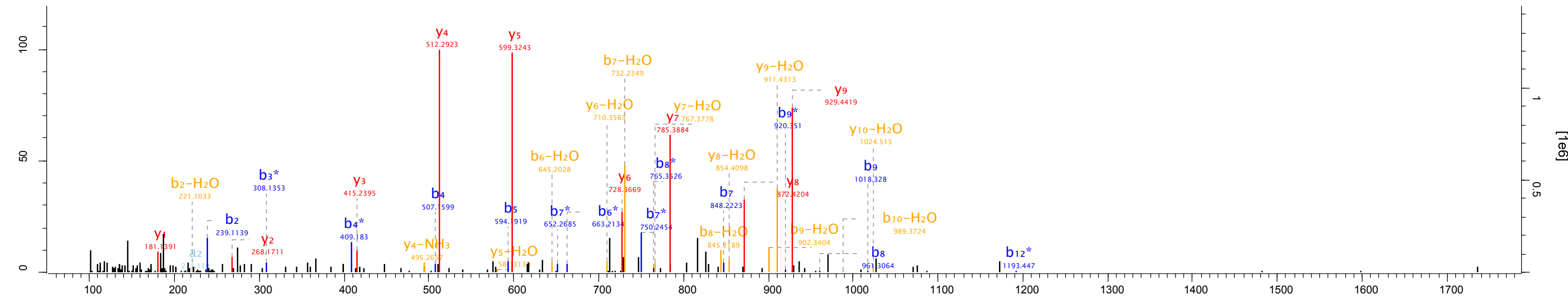


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 9252 Method: FTMS; HCD Score: 129.28 m/z: 964.37 Gene names: PSME3



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10162 Method FTMS; HCD Score 154.46 m/z 758.33 Gene names DDB2





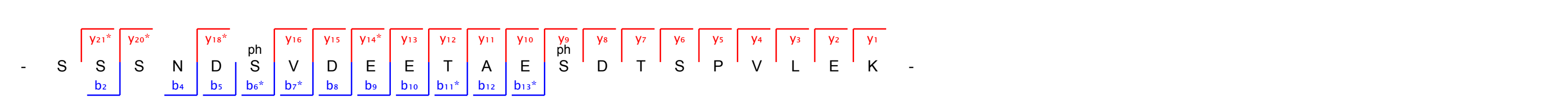
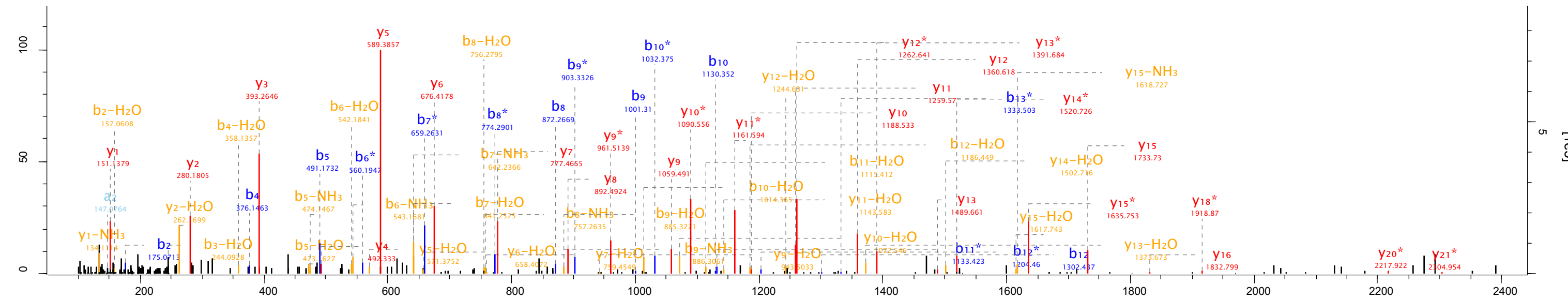
- T H S T S S L G S G E S P F S R -

ph ph

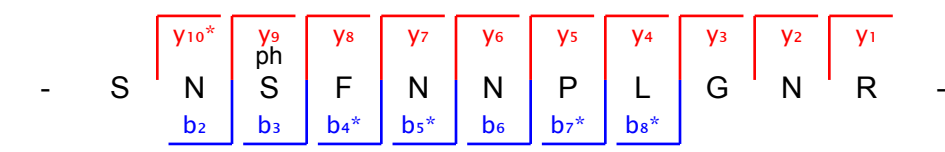
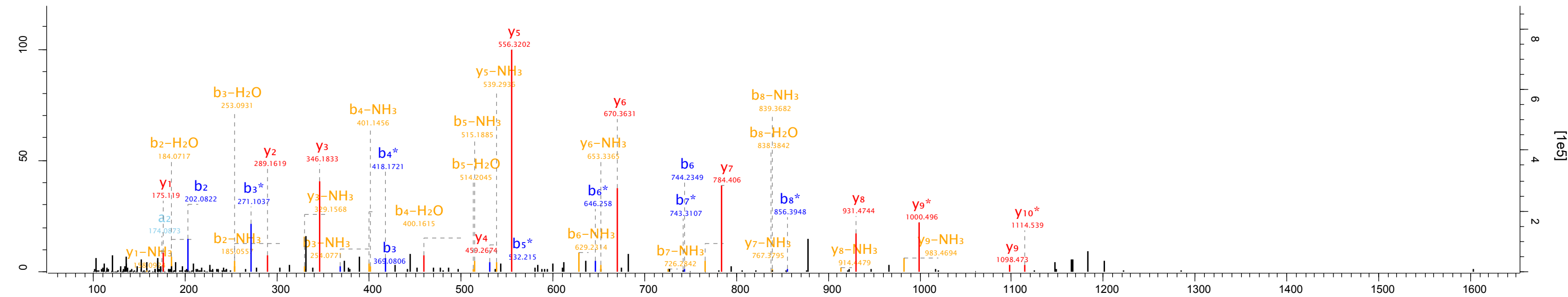
b₂ b₃* b₄ b₅ b₆* b₇ b₈ b₉ b₁₂*

y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

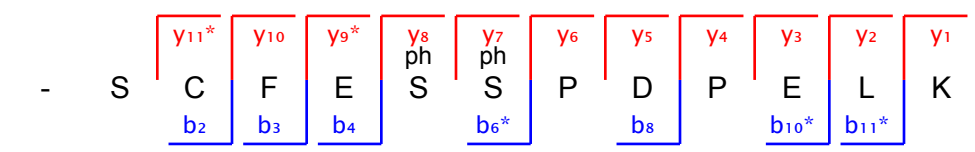
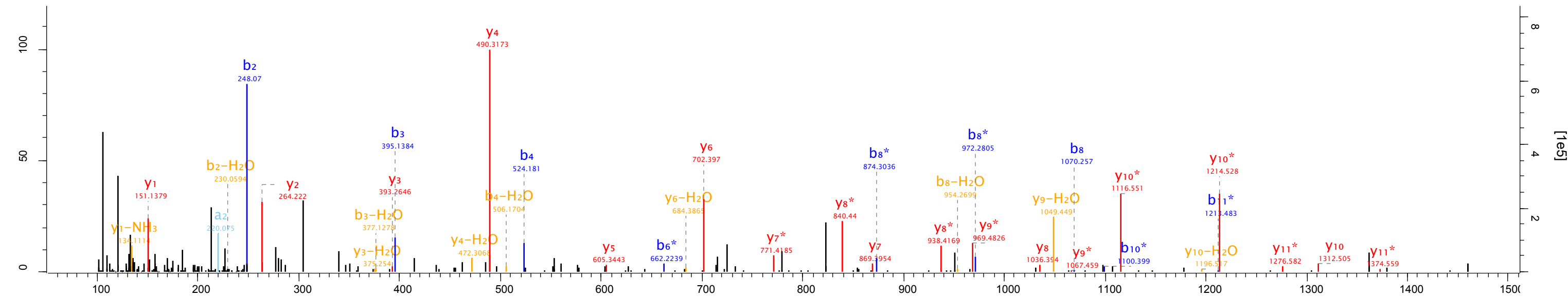
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10402 Method: FTMS; HCD Score: 276.8 m/z: 1245.99 Gene names: SCAF11

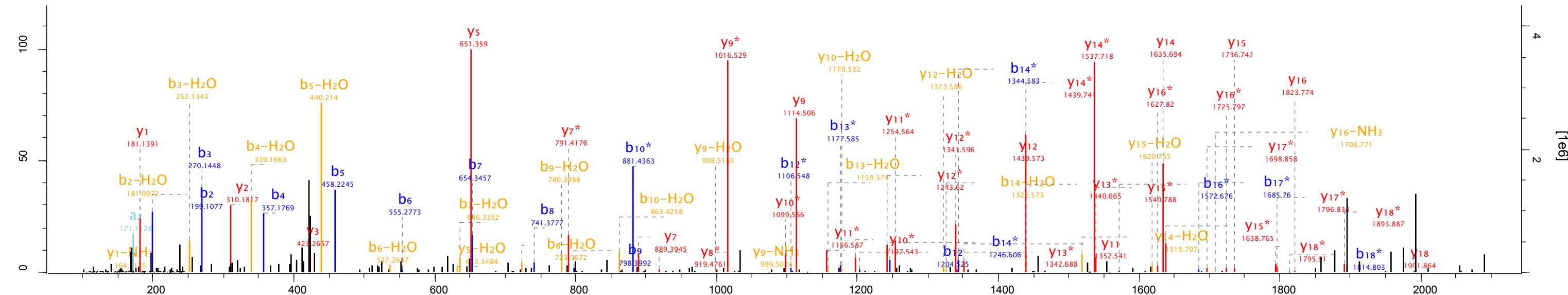


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10522 Method: FTMS; HCD Score: 179.21 m/z: 650.28 Gene names: LATS1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10602 Method FTMS; HCD Score 149.97 m/z 780.29 Gene names SRRM2

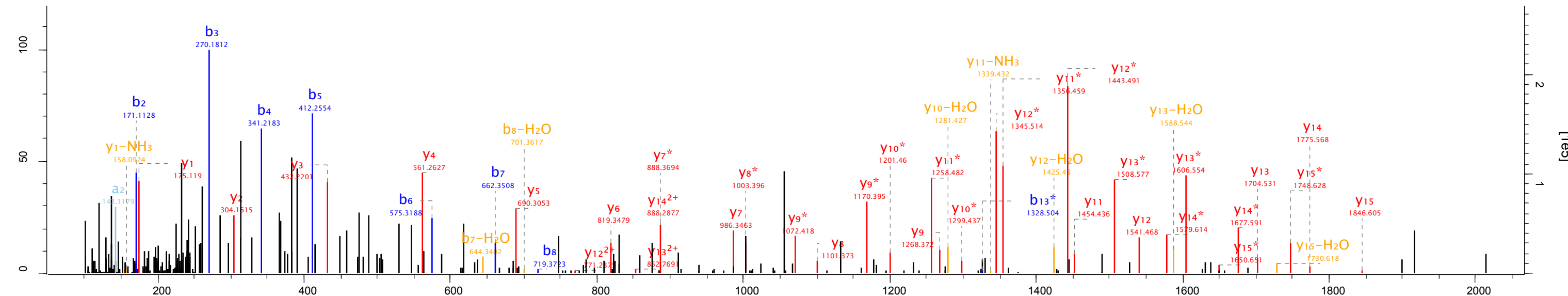




- T P A S T P V S G ph T P Q A S P M I E R -

y₁₈
y₁₇*
y₁₆
y₁₅
y₁₄
y₁₃*
y₁₂
y₁₁
y₁₀*
ph
T
P
y₉
y₈*
y₇
ph
y₅
M
y₃
y₂
y₁

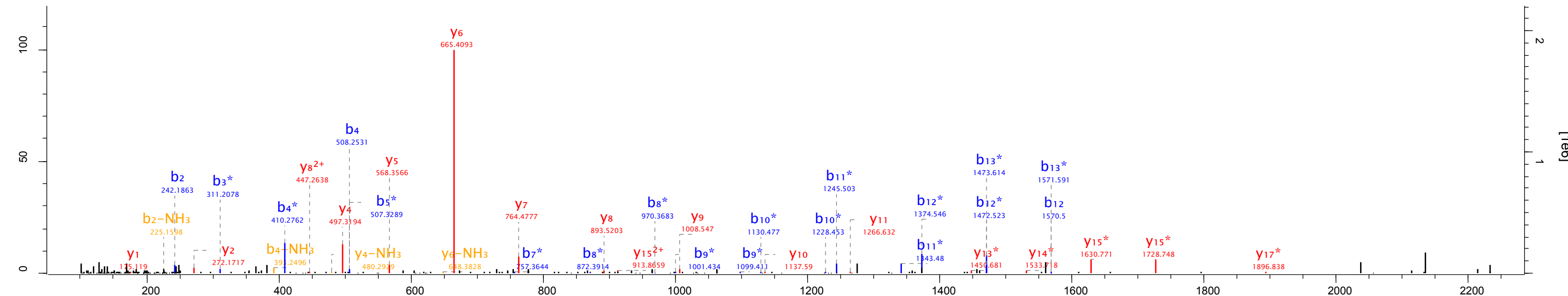
b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀*
b₁₂
b₁₃*
b₁₄*
b₁₆*
b₁₇*
b₁₈*



- G L V A A Y S G E S D S E E E Q E R -

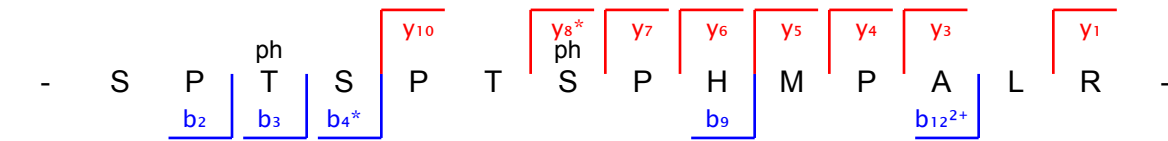
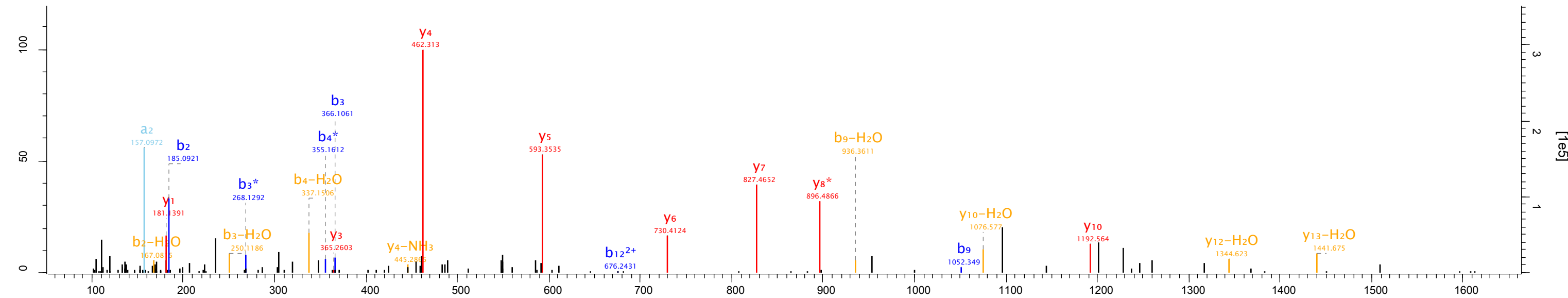
Fragmentation sites are indicated by boxes below the sequence:

- b₂ (L)
- b₃ (V)
- b₄ (A)
- b₅ (A)
- b₆ (Y)
- b₇ (S)
- b₈ (G)
- b₁₃^{*} (E)
- y₁₅ (A)
- y₁₄ (A)
- y₁₃ (Y)
- y₁₂ (S)
- y₁₁ (G)
- y₁₀^{*} (E)
- y₉ (S)
- y₈ (D)
- y₇ (S)
- y₆ (E)
- y₅ (E)
- y₄ (E)
- y₃ (Q)
- y₂ (E)
- y₁ (R)

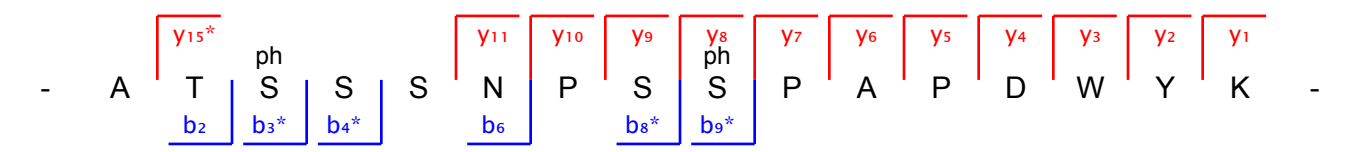
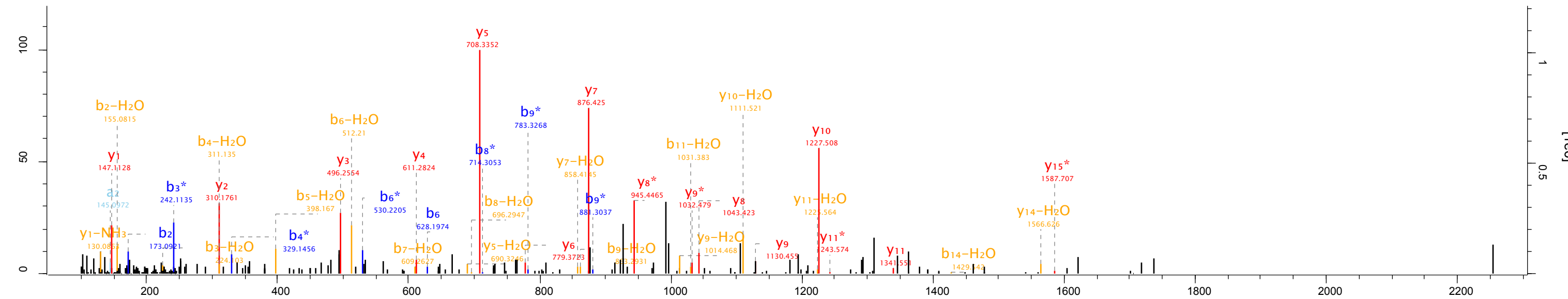


- K L S V P T S D E E D E V P A P K P R -

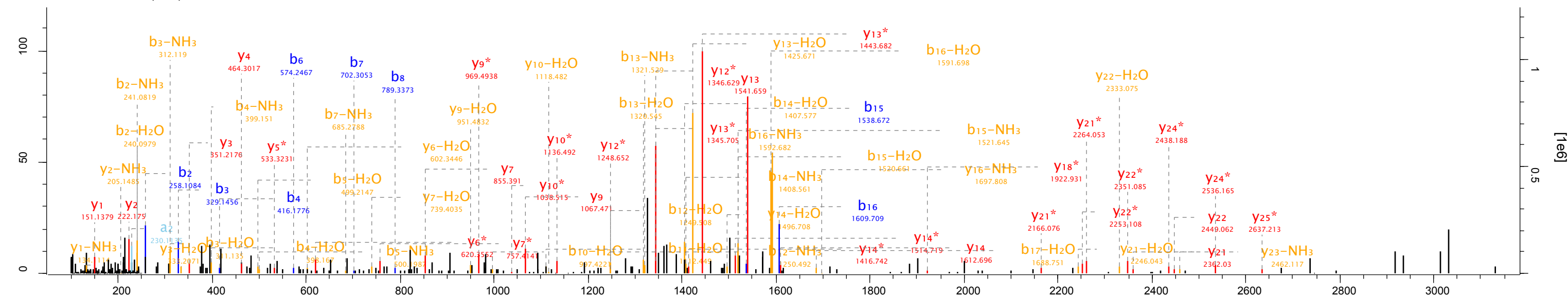
b₂
b₃*
b₄
b₅*
b₇*
b₈*
b₉*
b₁₀*
b₁₁*
b₁₂
b₁₃*
y₁₇*
y₁₅*
y₁₄*
y₁₃*
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₂
y₁



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11732 Method FTMS; HCD Score 108.37 m/z 927.85 Gene names ATRX

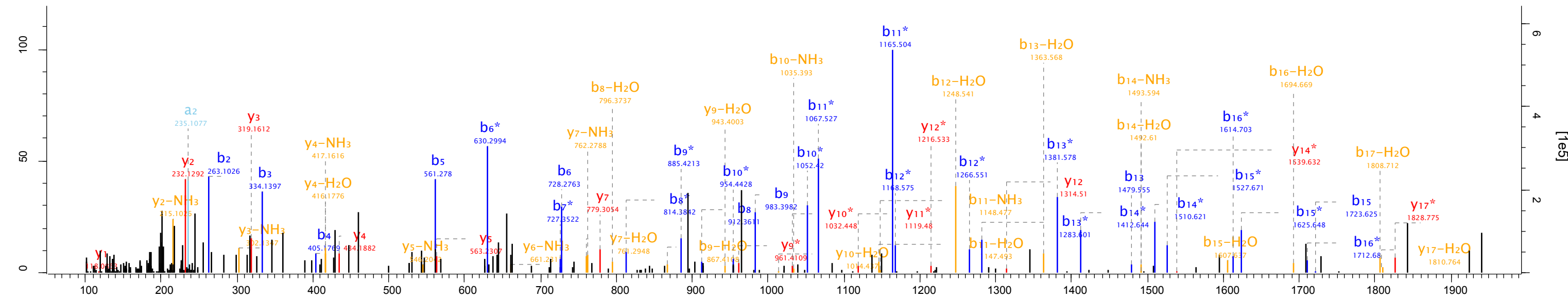


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 11772 Method: FTMS; HCD Score: 131.27 m/z: 1051.46 Gene names: NES



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

b₂ b₃ b₄ y₂₅* y₂₄* y₂₂ y₂₁
b₆ b₇ b₈ y₁₈* y₁₄ y₁₃ y₁₂* y₁₀* y₉ y₇ y₆* y₅* y₄ y₃ y₂ y₁

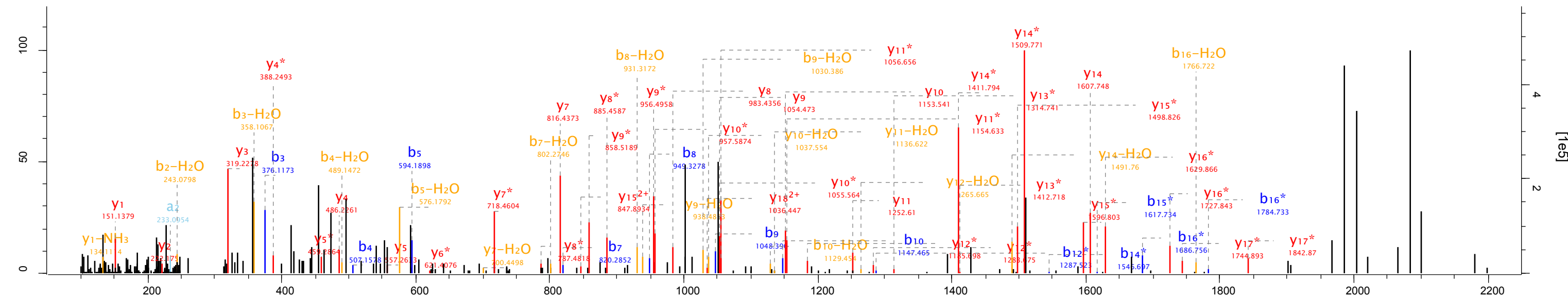


- D F A A R S P S A S I T D E D S N V -

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

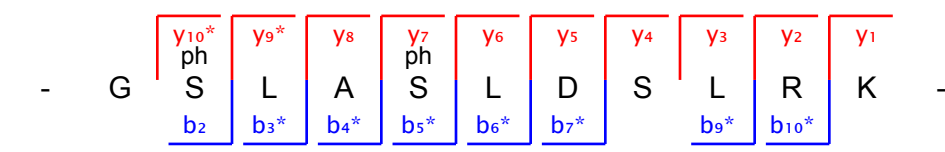
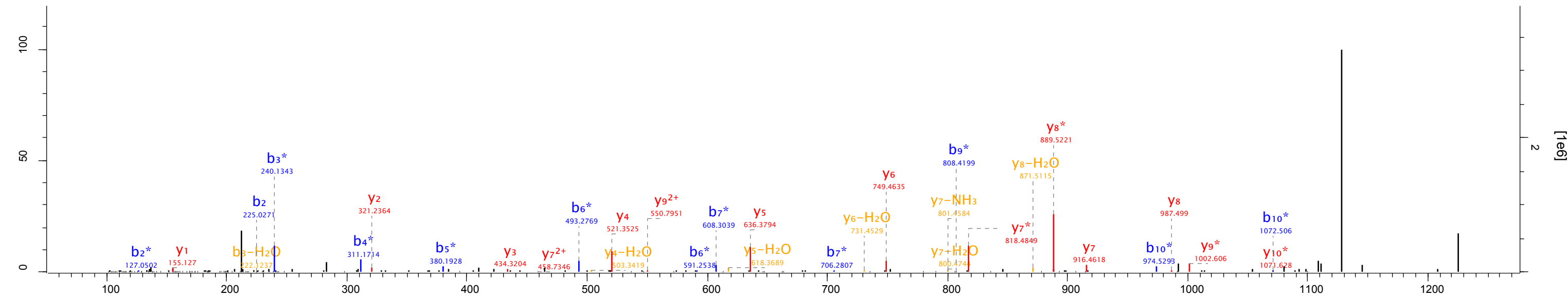
- F: b₂
- A: b₃
- A: b₄
- R: b₅
- S: b₆
- P: b₇*
- S: b₈
- A: b₉
- S: b₁₀*
- I: b₁₁*
- T: b₁₂*
- D: b₁₃
- E: b₁₄*
- D: b₁₅
- S: b₁₆*
- N: y₁₇*
- V: y₁₄*

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12342 Method FTMS; HCD Score 217.02 m/z 1100.97 Gene names TRIM32



E M D M S P E E V V A S P R A S P A K -
 a₂ b₃ b₄ b₅ b₇ b₈ b₉ b₁₀ b₁₂* b₁₄* b₁₅* b₁₆*

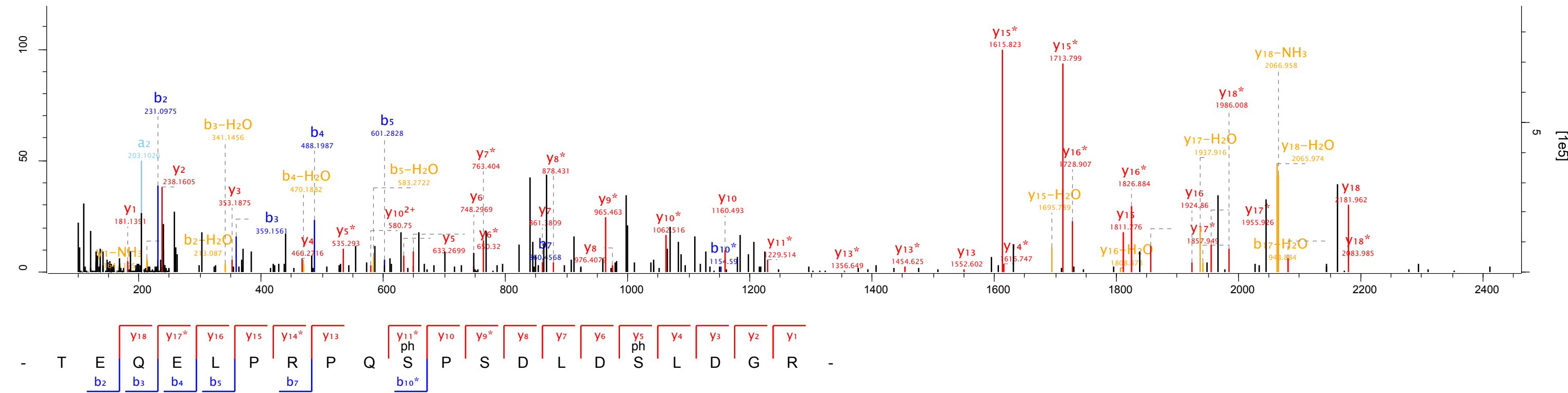
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12362 Method FTMS; HCD Score 115.26 m/z 662.81 Gene names CTNND1



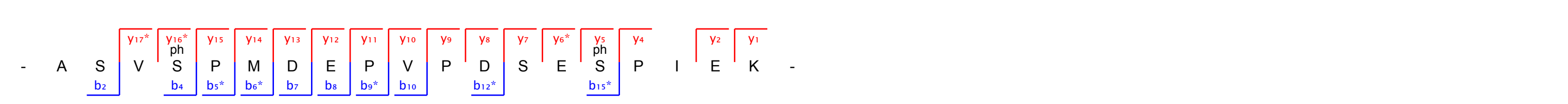
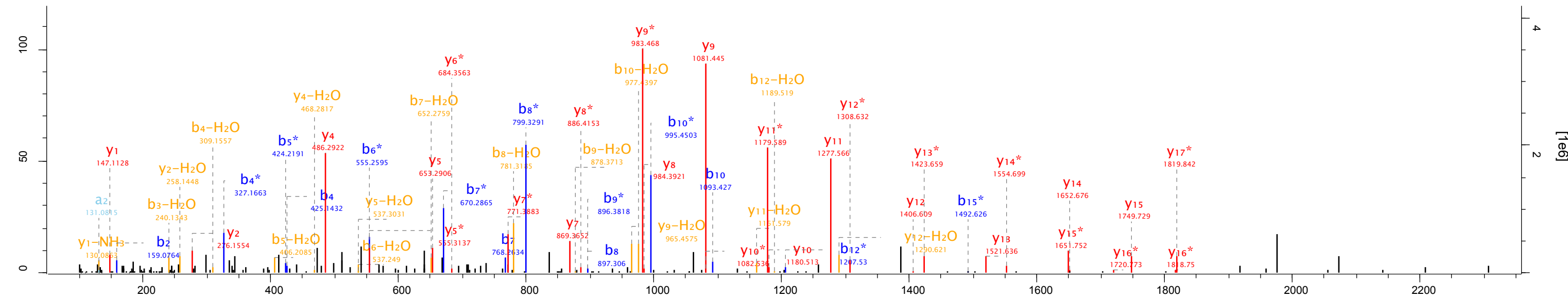
Raw file

20171215_MaS_33SR_LMH_phospho2_03

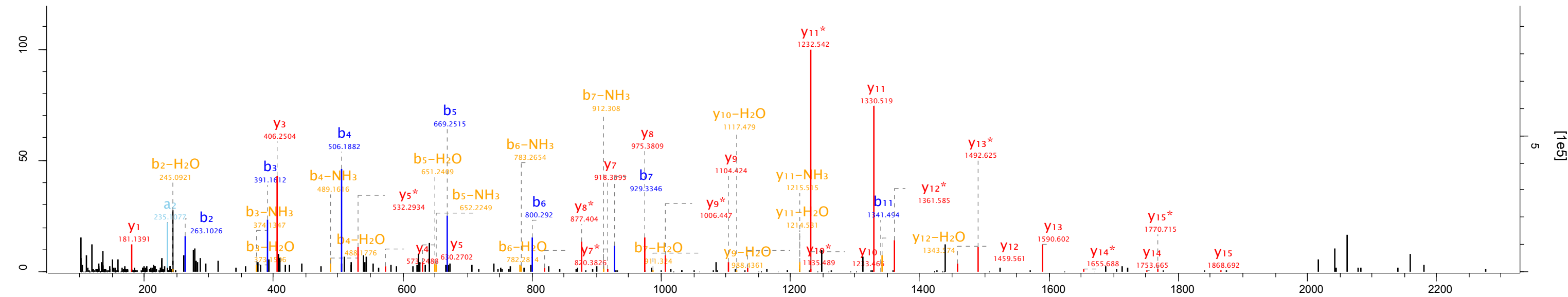
Scan	Method	Score	m/z	Gene names
12652	FTMS; HCD	114.76	805.03	ATN1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12732 Method FTMS; HCD Score 246.44 m/z 1087.94 Gene names MAP1B

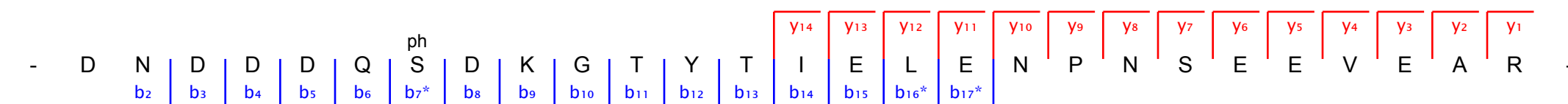
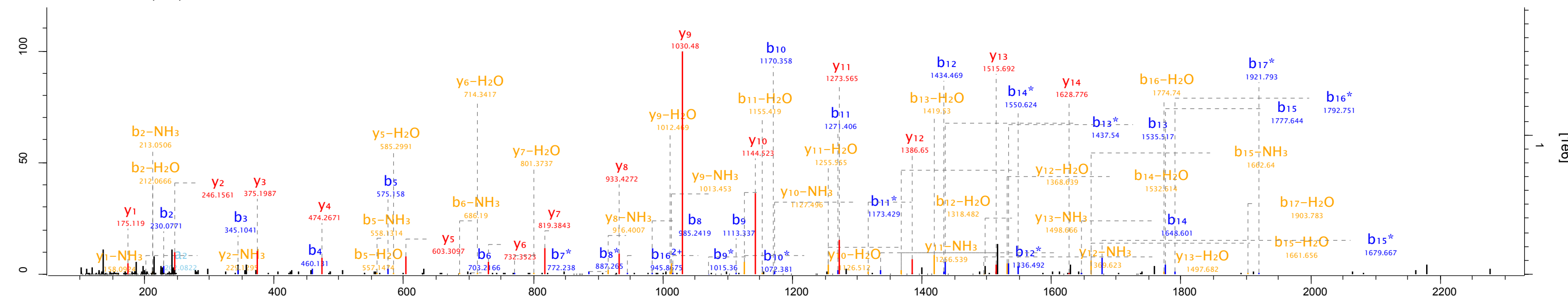


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13462 Method FTMS; HCD Score 181.81 m/z 1130.43 Gene names DYNC1LI2

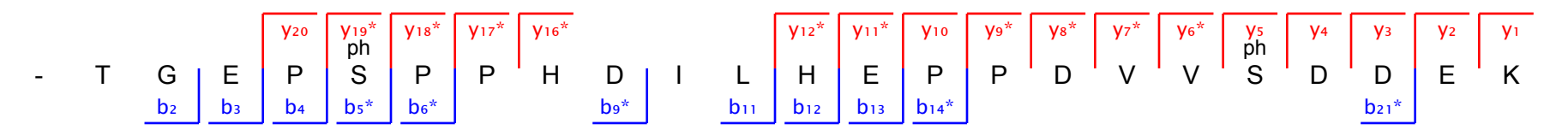
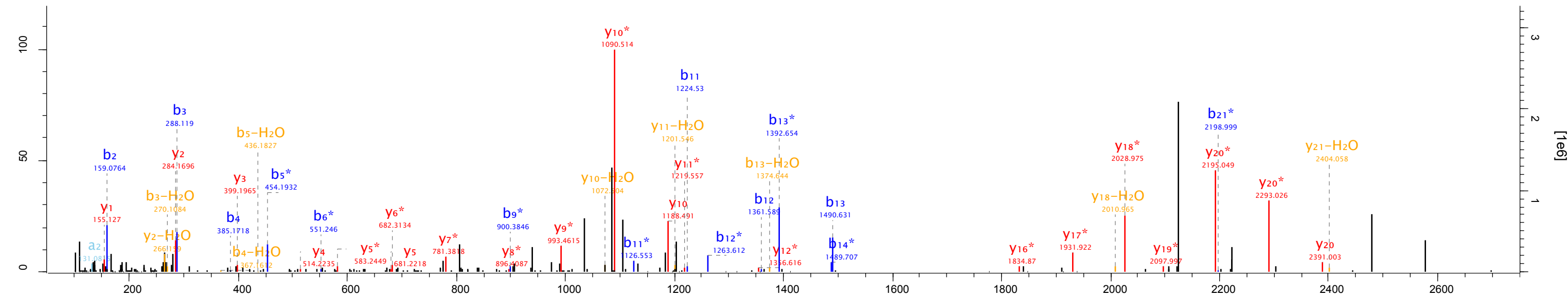


Raw file
20171215_MaS_33SR_LMH_phospho2_03

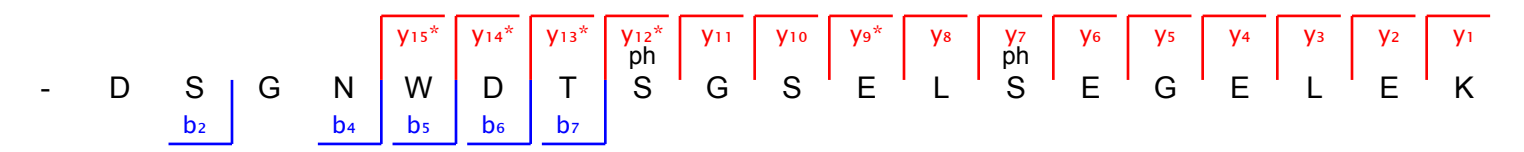
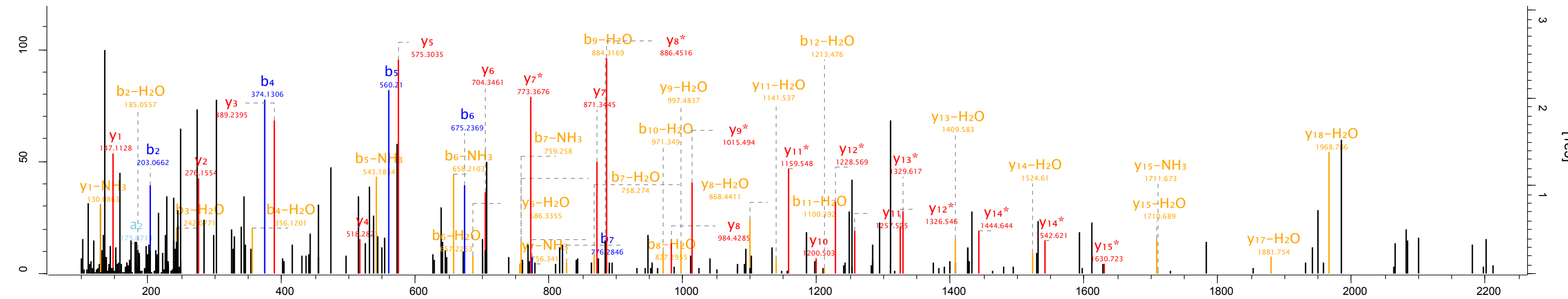
Scan 13522 Method FTMS; HCD Score 196.68 m/z 1055.43 Gene names CEP170



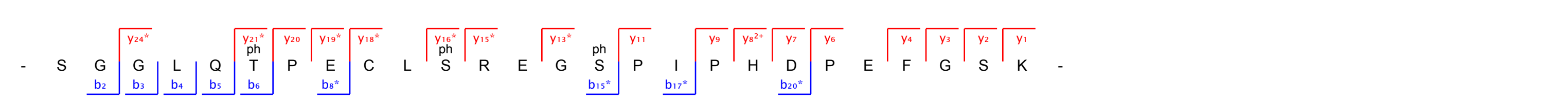
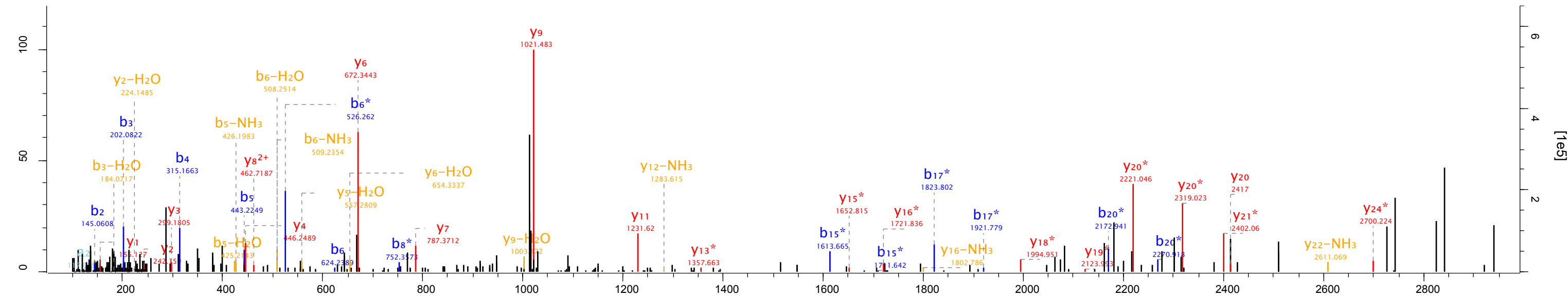
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13662 Method FTMS; HCD Score 118.77 m/z 893.71 Gene names RALBP1



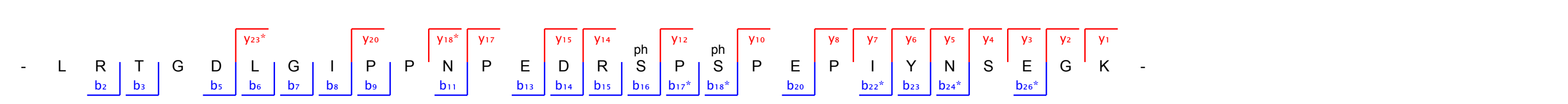
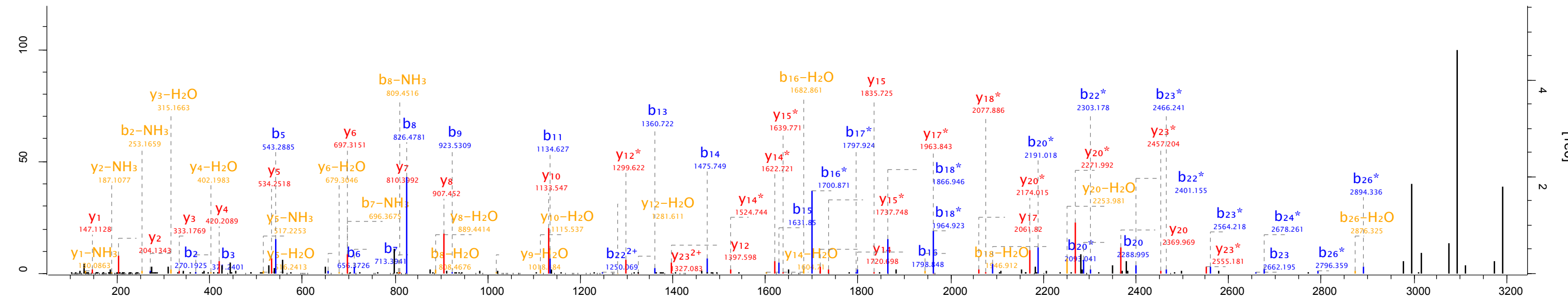
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13992 Method FTMS; HCD Score 94.4 m/z 1100.91 Gene names PRPF40A



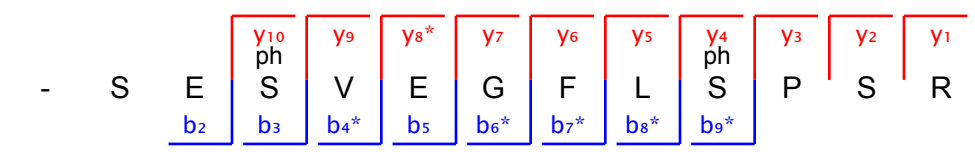
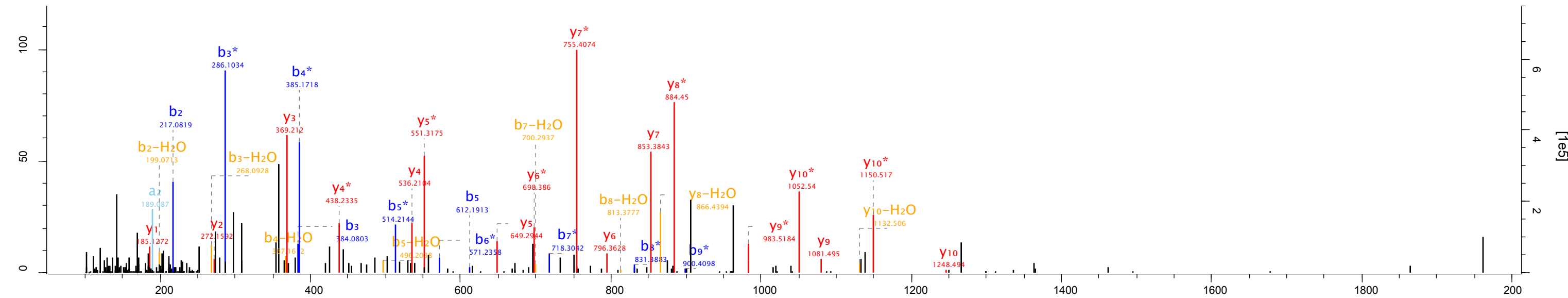
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 Scan: 14112 Method: FTMS; HCD Score: 59.53 m/z: 1014.08 Gene names: FOXK1



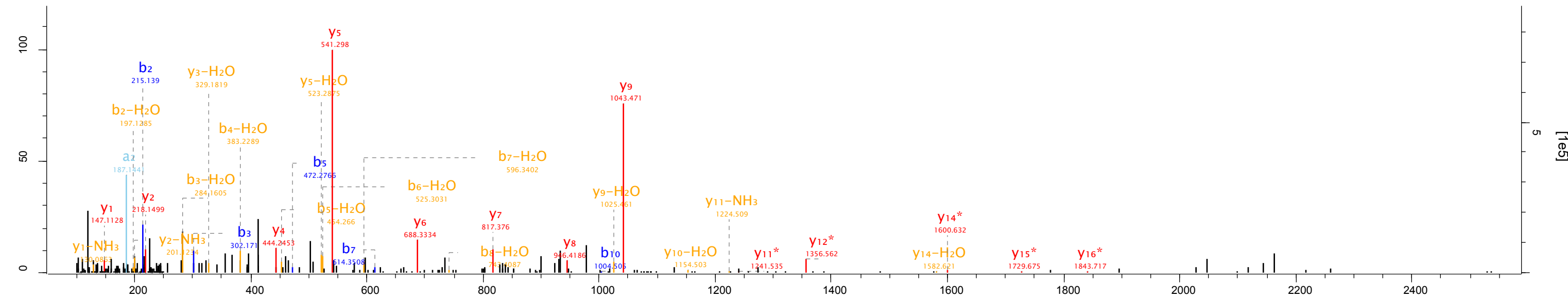
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14572 Method FTMS; HCD Score 276.3 m/z 1066.49 Gene names SF1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14742 Method FTMS; HCD Score 143.99 m/z 732.79 Gene names CAMSAP2



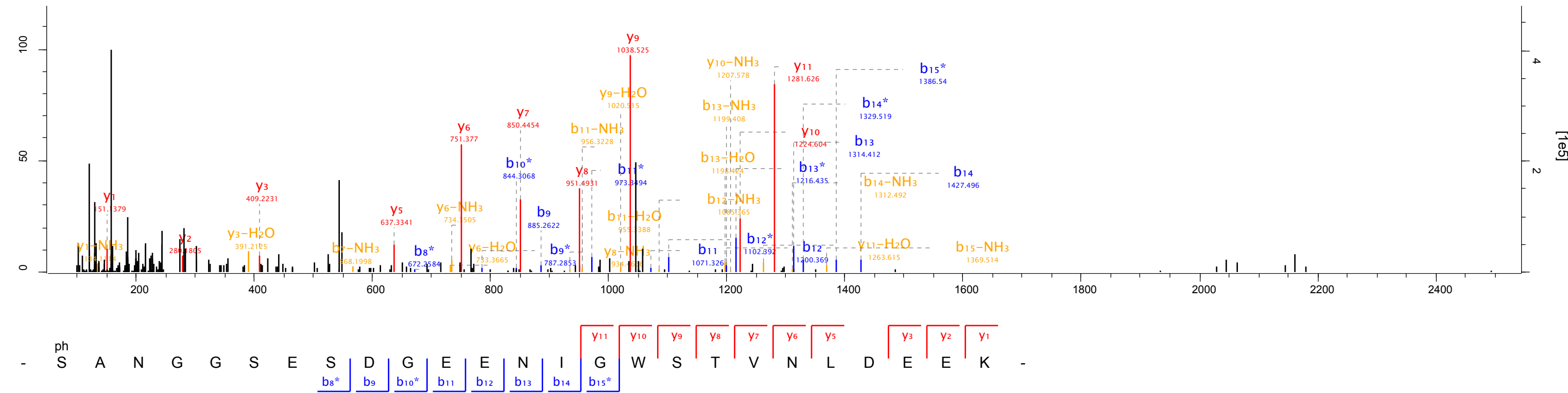
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15582 Method FTMS; HCD Score 43.36 m/z 901.71 Gene names PCNP



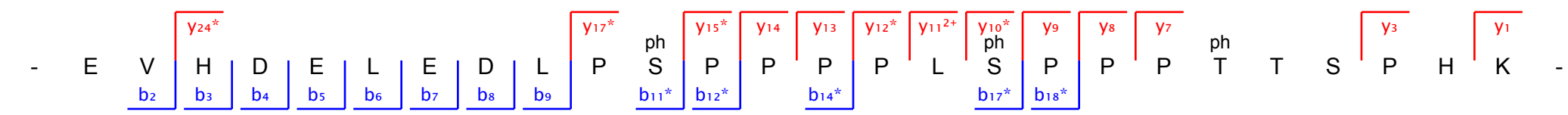
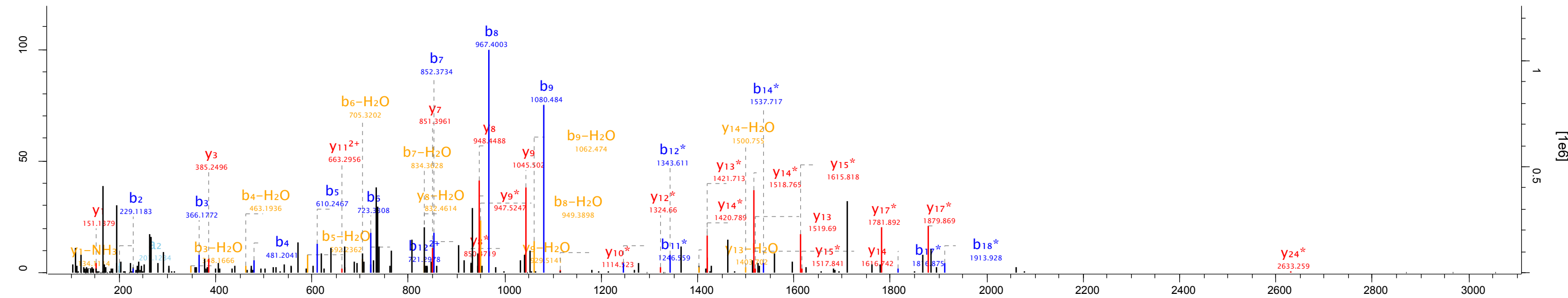
- T L S V A A F N E D E D S E P E E M P P E A K -

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

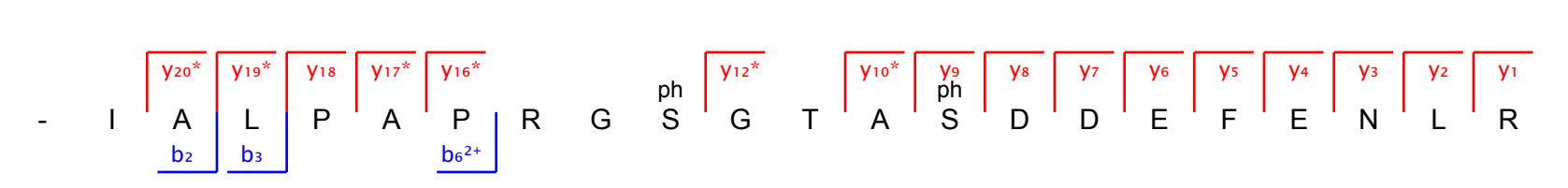
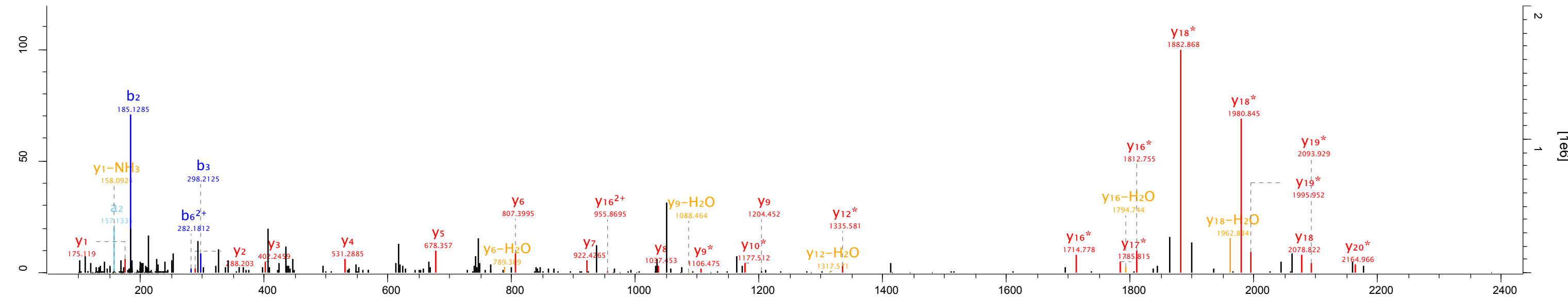
- b2: L, S
- b3: S, V
- b5: A, A
- b7: A, F
- b10: E, D, S
- y1: K
- y2: A
- y4: P, P
- y5: M, P
- y6: M
- y7: E
- y8: E
- y9: P
- y11: S
- y12: D
- y14: F
- y15: E
- y16: N



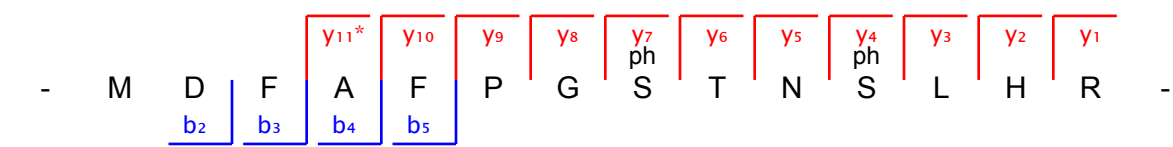
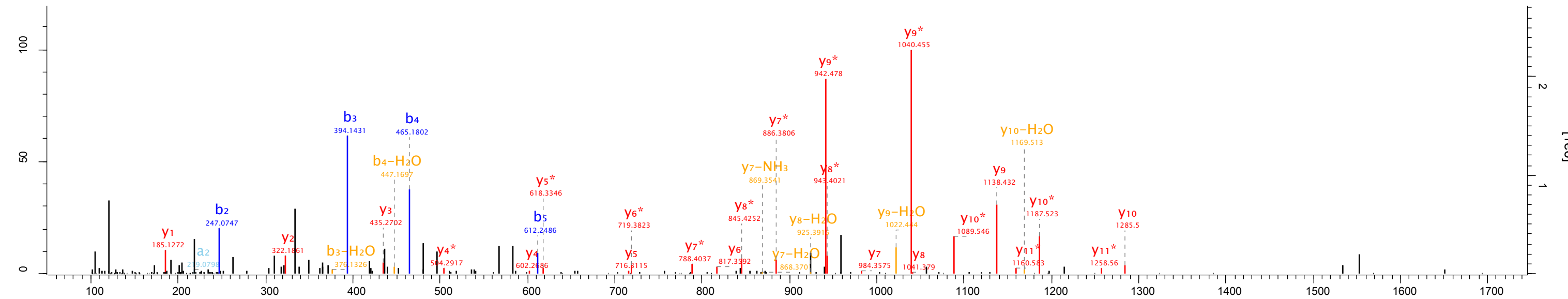
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16182 Method FTMS; HCD Score 79.18 m/z 765.34 Gene names GPHN

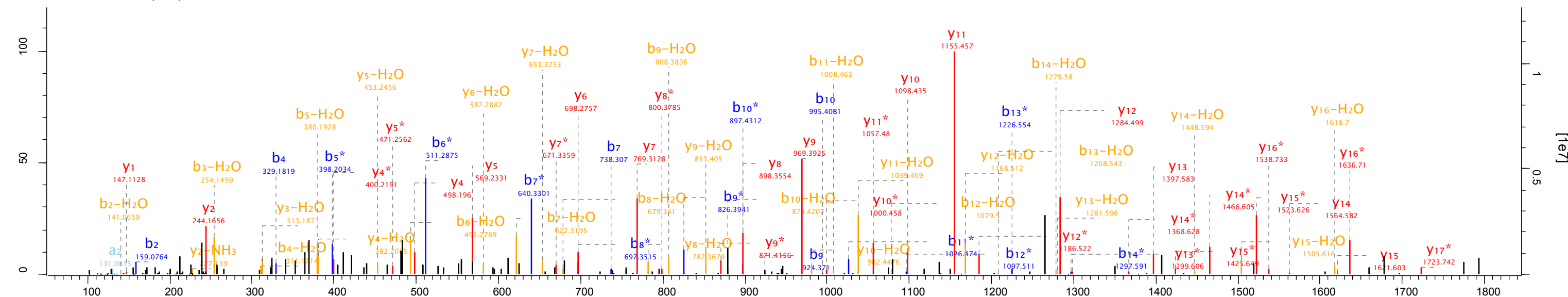


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16402 Method FTMS; HCD Score 79.51 m/z 793.02 Gene names HUWE1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16452 Method FTMS; HCD Score 114.53 m/z 875.34 Gene names ITGB4

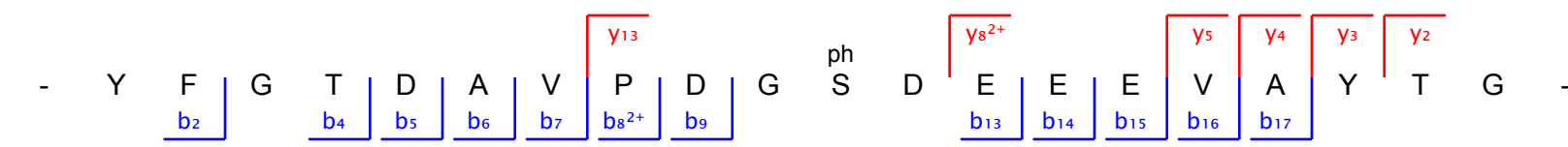
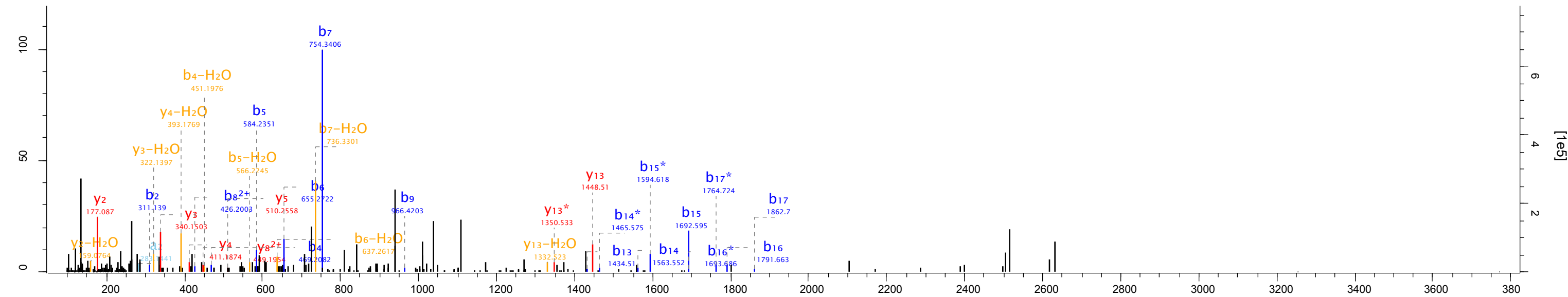




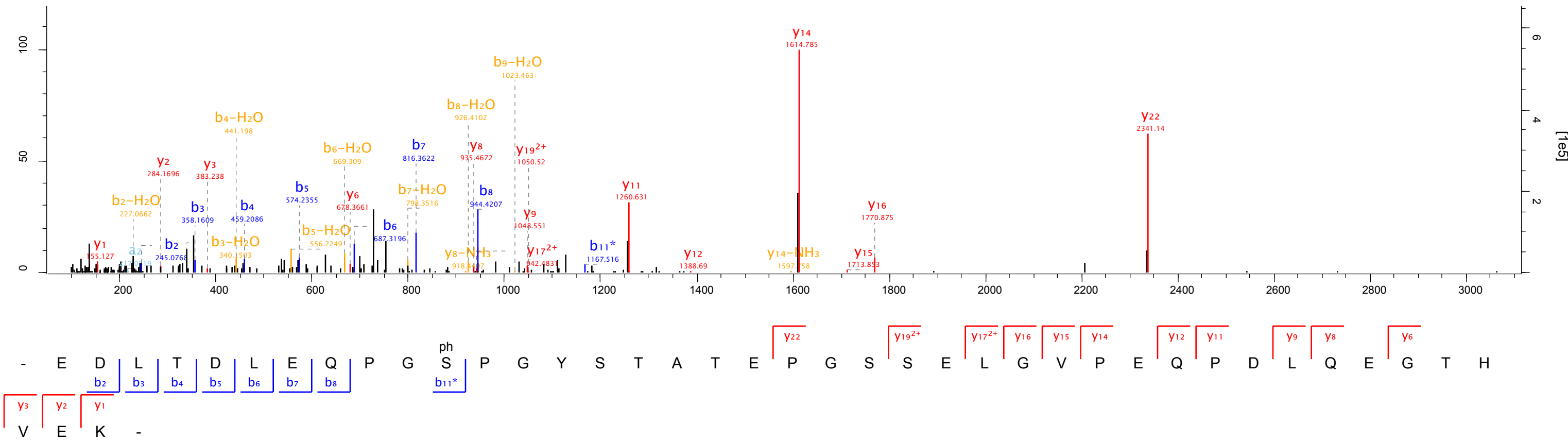
- A S L G S L E G E A E A S S P K -

b₂
b₄
b₅^{*}
b₆^{*}
b₇
b₈^{*}
b₉
b₁₀
b₁₁^{*}
b₁₂^{*}
b₁₃^{*}
b₁₄^{*}
y₄ph
y₅
y₆
y₇
y₈
y₉
y₁₀
y₁₁
y₁₂
y₁₃
y₁₄ph
y₁₅
y₁₆^{*}
y₁₇^{*}

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 16722 Method: FTMS; HCD Score: 115.88 m/z: 1101.93 Gene names: UCKL1

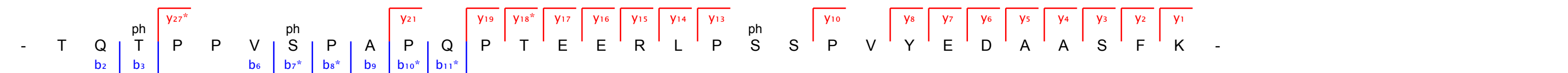
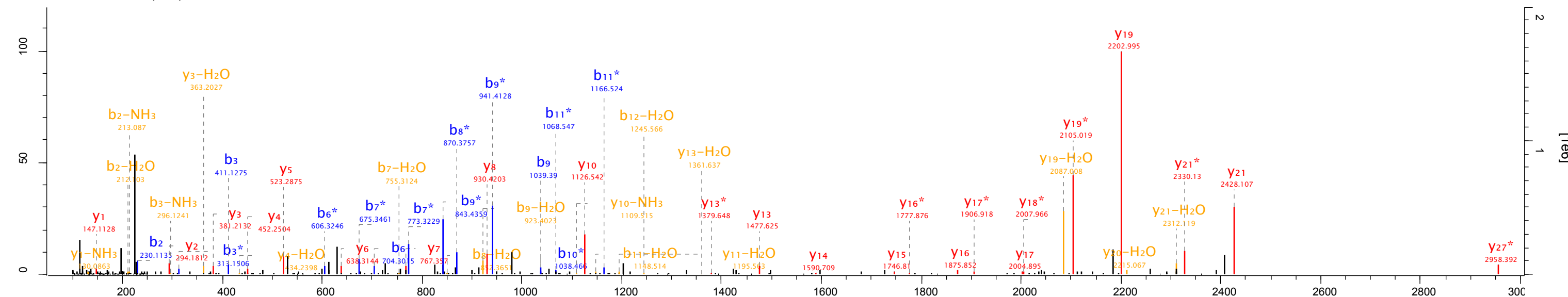


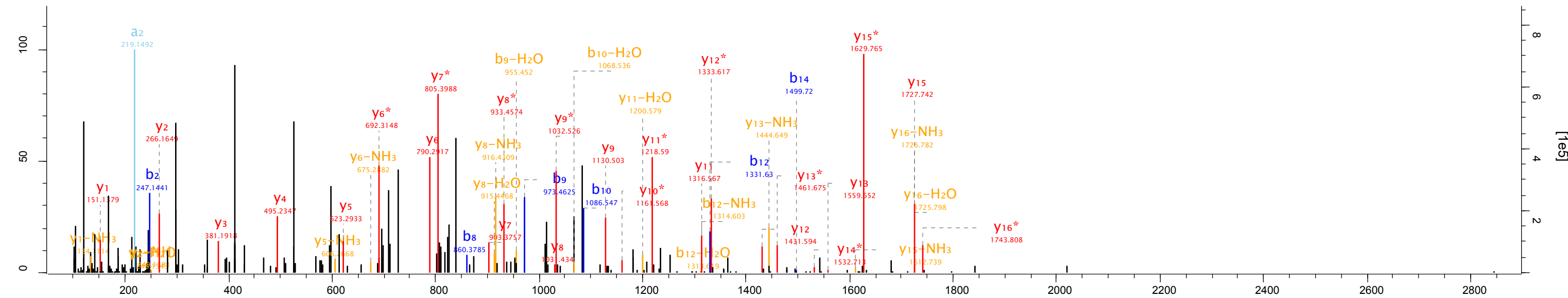
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16822 Method FTMS; HCD Score 48.61 m/z 1104.5 Gene names GBF1



Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 16882 Method FTMS; HCD Score 132 m/z 867.88 Gene names CTTN



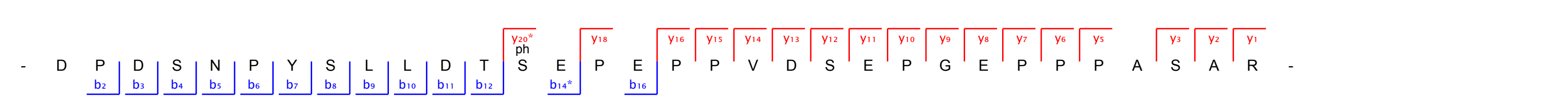
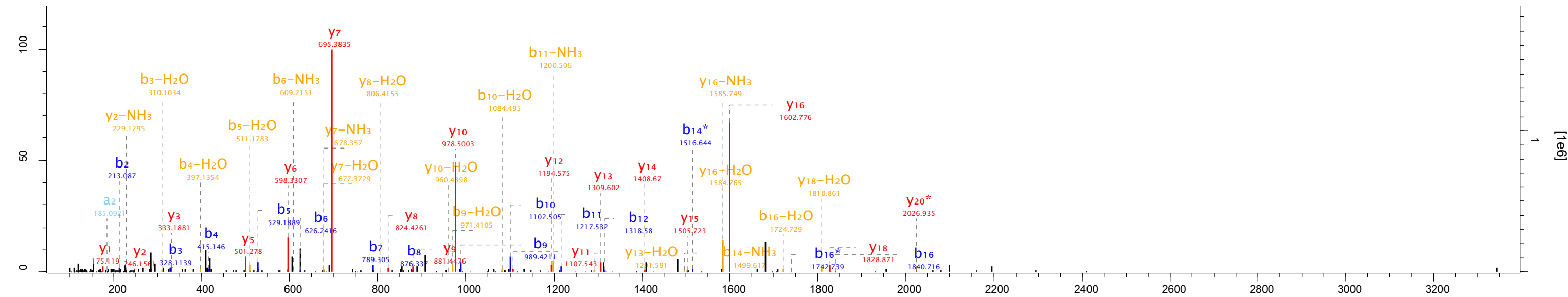


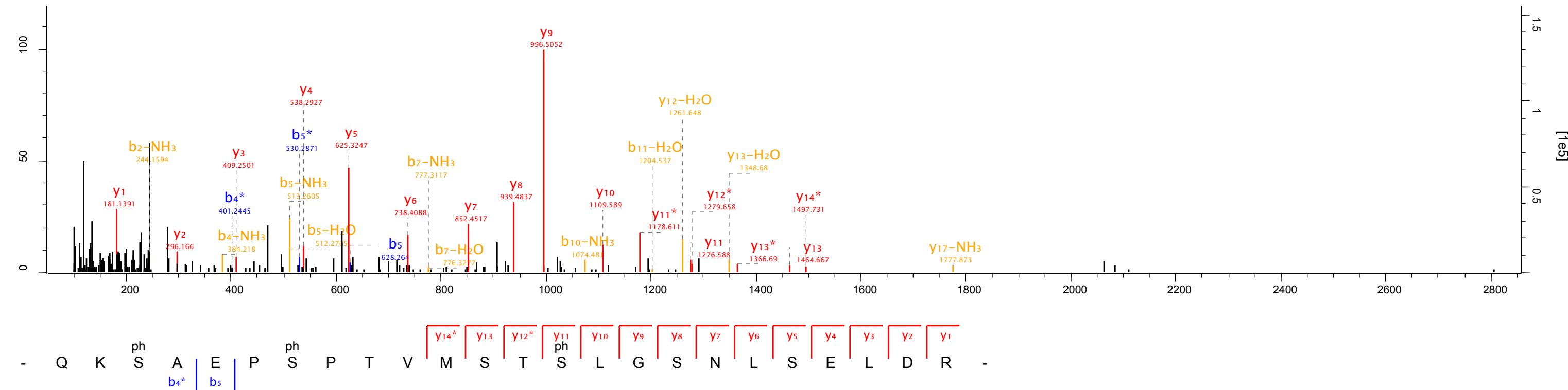
- F V P A E N D S I L M N P A Q D G E V Q L S Q N D D K -

Fragmentation sites are indicated by brackets below the sequence:

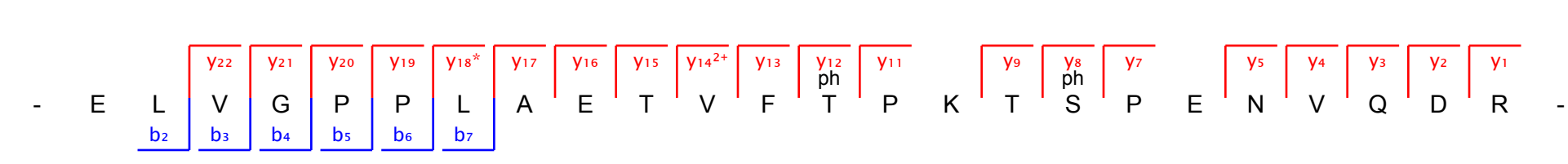
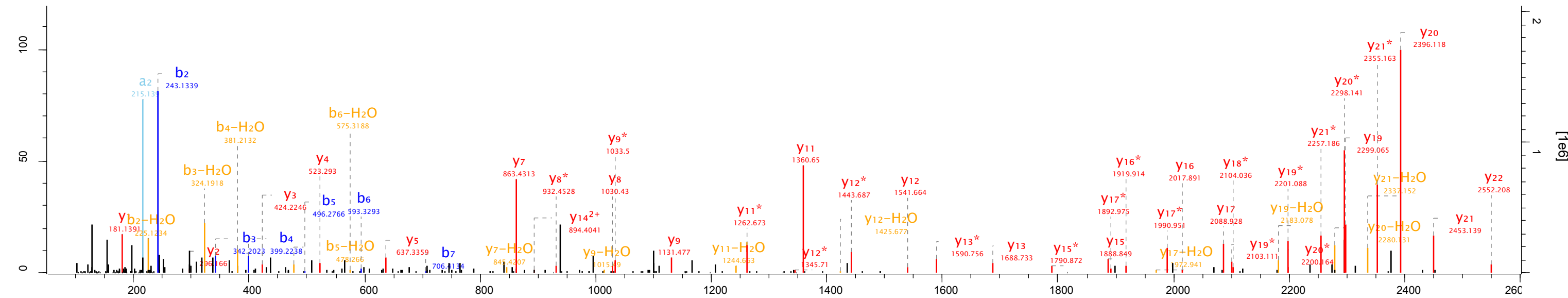
- b₂ (under V)
- b₈ (under S), b₉ (under I), b₁₀ (under L)
- b₁₂ (under N), b₁₄ (under A)
- y₁₆^{*} (under N), y₁₅ (under P), y₁₄^{*} (under A), y₁₃ (under Q), y₁₂ (under D), y₁₁ (under G), y₁₀^{*} (under E), y₉ (under V), y₈ (under Q), y₇ (under L), y₆^{ph} (under S), y₅ (under Q), y₄ (under N), y₃ (under D), y₂ (under D), y₁ (under K)

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18002 Method FTMS; HCD Score 117.15 m/z 1148.84 Gene names FXR2

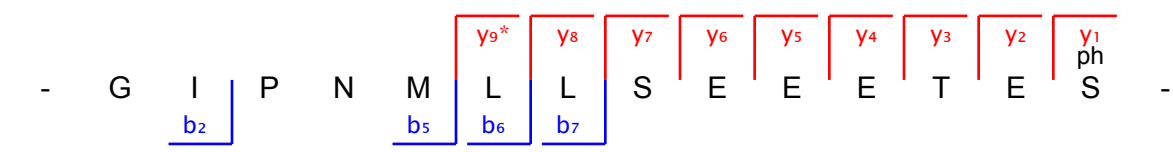
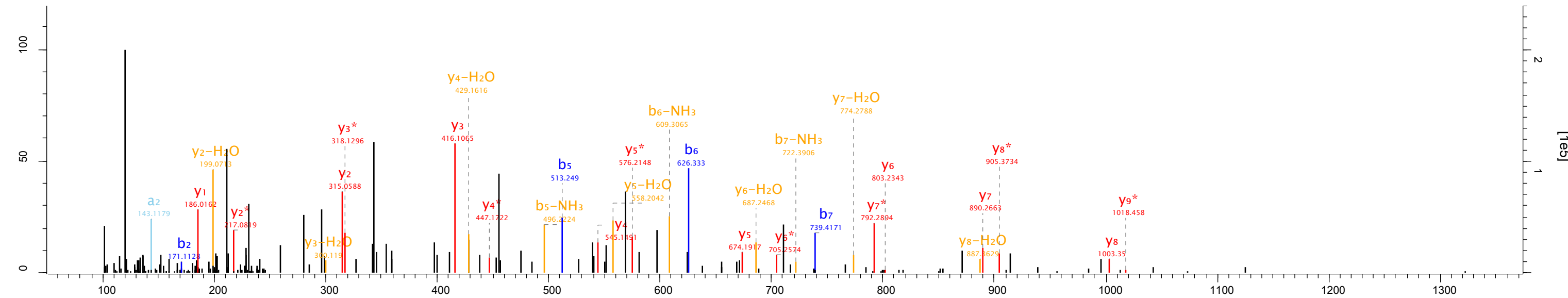


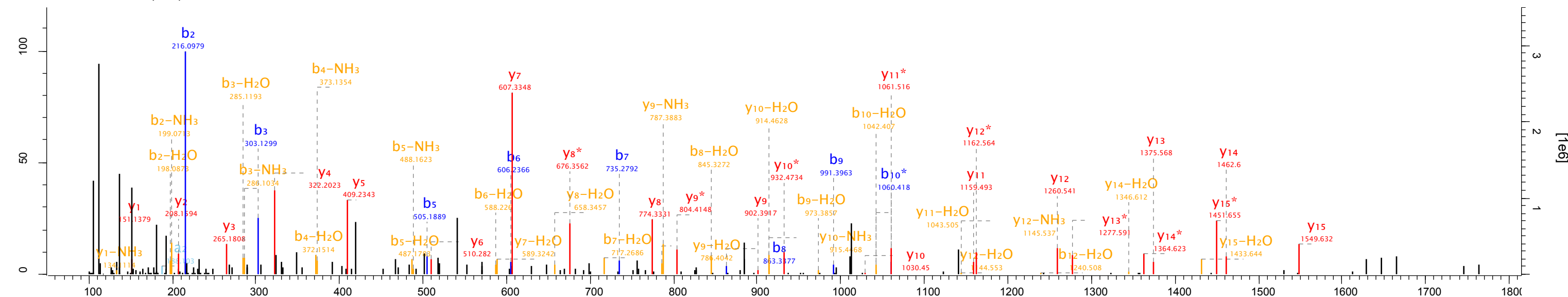


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 19132 Method: FTMS; HCD Score: 239.34 m/z: 932.45 Gene names: RANBP2



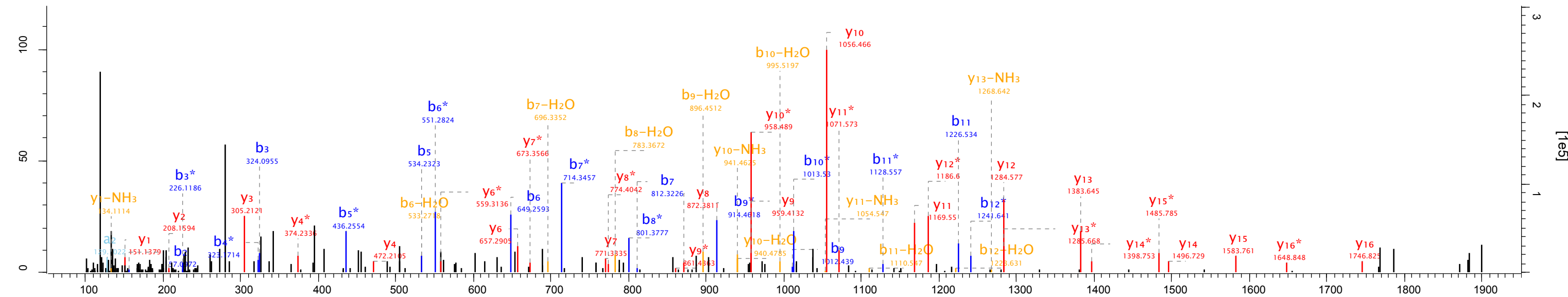
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 19142 Method FTMS; HCD Score 165.78 m/z 815.34 Gene names TRMT112





- S Q S S D T E Q Q S P T S G G G K -

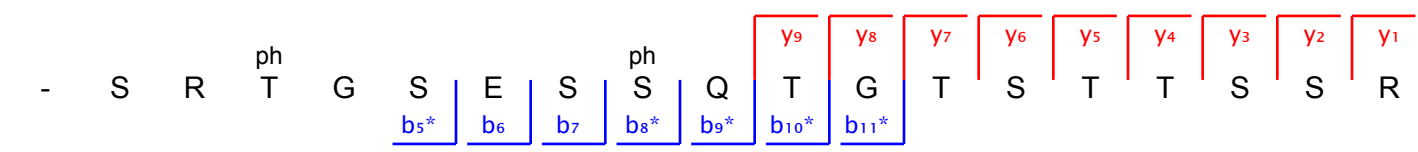
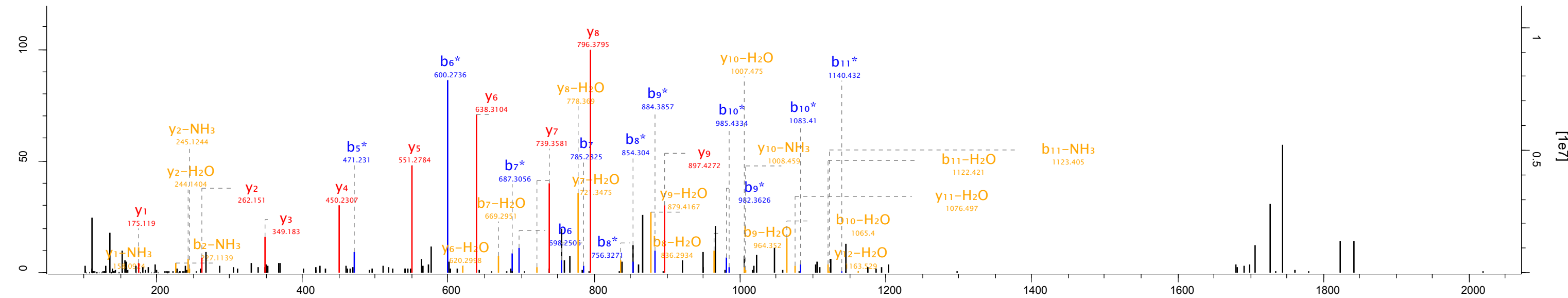
b₂
b₃
y₁₅
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈ph
S
y₇
y₆
y₅
y₄
y₃
y₂
y₁
b₅
b₆
b₇
b₈
b₉
b₁₀*



- V G S P L D Y S L V D L P S T N G Q S P G K -

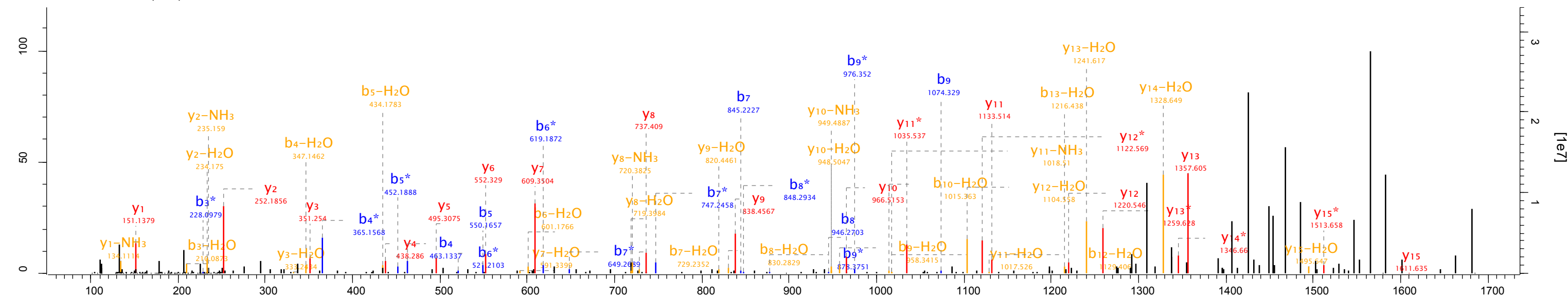
ph
 b₂ b₃ b₄^{*} b₅ b₆ b₇ b₈^{*} b₉ b₁₀^{*} b₁₁ b₁₂^{*} y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₄ ph y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 2052 Method FTMS; HCD Score 75.96 m/z 659.59 Gene names EIF4B



Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 2102 Method FTMS; HCD Score 202.52 m/z 841.84 Gene names LMNA

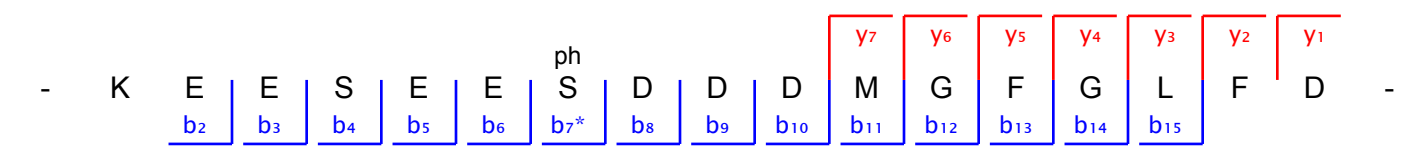
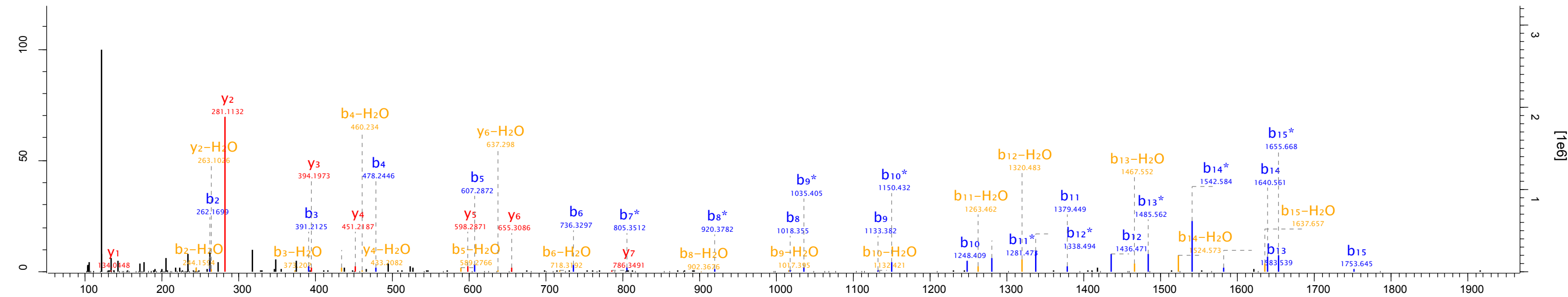


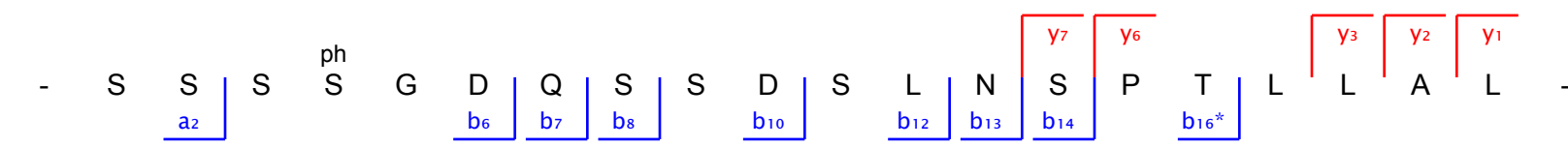
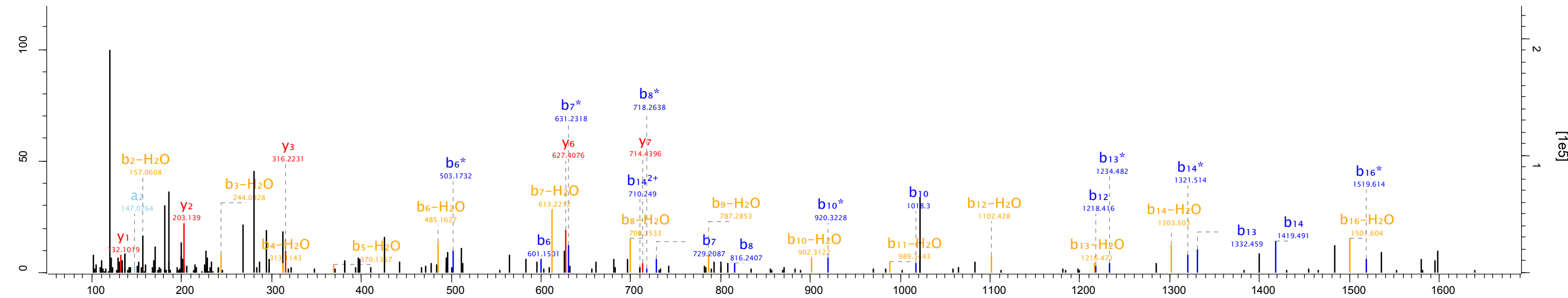
- A S S H S S Q T Q G G G S V T K -

y15 ph
y14*
y13
y12
y11 ph
y10
y9
y8
y7
y6
y5
y4
y3
y2
y1

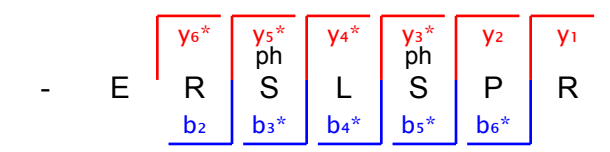
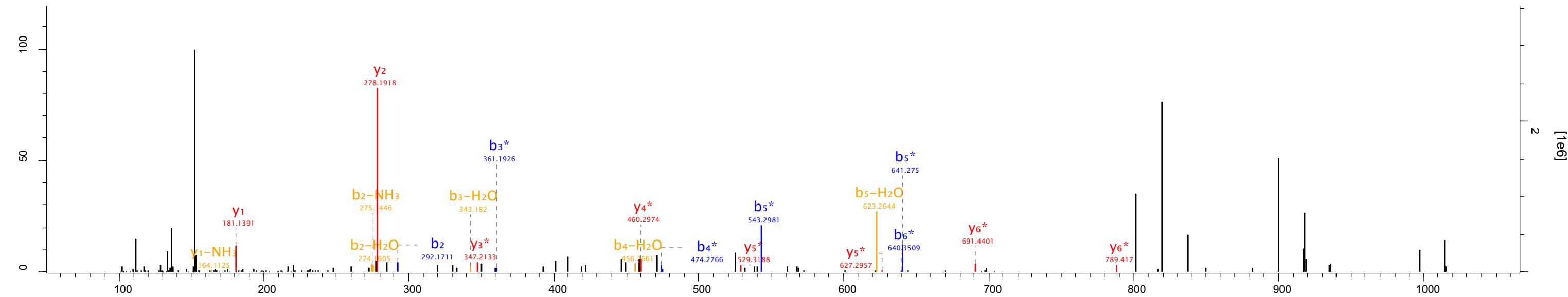
b3*
b4
b5
b6*
b7
b8
b9

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 21172 Method: FTMS; HCD Score: 235.5 m/z: 1017.88 Gene names: RPLP2;RPLP1

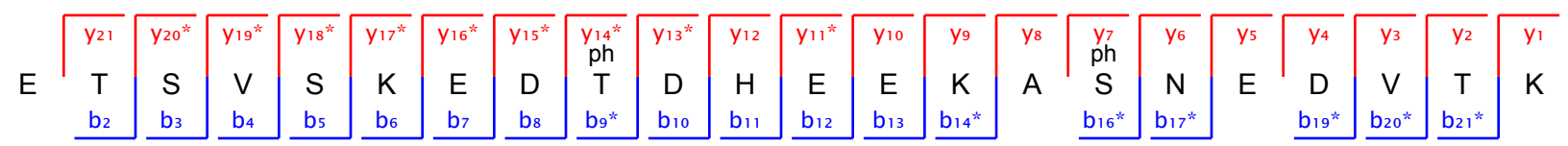
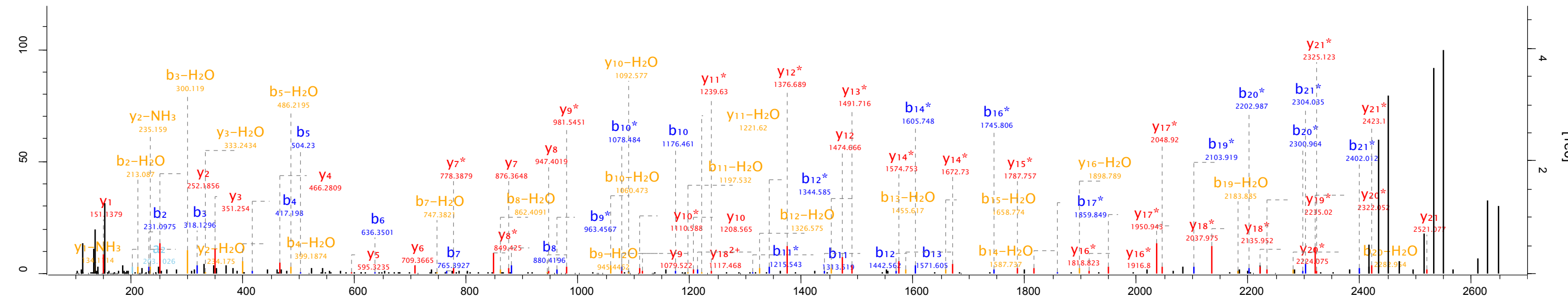




Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 2882 Method FTMS; HCD Score 72.58 m/z 508.72 Gene names TJP1

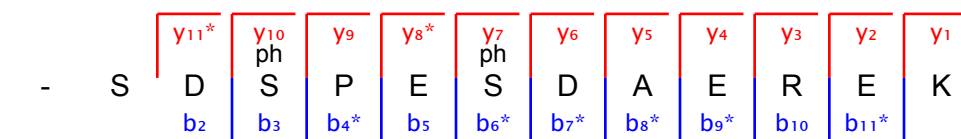
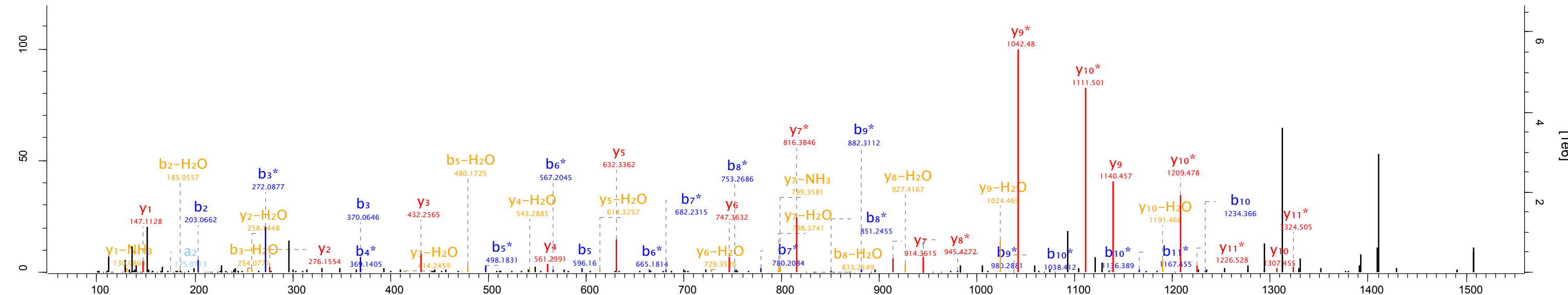


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 2932 Method: FTMS; HCD Score: 338.02 m/z: 884.38 Gene names: PSIP1

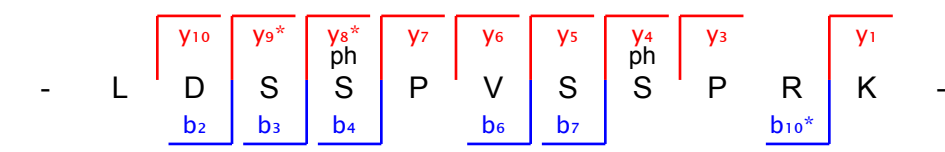
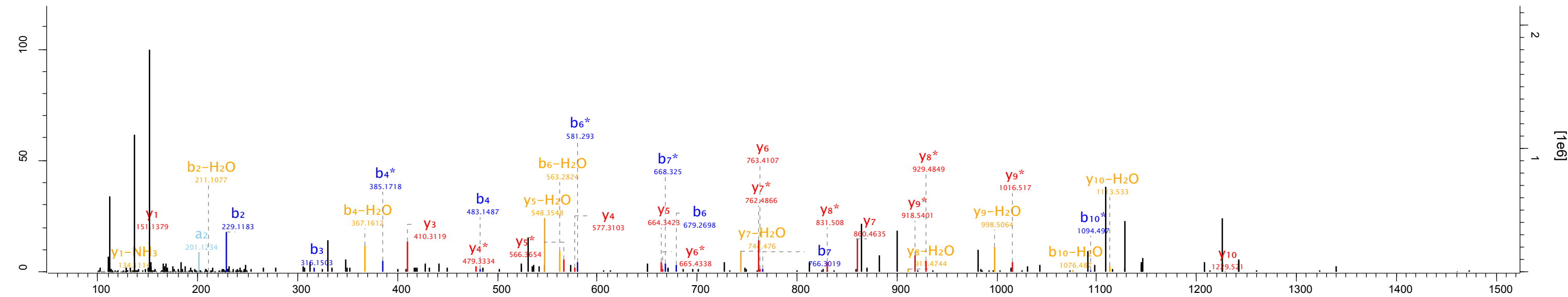


Raw file
20171215_MaS_33SR_LMH_phospho2_03

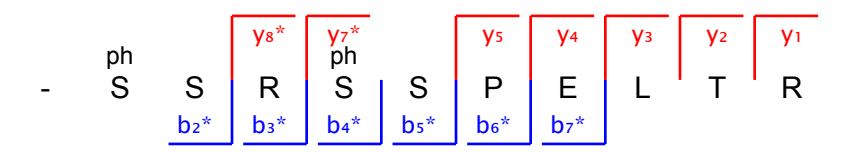
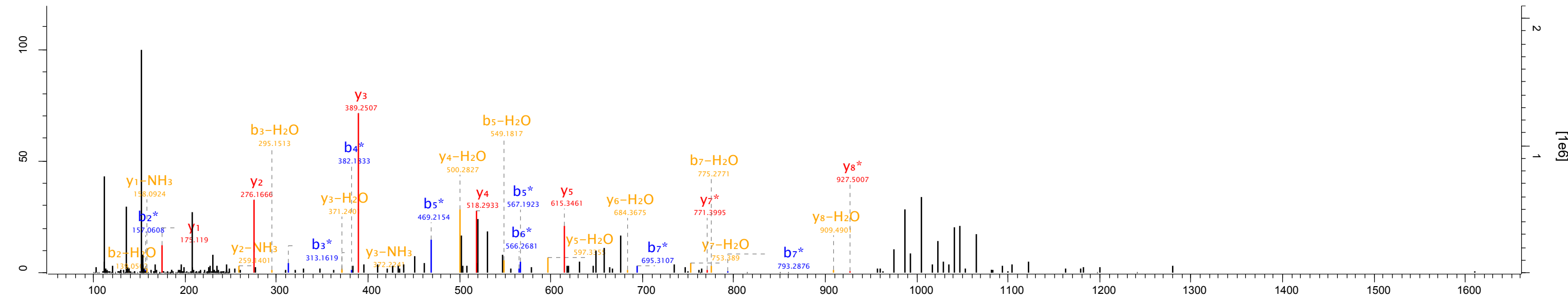
Scan Method Score m/z Gene names
3212 FTMS; HCD 231.15 755.26 PRPF40A



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3412 Method FTMS; HCD Score 84.94 m/z 671.81 Gene names ZFC3H1

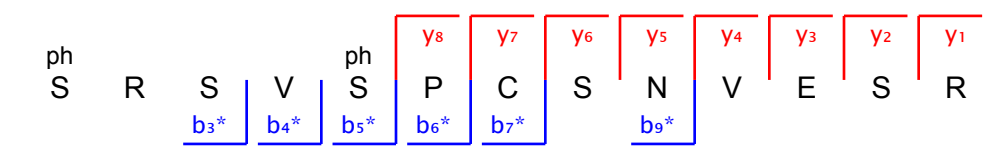
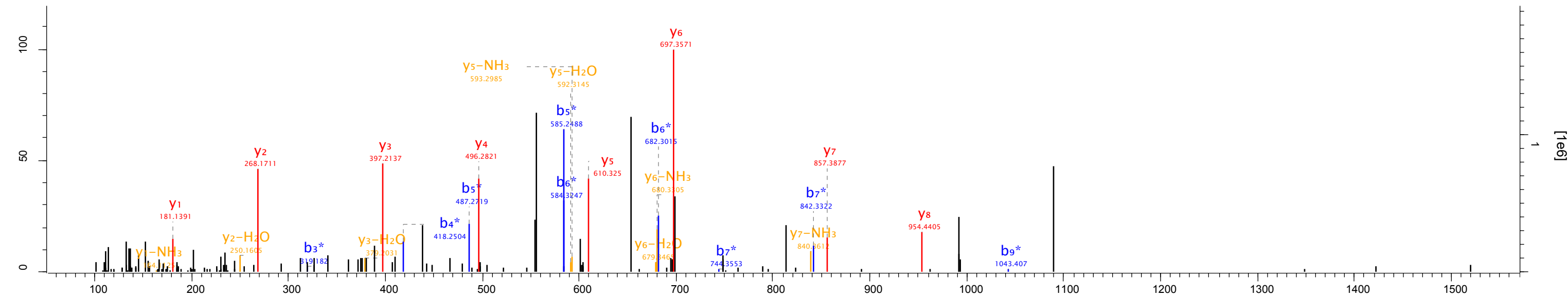


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3622 Method FTMS; HCD Score 76.01 m/z 427.17 Gene names SRRM2

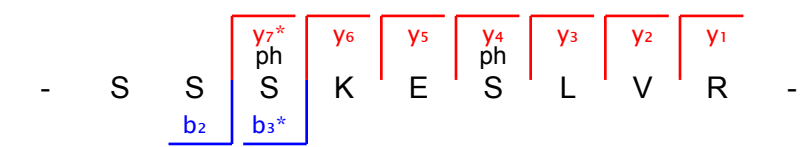
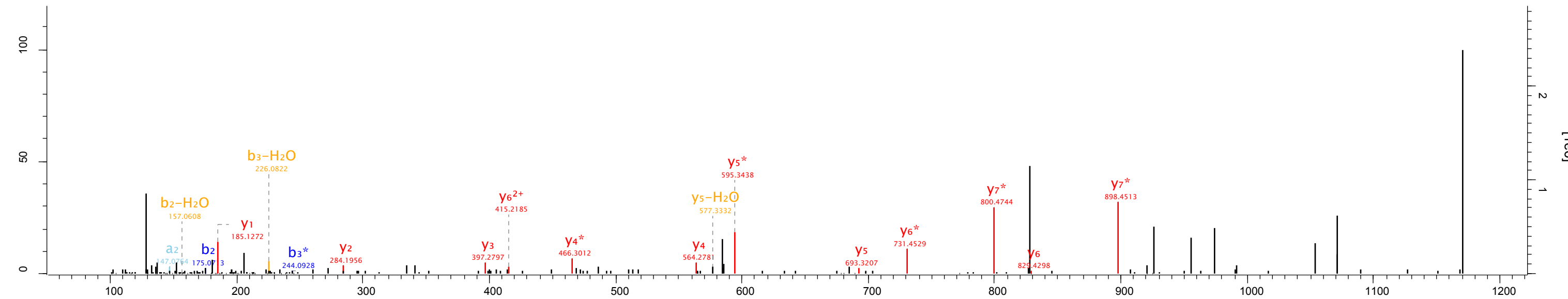


Raw file
20171215_MaS_33SR_LMH_phospho2_03

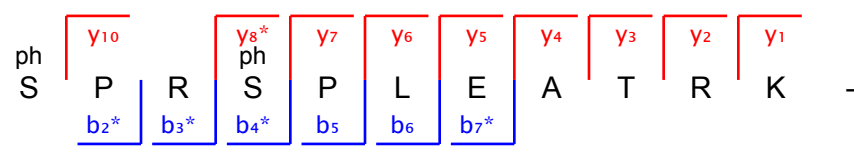
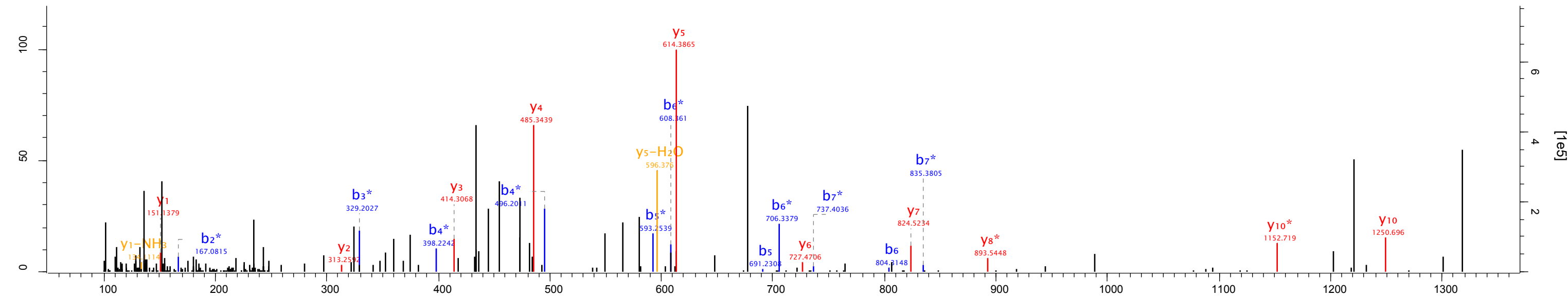
Scan 3922 Method FTMS; HCD Score 64.25 m/z 546.22 Gene names SRRM2



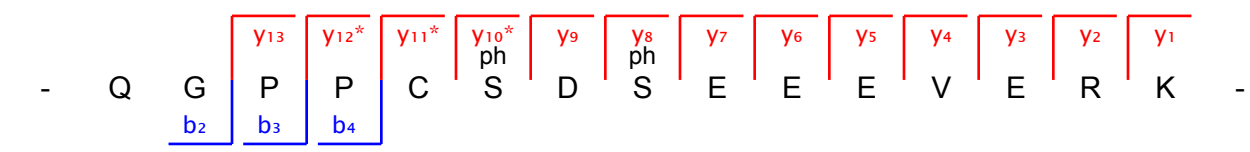
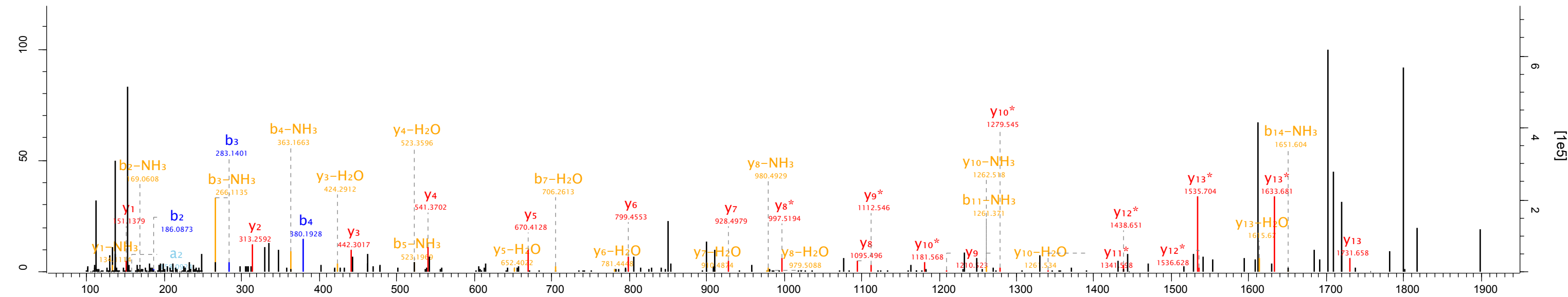
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4022 Method FTMS; HCD Score 56.57 m/z 585.75 Gene names GOLGA4

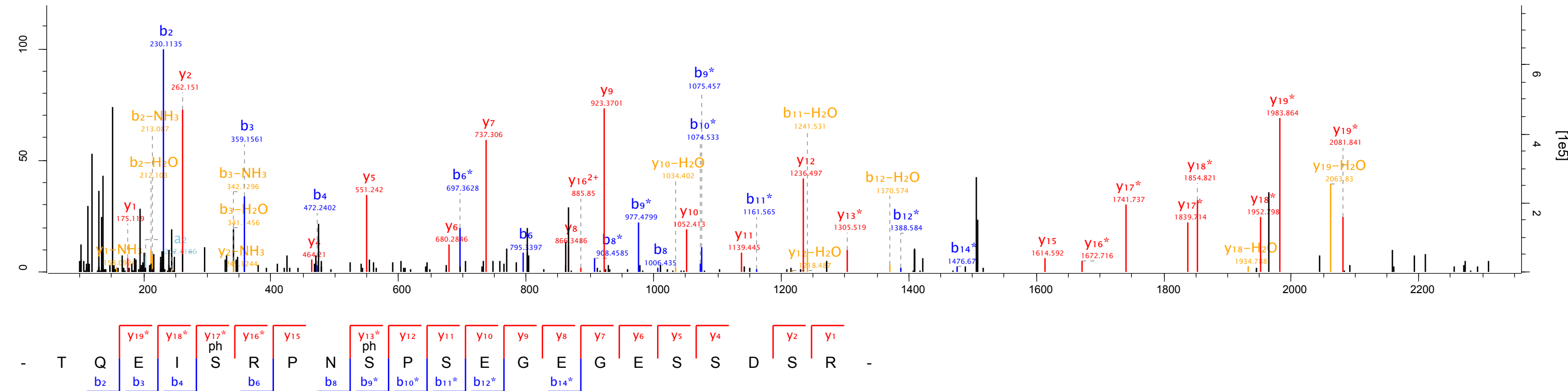


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4042 Method FTMS; HCD Score 60.62 m/z 473.24 Gene names ZNF592

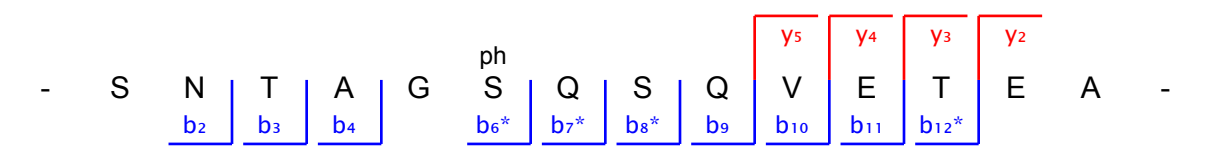
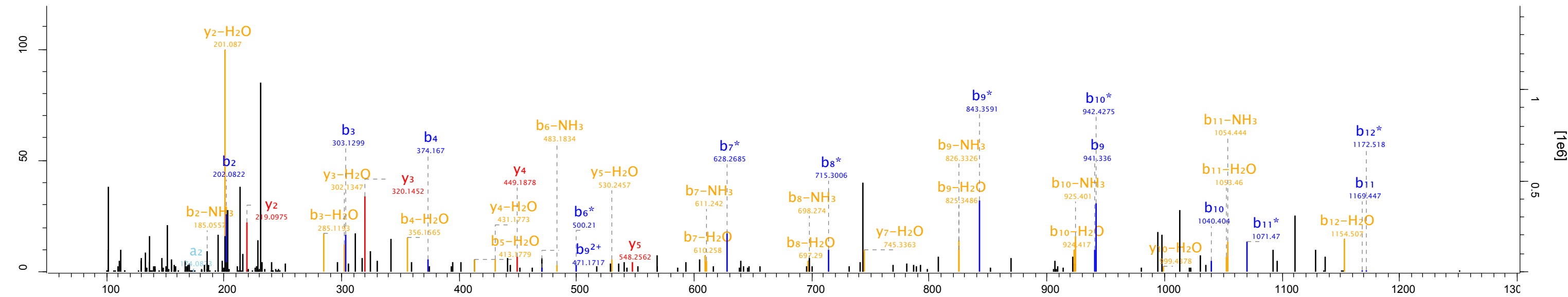


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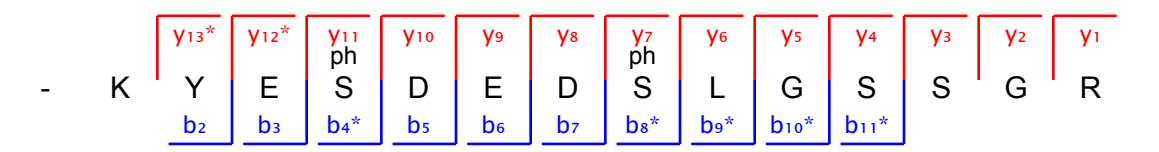
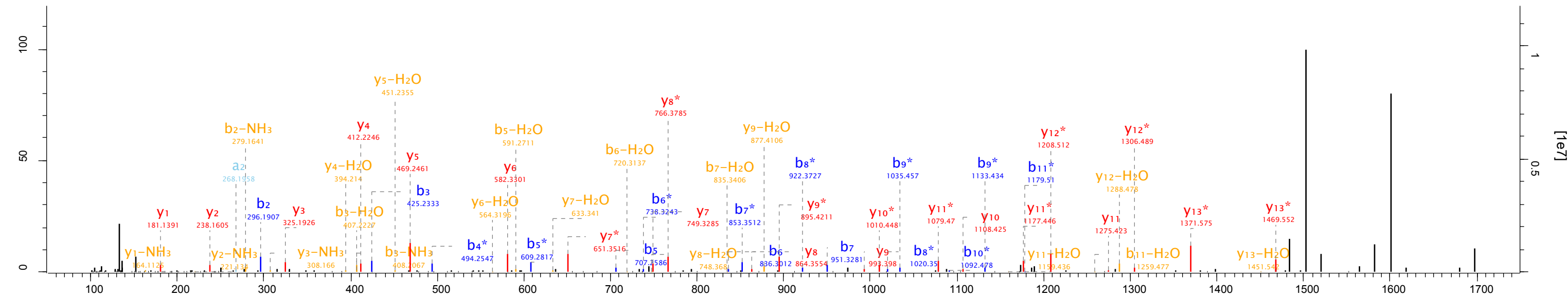




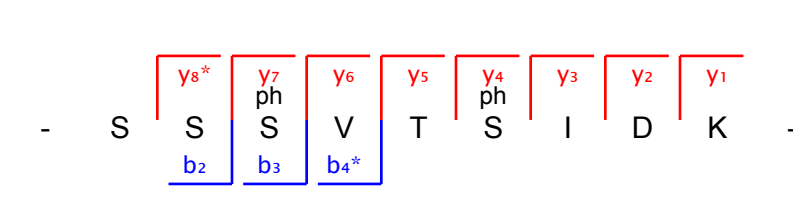
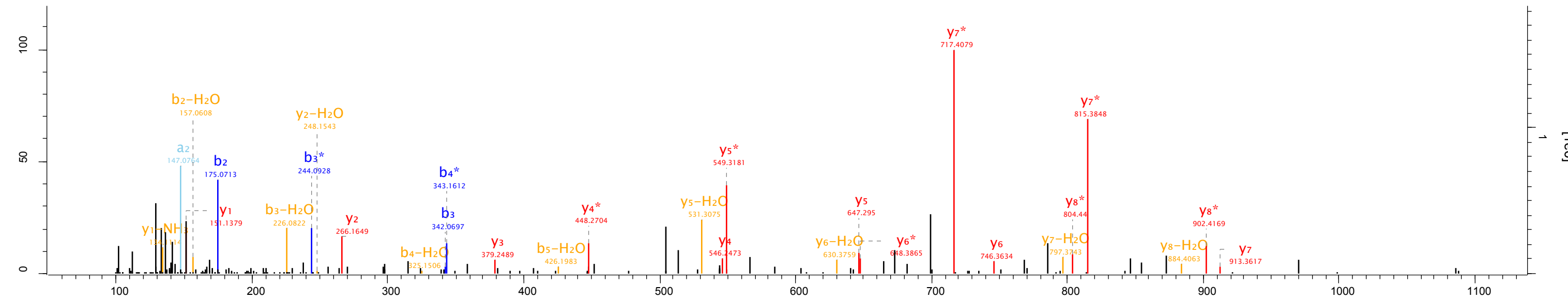
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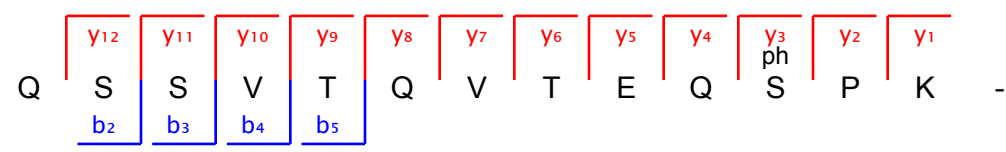
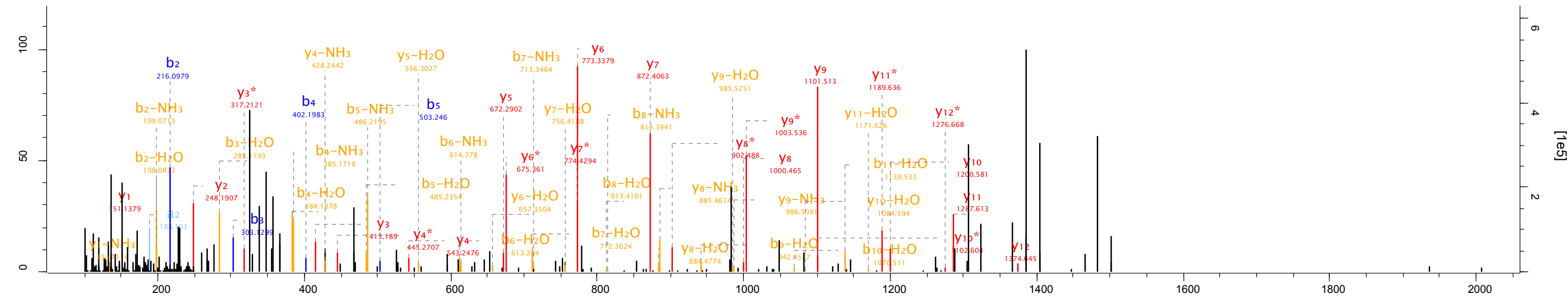


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 Scan: 4572 Method: FTMS; HCD Score: 118.24 m/z: 544.22 Gene names: STXBP5



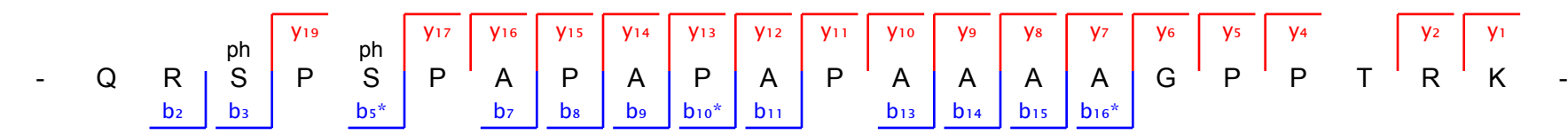
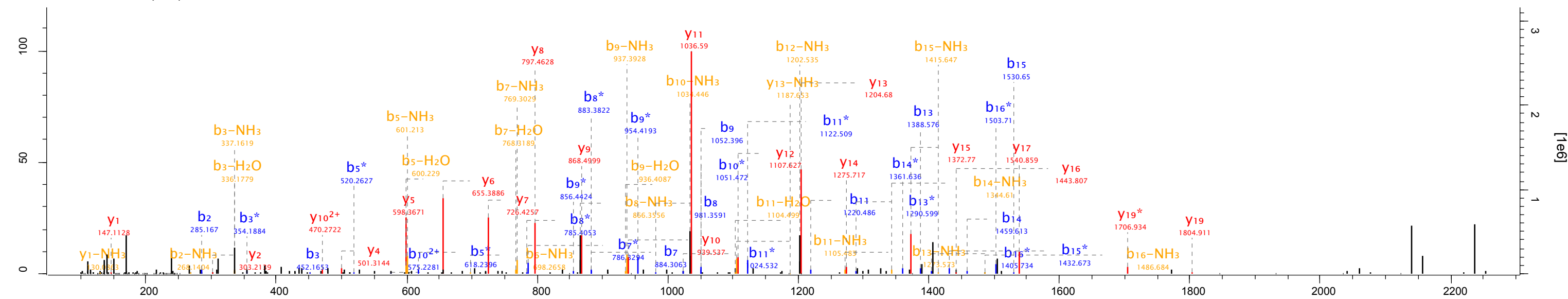
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20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
4822 FTMS; HCD 200.71 752.36 ZNF638

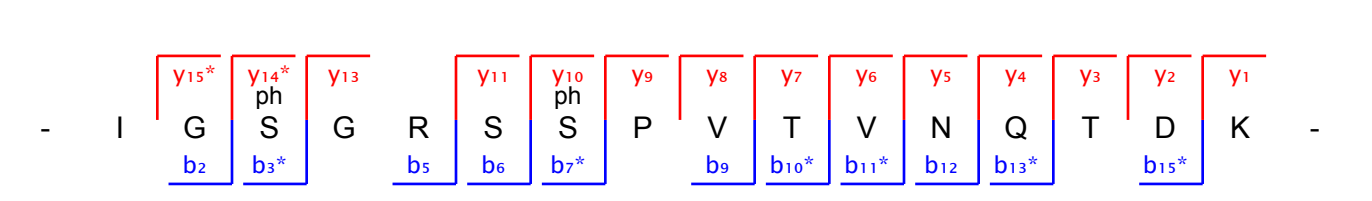
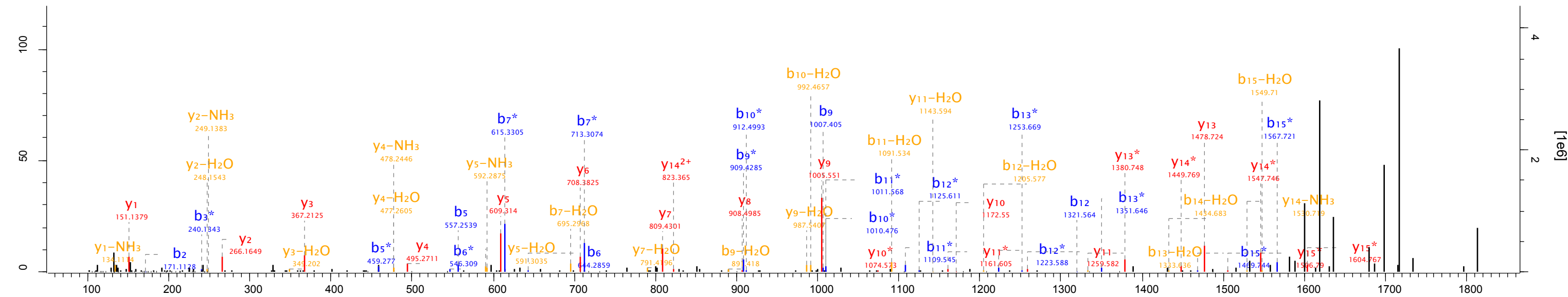


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20171215_MaS_33SR_LMH_phospho2_03

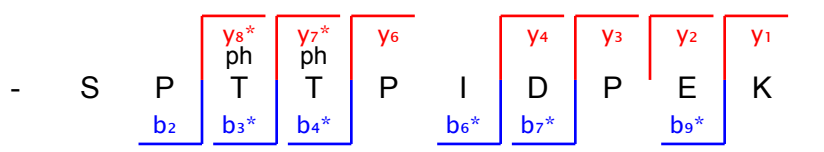
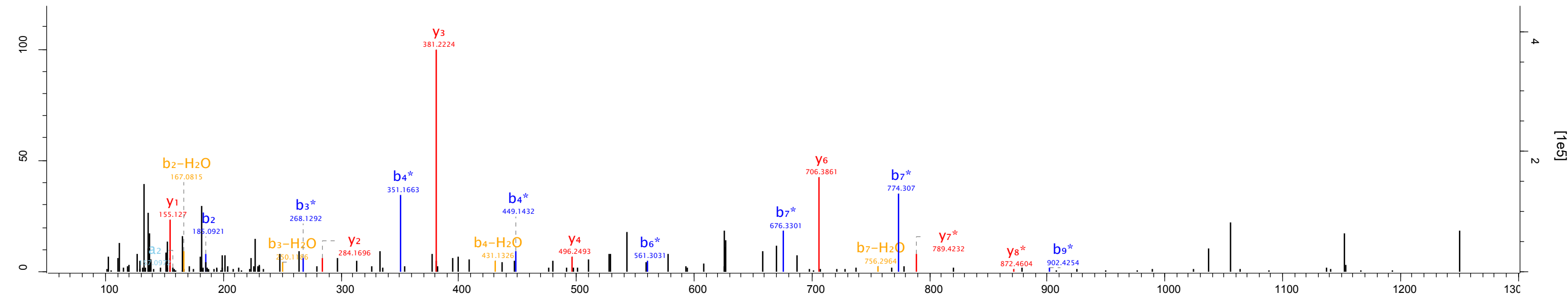
Scan 5222 Method FTMS; HCD Score 196.19 m/z 753.03 Gene names SCAF1



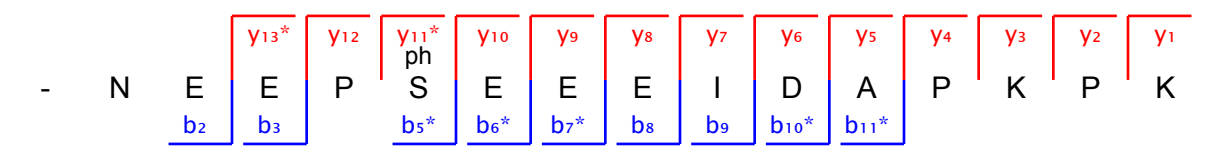
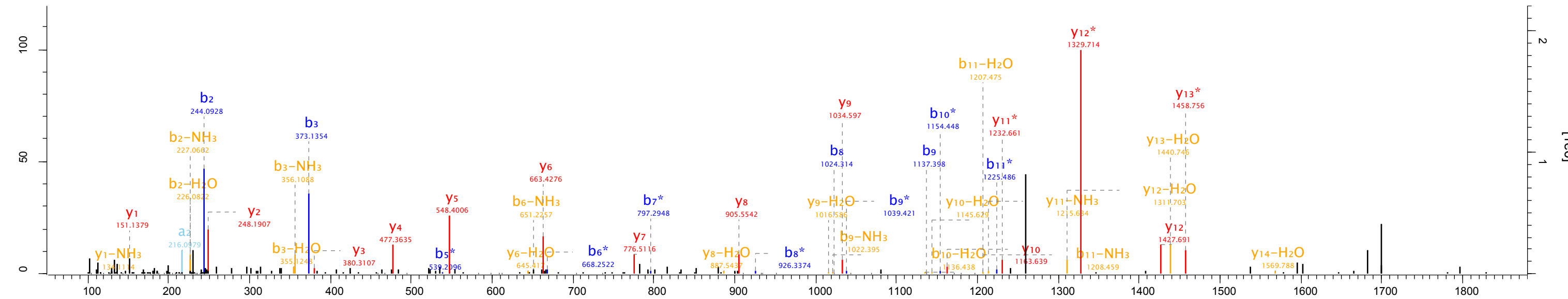
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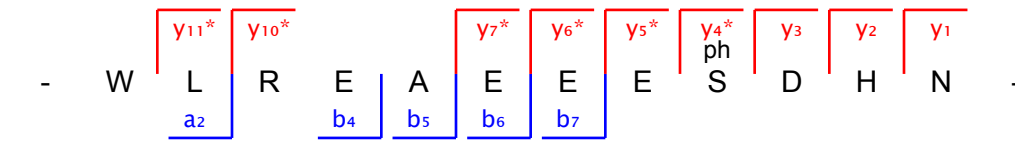
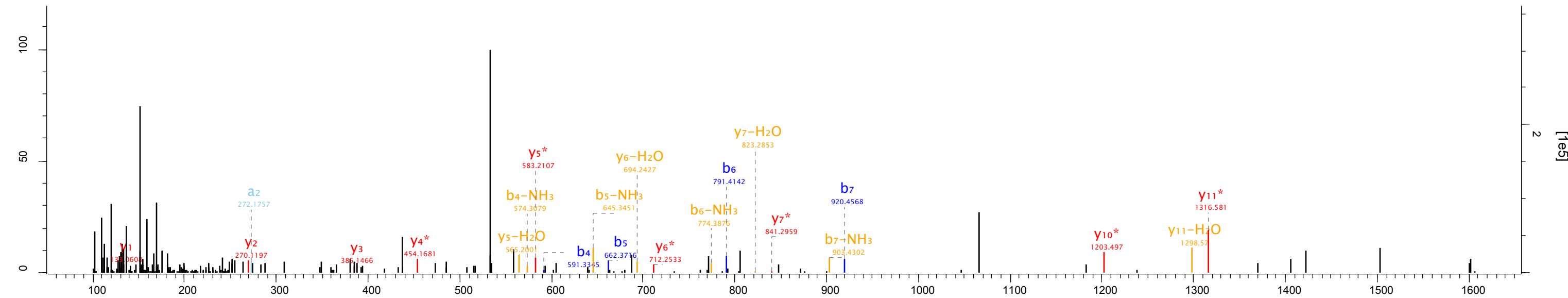


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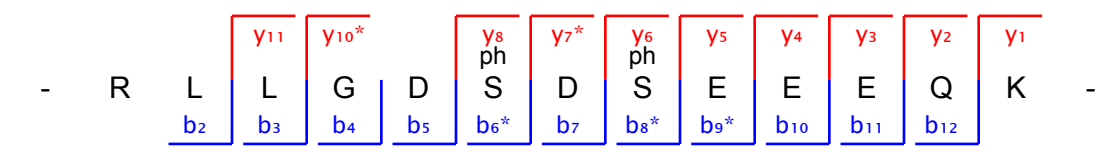
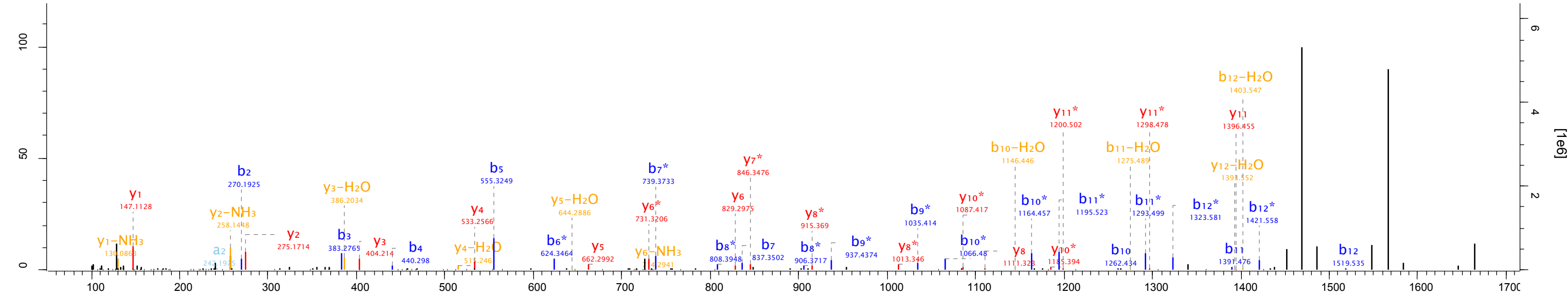


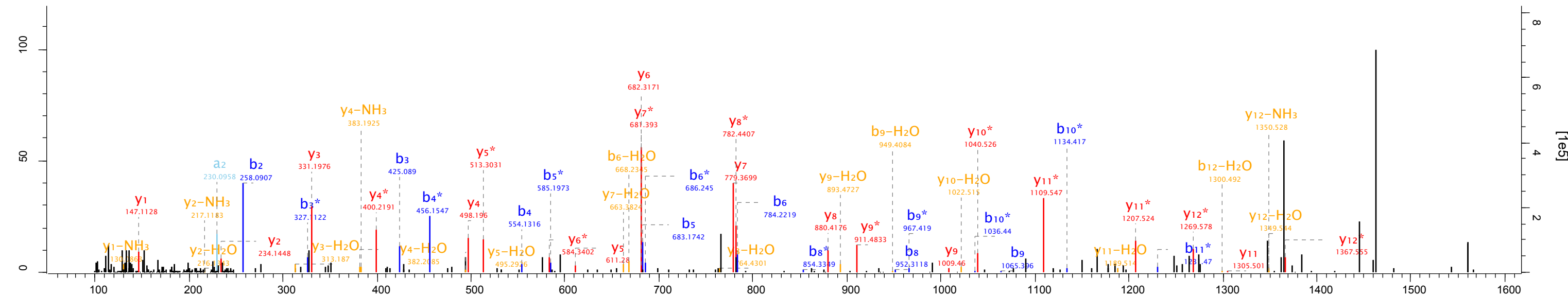
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20171215_MaS_33SR_LMH_phospho2_03 6342 FTMS; HCD 208.28 833.32 HIRIP3

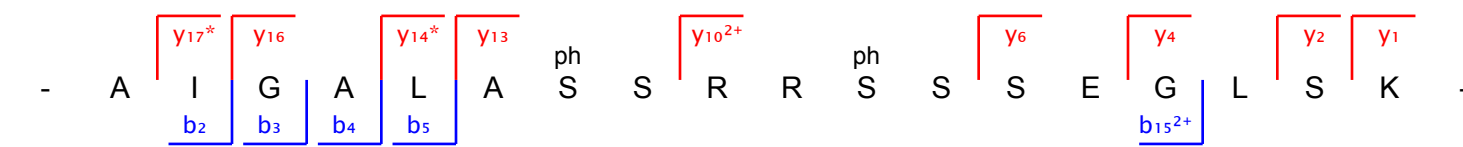
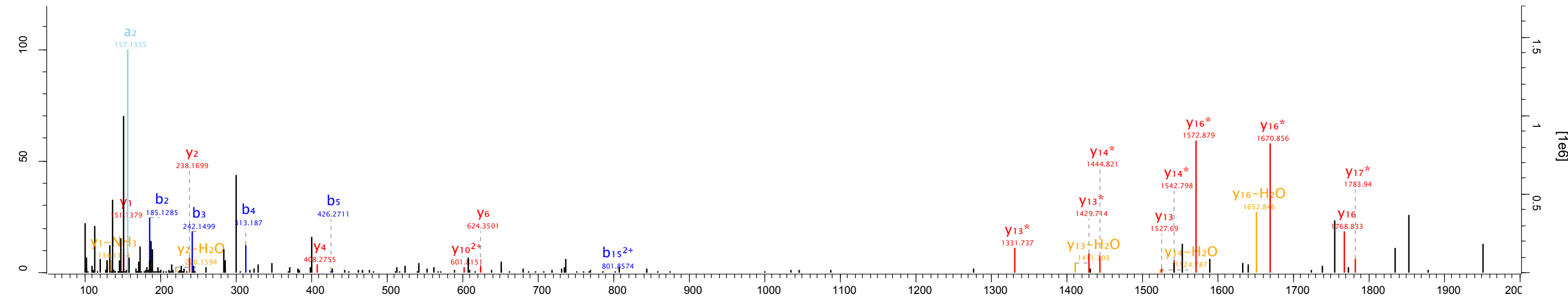


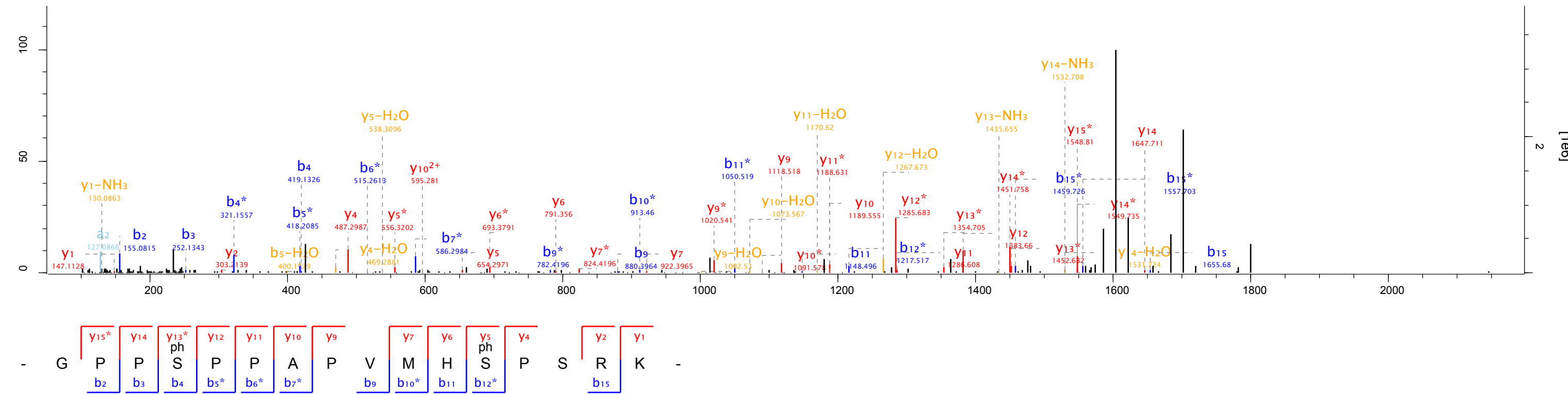


- P C S E E T P A I S P S K -

Fragmentation mapping (b and y ions):

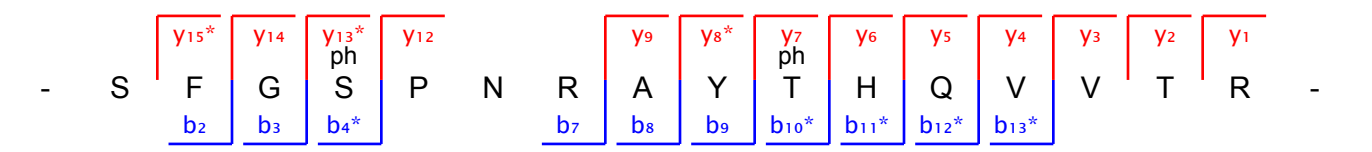
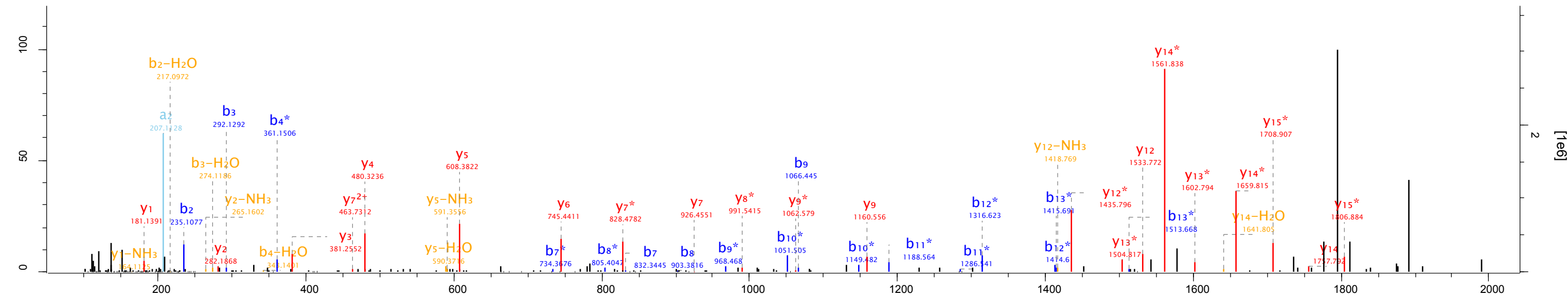
- Red boxes (y ions): y12*, y11 ph, y10*, y9, y8, y7, y6, y5, y4 ph, y3, y2, y1
- Blue boxes (b ions): b2, b3, b4, b5, b6, b8, b9, b10*, b11*





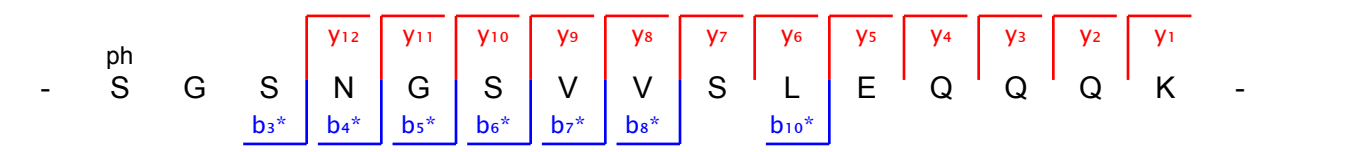
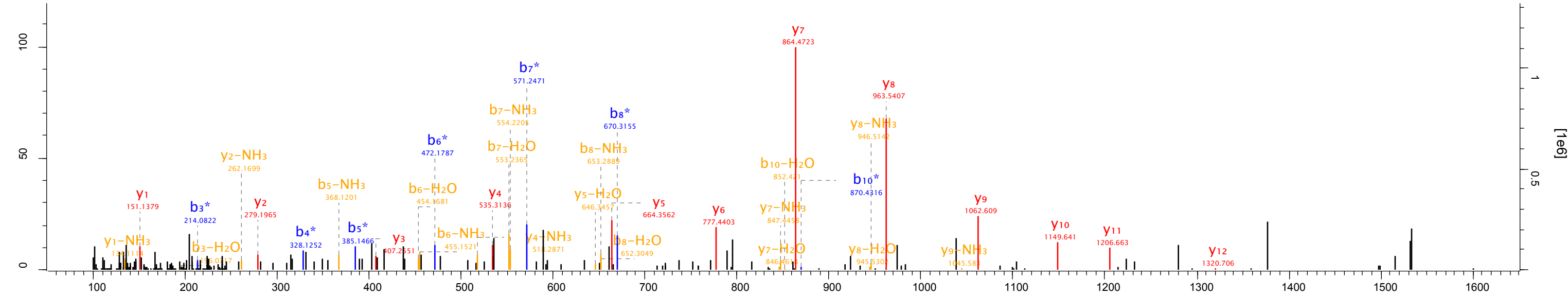
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 7802 Method FTMS; HCD Score 176.9 m/z 664.63 Gene names CDK7

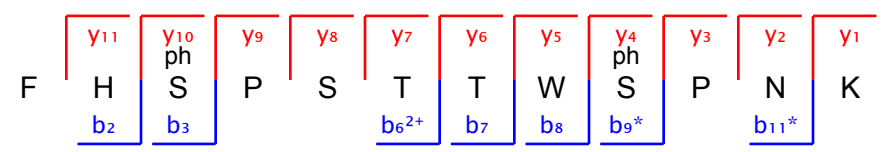
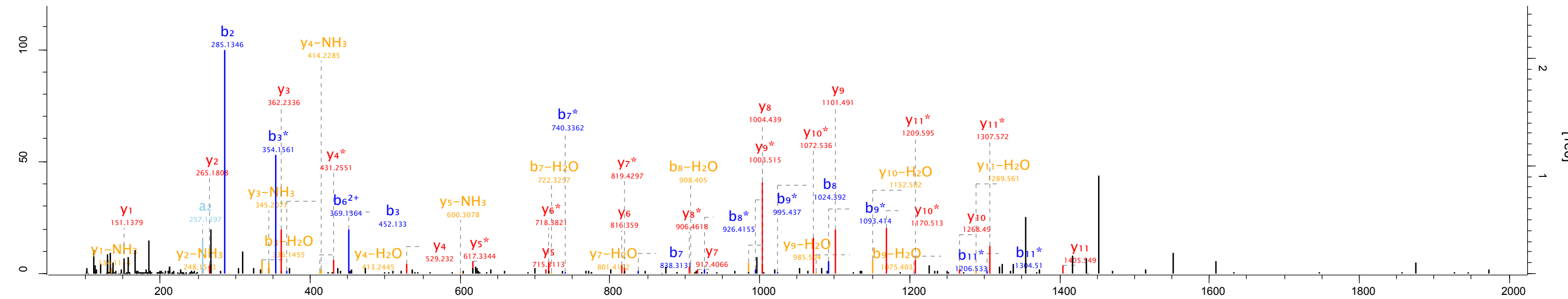


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 8062 FTMS; HCD 100.27 816.88 KIF7

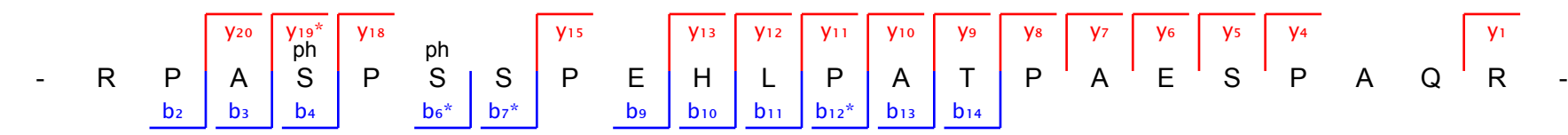
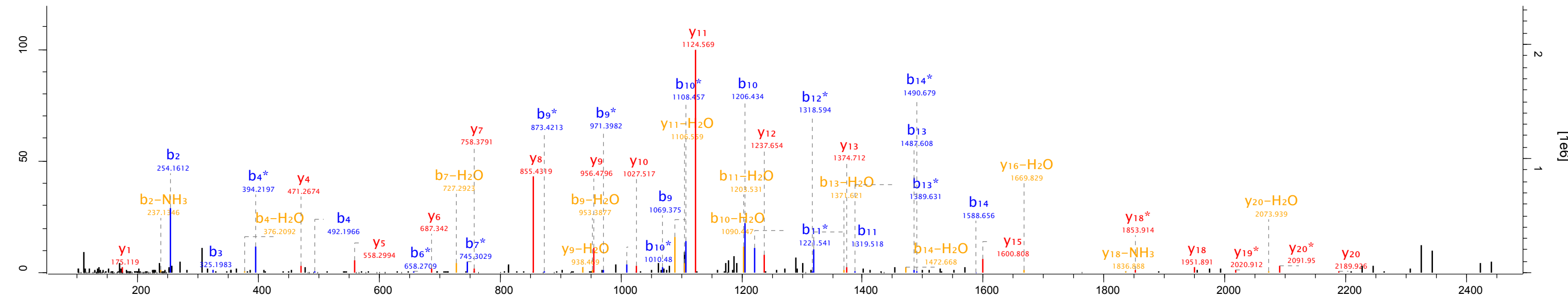


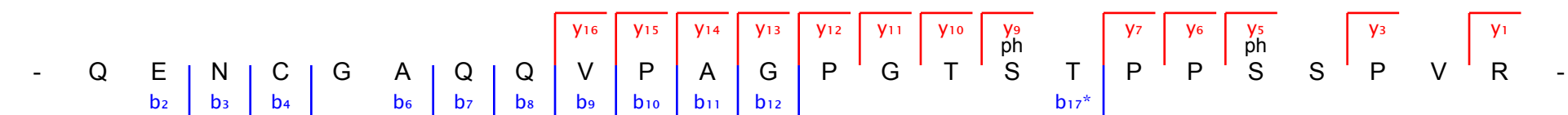
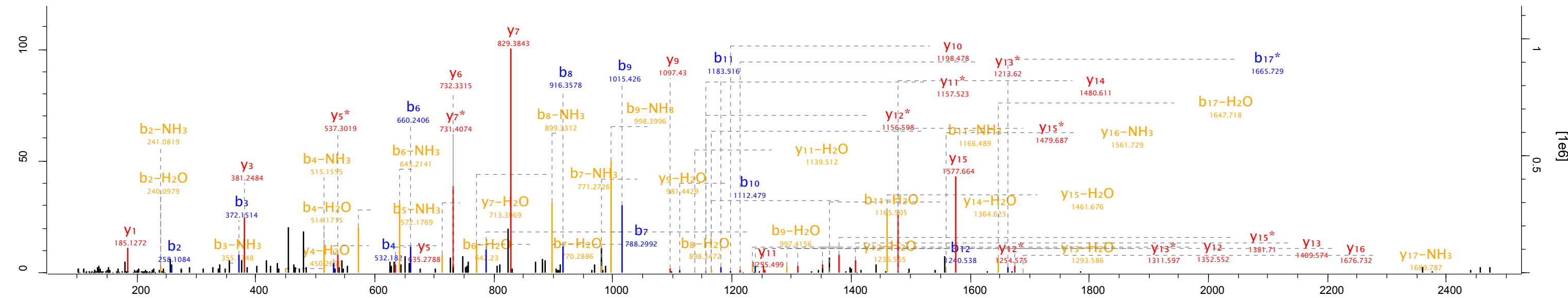
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 Scan: 8112 Method: FTMS; HCD Score: 197.51 m/z: 776.81 Gene names: SCAF11



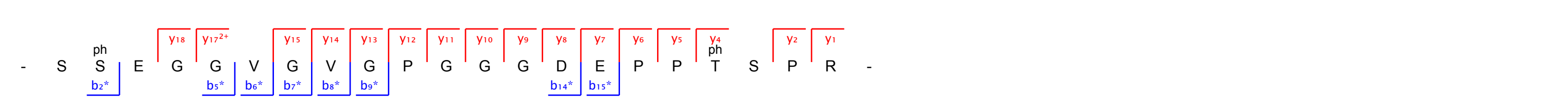
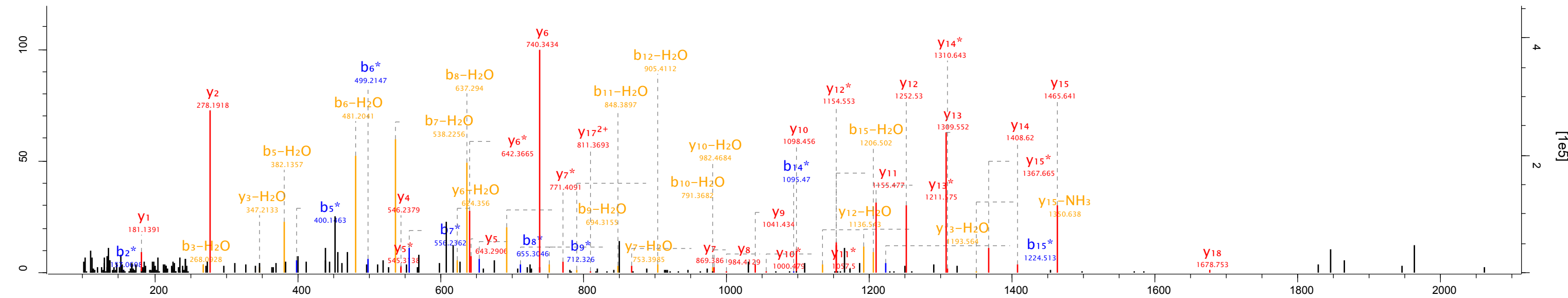
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20171215_MaS_33SR_LMH_phospho2_03

Scan 8152 Method FTMS; HCD Score 147.8 m/z 815.37 Gene names SUDS3

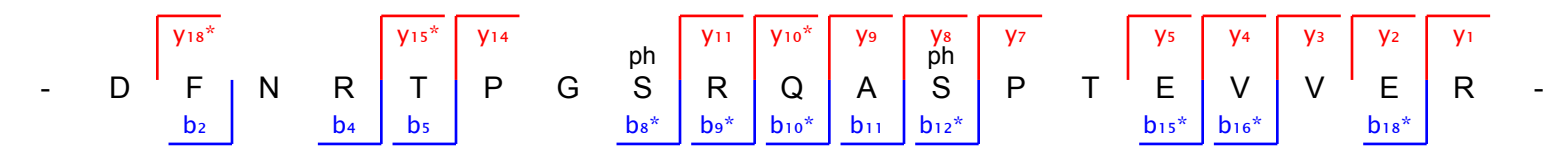
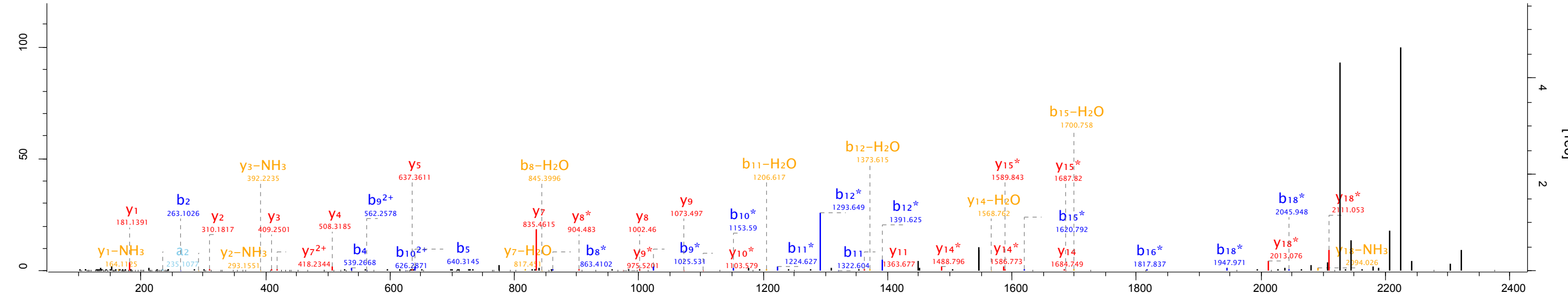


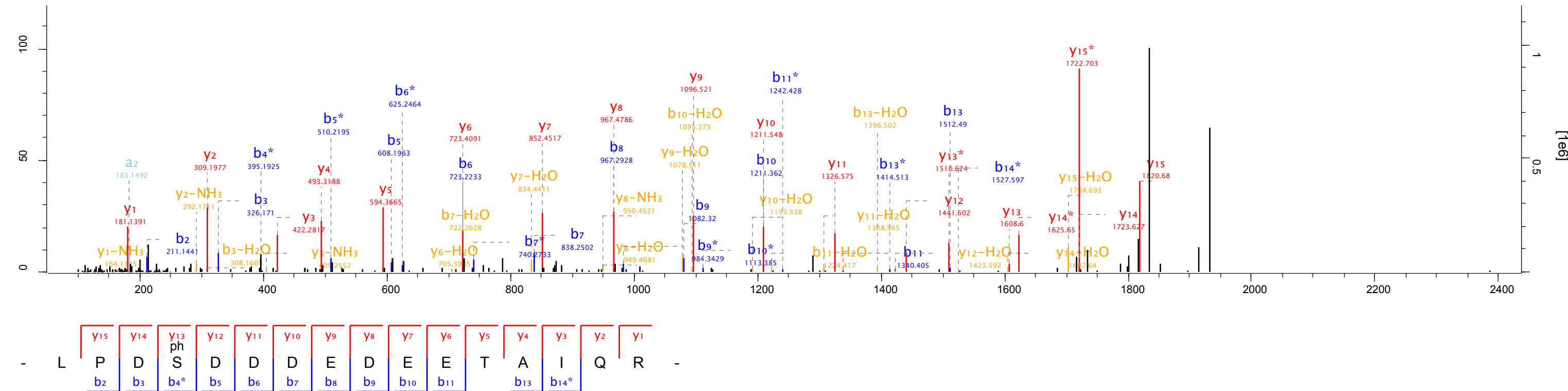


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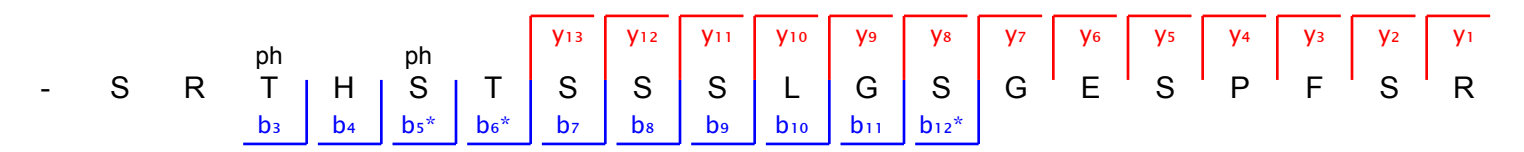
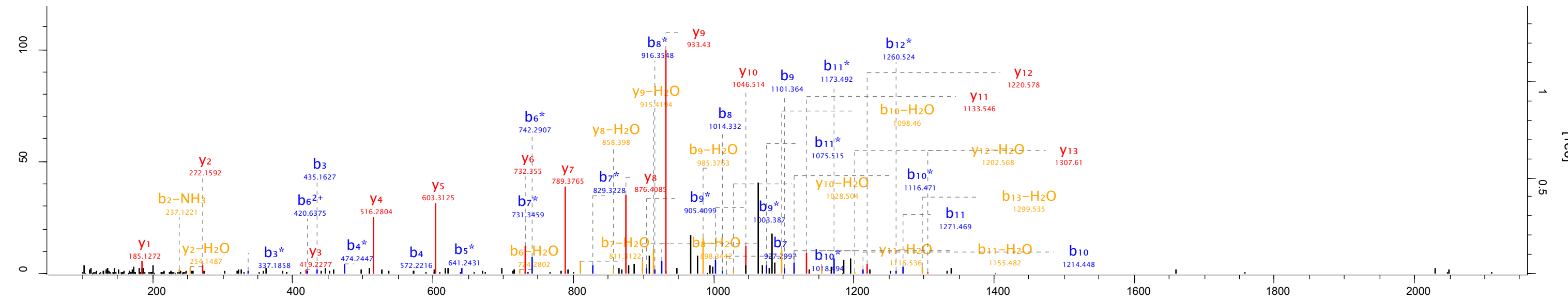


20171215_MaS_33SR_LMH_phospho2_03 8642 FTMS; HCD 124.82 775.36 PUM2

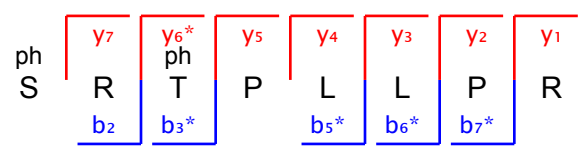
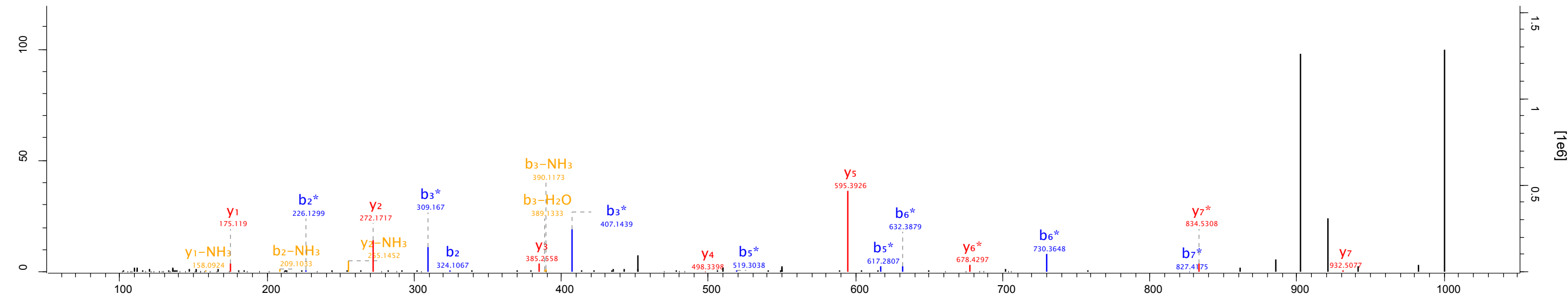




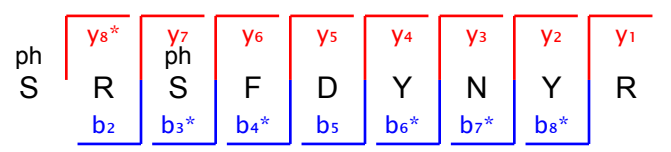
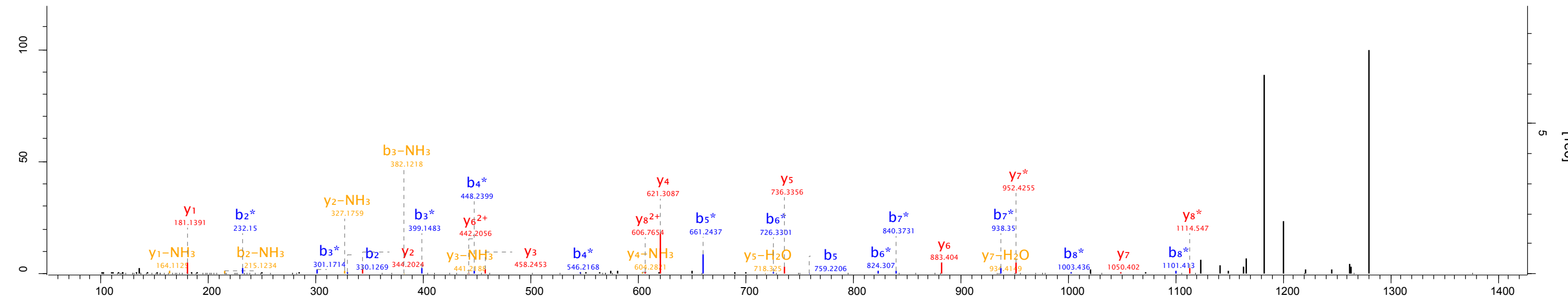
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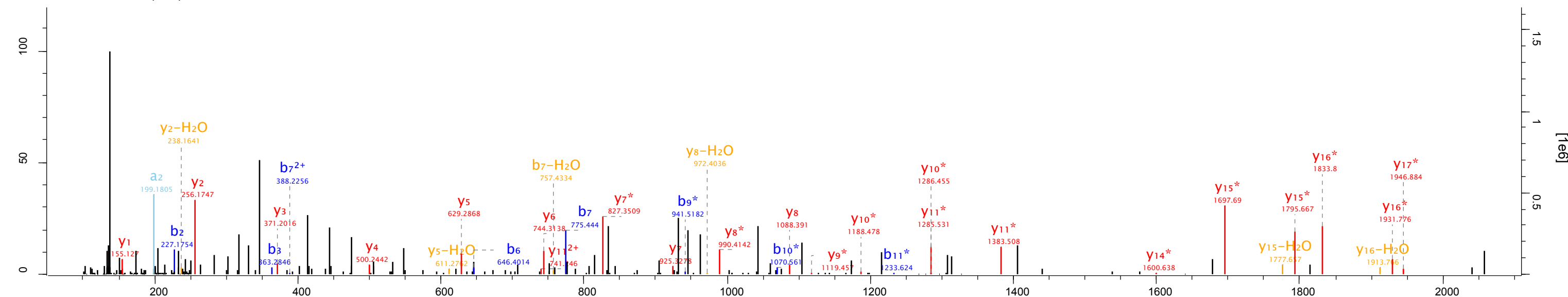


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8942 Method FTMS; HCD Score 85.67 m/z 550.25 Gene names SRRM2



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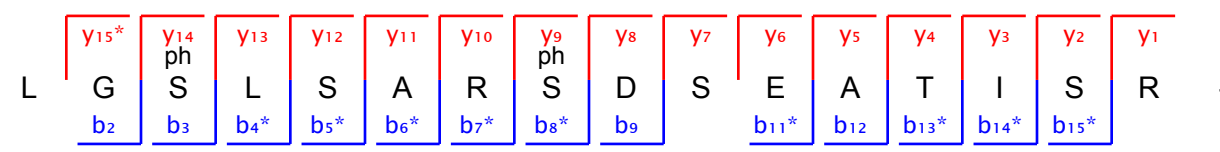
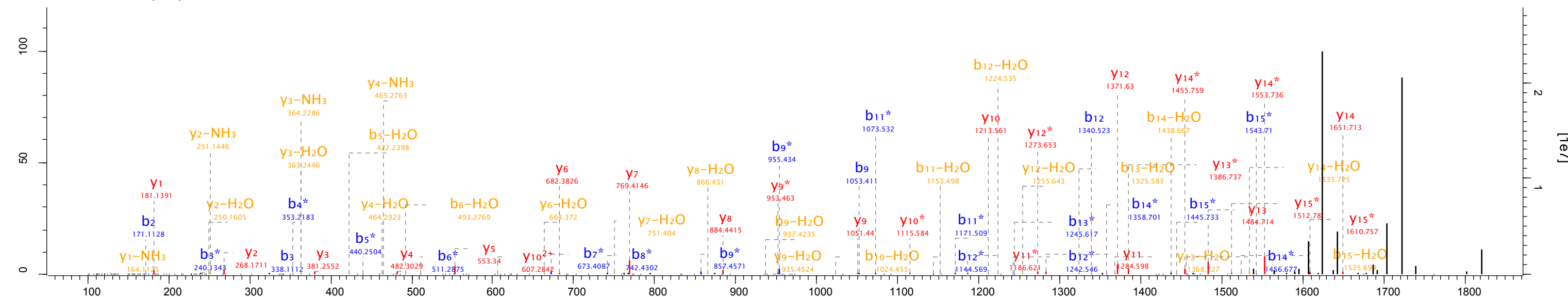




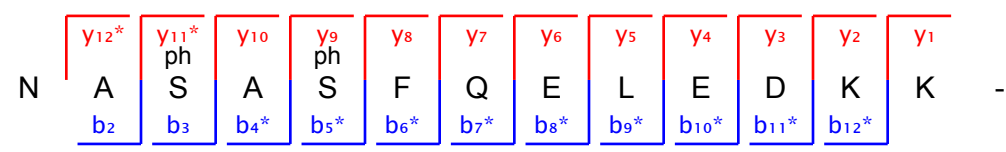
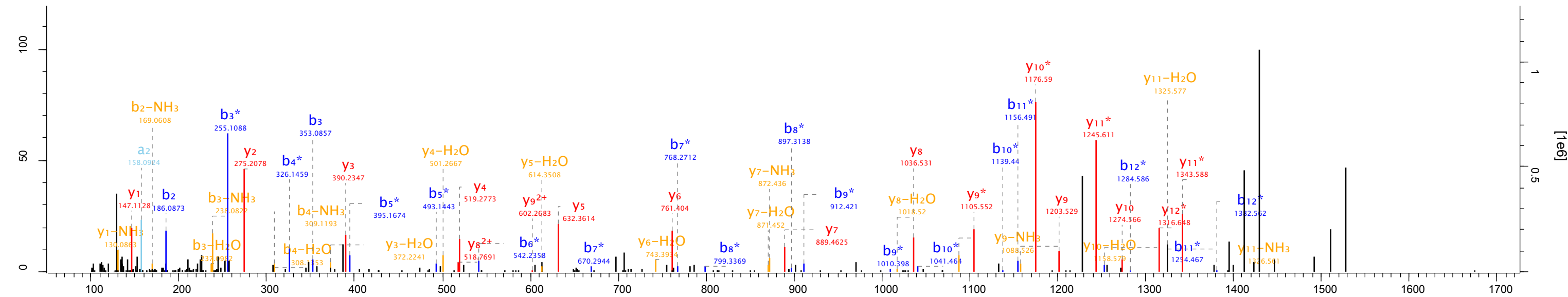
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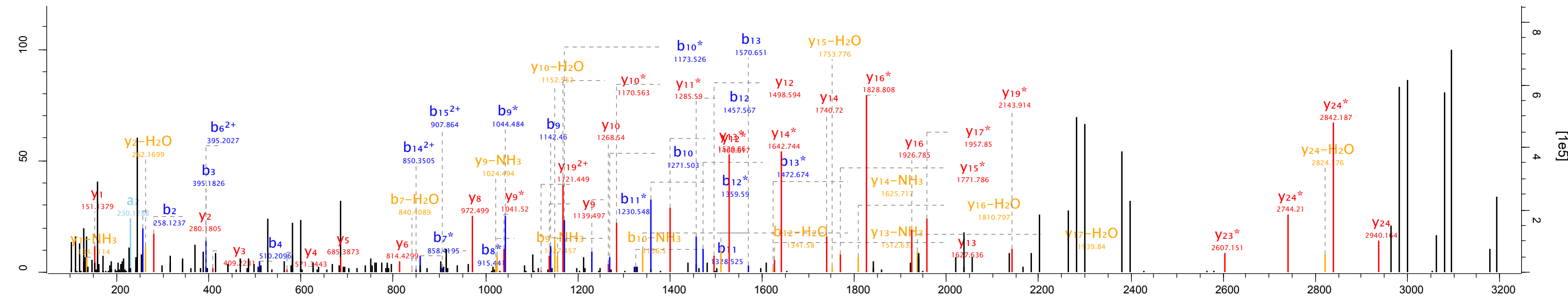
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 9202 Method FTMS; HCD Score 269.75 m/z 911.41 Gene names CEP170



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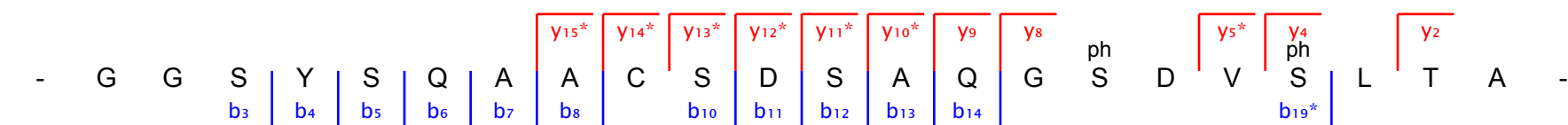
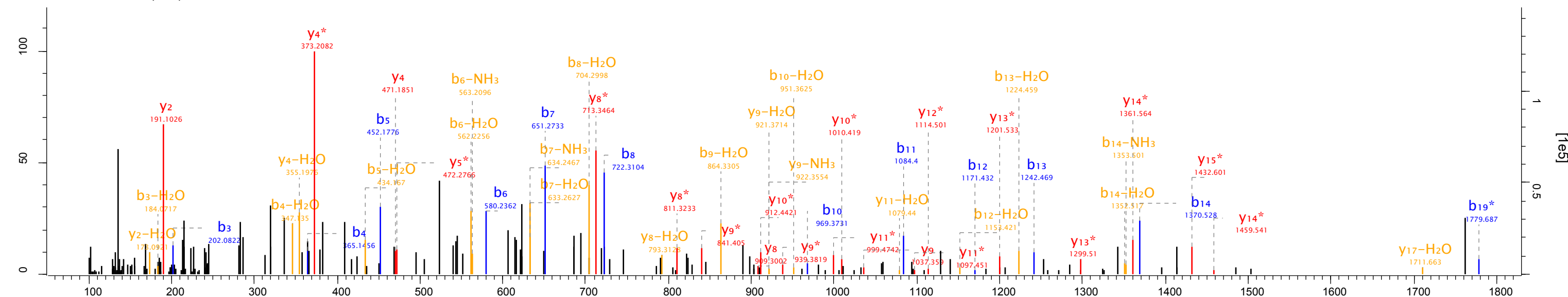


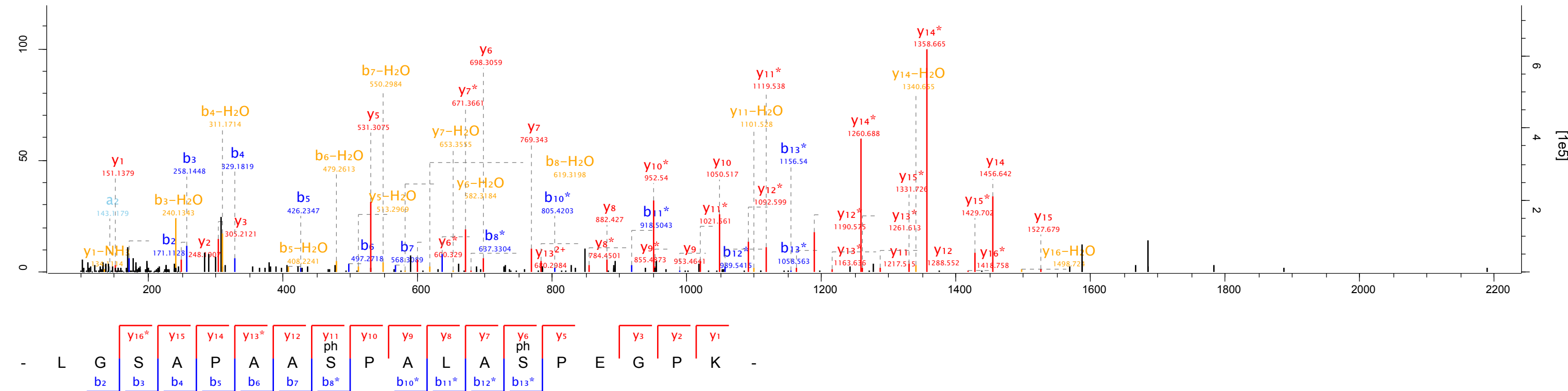


- W A H D K F S G E E G E I E D D E S G T E N R E E K -
 b₂ b₃ b₄ b₆²⁺ b₇^{*} b₈^{*} b₉ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄²⁺ b₁₅²⁺ y₁₉^{*} y₁₇^{*} y₁₆ y₁₅^{*} y₁₄ y₁₃ y₁₂ y₁₁^{*} y₁₀ y₉ y₈ y₆ y₅ y₄ y₃ y₂ y₁

Raw file
20171215_MaS_33SR_LMH_phospho2_03

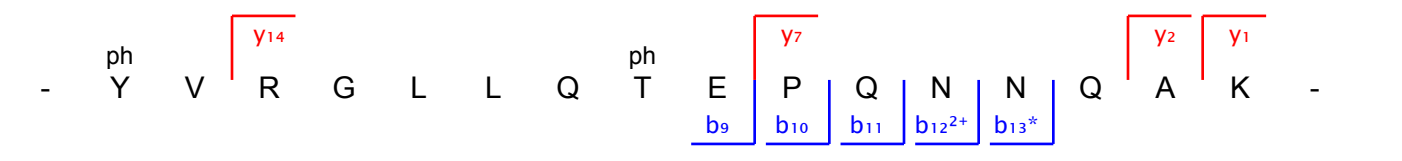
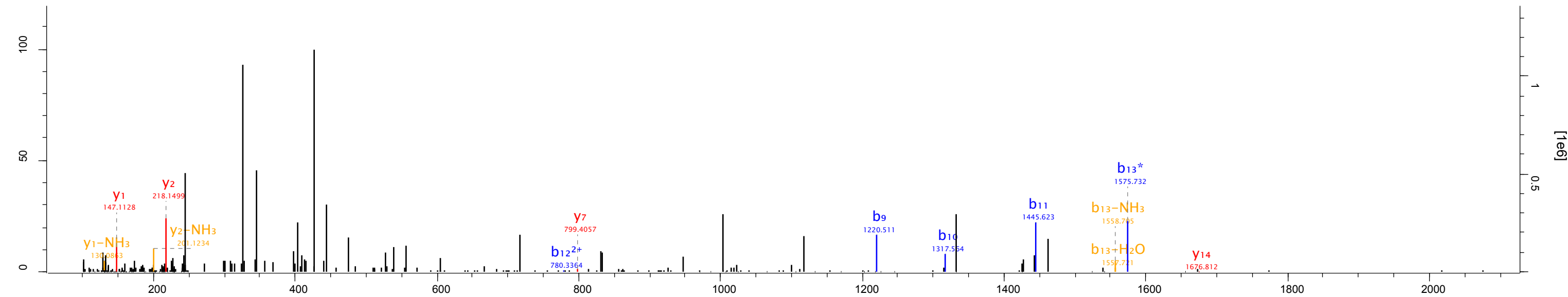
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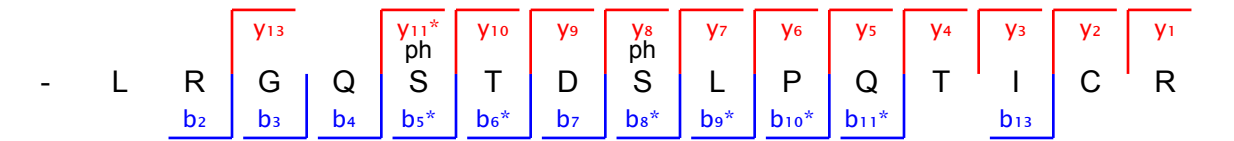
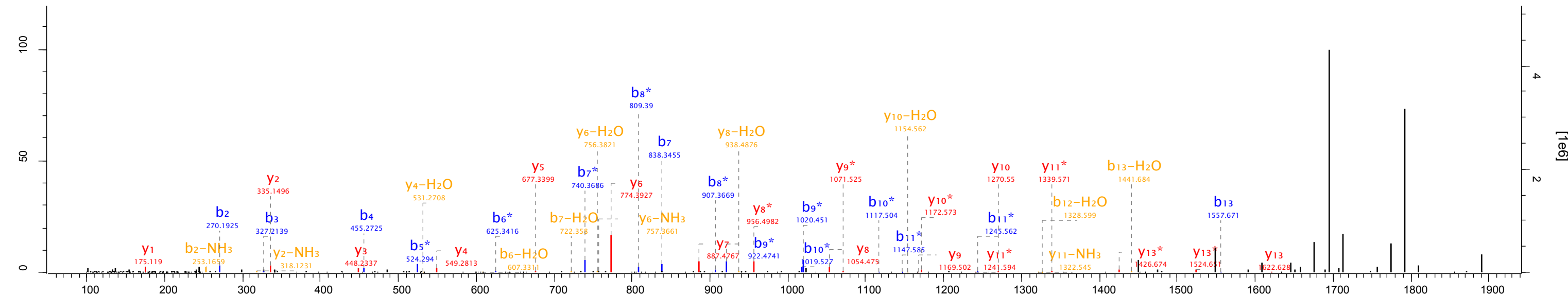




Raw file
20171215_MaS_33SR_LMH_phospho2_03

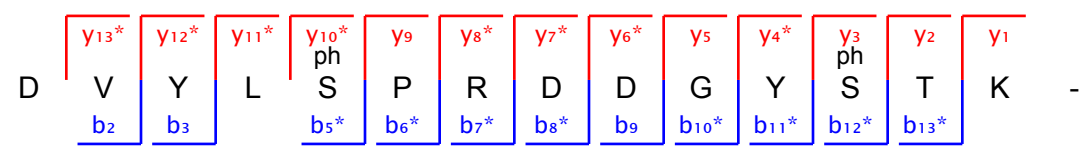
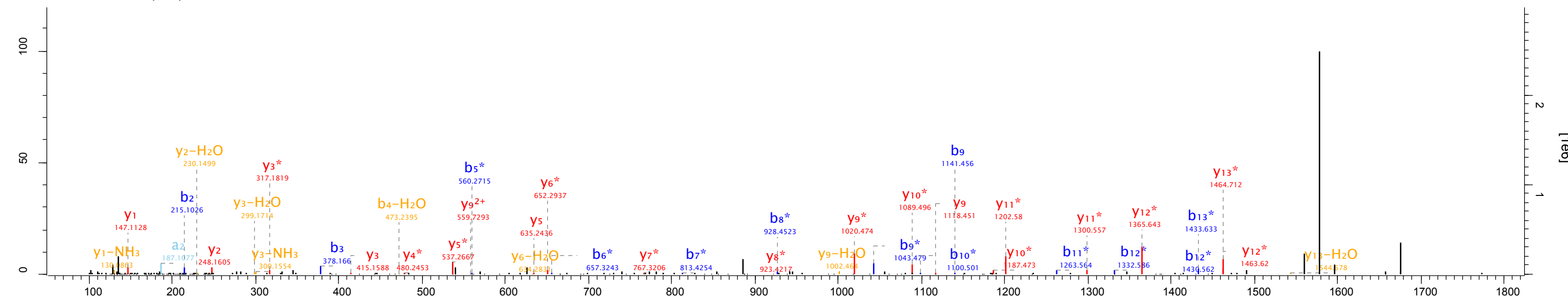
Scan	Method	Score	m/z	Gene names
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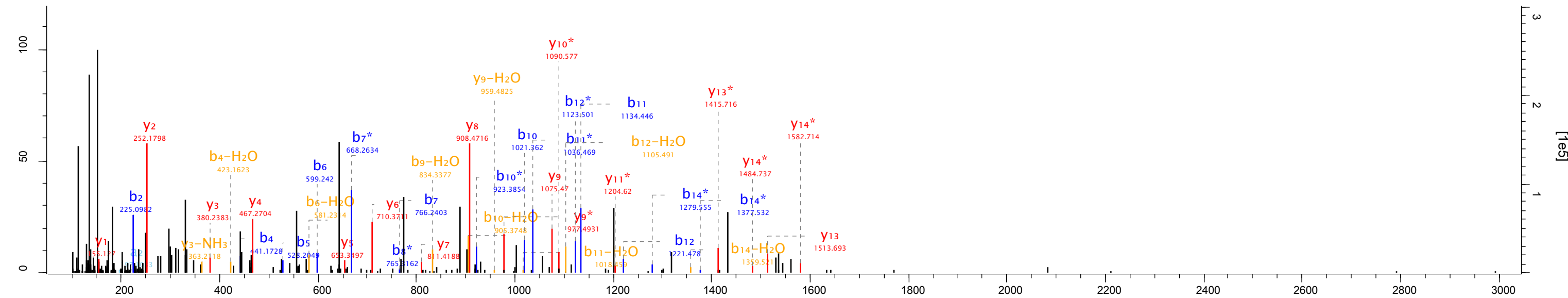




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20171215_MaS_33SR_LMH_phospho2_03

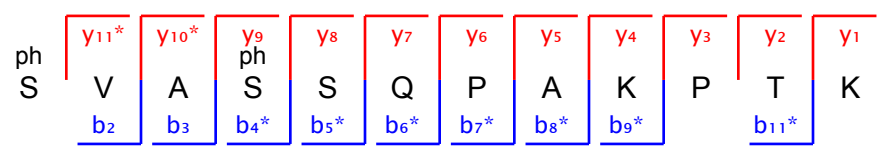
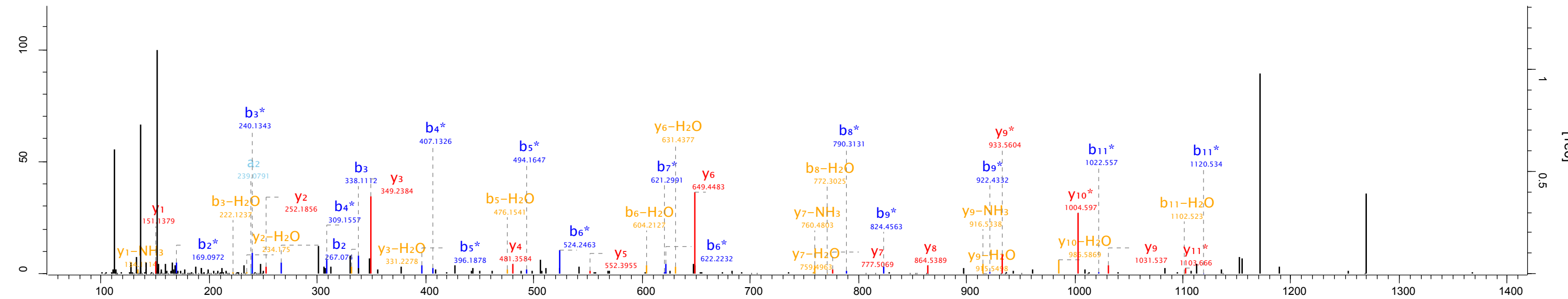
Scan 9972 Method FTMS; HCD Score 136.02 m/z 888.35 Gene names RBMX;RBMXL1



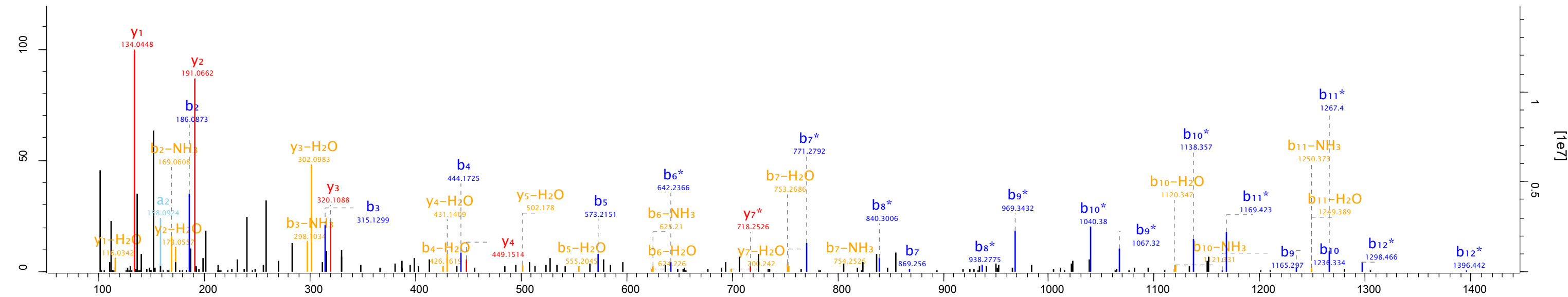


- S H S E S A S P S A L S S y14* ph y13 y11* y10* y9 ph y8 y7 y6 y5 y4 y3 y2 y1
 b2 b4 b5 b6 b7 b8* b10 b11 b12 b14*

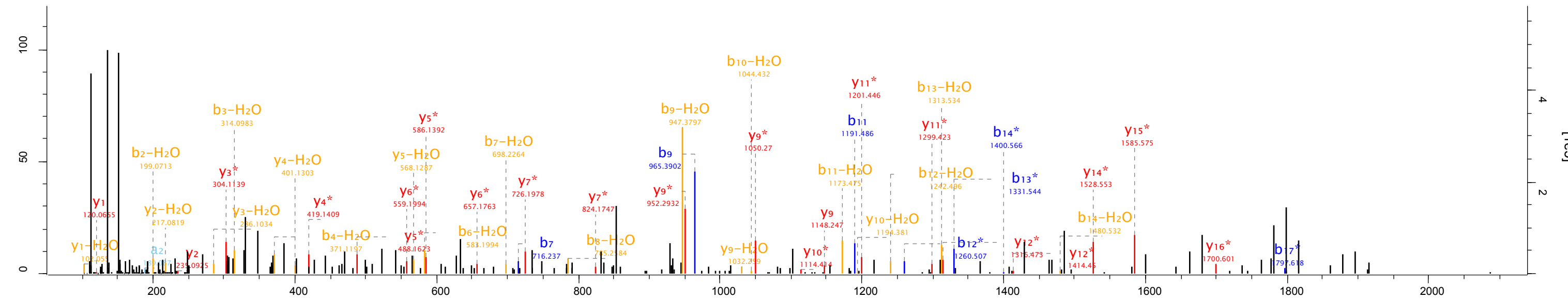
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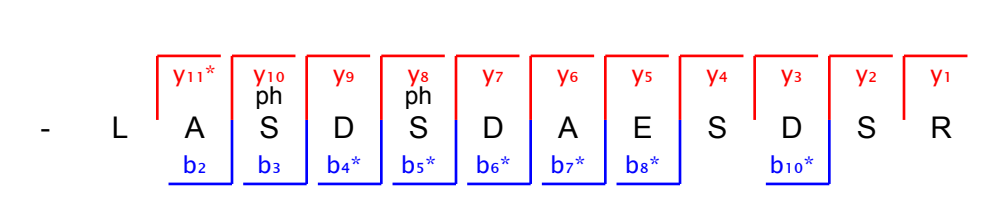
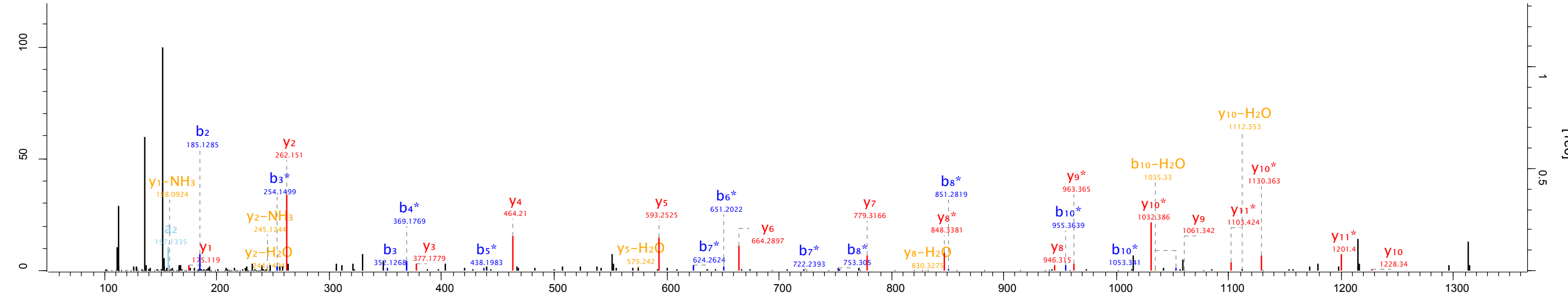


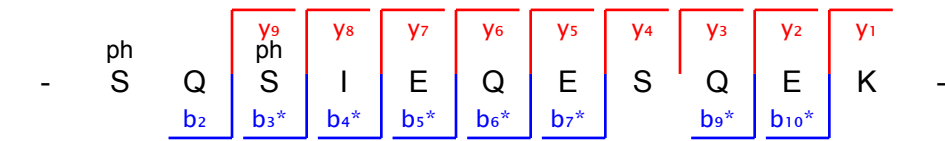
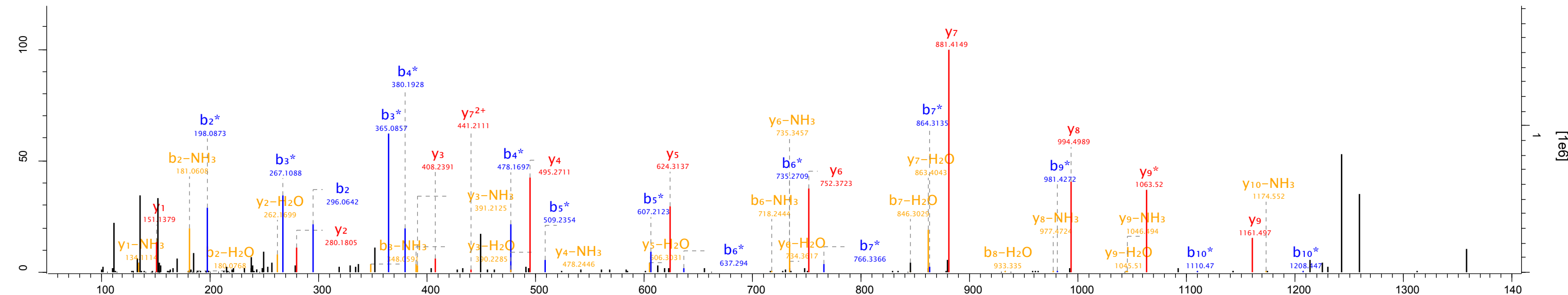
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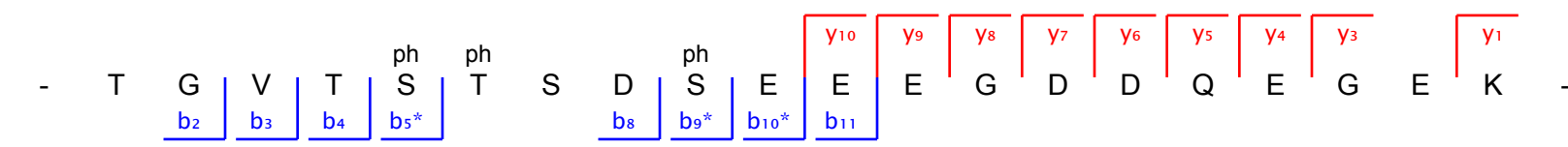
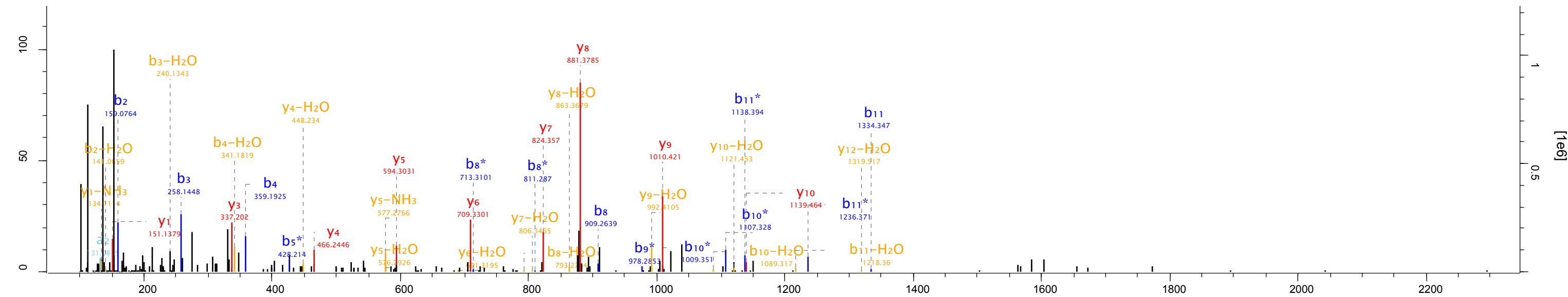
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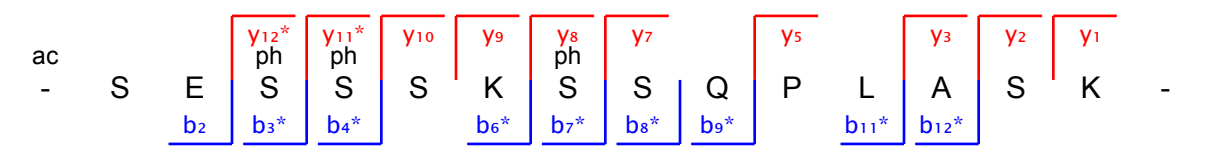
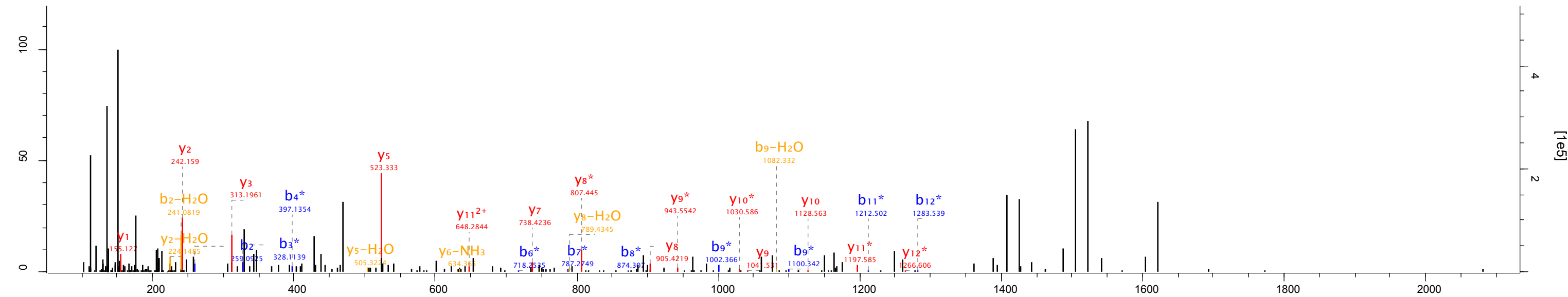


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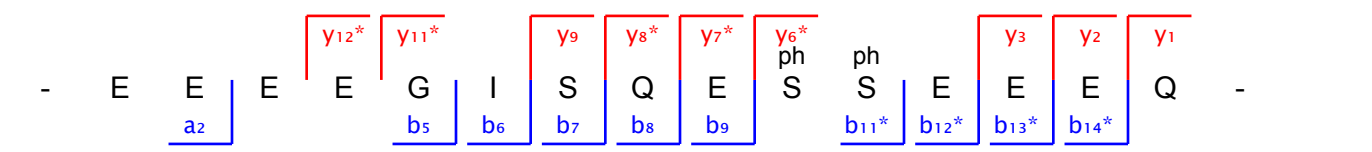
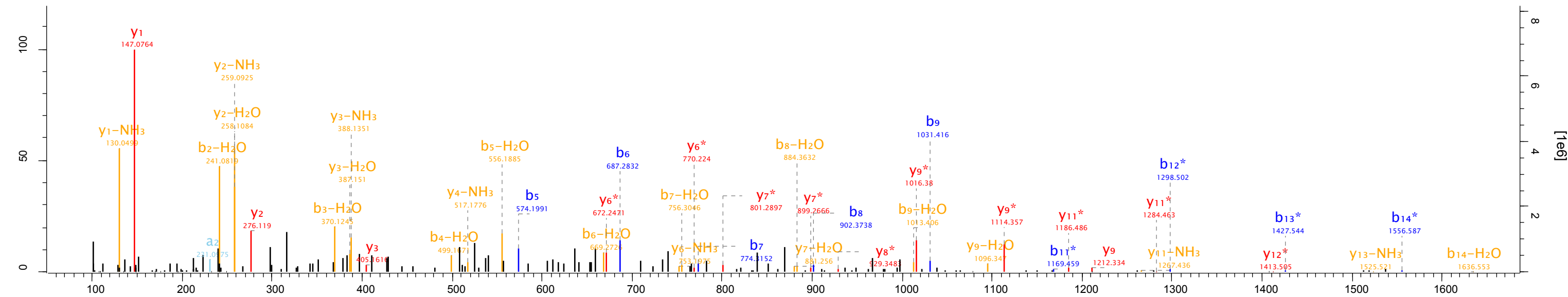
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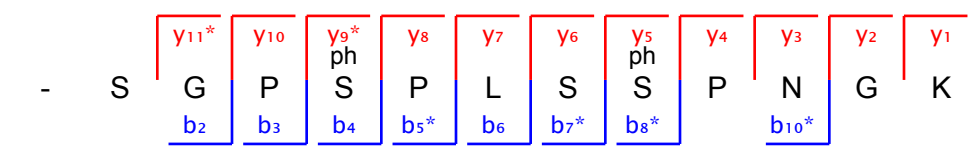
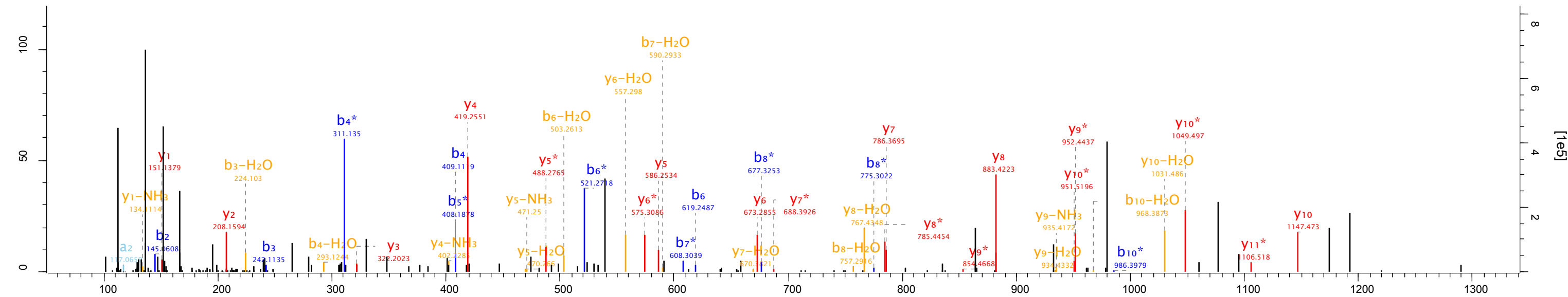
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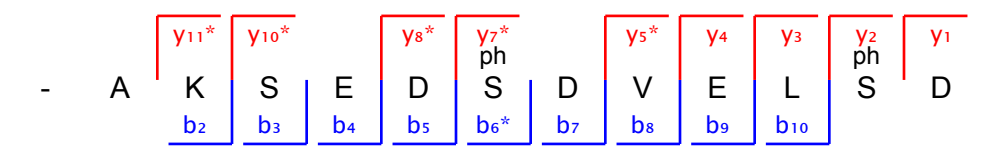
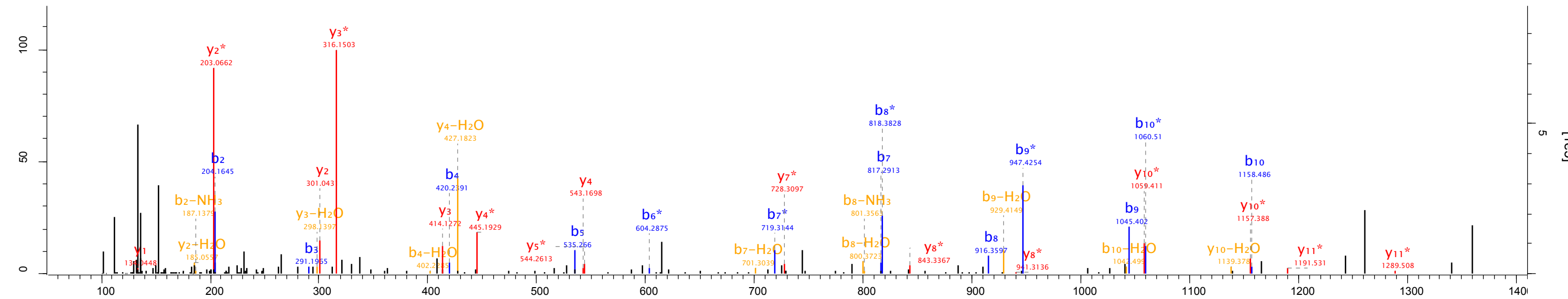
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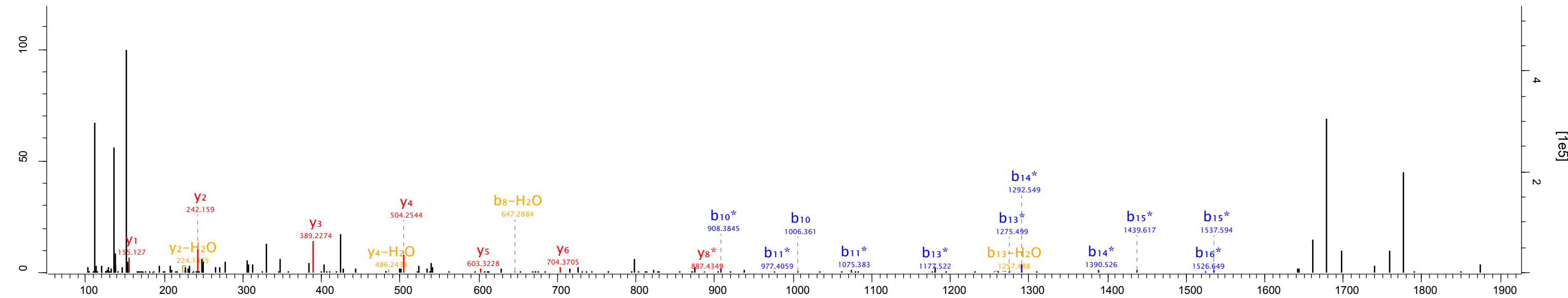


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 Scan: 4372 Method: FTMS; HCD Score: 164.57 m/z: 646.27 Gene names: ANKRD17



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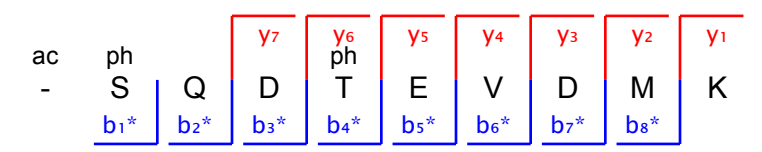
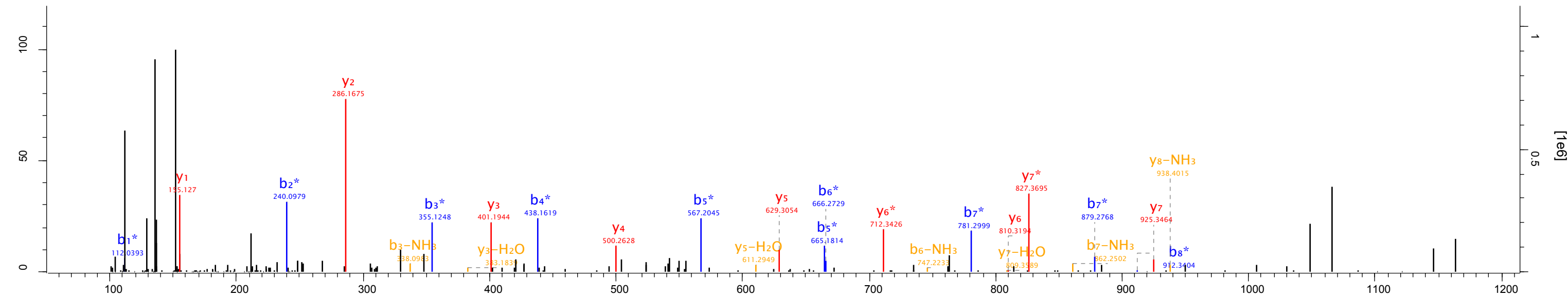
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ph ph

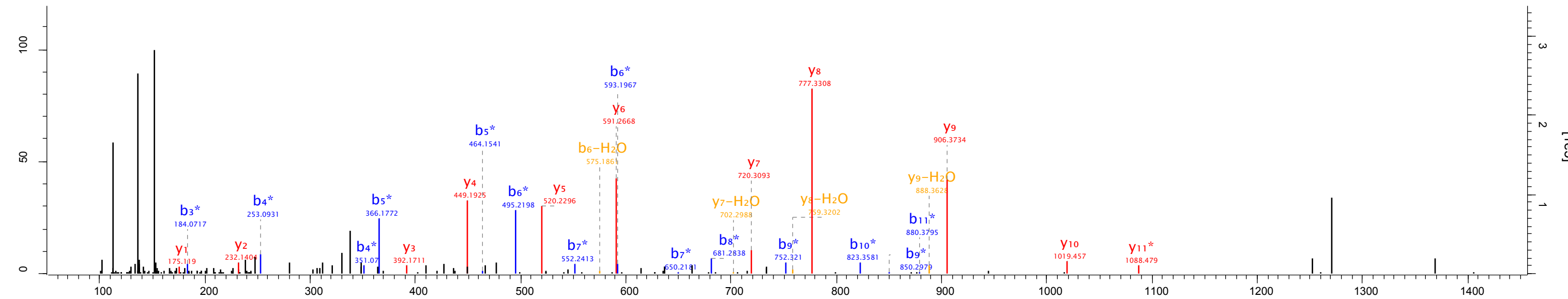
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b10 b11* b13* b14* b15* b16*

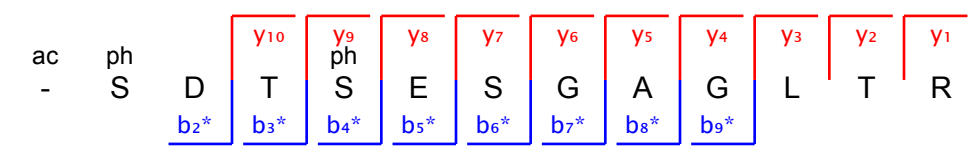
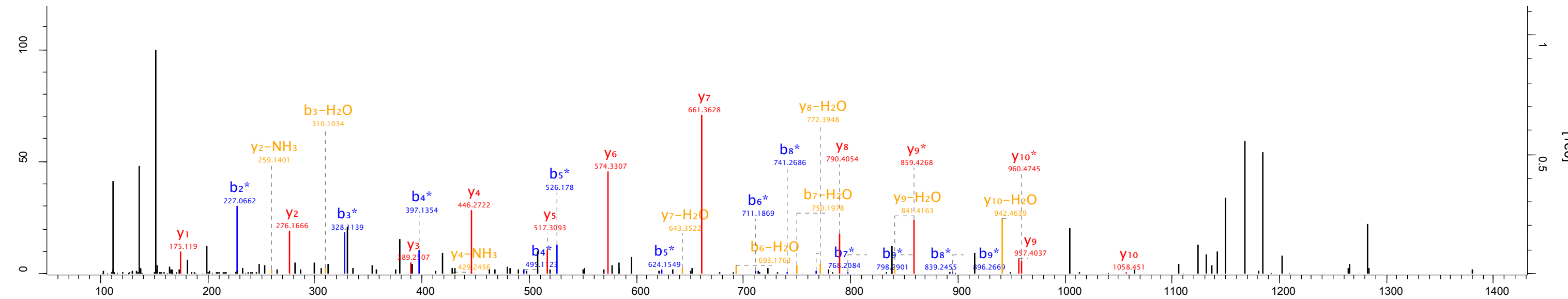
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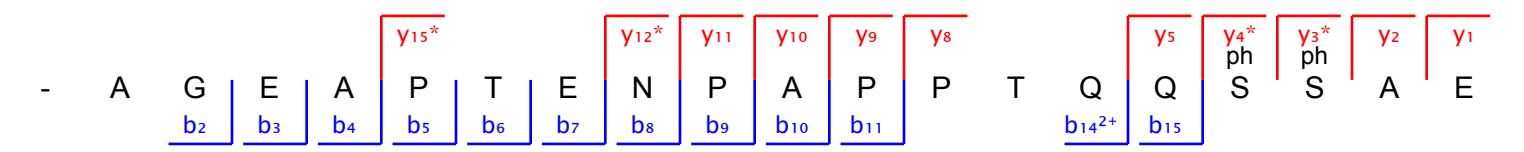
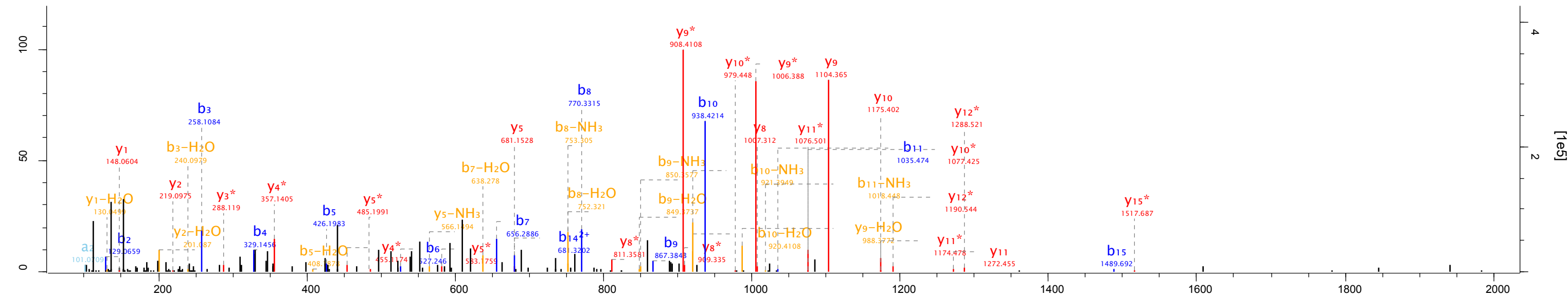
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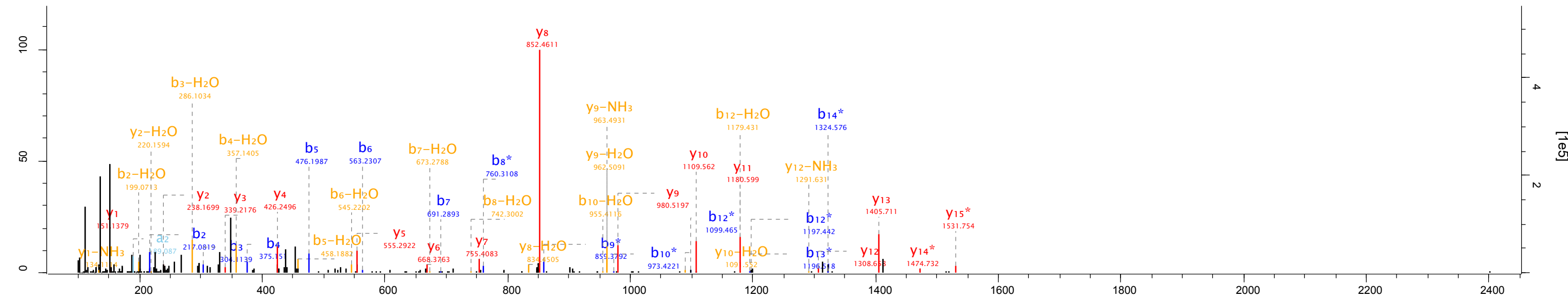
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 Scan: 5122 Method: FTMS; HCD Score: 98.57 m/z: 691.75 Gene names: MAGED2



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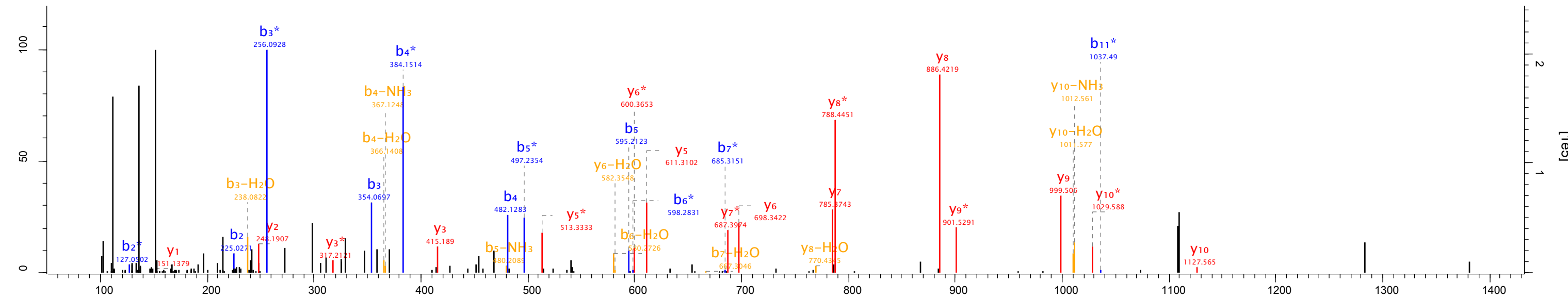


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- D T S A T S Q S V N G S P Q A E Q P S L E S T S K -

b₂
b₃
b₄
b₅
b₆
b₇
b₈^{*}
b₉^{*}
b₁₀^{*}
y₁₅^{*}
y₁₄^{*}
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁



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y₇

S

y₆

S

y₅

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y₃

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y₂

P

y₁

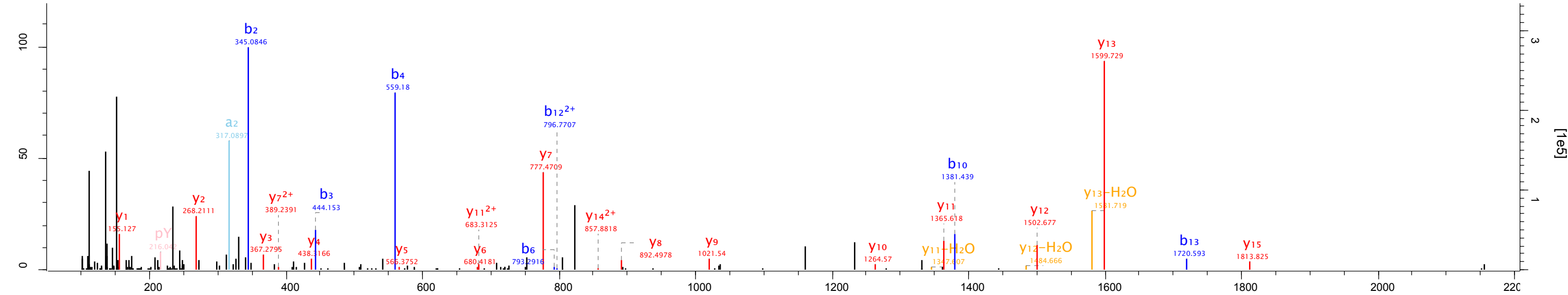
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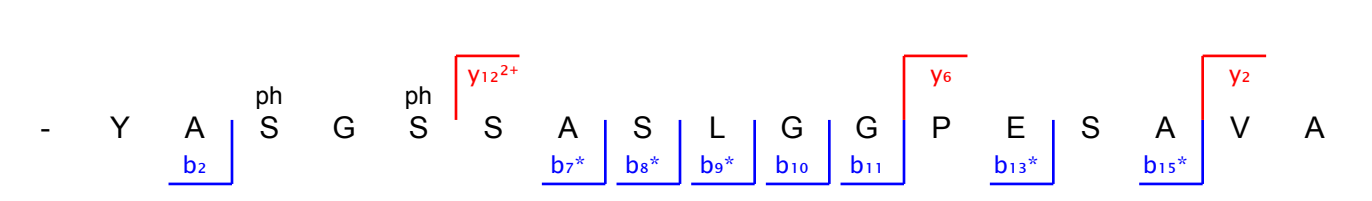
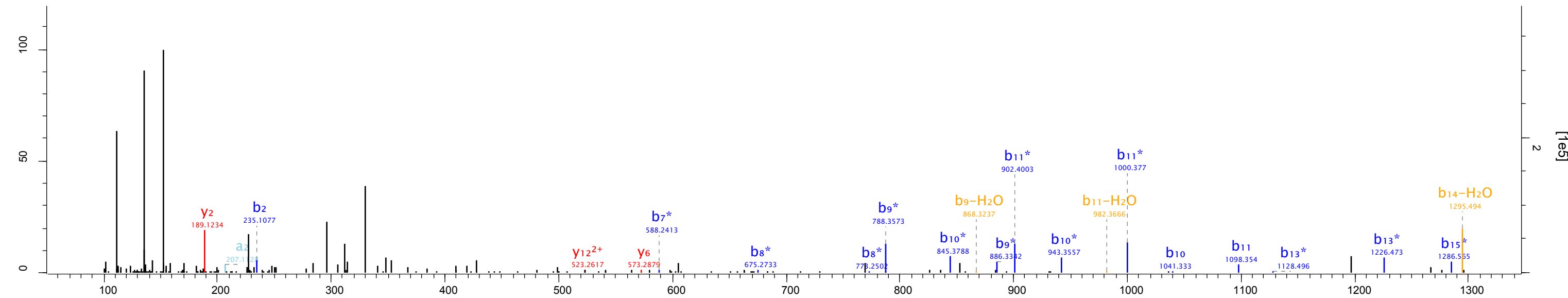
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[1e5]

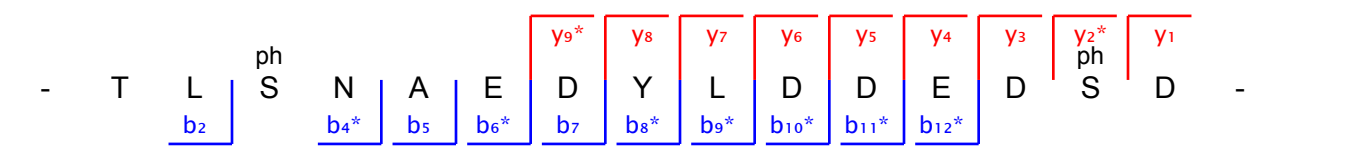
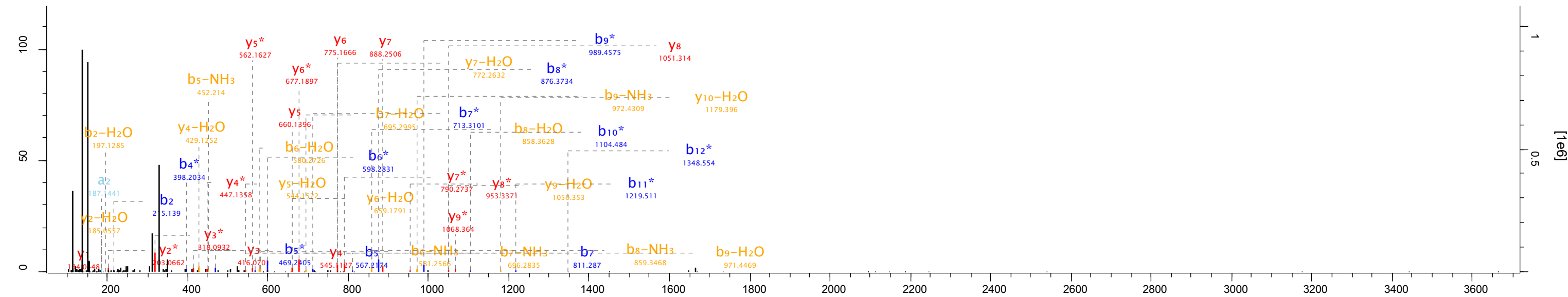
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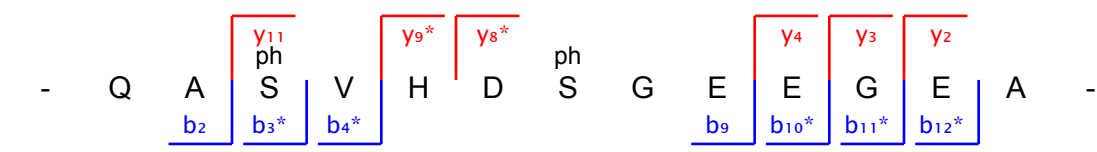
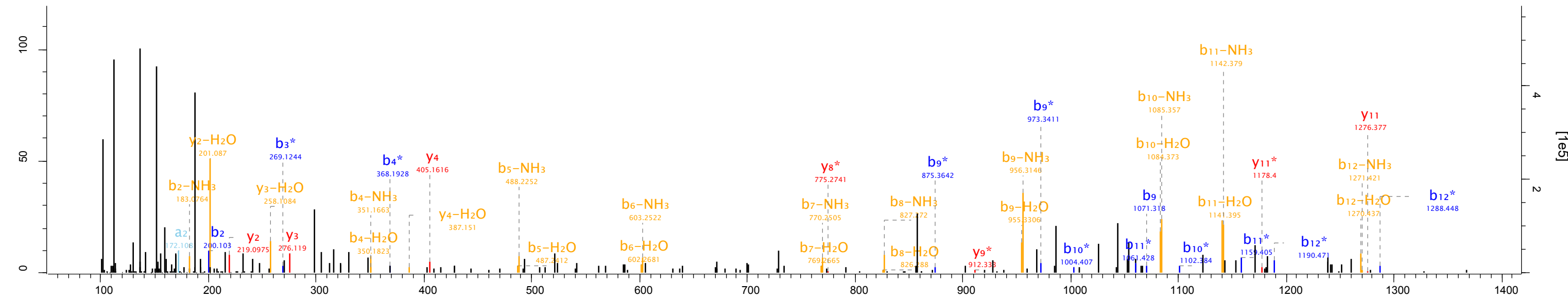
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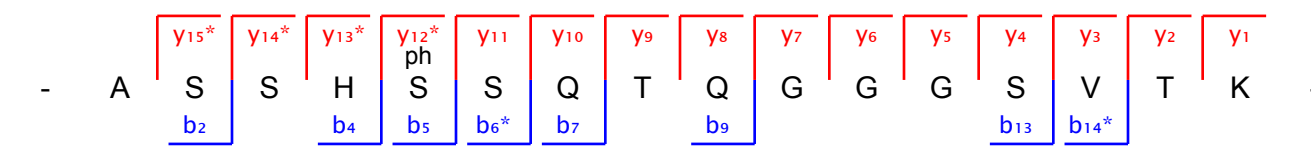
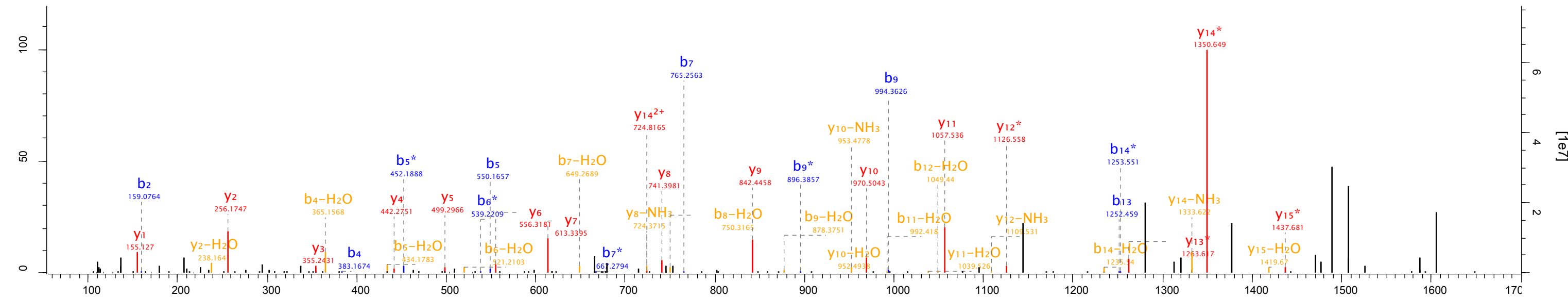
20171215_MaS_33SR_LMH_phospho2_05 16172 FTMS; HCD 165.49 931.3 OSTF1



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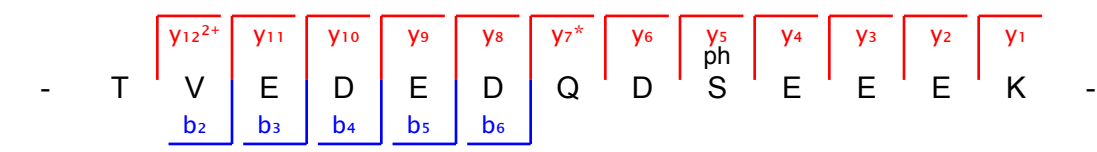
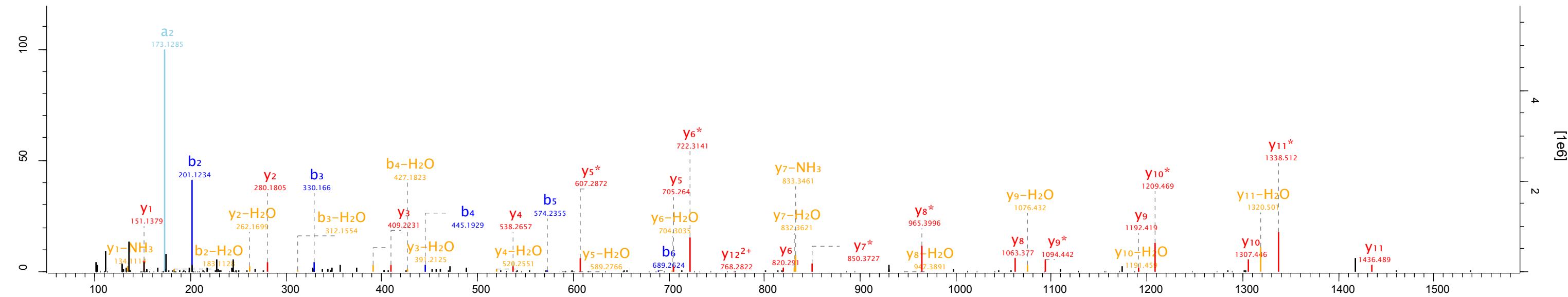


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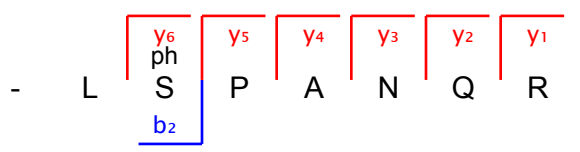
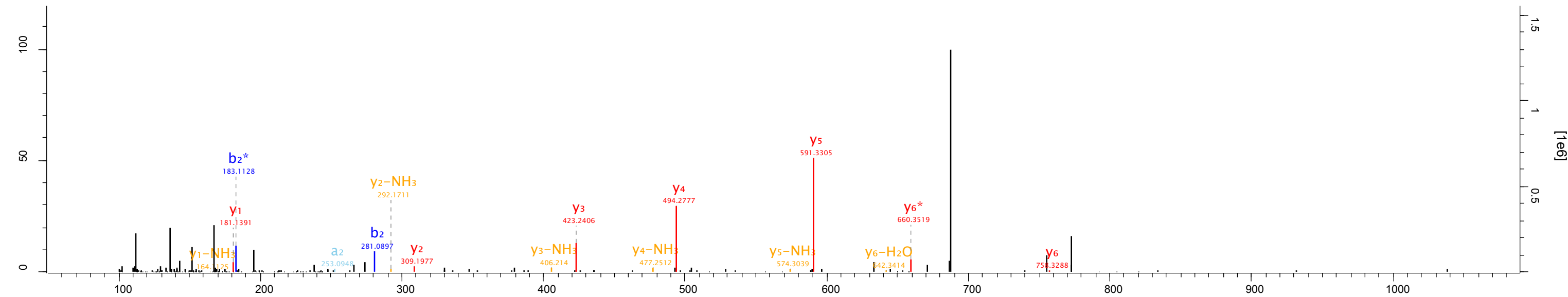


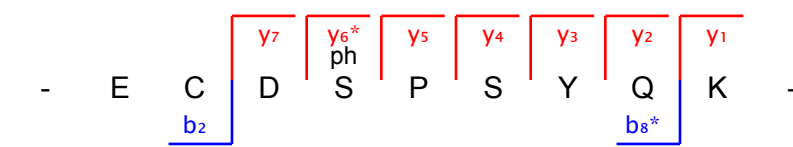
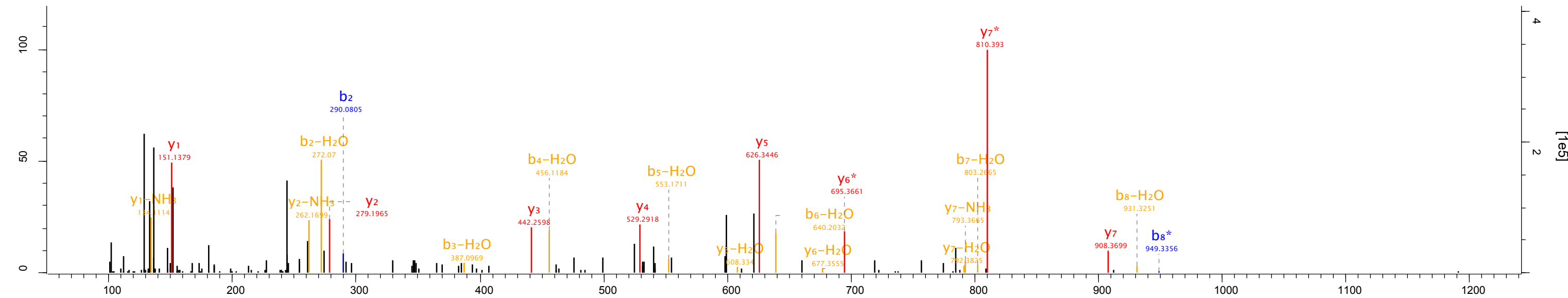
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20171215_MaS_33SR_LMH_phospho2_06

Scan 2372 Method FTMS; HCD Score 205.52 m/z 819.31 Gene names USP16



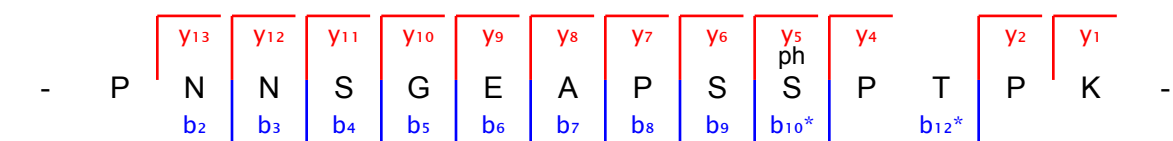
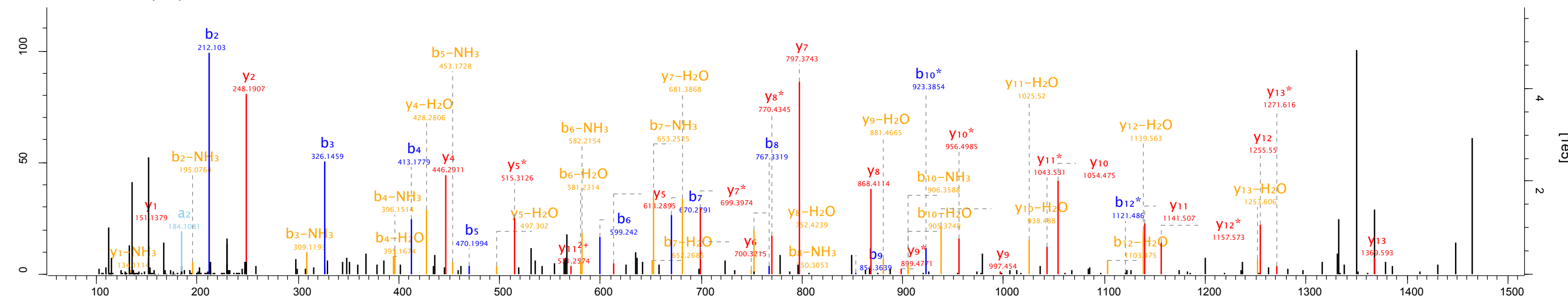
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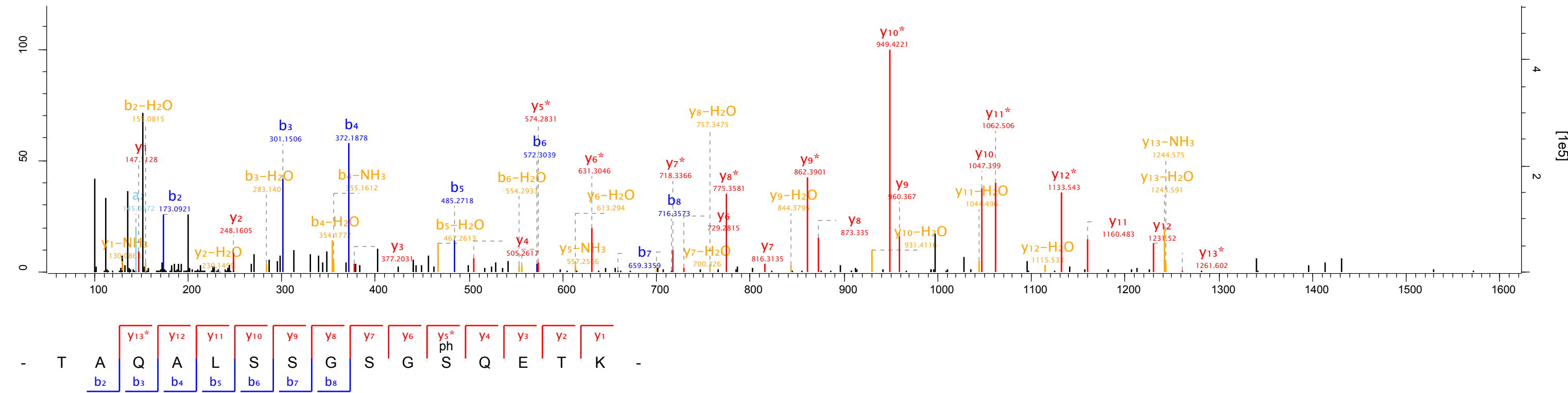




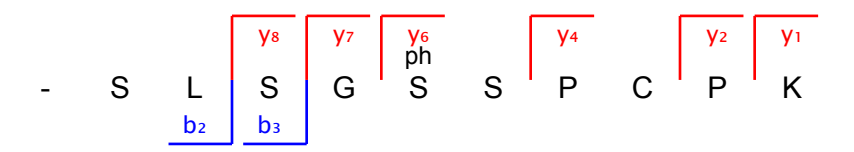
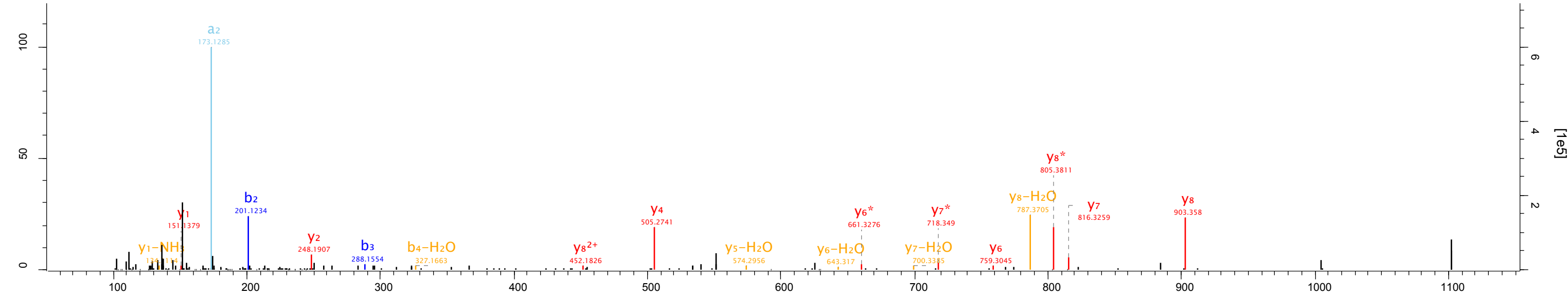
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20171215_MaS_33SR_LMH_phospho2_06

Scan 2512 Method FTMS; HCD Score 279.15 m/z 733.82 Gene names LIG3

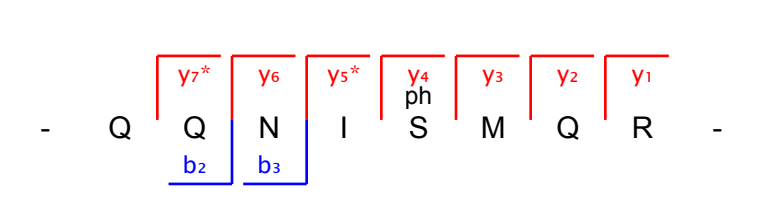
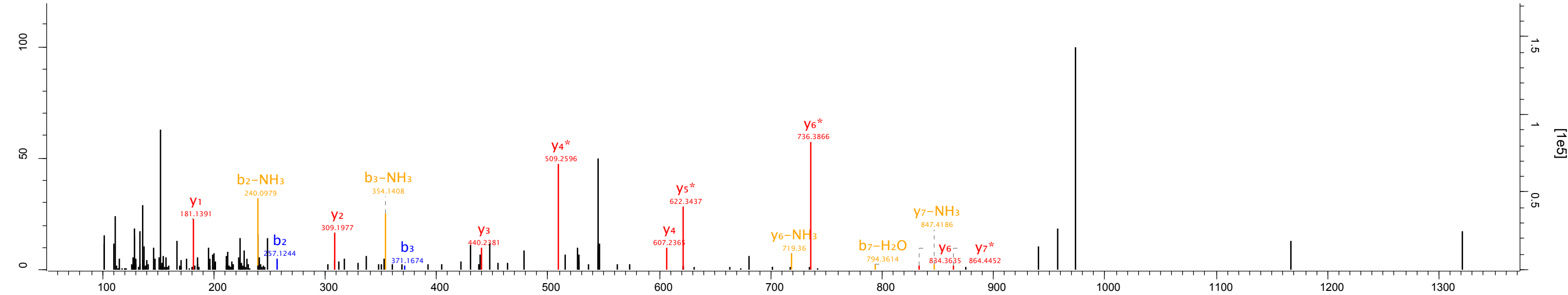




20171215_MaS_33SR_LMH_phospho2_06 2972 FTMS; HCD 89.3 552.24 SRRM2

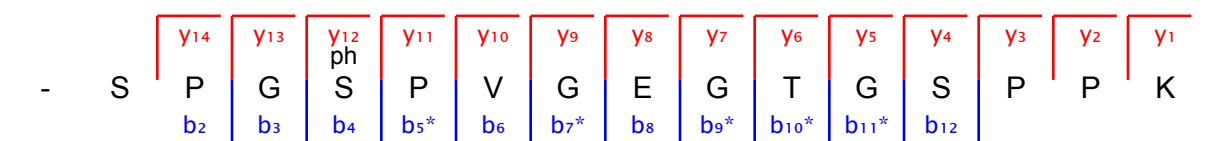
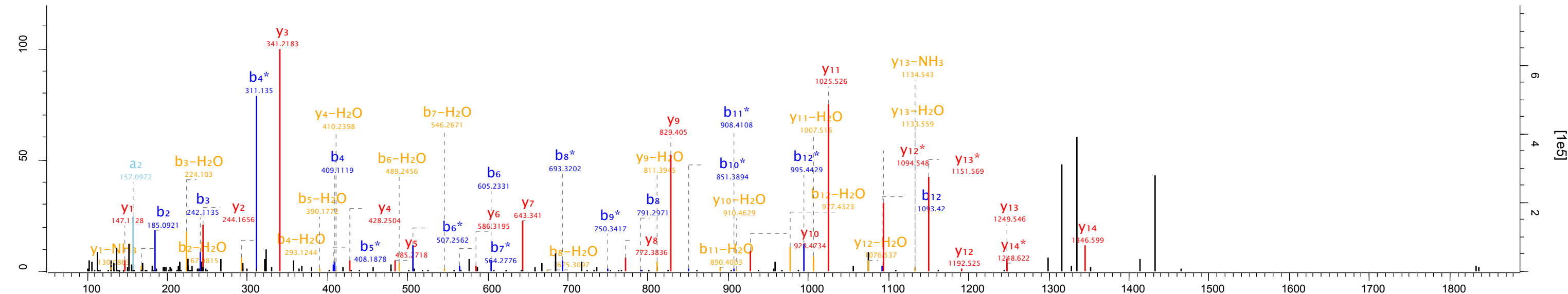


20171215_MaS_33SR_LMH_phospho2_06

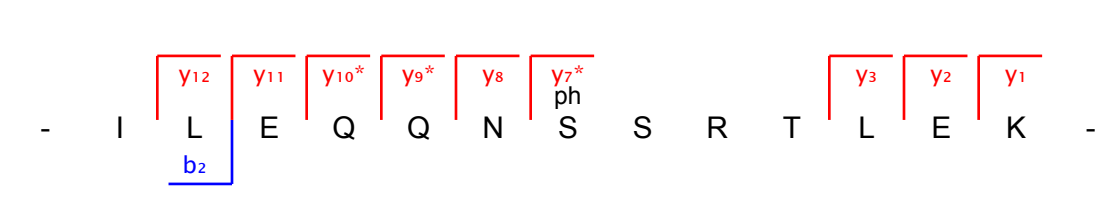
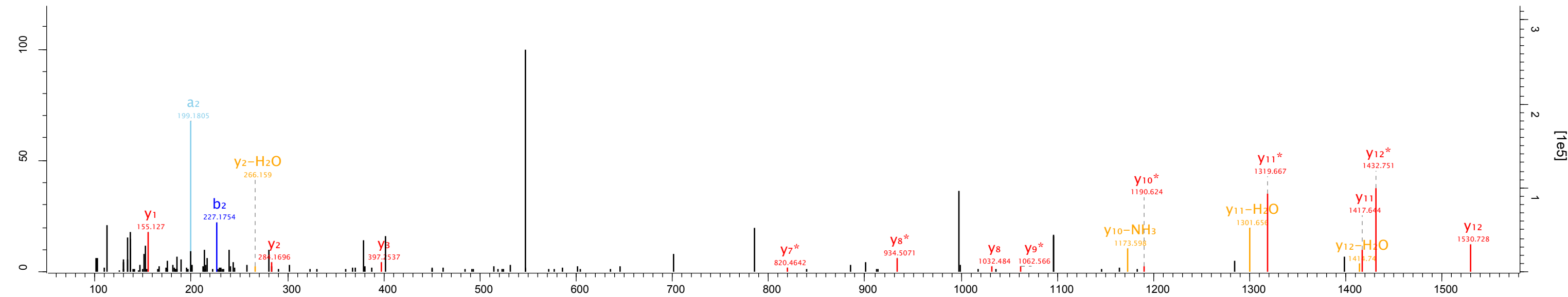


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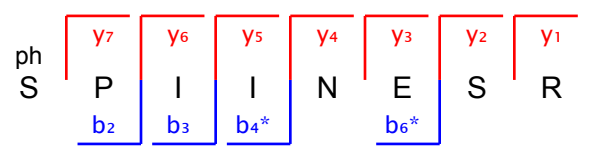
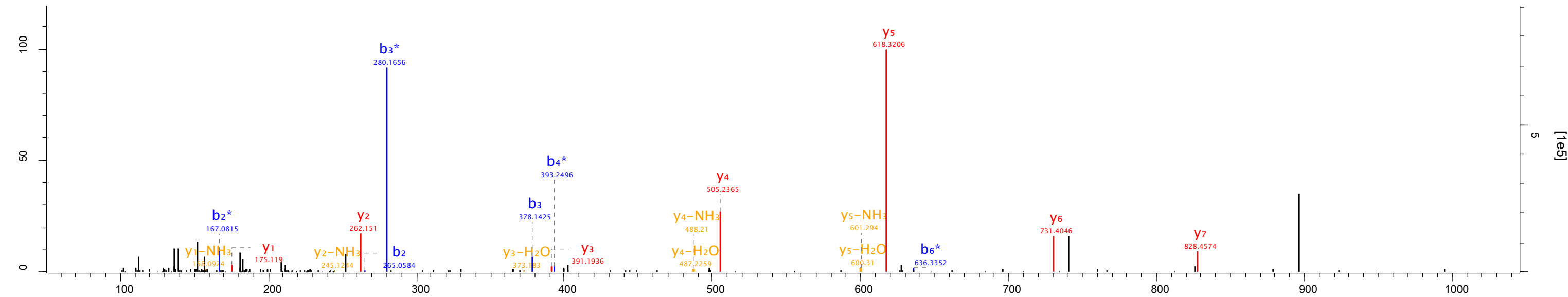
Scan 3972 Method FTMS; HCD Score 235.72 m/z 717.32 Gene names ADD1



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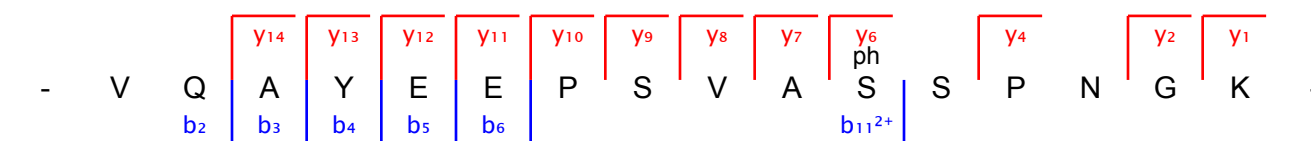
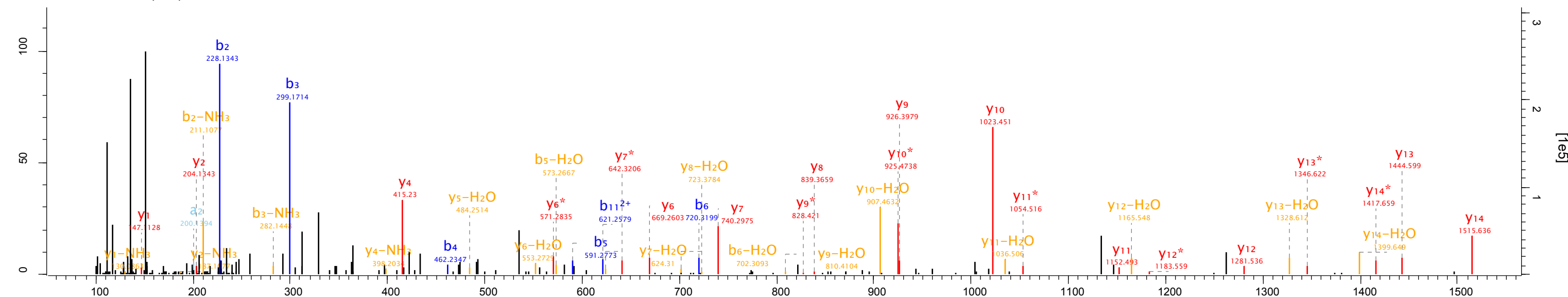


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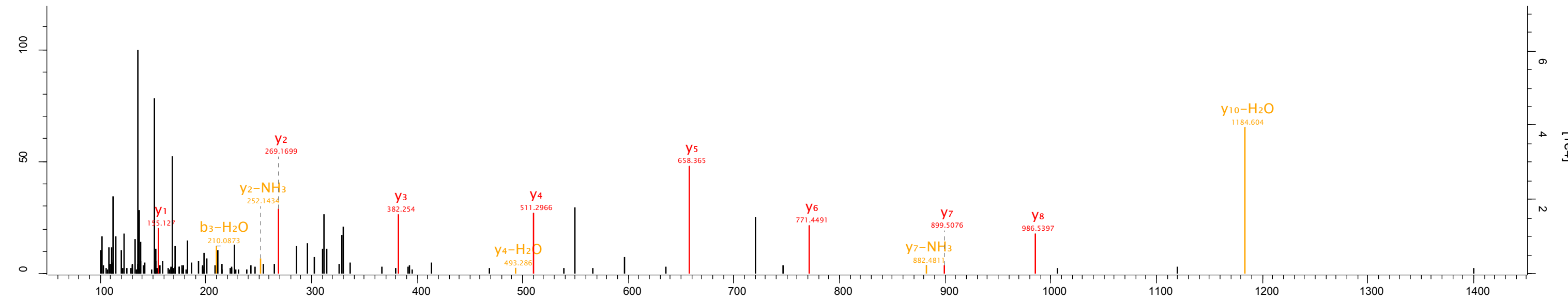


Raw file
20171215_MaS_33SR_LMH_phospho2_06

Scan 6382 Method FTMS; HCD Score 184.78 m/z 871.88 Gene names POP1



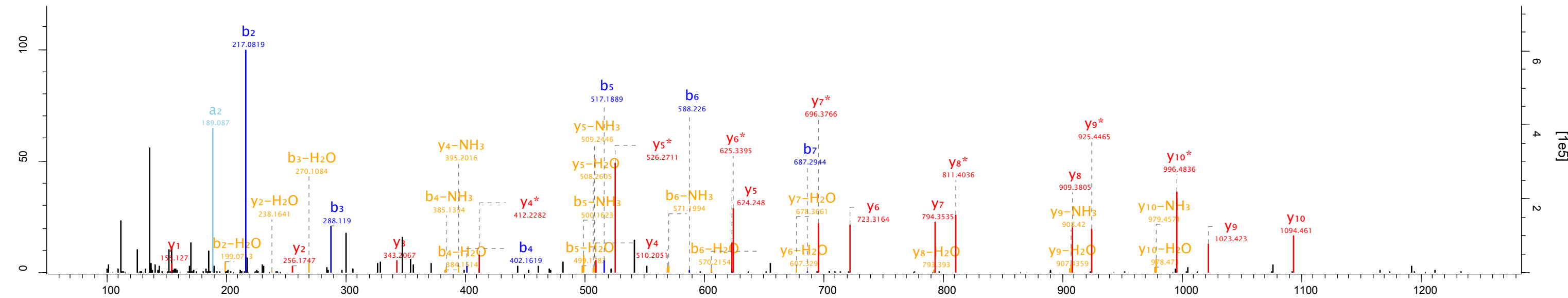
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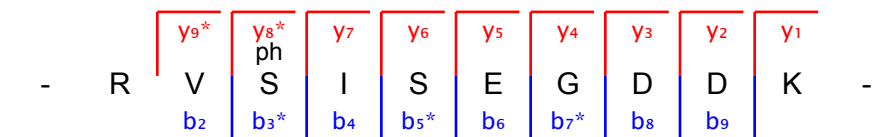
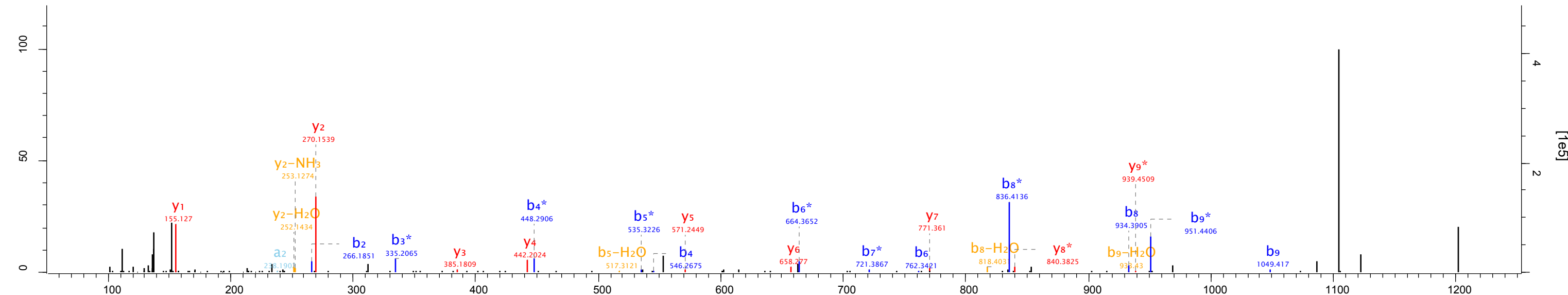
Red brackets above the sequence indicate the fragmentation sites for the labeled ions:

- y8: S
- y7: Q
- y6: I
- y5: F
- y4: E
- y3: L
- y2: N
- y1: K

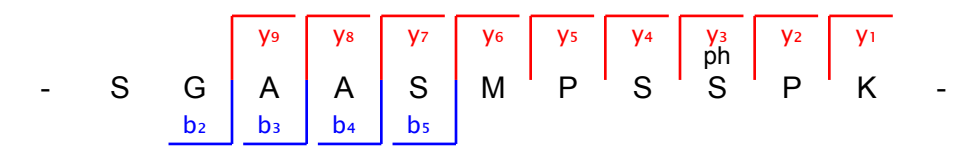
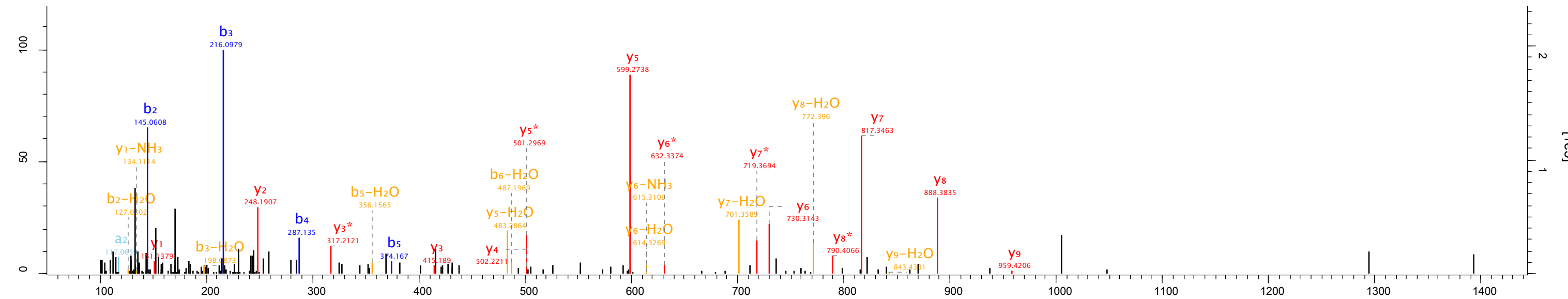


- S E A N D A V N S S T K -

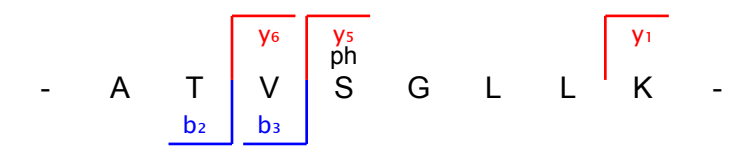
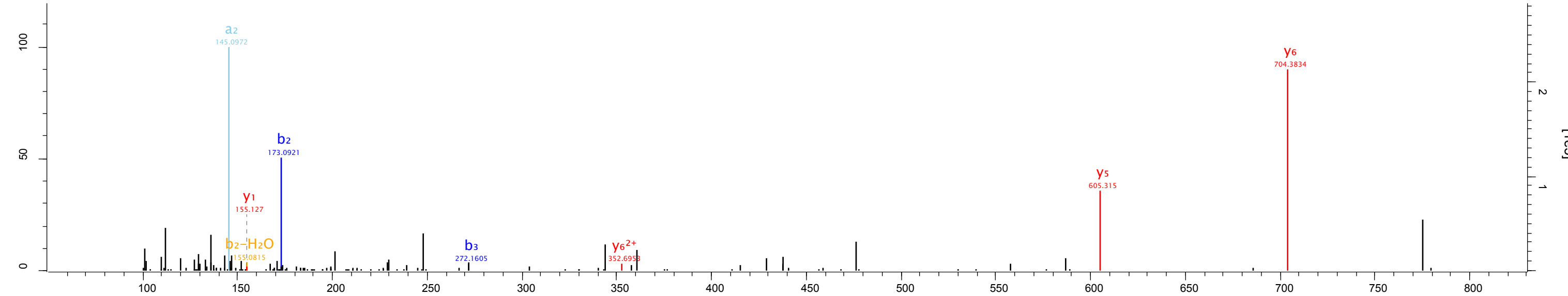
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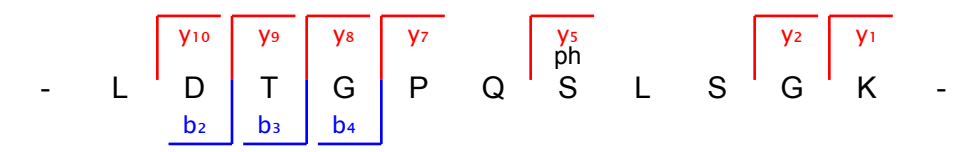
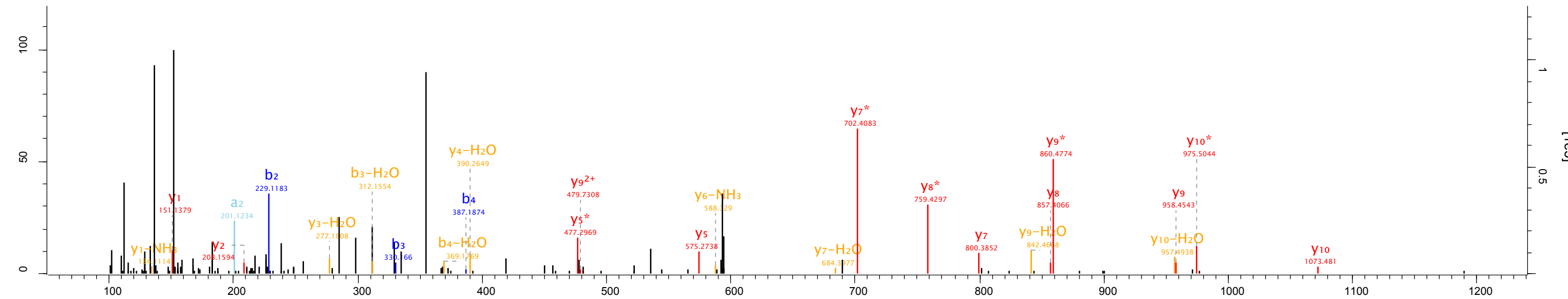
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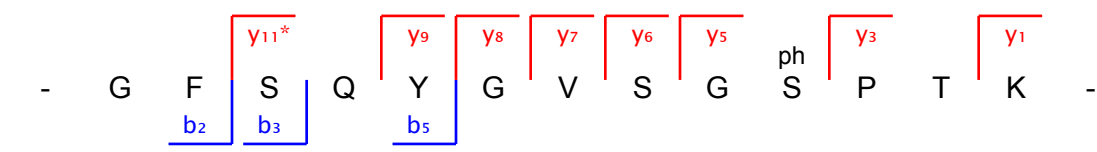
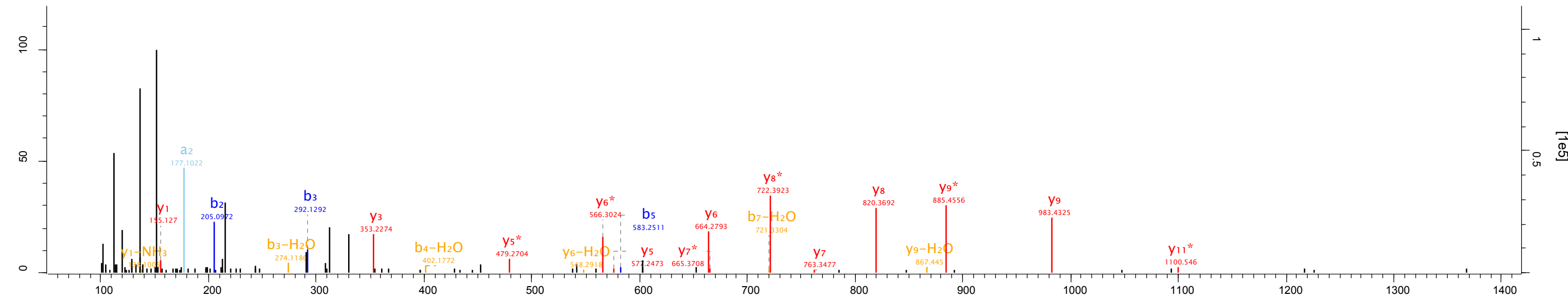
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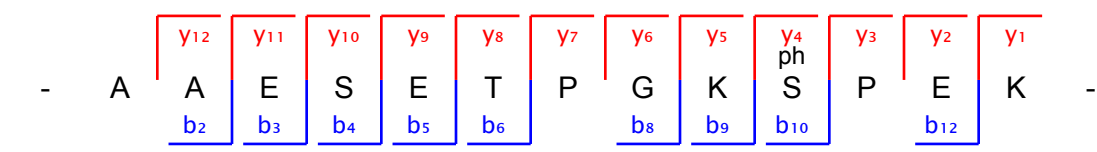
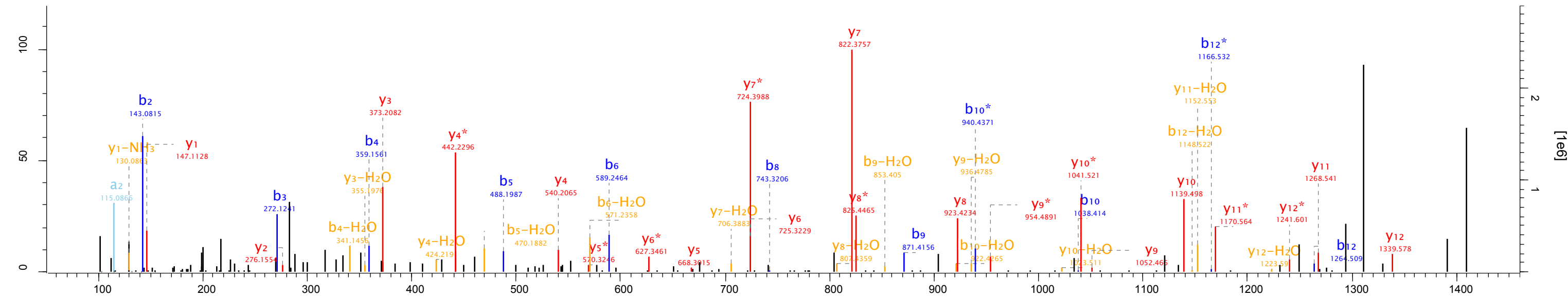
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Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 7522 Method FTMS; HCD Score 56.12 m/z 701.81 Gene names MIOS



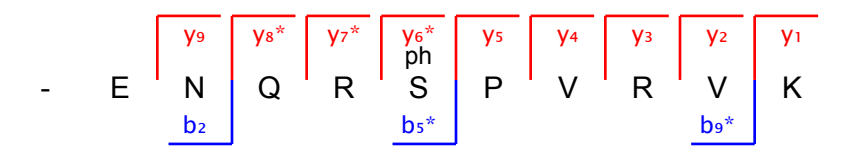
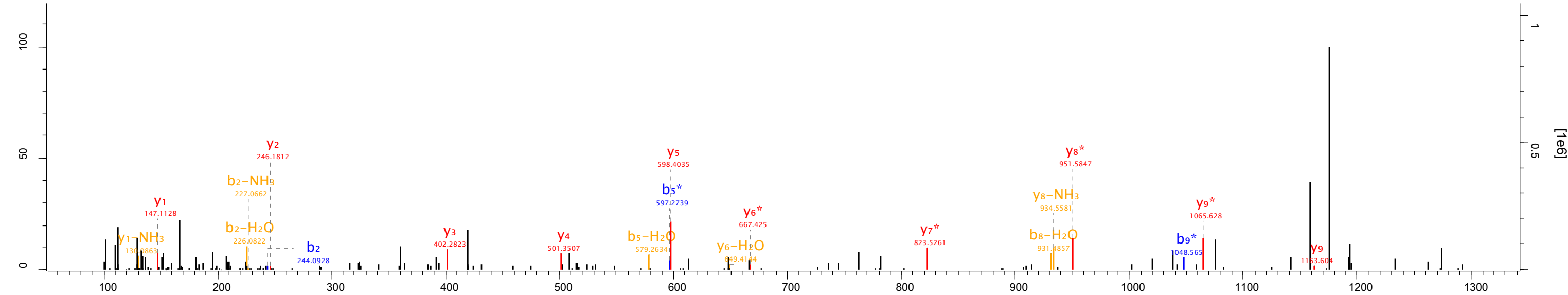
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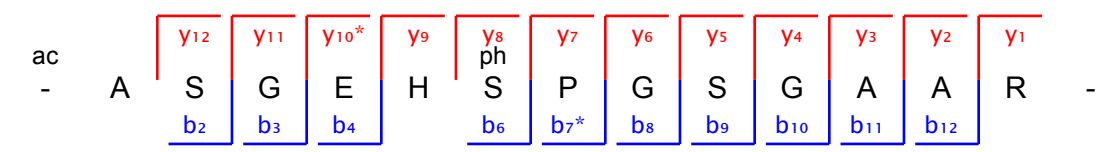
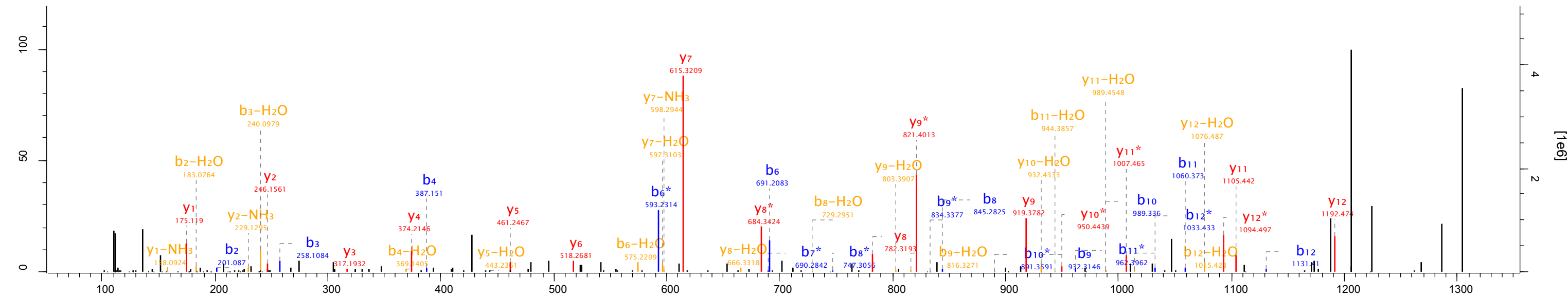
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20171215_MaS_33SR_LMH_phospho2_09

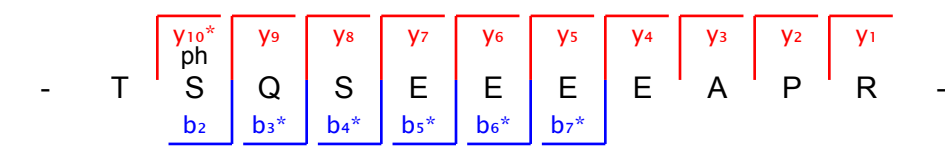
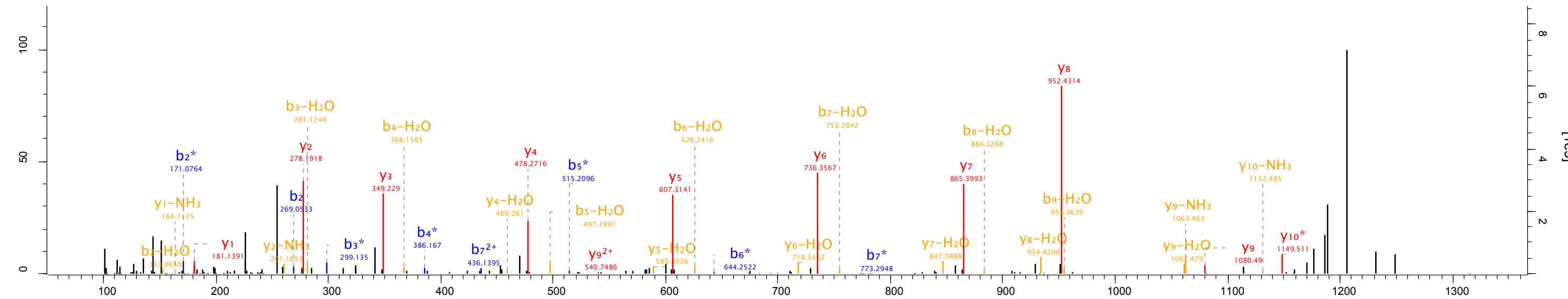
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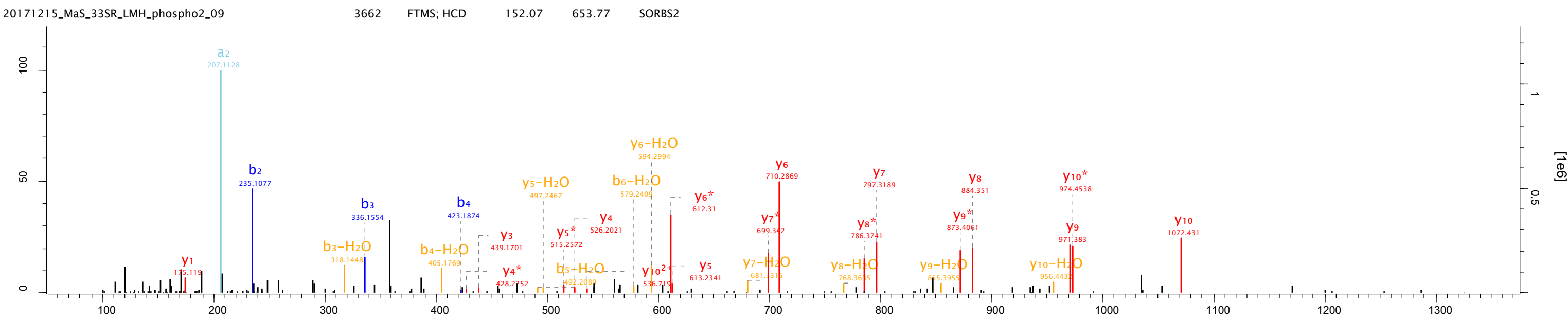


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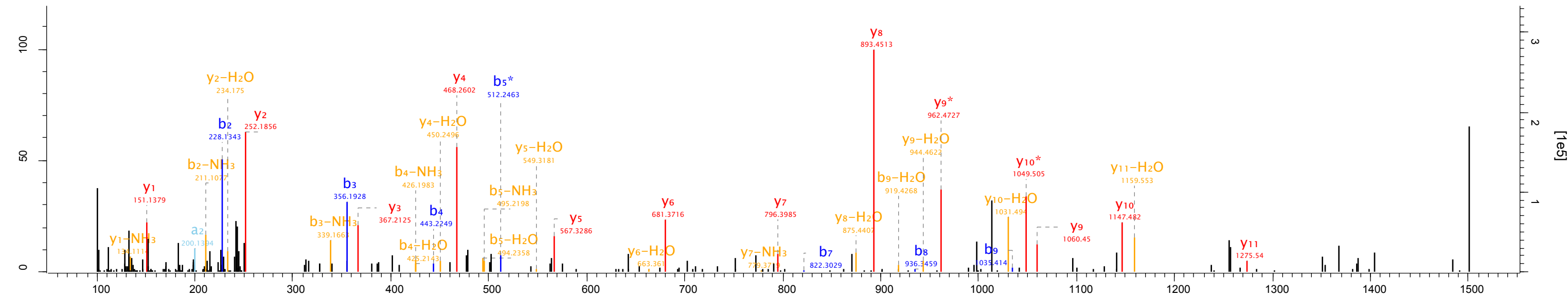


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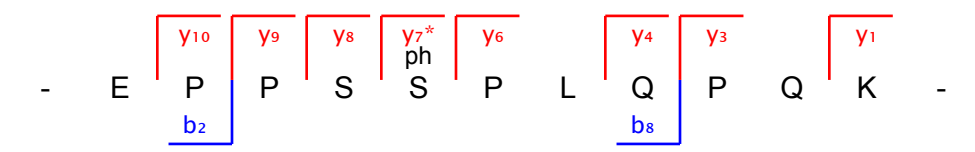
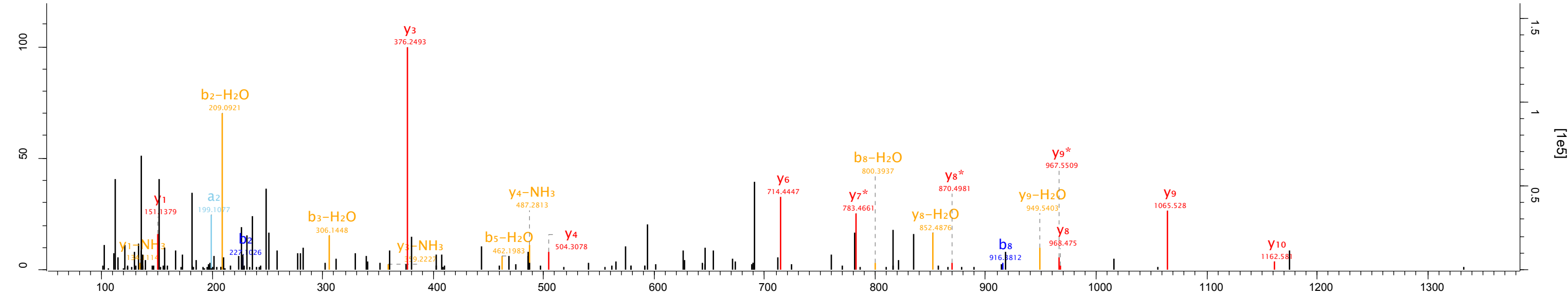




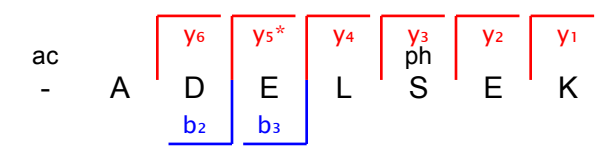
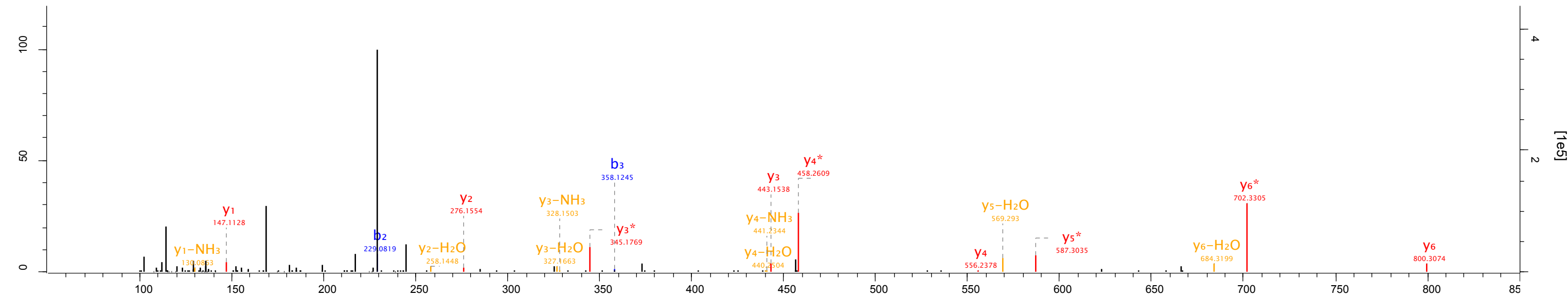
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 Scan: 3702 Method: FTMS; HCD Score: 156.58 m/z: 752.34 Gene names: CAMSAP2



20171215_MaS_33SR_LMH_phospho2_09 4622 FTMS; HCD 57.03 646.31 LARP4B



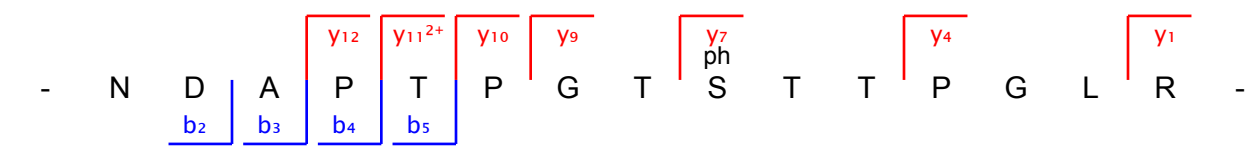
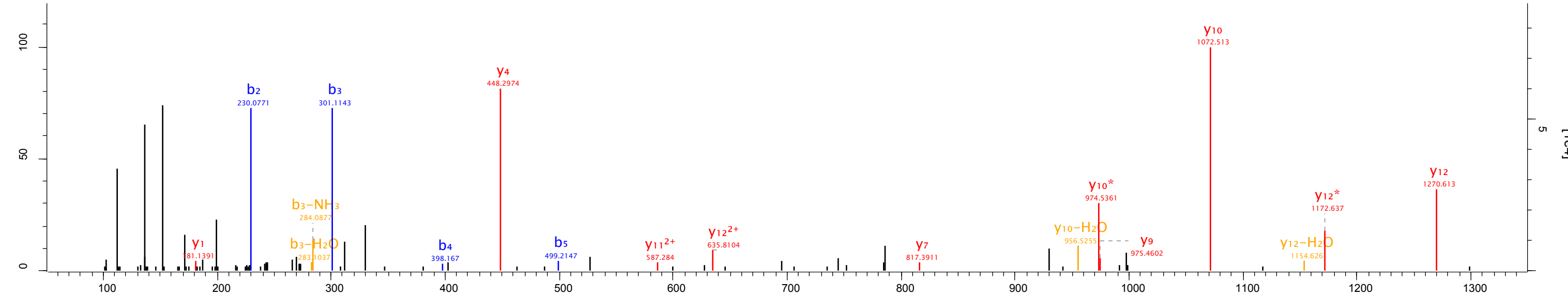
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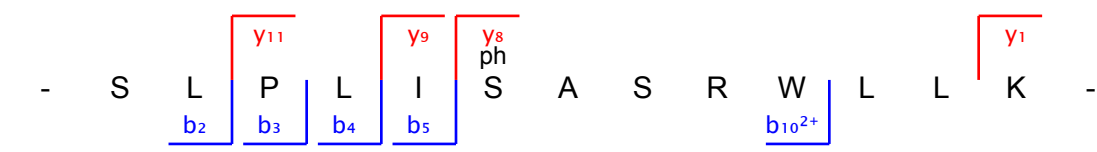
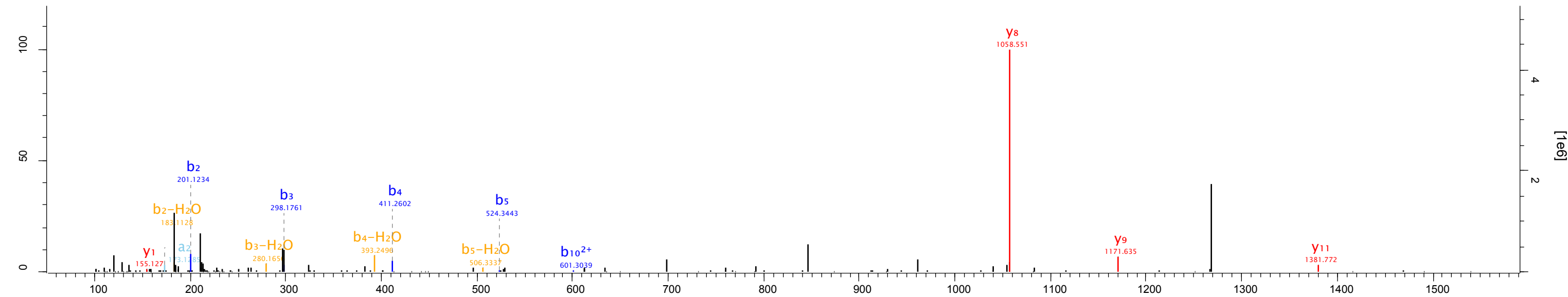
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20171215_MaS_33SR_LMH_phospho2_09

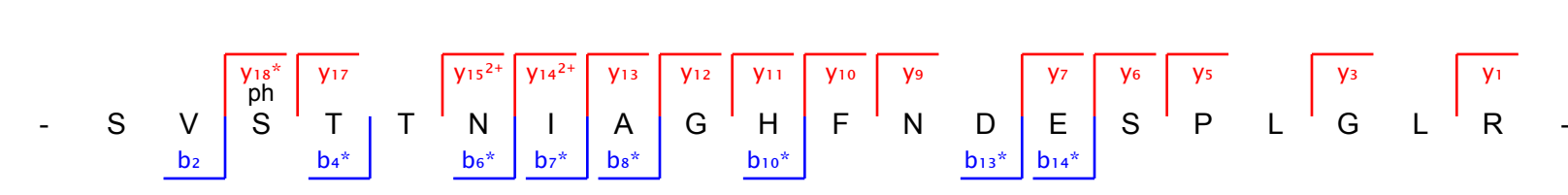
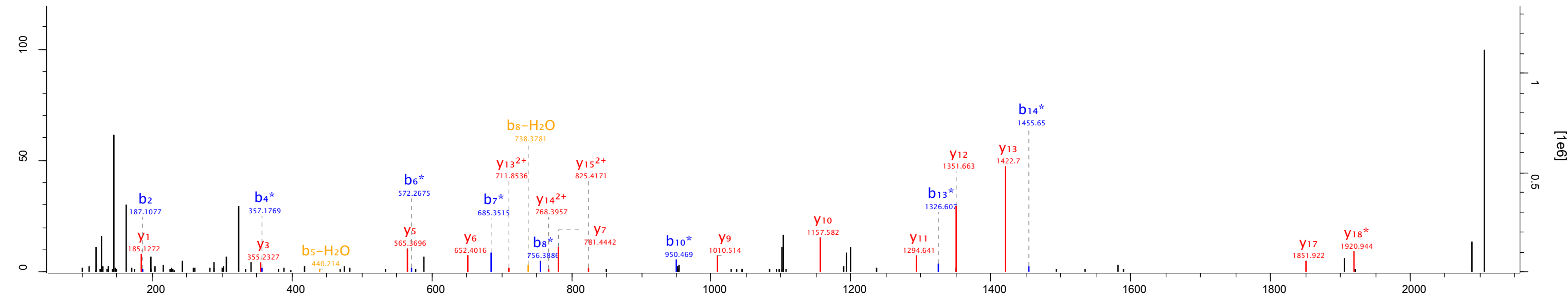
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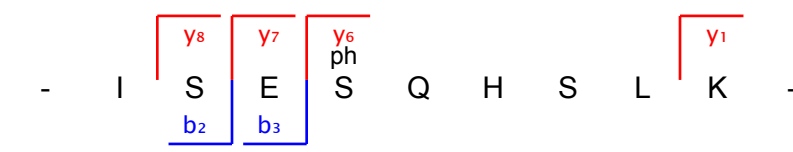
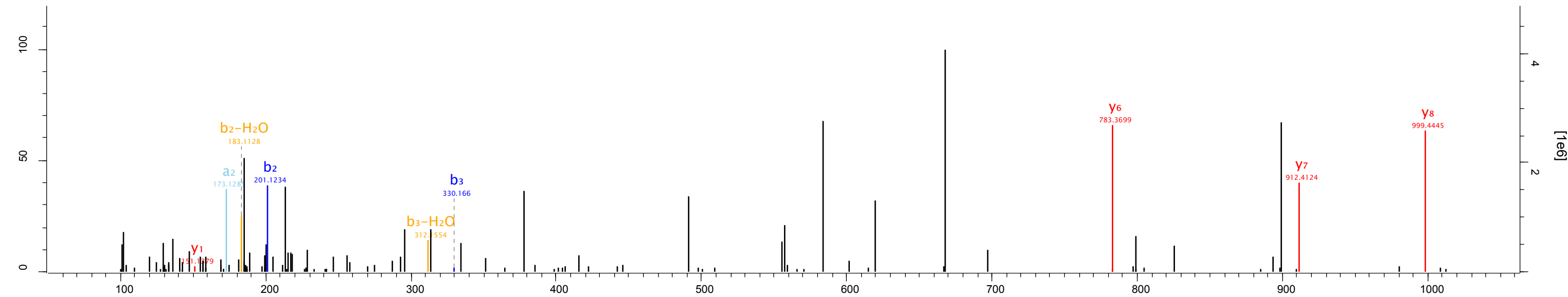
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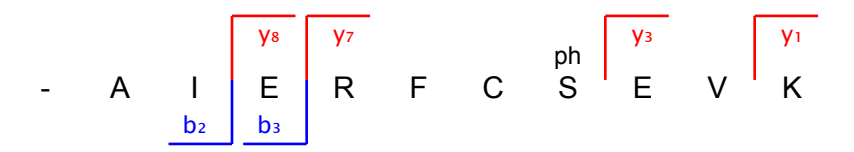
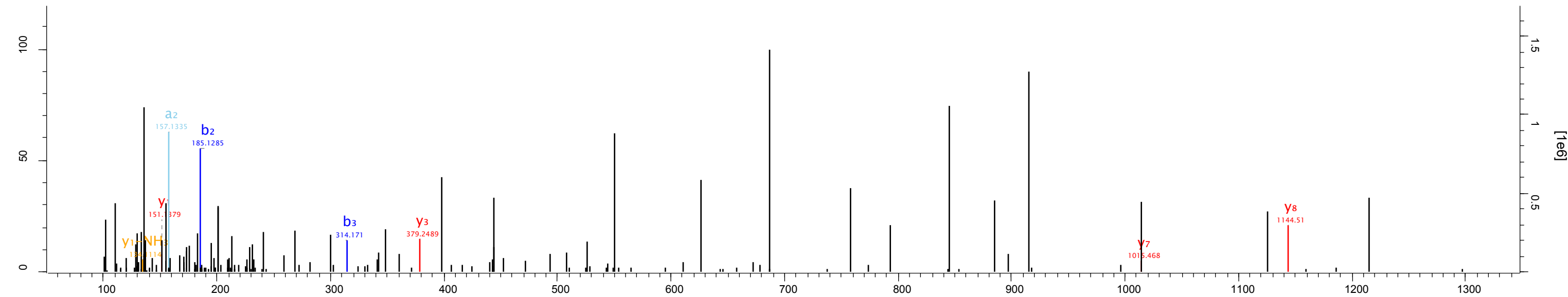
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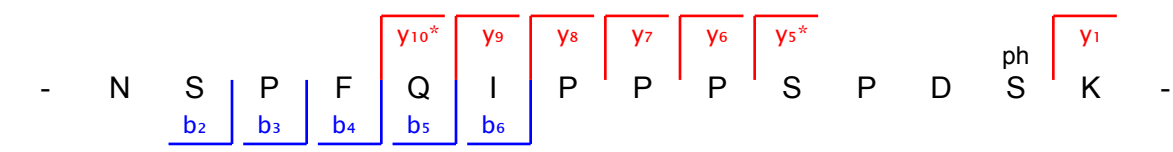
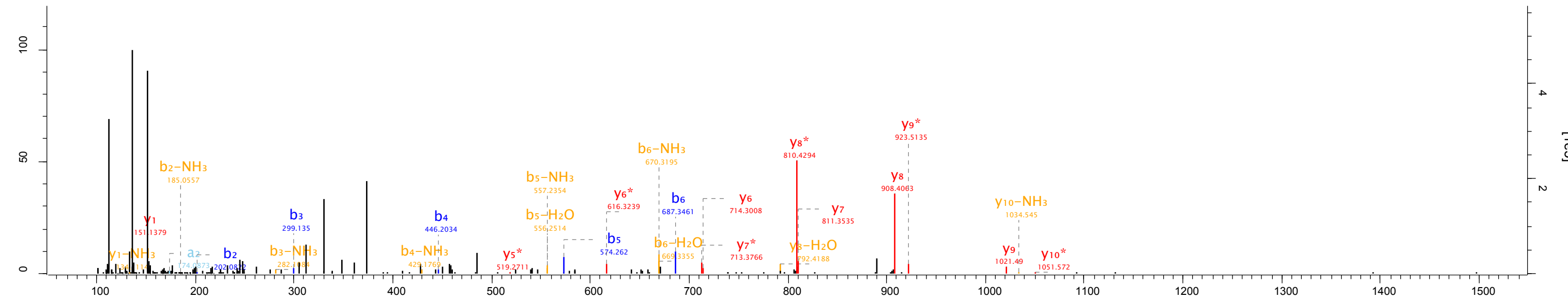
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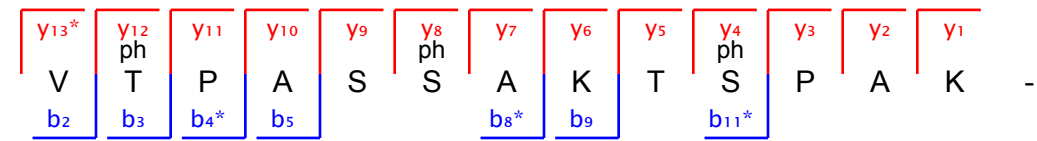
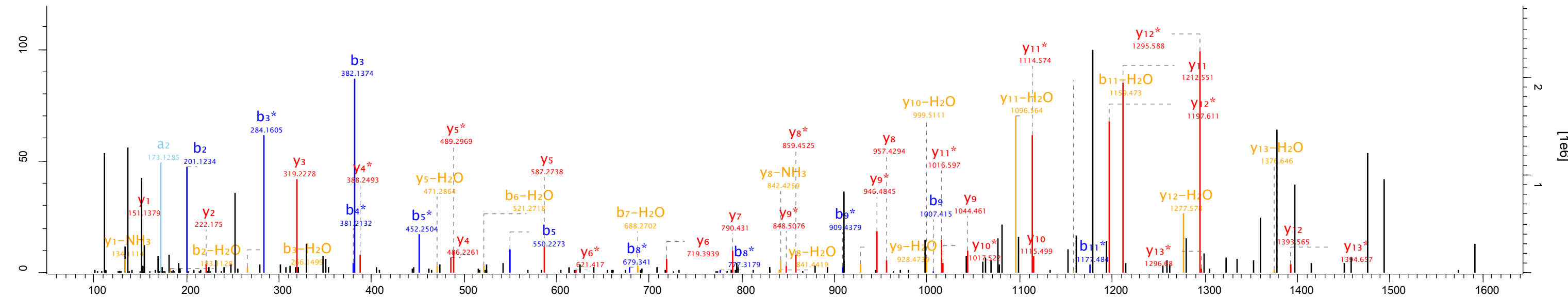
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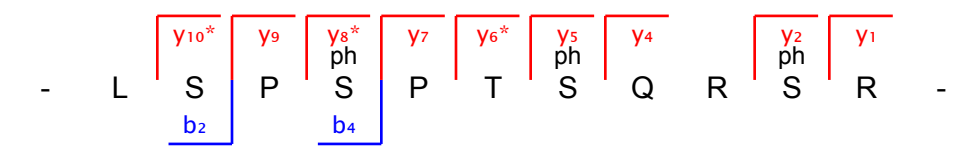
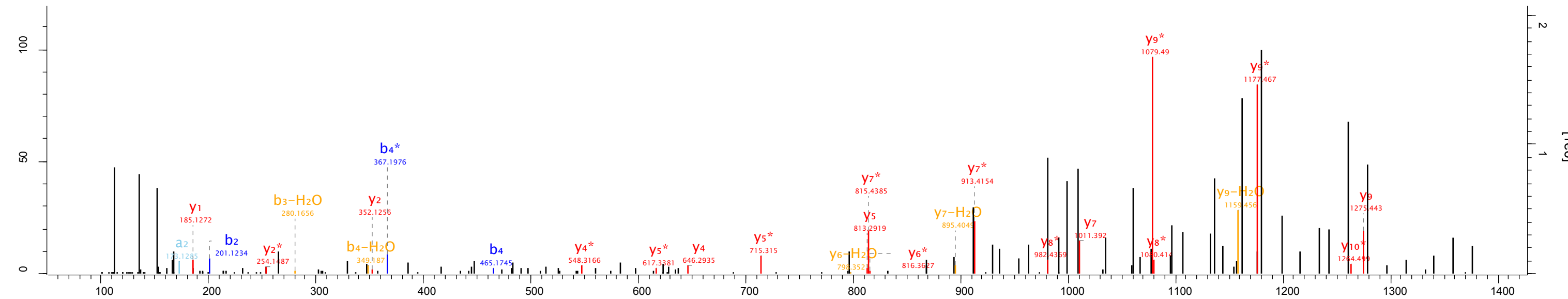
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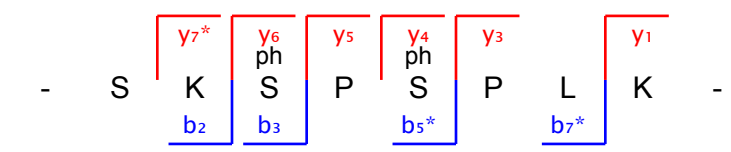
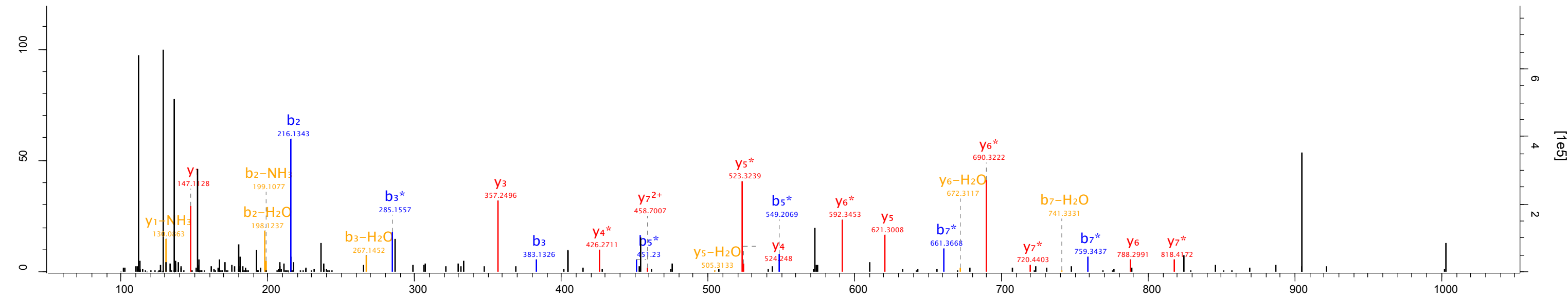
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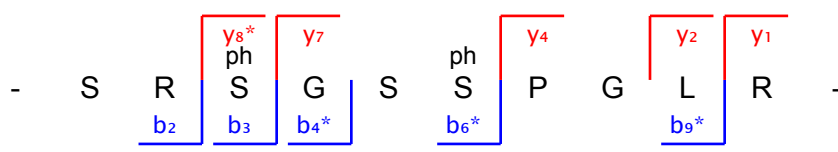
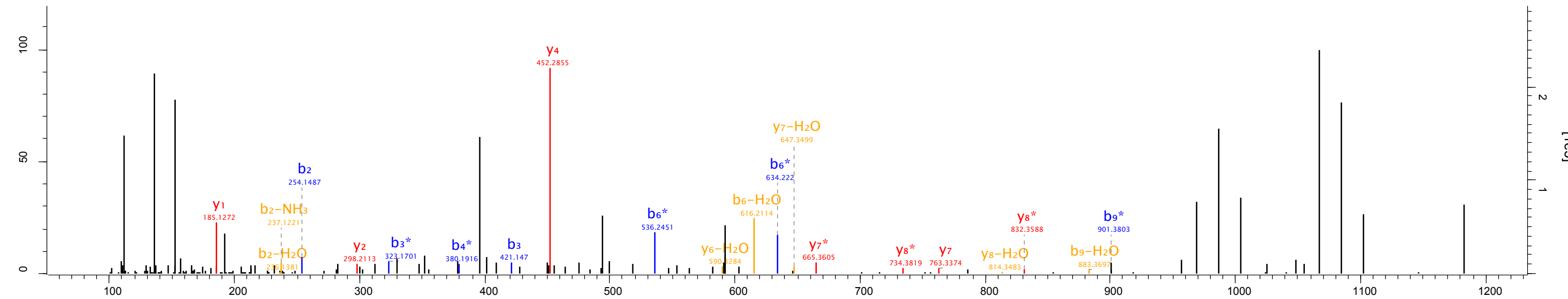
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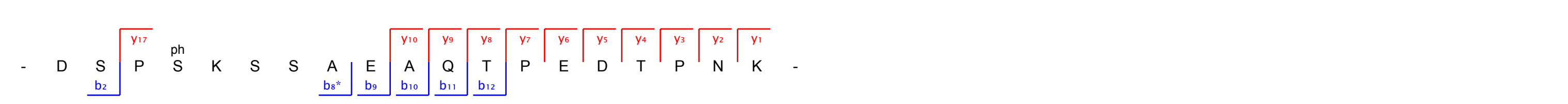
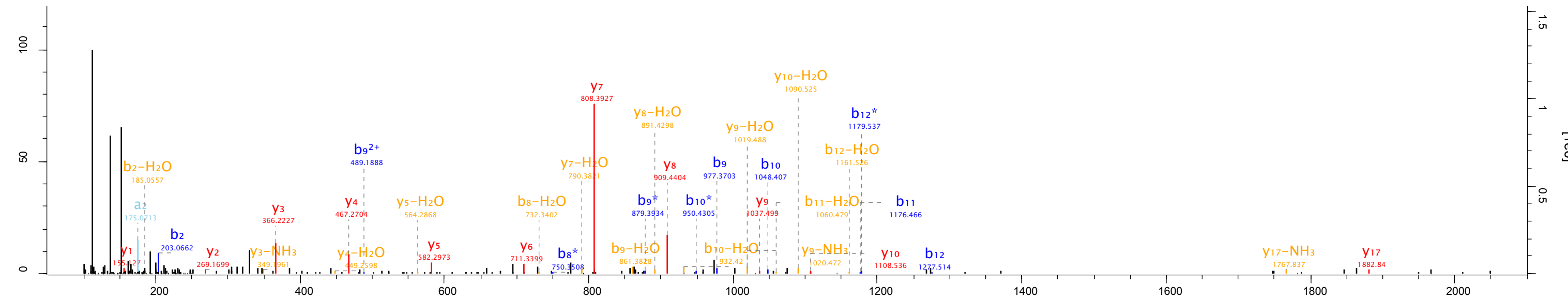
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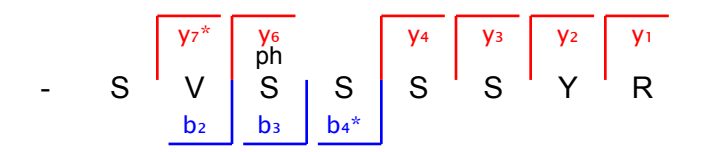
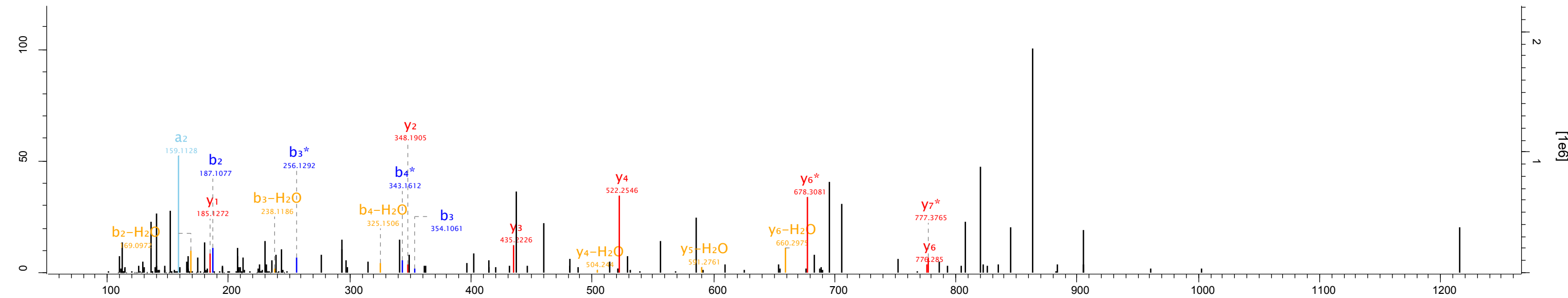
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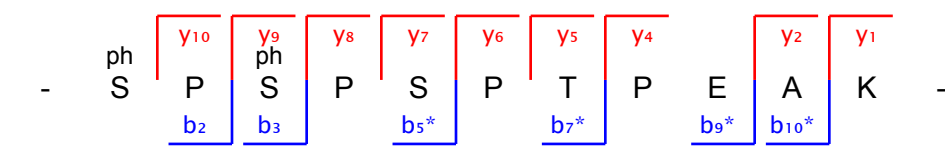
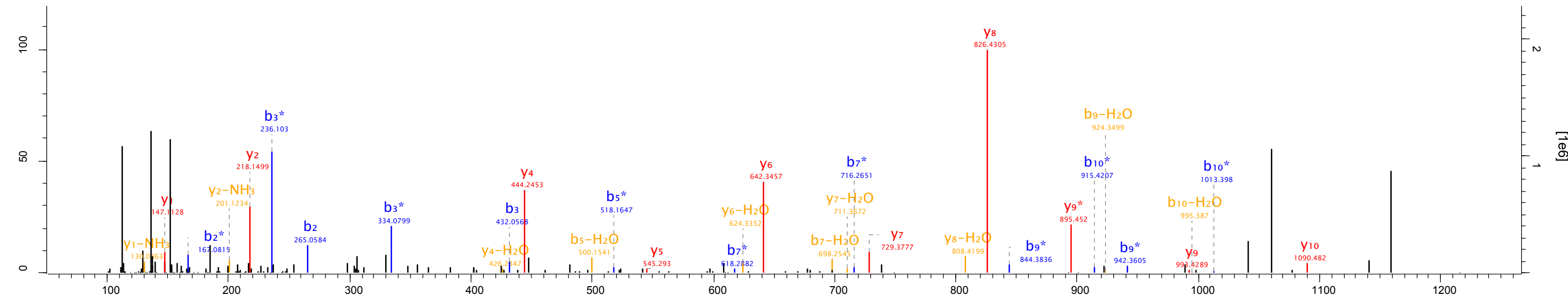
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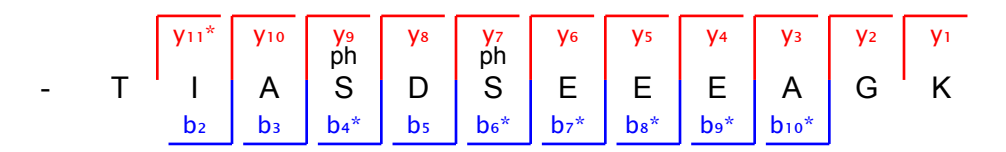
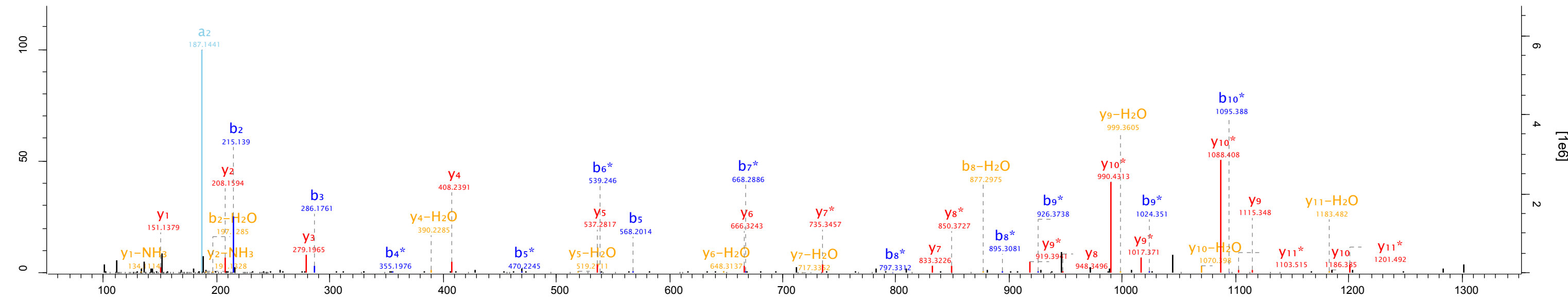
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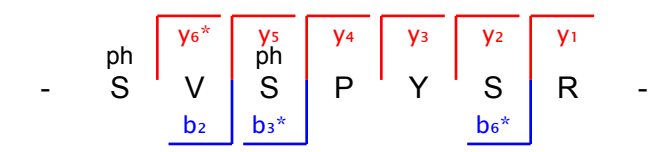
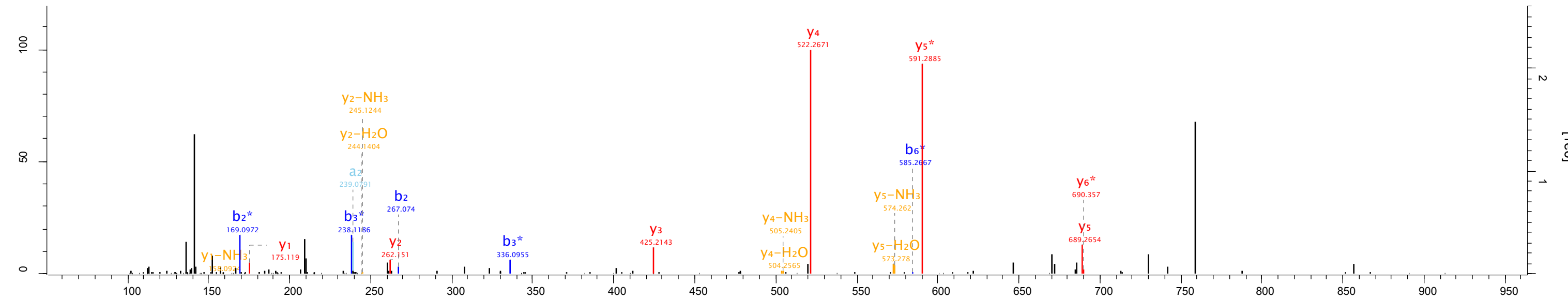


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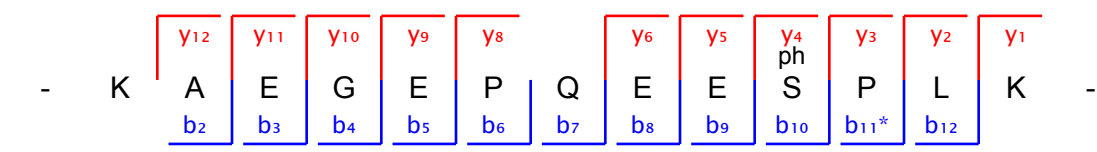
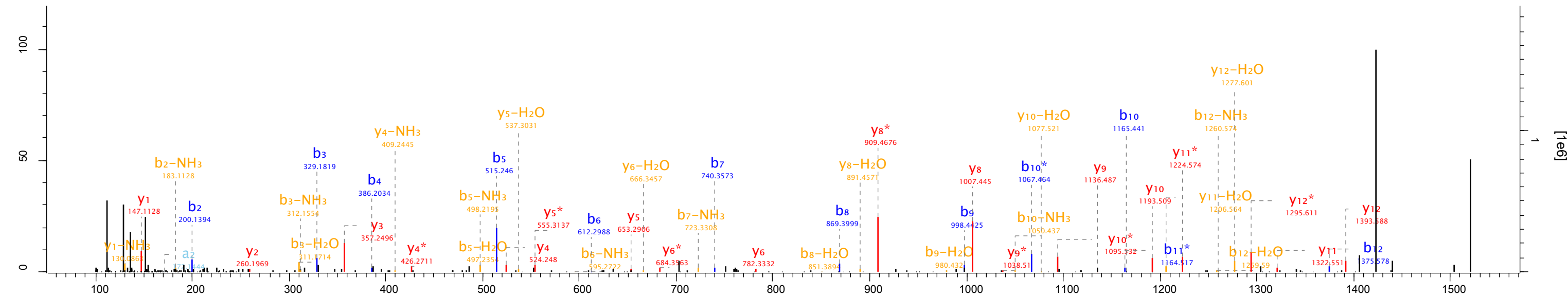


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20171215_MaS_33SR_LMH_phospho_01

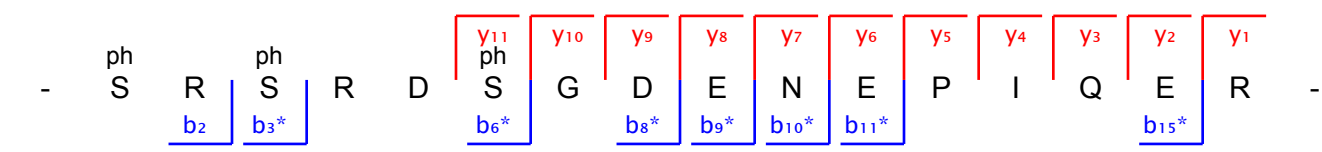
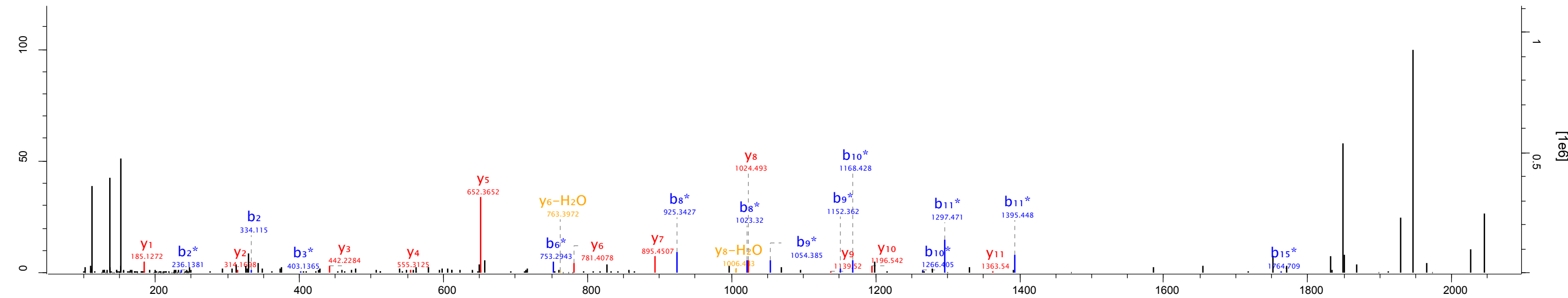
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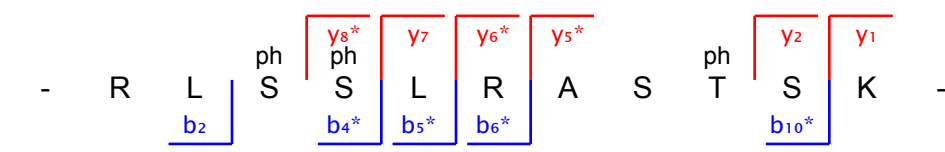
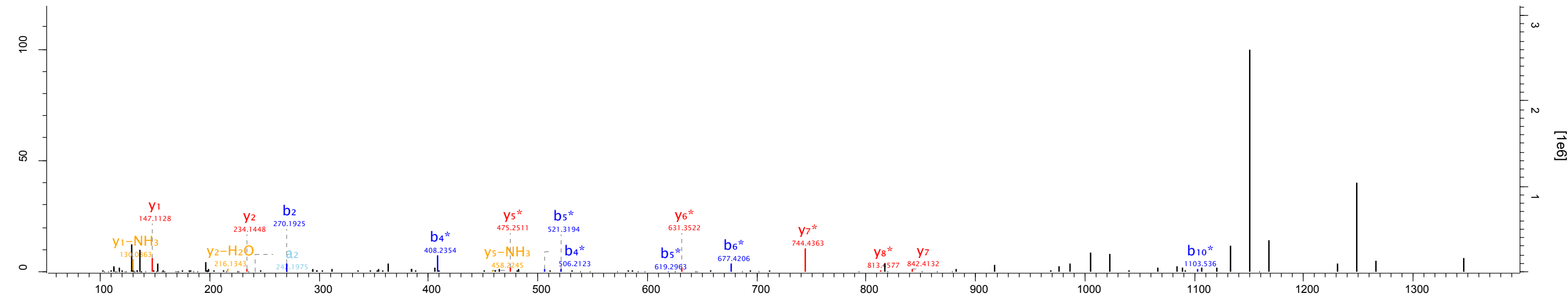
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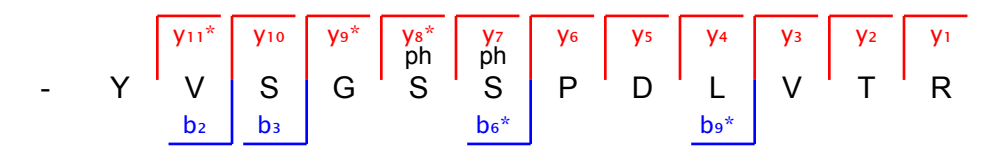
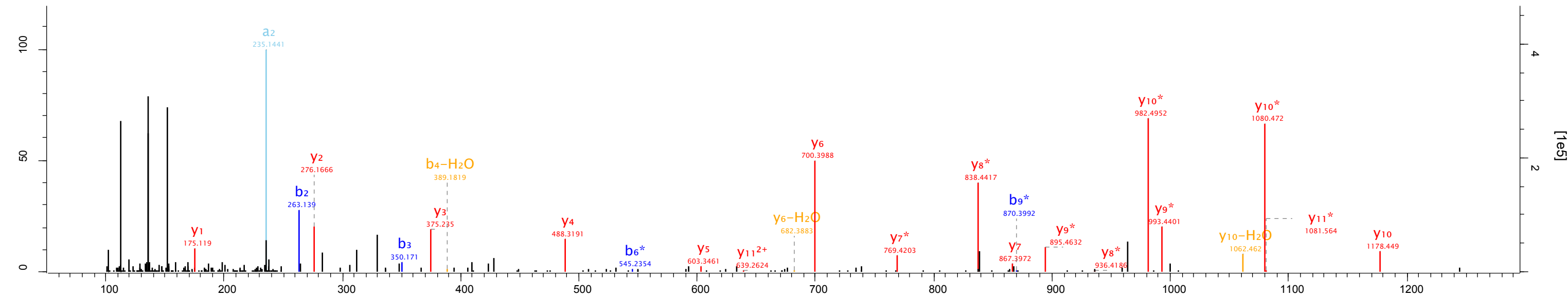
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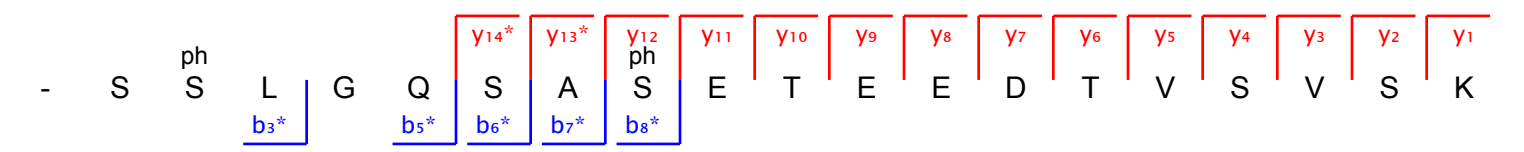
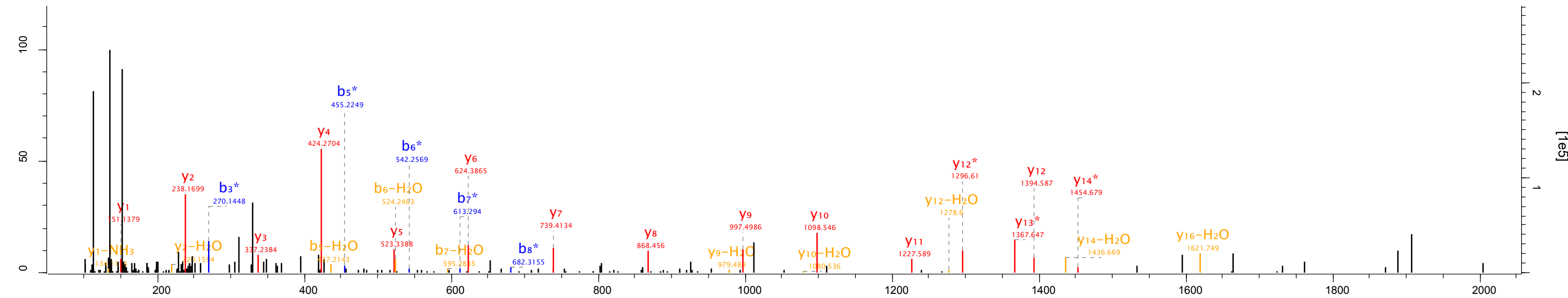
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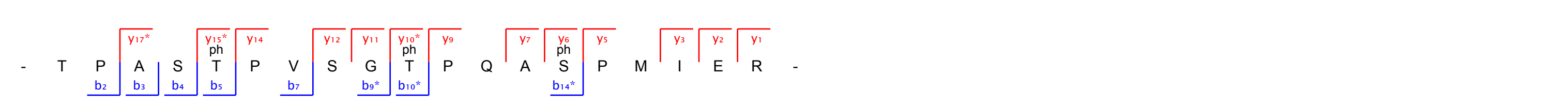
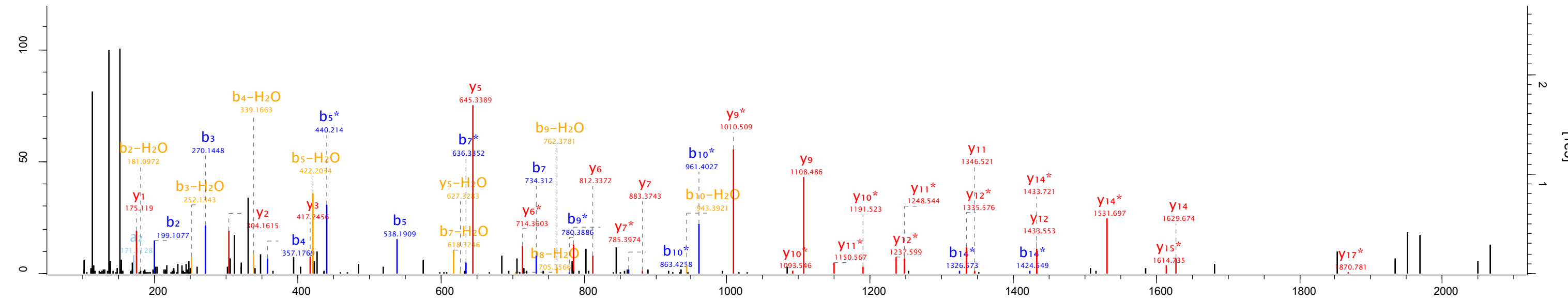
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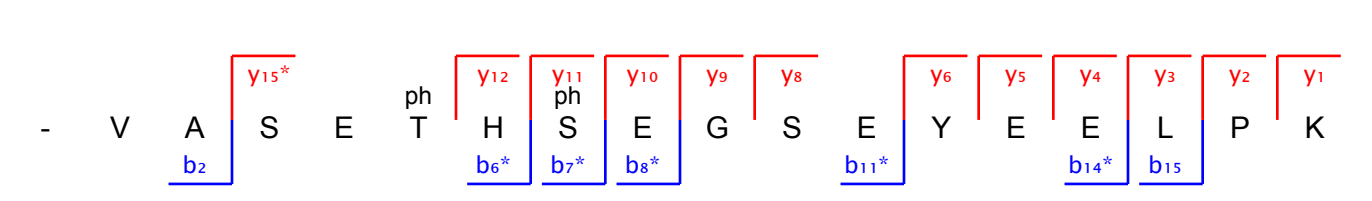
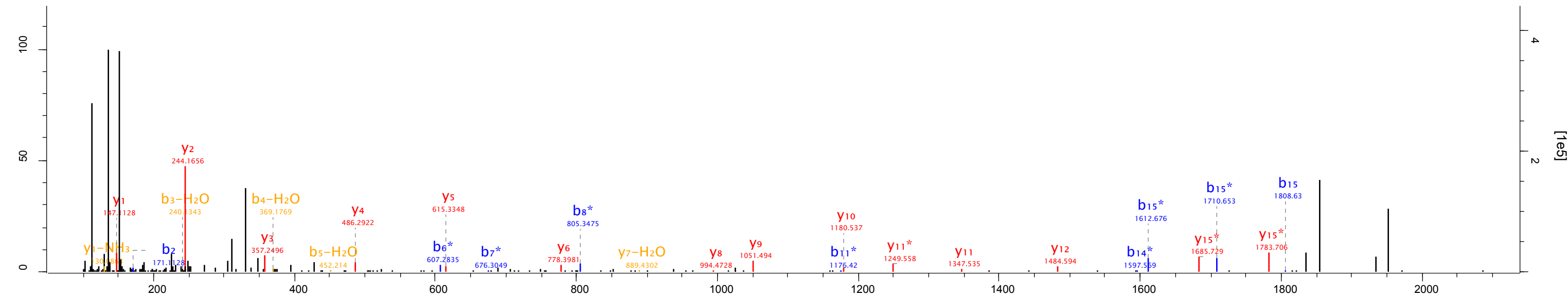
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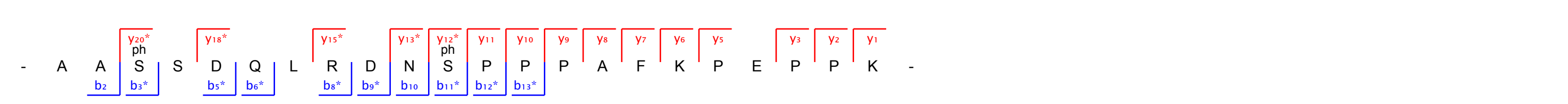
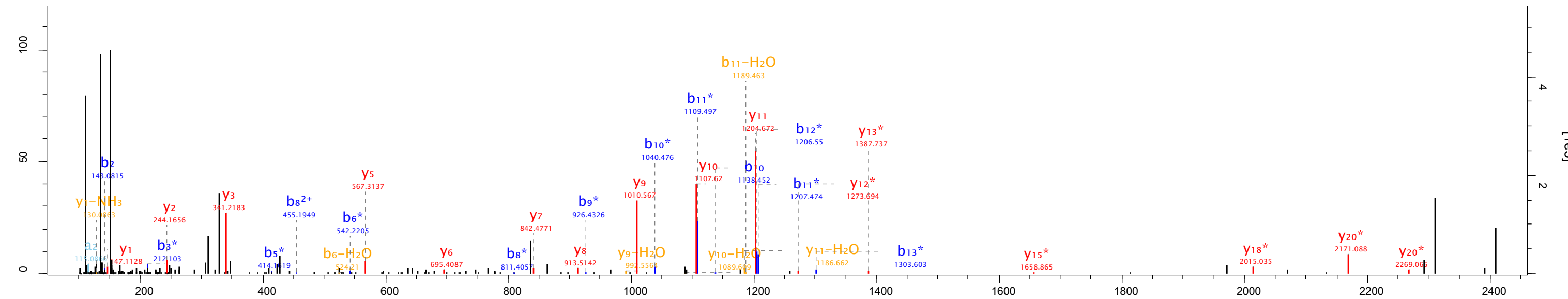
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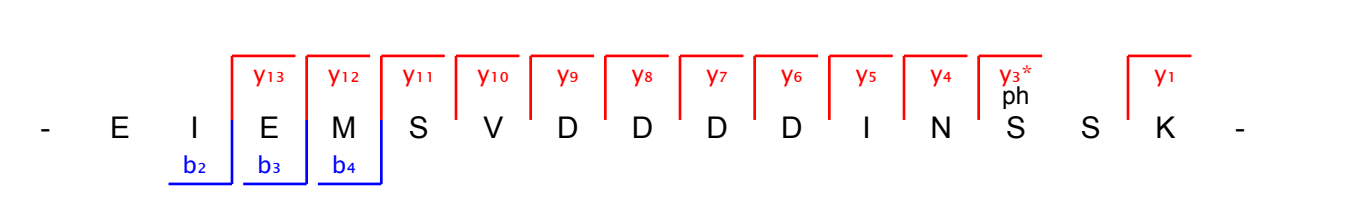
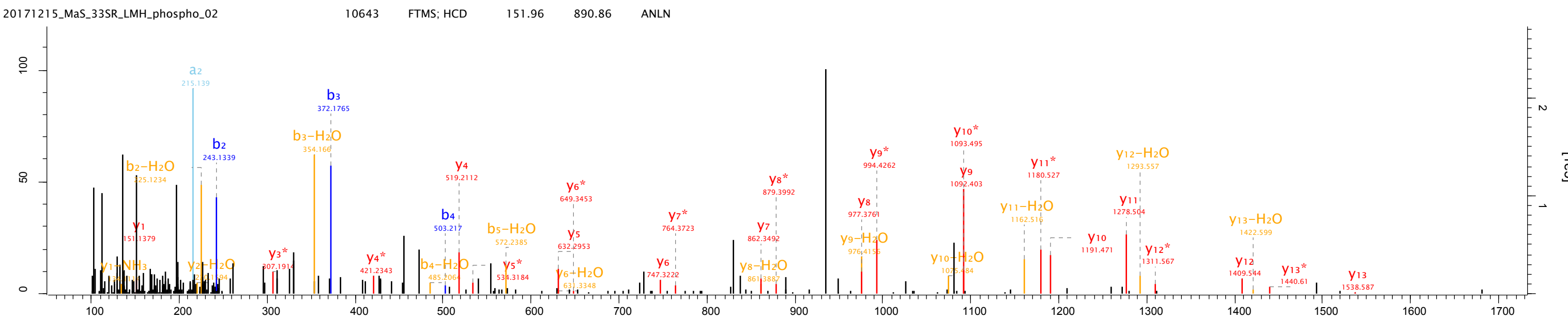
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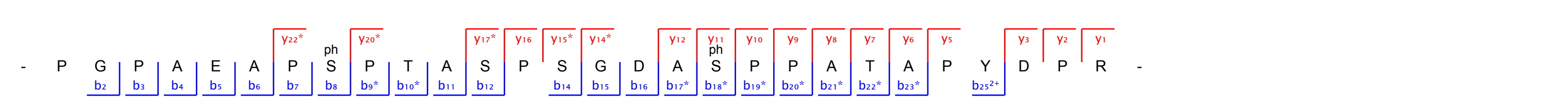
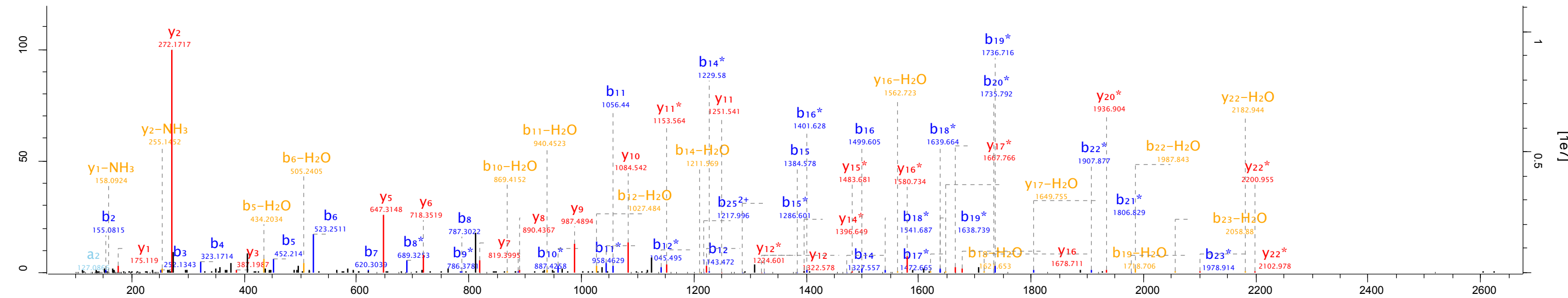
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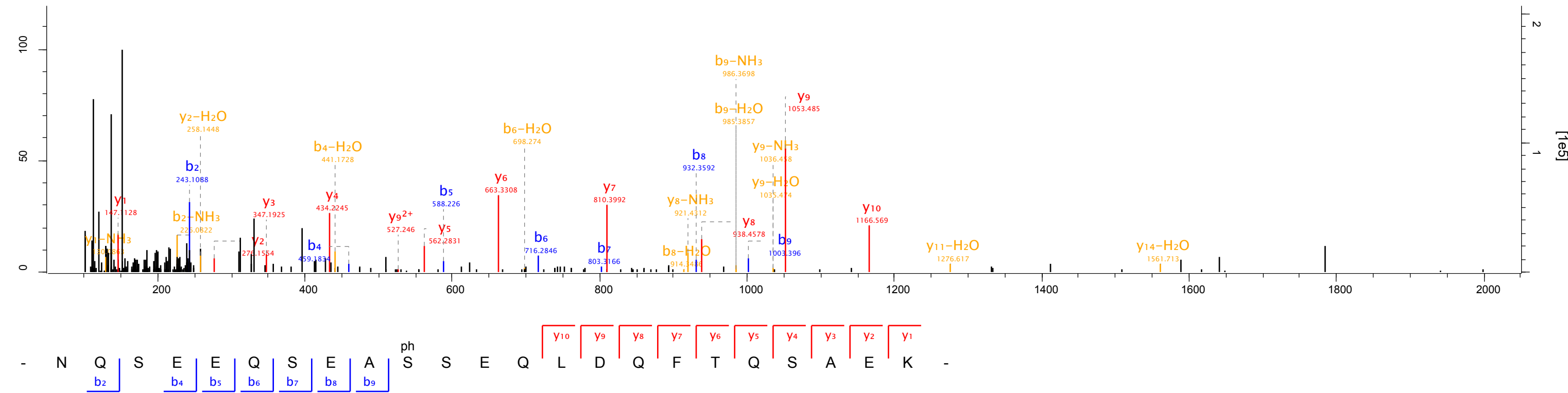
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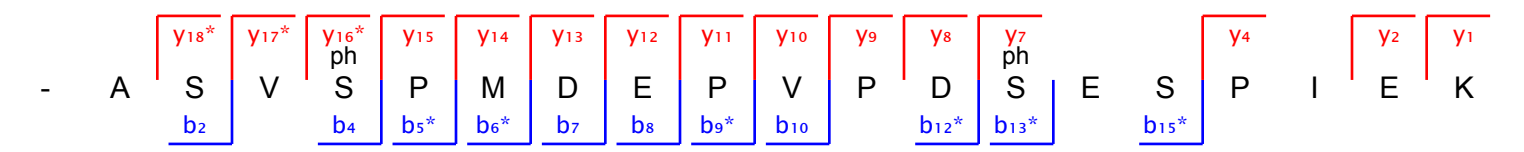
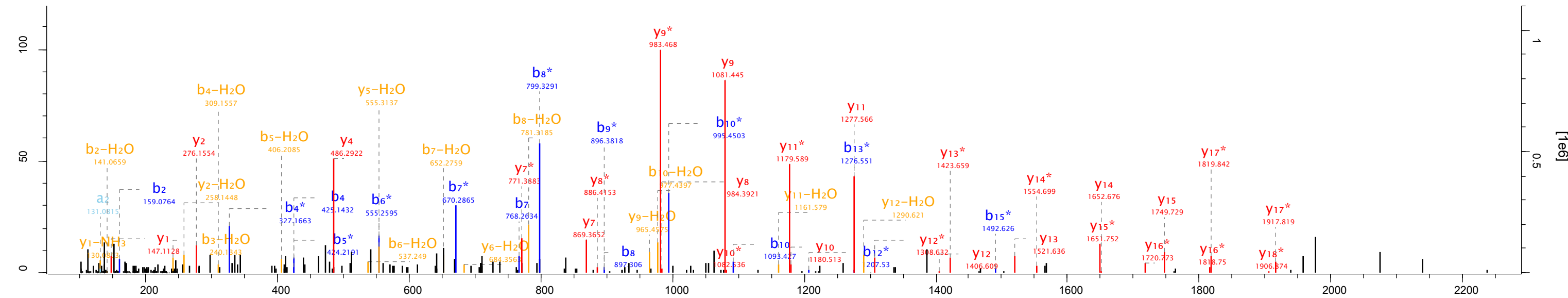
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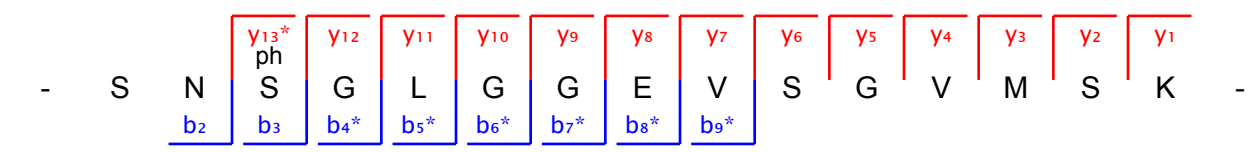
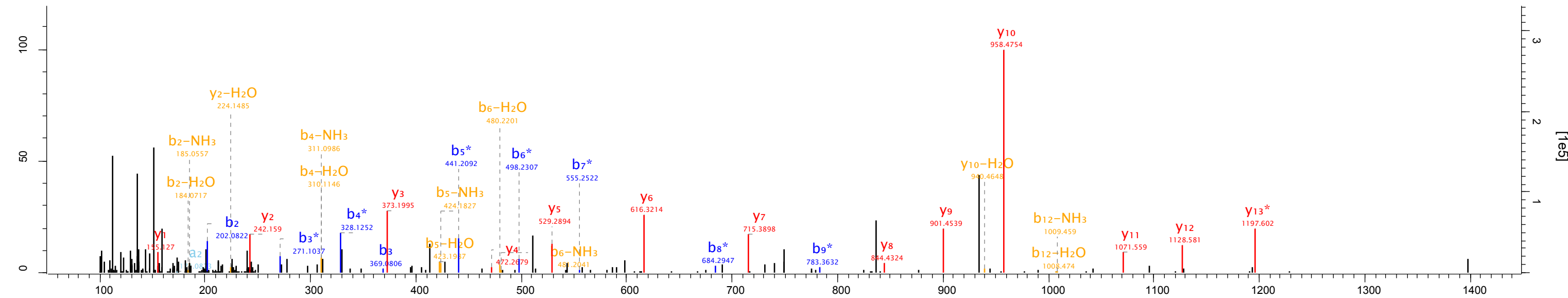
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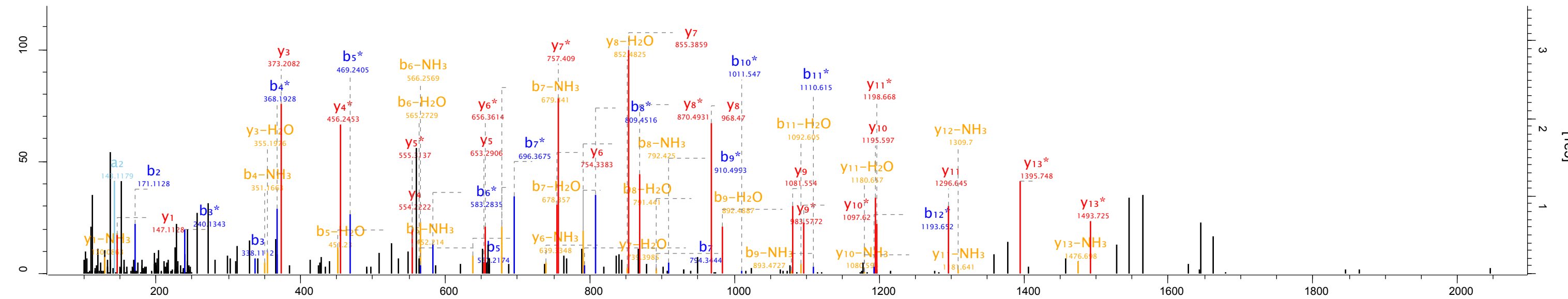
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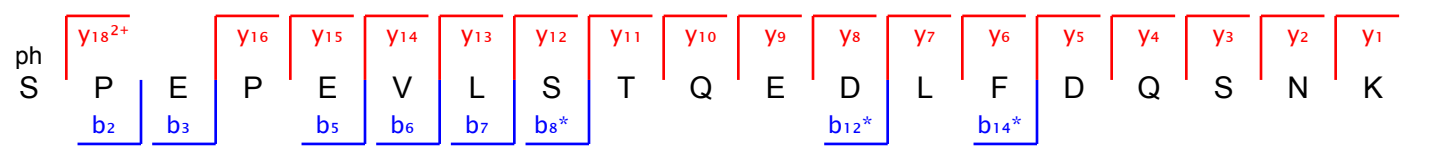
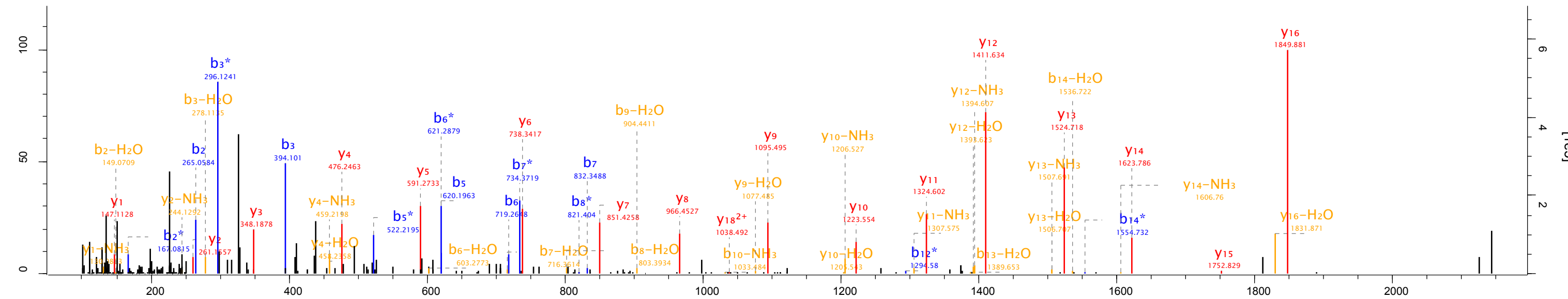
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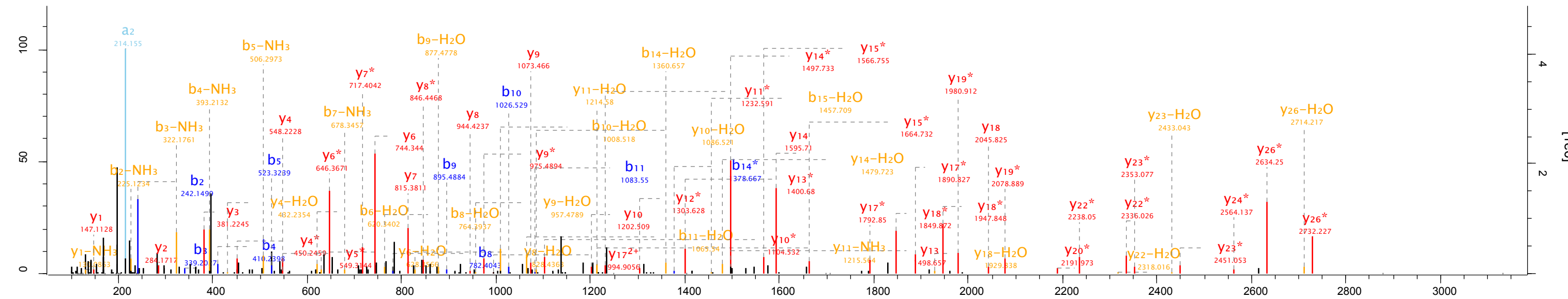
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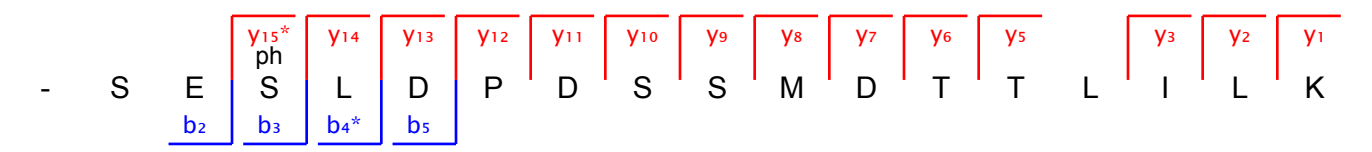
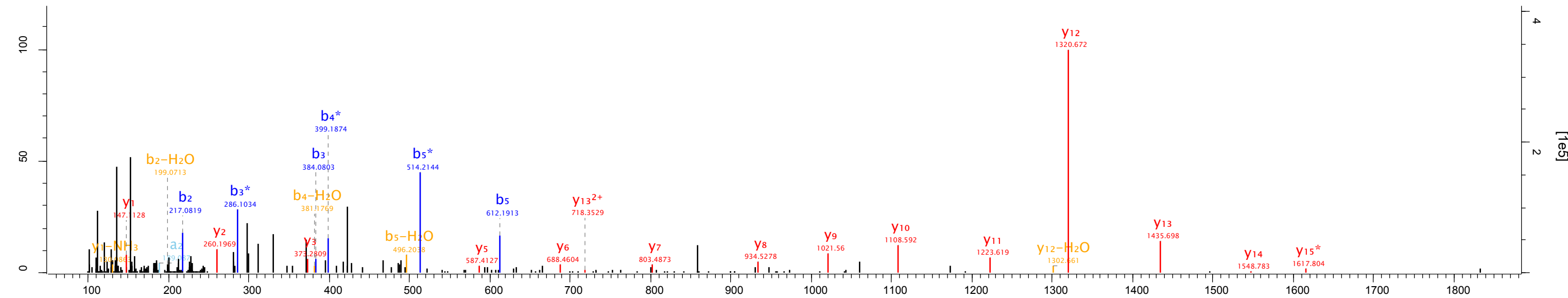


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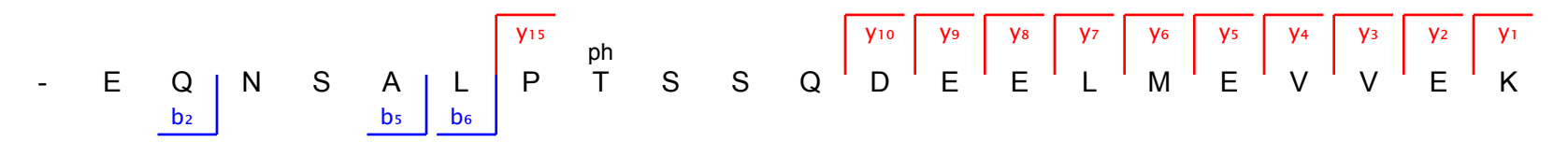
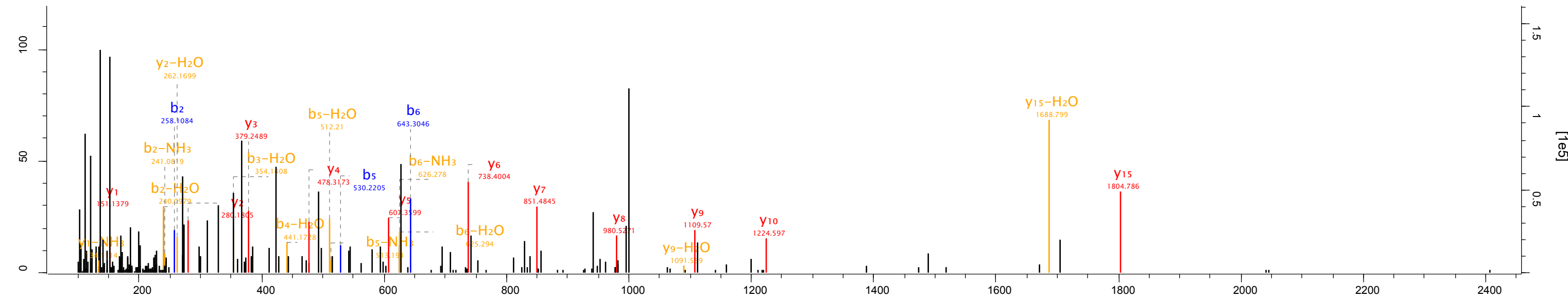
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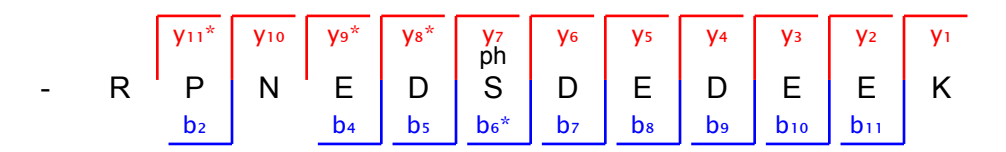
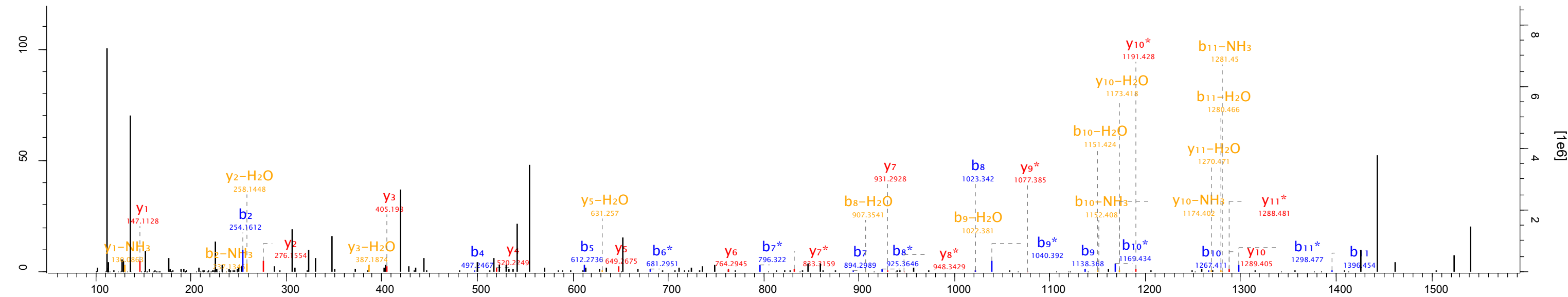
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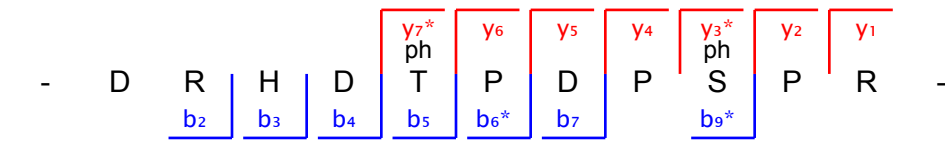
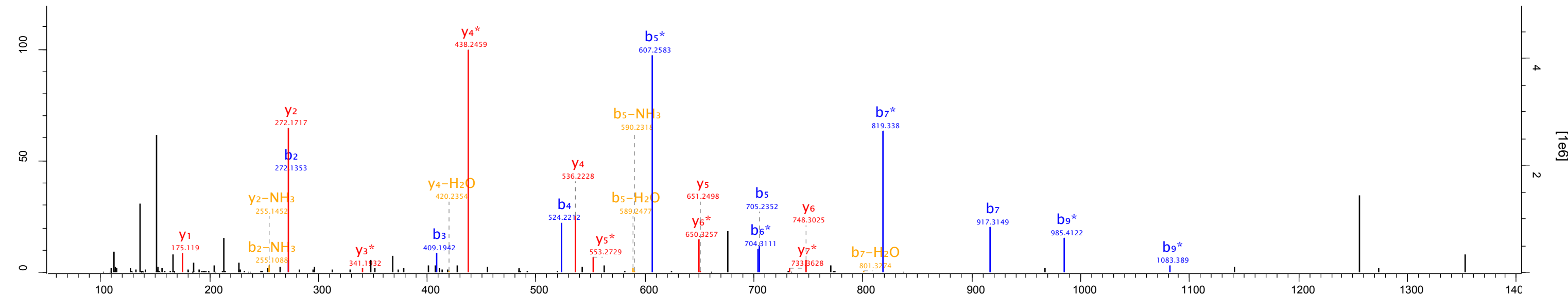


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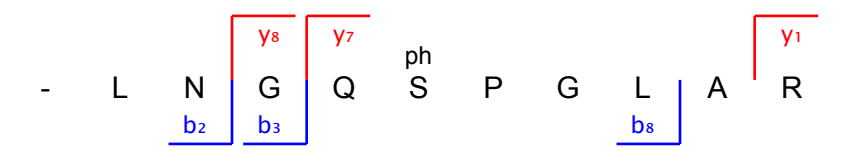
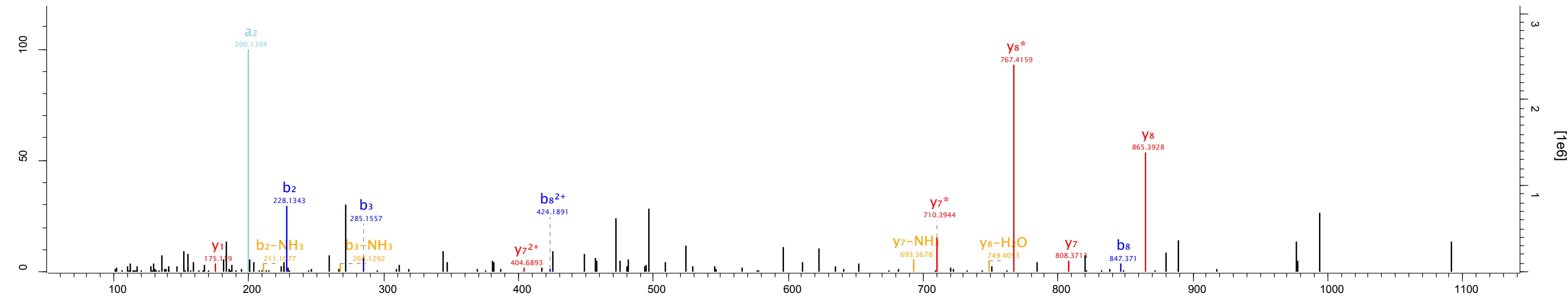


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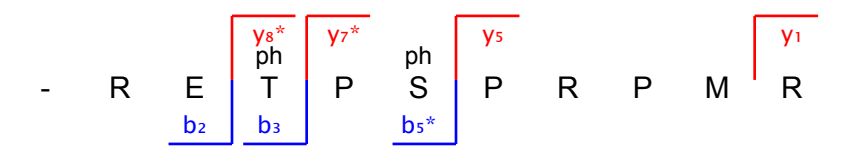
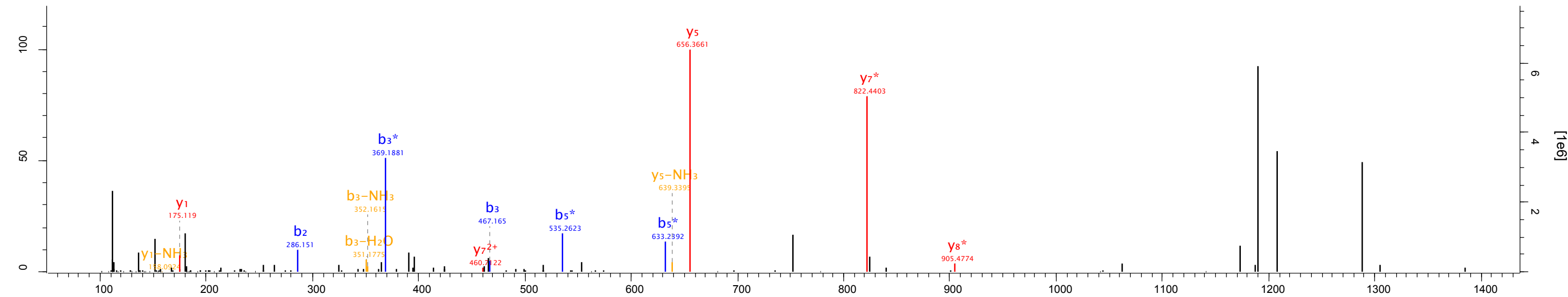




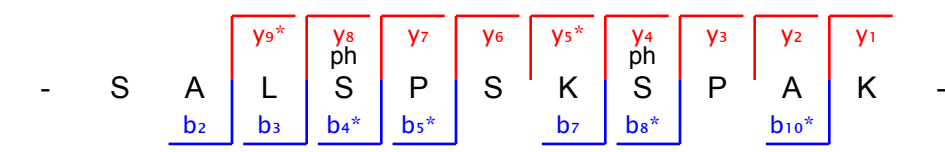
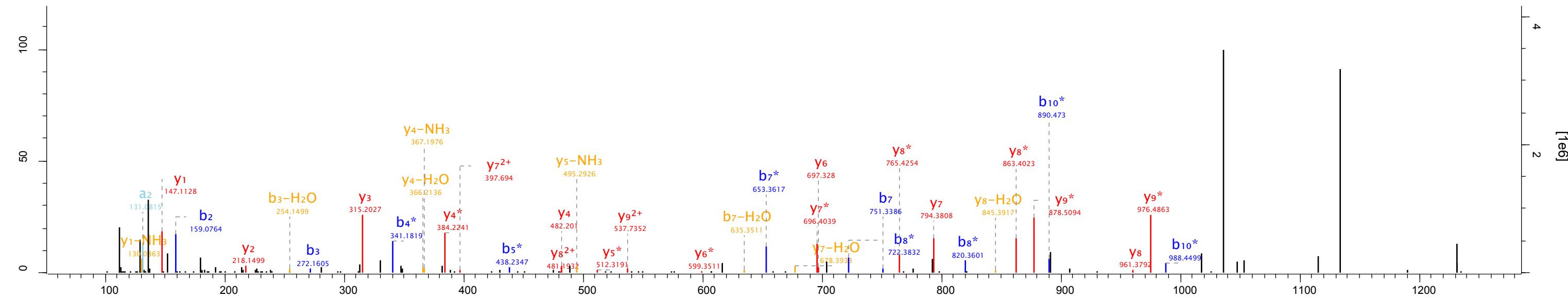
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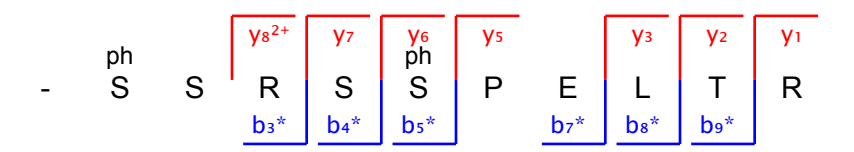
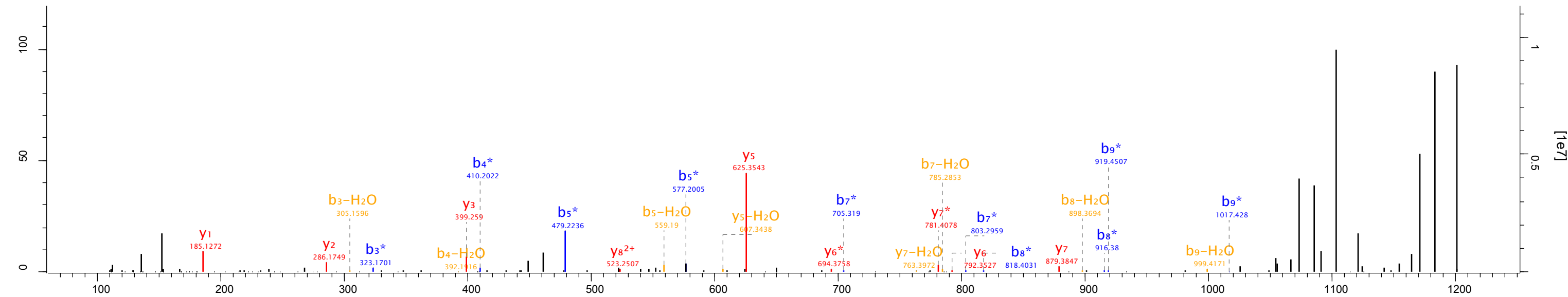
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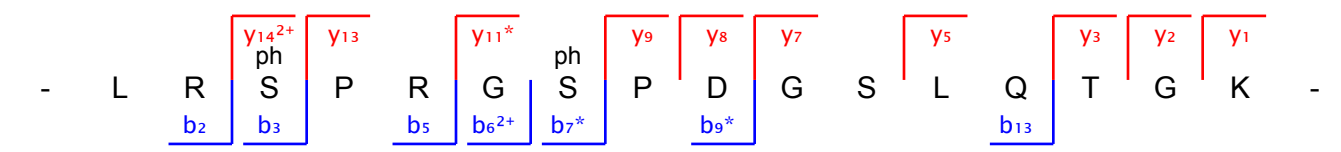
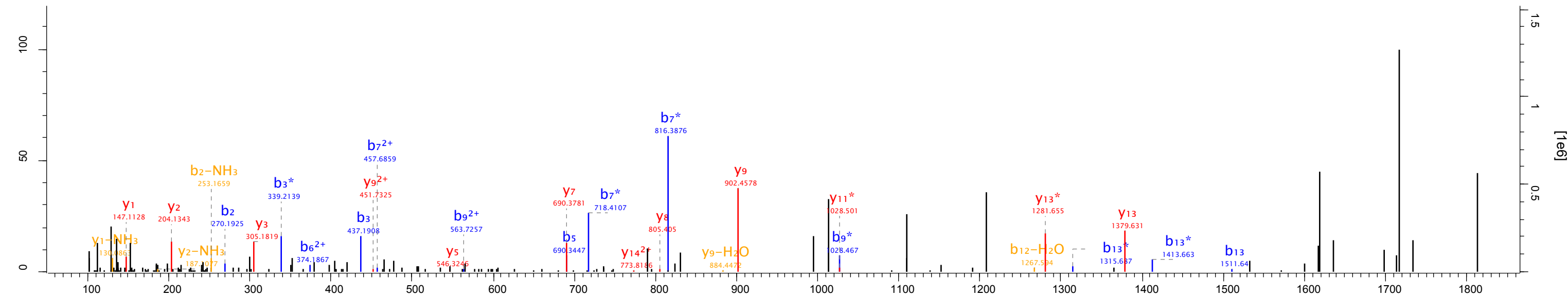
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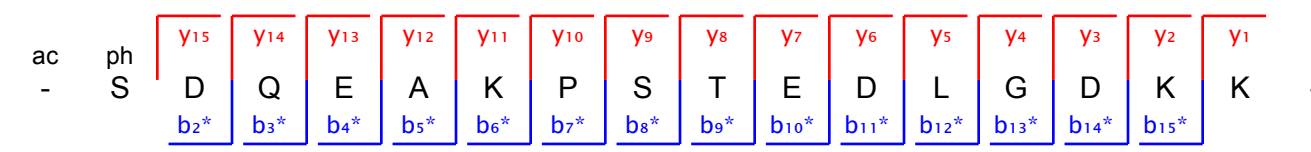
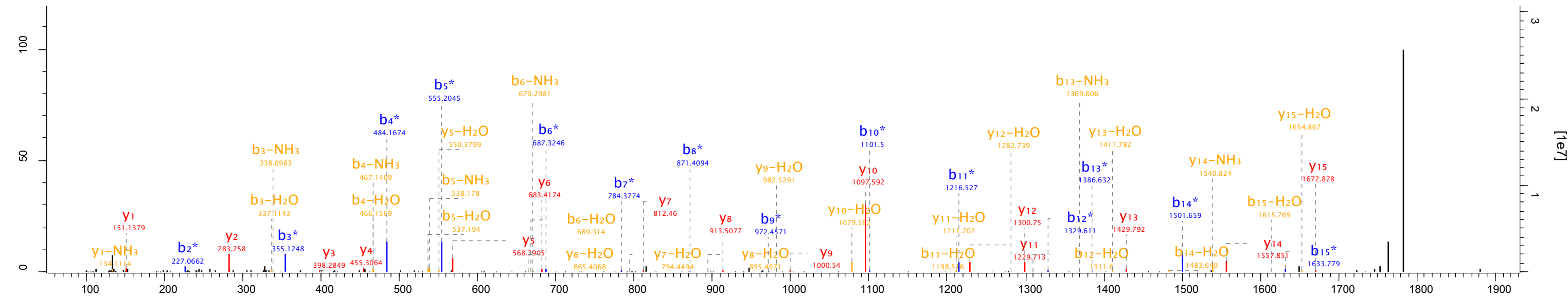
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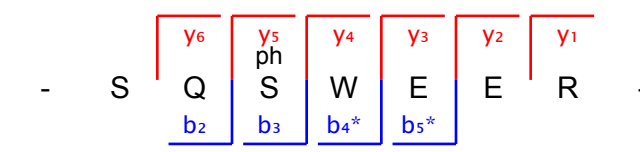
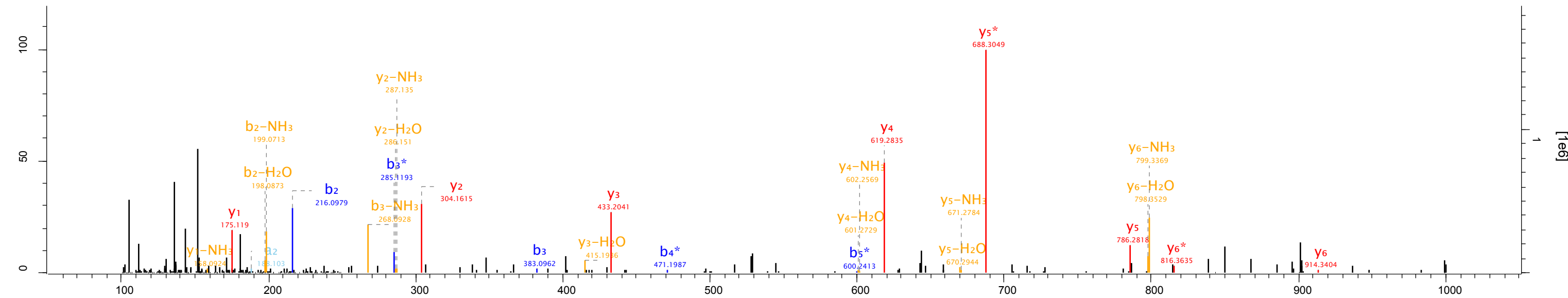


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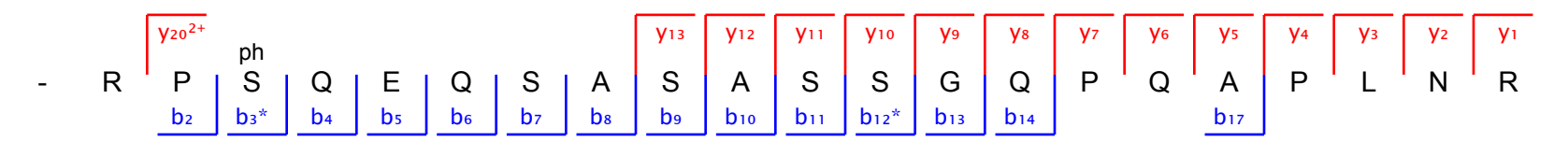
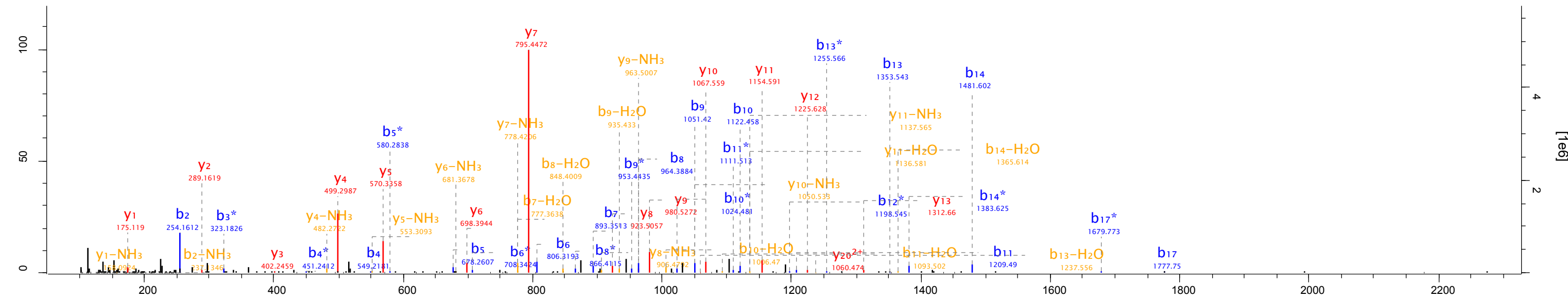


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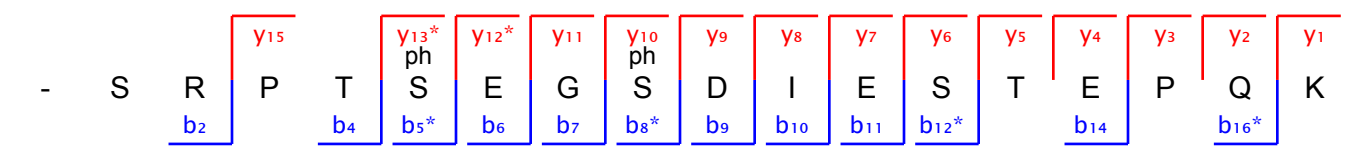
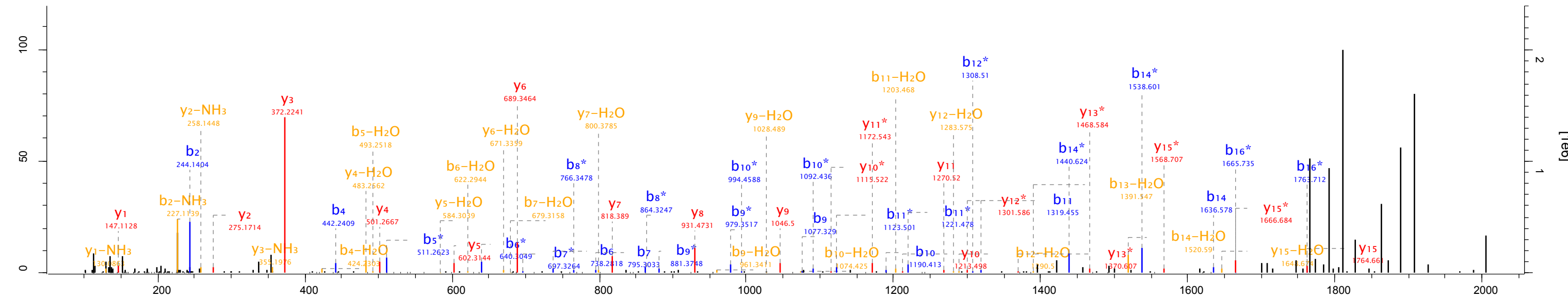




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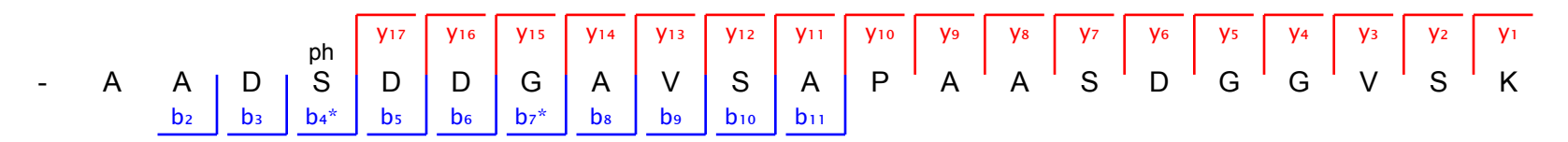
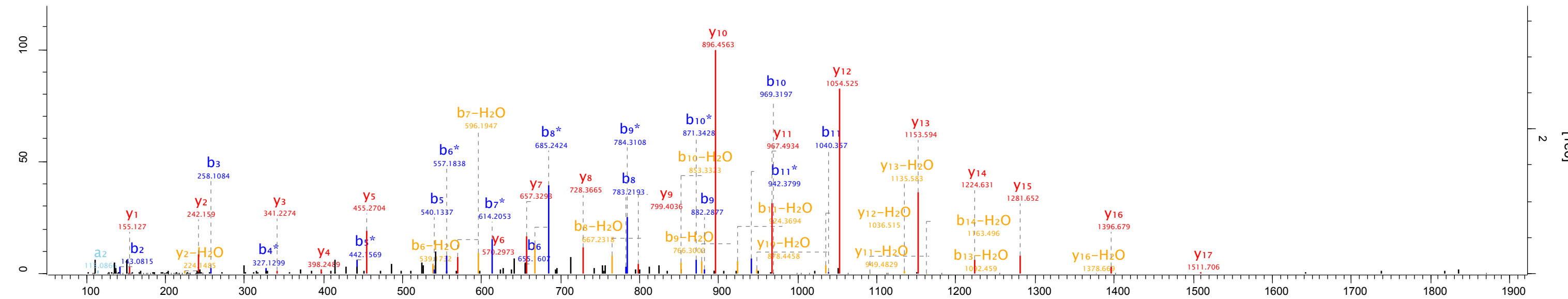


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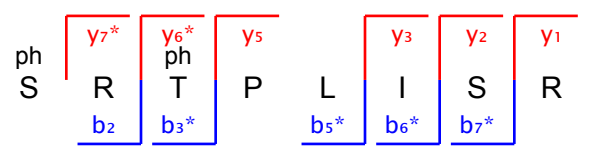
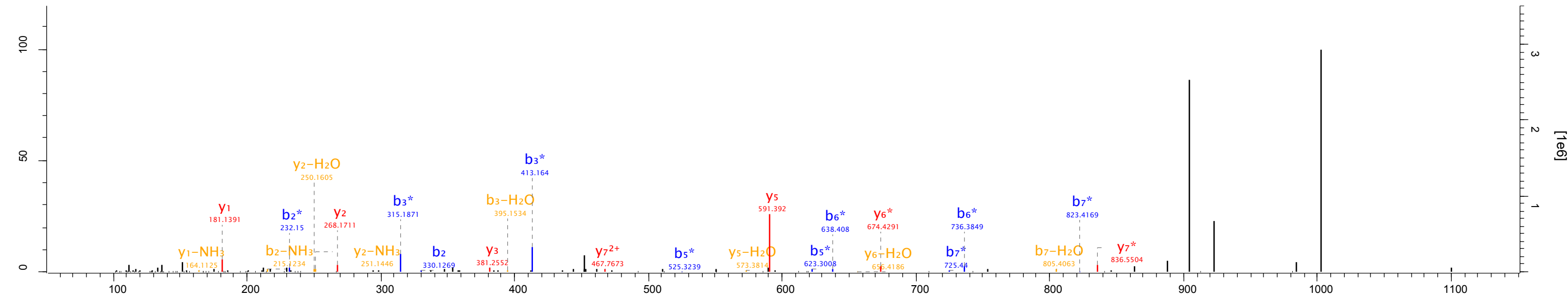


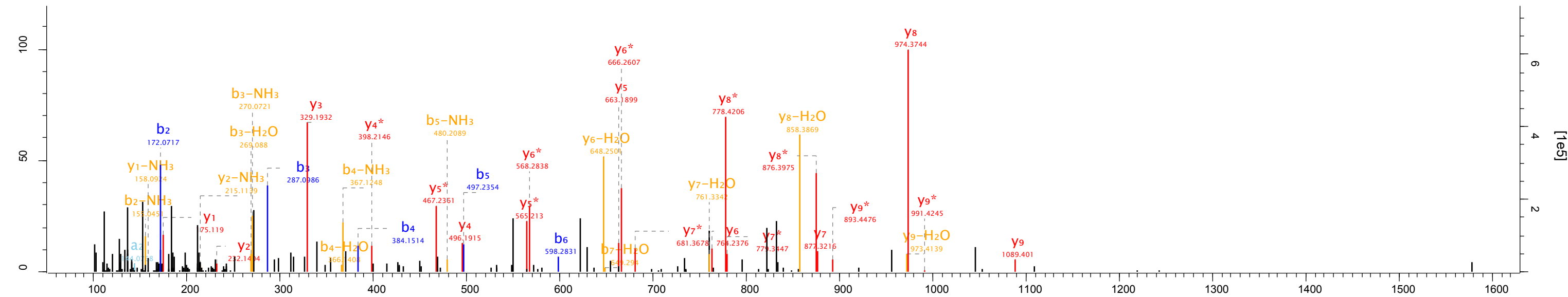
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20171215_MaS_33SR_LMH_phospho_02

Scan 5643 Method FTMS; HCD Score 183.25 m/z 968.91 Gene names TOE1



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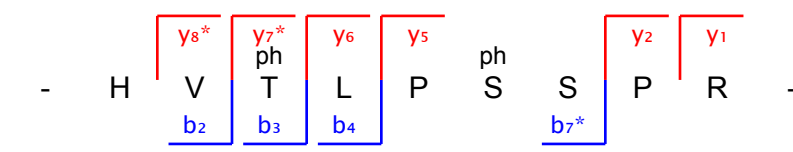
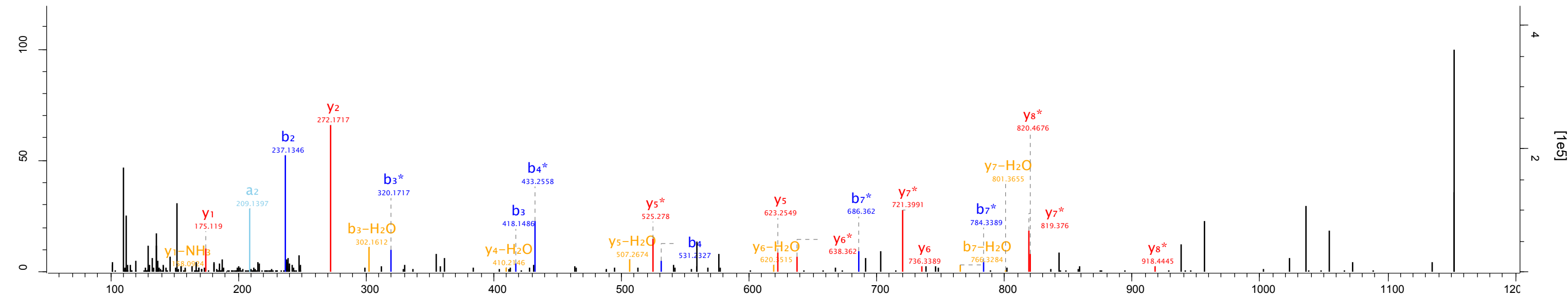




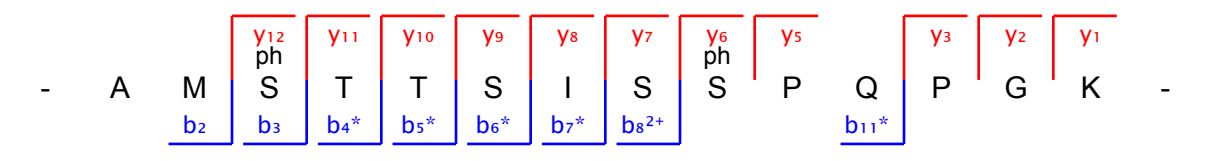
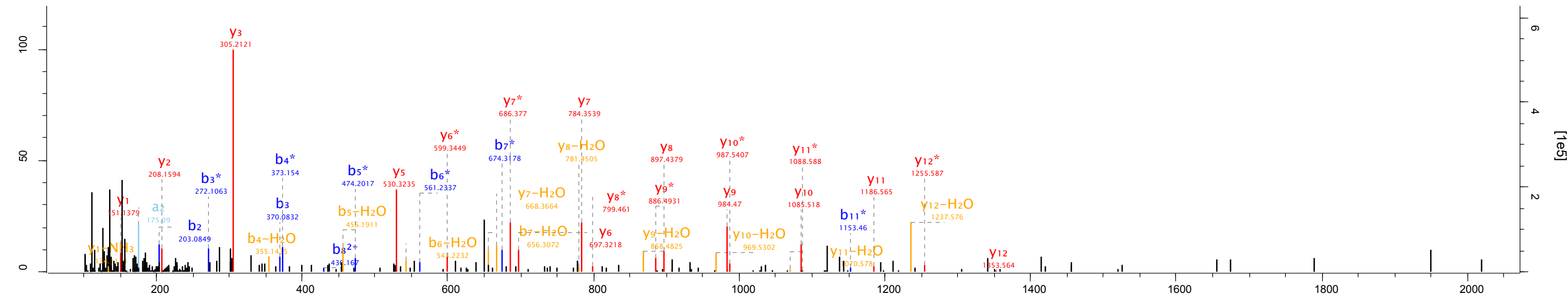
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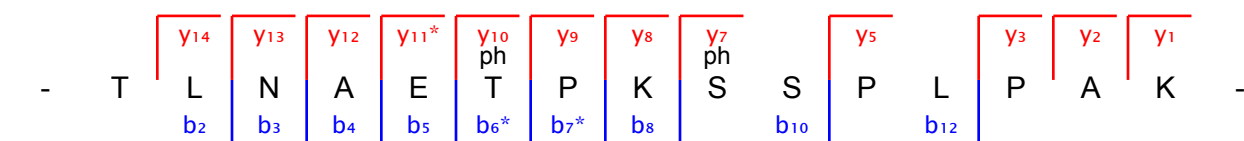
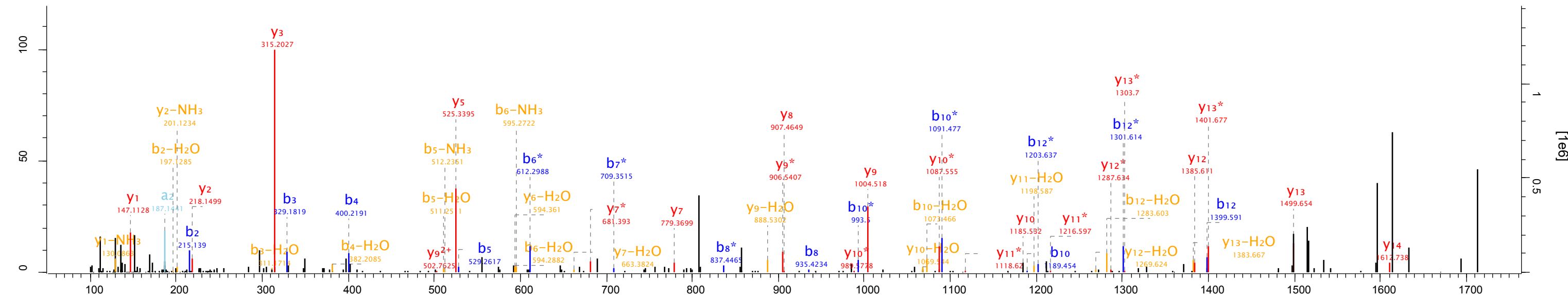
Fragmentation scheme diagram showing b and y ions for the peptide sequence: G N D P L T S S P G R. The b ions (b₂ to b₆) are shown in blue, and the y ions (y₁ to y₉) are shown in red. The b ions are labeled below the amino acids, and the y ions are labeled above the amino acids. The b₂ ion is shown below the N, b₃ below D, b₄ below P, b₅ below L, and b₆ below T. The y₁ ion is above R, y₂ above G, y₃ above P, y₄ above S, y₅ above S, y₆ above T, y₇ above L, y₈ above P, and y₉ above D.

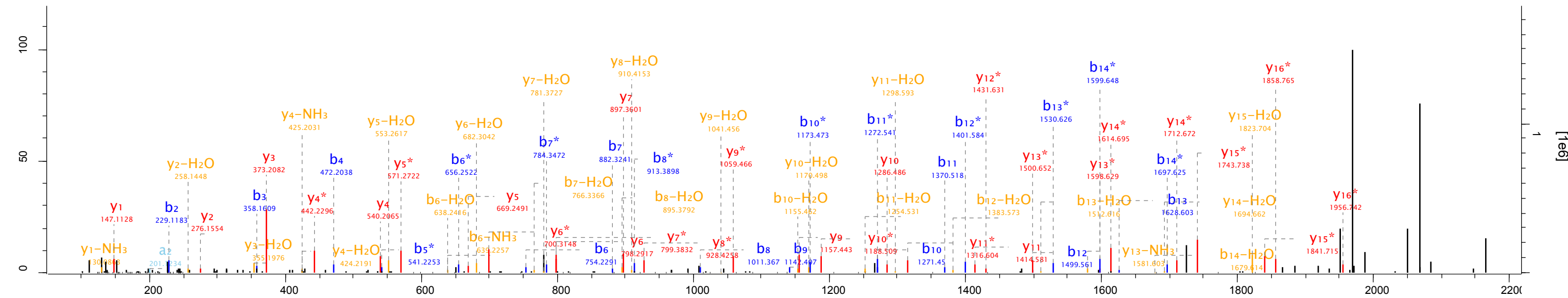
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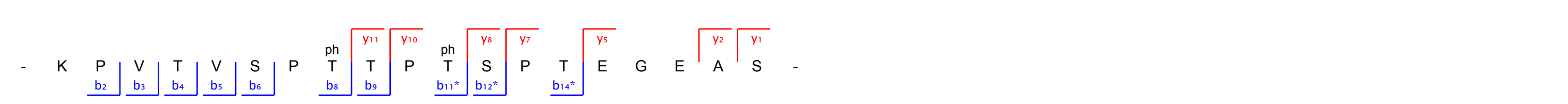
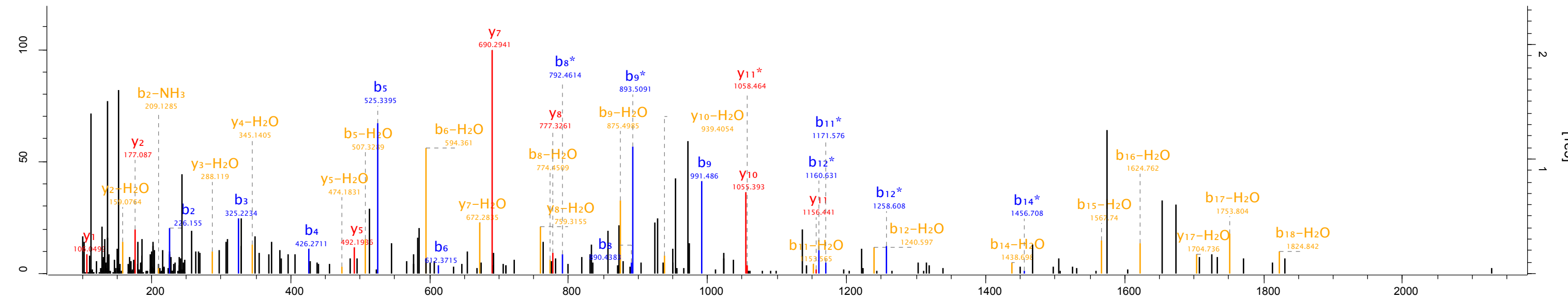




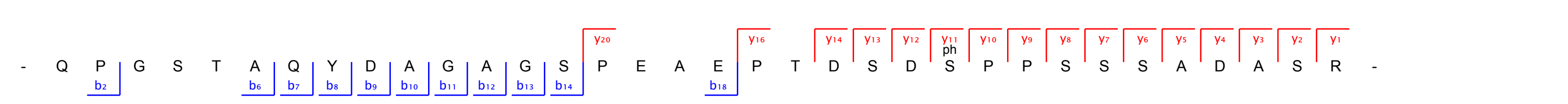
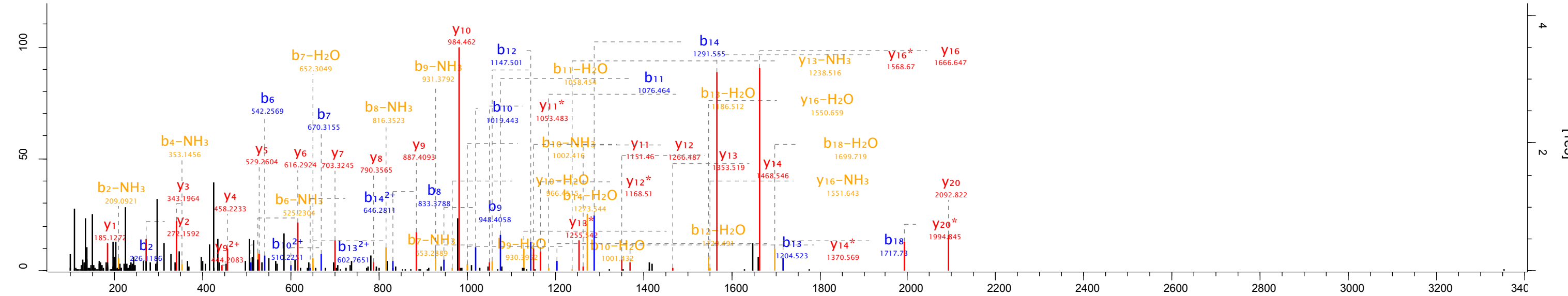


y16*	y15*	y14*	y13* ph	y12*	y11	y10	y9	y8*	y7	y6	y5	y4 ph	y3	y2	y1
D	E	N	S	D	K	E	M	E	V	E	E	S	P	E	K
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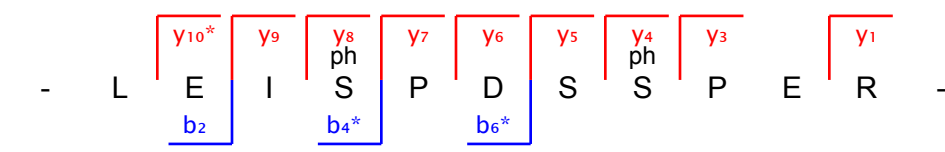
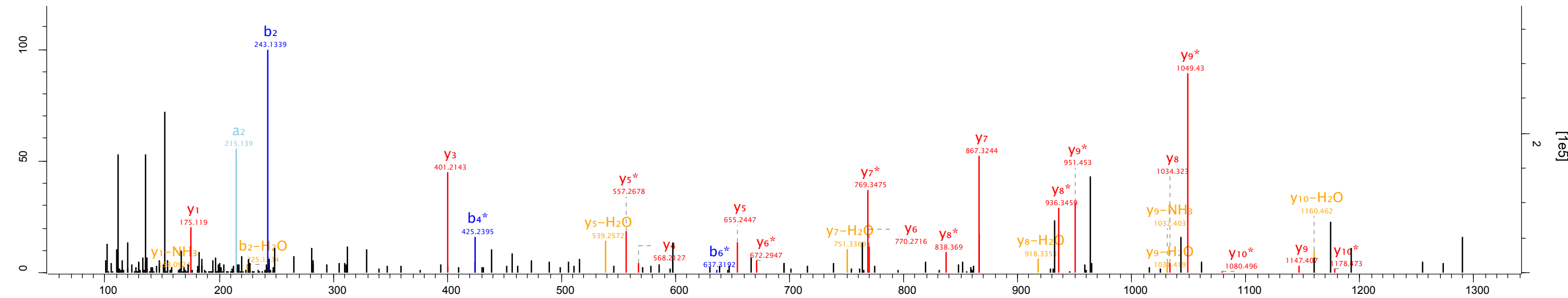
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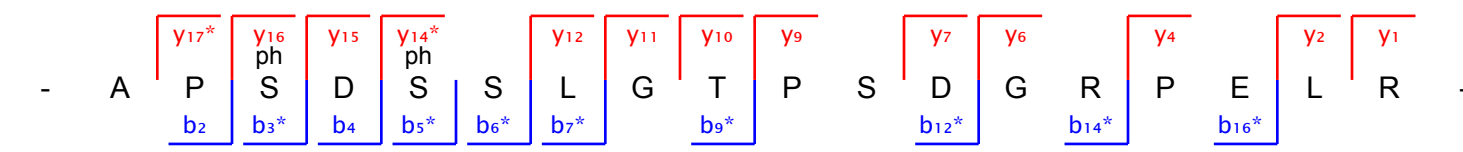
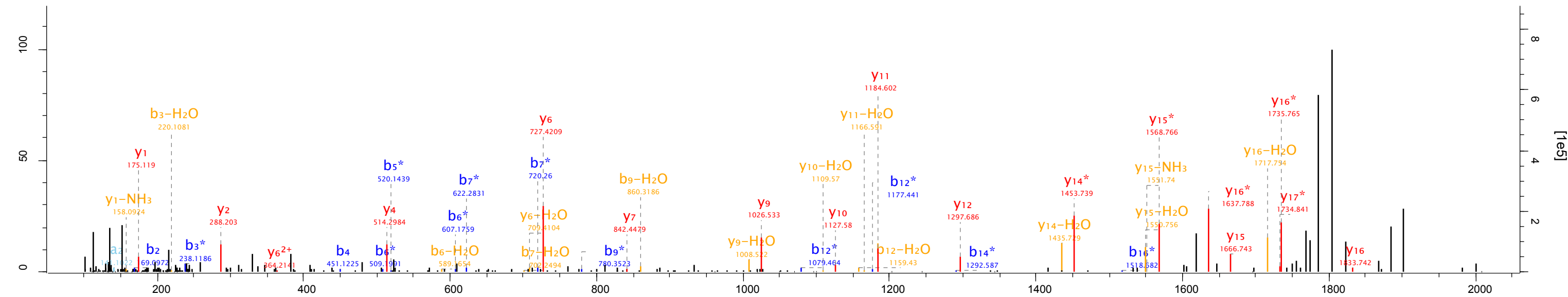
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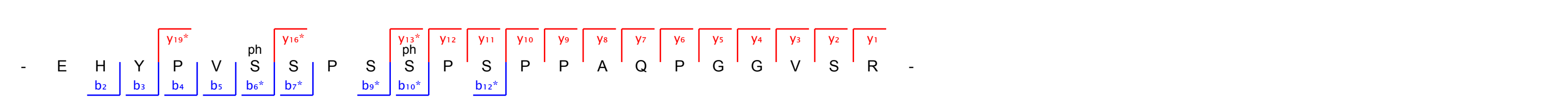
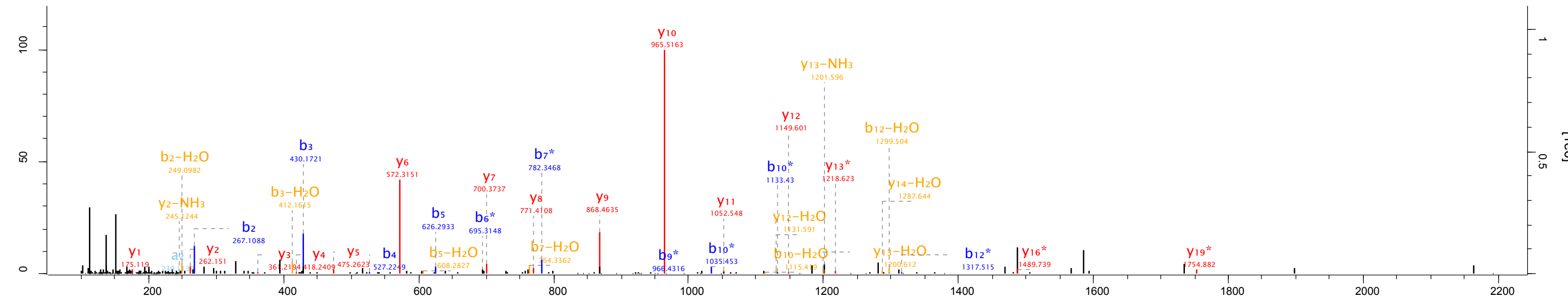
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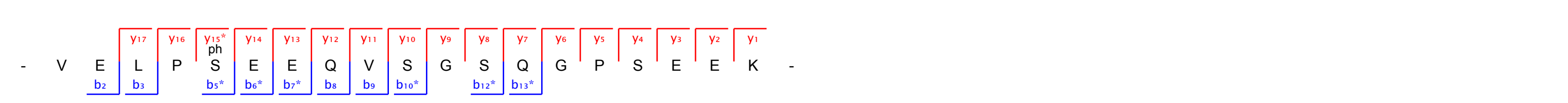
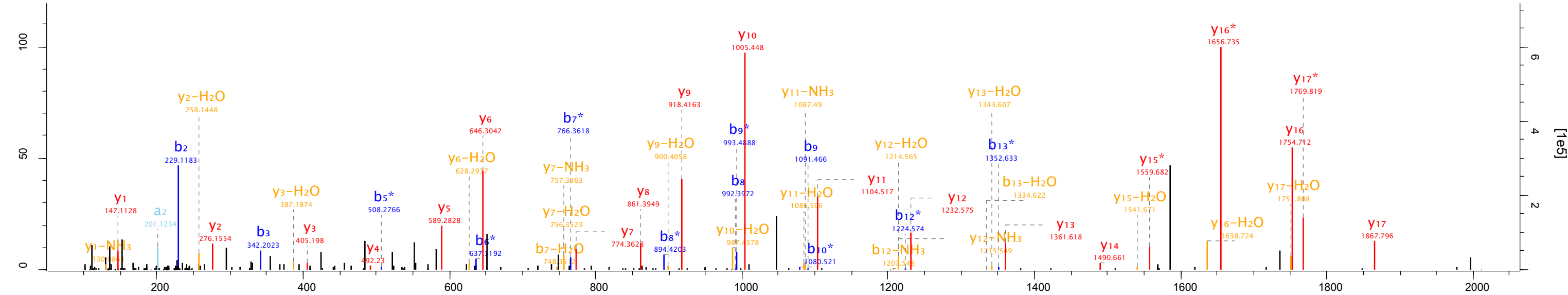
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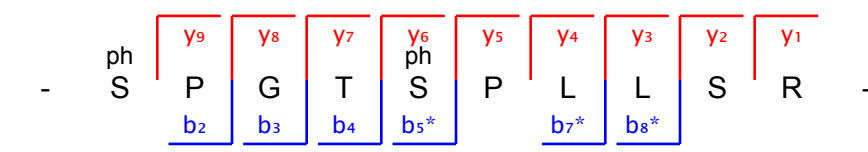
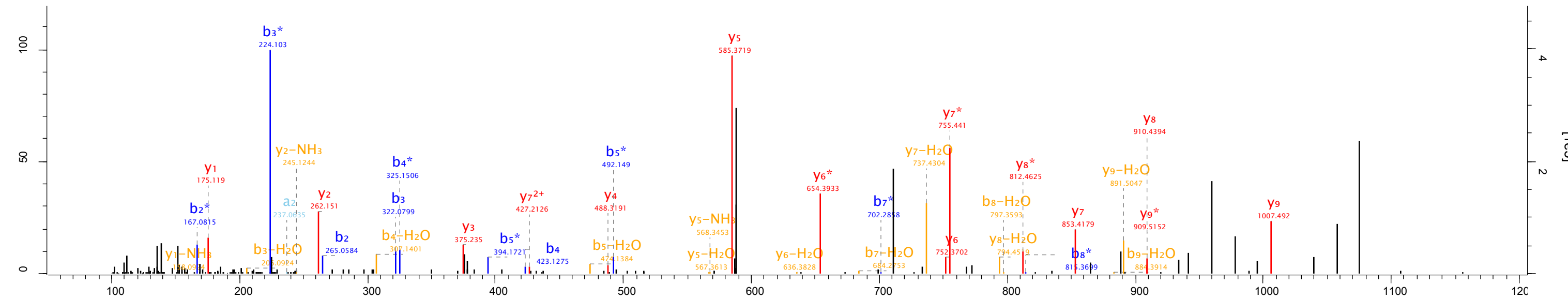
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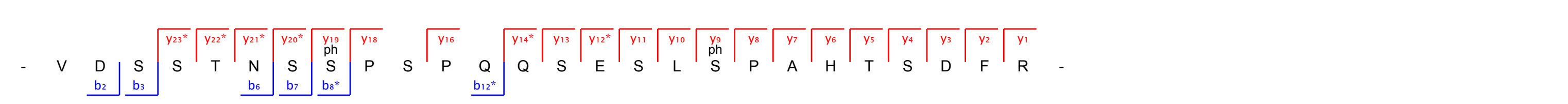
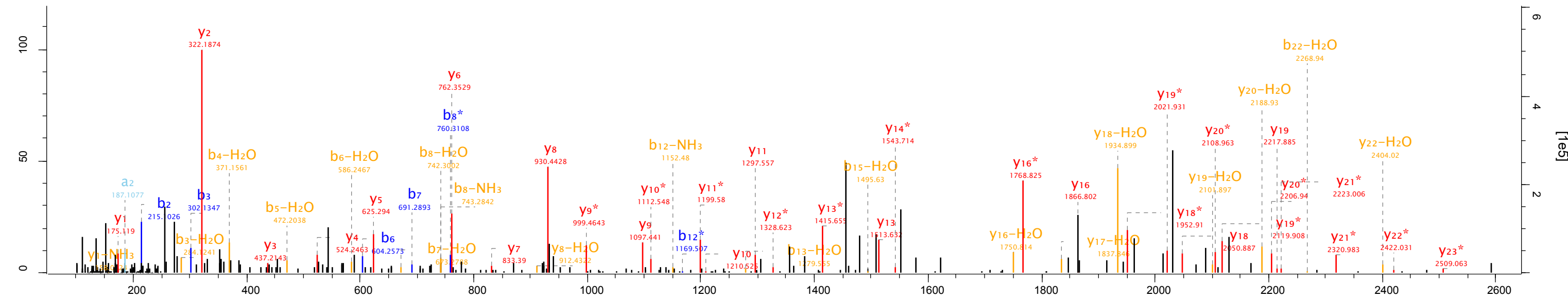
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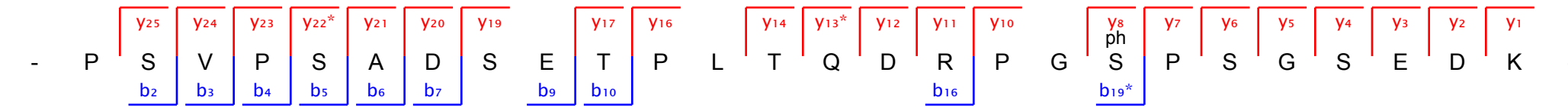
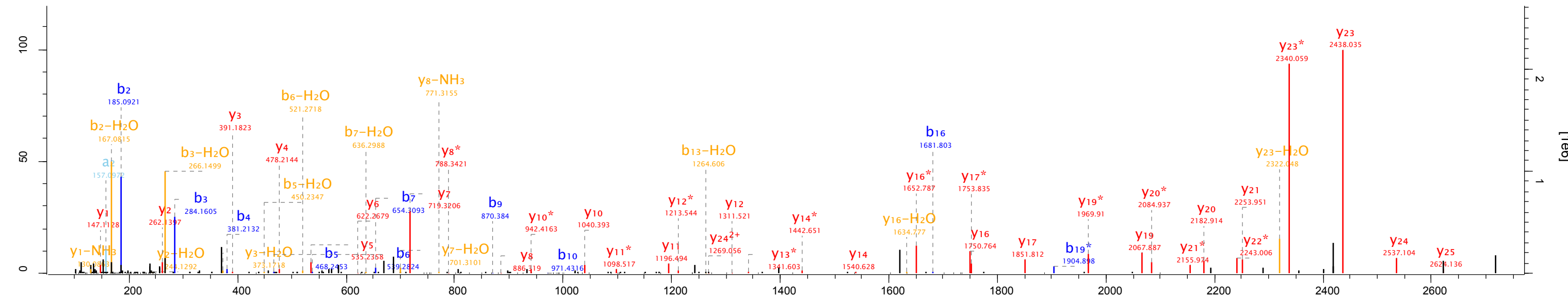


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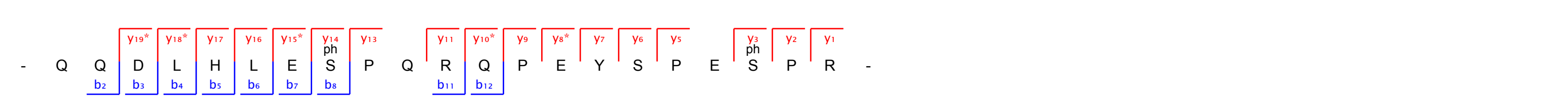
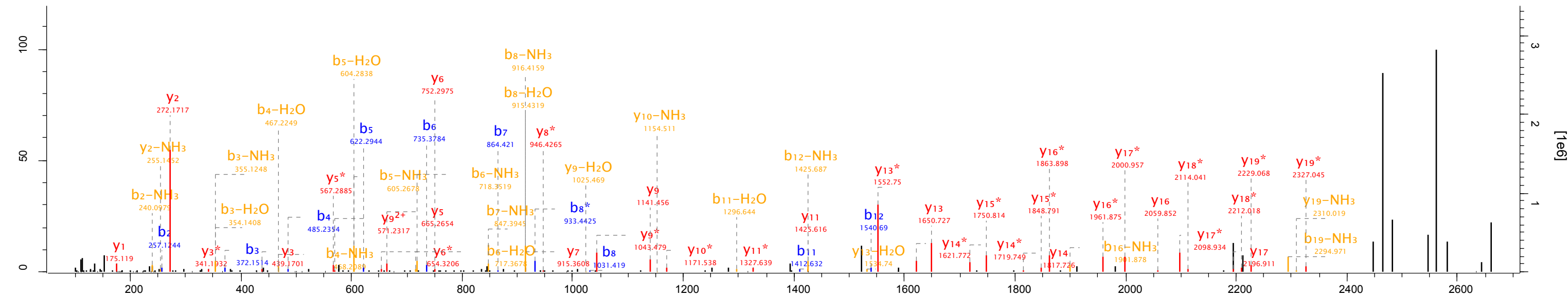


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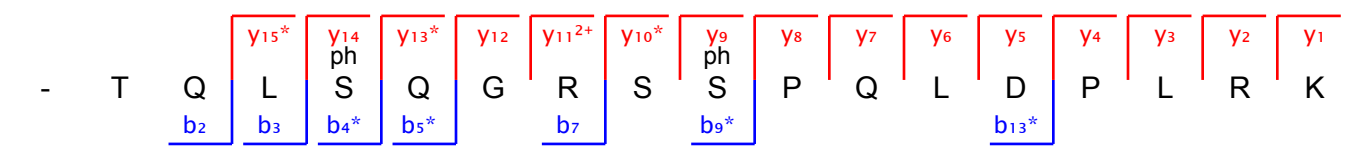
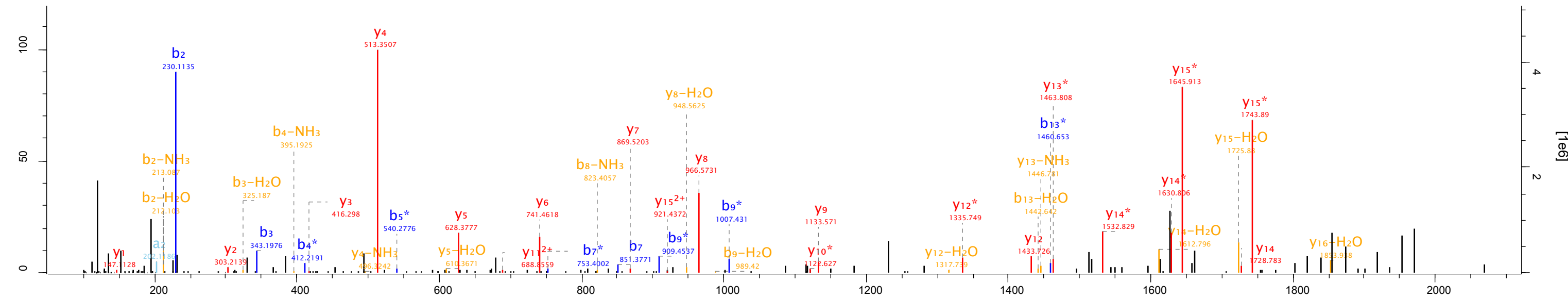




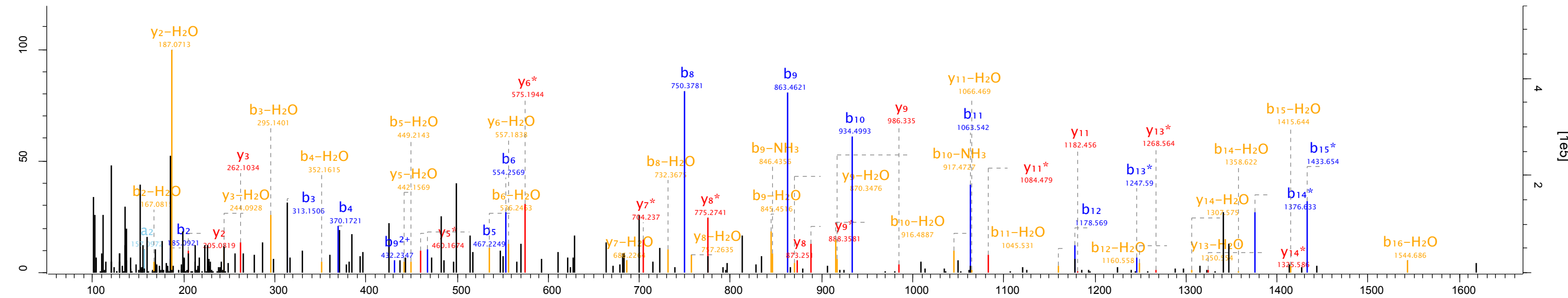
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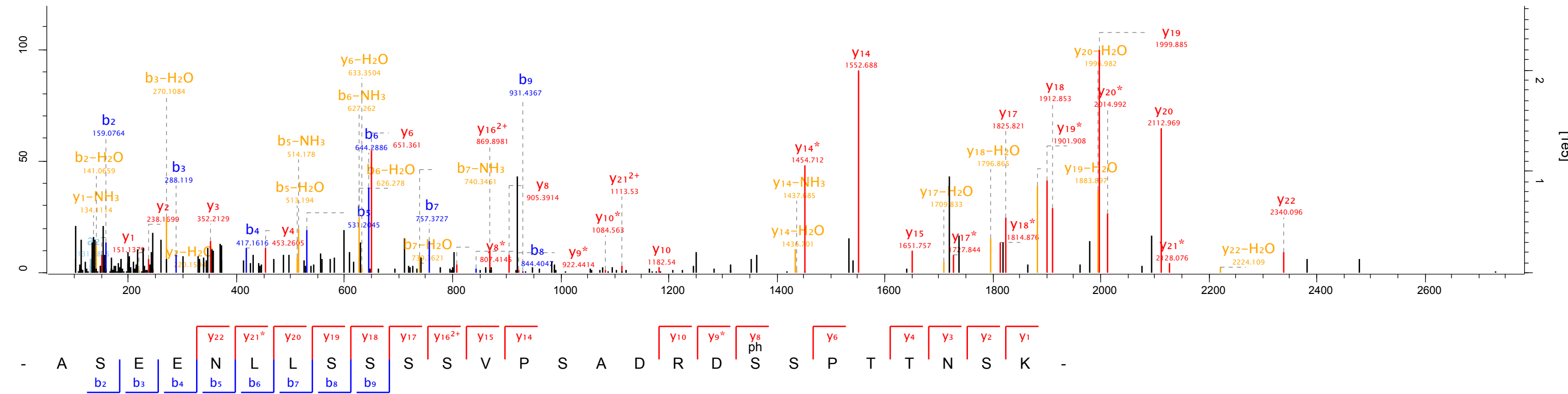
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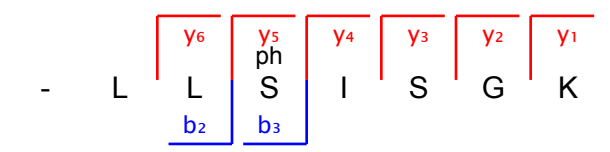
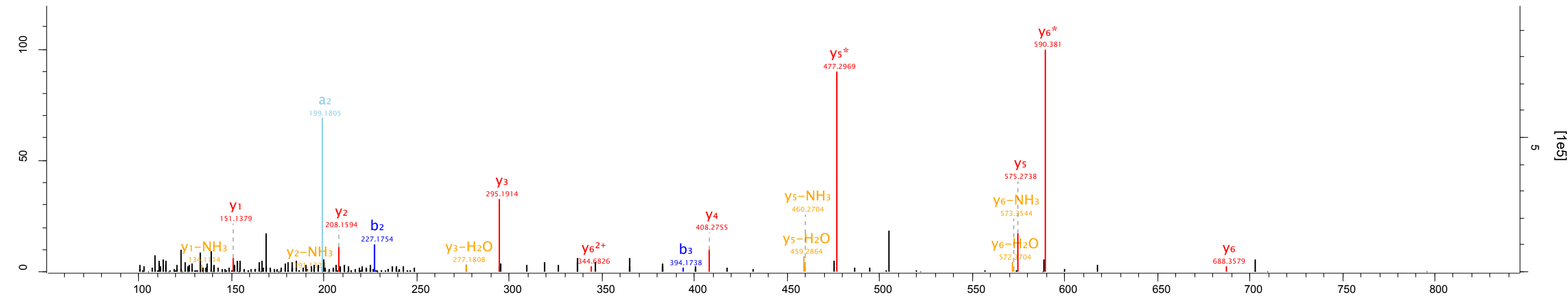
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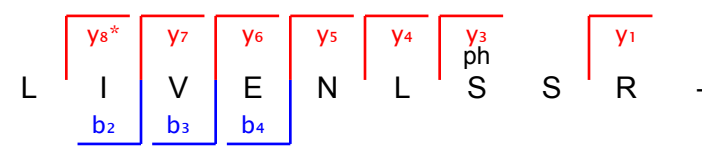
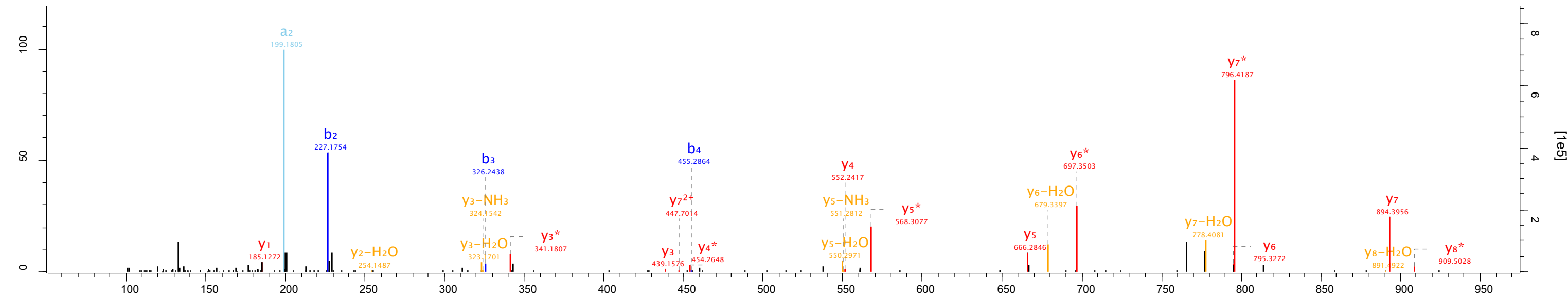
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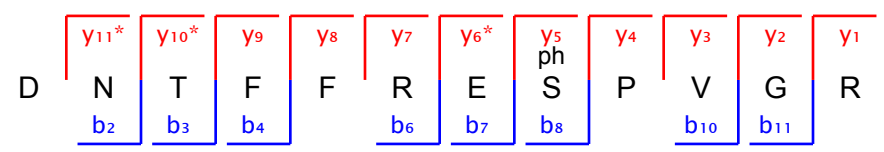
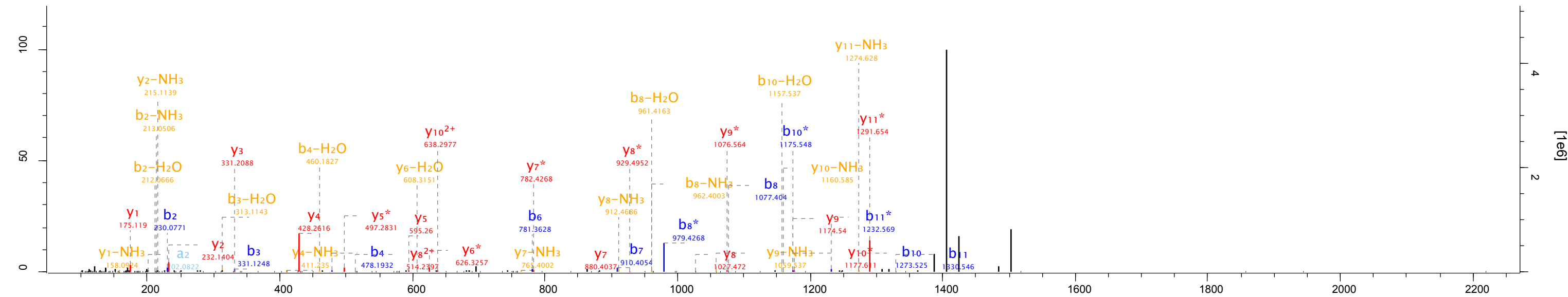
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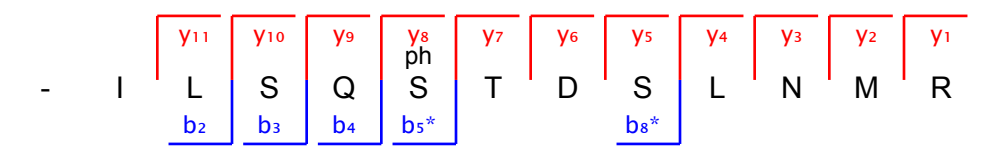
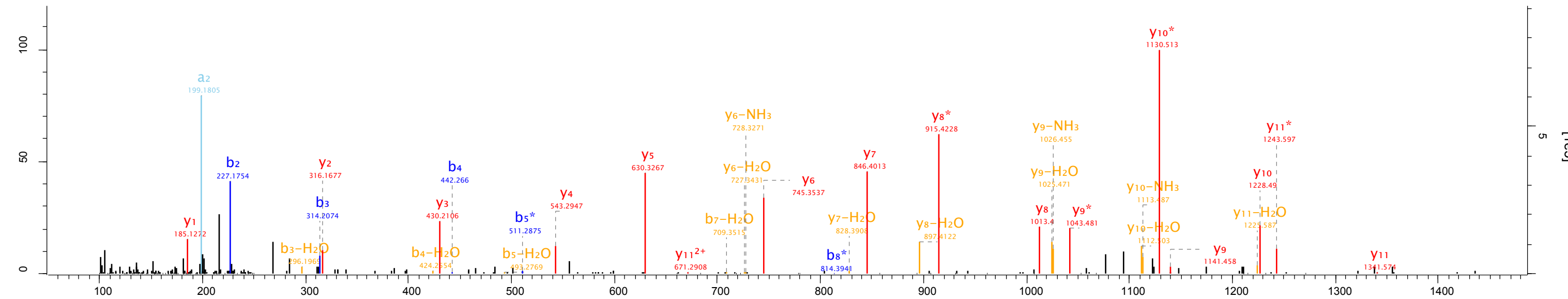
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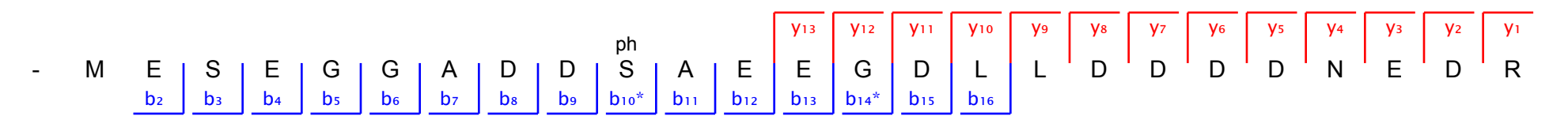
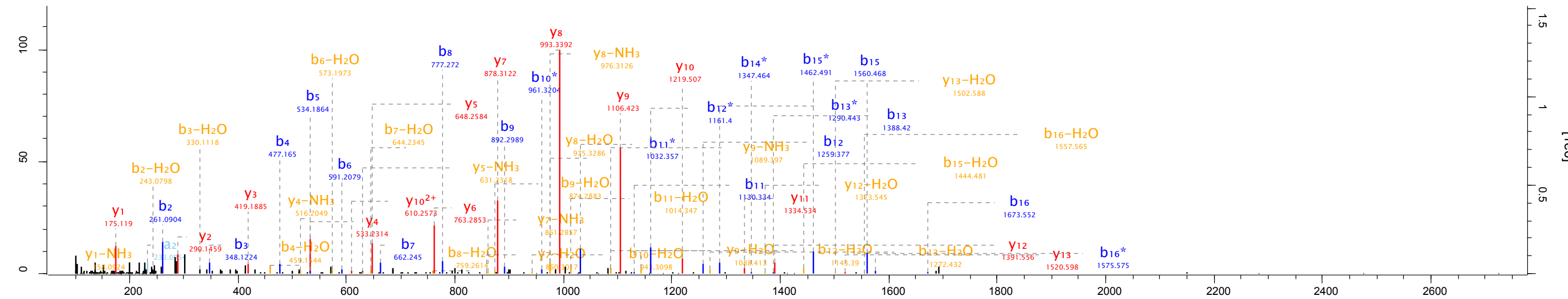
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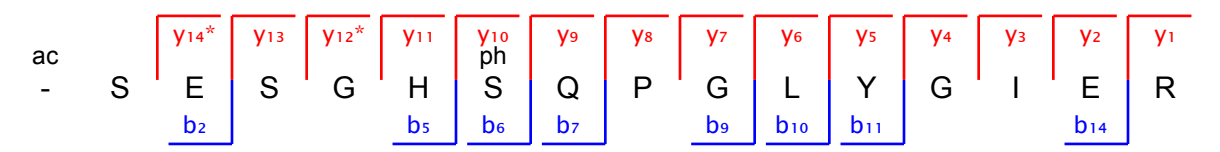
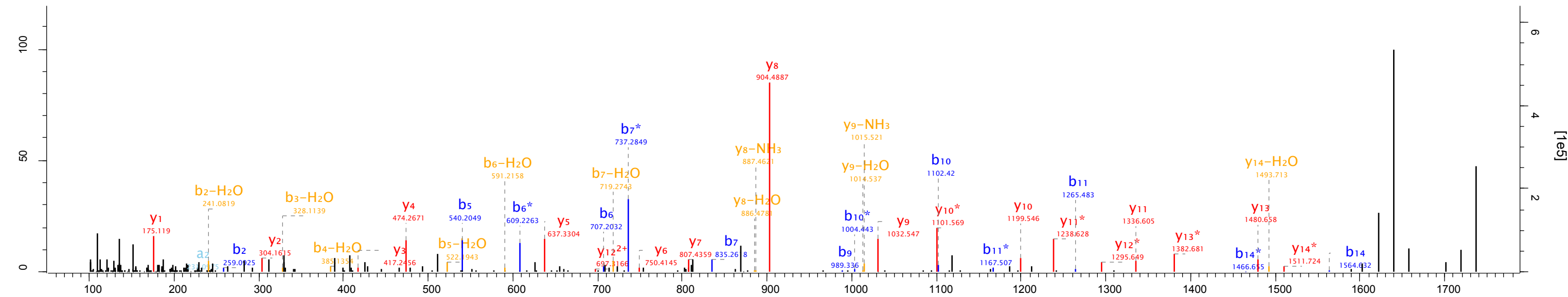
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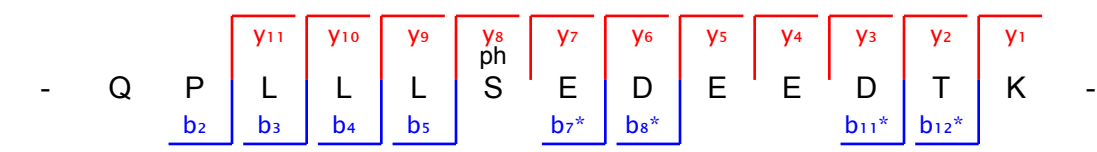
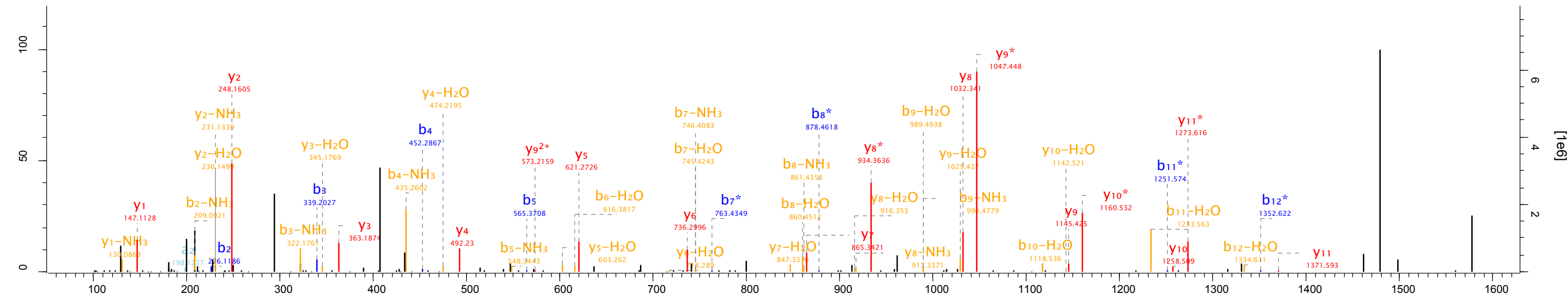
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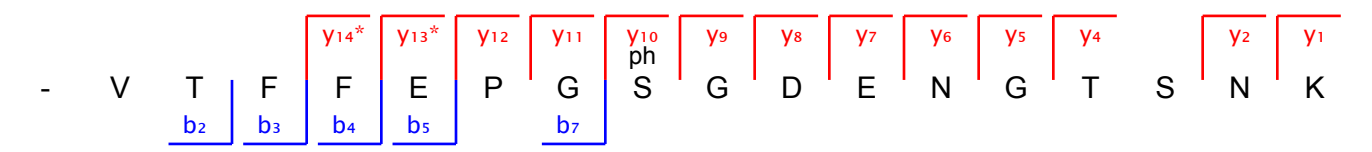
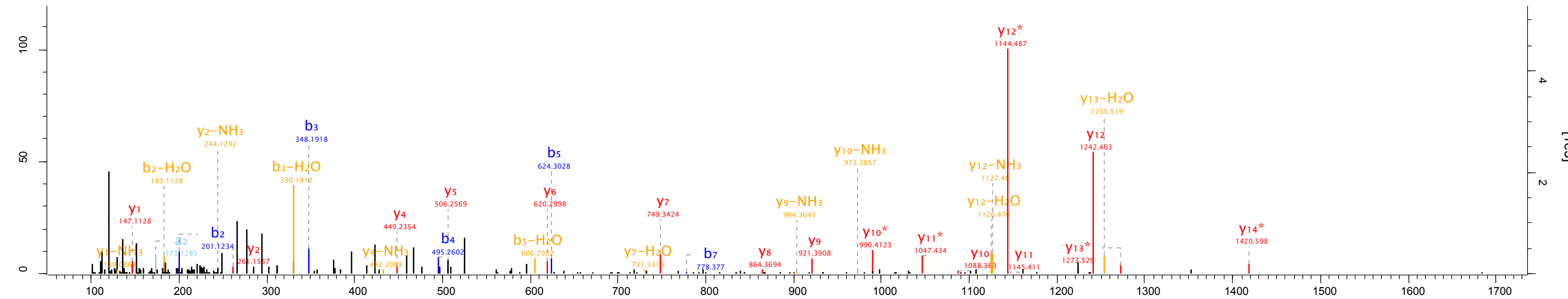
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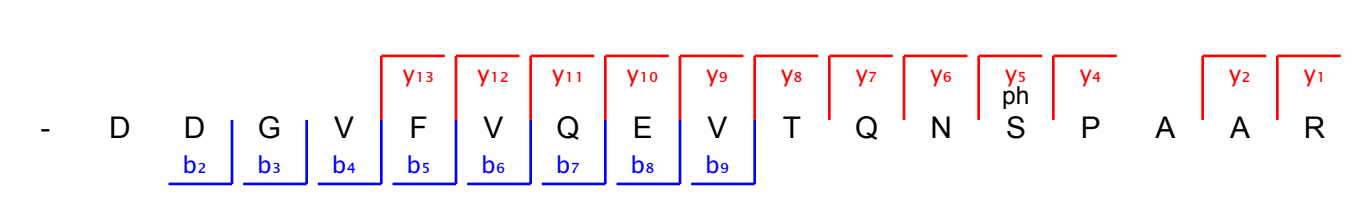
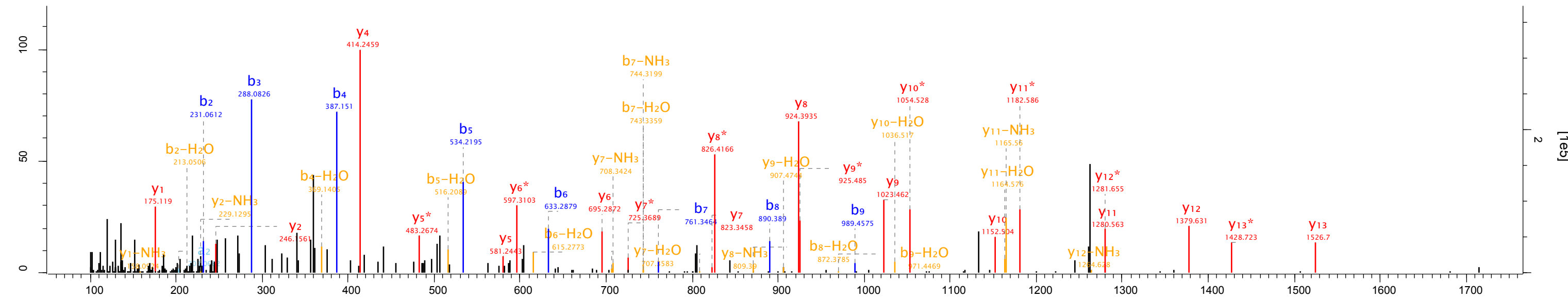
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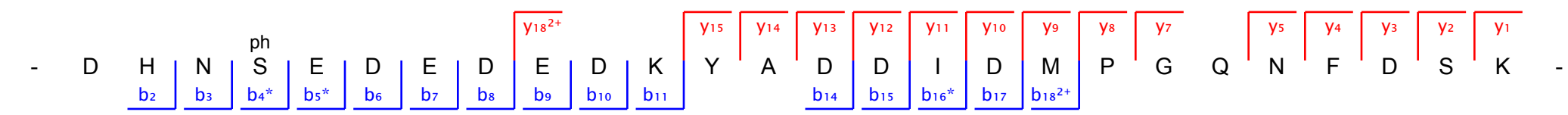
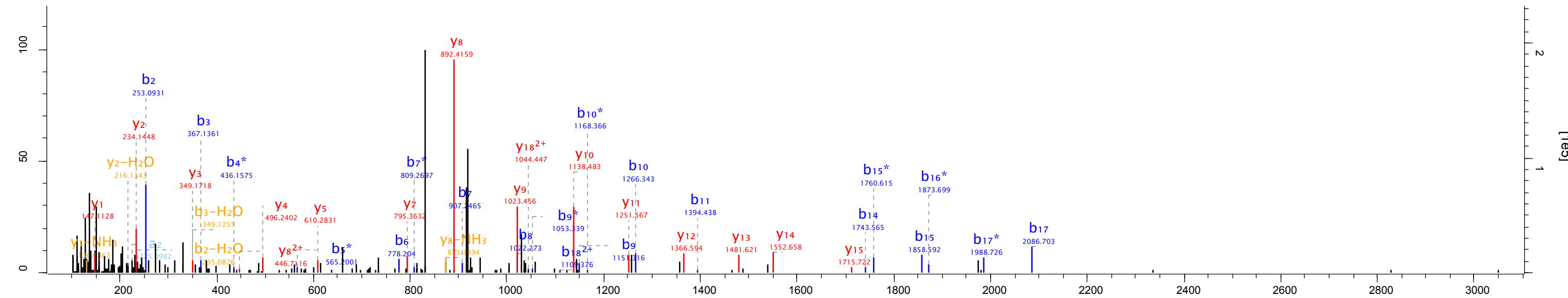
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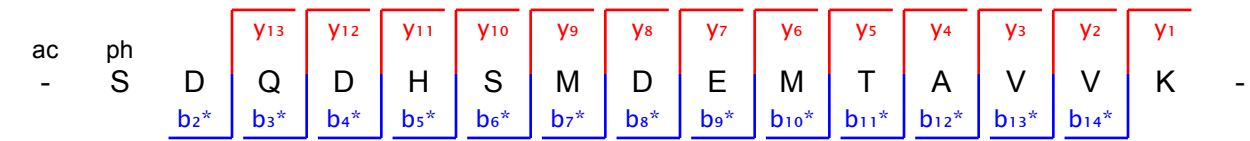
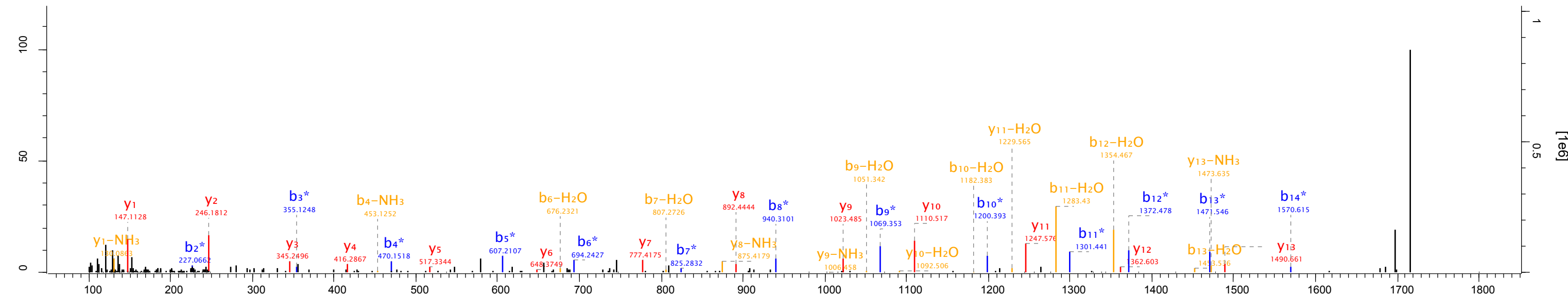
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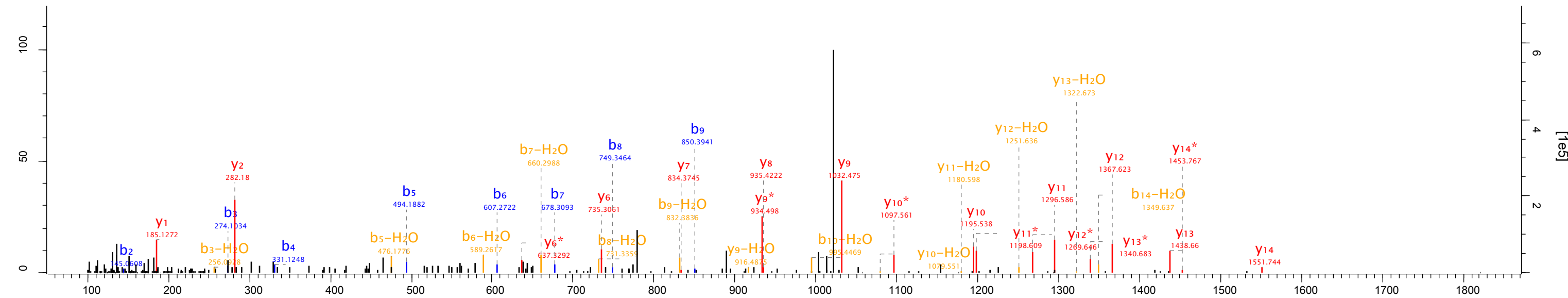


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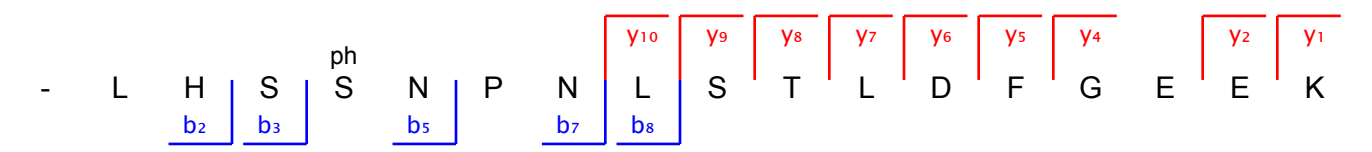
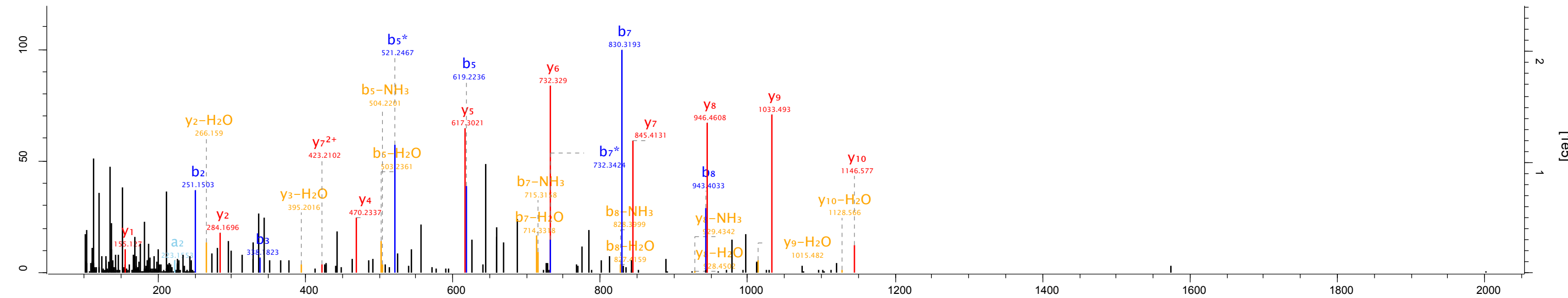




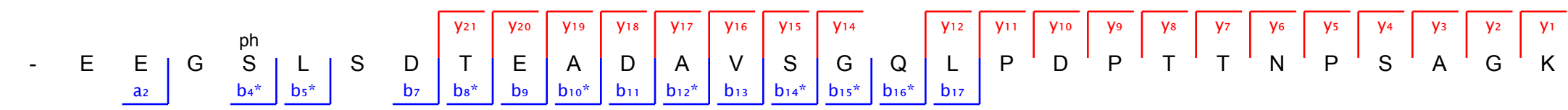
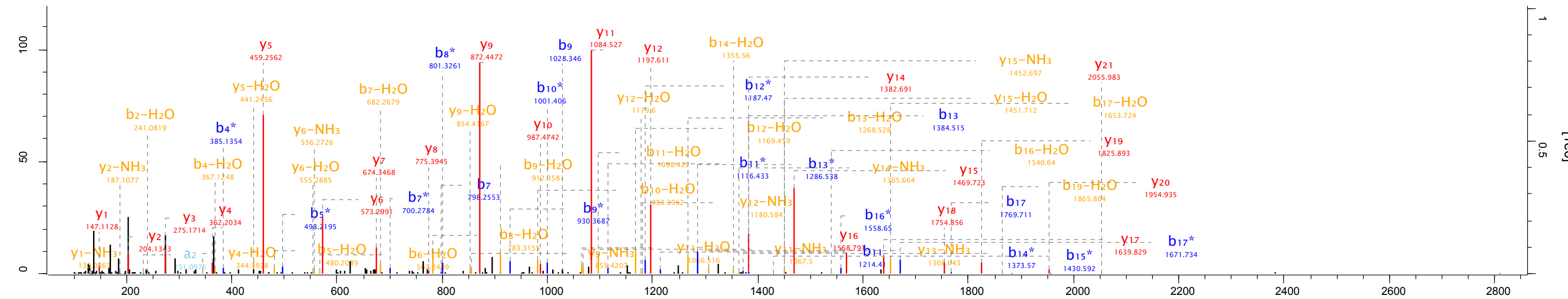
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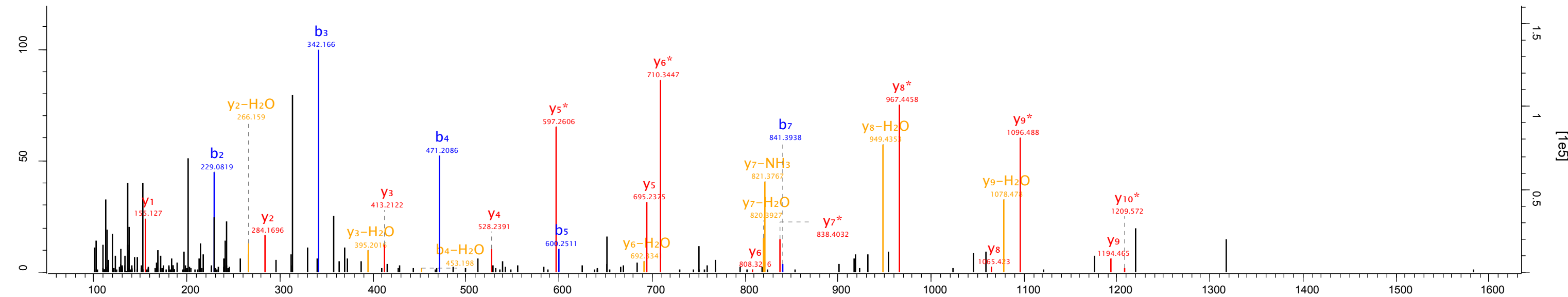
b₂
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b₈
b₉
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₂
y₁

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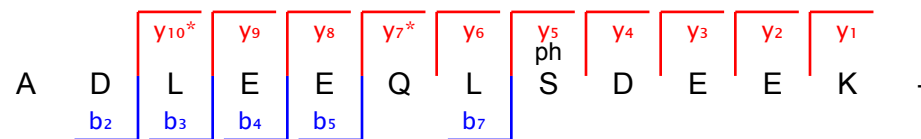
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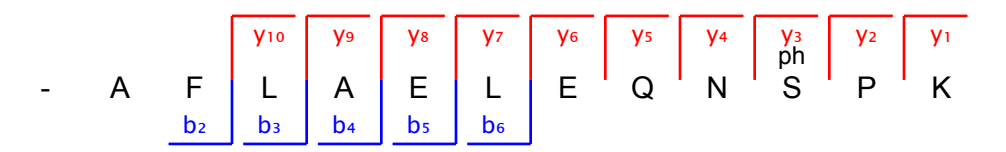
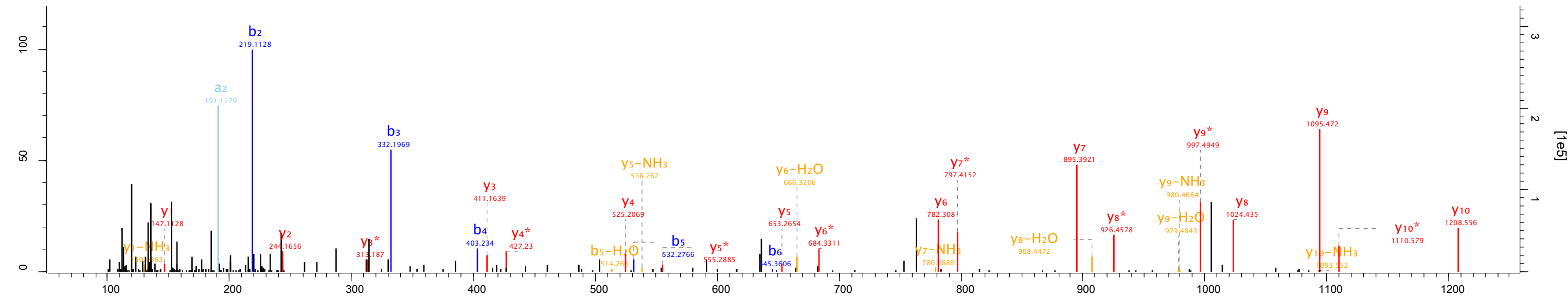
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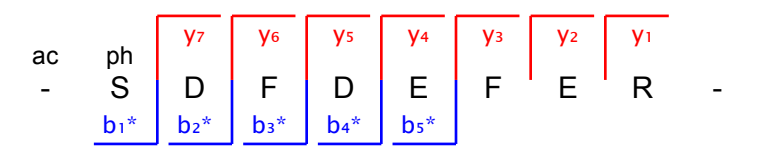
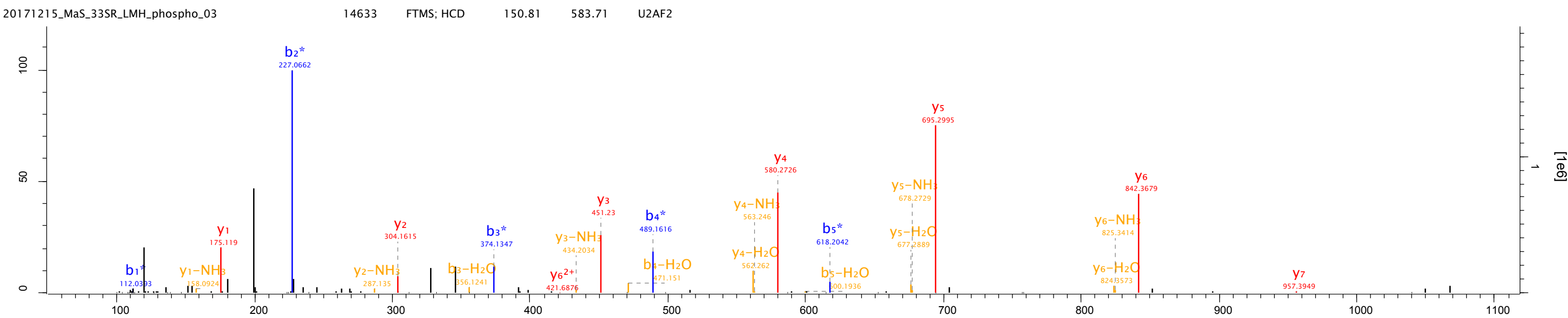


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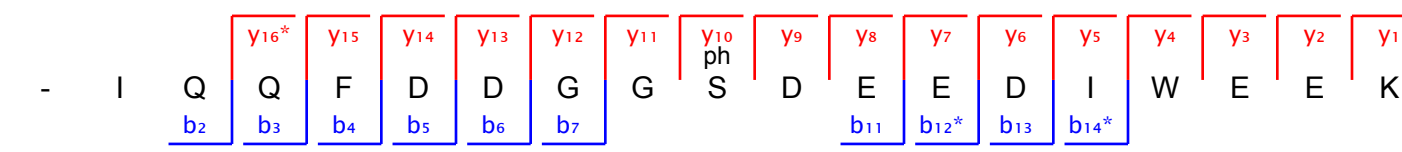
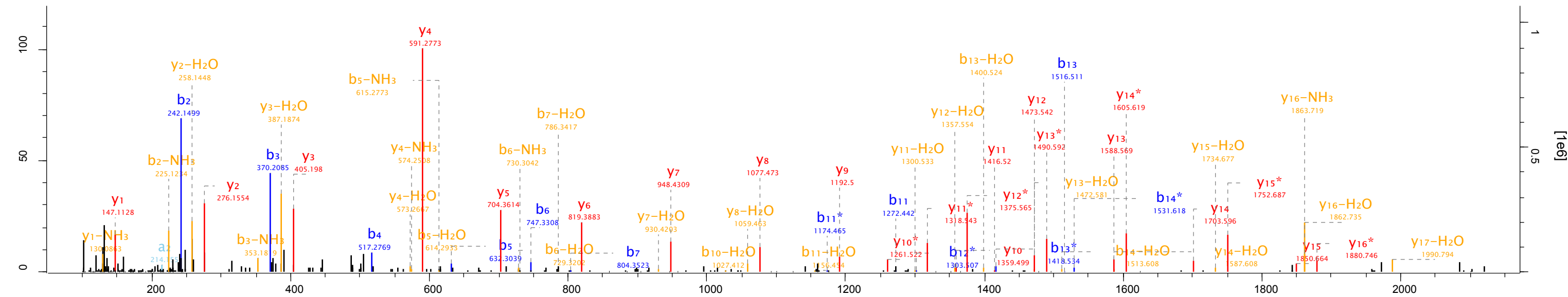
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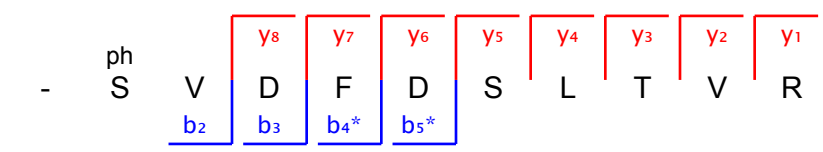
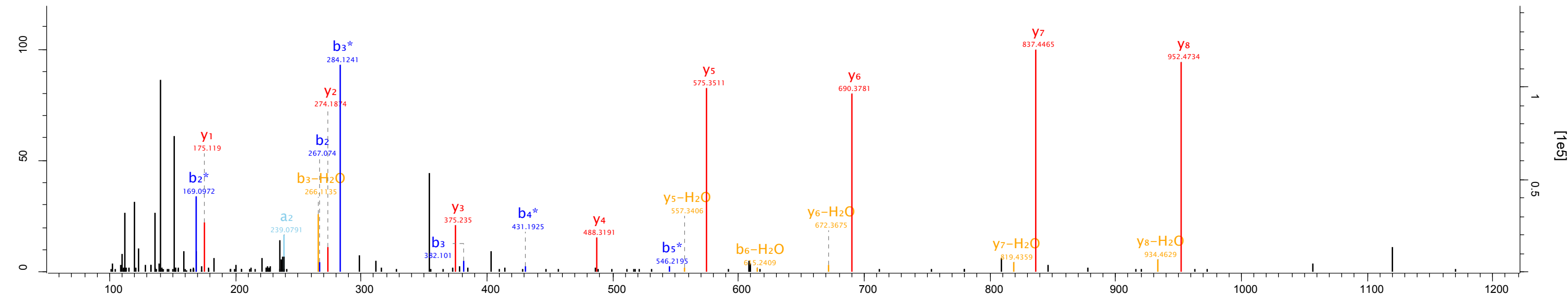
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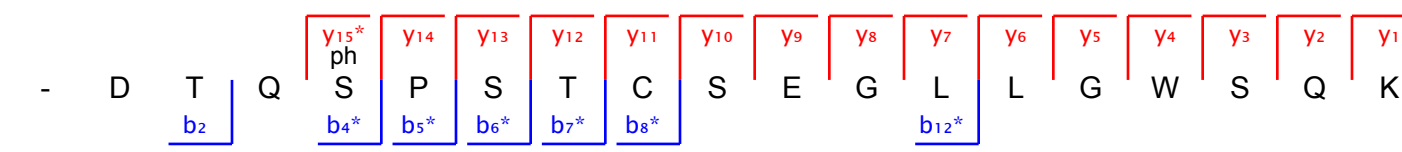
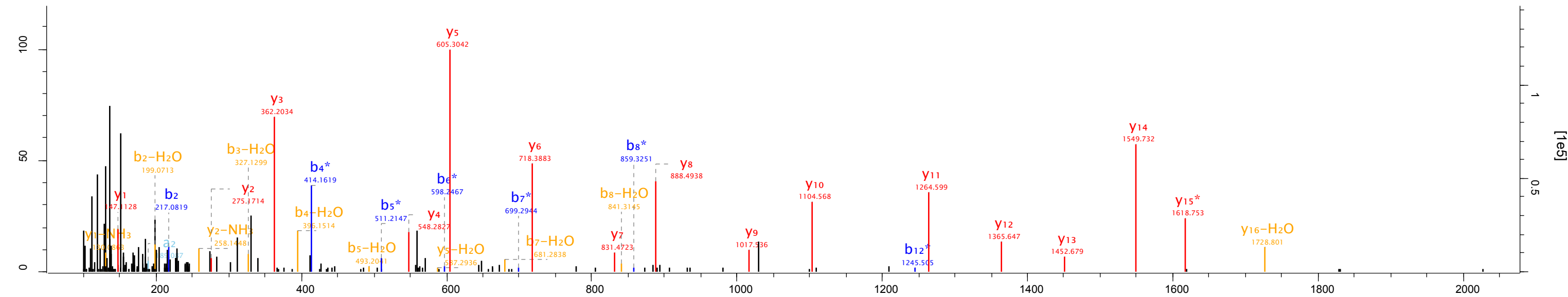
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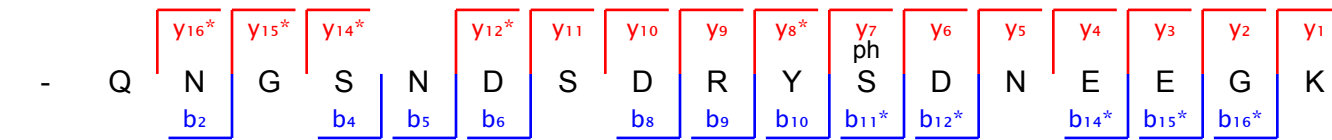
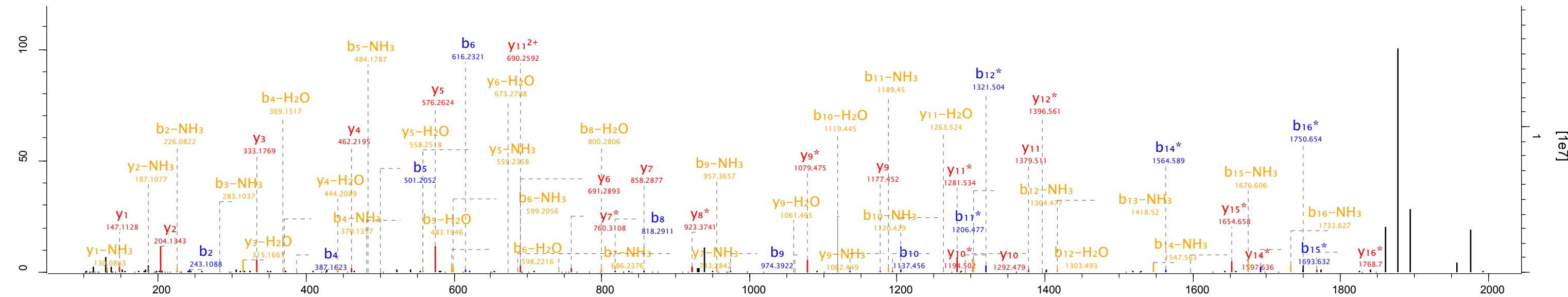


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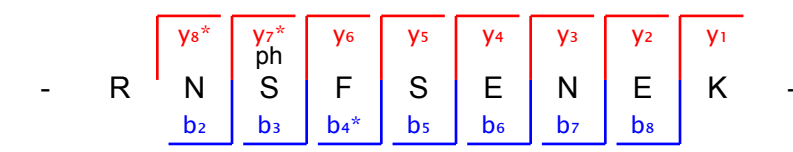
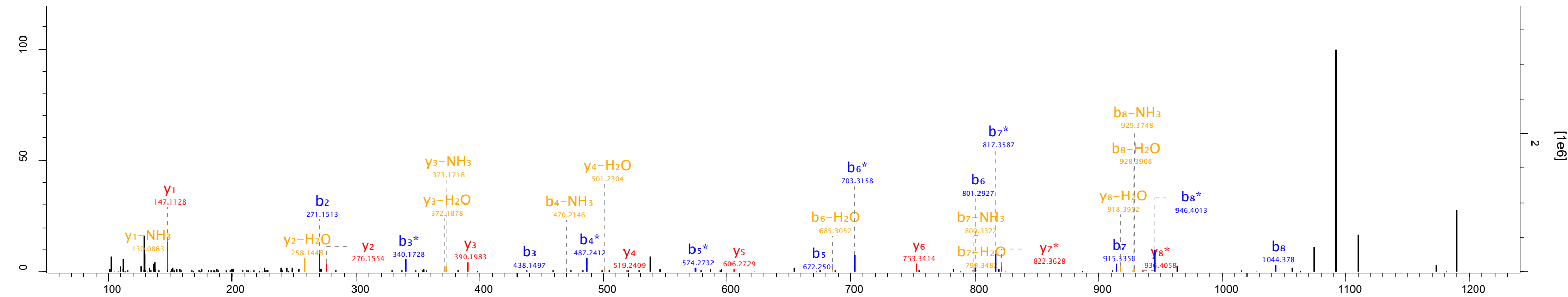


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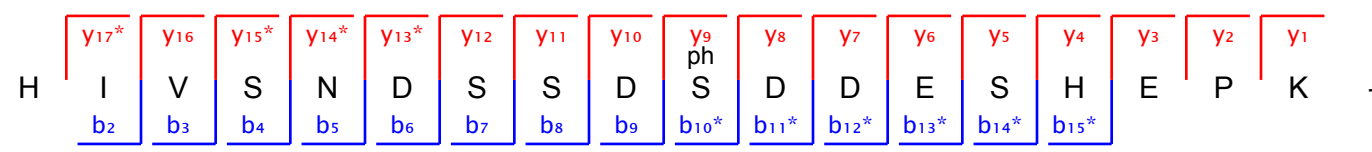
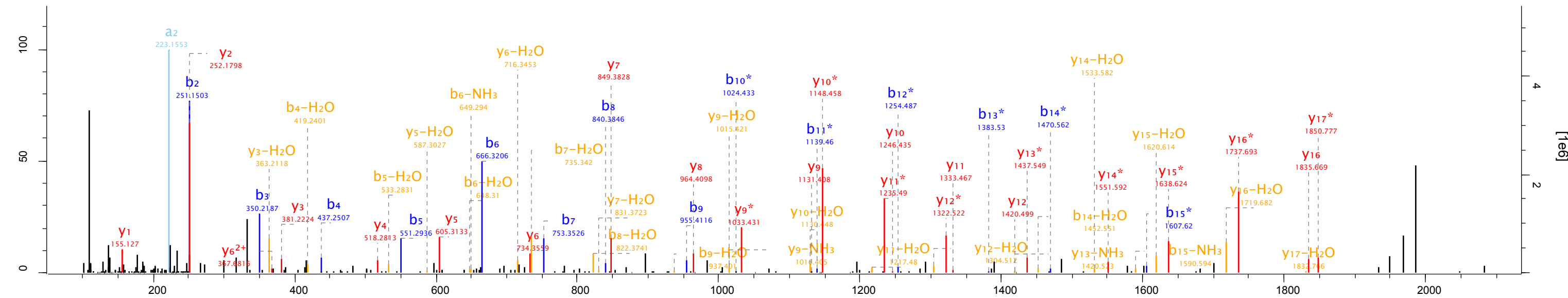




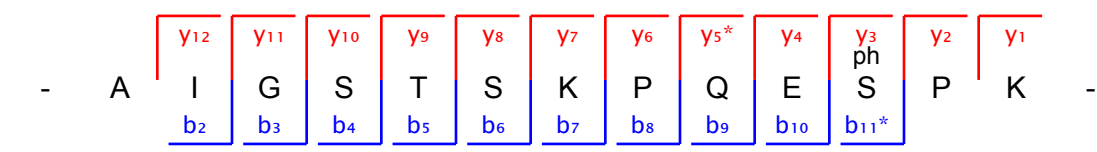
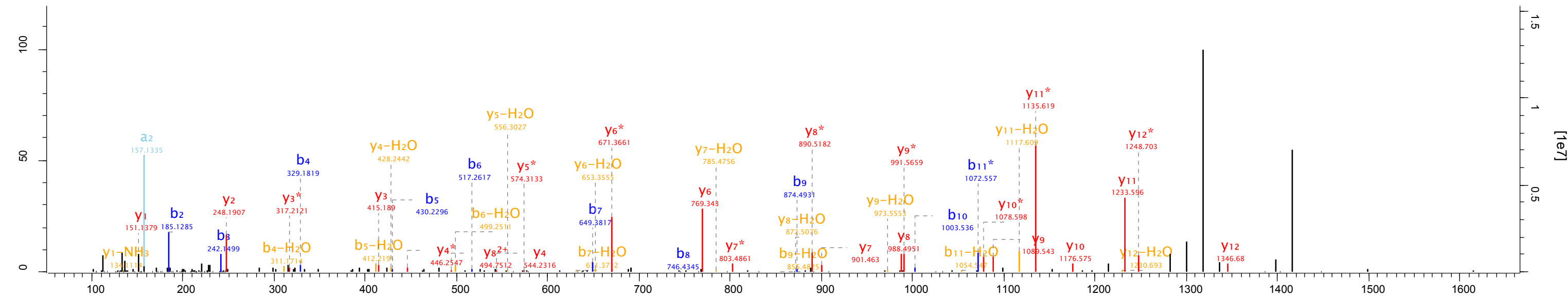
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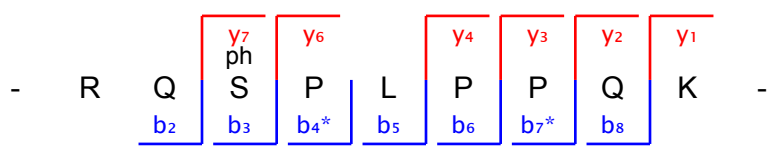
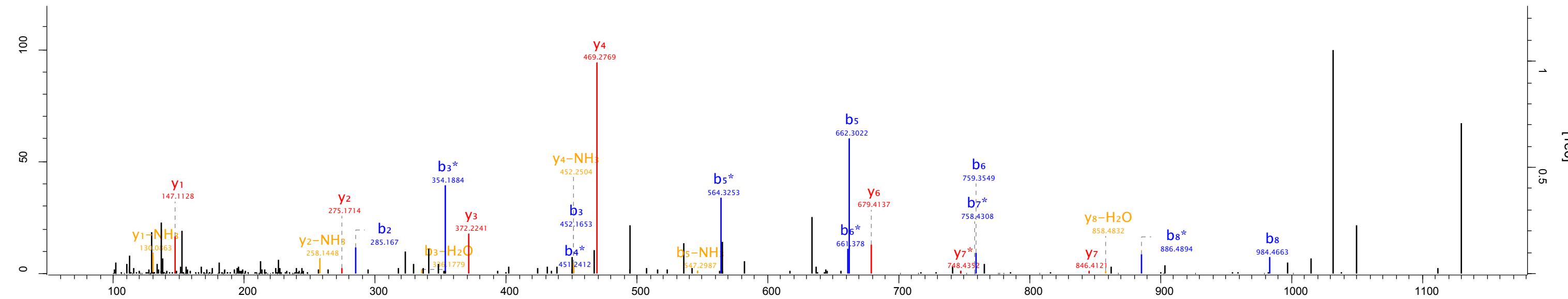
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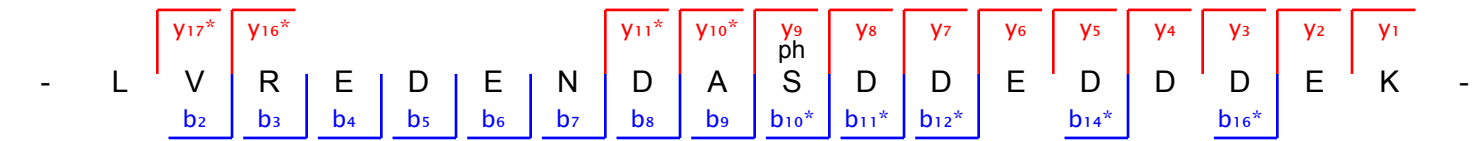
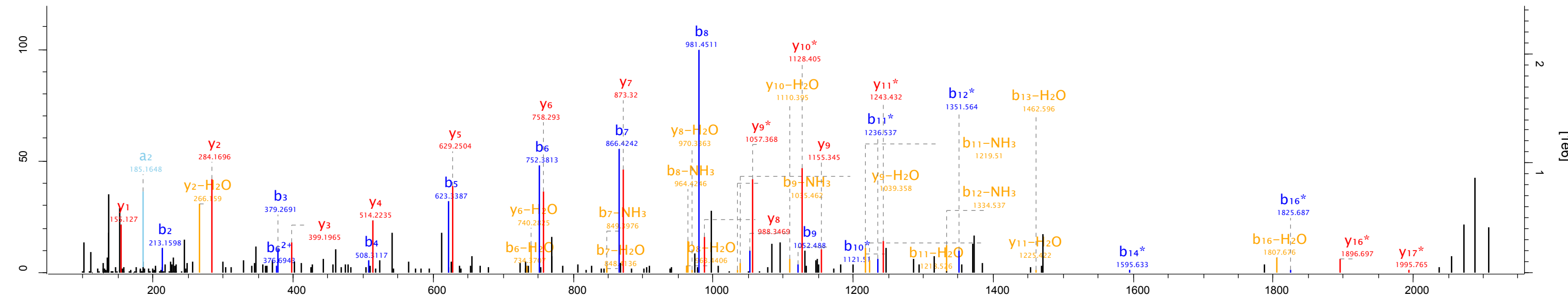


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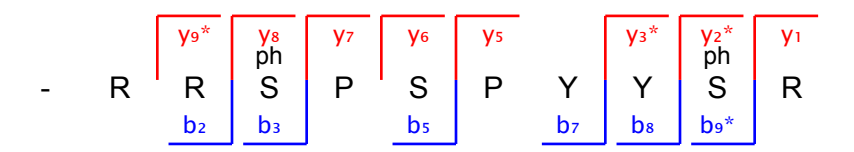
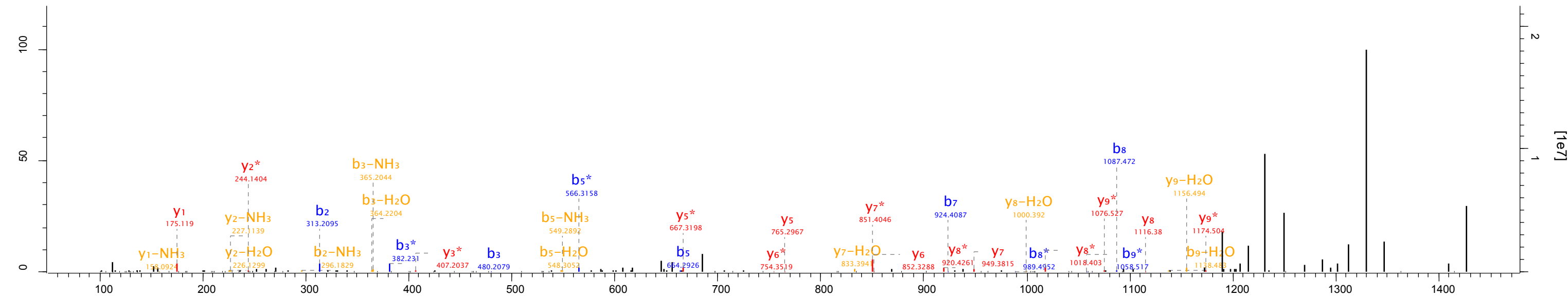


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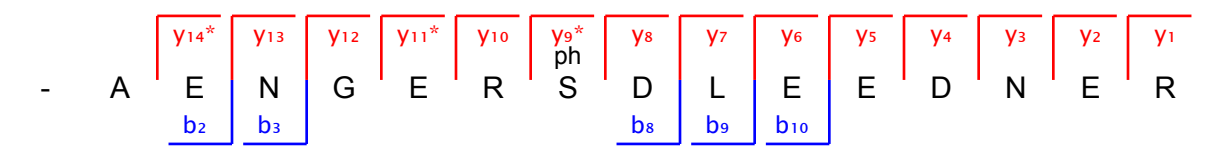
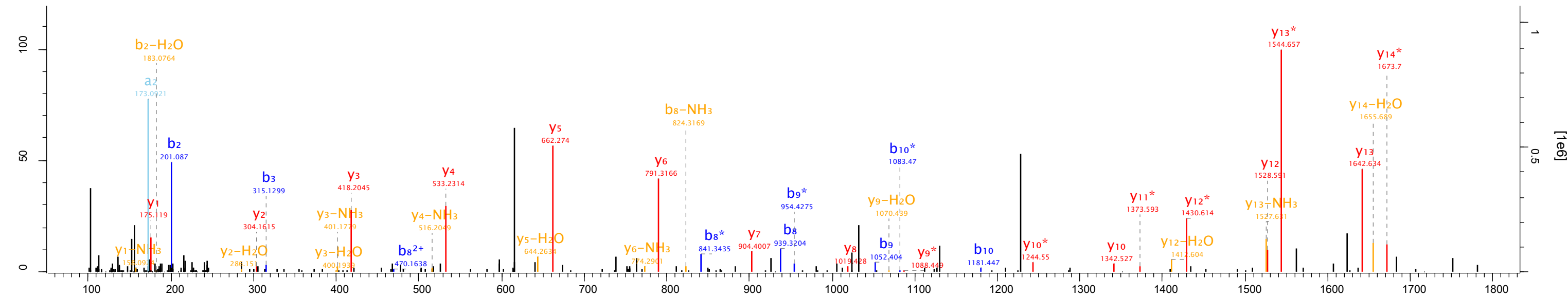




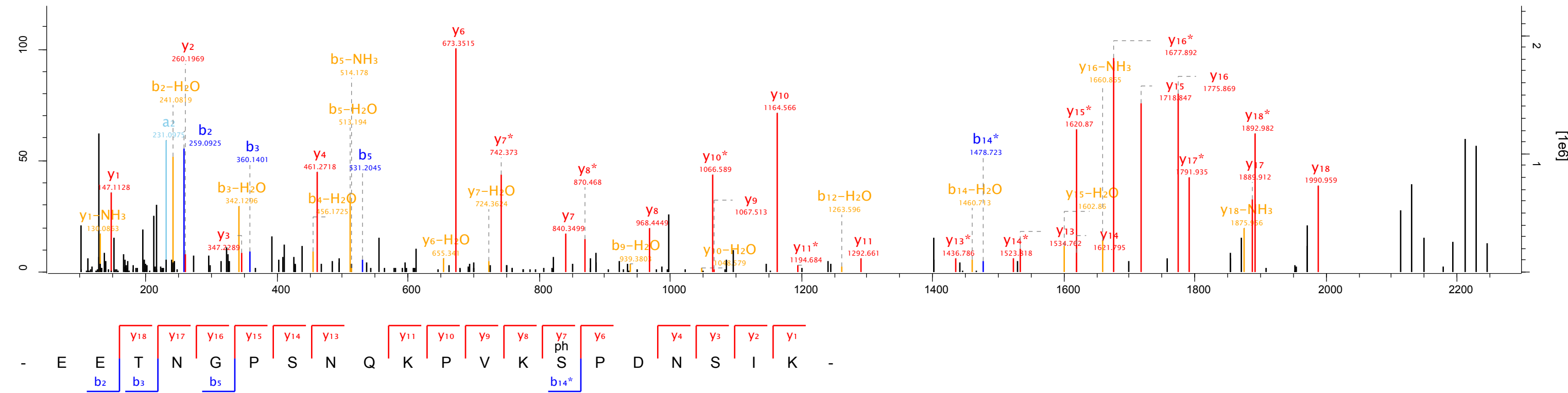
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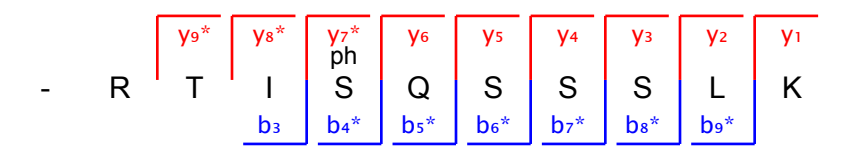
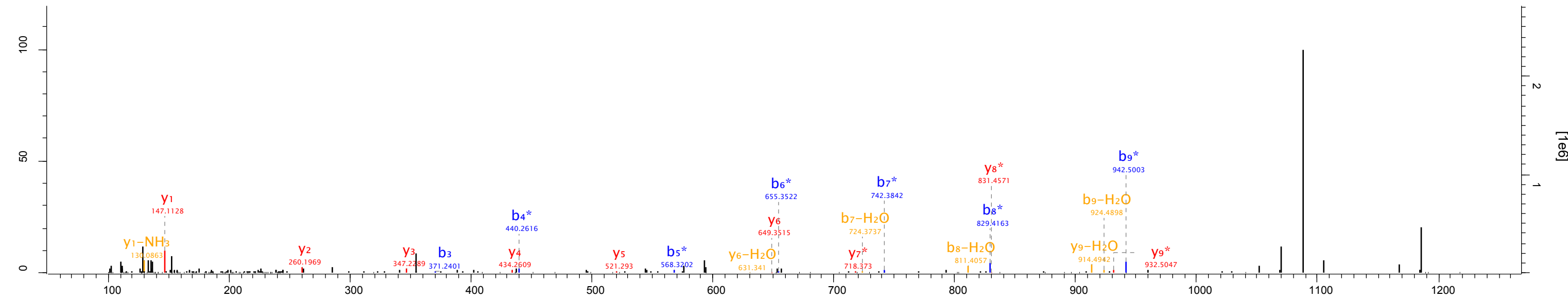
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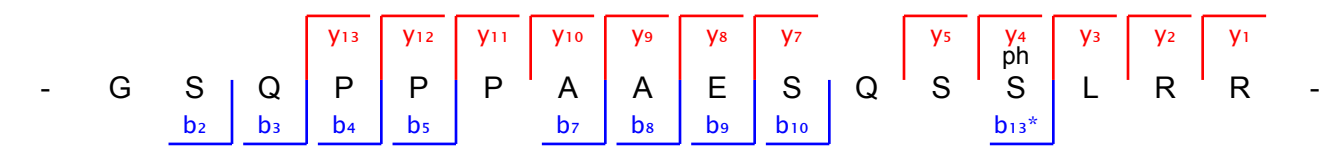
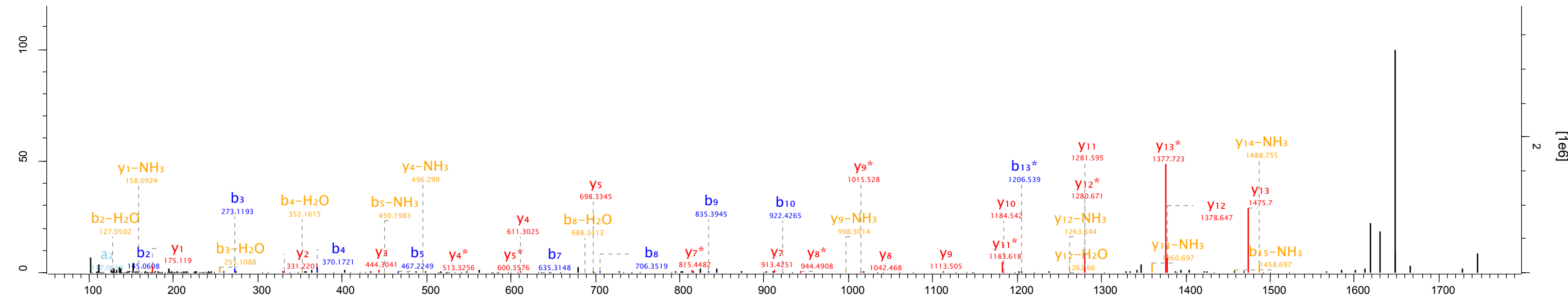
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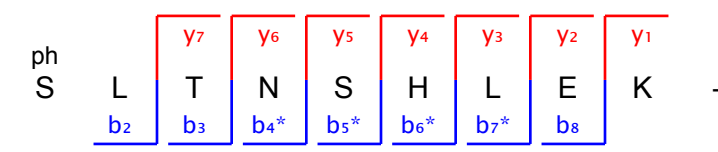
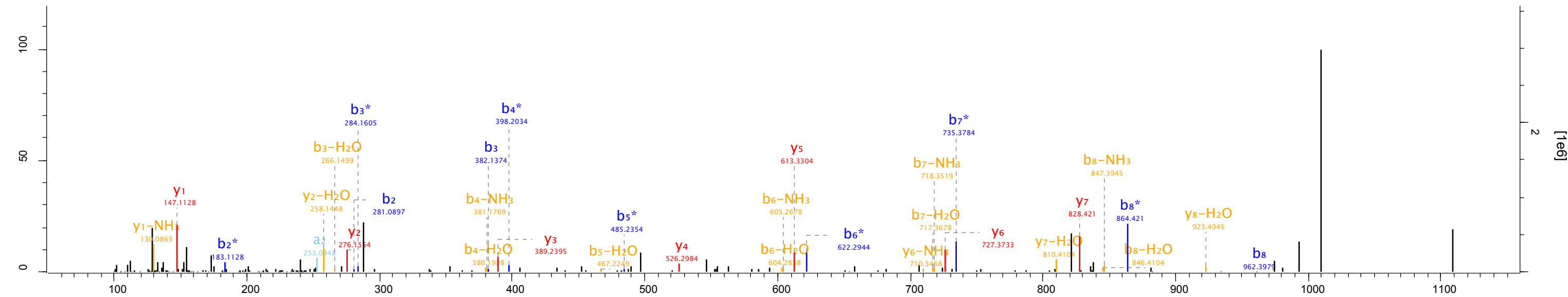
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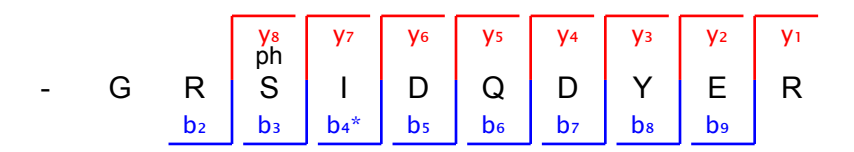
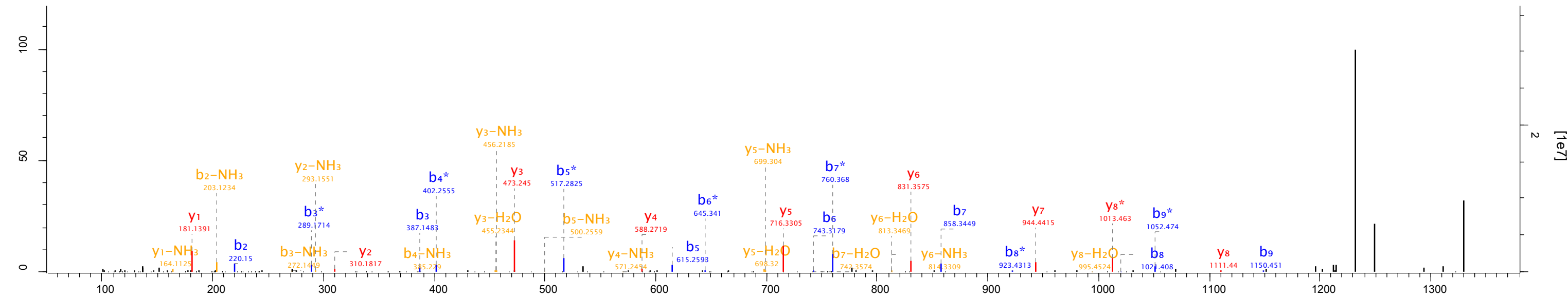
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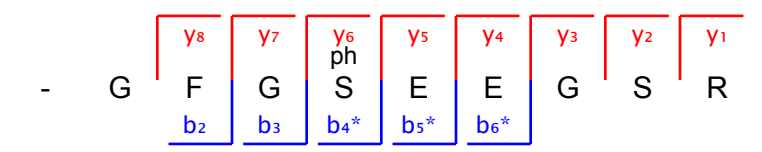
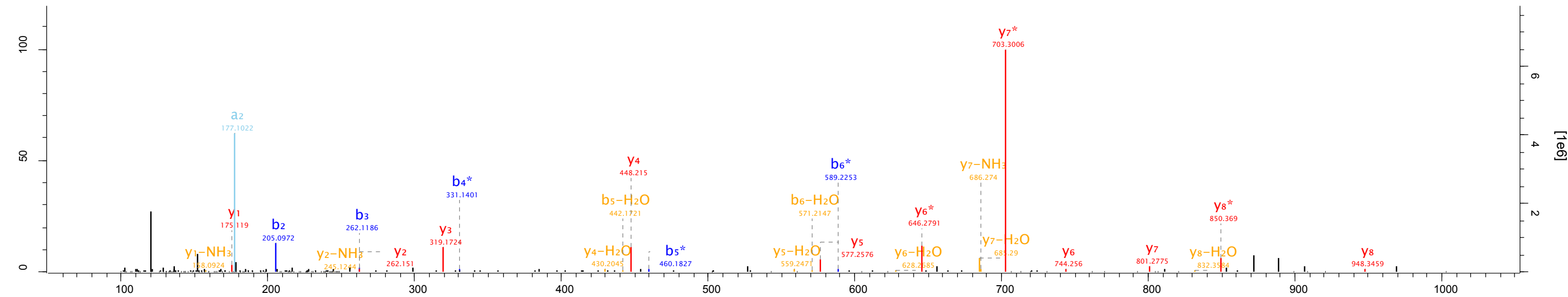
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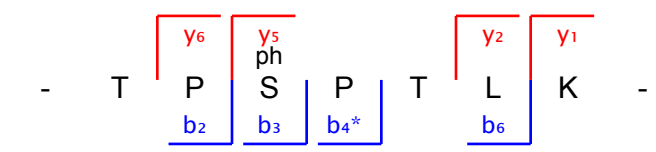
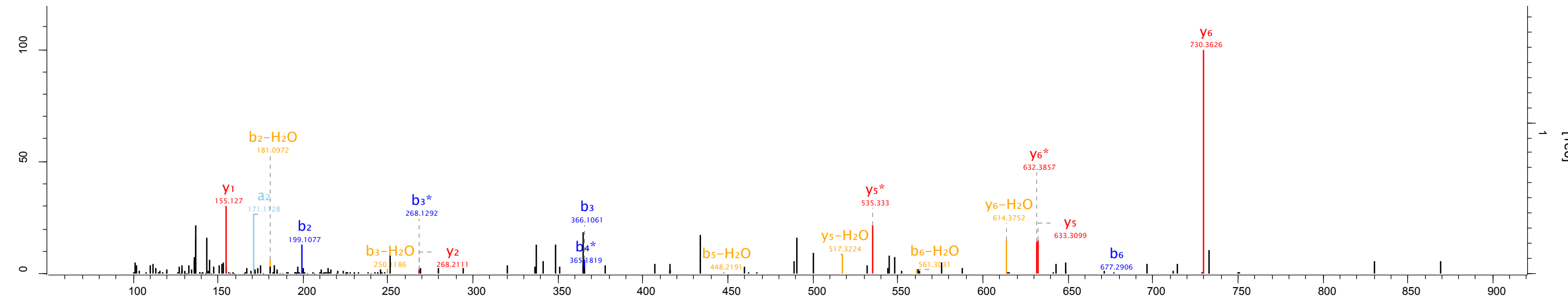
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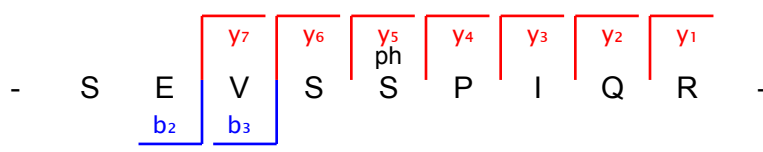
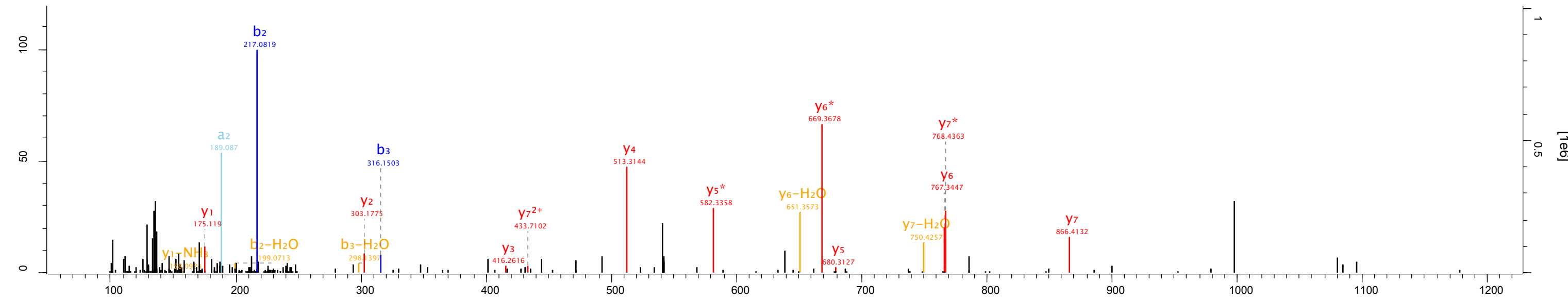
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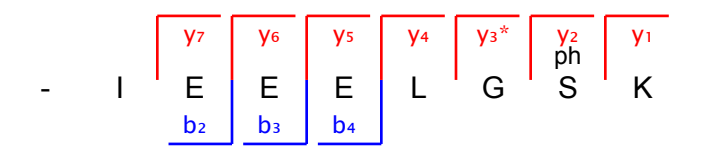
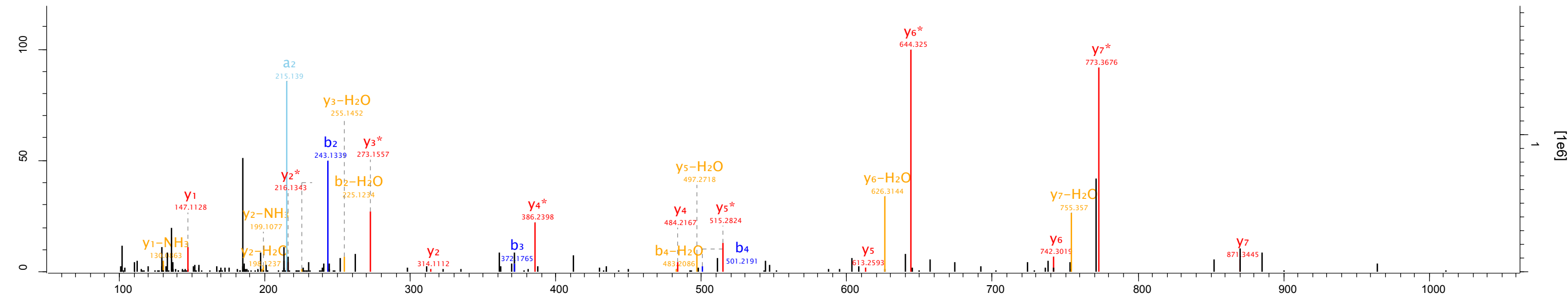
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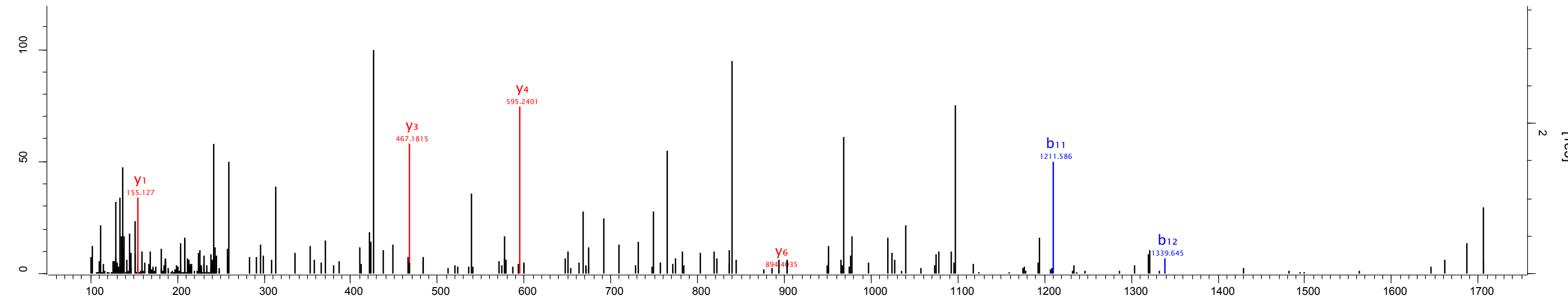
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Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 4653 Method FTMS; HCD Score 106.67 m/z 492.72 Gene names ENO1



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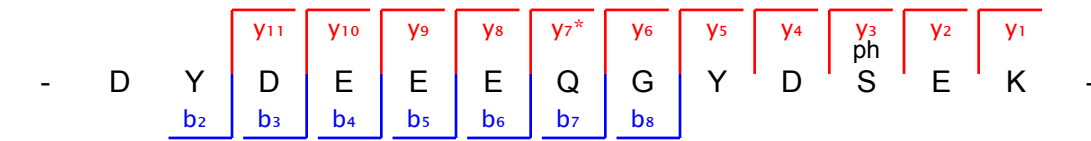
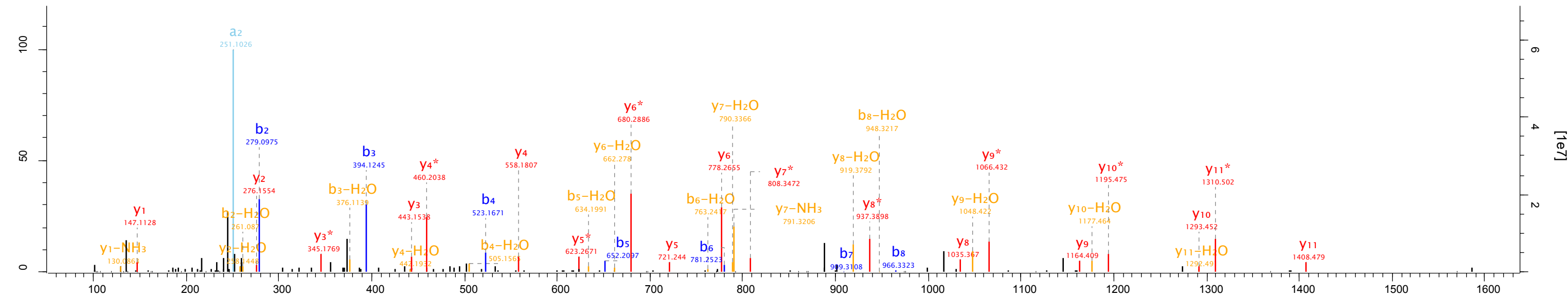


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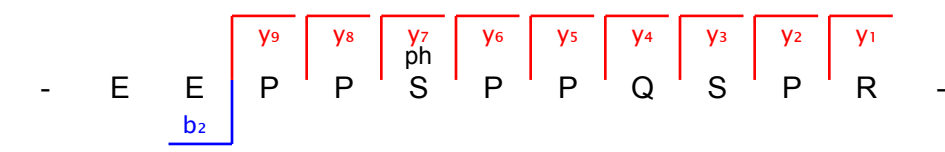
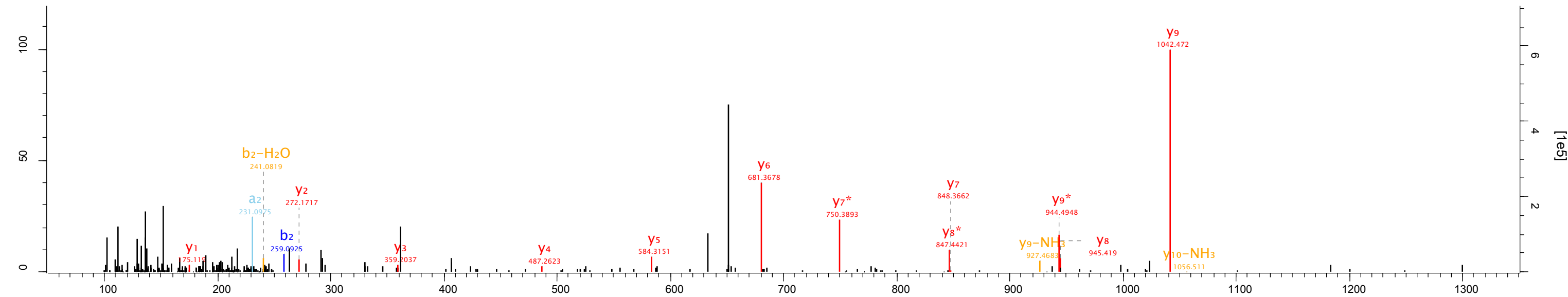
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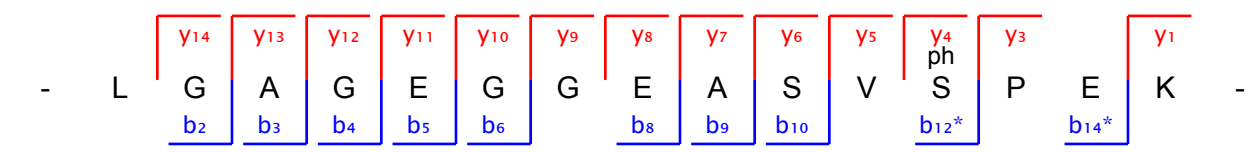
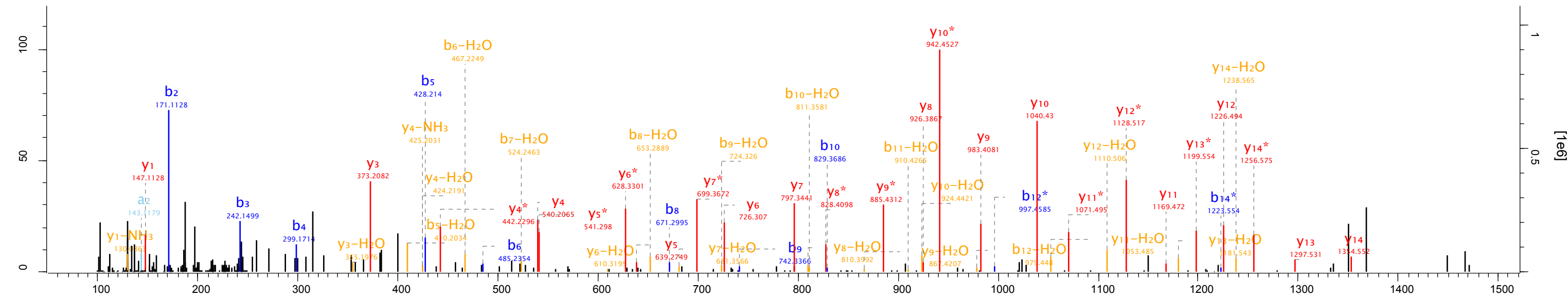
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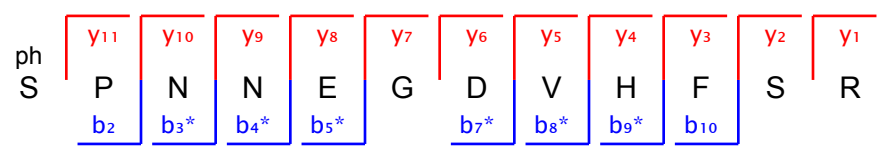
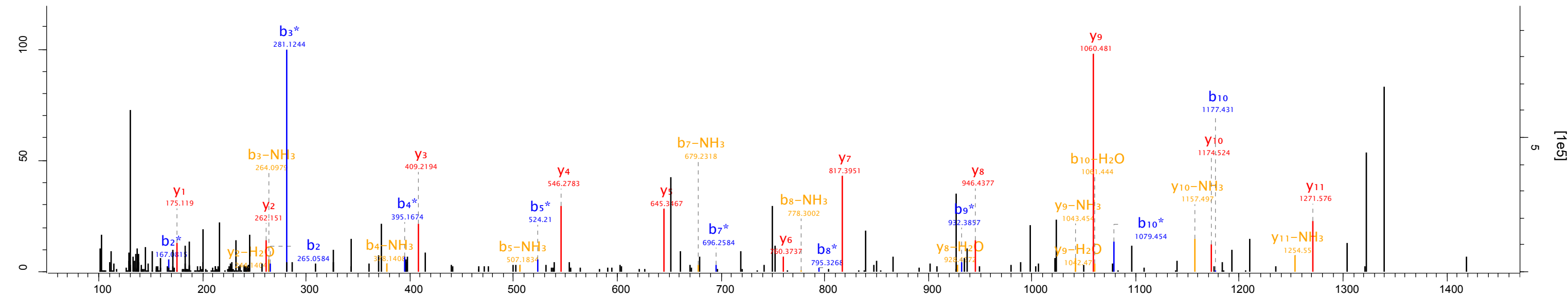
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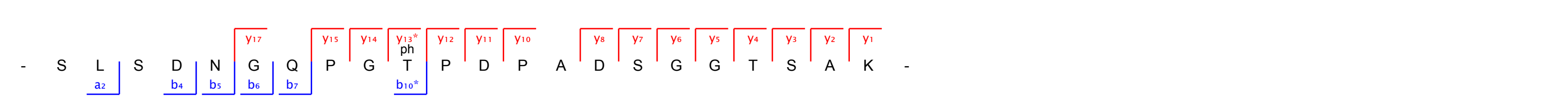
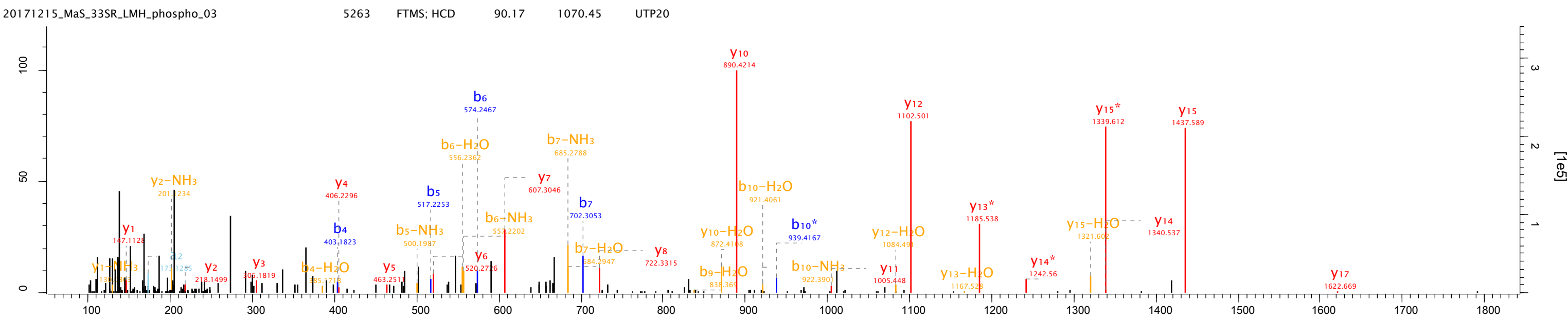
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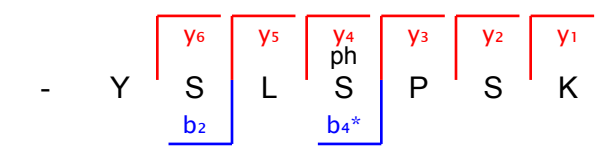
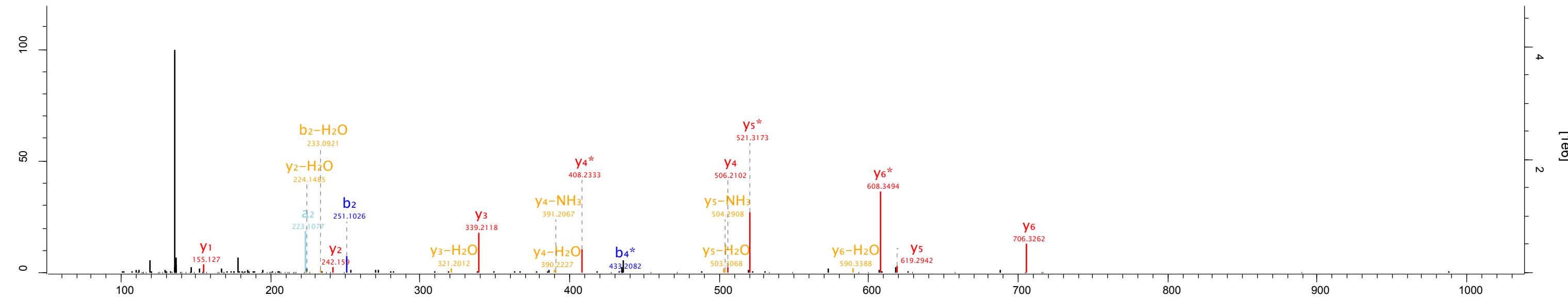
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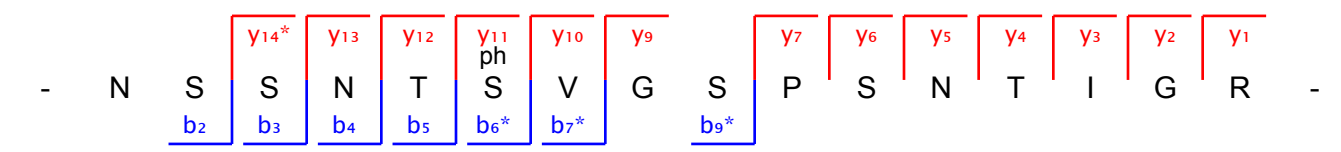
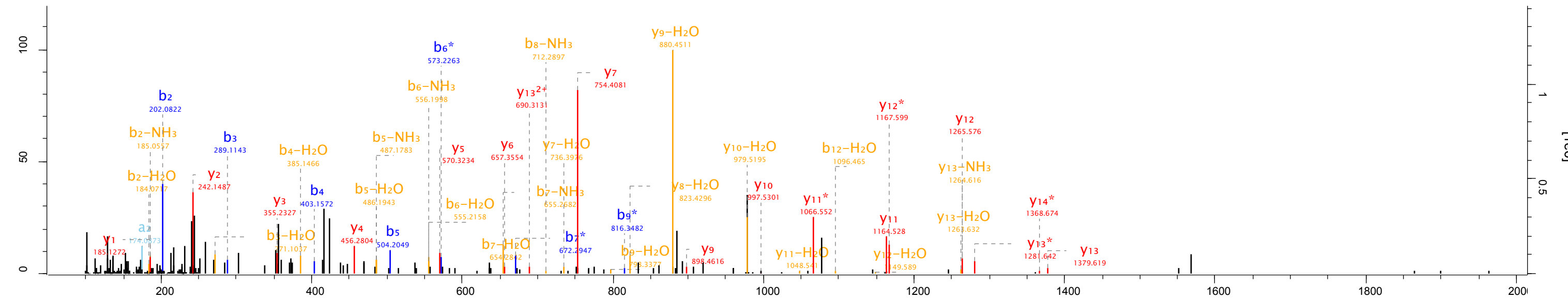
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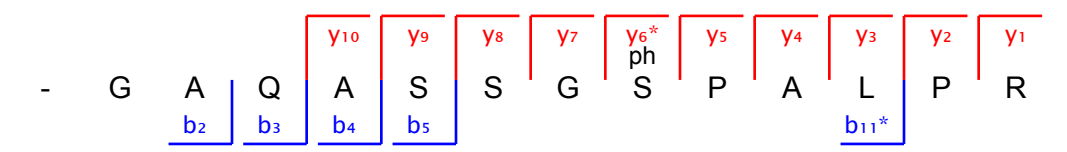
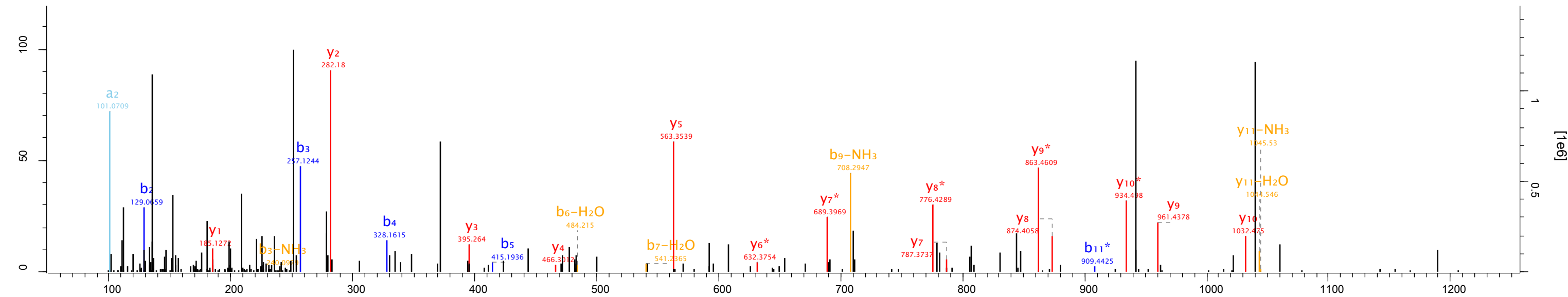
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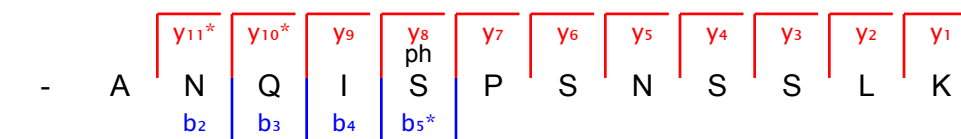
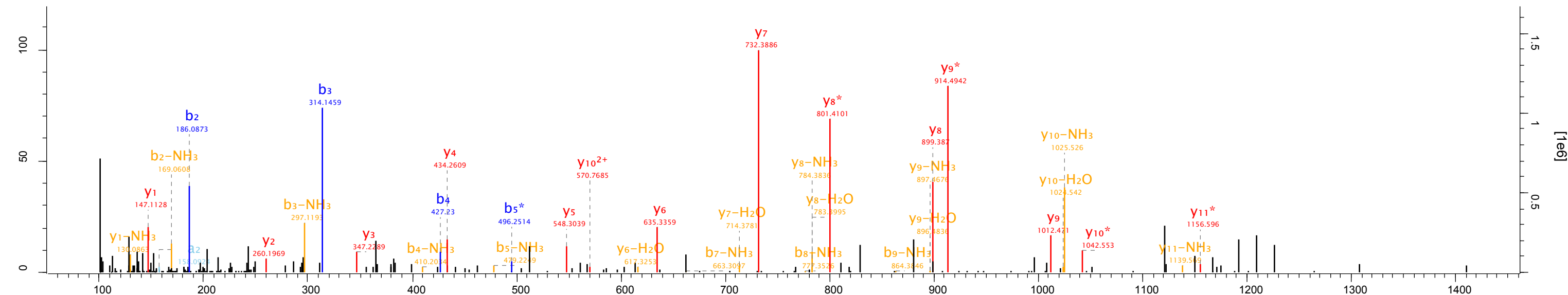


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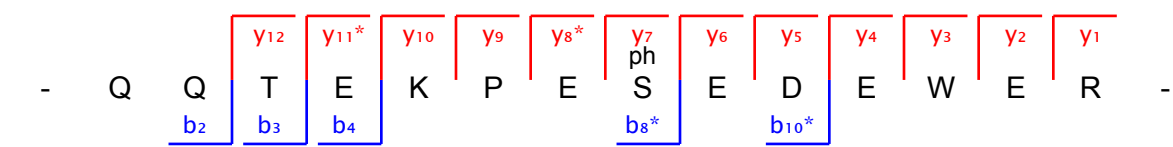
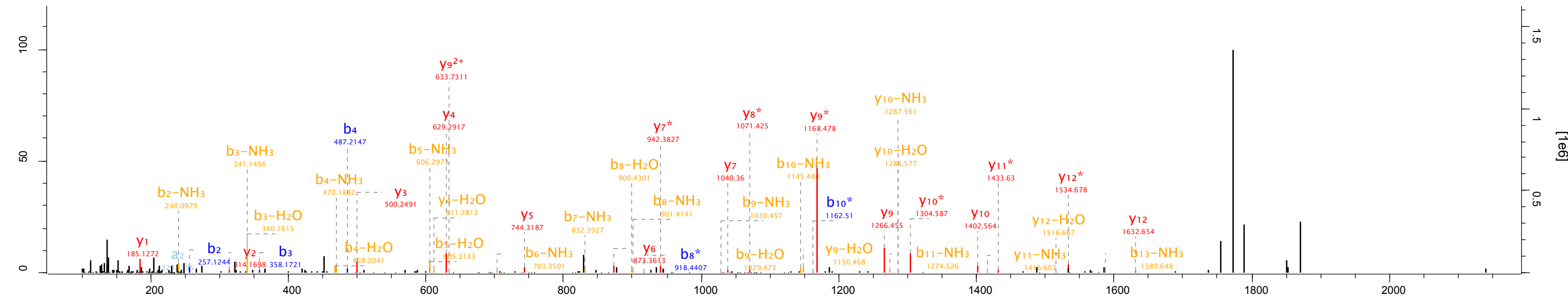


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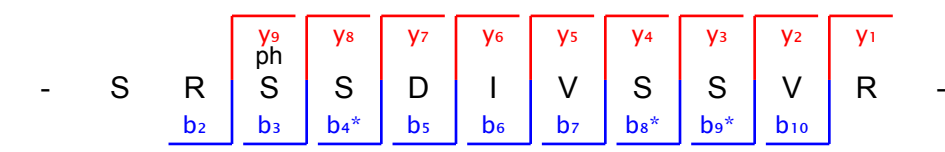
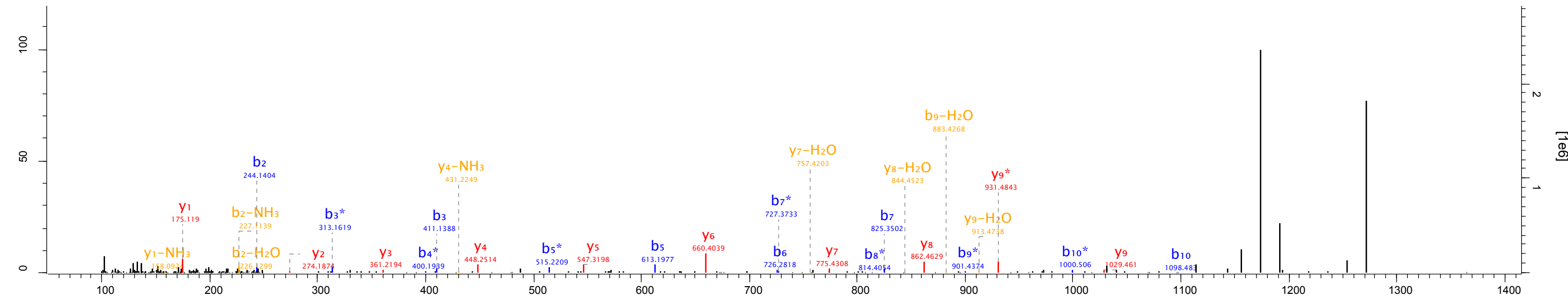




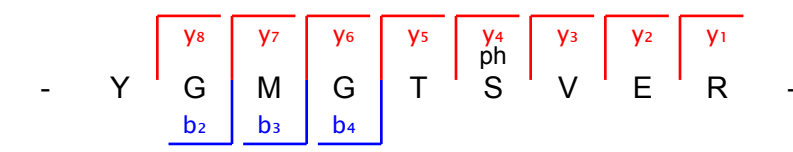
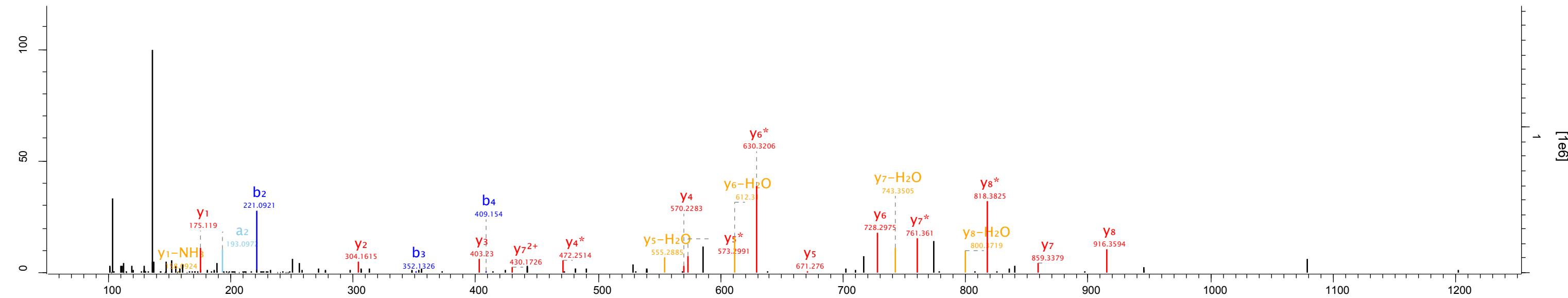
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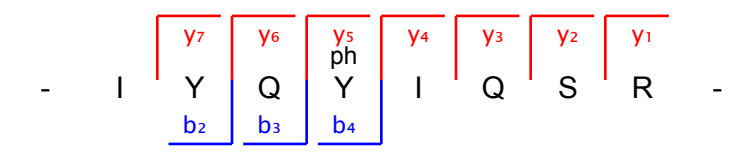
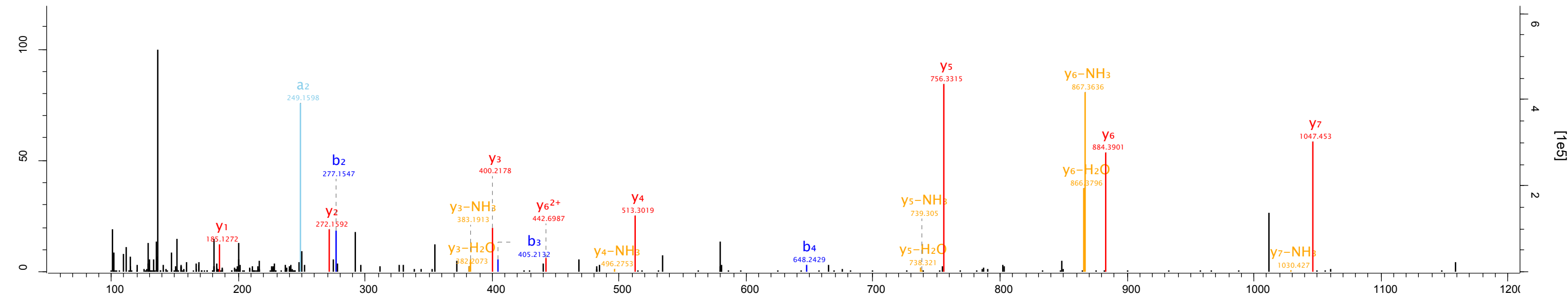
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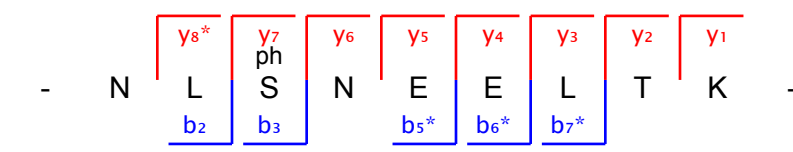
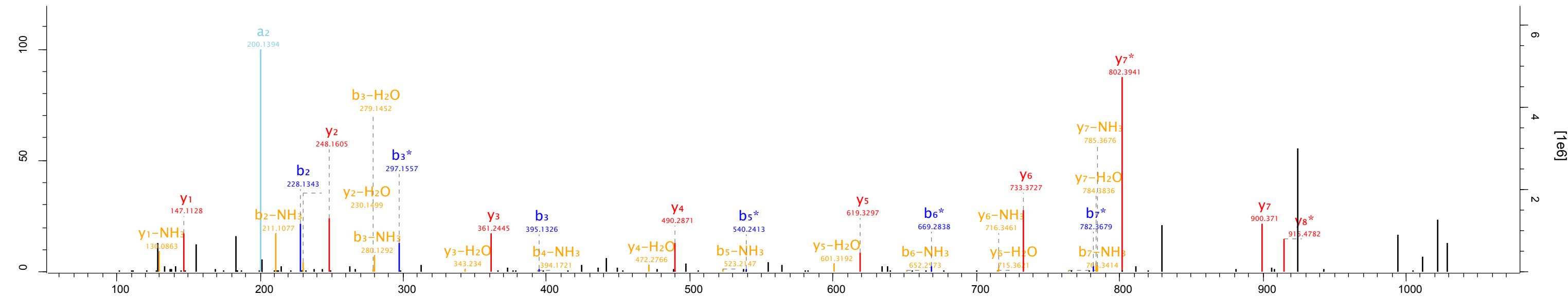
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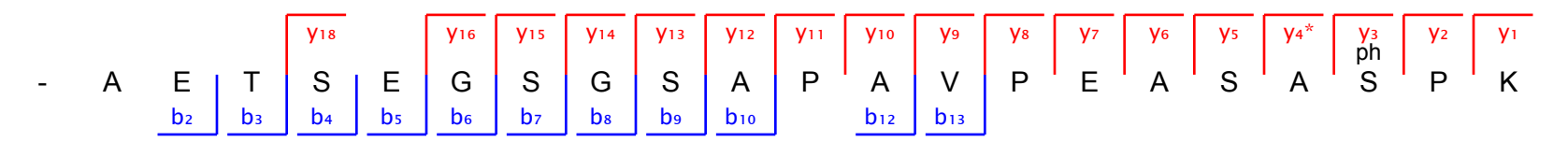
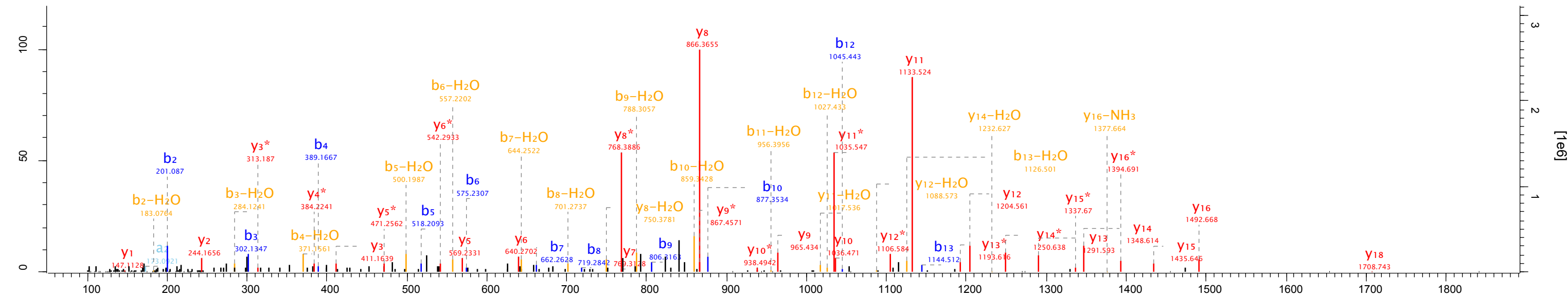
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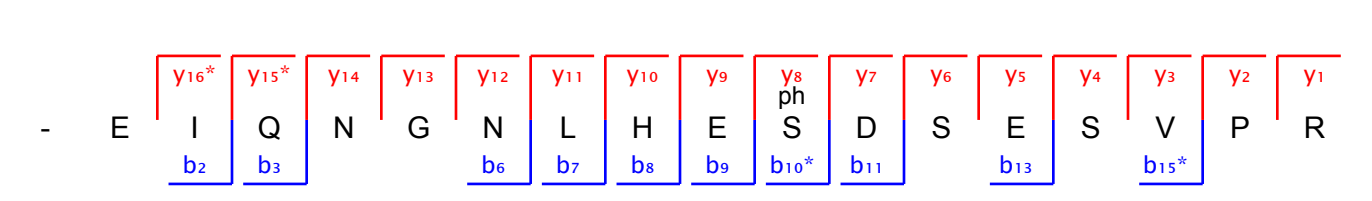
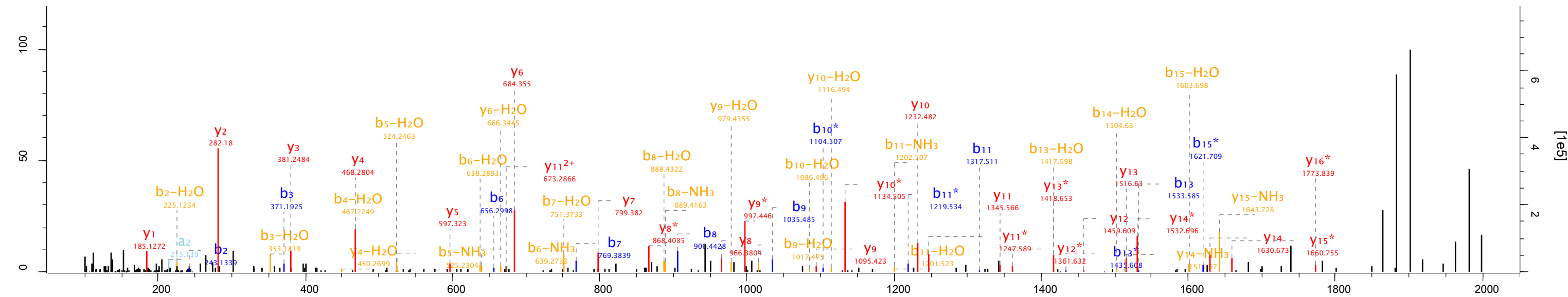
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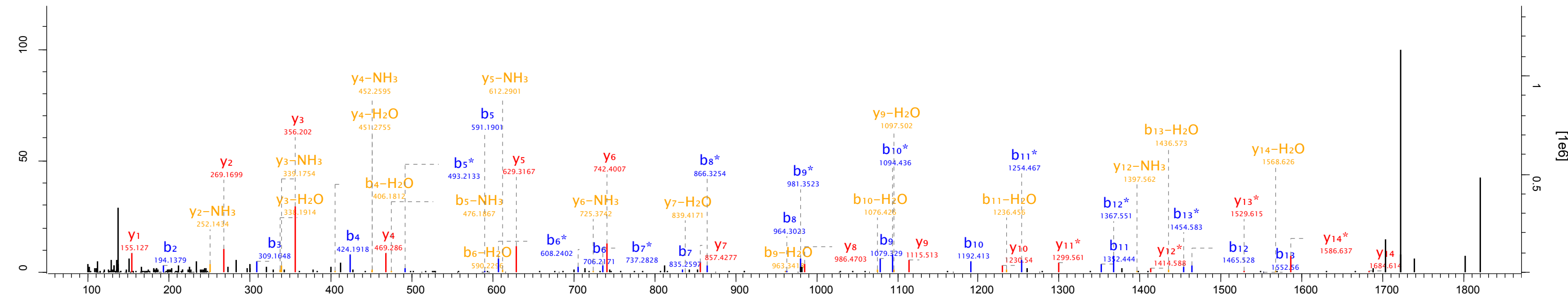
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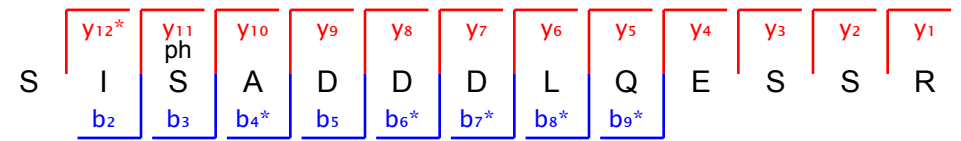
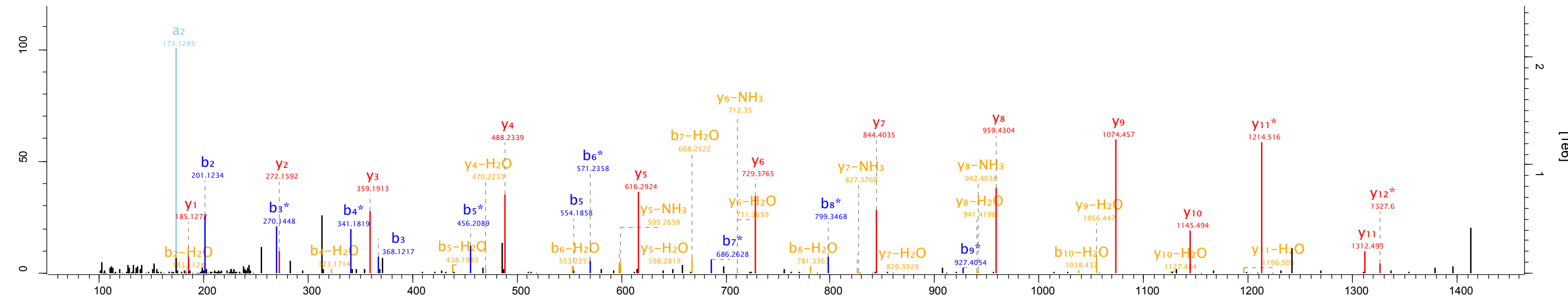


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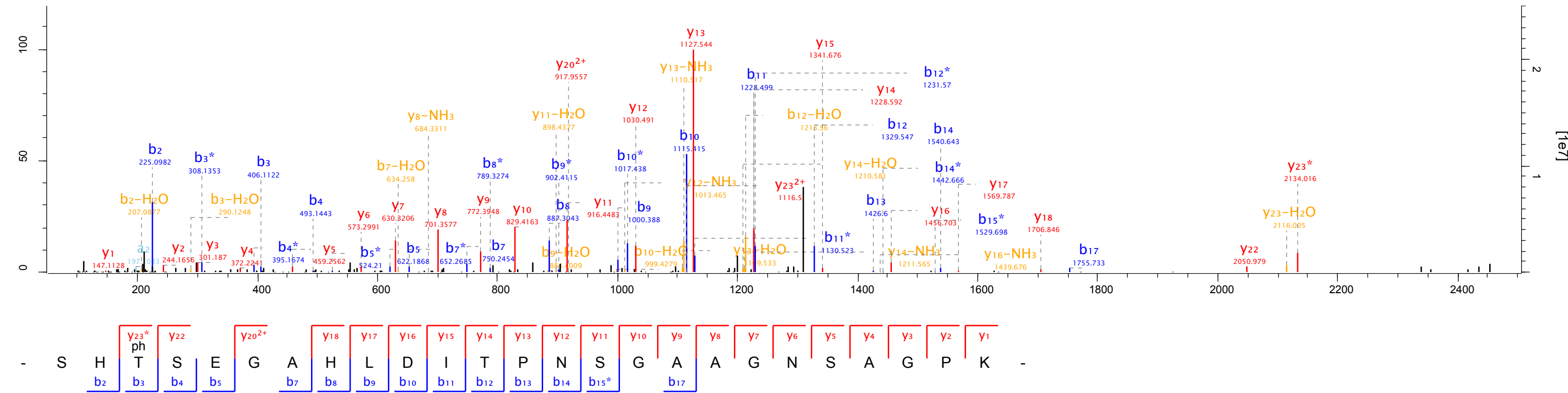
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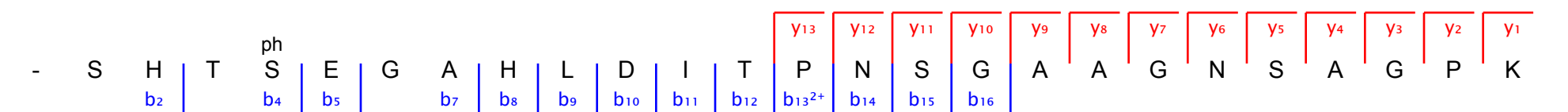
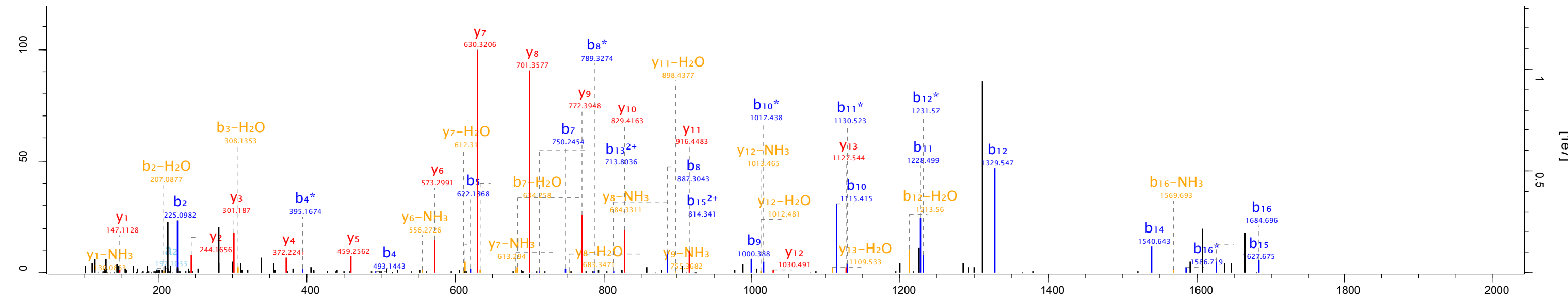
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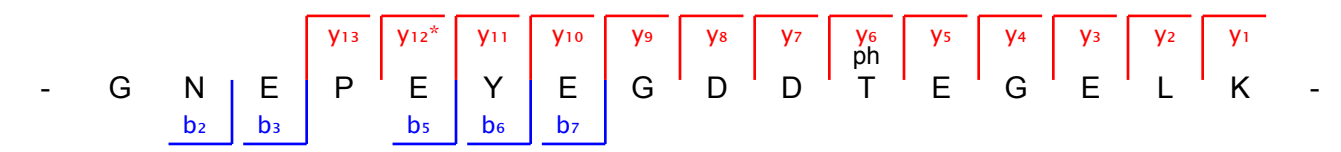
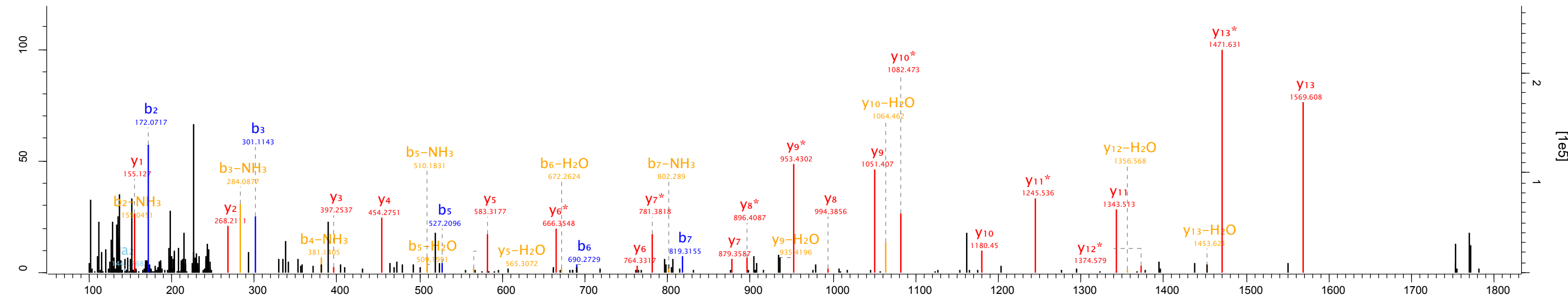


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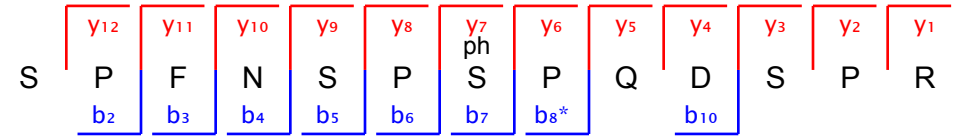
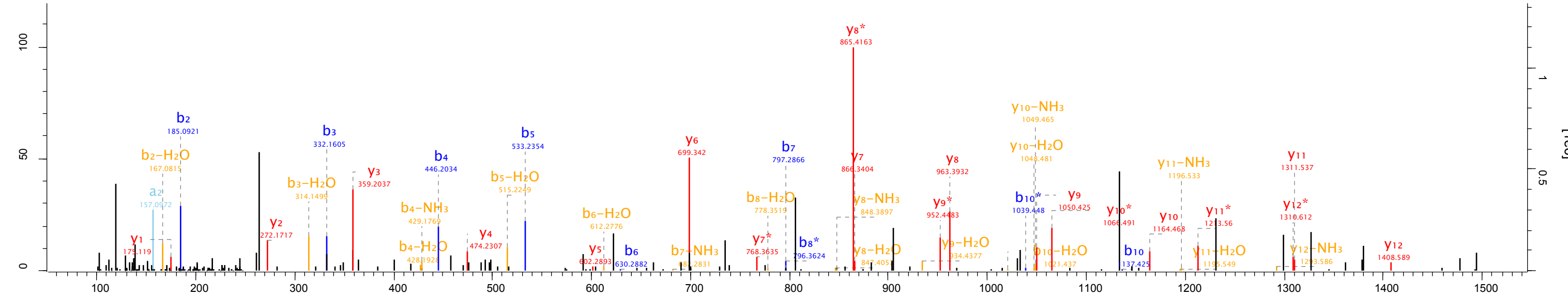


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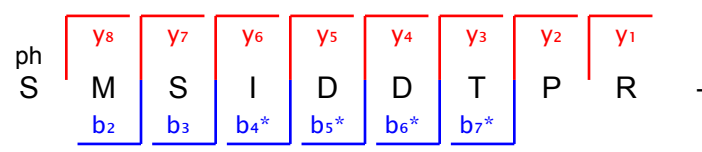
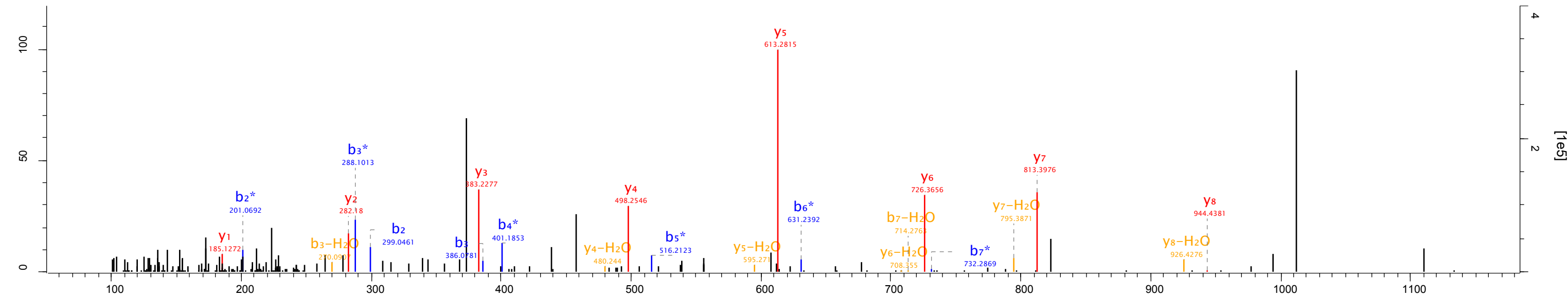


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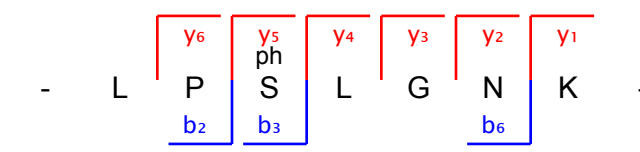
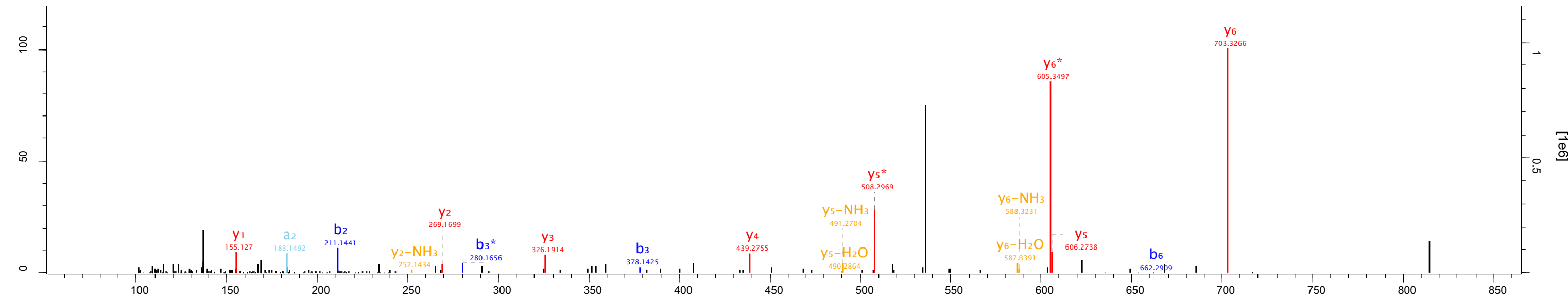
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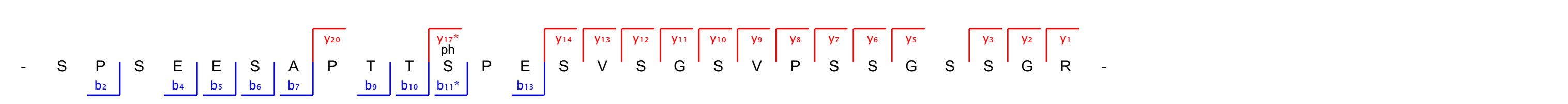
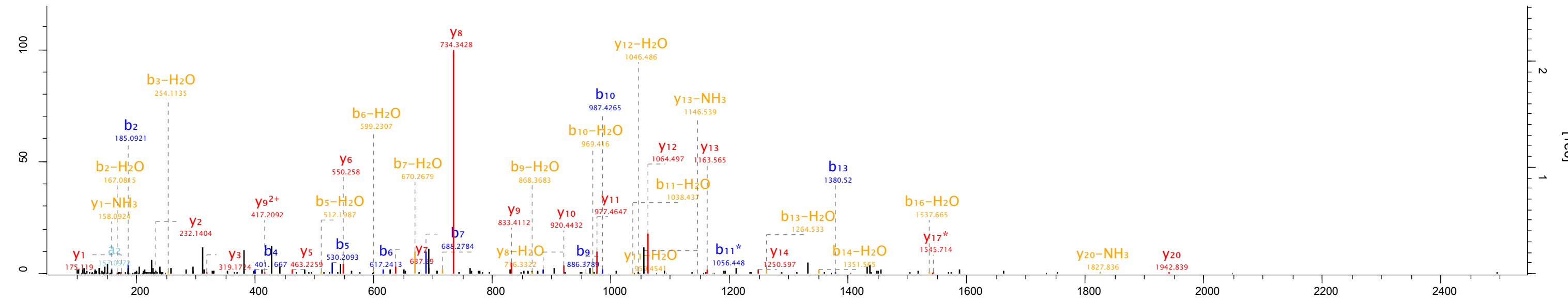
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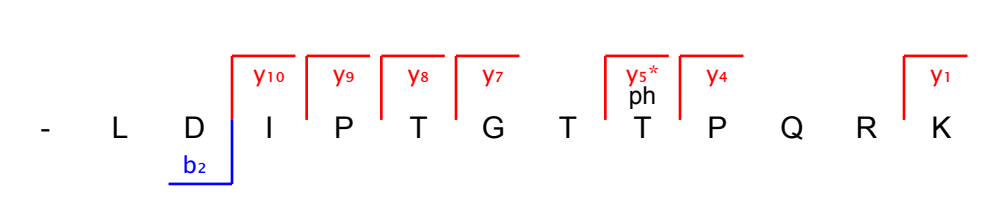
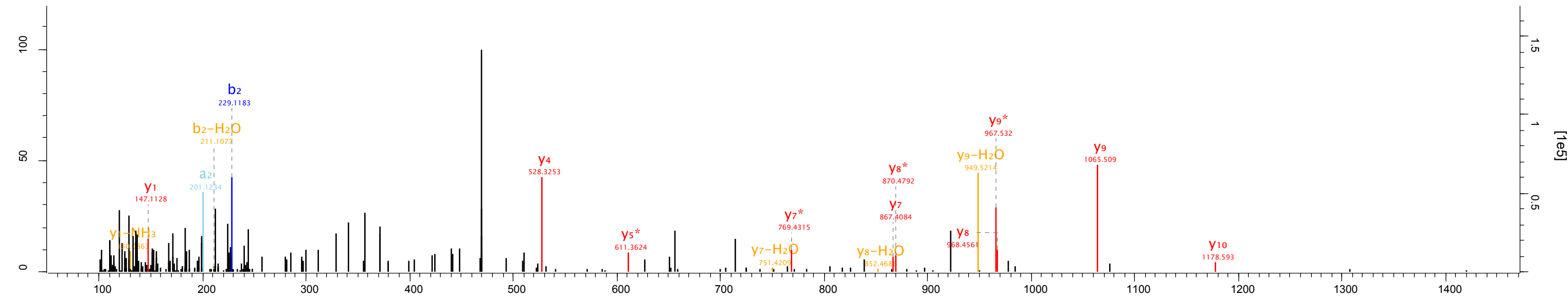
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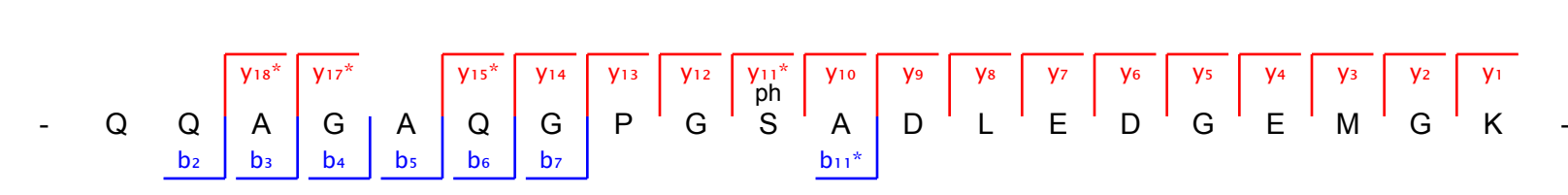
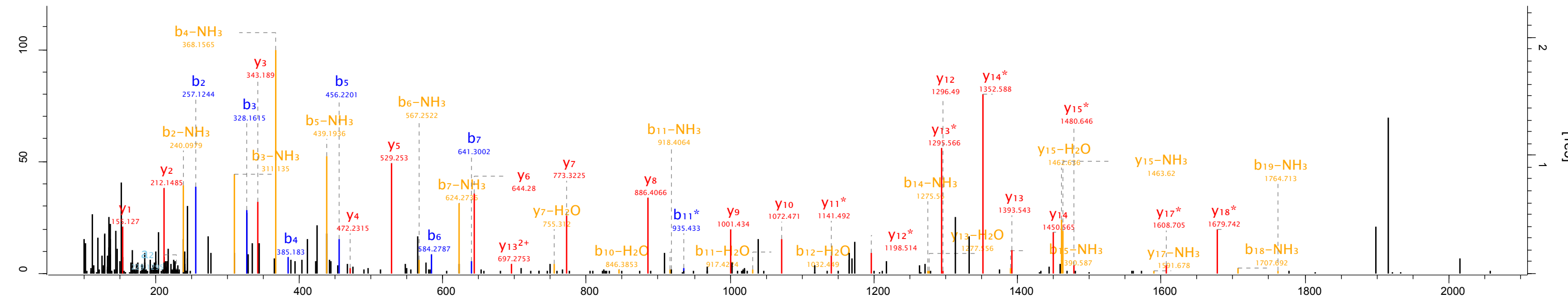
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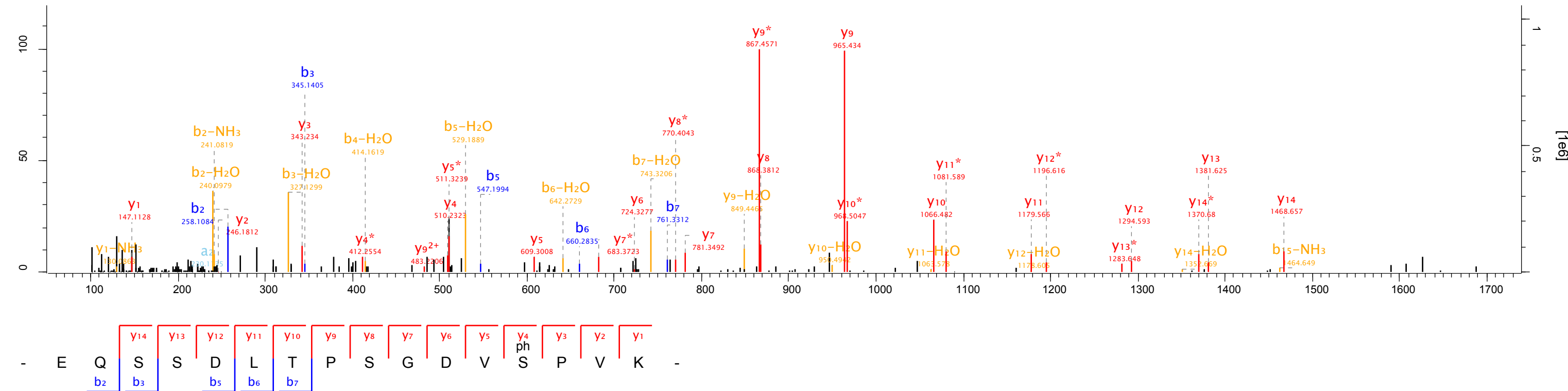


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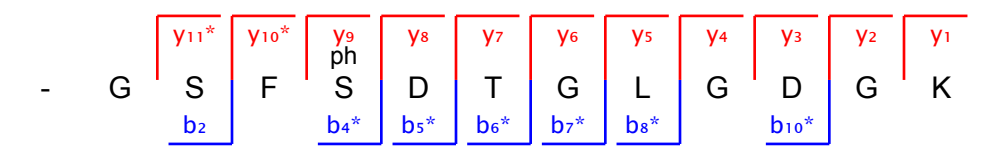
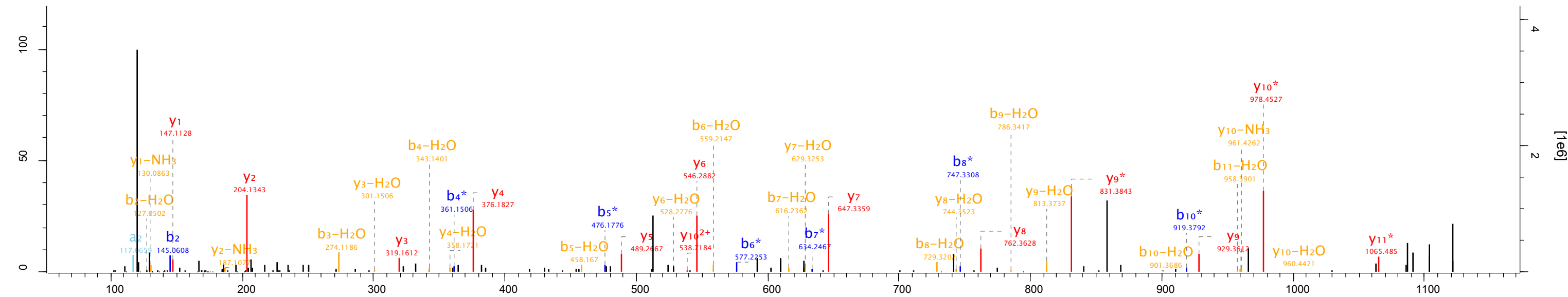


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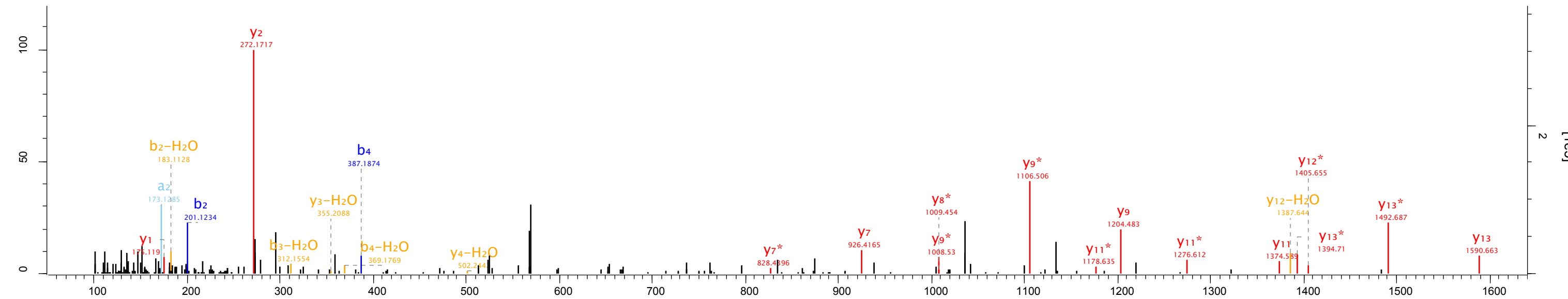




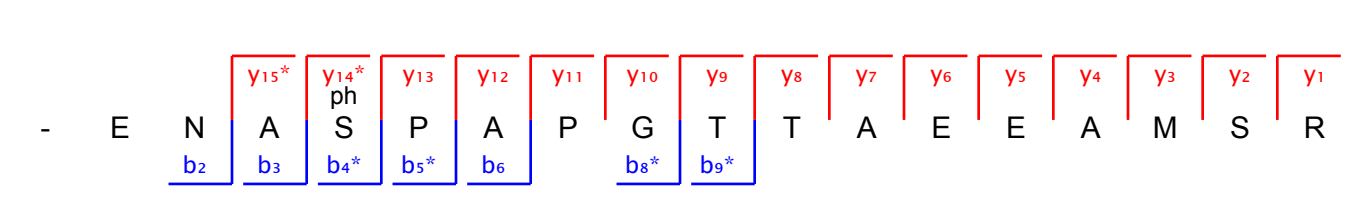
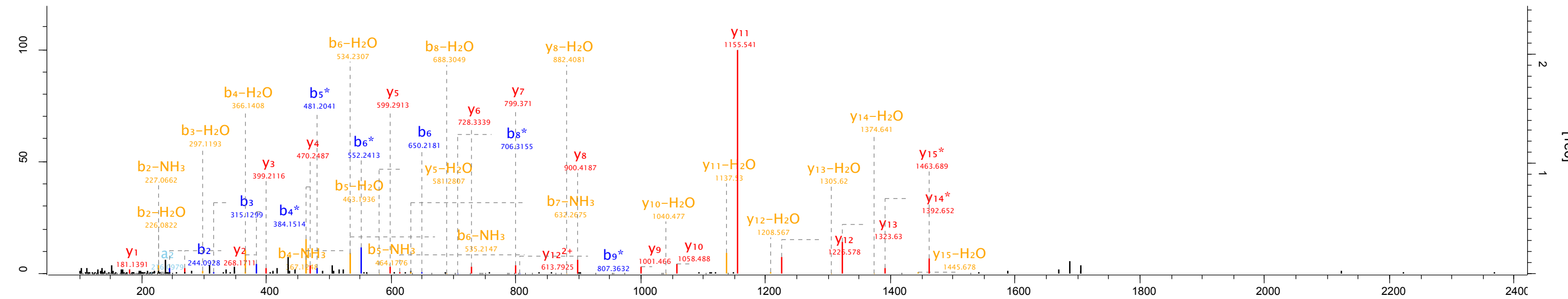
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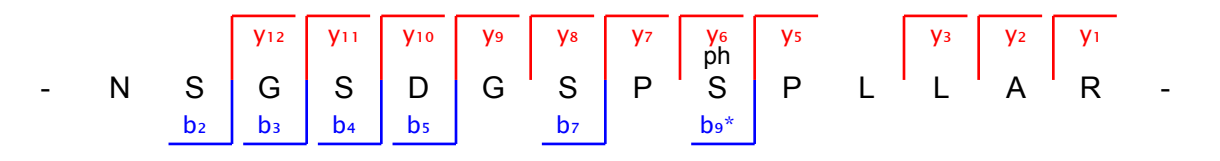
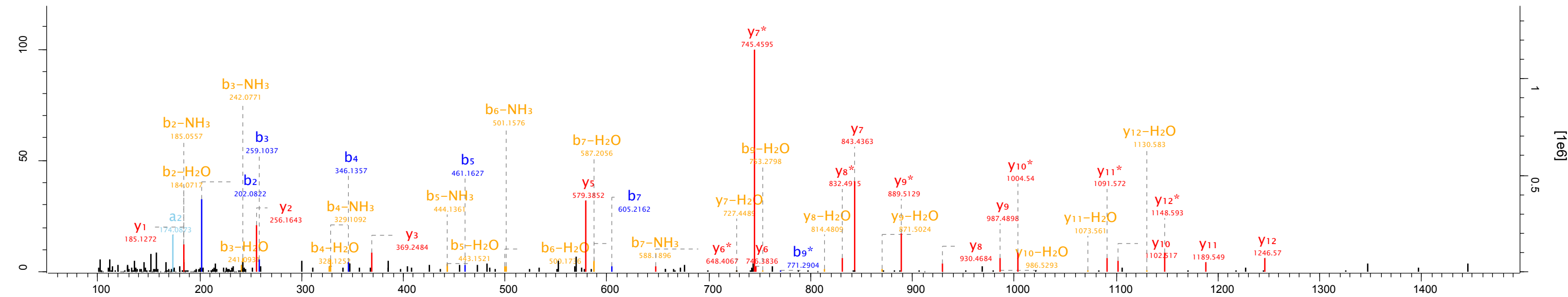
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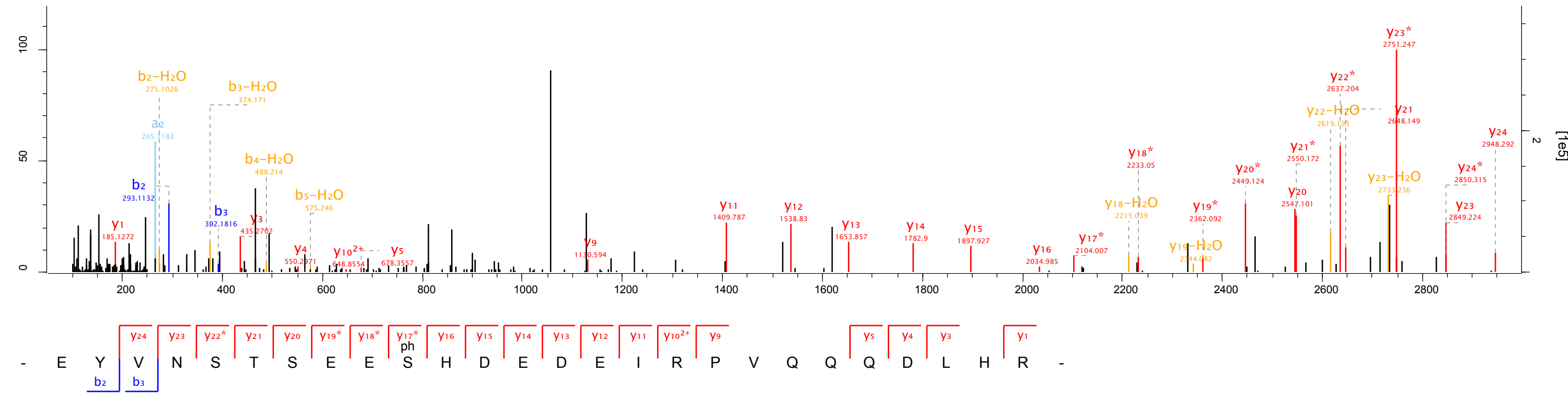
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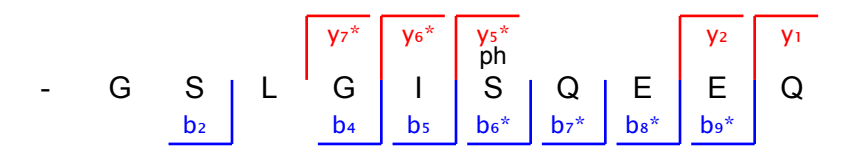
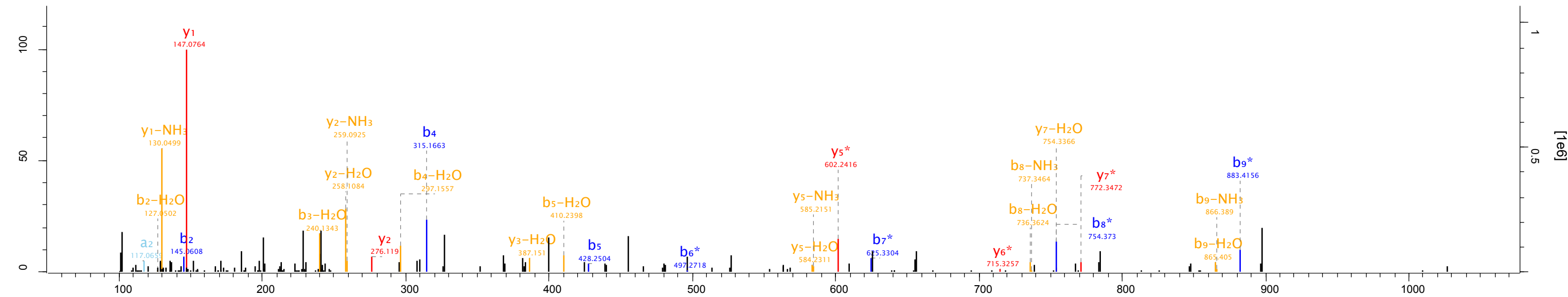
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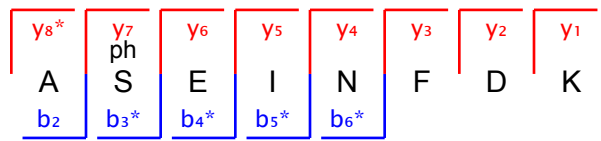
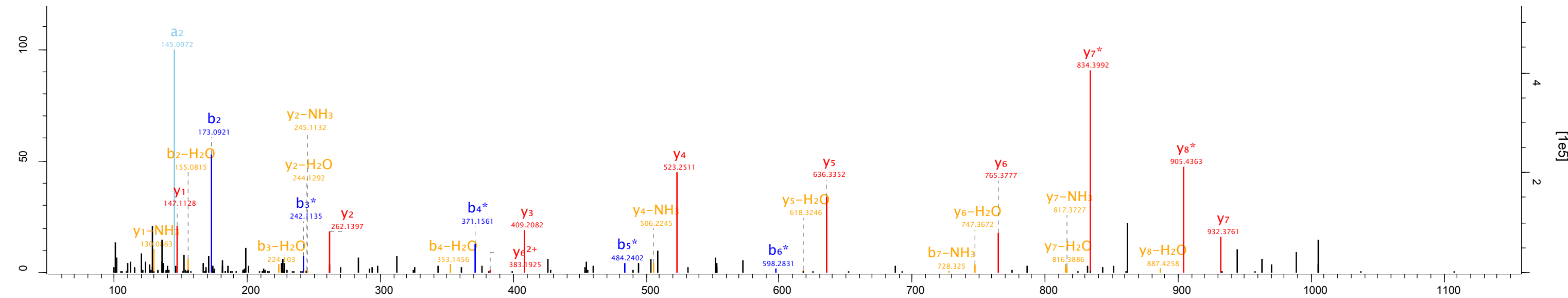
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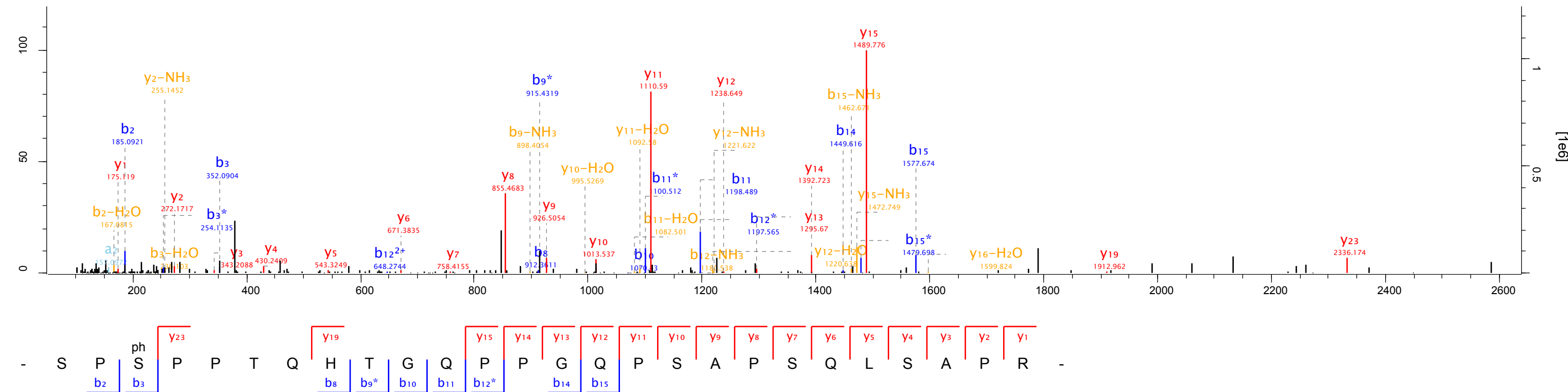
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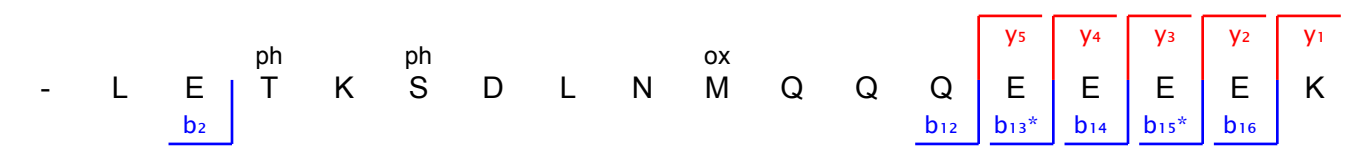
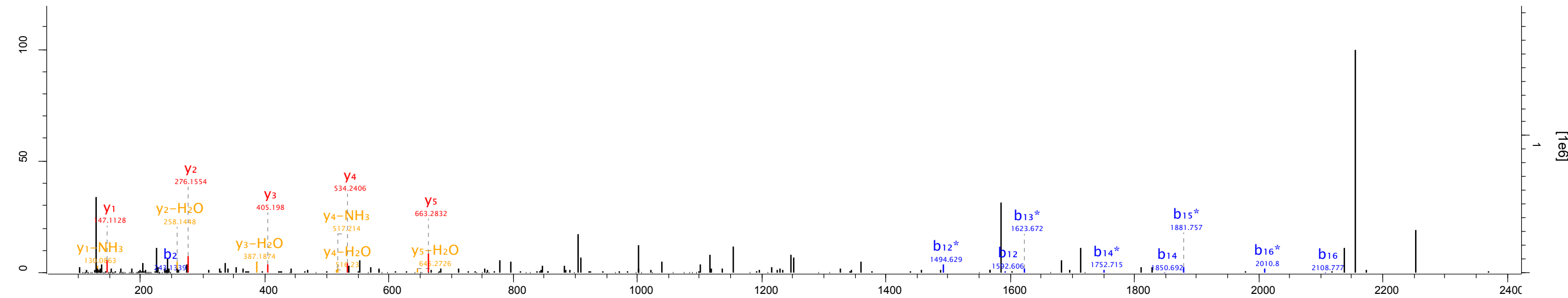
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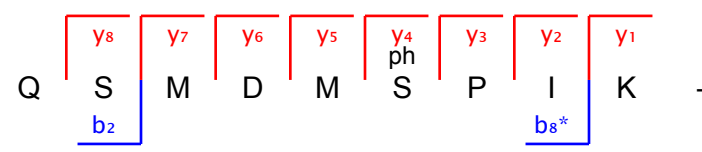
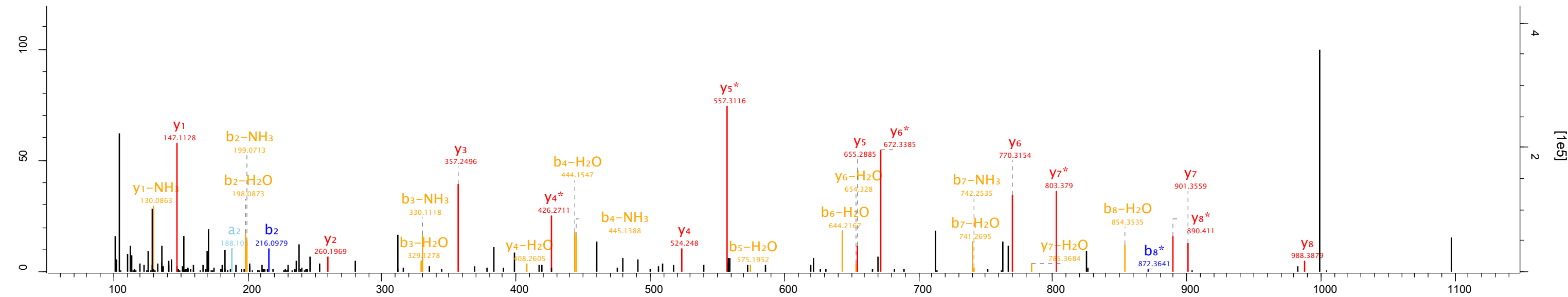
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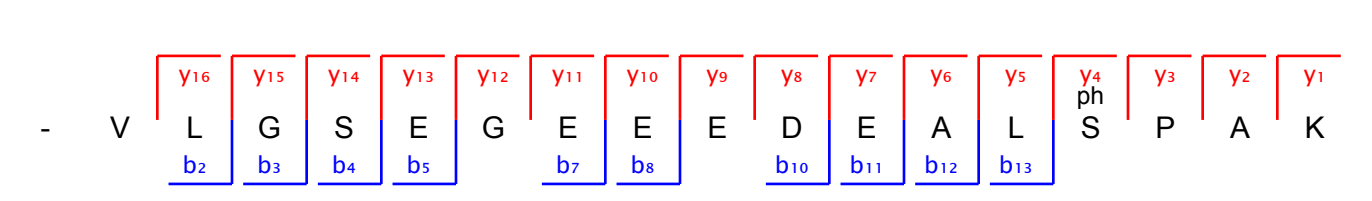
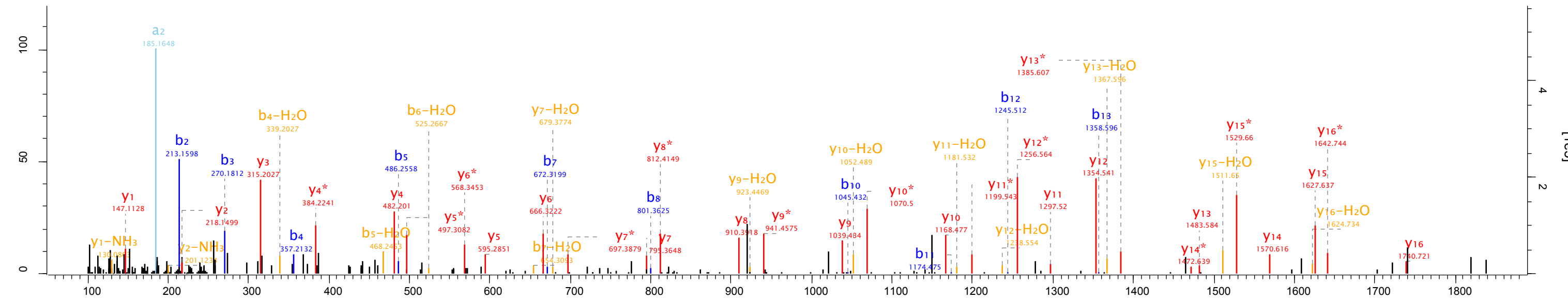


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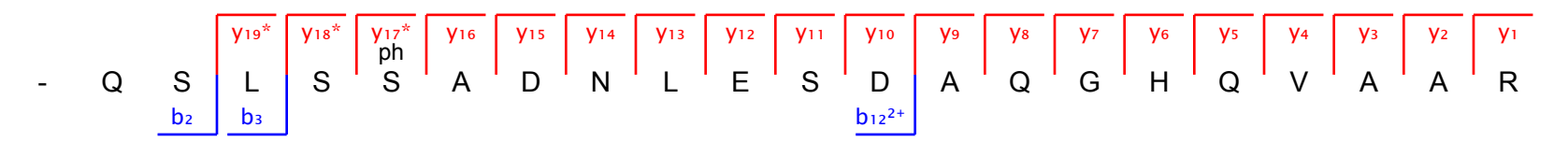
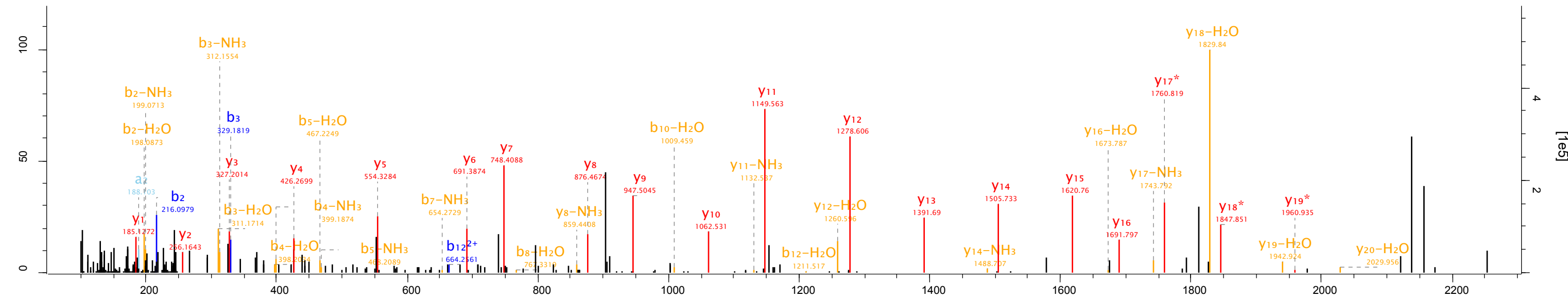


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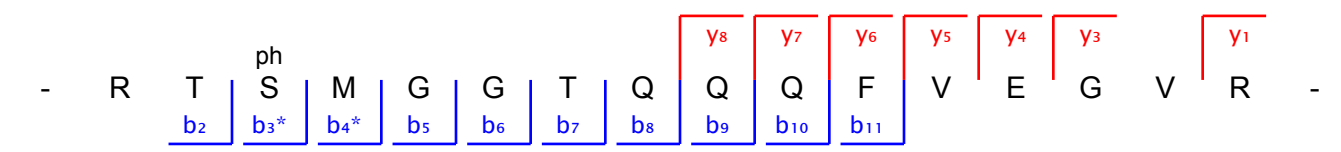
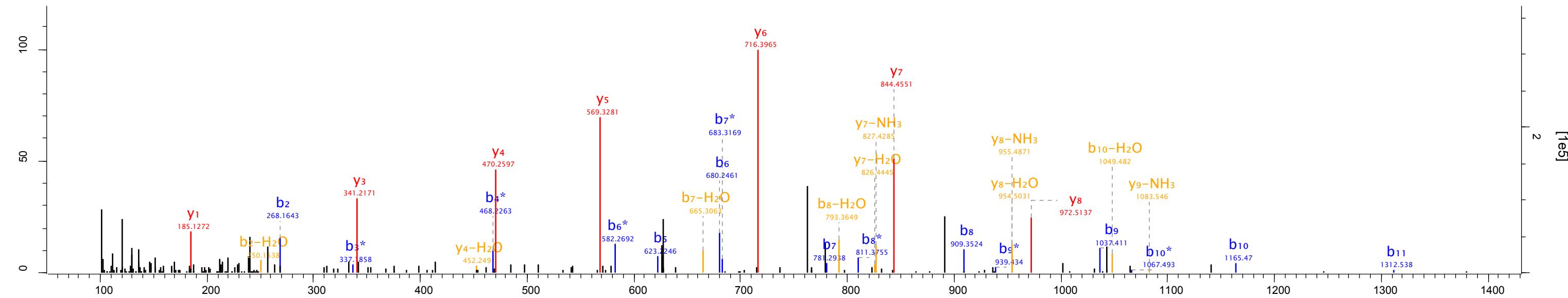




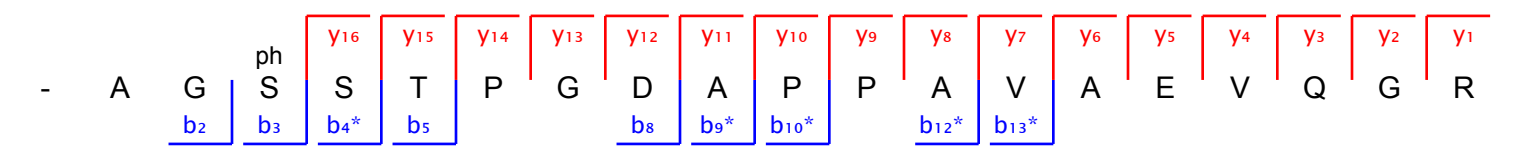
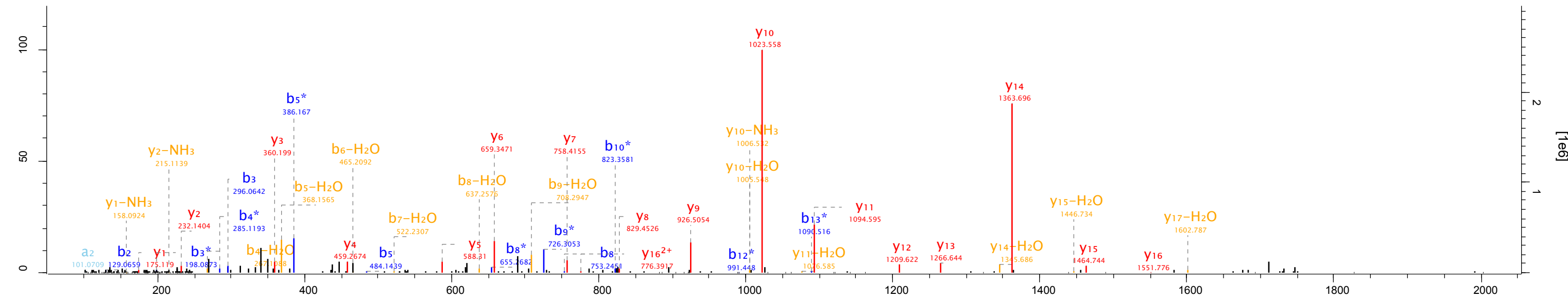
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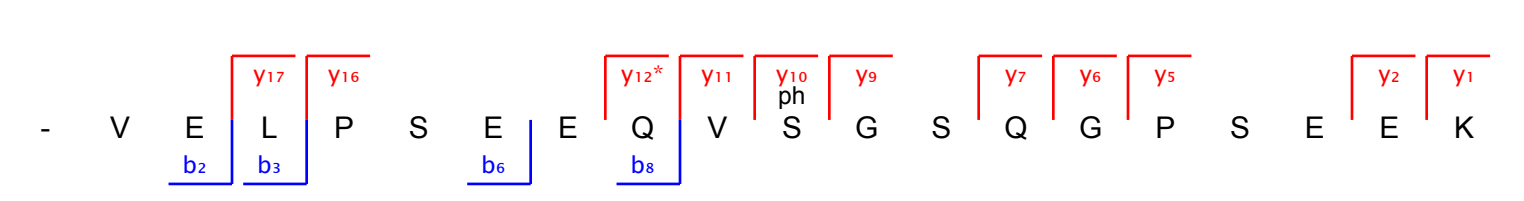
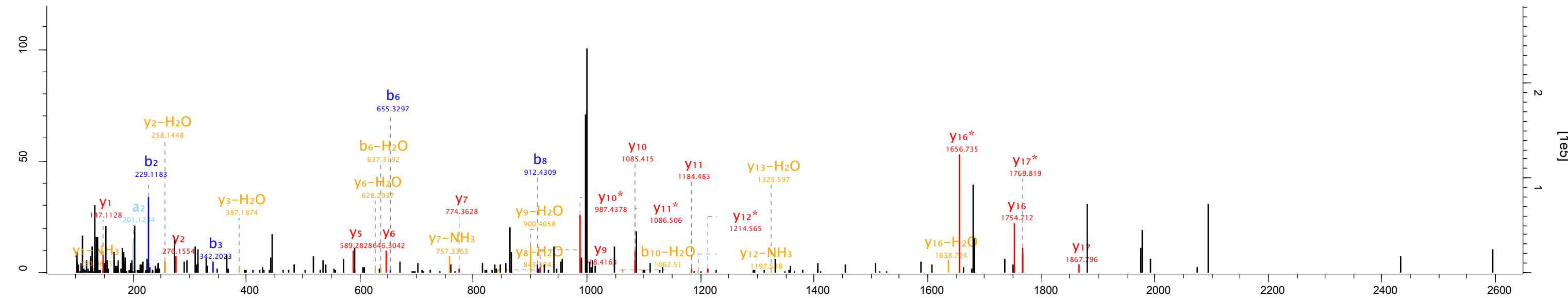
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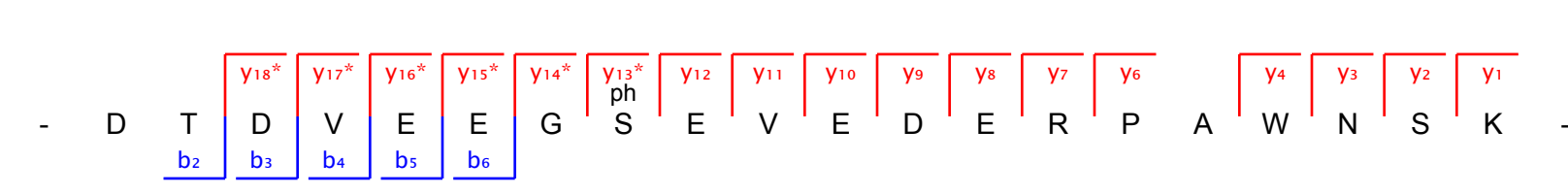
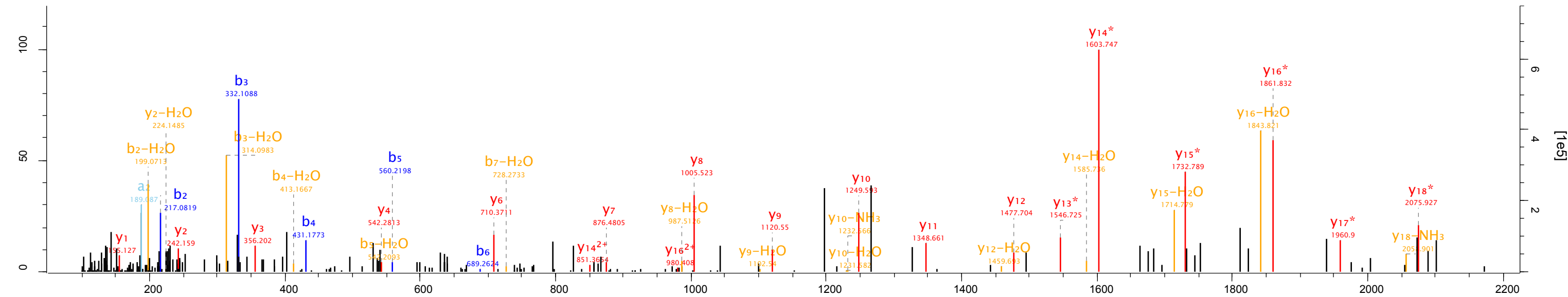
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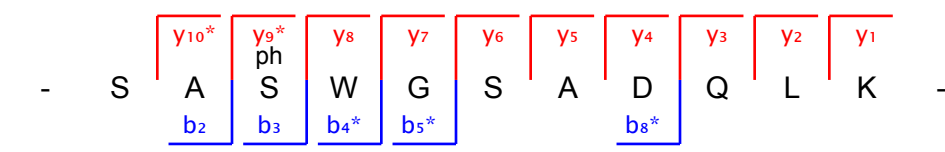
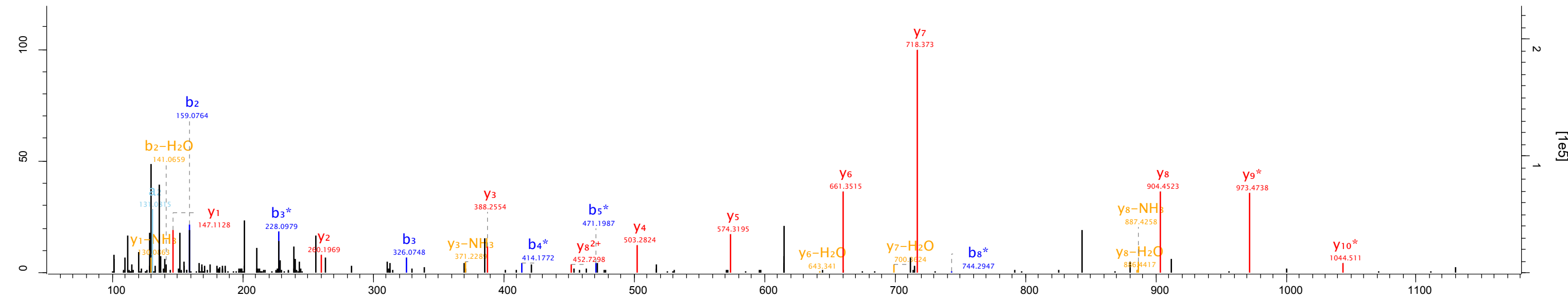
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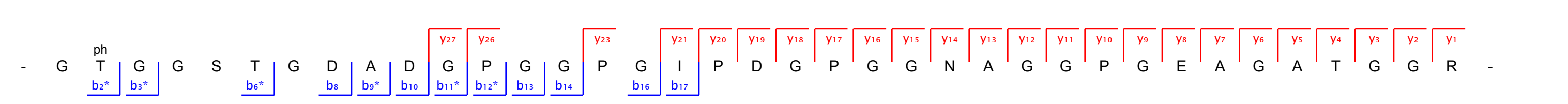
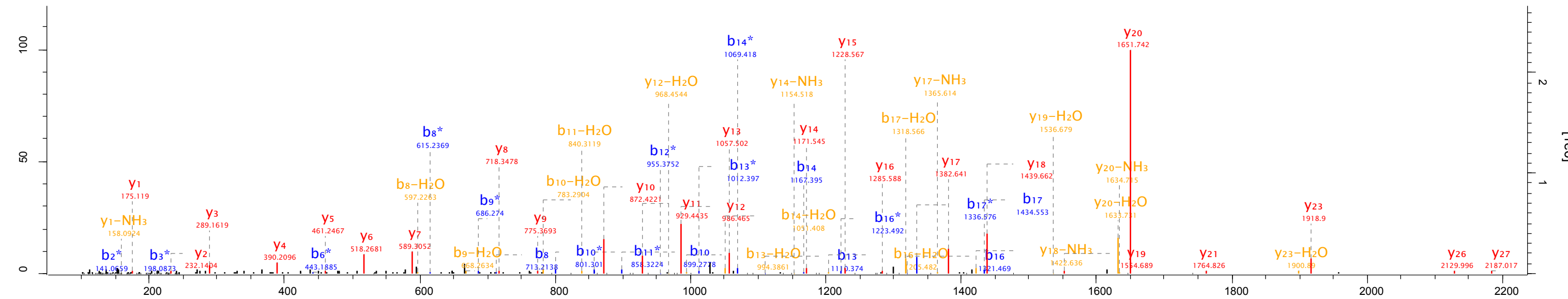
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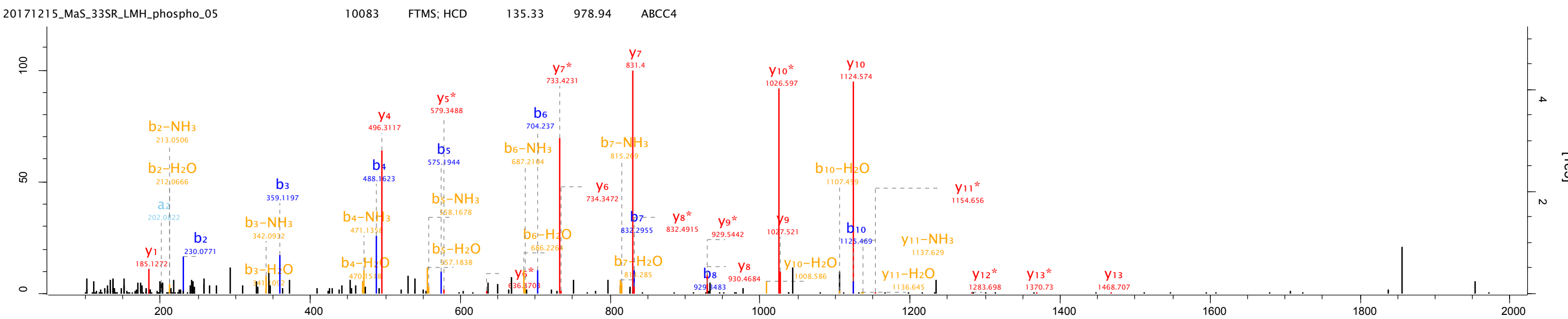
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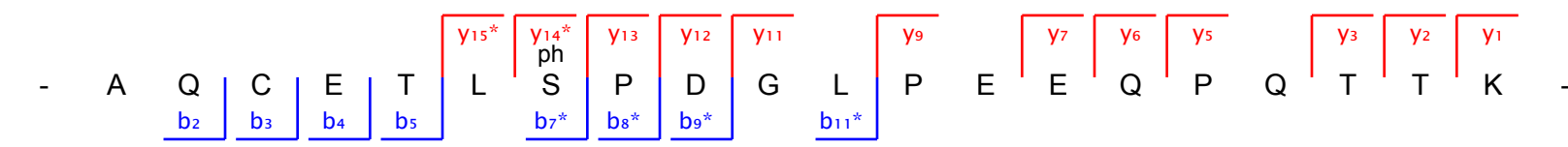
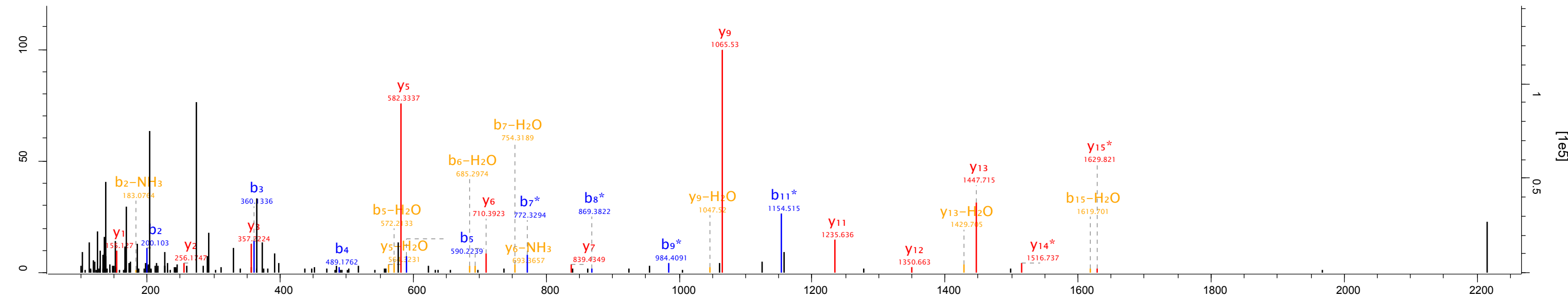
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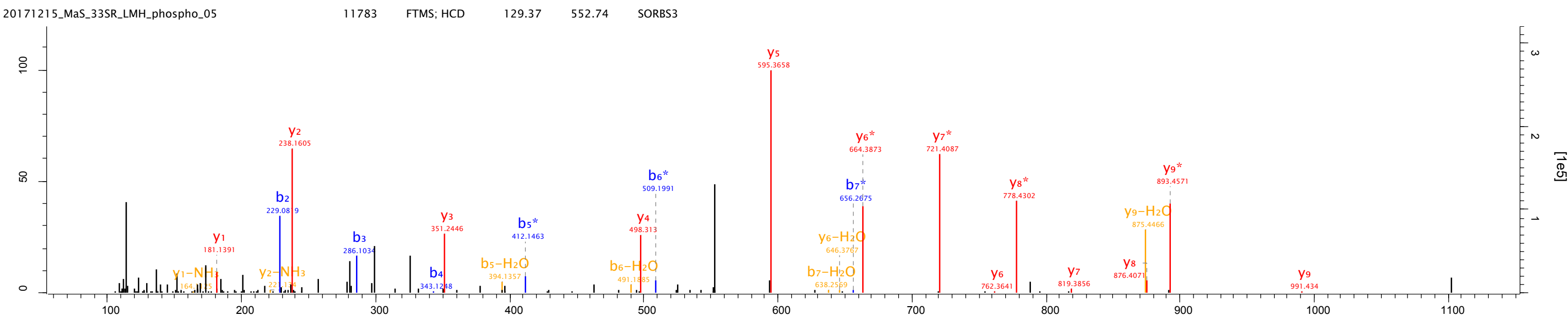
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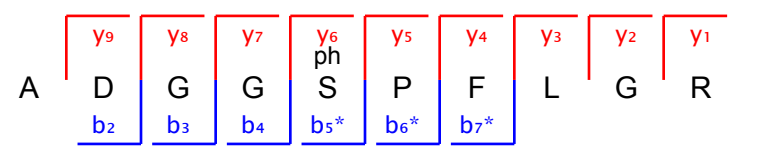
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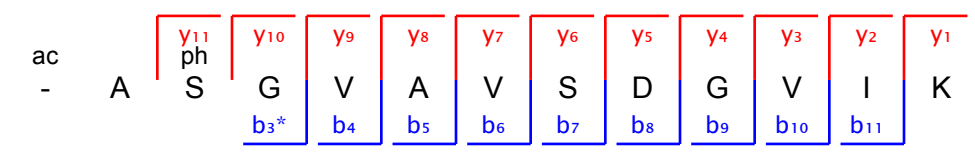
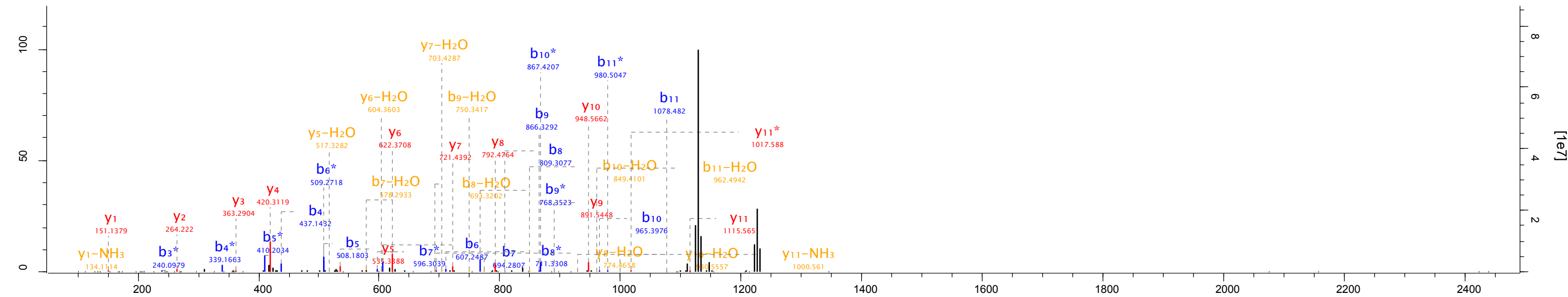
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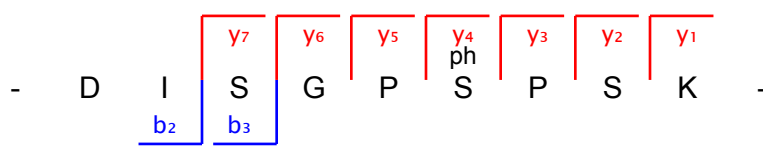
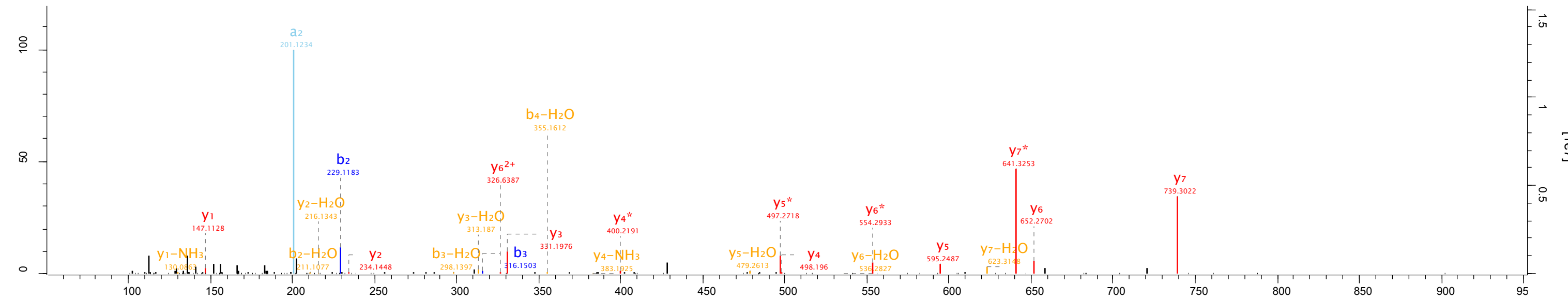
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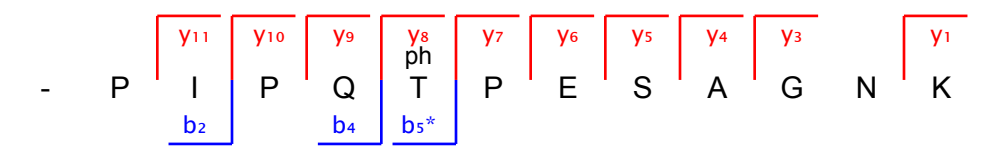
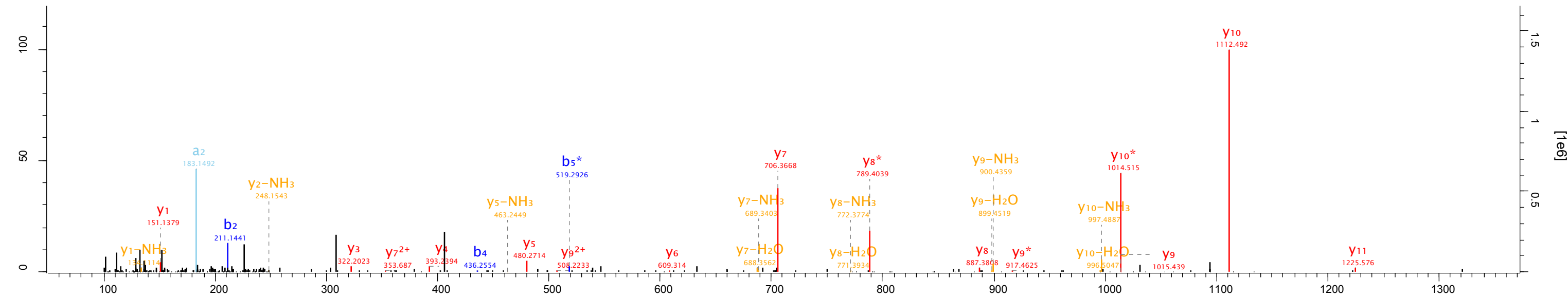
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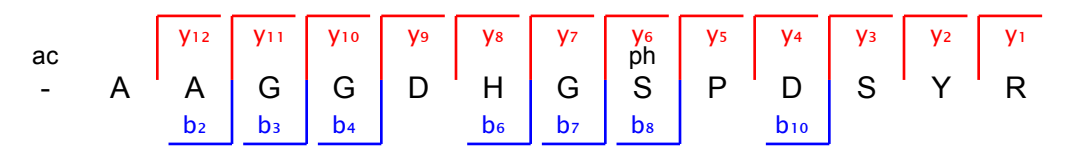
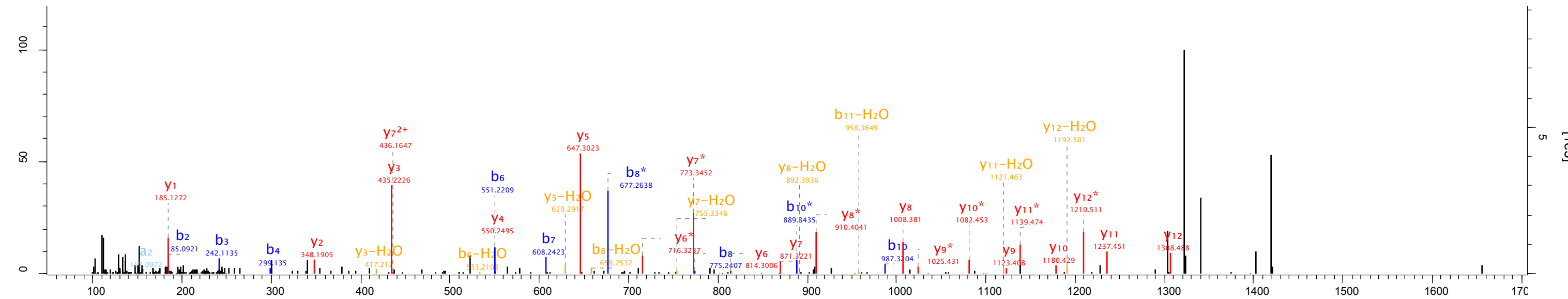
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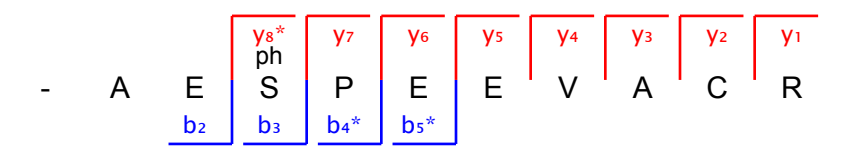
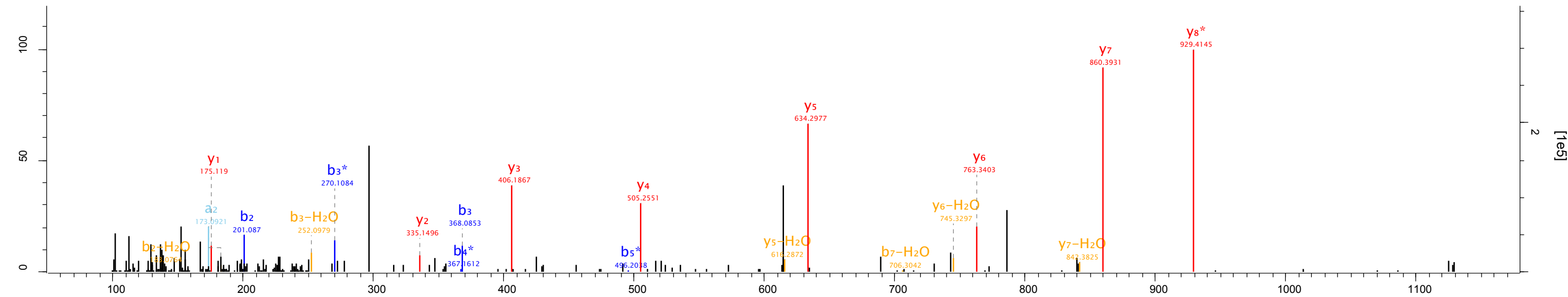
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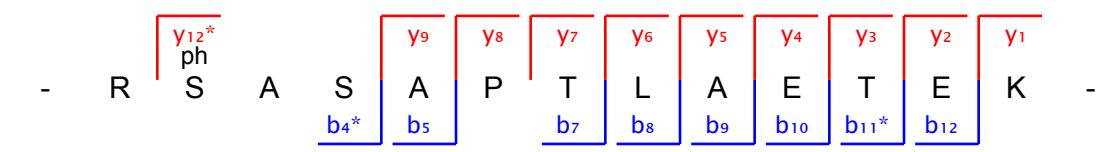
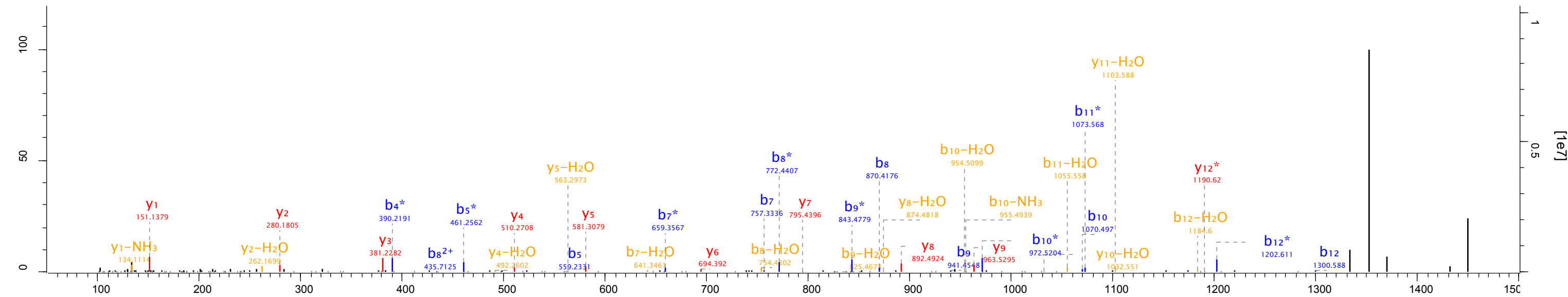
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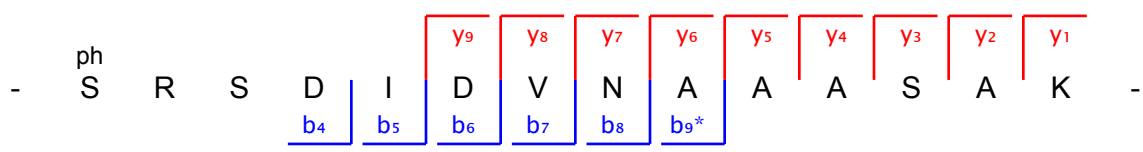
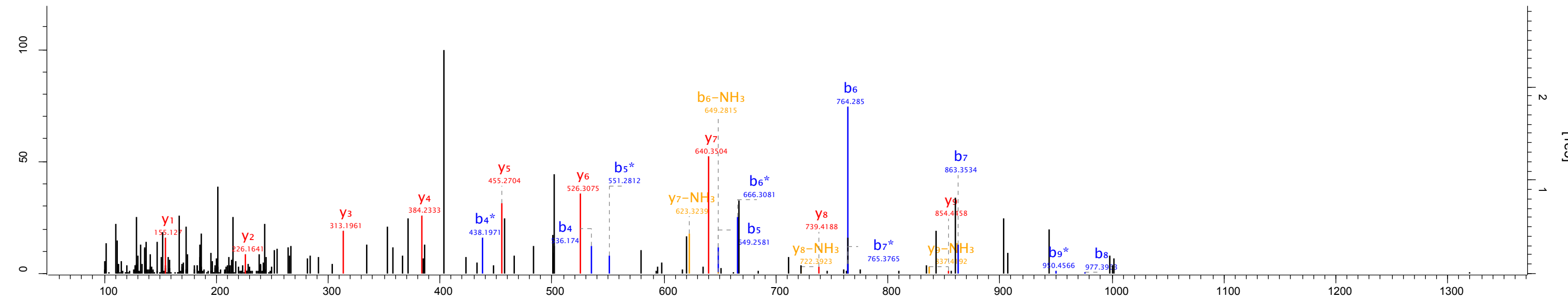
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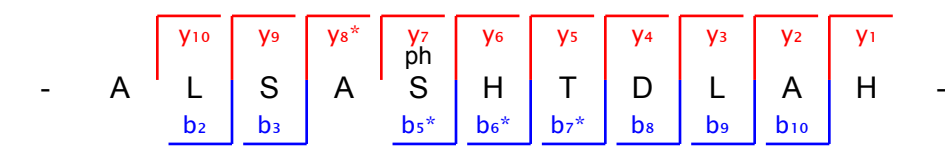
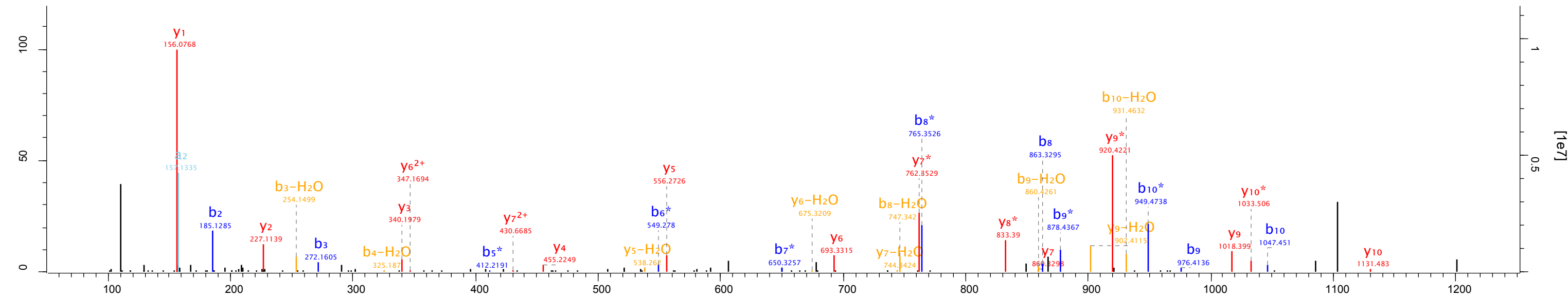
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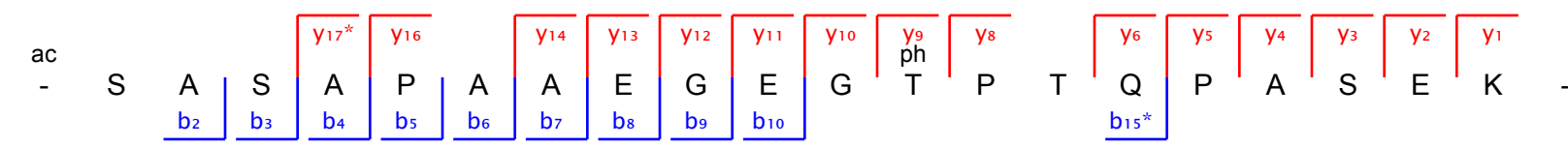
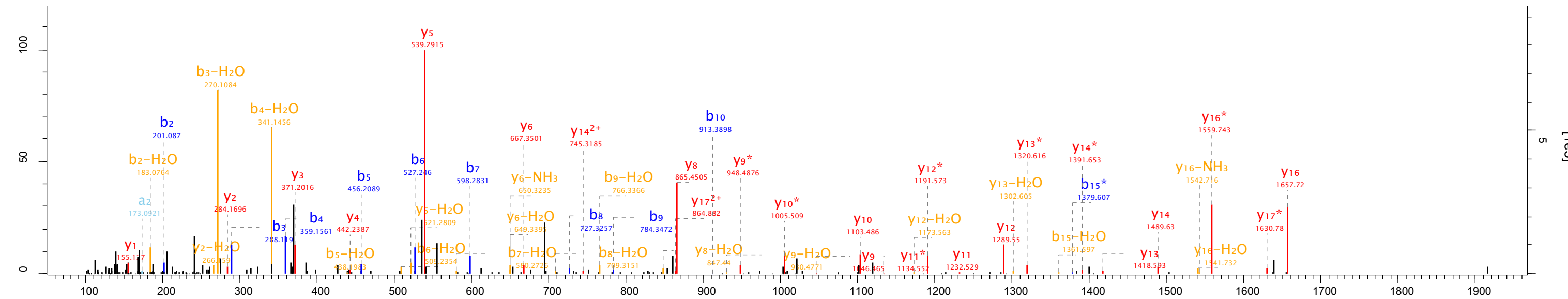
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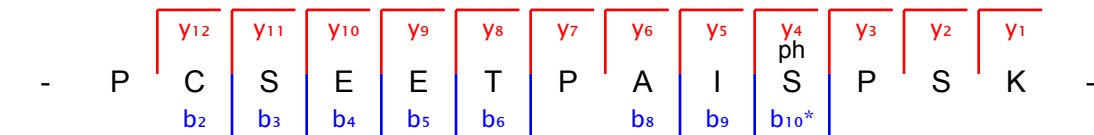
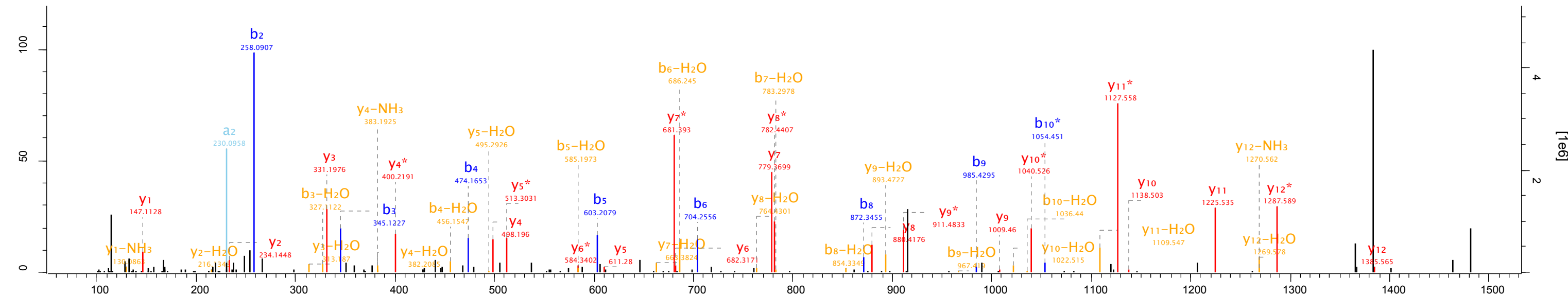


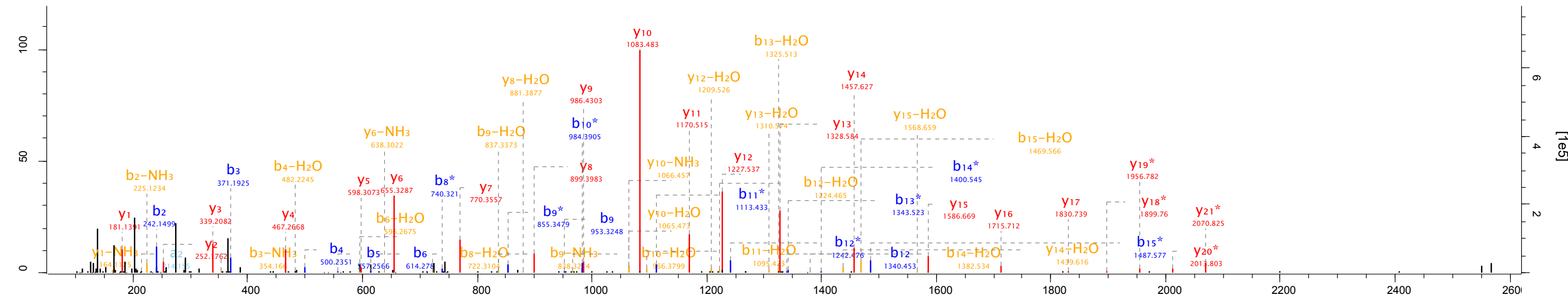
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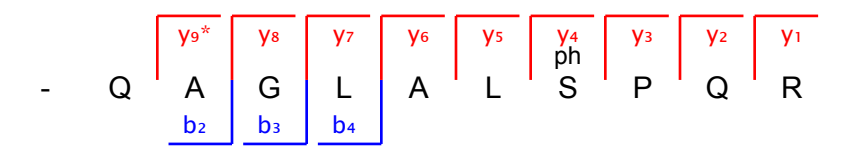
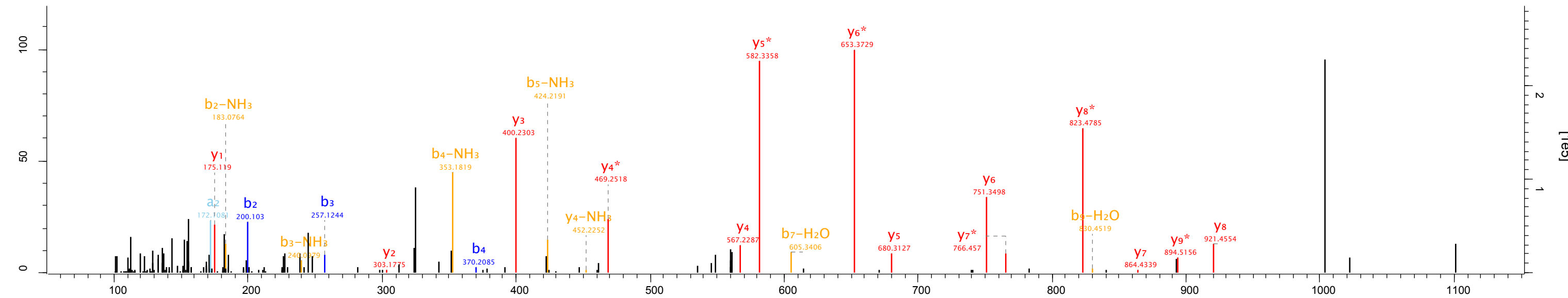


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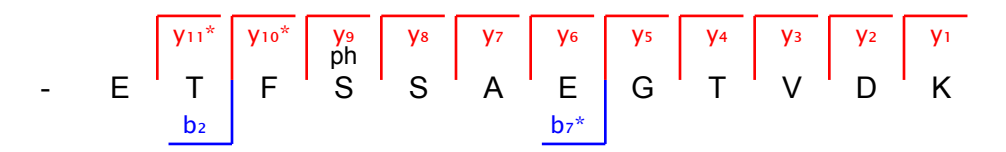
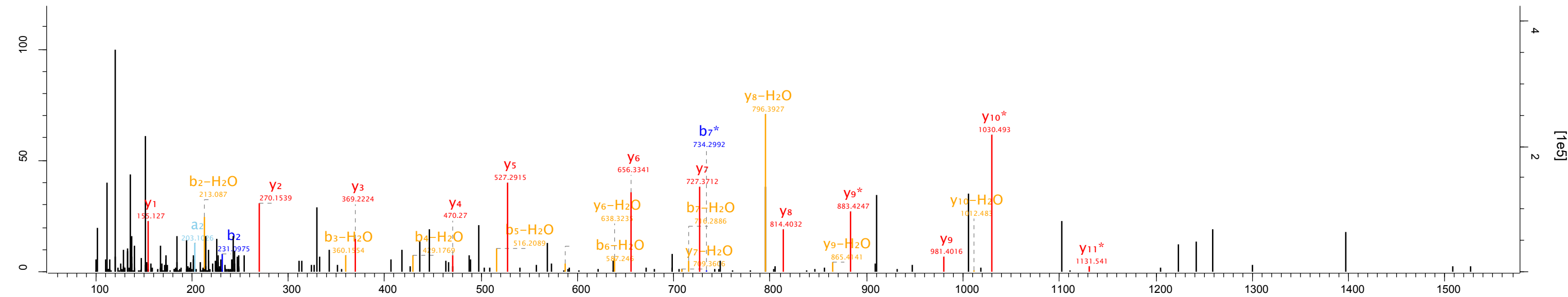
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b₄
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y₂₀*
y₁₉*
y₁₈*
ph
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y₁₅
y₁₄
y₁₃
y₁₂
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y₁

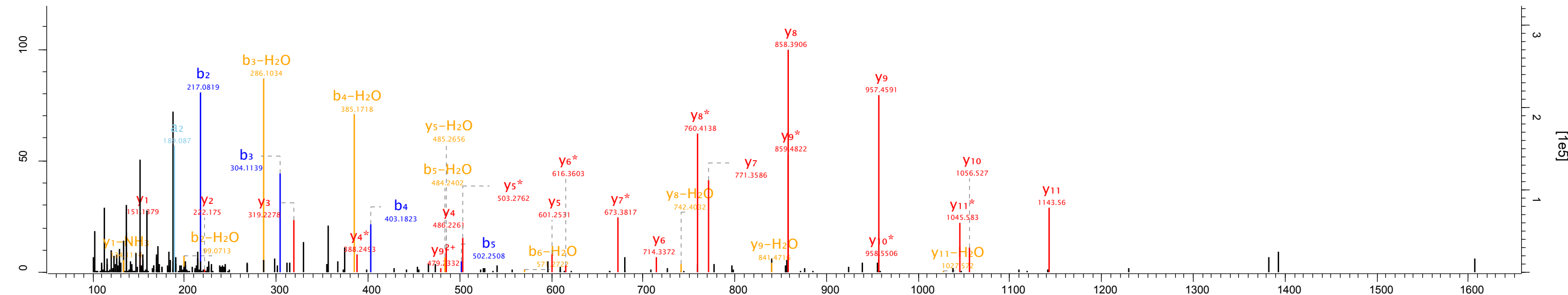
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b₉
b₁₀*
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b₁₃*
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b₁₅*

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Raw file 20171215_MaS_33SR_LMH_phospho_05 Scan 7983 Method FTMS; HCD Score 77.07 m/z 679.78 Gene names ATRX





- S E S V V S G L D S P A K -

b₂ b₃ b₄ b₅

y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

y₁₁-H₂O y₁₀-H₂O y₉-H₂O y₈-H₂O y₇-H₂O y₆-H₂O y₅-H₂O y₄-H₂O y₃-H₂O y₂-H₂O y₁-H₂O

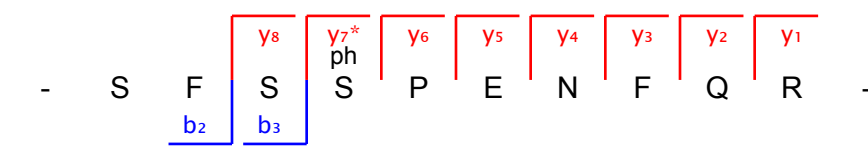
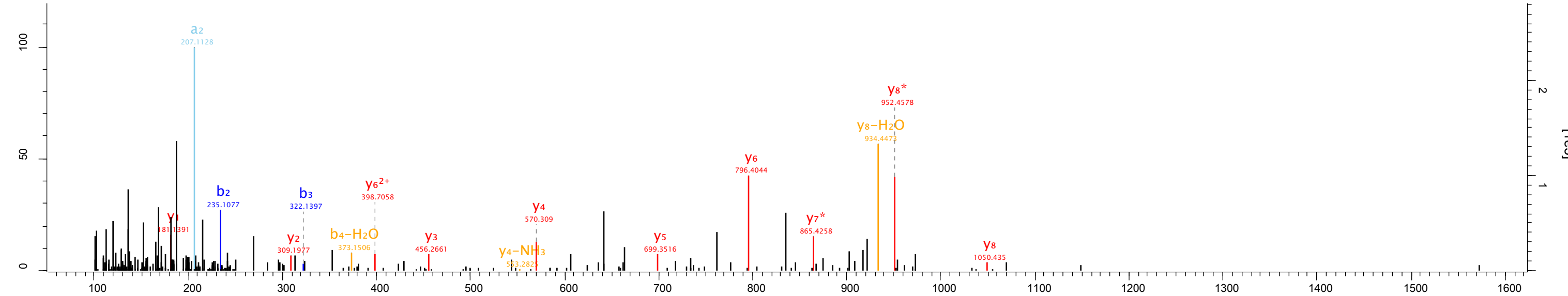
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y₁-NH₃

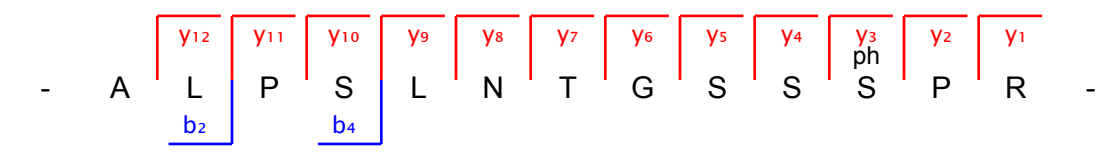
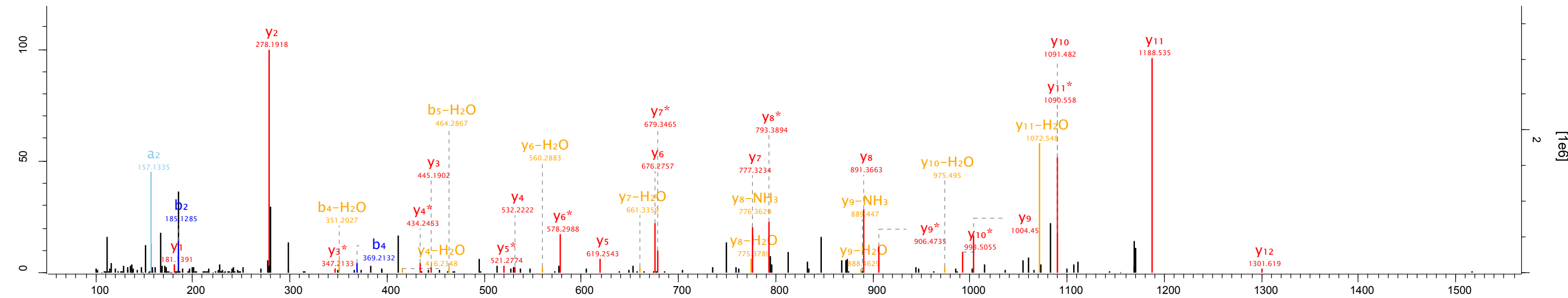
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20171215_MaS_33SR_LMH_phospho_05

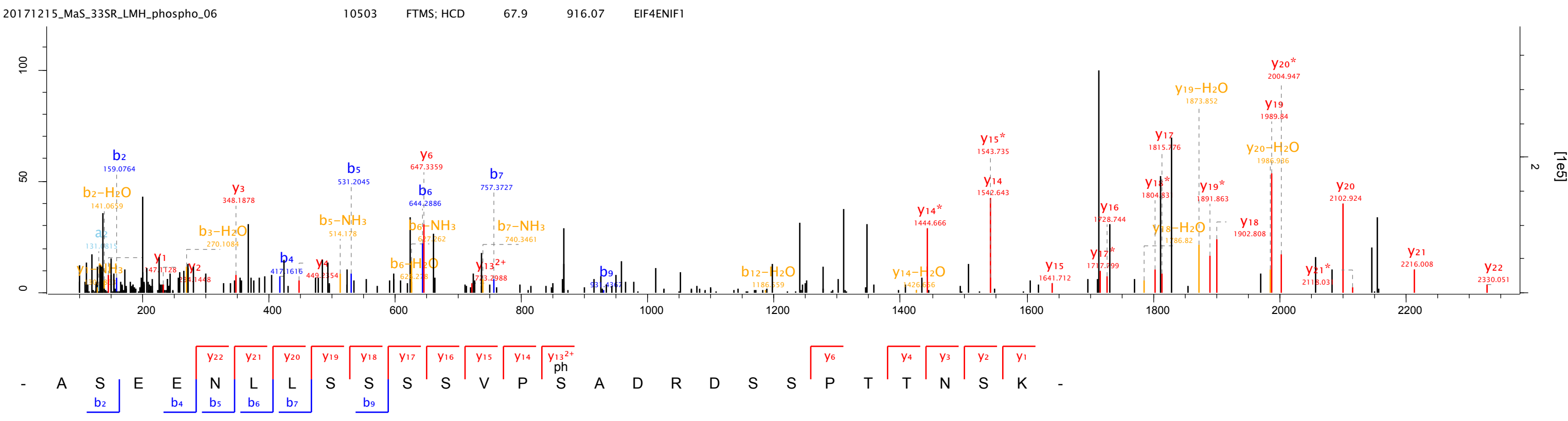
Scan 9023 Method FTMS; HCD Score 53.45 m/z 642.77 Gene names RBM7



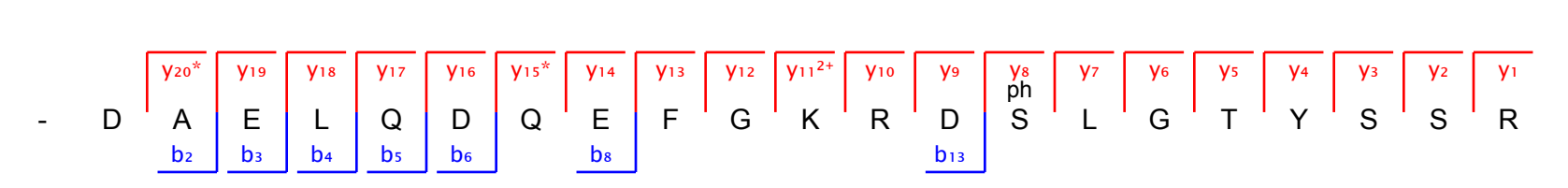
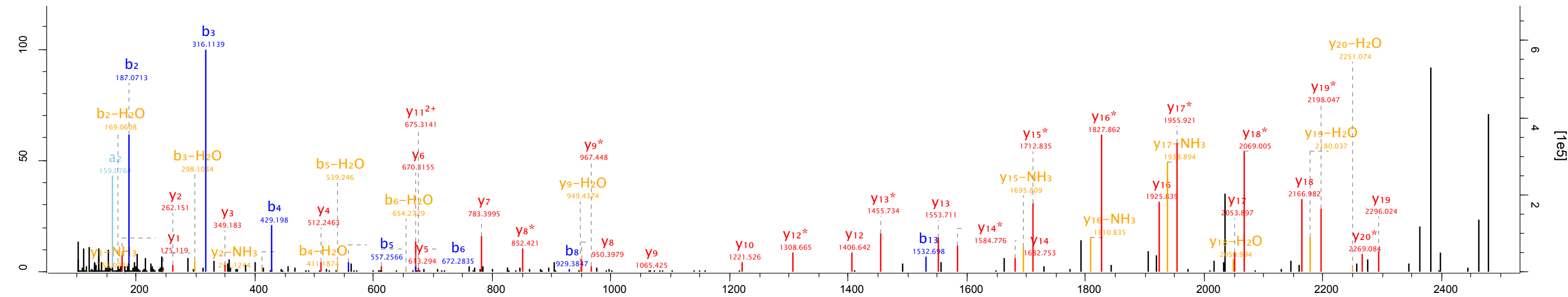
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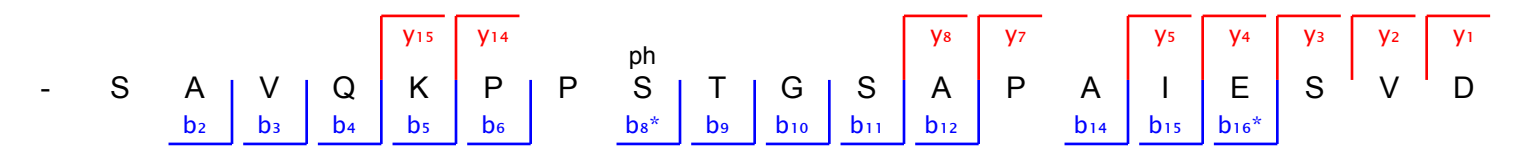
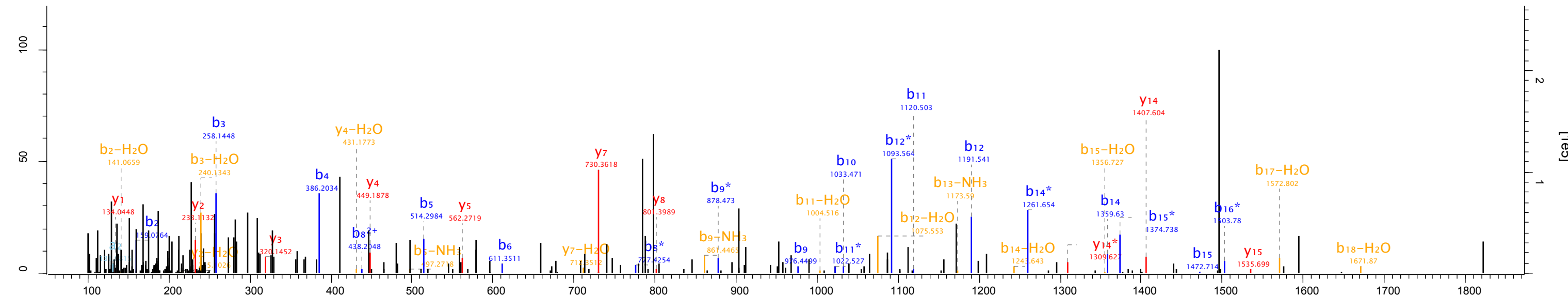
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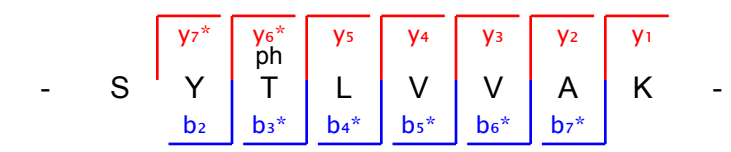
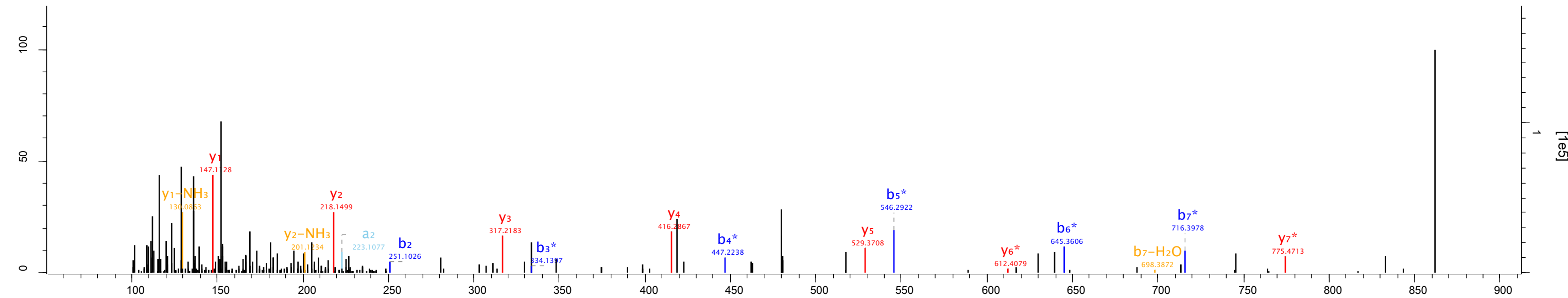
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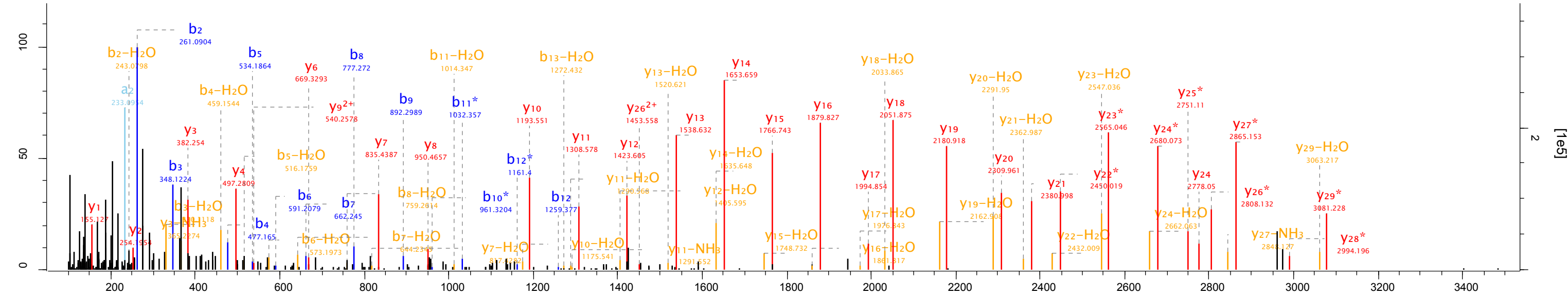
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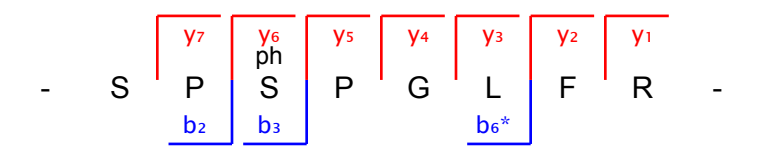
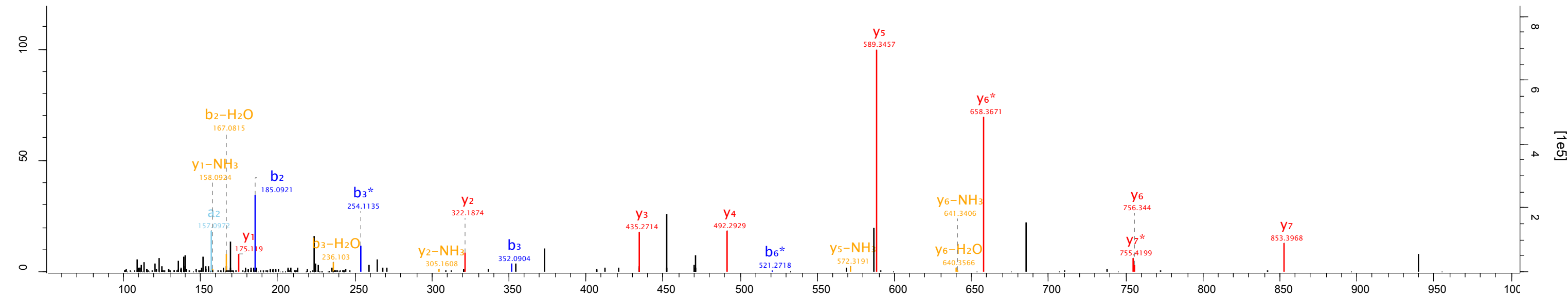
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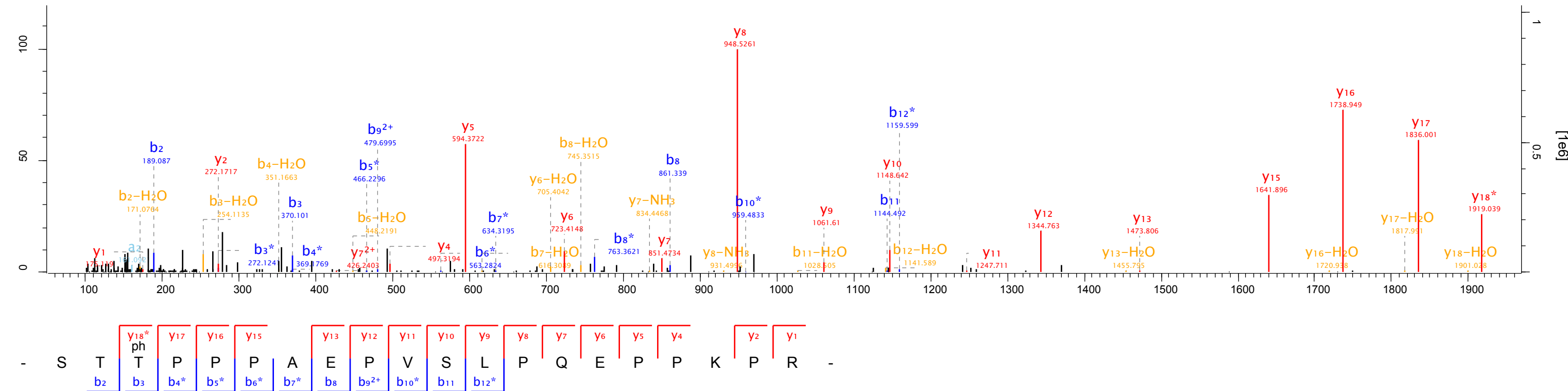


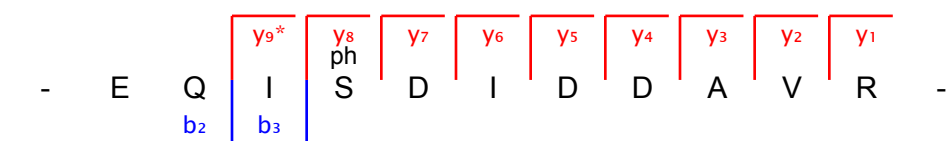
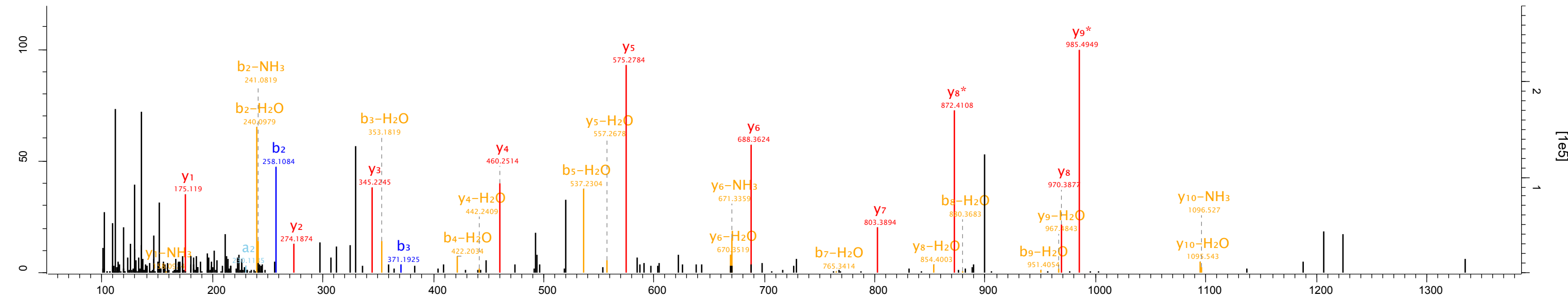
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b₂
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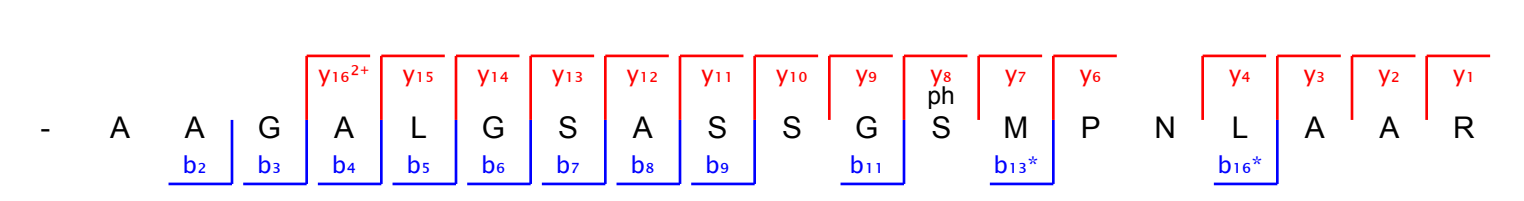
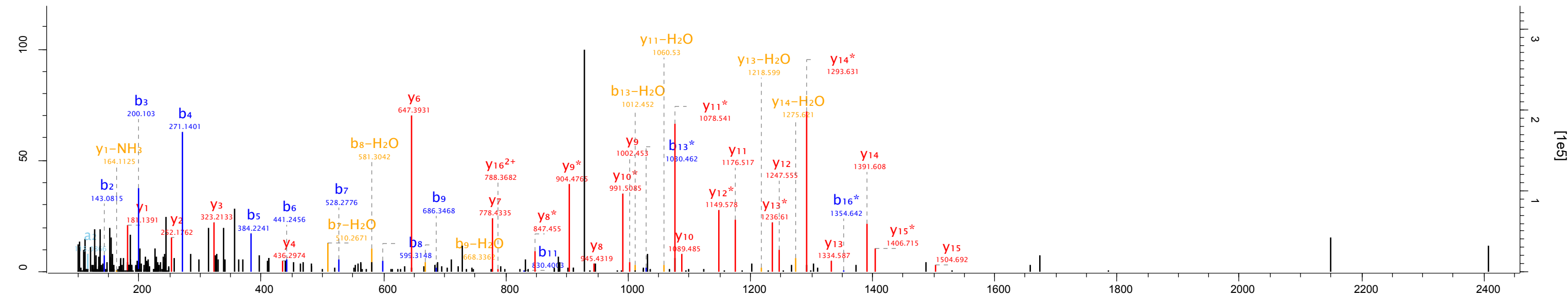
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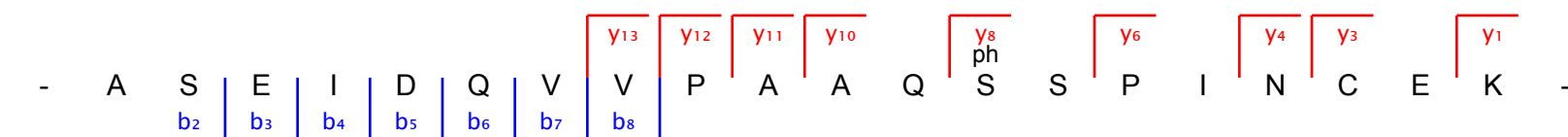
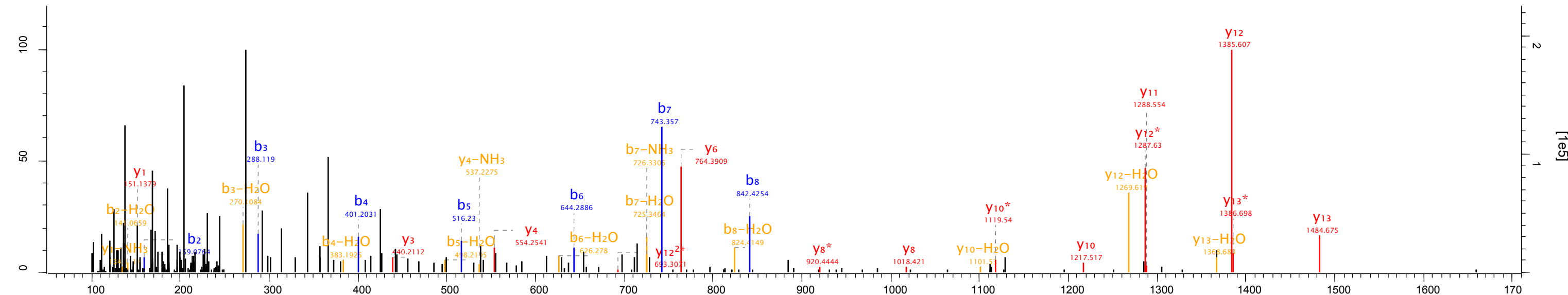




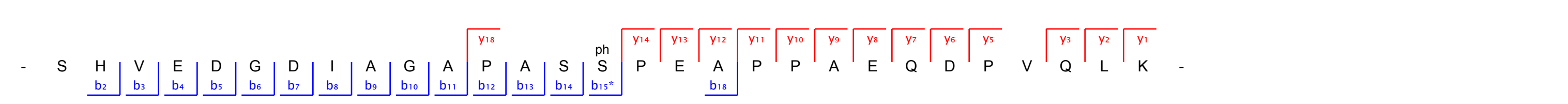
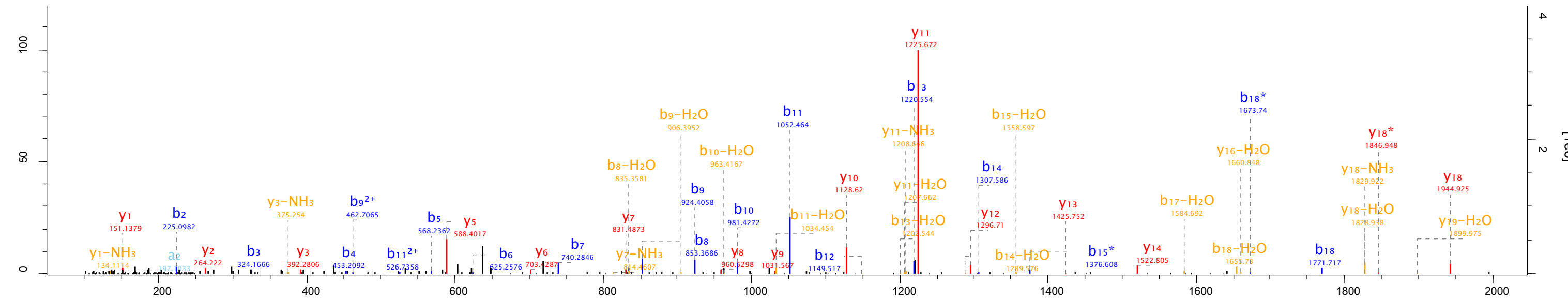
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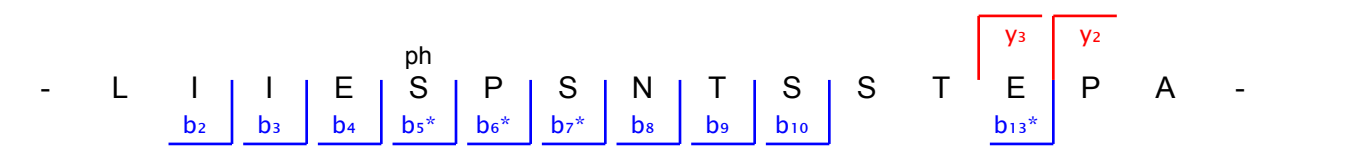
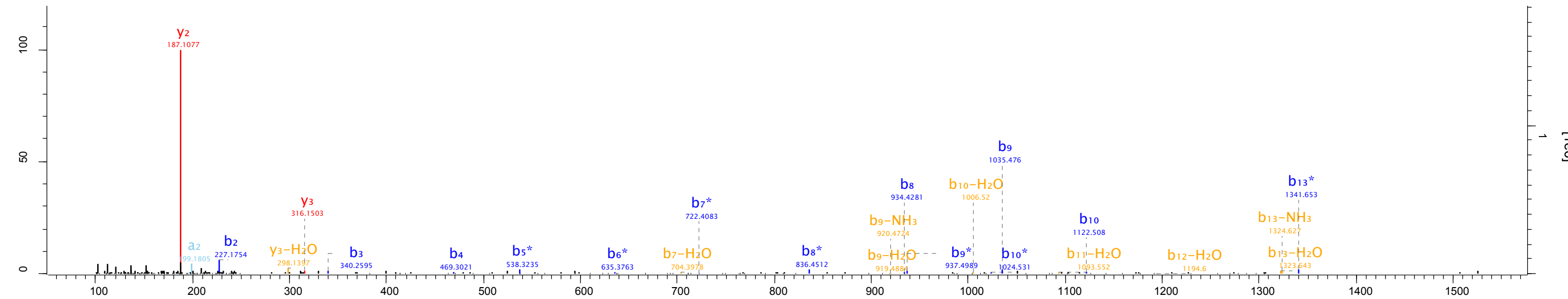
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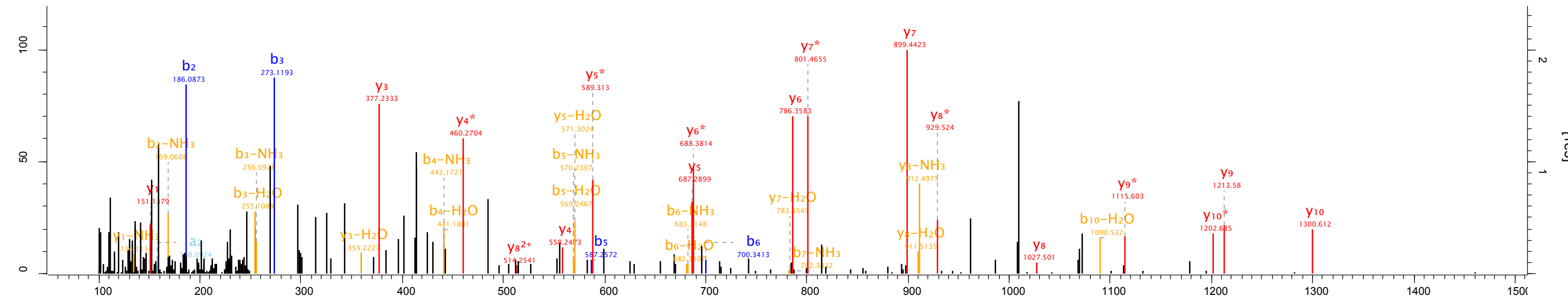
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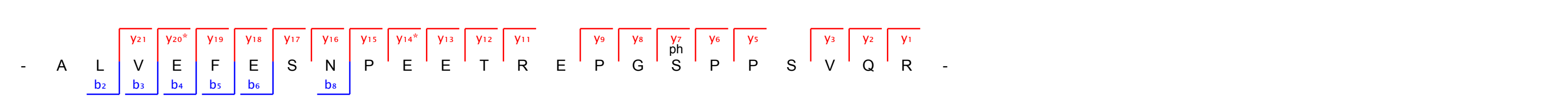
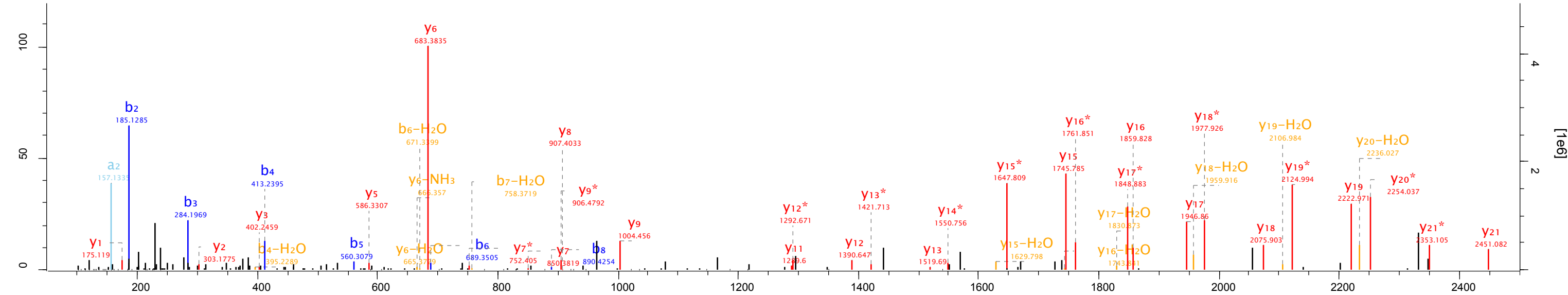
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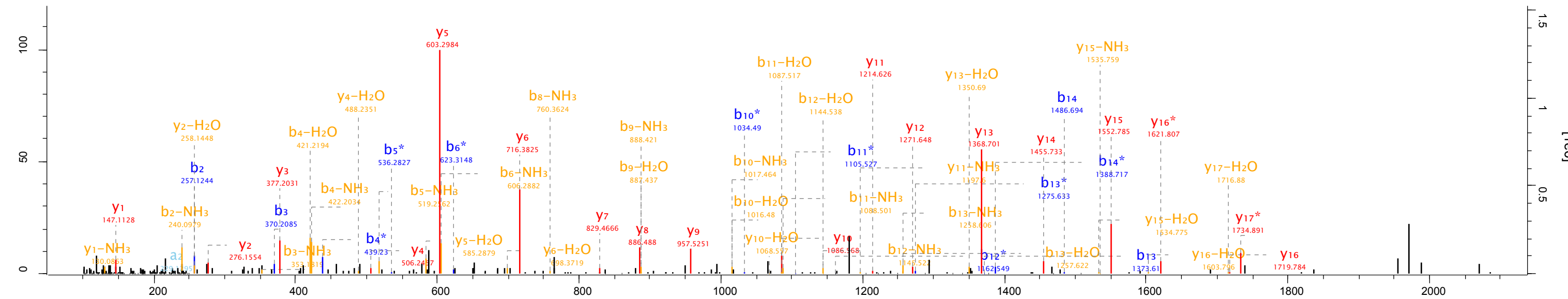
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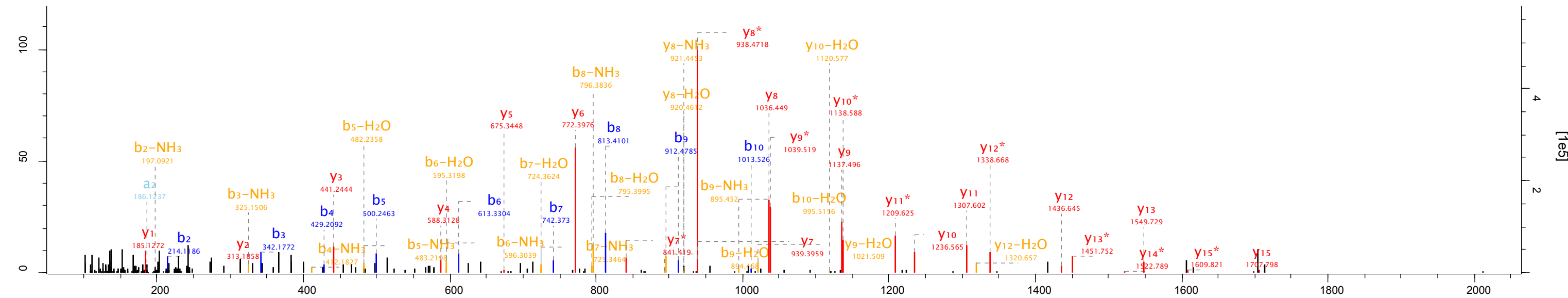
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b₂ b₃ b₄^{*} b₅^{*} b₆^{*} b₁₀^{*} b₁₁^{*} b₁₂^{*} b₁₃ b₁₄

y₁₇^{*} y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁



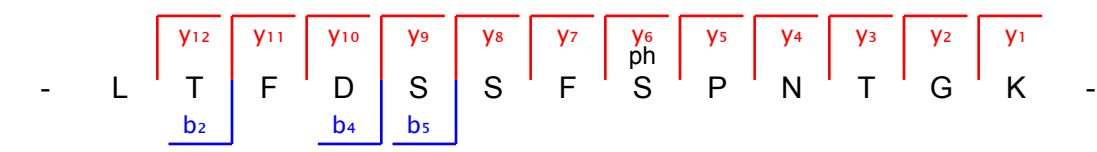
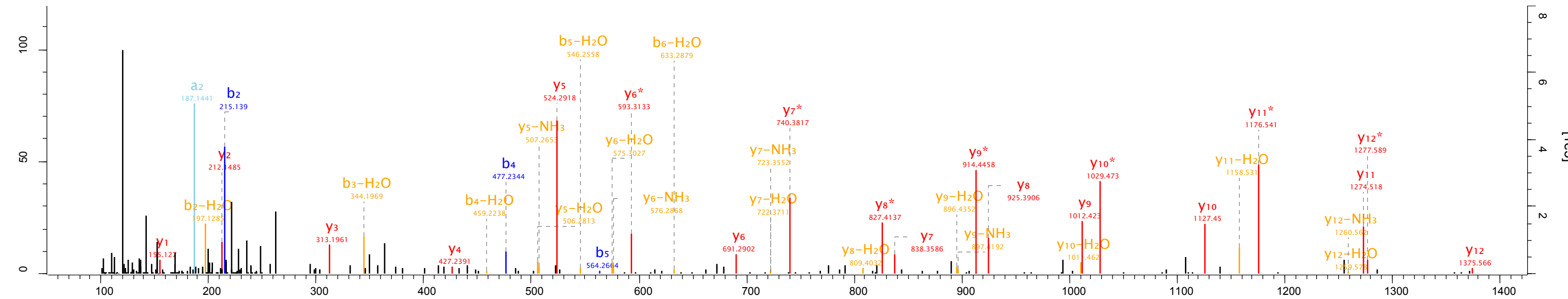
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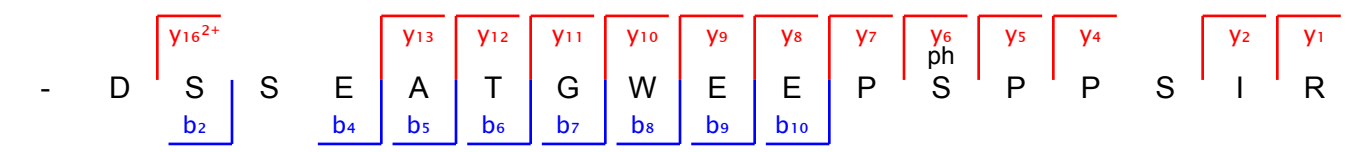
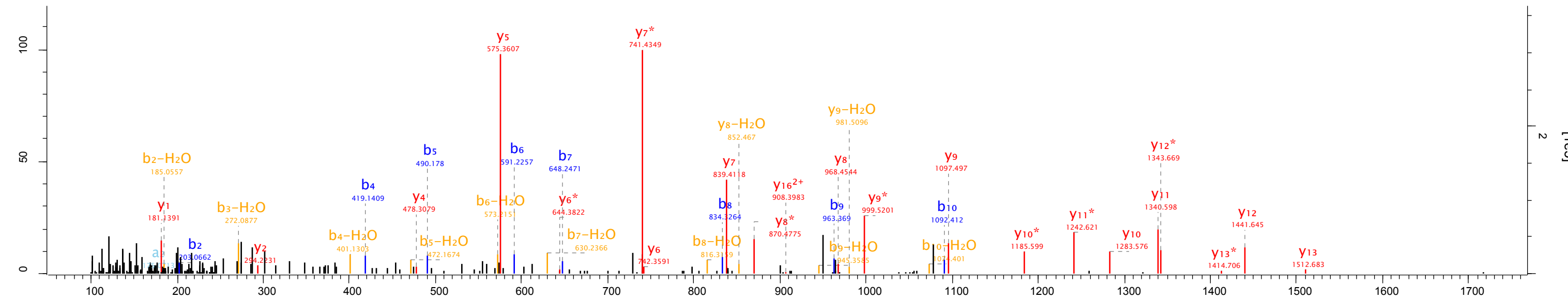
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ph

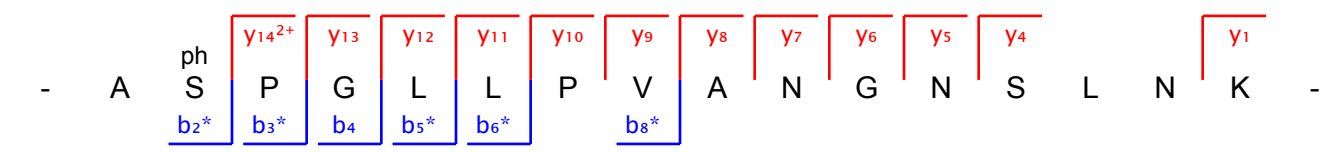
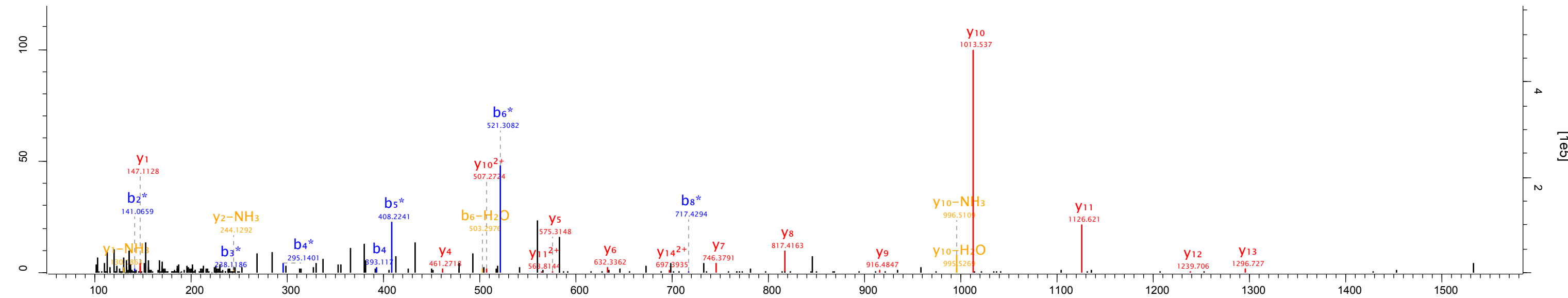
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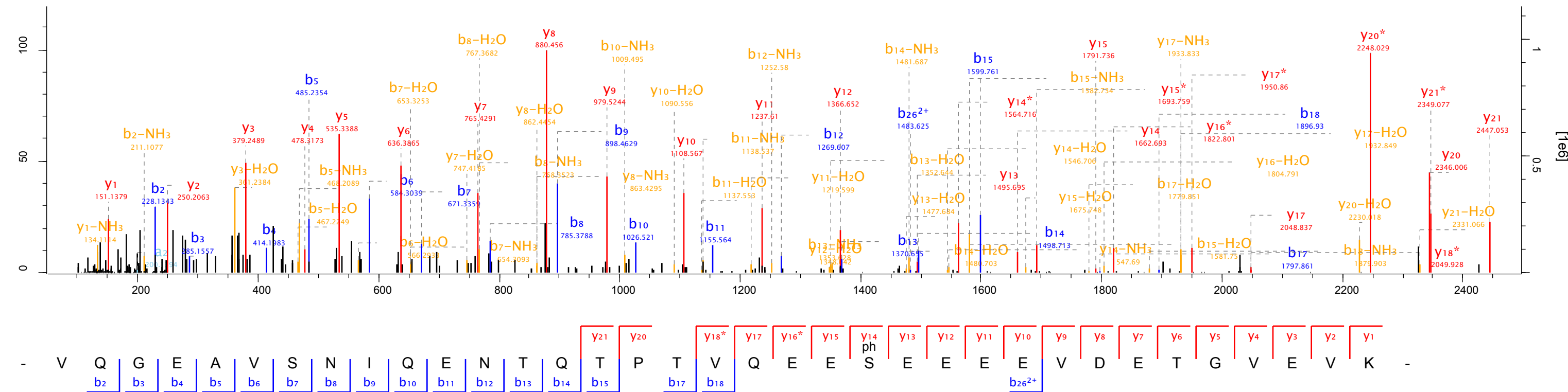
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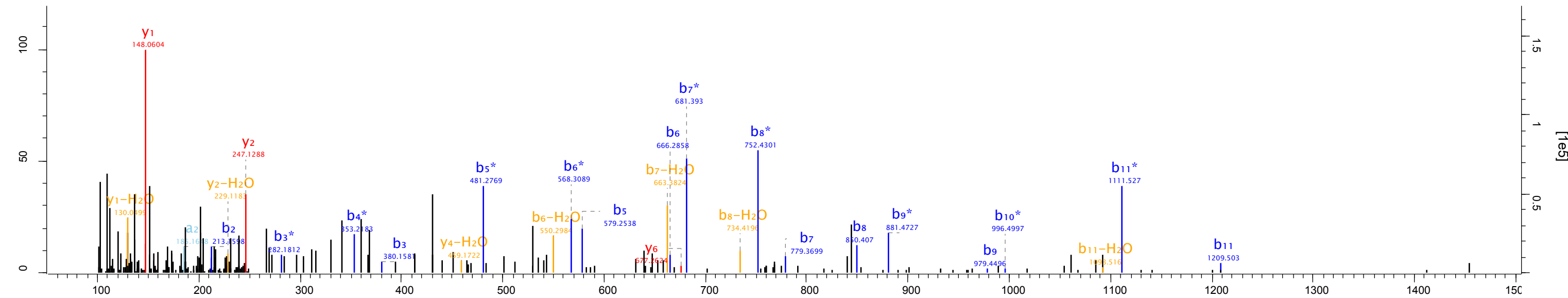


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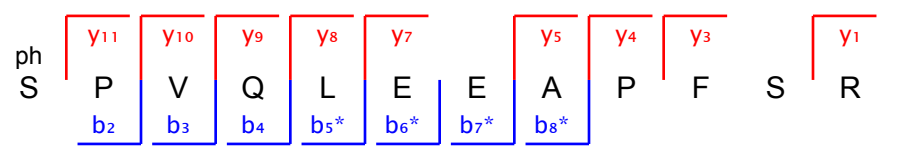
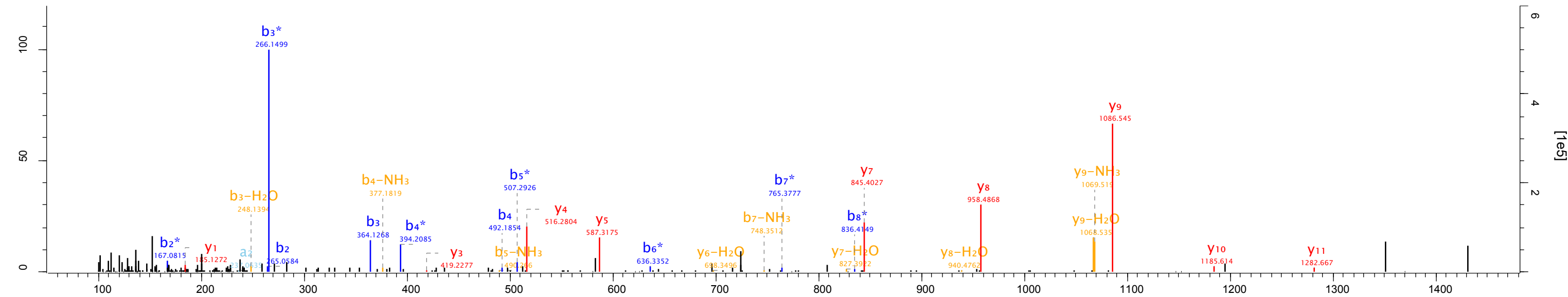


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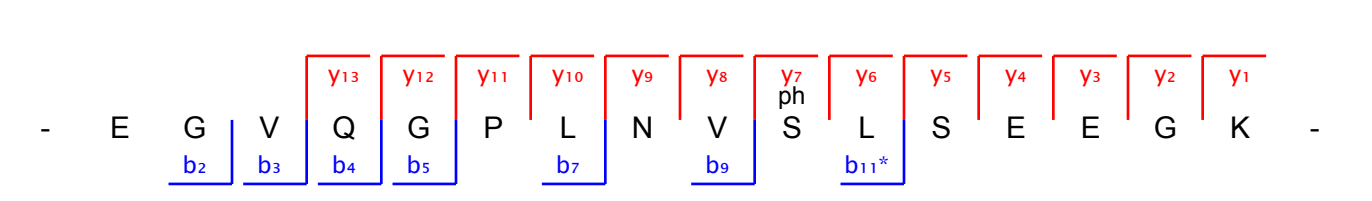
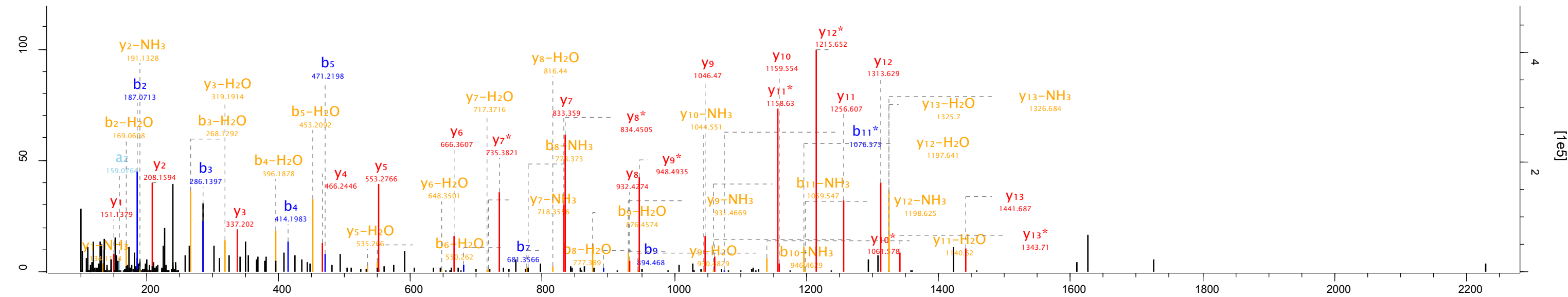
ph
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y₂
y₁

b₂ b₃ b₄* b₅ b₆ b₇ b₈ b₉ b₁₀* b₁₁

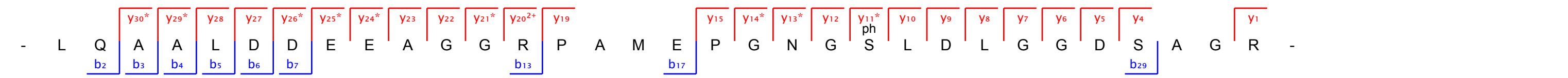
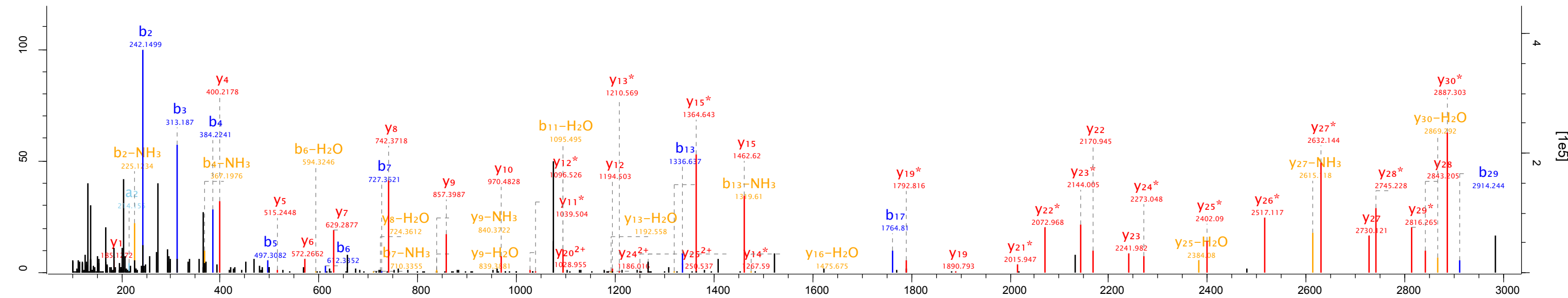
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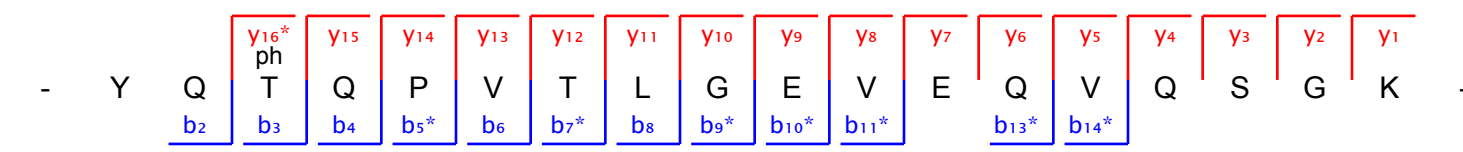
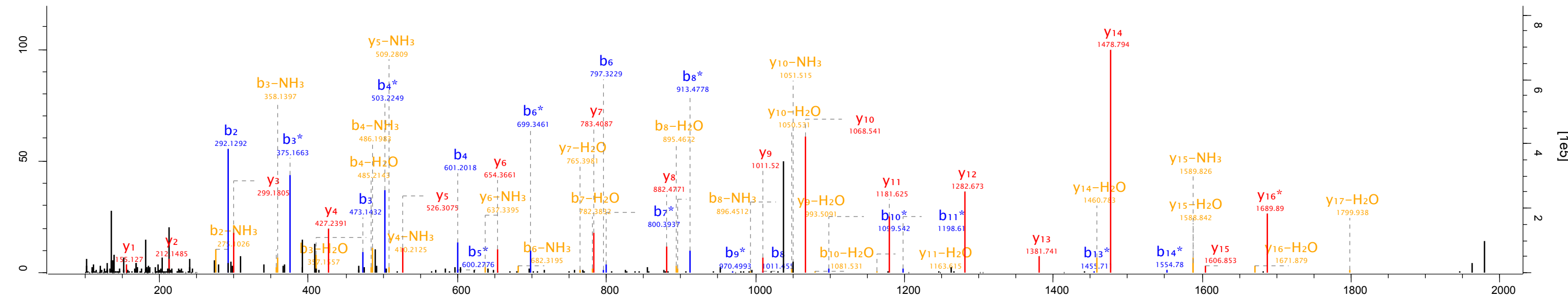
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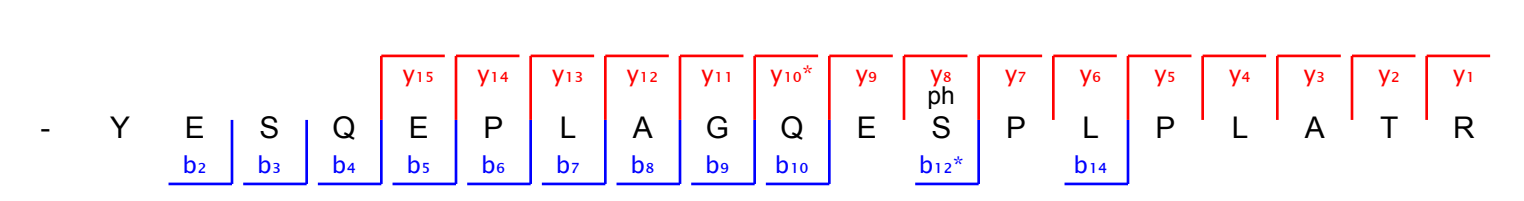
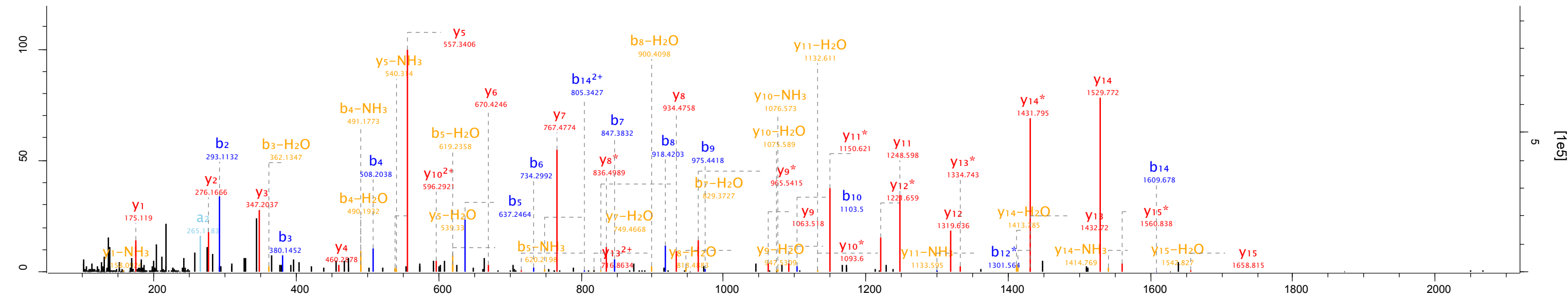
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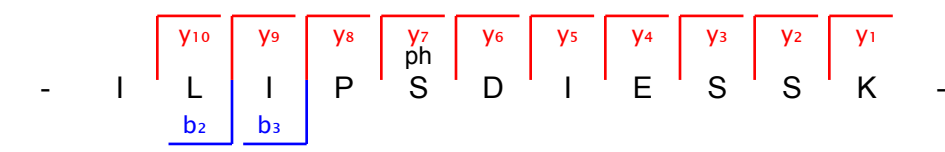
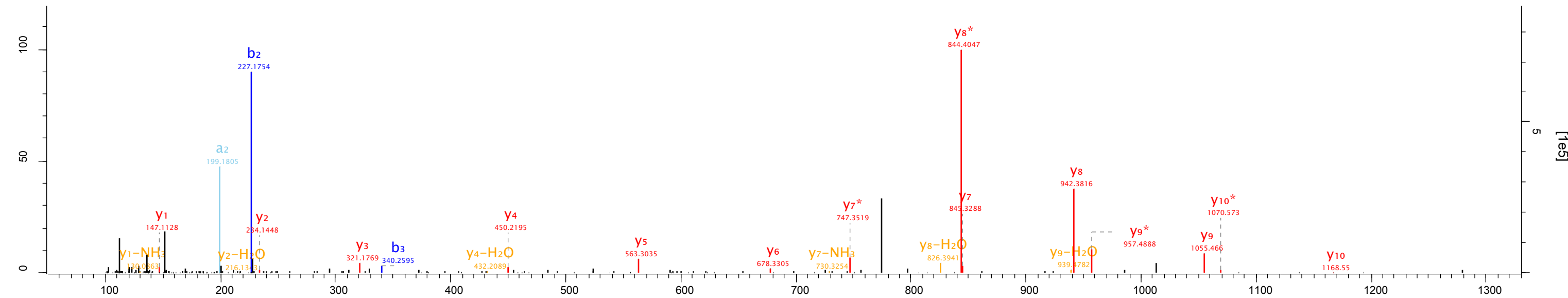
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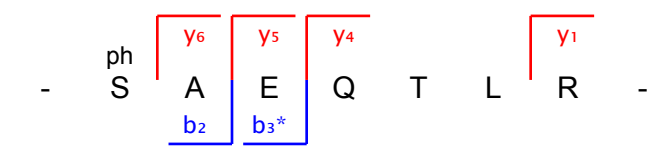
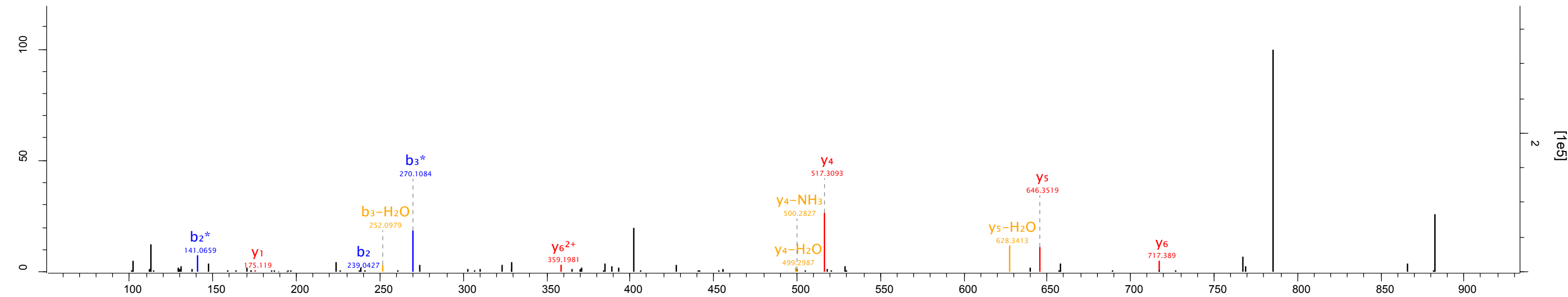
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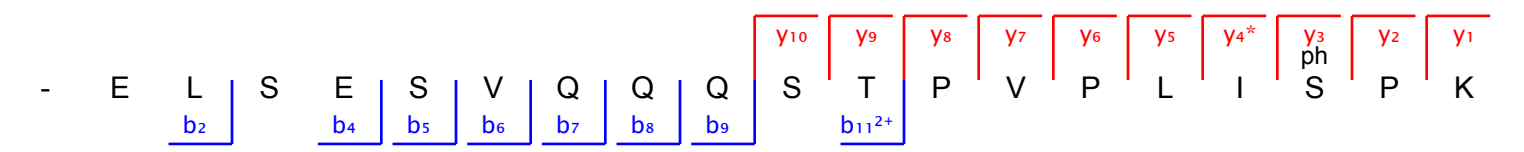
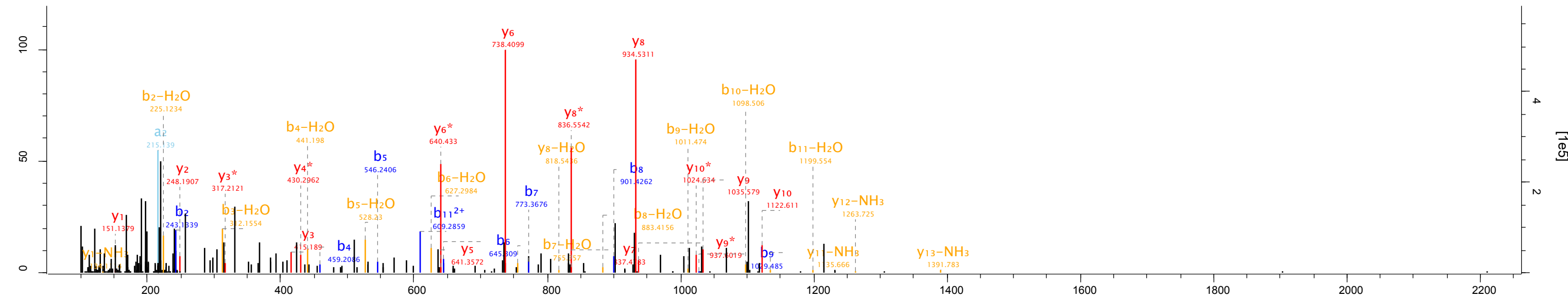
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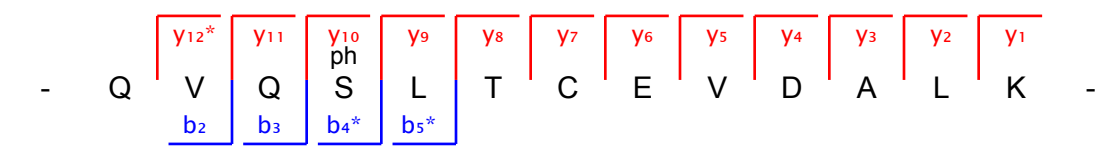
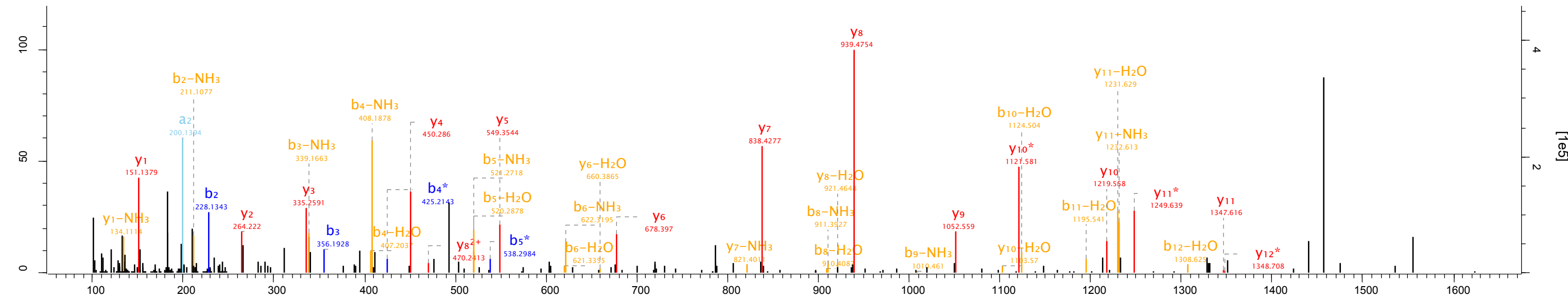
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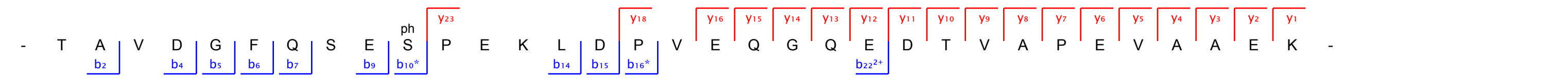
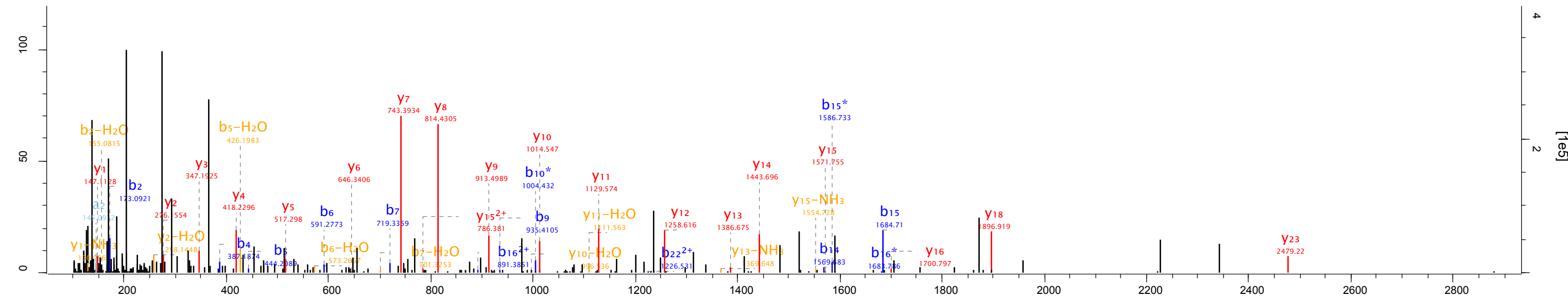
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 14893 Method FTMS; HCD Score 52.96 m/z 717.7 Gene names ZMYND8



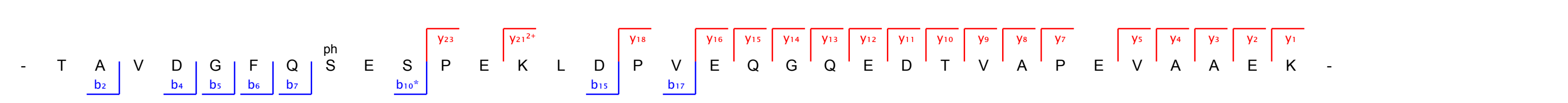
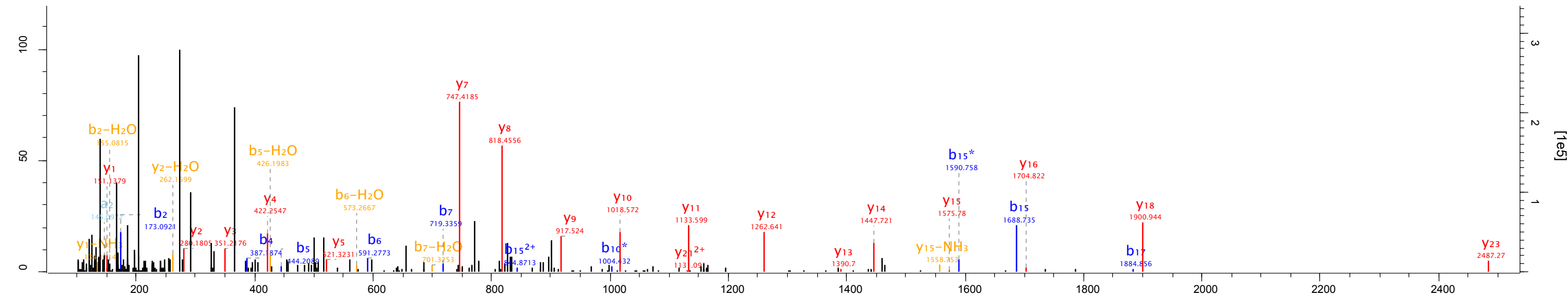
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Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 15363 Method FTMS; HCD Score 68.53 m/z 1194.54 Gene names CDYL



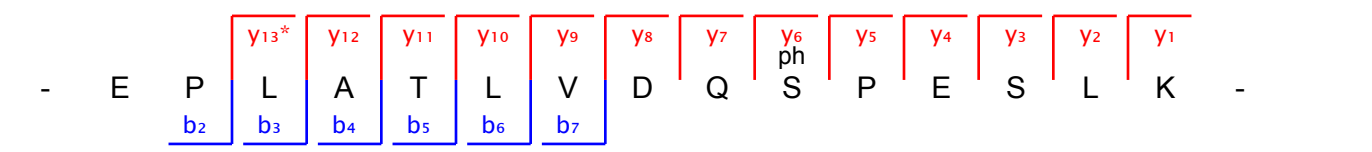
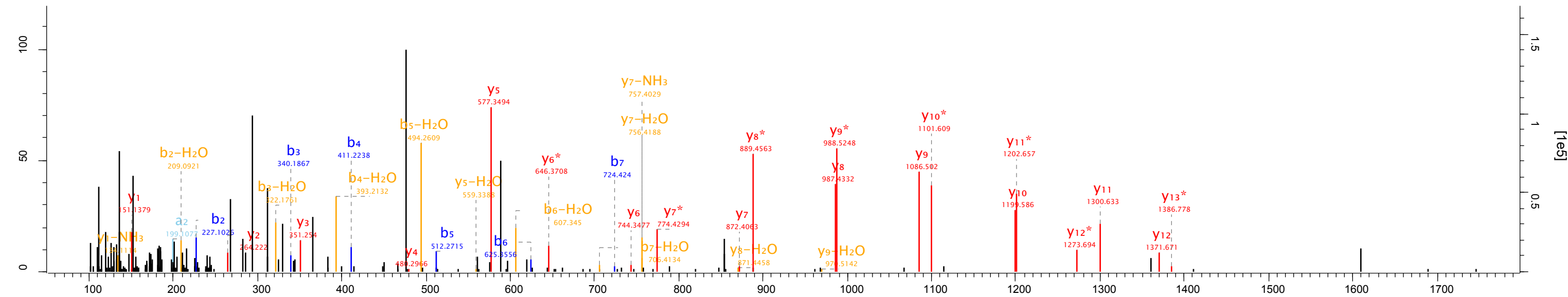
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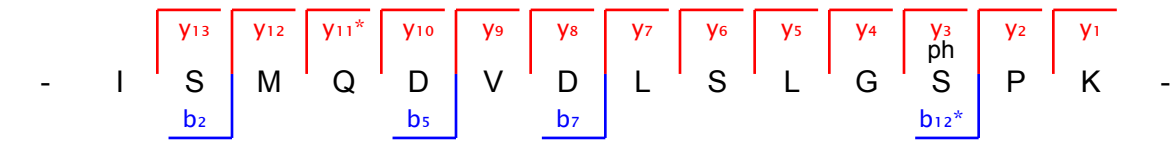
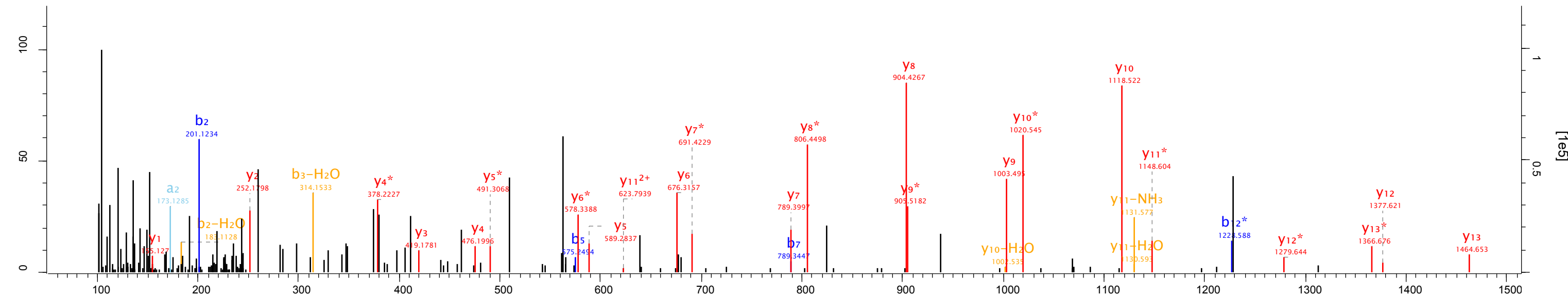


Fragmentation patterns shown in the diagram:

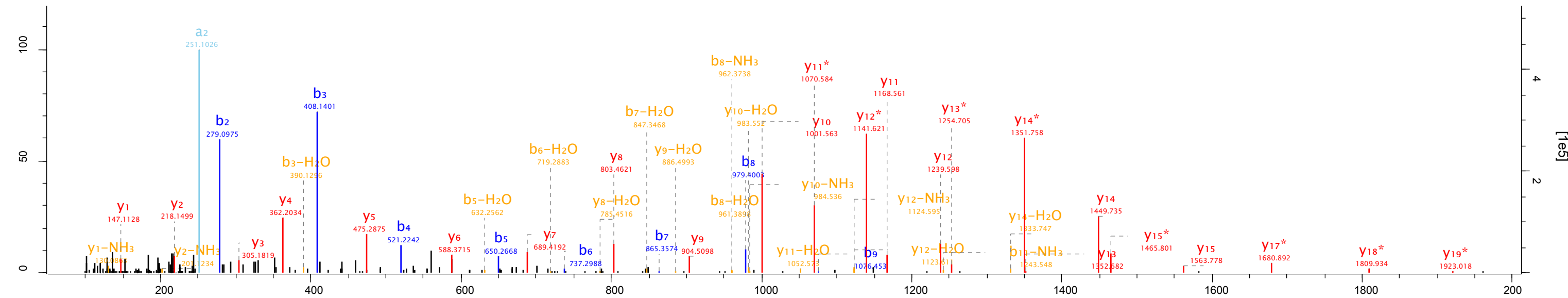
- Blue brackets (b ions): b₂ (A), b₄ (D), b₅ (G), b₆ (F), b₇ (Q), b₁₀^{*} (S), b₁₅ (D), b₁₇ (V).
- Red lines (y ions): y₁ (Q), y₂ (E), y₃ (A), y₄ (A), y₅ (V), y₇ (A), y₈ (V), y₉ (T), y₁₀ (D), y₁₁ (E), y₁₂ (Q), y₁₃ (G), y₁₄ (E), y₁₅ (Q), y₁₆ (V), y₁₈ (P), y₂₁²⁺ (K), y₂₃ (P).

Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 15593 Method FTMS; HCD Score 173.49 m/z 855.93 Gene names ASXL2



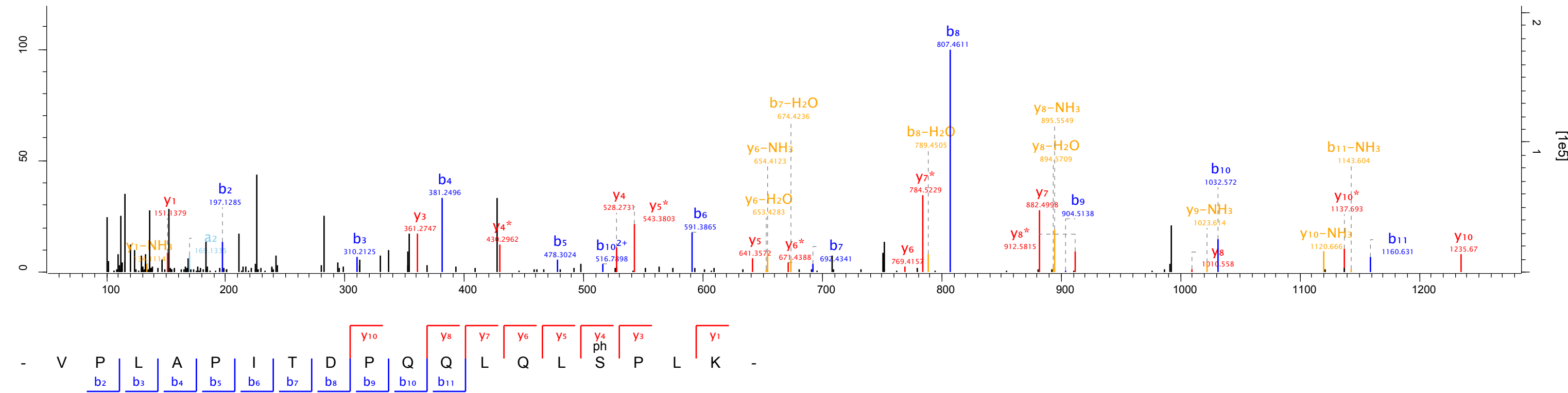


Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 18893 Method FTMS; HCD Score 140.9 m/z 810.05 Gene names NUFIP2

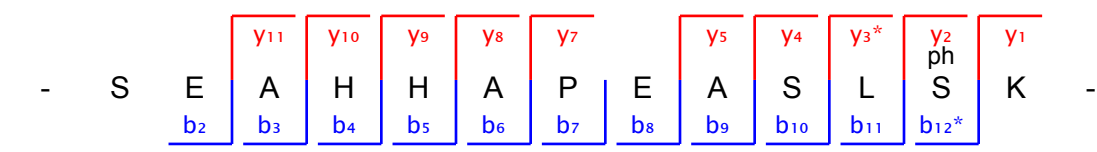
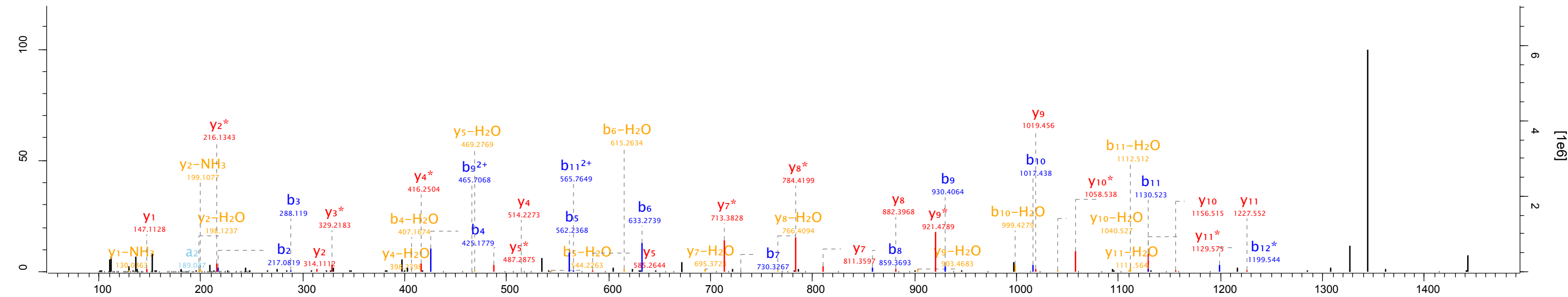


- D Y E I E S Q N P L A S P T N T L L G S A K -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
y₁₉*
y₁₈*
y₁₇*
y₁₅
y₁₄
y₁₃
y₁₂
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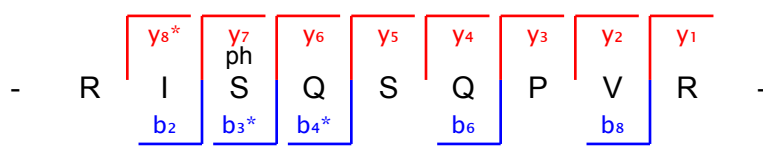
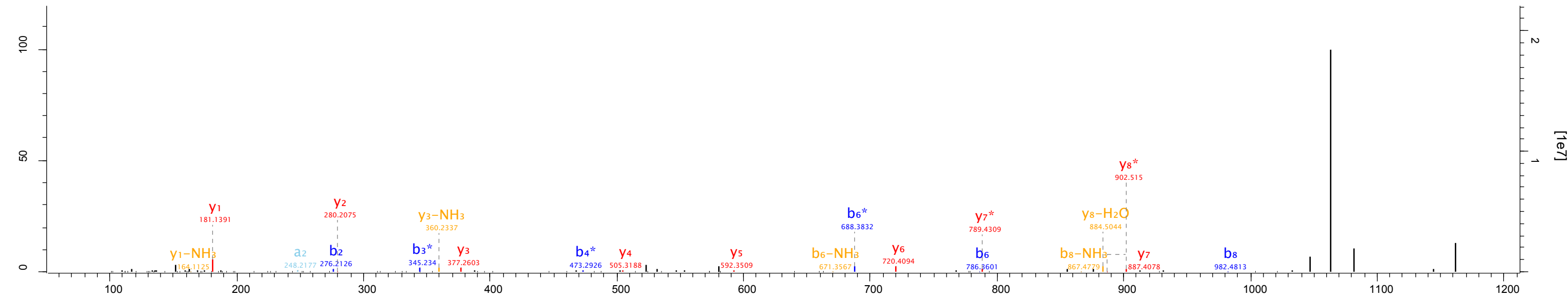
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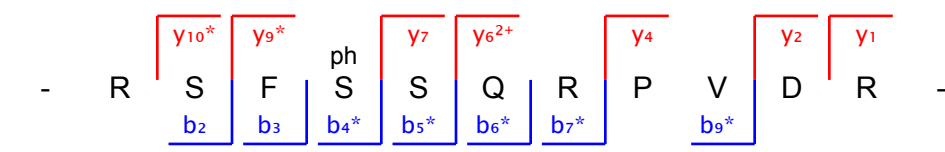
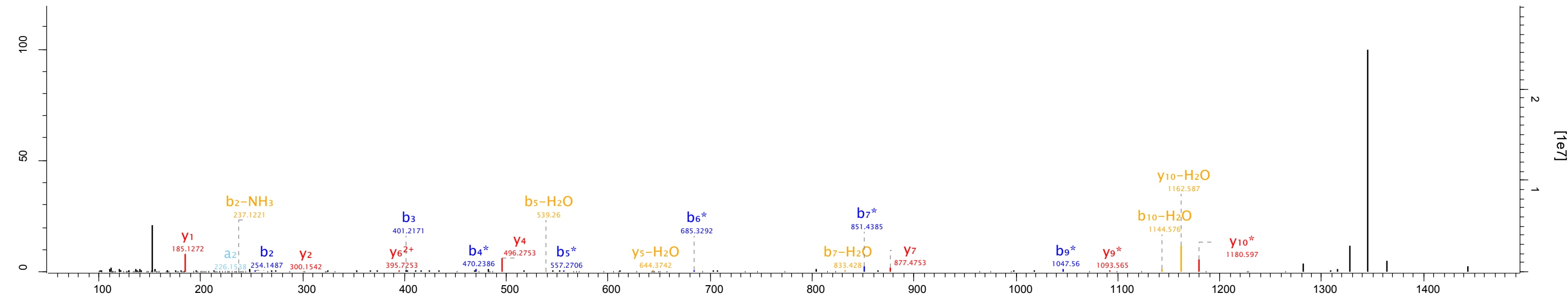
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20171215_MaS_33SR_LMH_phospho_06

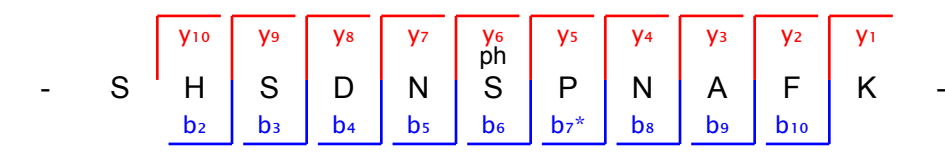
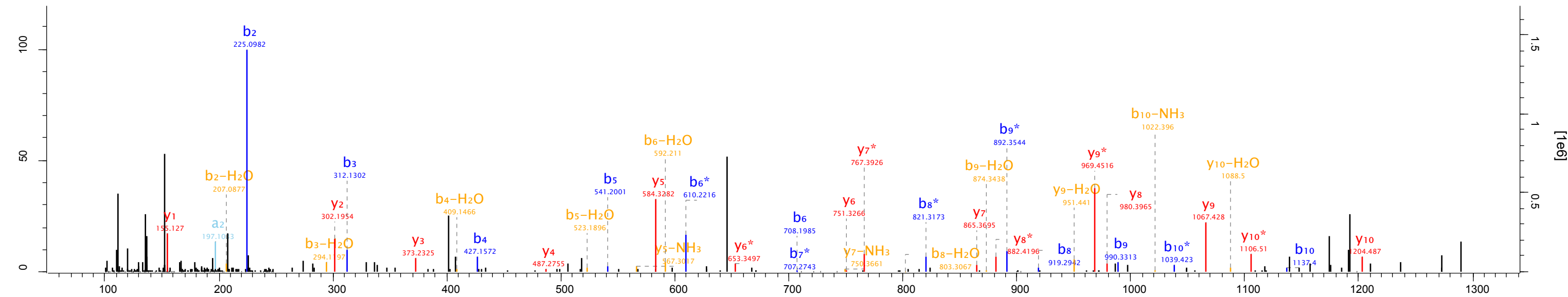
Scan 2703 Method FTMS; HCD Score 88.1 m/z 581.81 Gene names UBR5



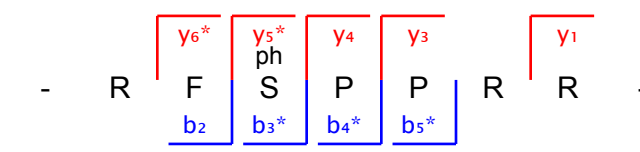
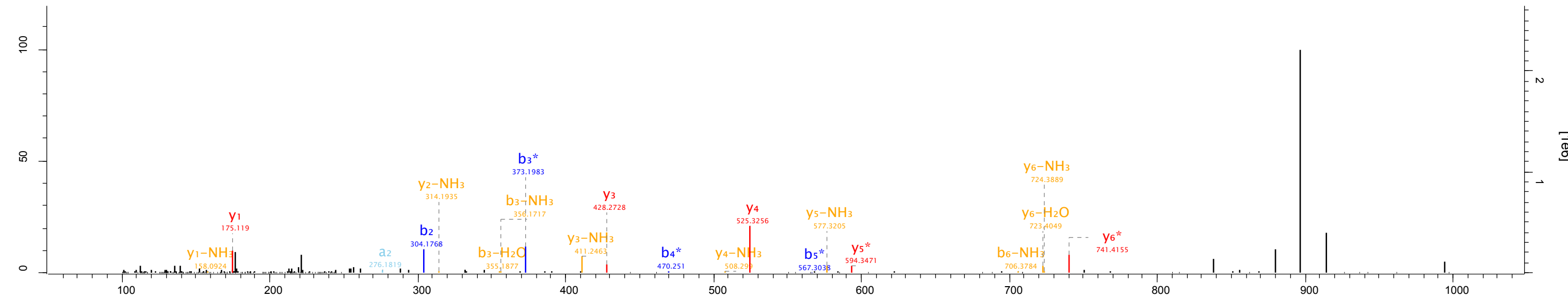
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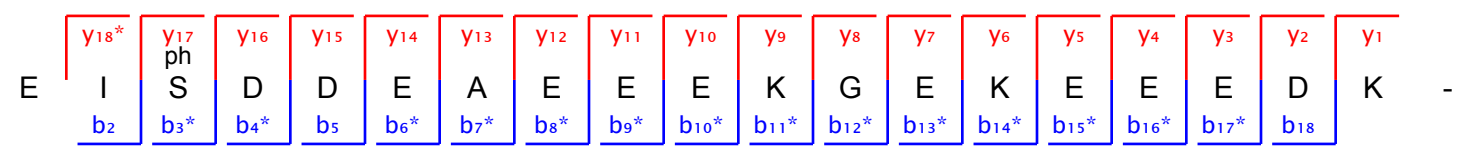
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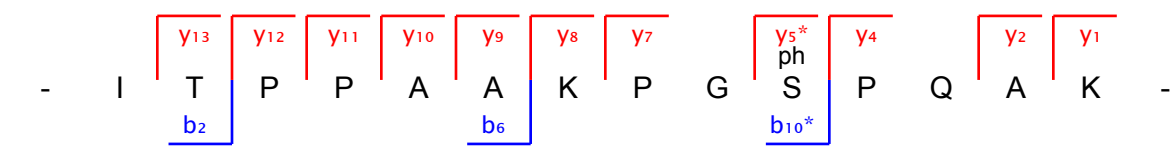
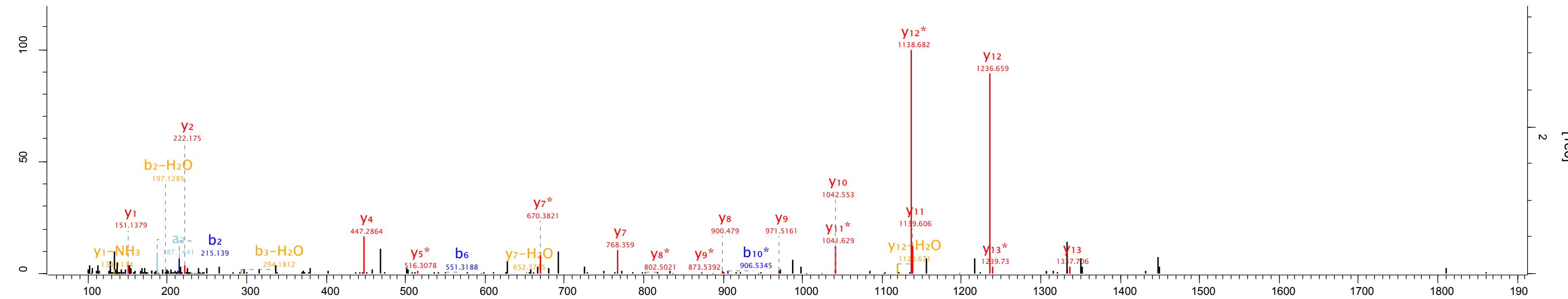
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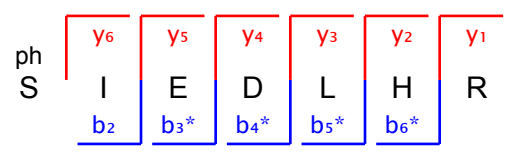
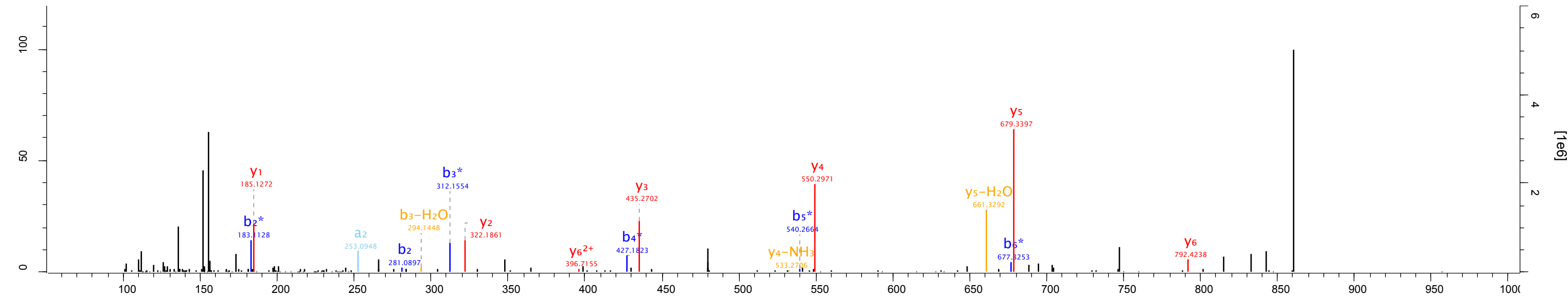
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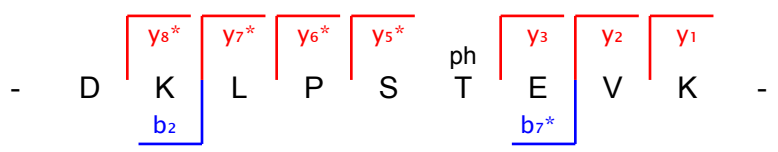
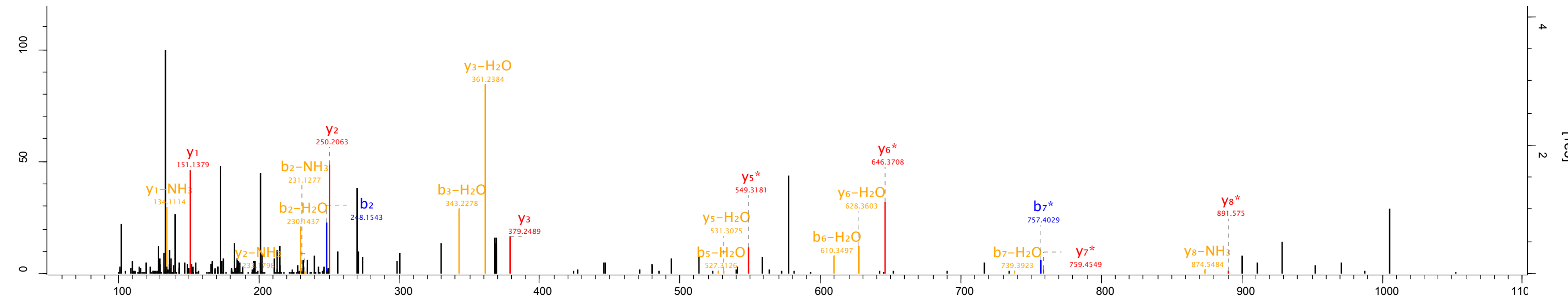
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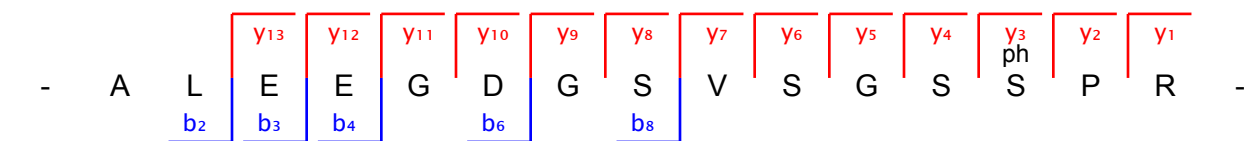
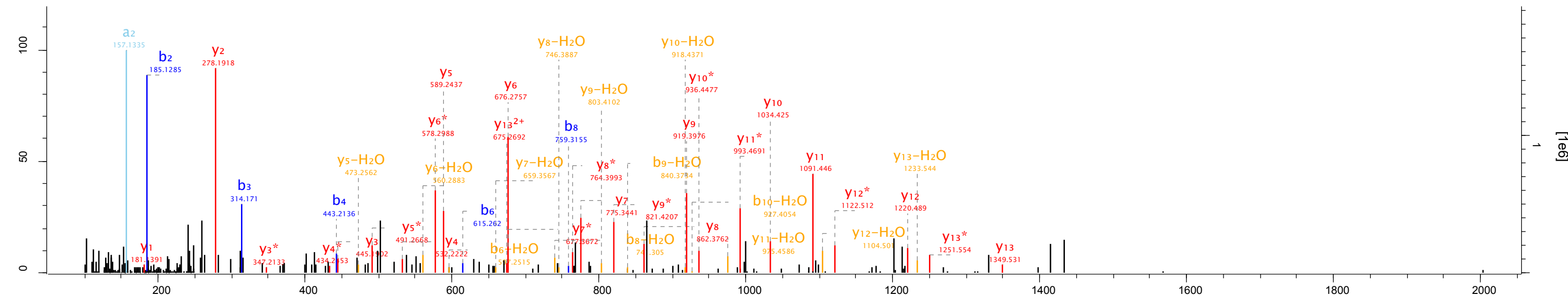


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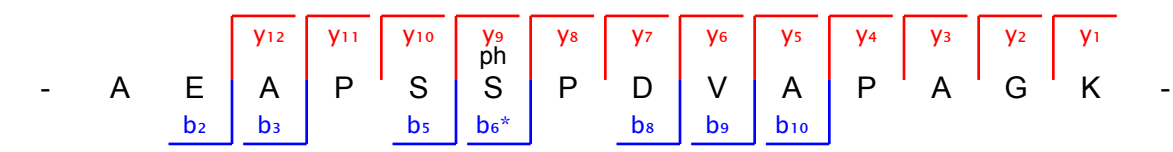
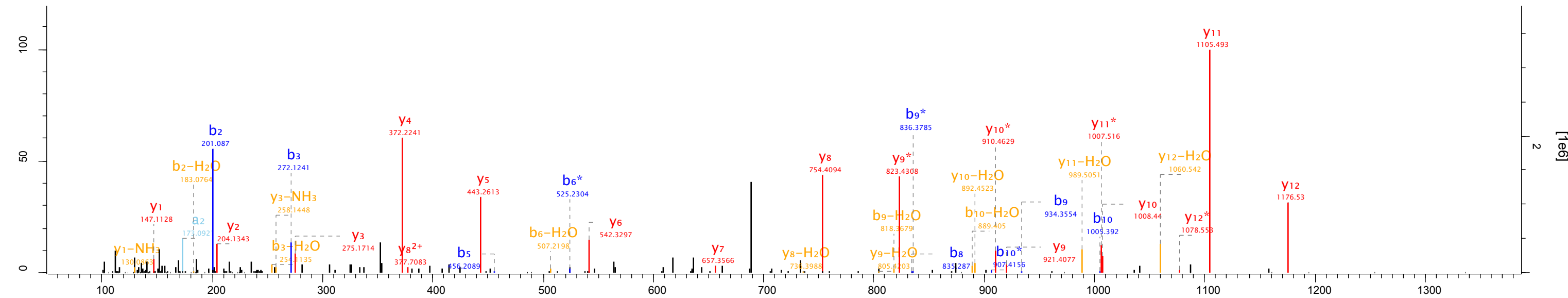


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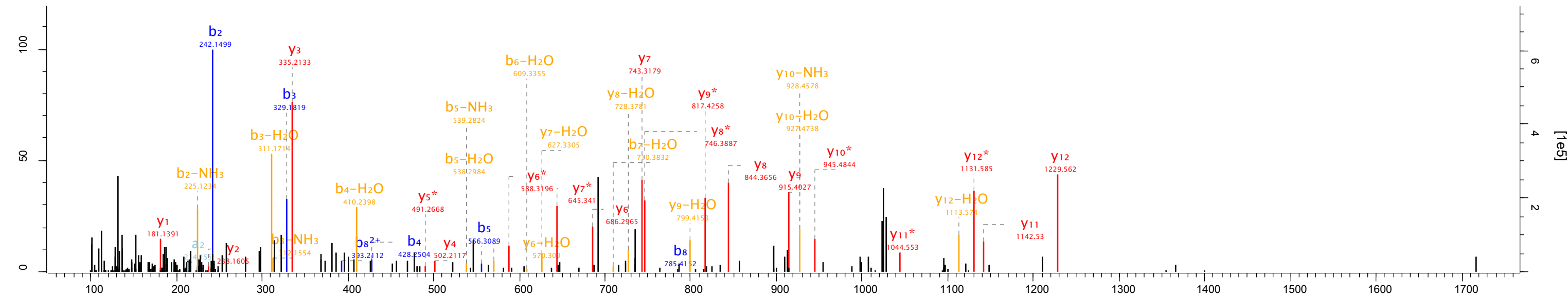




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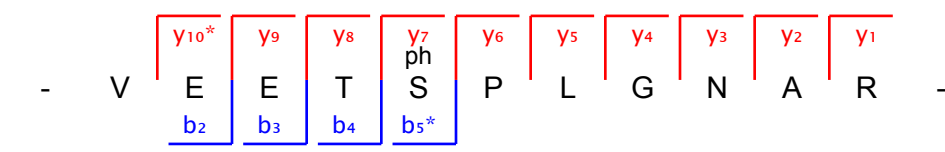
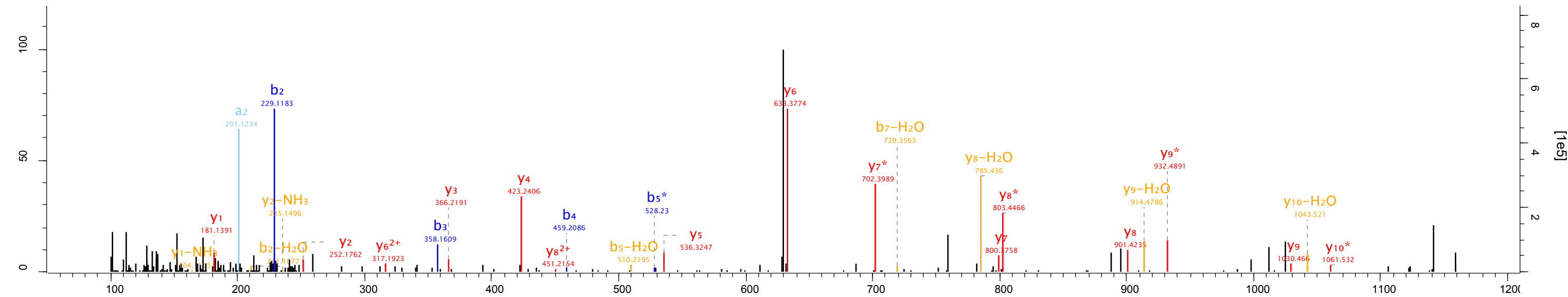


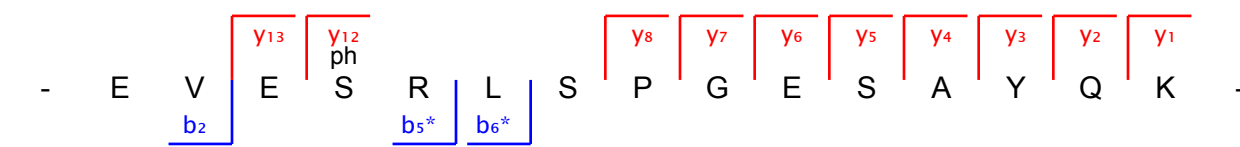
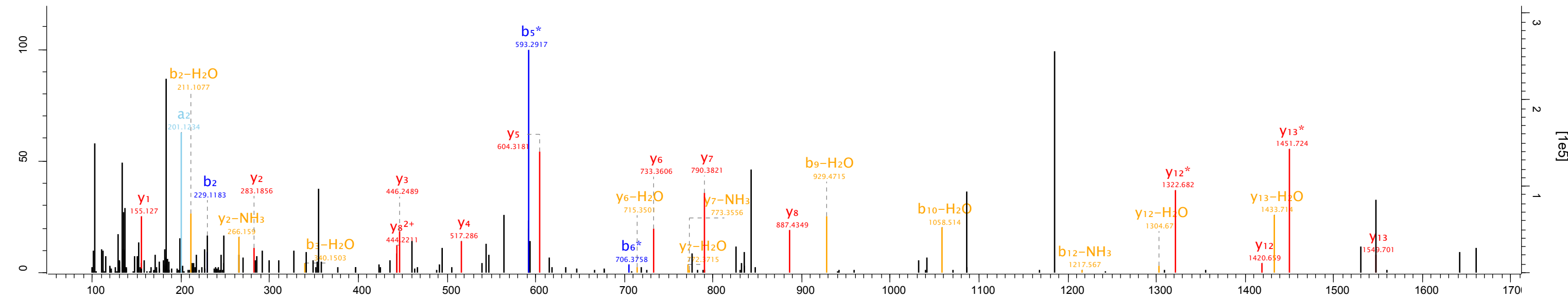
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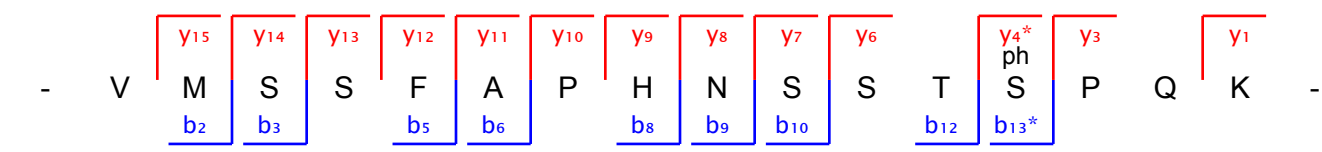
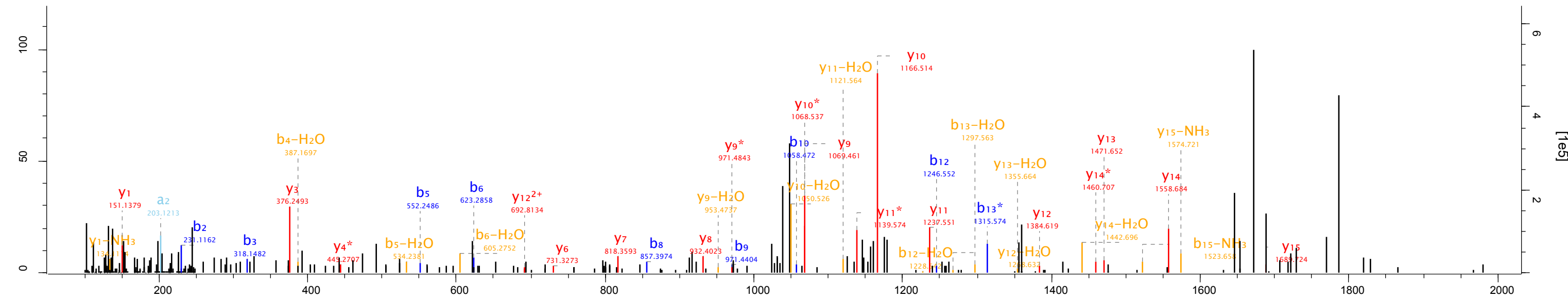
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 b₂ b₃ b₄ b₅ b₈
 y₁₂ y₁₁ y₁₀* y₉ y₈ y₇ y₆ y₅* y₄ y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 5833 Method FTMS; HCD Score 136.3 m/z 629.79 Gene names NKTR

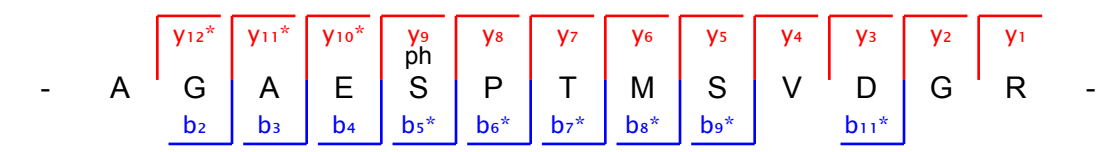
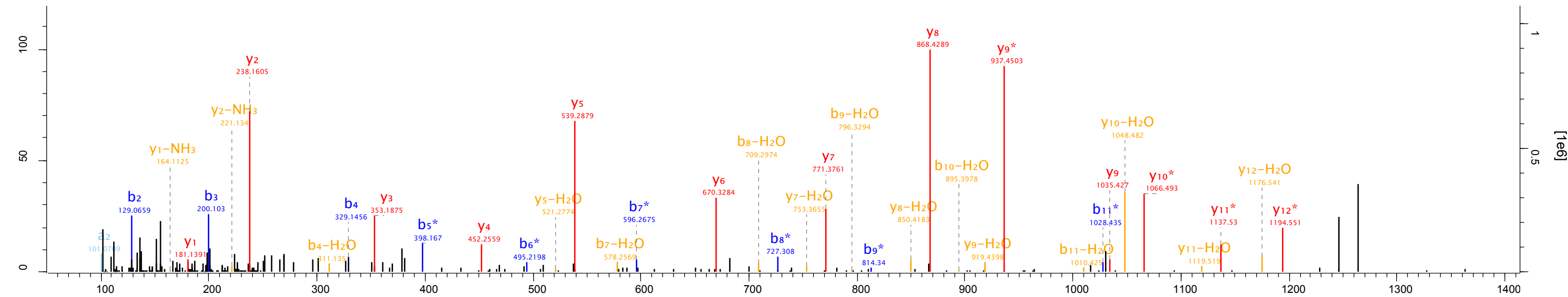




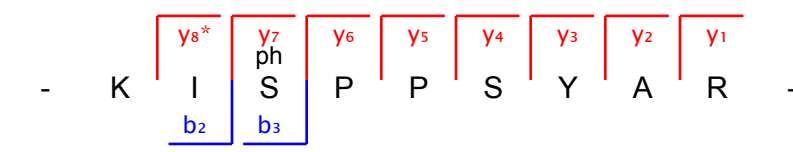
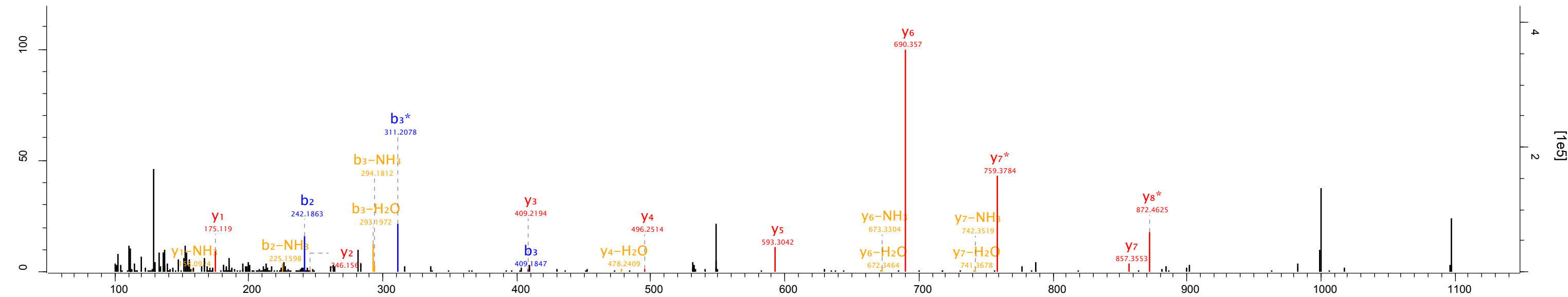
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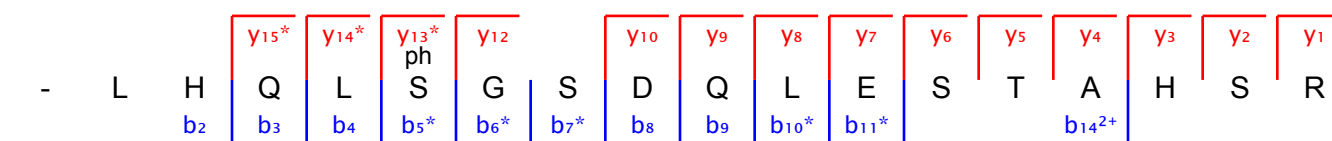
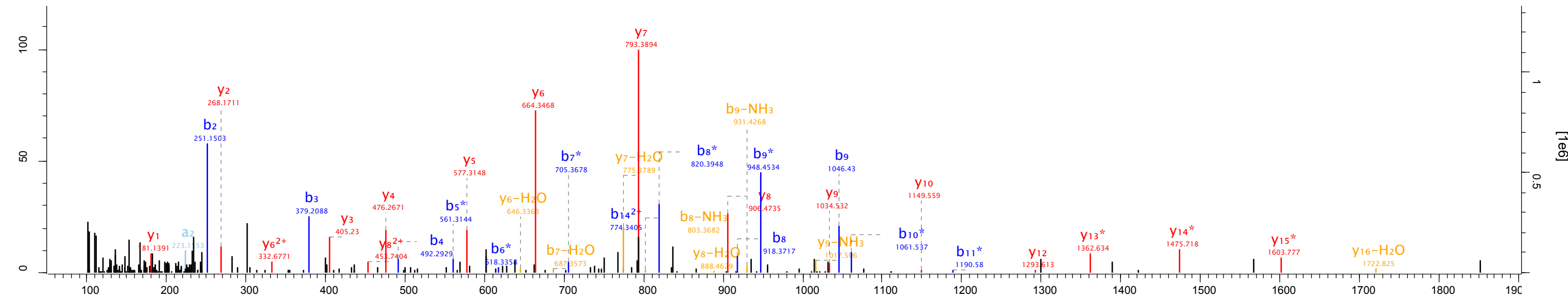
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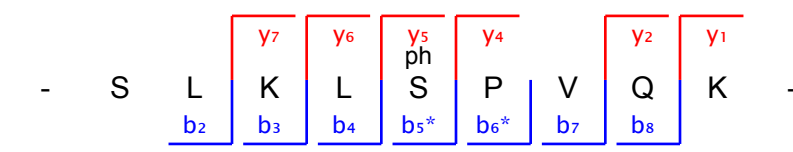
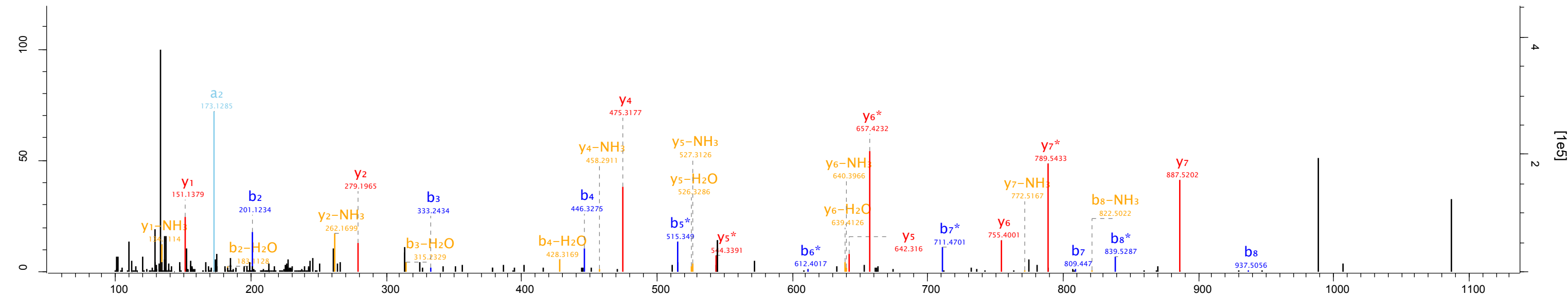
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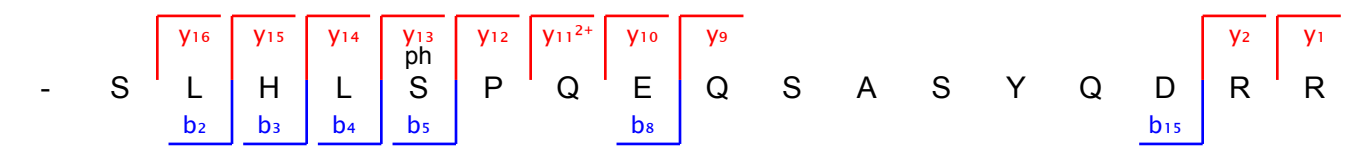
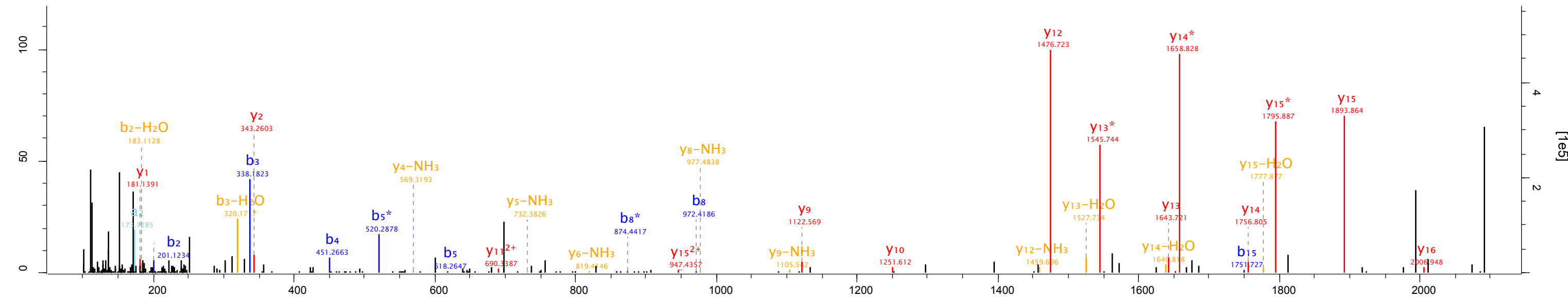
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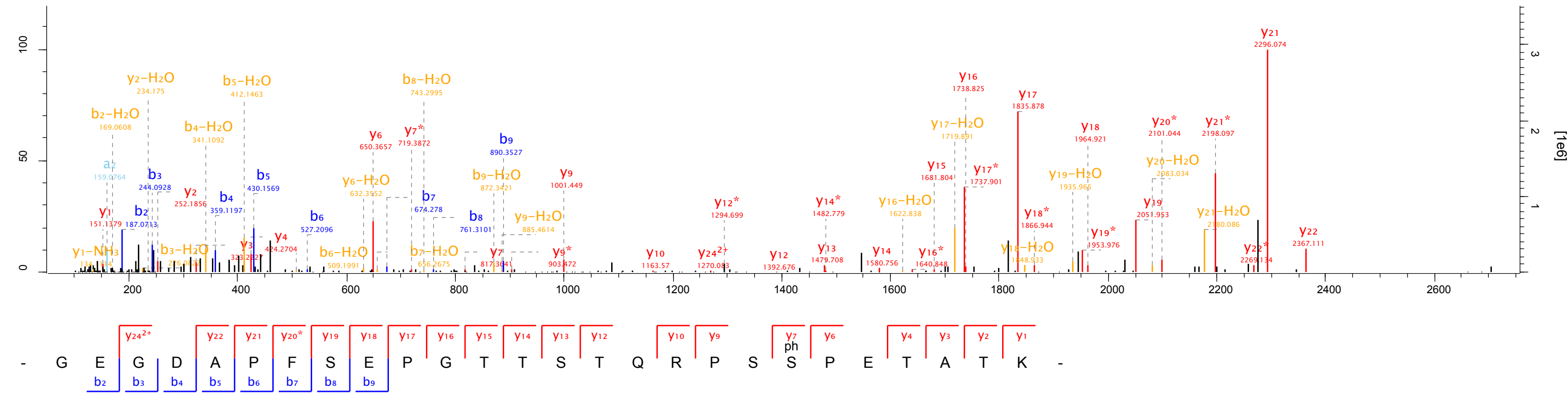
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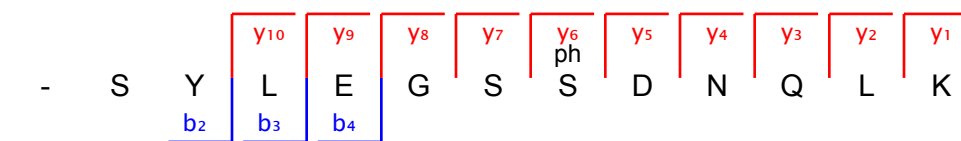
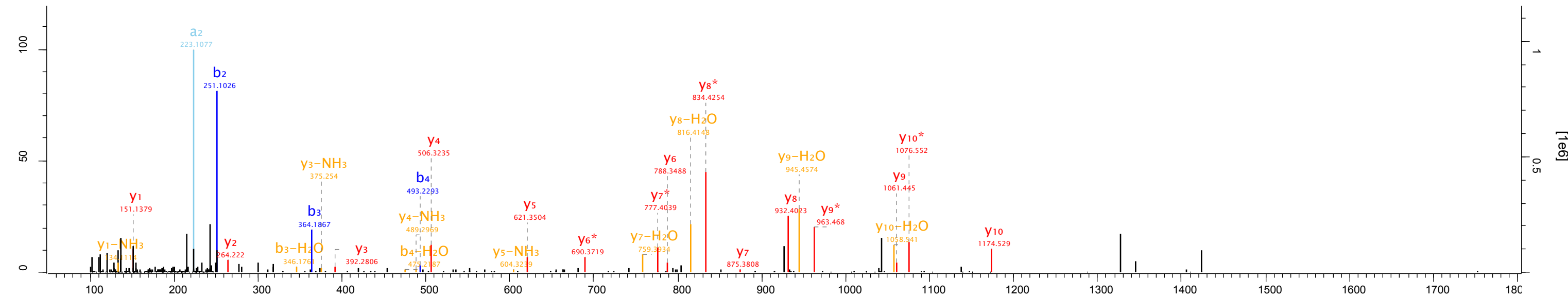


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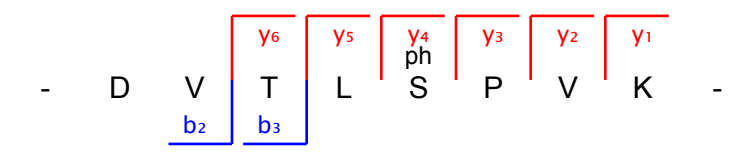
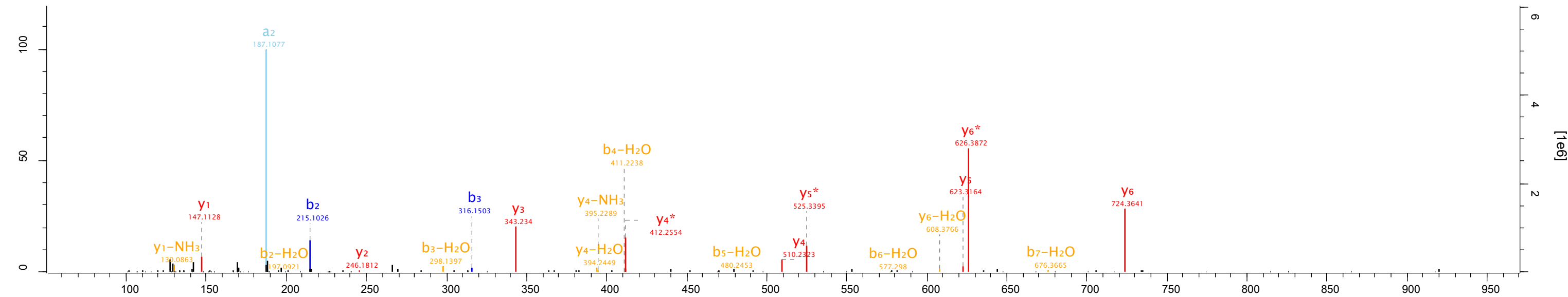


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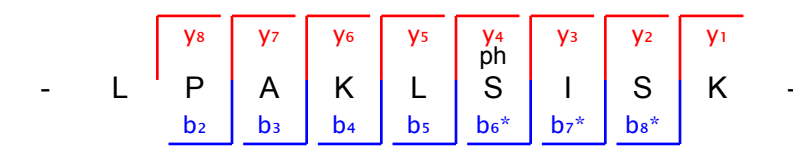
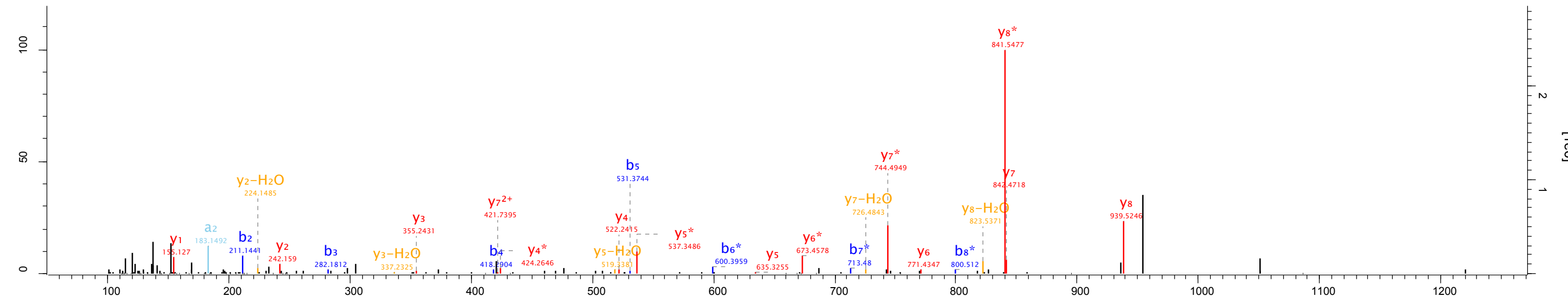
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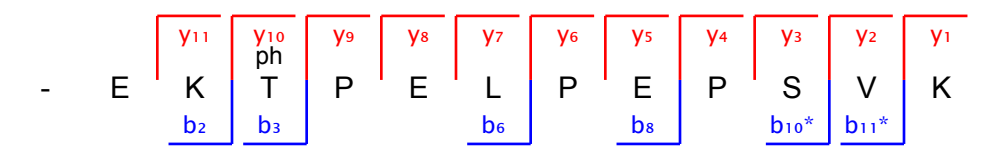
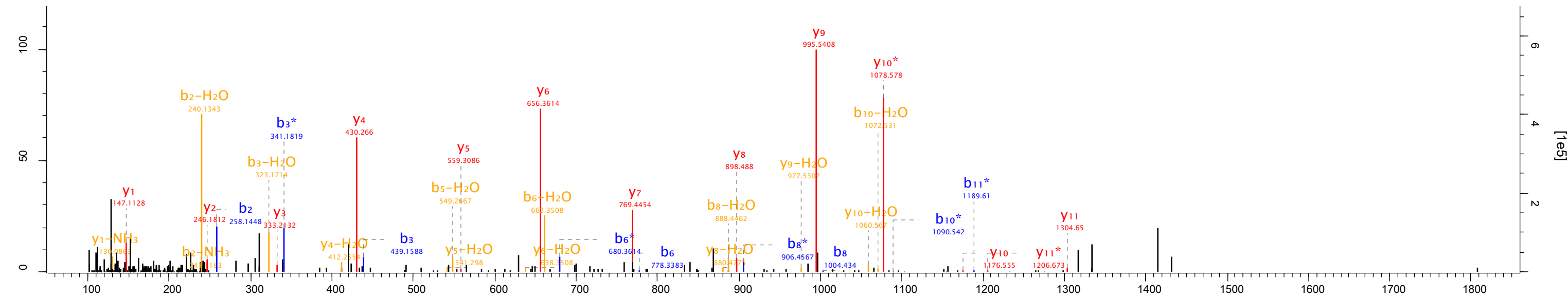
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20171215_MaS_33SR_LMH_phospho_06

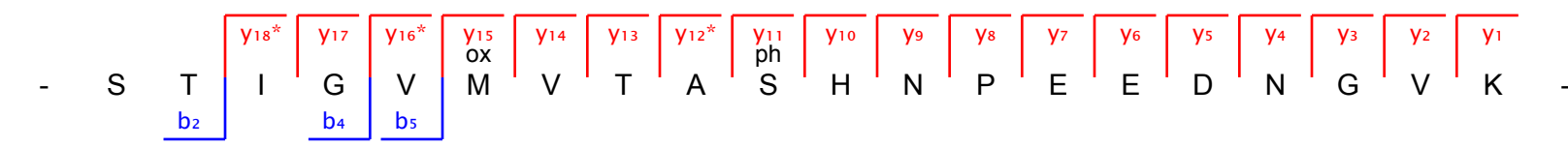
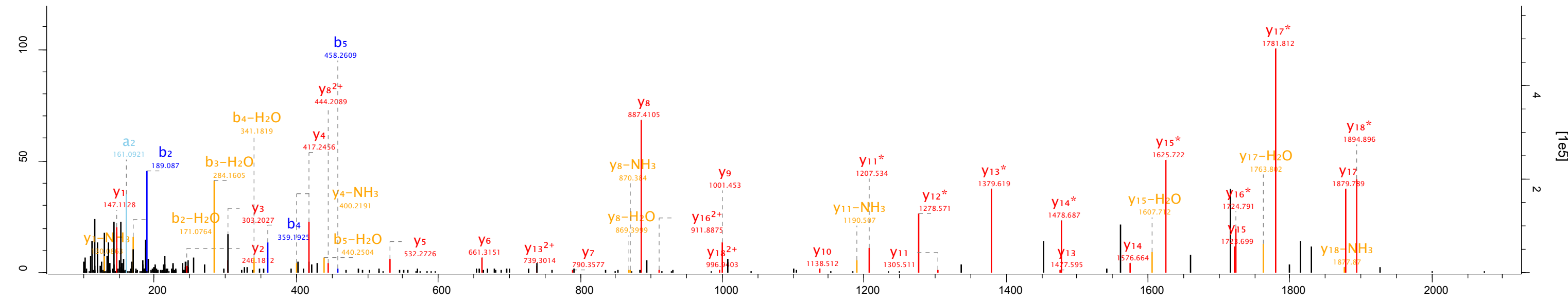
Scan	Method	Score	m/z	Gene names
8873	FTMS; HCD	135.94	526.81	PTRF



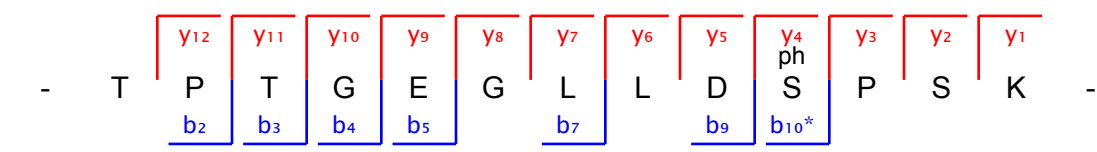
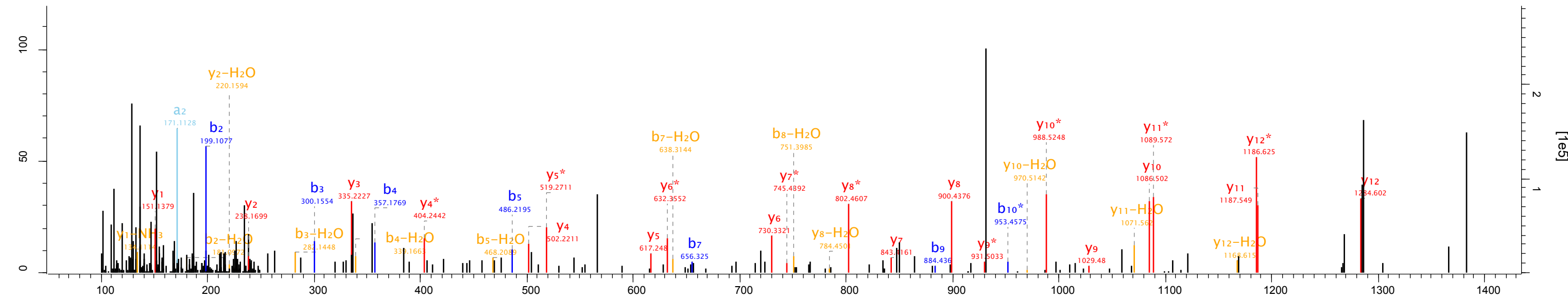
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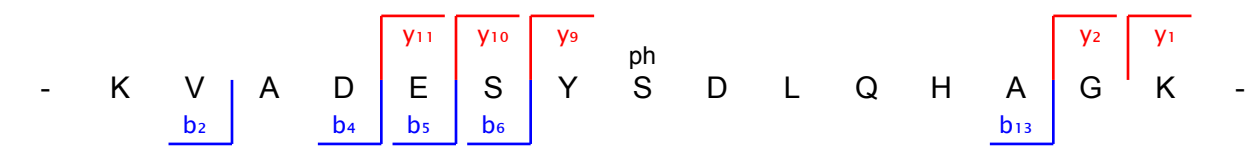
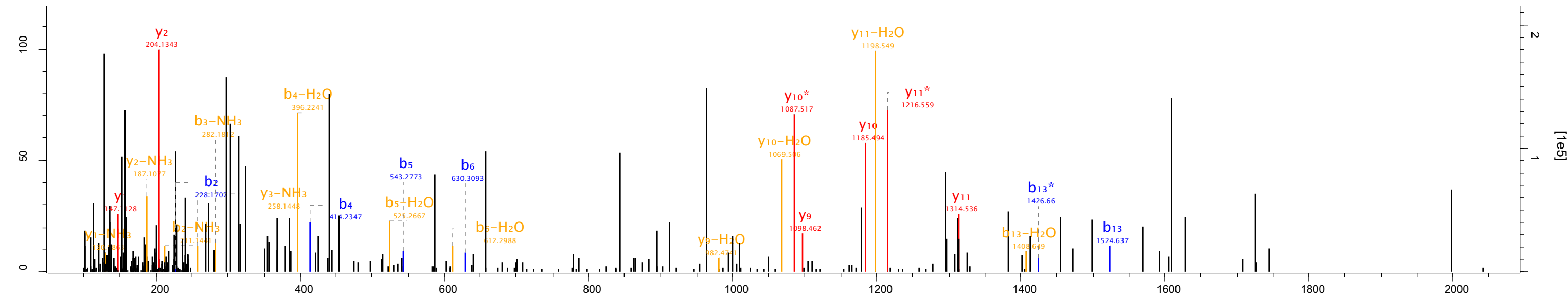
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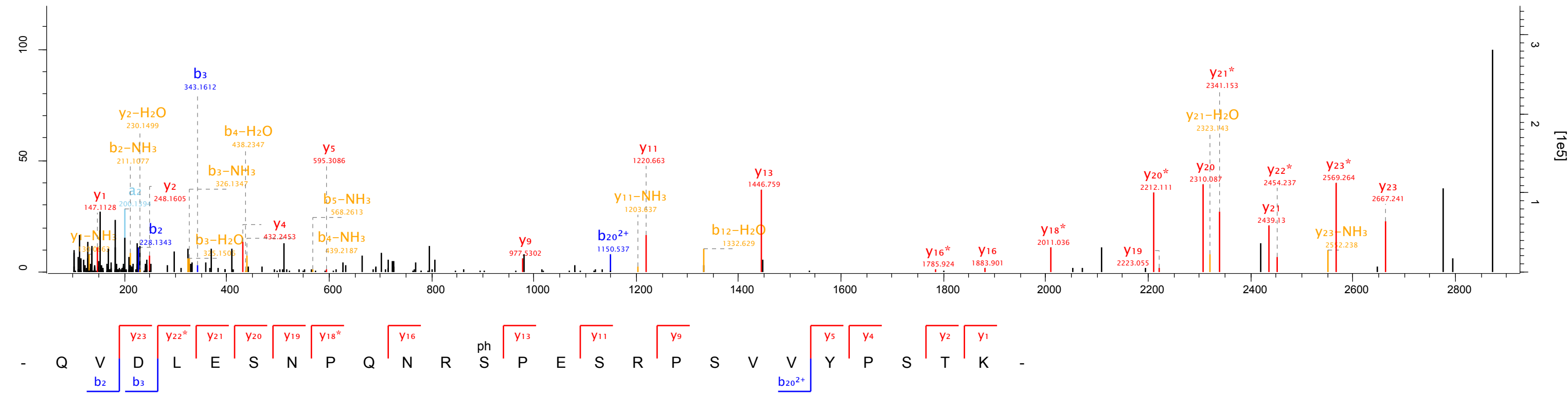
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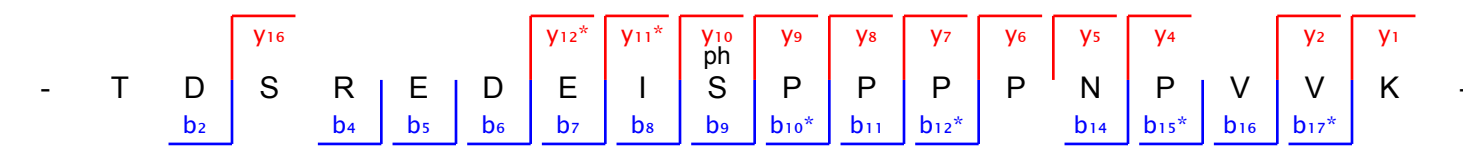
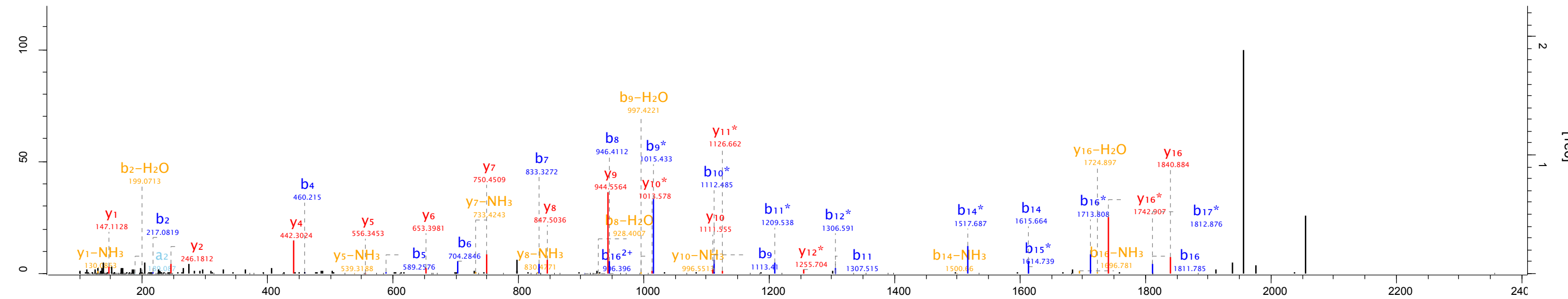
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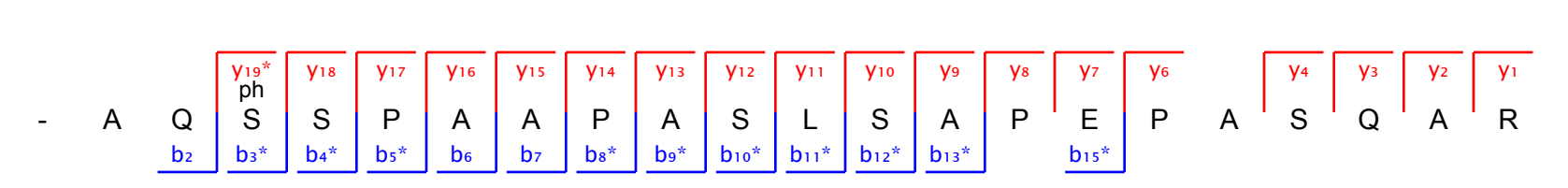
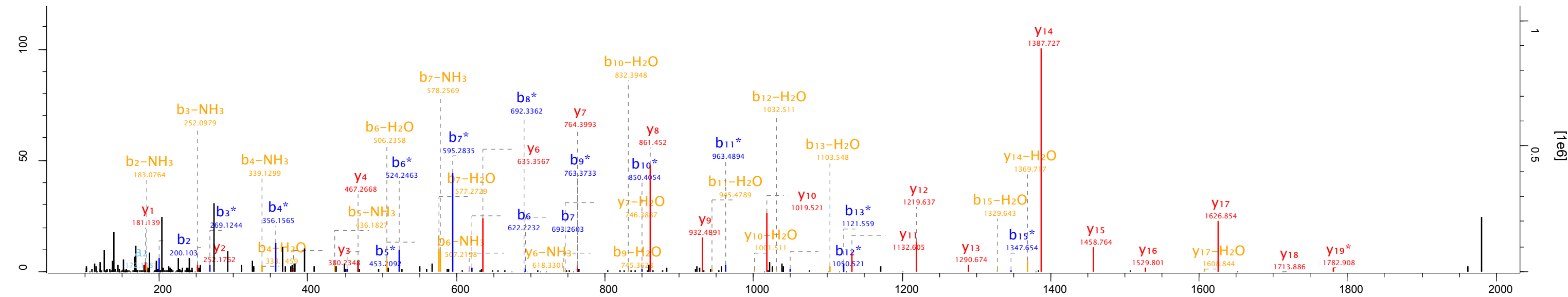
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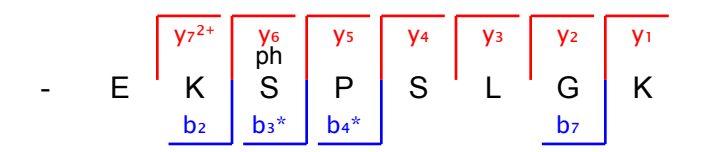
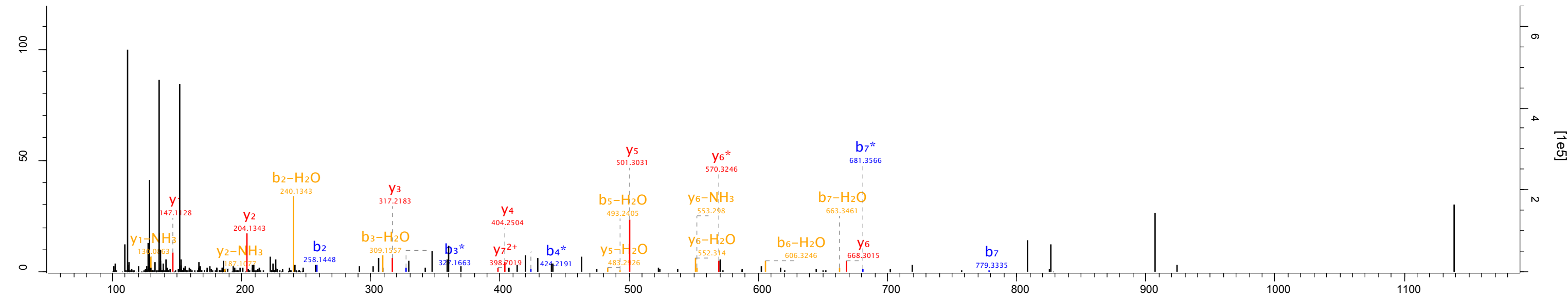
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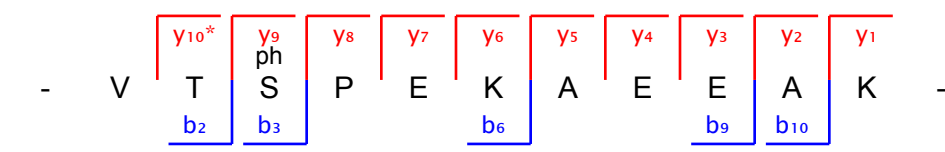
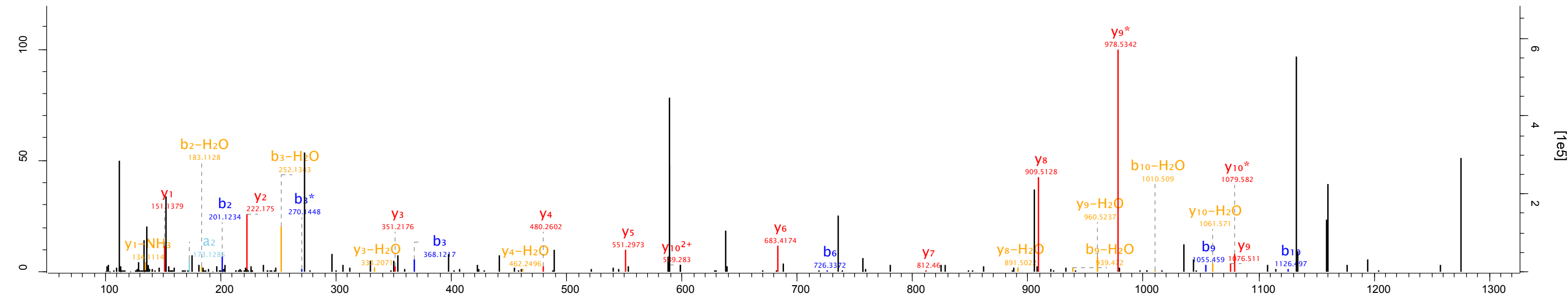
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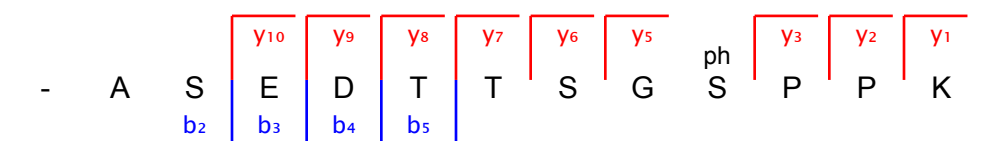
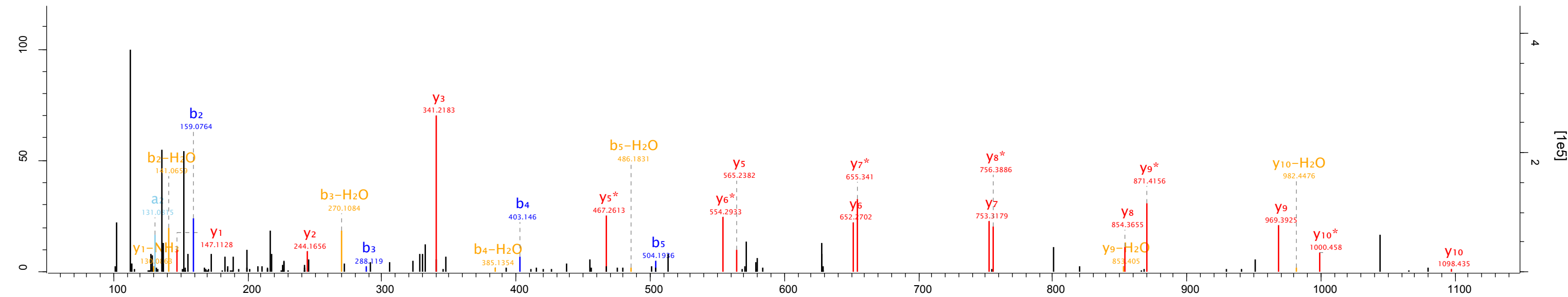
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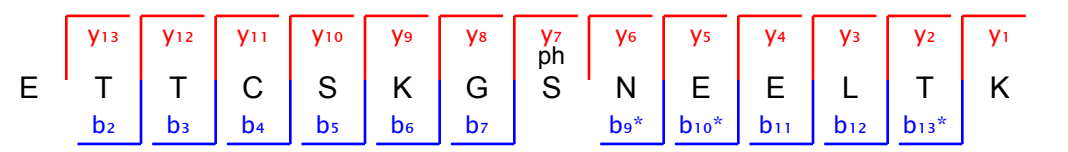
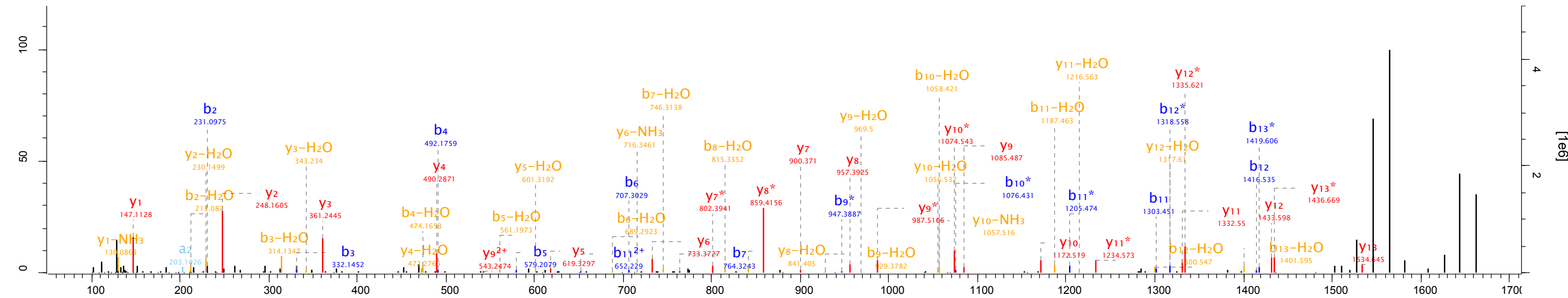
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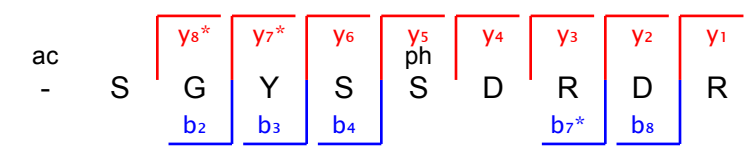
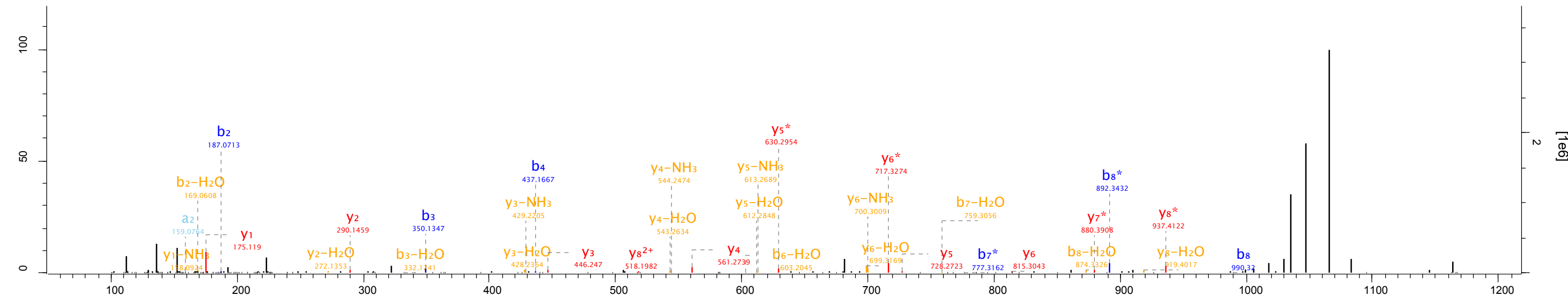
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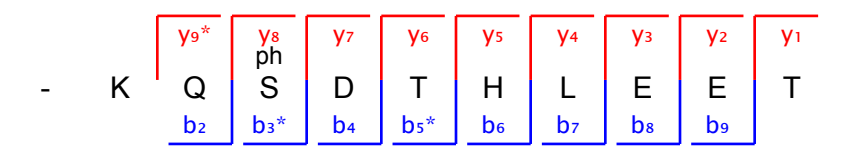
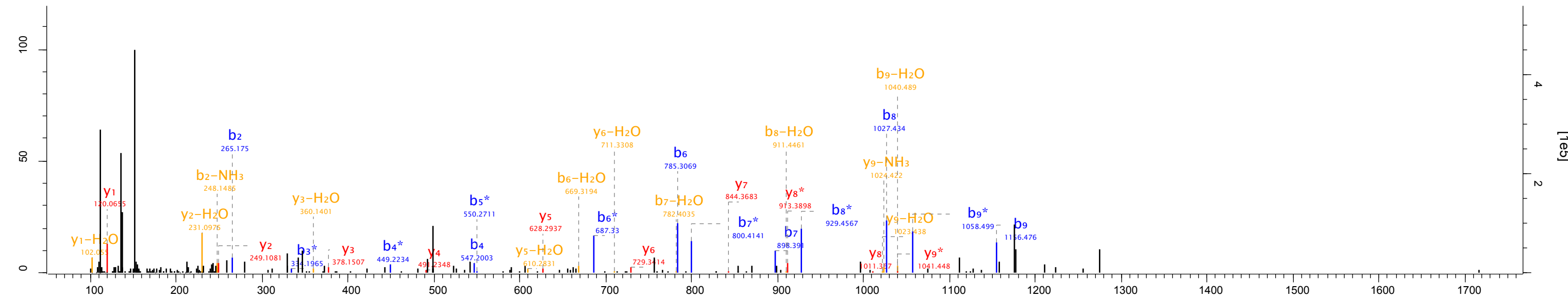
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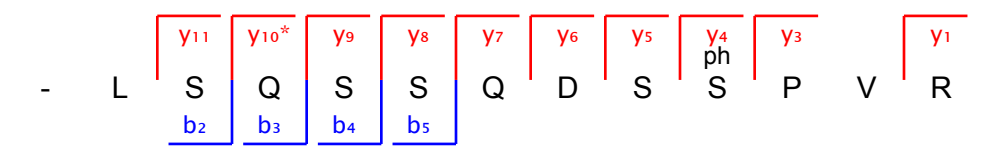
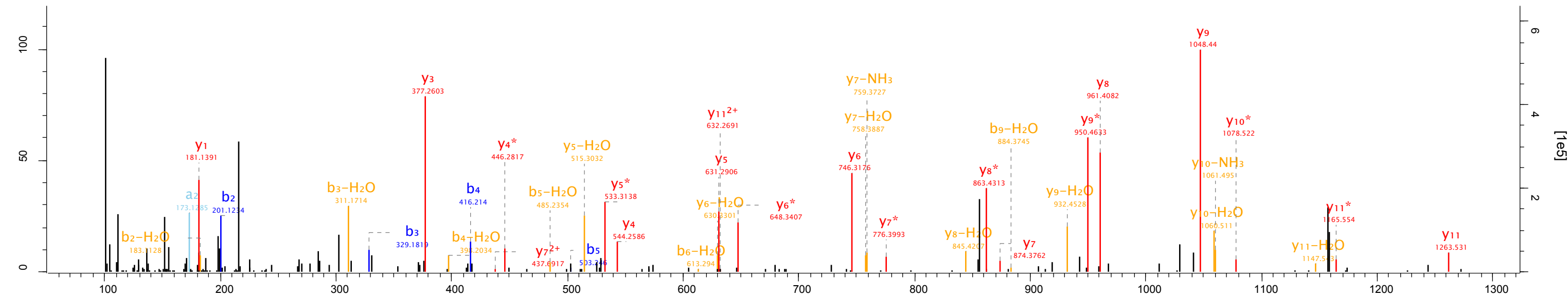
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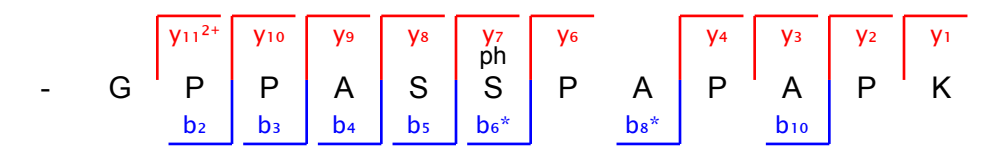
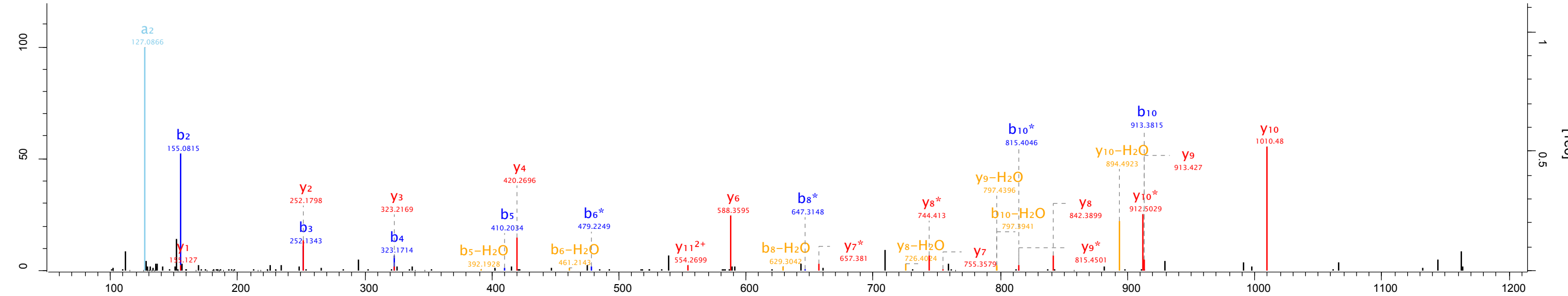


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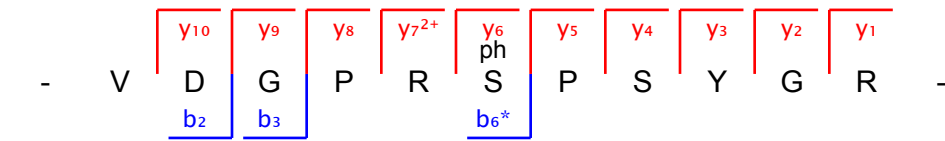
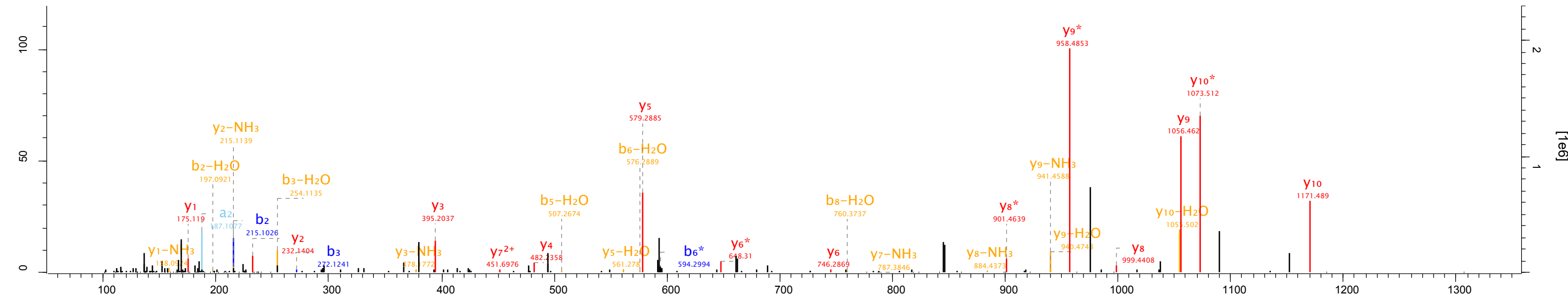


20171215_MaS_33SR_LMH_phospho_07

2813 FTMS; HCD 113.1 582.78 ZYX

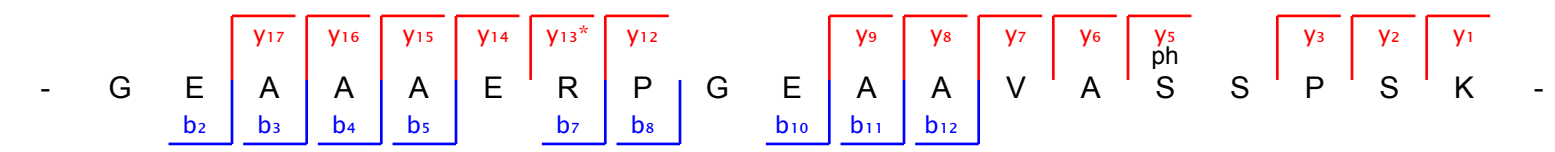
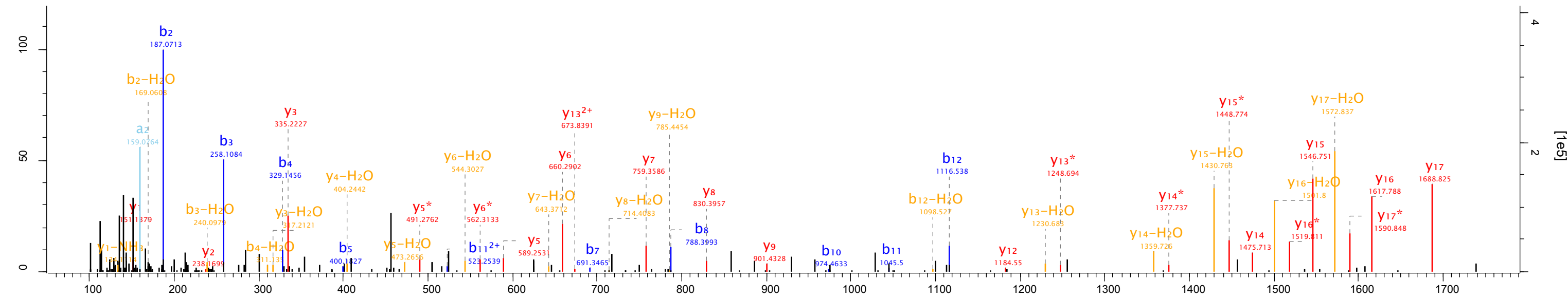


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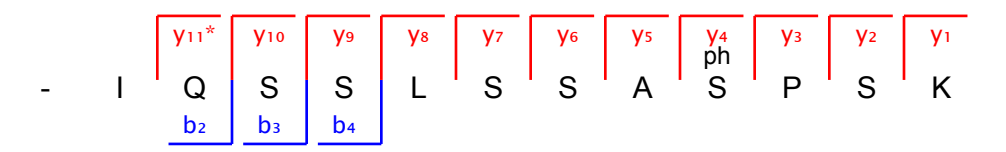
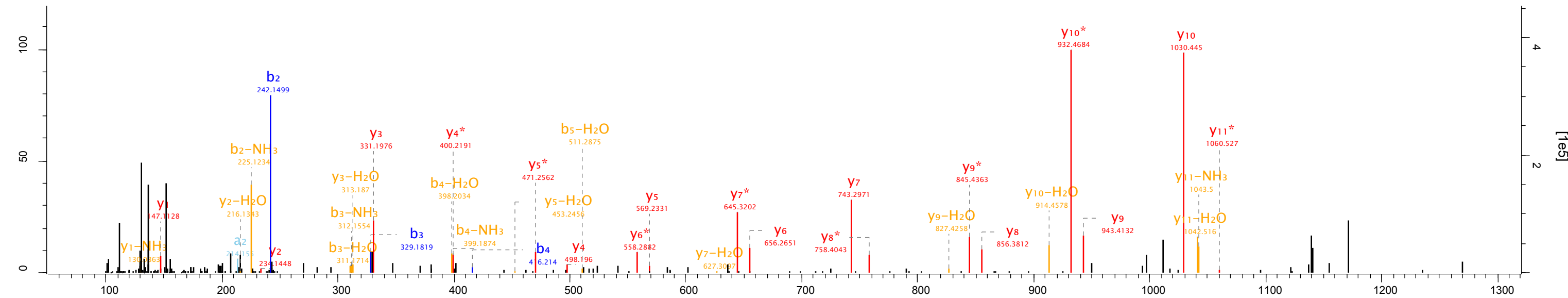


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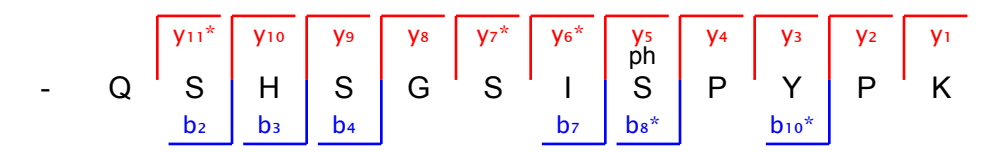
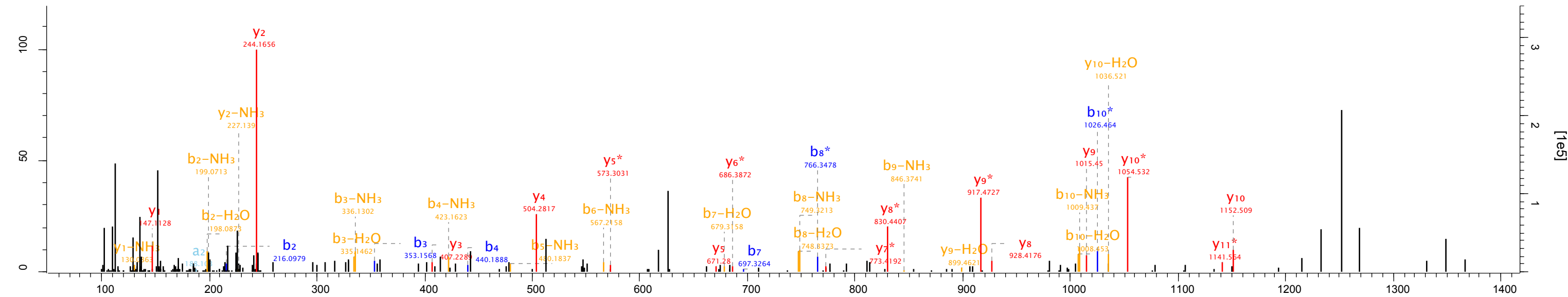
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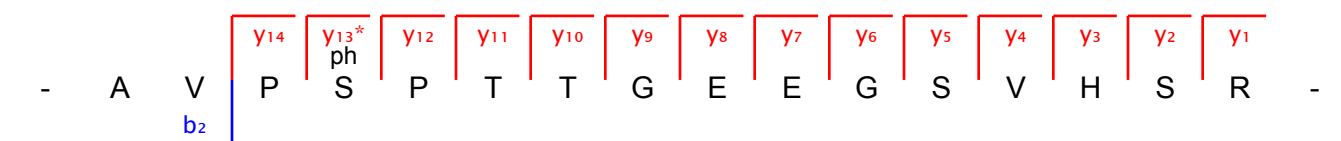
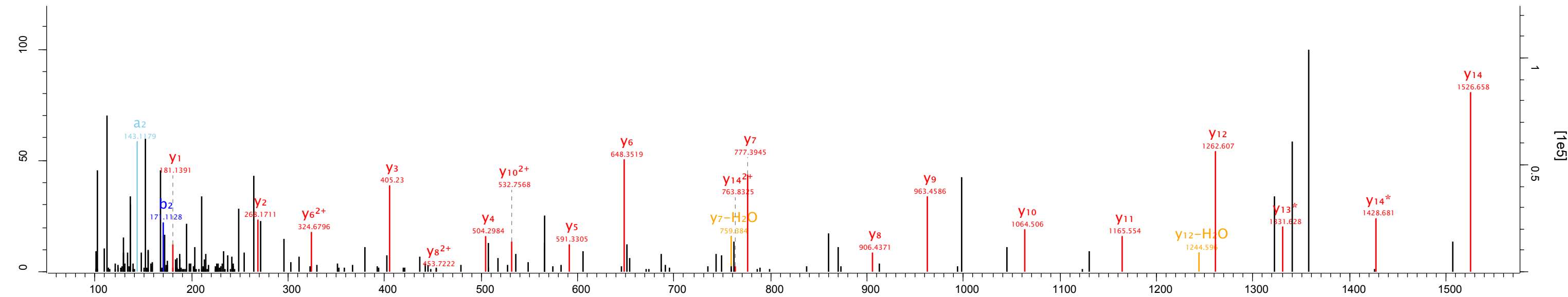
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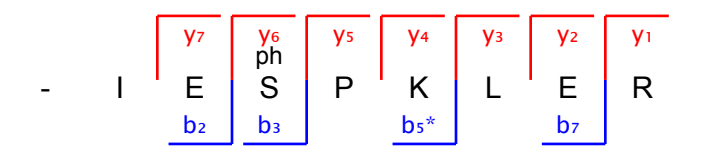
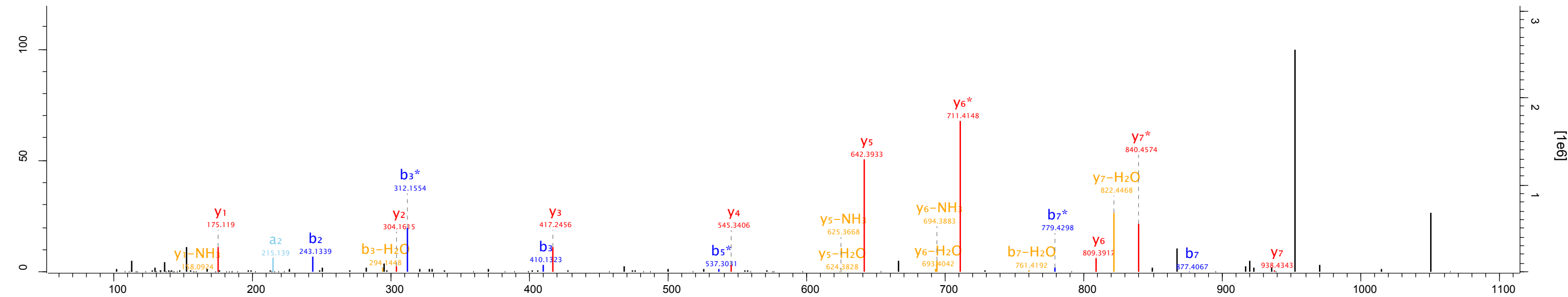
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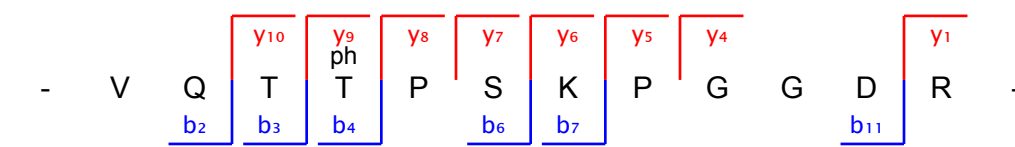
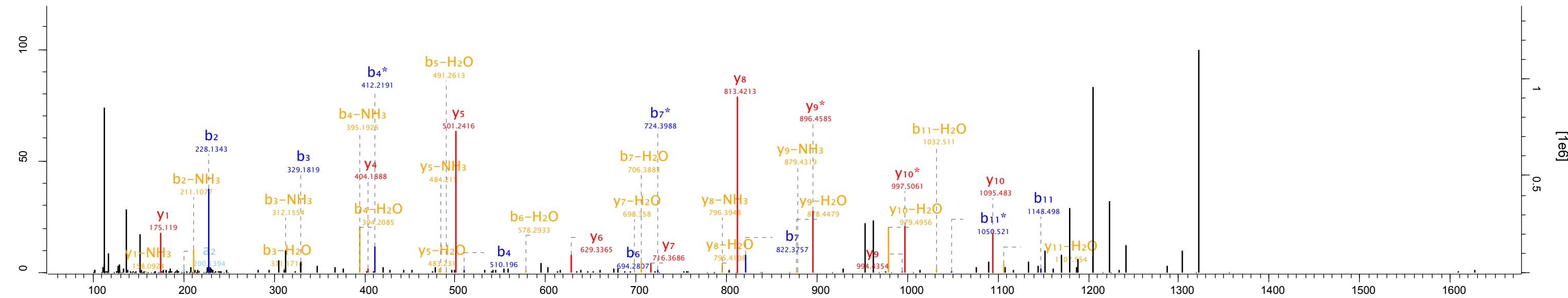


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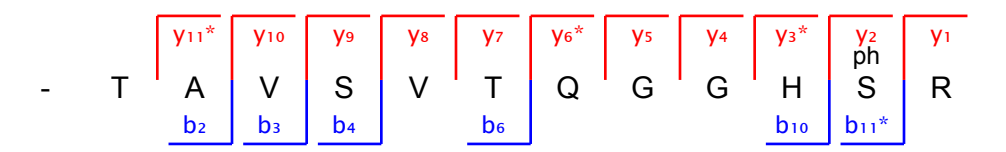
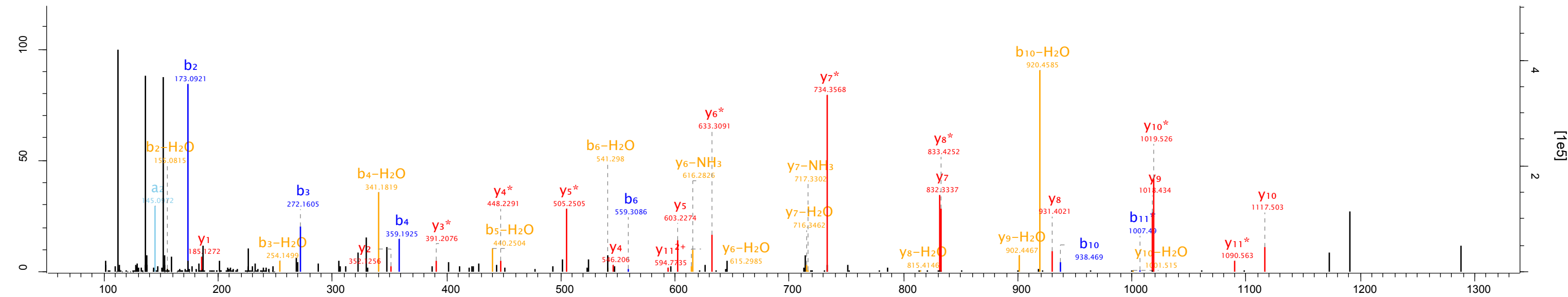


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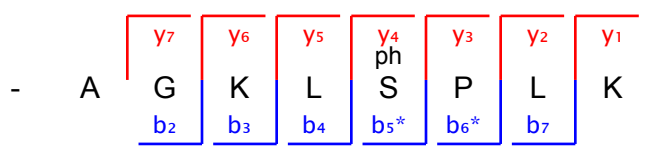
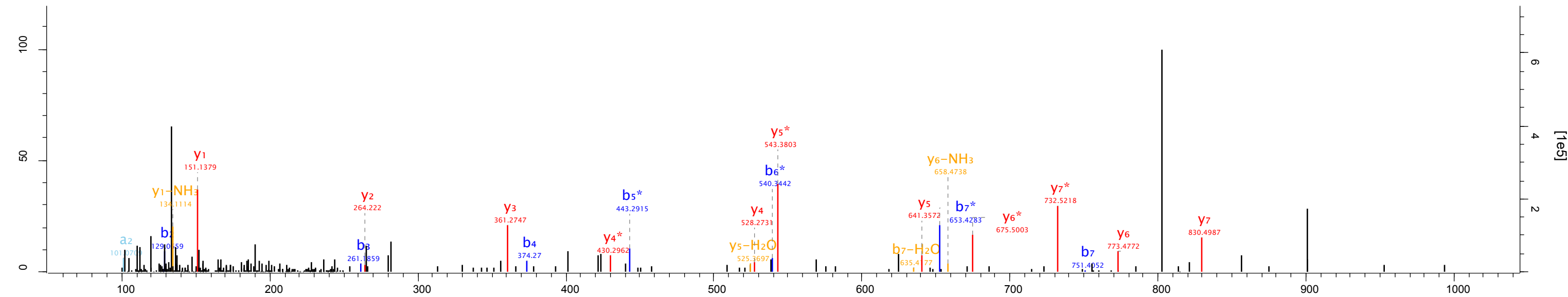




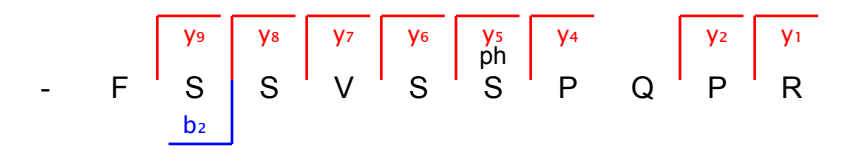
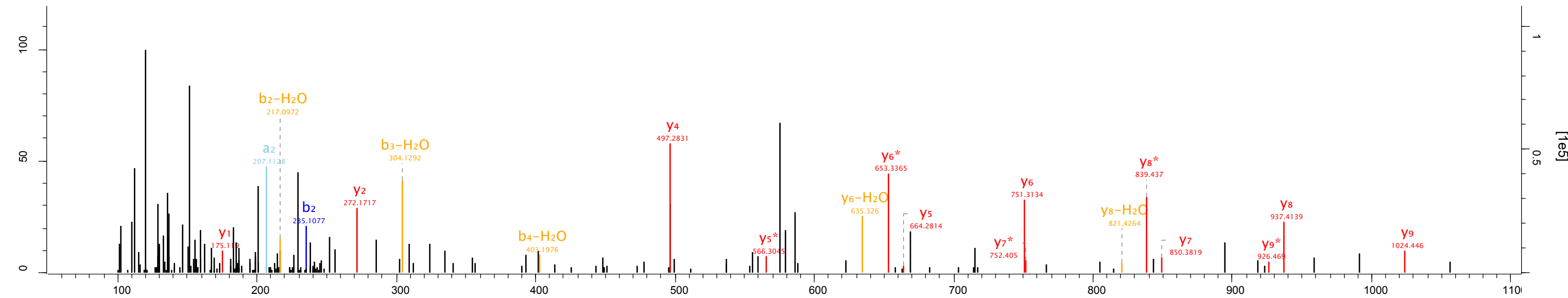
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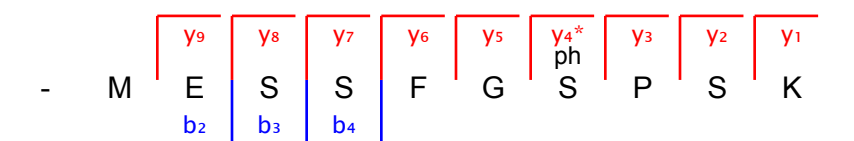
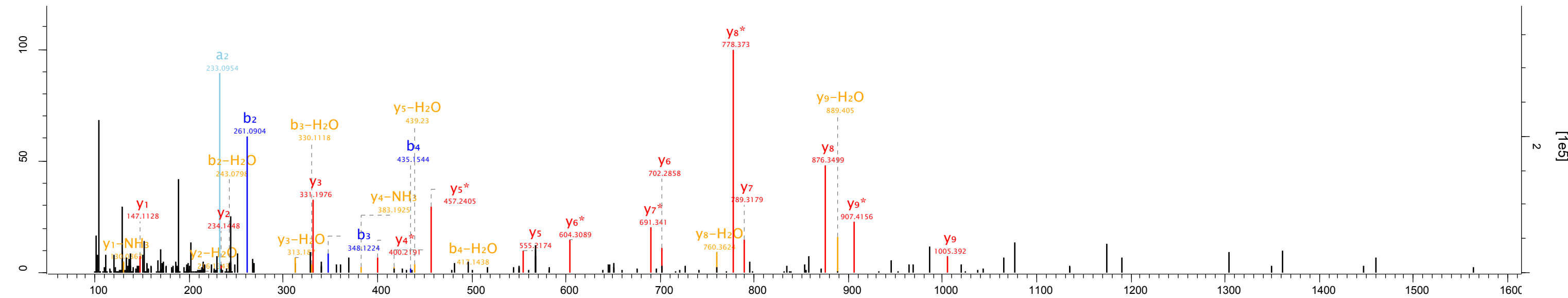
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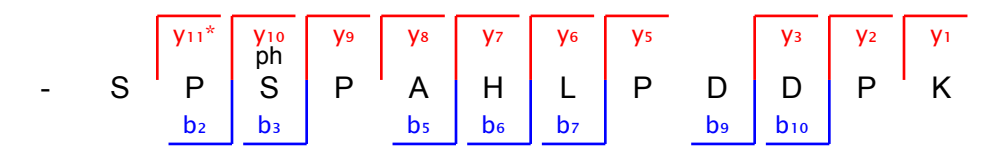
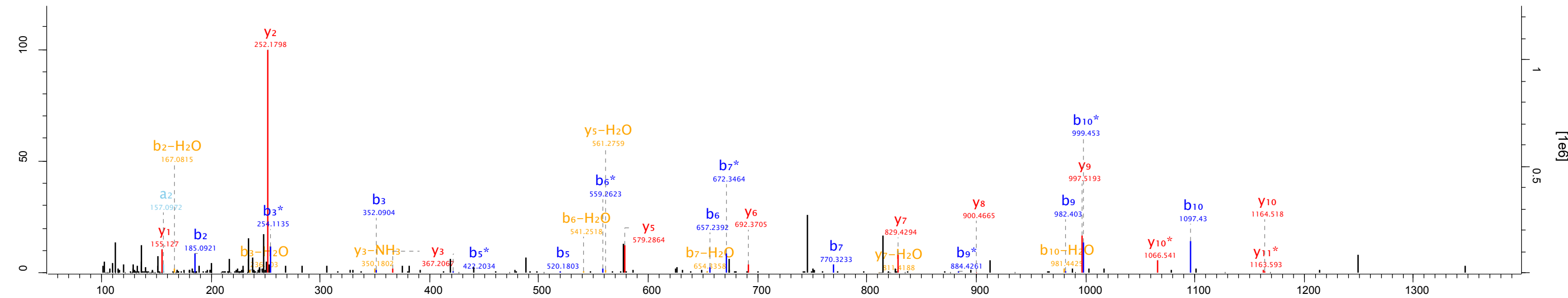
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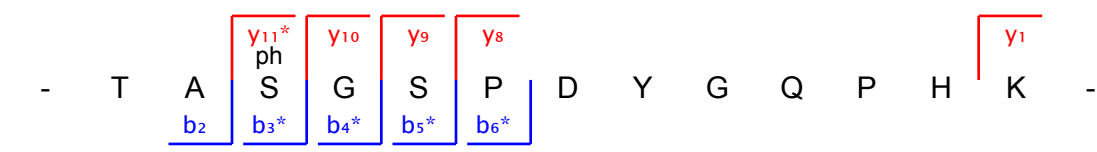
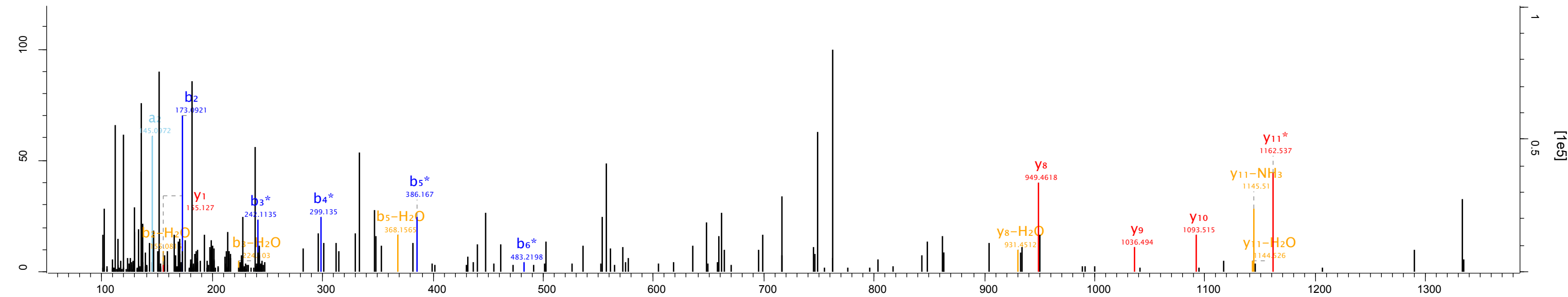
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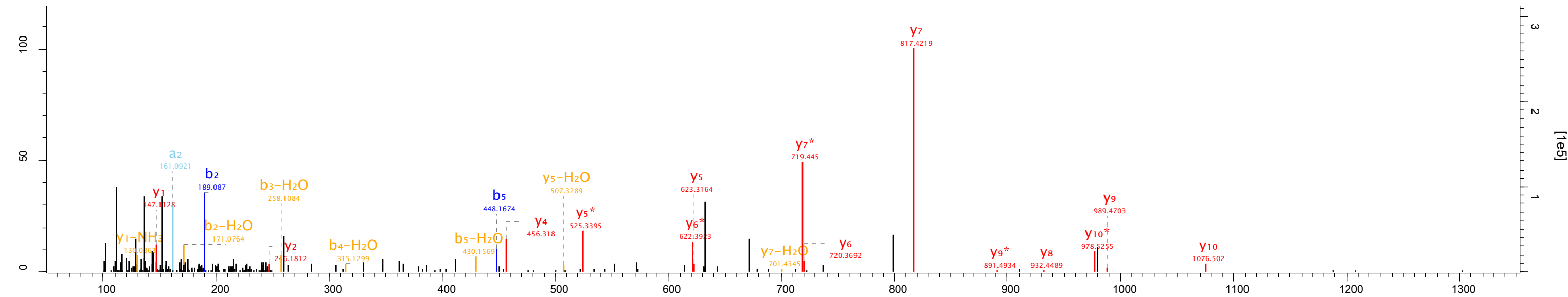
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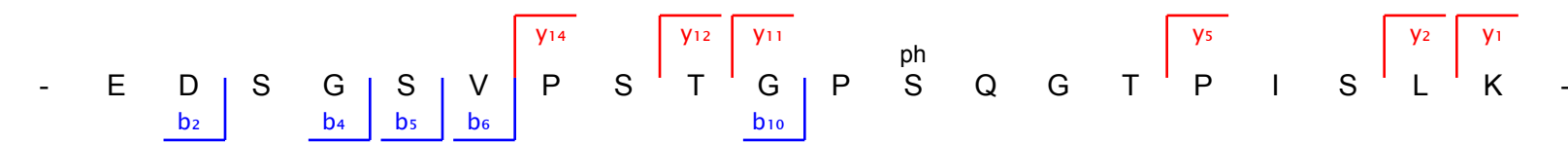
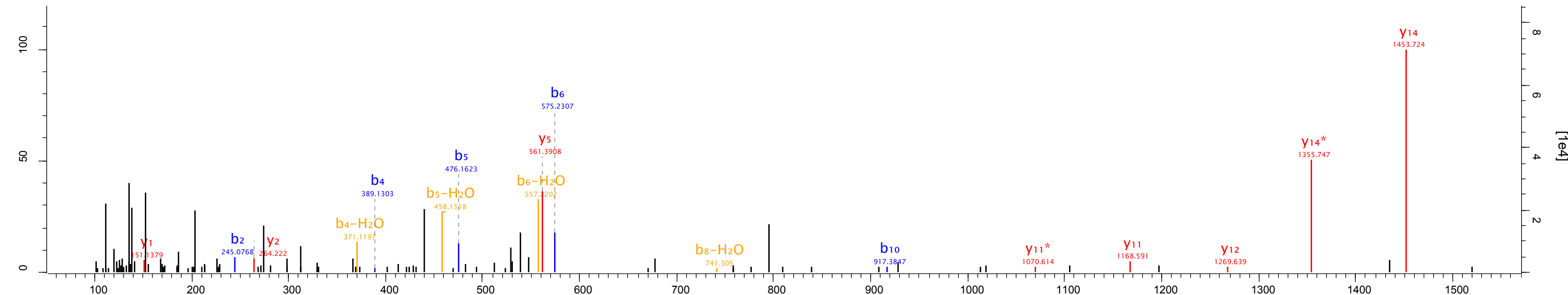


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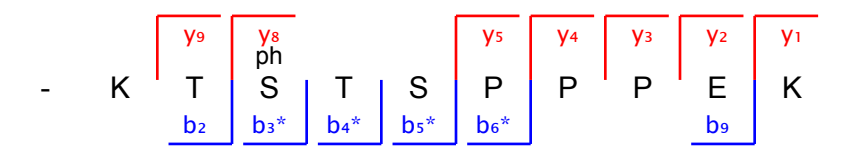
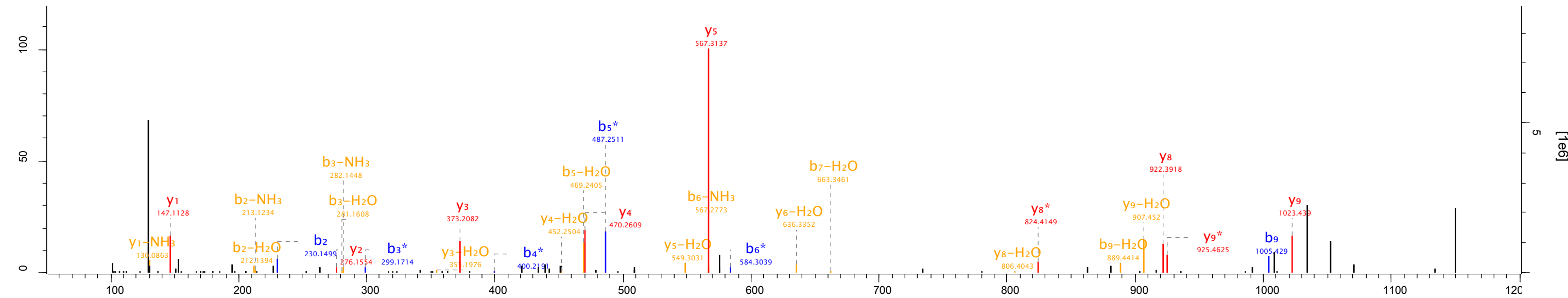


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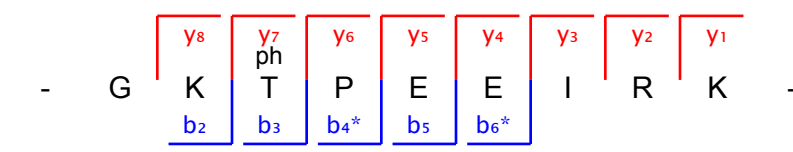
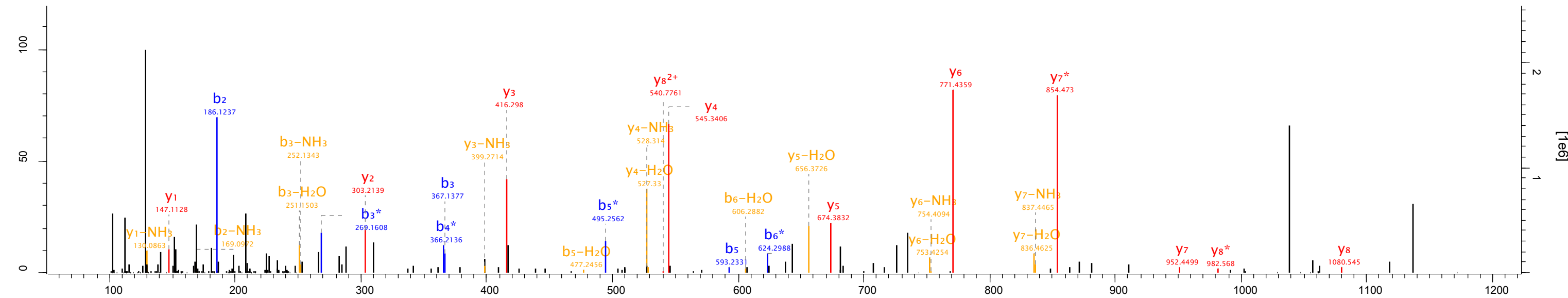




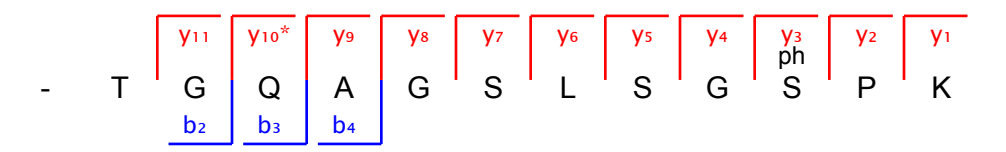
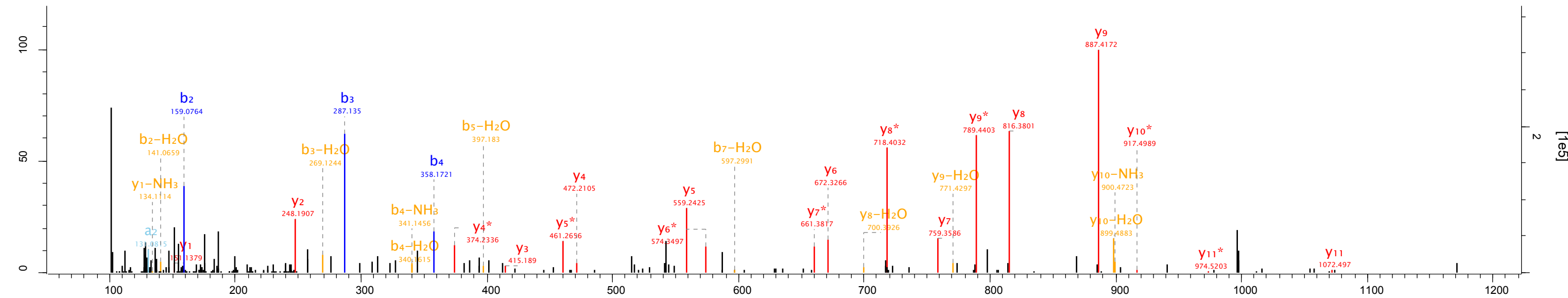
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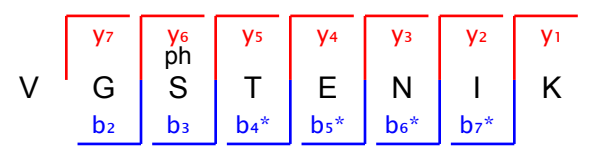
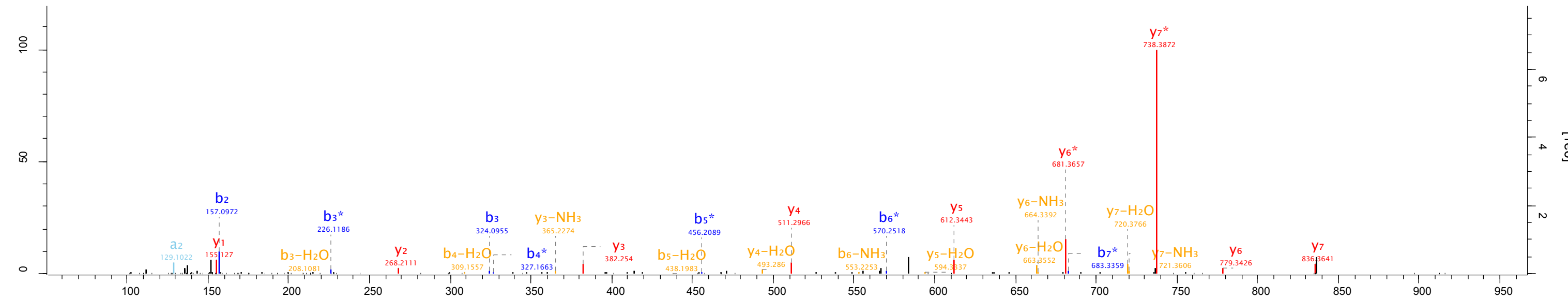
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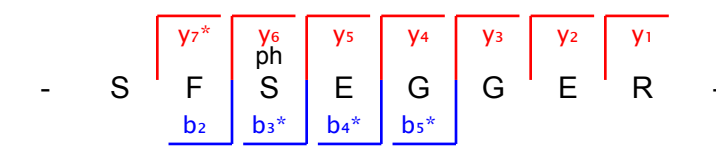
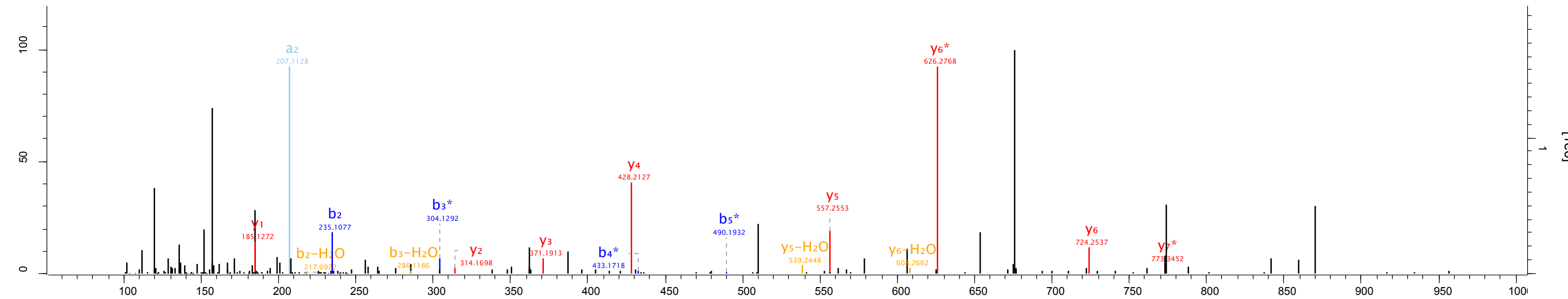
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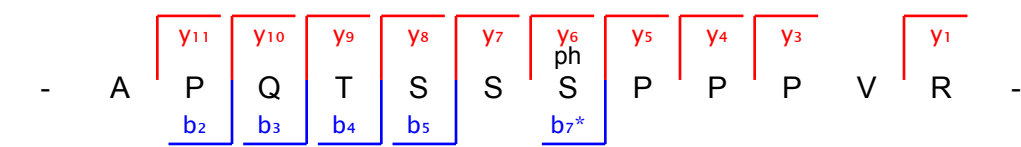
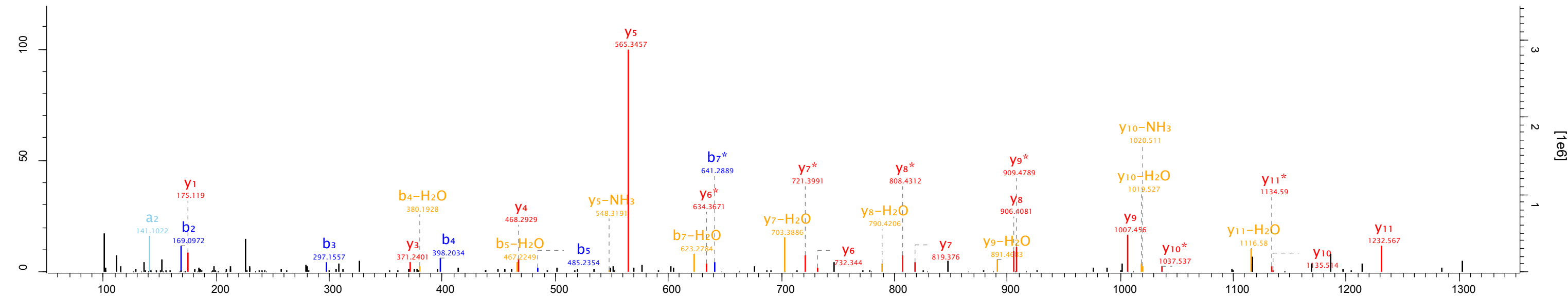


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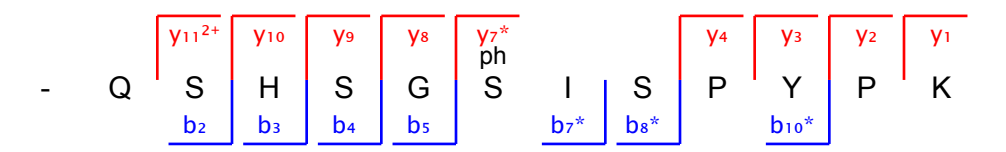
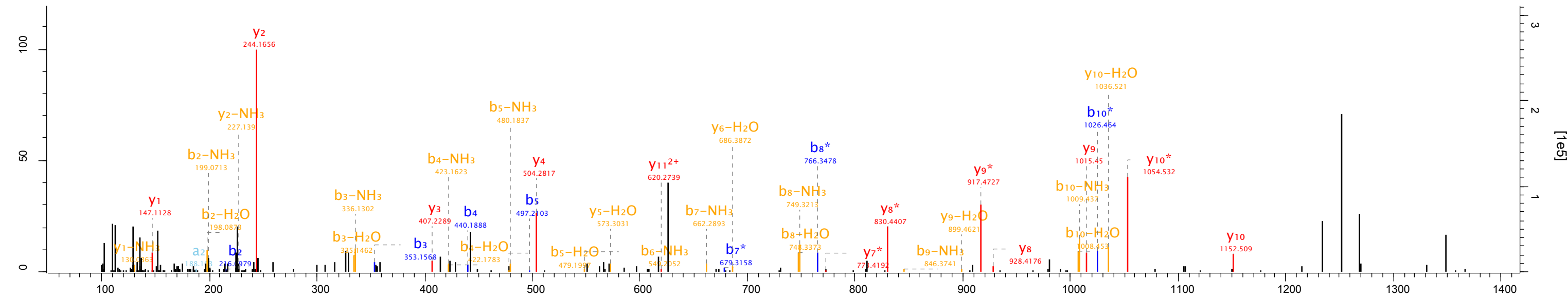
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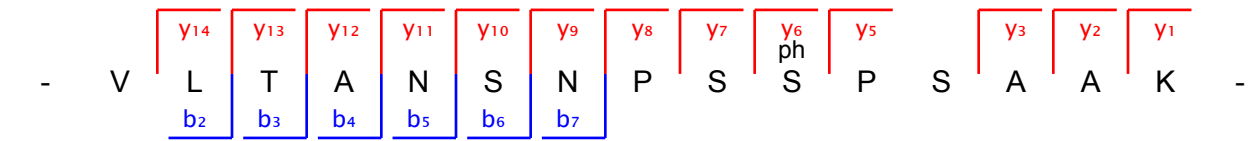
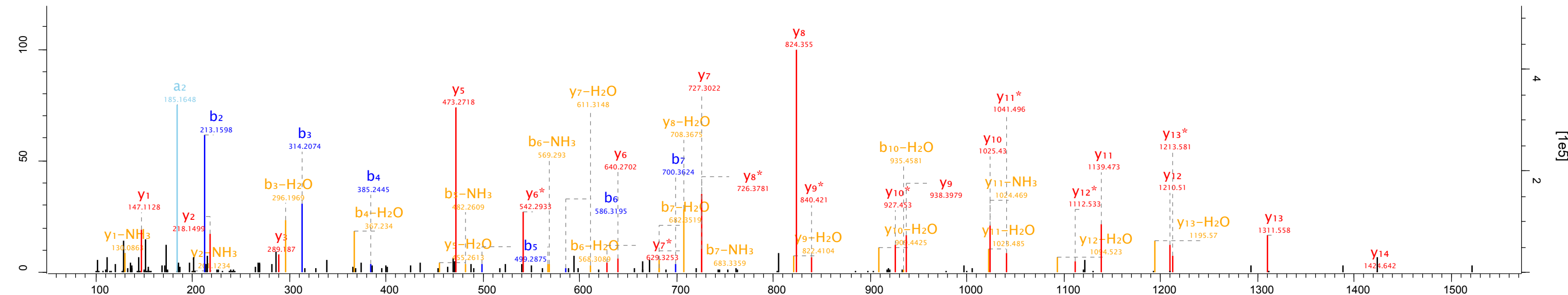




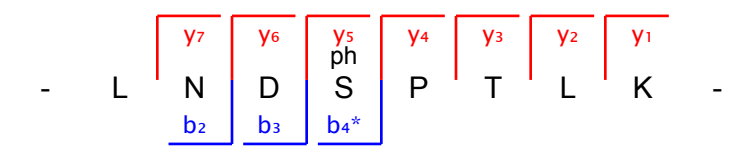
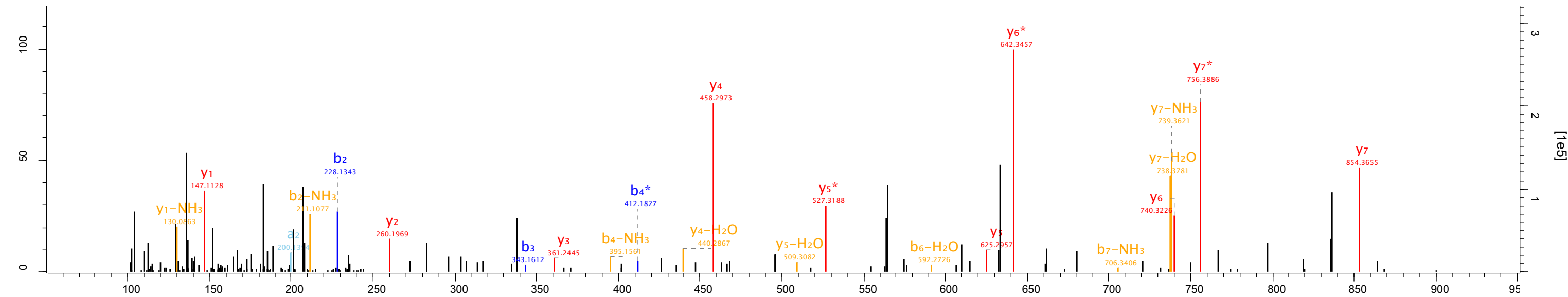
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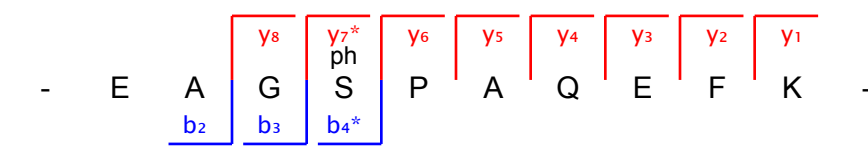
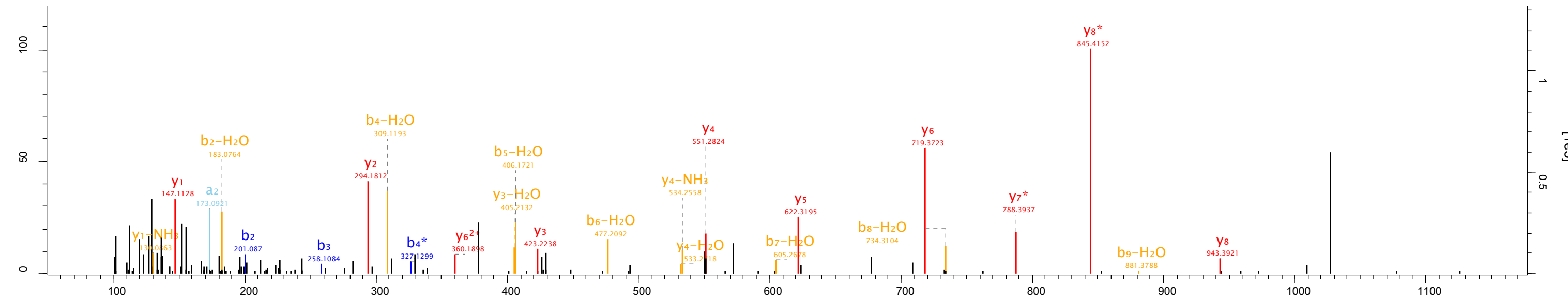




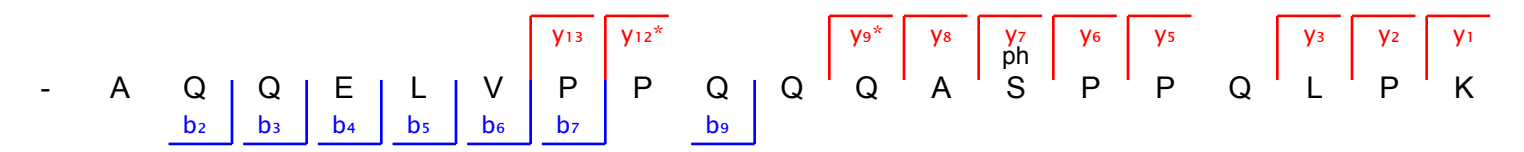
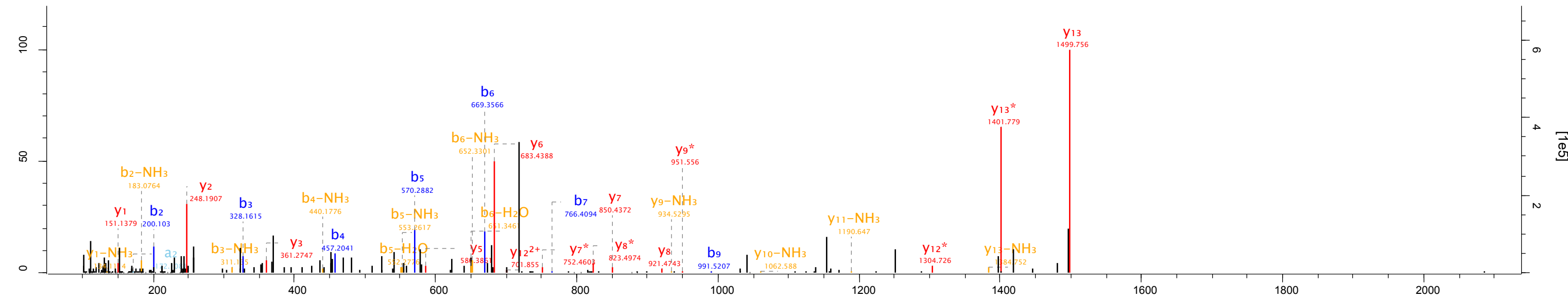
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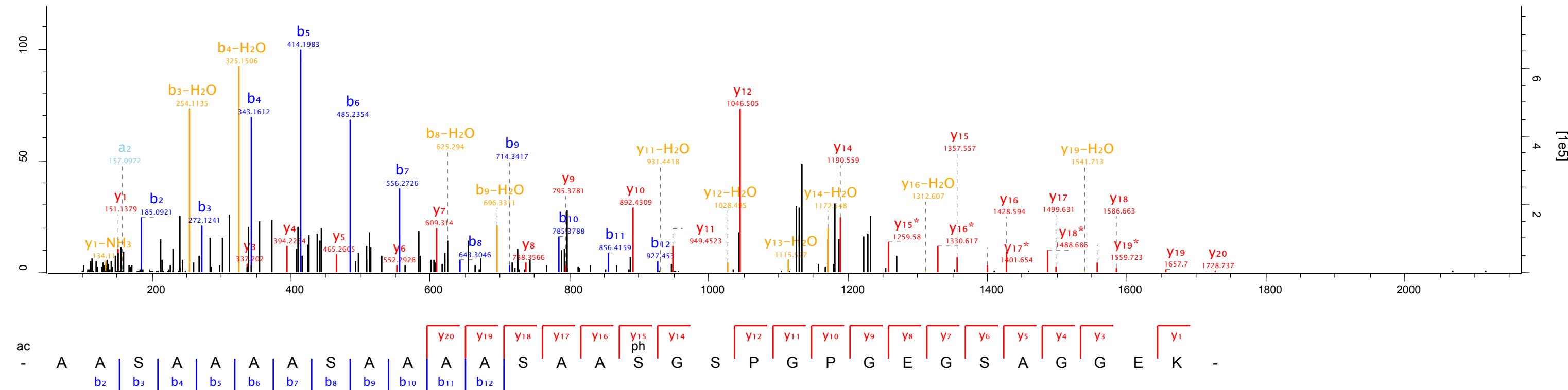
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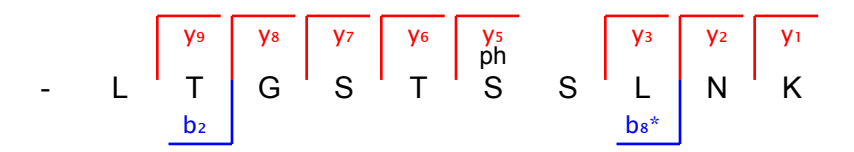
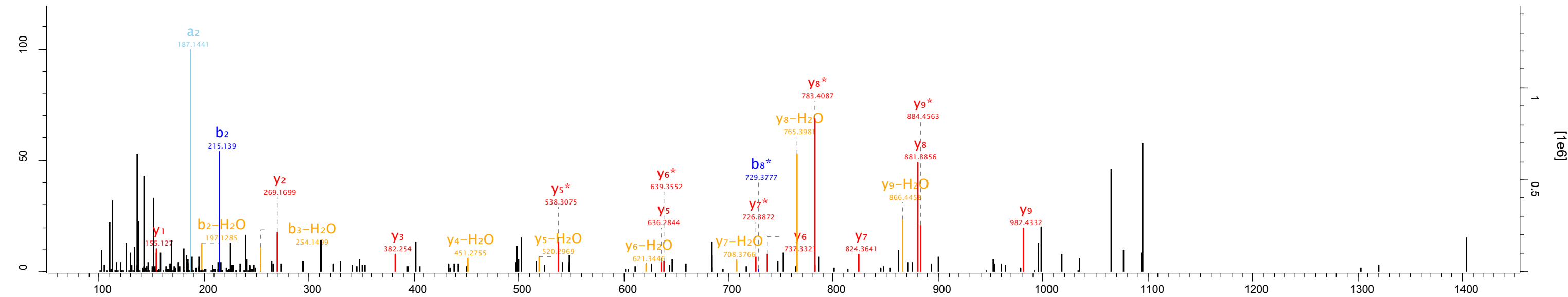
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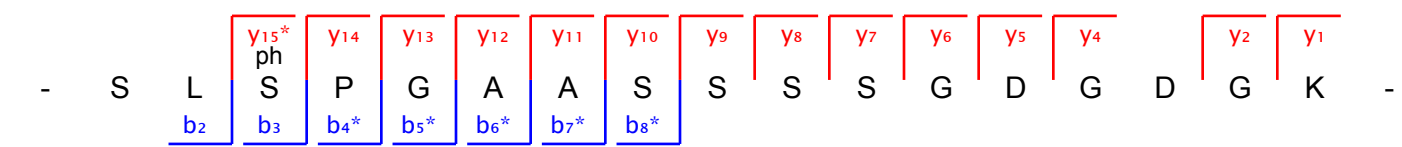
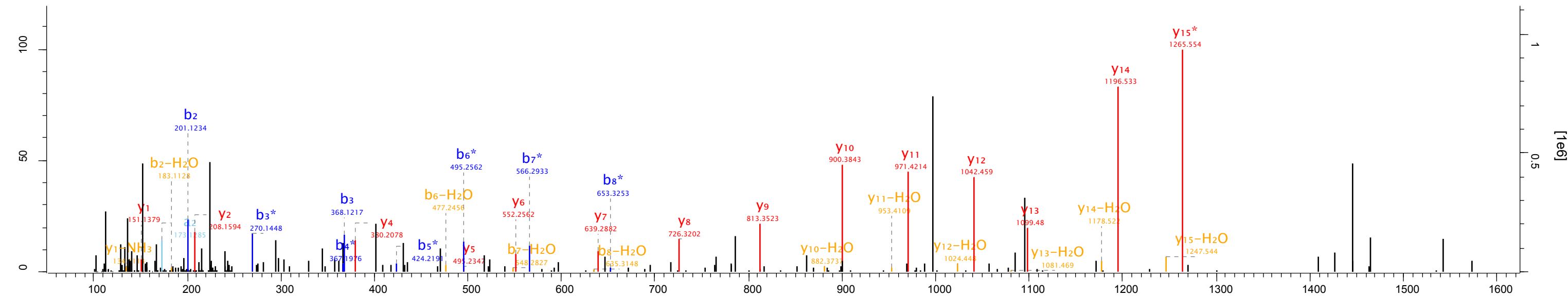
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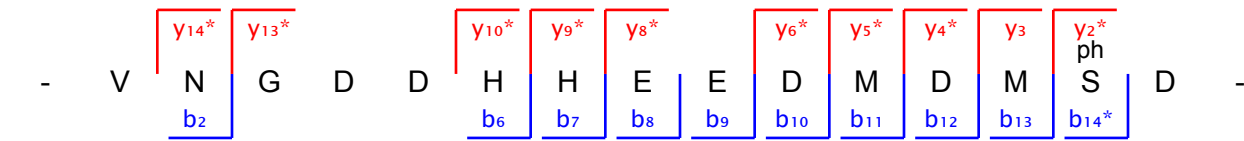
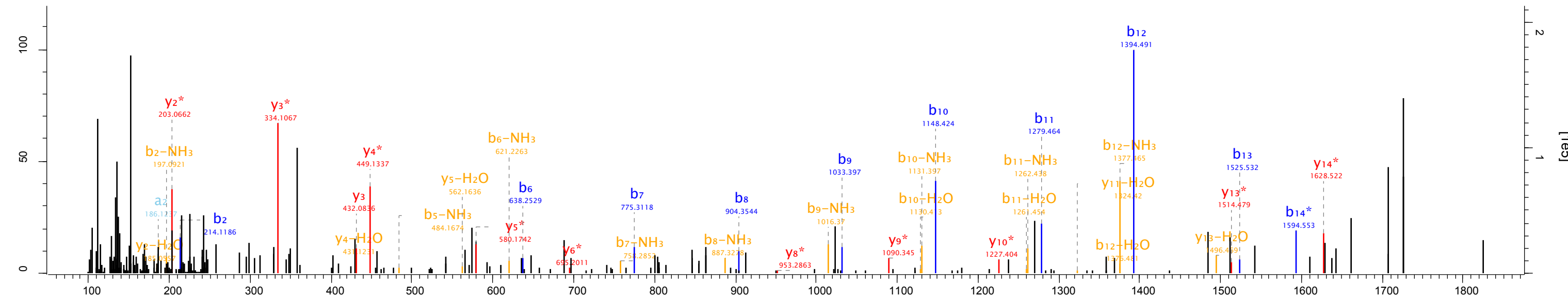


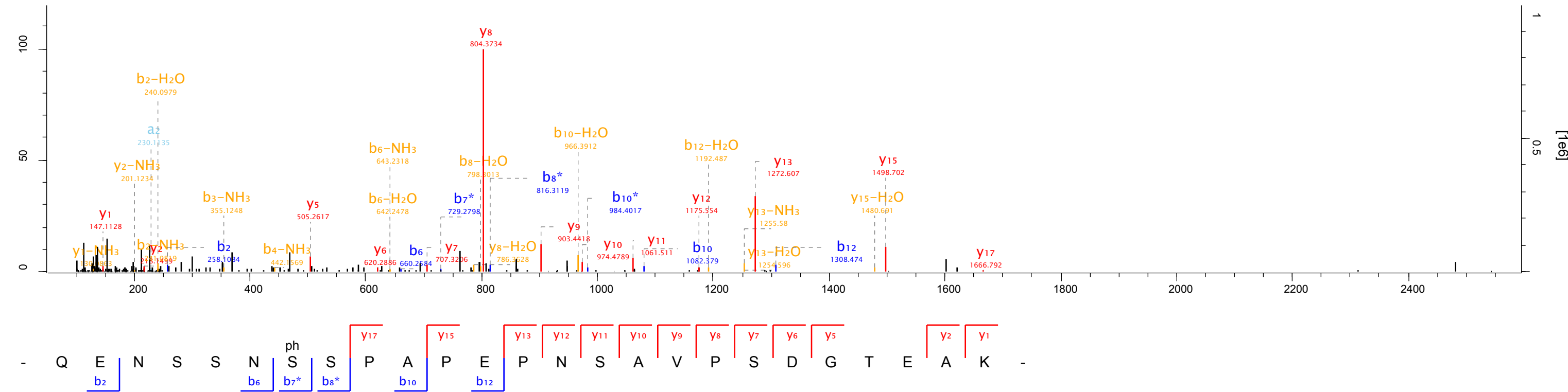
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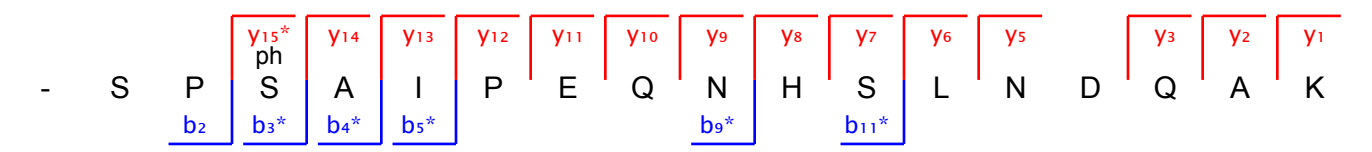
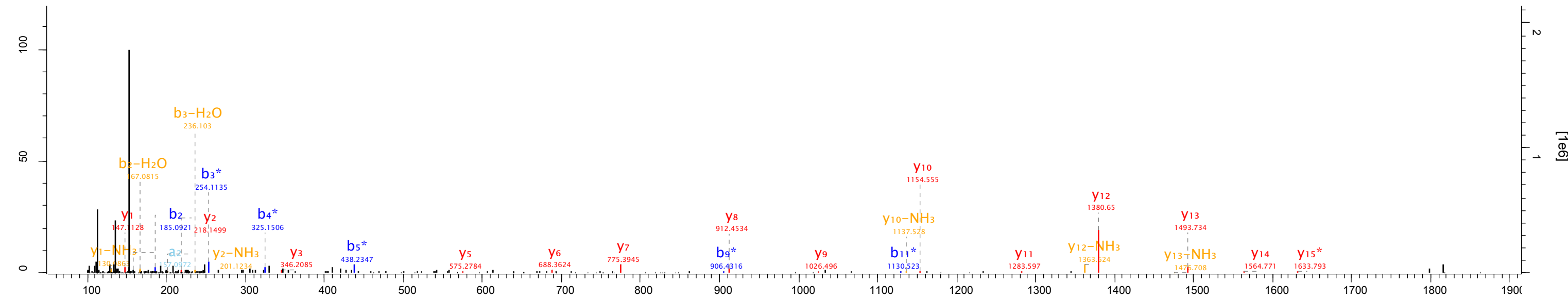
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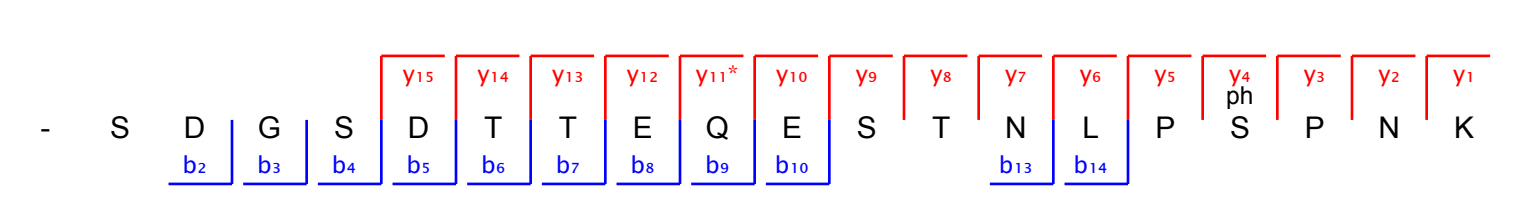
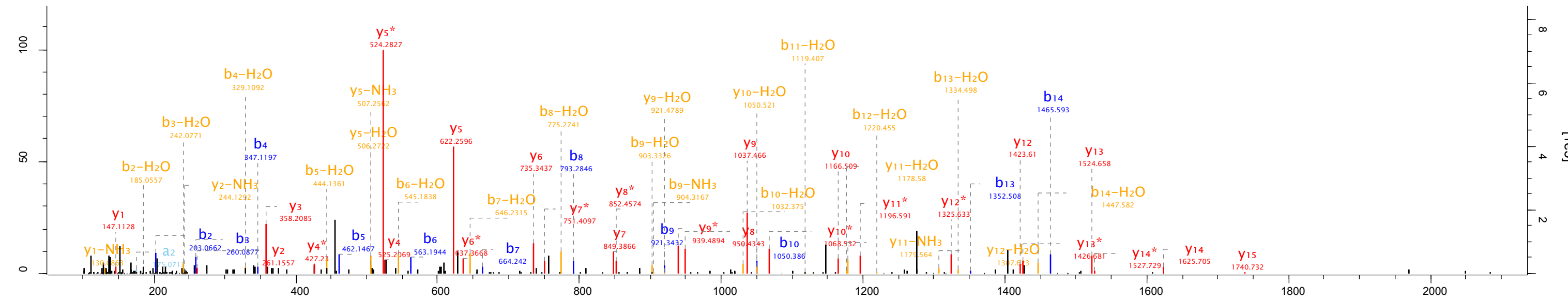




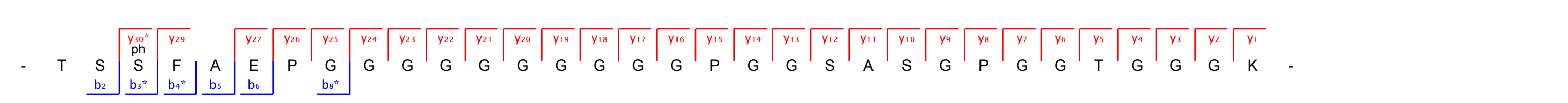
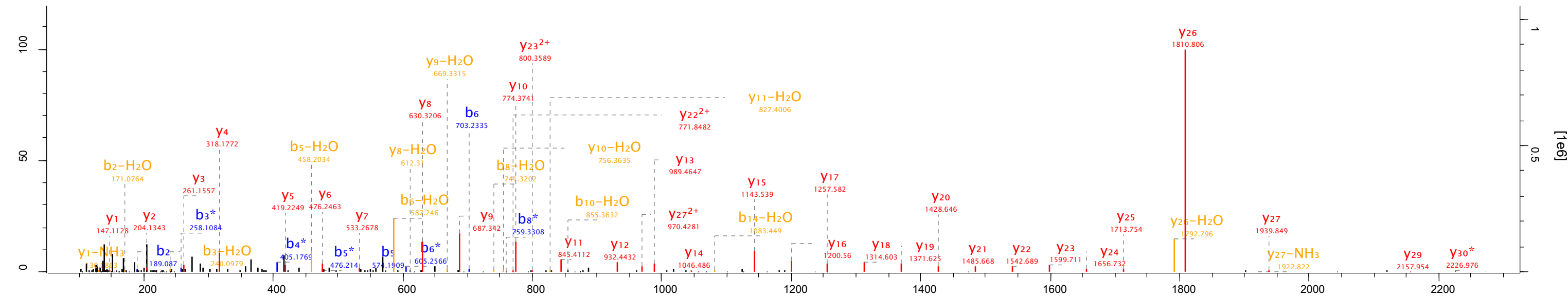
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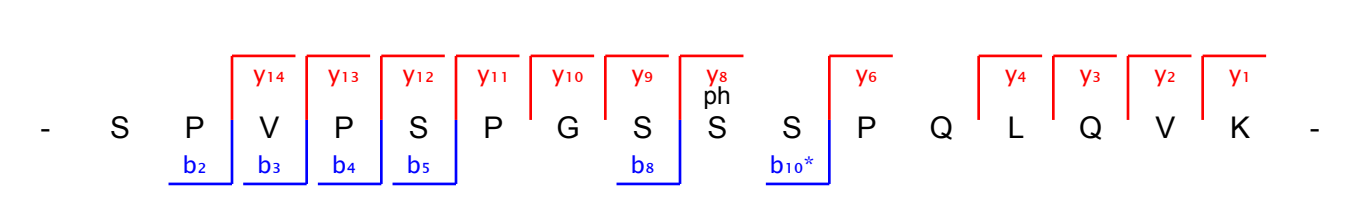
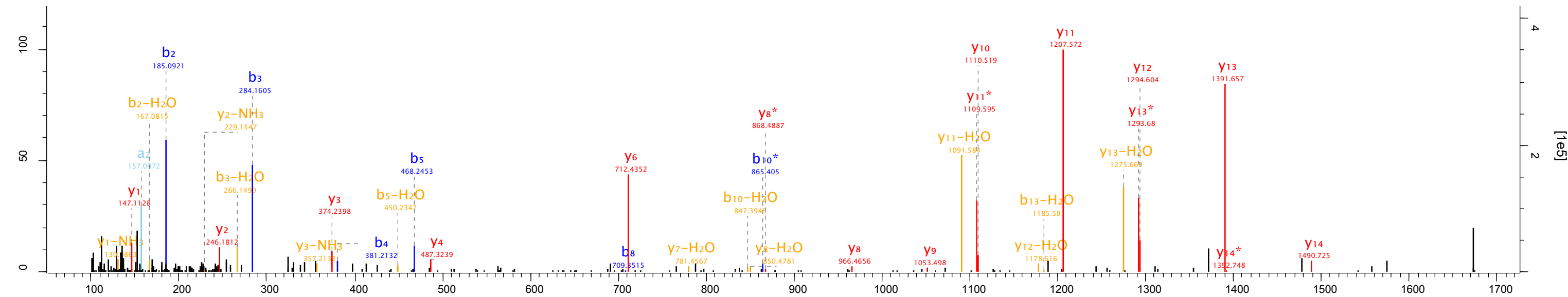
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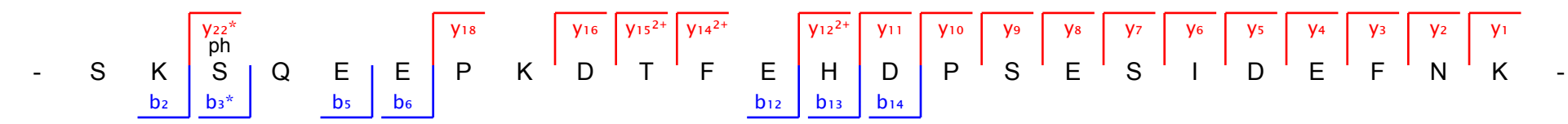
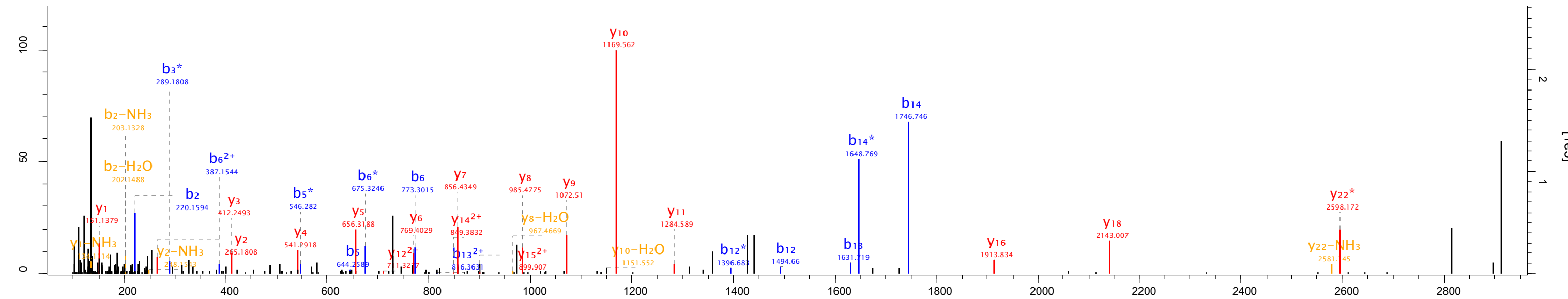
Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 5993 Method FTMS; HCD Score 135.16 m/z 1257.02 Gene names GSK3A



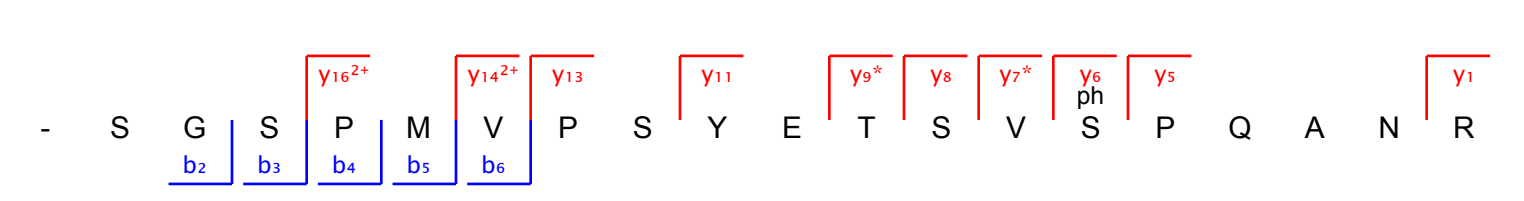
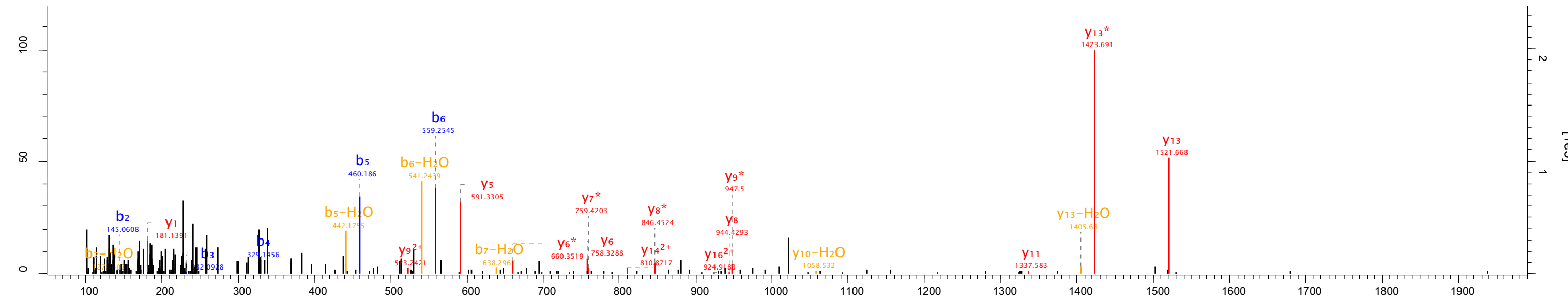
Raw file: 20171215_MaS_33SR_LMH_phospho2_01
 Scan: 9273 Method: FTMS; HCD Score: 149.47 m/z: 838.41 Gene names: MICALL1



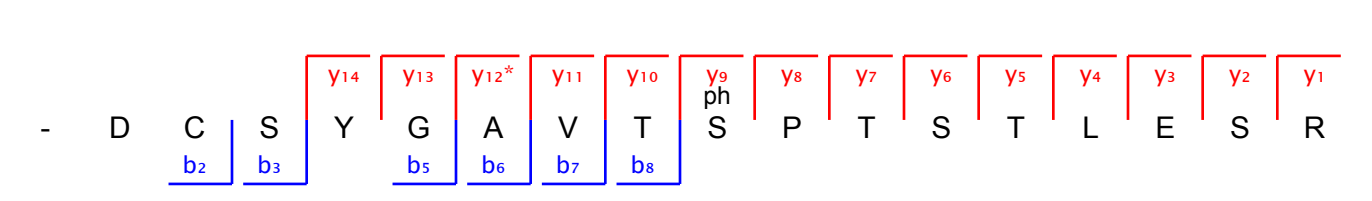
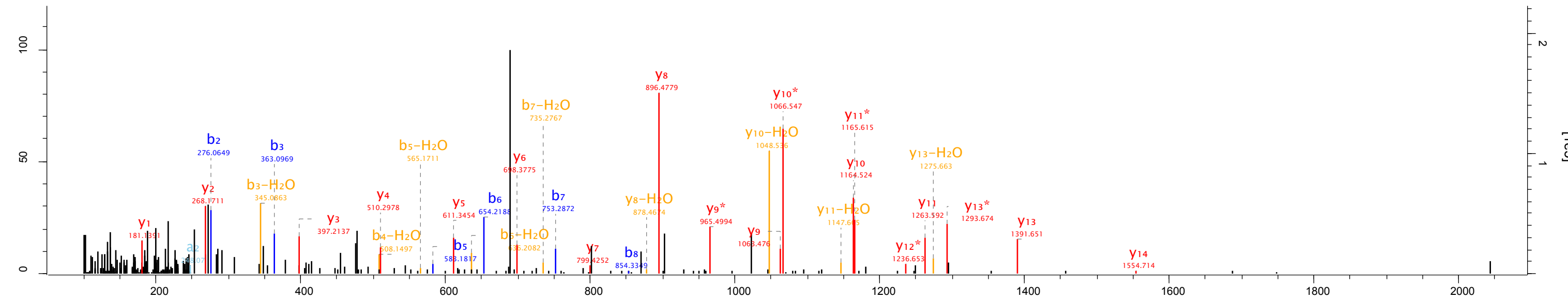
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 10223 Method: FTMS; HCD Score: 99.32 m/z: 729.83 Gene names: BCLAF1



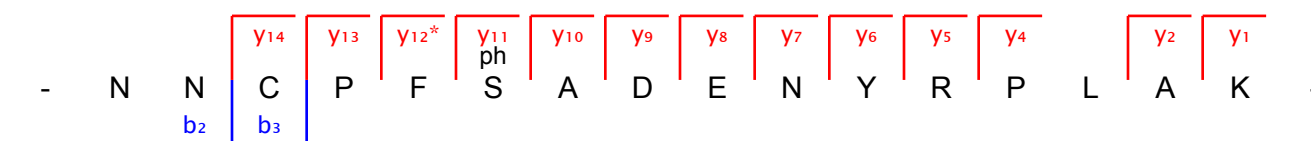
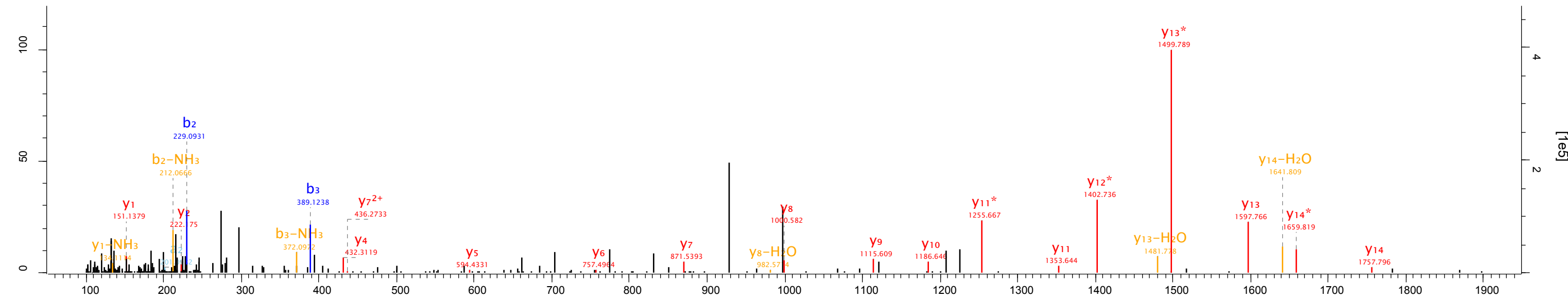
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 10713 Method FTMS; HCD Score 60.13 m/z 1040.47 Gene names PIKFYVE



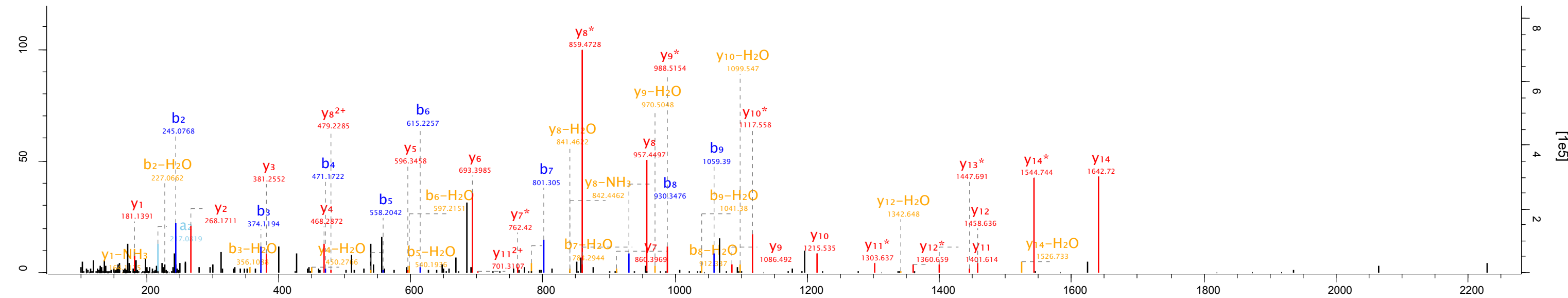
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 10993 Method FTMS; HCD Score 140.95 m/z 959.4 Gene names TANC2



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11053 Method FTMS; HCD Score 83.42 m/z 662.97 Gene names PCM1



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11713 Method FTMS; HCD Score 190.57 m/z 1008.42 Gene names TNRC6B

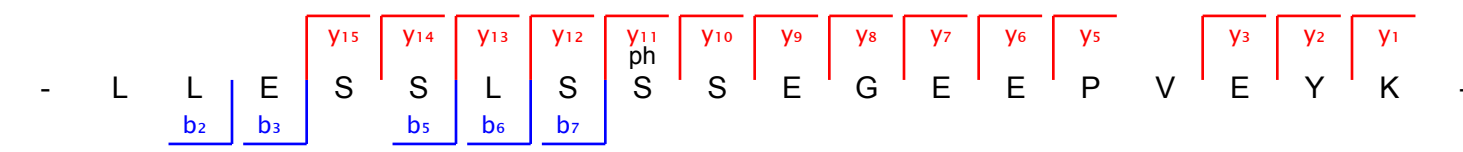
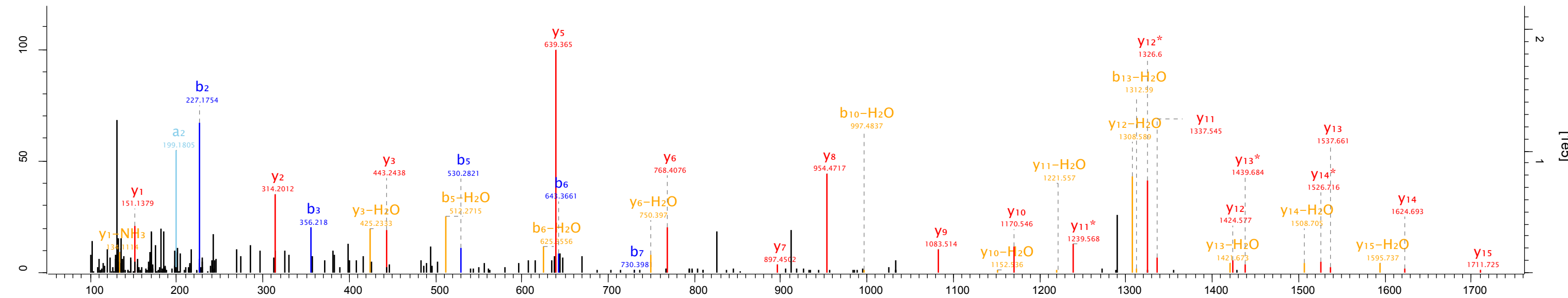


- D E E P S G W E E P S P Q S I S R -

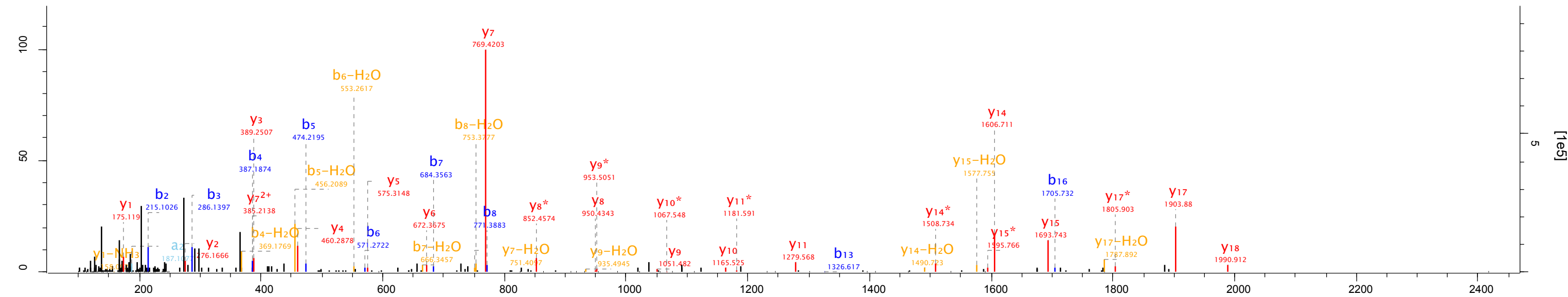
Fragmentation mapping (b-ions in blue, y-ions in red):

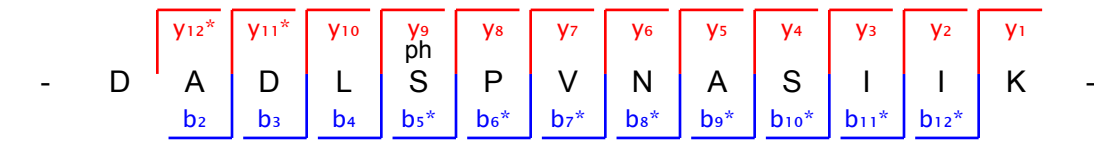
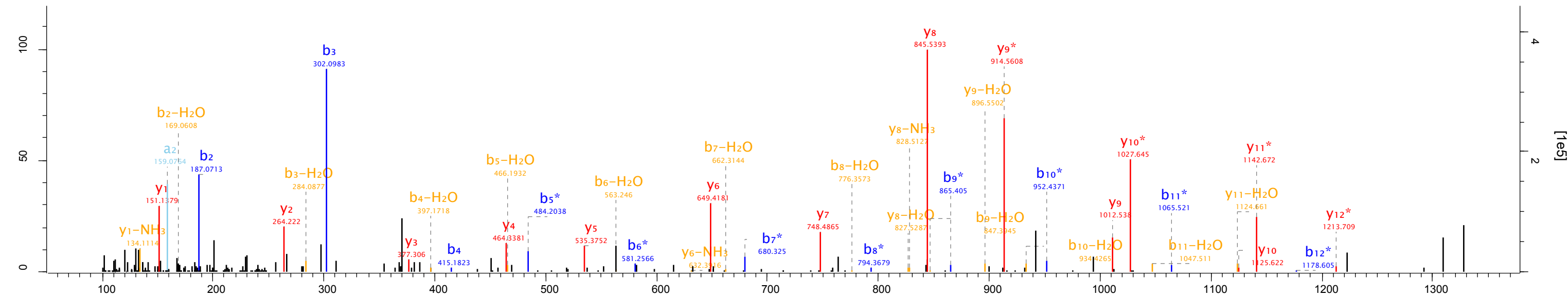
- b2: E
- b3: E
- b4: P
- b5: S
- b6: G
- b7: W
- b8: E
- b9: E
- y1: R
- y2: S
- y3: I
- y4: S
- y5: Q
- y6: P
- y7: S
- y8: P
- y9: E
- y10: W
- y11: G
- y12: S
- y13: P
- y14: E

Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 12223 Method FTMS; HCD Score 156.87 m/z 1033.97 Gene names ITGA5

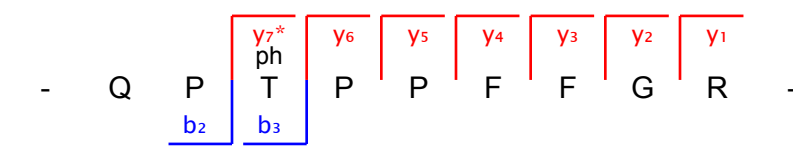
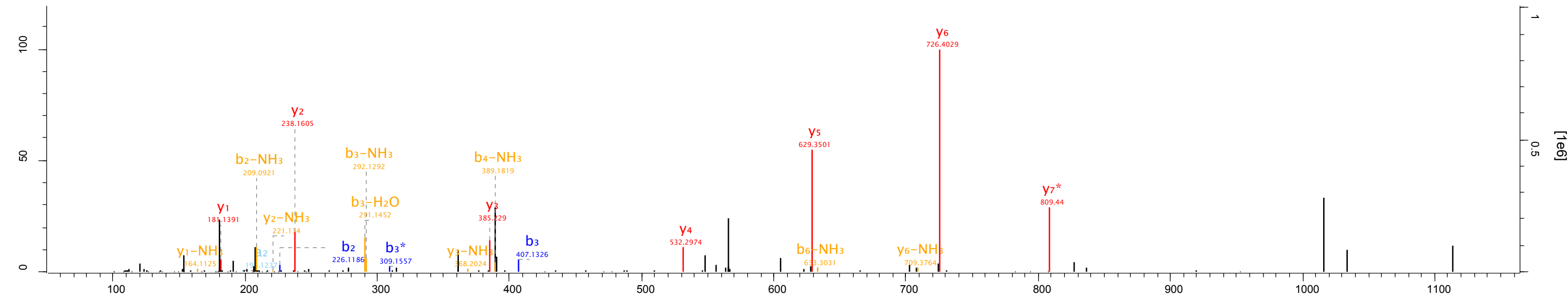


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 12413 Method FTMS; HCD Score 187.51 m/z 1189.55 Gene names PAK1





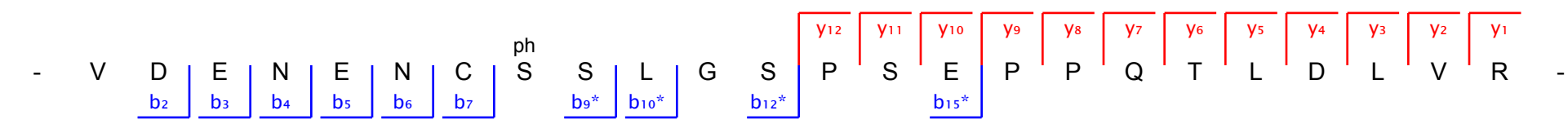
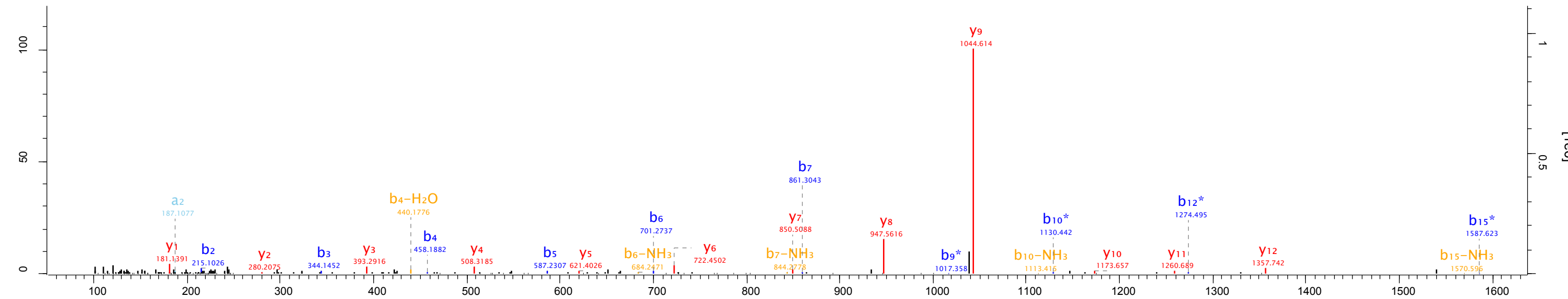
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 13523 Method: FTMS; HCD Score: 80.04 m/z: 566.77 Gene names: RBM14

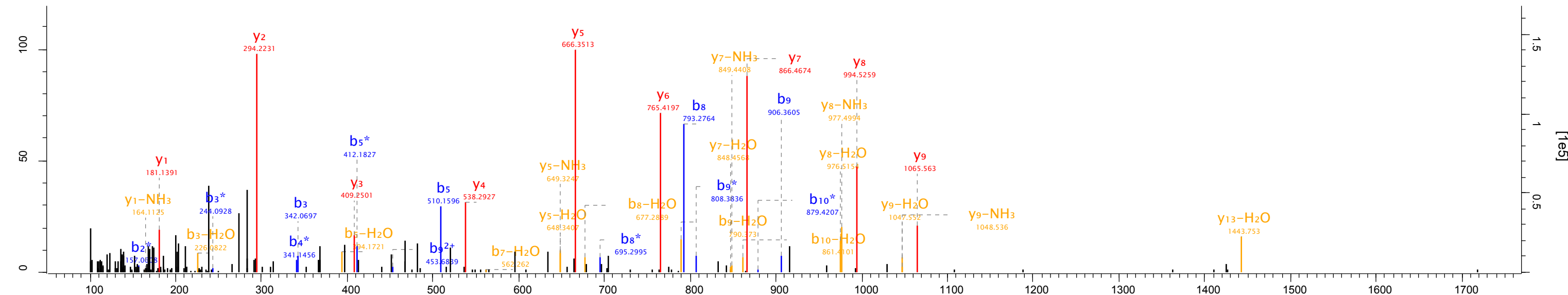


Raw file

20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
14653	FTMS; HCD	91.6	910.41	RPRD1A

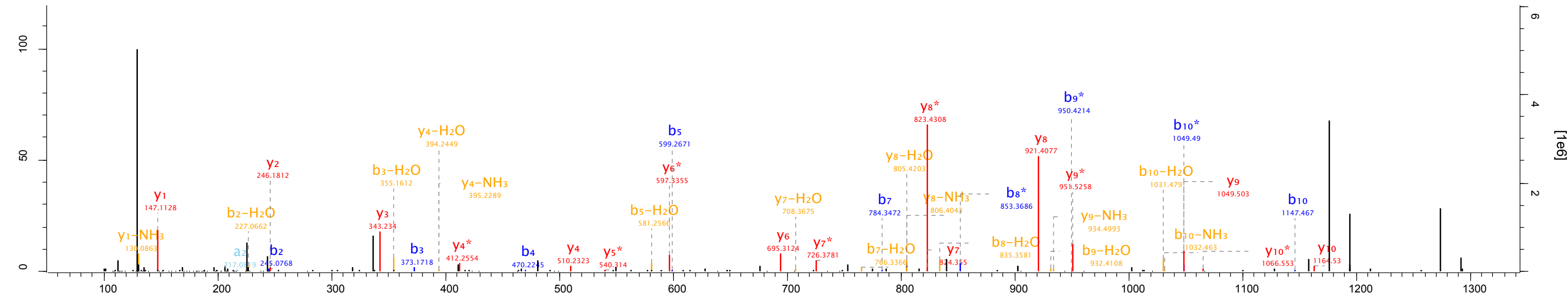




ph
- S S S P A P A D I A Q T V Q E D L R -

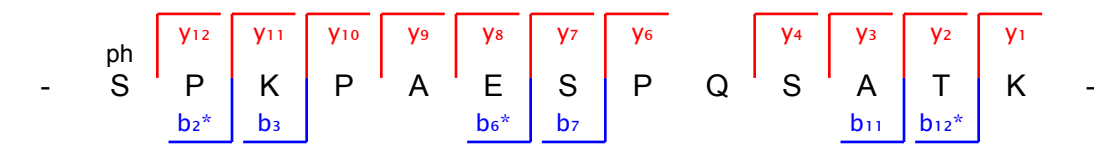
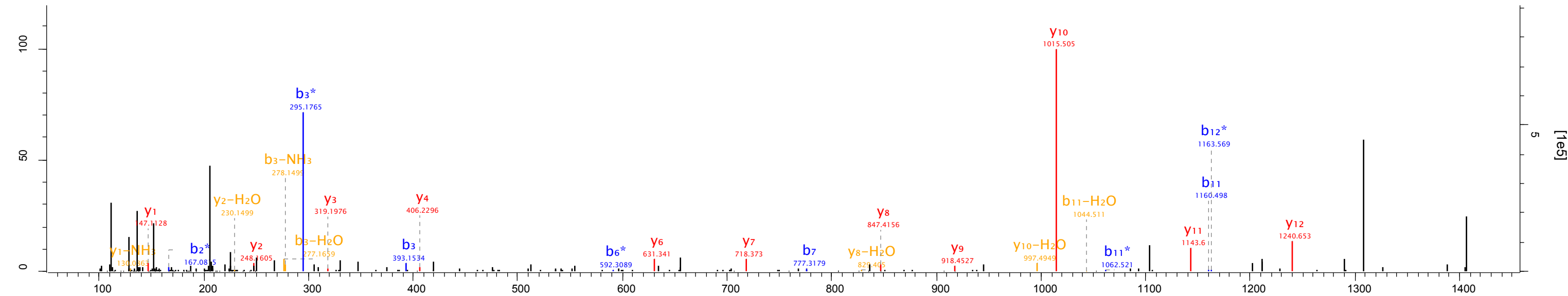
b2* b3 b4* b5 b8 b9 b10*

y9 y8 y7 y6 y5 y4 y3 y2 y1



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

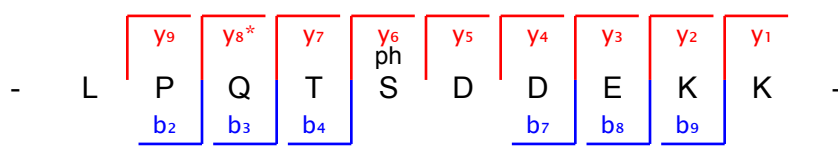
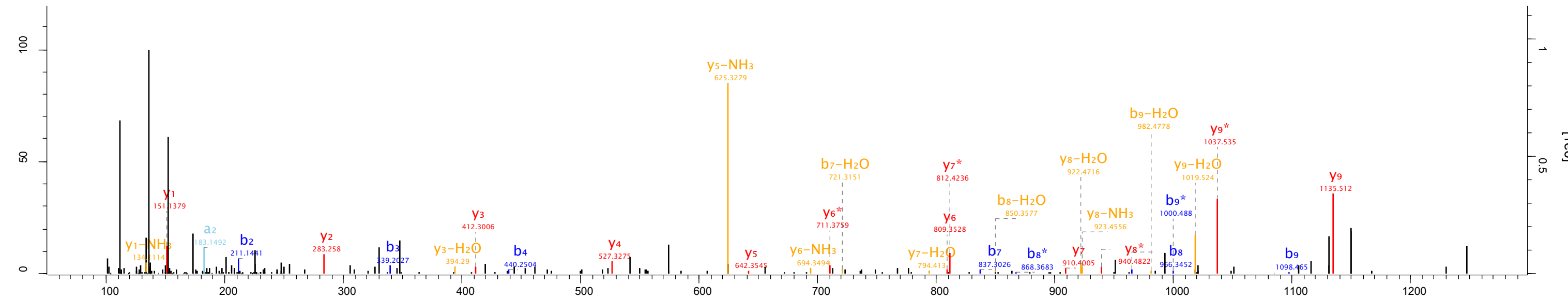
y10 y9 y8 y7 y6 y5* y4 y3 y2 y1
b2 b3 b4 b5 b7 b8* b9* b10



Raw file Scan Method Score m/z Gene names

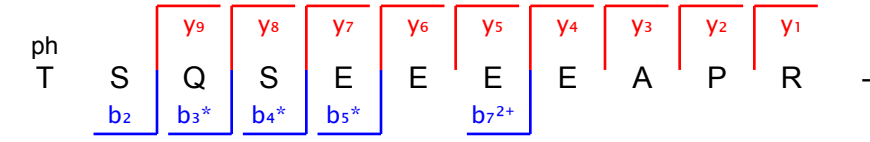
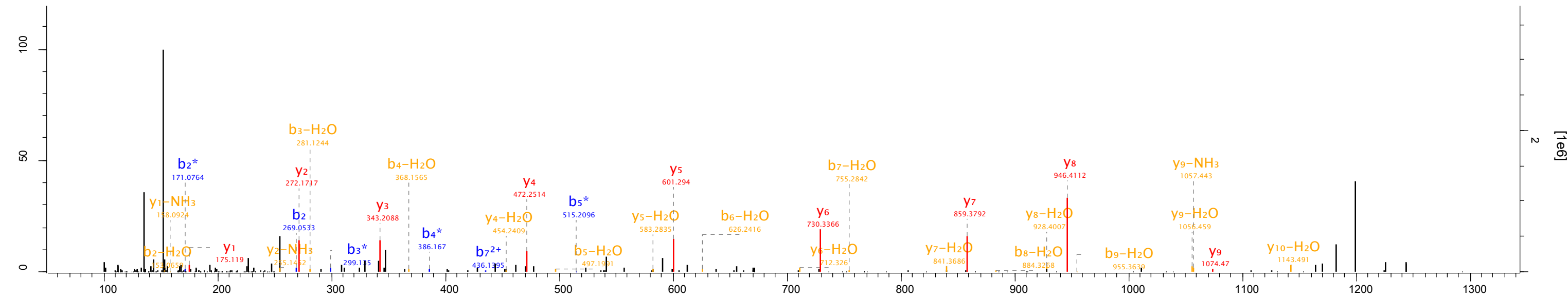
20171215_MaS_33SR_LMH_phospho2_02

2293 FTMS; HCD 123.1 624.8 SLIRP



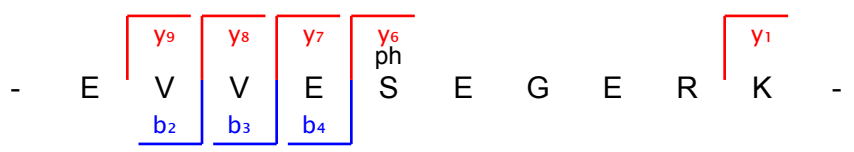
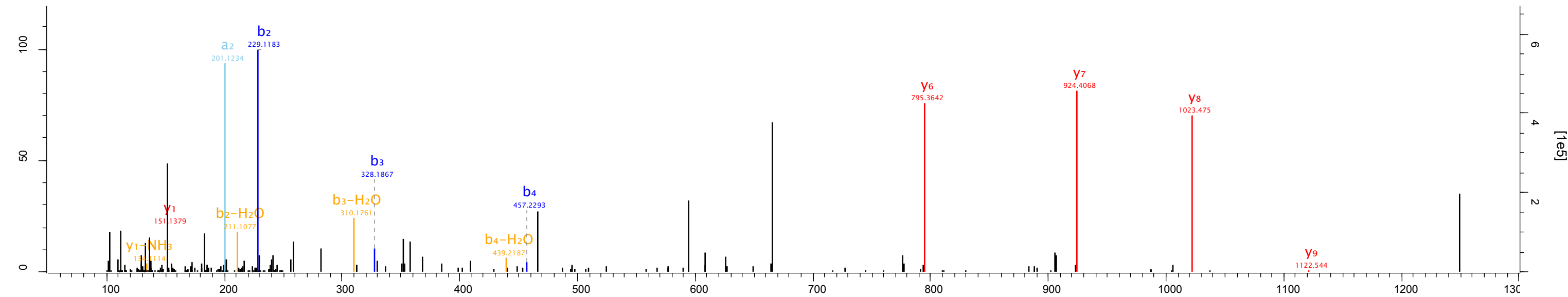
Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 2753 Method FTMS; HCD Score 77.06 m/z 671.76 Gene names MICAL3

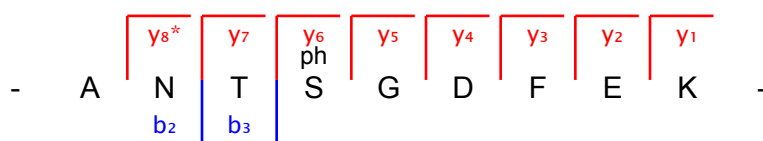
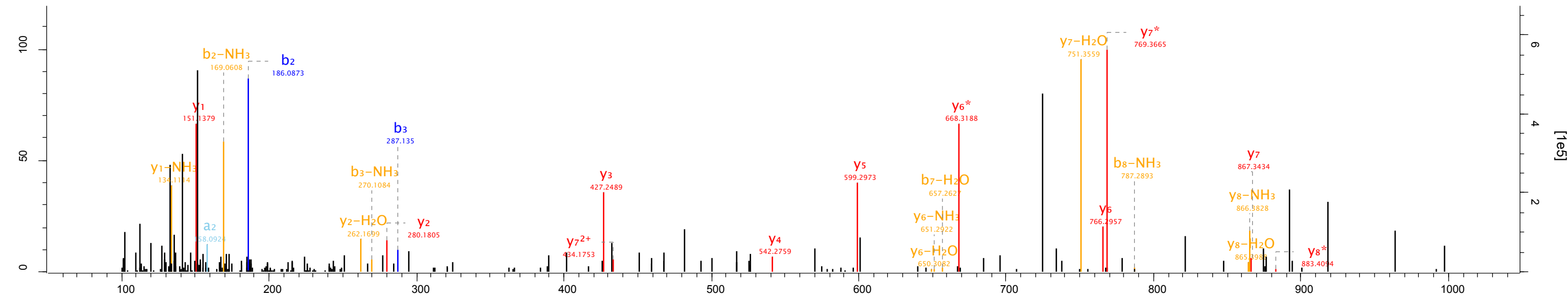


Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 3293 Method FTMS; HCD Score 136.57 m/z 626.3 Gene names SMARCC2

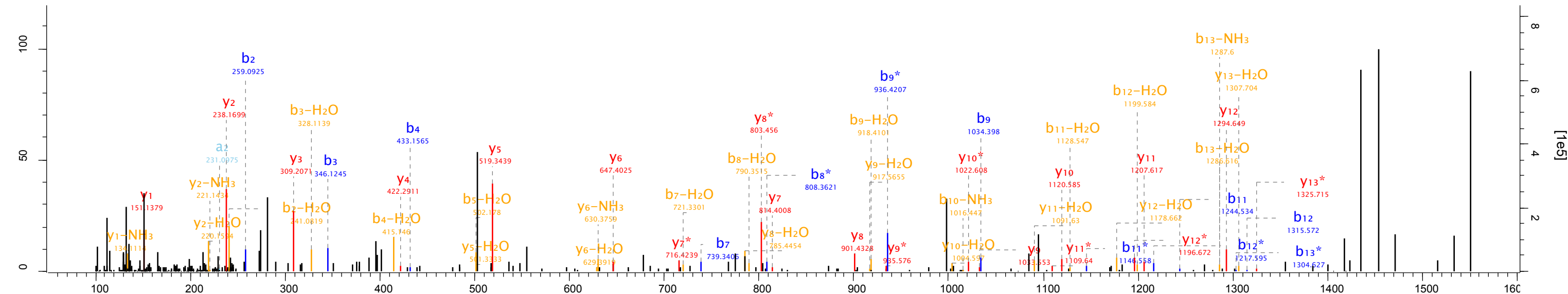


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3363 Method FTMS; HCD Score 74.08 m/z 526.72 Gene names RANBP2;RGPD4;RGPD5;RGPD8



Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 3403 Method FTMS; HCD Score 201.32 m/z 776.87 Gene names HMGA1;C2orf81

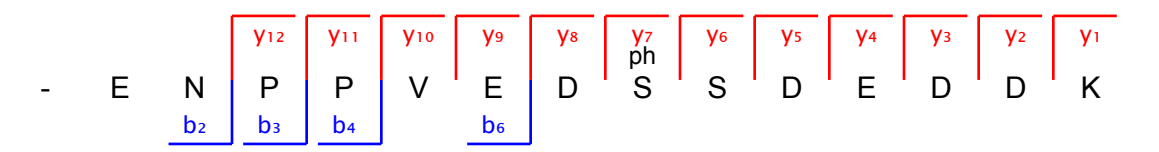
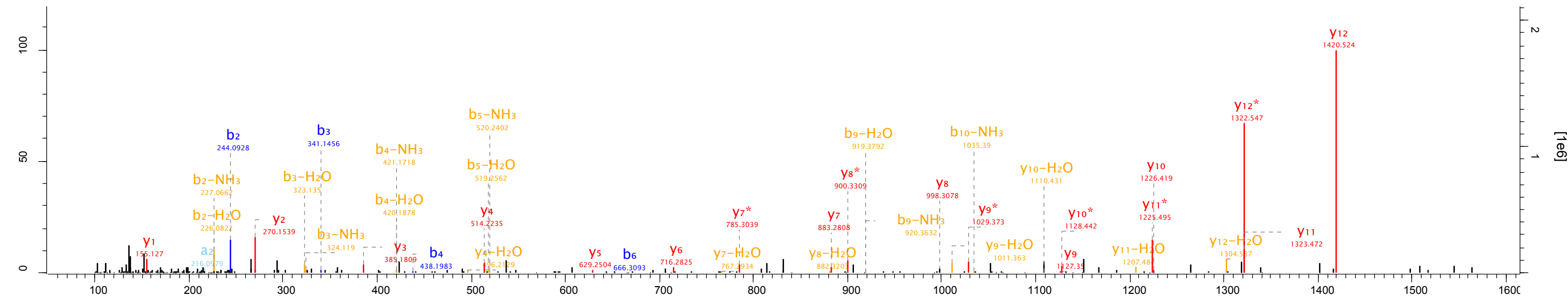


ac
- S E S S S K S ph S Q P L A S K -

Fragmentation scheme diagram showing amino acid residues (E, S, S, S, K, S, ph, S, Q, P, L, A, S, K) and their corresponding b and y series labels (b2, b3, b4, b7, b8*, b9, b11, b12, b13*) connected by lines, indicating the fragmentation pattern.

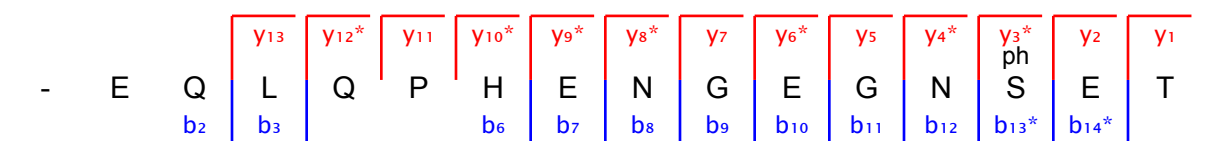
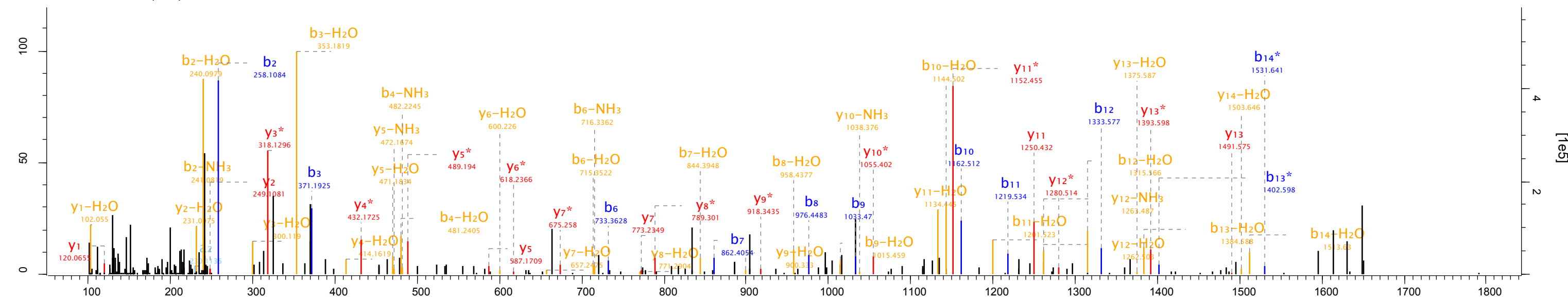
Raw file
20171215_MaS_33SR_LMH_phospho2_02

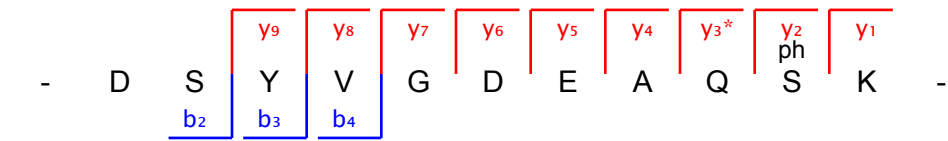
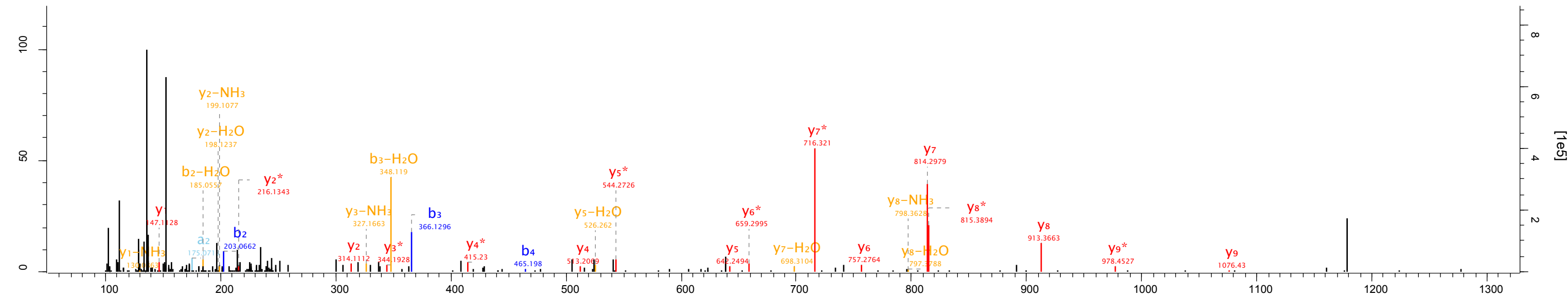
Scan Method Score m/z Gene names
3463 FTMS; HCD 124.25 832.31 STT3B

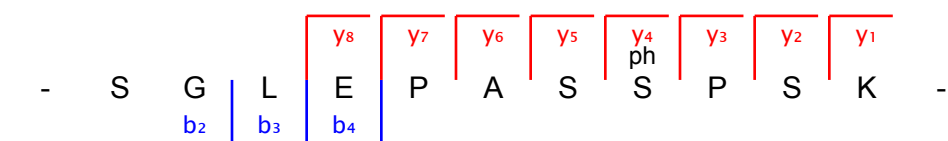
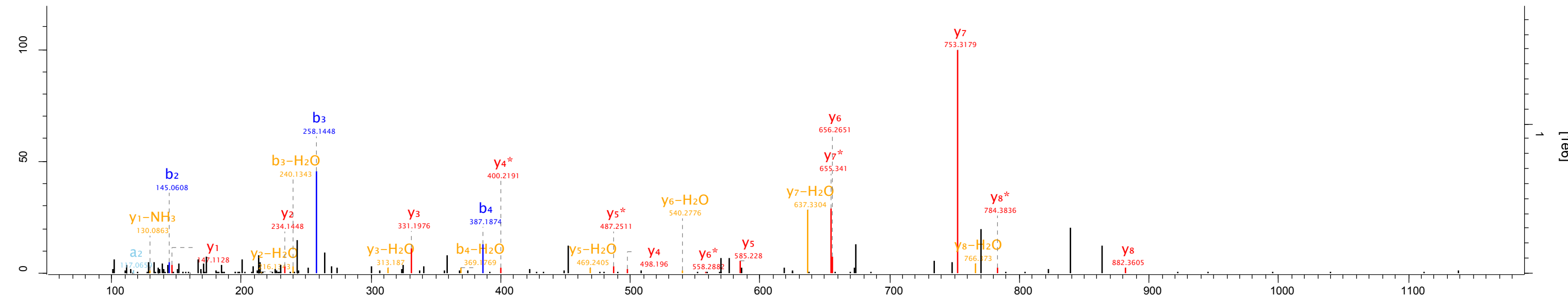


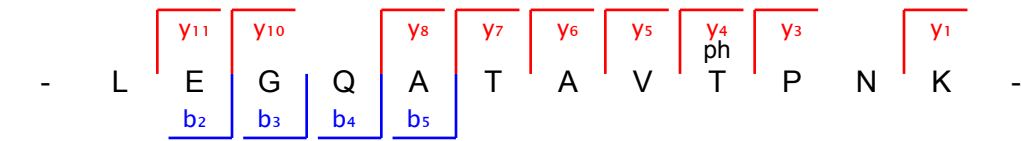
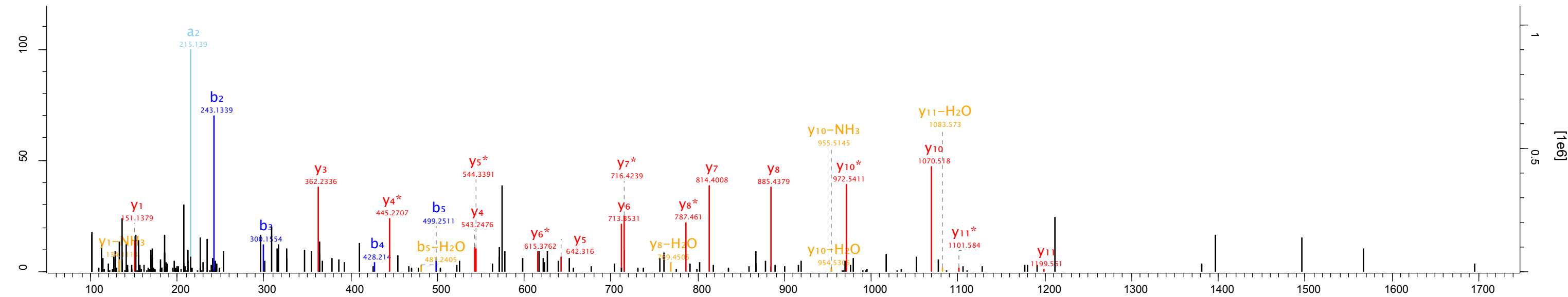
Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 3733 Method FTMS; HCD Score 248.91 m/z 875.34 Gene names ITGAV

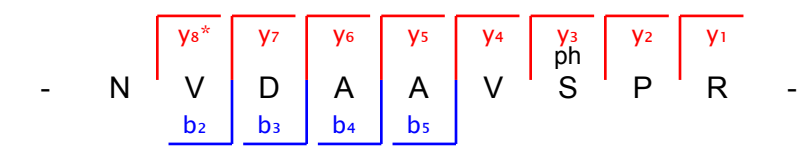
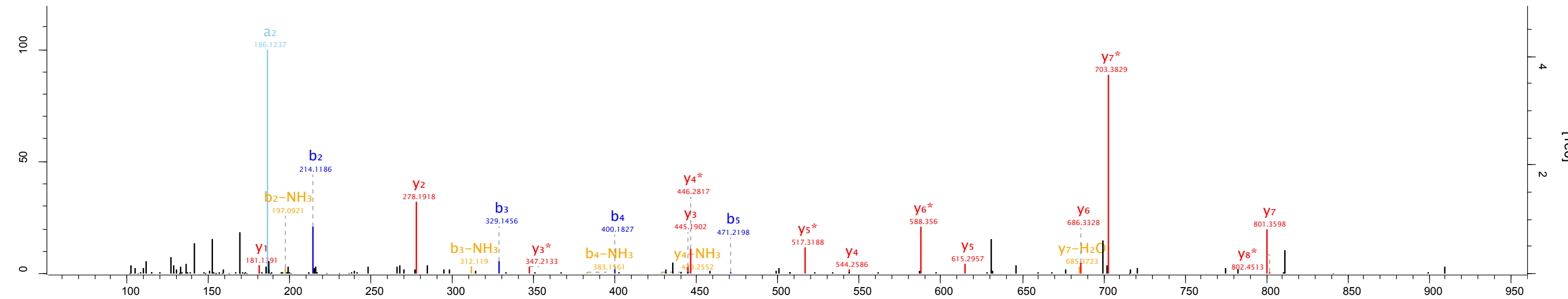




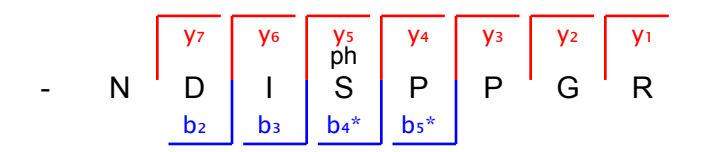
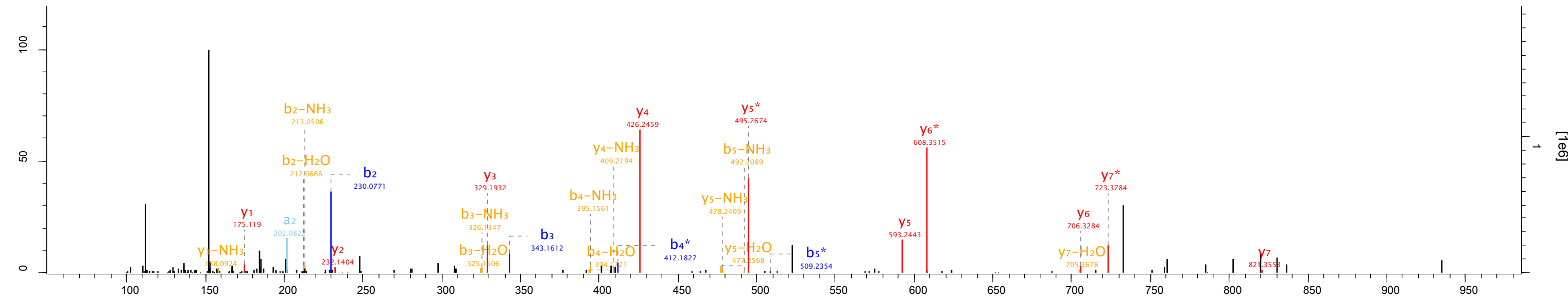




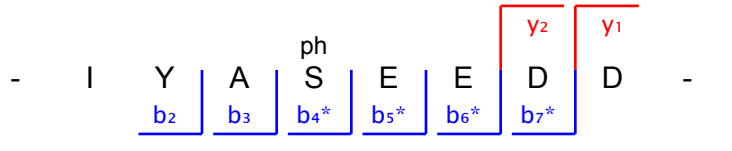
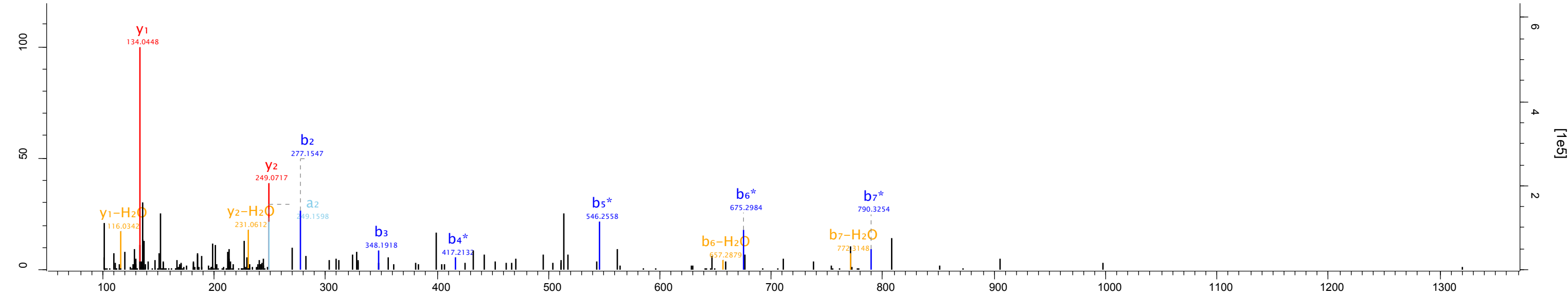
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 4113 Method FTMS; HCD Score 105.95 m/z 507.74 Gene names SPEN



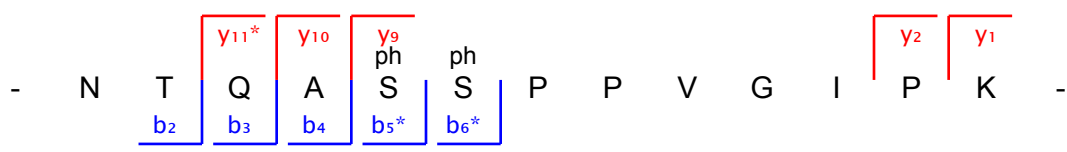
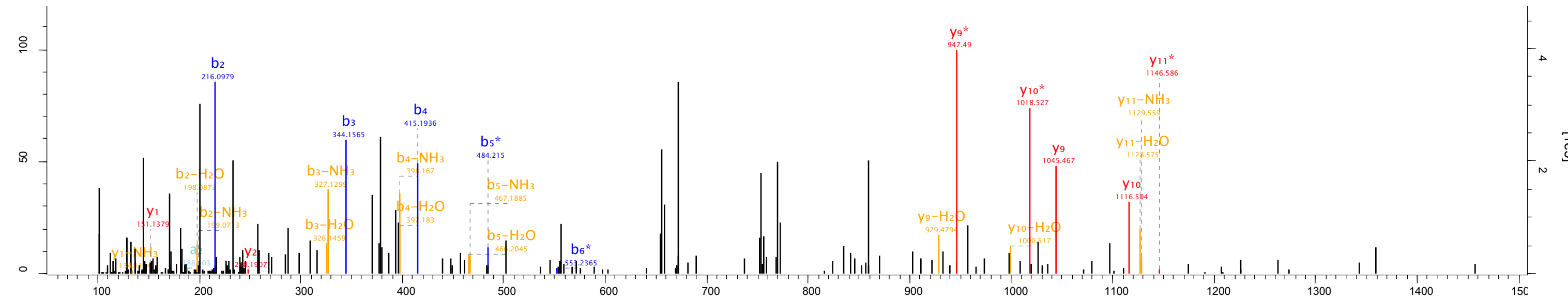
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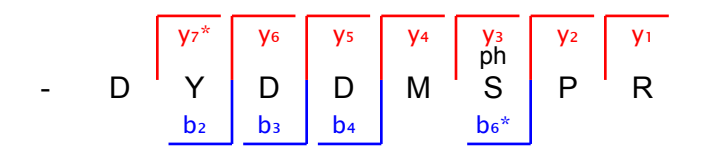
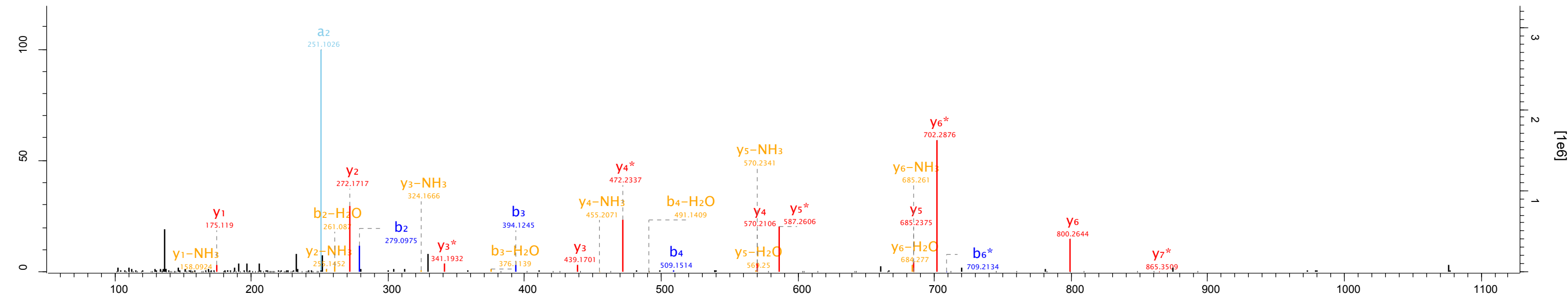
20171215_MaS_33SR_LMH_phospho2_02 4683 FTMS; HCD 80.17 511.17 MISP



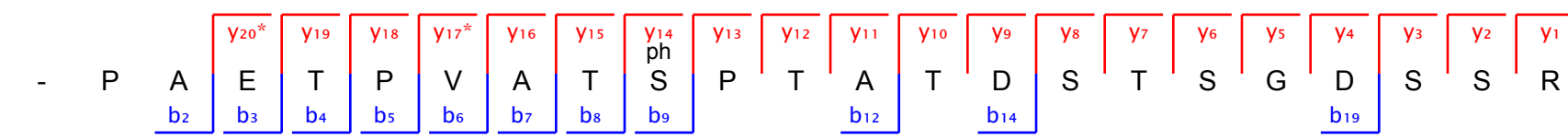
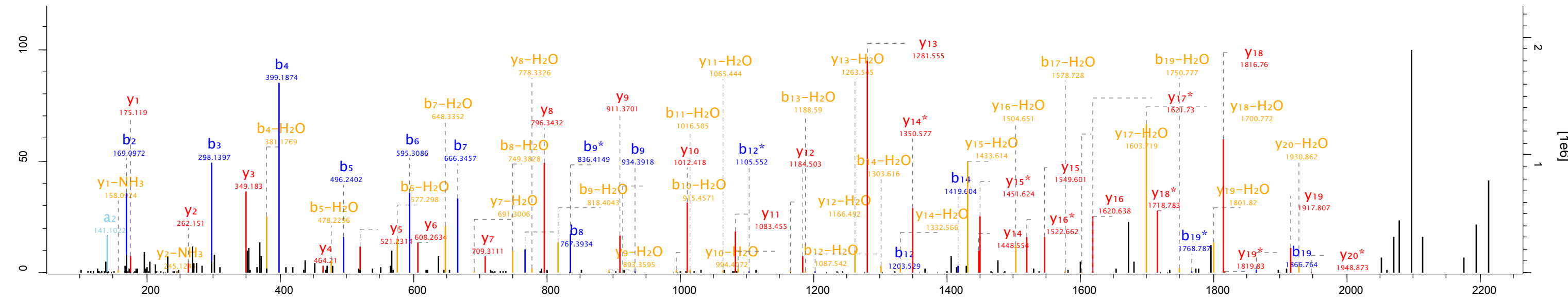
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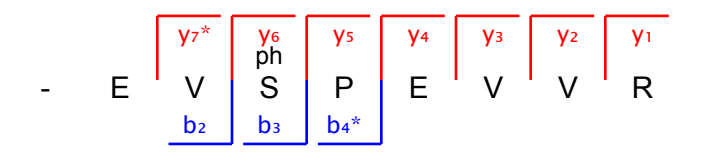
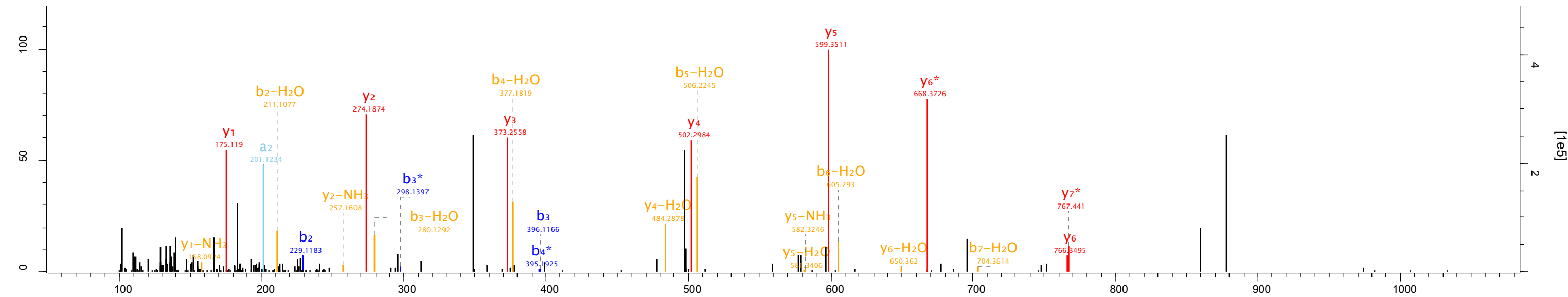
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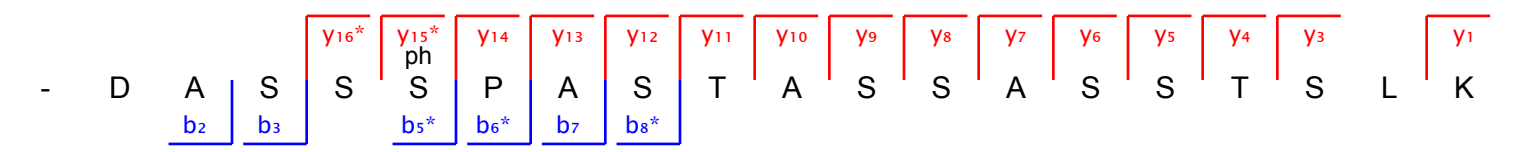
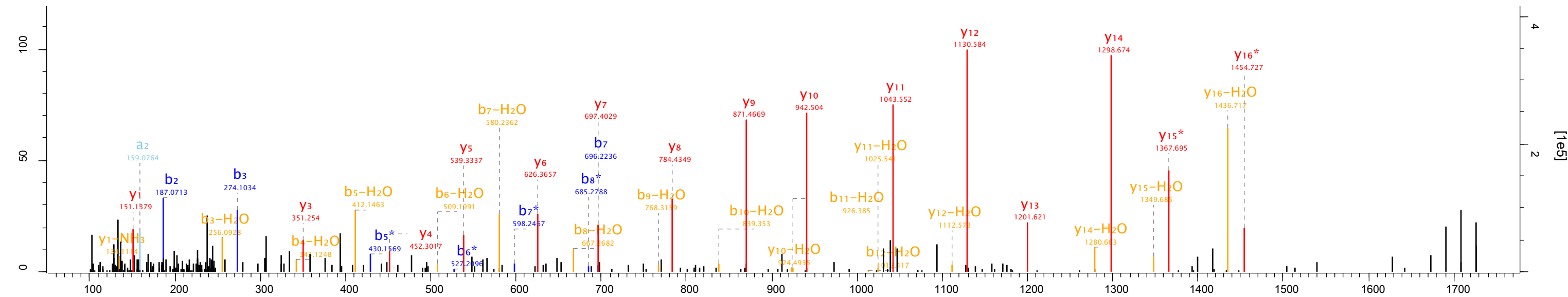
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 5633 Method FTMS; HCD Score 347.24 m/z 1108.48 Gene names RAD23B



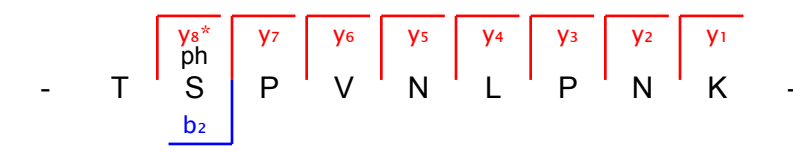
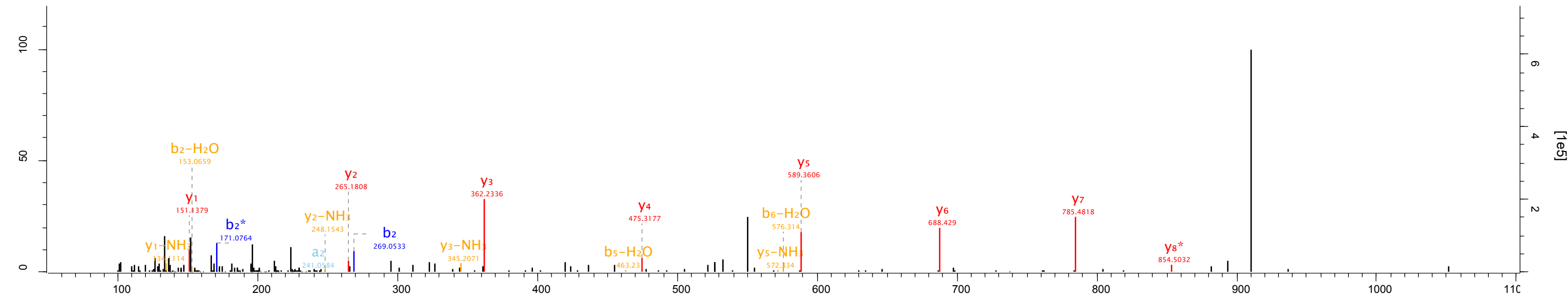
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 5783 Method: FTMS; HCD Score: 99.97 m/z: 497.73 Gene names: ZC3H13

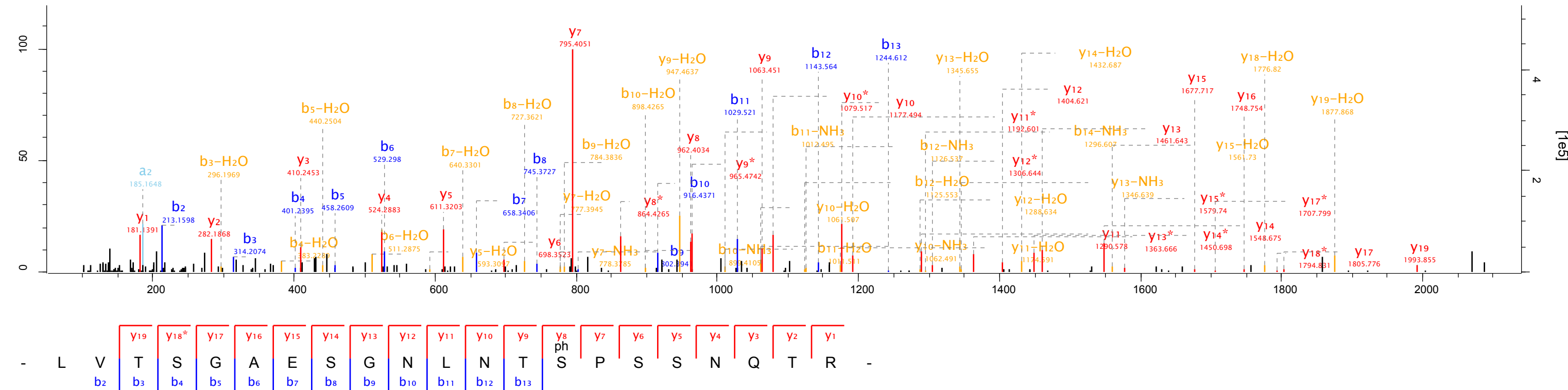


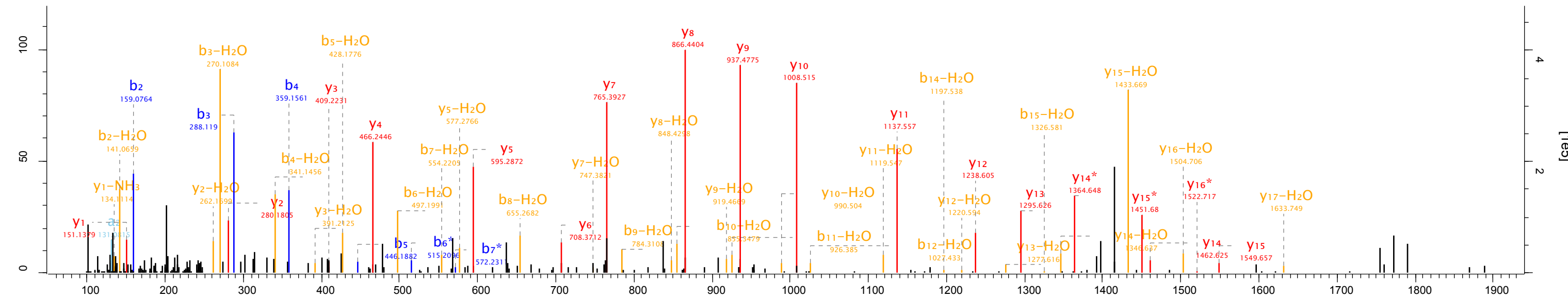
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6003 Method FTMS; HCD Score 129.85 m/z 913.4 Gene names TLE1



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6073 Method FTMS; HCD Score 54.2 m/z 527.27 Gene names SOX6



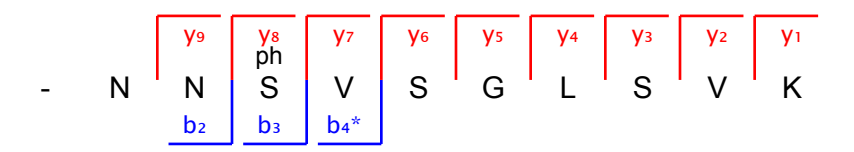
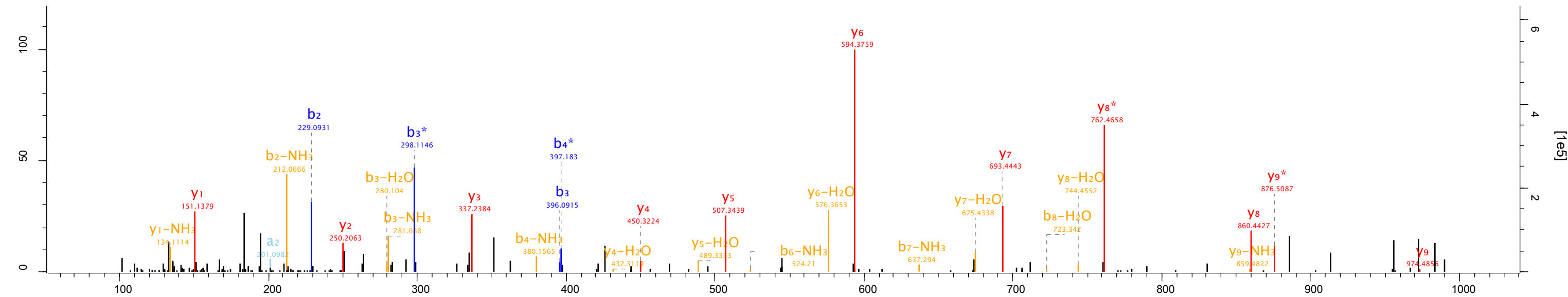




- G T E A S ph S G T E A A T G L E G E E K -

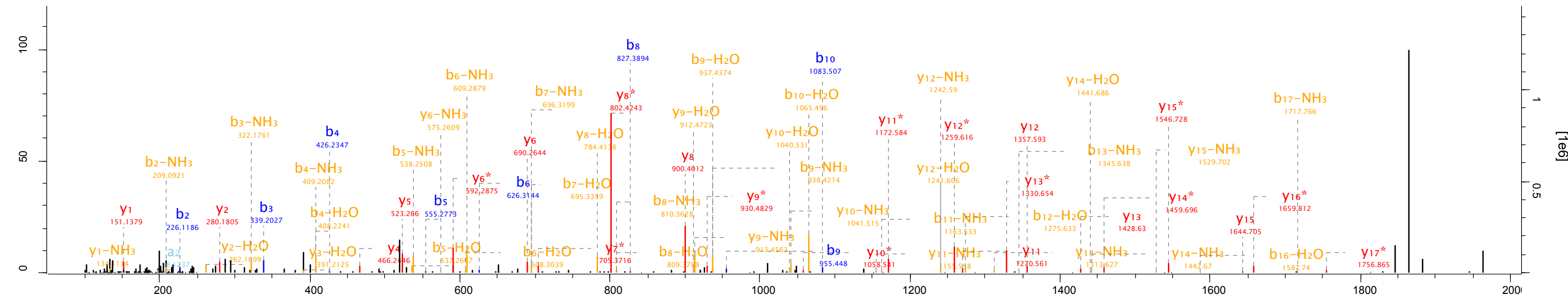
b₂
b₃
b₄
b₅
b₆*
b₇*
y₁₆*
y₁₅
y₁₄ph
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 6783 Method: FTMS; HCD Score: 115.37 m/z: 544.77 Gene names: DDX20



Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 6873 Method FTMS; HCD Score 233.85 m/z 992.46 Gene names ANLN

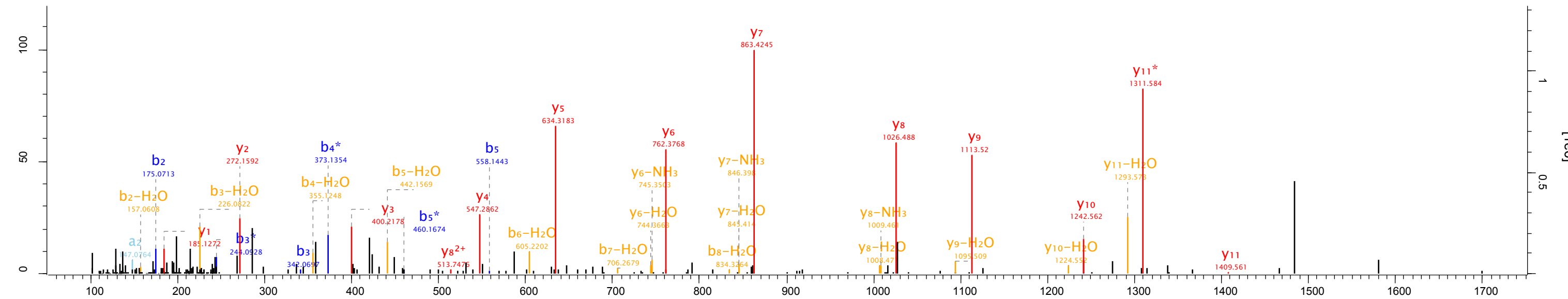


- Q P L S E A S N Q Q P L S G G E E K -

Fragmentation mapping:
b2 (P), b3 (L), b4 (S), b5 (E), b6 (A), b8 (N), b9 (Q), b10 (Q)
y1 (K), y2 (E), y4 (G), y5 (G), y6 (S), y7 (L), y8 (P), y9 (Q), y10 (Q), y11 (S), y12 (S), y13 (A), y14 (E), y15 (S), y16 (L), y17 (P)

Raw file
20171215_MaS_33SR_LMH_phospho2_02

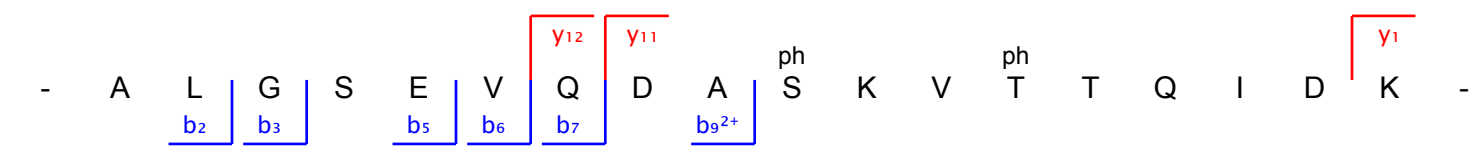
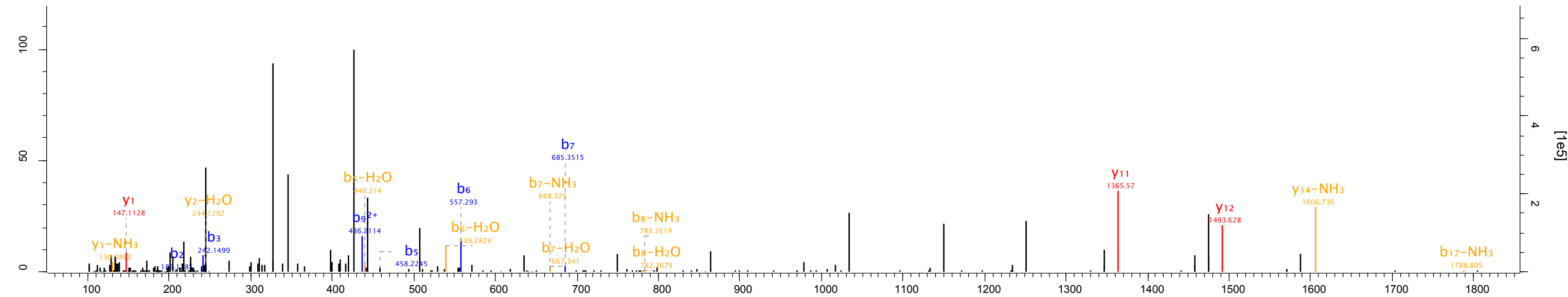
Scan 7503 Method FTMS; HCD Score 134.88 m/z 792.32 Gene names PI4K2A



- S S S y11 ph S y10 E S y9 S y8 Y T Q y6 S y5 S F Q y4 Q y3 S y2 S R -

Below the sequence, blue boxes highlight the b ions corresponding to the peaks in the spectrum: b2 (under the first S), b3 (under the second S), b4* (under the E), and b5 (under the third S).

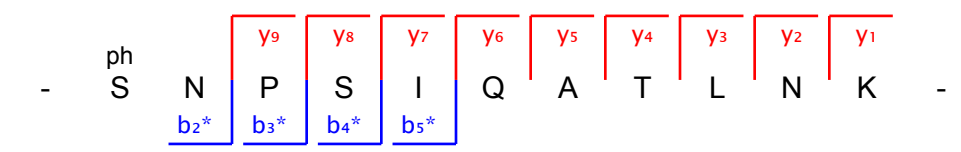
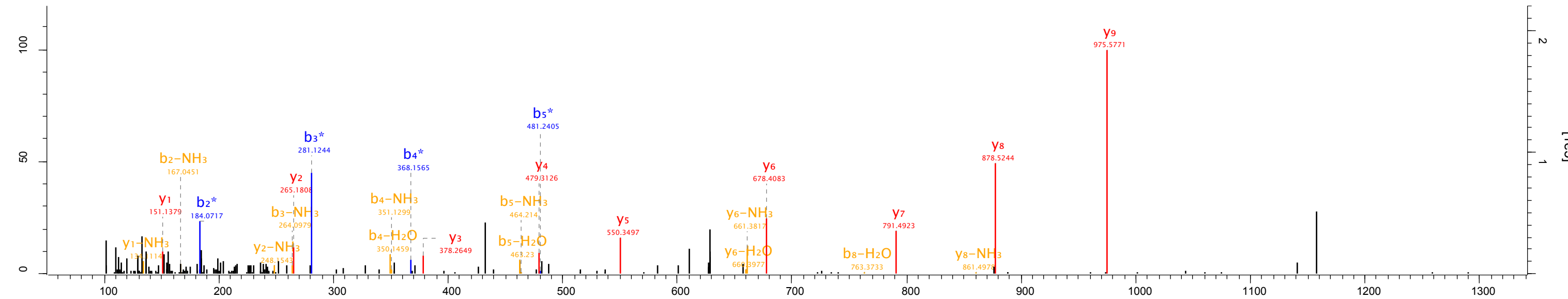
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 7593 Method: FTMS; HCD Score: 62.86 m/z: 1025.96 Gene names: SLK



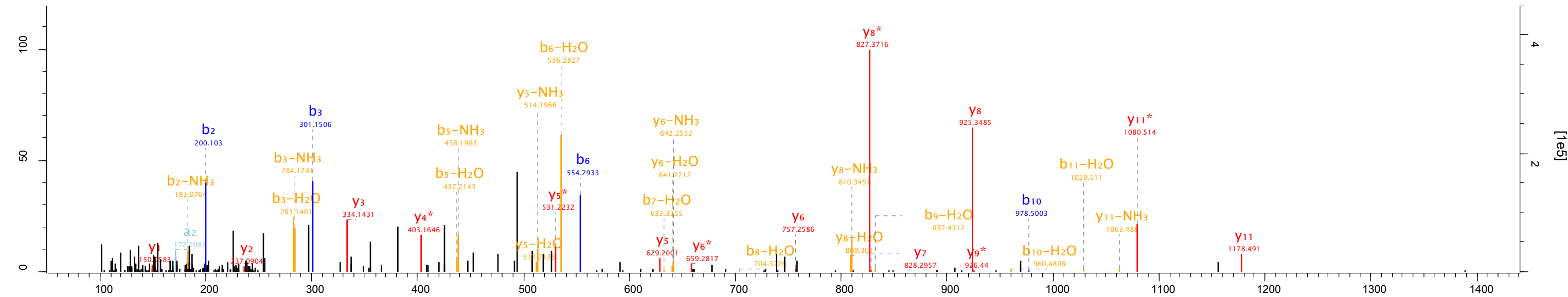
Raw file

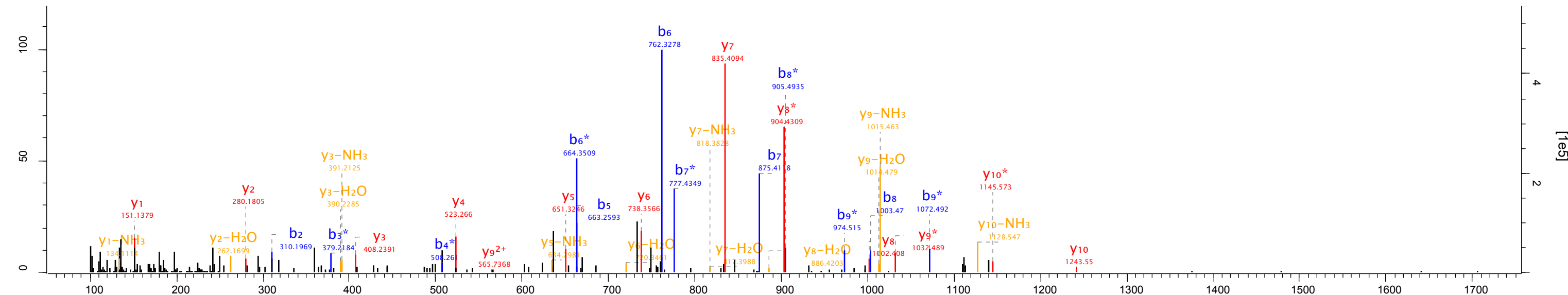
20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
8443	FTMS; HCD	76.76	628.81	CRTC3



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 8633 Method FTMS; HCD Score 115.87 m/z 739.82 Gene names KDM1A





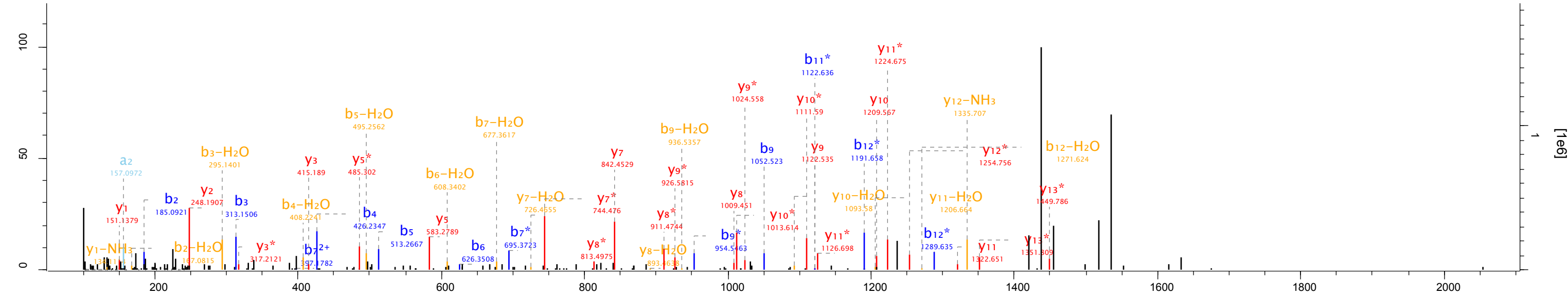
- R F S ph E G V L Q S ph S P S Q D Q E K -

b₂ b₃^{*} b₄^{*} b₅ b₆ b₇ b₈ b₉^{*}

y₁₀ y₉^{*} y₈ ph y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 10123 FTMS; HCD 175.77 817.9 WIZ



Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan

10153

Method

FTMS; HCD

Score

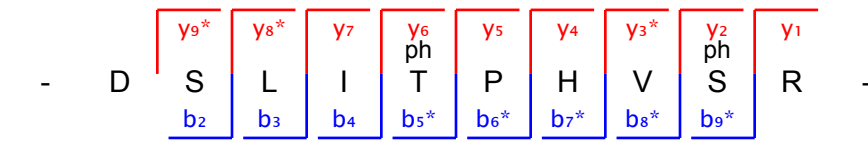
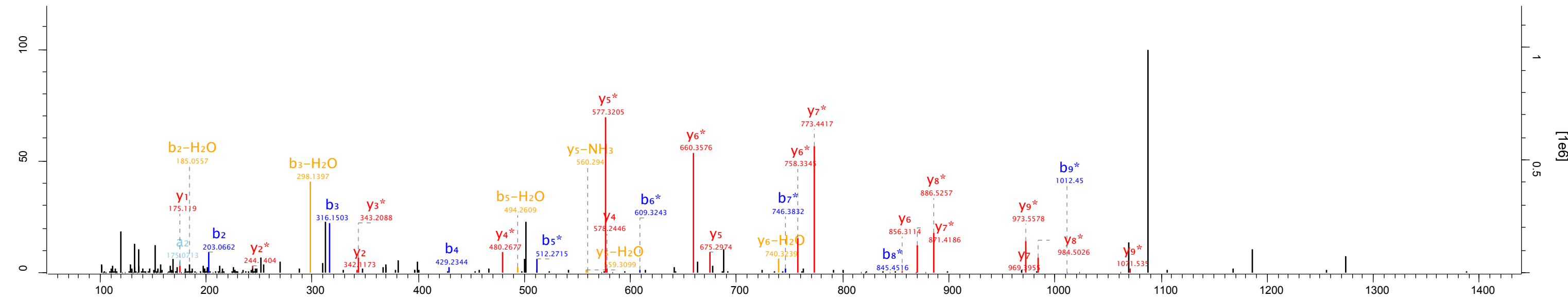
128.74

m/z

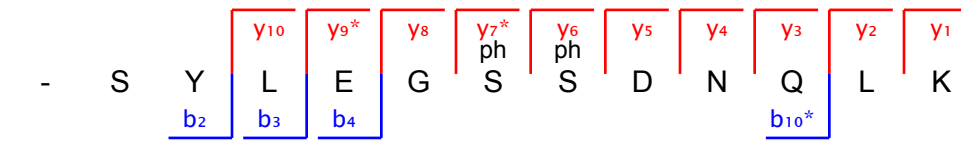
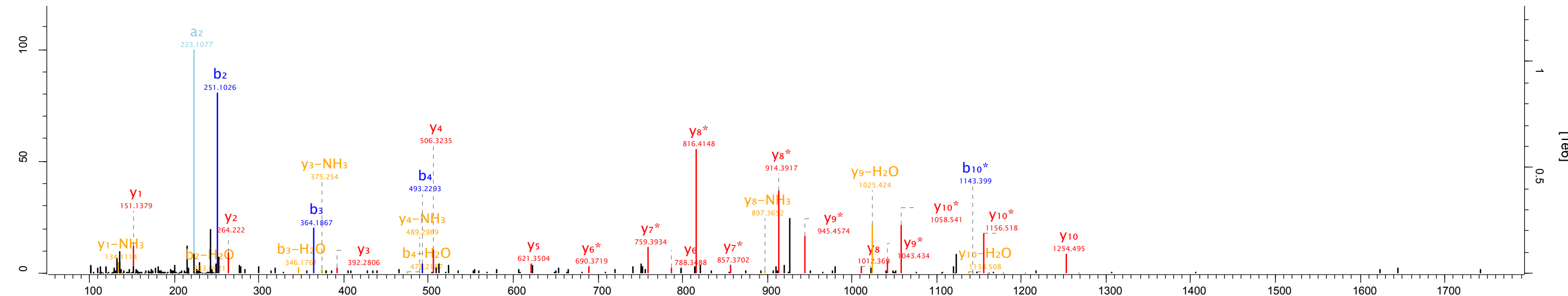
643.27

Gene names

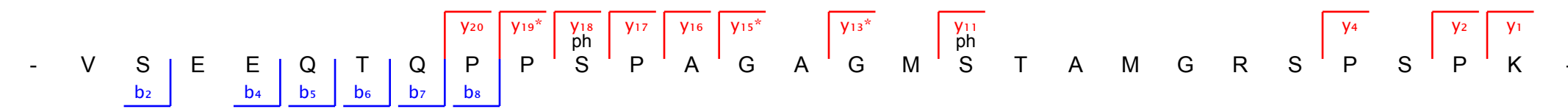
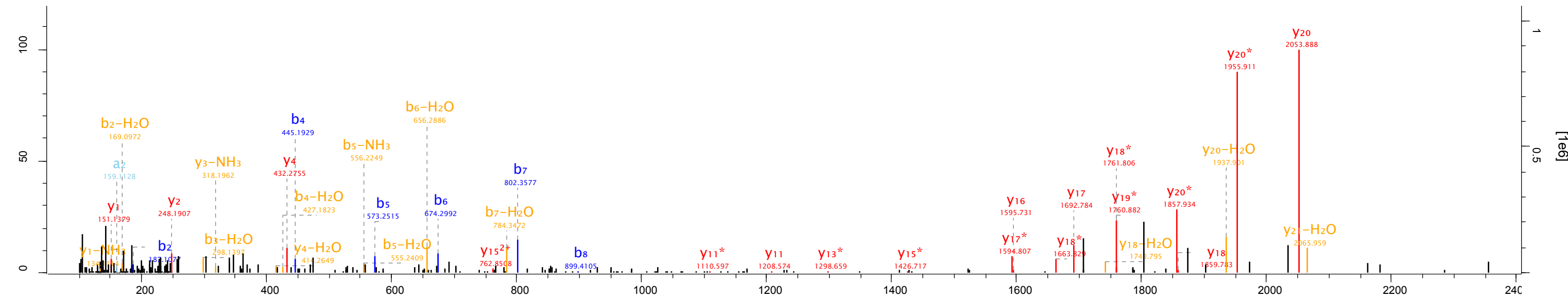
RANBP2;RGPD6;RGPD4;RGPD5;RGPD8



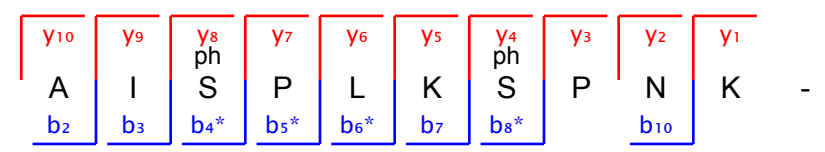
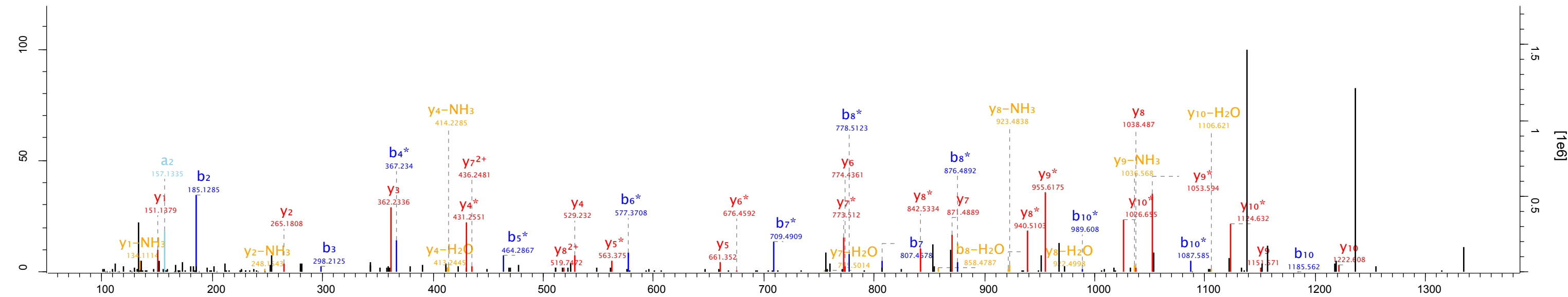
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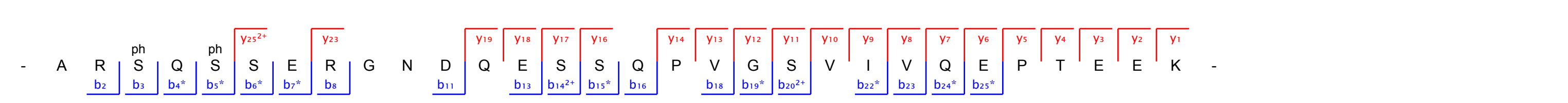
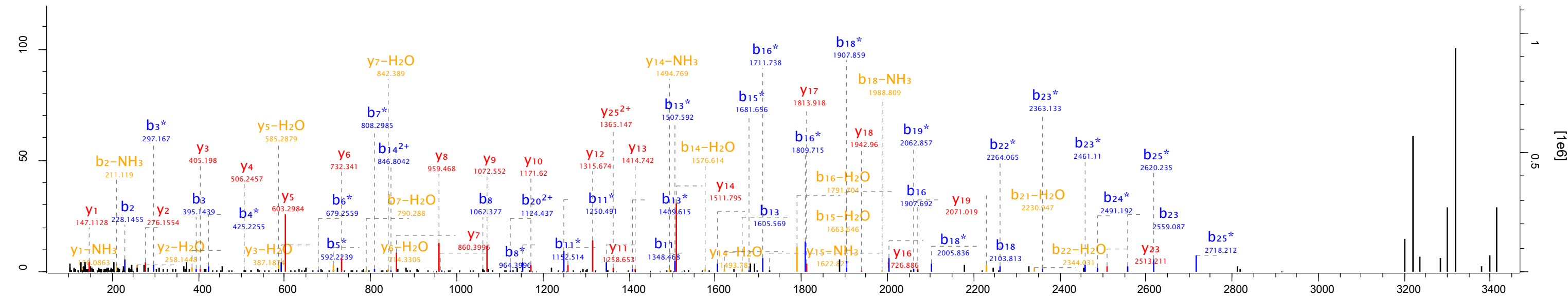
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 Scan: 10233 Method: FTMS; HCD Score: 53.49 m/z: 952.42 Gene names: IFI16



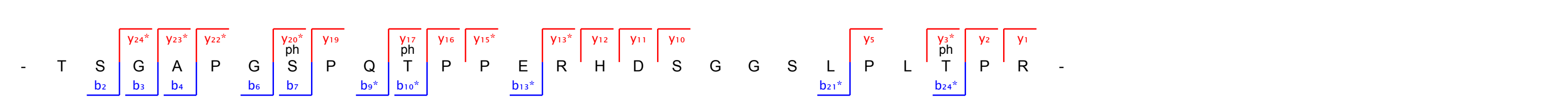
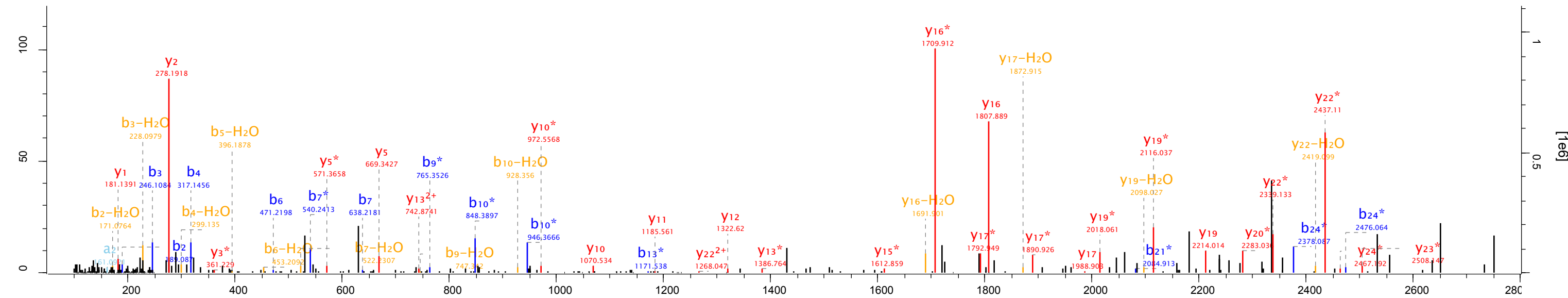
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10293 Method FTMS; HCD Score 183.82 m/z 668.35 Gene names LIN54



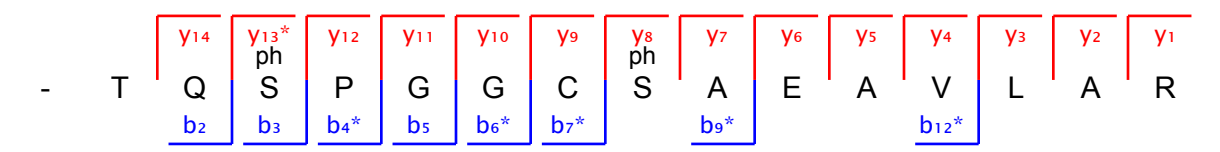
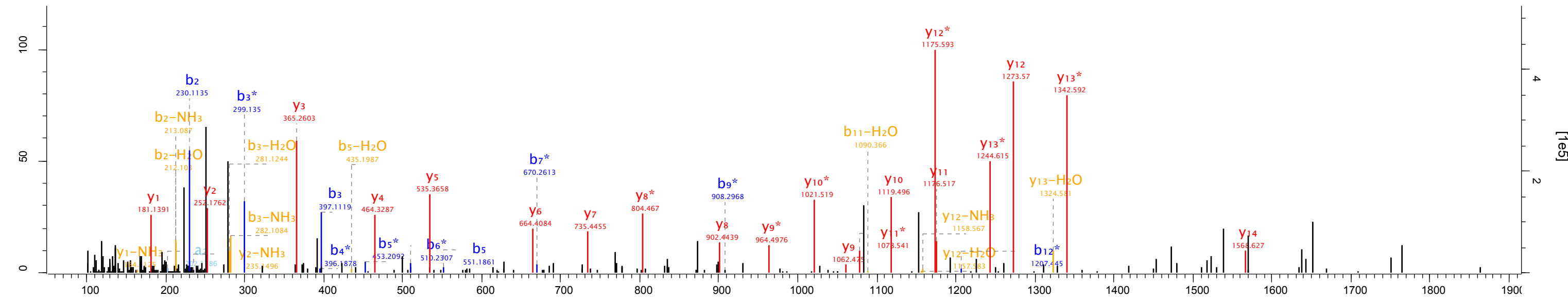
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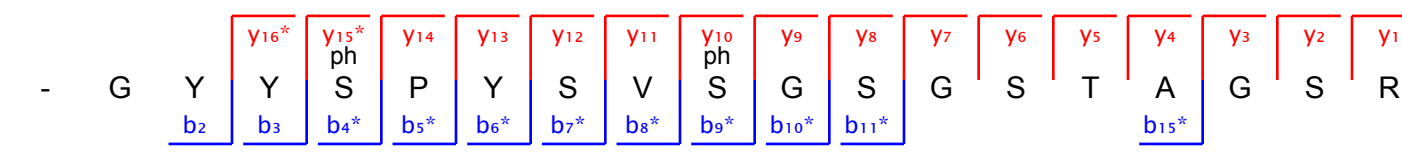
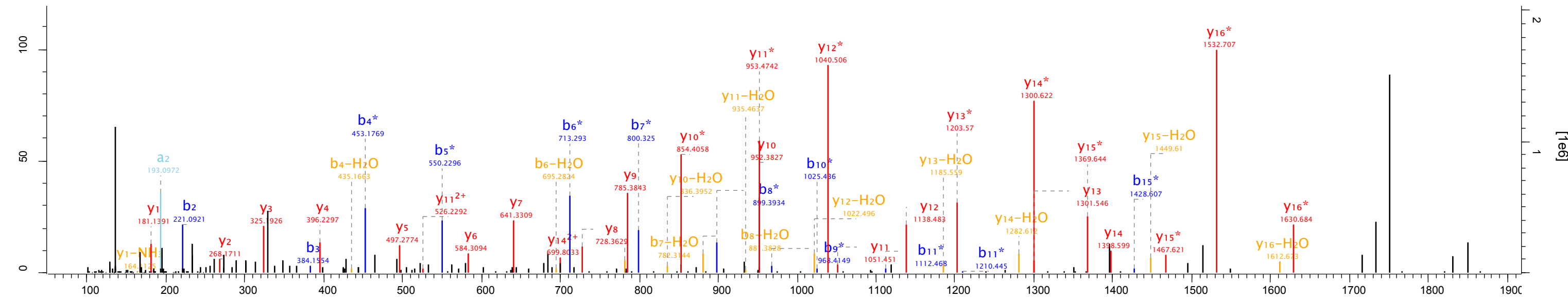
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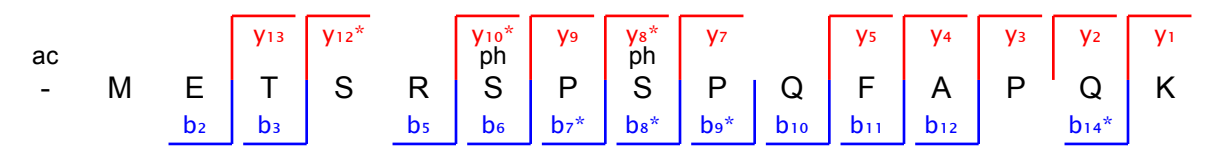
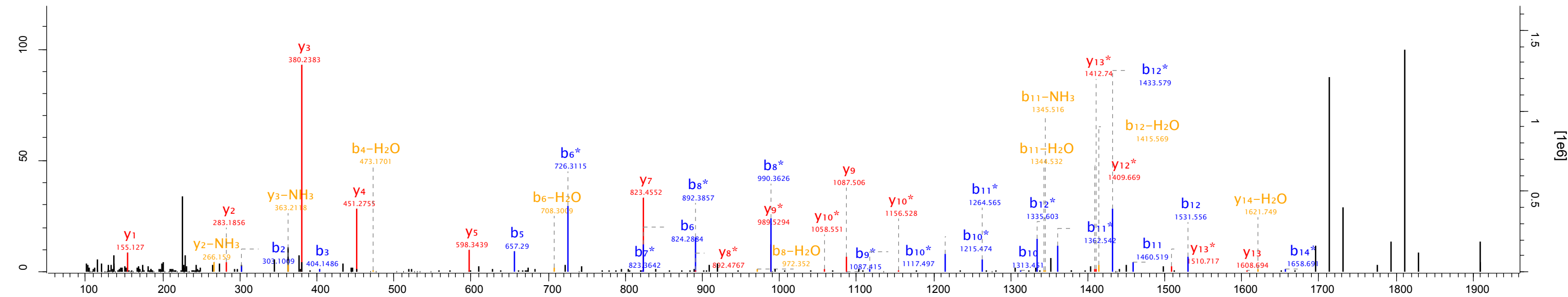
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 Scan: 10403 Method: FTMS; HCD Score: 105.56 m/z: 835.34 Gene names: HEXIM2



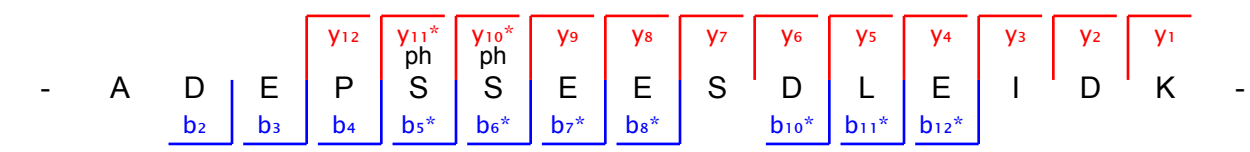
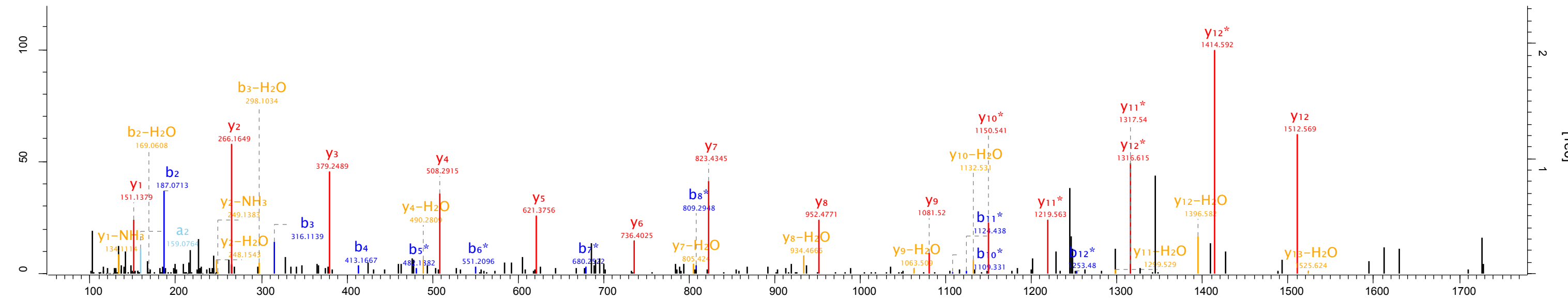
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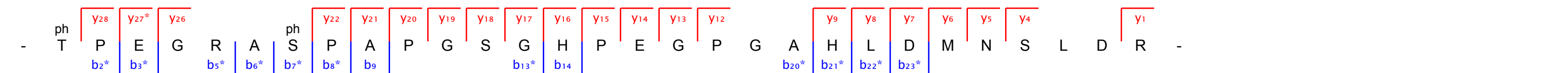
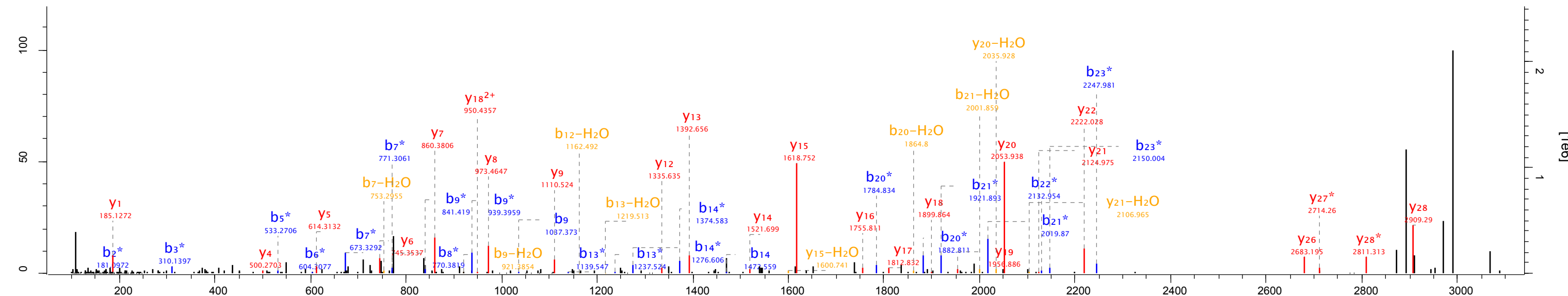
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 Scan: 10553 Method: FTMS; HCD Score: 141.19 m/z: 956.4 Gene names: SHROOM2



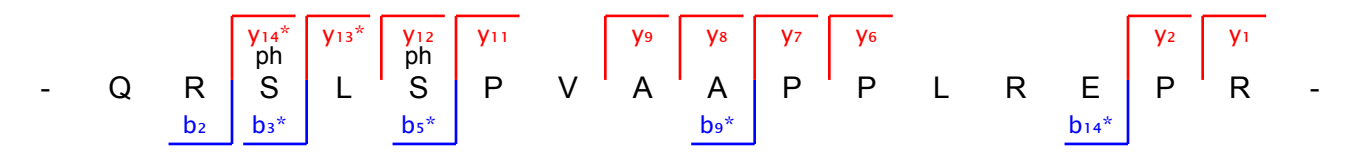
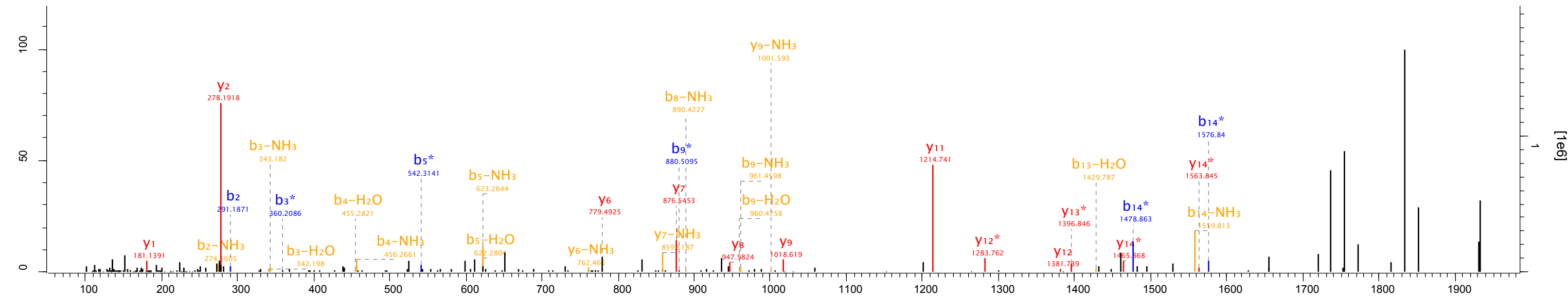
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10623 Method: FTMS; HCD Score: 115.38 m/z: 914.34 Gene names: ST13;ST13P4

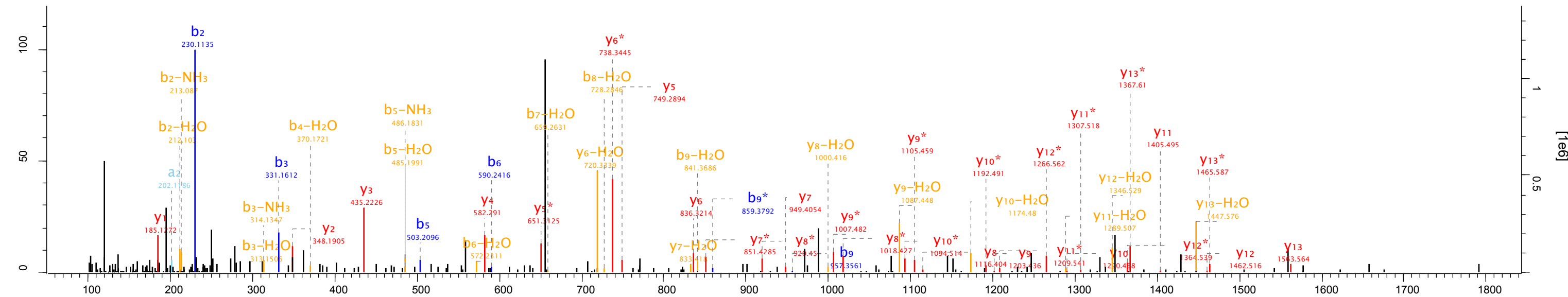


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 Scan: 10733 Method: FTMS; HCD Score: 101.38 m/z: 773.58 Gene names: TOMM70A



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 Scan: 10773 Method: FTMS; HCD Score: 74.36 m/z: 651.34 Gene names: RBM15B



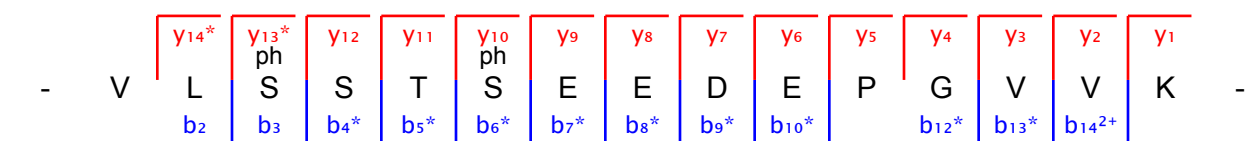
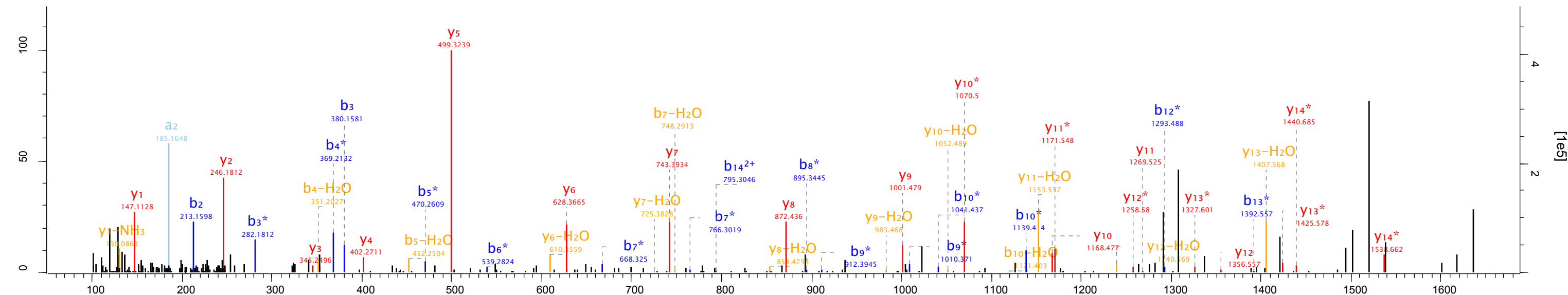


- T Q T G D S S S I S S F S Y R -

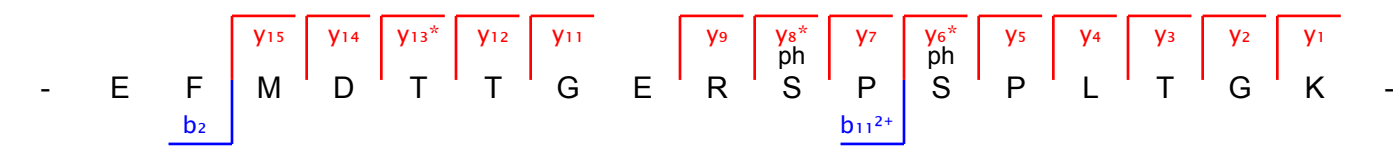
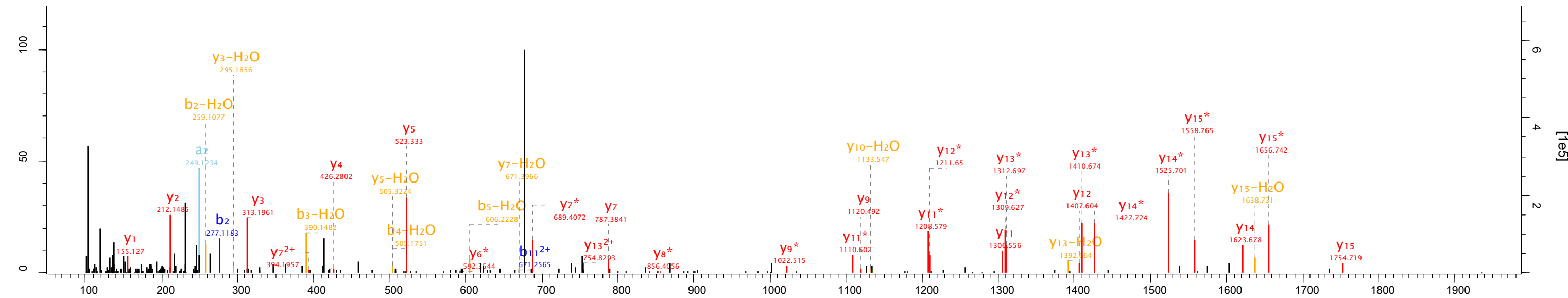
Fragmentation mapping (b and y ions):

- b2: T
- b3: T, G
- b5: D
- b6: S
- b9: I
- y1: R
- y2: Y
- y3: S
- y4: F
- y5: S
- y6: S
- y7: I
- y8: S
- y9: S
- y10: S
- y11: D
- y12: G
- y13: T

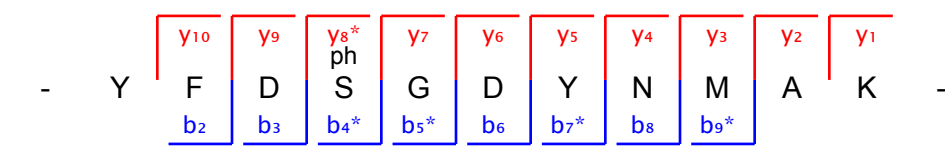
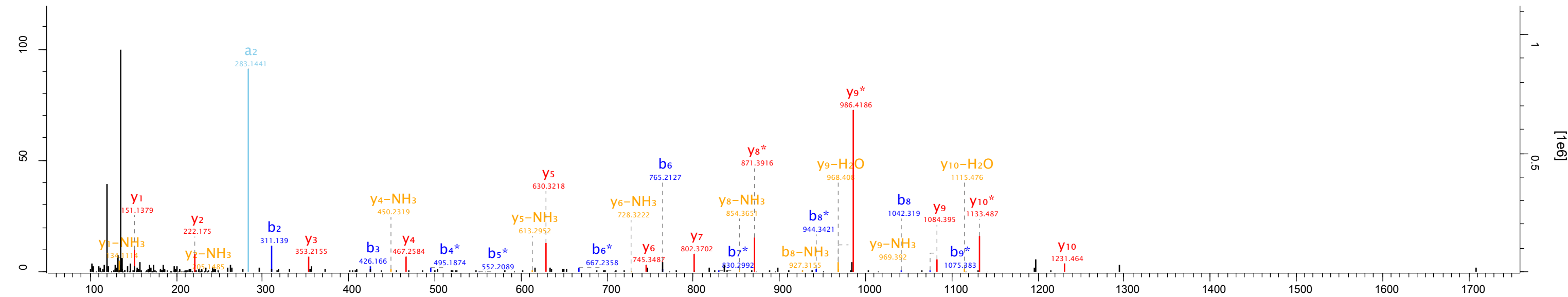
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10933 Method FTMS; HCD Score 163.78 m/z 868.35 Gene names NCOA7



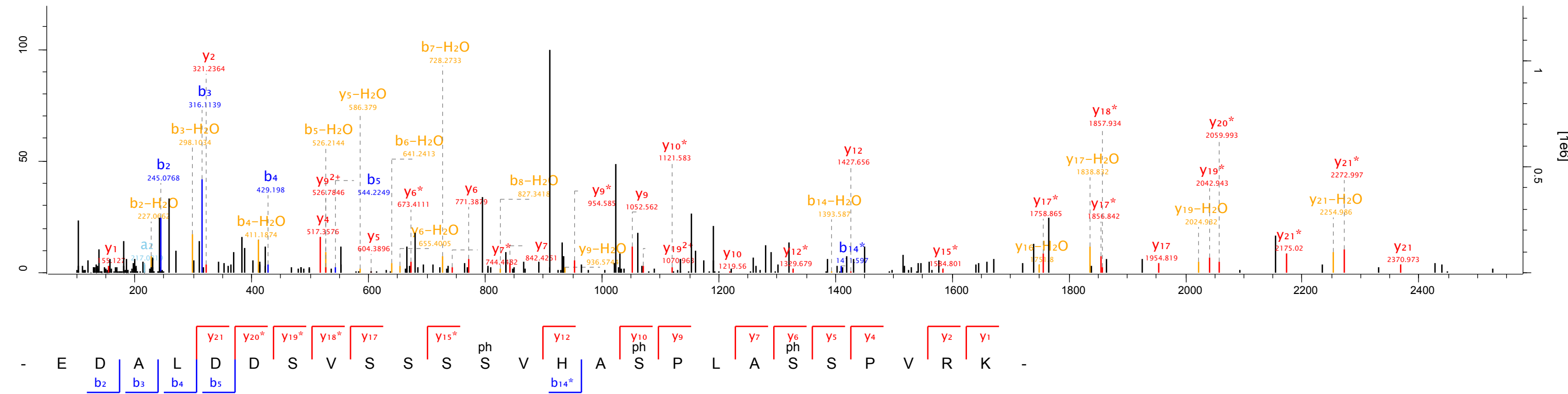
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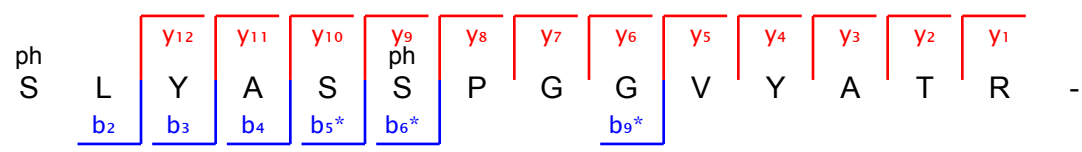
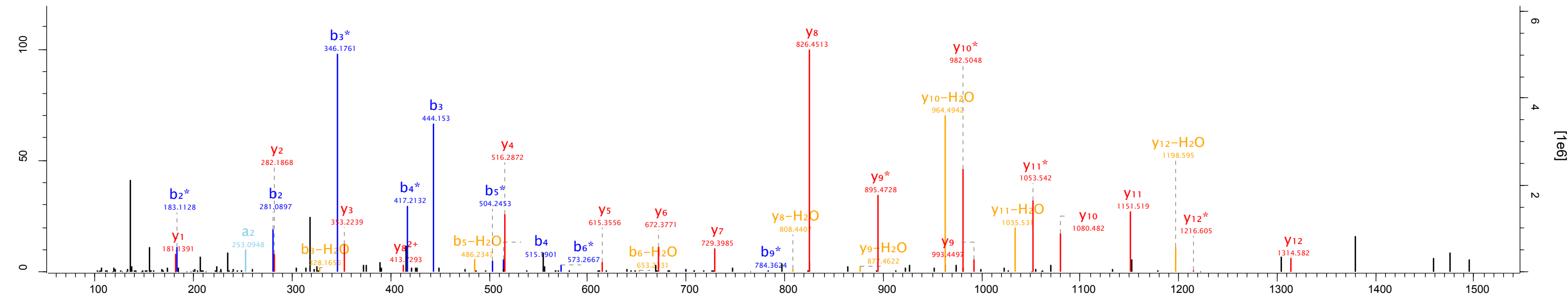
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 11393 Method: FTMS; HCD Score: 156.6 m/z: 697.77 Gene names: ARPP19;ENSA



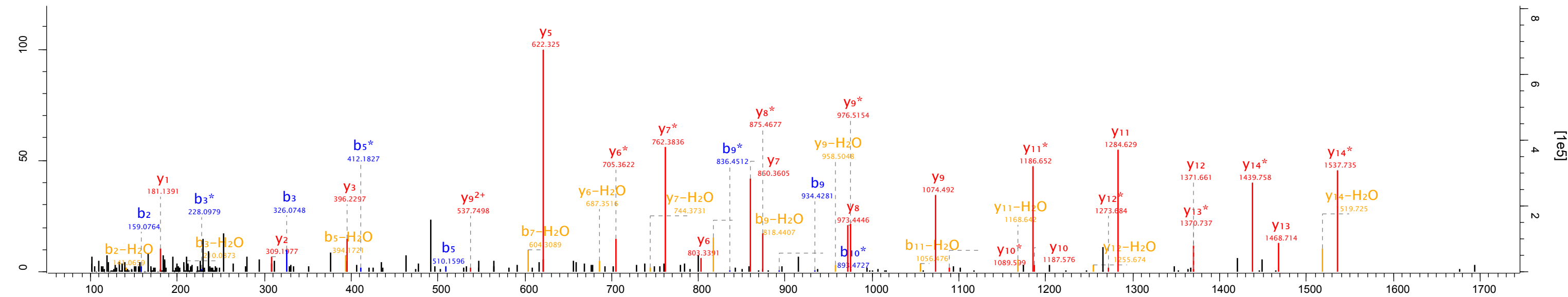
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11513 Method FTMS; HCD Score 63.3 m/z 934.06 Gene names RANBP2;RGPD4;RGPD5;RGPD8



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 11553 Method: FTMS; HCD Score: 149.95 m/z: 797.84 Gene names: VIM



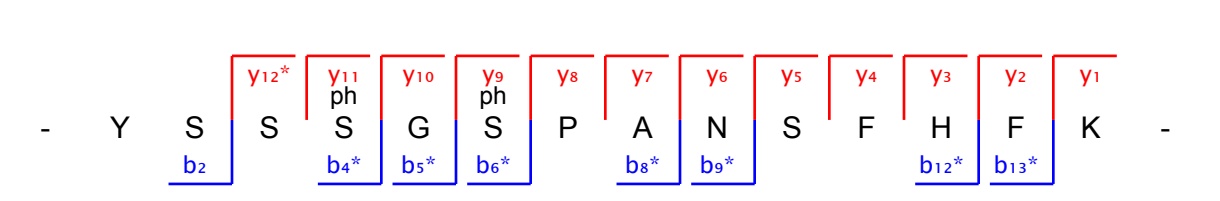
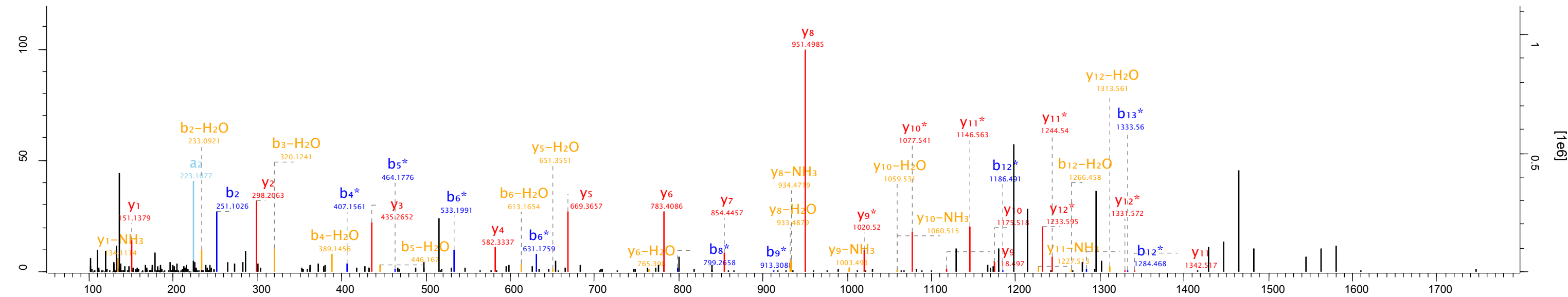
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11623 Method FTMS; HCD Score 166.65 m/z 897.39 Gene names DCP1A



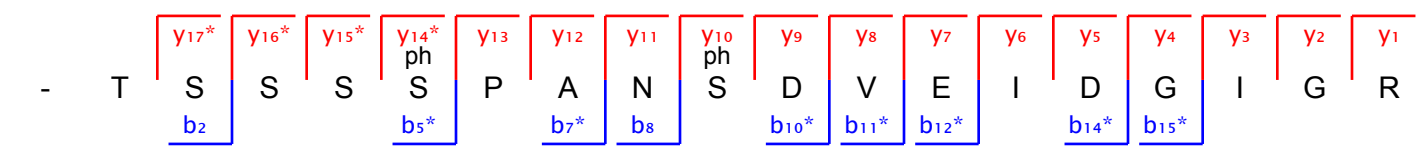
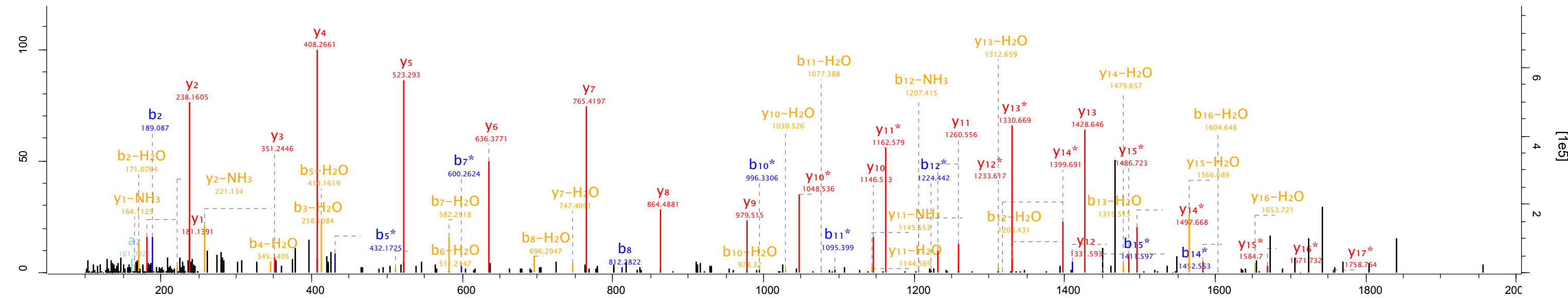
- A S S P S P L T I G T P E S Q R -

Fragmentation scheme showing b and y ions for the peptide sequence: A-S-S-P-S-P-L-T-I-G-T-P-E-S-Q-R. The b ions are labeled b2, b3, b5, b9, and b10*. The y ions are labeled y1, y2, y3, y5, y6, y7, y8, y9, y10, y11, y12, y13, and y14*.

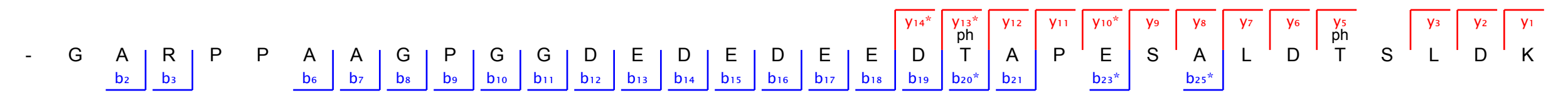
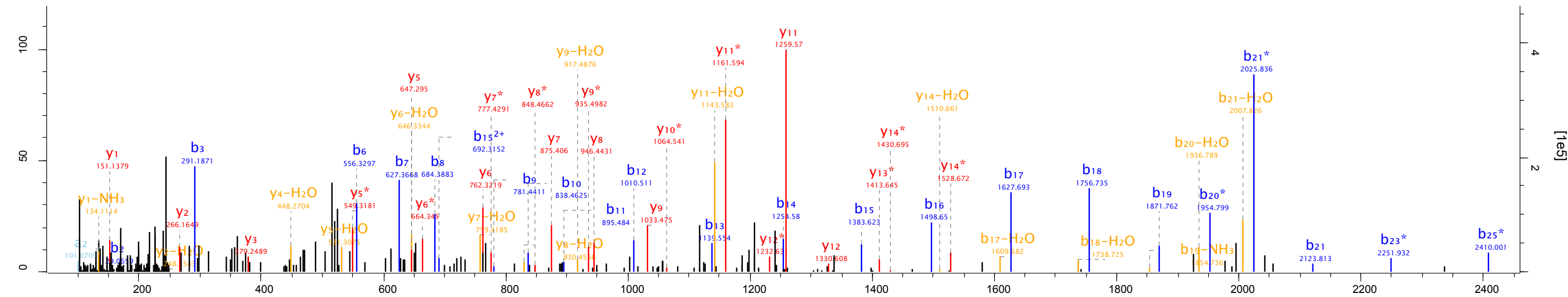
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 Scan: 11653 Method: FTMS; HCD Score: 147.86 m/z: 840.83 Gene names: EEF2K



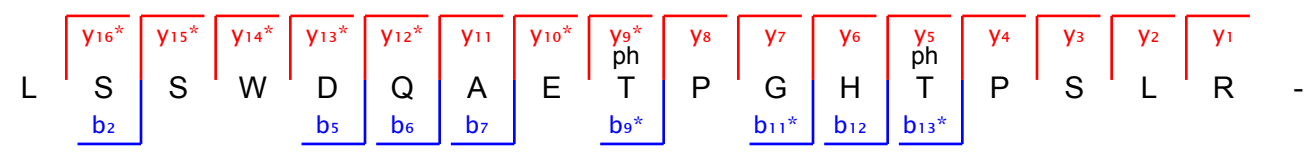
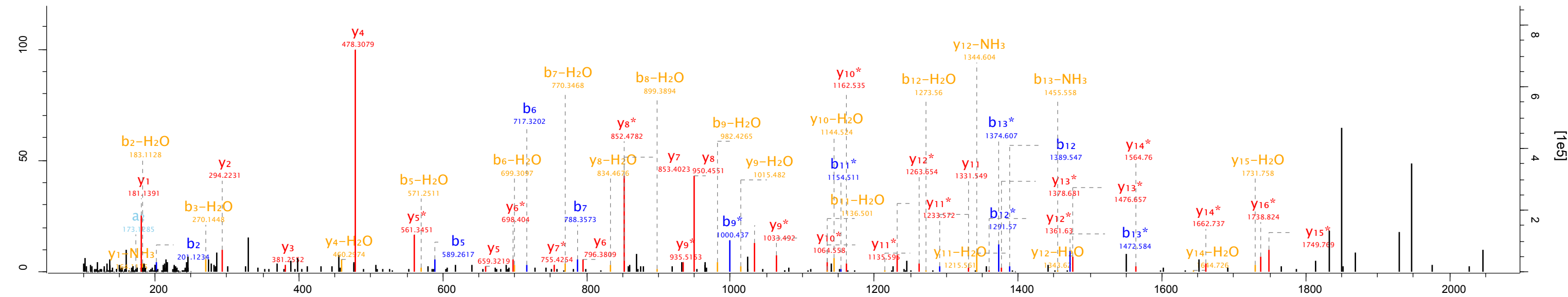
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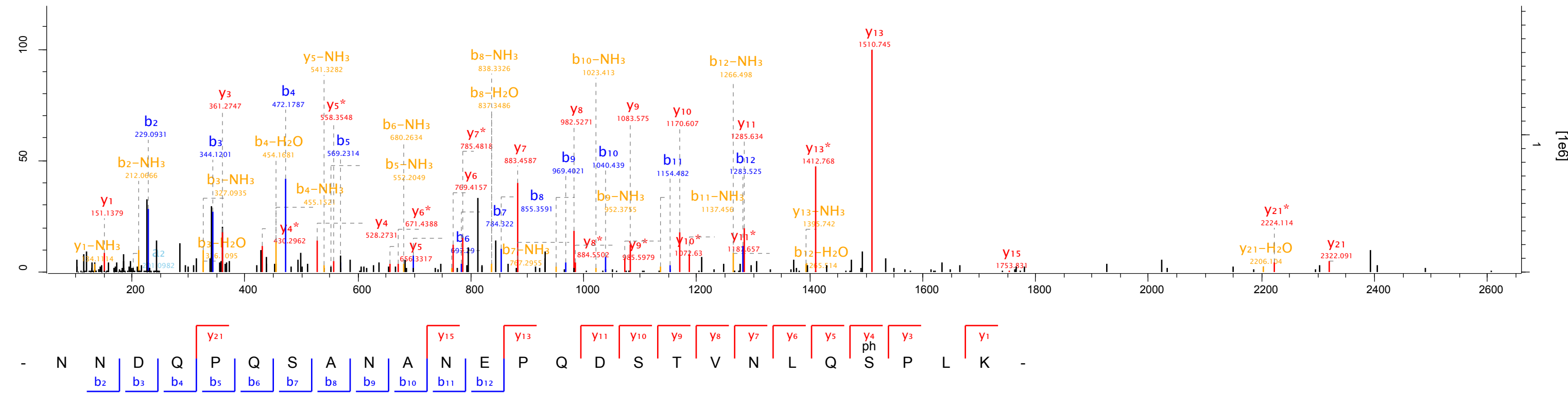


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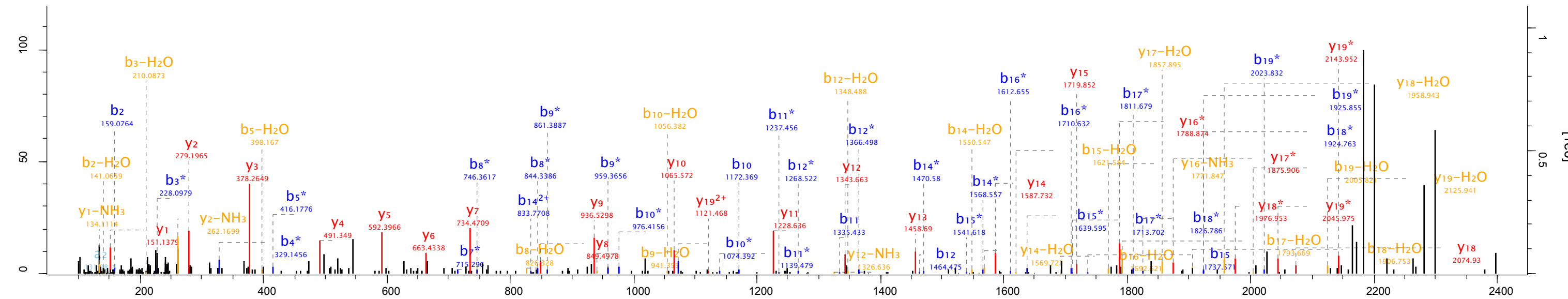


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11903 Method FTMS; HCD Score 220.46 m/z 1024.93 Gene names SF3B1





Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12213 Method FTMS; HCD Score 217.54 m/z 1200.5 Gene names UBR4

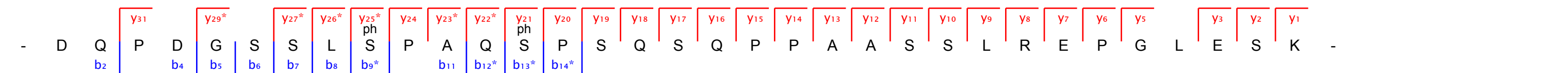
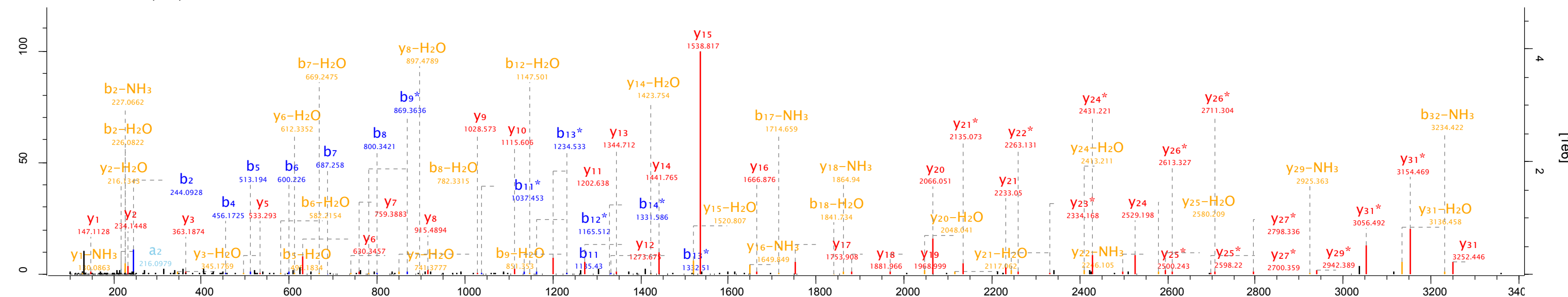


- T G Y₁₉*
ph
S Y₁₈ Y₁₇*
S Y₁₆*
ph
S Y₁₅ Y₁₄ Y₁₃ Y₁₂ Y₁₁ Y₁₀ Y₉ Y₈ Y₇ Y₆ Y₅ Y₄ Y₃ Y₂ Y₁ -

b₂ b₃*
b₃*-H₂O b₄*
b₄*-H₂O b₅*
b₅*-H₂O b₇*
b₇*-H₂O b₈*
b₈*-H₂O b₉*
b₉*-H₂O b₁₀ b₁₁ b₁₂ b₁₄*
b₁₄*-H₂O b₁₅ b₁₆*
b₁₆*-H₂O b₁₇*
b₁₇*-H₂O b₁₈*
b₁₈*-H₂O b₁₉*
b₁₉*-H₂O Q K -

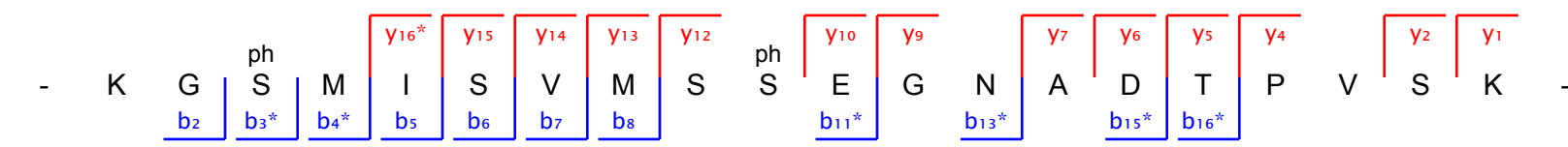
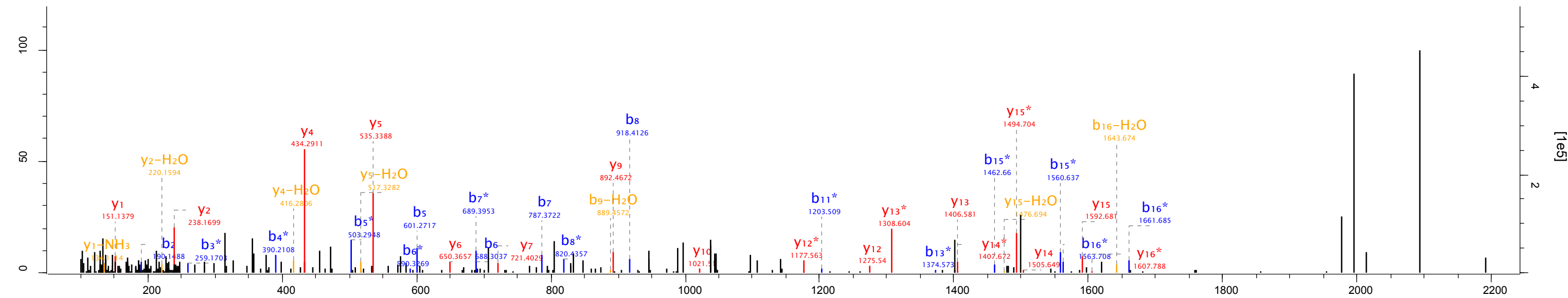
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20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
12293 FTMS; HCD 237.33 1166.52 MPRIP

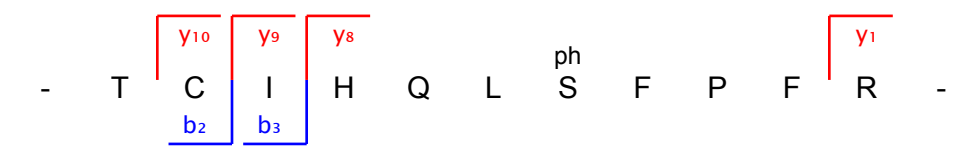
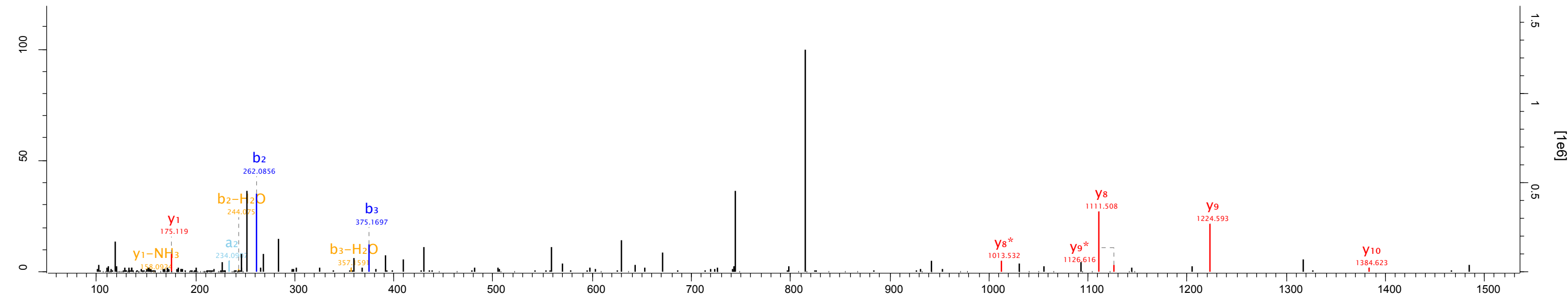


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20171215_MaS_33SR_LMH_phospho2_03

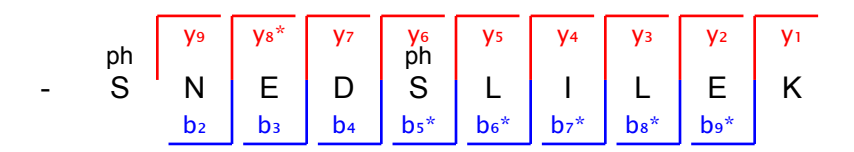
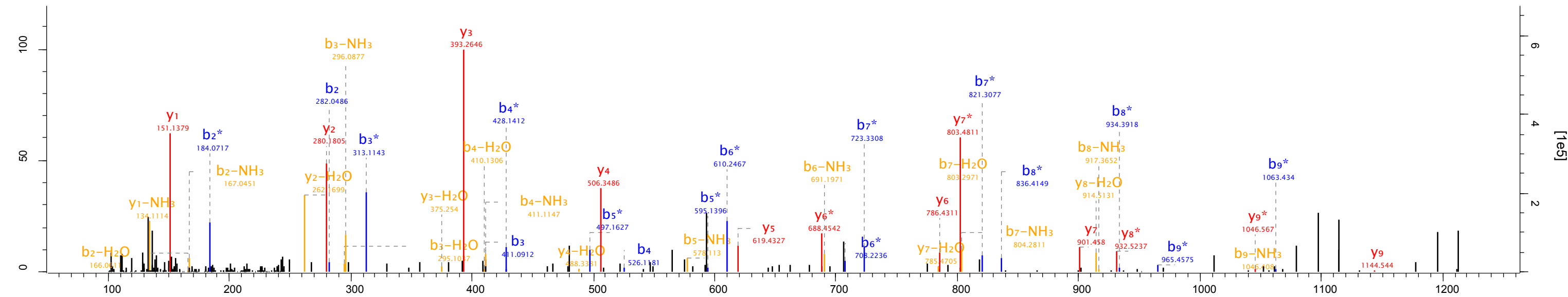
Scan 12393 Method FTMS; HCD Score 77.61 m/z 1096.98 Gene names NF1



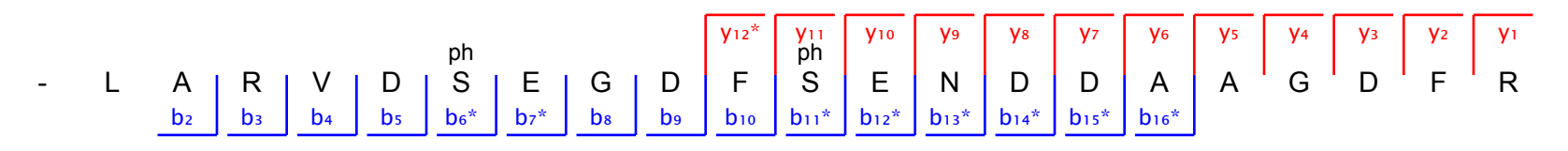
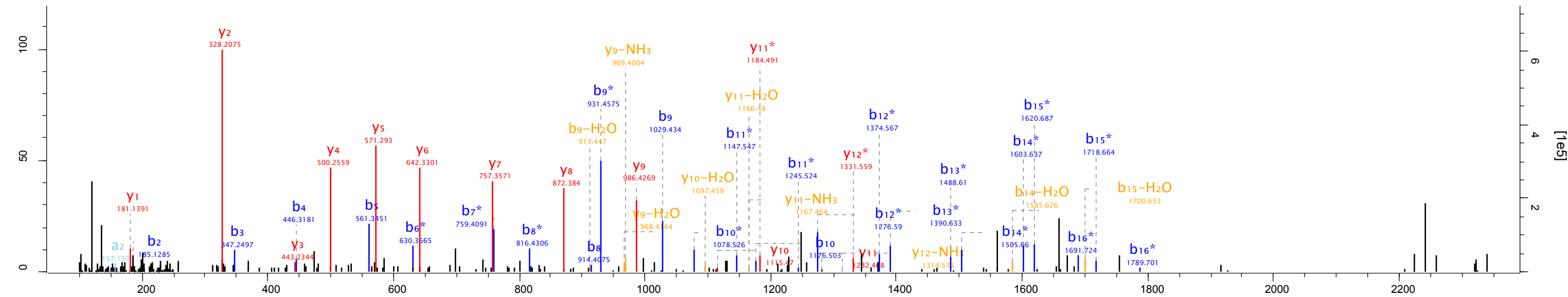
Raw file
20171215_MaS_33SR_LMH_phospho2_03
Scan 12443 Method FTMS; HCD Score 43.76 m/z 743.34



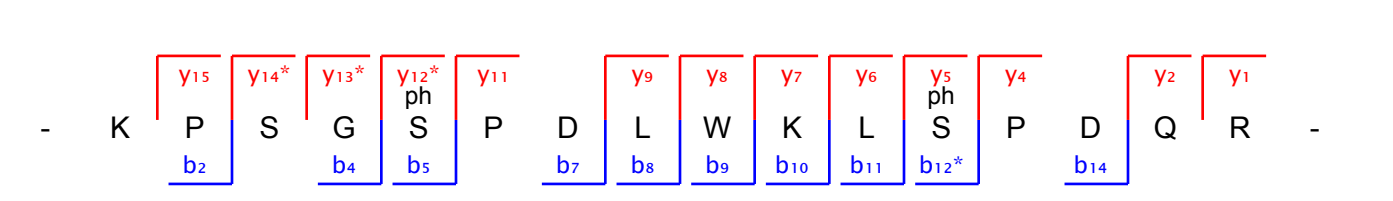
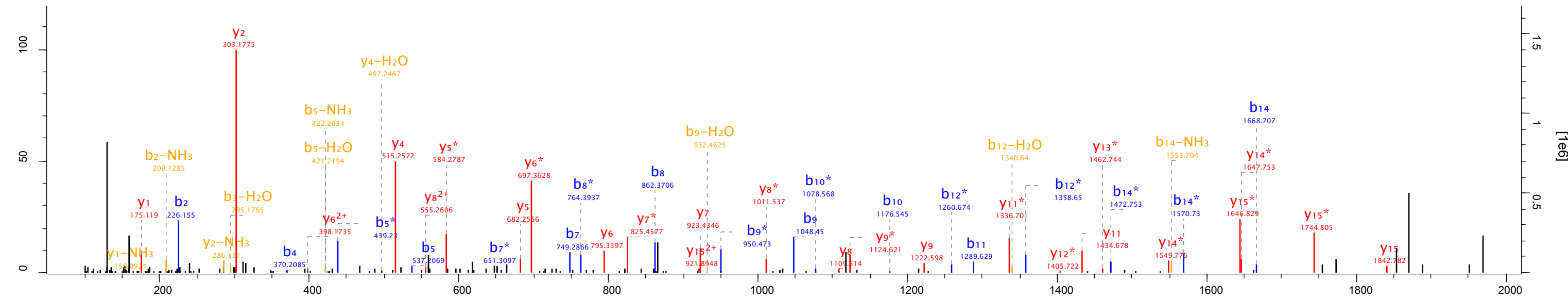
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12793 Method FTMS; HCD Score 130.72 m/z 820.33 Gene names AKAP8

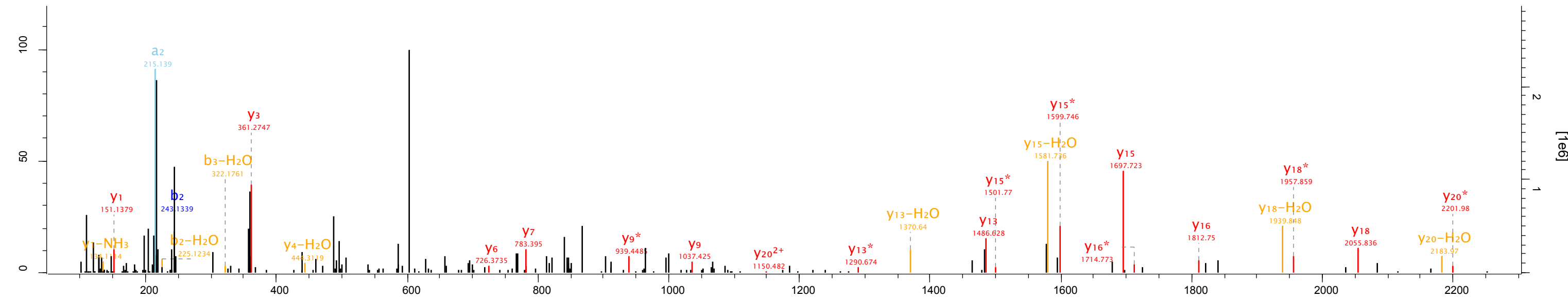


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 Scan: 12853 Method: FTMS; HCD Score: 228.64 m/z: 657.63 Gene names: CHAMP1



Raw file
20171215_MaS_33SR_LMH_phospho2_03

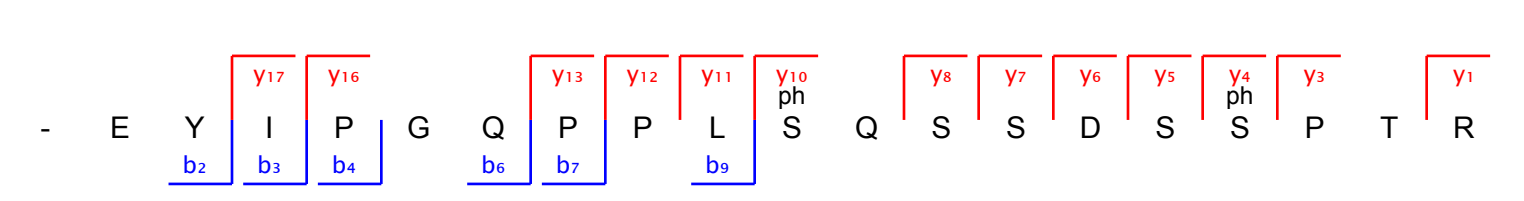
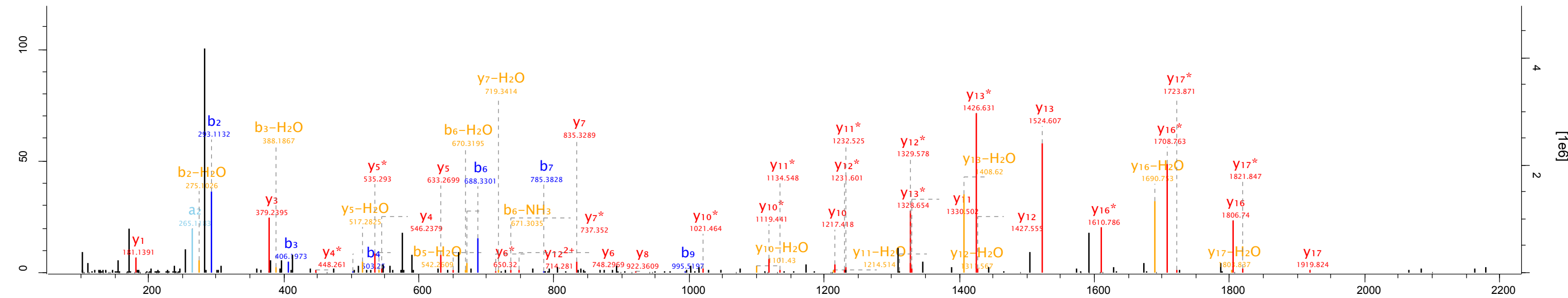
Scan 12923 Method FTMS; HCD Score 61.49 m/z 848.03 Gene names C2CD5



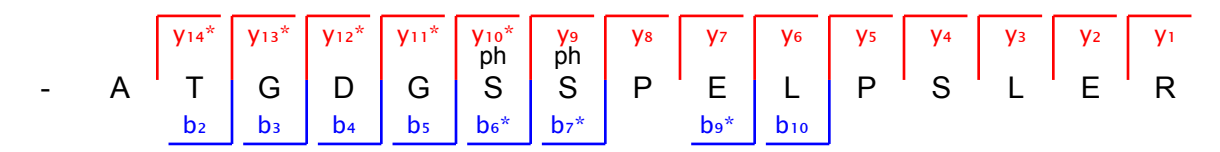
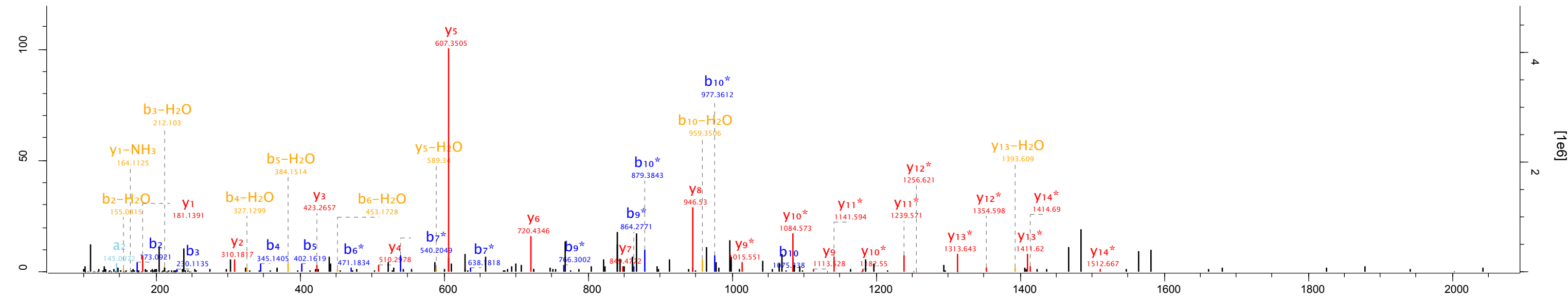
- E I P F N E D P N T P N T P L K -

Fragmentation diagram showing b2 (blue) and y1 through y20* (red) ions. The b2 ion is at m/z 243.1339. The y ions are labeled with their m/z values: y20* (1150.482), y18 (2055.836), y16 (1812.75), y15 (1697.723), y13 (1486.628), y9 (1037.425), y7 (783.395), y6 (726.3735), y3 (361.2747), and y1 (151.1379).

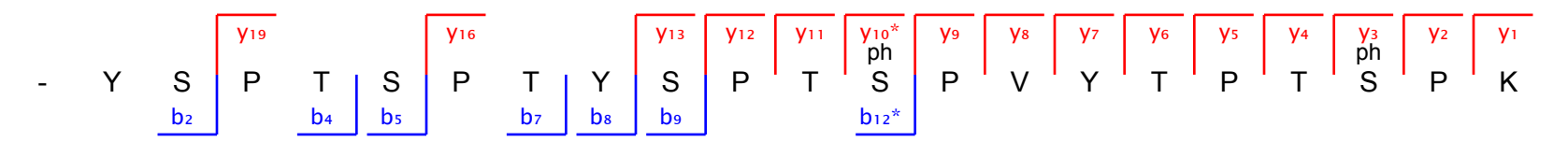
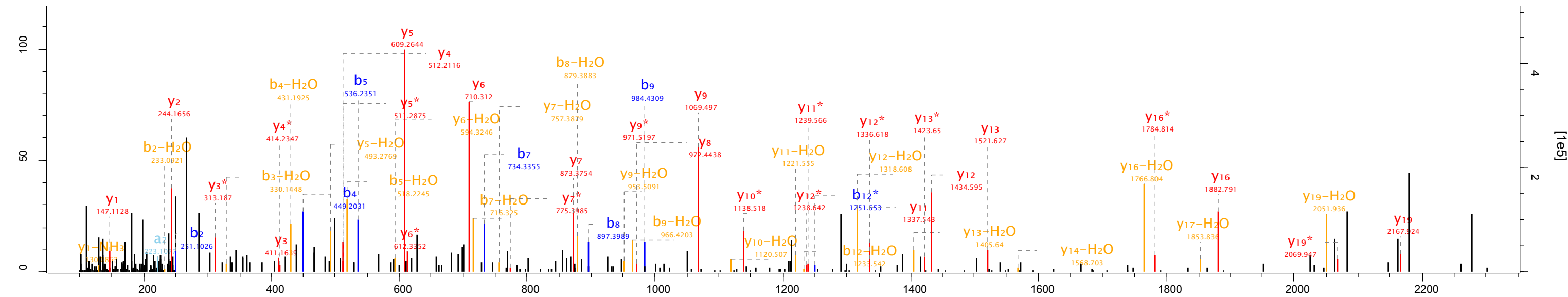
Raw file
 20171215_MaS_33SR_LMH_phospho2_03
 Scan 12953 Method FTMS; HCD Score 163.19 m/z 1106.97 Gene names EPRS



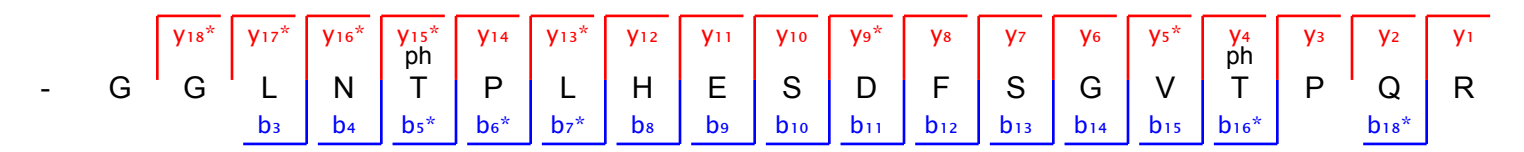
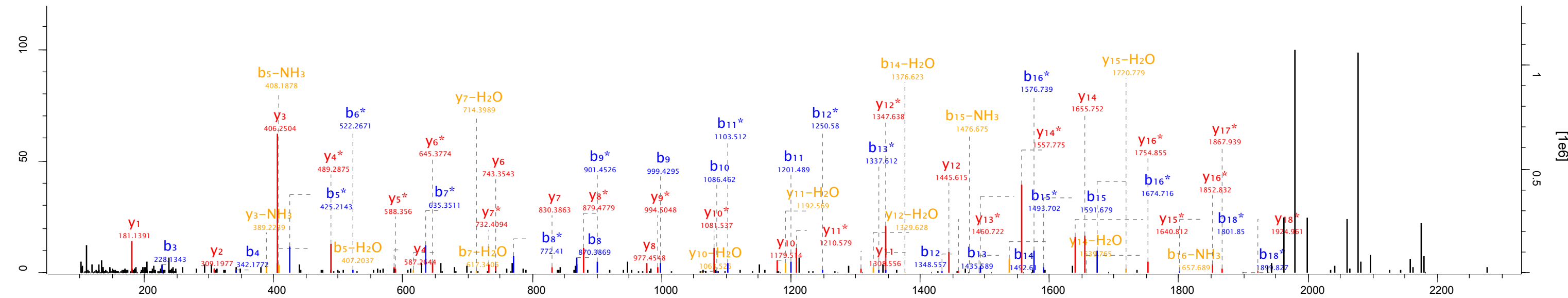
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13003 Method FTMS; HCD Score 136.53 m/z 841.34 Gene names ZNF106



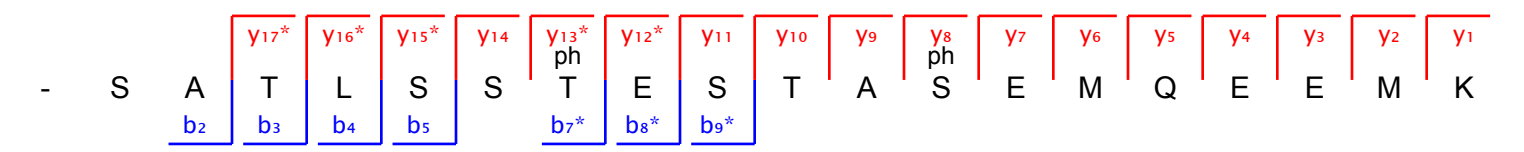
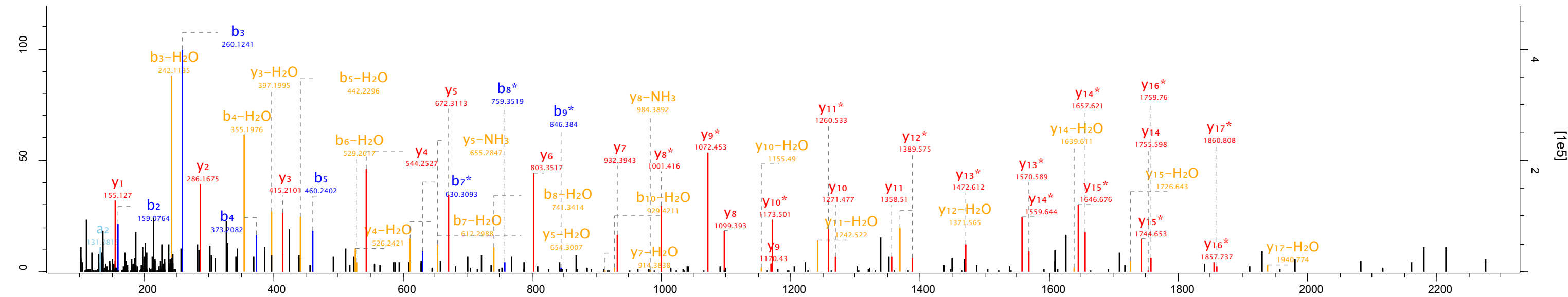
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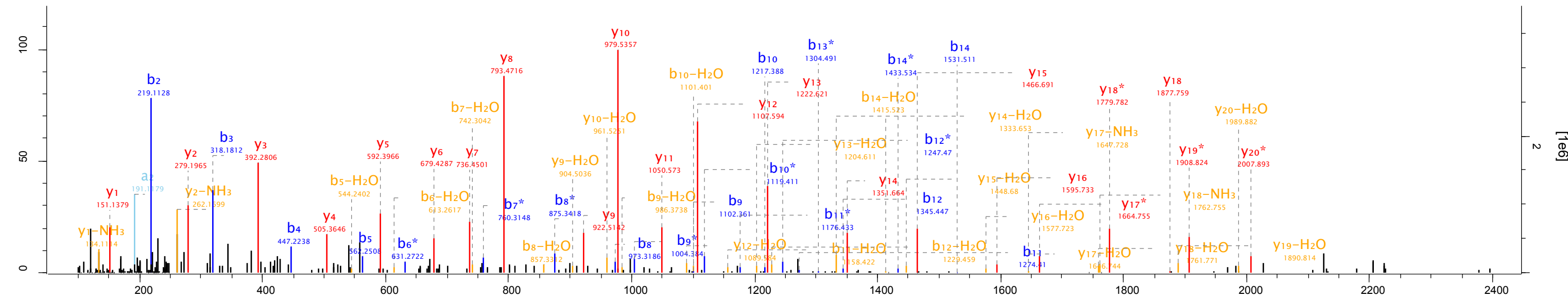
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Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13263 Method: FTMS; HCD Score: 247.34 m/z: 1108.42 Gene names: AKAP12



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13283 Method FTMS; HCD Score 320.96 m/z 1162.99 Gene names KRI1

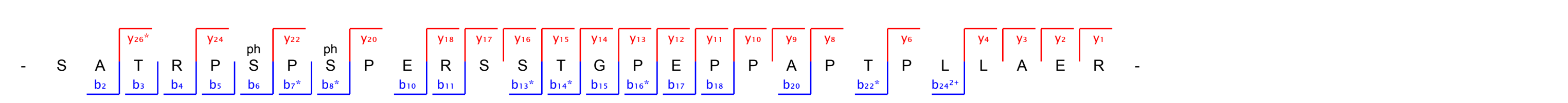
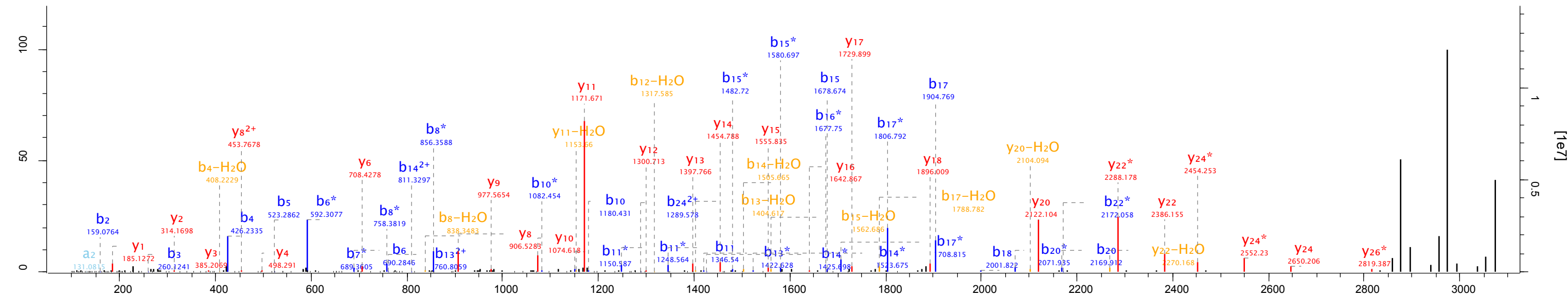


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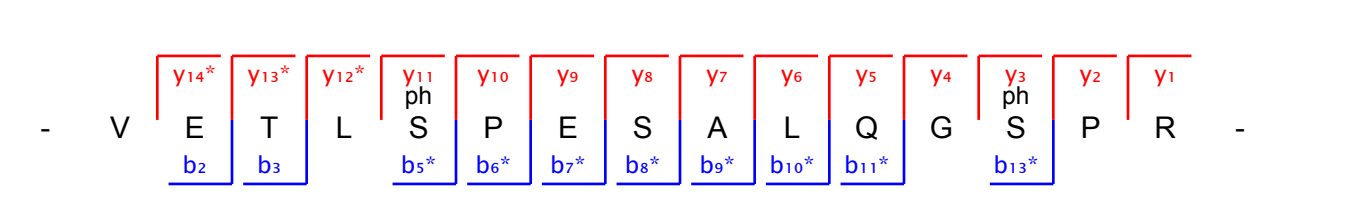
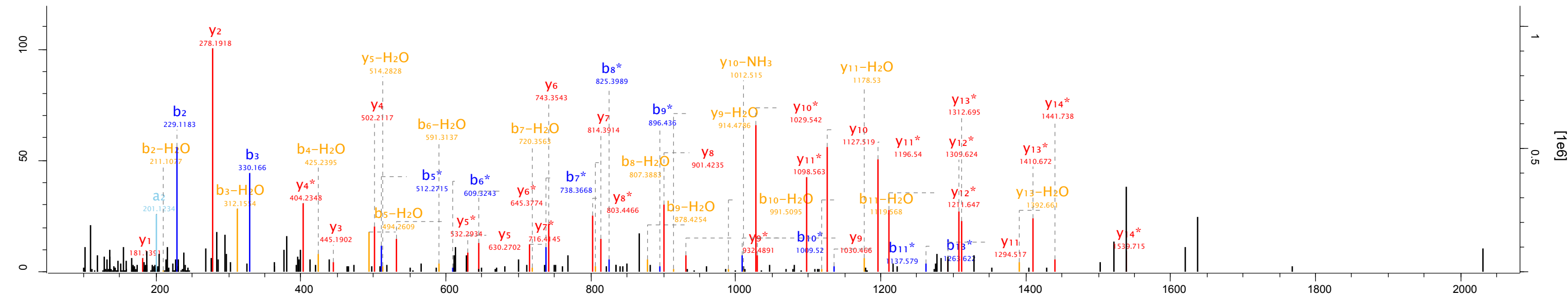
b₂
b₃
b₄
b₅
b₆^{*}
b₇^{*}
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃^{*}
b₁₄

y₂₀^{*}
y₁₉^{*}
y₁₈
y₁₇^{*}
ph
y₁₆
y₁₅
y₁₄
y₁₃
y₁₂
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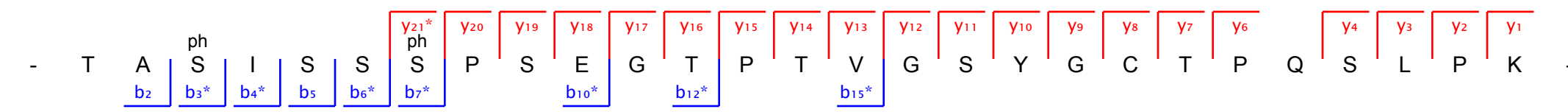
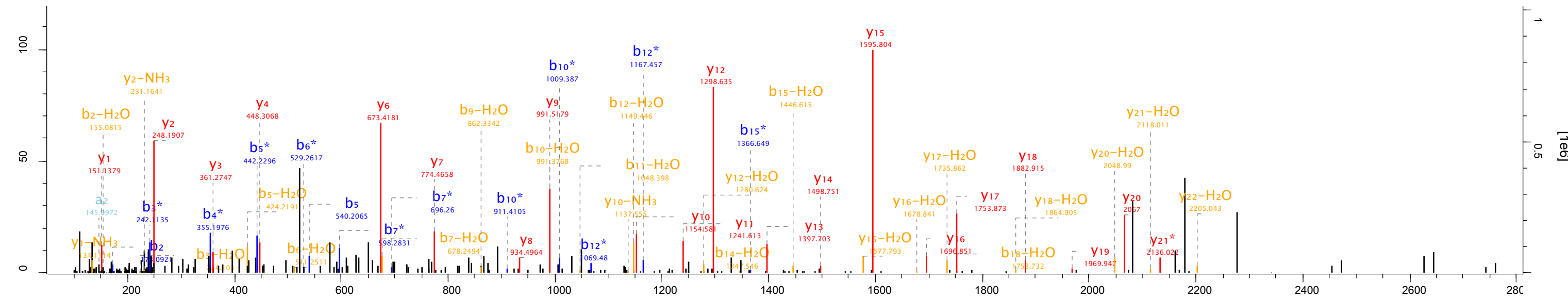
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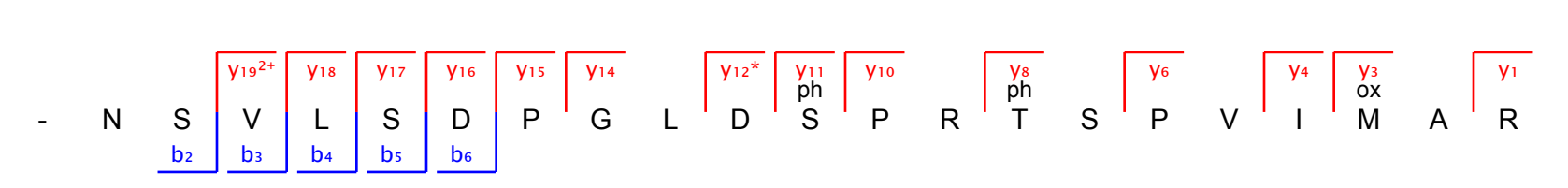
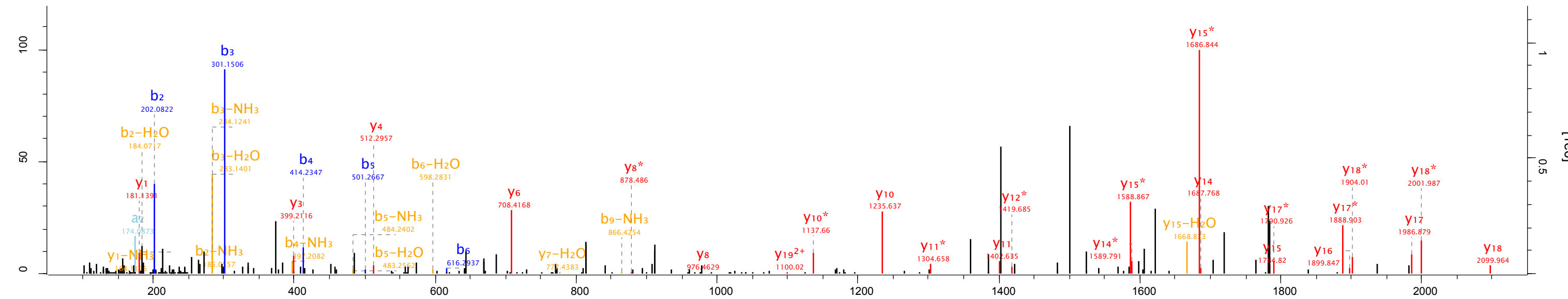
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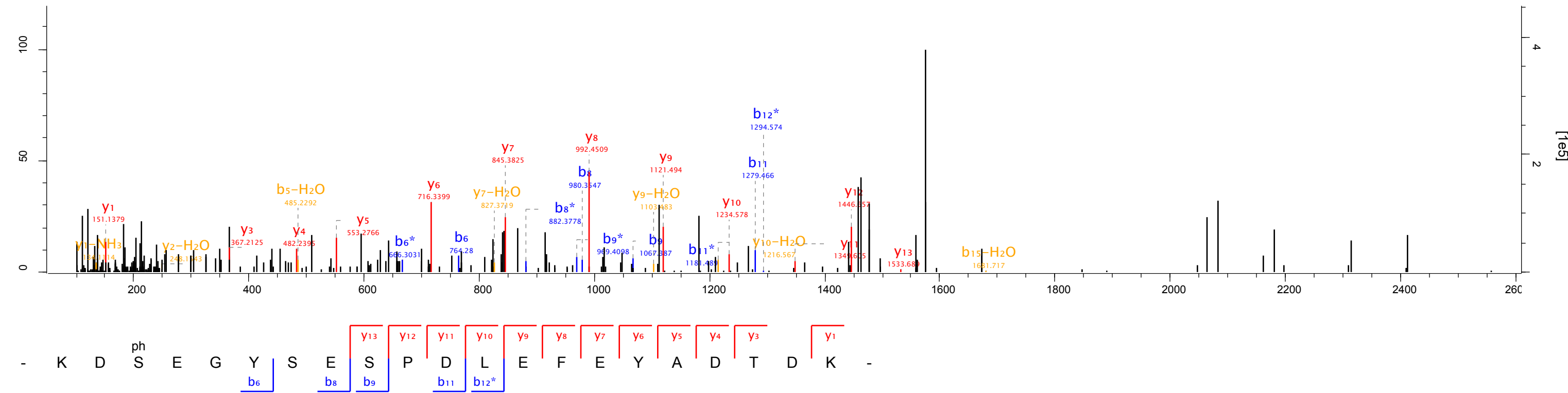


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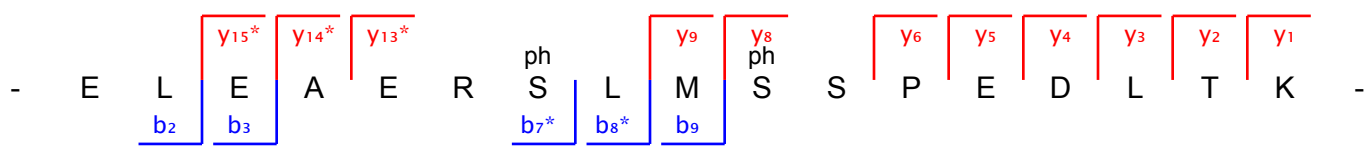
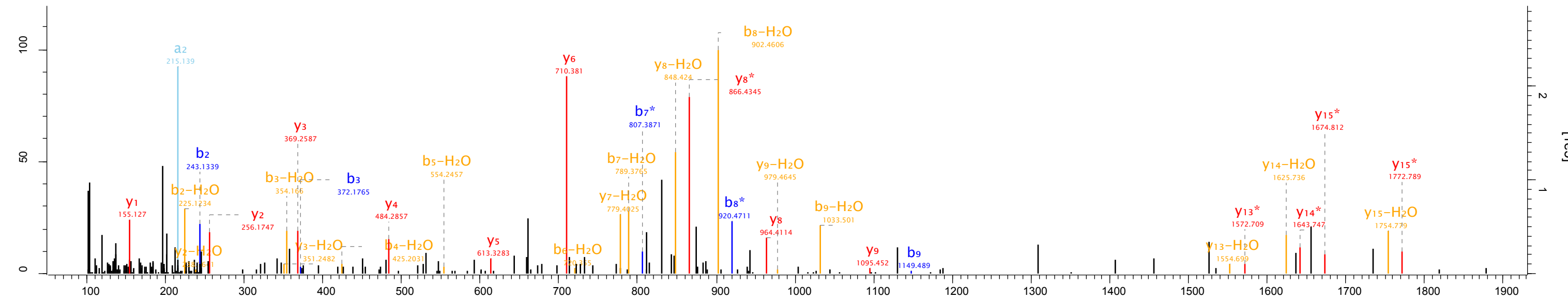
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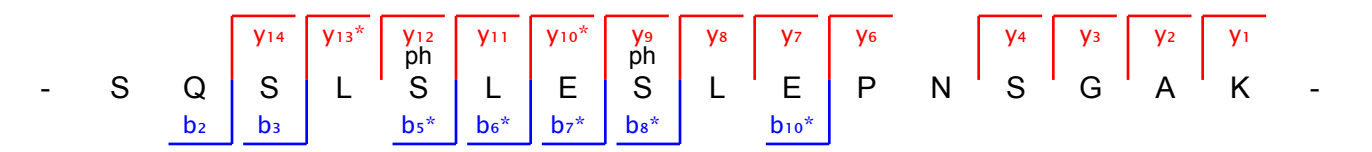
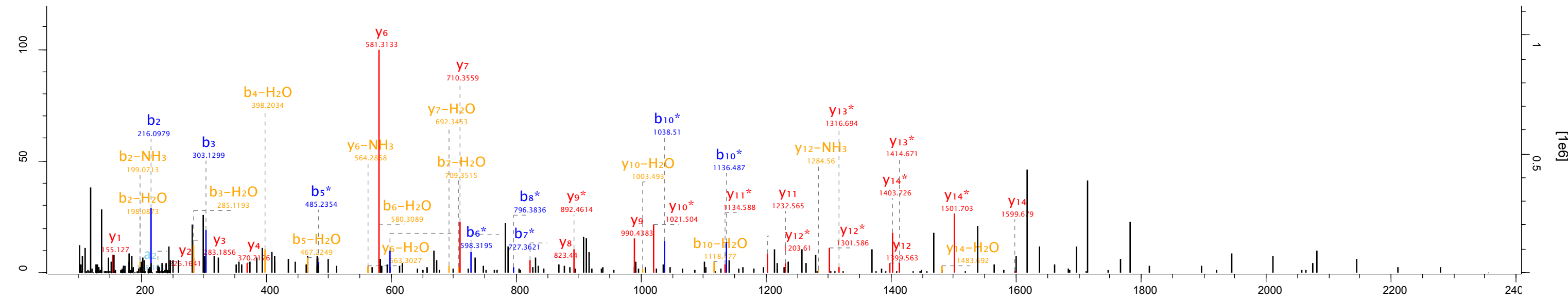


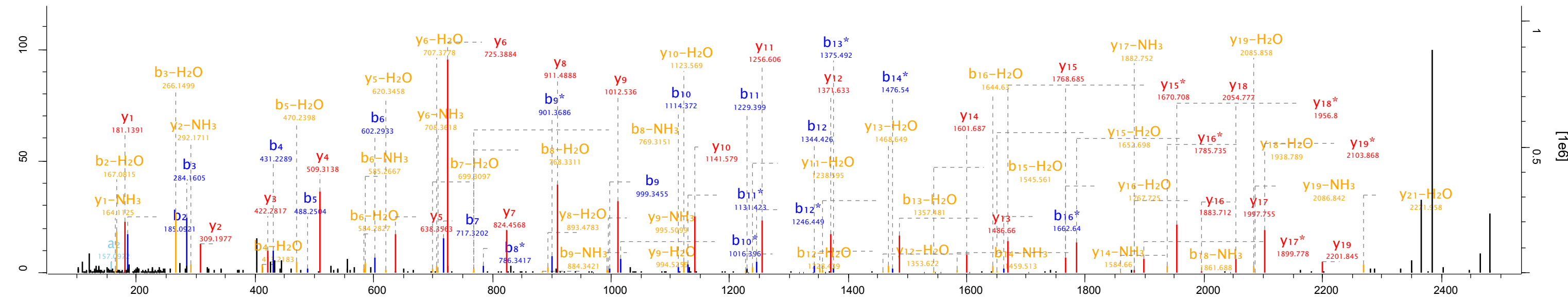
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 14573 Method FTMS; HCD Score 115.42 m/z 704.97 Gene names MAP1B



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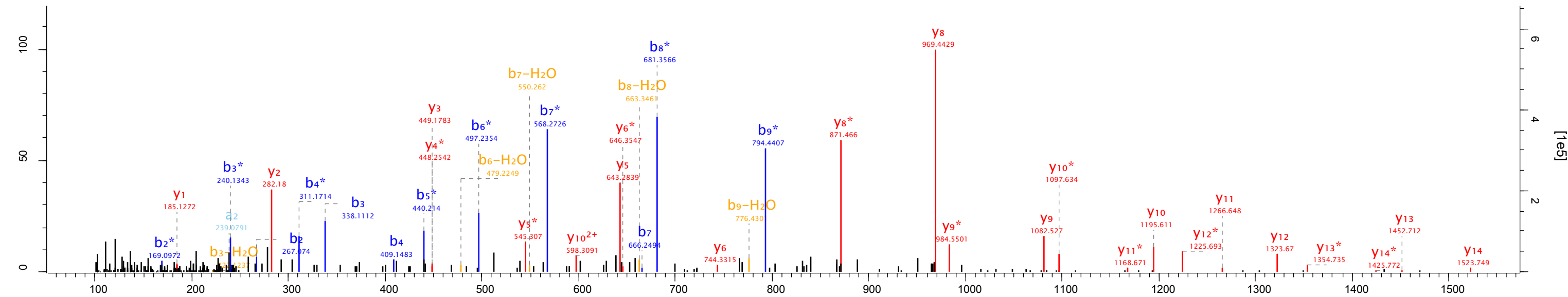


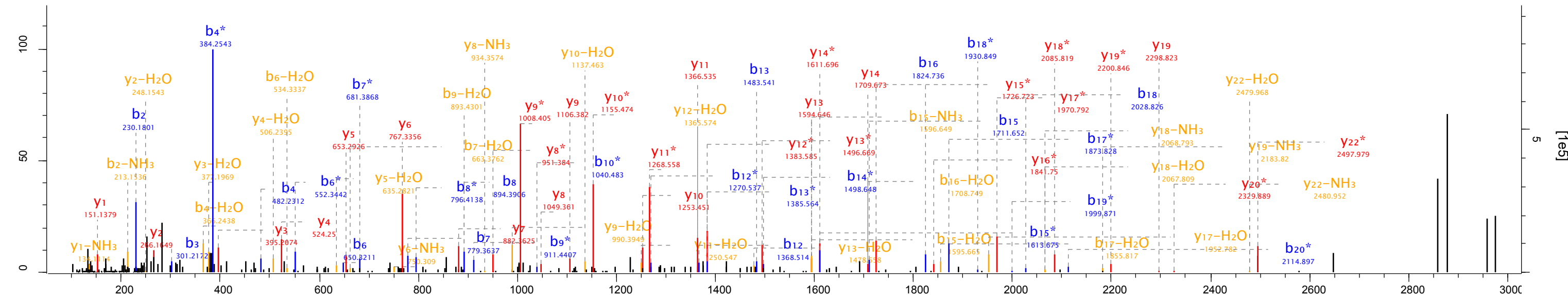
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b₂ b₃ b₄ b₅ b₆ b₇ b₈^{*} b₉ b₁₀ b₁₁ b₁₂ b₁₃^{*} b₁₄^{*} b₁₆^{*}

y₁₉ y₁₈ y₁₇ y₁₆ y₁₅ ph y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

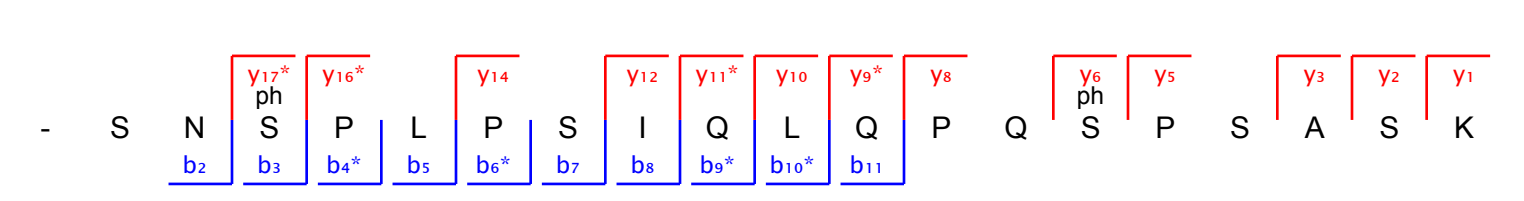
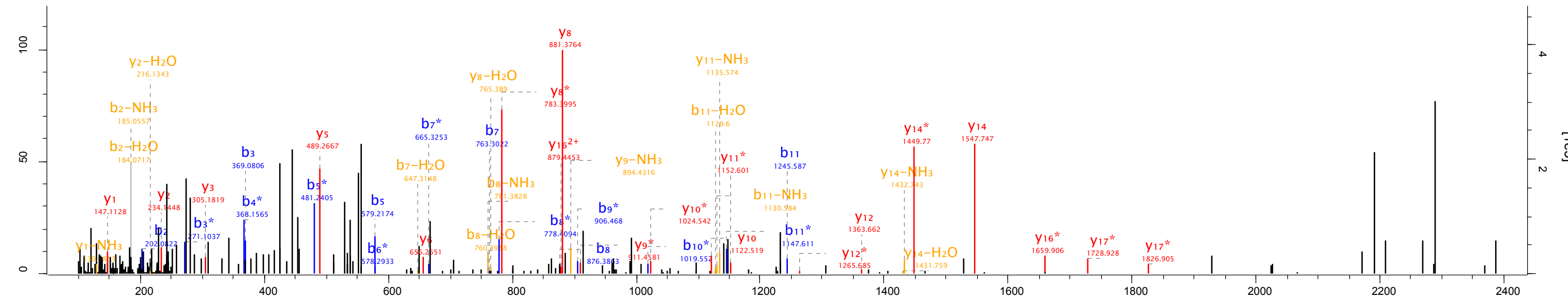
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 Scan: 14943 Method: FTMS; HCD Score: 126.68 m/z: 930.93 Gene names: RALGPS2



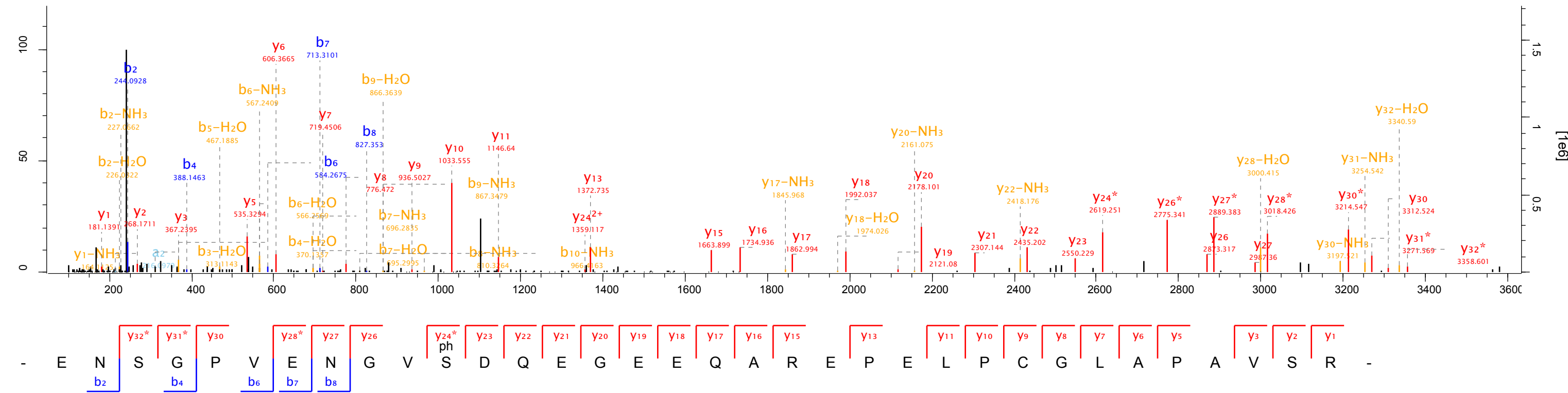


- K P A T P A E D D E D D D I D L F G S D N E E E D K -
 b₂ b₃ b₄ y₂₂* b₆ b₇ b₈ b₉* b₁₀* b₁₂ b₁₃ b₁₄* b₁₅ b₁₆ b₁₇* b₁₈ b₁₉* b₂₀*

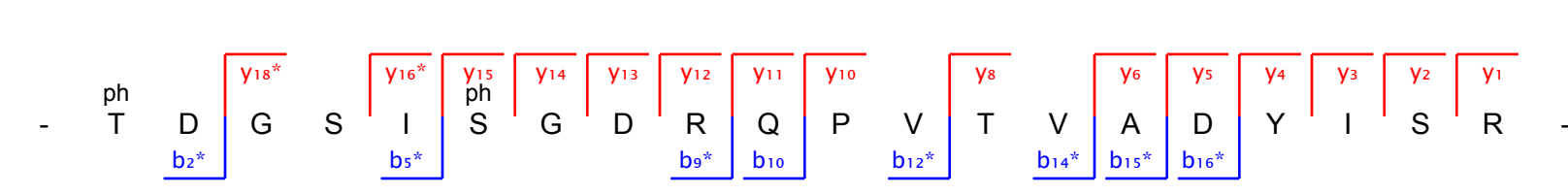
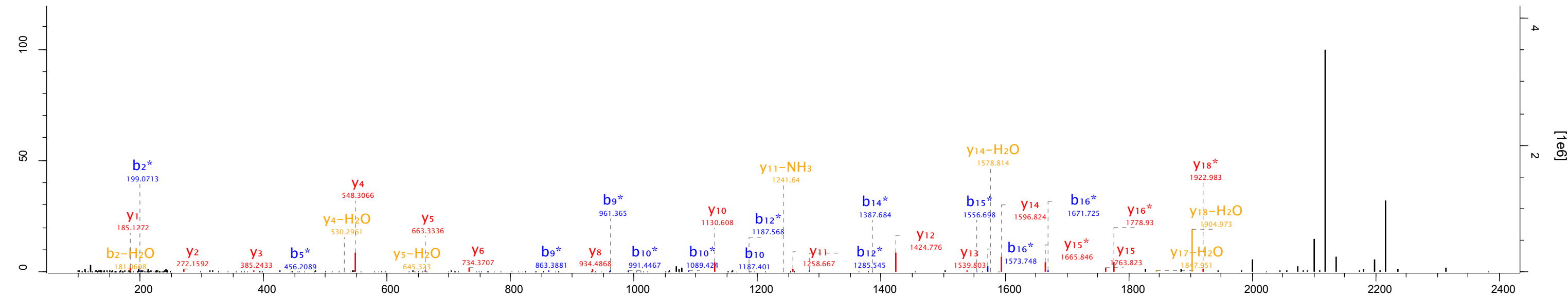
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 Scan: 15233 Method: FTMS; HCD Score: 111.98 m/z: 1063.48 Gene names: PCDH1



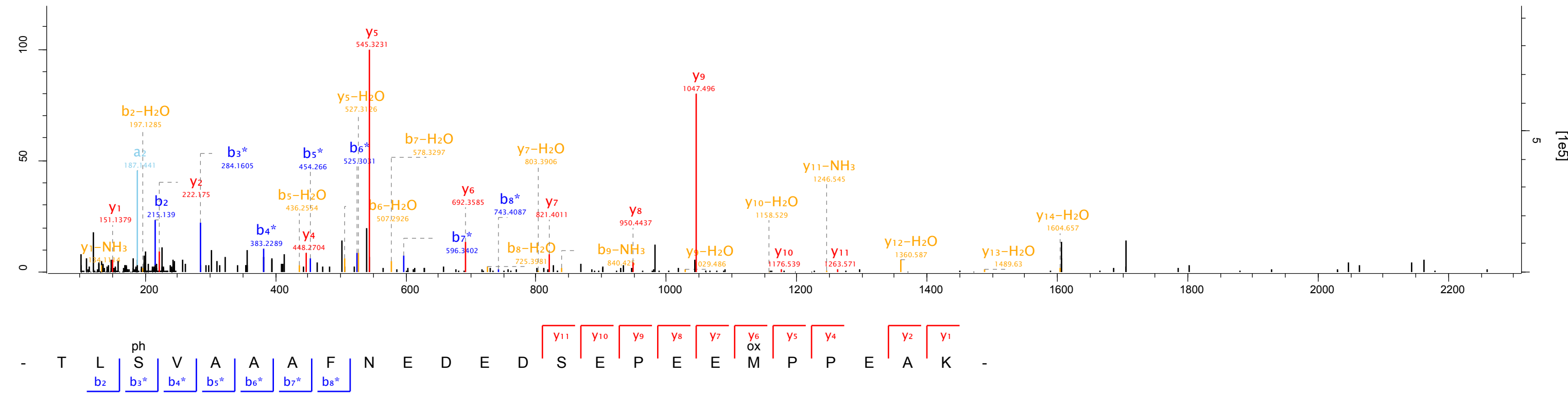
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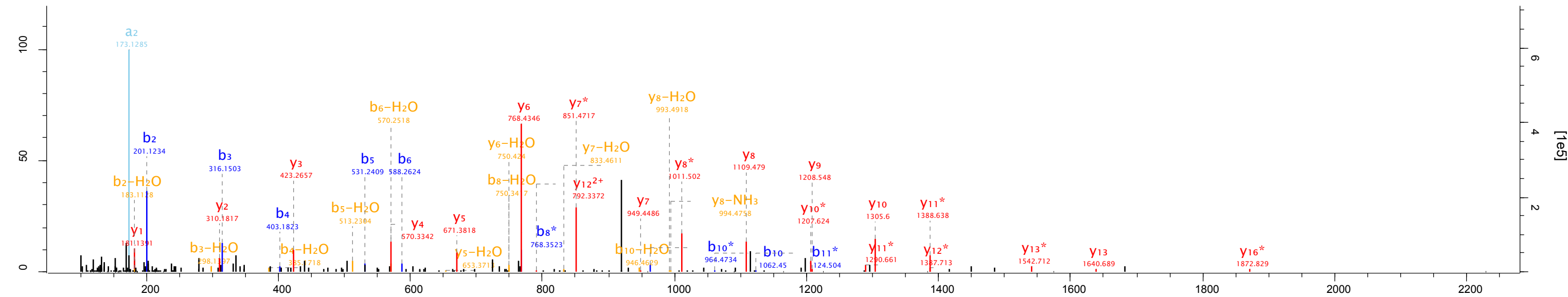
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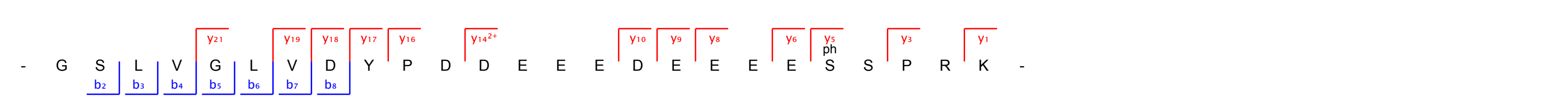
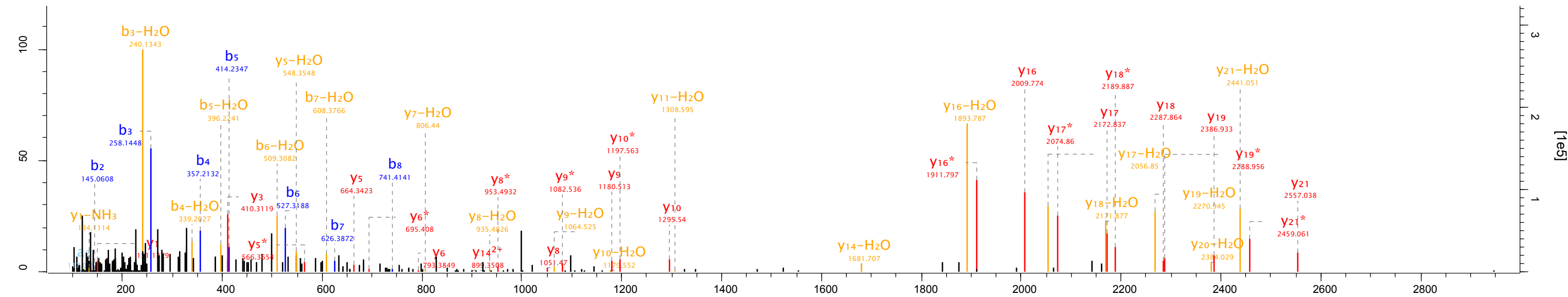
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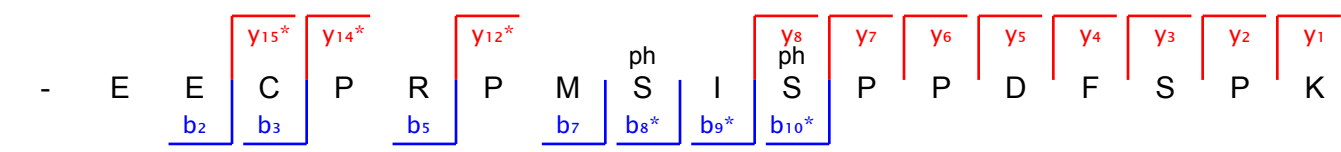
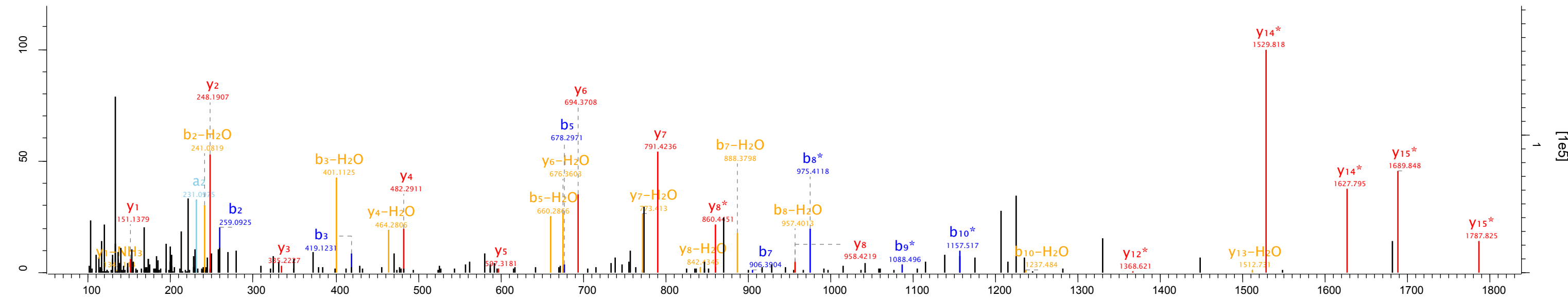
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 15663 Method: FTMS; HCD Score: 139.22 m/z: 724.65 Gene names: NIFK



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 Scan: 15783 Method: FTMS; HCD Score: 129.35 m/z: 972.42 Gene names: SMEK2

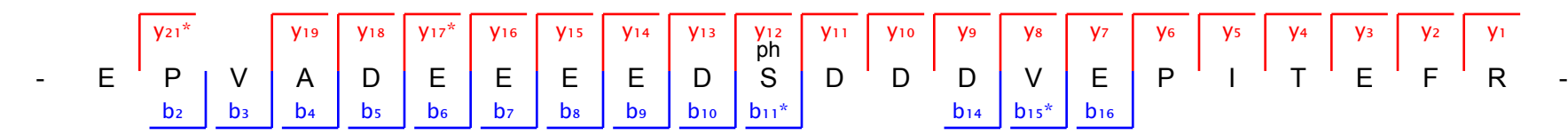
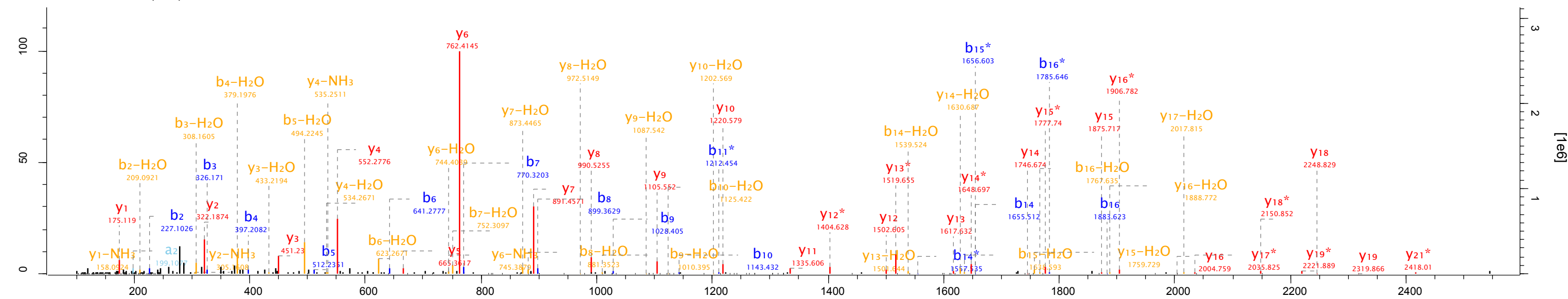


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 Scan: 15933 Method: FTMS; HCD Score: 87.51 m/z: 715.3 Gene names: MAP1B

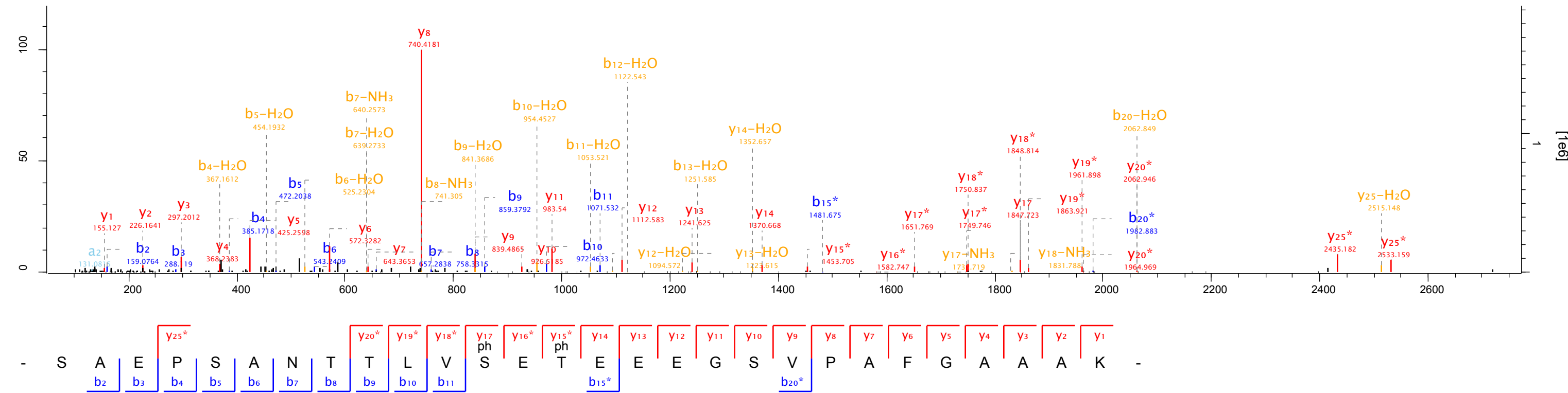


Raw file
20171215_MaS_33SR_LMH_phospho2_03

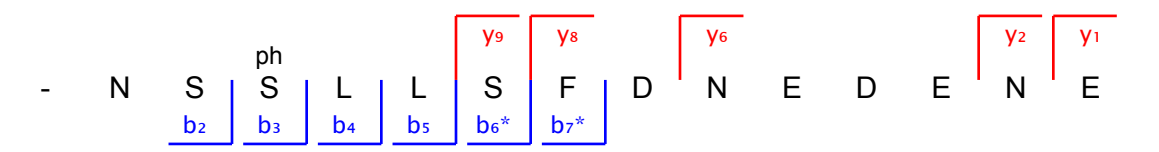
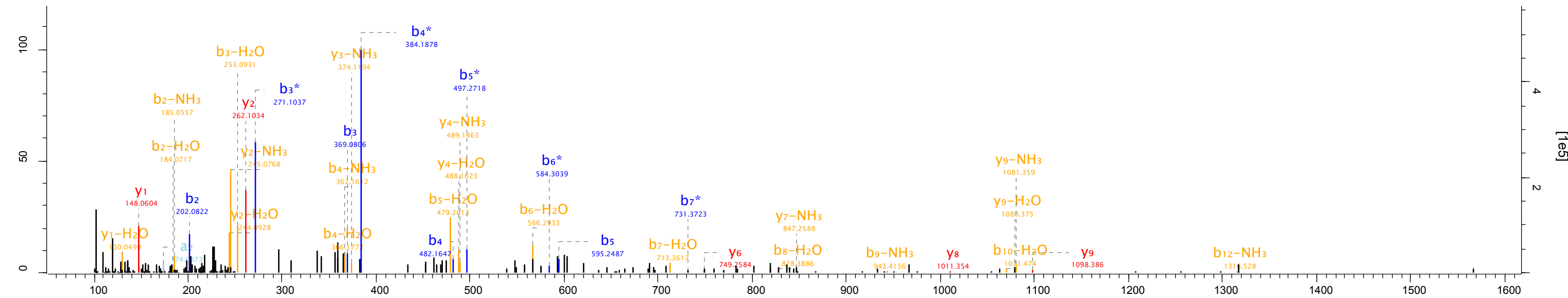
Scan 15953 Method FTMS; HCD Score 328.42 m/z 1323.52 Gene names CLNS1A



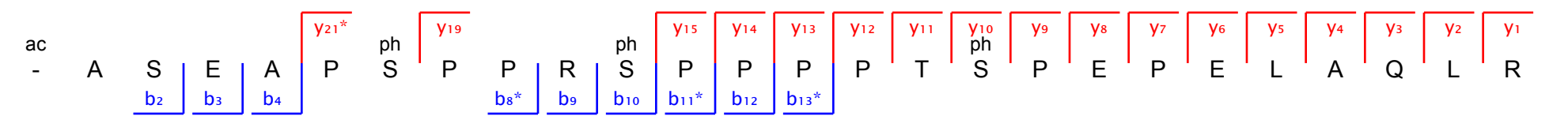
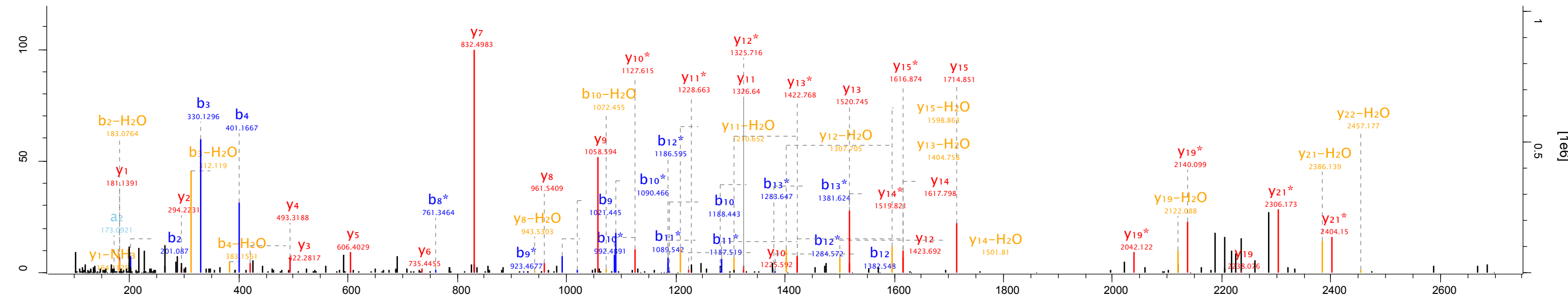
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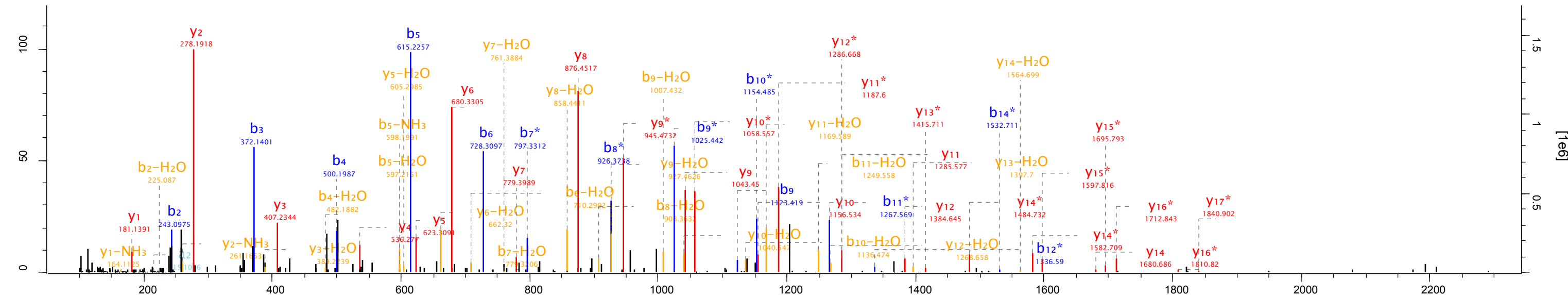


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16023 Method FTMS; HCD Score 79.51 m/z 847.32 Gene names KIAA1143



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16753 Method FTMS; HCD Score 143.17 m/z 968.44 Gene names AGGF1





ac

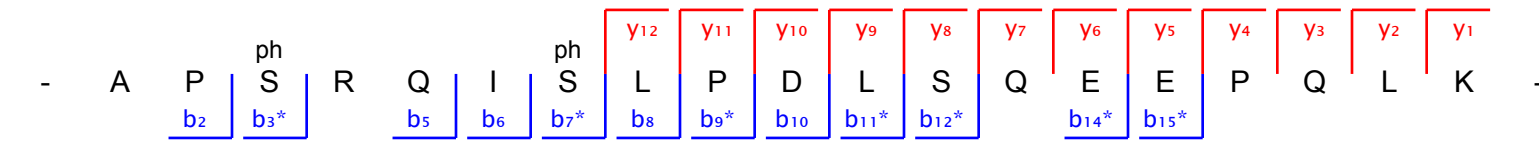
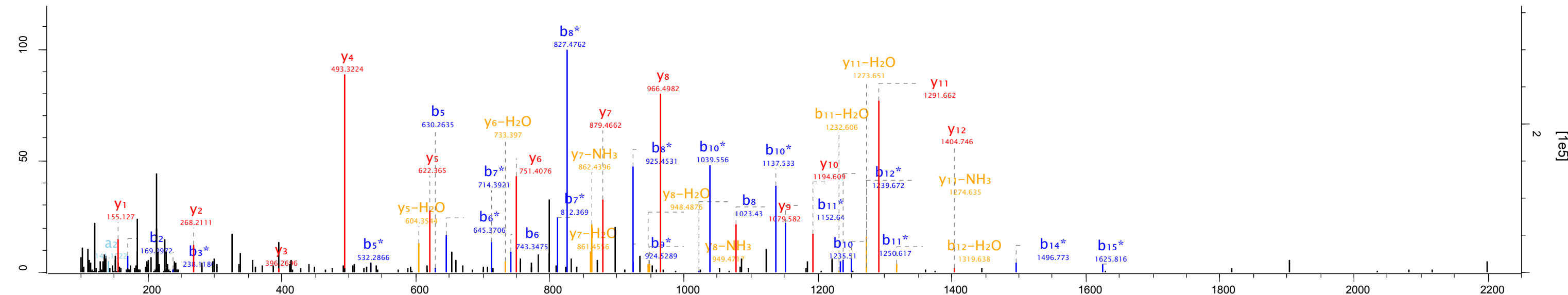
- A E E Q D L S E V E L S P V G S E E P R -

Fragmentation sites are indicated by brackets below the sequence:

- b₂ (under E)
- b₃ (under E)
- b₄ (under Q)
- b₅ (under D)
- b₆ (under L)
- b₇^{*} (under S)
- b₈^{*} (under E)
- b₉ (under V)
- b₁₀^{*} (under E)
- b₁₁^{*} (under L)
- b₁₂^{*} (under S)
- b₁₄^{*} (under V)

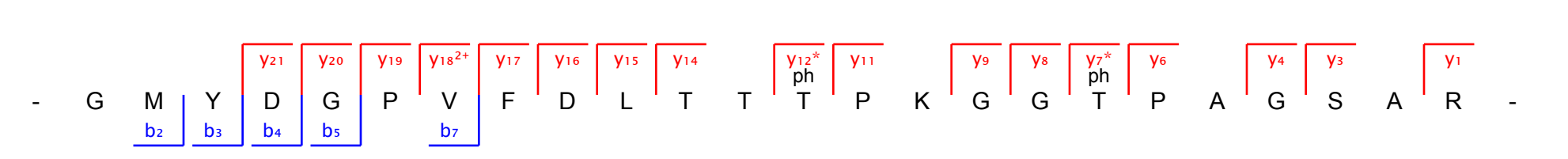
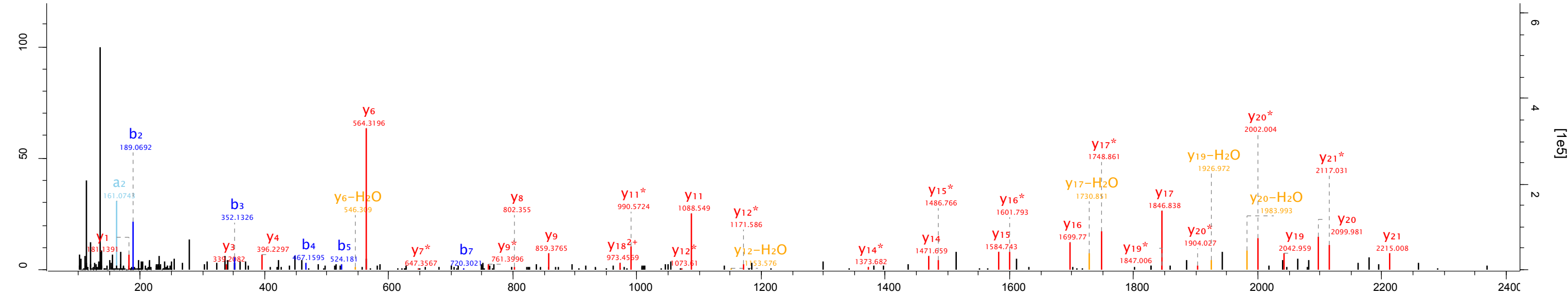
Fragmentation sites are also indicated by brackets above the sequence:

- y₁₇^{*} (over Q)
- y₁₆^{*} (over D)
- y₁₅^{*} (over L)
- y₁₄ (over S)
- y₁₃^{*} (over E)
- y₁₂ (over V)
- y₁₁ (over E)
- y₁₀ (over L)
- y₉ (over S)
- y₈ (over P)
- y₇ (over V)
- y₆ (over G)
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- y₂ (over P)
- y₁ (over R)

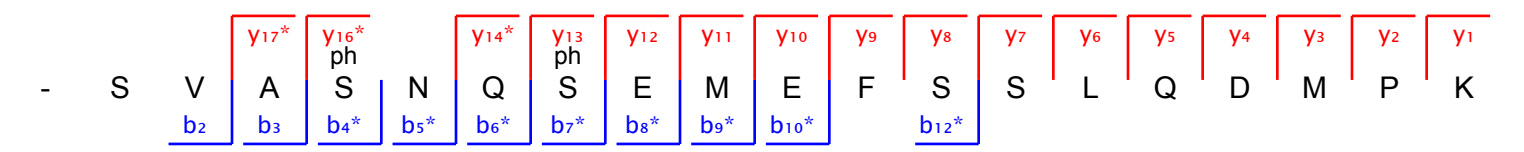
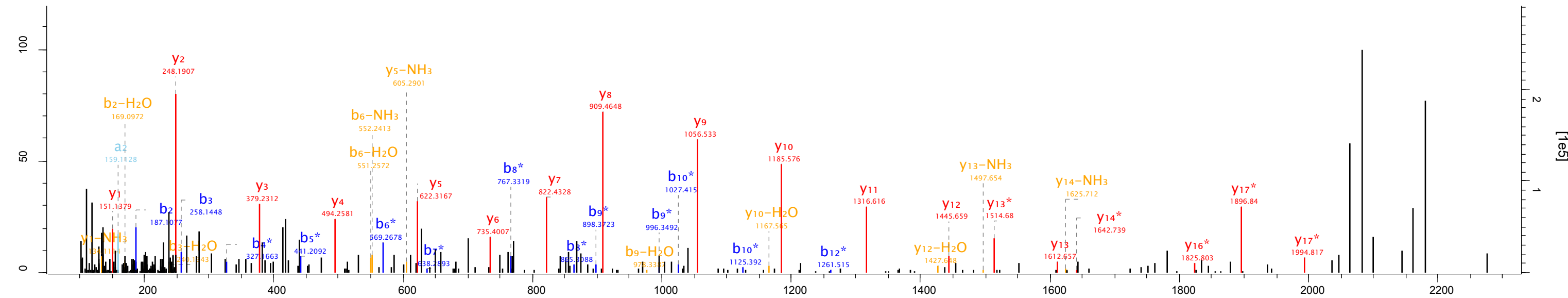


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 17913 FTMS; HCD 102.51 856.38 DPYSL3

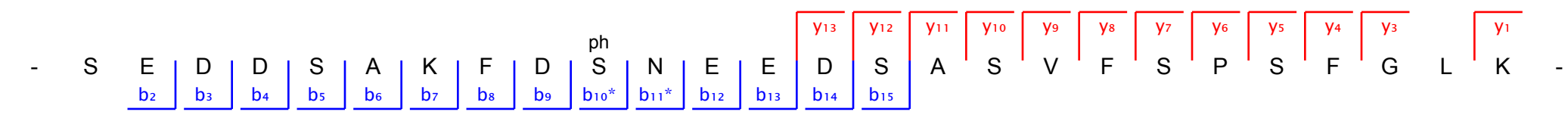
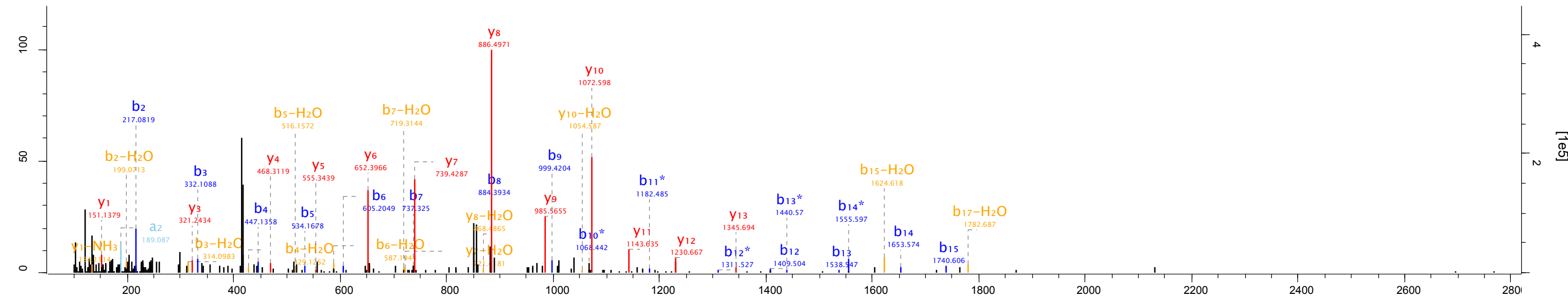


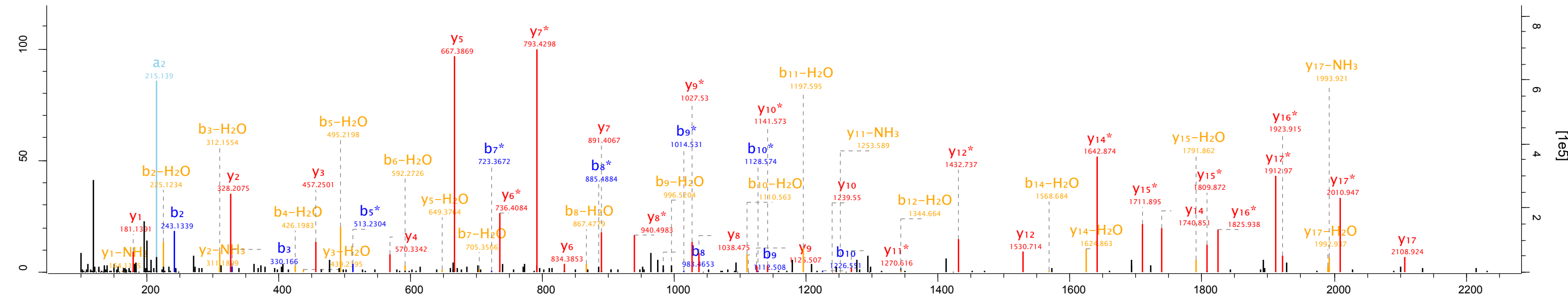
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 17983 Method FTMS; HCD Score 109.98 m/z 1140.46 Gene names CCAR2



Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
18203 FTMS; HCD 92.35 961.75 TOP2B



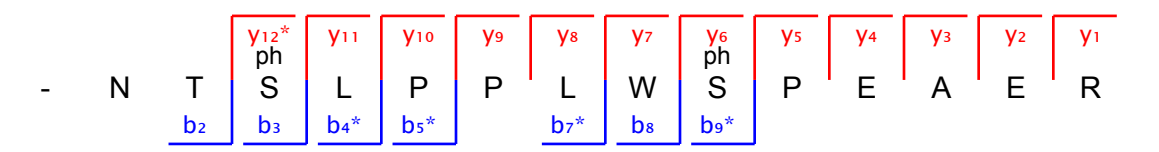
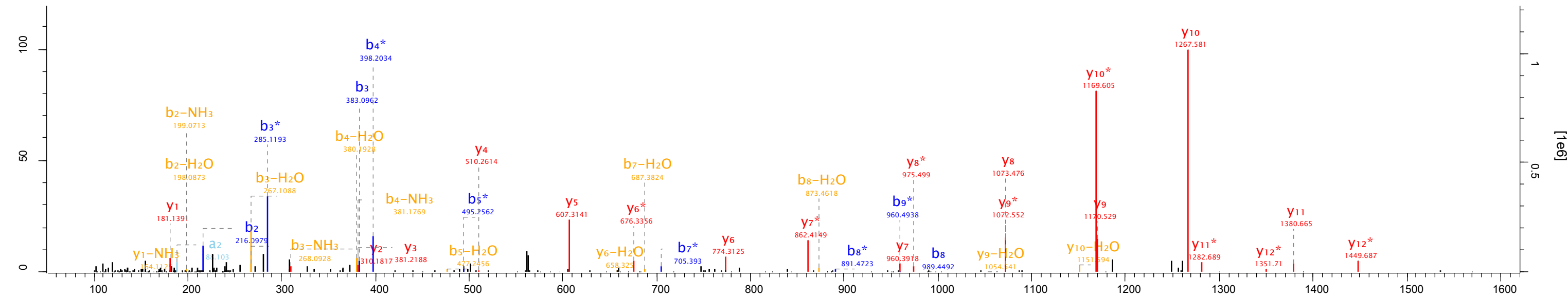


- E L S N P L R E N S F G S P L E F R -

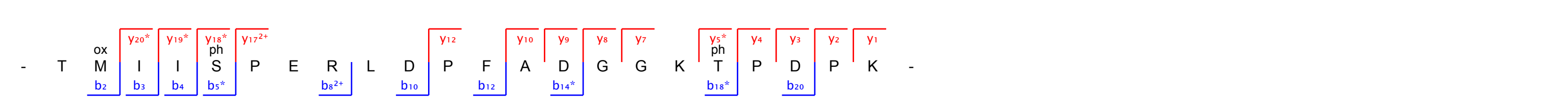
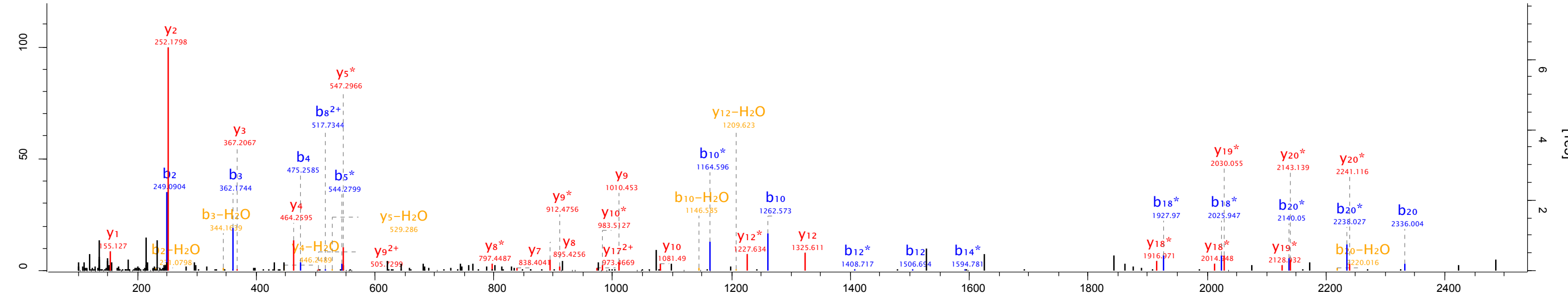
Fragmentation mapping (b and y ions) is shown below the sequence:

- Blue boxes (b ions):** b₂ (L), b₃ (S), b₅* (N), b₇* (L), b₈ (R), b₉ (E), b₁₀ (N)
- Red boxes (y ions):** y₁₇ (S), y₁₆* (N), y₁₅* (ph), y₁₄ (S), y₁₂ (R), y₁₁* (E), y₁₀ (N), y₉ (S), y₈ (F), y₇ (G), y₆ (ph), y₅ (S), y₄ (L), y₃ (E), y₂ (F), y₁ (R)

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18433 Method FTMS; HCD Score 152.06 m/z 882.38 Gene names NUP153



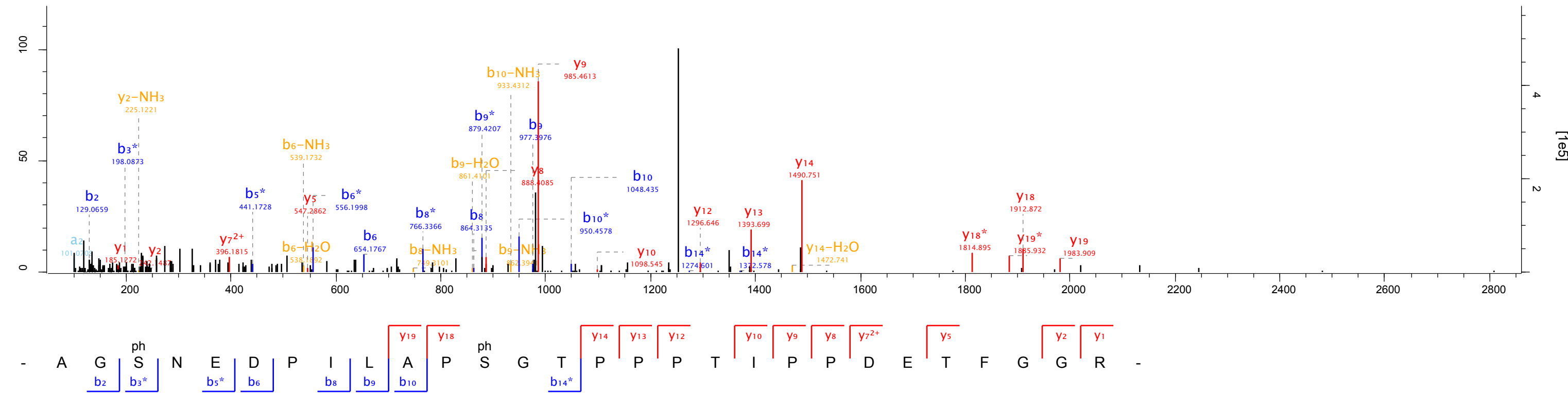
20171215_MaS_33SR_LMH_phospho2_03 18443 FTMS; HCD 143.79 863.4 SF3B1



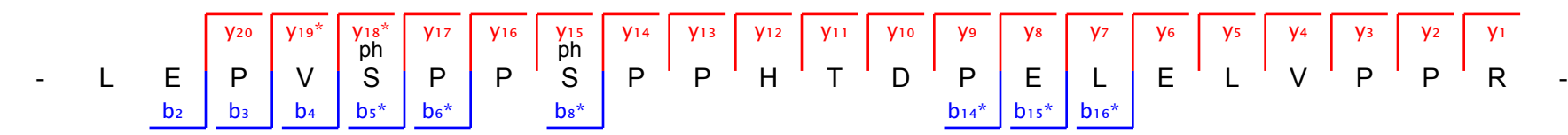
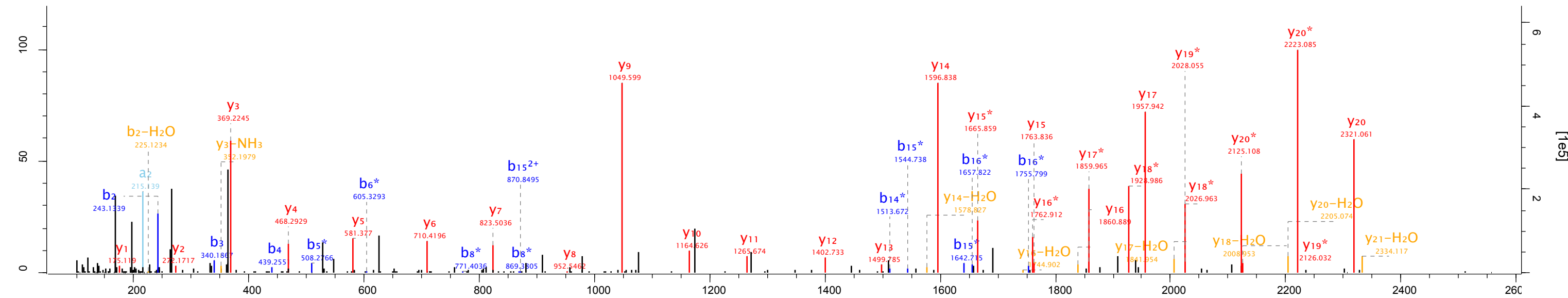
Raw file

20171215_MaS_33SR_LMH_phospho2_03

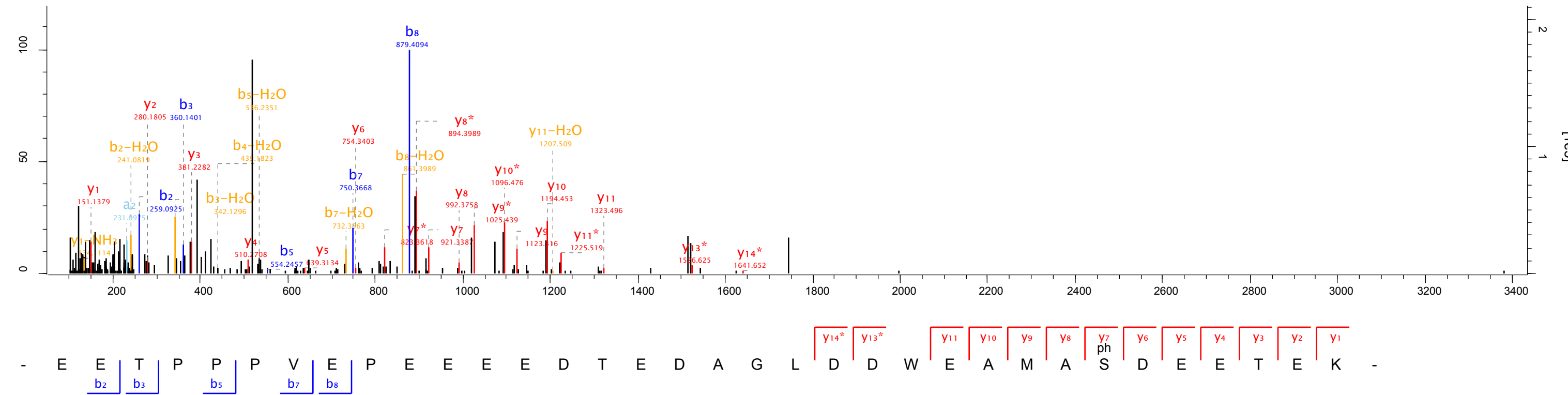
Scan	Method	Score	m/z	Gene names
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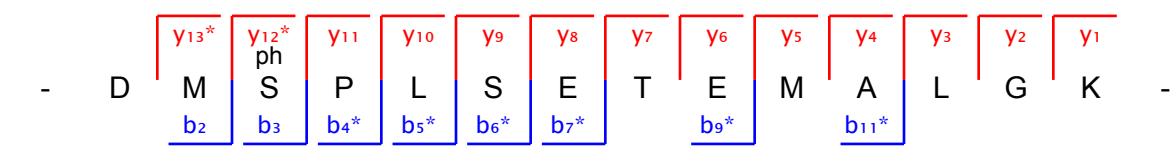
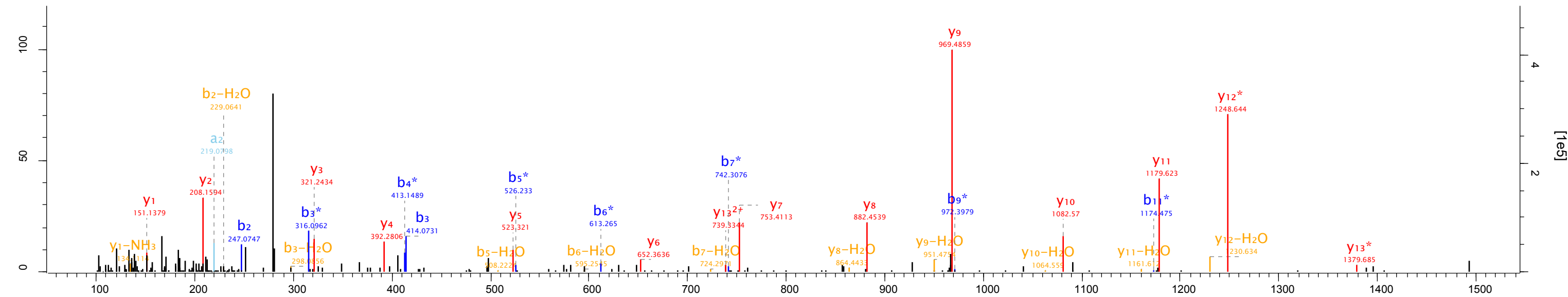
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18623 Method FTMS; HCD Score 158.13 m/z 855.07 Gene names NCOR2

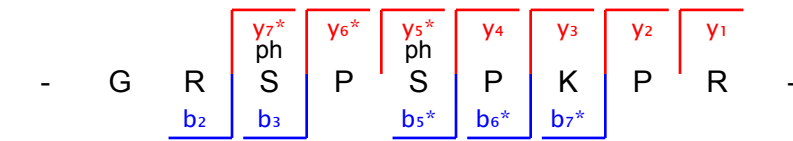
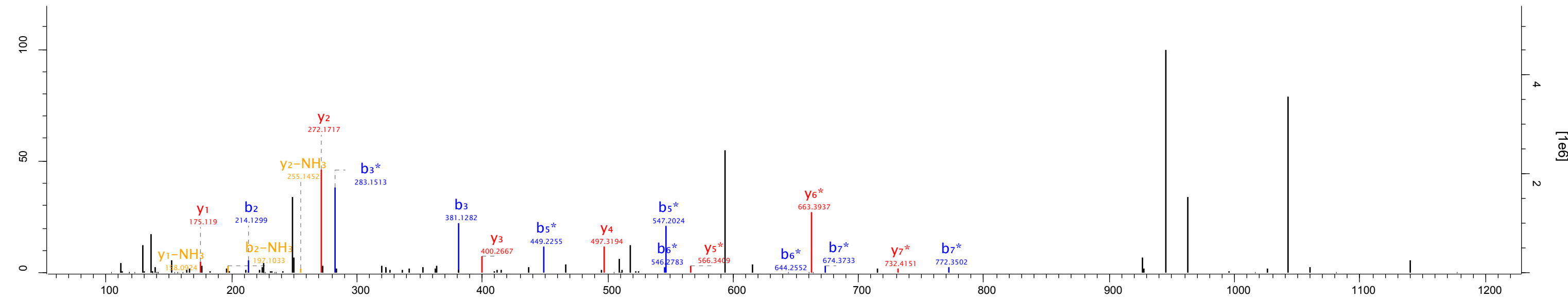


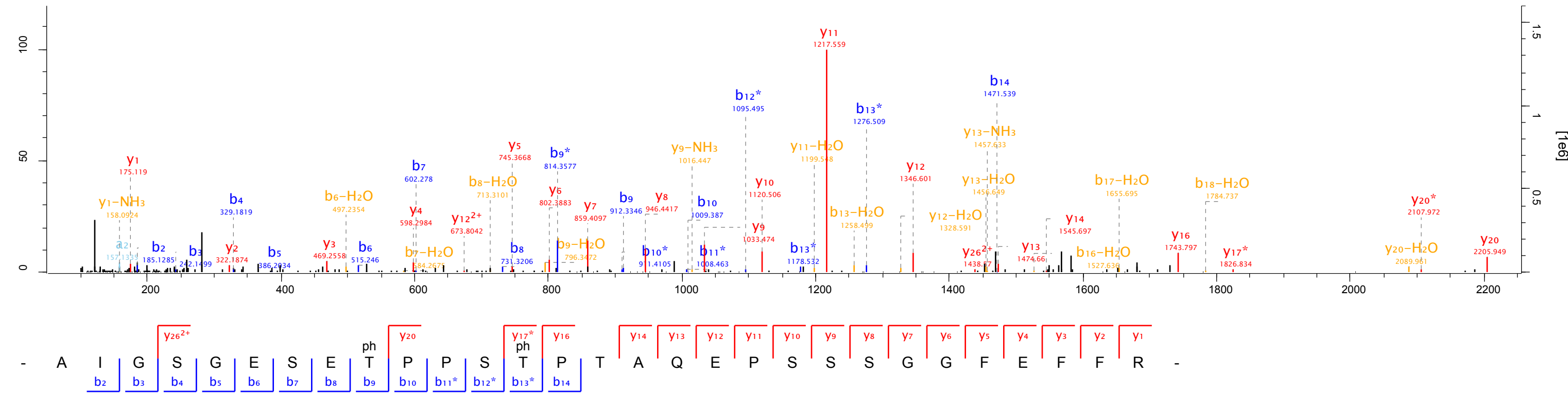
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 18683 Method: FTMS; HCD Score: 47.72 m/z: 1311.52 Gene names: EIF5B



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18713 Method FTMS; HCD Score 133.86 m/z 796.85 Gene names MAP4

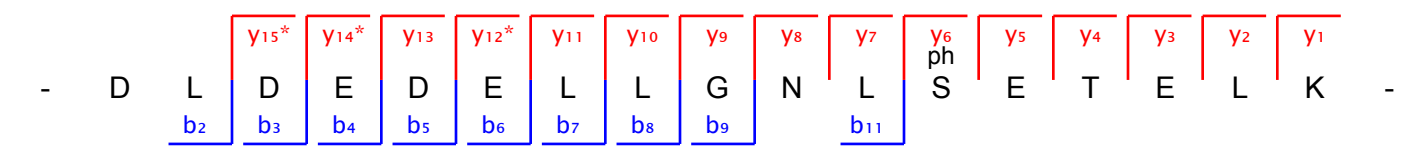
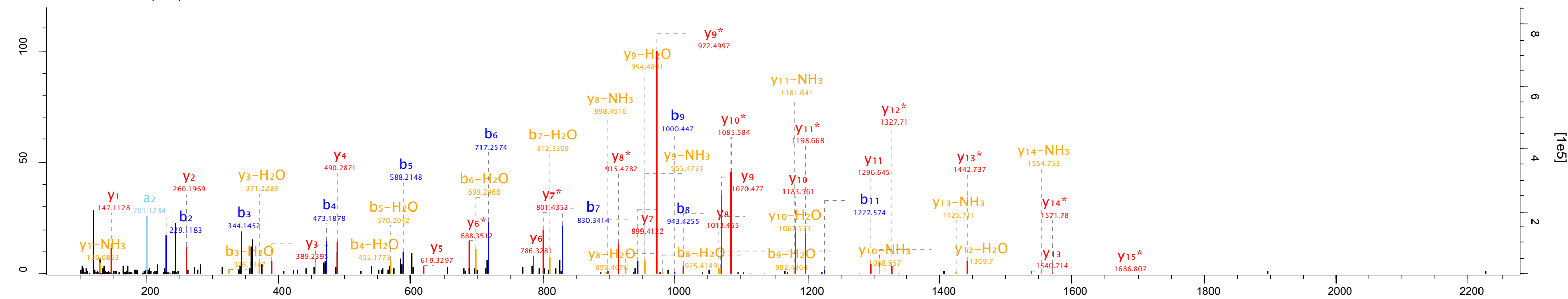


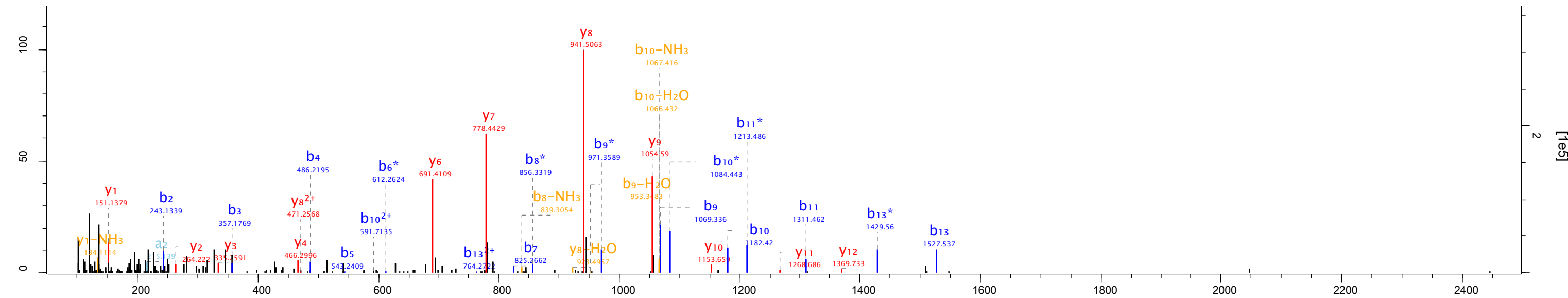




Raw file
20171215_MaS_33SR_LMH_phospho2_03

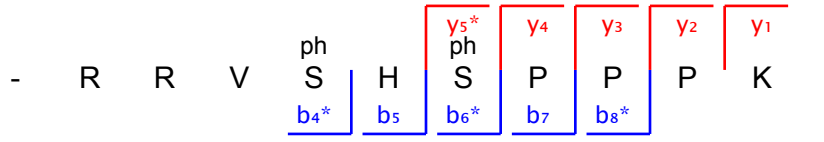
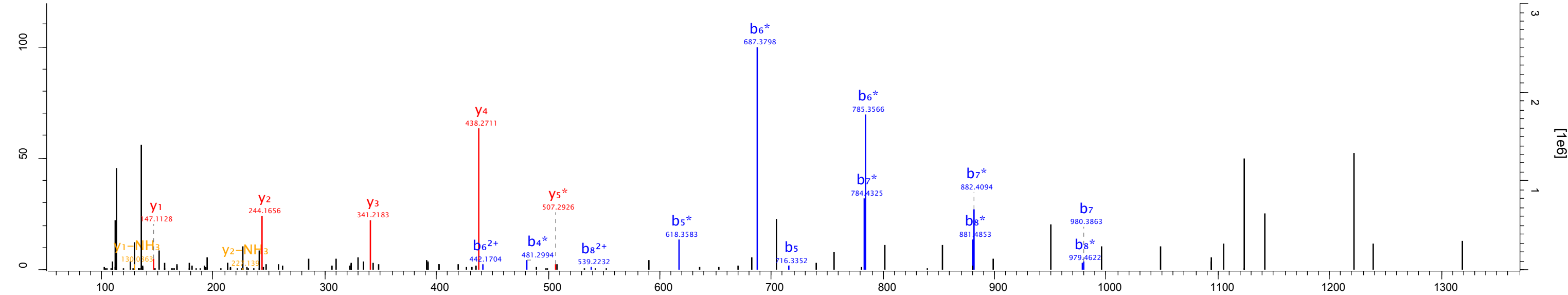
Scan 20023 Method FTMS; HCD Score 250.86 m/z 1006.95 Gene names TMOD3

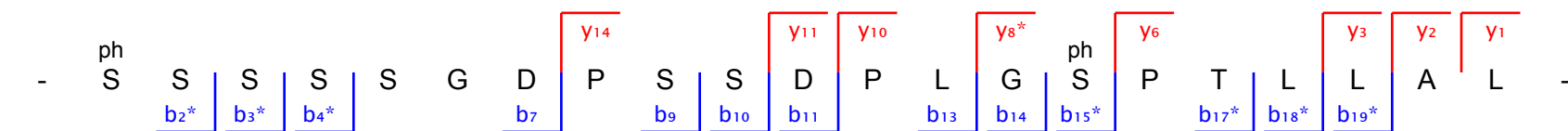
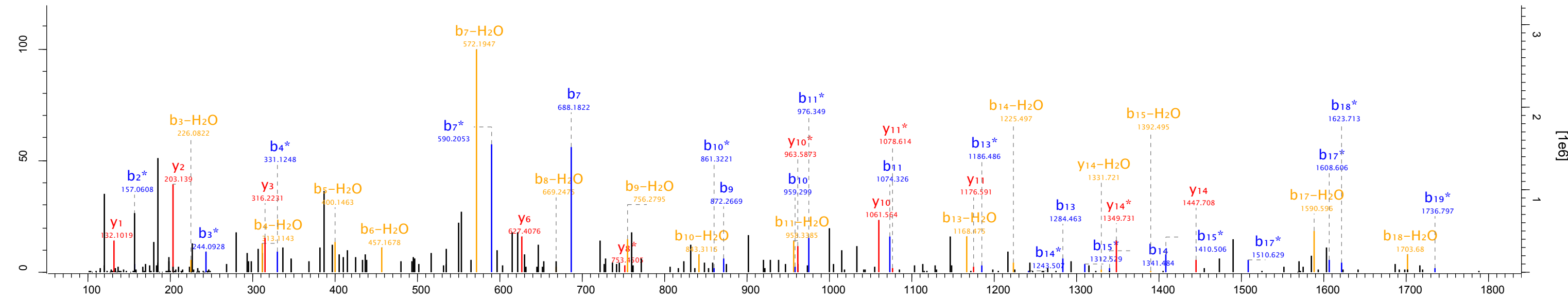


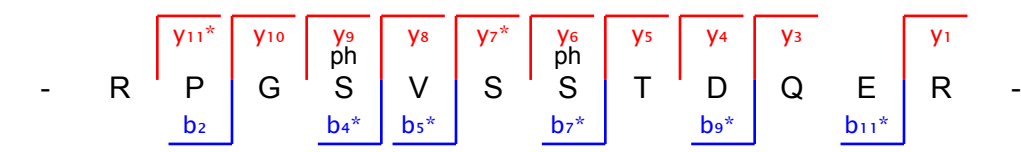
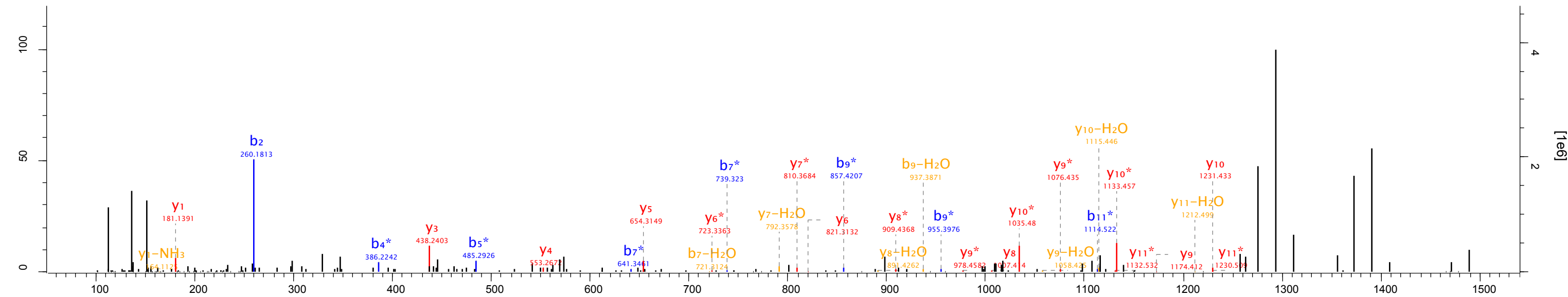


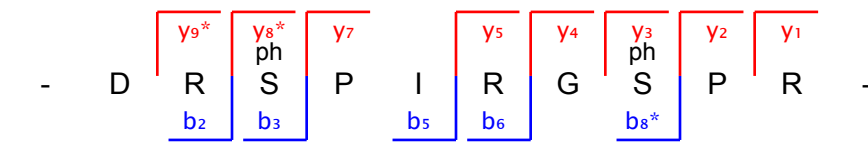
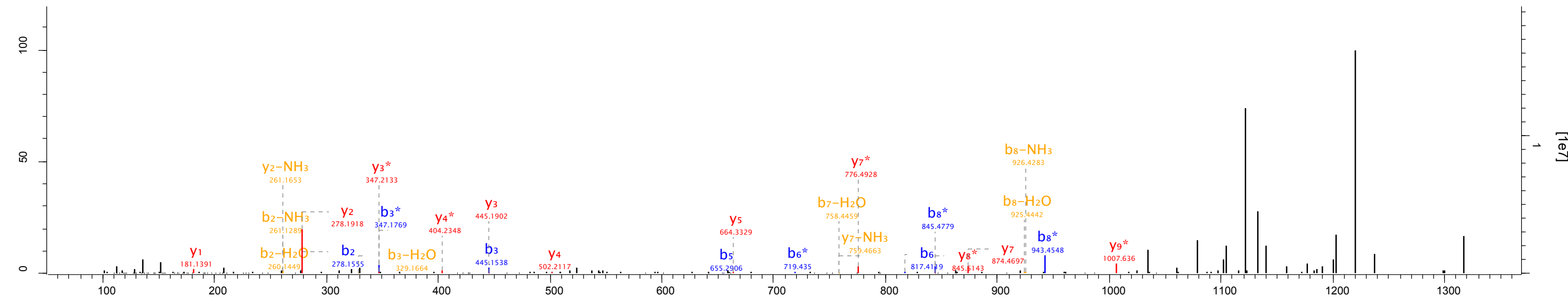
- L E N E G S D E D I E T D V L Y S P Q M A L K -
 b₂ b₃ b₄ b₅ b₆^{*} b₇ b₈^{*} b₉ b₁₀ b₁₁ b₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₄ y₃ y₂ y₁

20171215_MaS_33SR_LMH_phospho2_03 2263 FTMS; HCD 60.66 440.87 SRRM1

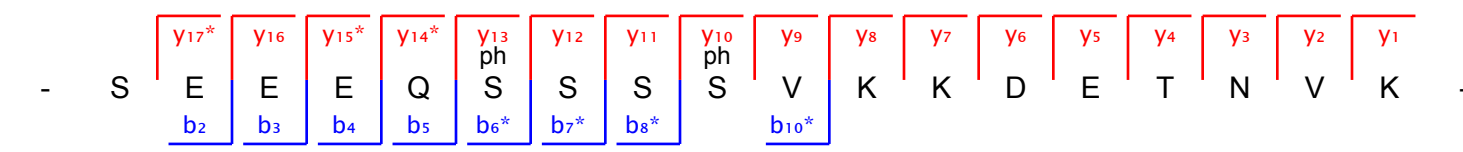
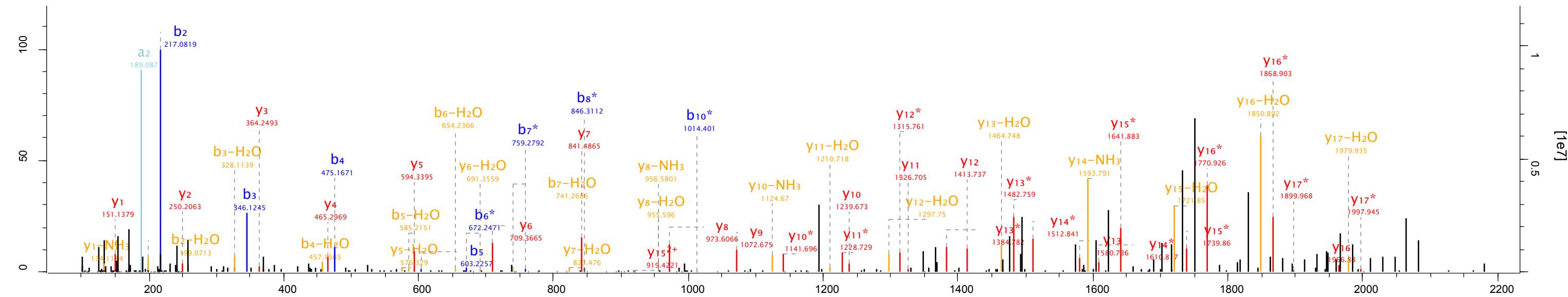




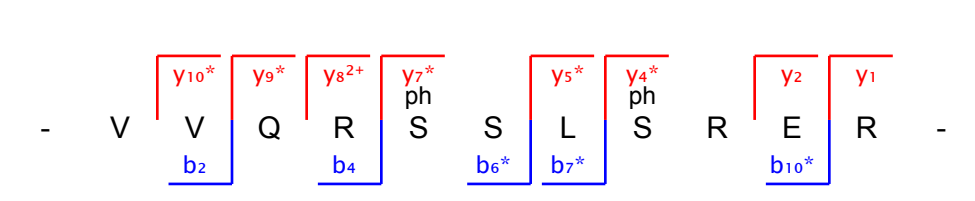
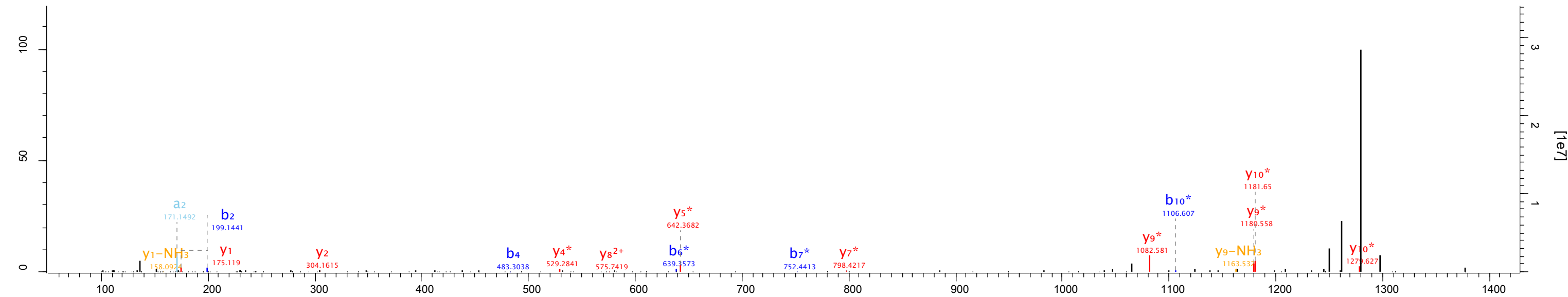


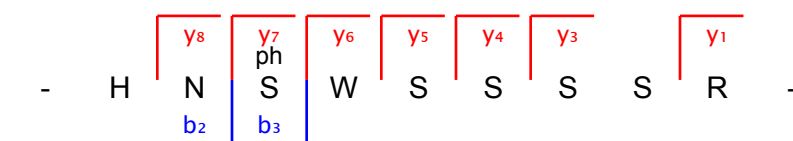
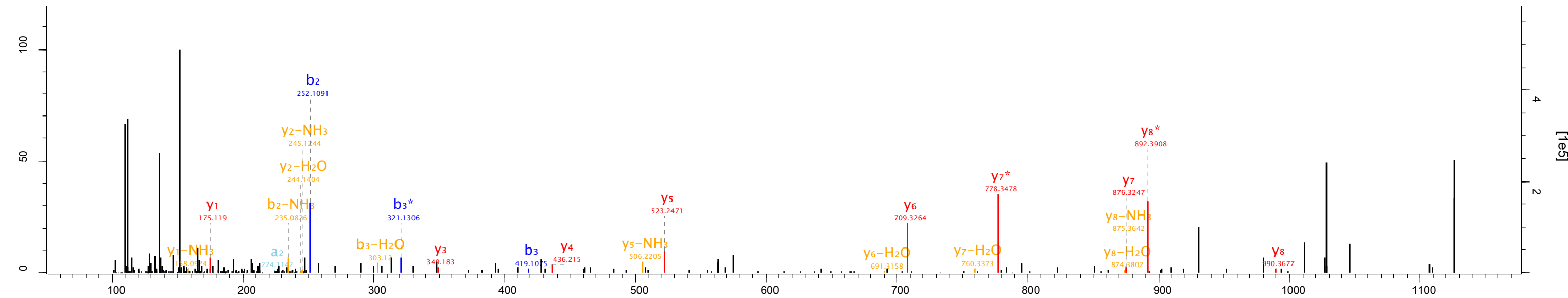


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 Scan: 3063 Method: FTMS; HCD Score: 198.83 m/z: 728.66 Gene names: HNRNPC

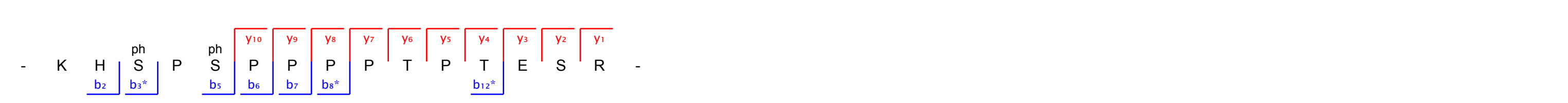
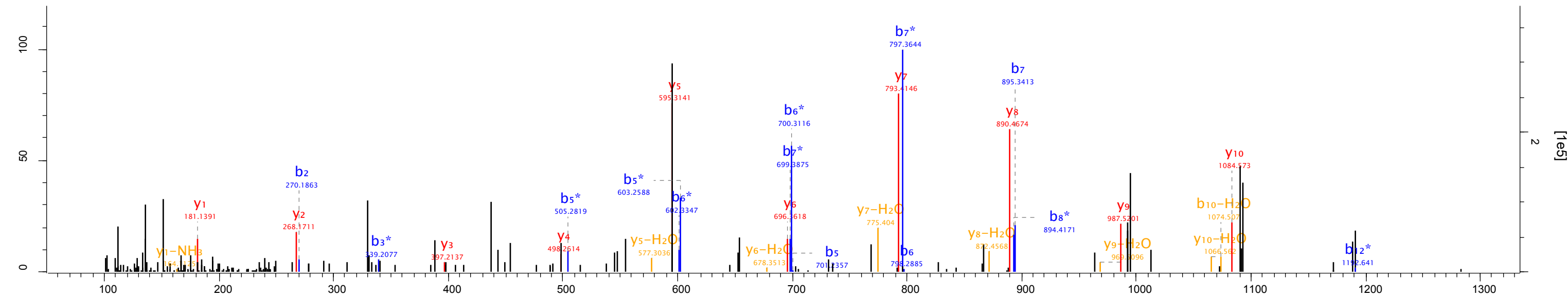


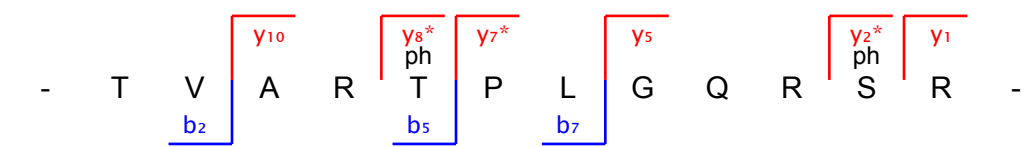
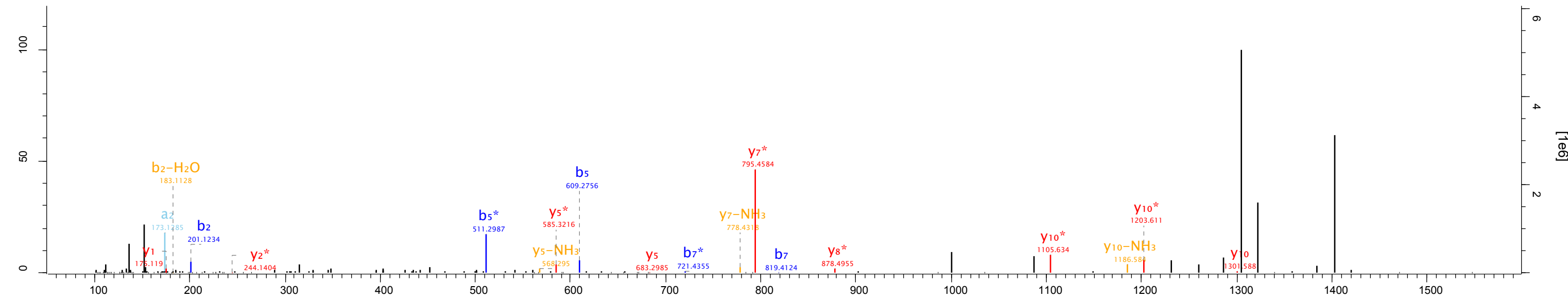
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3123 Method FTMS; HCD Score 61.44 m/z 492.9 Gene names EIF4G1

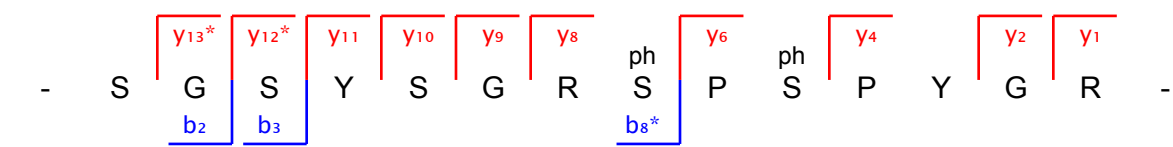
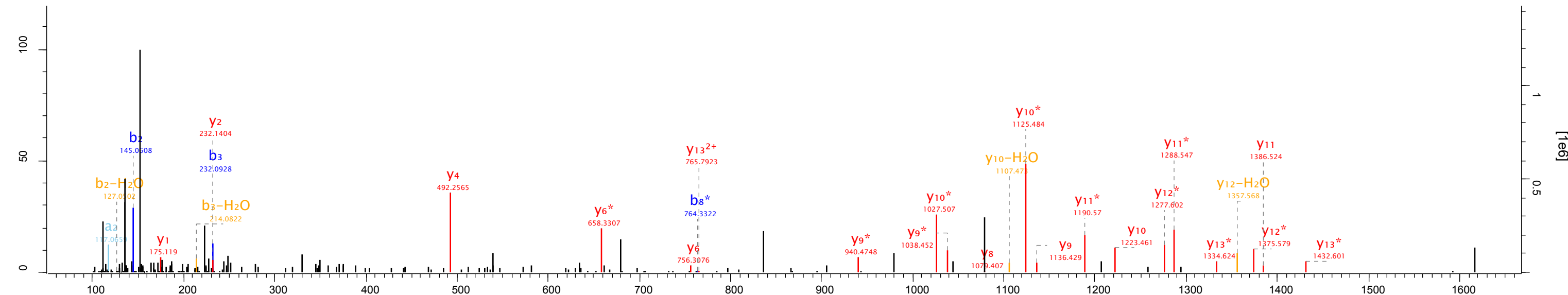


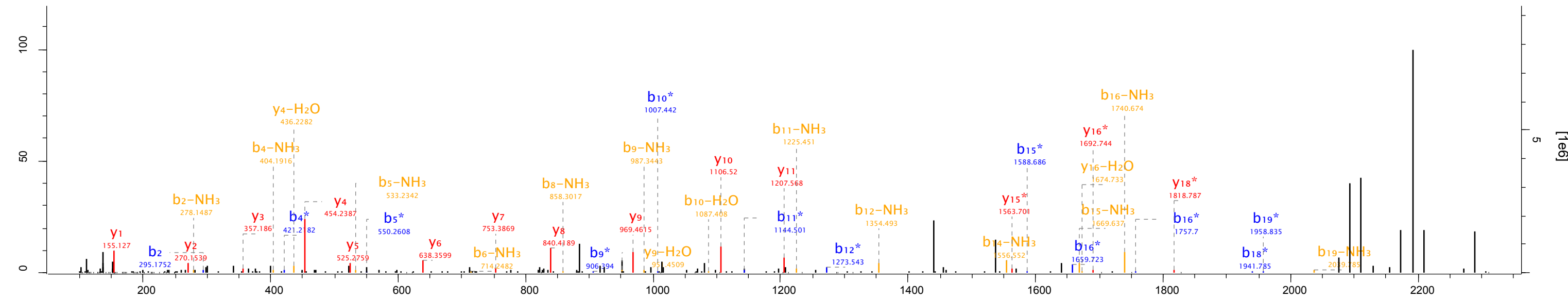


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 Scan: 3393 Method: FTMS; HCD Score: 62.74 m/z: 595.94 Gene names: SMARCC1







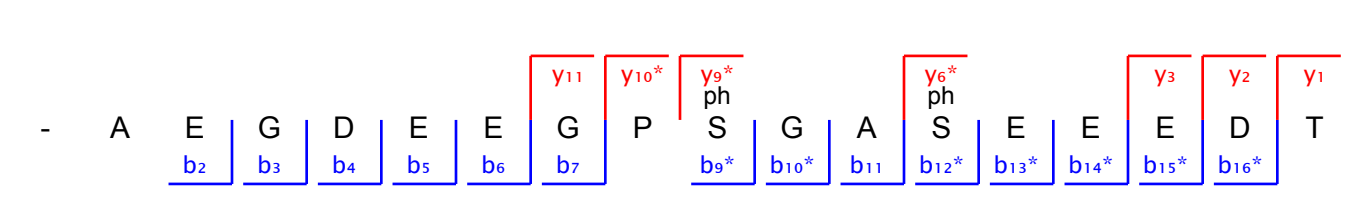
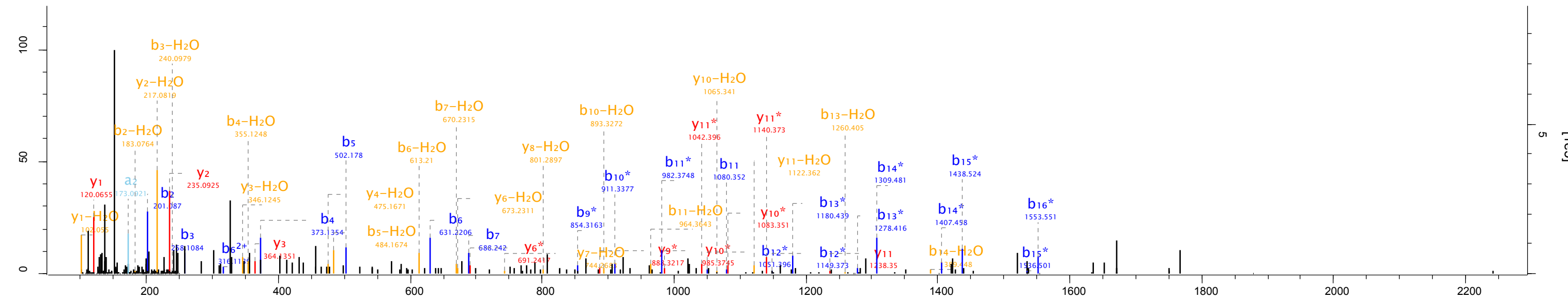


- Q R G S E T H E S D L A P S D K -

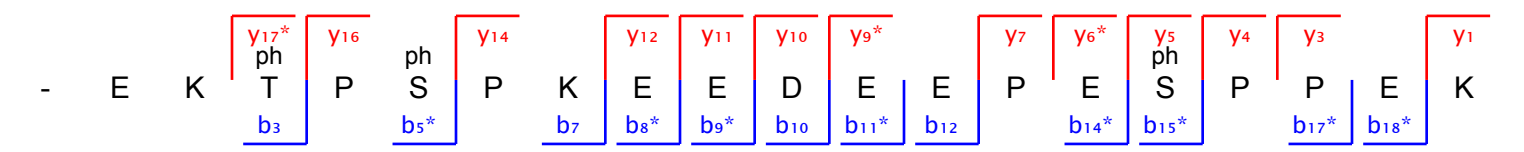
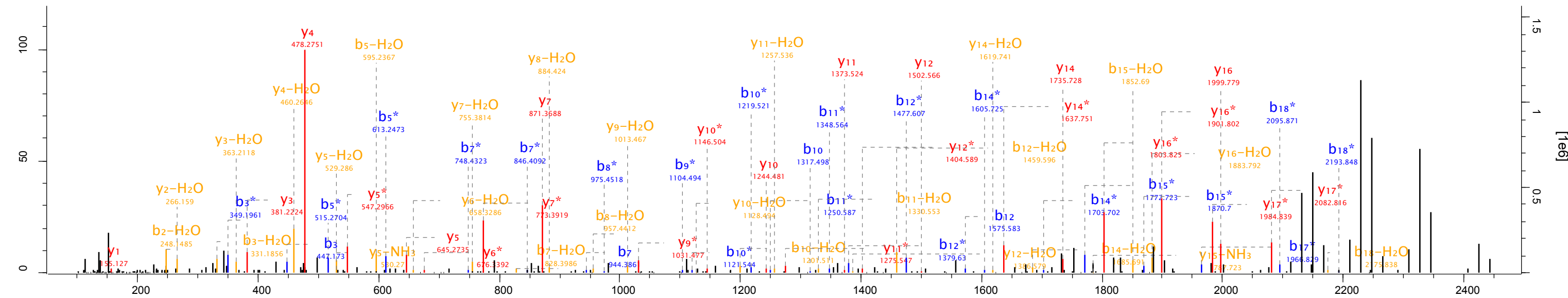
Fragmentation mapping:

- Red boxes: y18* (G), y16* (E), y15* (ph), y11 (T), y10 (H), y9 (E), y8 (S), y7 (D), y6 (L), y5 (A), y4 (P), y3 (S), y2 (D), y1 (K)
- Blue boxes: b2 (R), b4* (S), b5* (E), b9* (E), b10* (T), b11* (H), b12* (E), b15* (L), b16* (A), b18* (S), b19* (D)

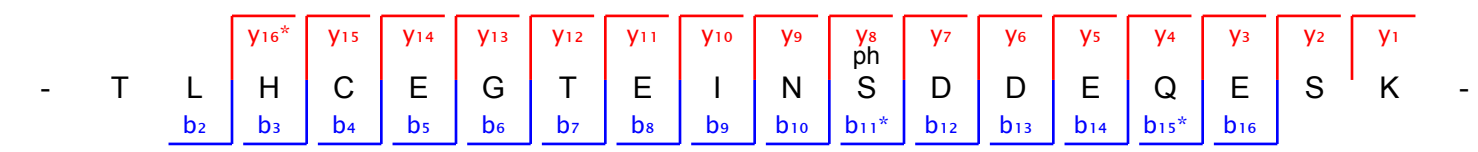
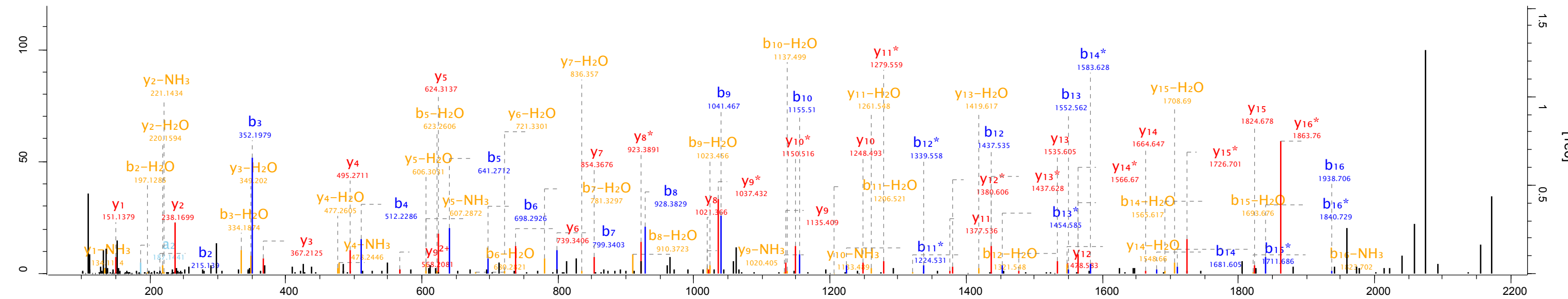
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4113 Method FTMS; HCD Score 156.48 m/z 934.79 Gene names TRIM44



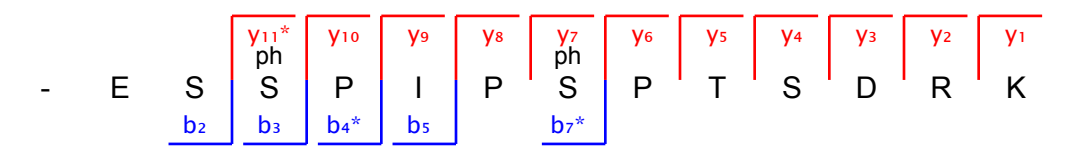
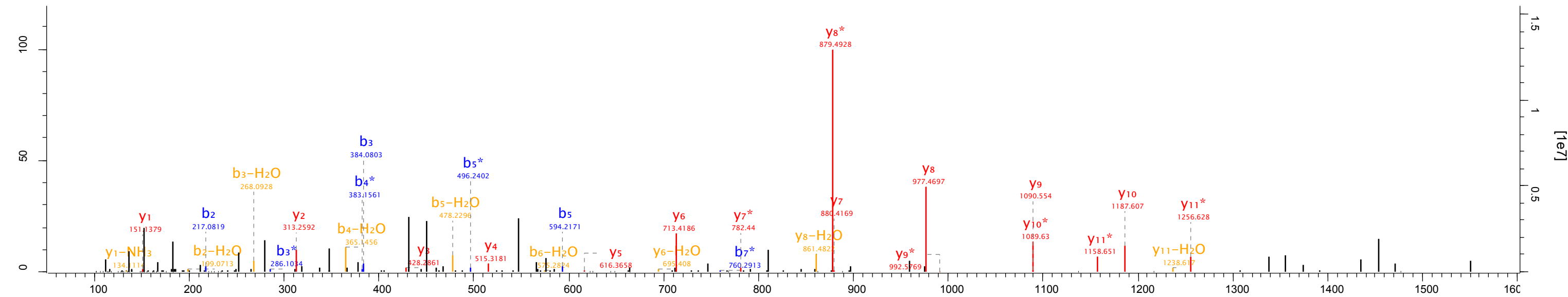
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4303 Method FTMS; HCD Score 321.31 m/z 1223.97 Gene names NUCKS1

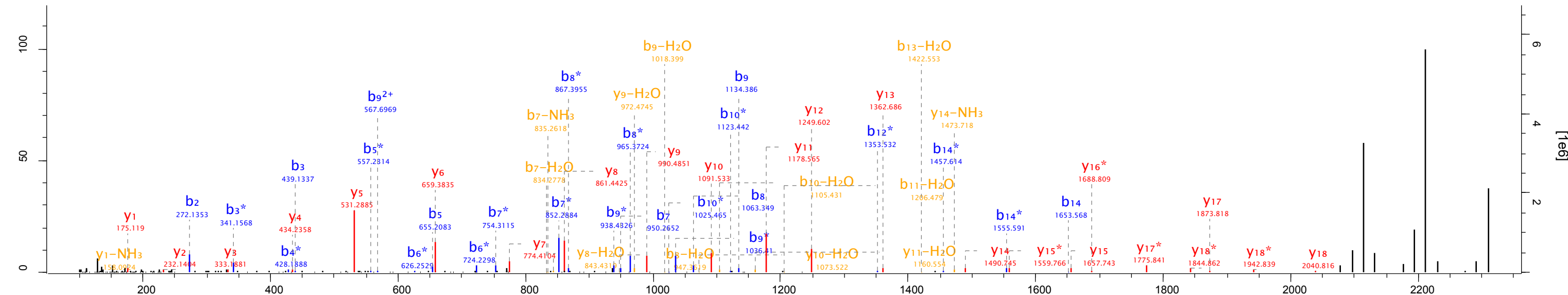


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4613 Method FTMS; HCD Score 320.44 m/z 1088.44 Gene names NCAPG



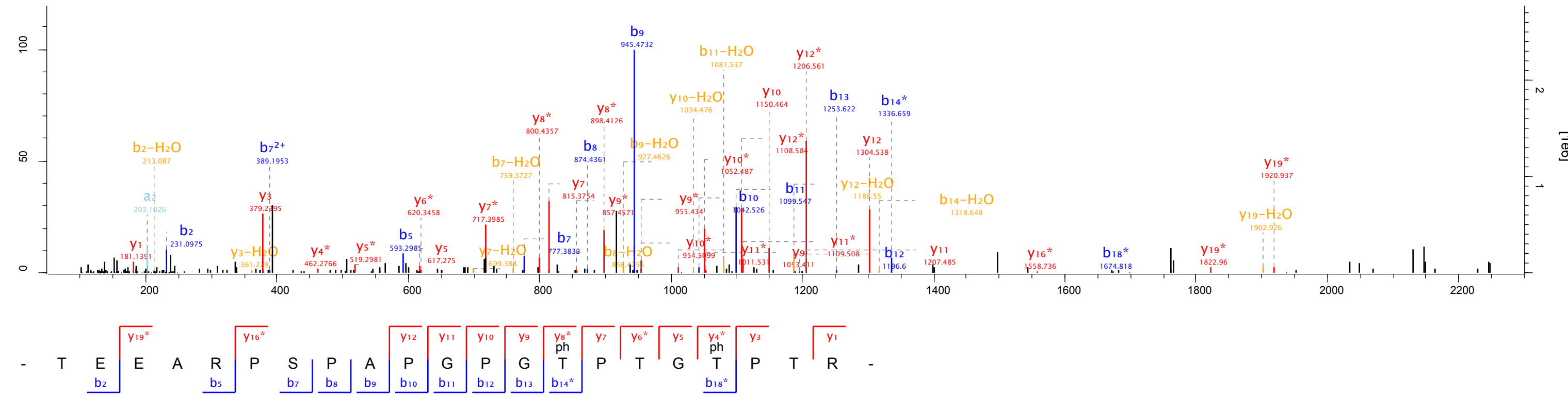
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4633 Method FTMS; HCD Score 105.5 m/z 785.84 Gene names SPTBN1



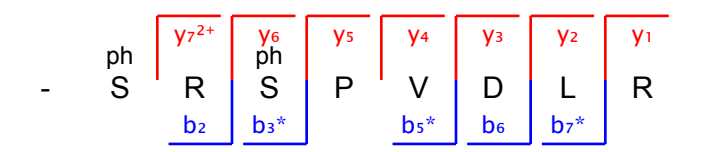
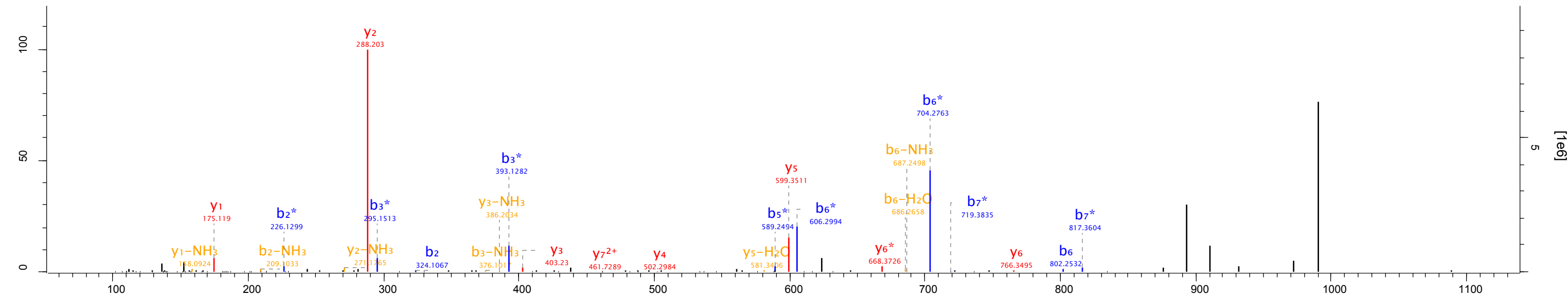


- R D S ph S E S ph S Q L A S T E S D K P T T G R -

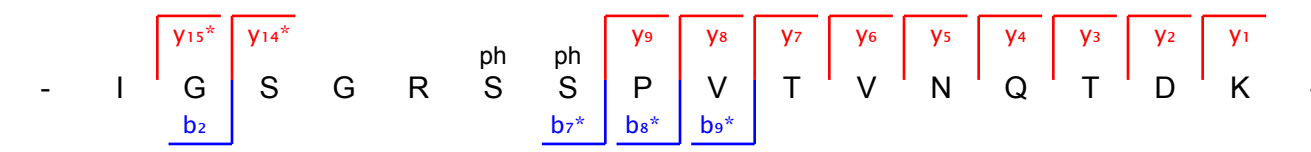
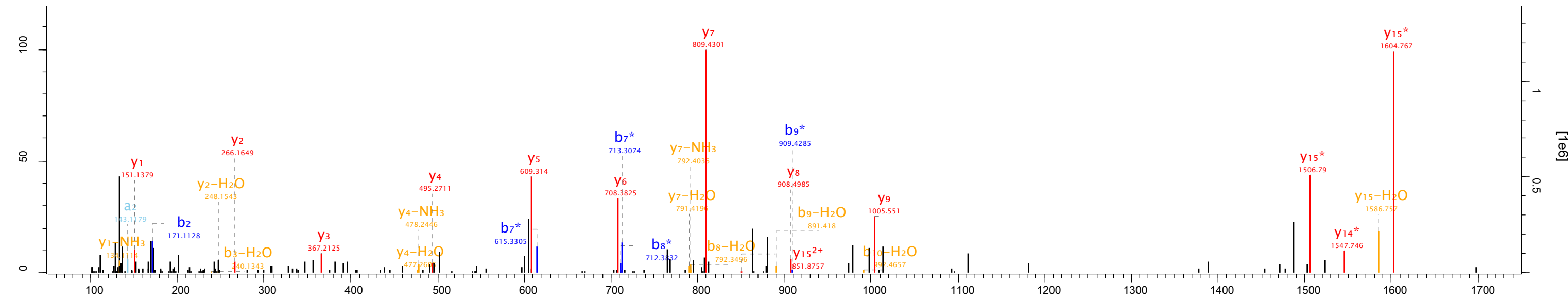
b₂
b₃
b₄^{*}
b₅
b₆^{*}
b₇
b₈
b₉
b₁₀^{*}
b₁₂^{*}
b₁₄



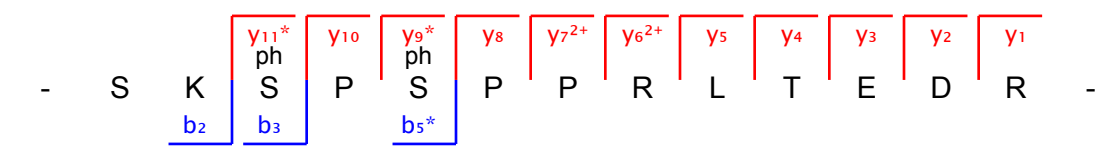
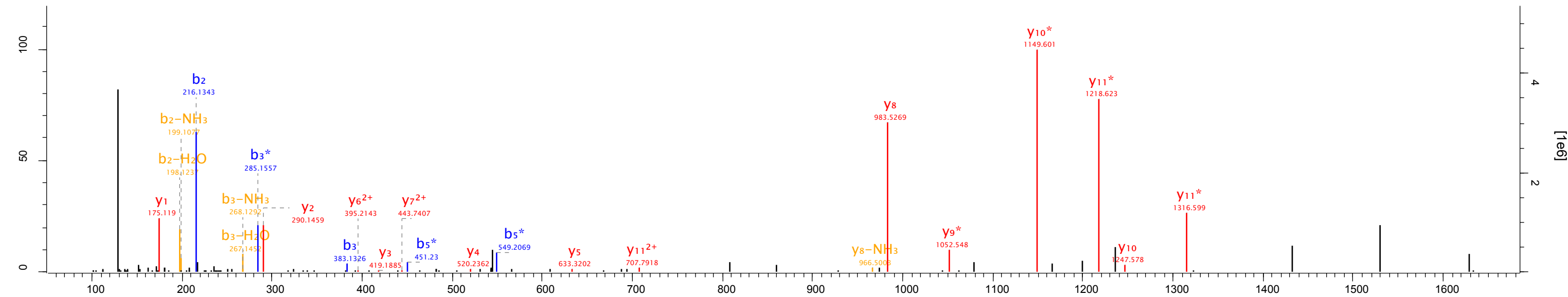
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 5363 Method: FTMS; HCD Score: 111.96 m/z: 545.23 Gene names: PRPF4B

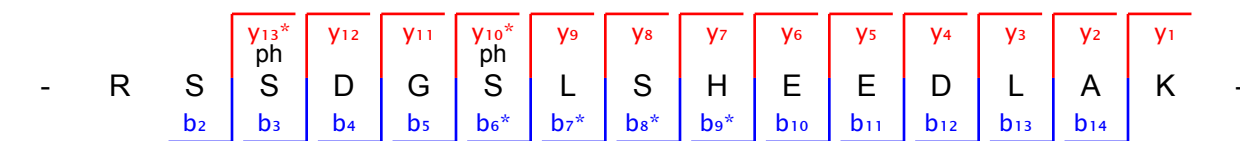
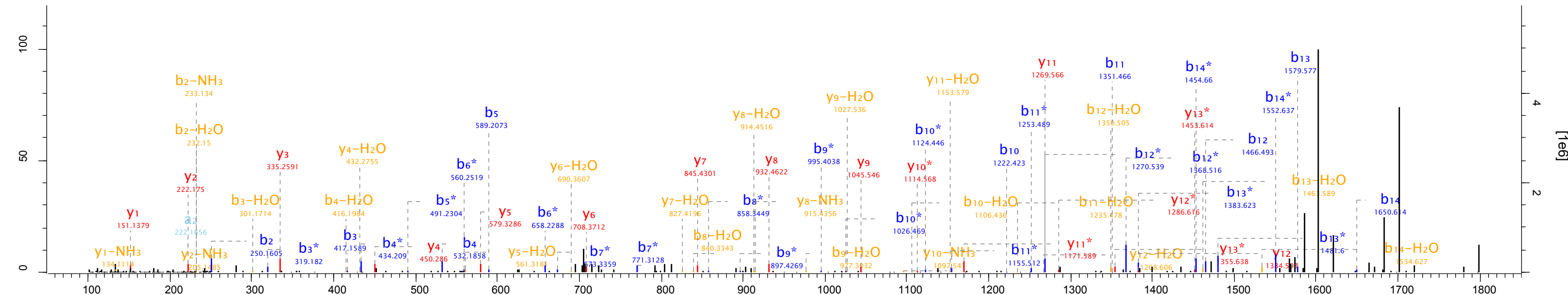


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5533 Method FTMS; HCD Score 53.35 m/z 605.95 Gene names NAV3



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5713 Method FTMS; HCD Score 78.67 m/z 543.91 Gene names ACIN1

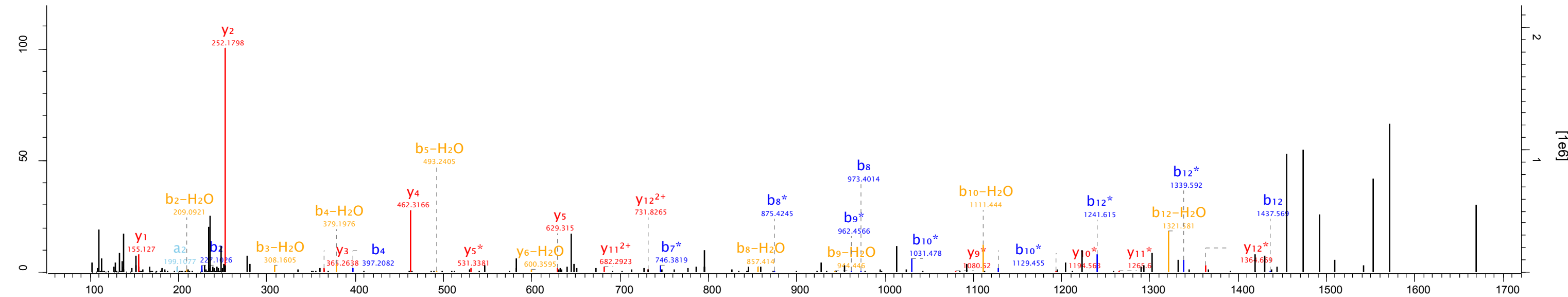




Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
6053	FTMS; HCD	74.11	844.87	ZNF532



- E P V A N S R E S S P L P K -

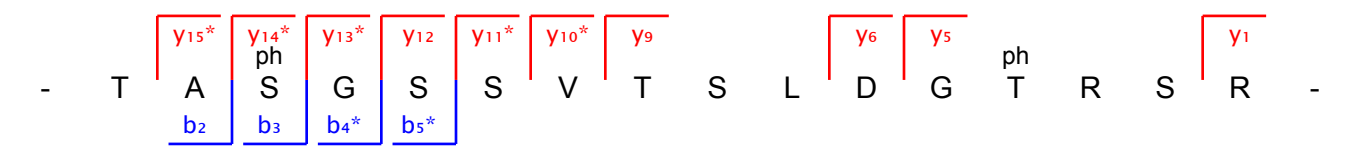
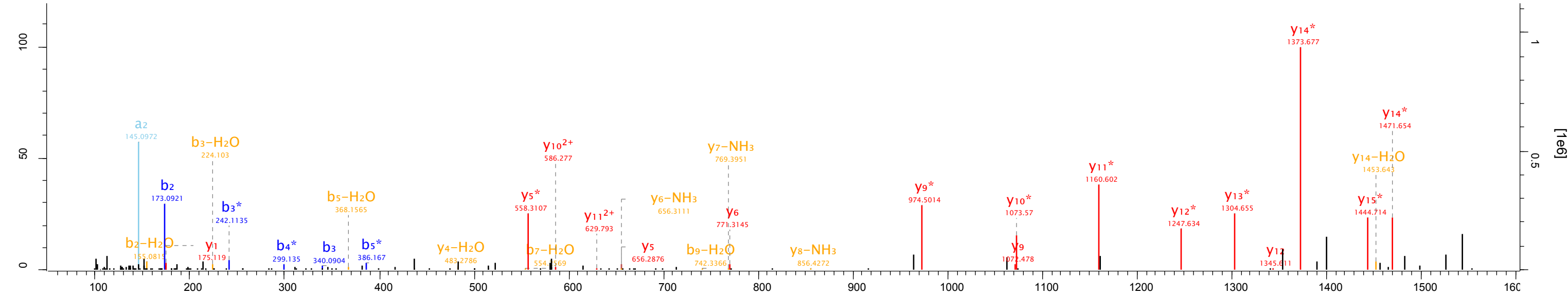
b₂
y₁₂^{*}
y₁₁^{*}
y₁₀^{*}
y₉^{ph}
y₄
y₃
y₂
y₁

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b₇^{*}
b₈
b₉^{*}
b₁₀^{*}
b₁₂

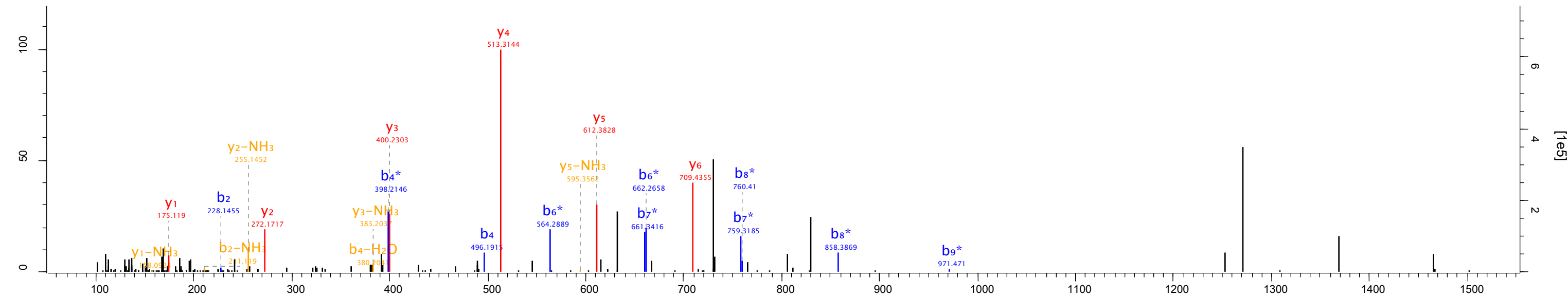
Raw file

20171215_MaS_33SR_LMH_phospho2_03

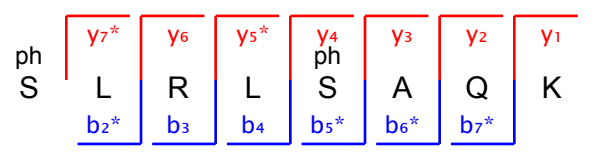
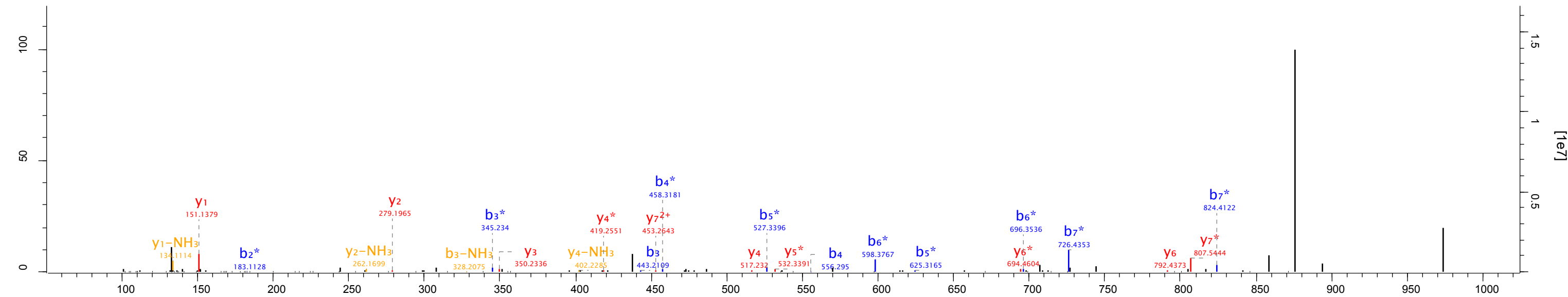
Scan	Method	Score	m/z	Gene names
6233	FTMS; HCD	79.69	581.58	NDRG1

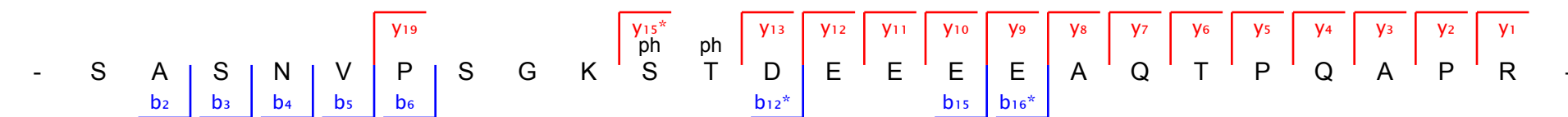
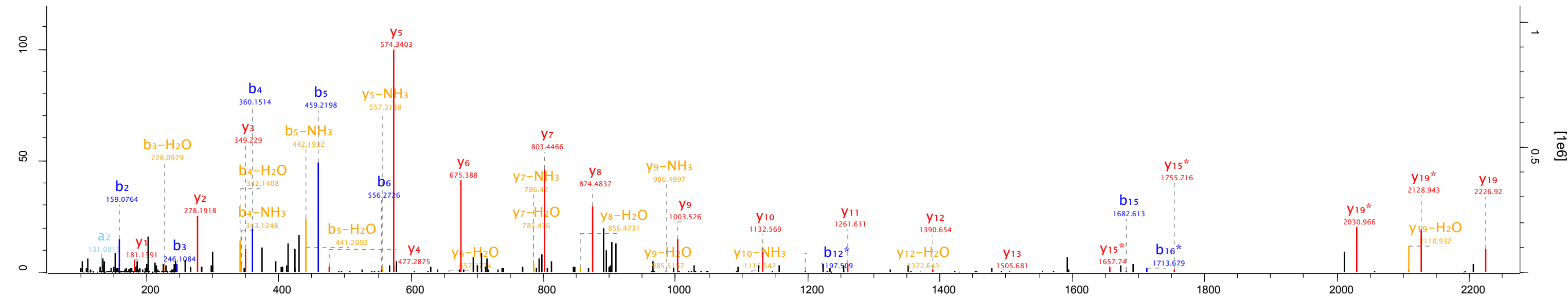


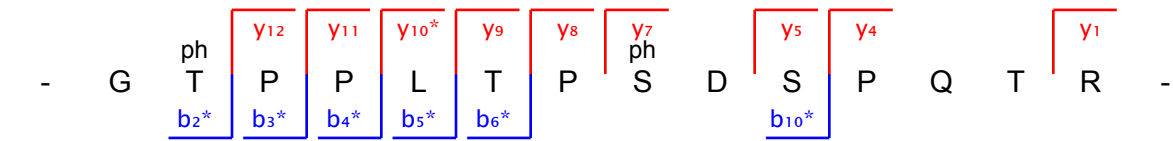
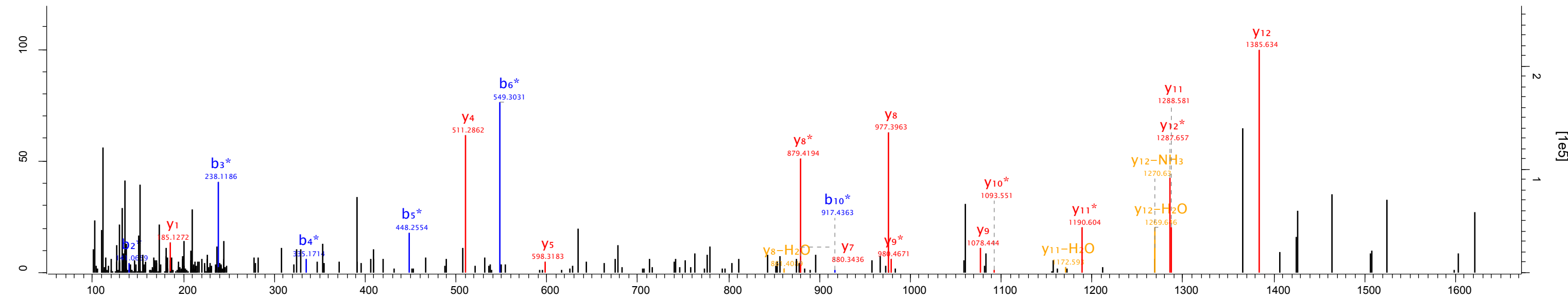
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 Scan: 6263 Method: FTMS; HCD Score: 68.58 m/z: 490.23 Gene names: DOT1L



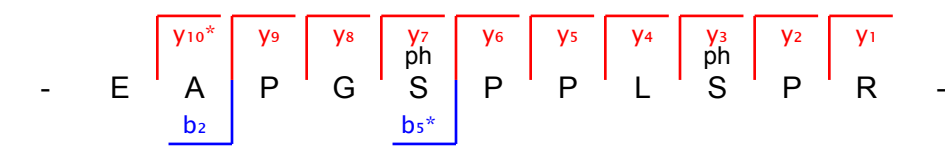
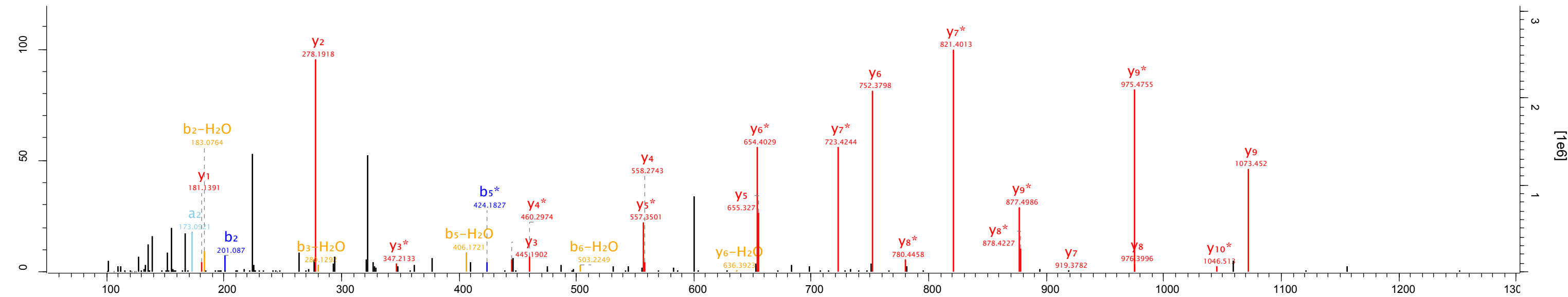
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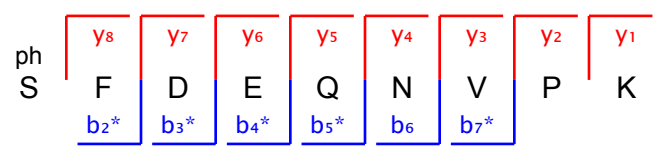
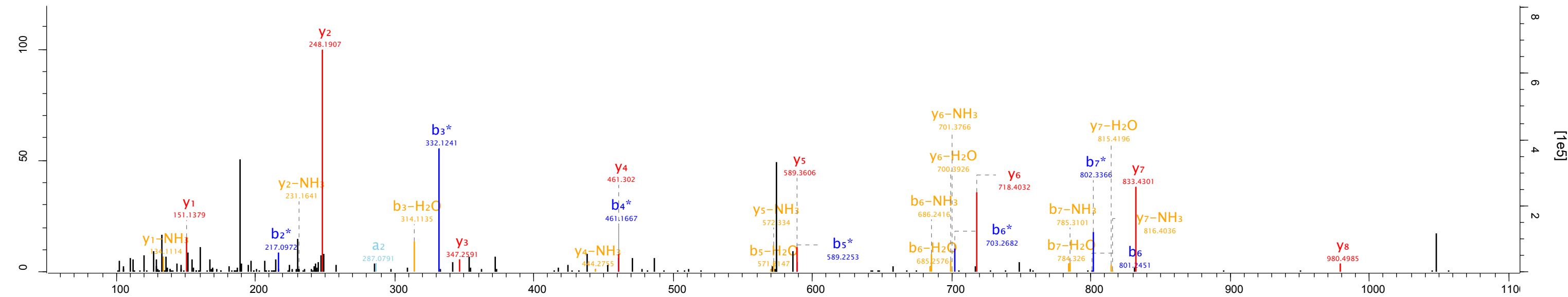




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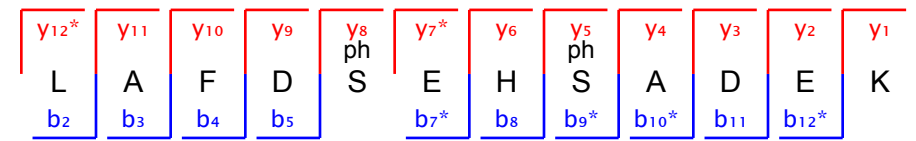
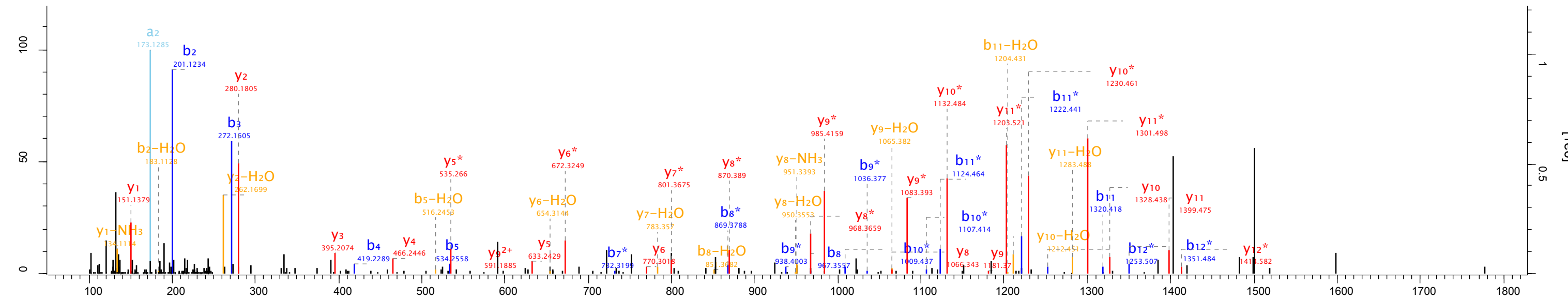


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 Scan: 7123 Method: FTMS; HCD Score: 135.16 m/z: 574.25 Gene names: SVIL

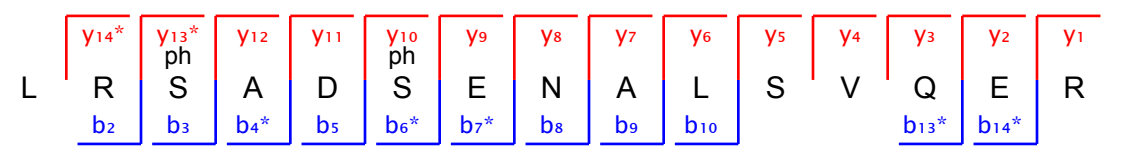
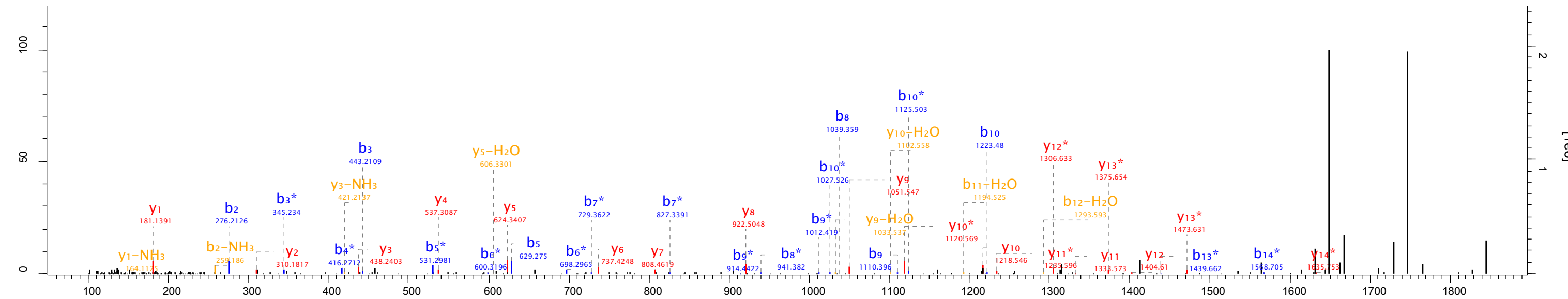


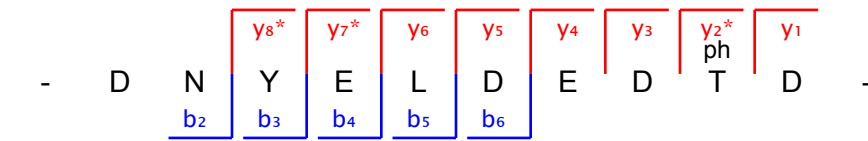
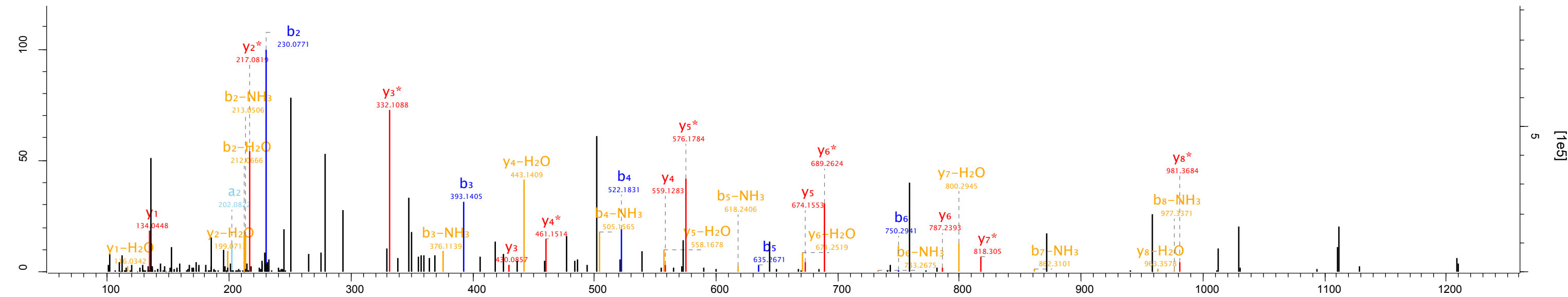
Raw file
20171215_MaS_33SR_LMH_phospho2_03

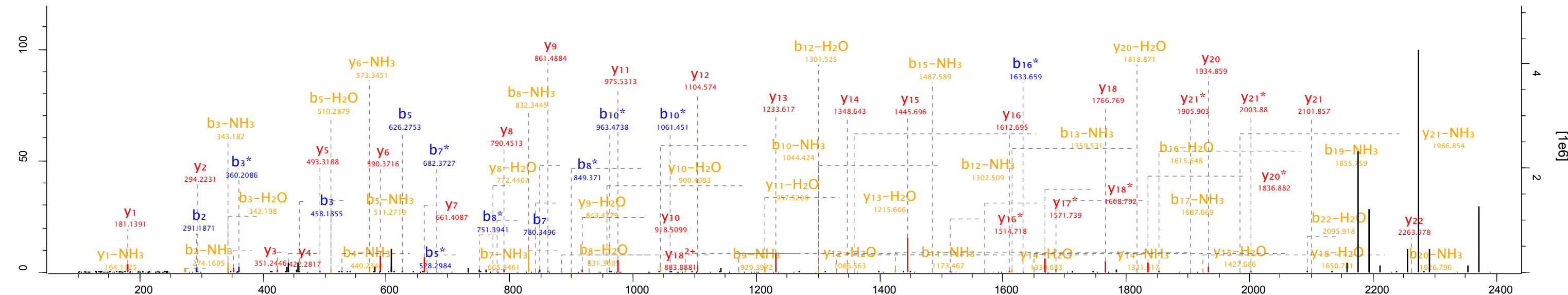
Scan 7753 Method FTMS; HCD Score 179.84 m/z 800.29 Gene names NSD1



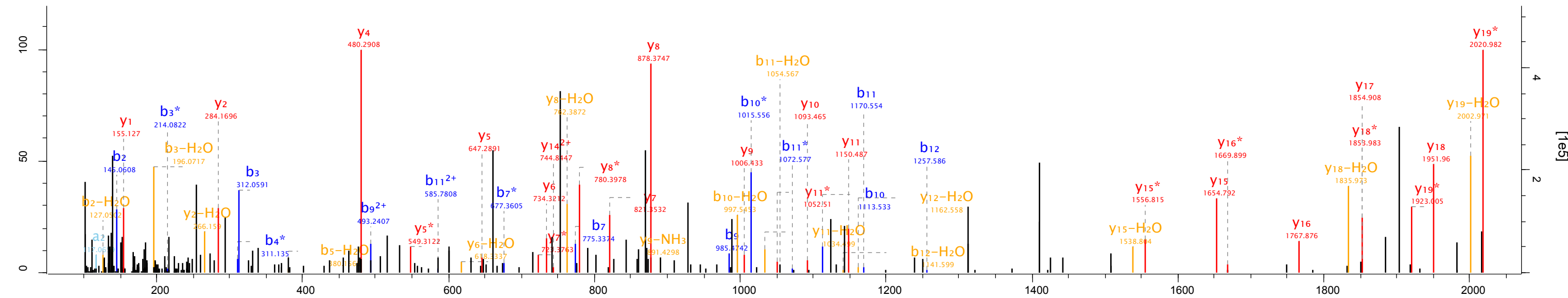
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 7893 Method FTMS; HCD Score 142.45 m/z 923.91 Gene names MAP3K3







- Q R S P A P G S P D E E G G A E A P A A G I R -
 y22 y21 ph y20 y18 y17* y16 ph y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1
 b2 b3 b5 b7 b8* b10* b16*



- G S S P S I R P I Q G S Q G S S S P V E K -

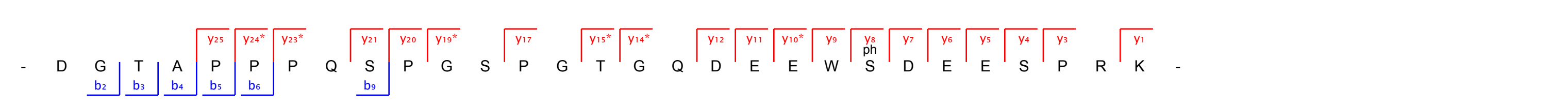
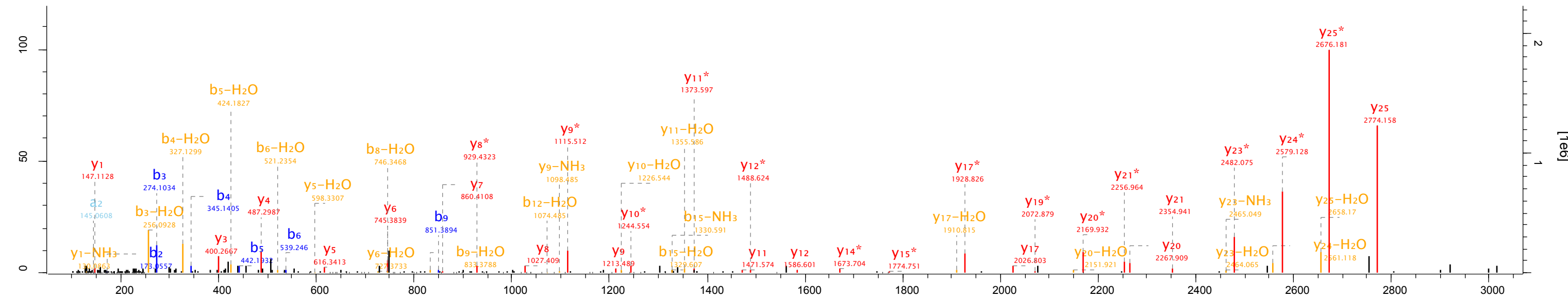
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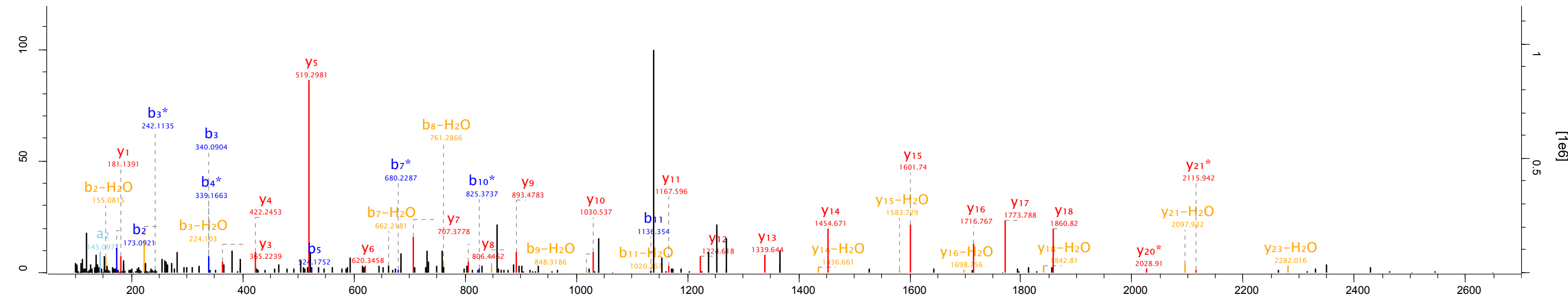
- b₂ (under S)
- b₃ (under S)
- b₄^{*} (under P)
- b₇ (under R)
- b₉ (under I)
- b₁₀ (under Q)
- b₁₁ (under G)
- b₁₂ (under S)

Labels above the sequence:

- y₁₉^{*} ph (above S)
- y₁₈ (above P)
- y₁₇ (above S)
- y₁₆ (above I)
- y₁₅ (above R)
- y₁₄²⁺ (above P)
- y₁₁ (above G)
- y₁₀ (above S)
- y₉ (above Q)
- y₈ (above G)
- y₇ (above S)
- y₆ (above S)
- y₅ ph (above S)
- y₄ (above P)
- y₂ (above E)
- y₁ (above K)

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8493 Method FTMS; HCD Score 213.15 m/z 1040.44 Gene names PACSIN3





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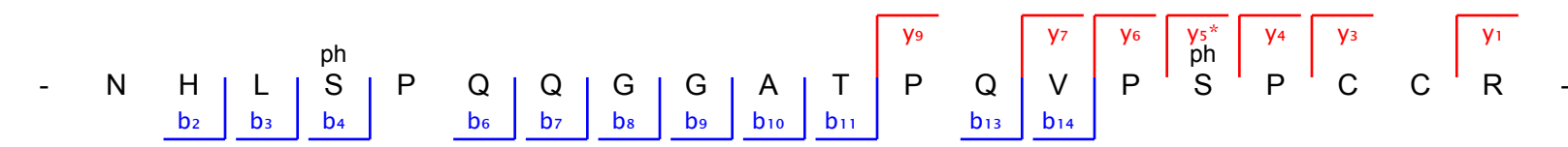
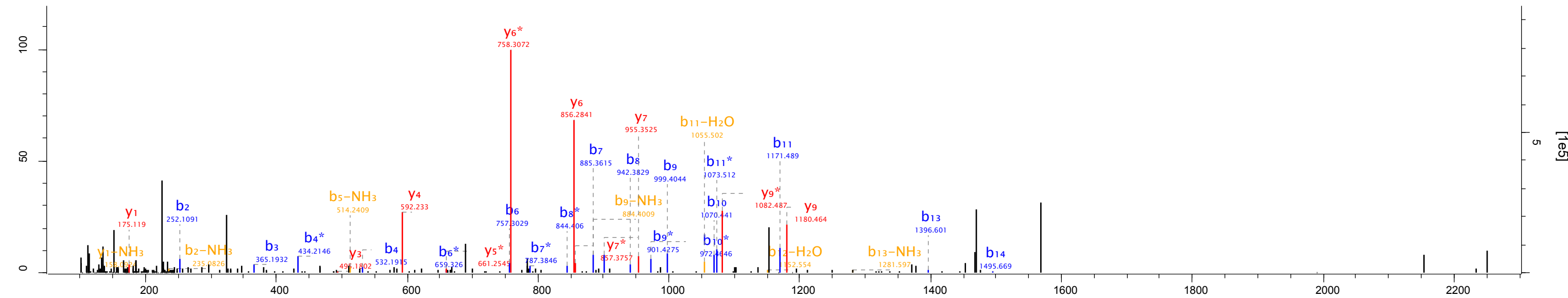
ph ph

b₂ b₃ b₄* b₅ b₇*

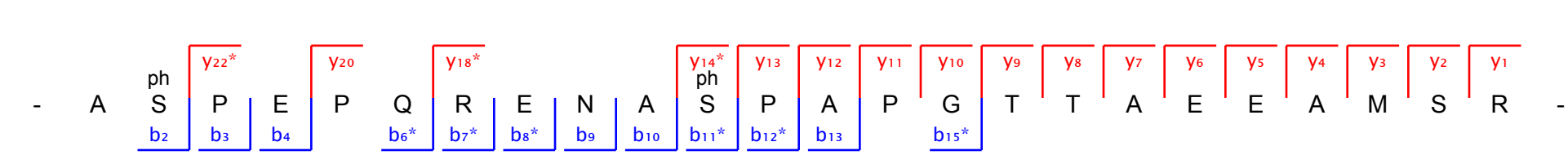
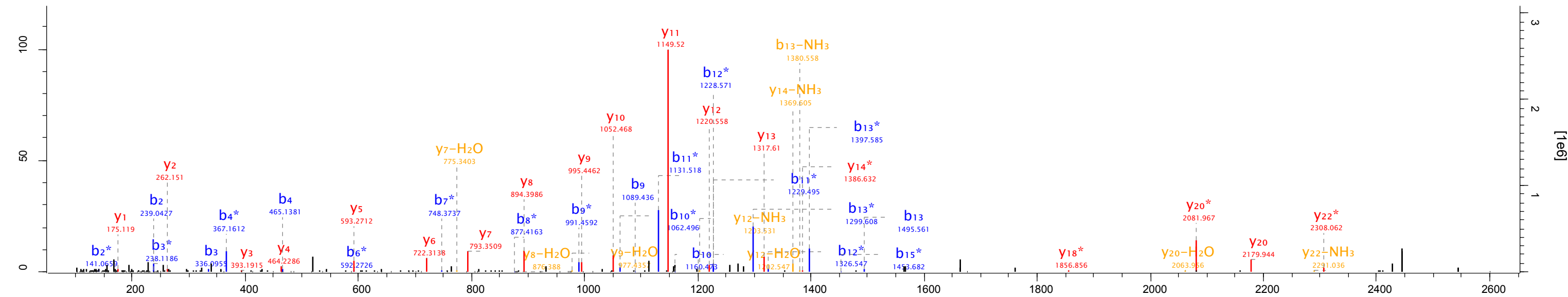
y₂₁* y₂₀* y₁₈ y₁₇ y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃

b₁₀* b₁₁

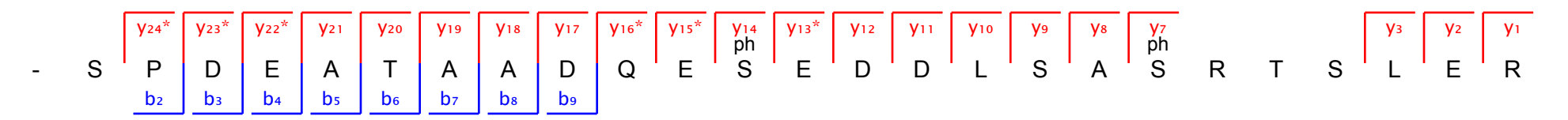
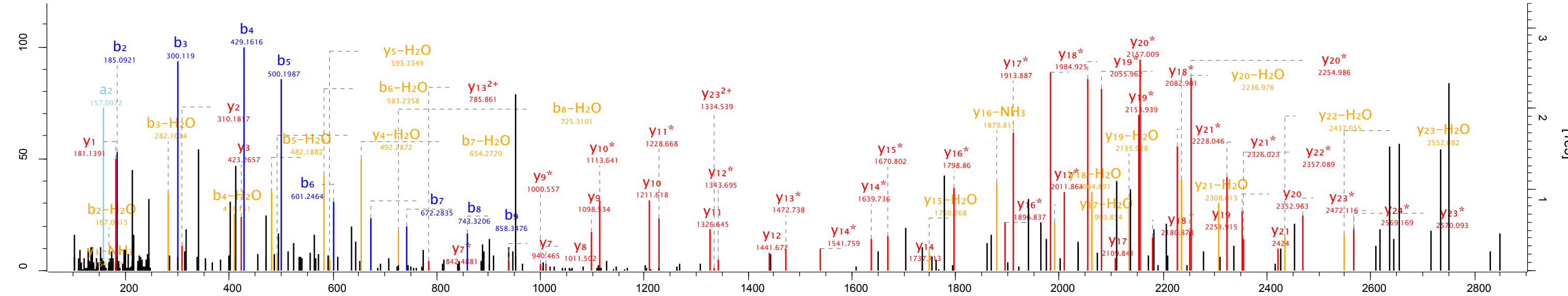
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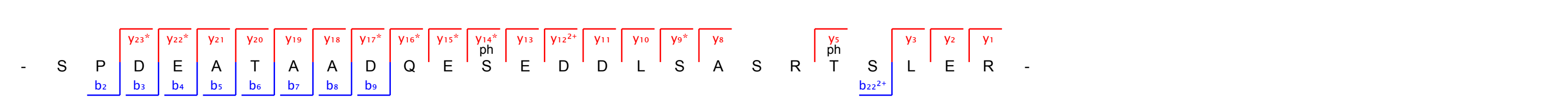
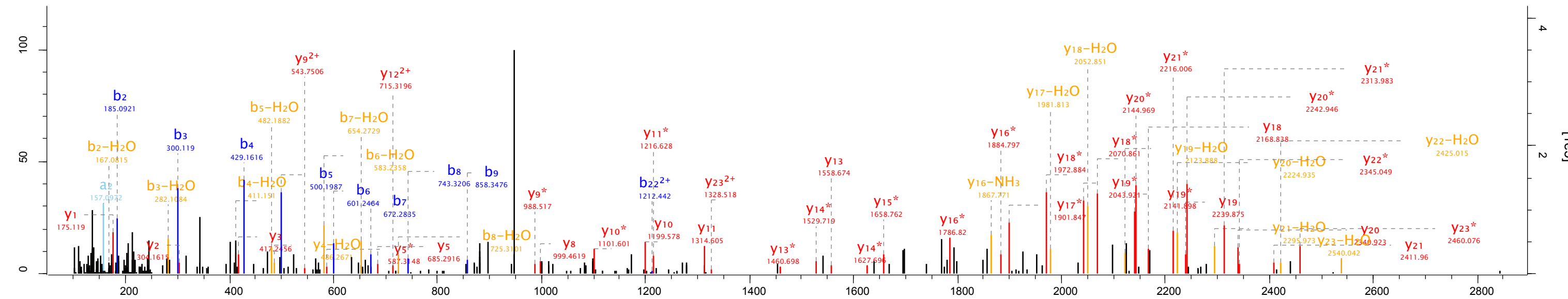
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8953 Method FTMS; HCD Score 105.66 m/z 882.7 Gene names BAT3;BAG6



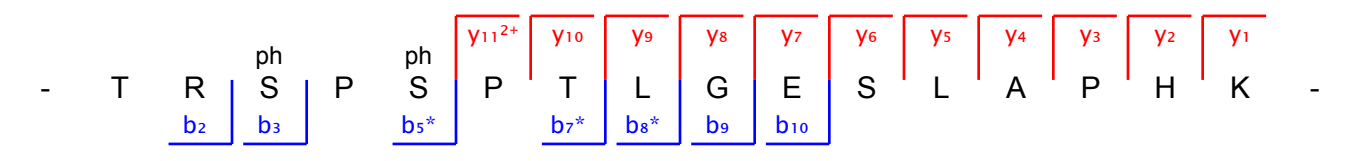
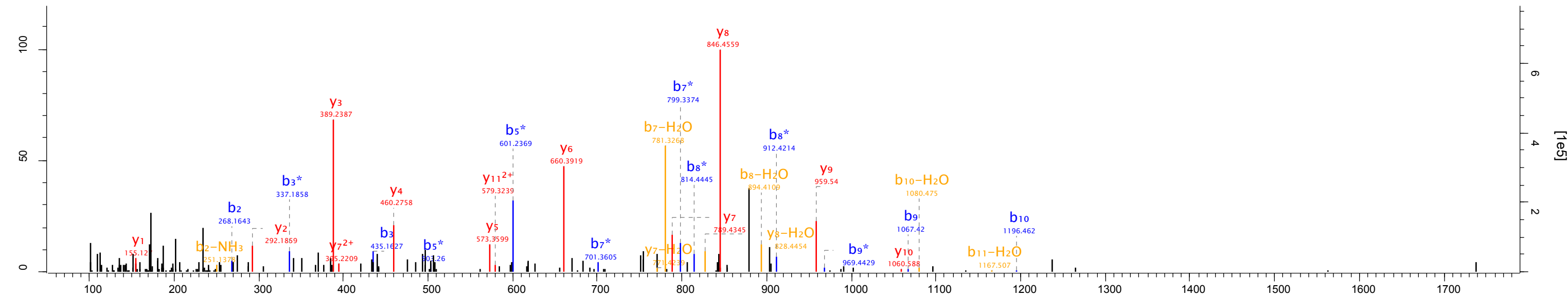
20171215_MaS_33SR_LMH_phospho2_03 9113 FTMS; HCD 249.54 951.72 FARP1



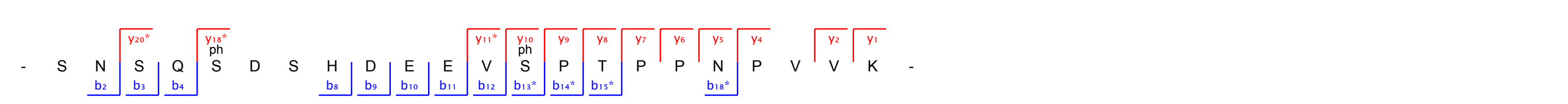
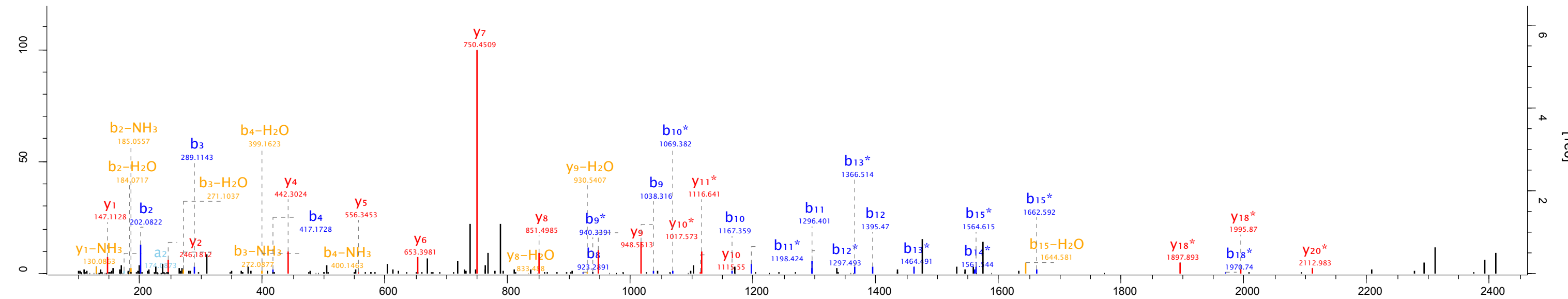
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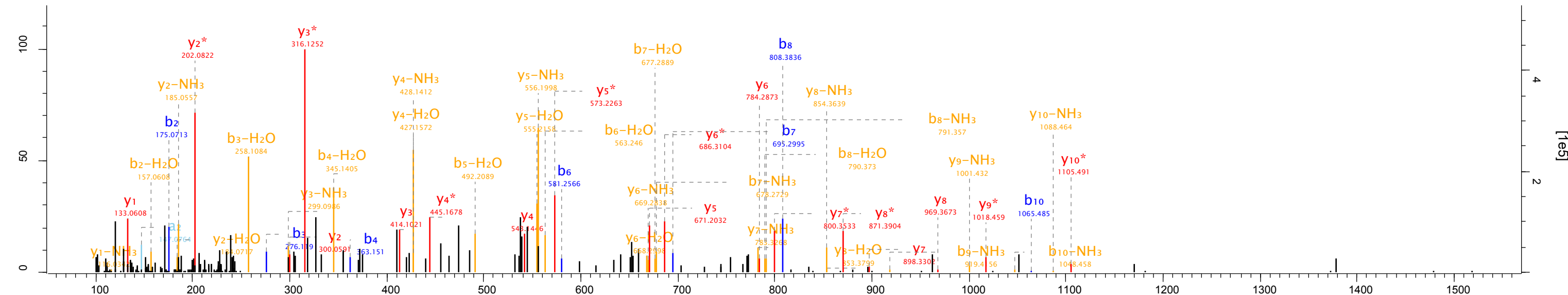


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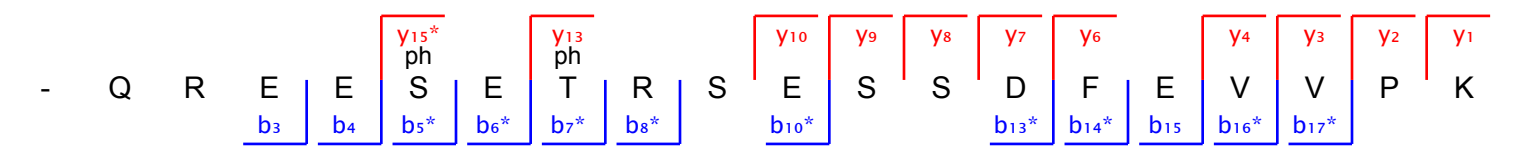
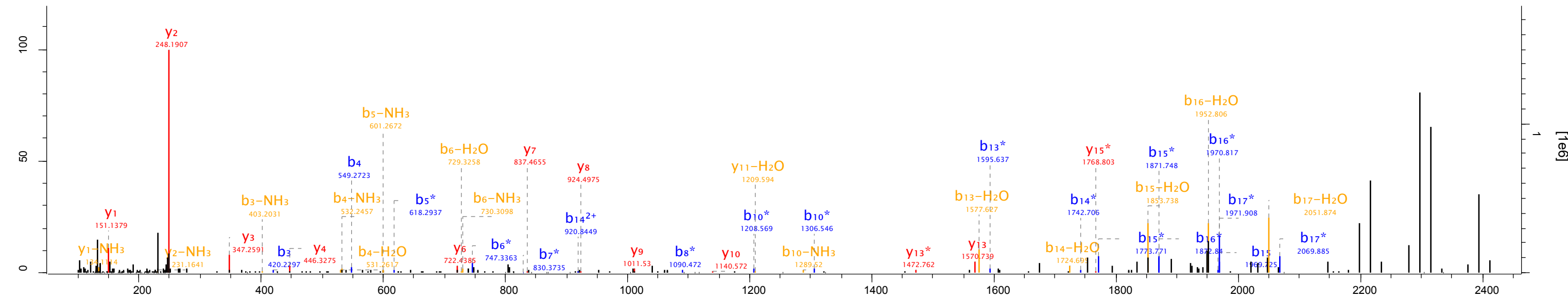




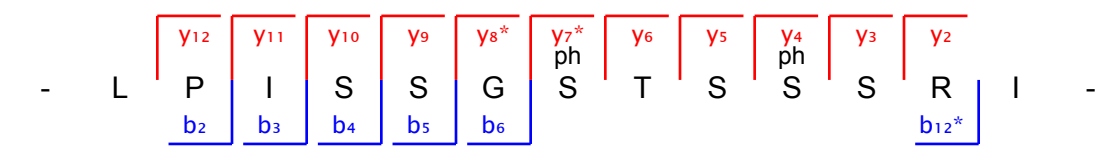
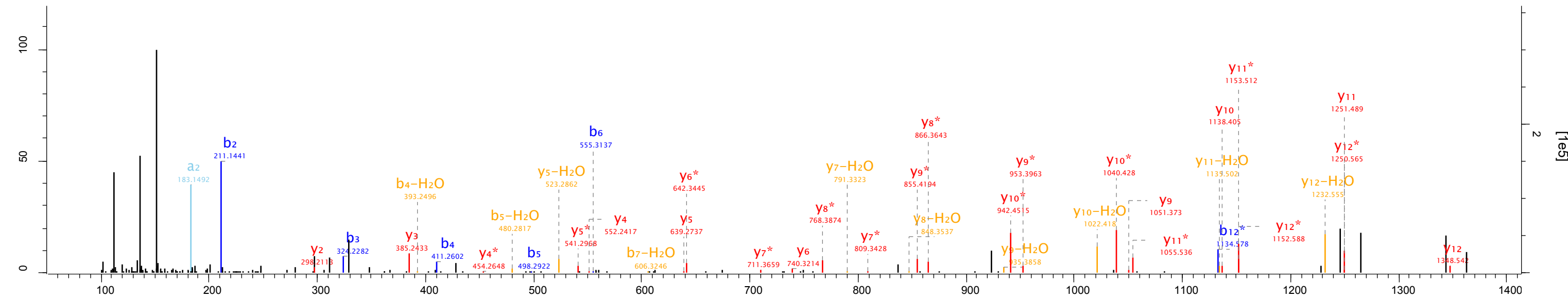
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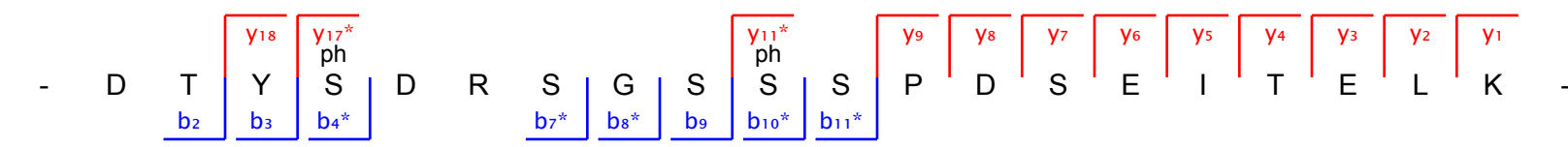
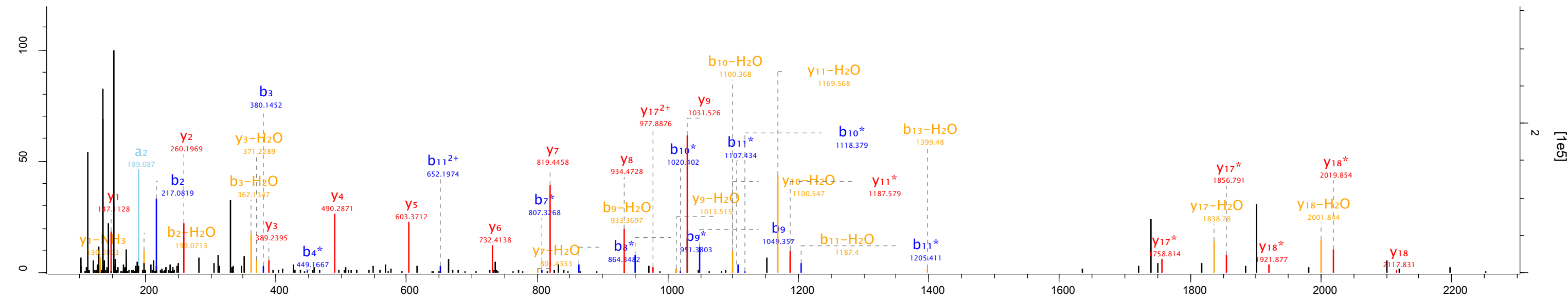


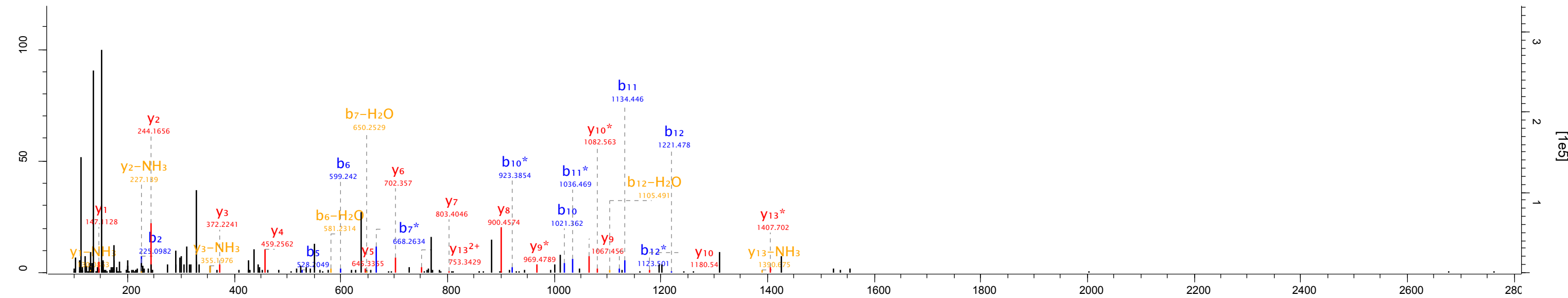
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Raw file
20171215_MaS_33SR_LMH_phospho2_04

Scan 10403 Method FTMS; HCD Score 128.58 m/z 778.64 Gene names CTPS1



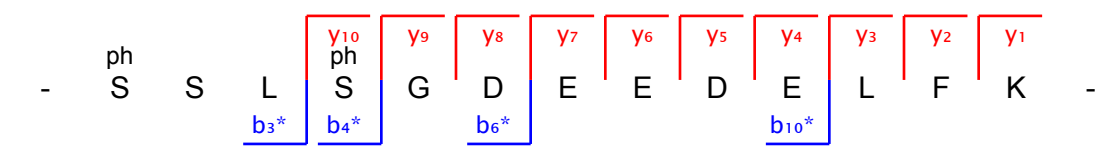
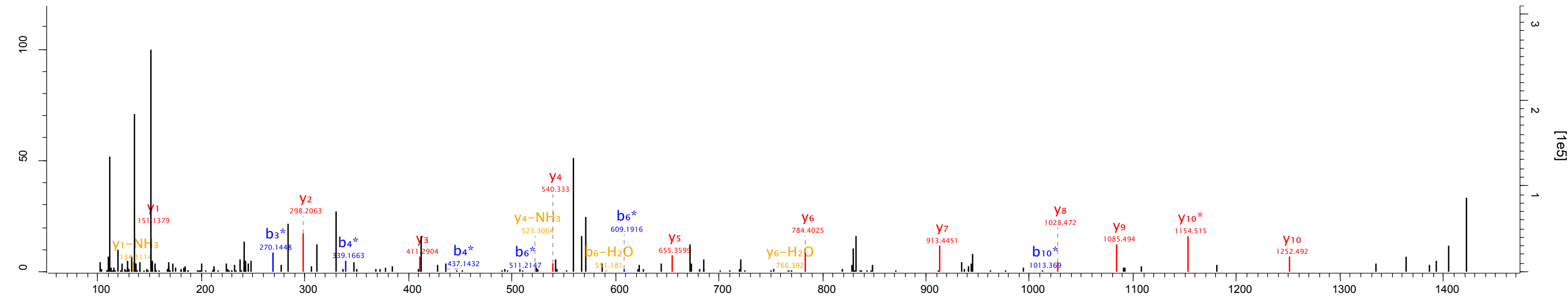


- S H S E S A S P S A L S S P N N L S P T G W S Q P K -

Annotations below the sequence:

- b2 (under H)
- b5 (under S), b6 (under A), b7* (under S)
- b10 (under A), b11 (under L), b12 (under S)
- y13* (under P)
- y10 (under L), y9 ph (under S), y8 (under P), y7 (under T), y6 (under G), y5 (under W), y4 (under S), y3 (under Q), y2 (under P), y1 (under K)

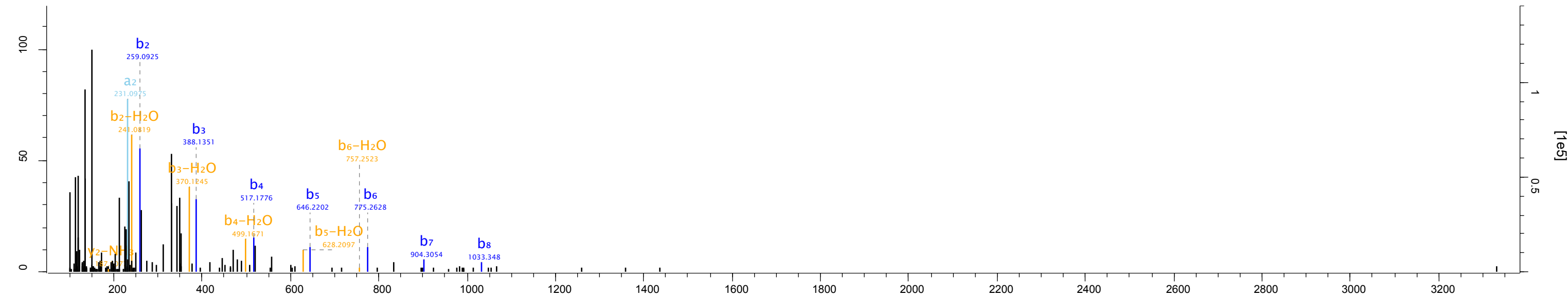
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Raw file

20171215_MaS_33SR_LMH_phospho2_04

Scan	Method	Score	m/z	Gene names
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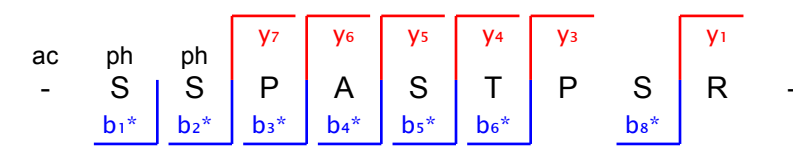
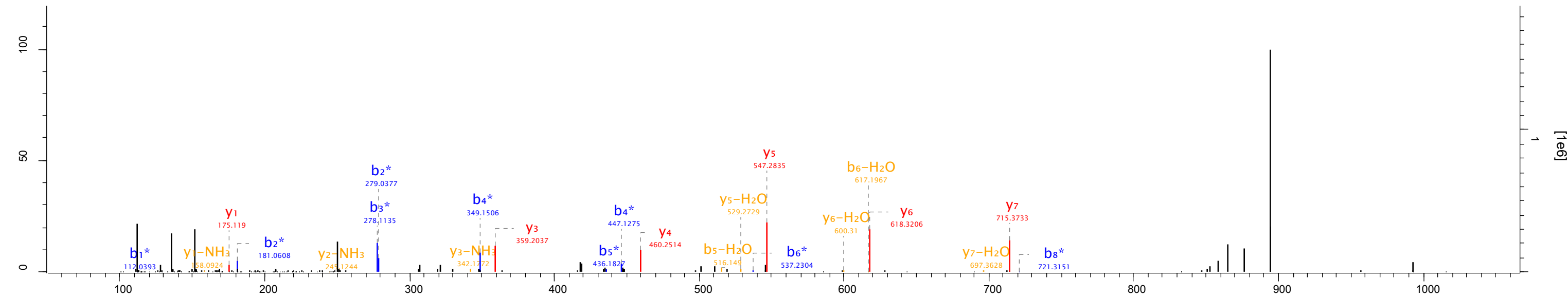


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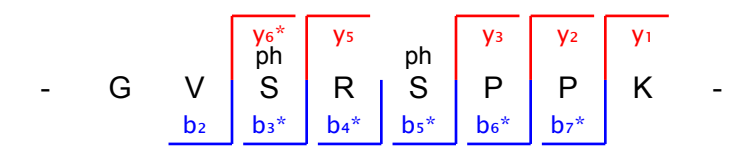
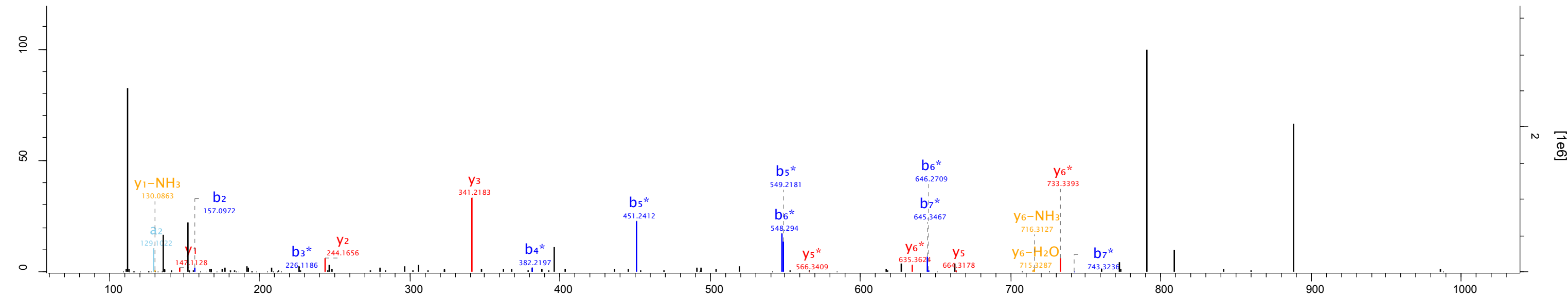
ph

b2 b3 b4 b5 b6 b7 b8

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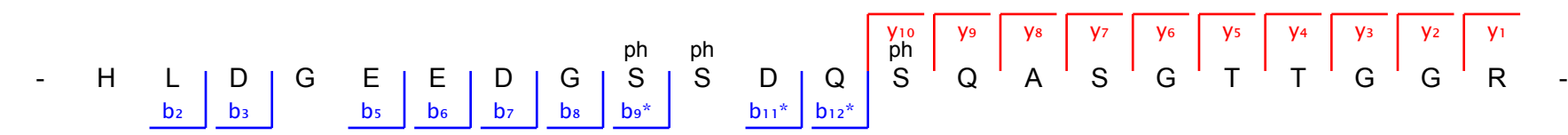
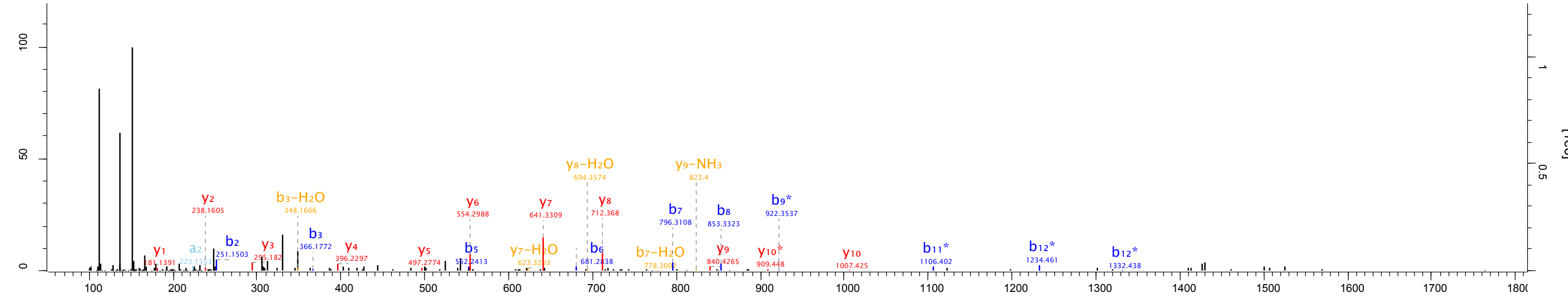
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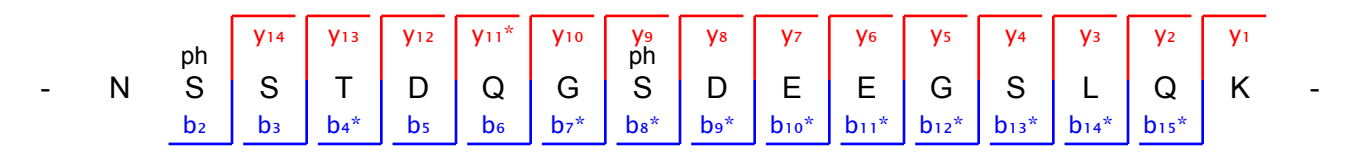
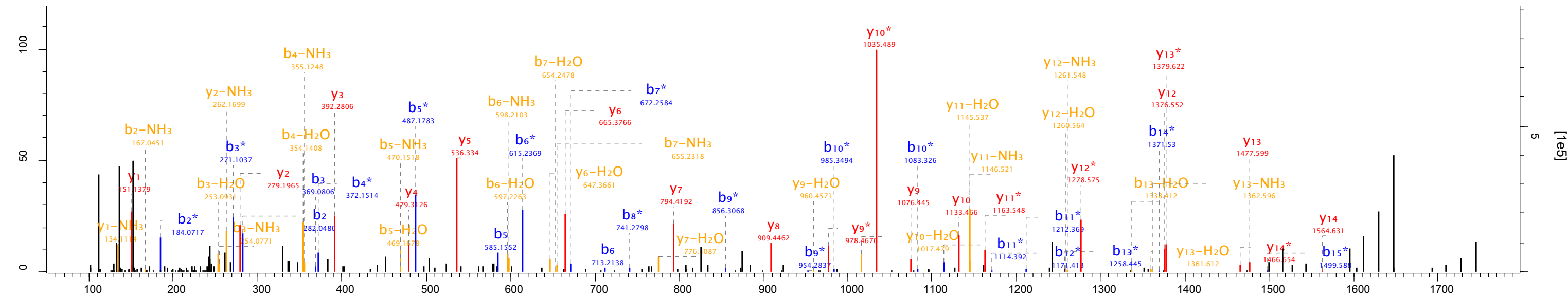
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20171215_MaS_33SR_LMH_phospho2_04

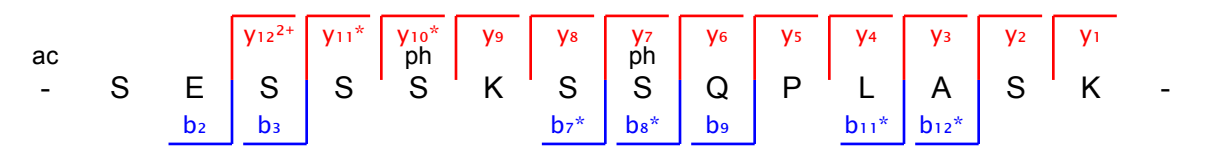
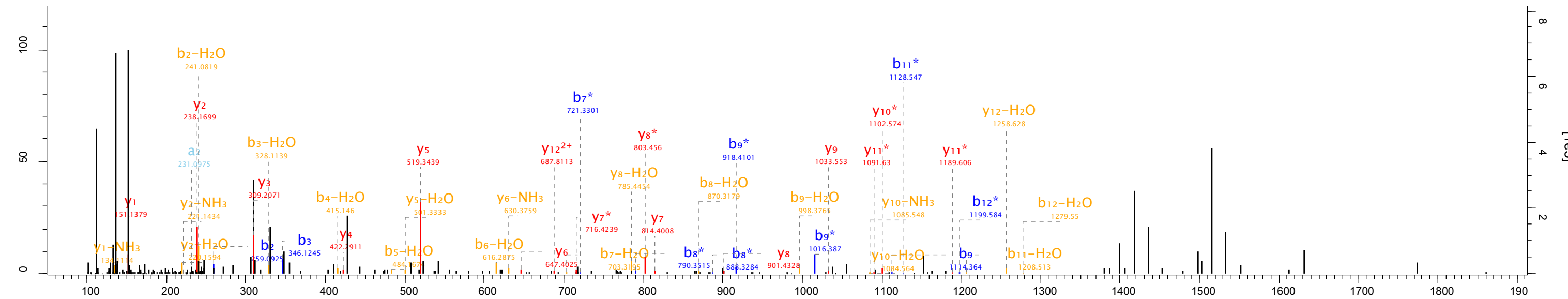
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3433	FTMS; HCD	45.75	812.95	MAGED2



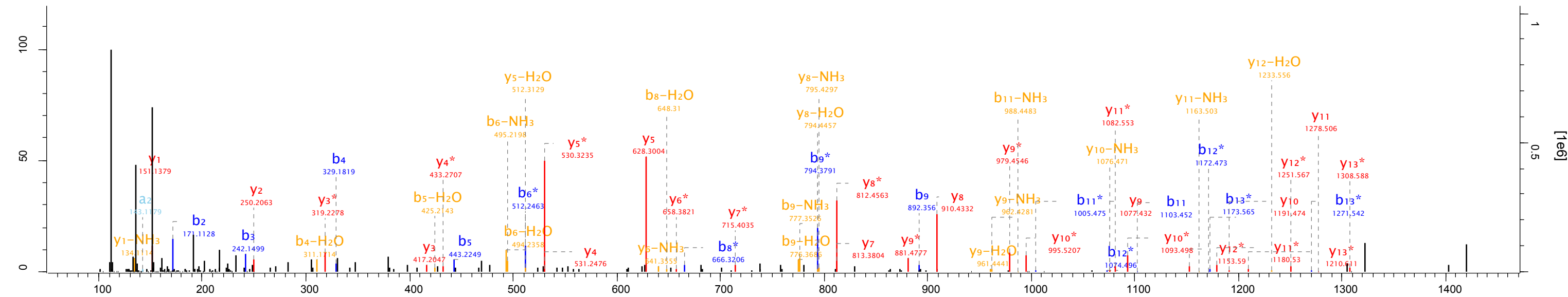
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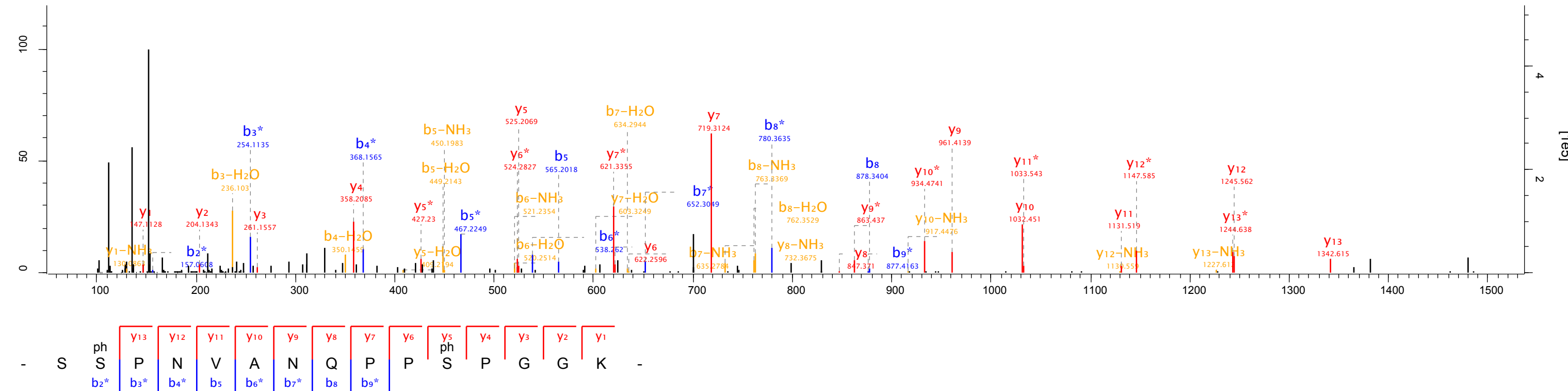


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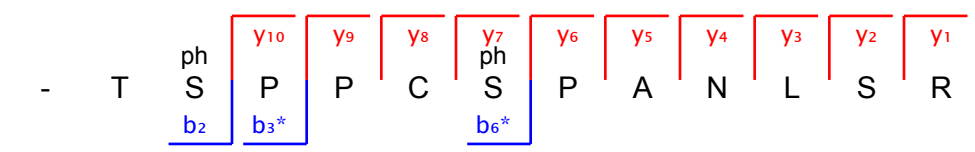
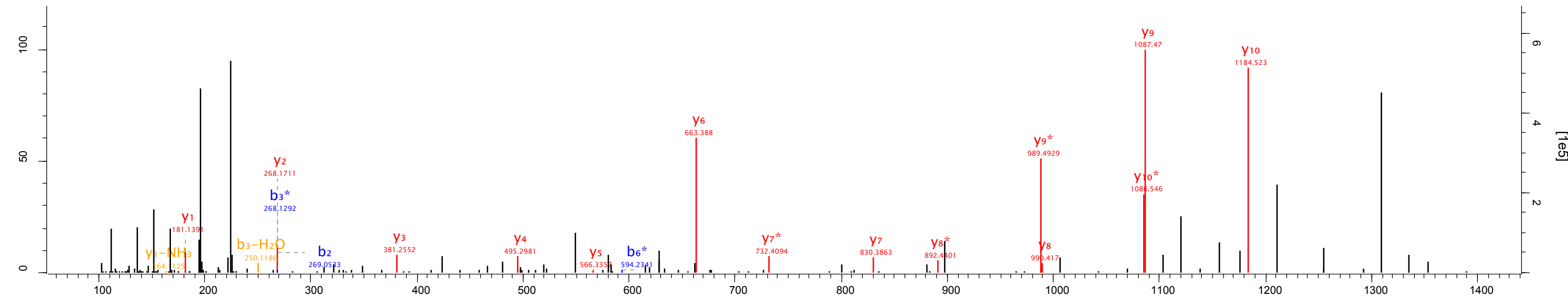


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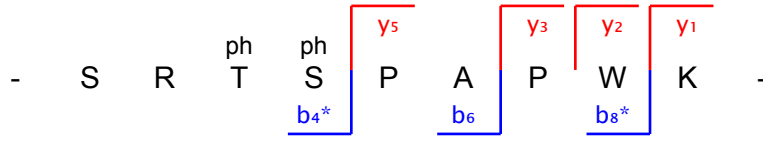
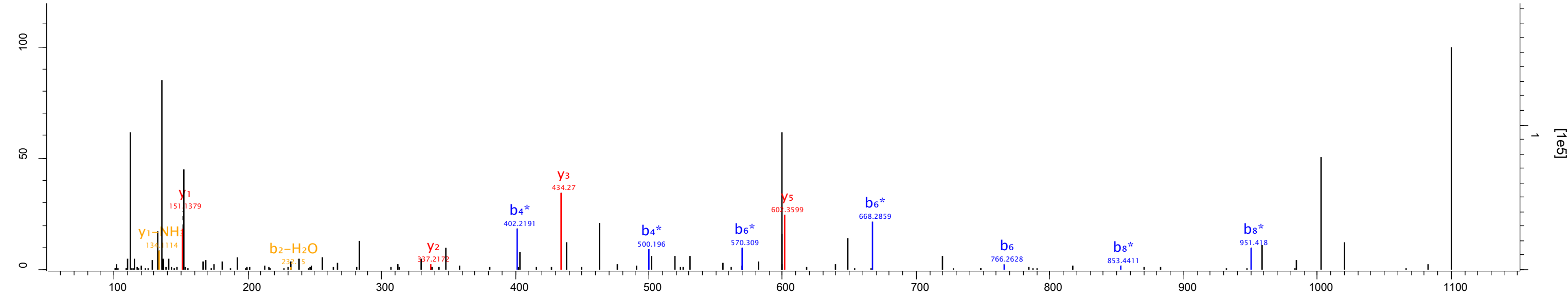
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Raw file

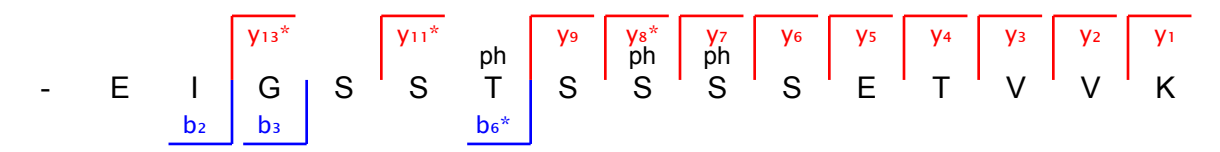
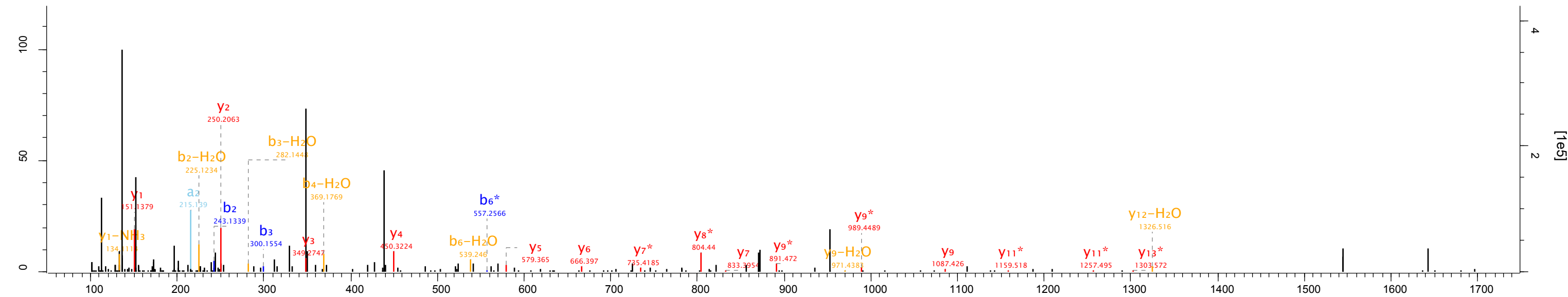
20171215_MaS_33SR_LMH_phospho2_04

Scan	Method	Score	m/z	Gene names
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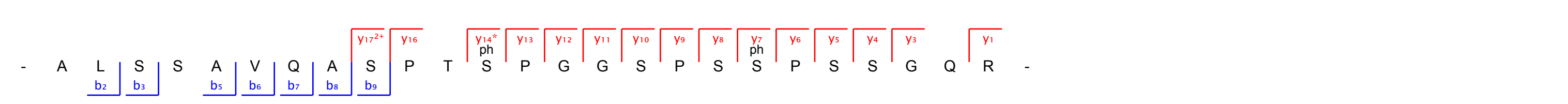
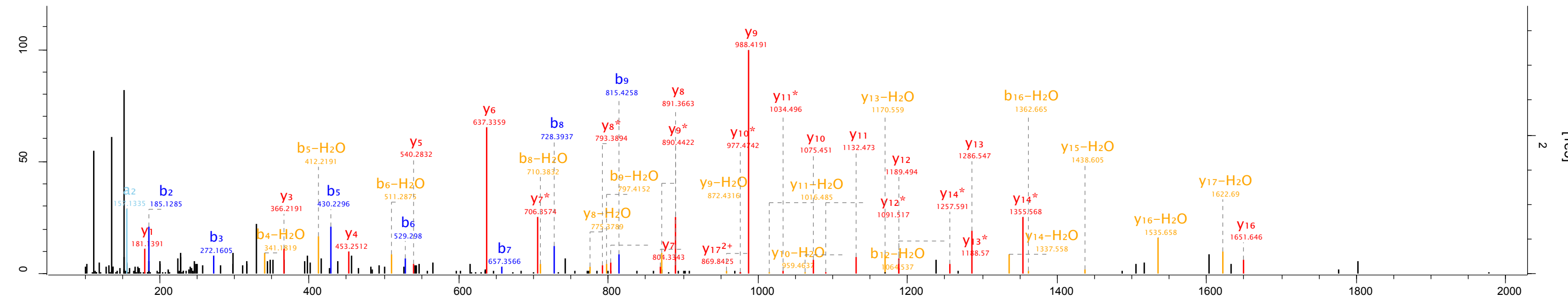


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20171215_MaS_33SR_LMH_phospho2_04

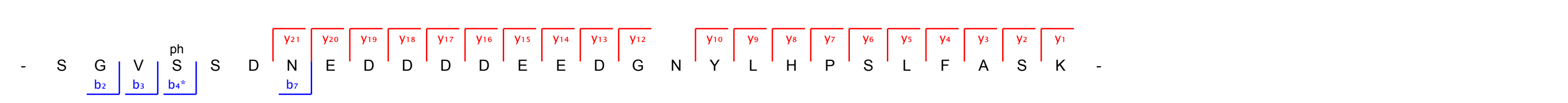
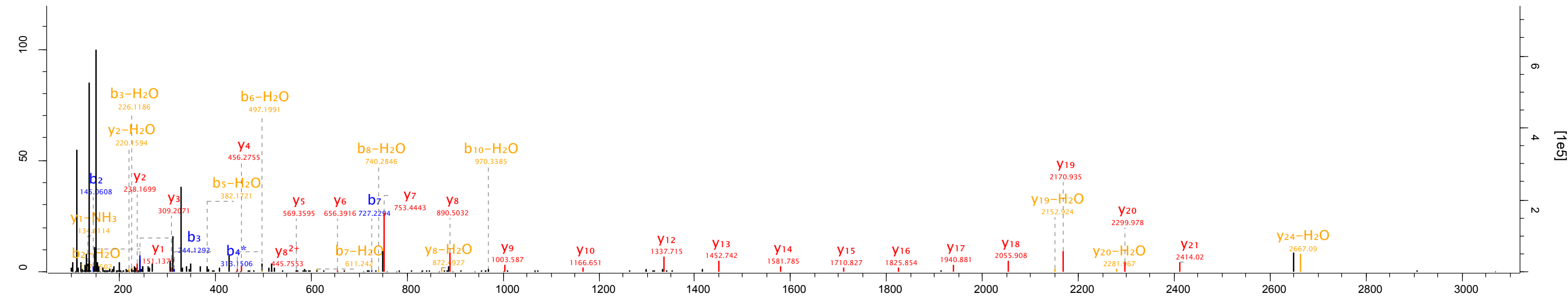
Scan 6273 Method FTMS; HCD Score 56.88 m/z 871.32 Gene names FRMD6



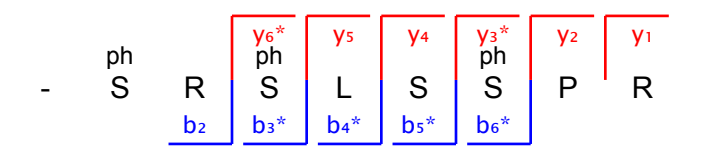
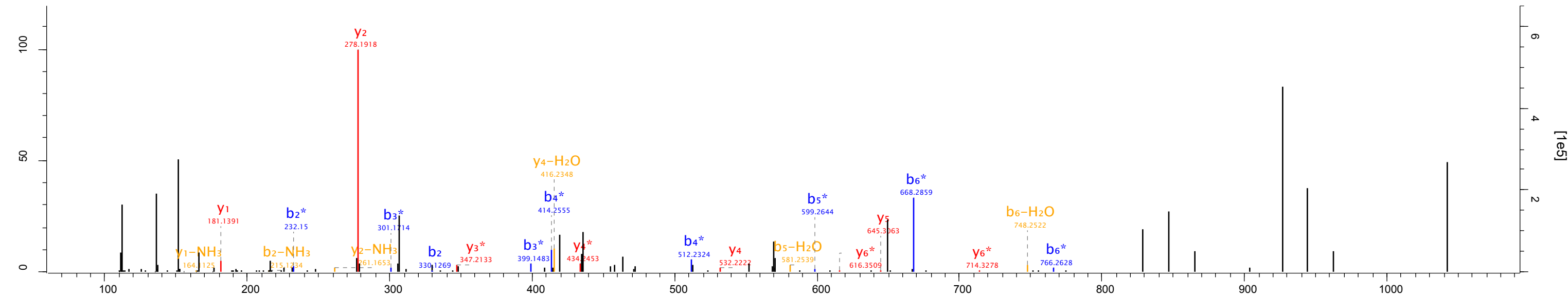
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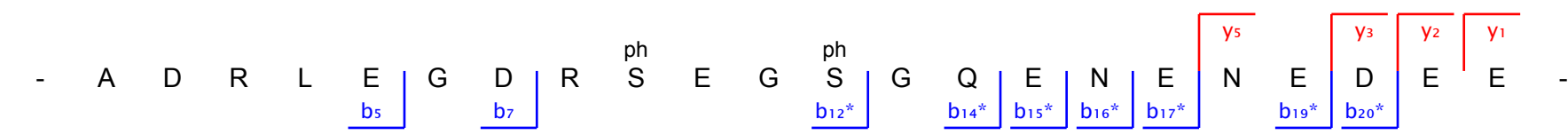
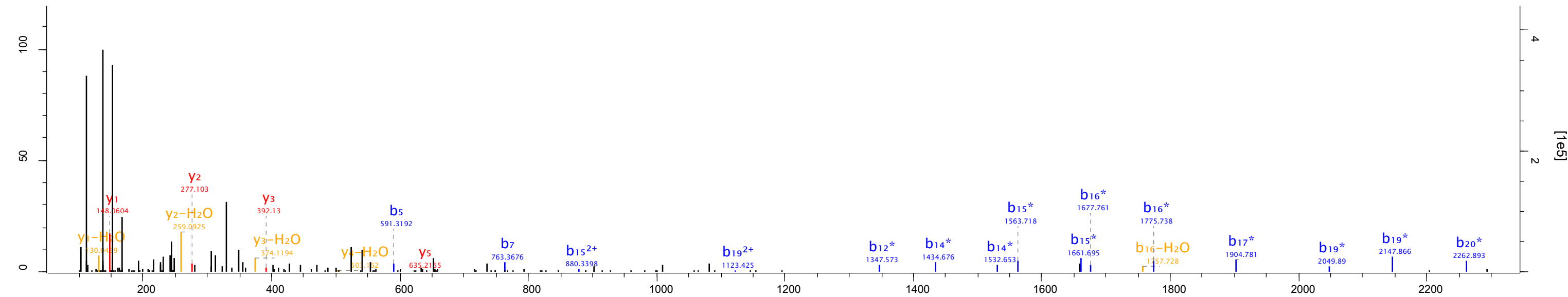
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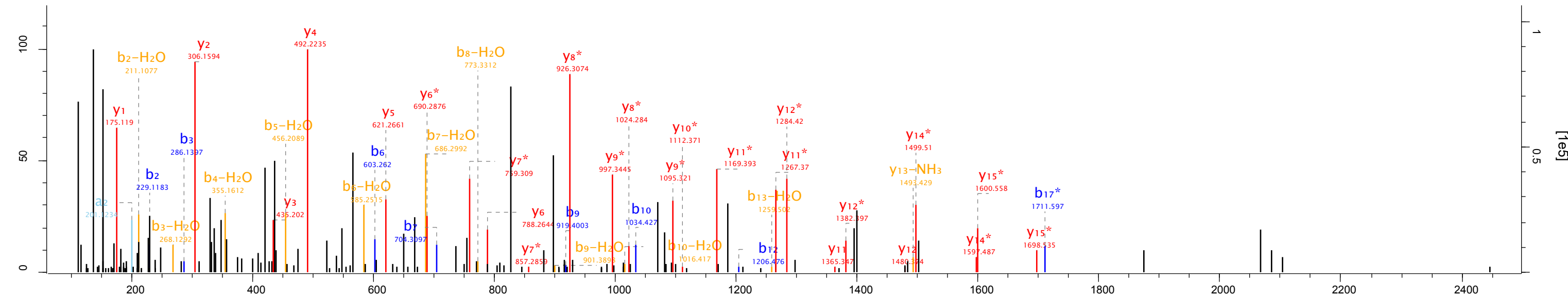


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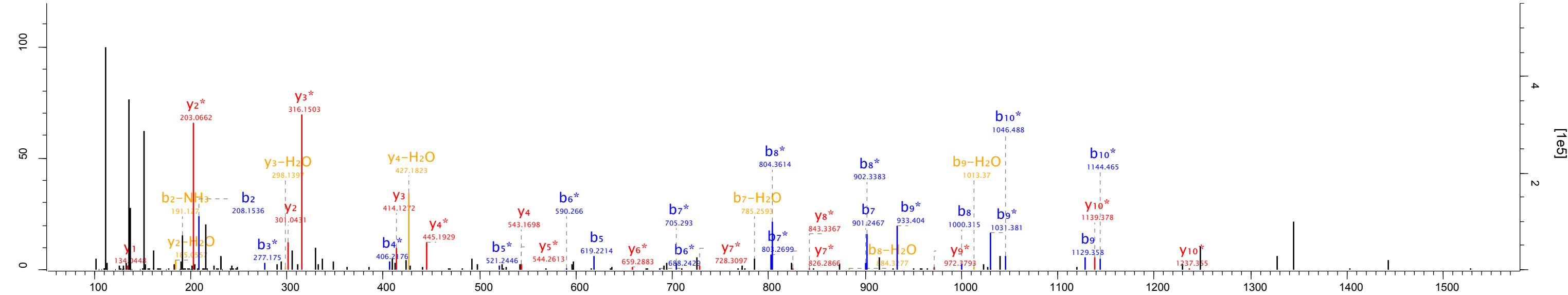


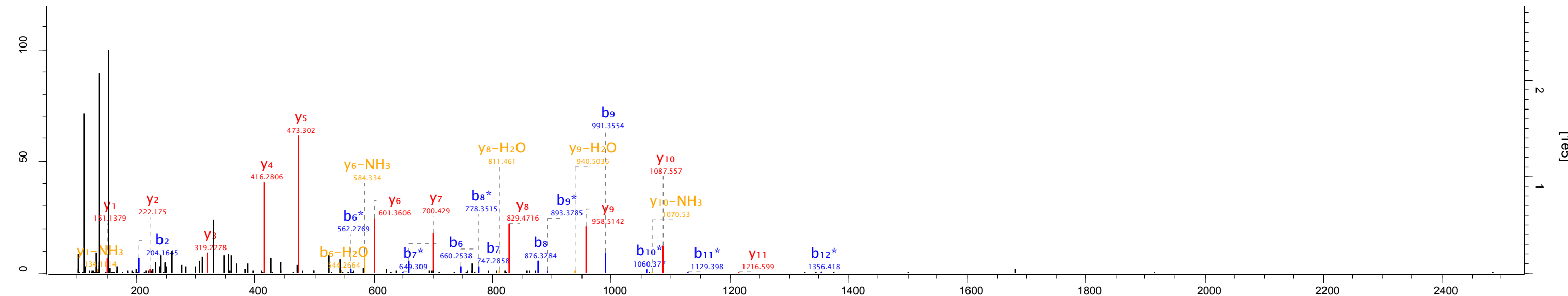


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20171215_MaS_33SR_LMH_phospho2_05 4763 FTMS; HCD 136.62 771.74 ZMYM4



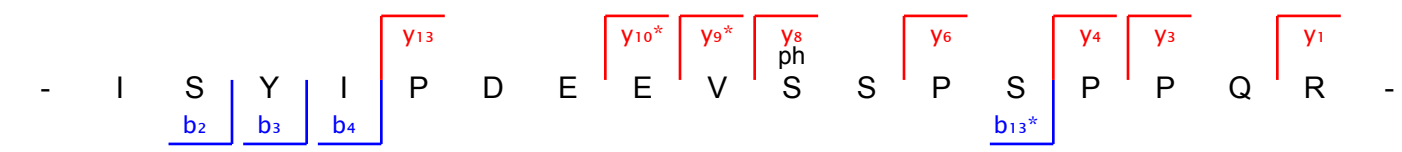
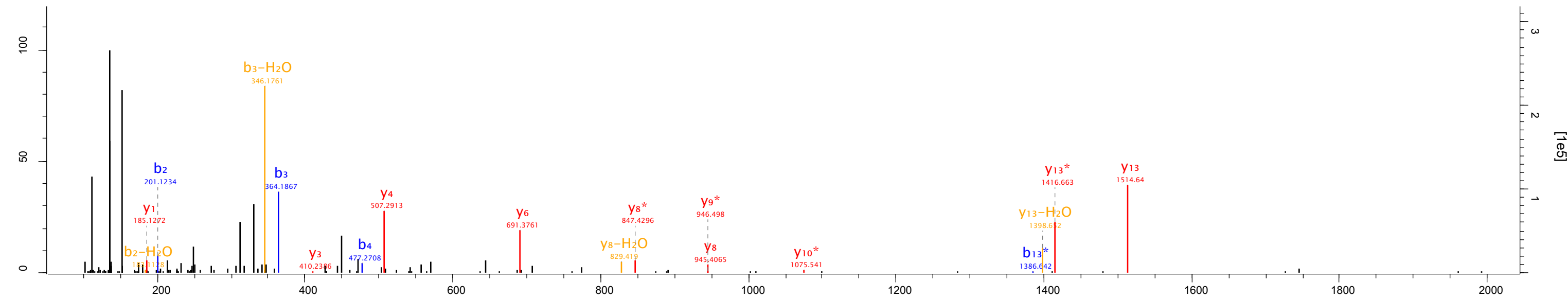


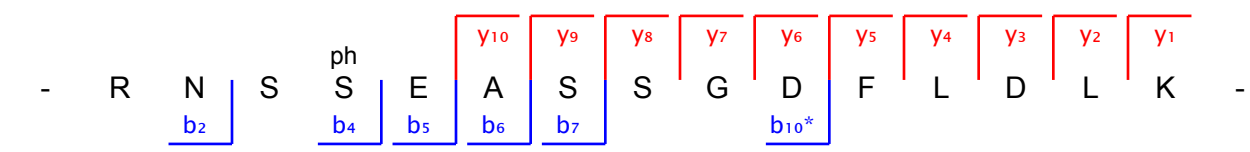
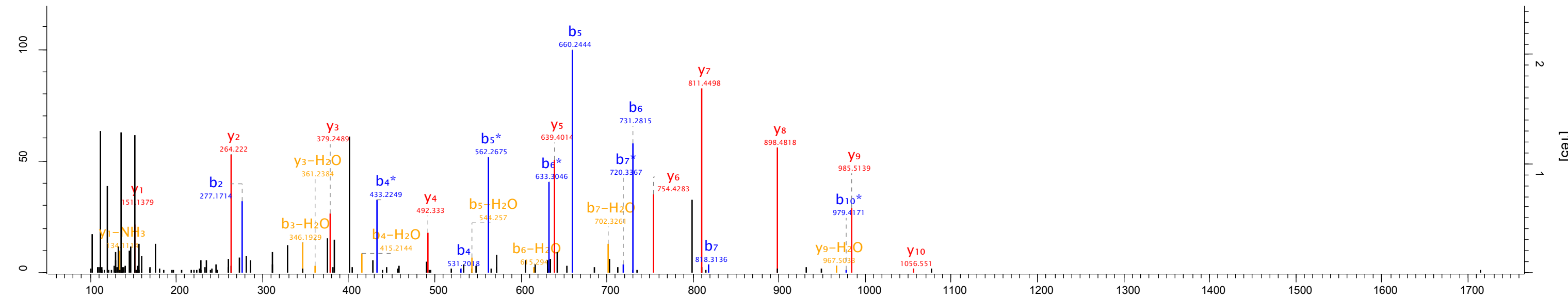
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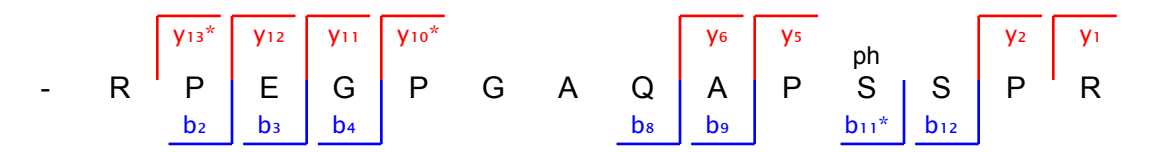
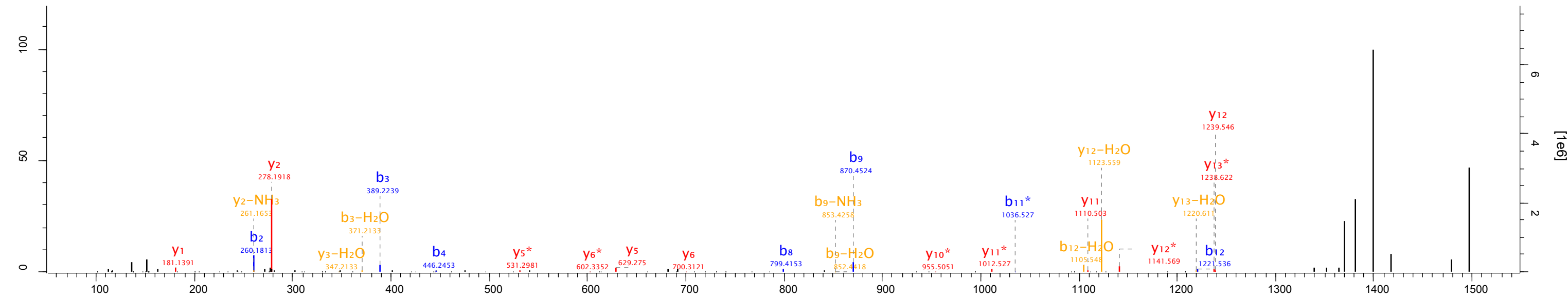
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20171215_MaS_33SR_LMH_phospho2_06

Scan 11143 Method FTMS; HCD Score 41.62 m/z 996.45 Gene names IGF2BP2

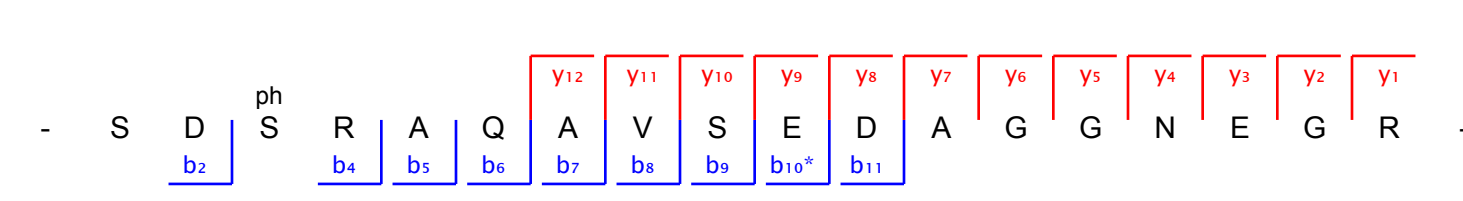
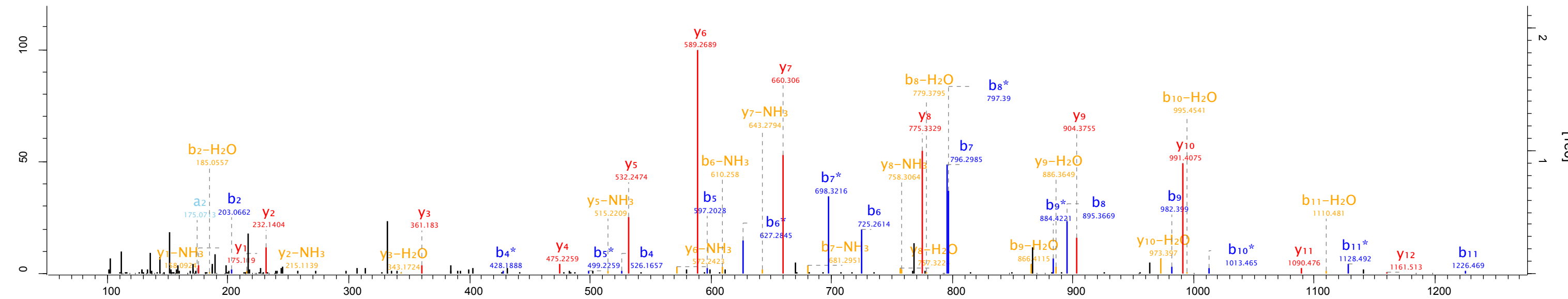




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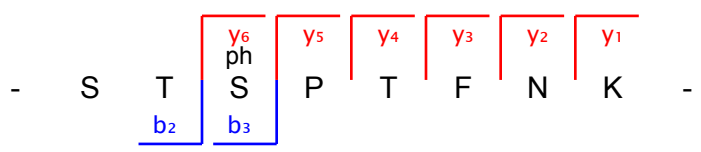
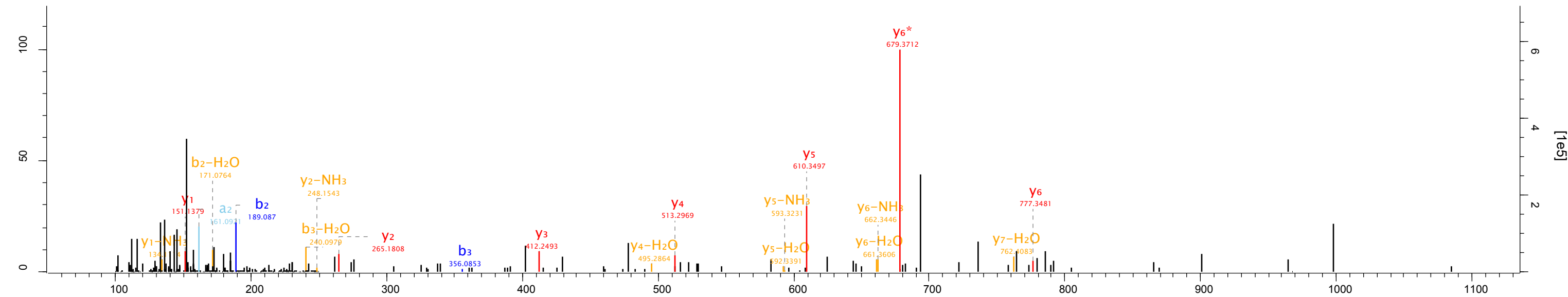


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Raw file
20171215_MaS_33SR_LMH_phospho2_06

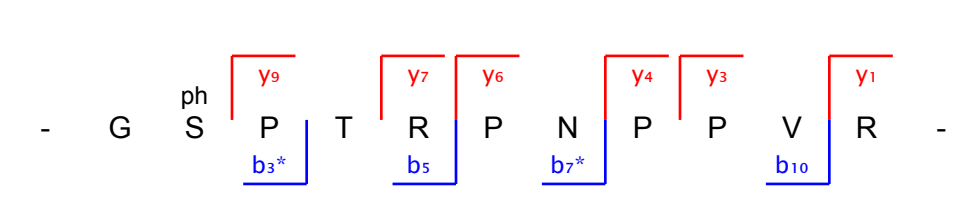
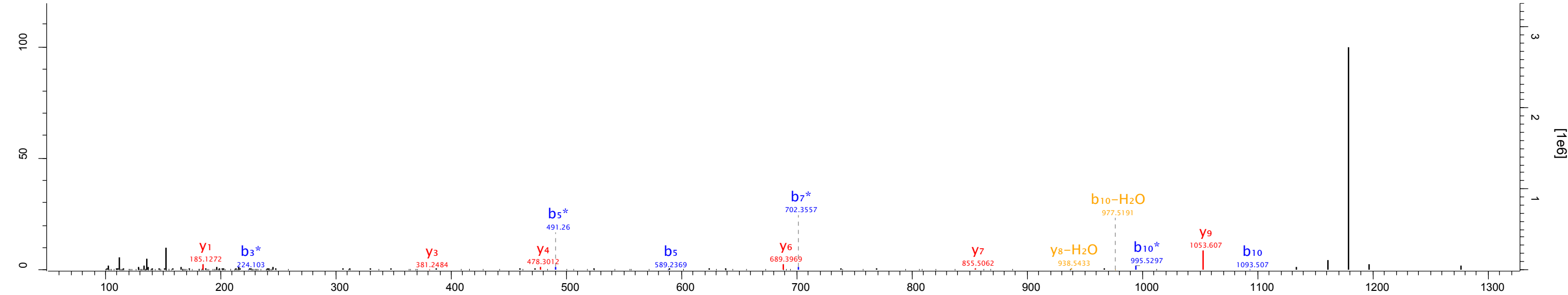
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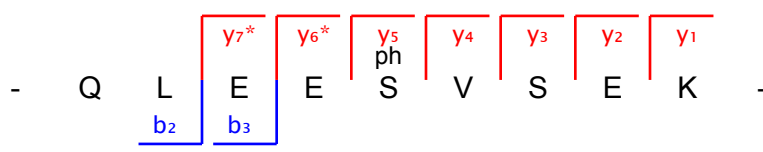
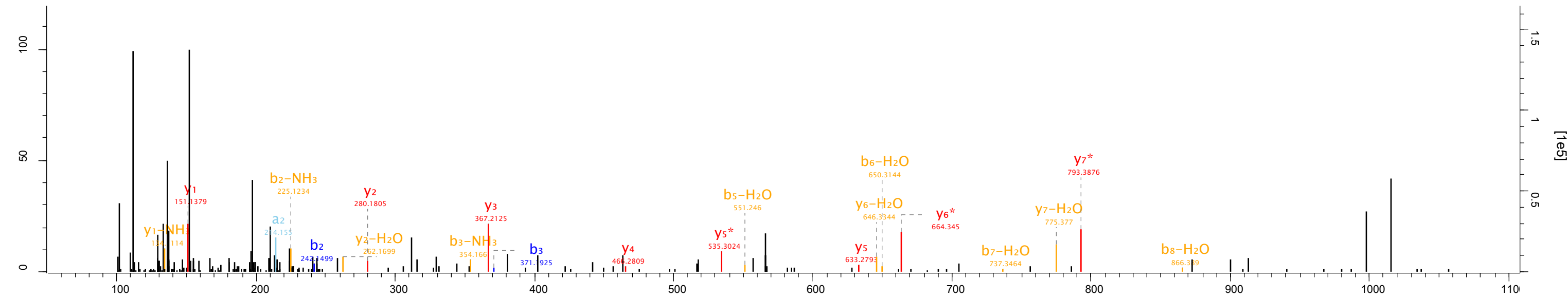
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20171215_MaS_33SR_LMH_phospho2_06

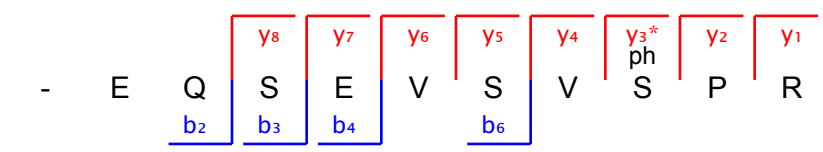
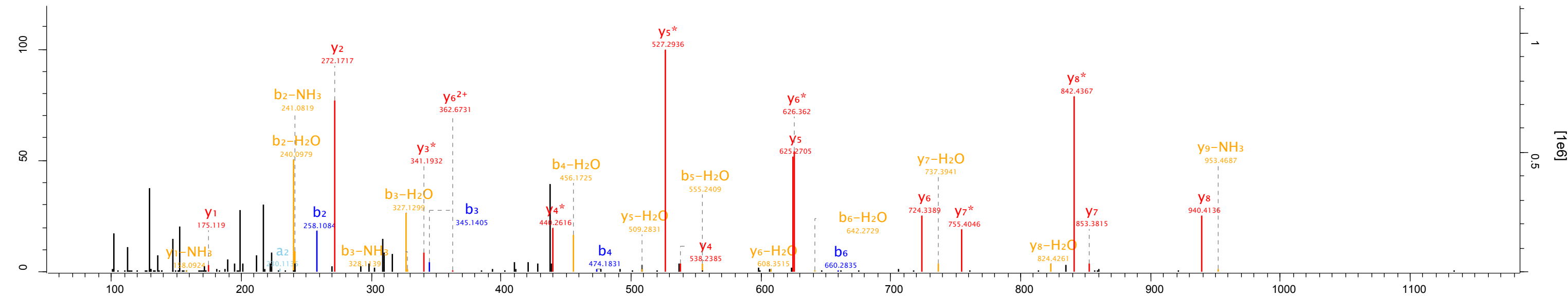
Scan	Method	Score	m/z	Gene names
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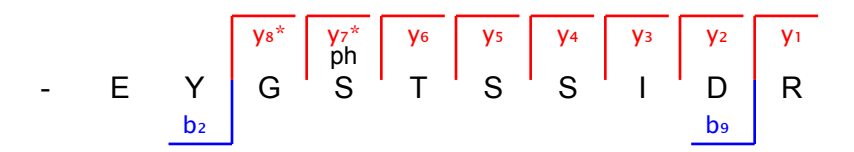
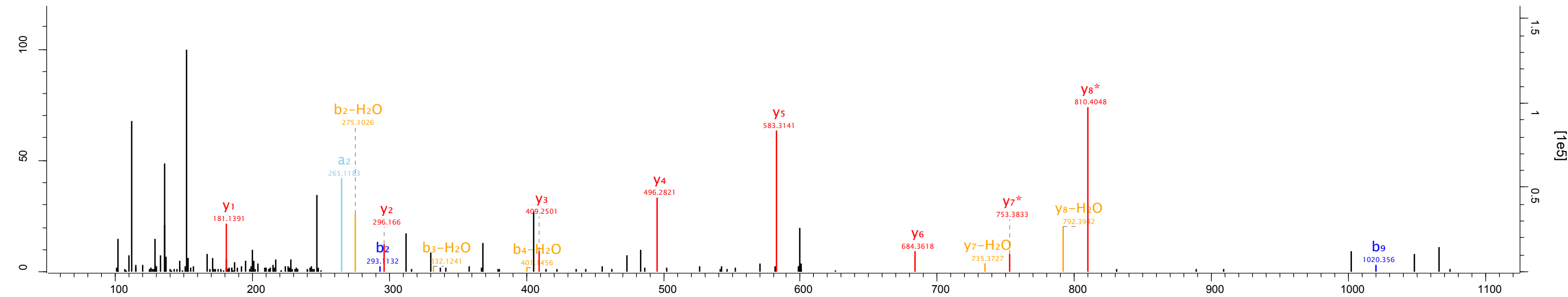
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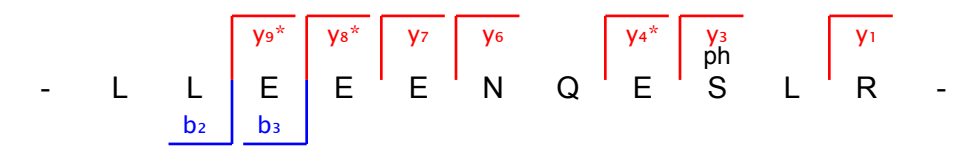
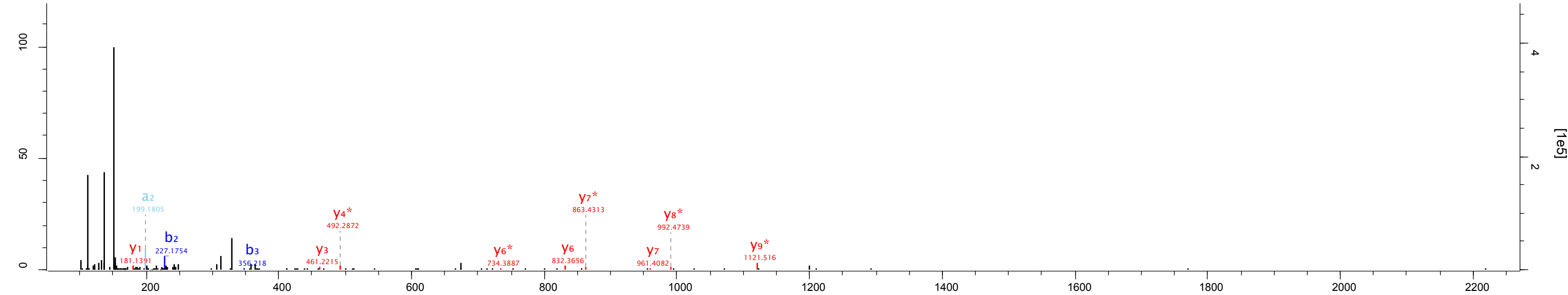
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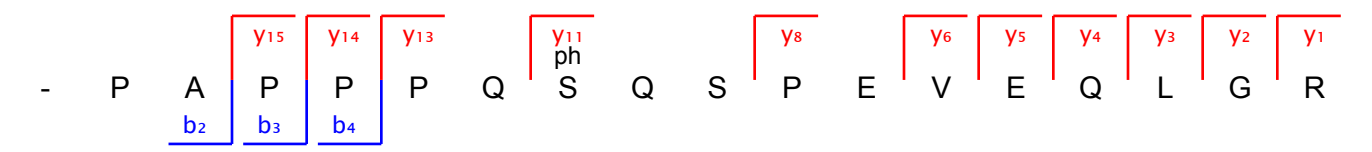
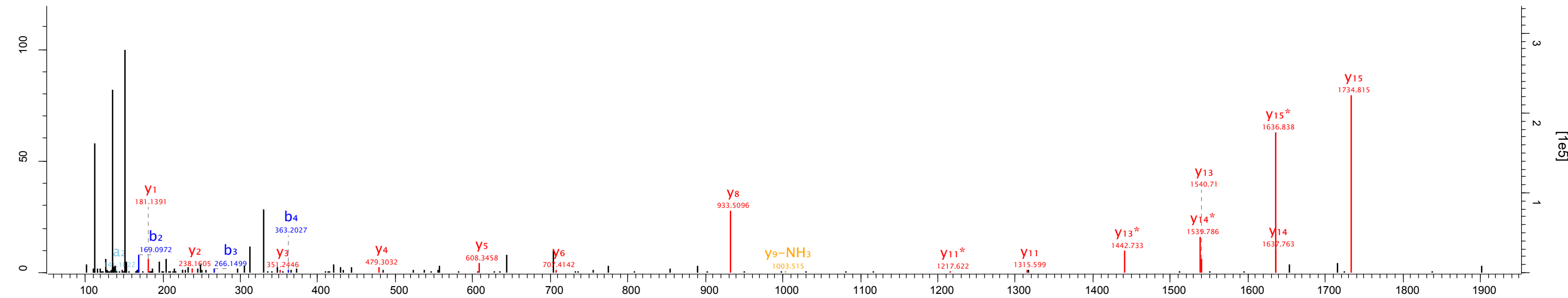
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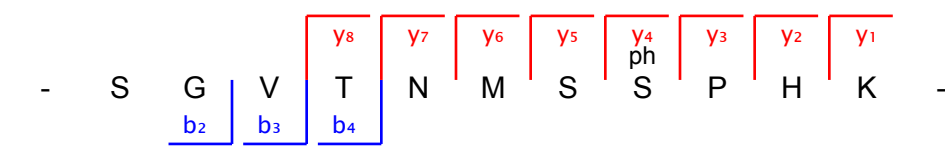
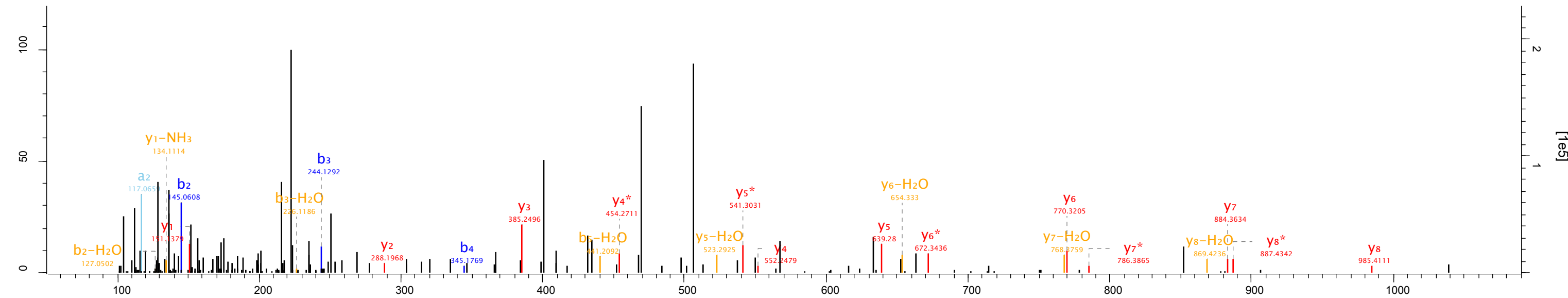
20171215_MaS_33SR_LMH_phospho2_06

Scan	Method	Score	m/z	Gene names
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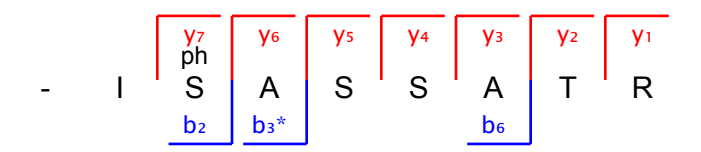
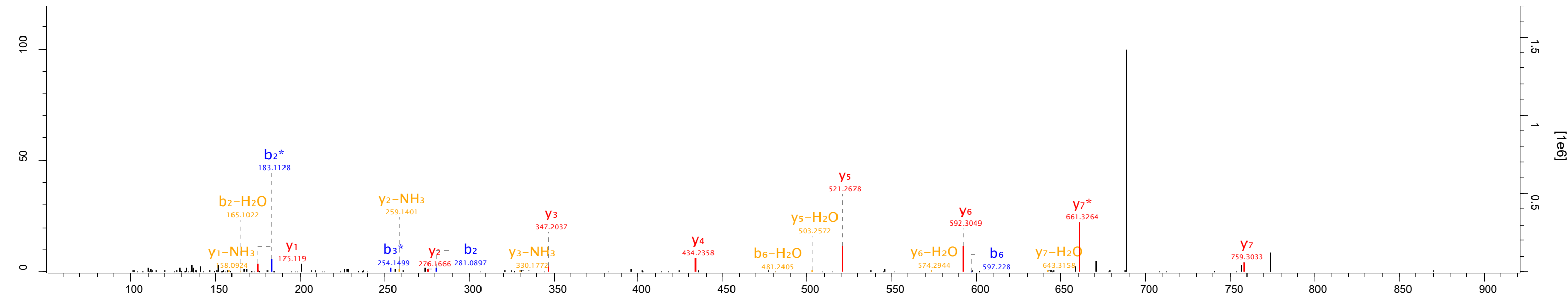


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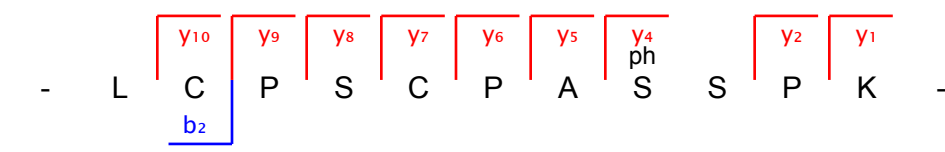
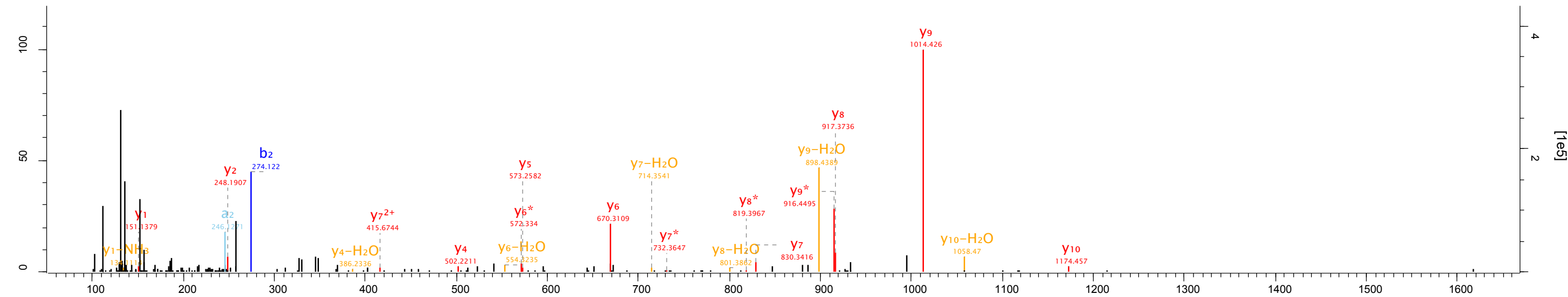




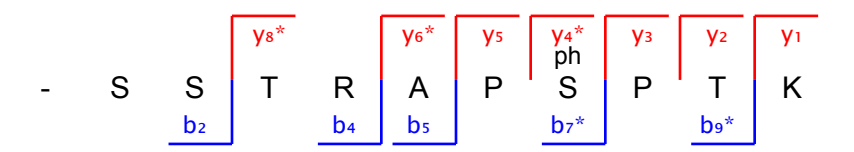
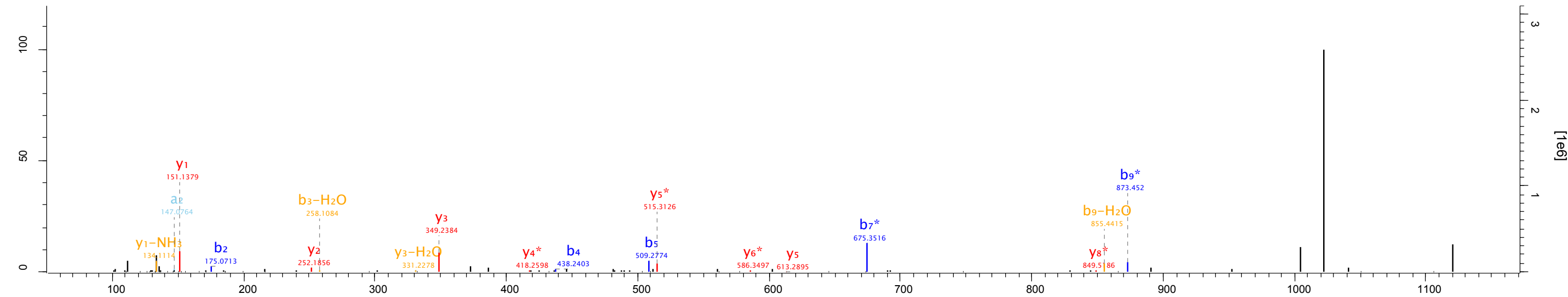
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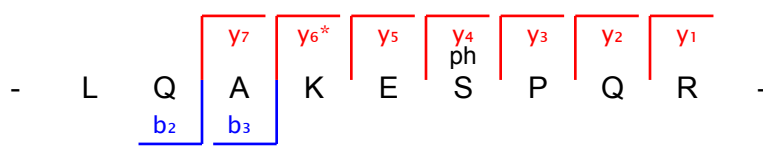
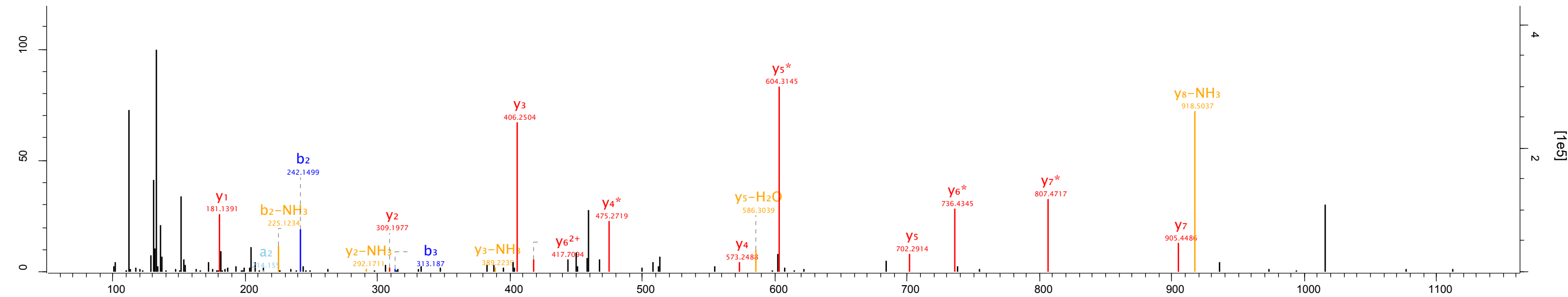
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Raw file

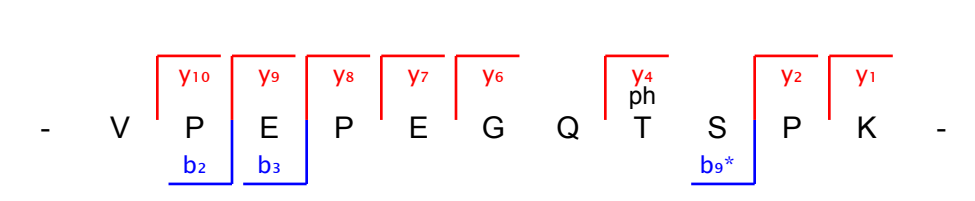
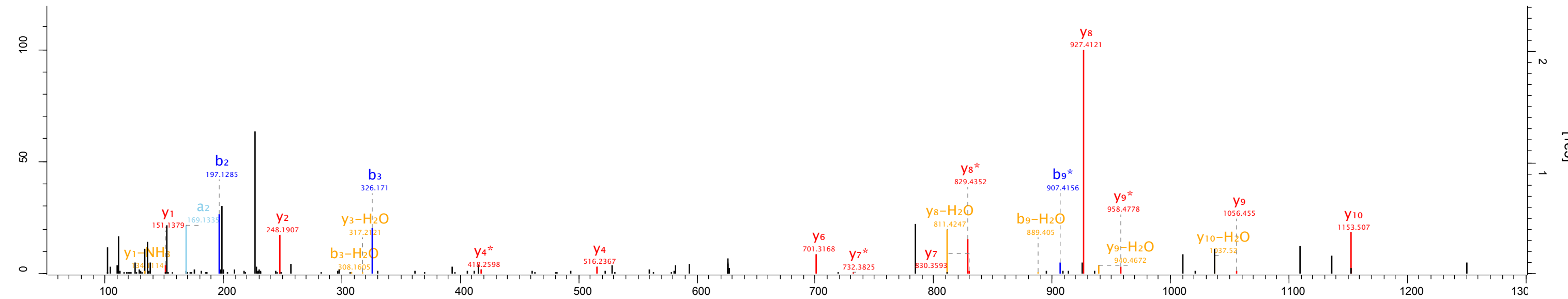
20171215_MaS_33SR_LMH_phospho2_09

Scan	Method	Score	m/z	Gene names
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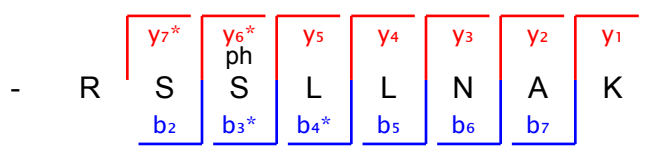
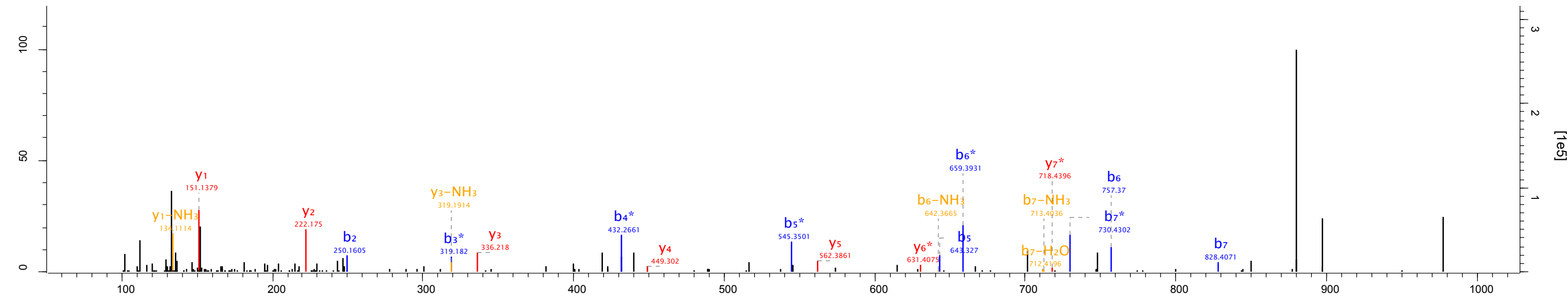


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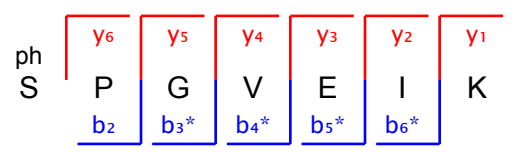
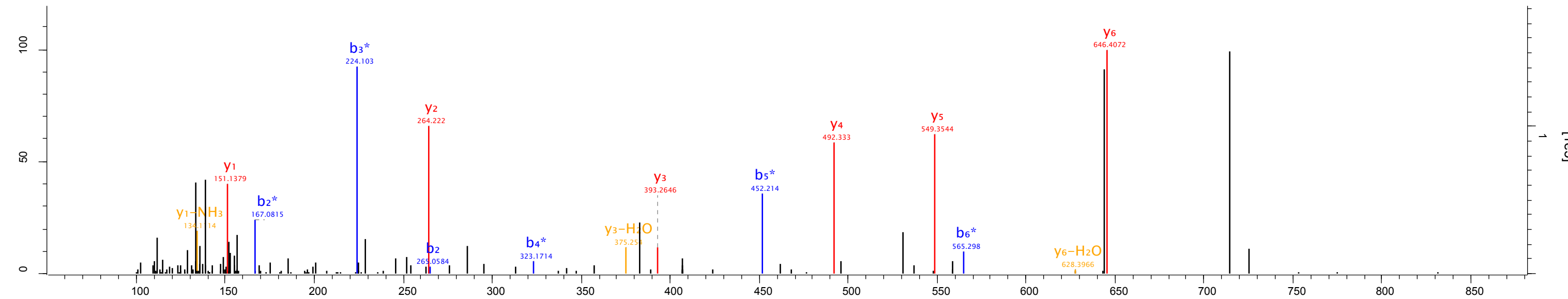
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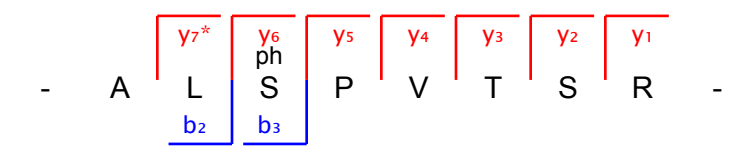
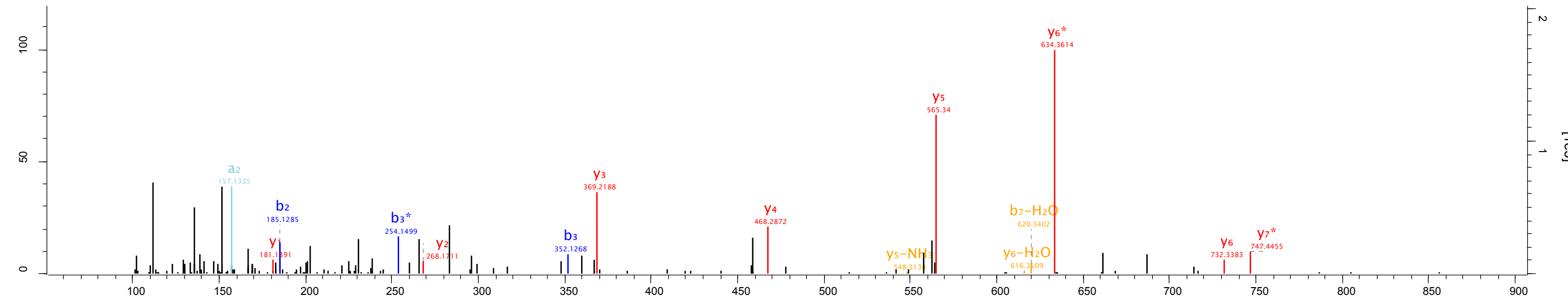
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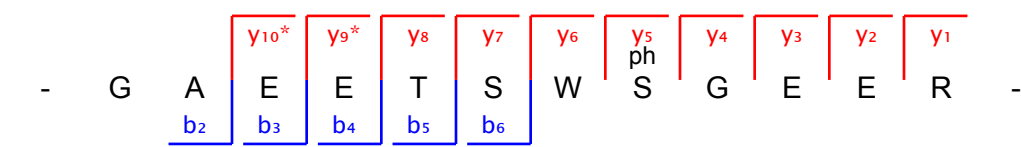
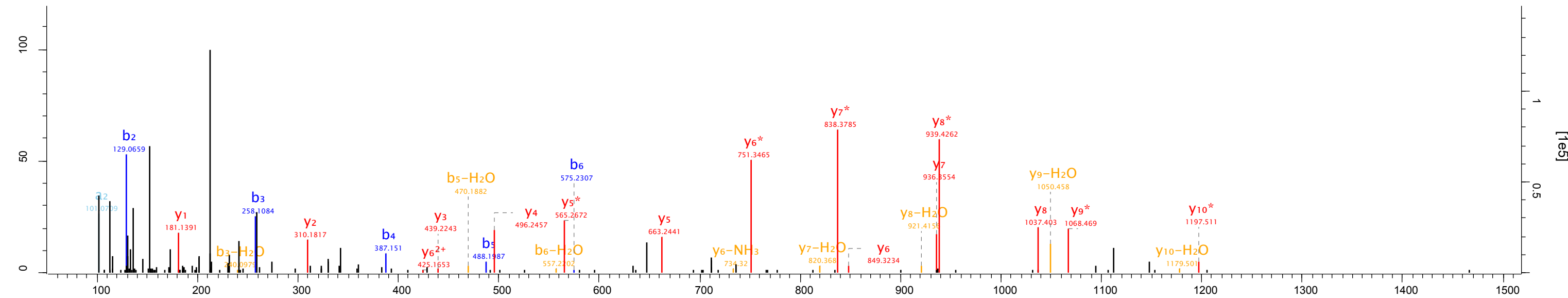


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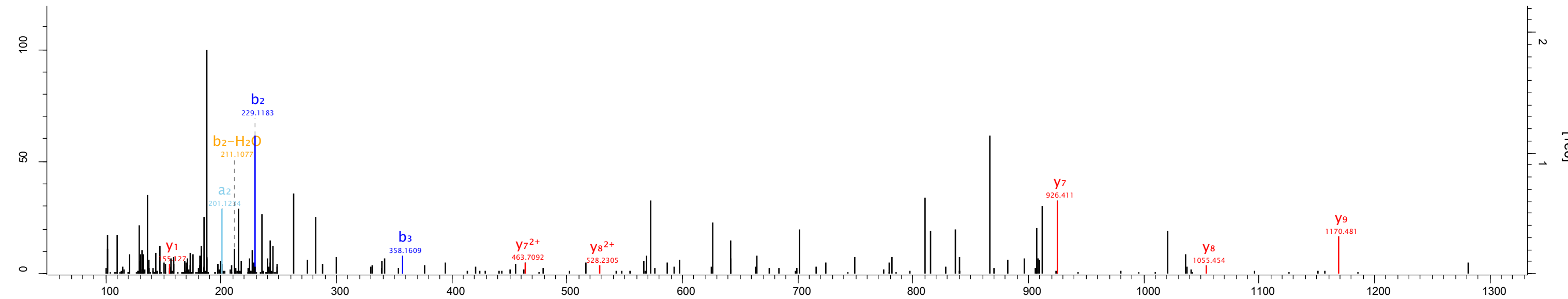


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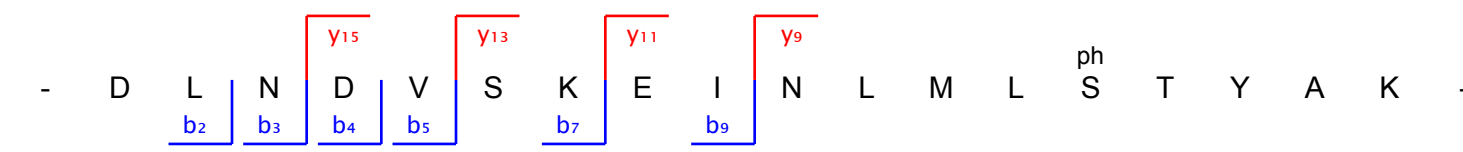
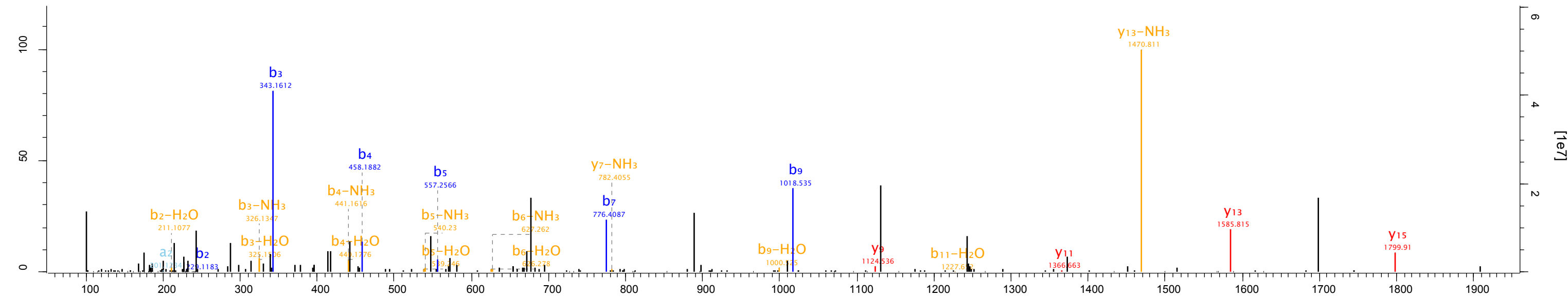




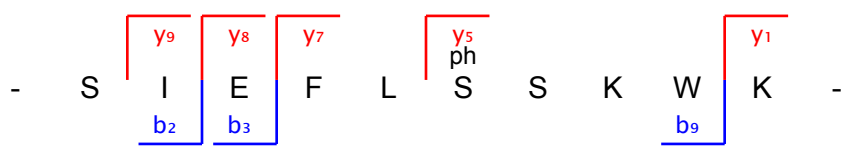
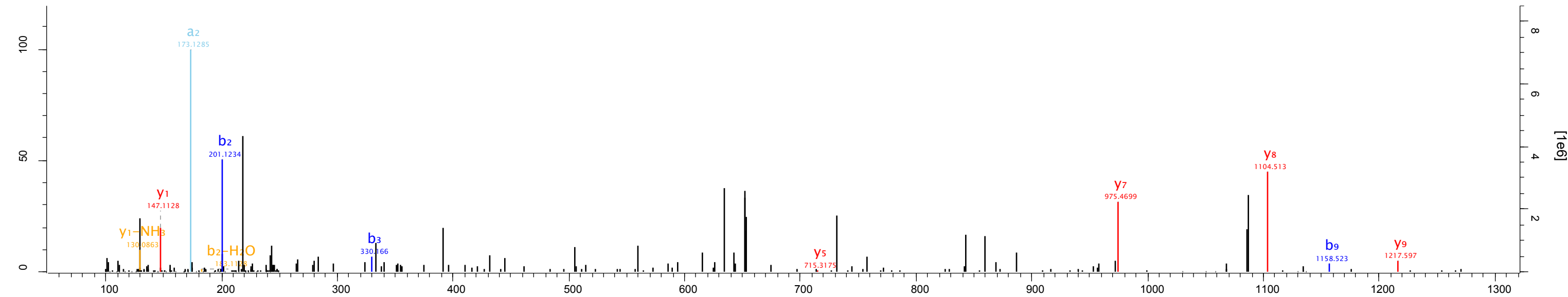
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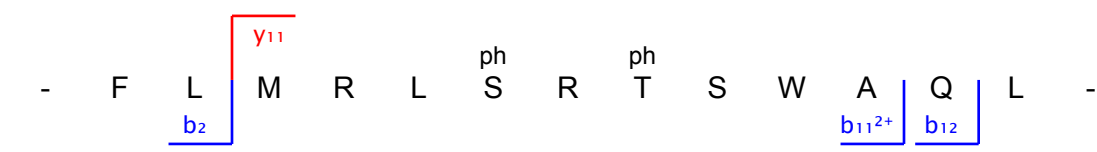
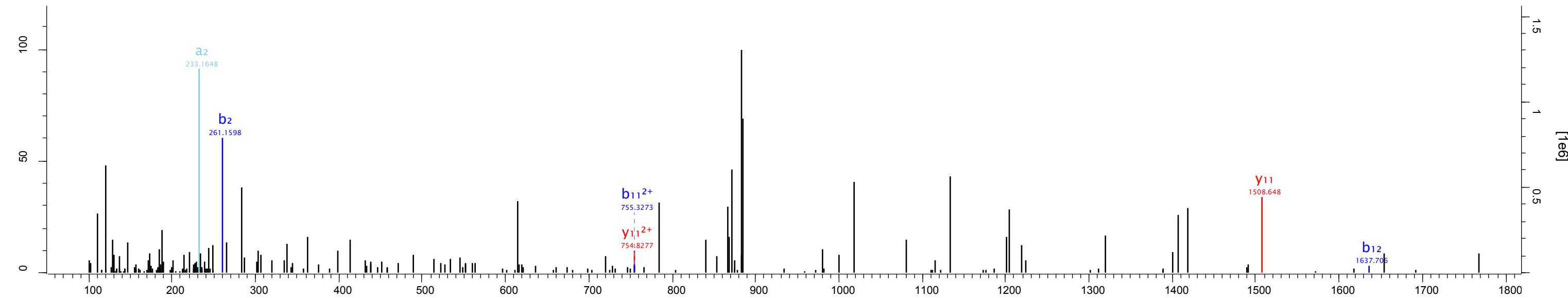
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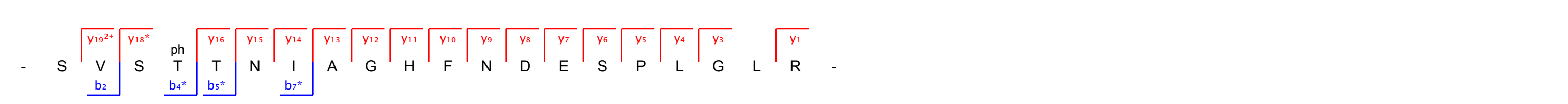
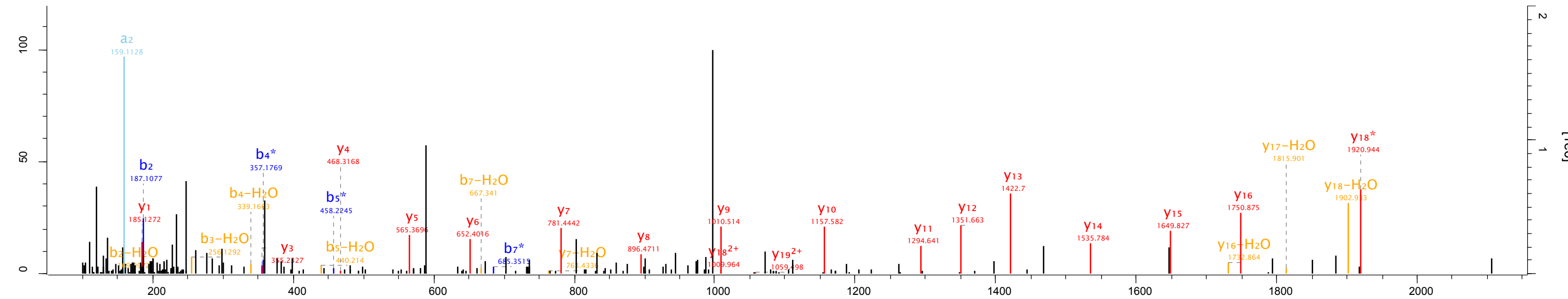
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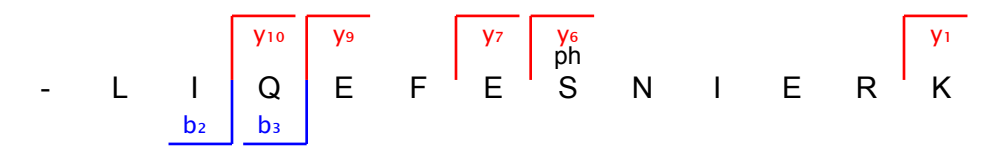
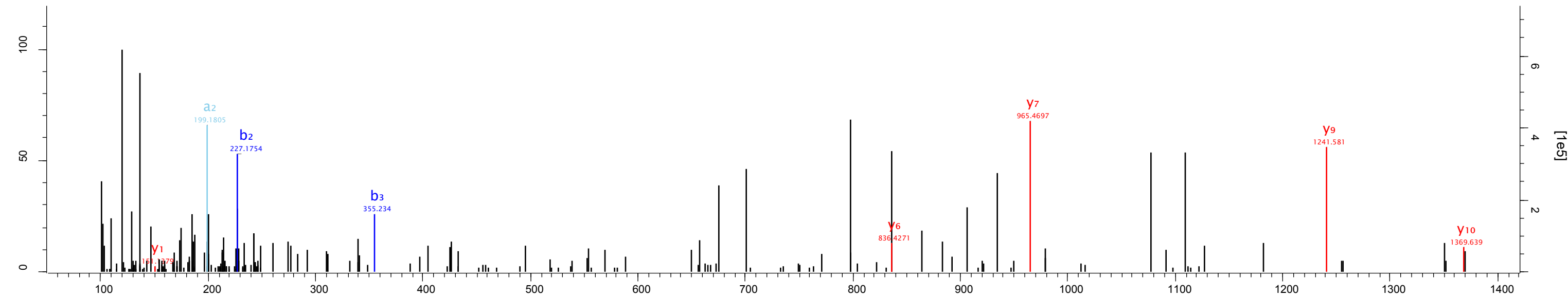
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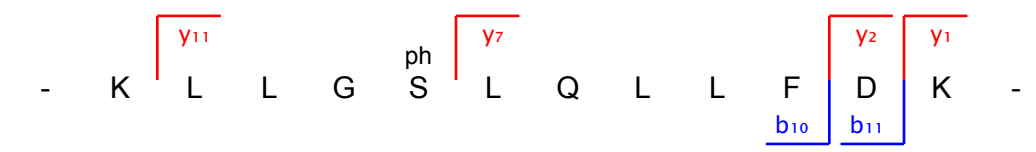
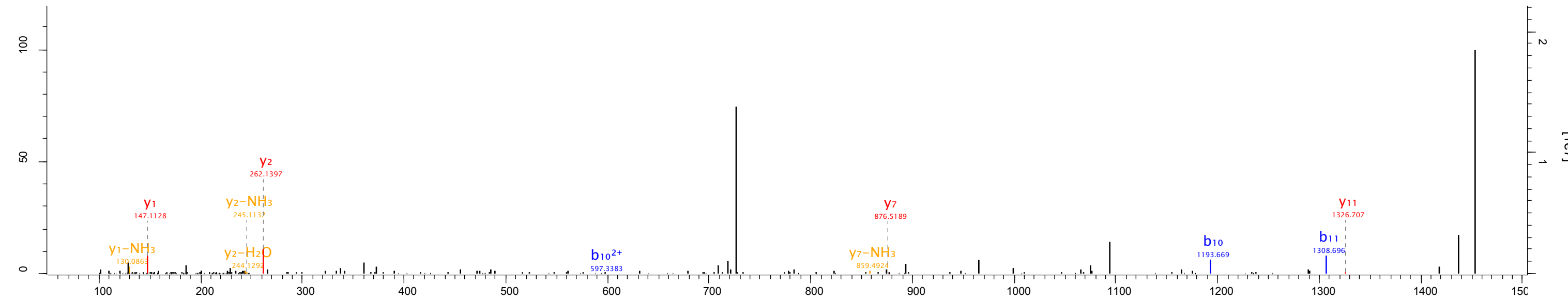
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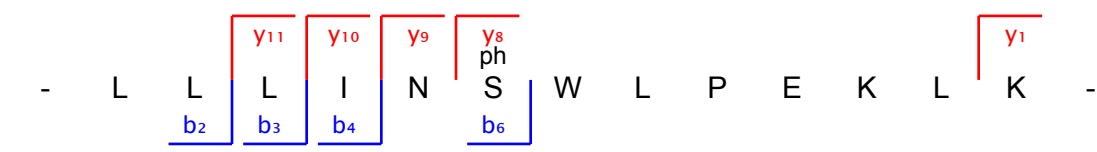
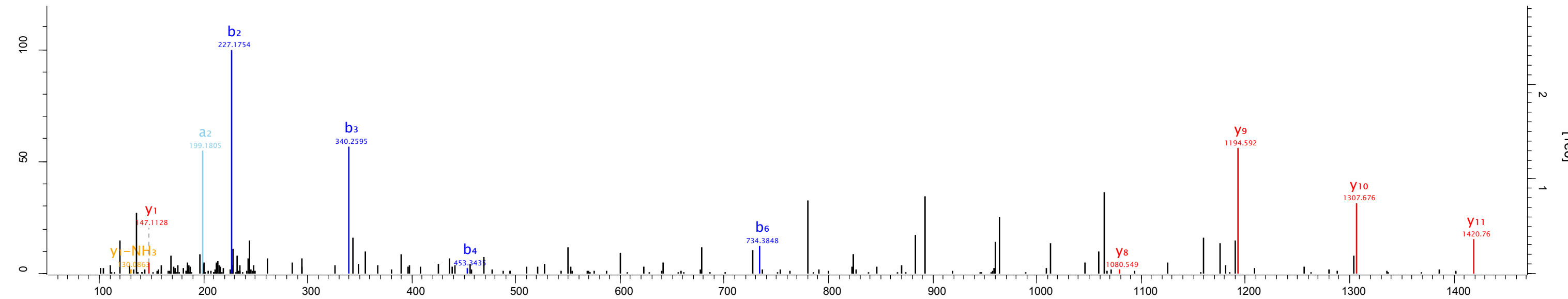
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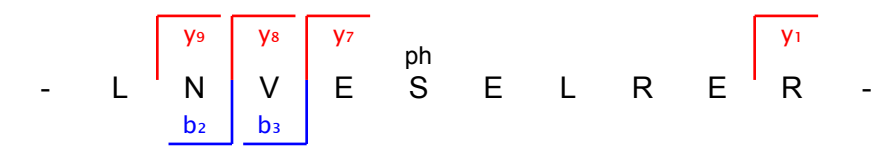
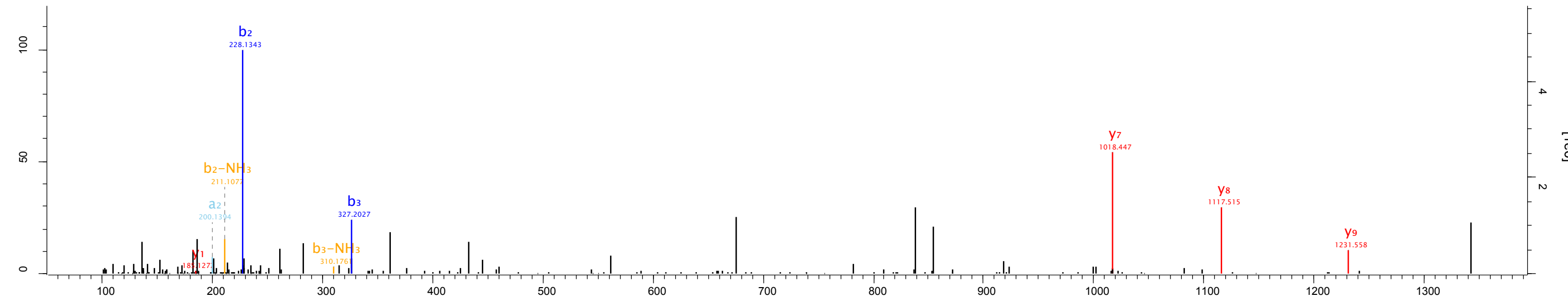
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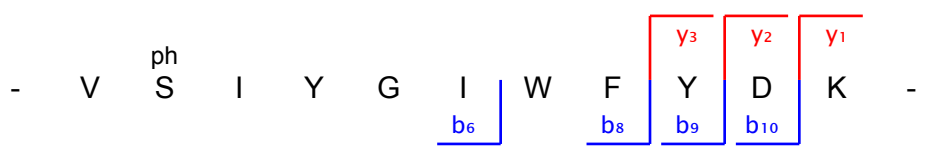
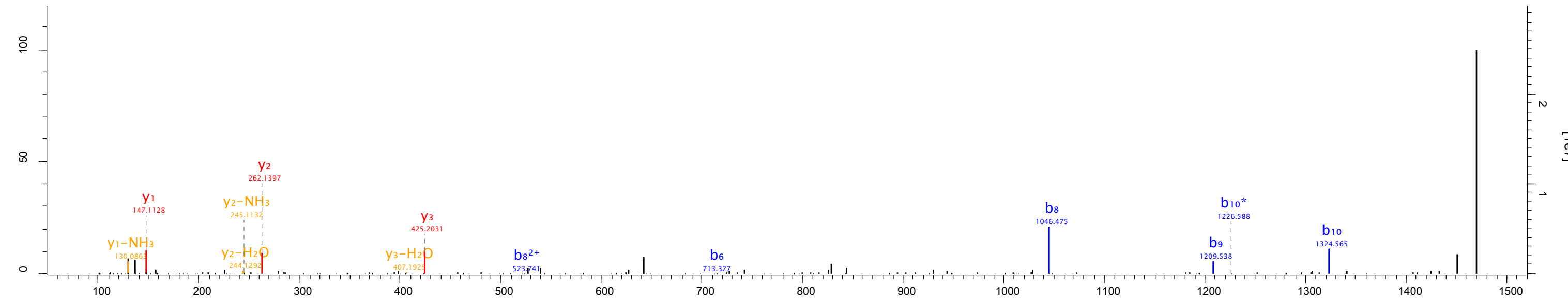
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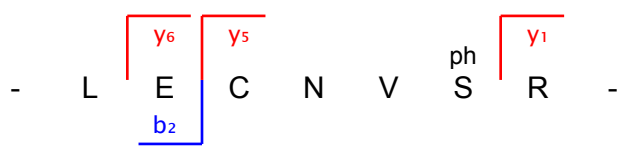
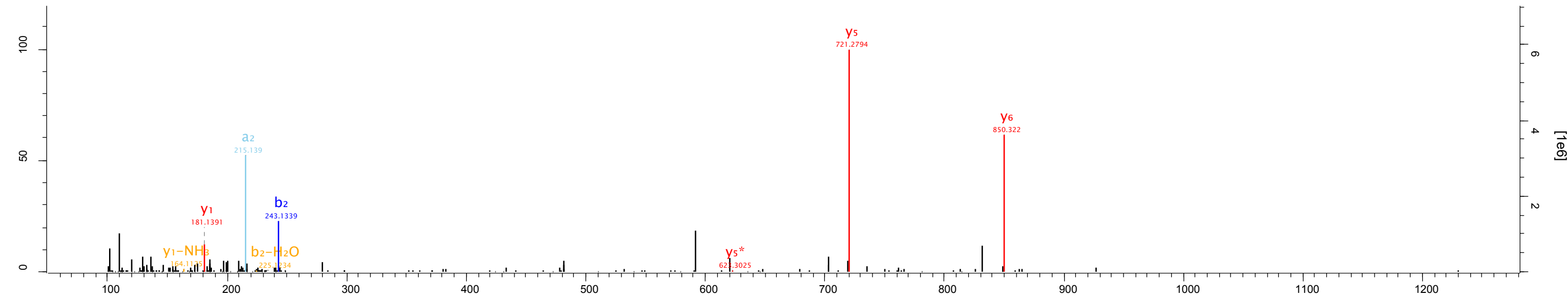
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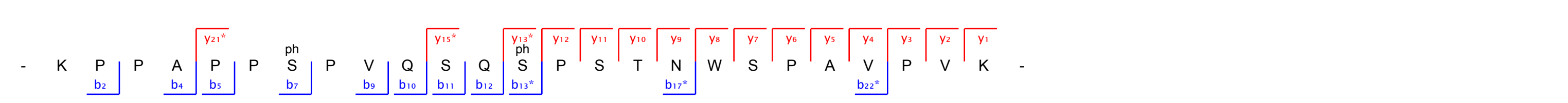
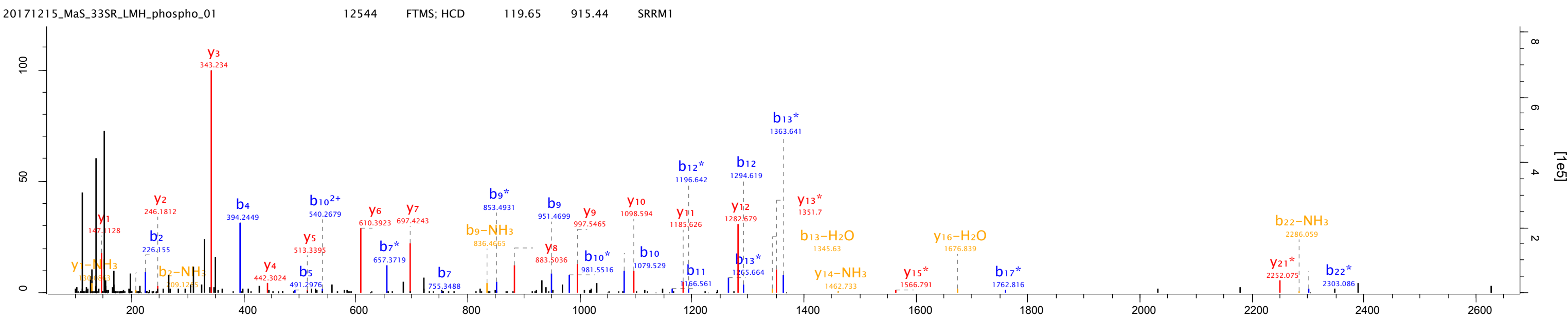
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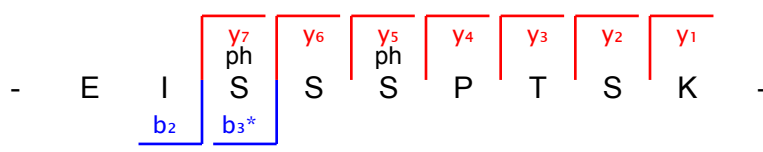
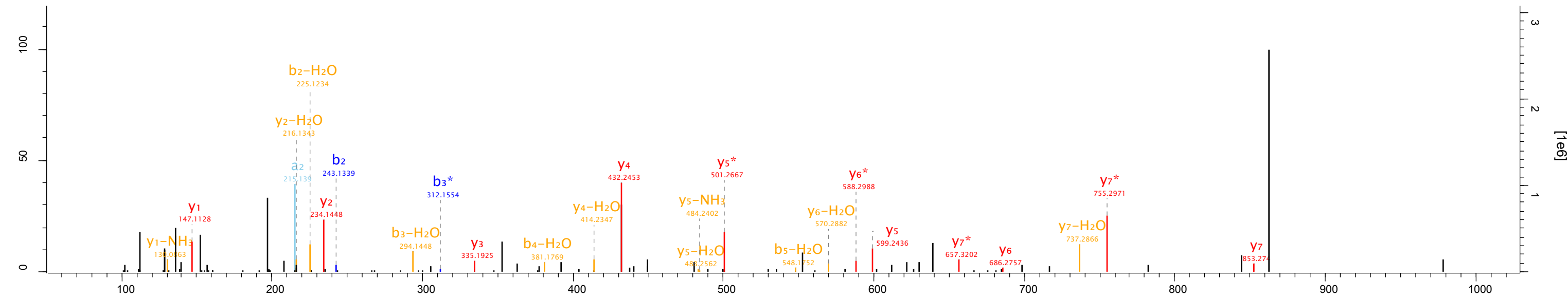
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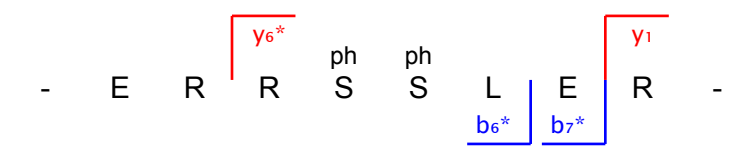
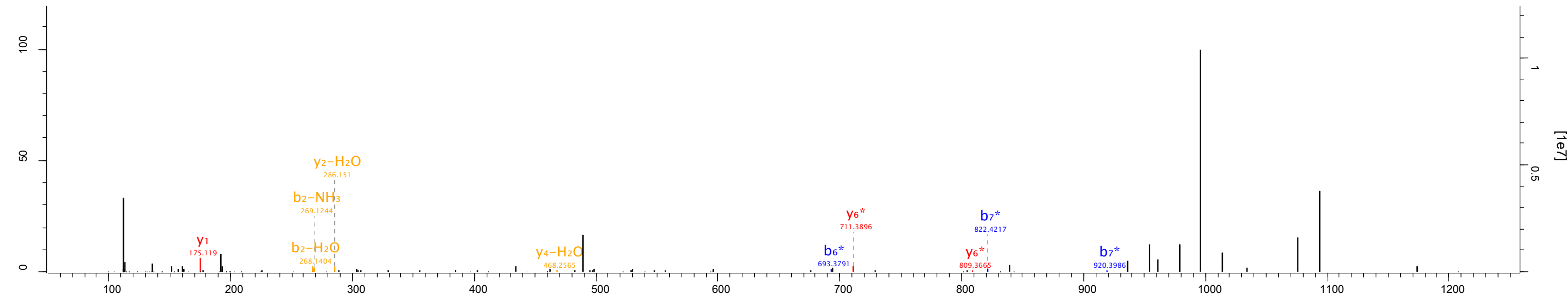
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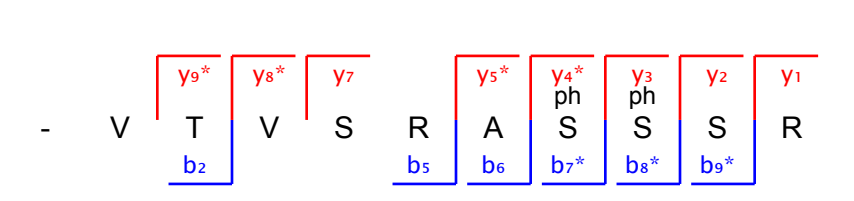
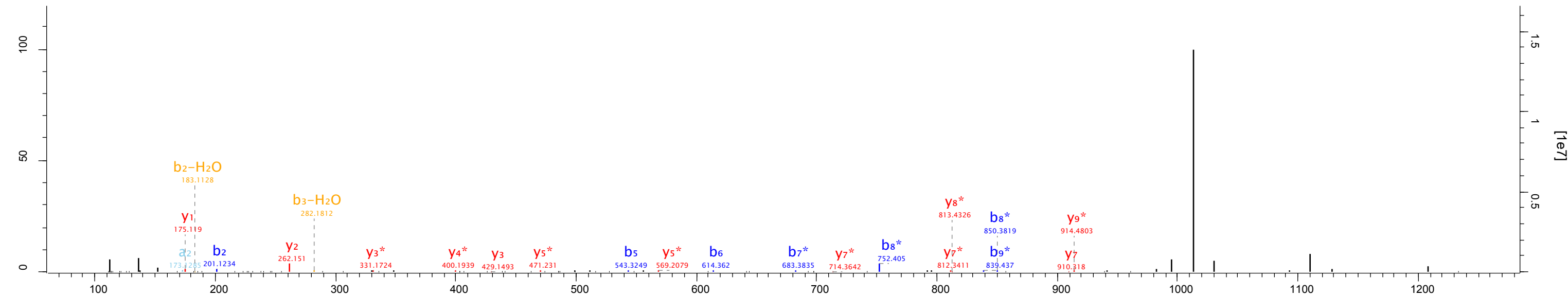


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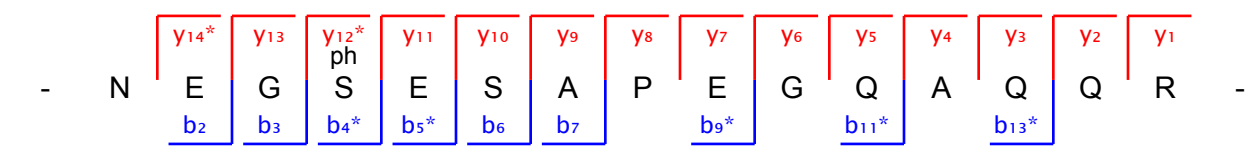
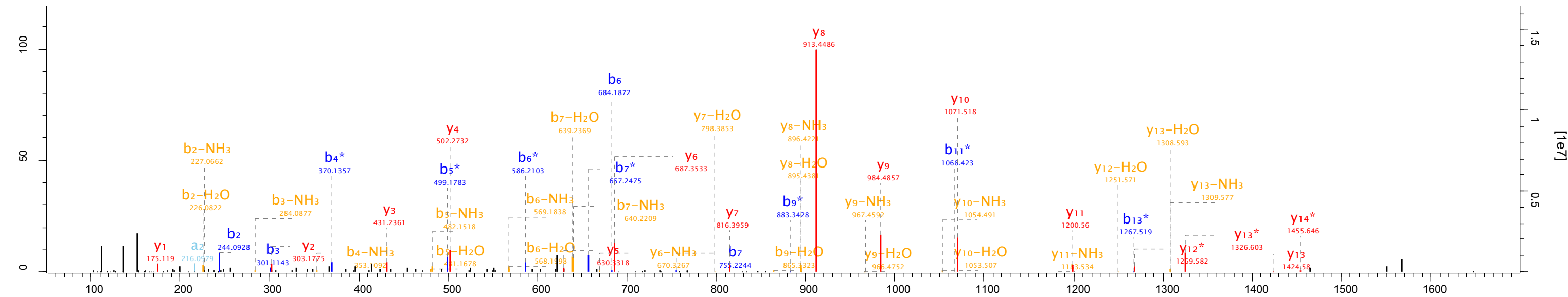


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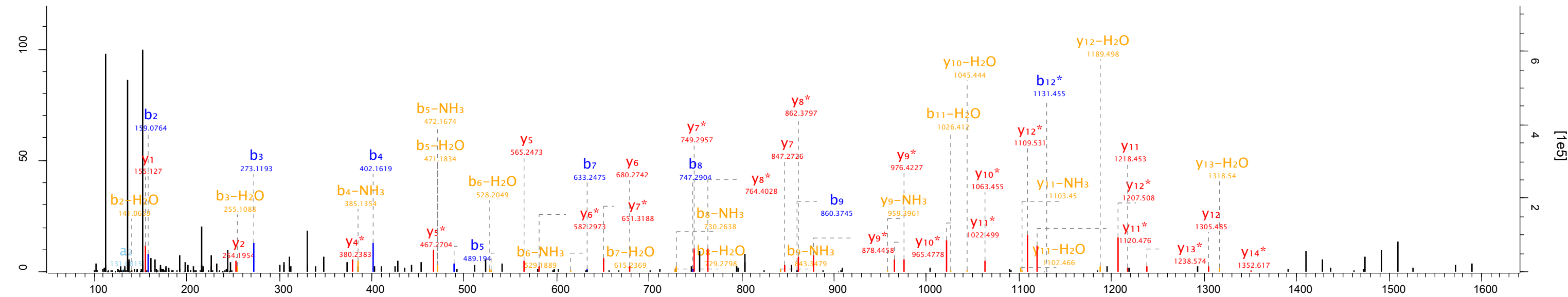
20171215_MaS_33SR_LMH_phospho_01



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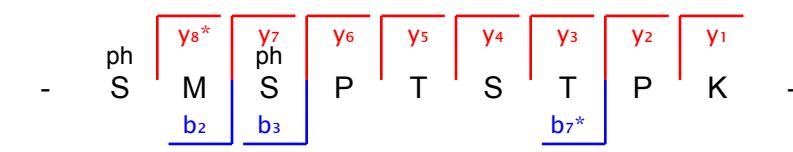
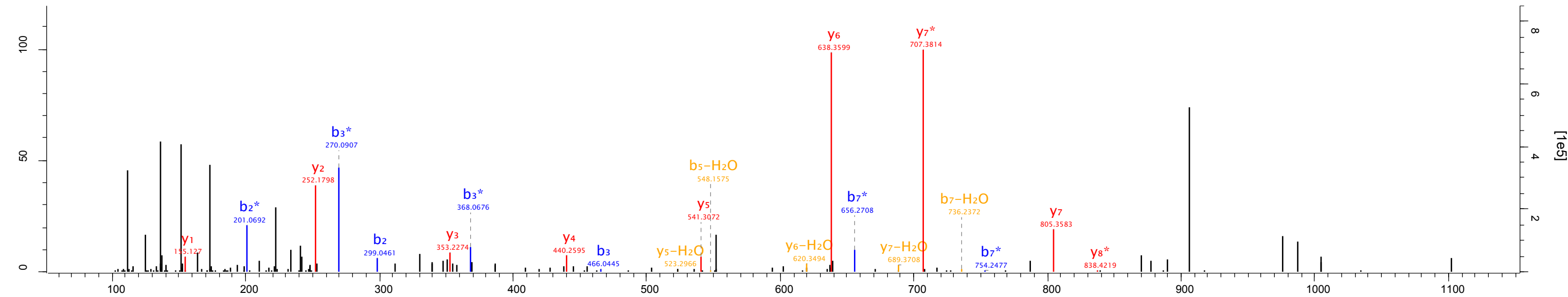


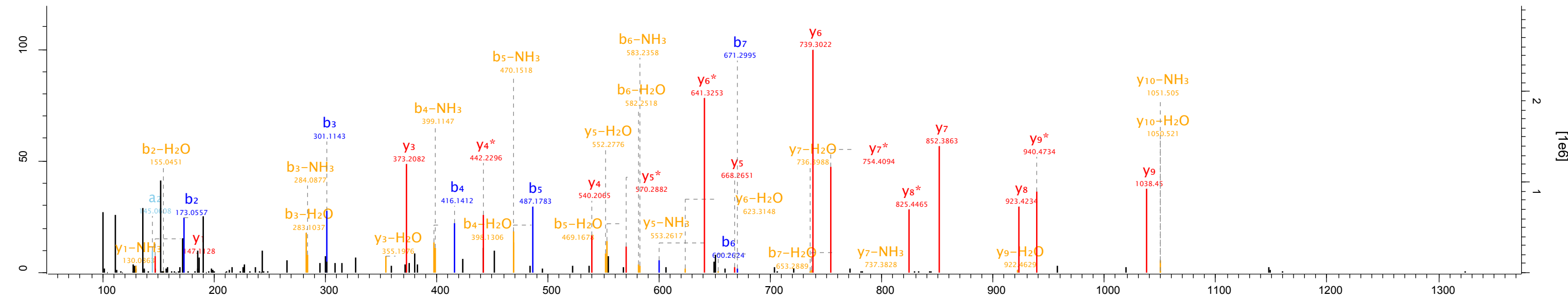
- T G N E S G S N L S G S V K -

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

- b₂ (under G)
- b₃ (under N)
- b₄ (under E)
- b₅ (under S)
- b₇ (under S)
- b₈ (under N)
- b₉ (under L)
- b₁₂* (under S)
- y₁₄* (over N)
- y₁₃* (over E)
- y₁₂ (over S)
- y₁₁ (over G)
- y₁₀* (over S)
- y₉* (over N)
- y₈* (over L)
- y₇ (over ph)
- y₆ (over D)
- y₅ (over S)
- y₄* (over G)
- y₂ (over V)
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Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 3744 Method FTMS; HCD Score 79.89 m/z 552.2 Gene names PCF11

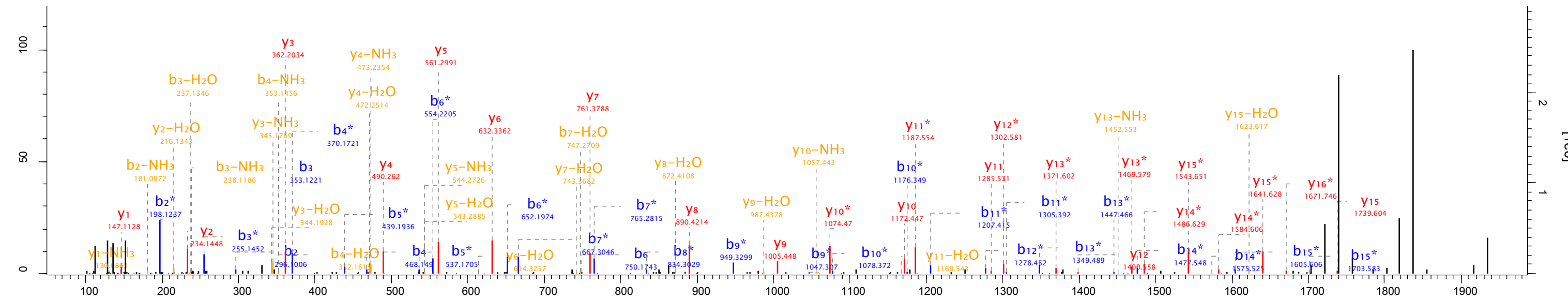




- D G Q D A I A Q S P E K -

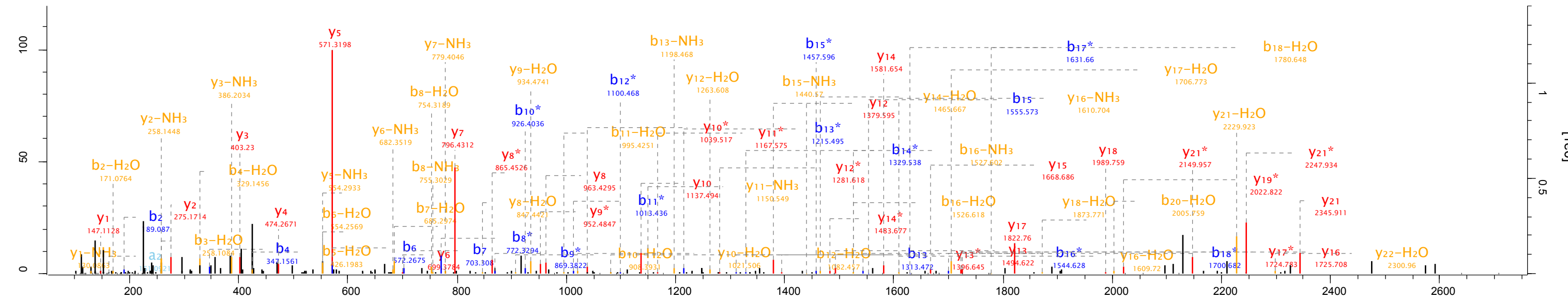
b₂
b₃
b₄
b₅
b₆
b₇
y₉
y₈
y₇
y₆
y₅
y₄
ph
y₃
y₁

Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 4044 Method FTMS; HCD Score 259.44 m/z 1017.85 Gene names ZC3H13



ph S
 - S
 K G D D I S D E E A A Q Q S K
 b₂ b₃ b₄ b₅* b₆ b₇* b₈* b₉* b₁₀* b₁₁* b₁₂* b₁₃* b₁₄* b₁₅*
 y₁₆* y₁₅ y₁₄* y₁₃* ph y₁₂ y₁₁ y₁₀ ph y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

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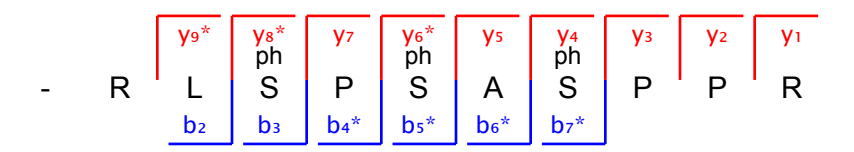
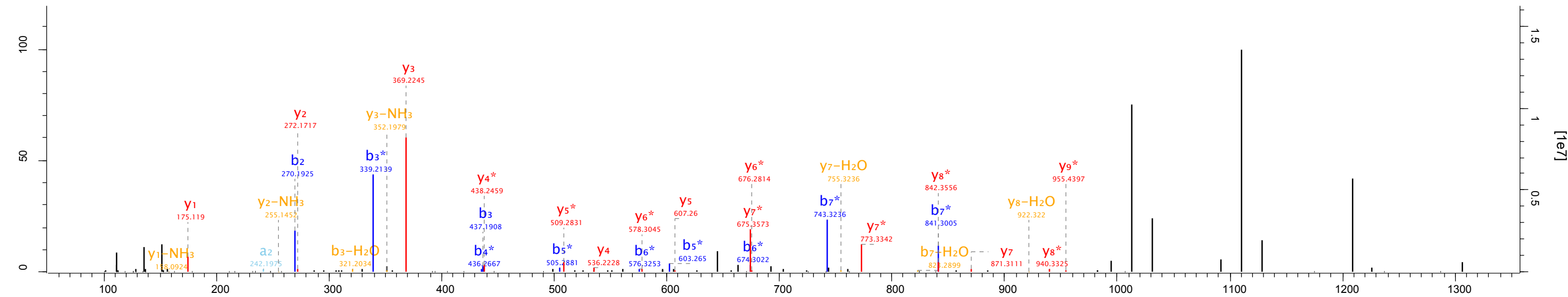


- S T S A P Q M S P G S S D N Q S S P Q P A Q Q K -

b₂
b₄
b₆
b₇
b₈^{*}
b₉^{*}
b₁₀^{*}
b₁₁^{*}
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b₁₃
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b₁₈^{*}

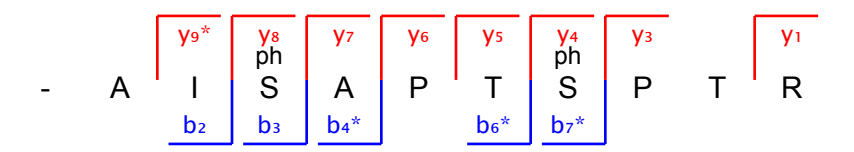
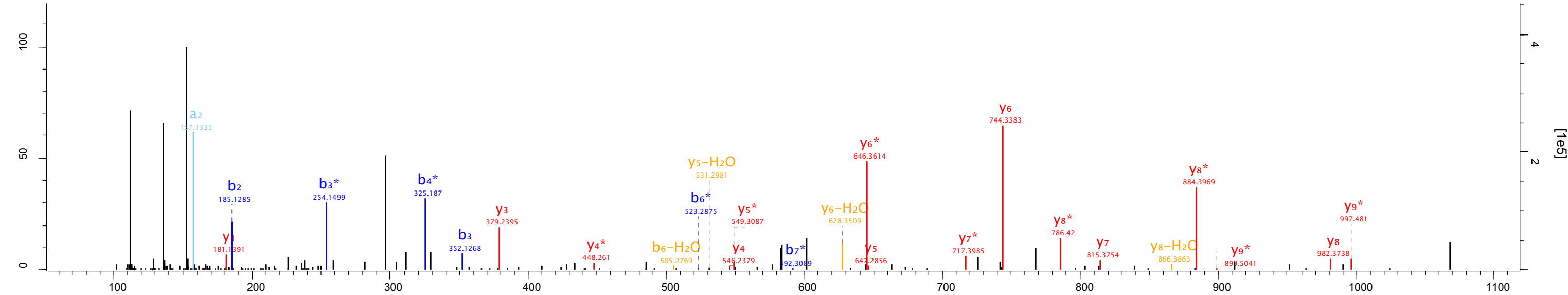
y₂₁
y₁₉^{*}
y₁₈^{ph}
y₁₇
y₁₆
y₁₅
y₁₄
y₁₃
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y₁₁^{*}
y₁₀
y₉^{*}
y₈^{ph}
y₇
y₆
y₅
y₄
y₃
y₂
y₁

Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 4594 Method FTMS; HCD Score 124.5 m/z 654.25 Gene names SRRM1

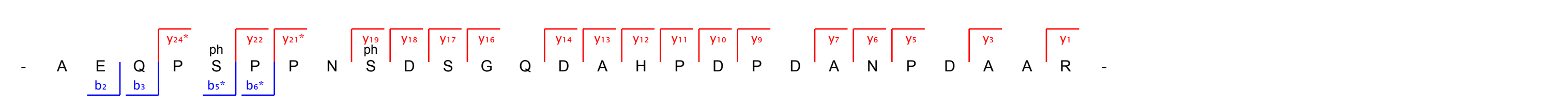
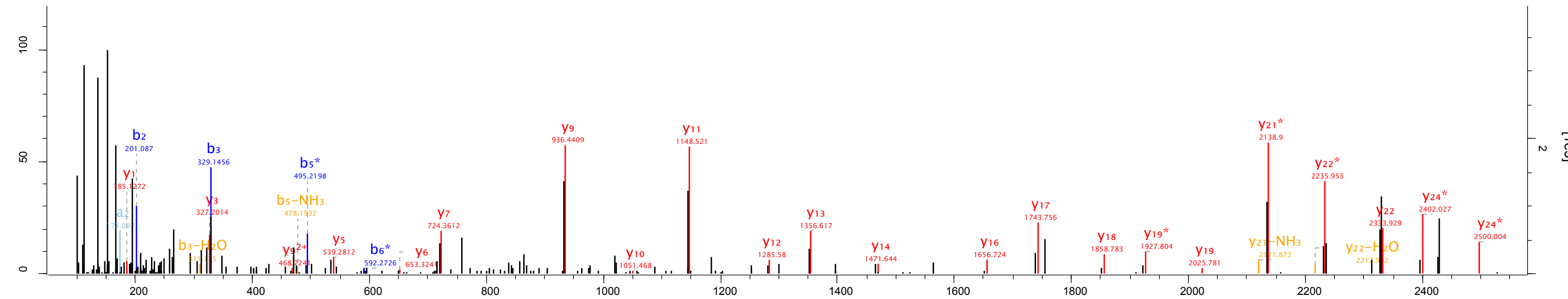


Raw file Scan Method Score m/z Gene names

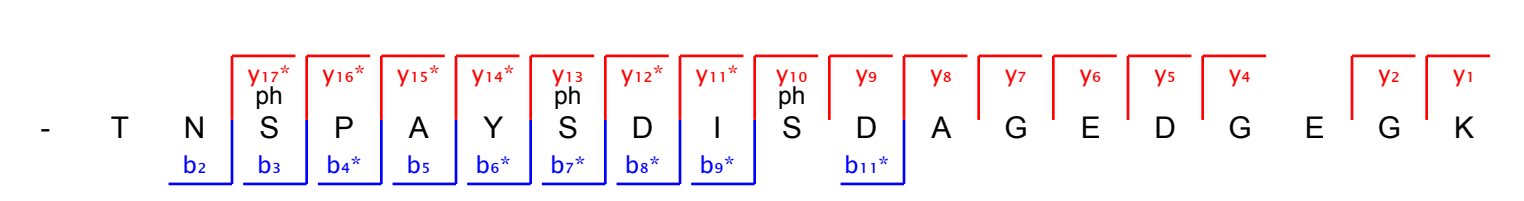
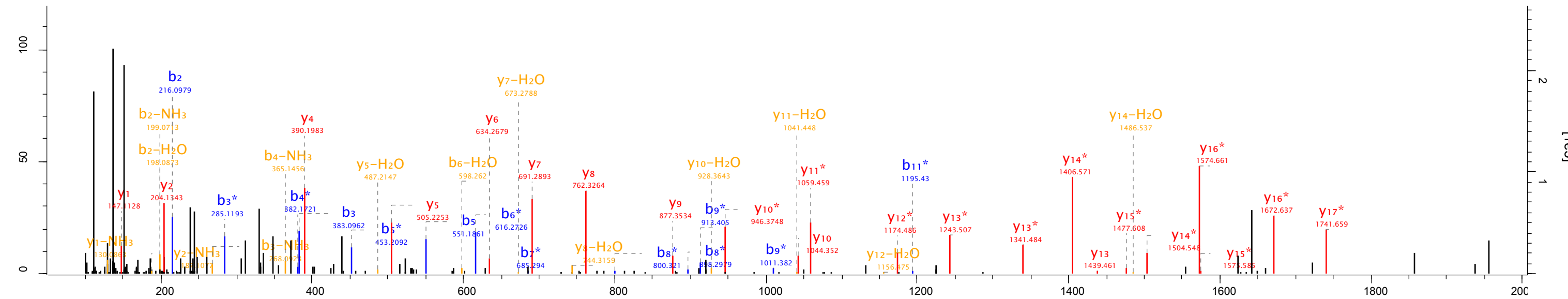
20171215_MaS_33SR_LMH_phospho_01 4934 FTMS; HCD 115.1 583.75 MIEF1



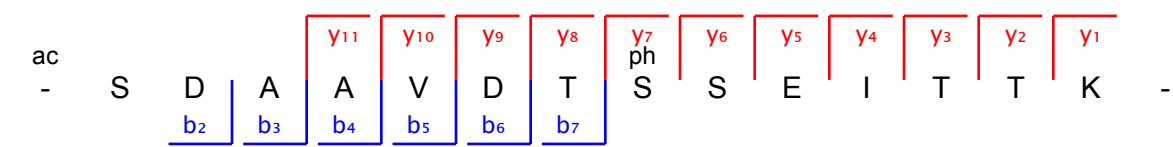
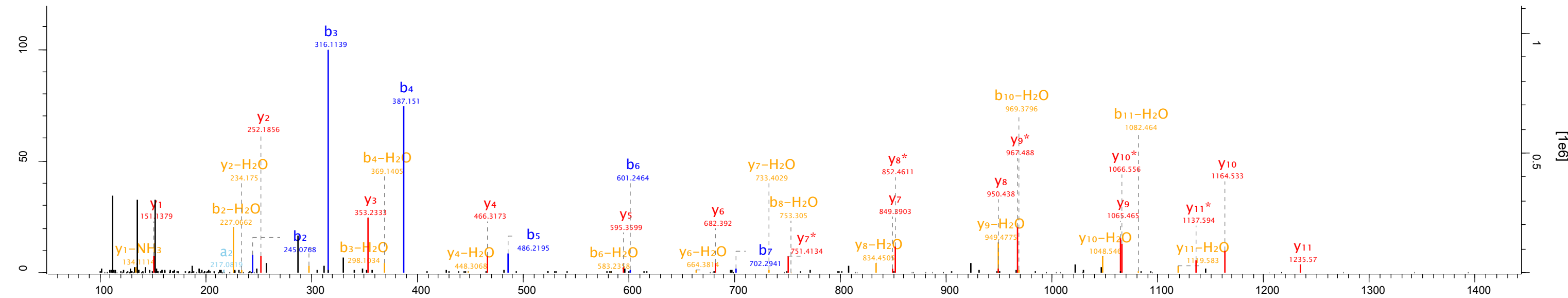
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 20171215_MaS_33SR_LMH_phospho_01 5314 FTMS; HCD 47.88 976.05 C11orf84



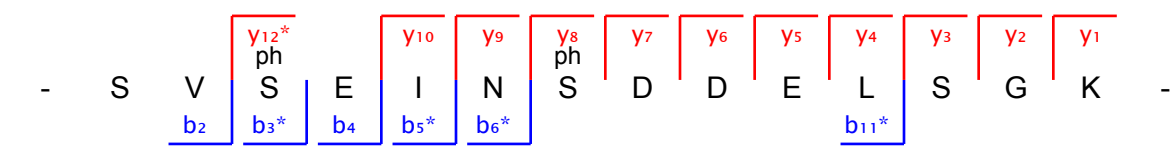
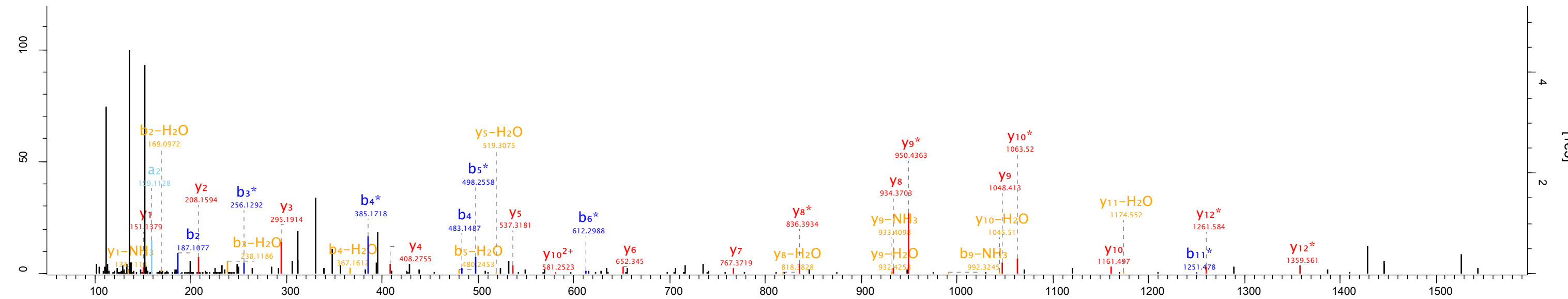
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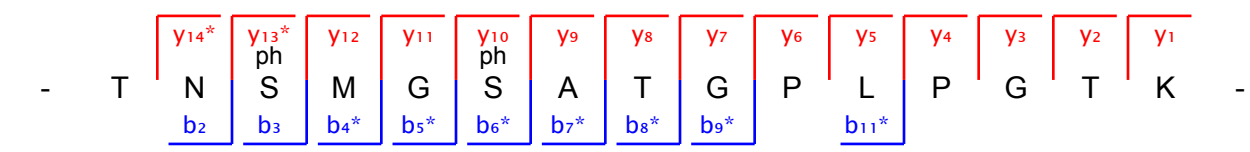
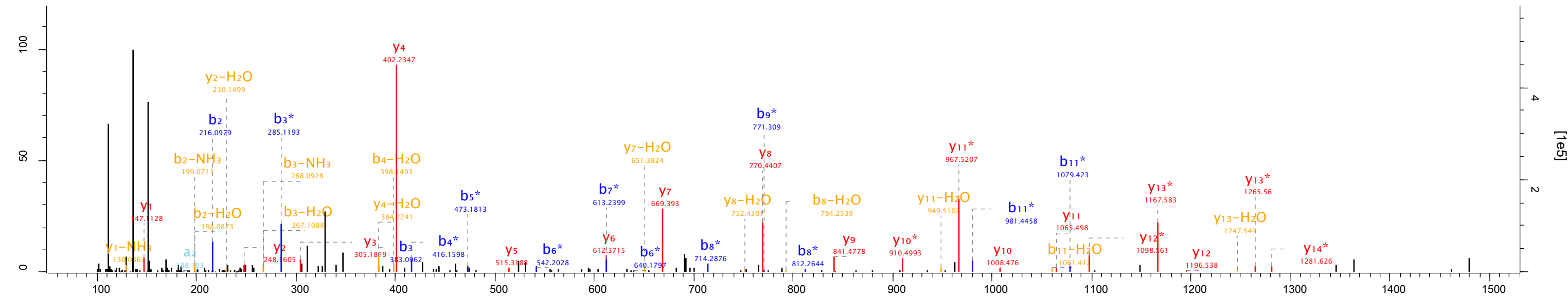
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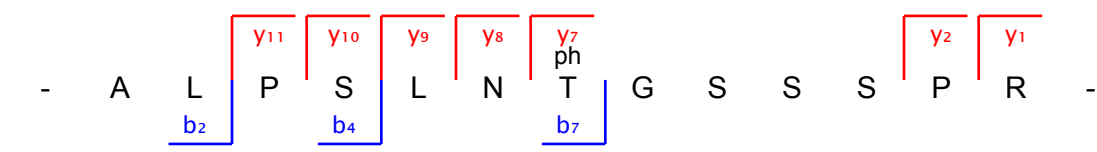
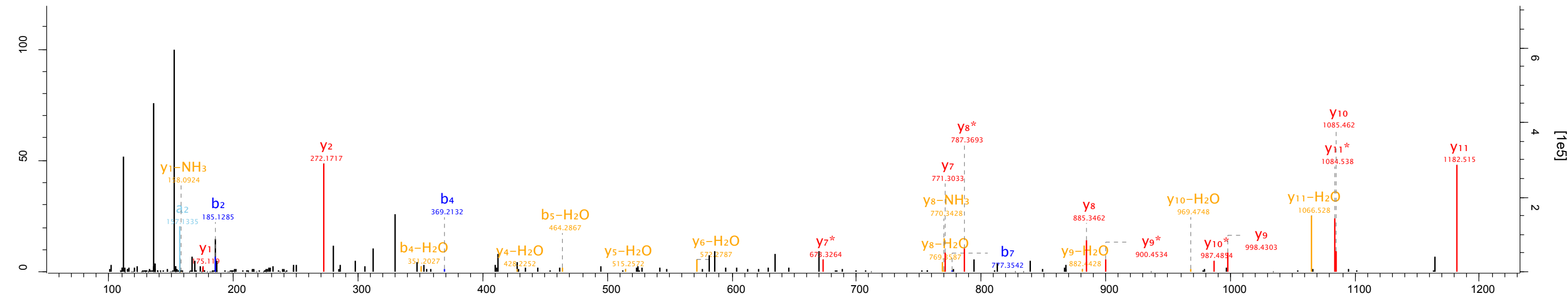
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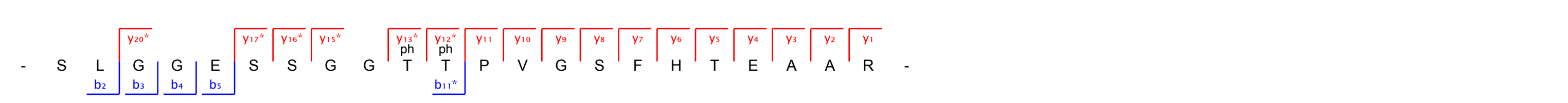
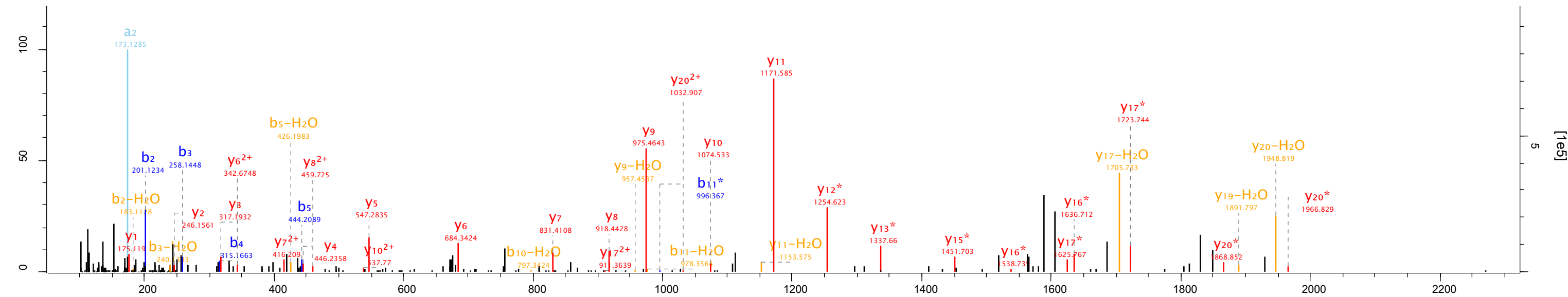
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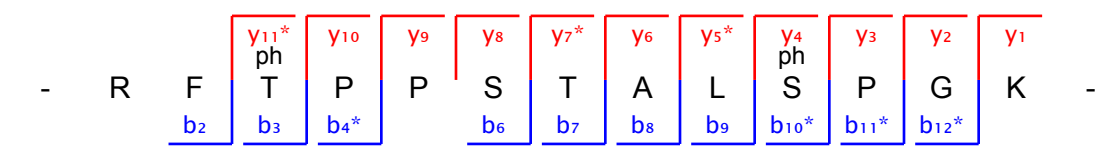
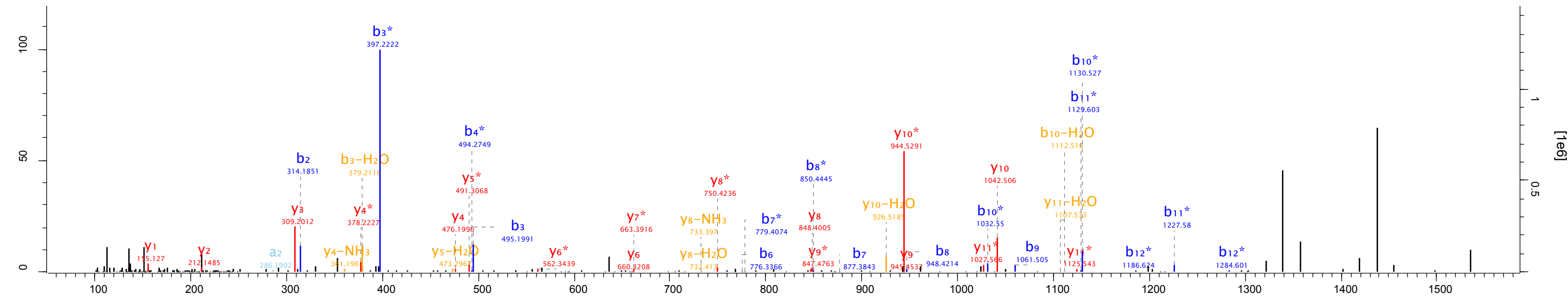
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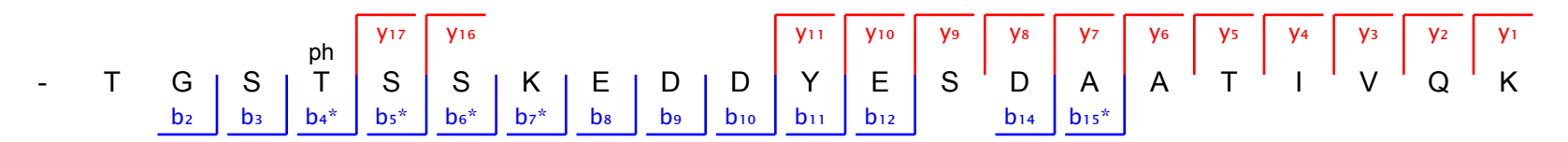
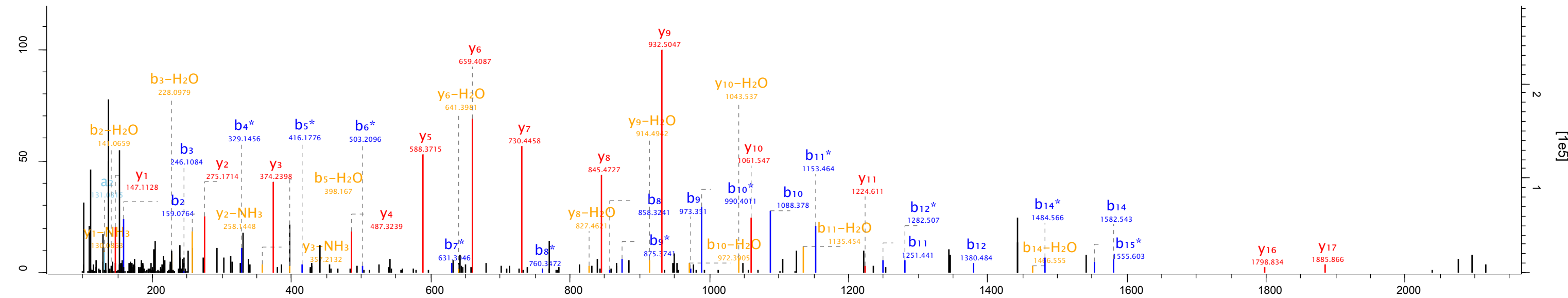
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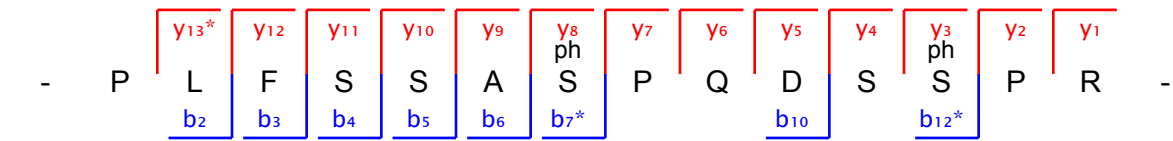
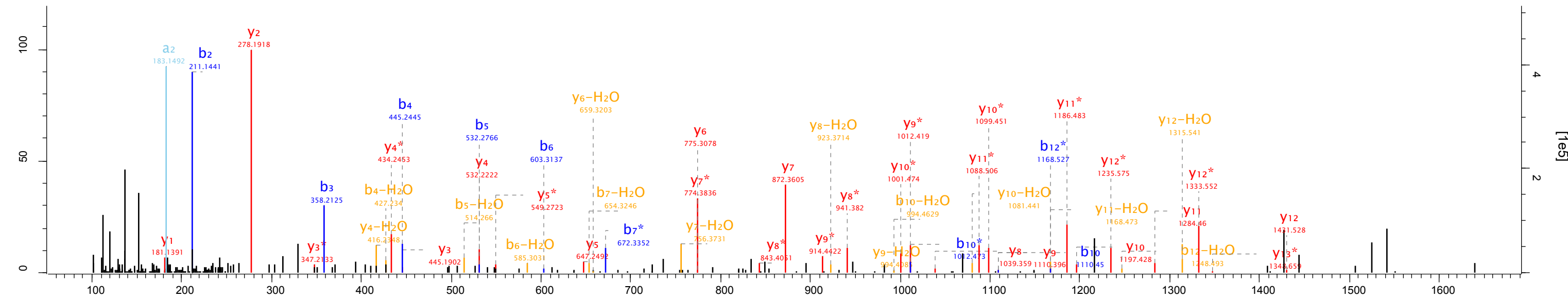


20171215_MaS_33SR_LMH_phospho_02 10174 FTMS; HCD 127.54 768.85 RUNX1

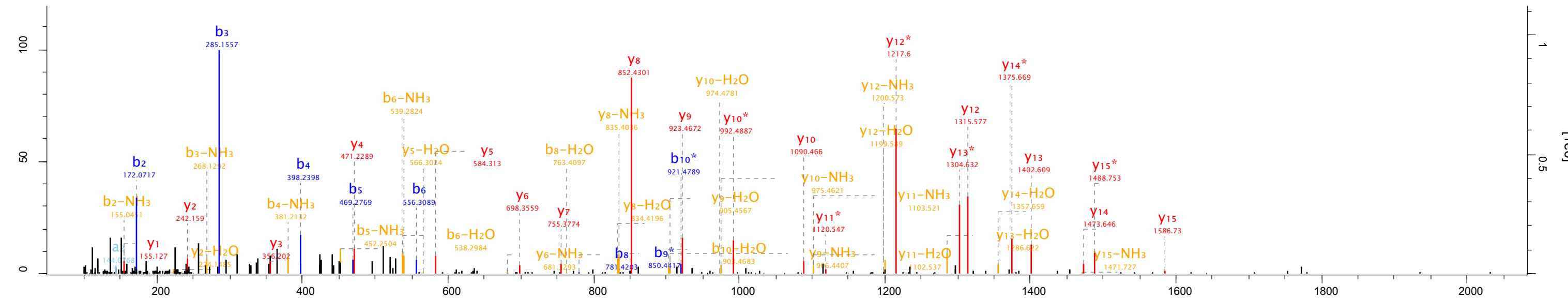


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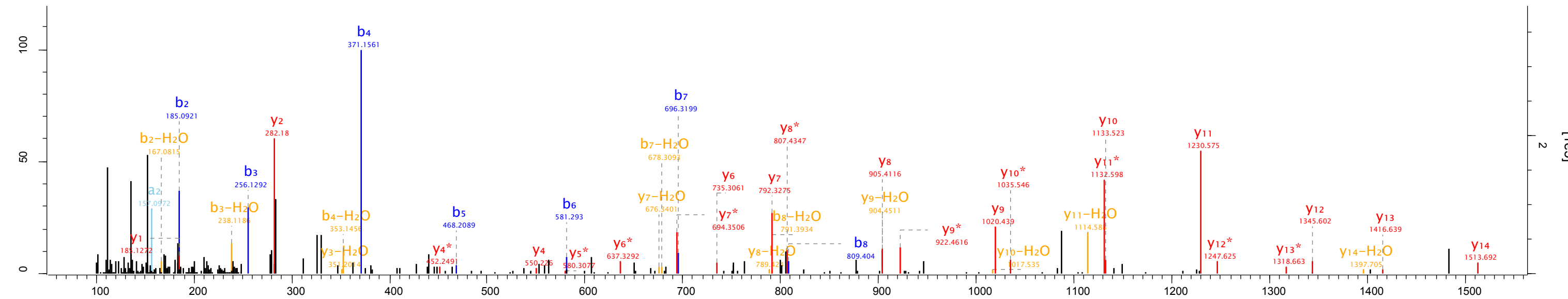




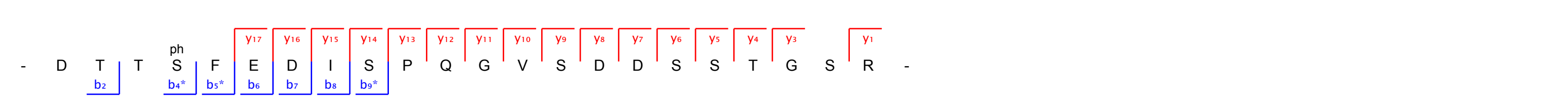
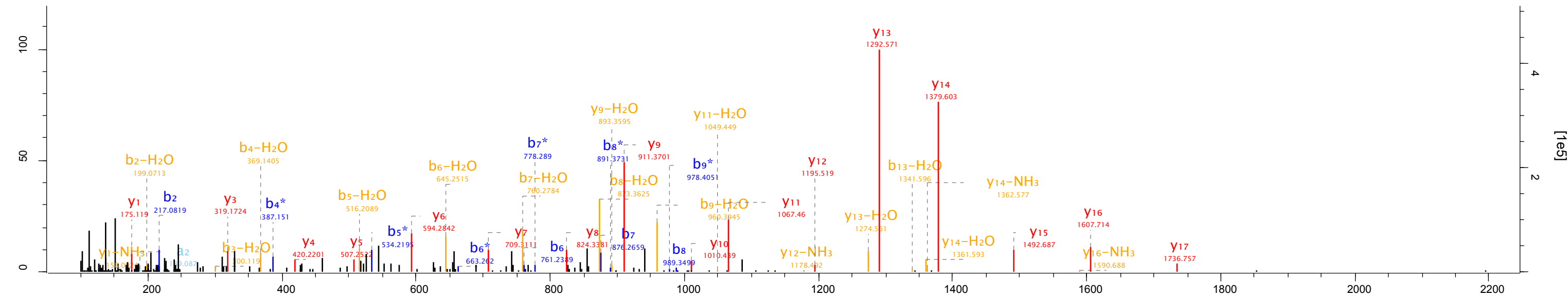
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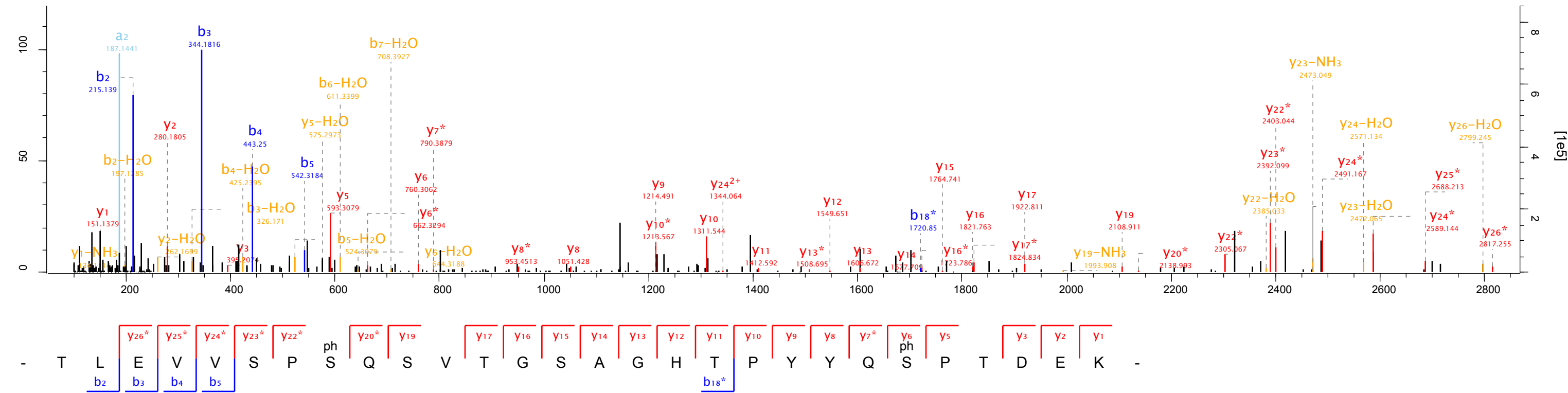
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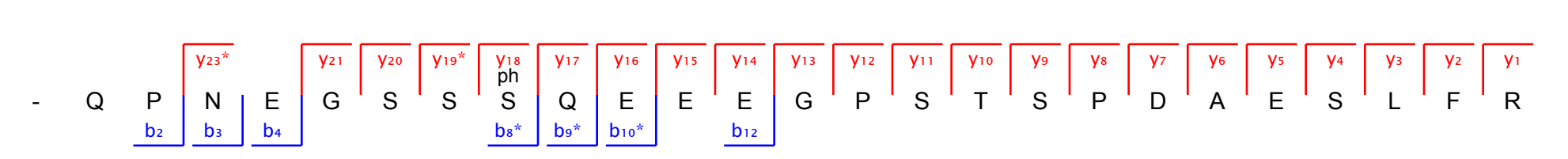
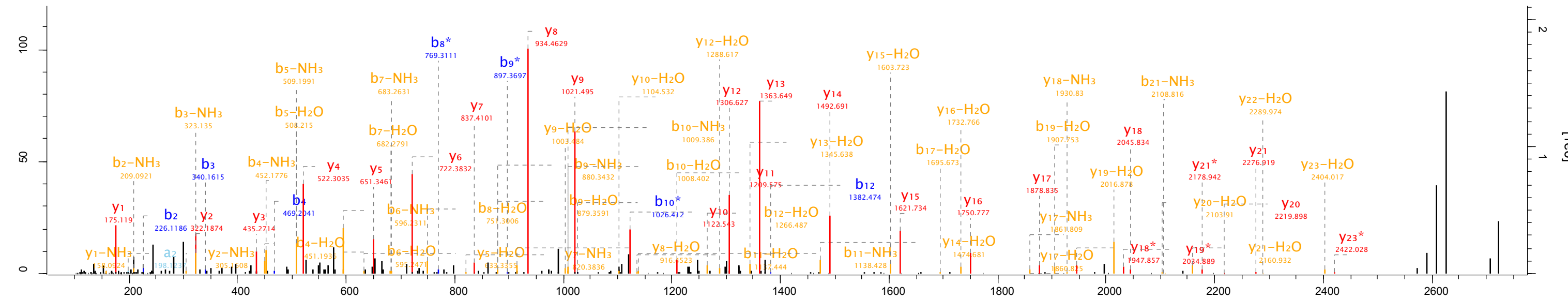
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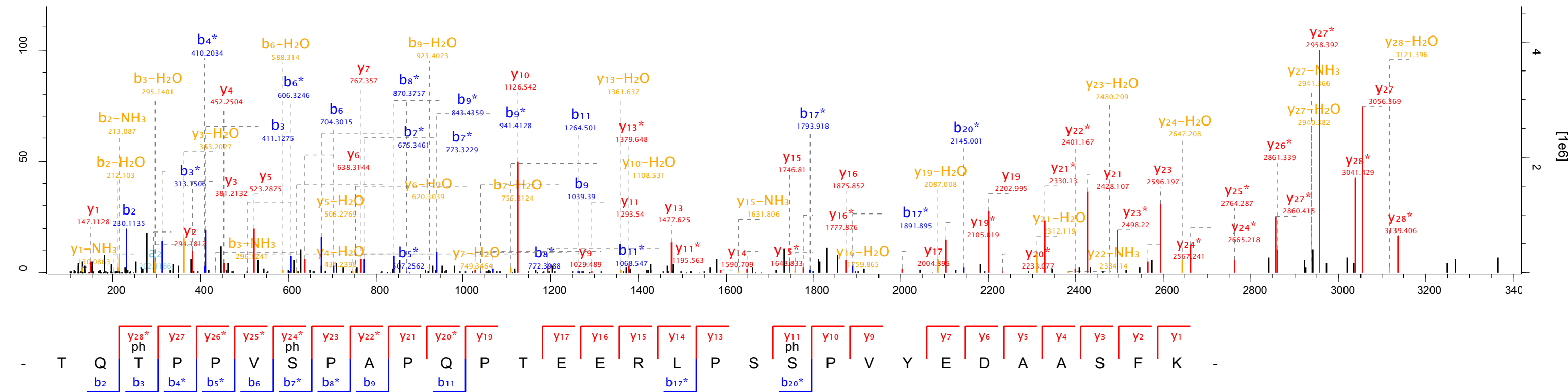
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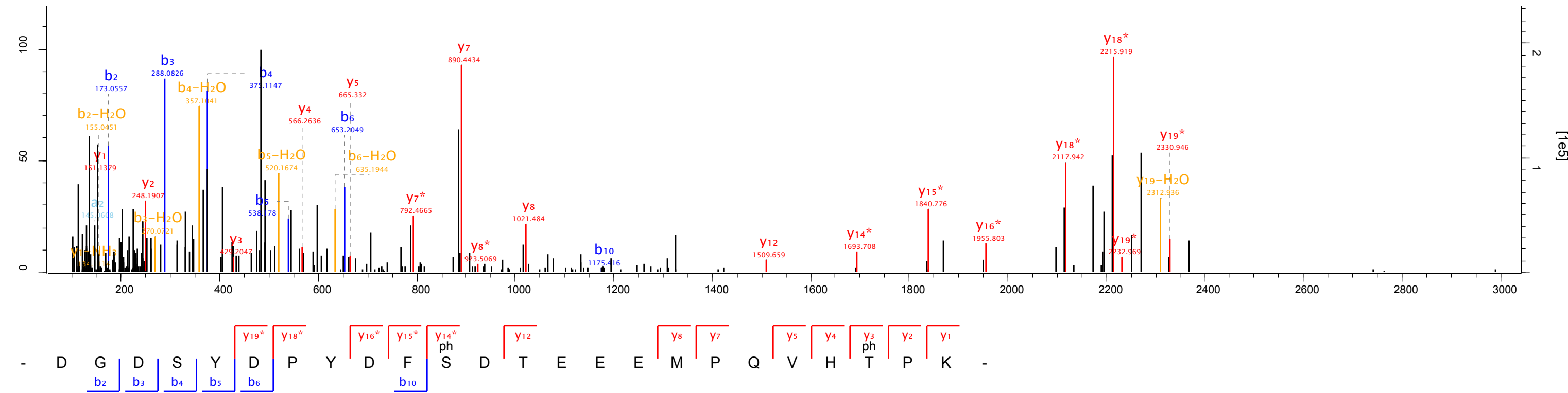
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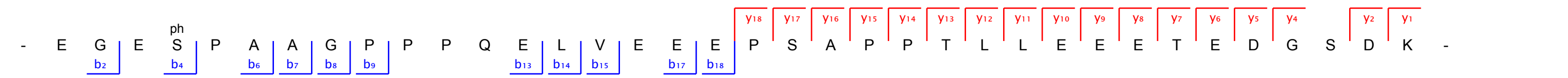
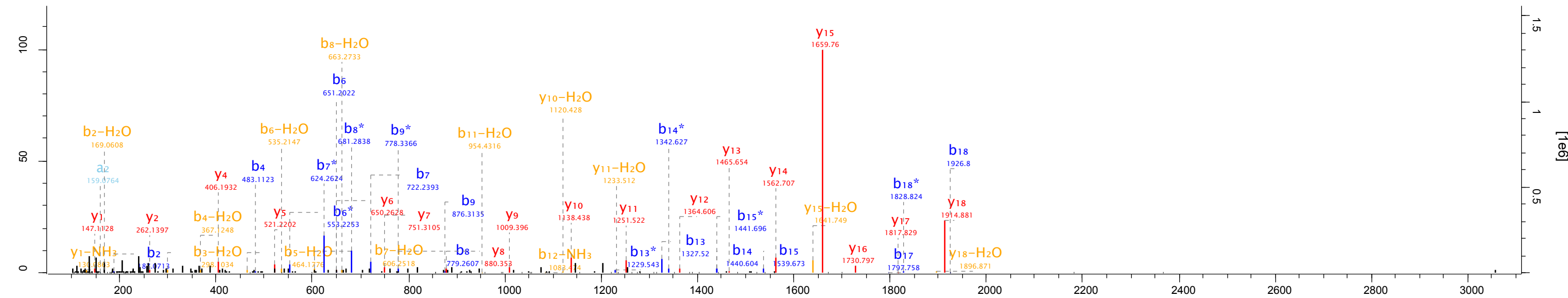
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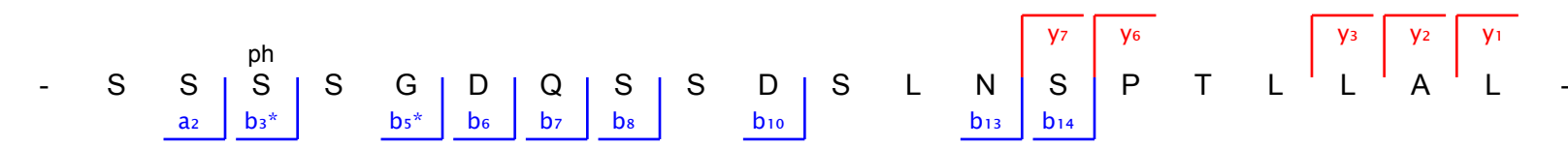
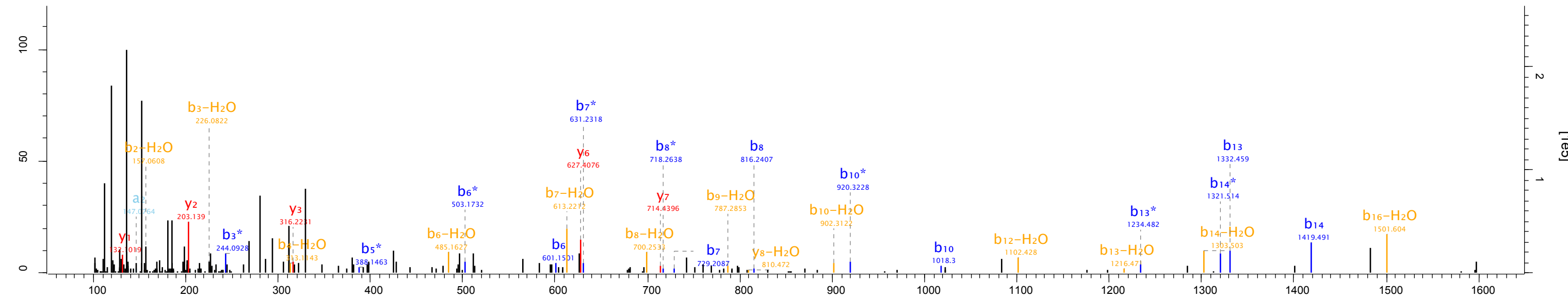
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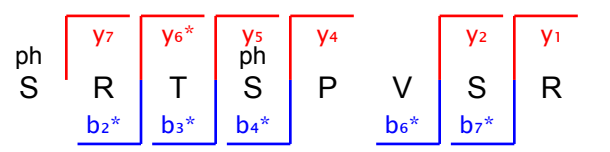
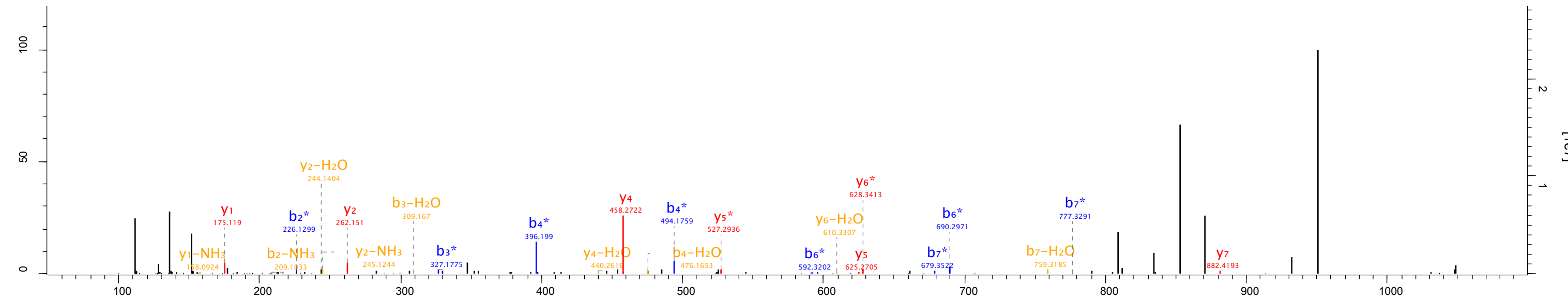
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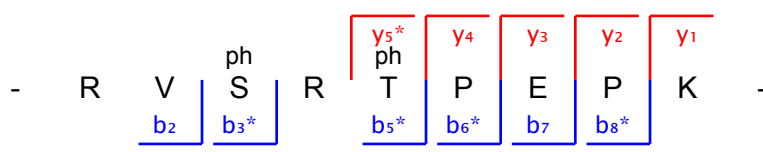
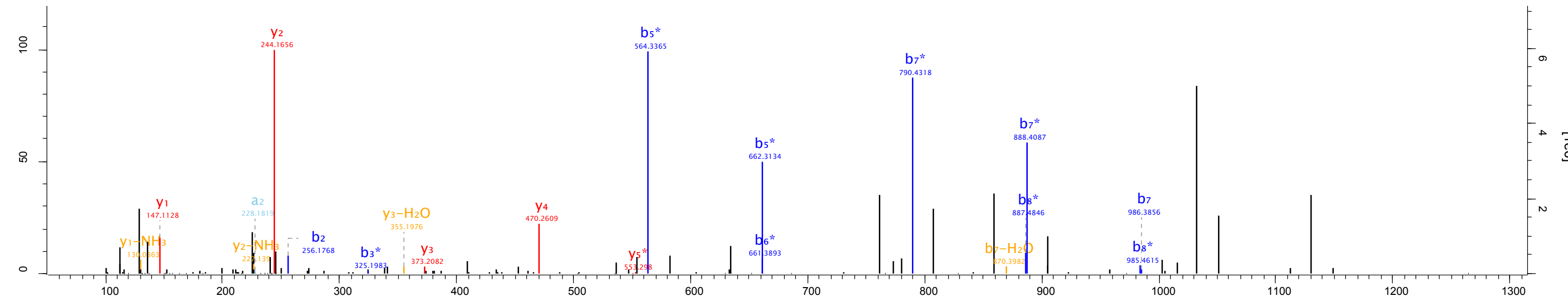
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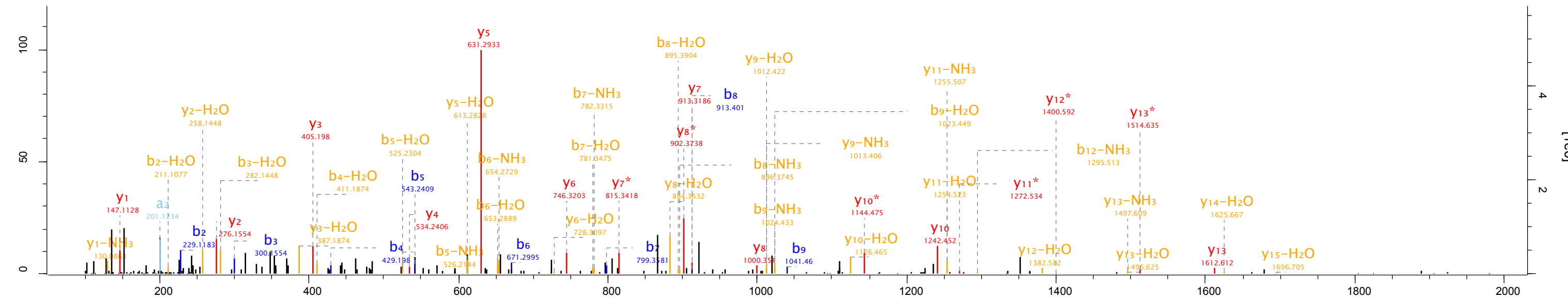
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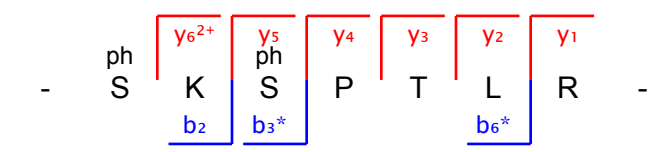
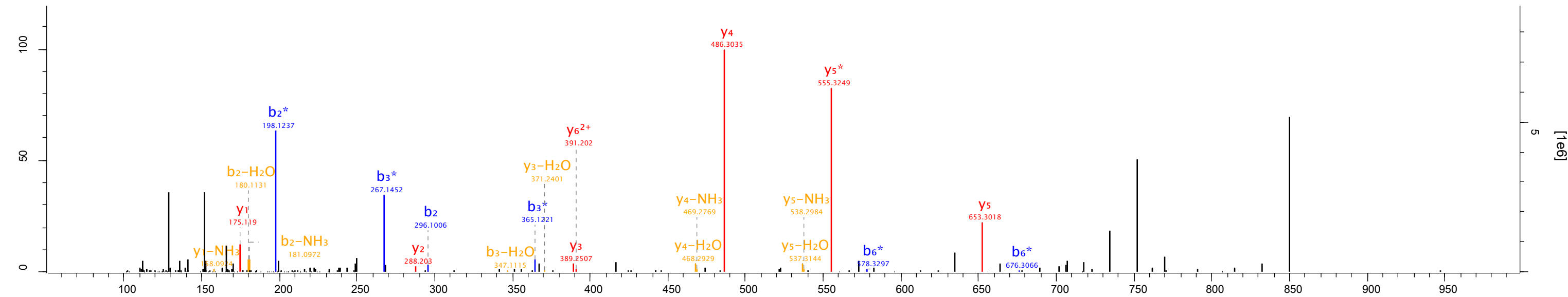
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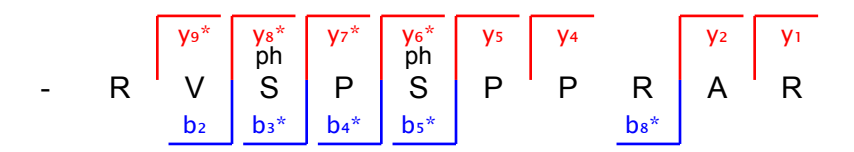
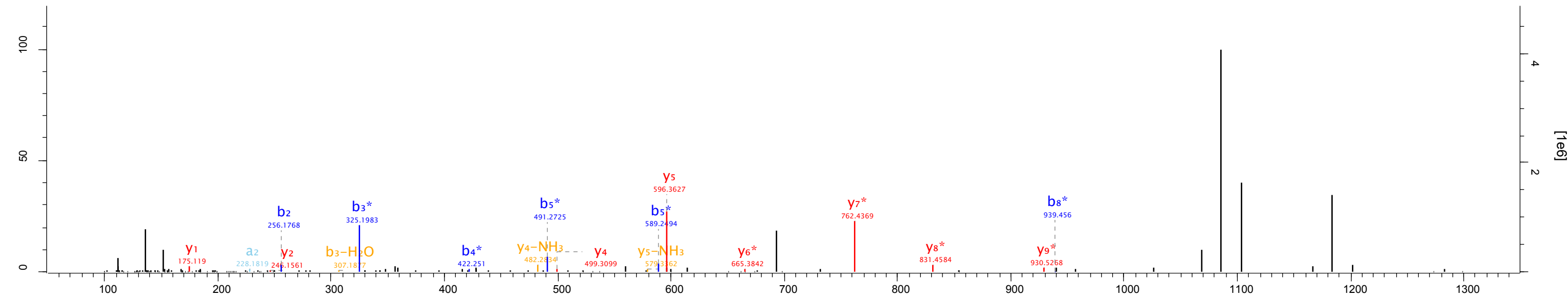
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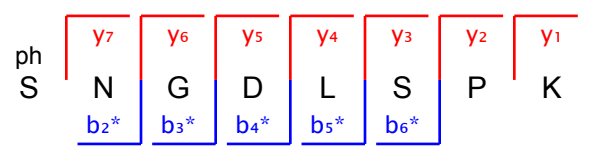
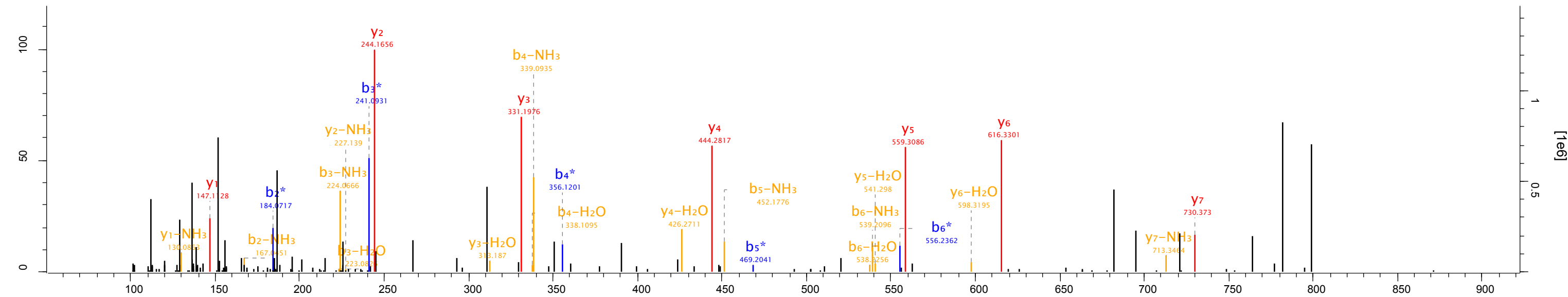
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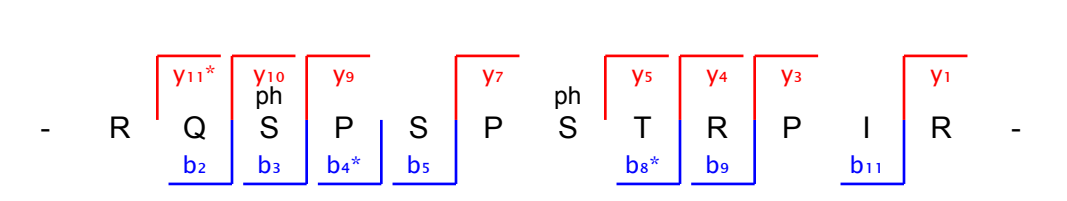
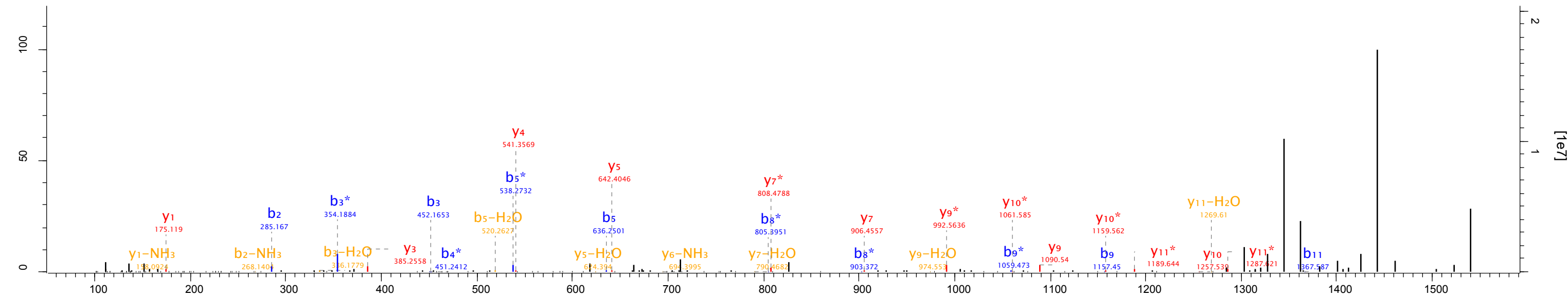
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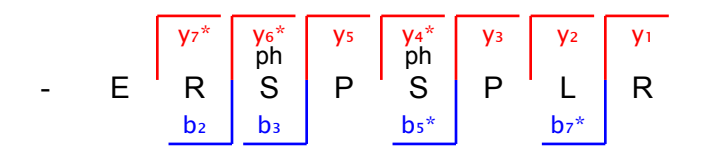
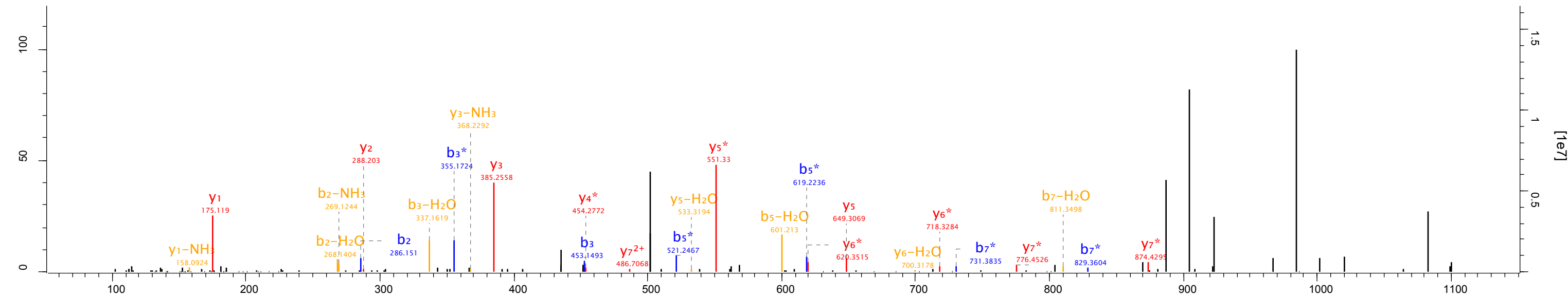
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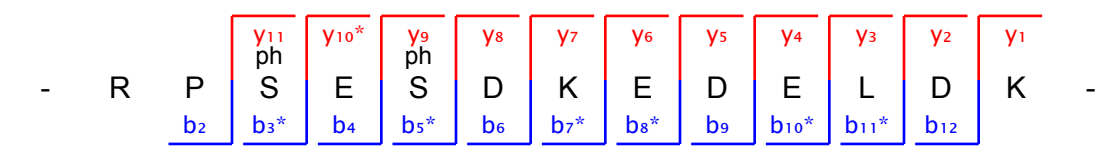
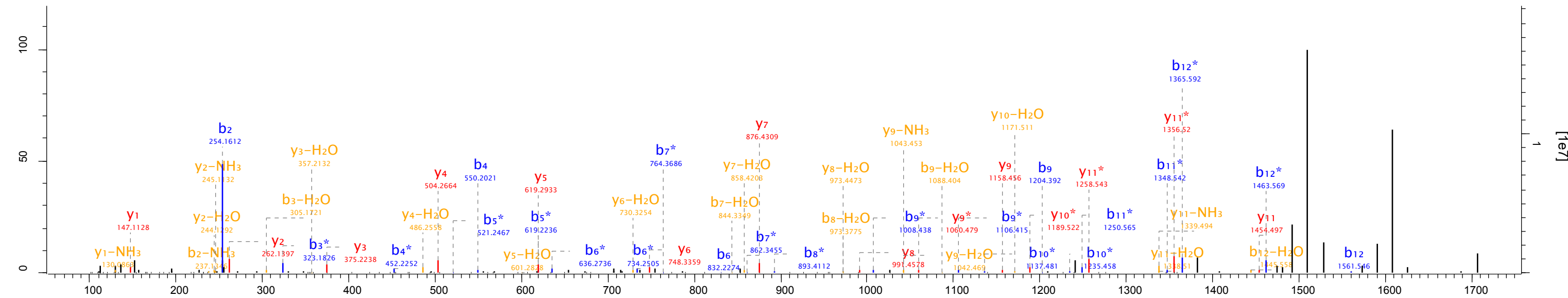
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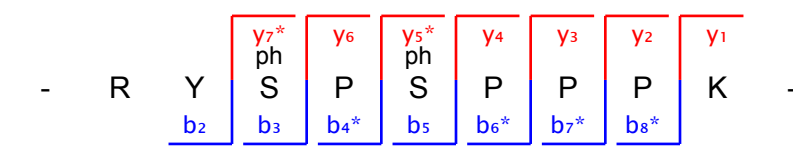
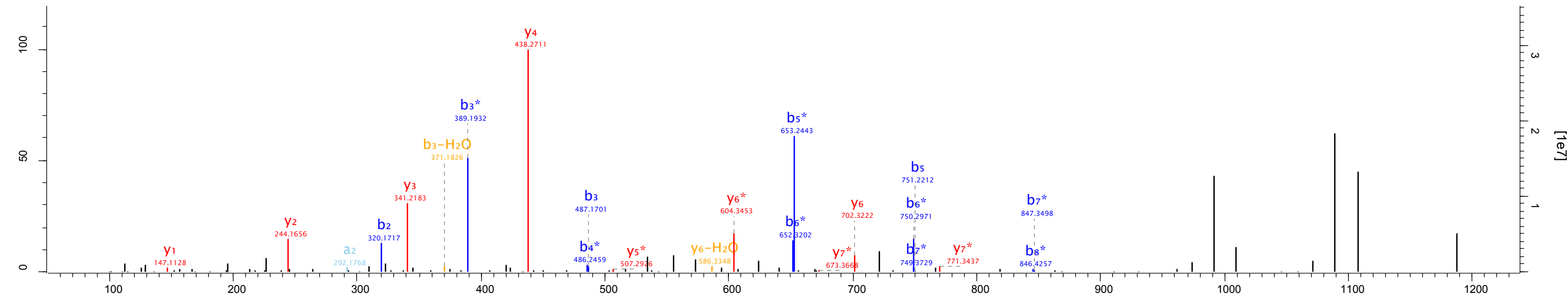
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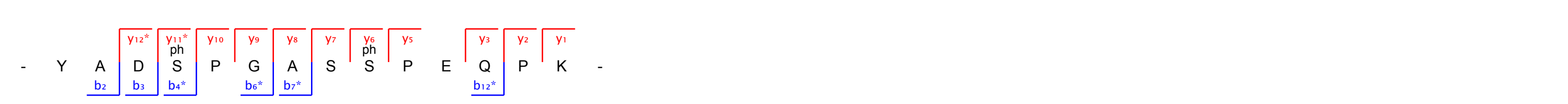
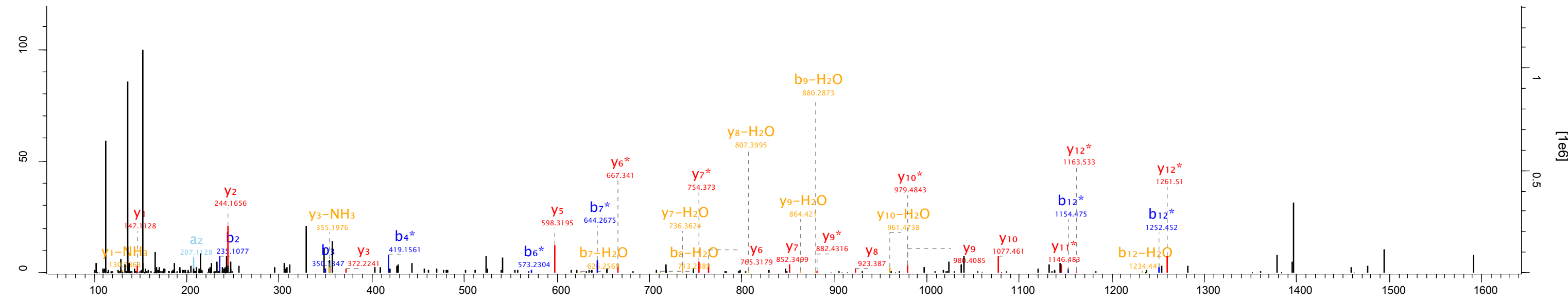
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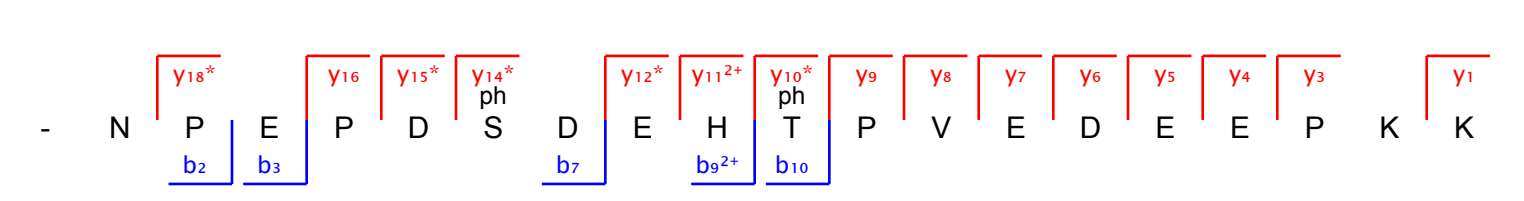
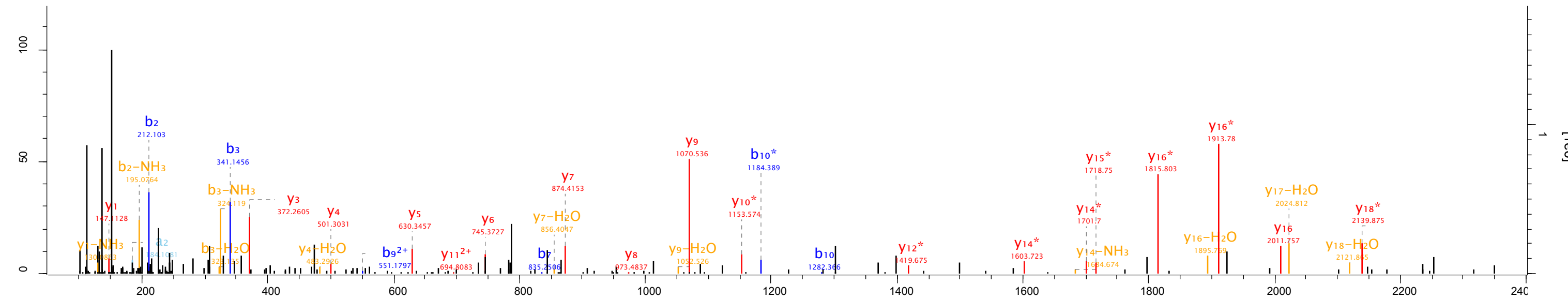
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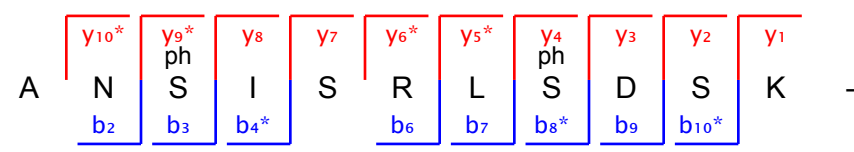
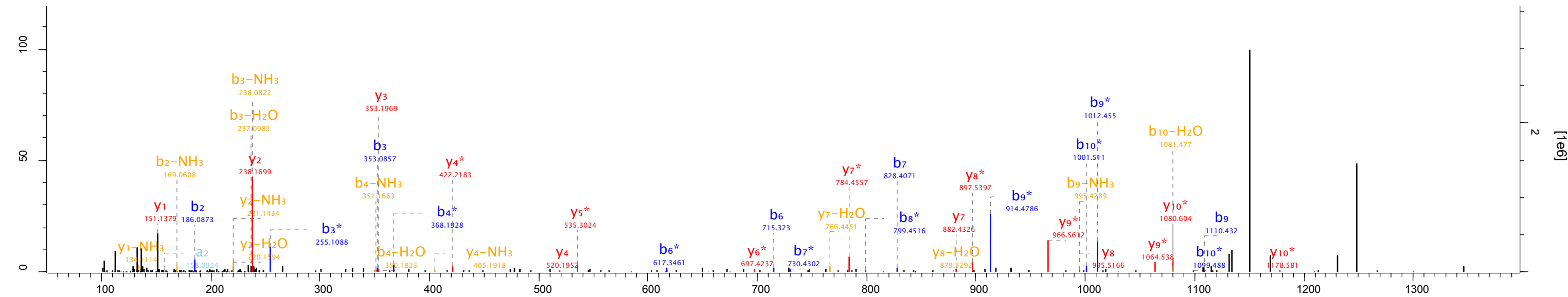
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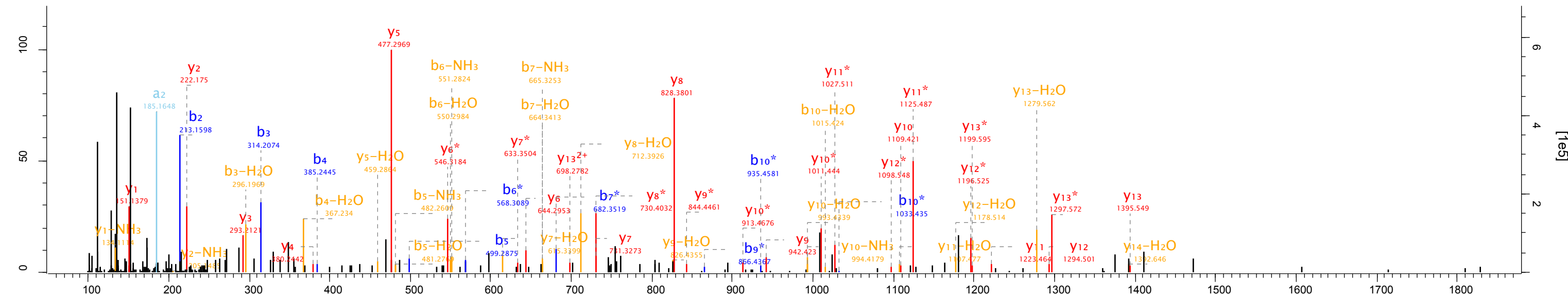
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Raw file

20171215_MaS_33SR_LMH_phospho_02

Scan	Method	Score	m/z	Gene names
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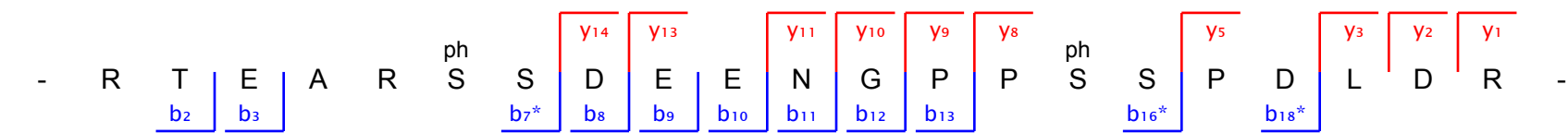
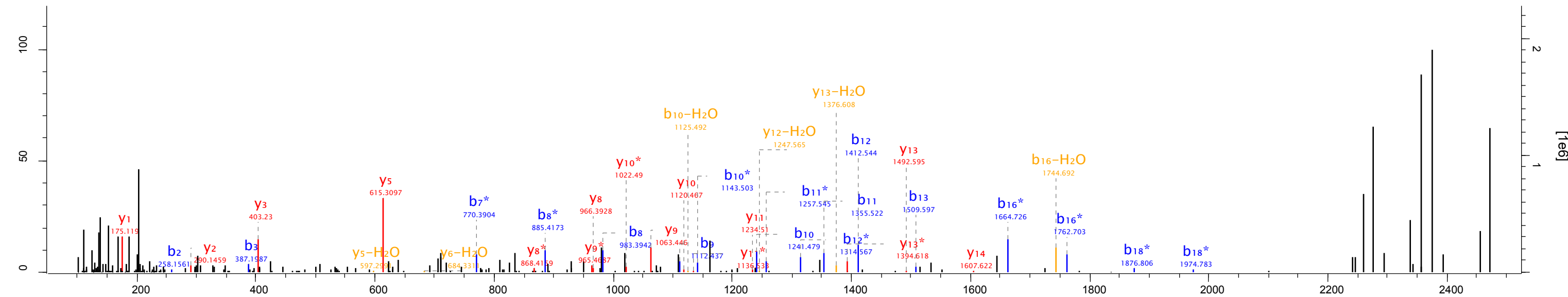
- V L T A N S N P S P S A A K -

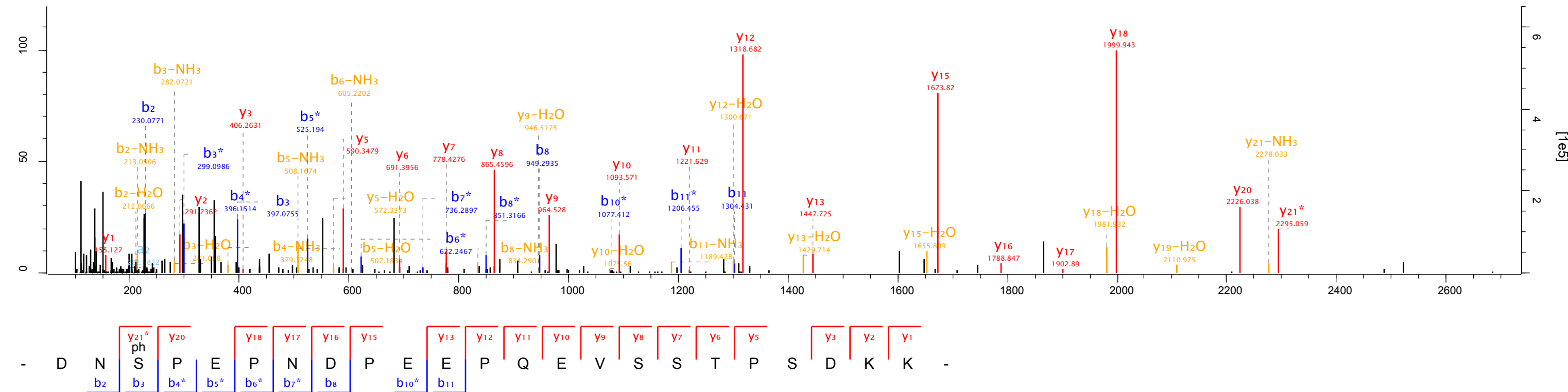
Fragmentation mapping (b and y ions) is shown below the sequence:

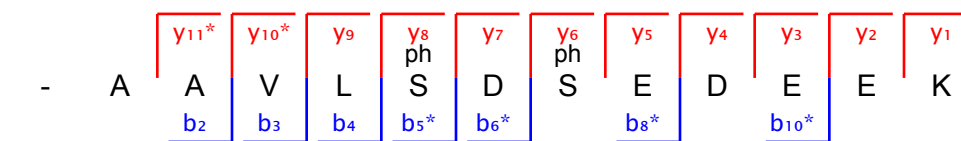
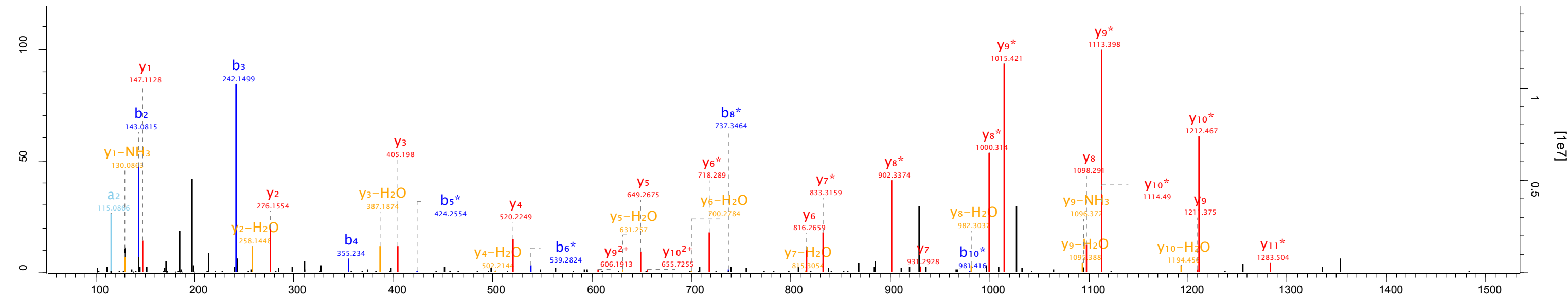
- b2: L
- b3: T
- b4: A
- b5: N
- b6*: S
- b7*: N
- b9*: S
- b10*: S

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

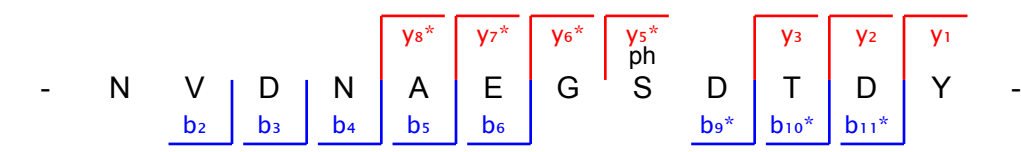
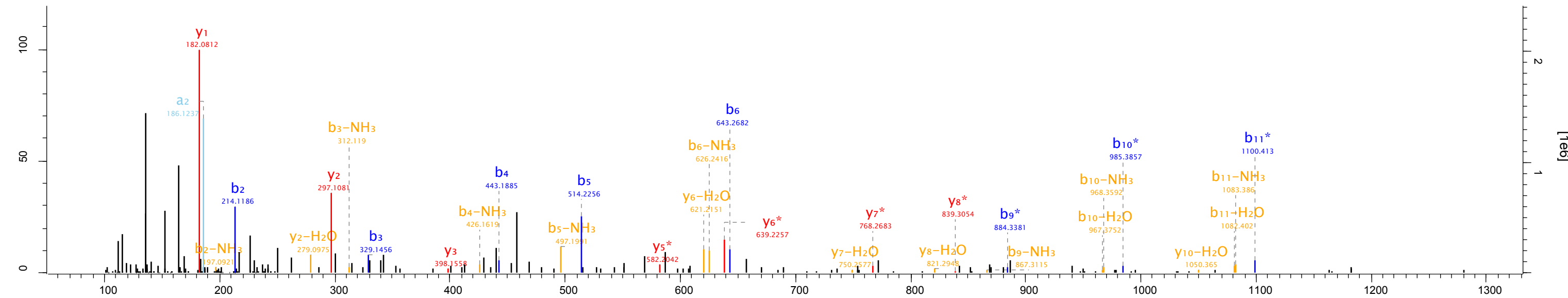
- y1: K
- y2: A
- y3: A
- y4: P
- y5: P
- y6: S
- y7: S
- y8: P
- y9: N
- y10: S
- y11: N
- y12: A
- y13: T
- y14: L



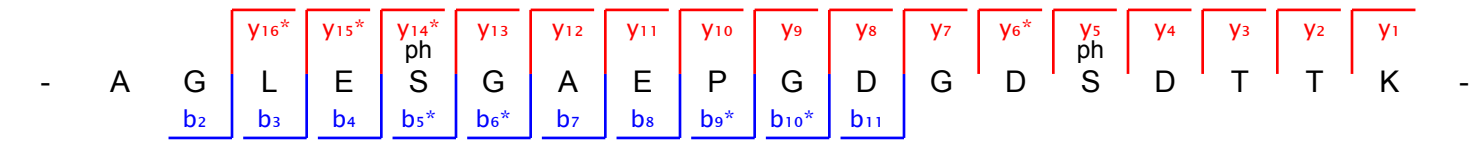
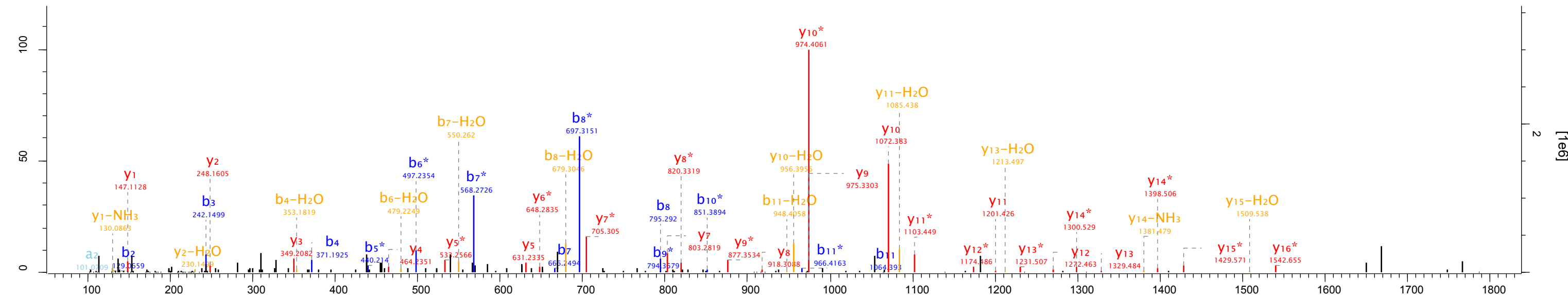




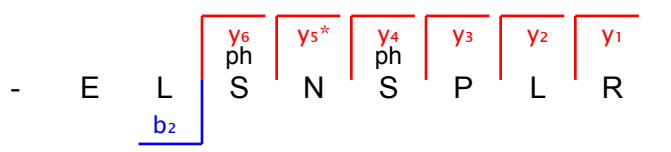
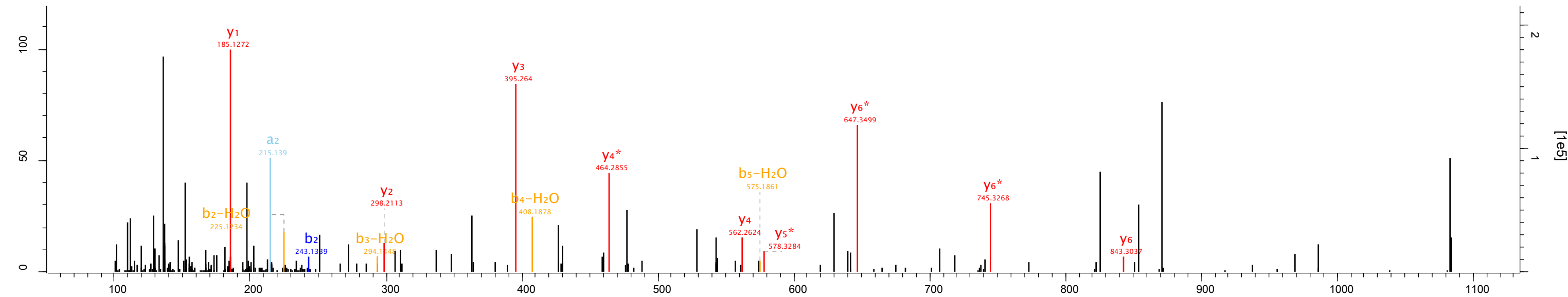
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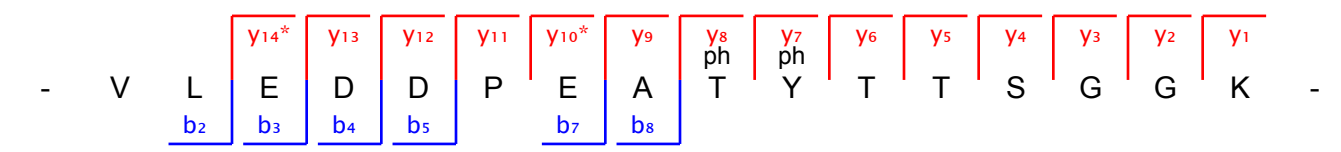
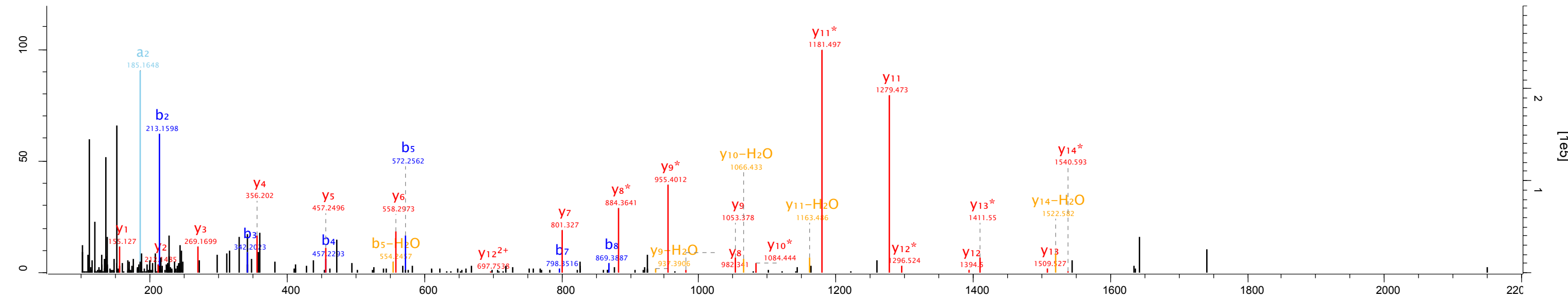
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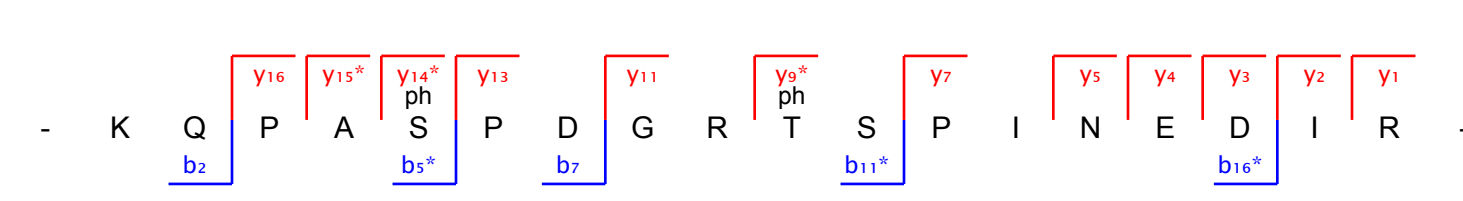
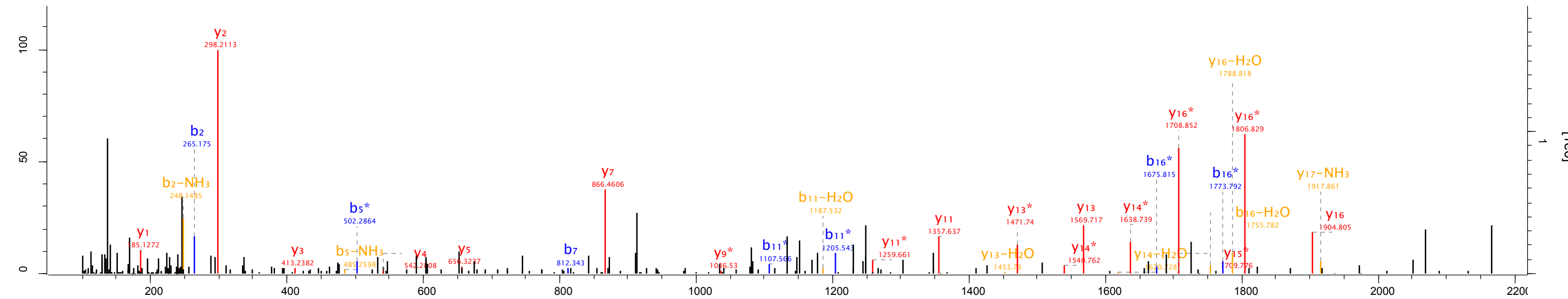
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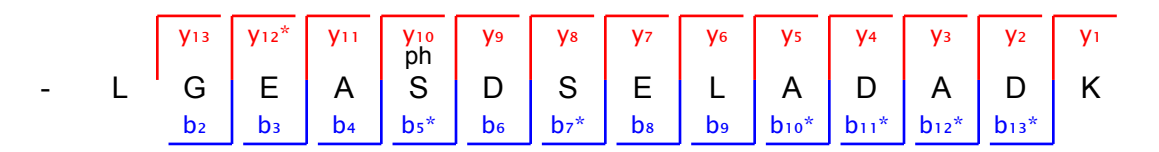
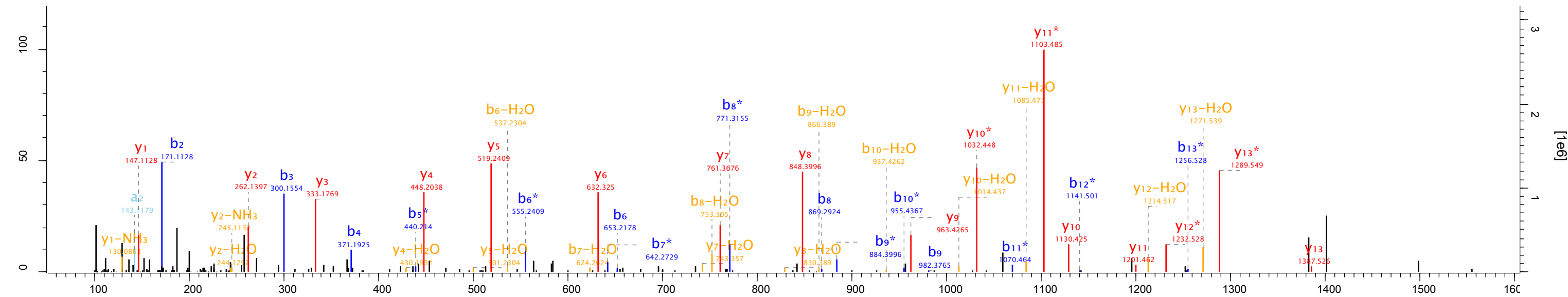
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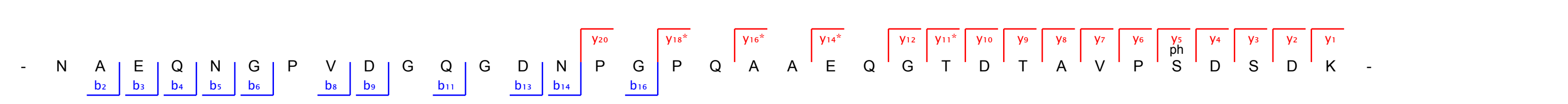
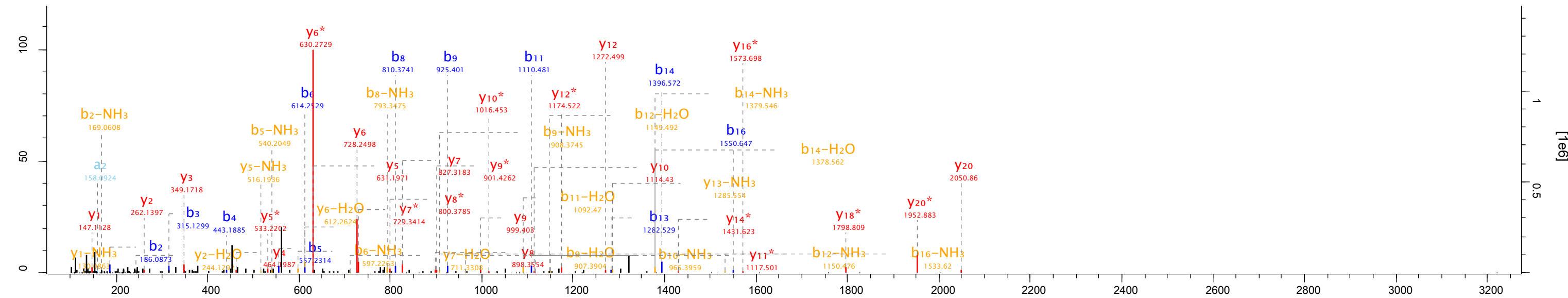
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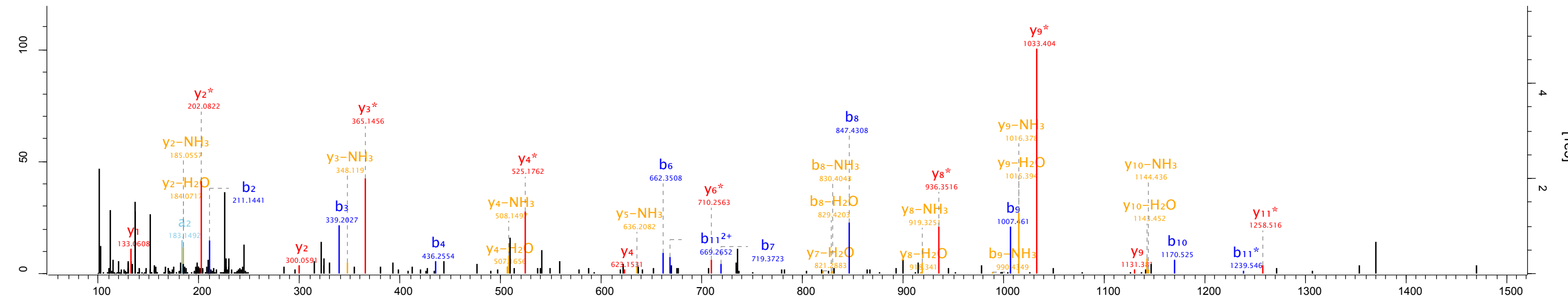
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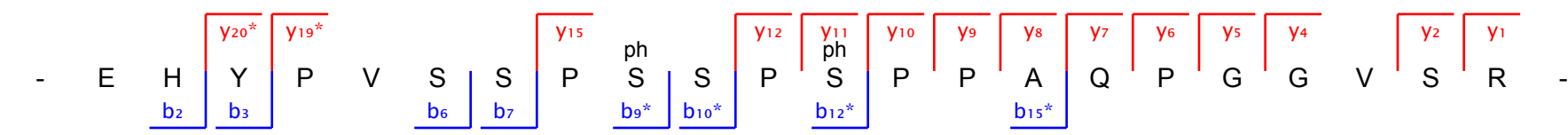
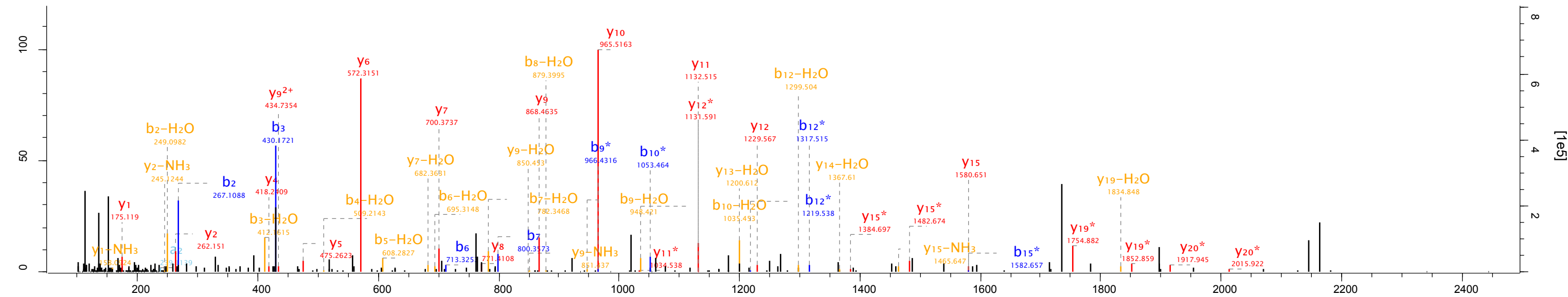


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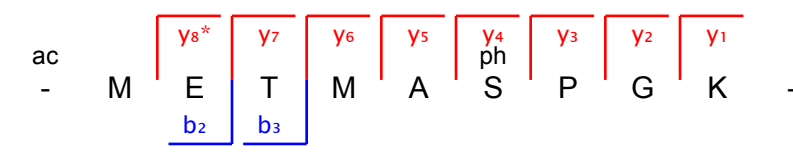
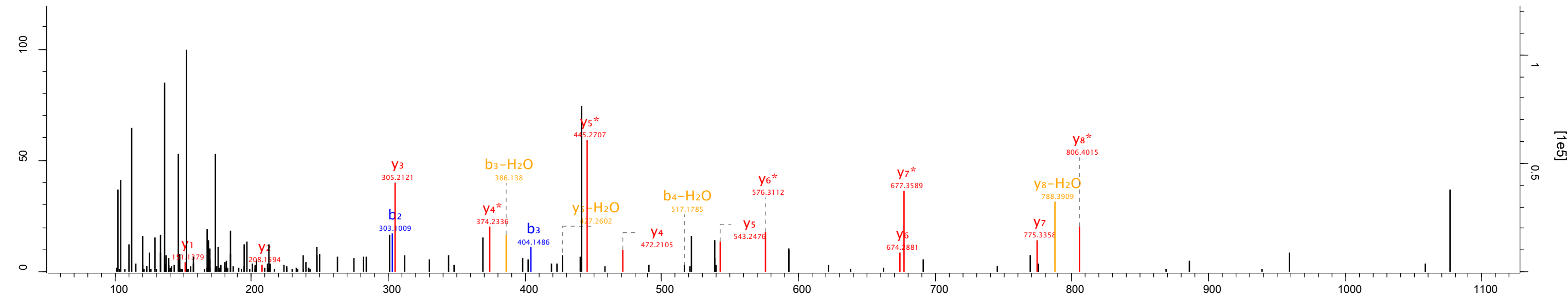


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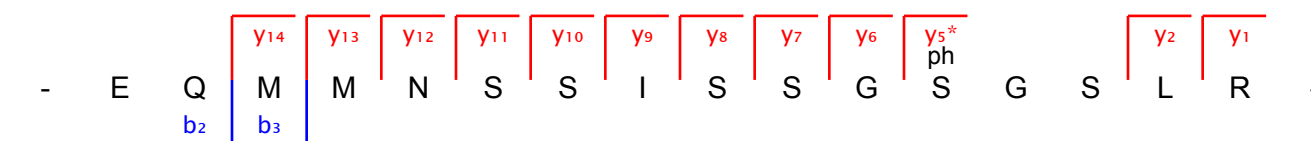
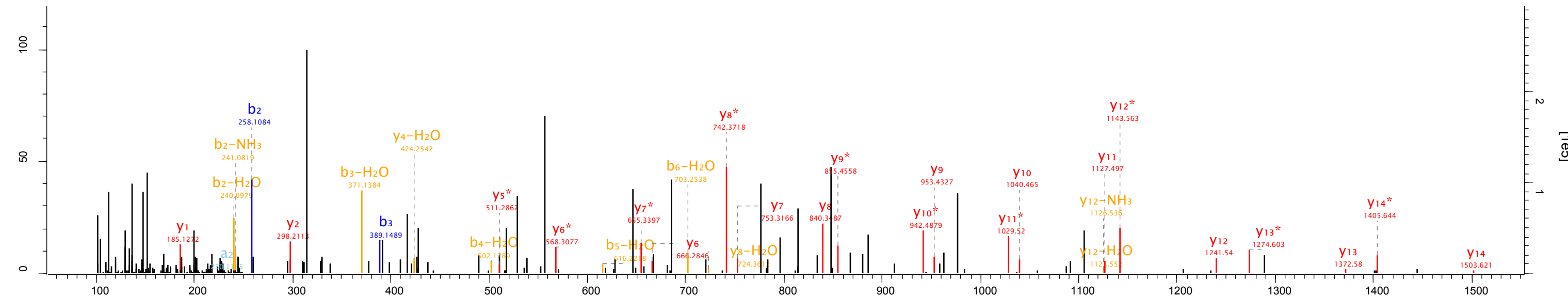




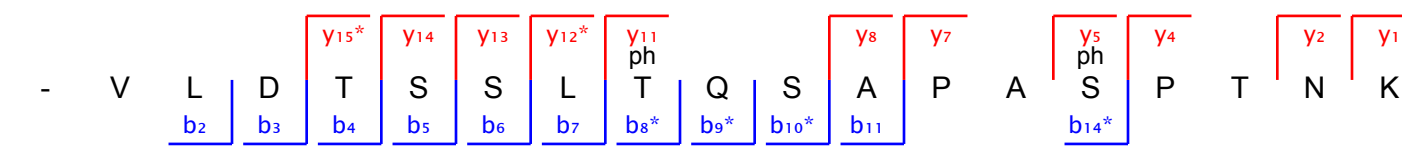
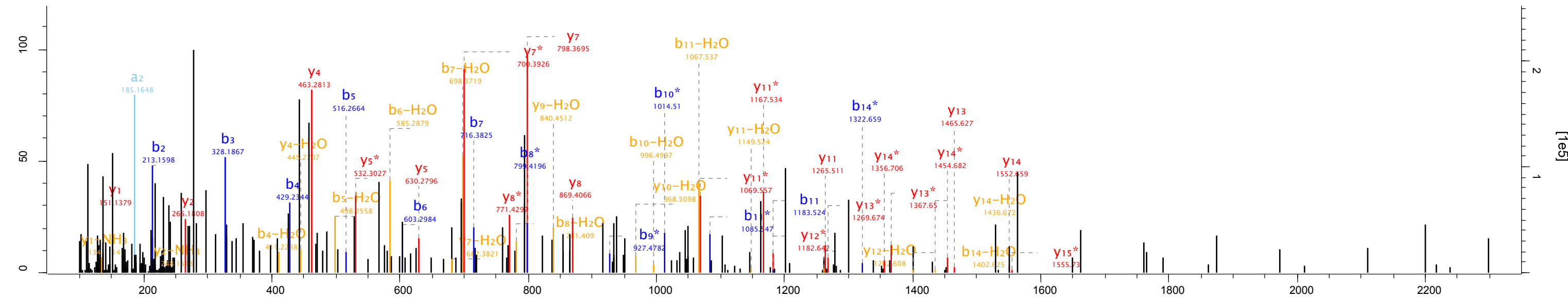
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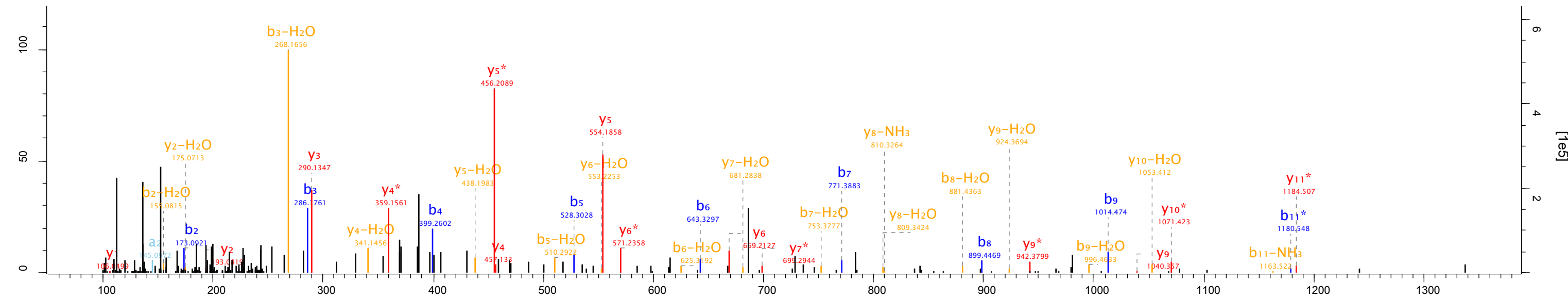


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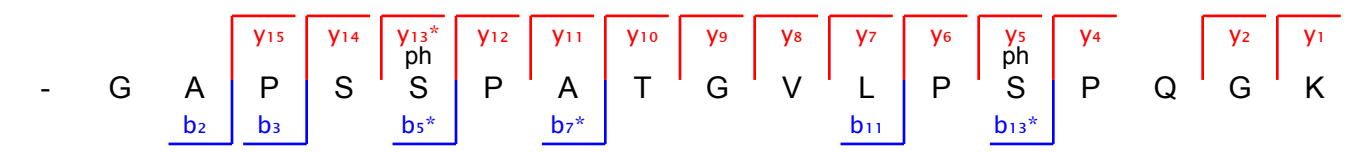
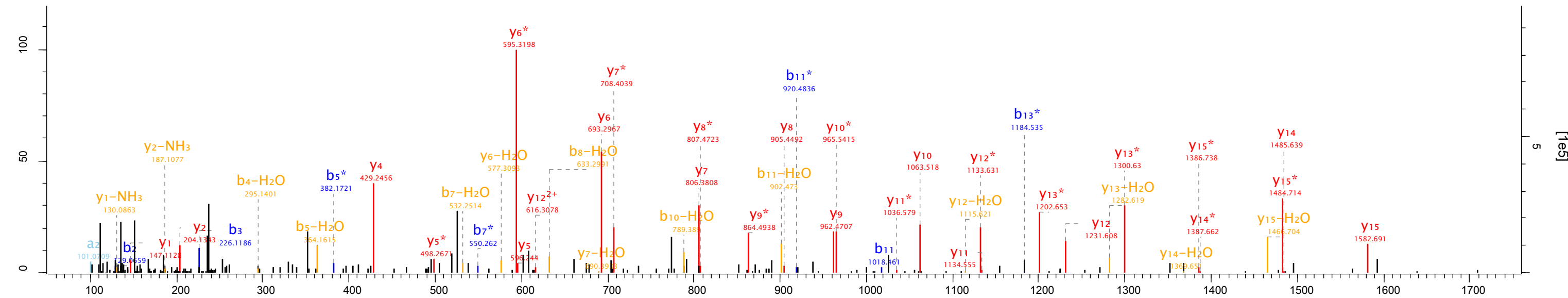


- A T L L E D Q Q D P S P S -

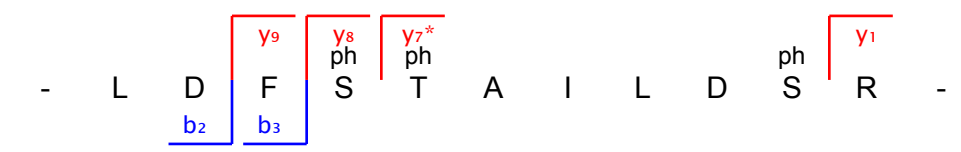
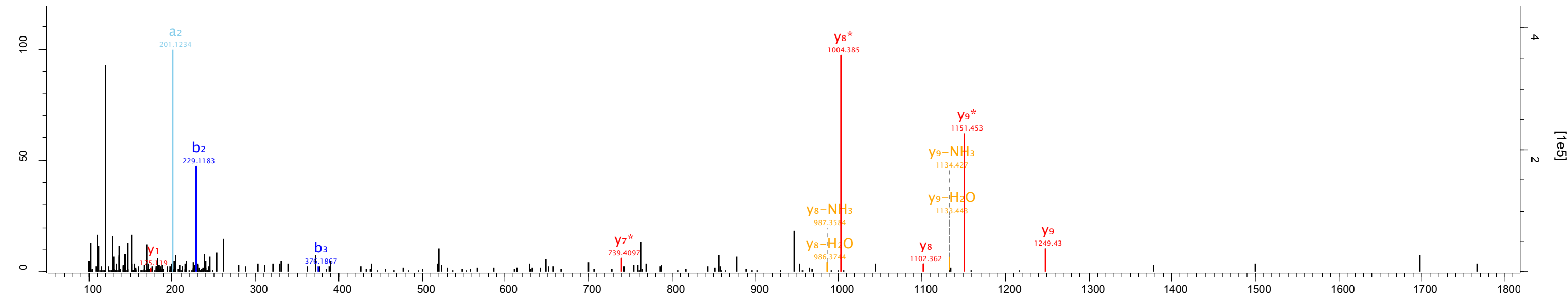
Fragmentation mapping (b and y ions) is shown below the sequence:

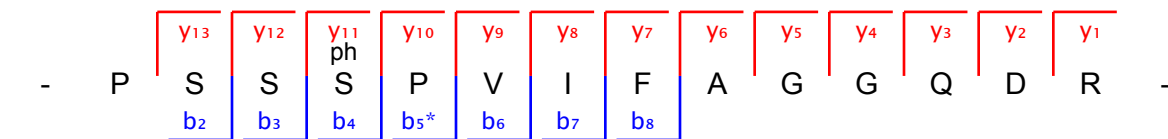
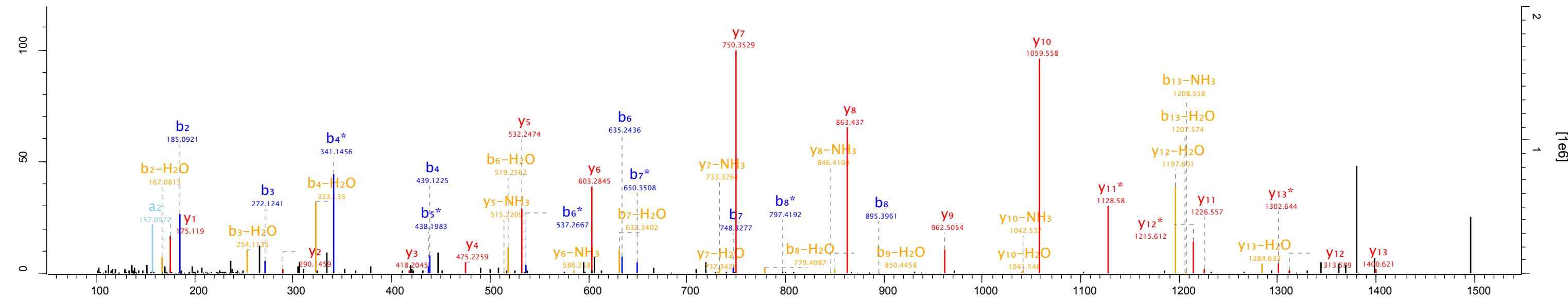
- b₂ (under T)
- b₃ (under L)
- b₄ (under L)
- b₅ (under E)
- b₆ (under D)
- b₇ (under Q)
- b₈ (under Q)
- b₉ (under D)
- b₁₁* (under S)
- y₁₁* (above L)
- y₁₀* (above E)
- y₉ (above D)
- y₇* (above Q)
- y₆ (above D)
- y₅ (above P)
- y₄ (above S)
- y₃ (above P)
- y₂ (above S)
- y₁ (above S)

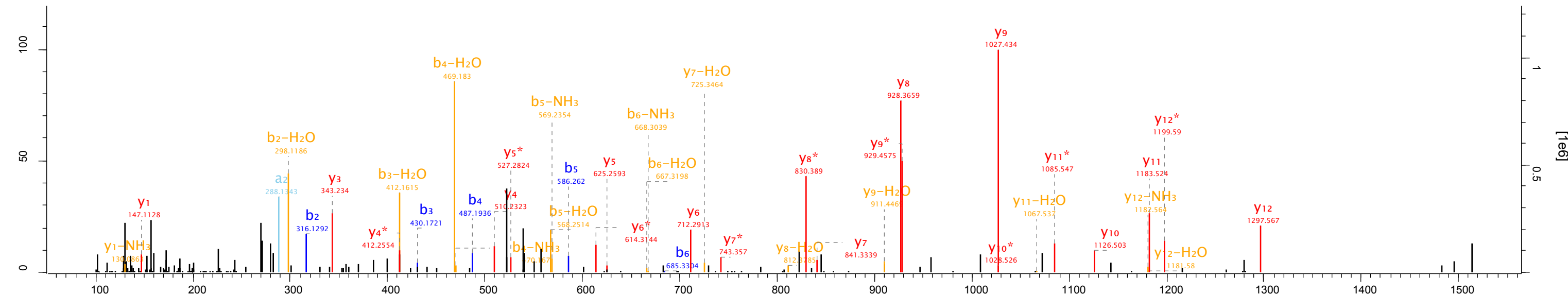
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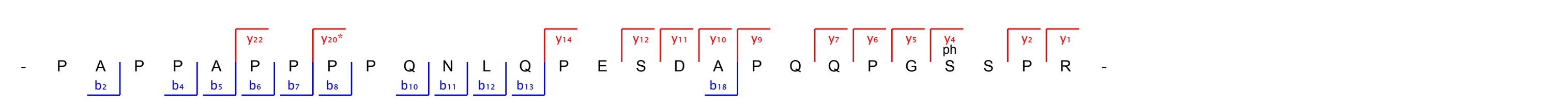
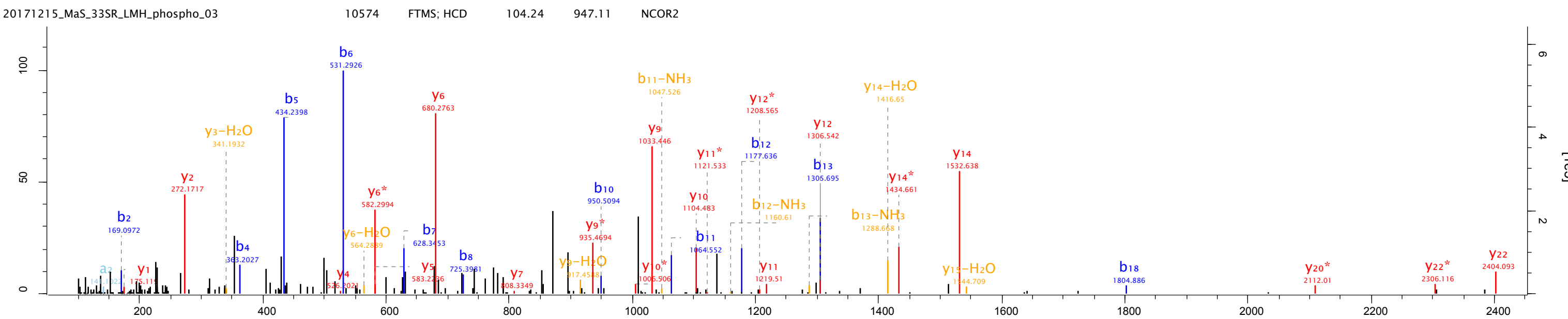


- E W N G V V S E S D S P V K -

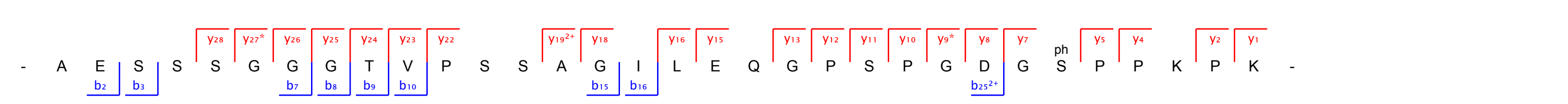
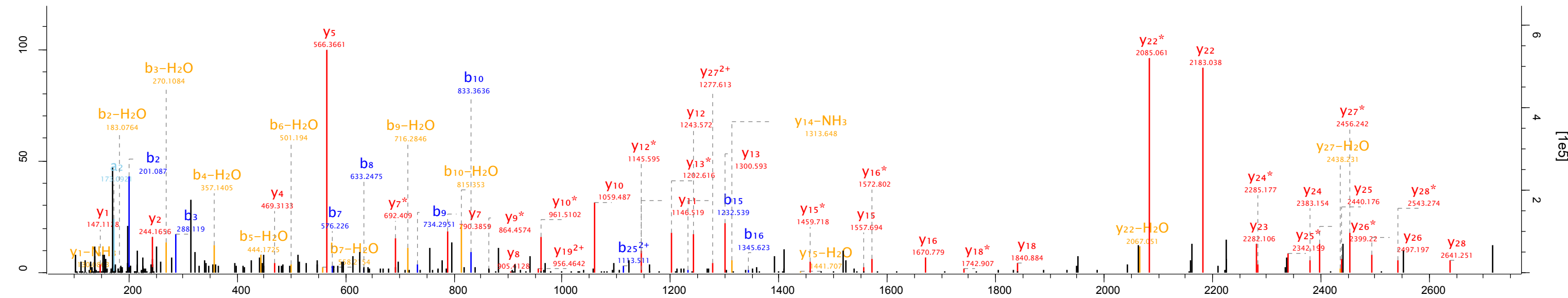
Fragmentation mapping (b and y ions):

- b₂ (under W)
- b₃ (under N)
- b₄ (under G)
- b₅ (under V)
- b₆ (under V)
- y₁ (under K)
- y₃ (under P)
- y₄ (under S)
- y₅ (under D)
- y₆ (under S)
- y₇ (under E)
- y₈ (under S)
- y₉ (under V)
- y₁₀ (under V)
- y₁₁ (under G)
- y₁₂ (under N)

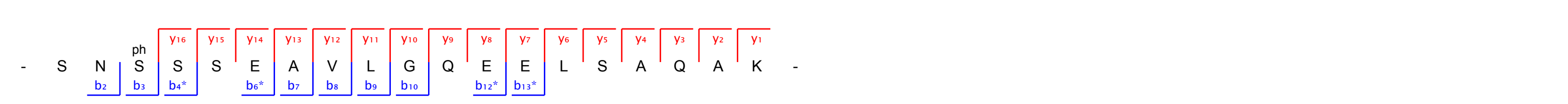
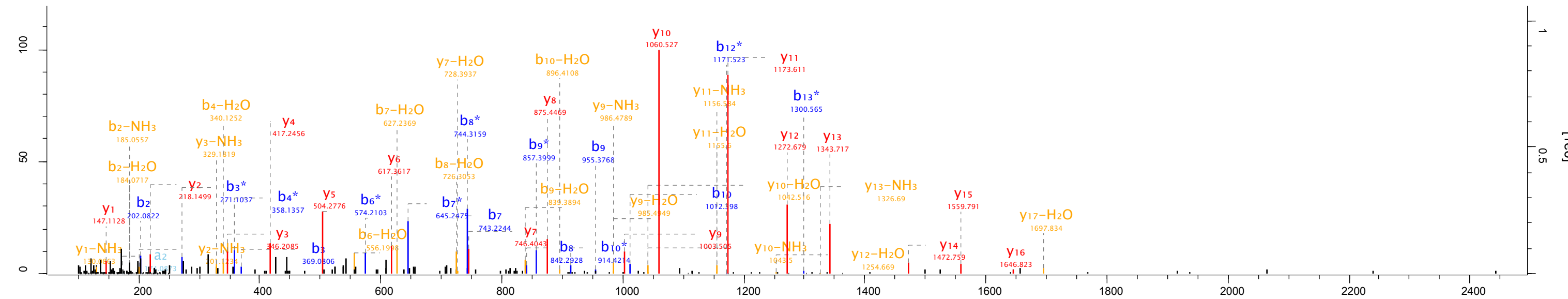
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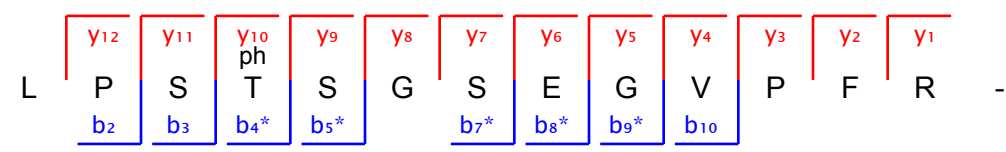
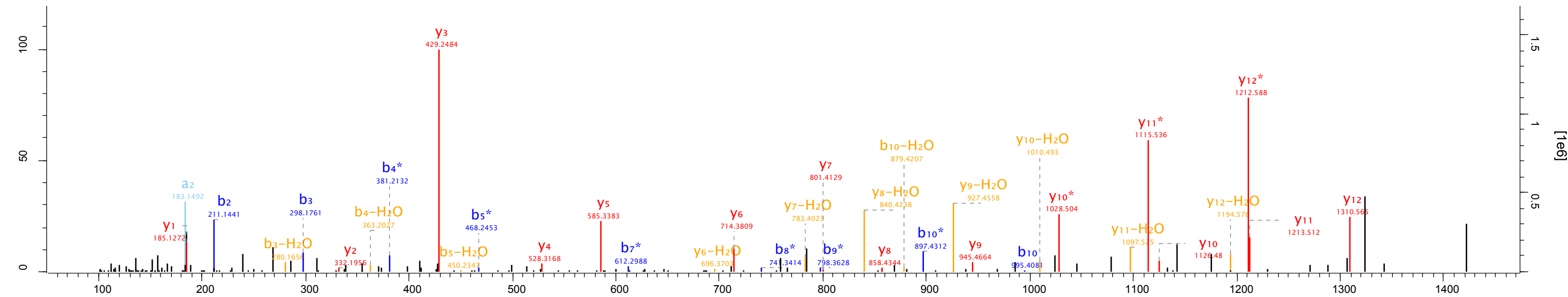
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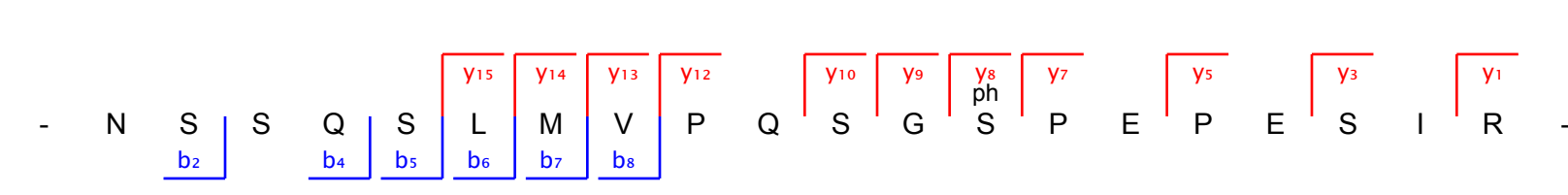
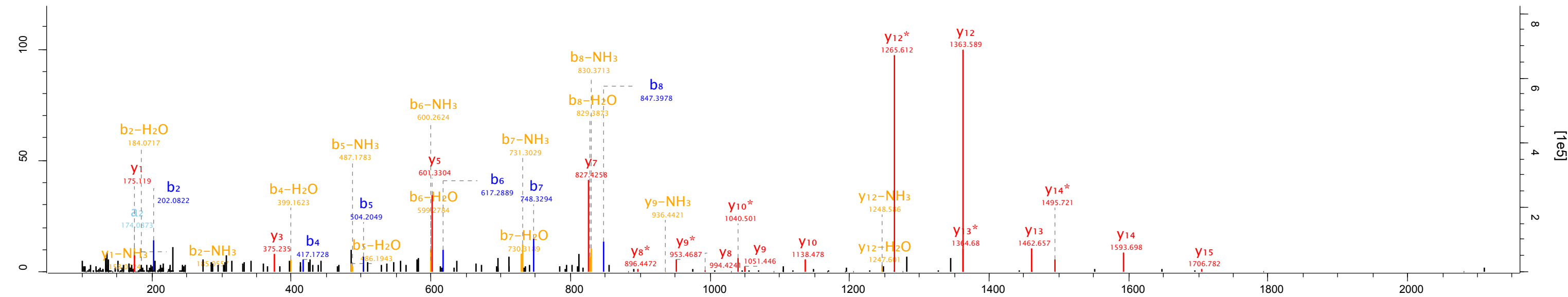
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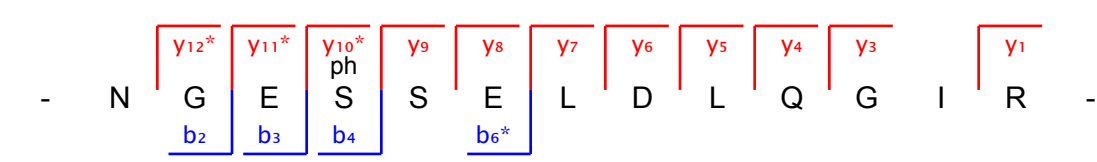
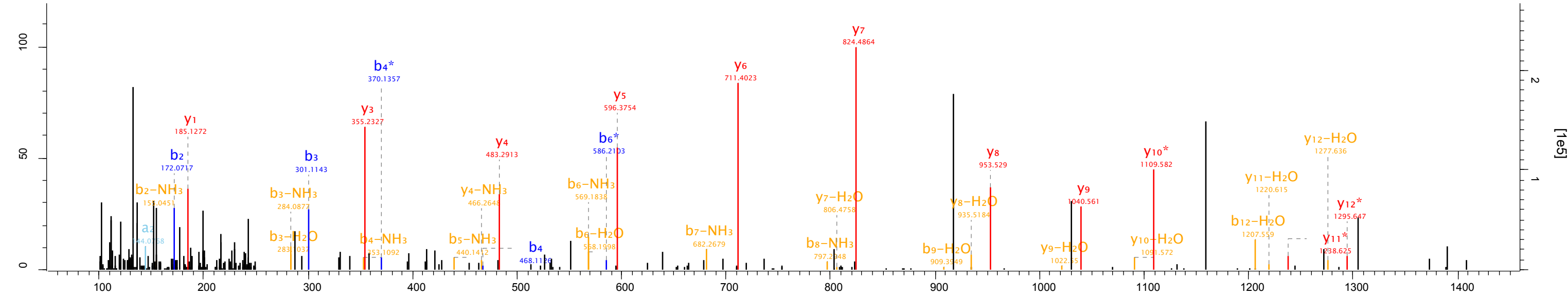
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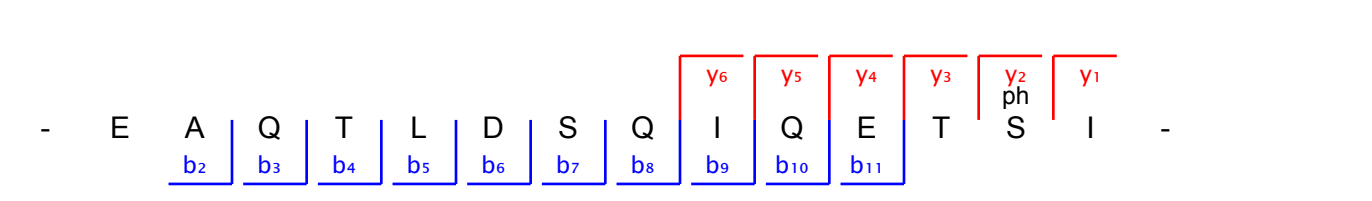
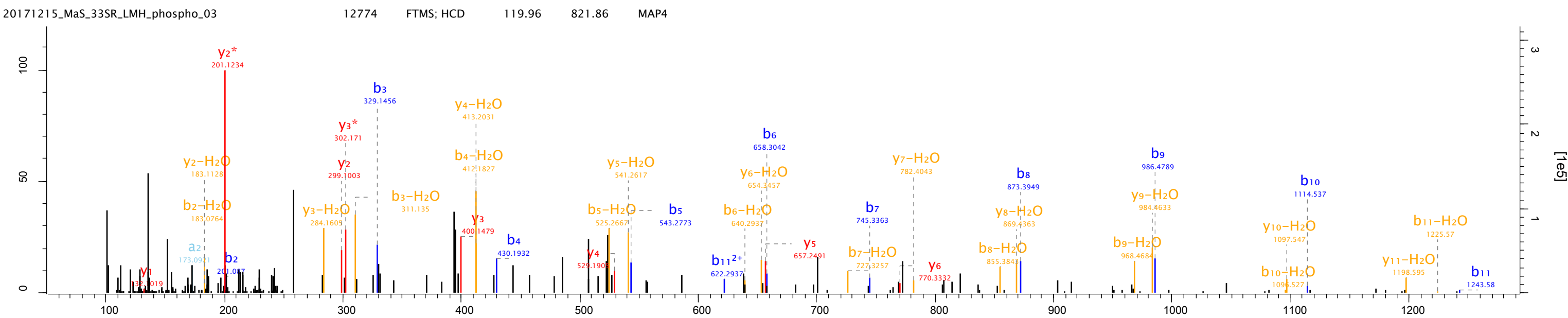


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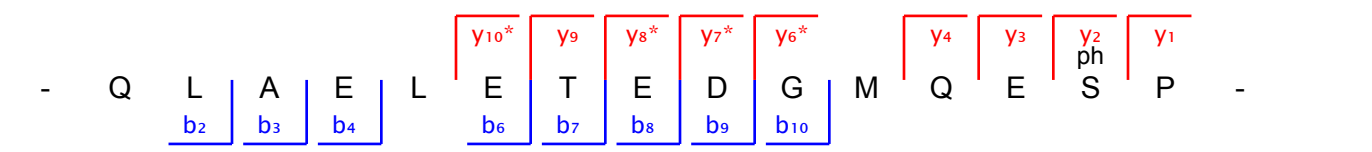
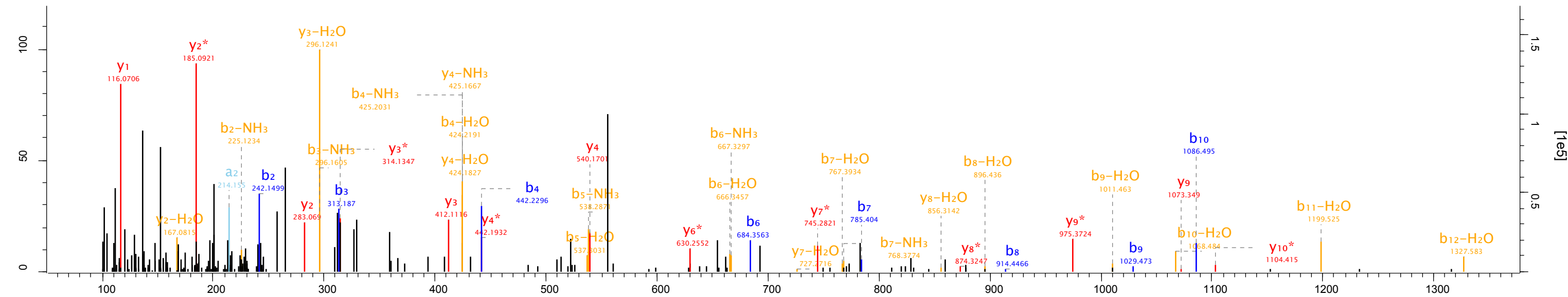


20171215_MaS_33SR_LMH_phospho_03 12744 FTMS; HCD 109.14 754.34 CNPY2

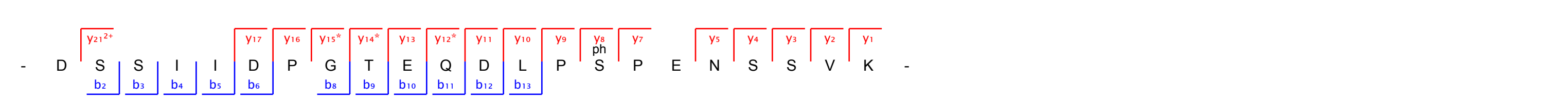
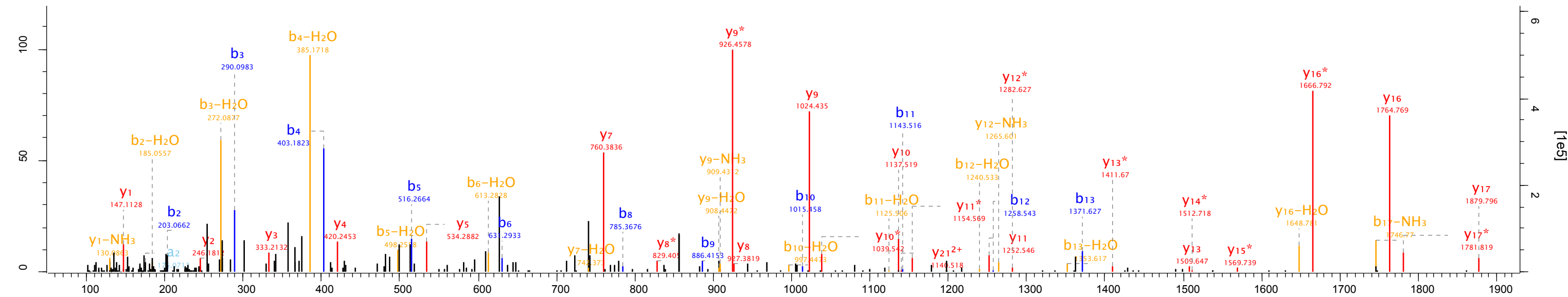




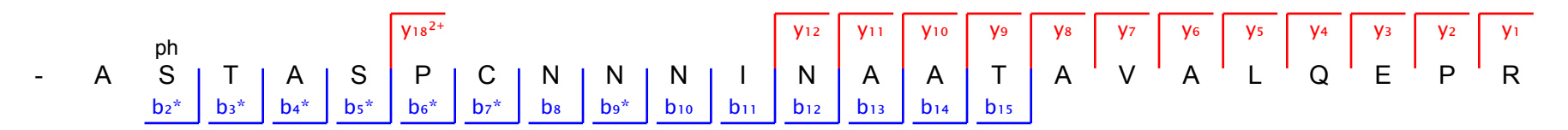
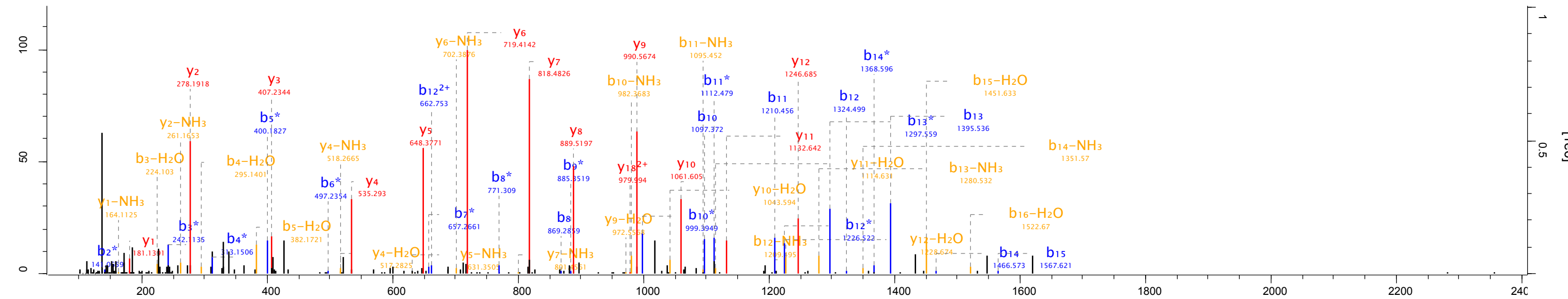
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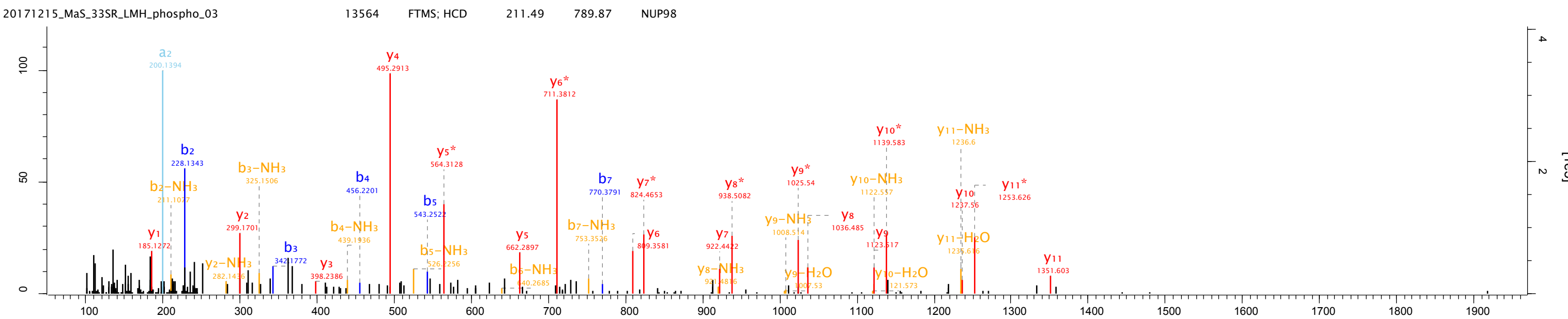
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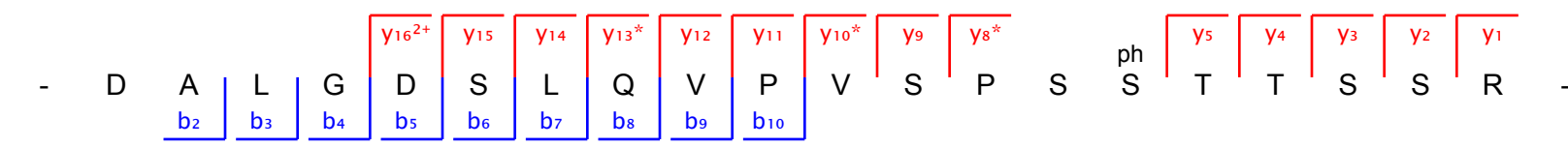
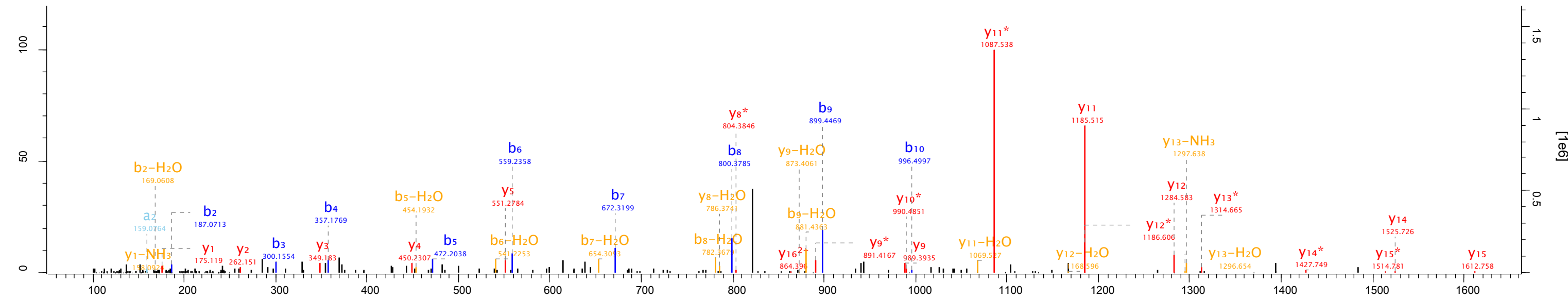
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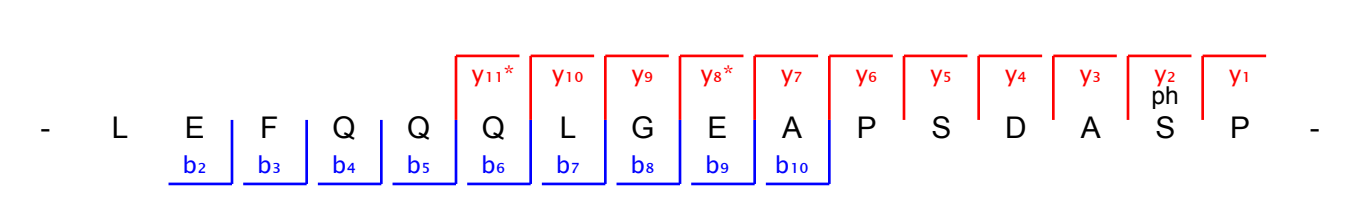
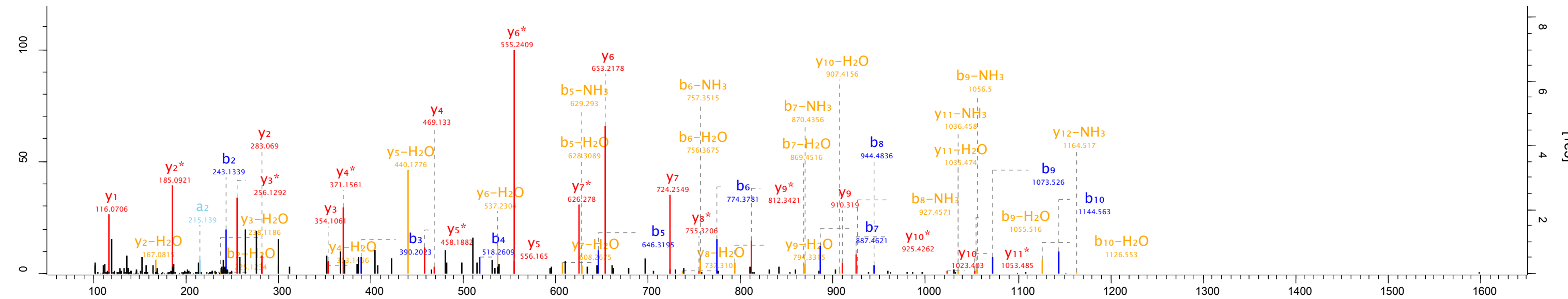
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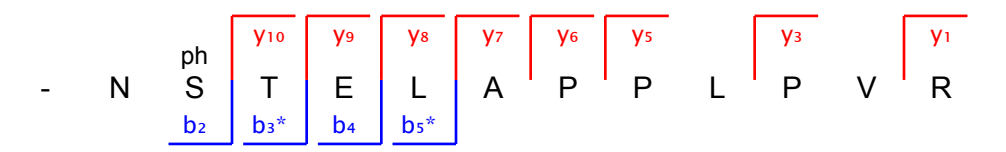
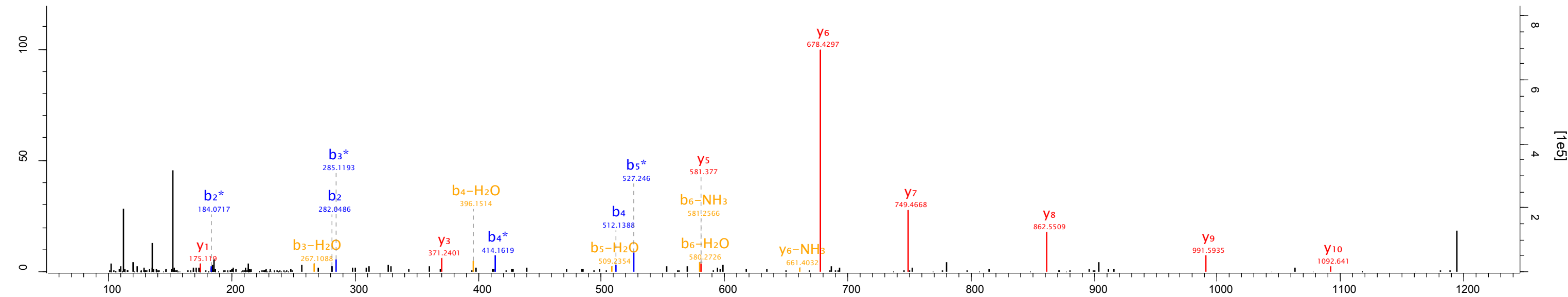
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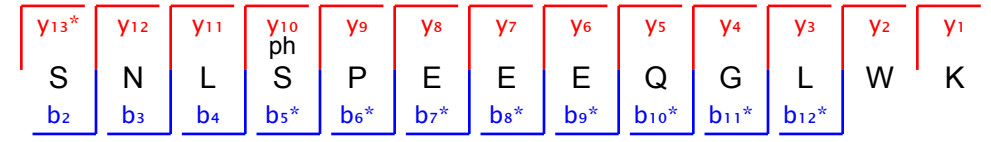
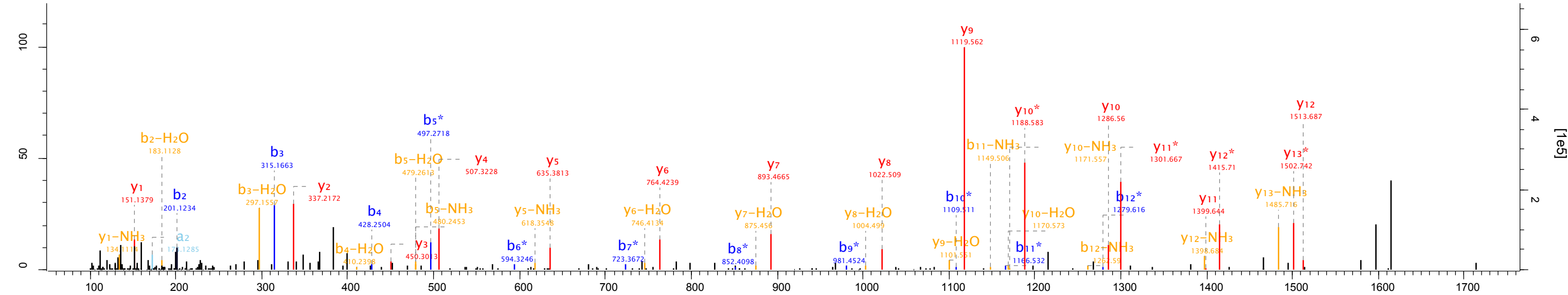
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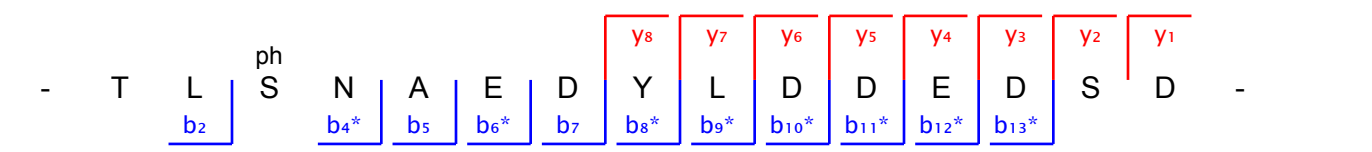
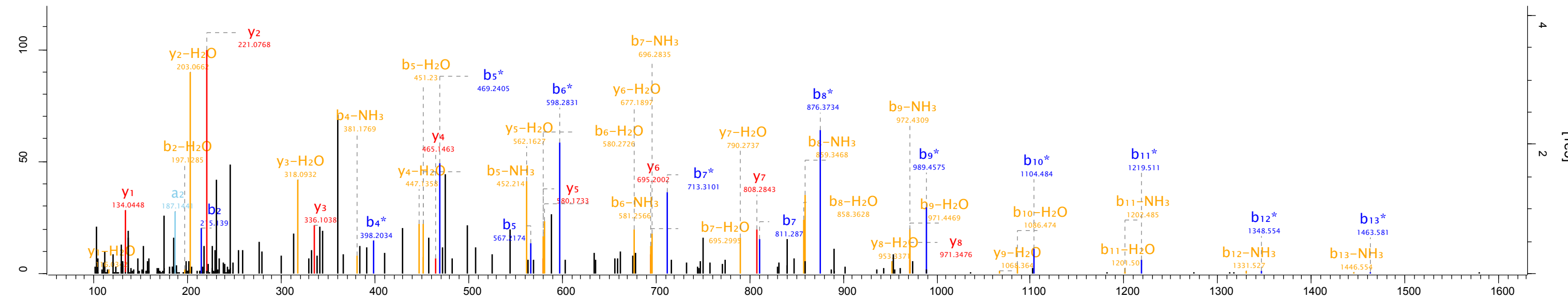
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20171215_MaS_33SR_LMH_phospho_03 14404 FTMS; HCD 218.64 857.91 FAM76B

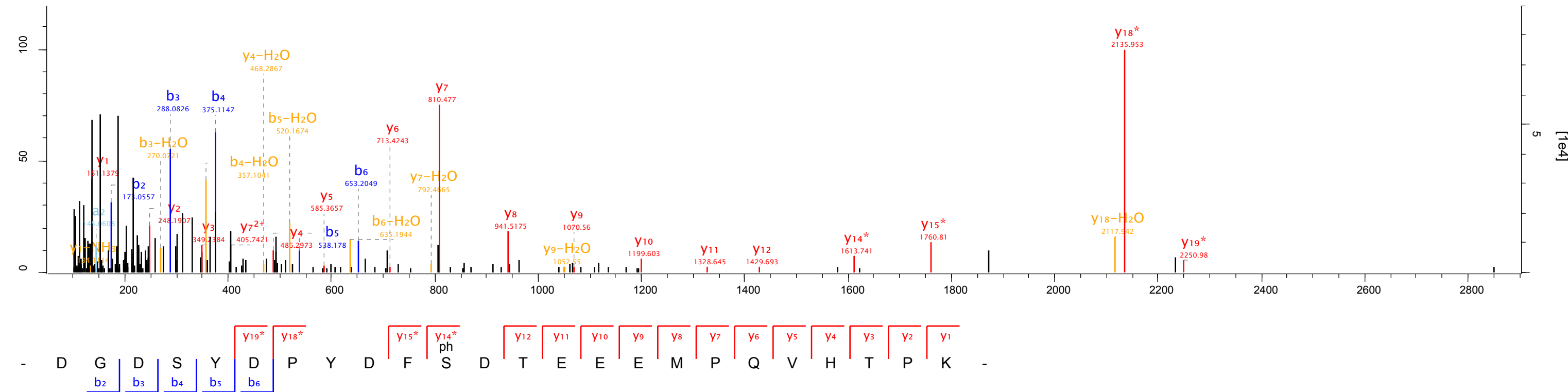


20171215_MaS_33SR_LMH_phospho_03 14794 FTMS; HCD 232.78 891.32 OSTF1

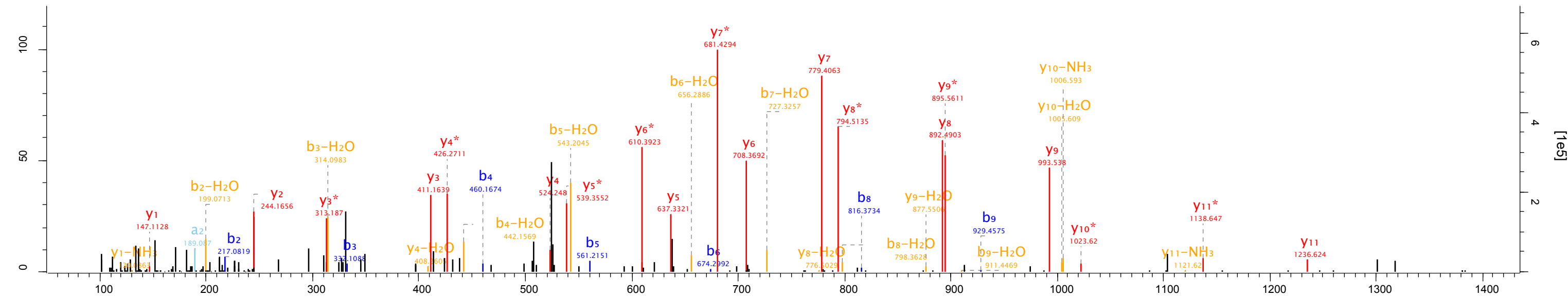


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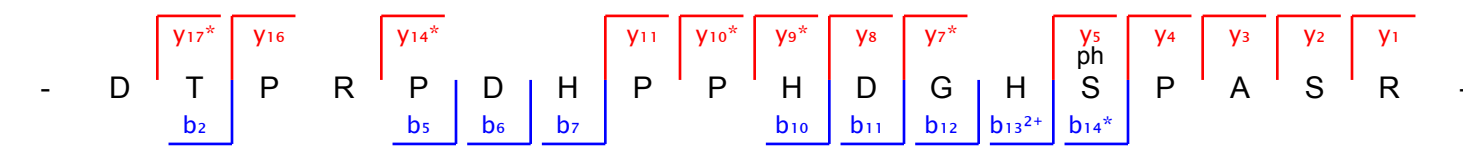
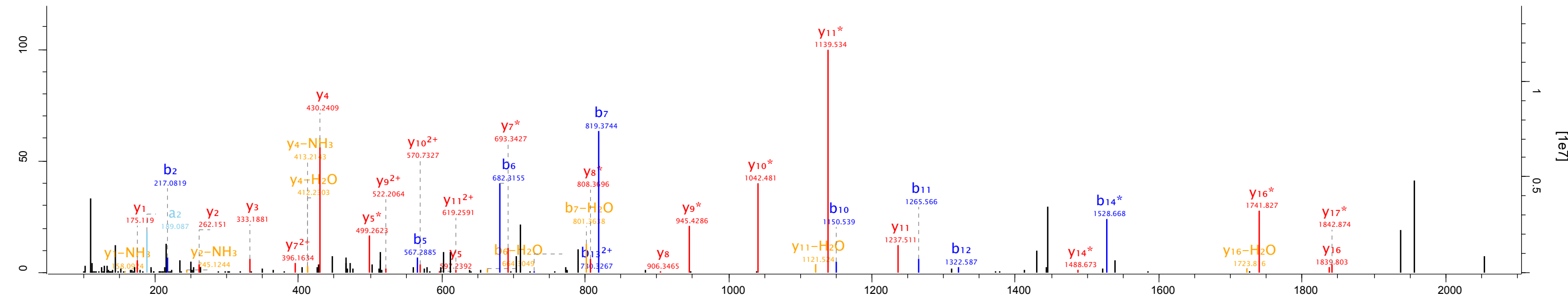
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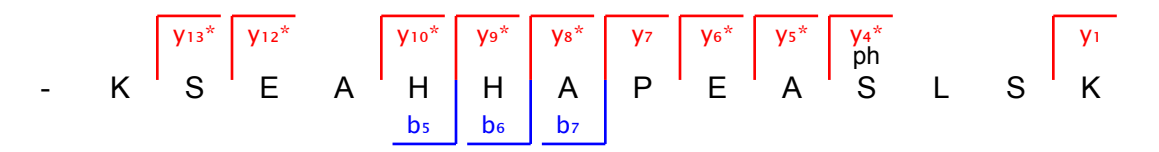
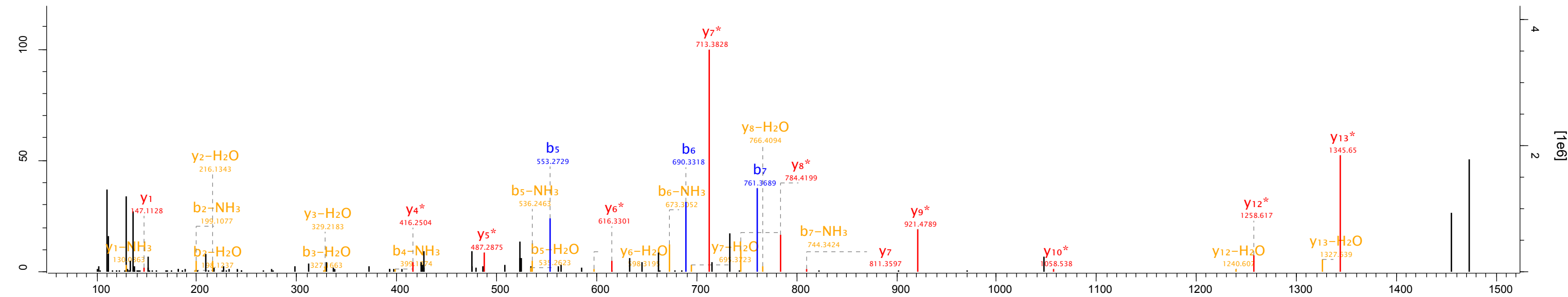
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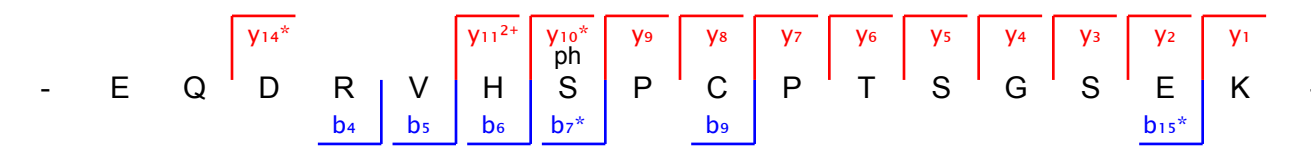
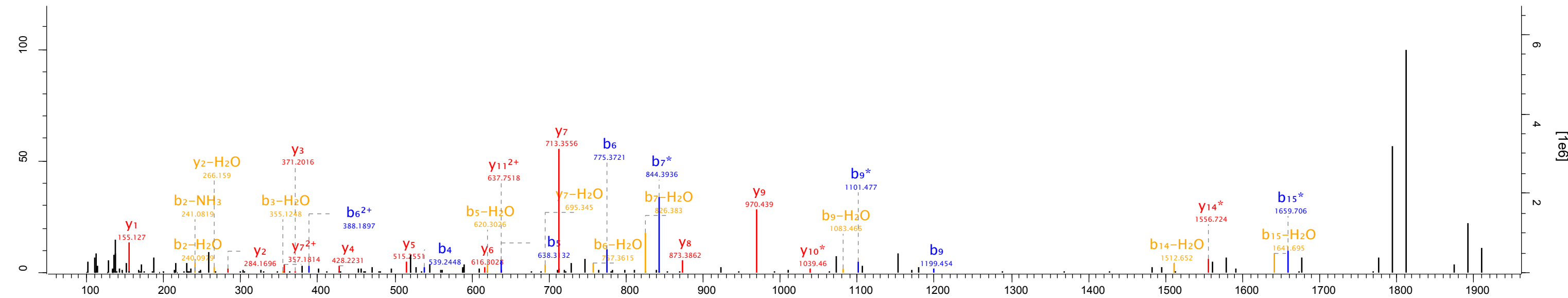
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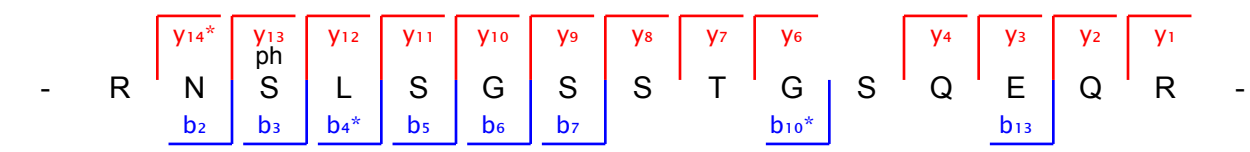
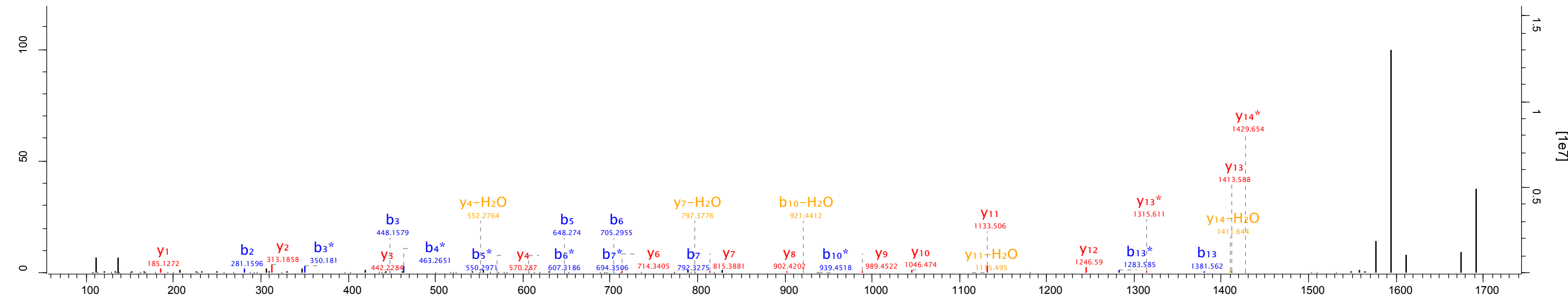
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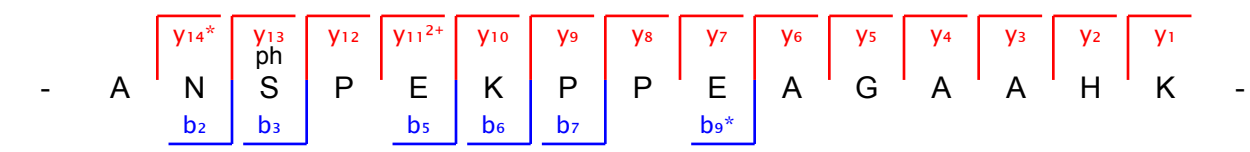
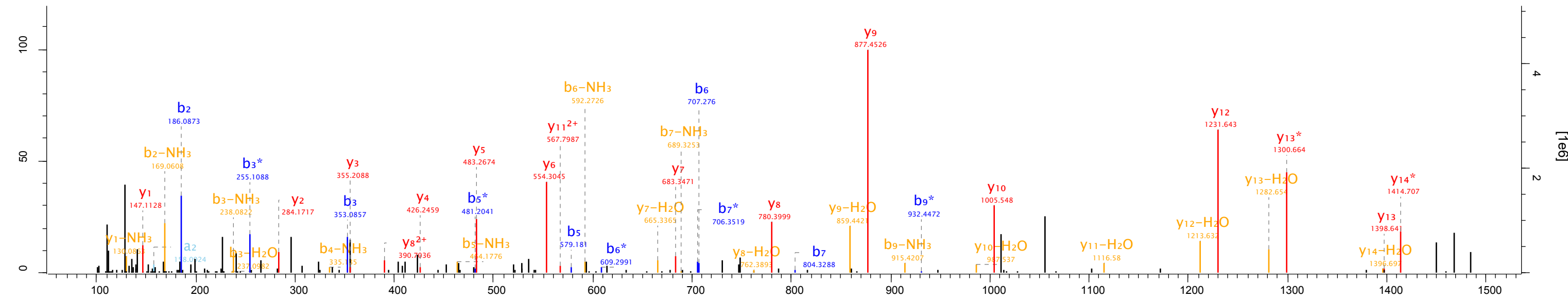
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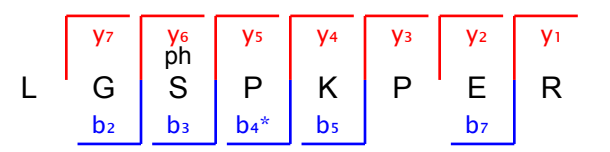
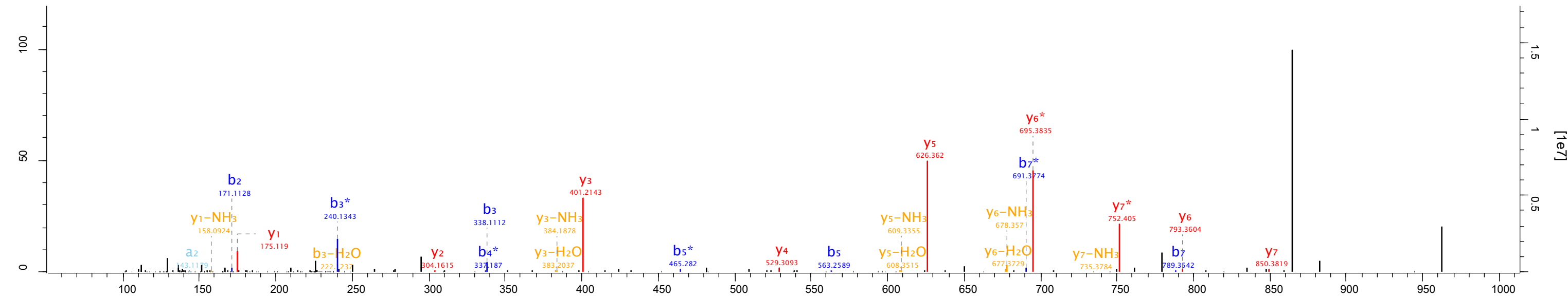
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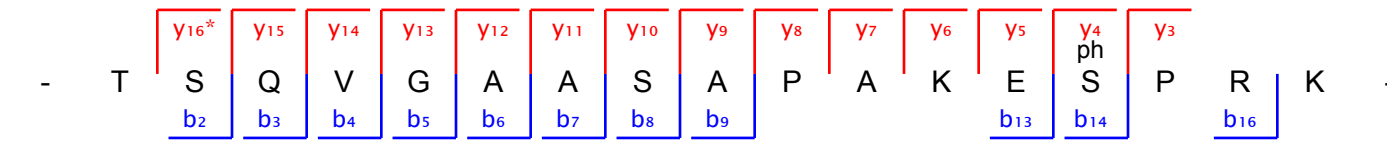
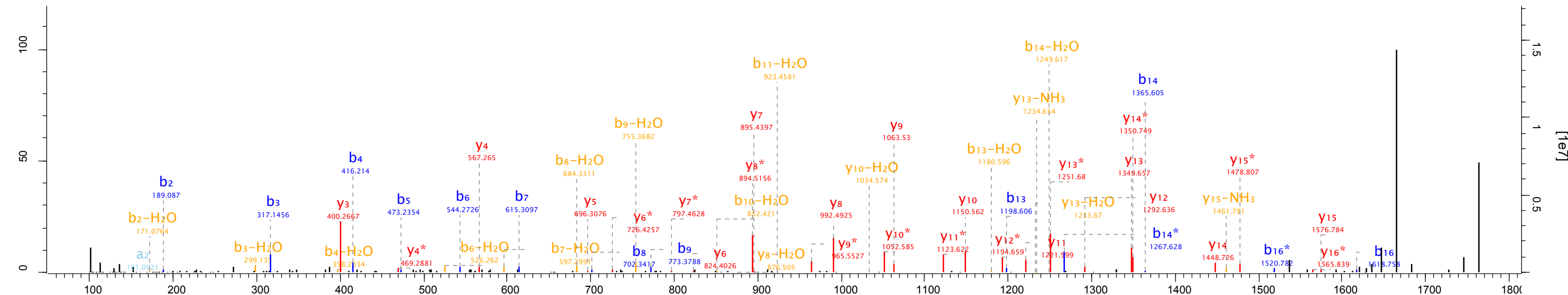
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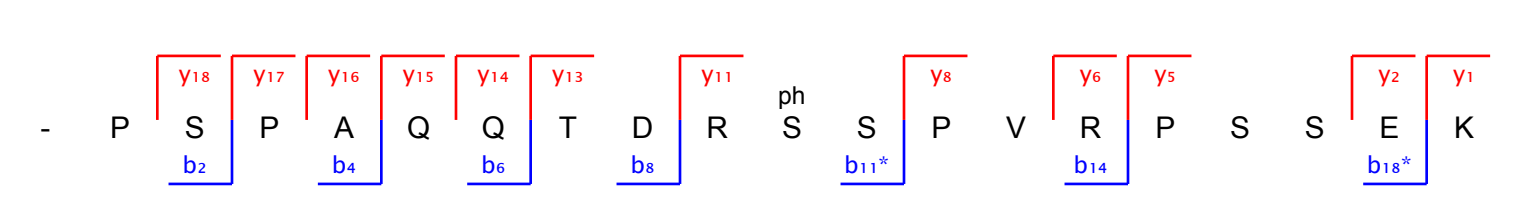
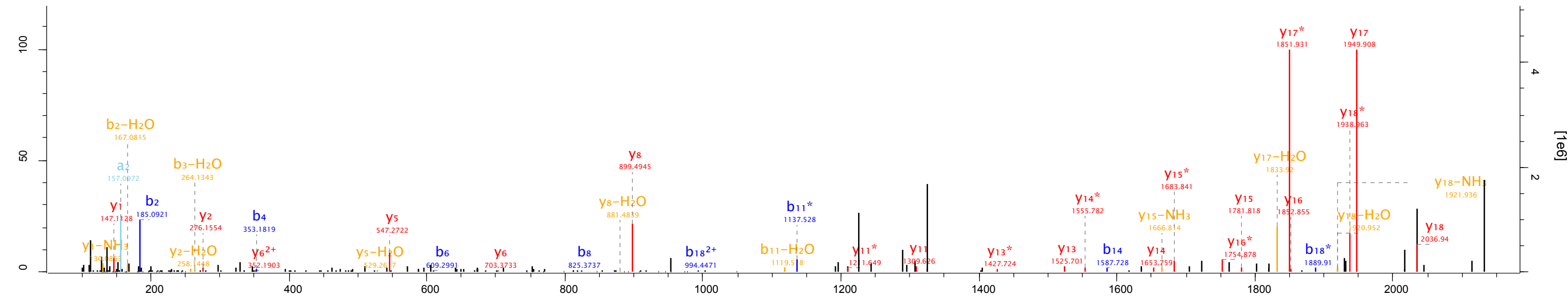
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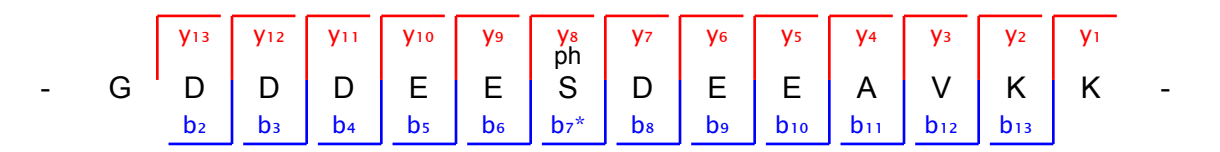
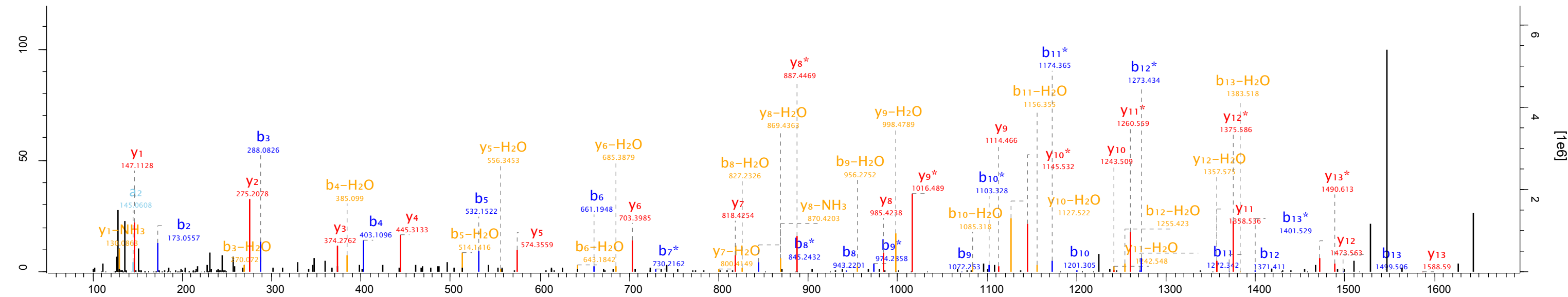
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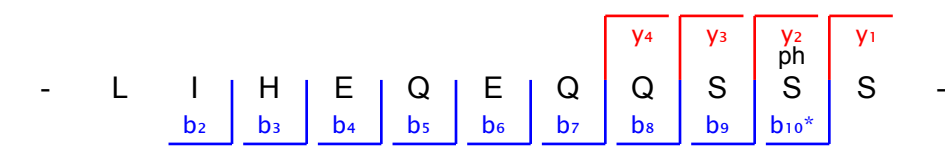
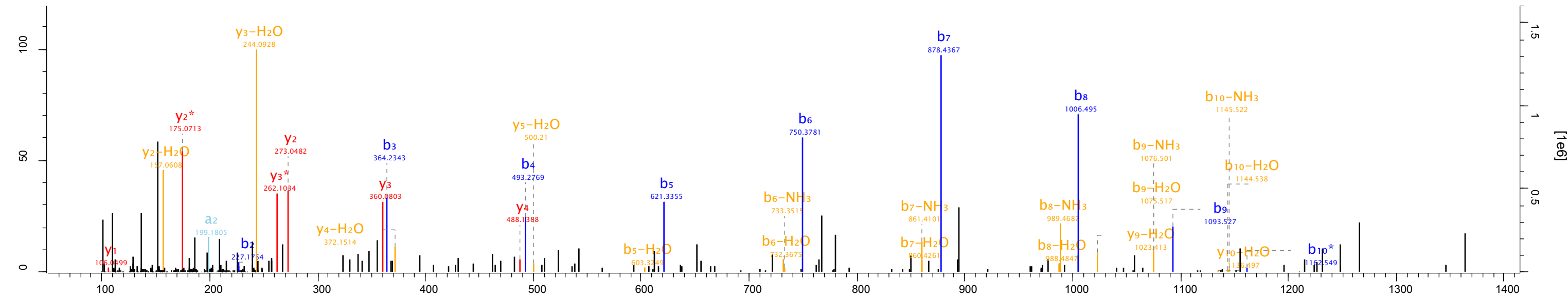
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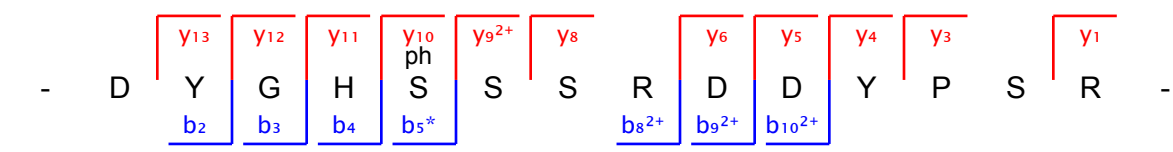
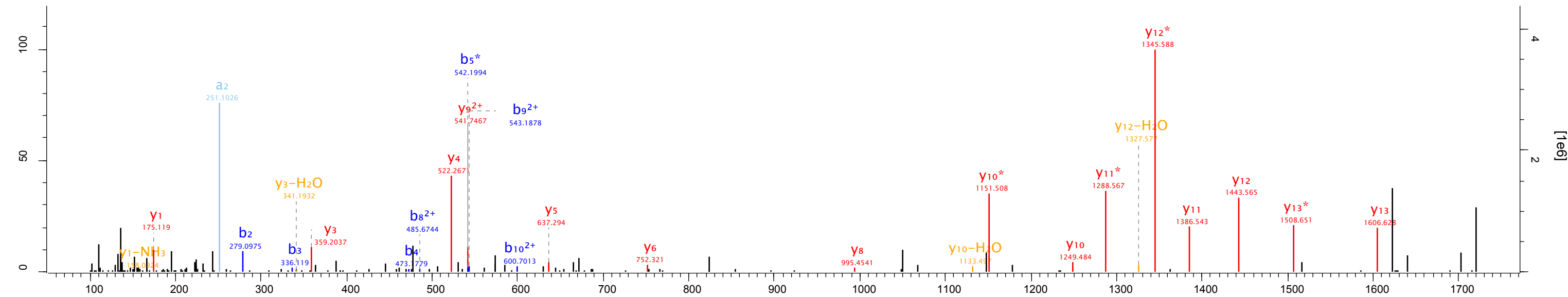
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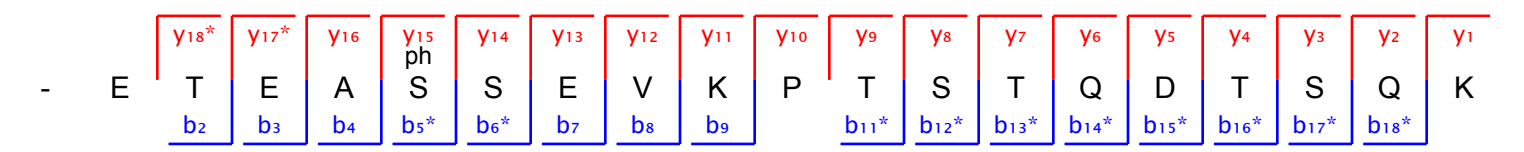
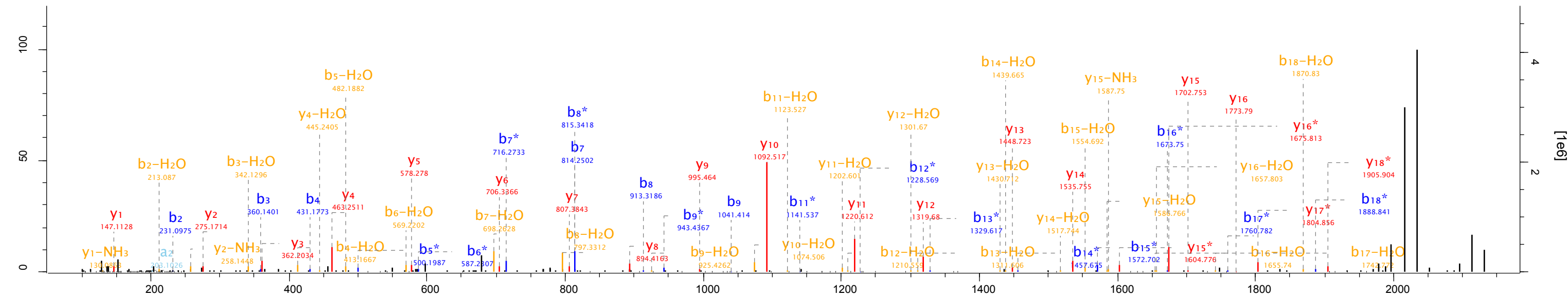
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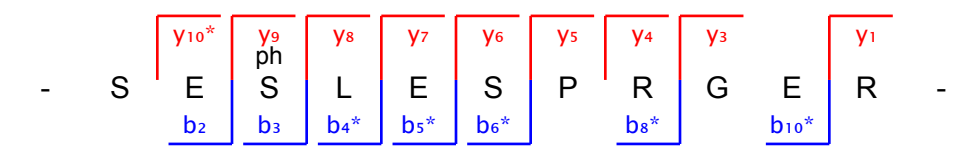
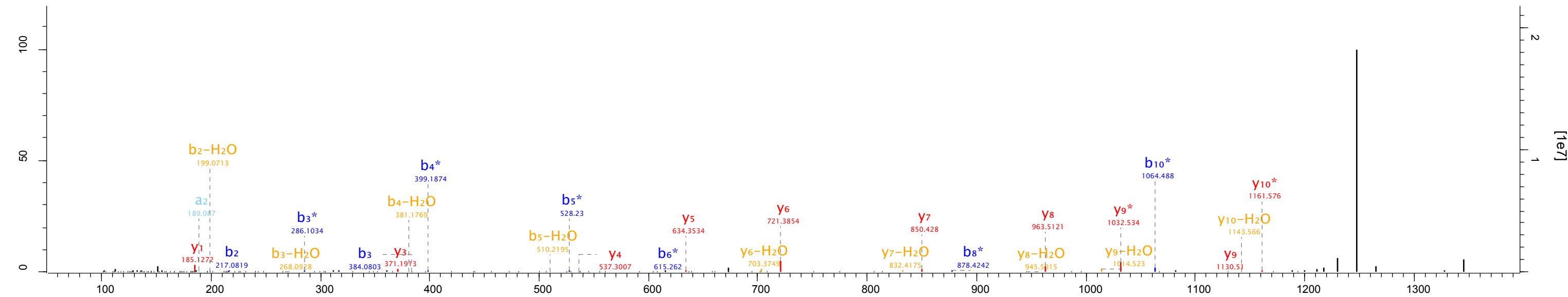
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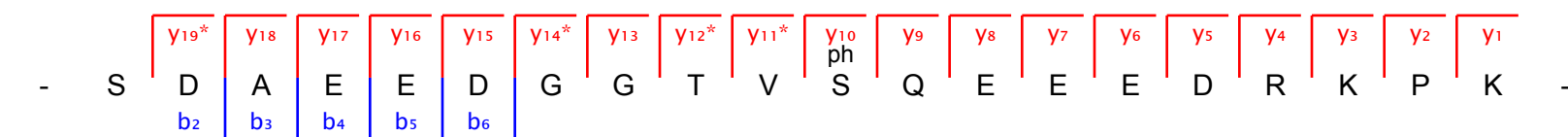
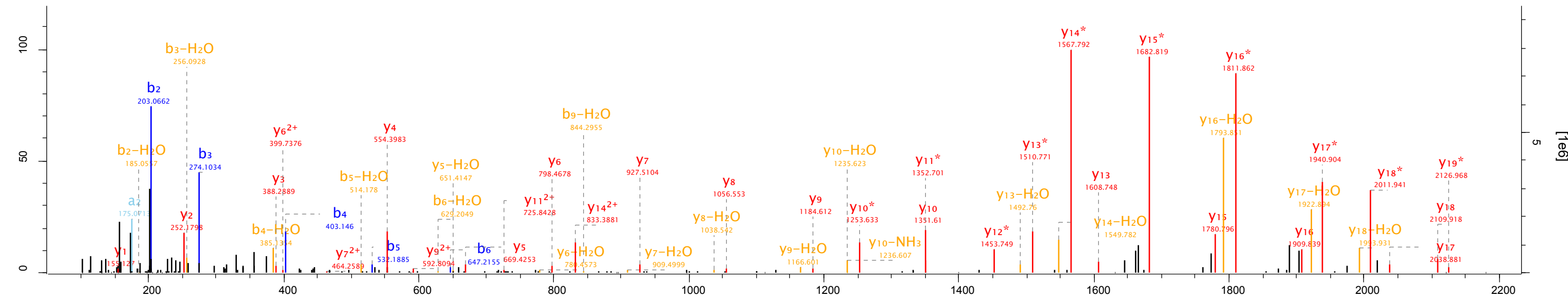
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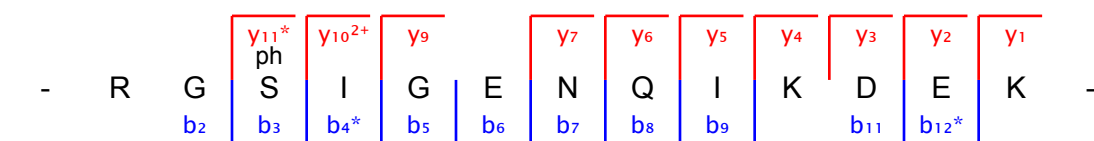
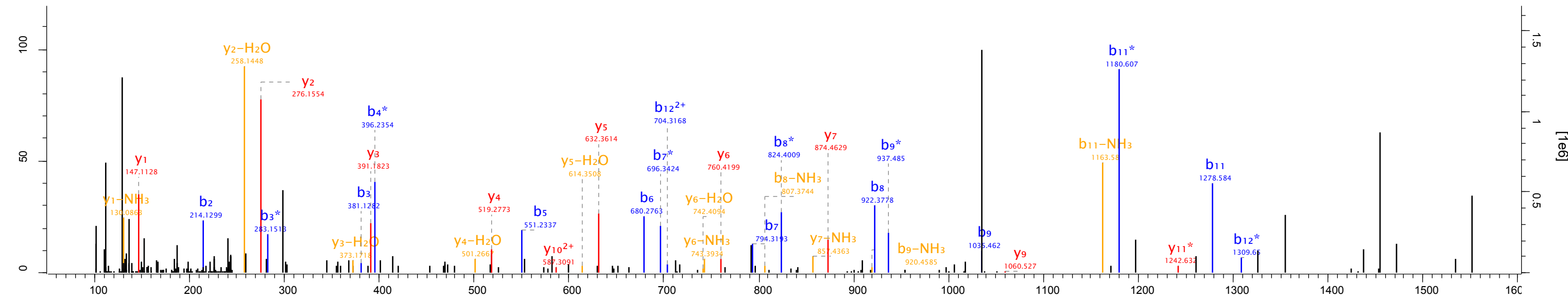


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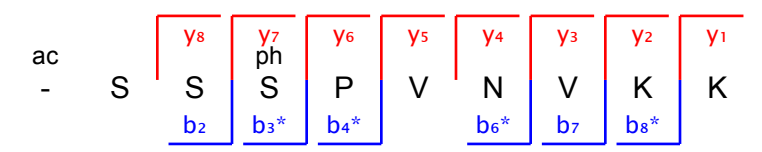
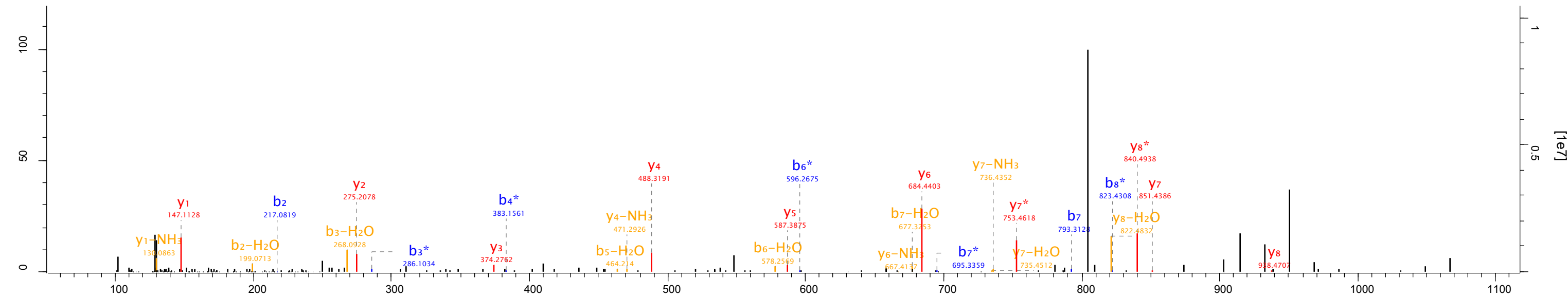


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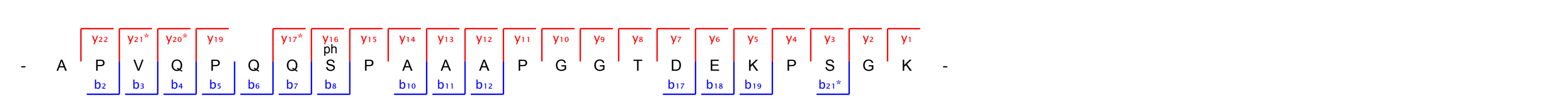
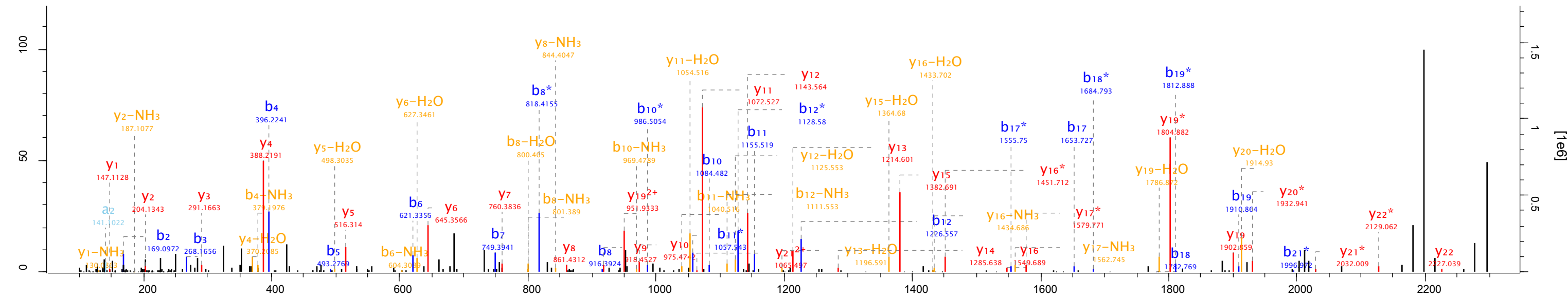




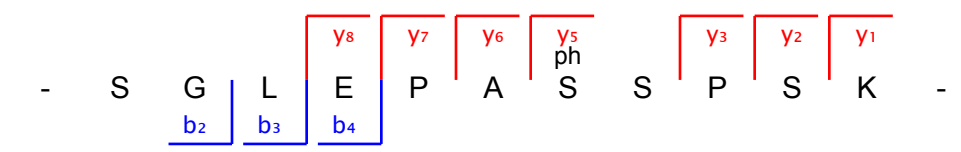
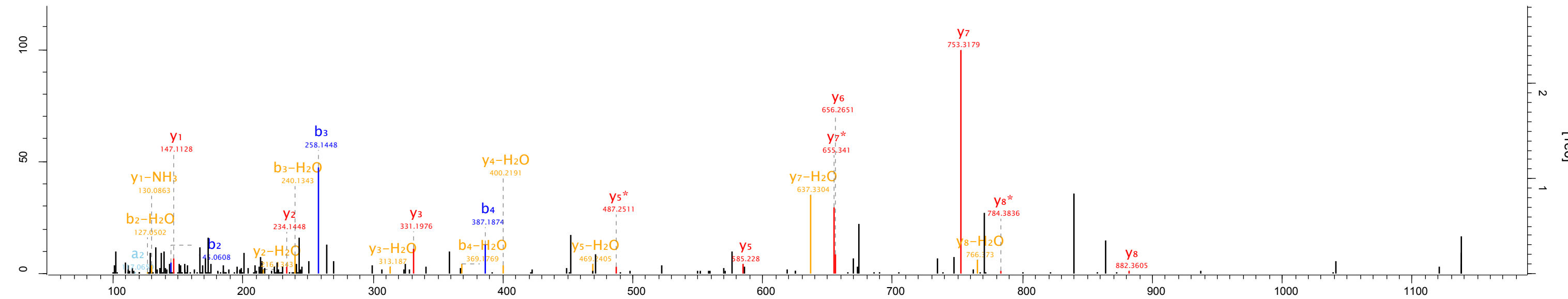
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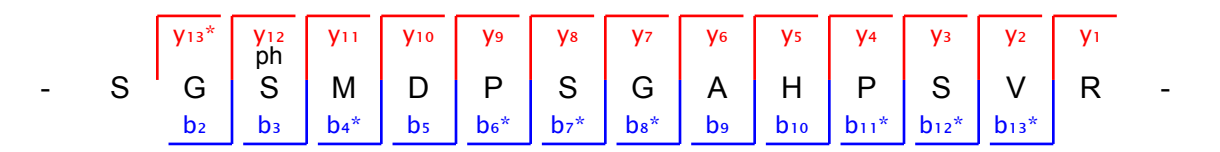
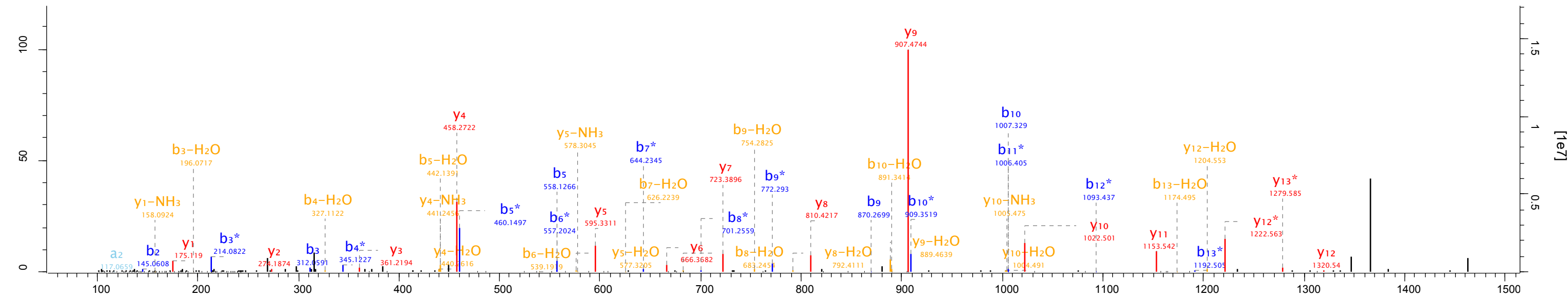
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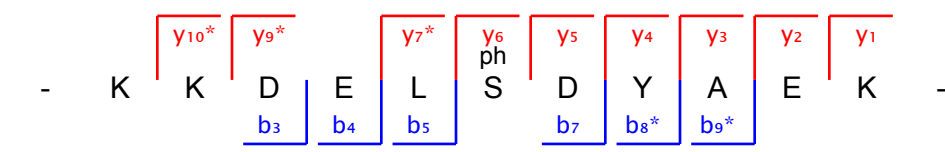
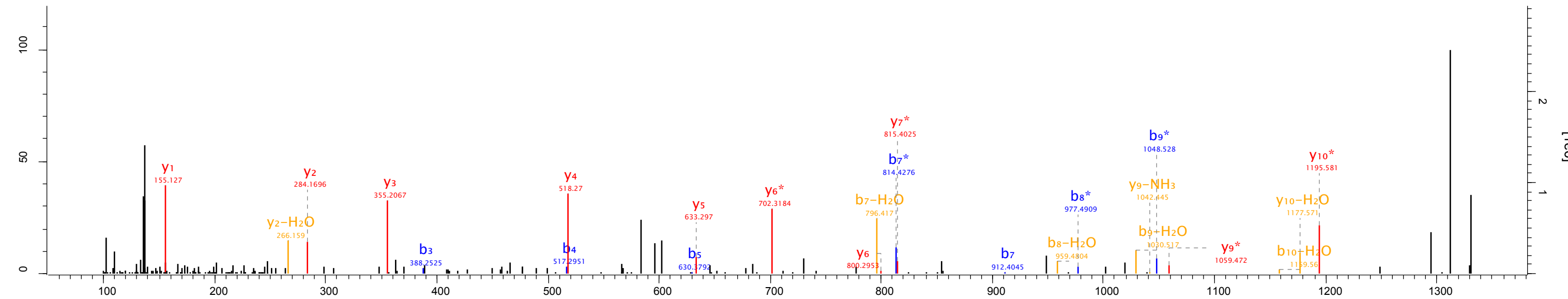
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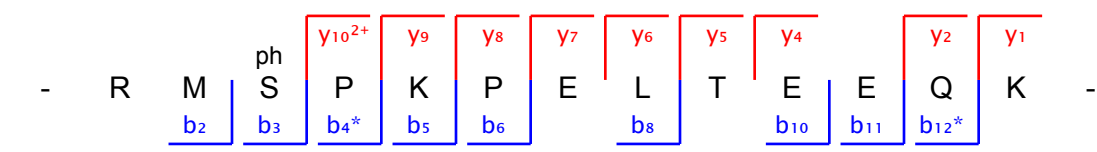
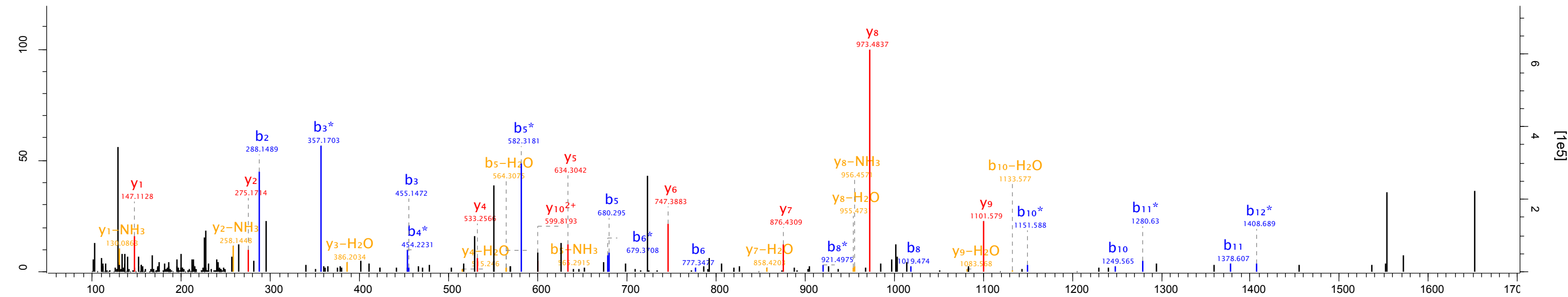
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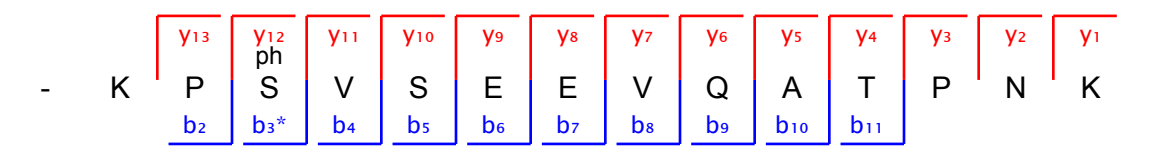
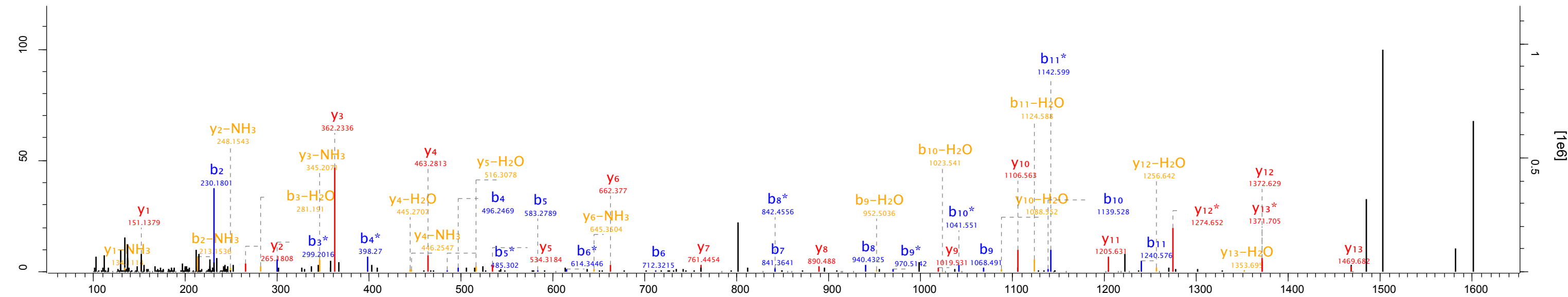
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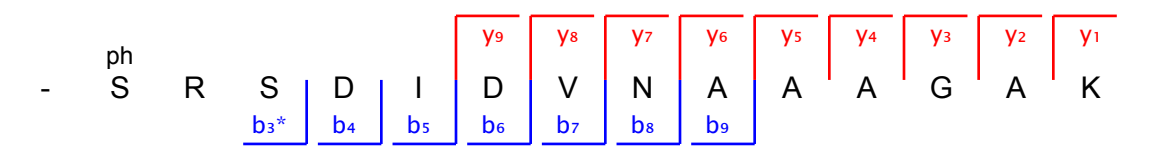
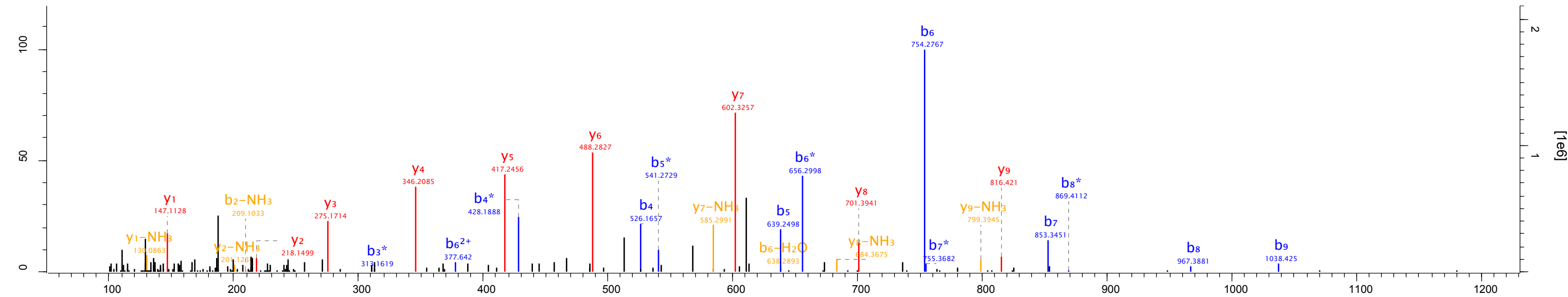
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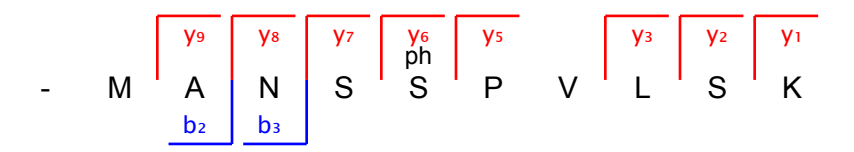
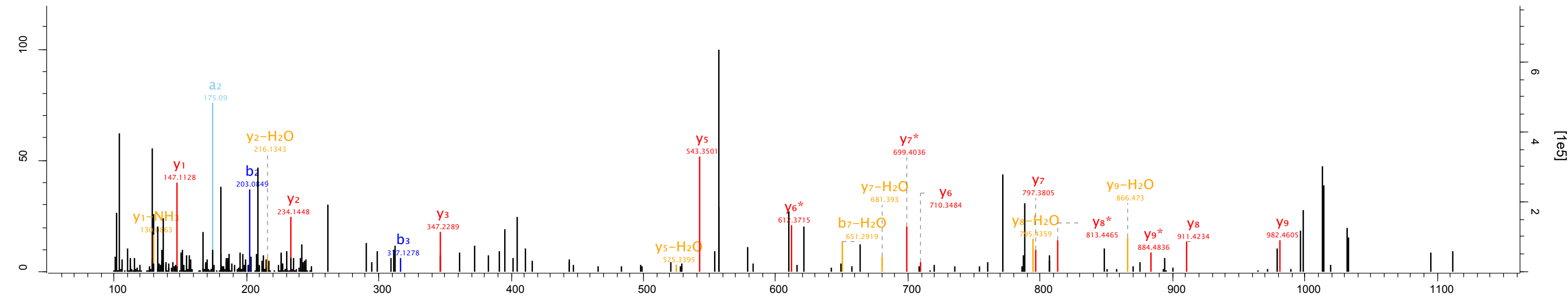
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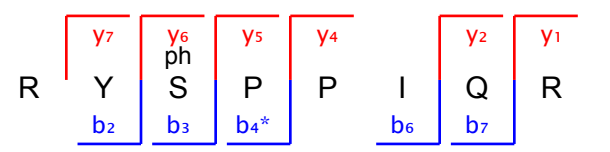
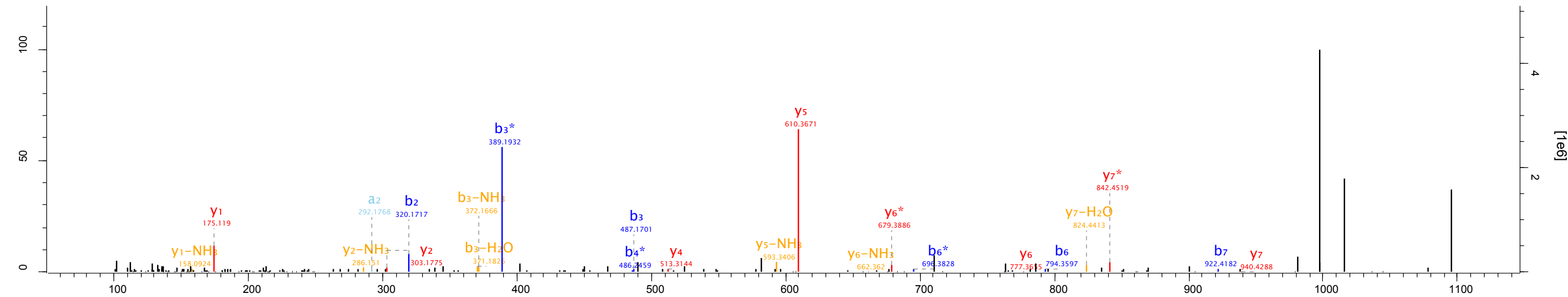
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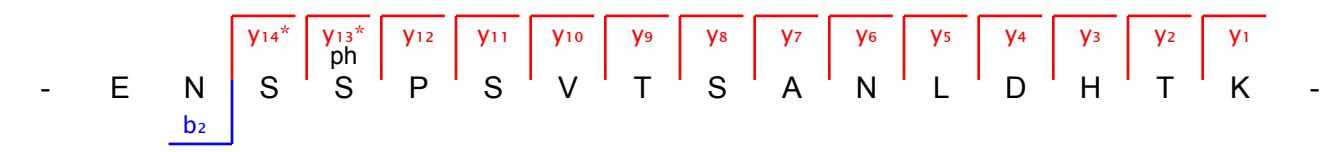
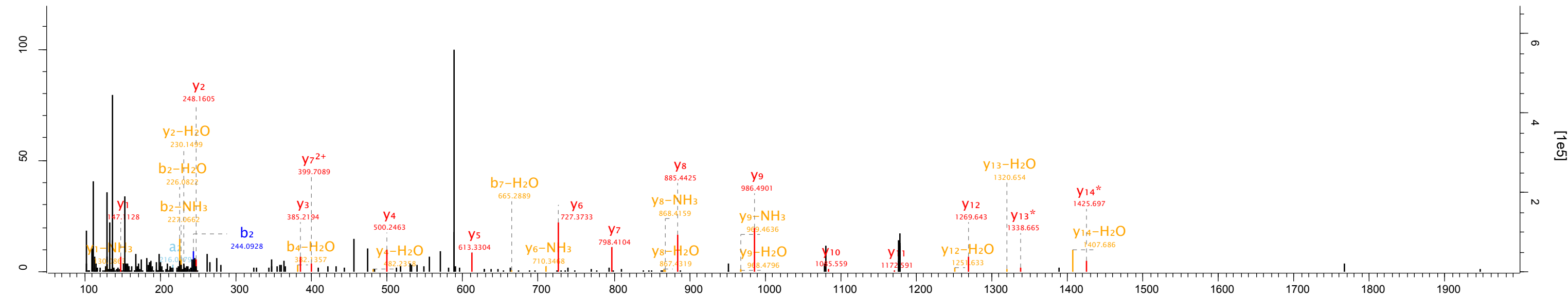
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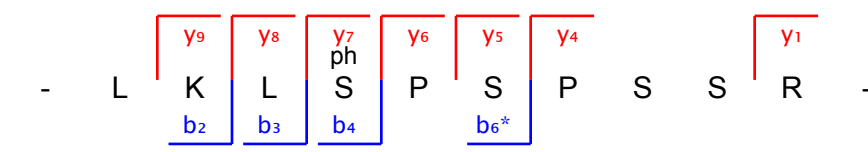
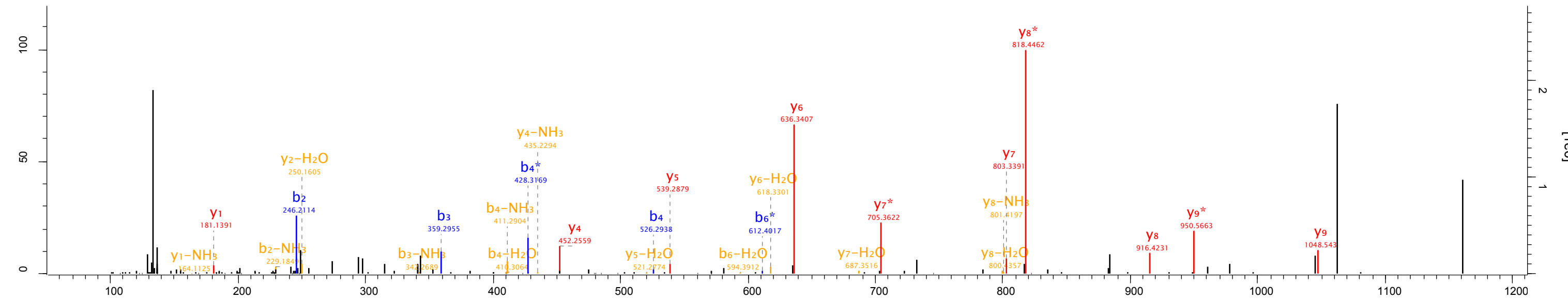
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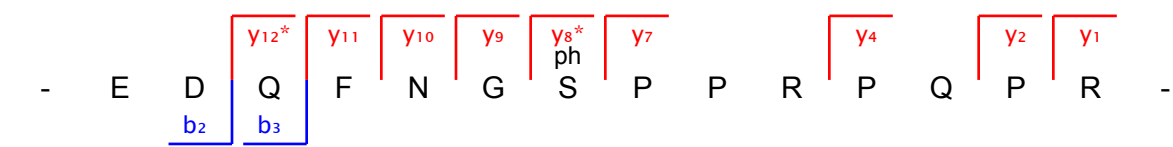
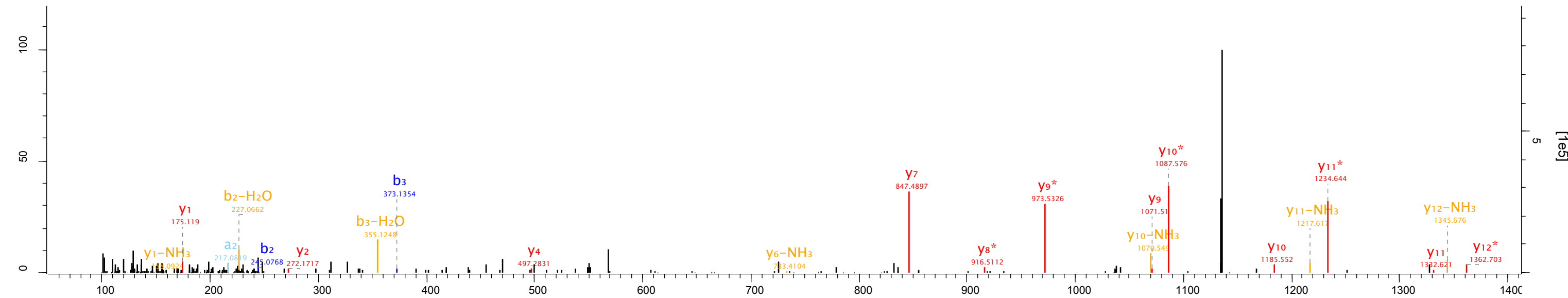
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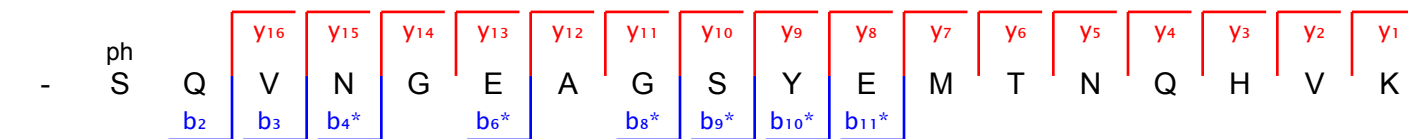
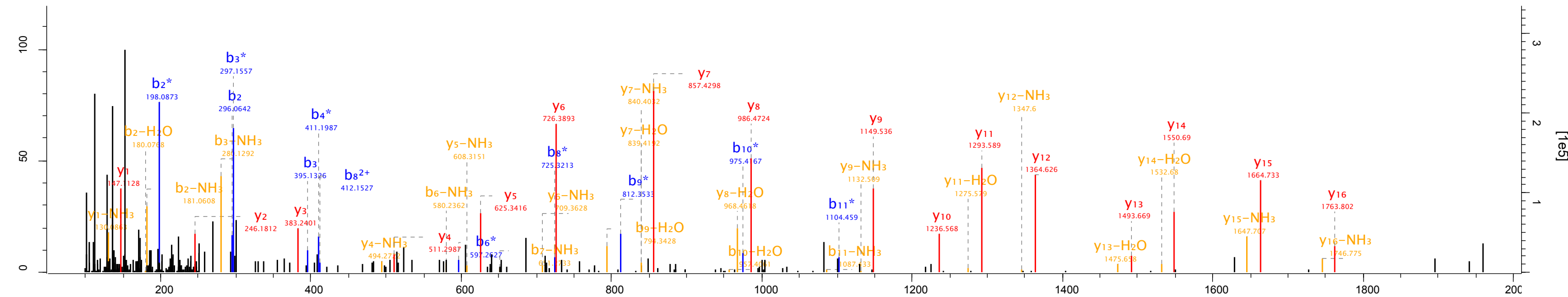


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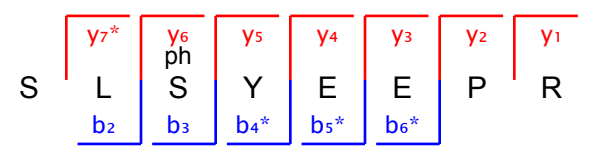
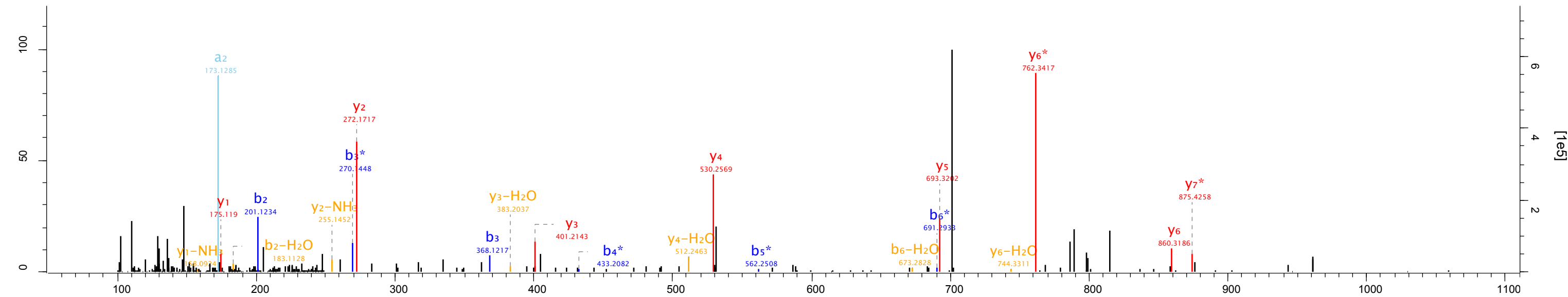


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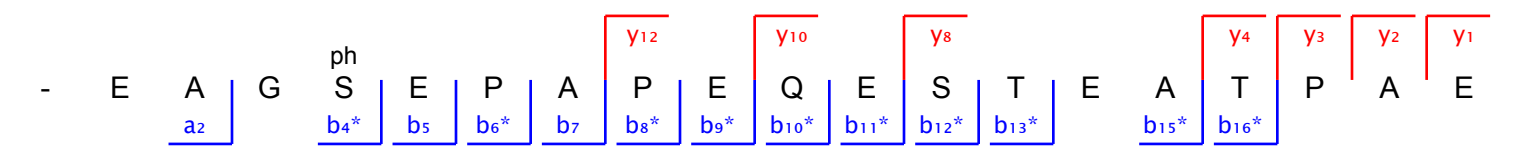
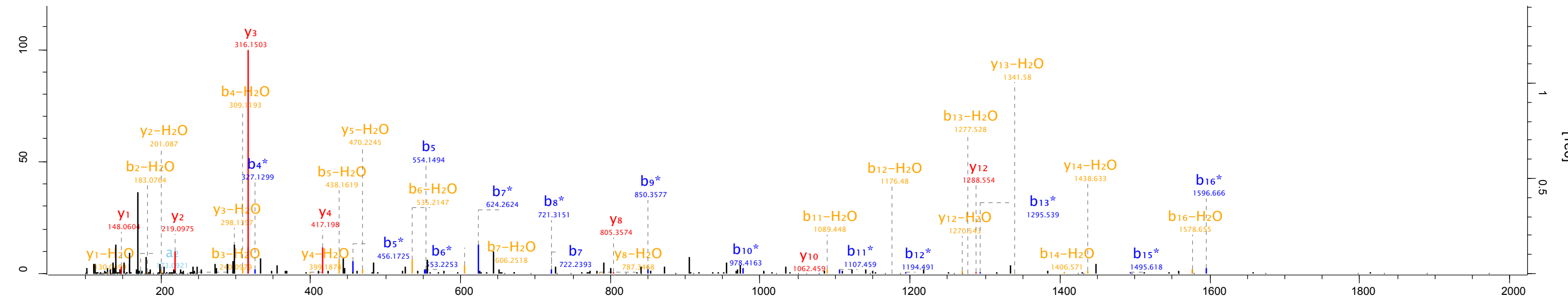




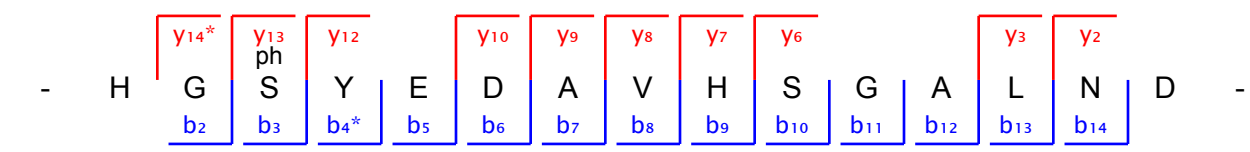
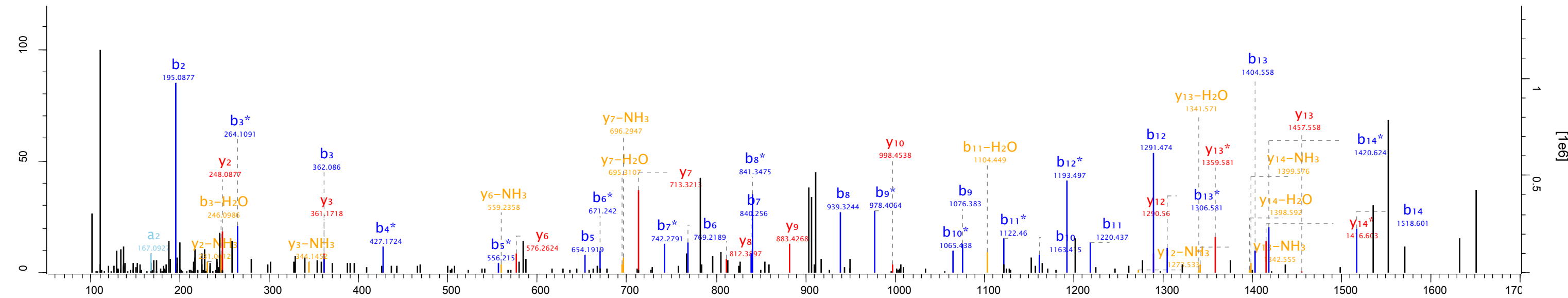
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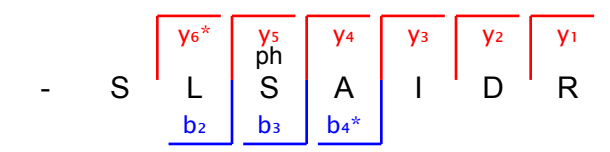
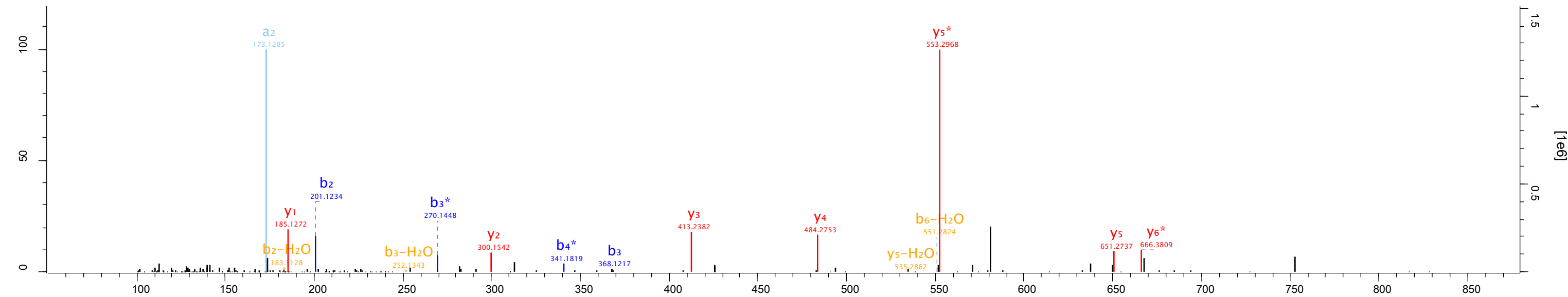
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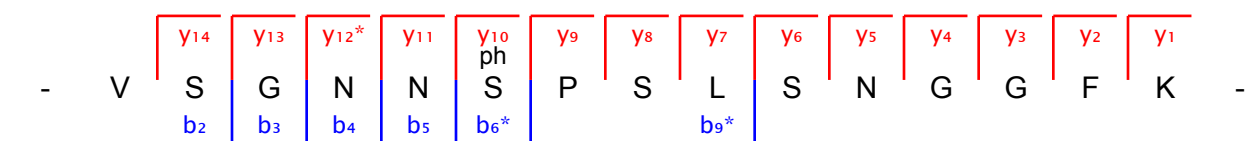
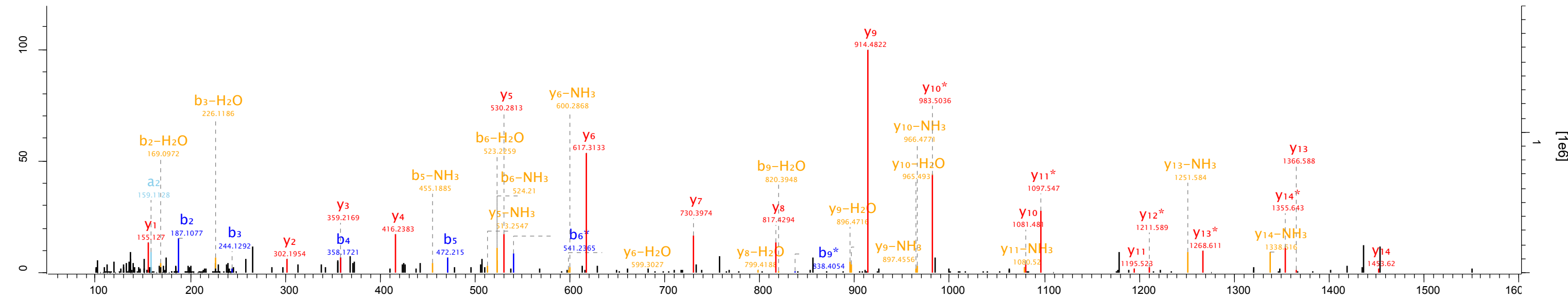
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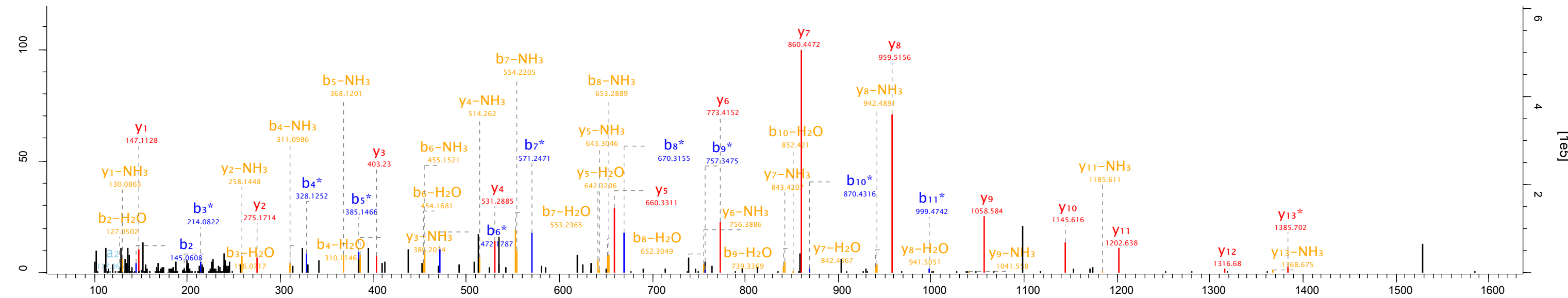
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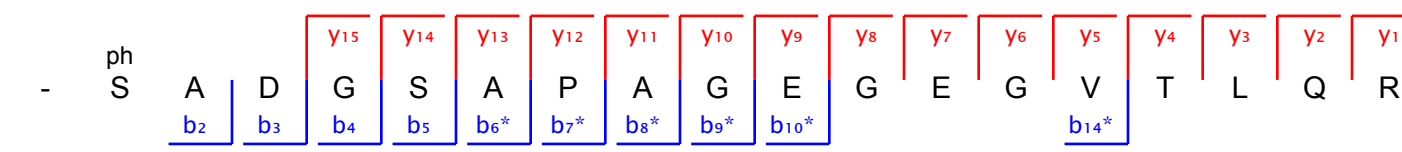
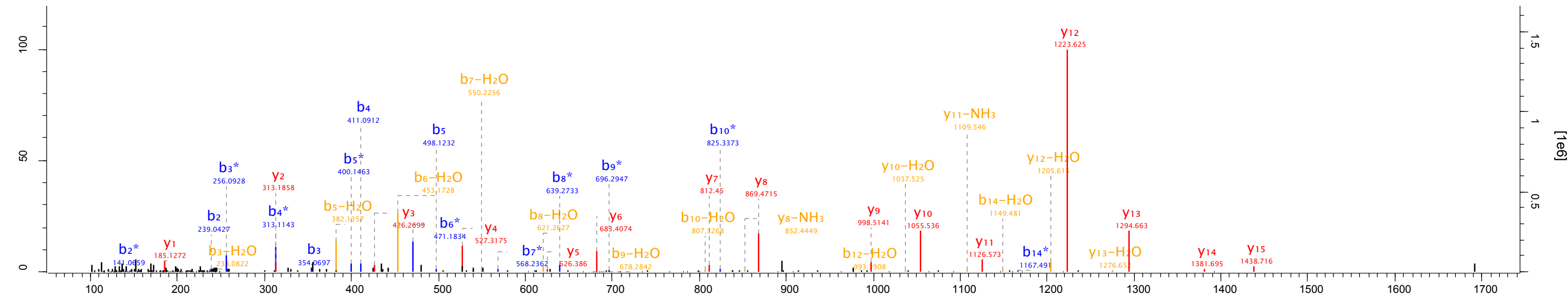
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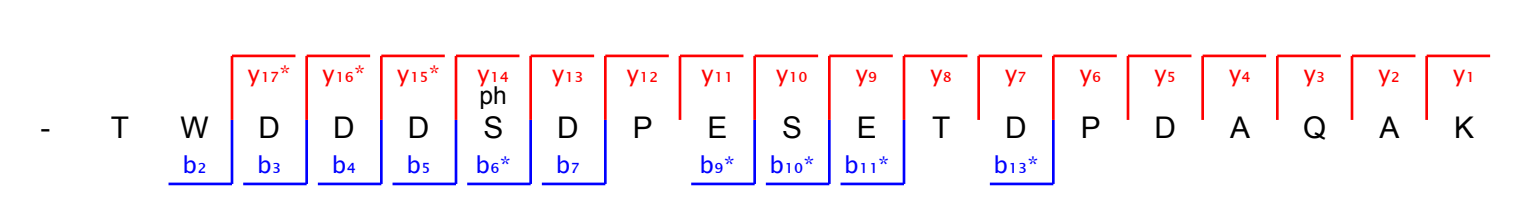
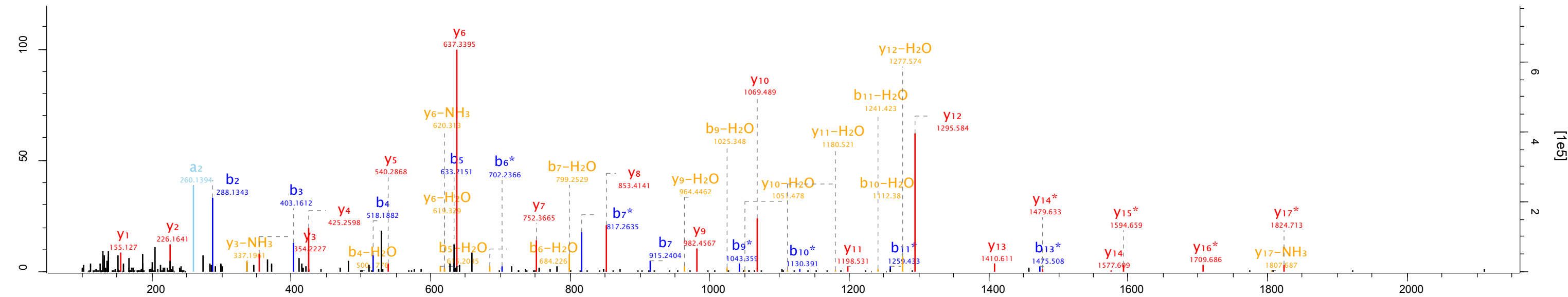
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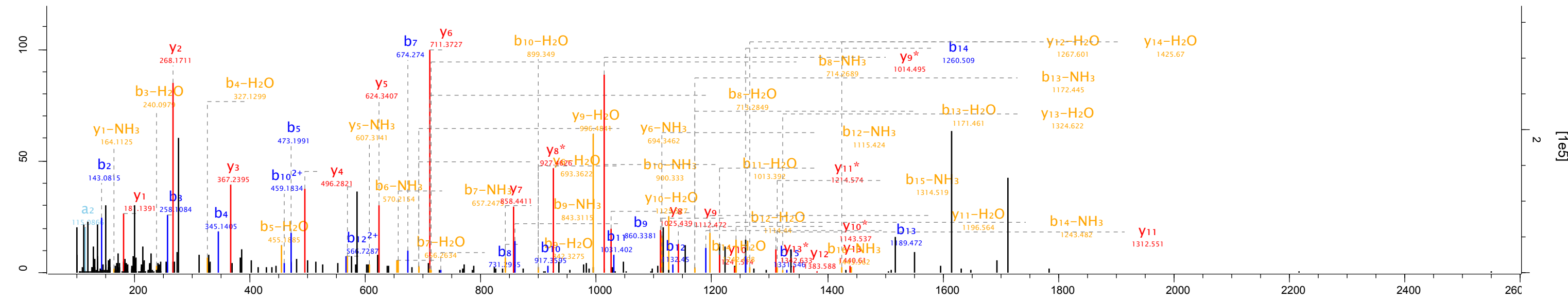
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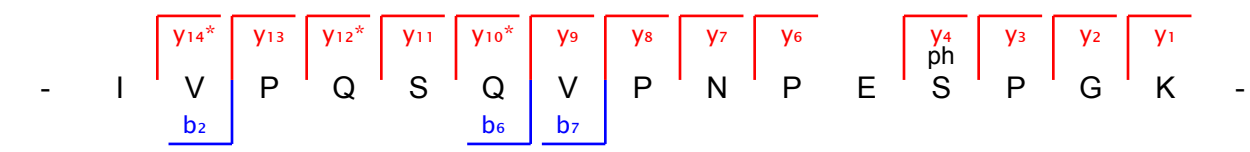
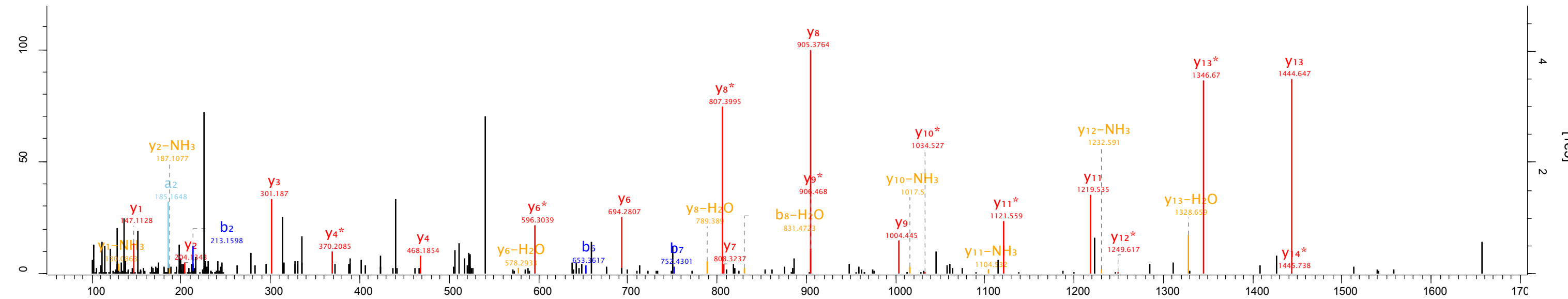


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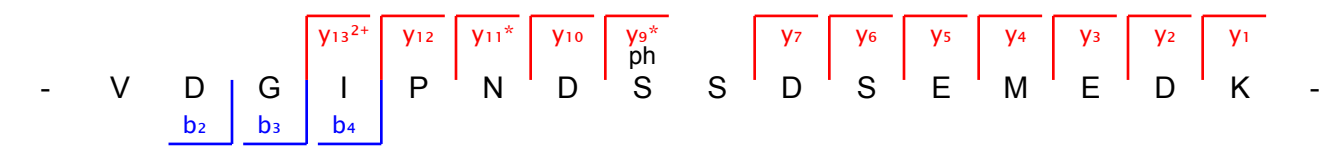
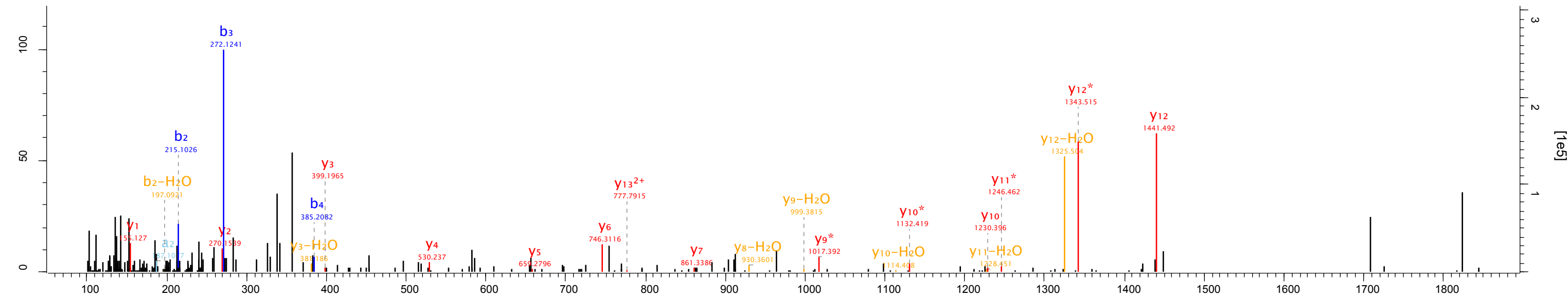




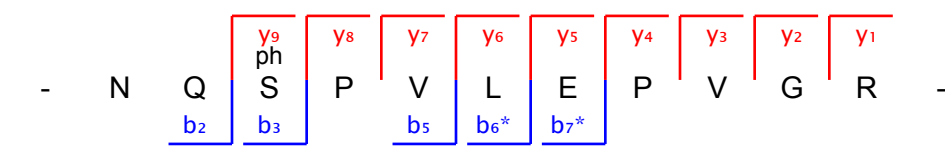
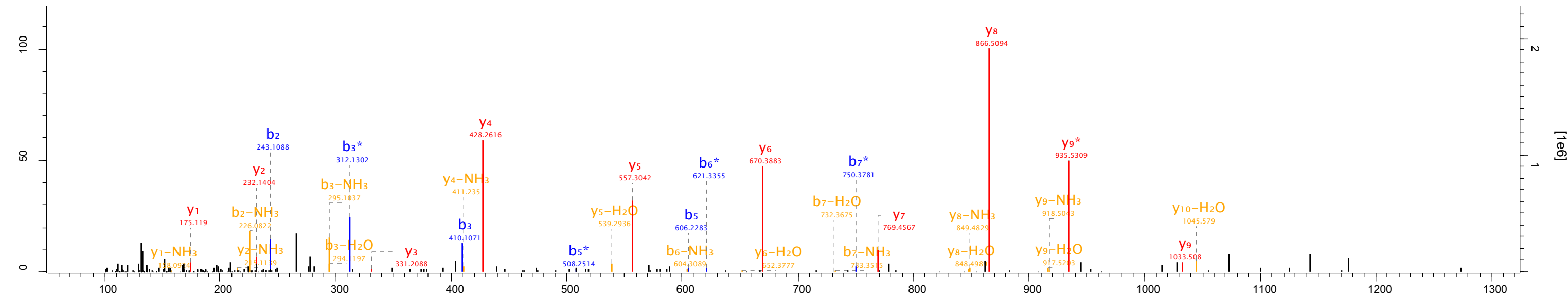
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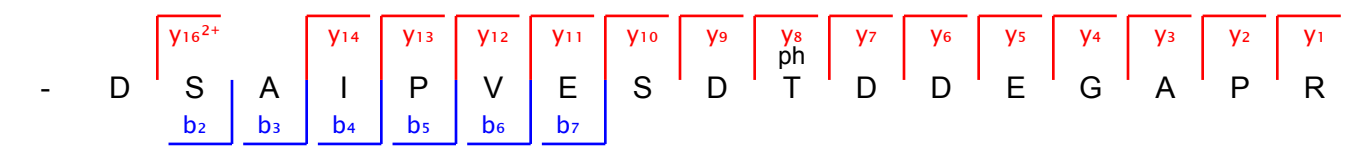
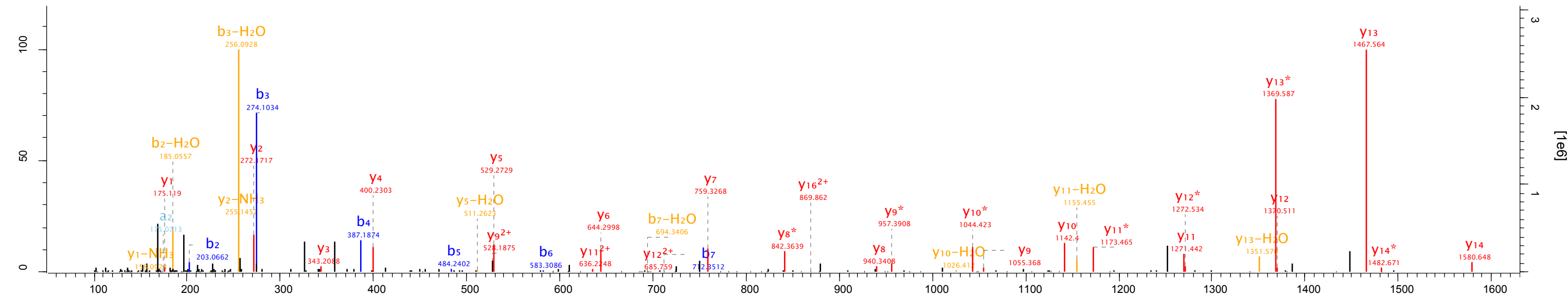
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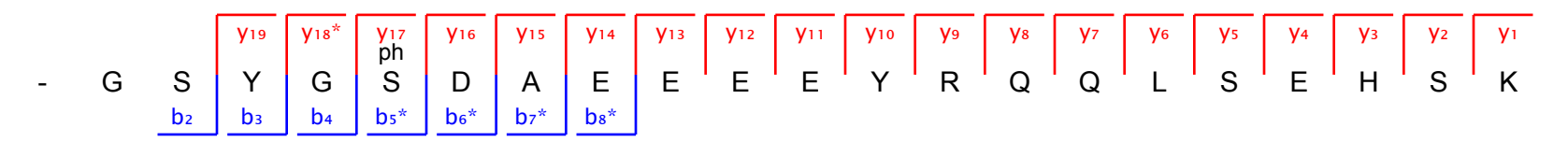
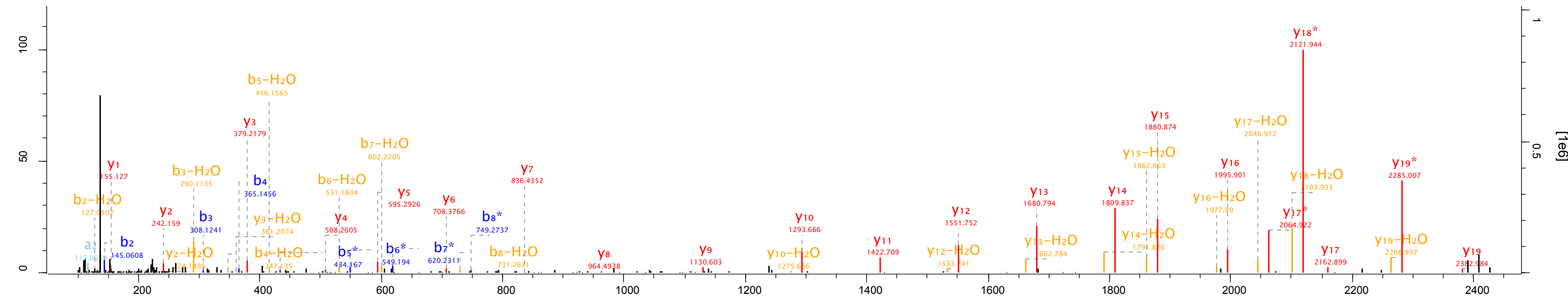
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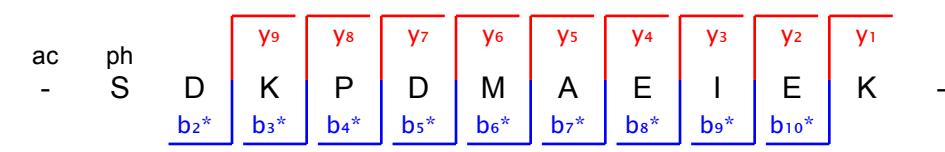
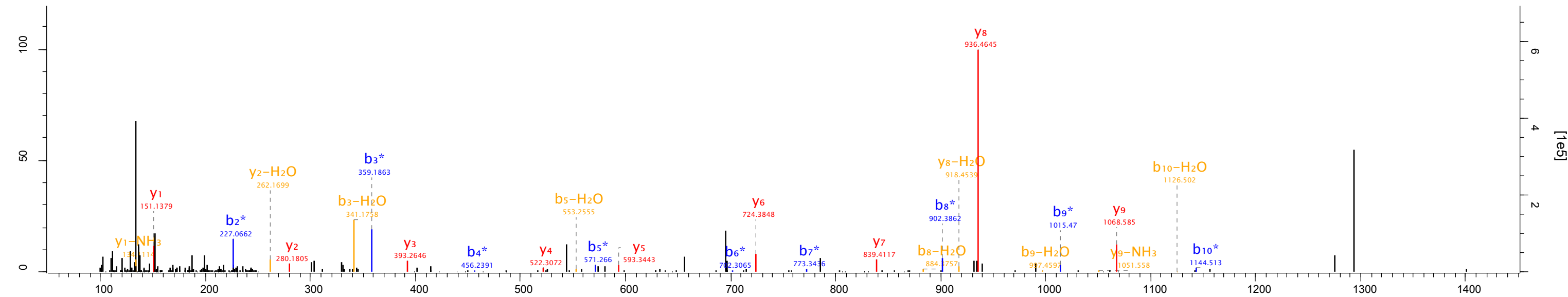
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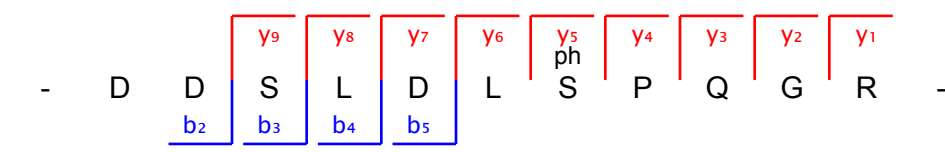
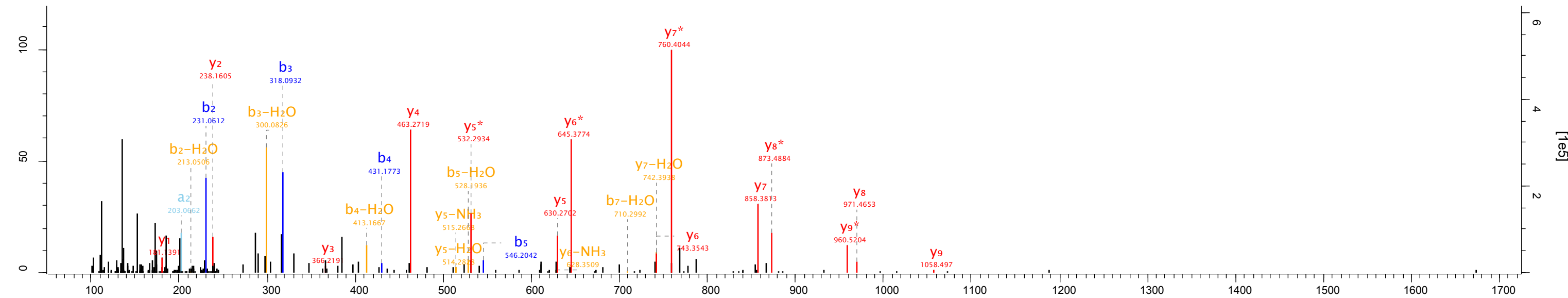
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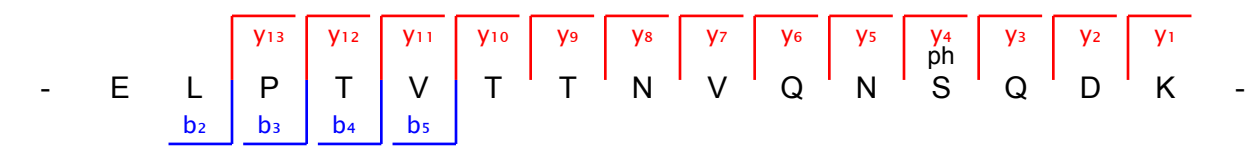
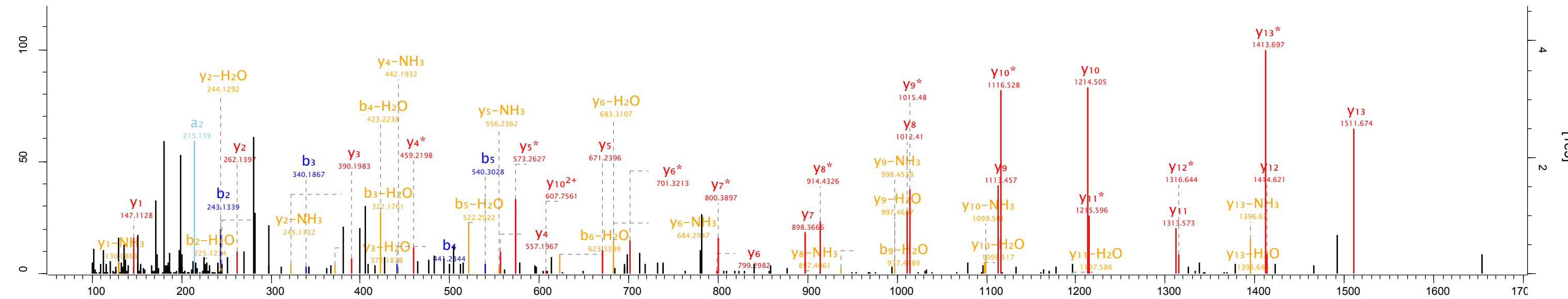
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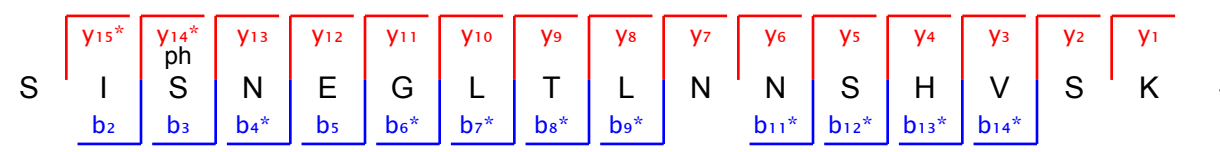
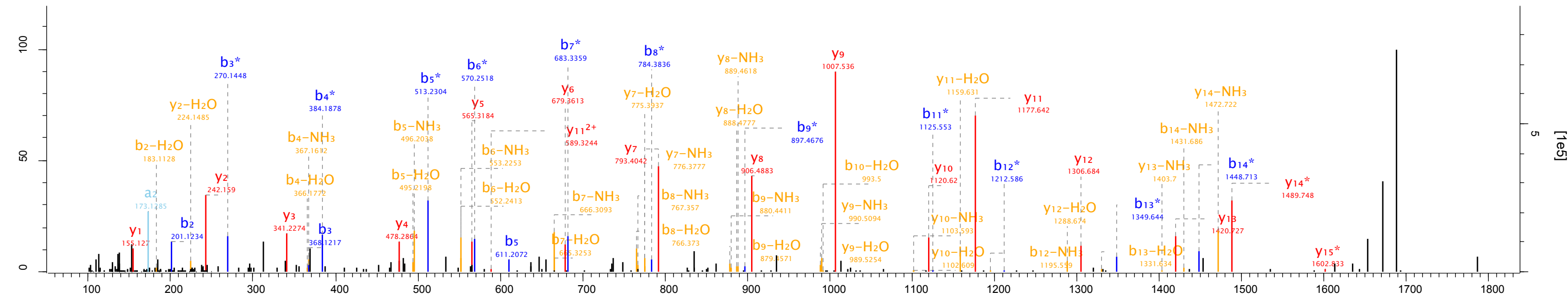
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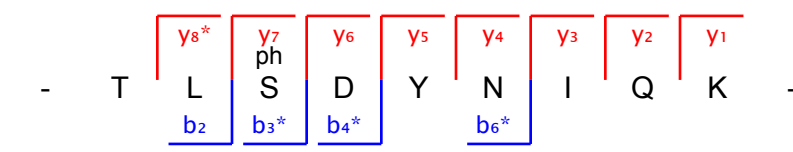
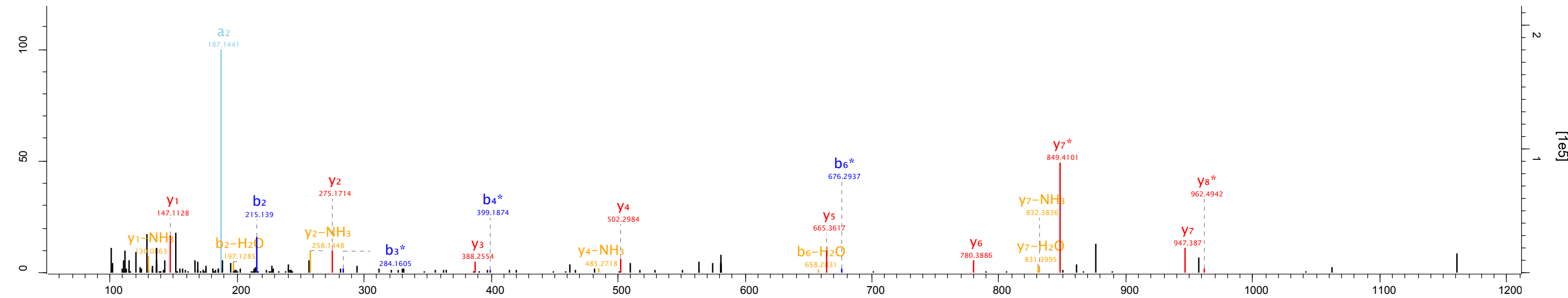
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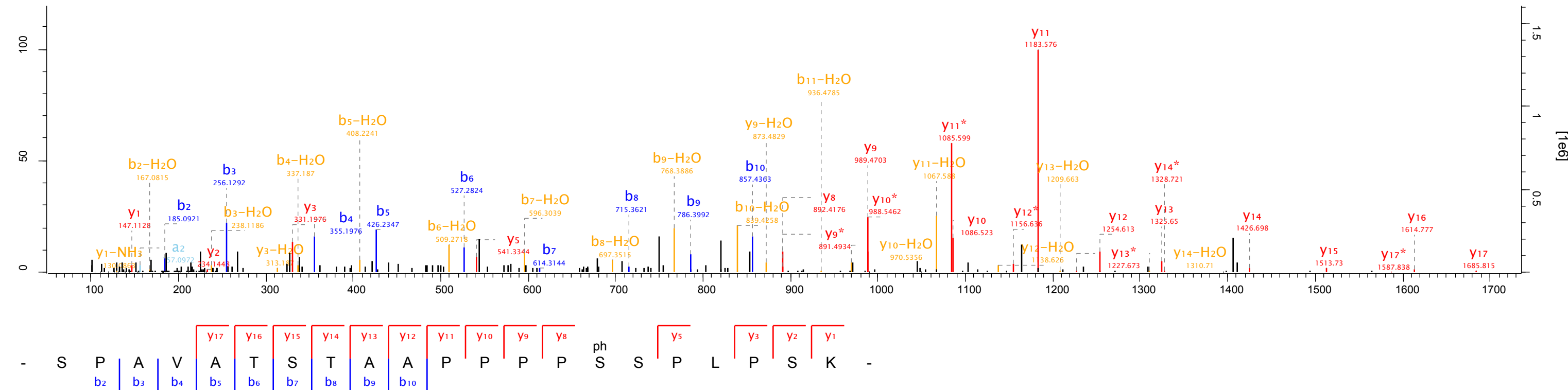


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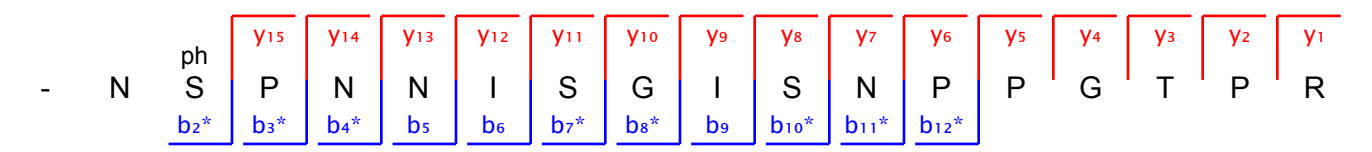
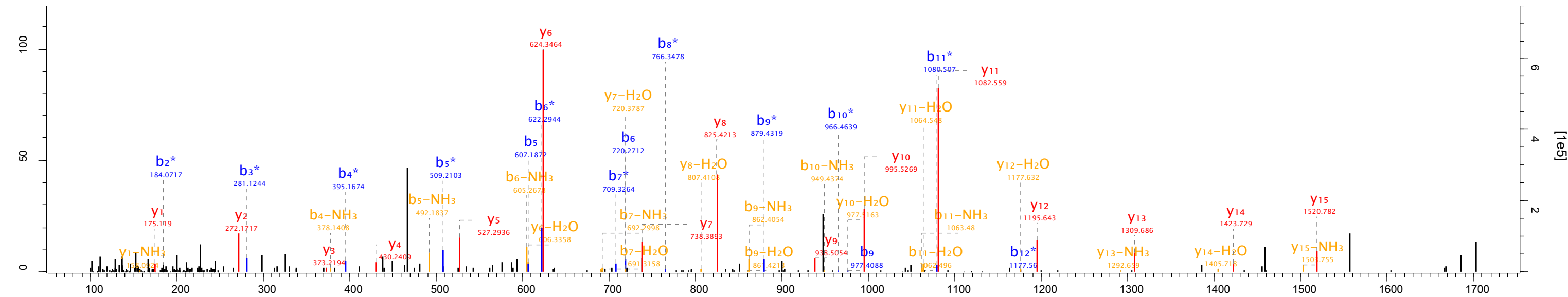


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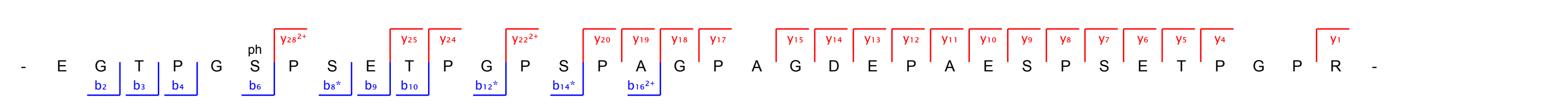
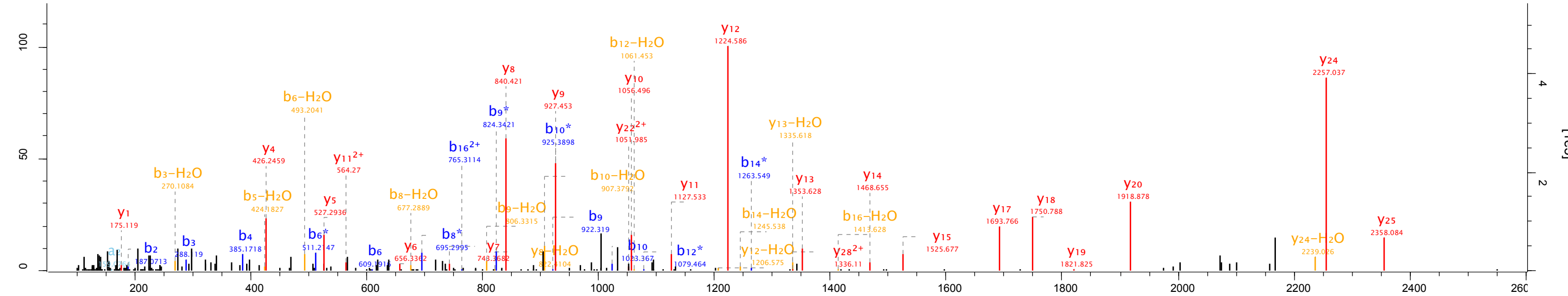




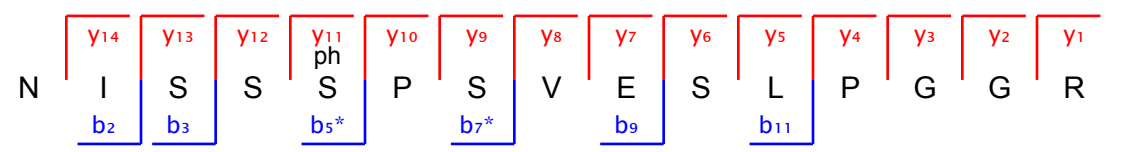
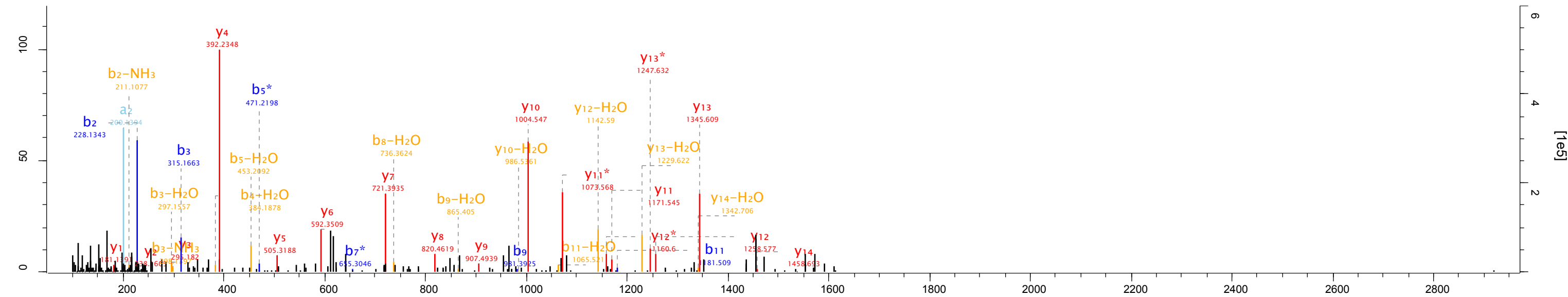
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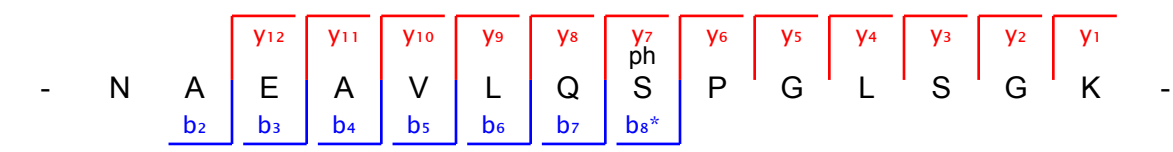
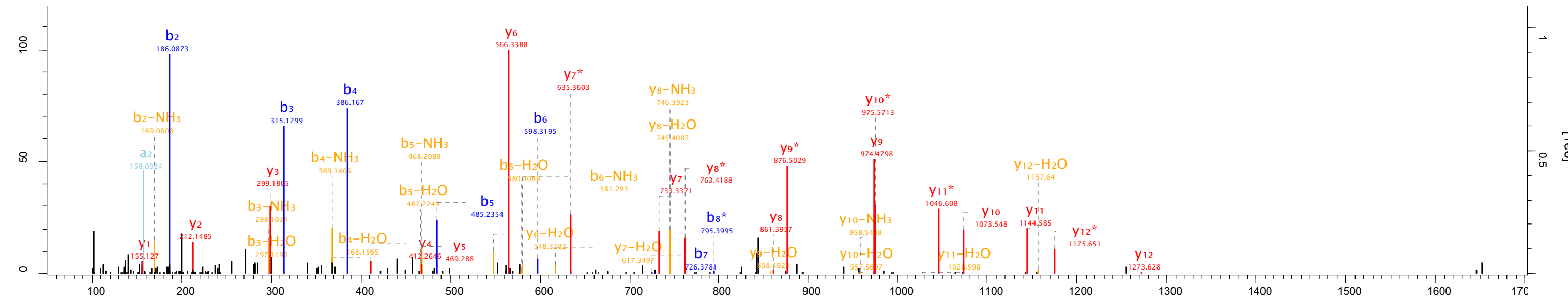
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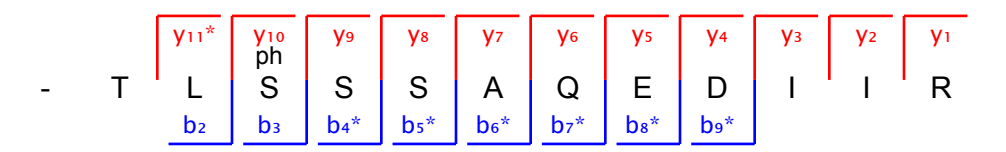
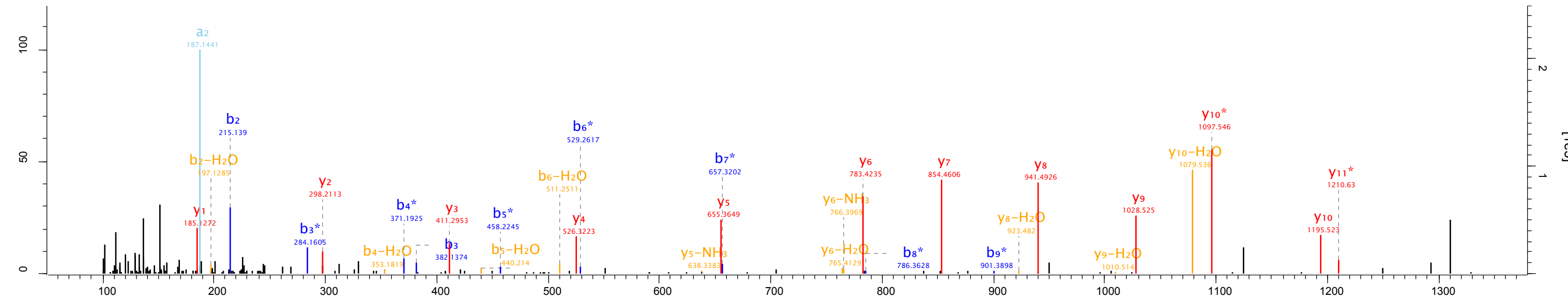
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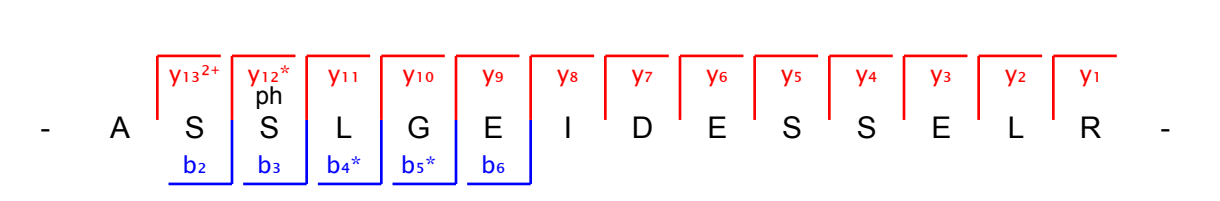
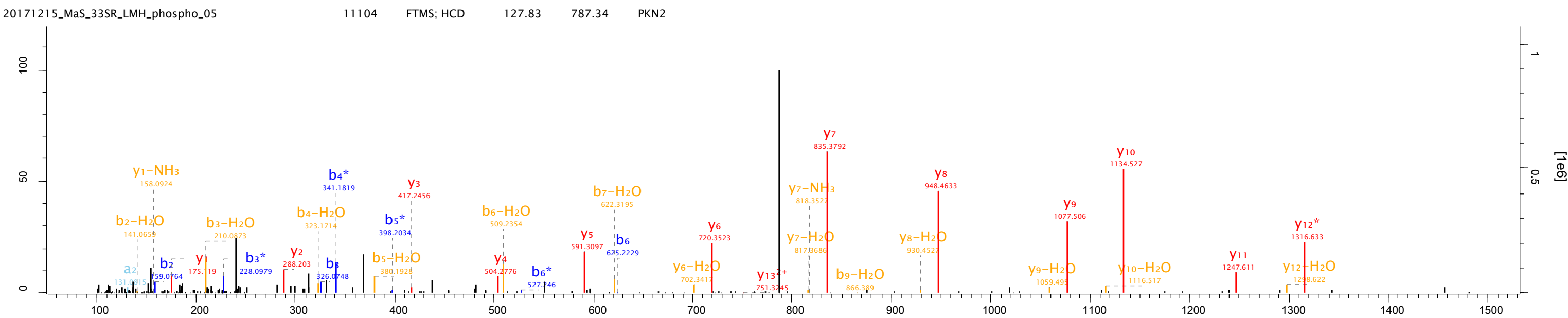
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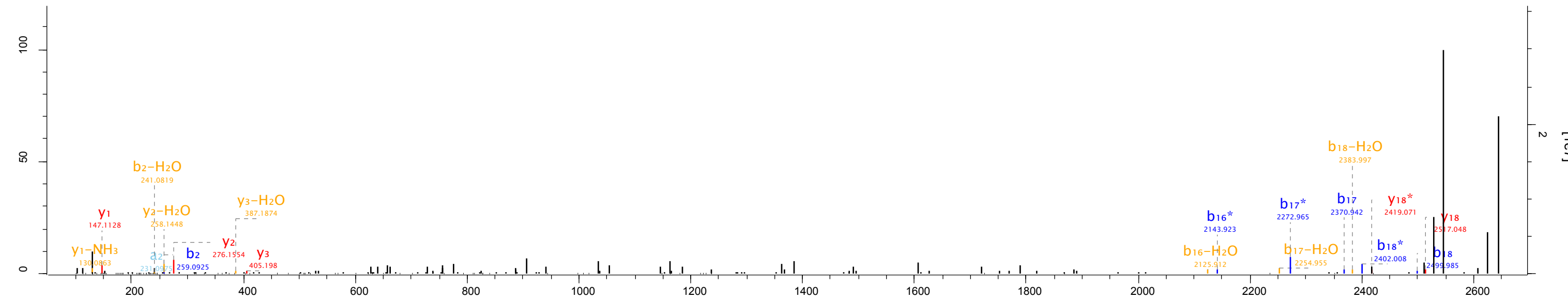
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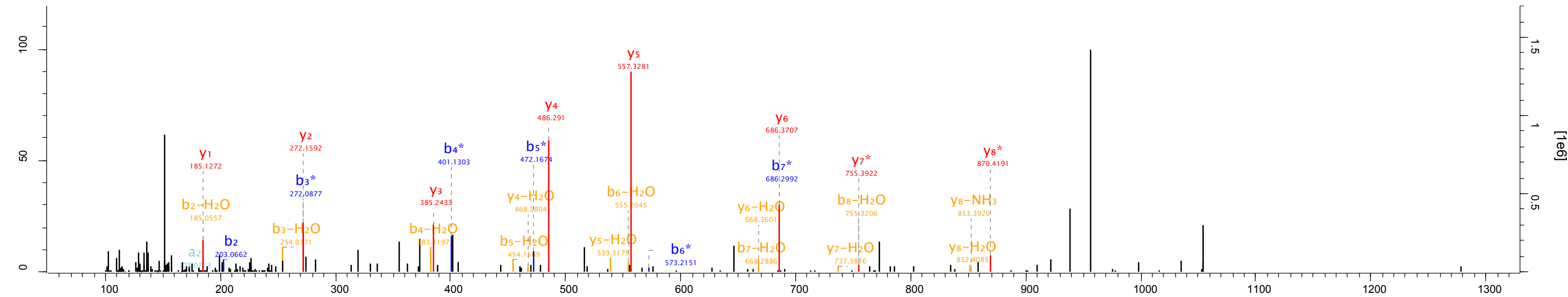
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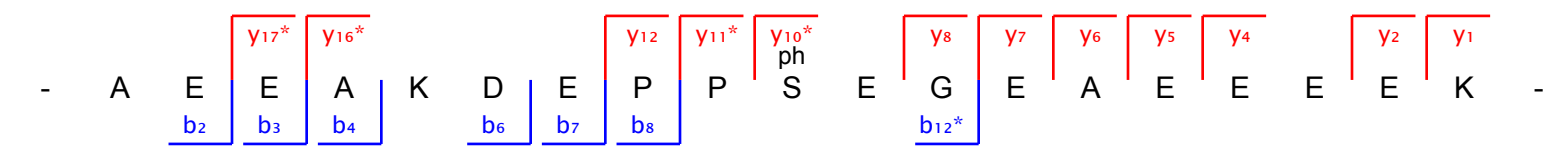
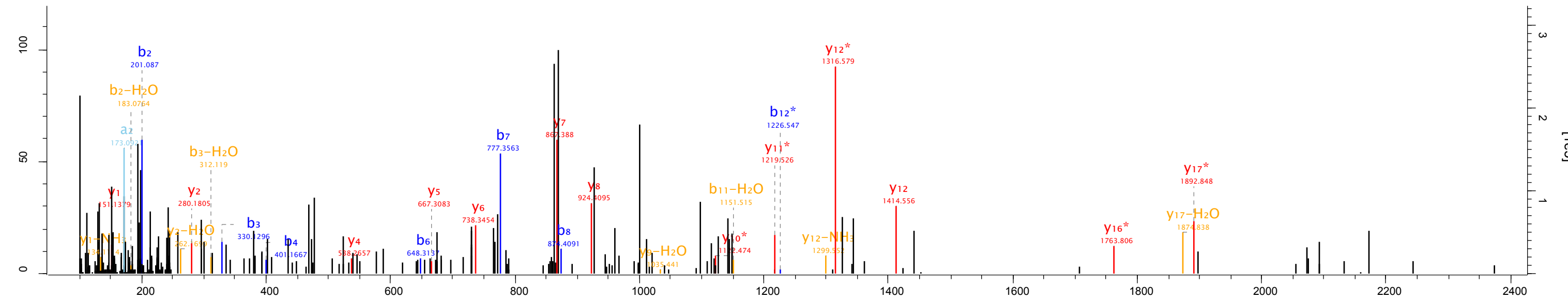
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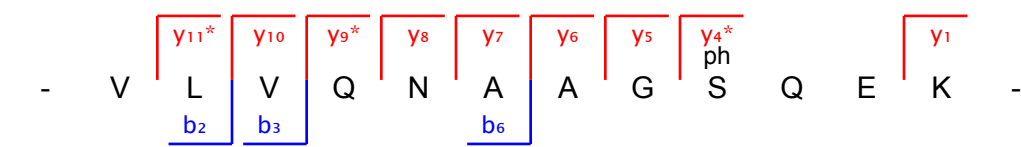
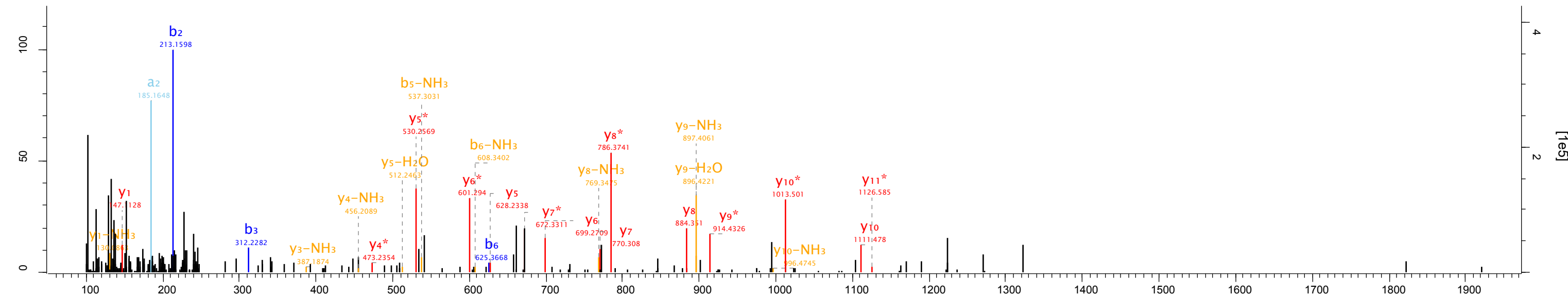
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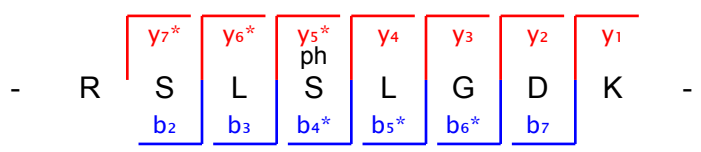
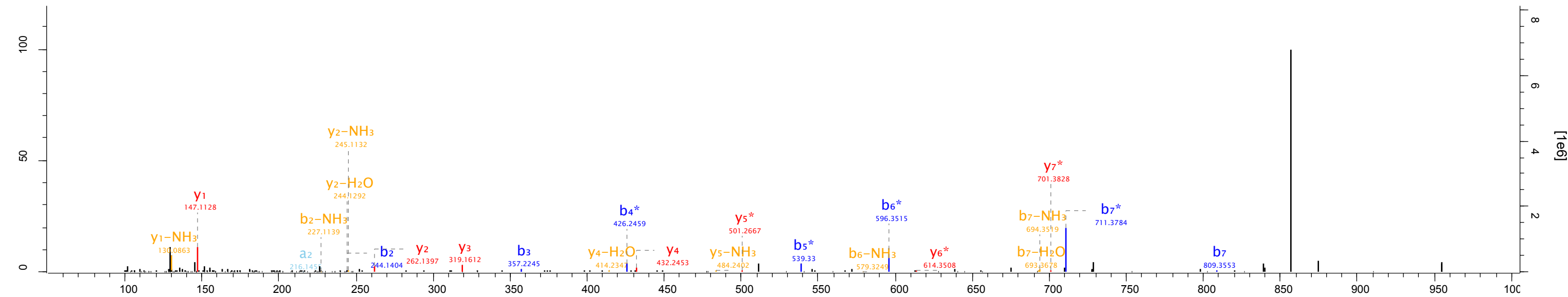
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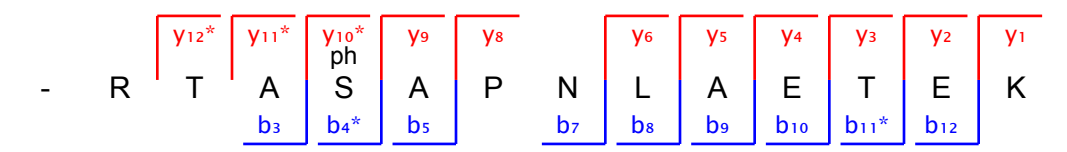
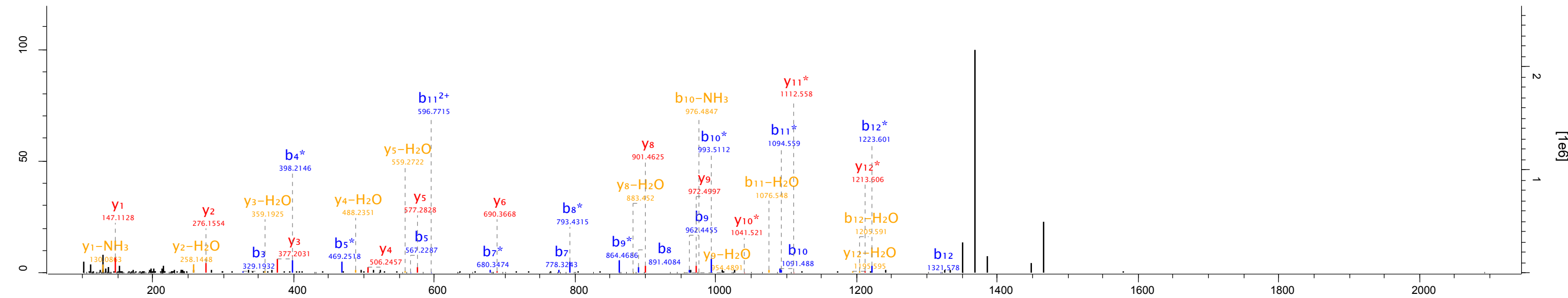
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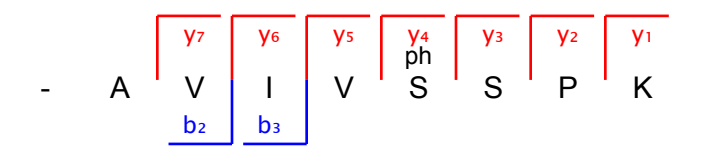
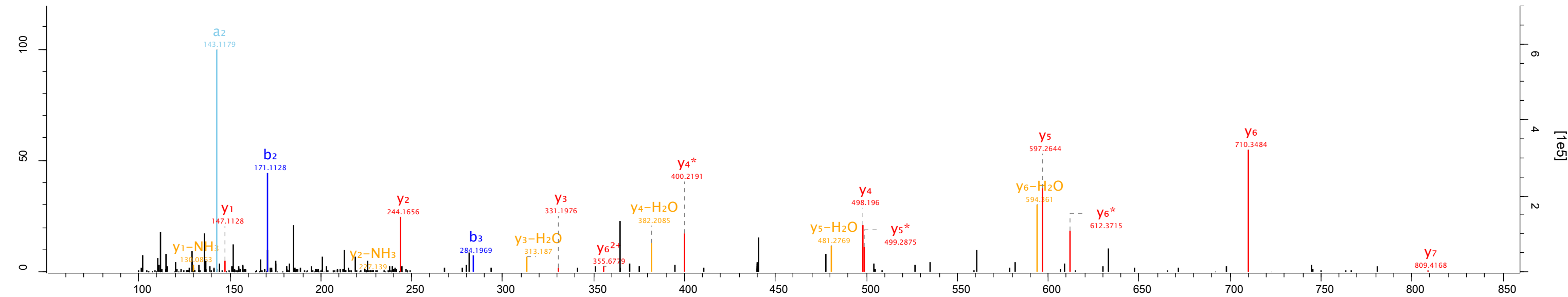
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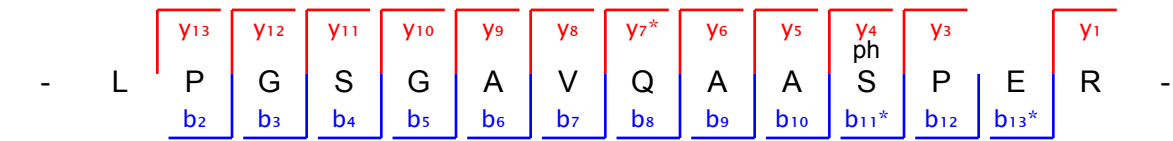
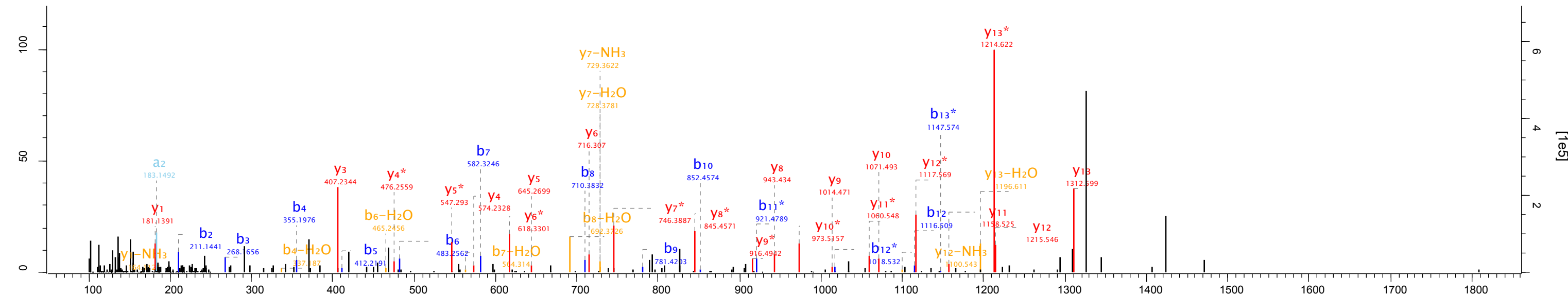


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L

y13

y12

y11

y10

y9

y8

y7*

y6

y5

y4

y3

y1

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b2

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b5

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b7

b8

b9

b10

b11*

b12

b13*

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L

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y12

y11

y10

y9

y8

y7*

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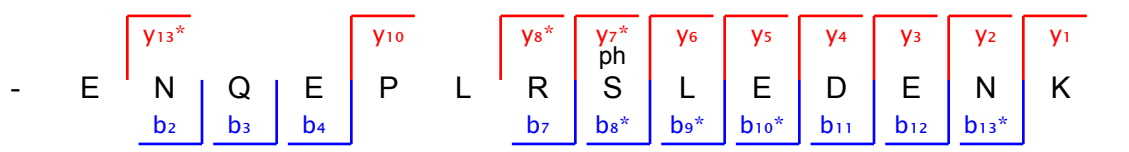
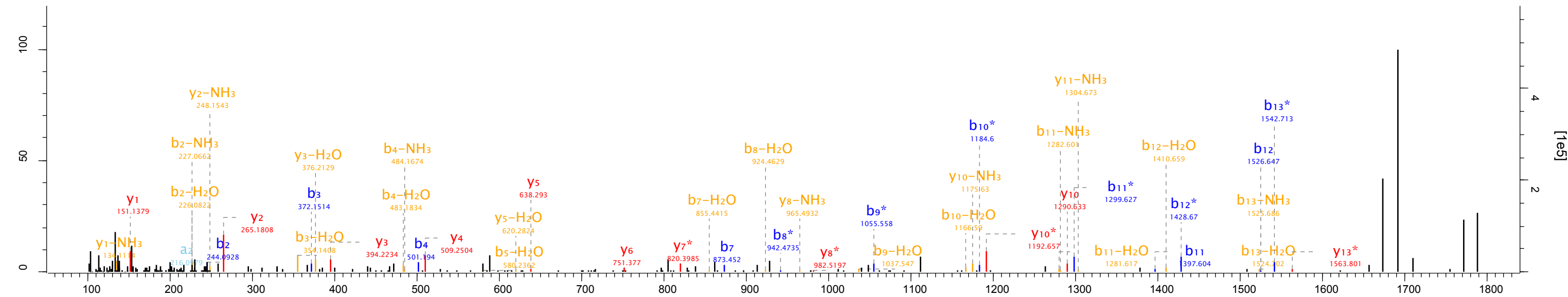
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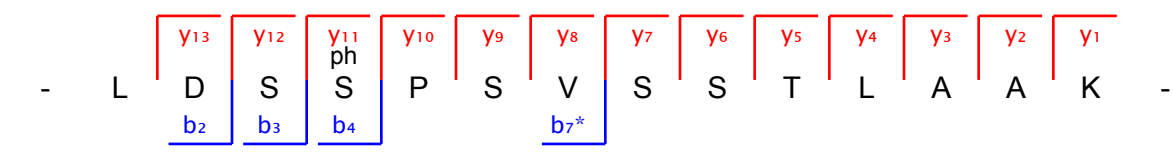
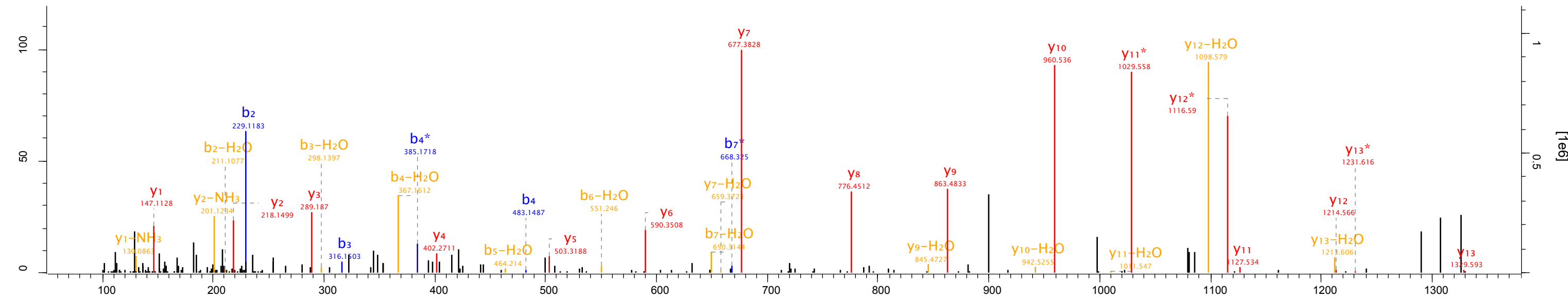
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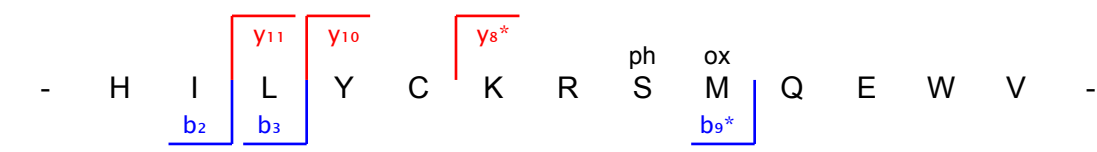
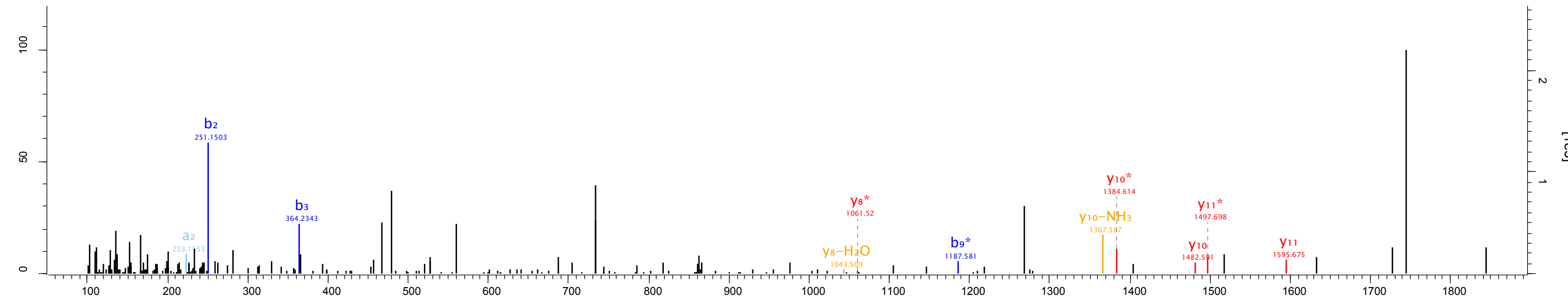
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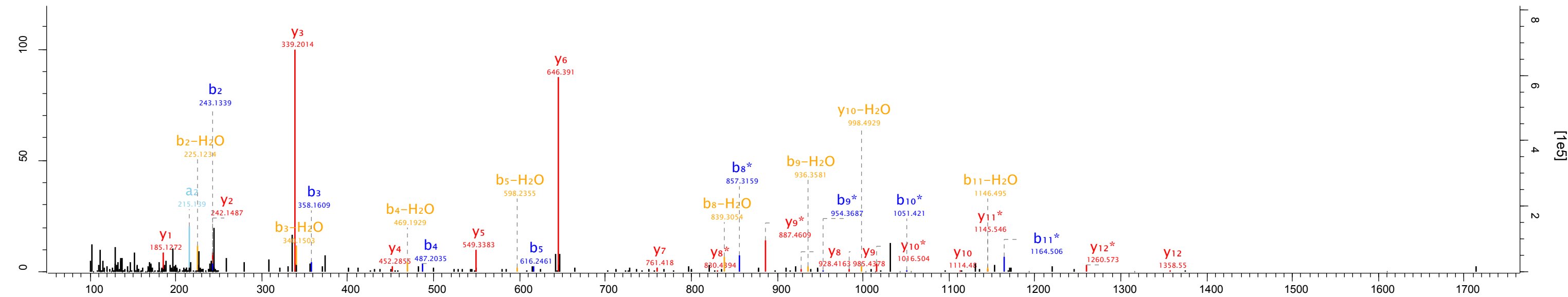
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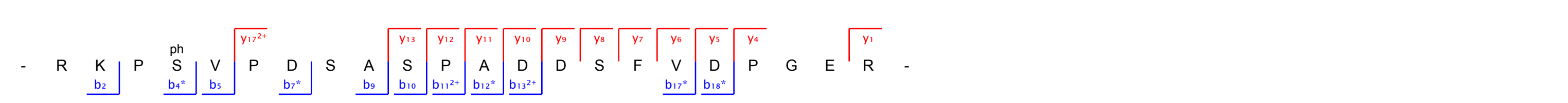
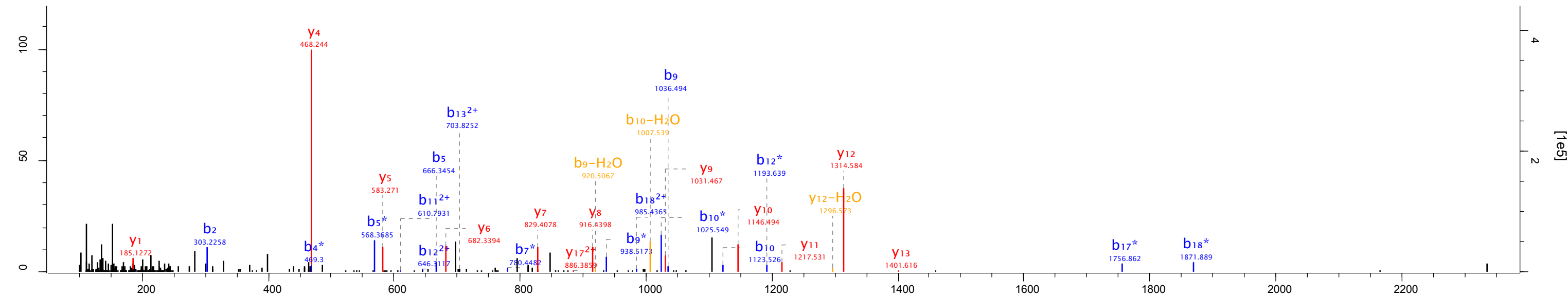
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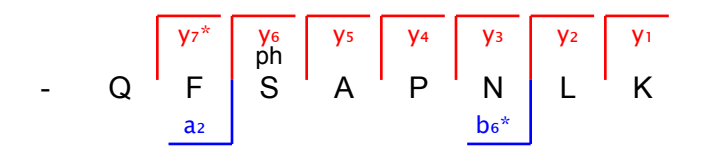
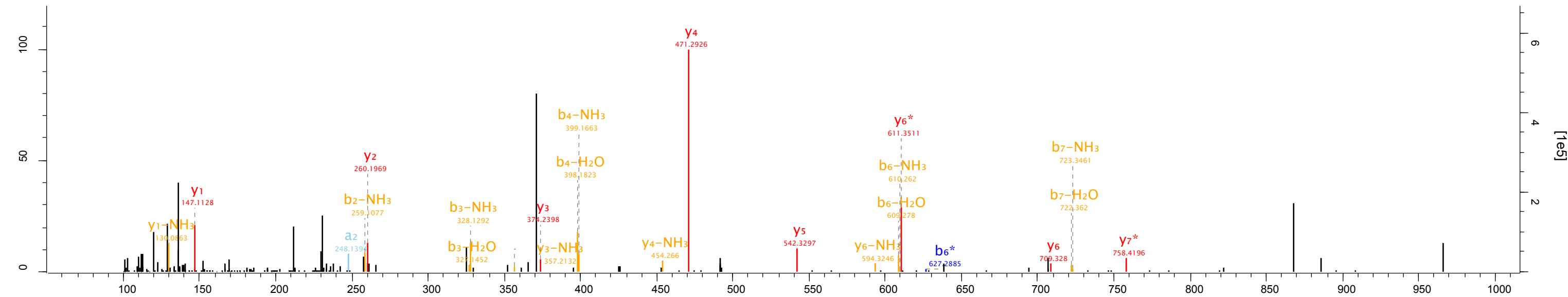
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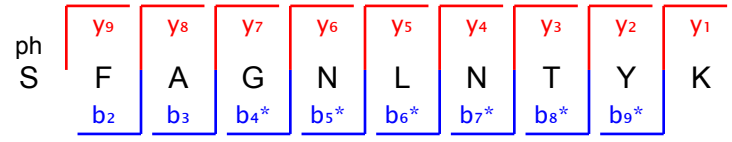
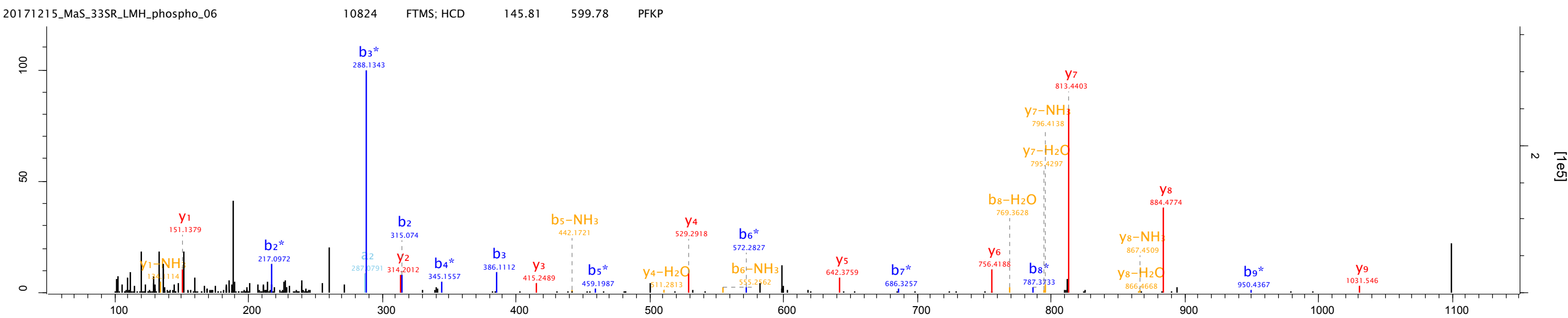
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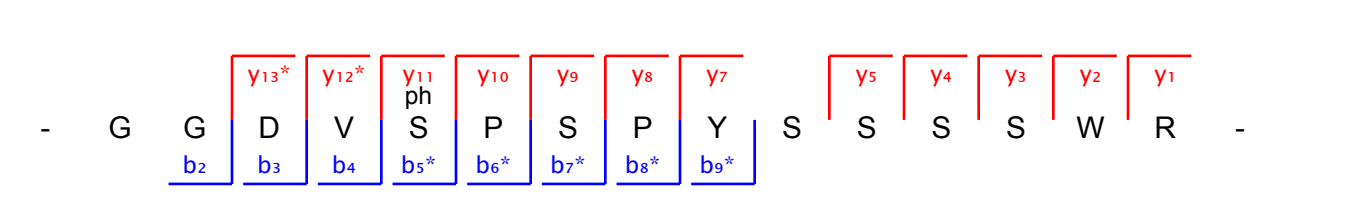
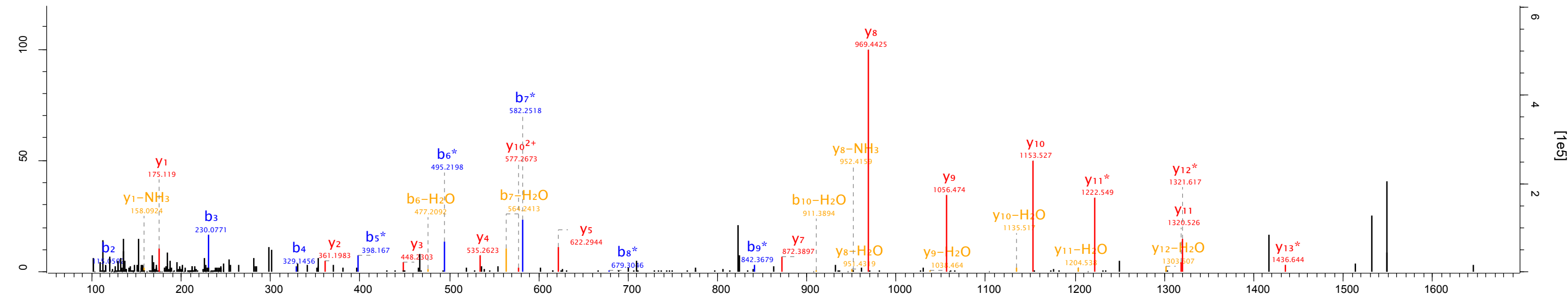
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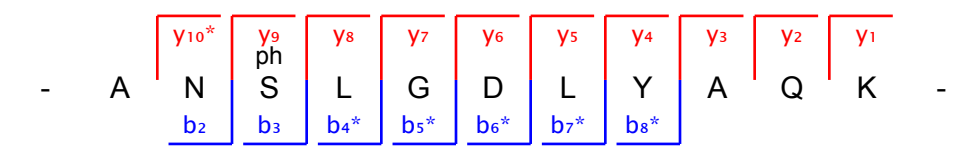
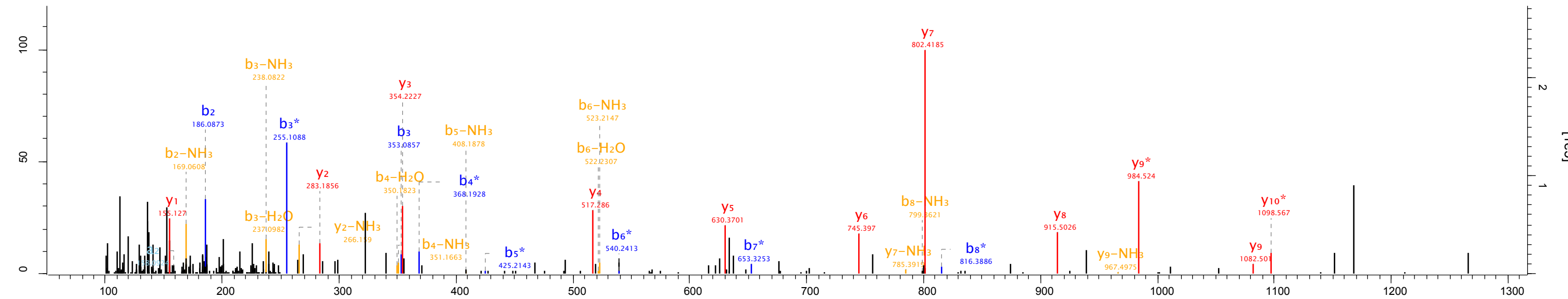
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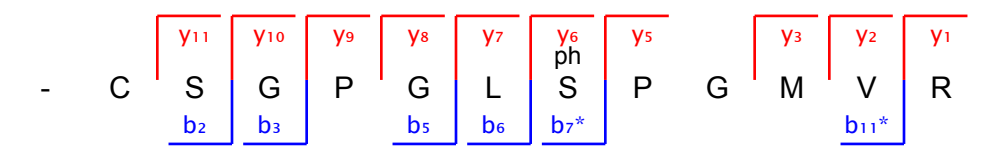
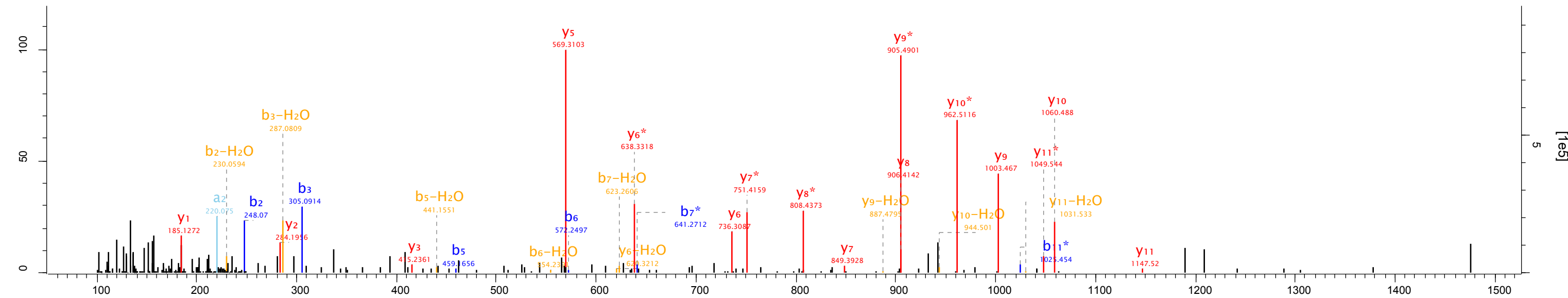
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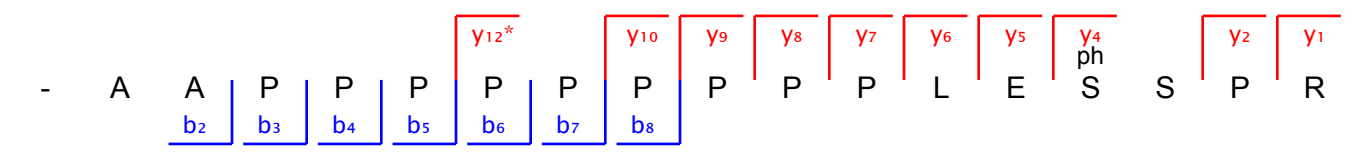
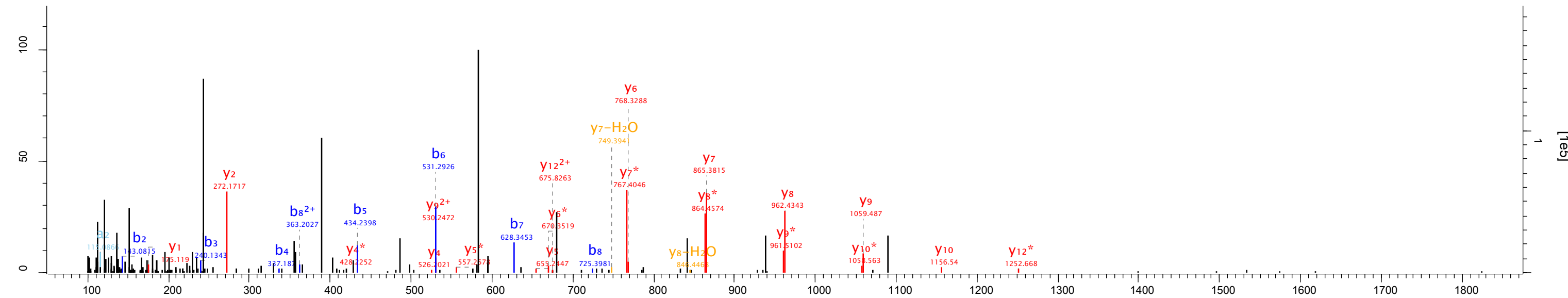
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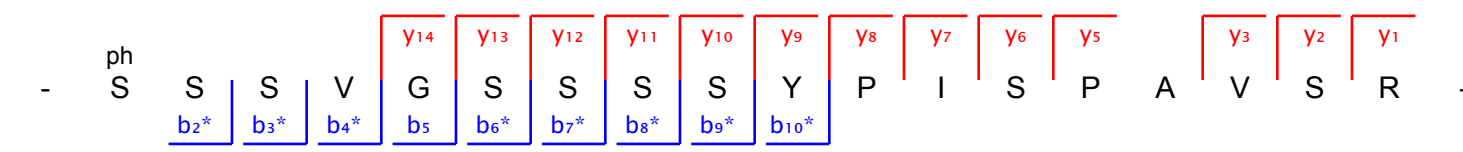
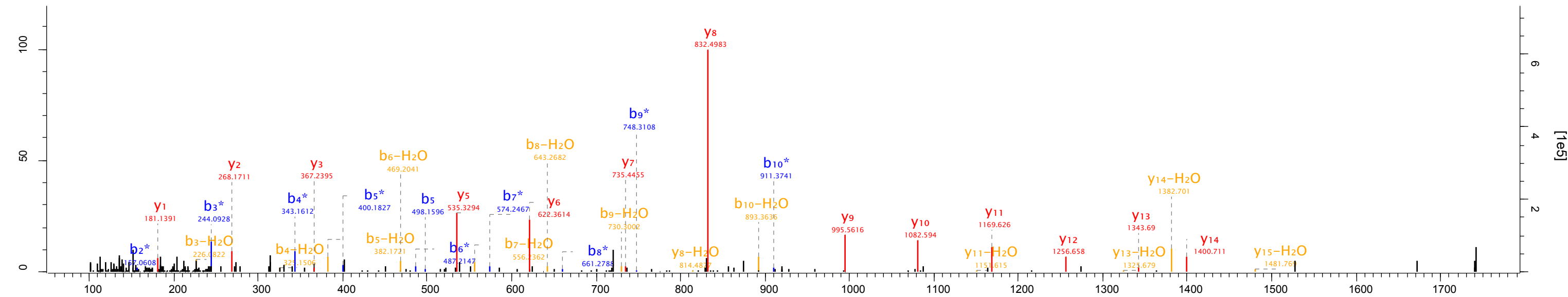
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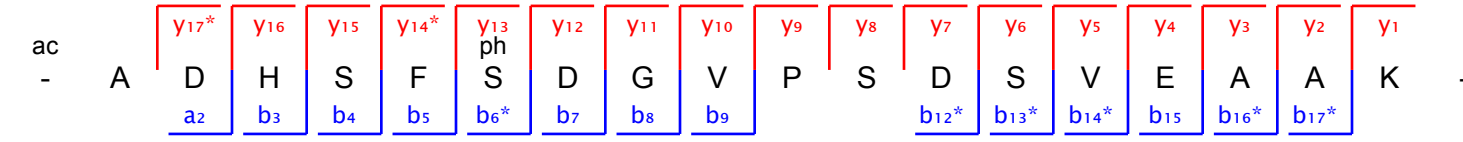
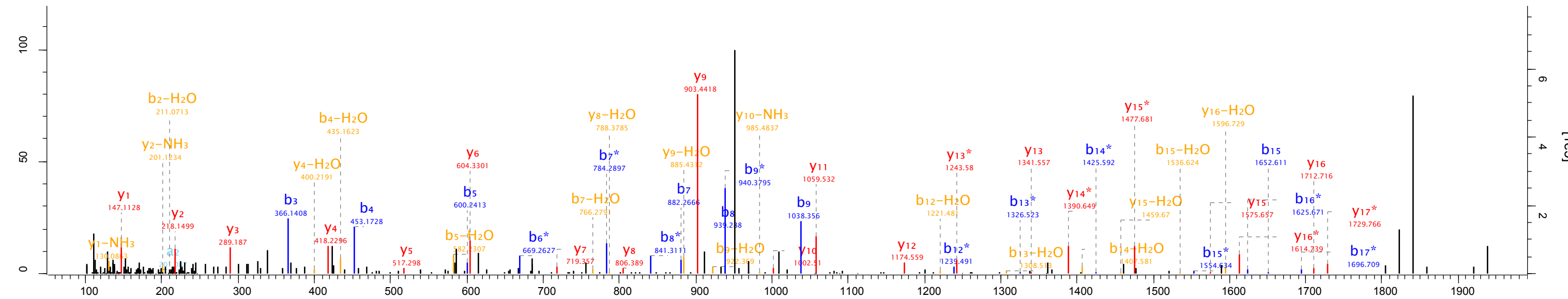


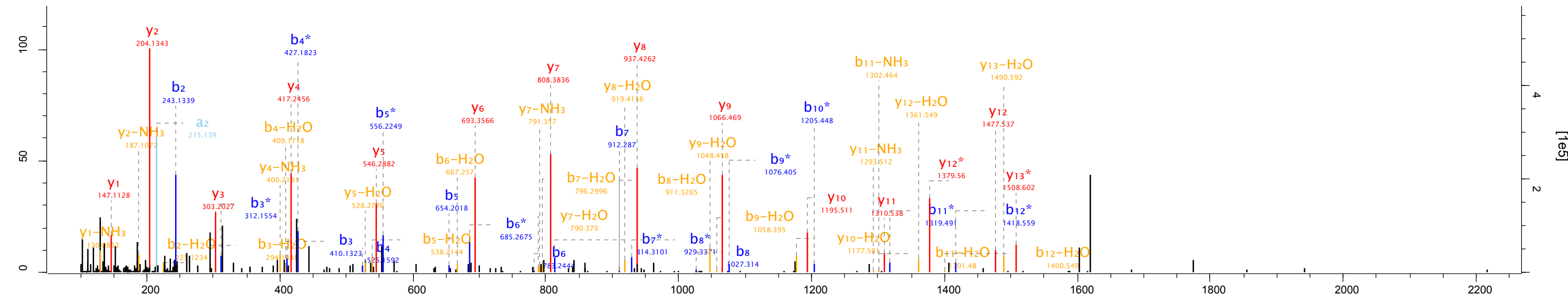
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20171215_MaS_33SR_LMH_phospho_06



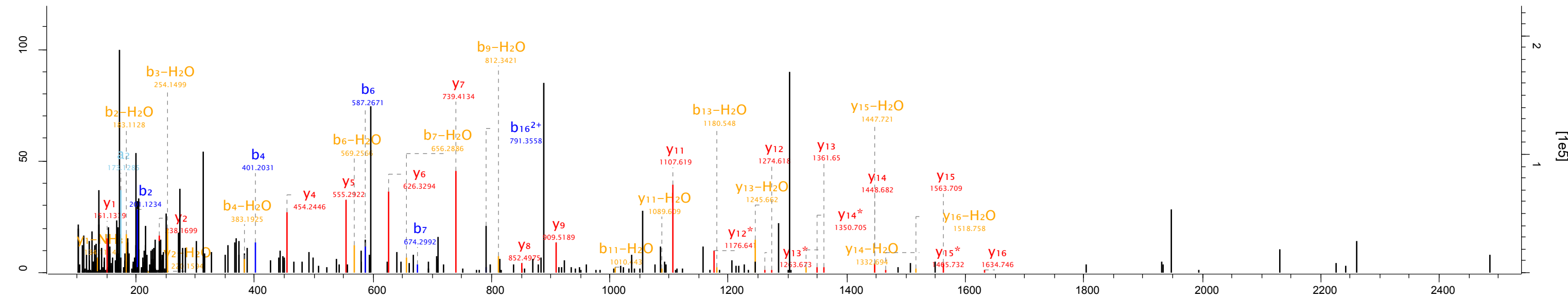


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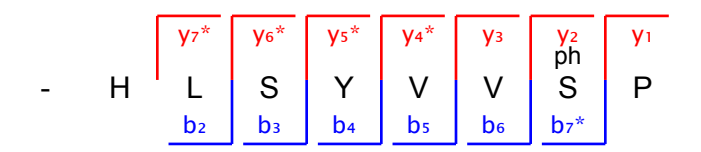
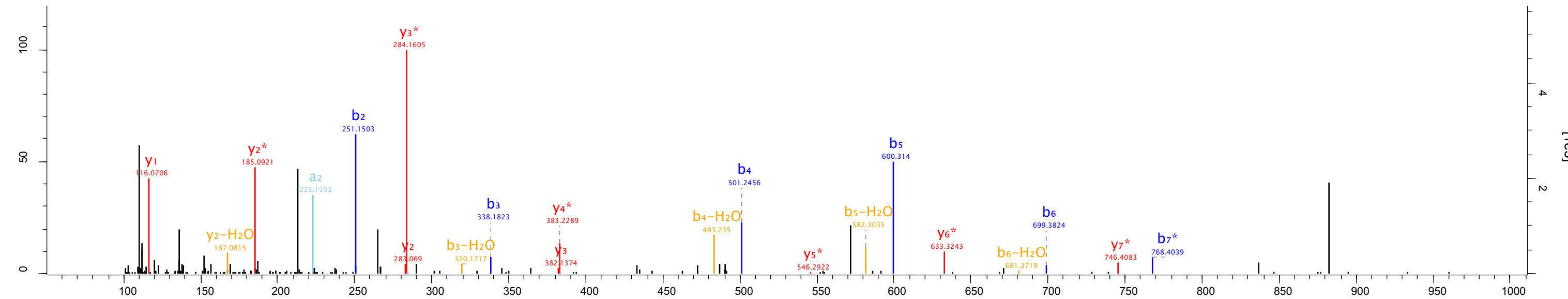
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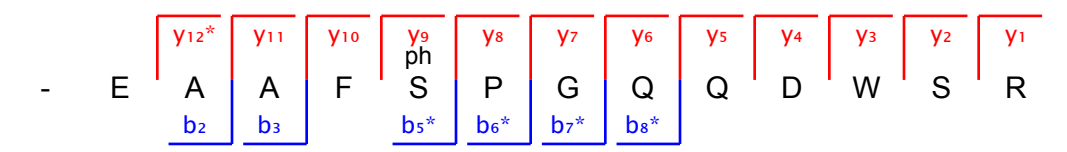
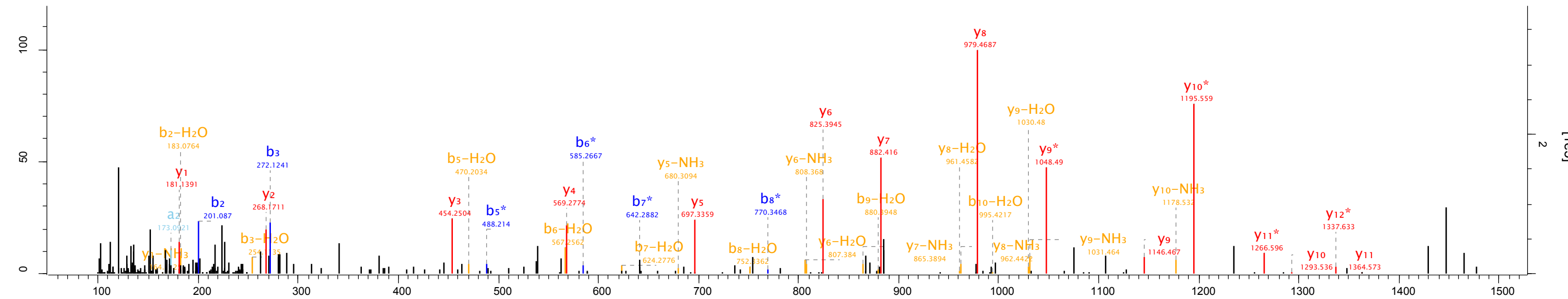
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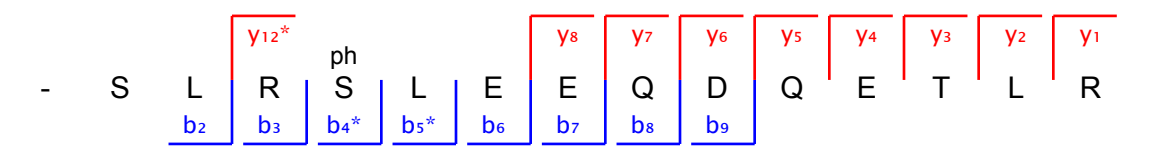
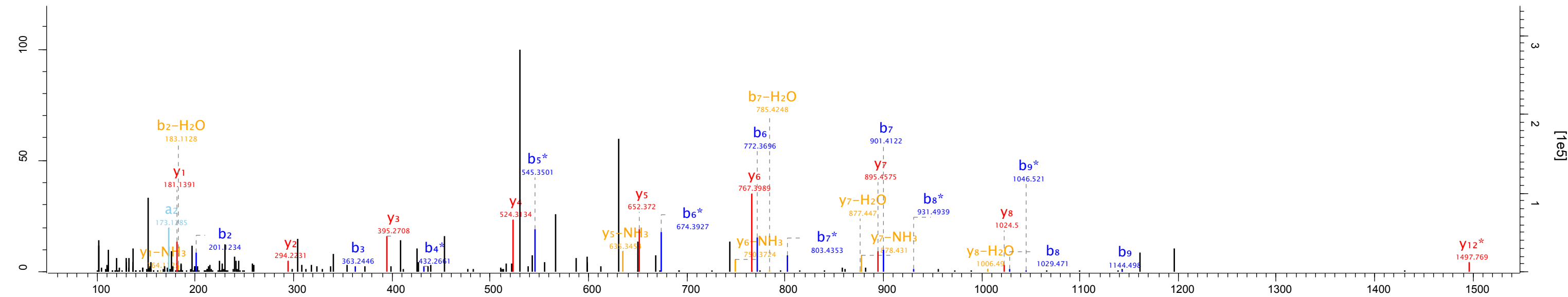
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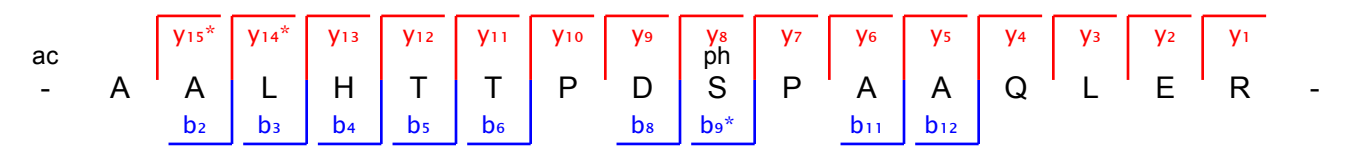
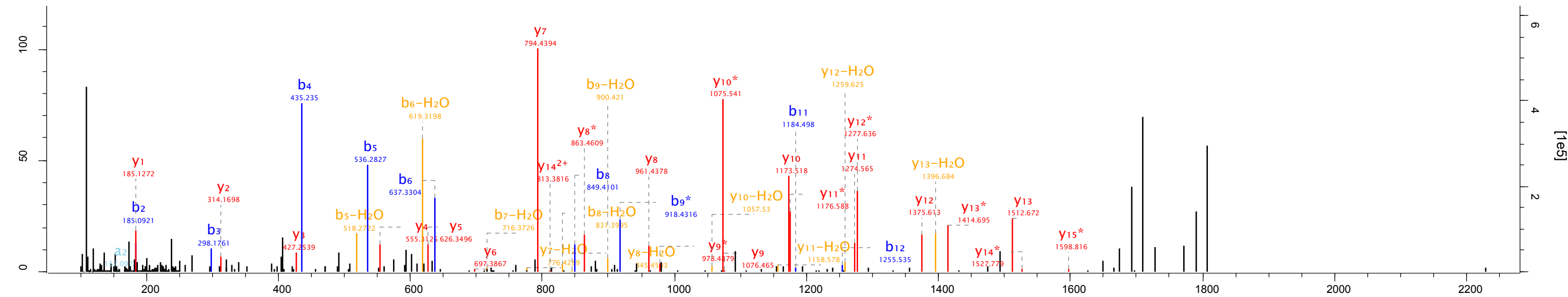
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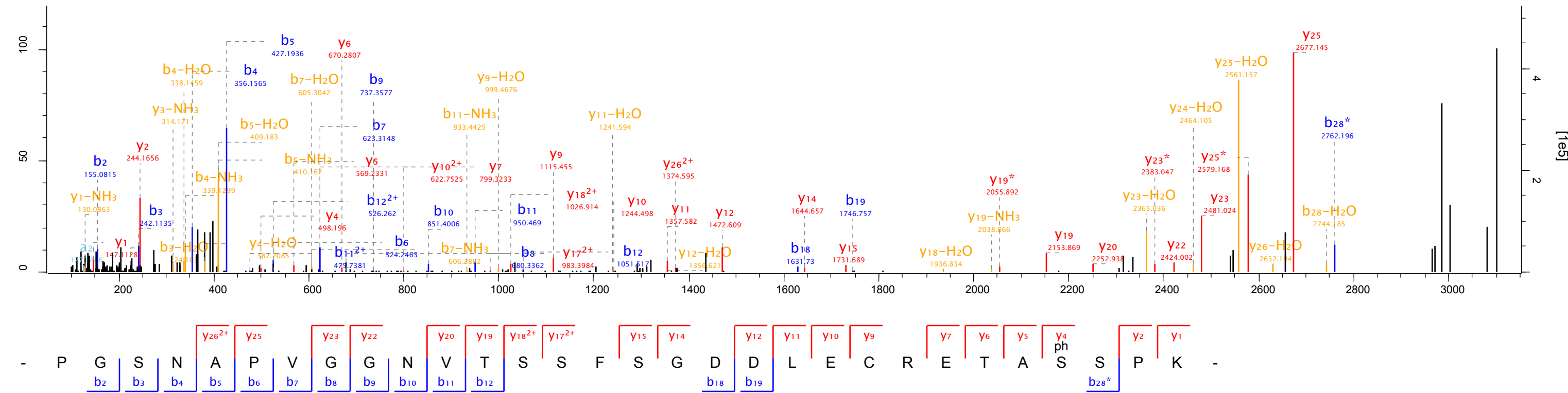
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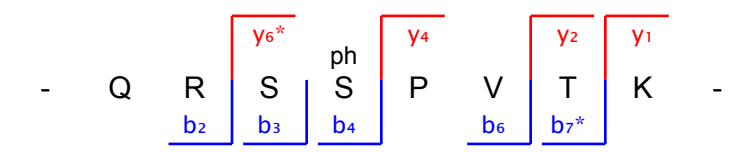
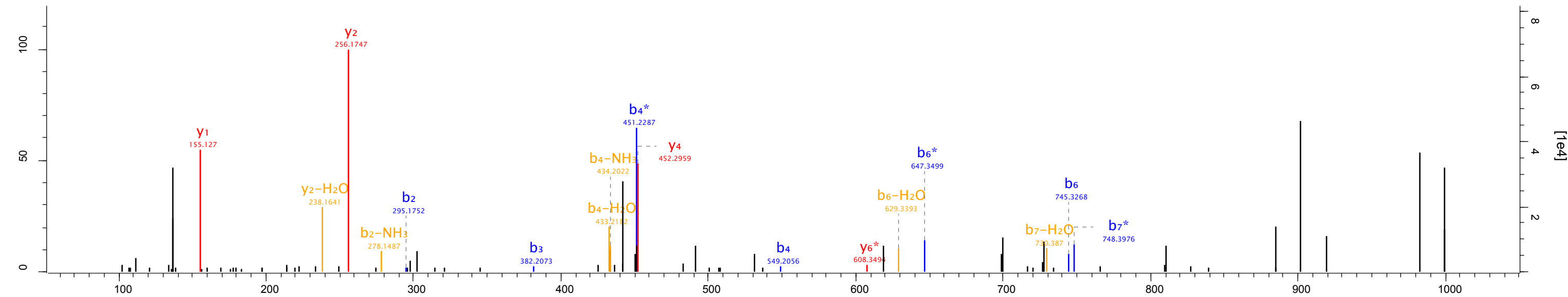
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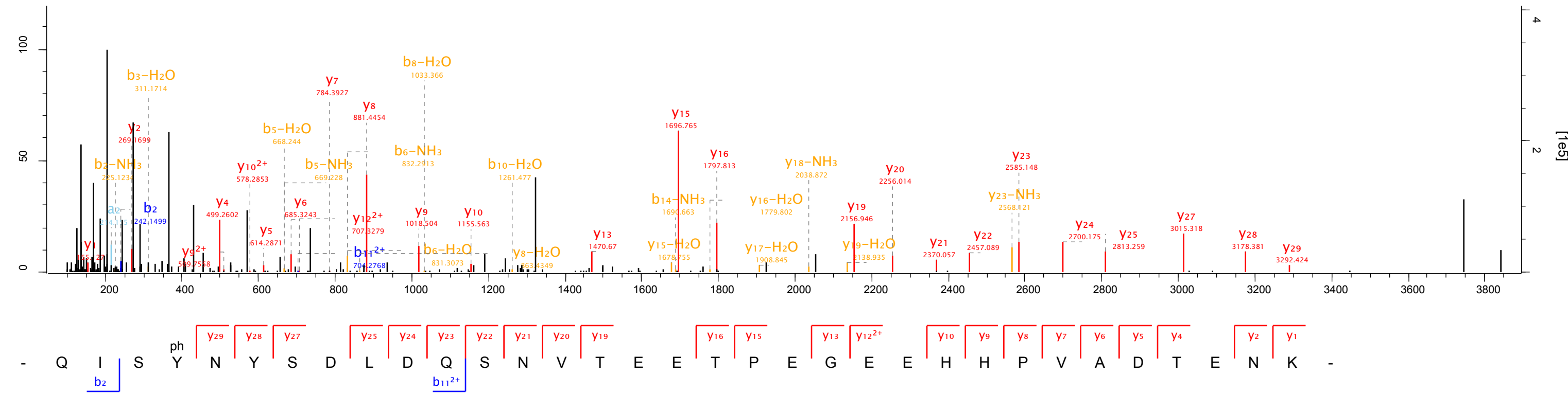
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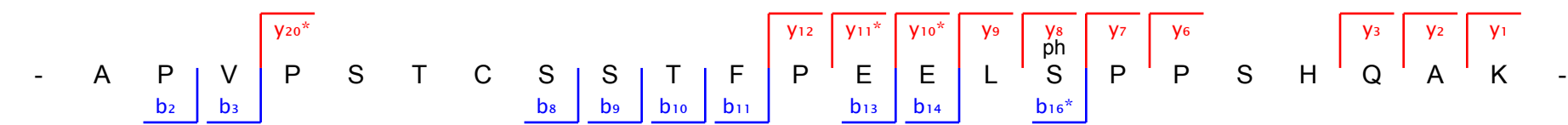
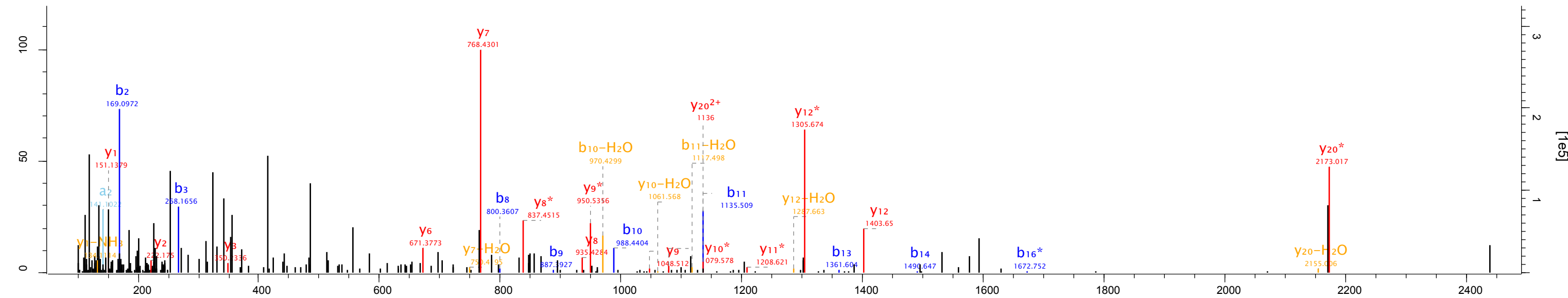


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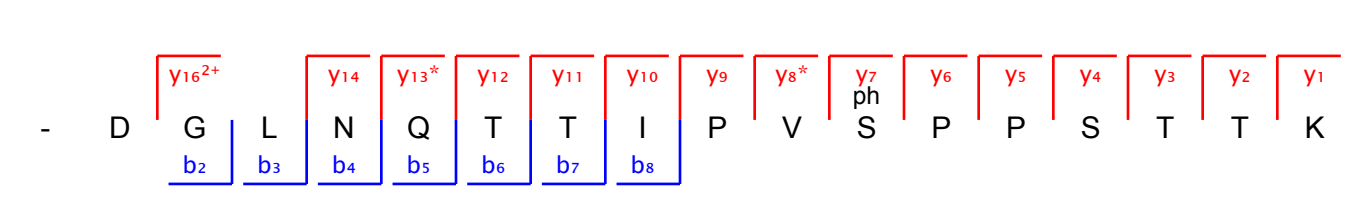
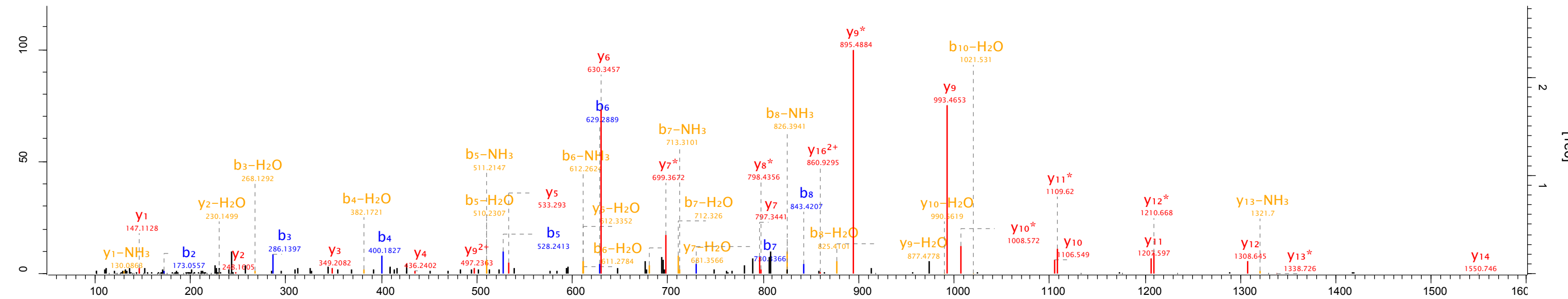


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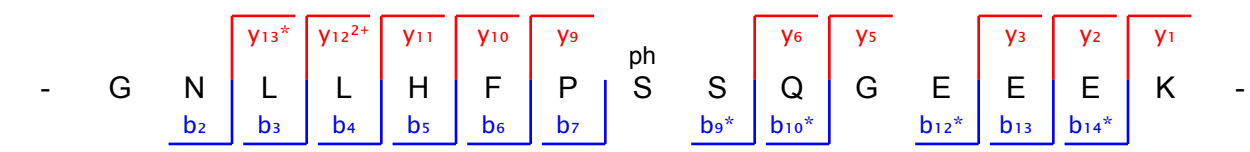
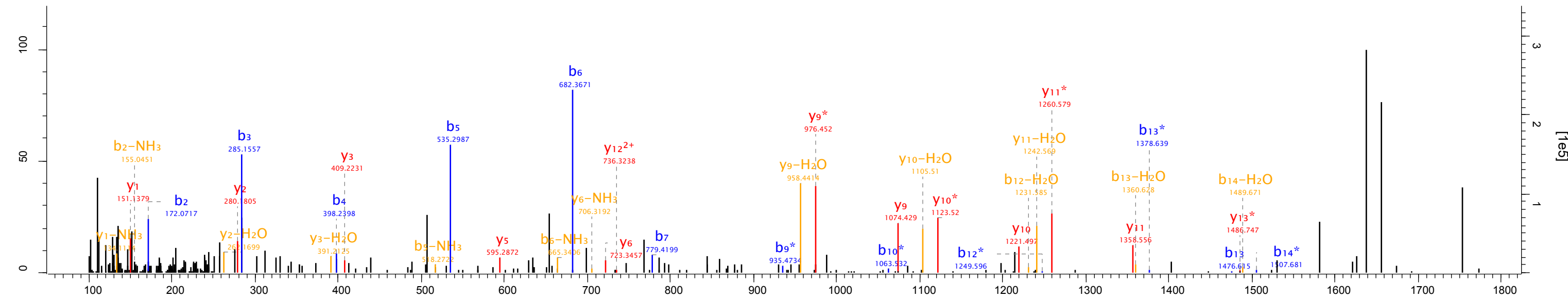


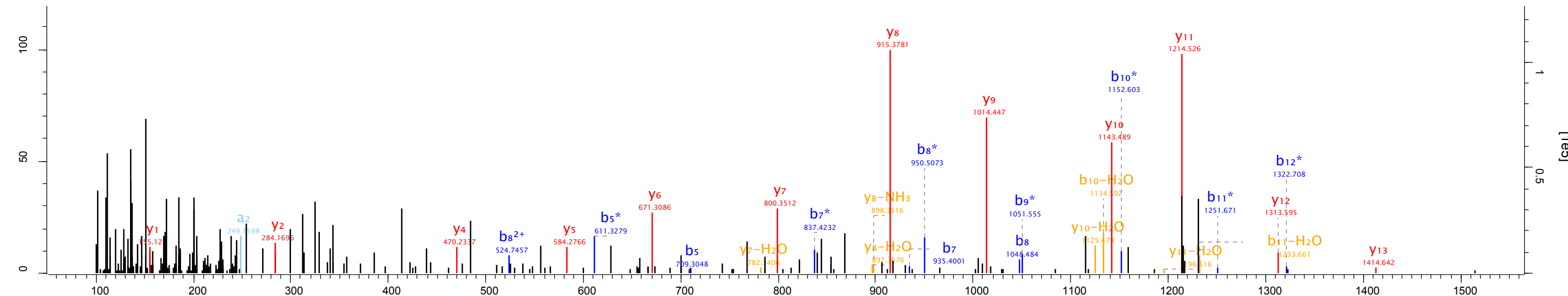


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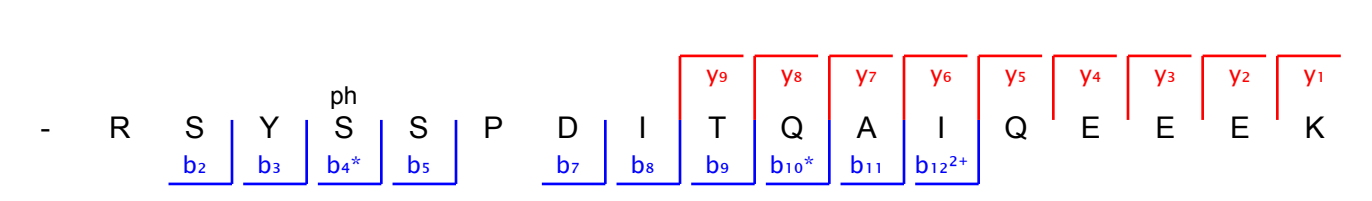
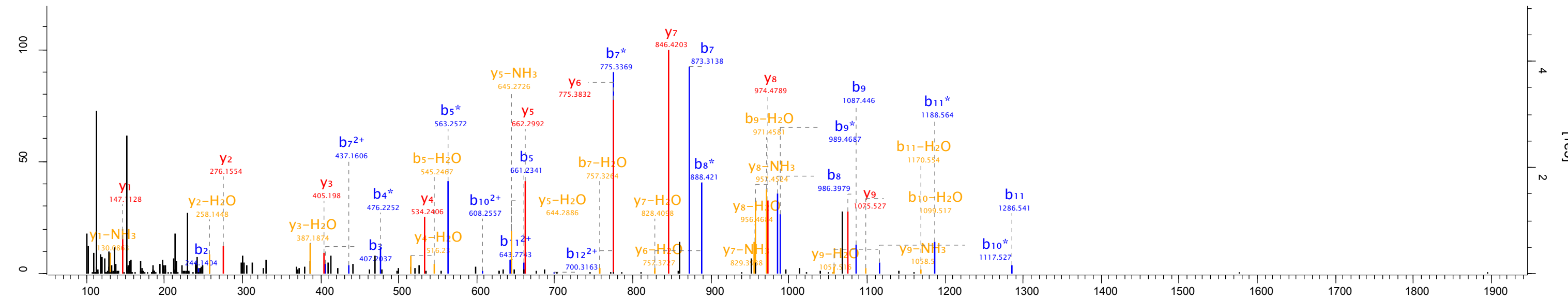
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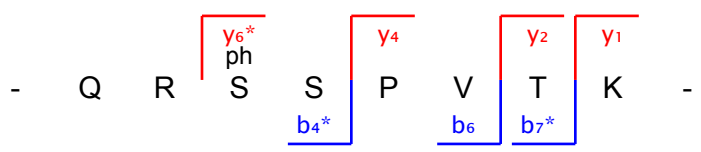
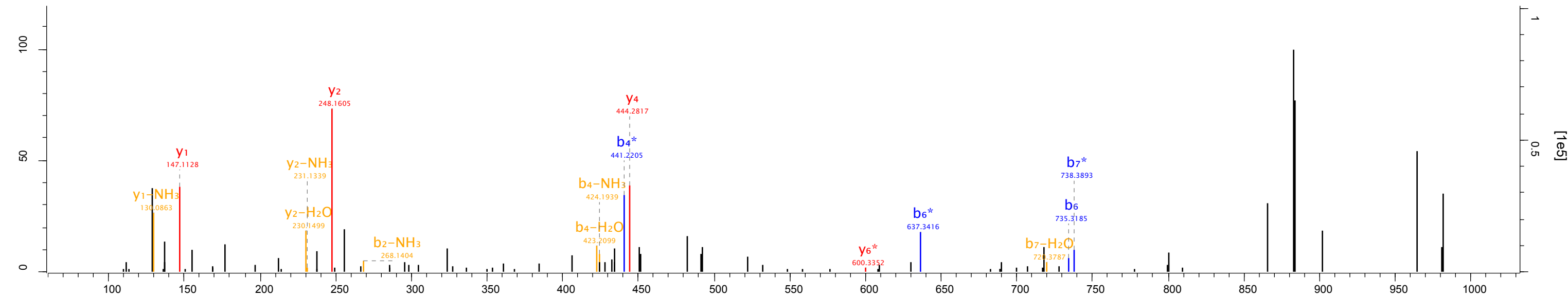


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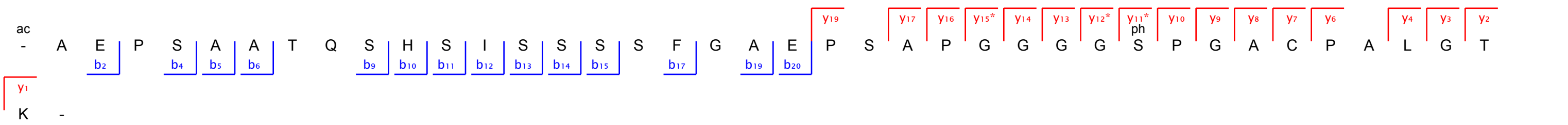
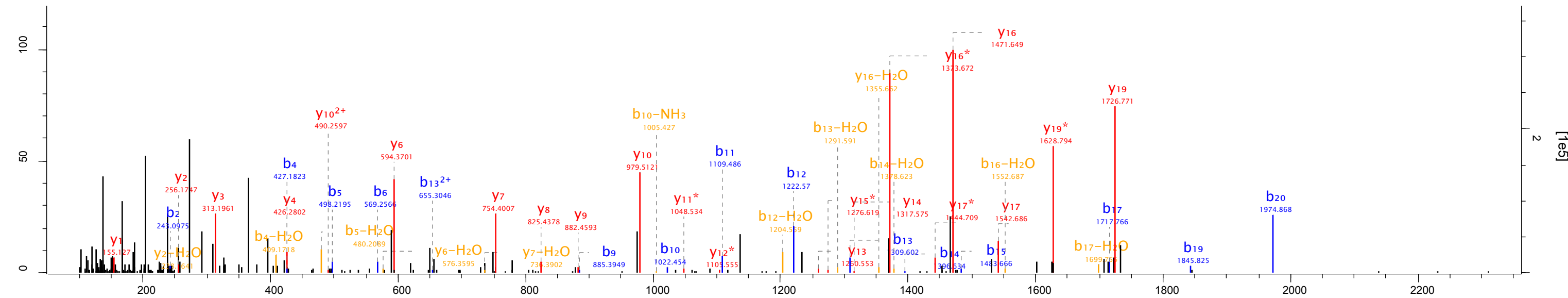
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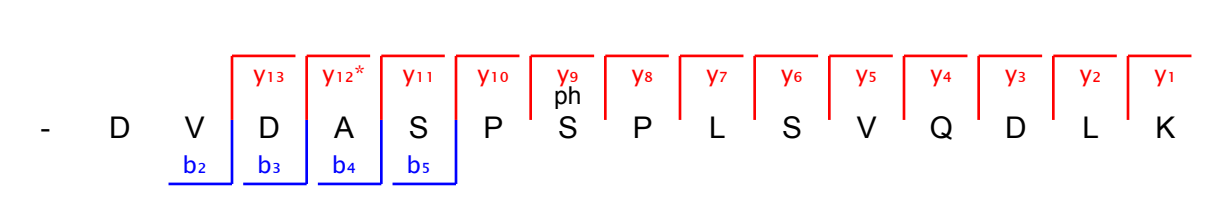
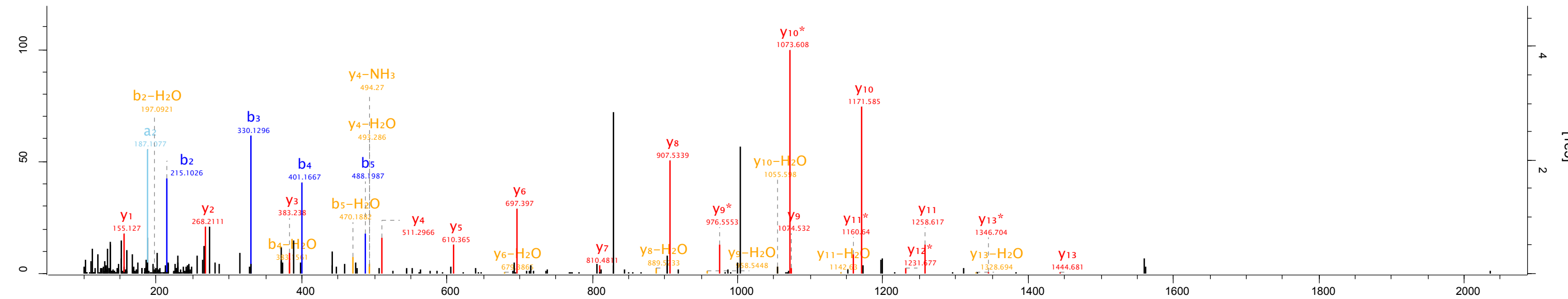
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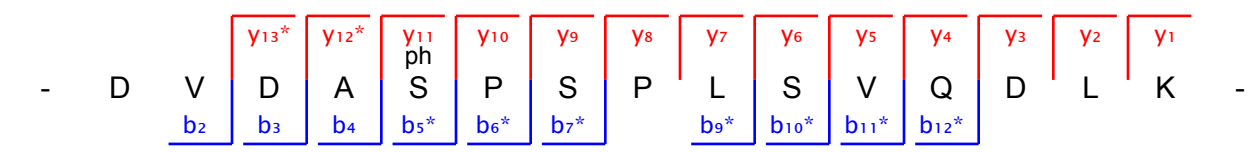
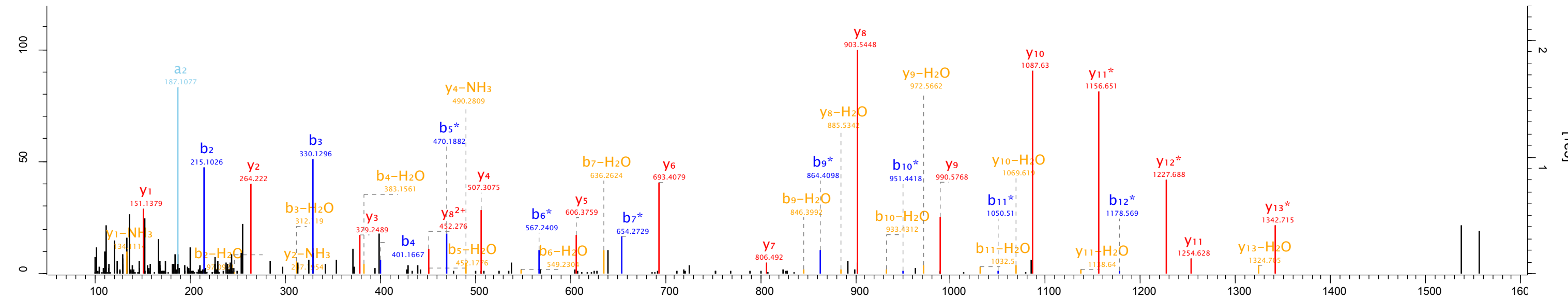
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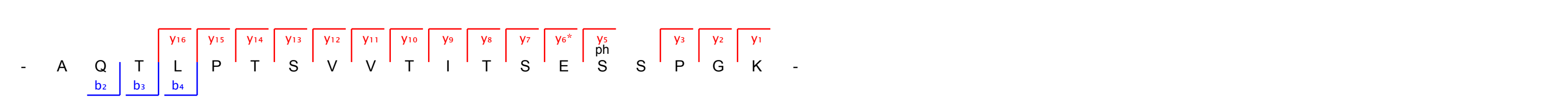
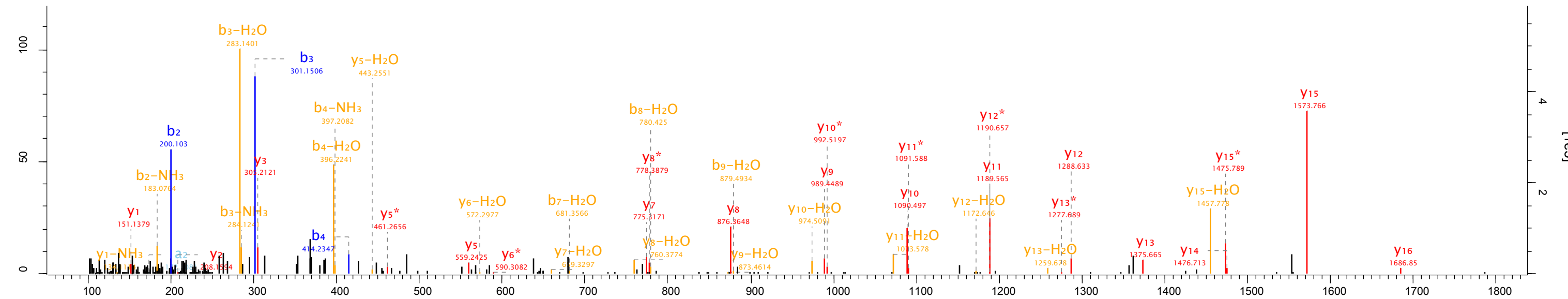
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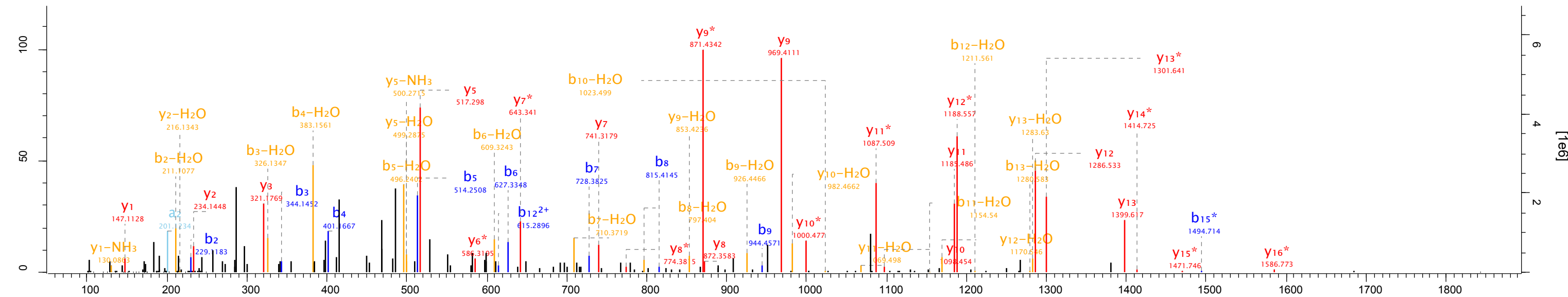


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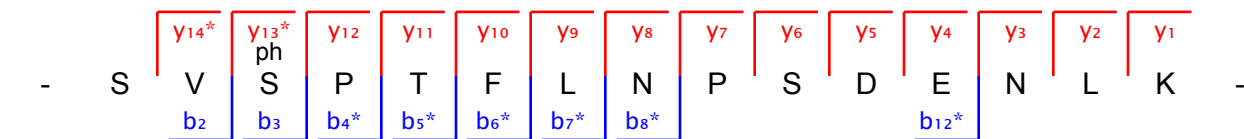
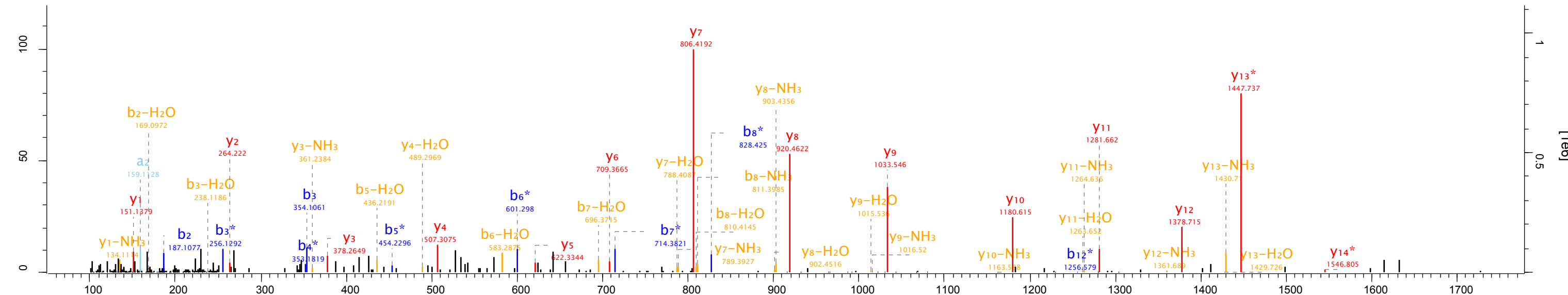




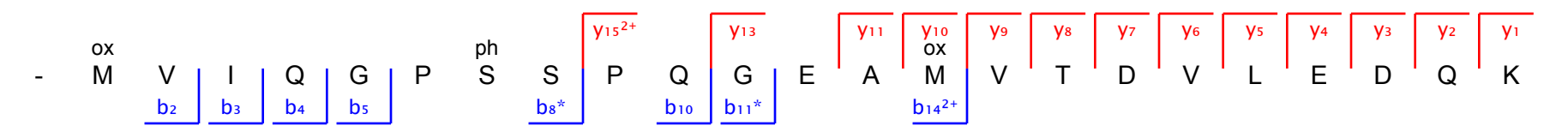
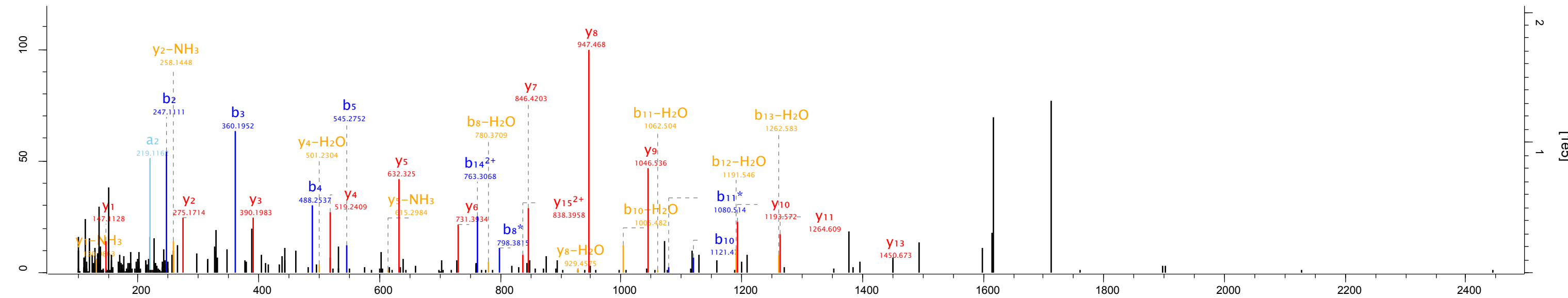
- E V D G L L T S E P M G S P V S S K -

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

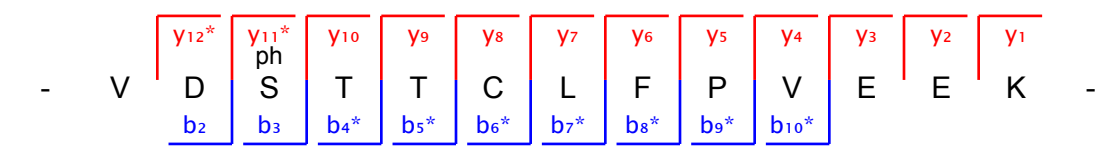
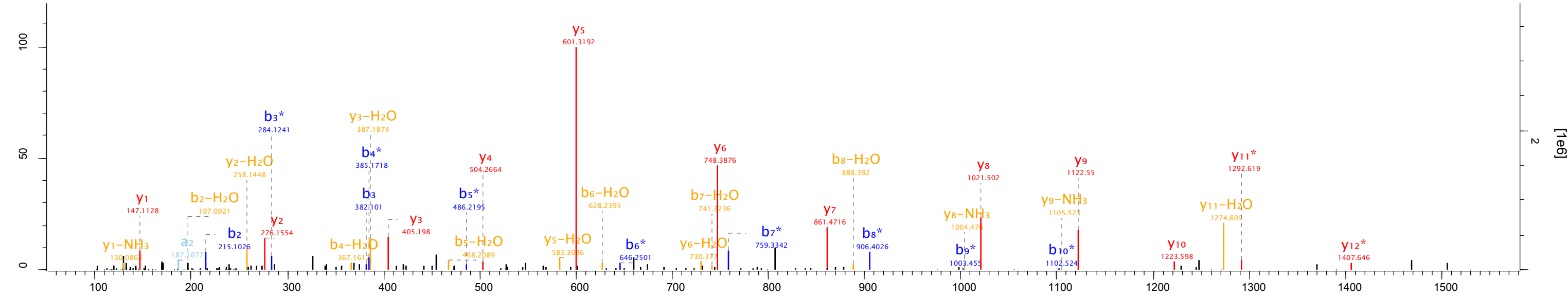
- b₂ (under V)
- b₃ (under D)
- b₄ (under G)
- b₅ (under L)
- b₆ (under L)
- b₇ (under T)
- b₈ (under S)
- b₉ (under E)
- b₁₂²⁺ (under G)
- b₁₅^{*} (under V)
- y₁₆^{*} (above D)
- y₁₅^{*} (above G)
- y₁₄^{*} (above L)
- y₁₃ (above L)
- y₁₂ (above T)
- y₁₁ (above S)
- y₁₀ (above E)
- y₉ (above P)
- y₈ (above M)
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- y₁ (above K)



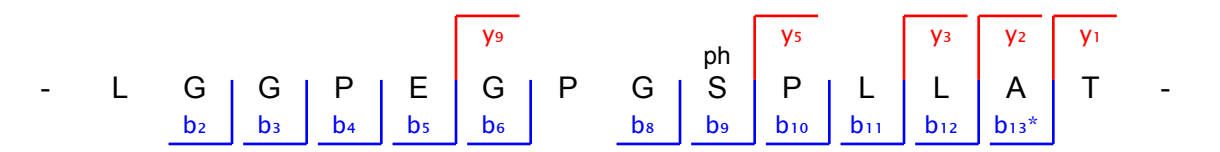
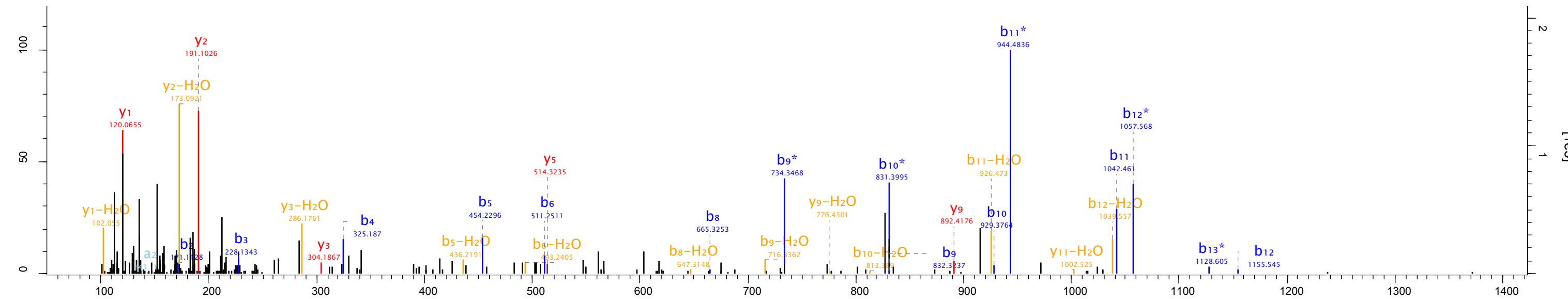
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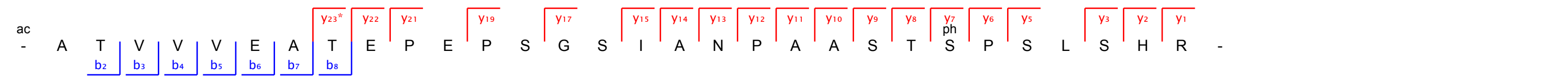
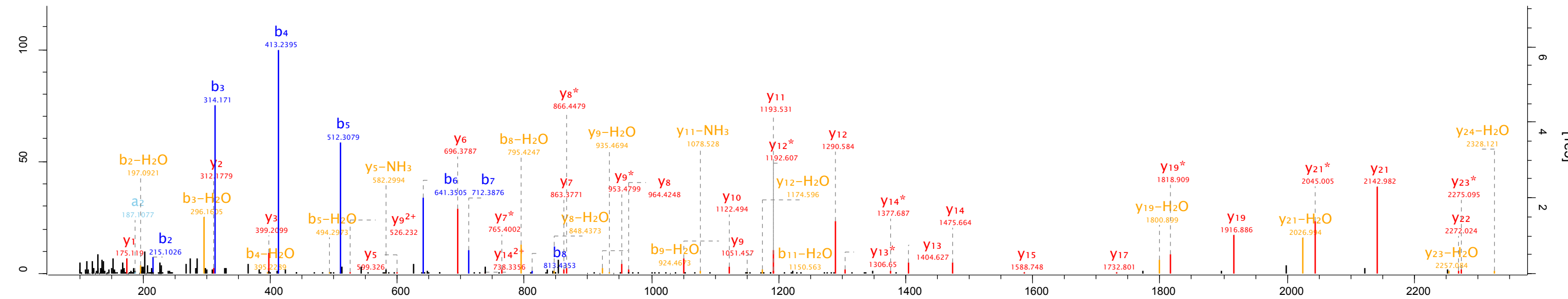
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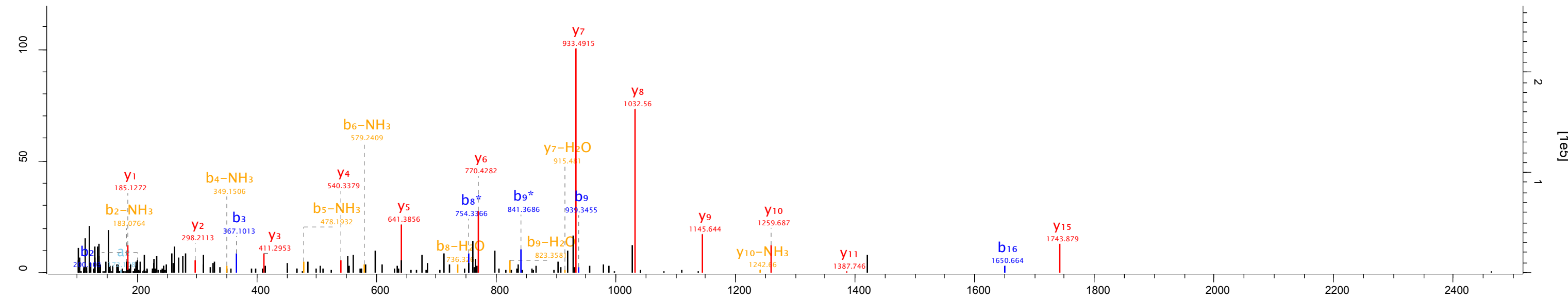
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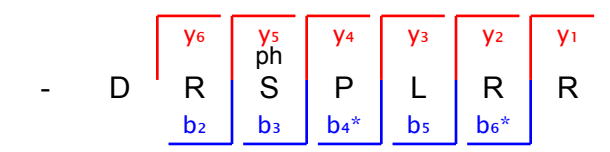
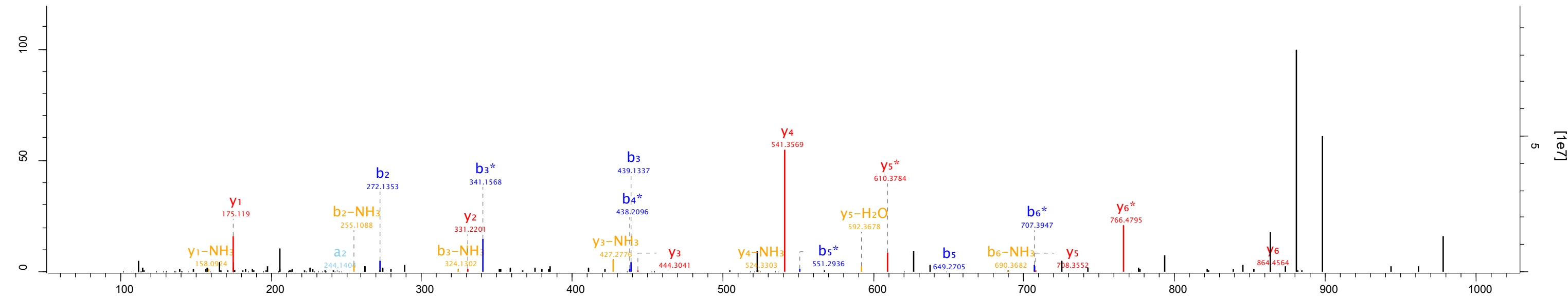
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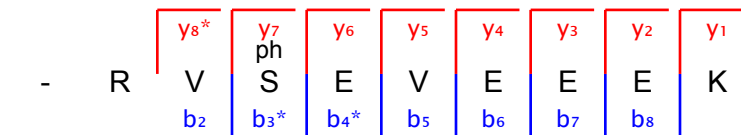
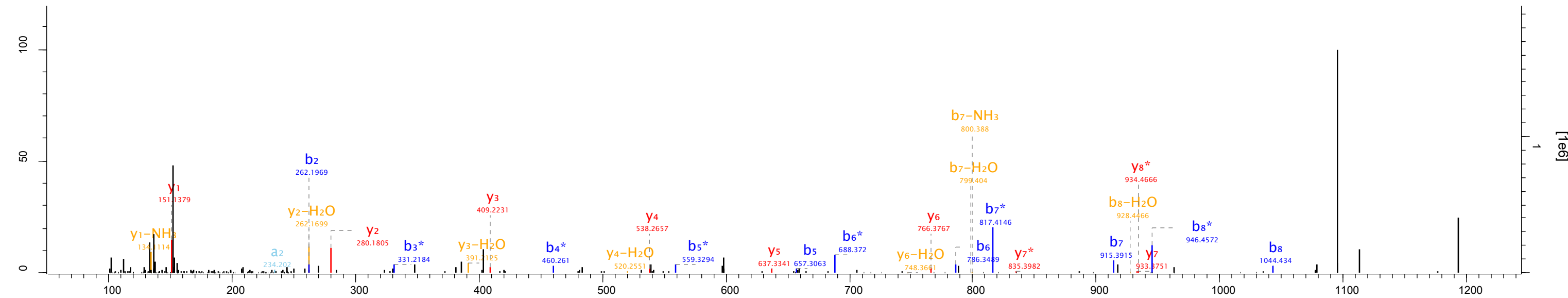


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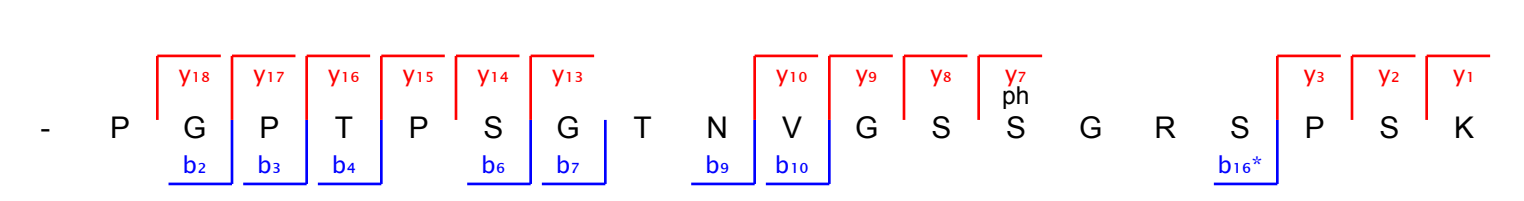
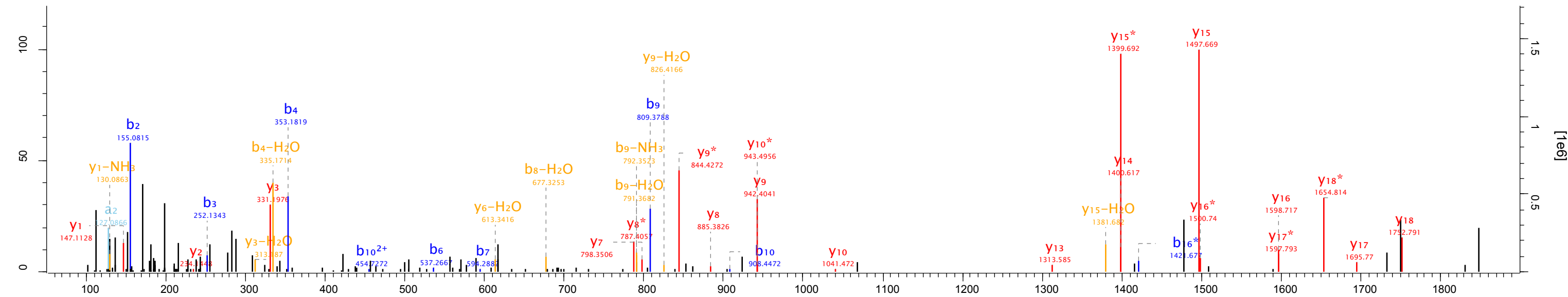


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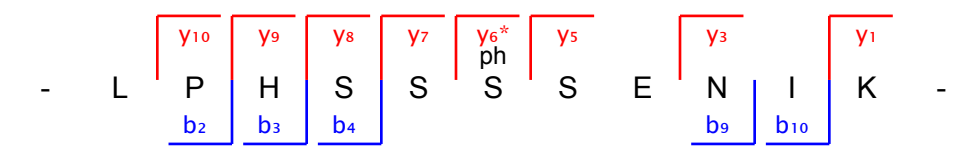
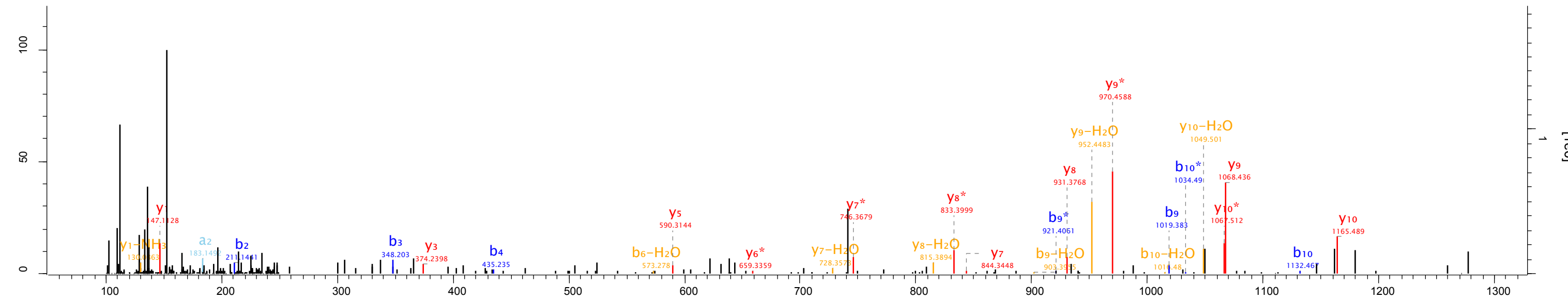




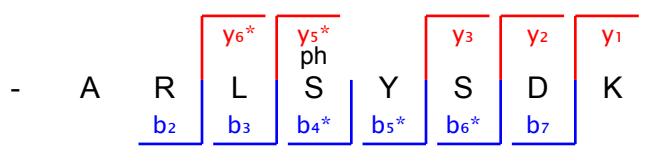
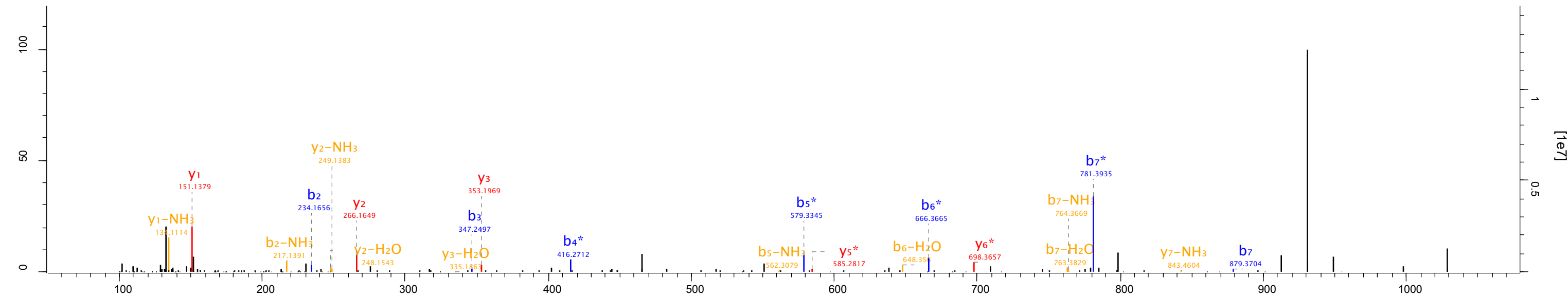
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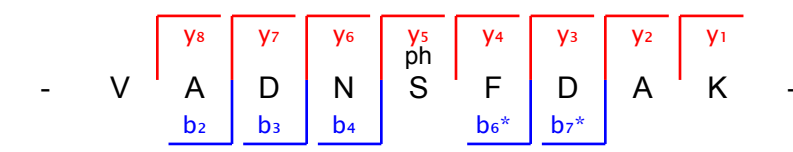
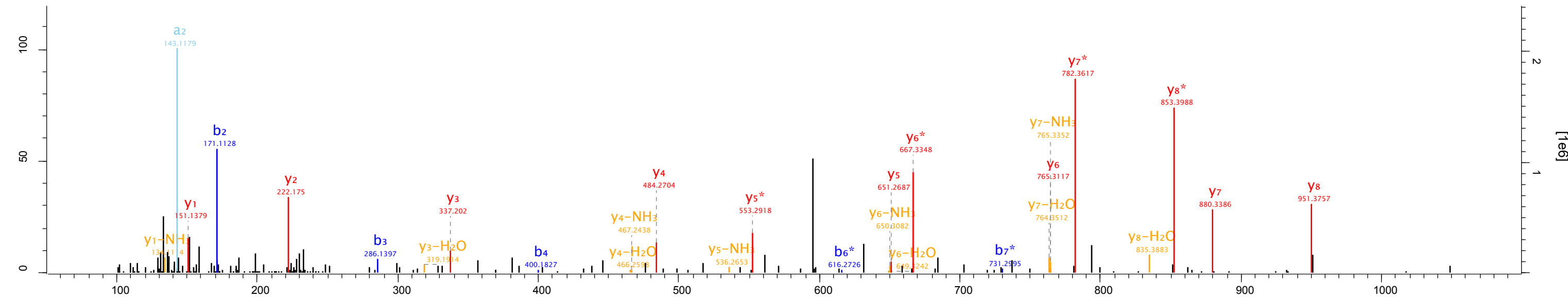
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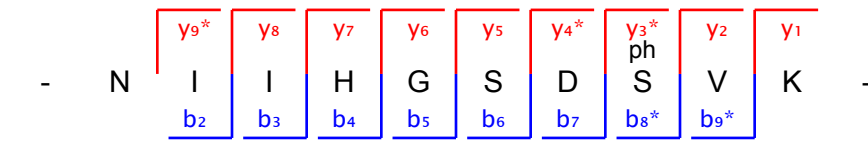
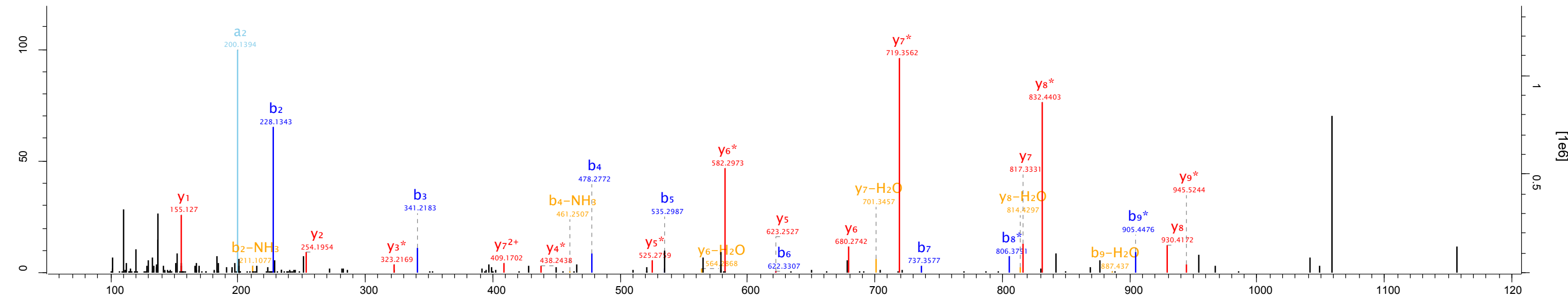
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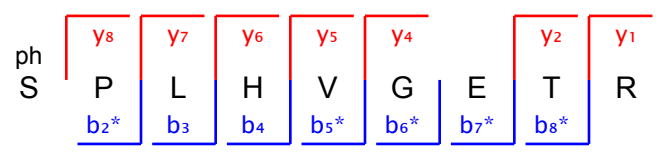
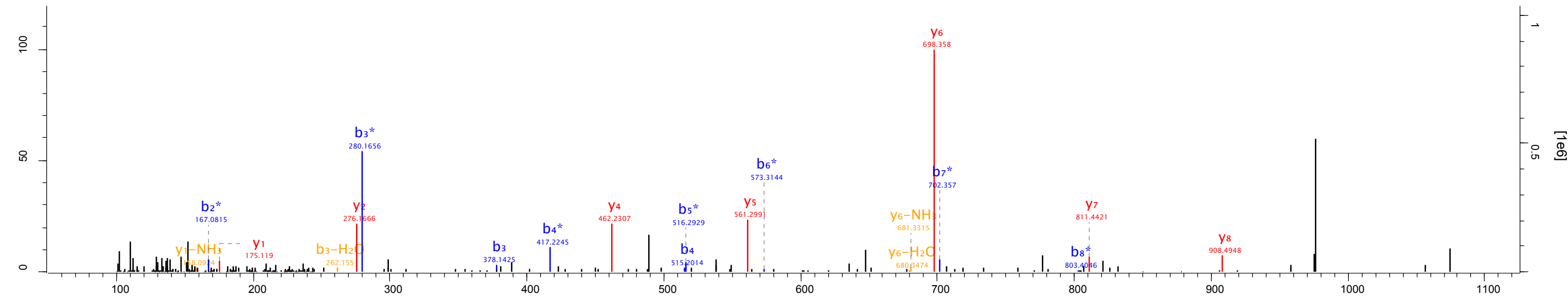
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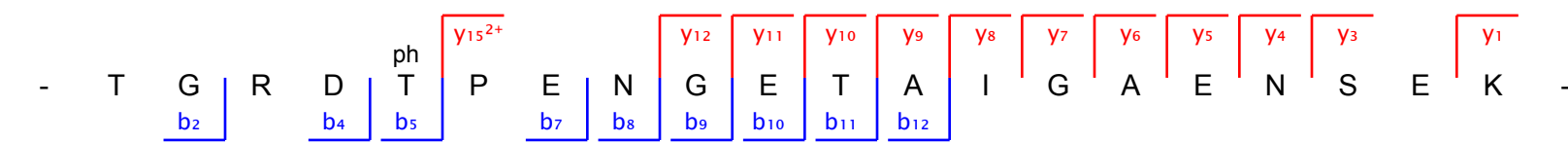
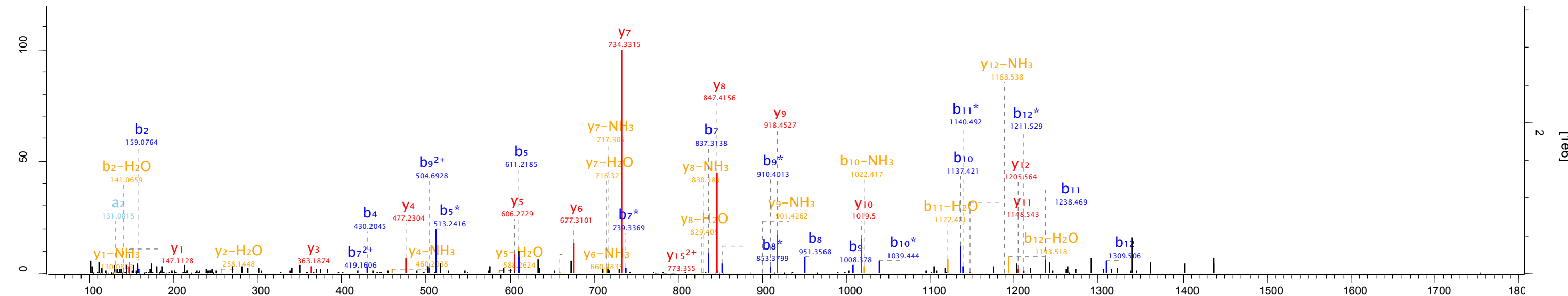


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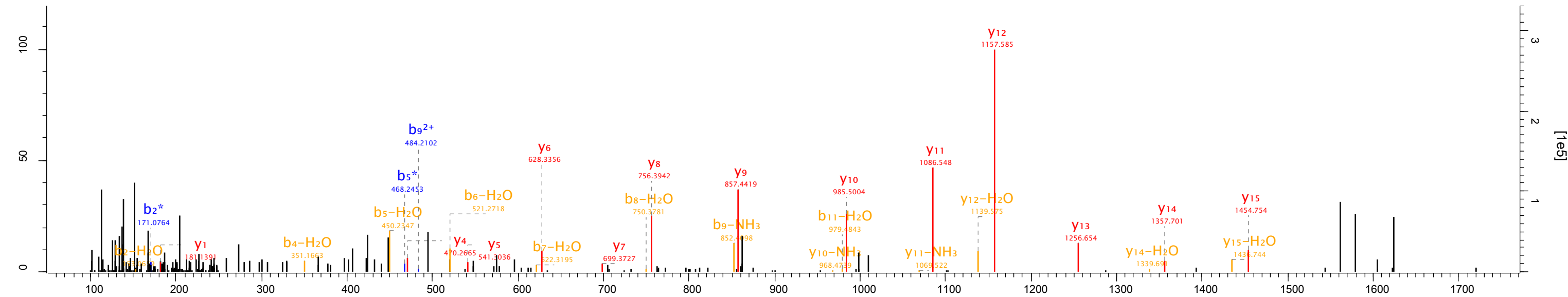


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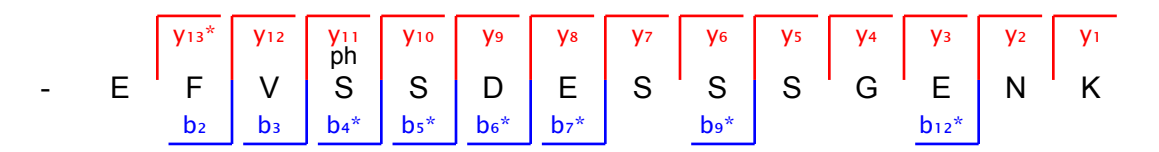
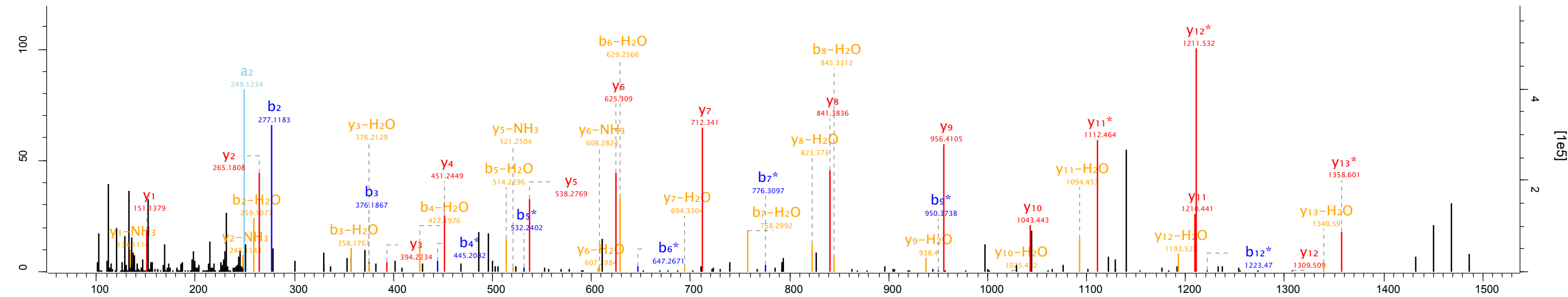


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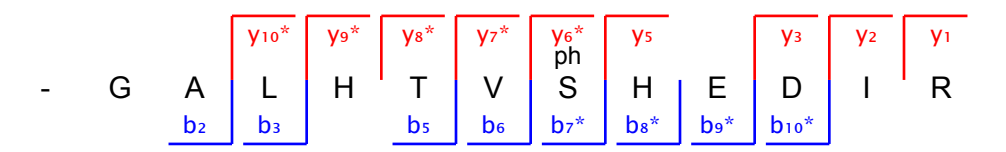
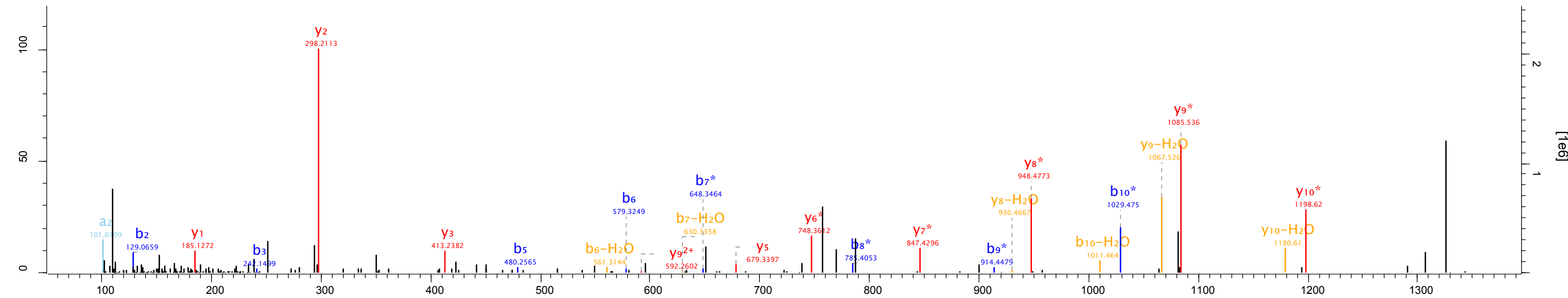


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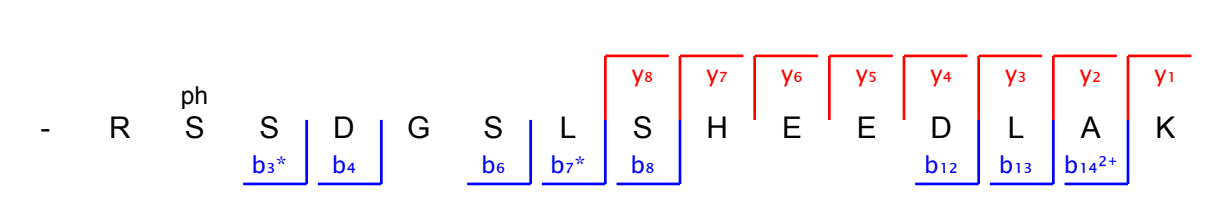
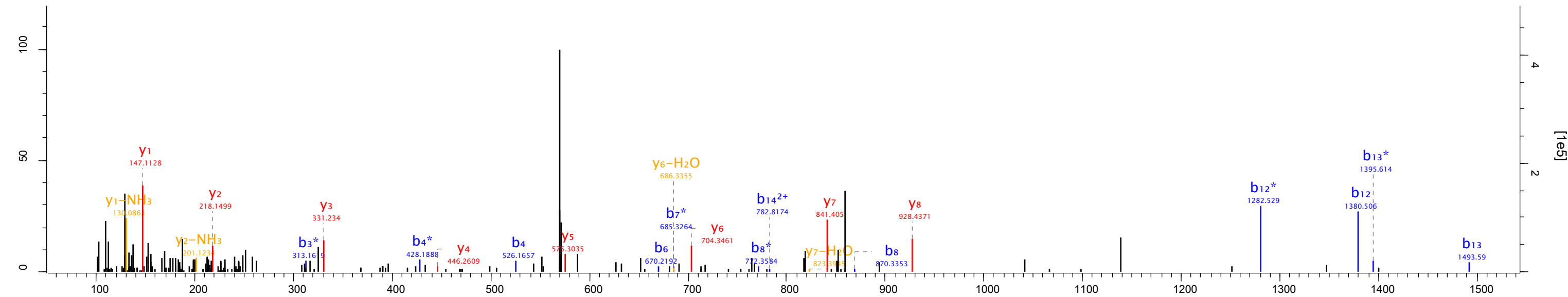
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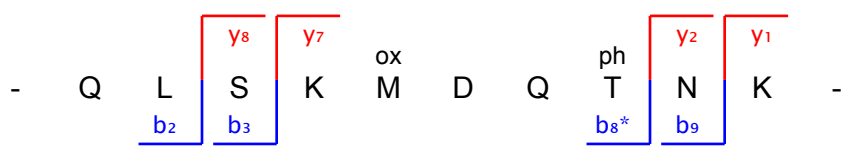
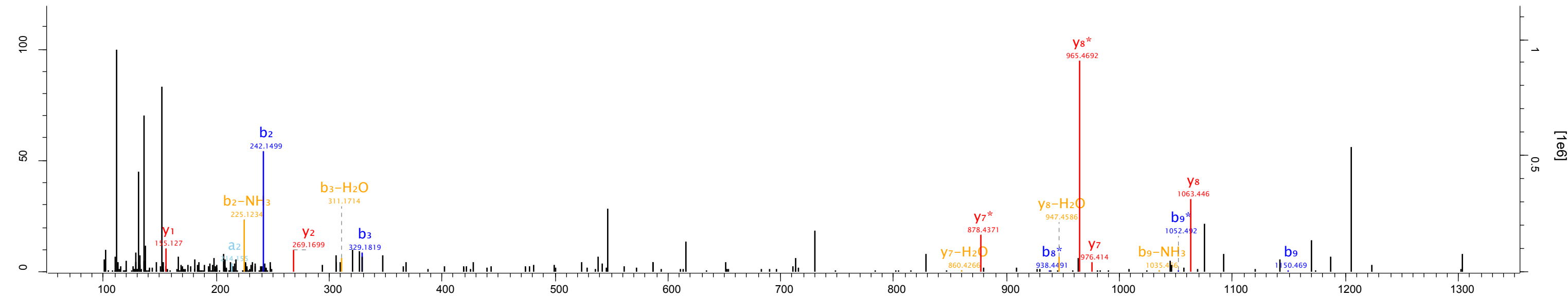
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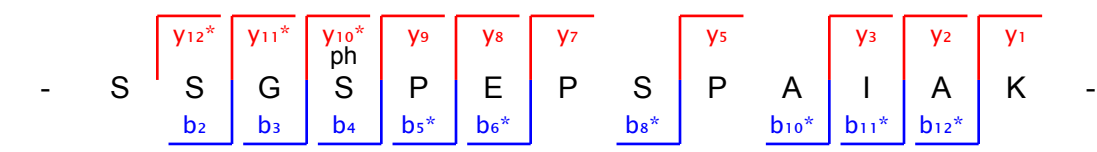
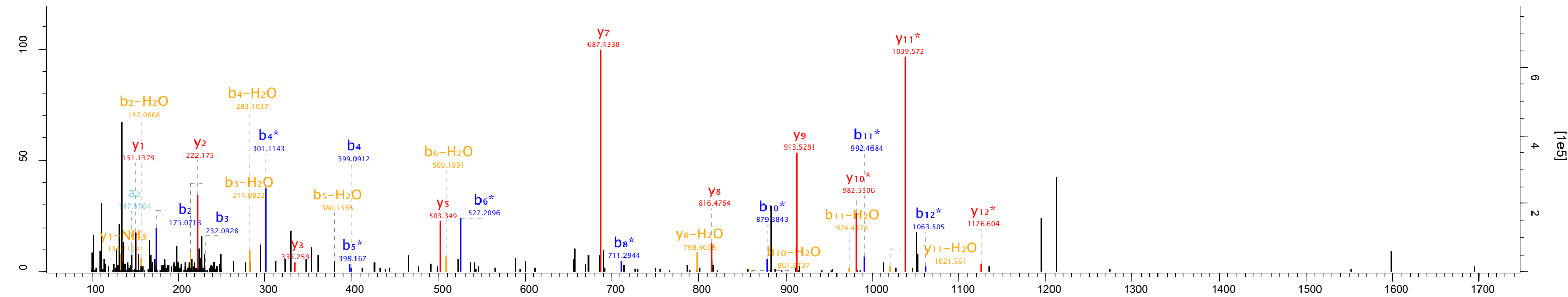
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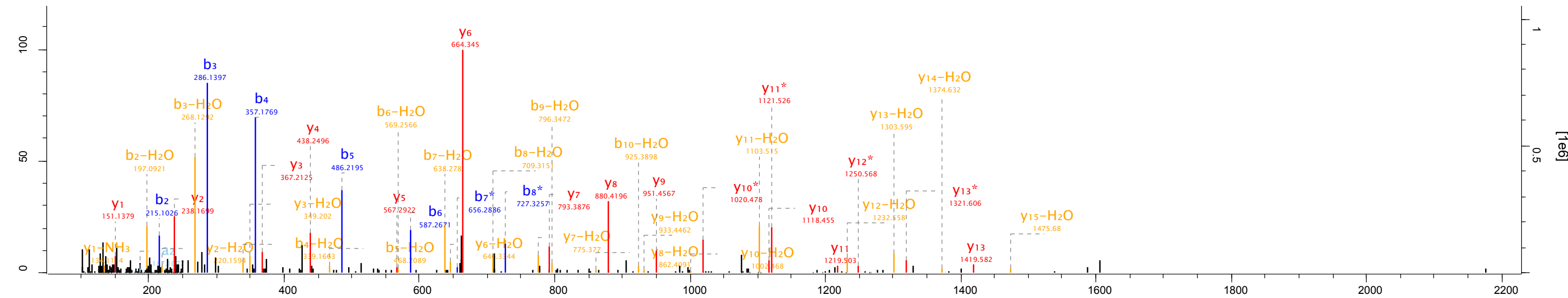
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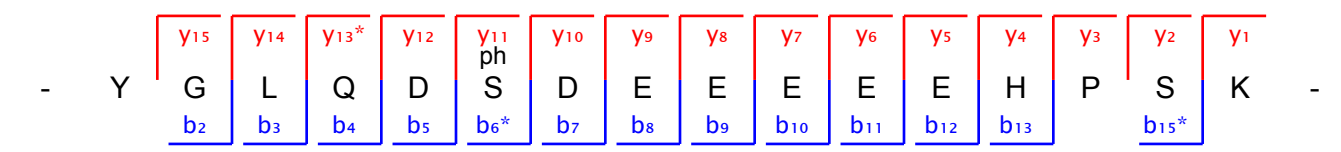
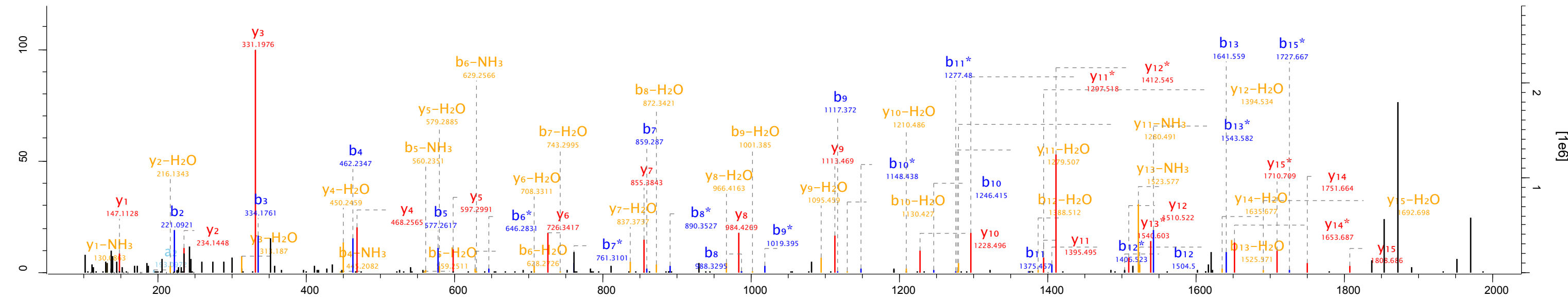


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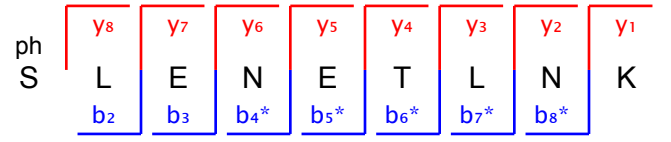
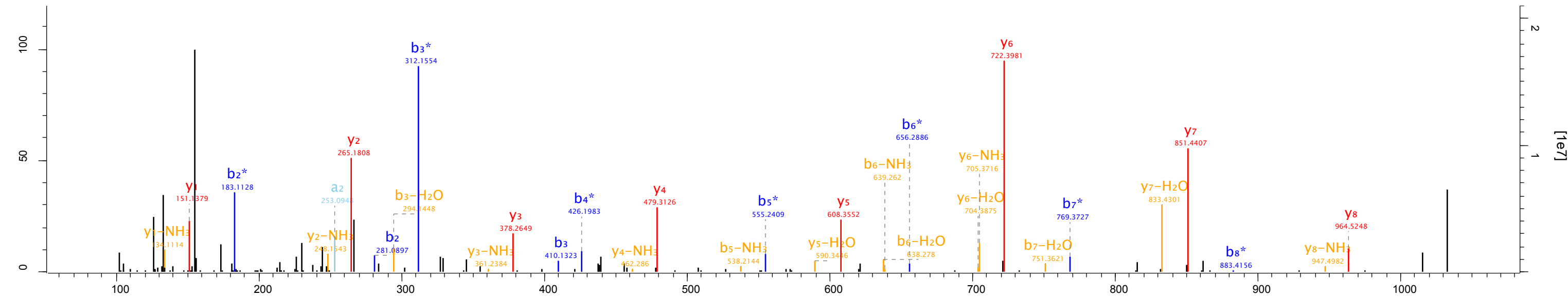


ac
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 b2 b3 b4 b5 b6 b7* b8*

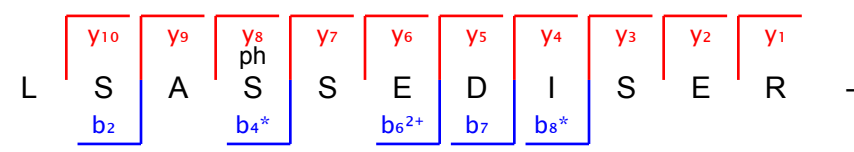
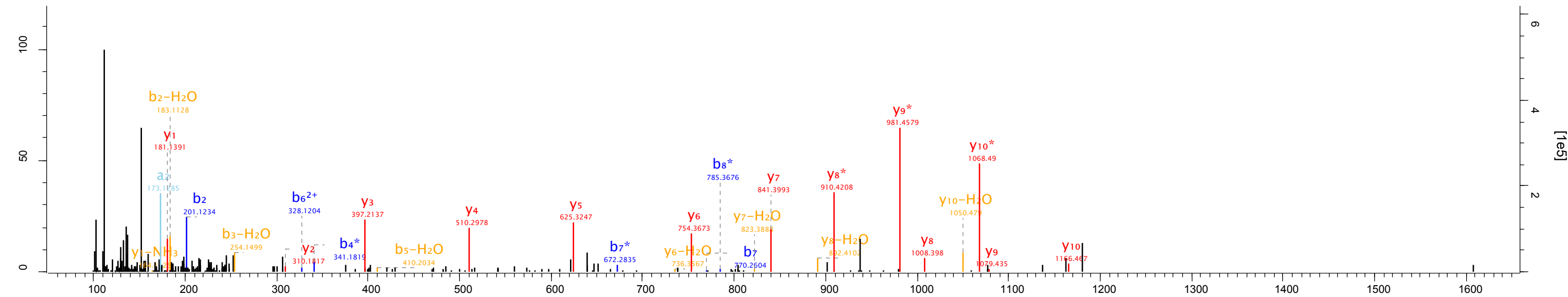
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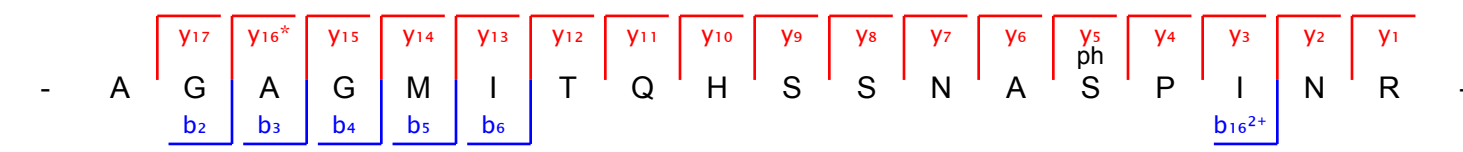
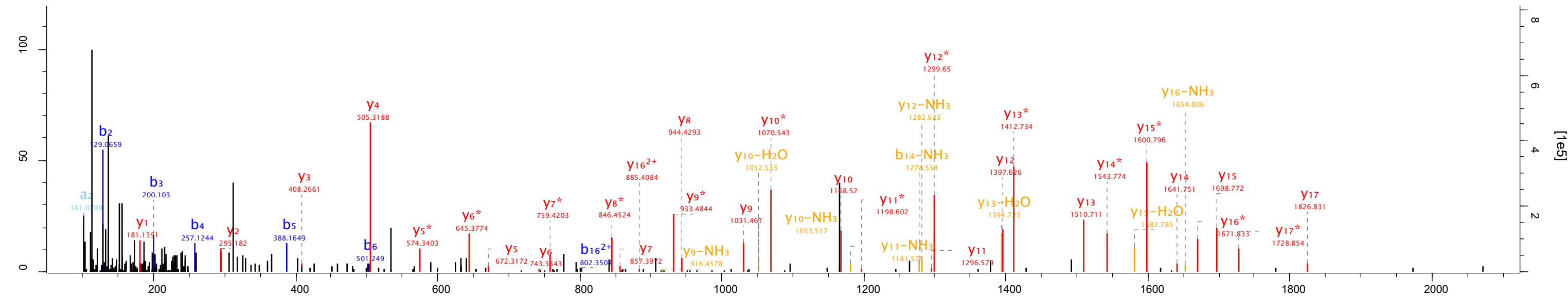


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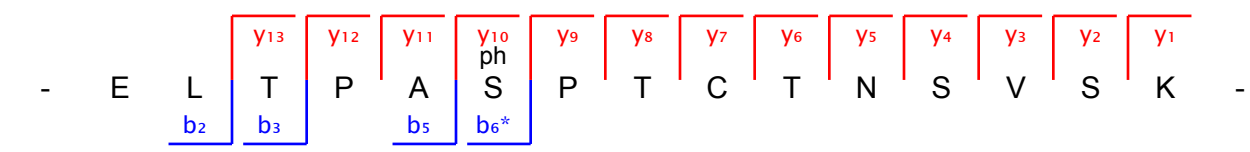
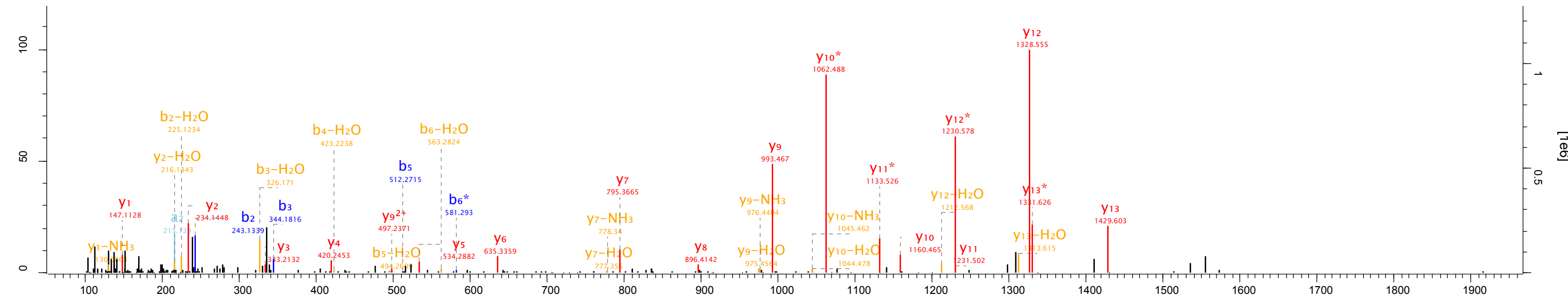


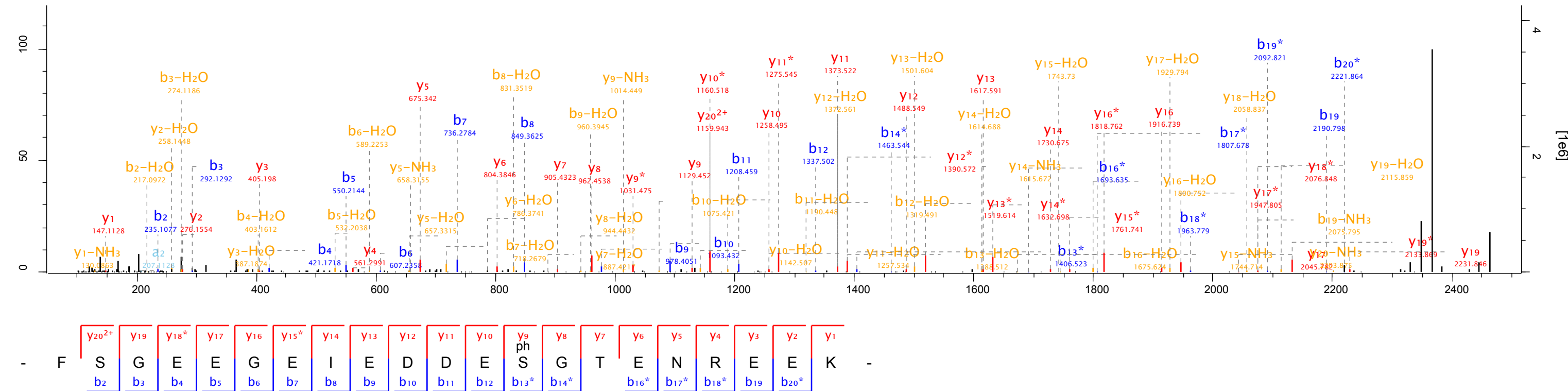
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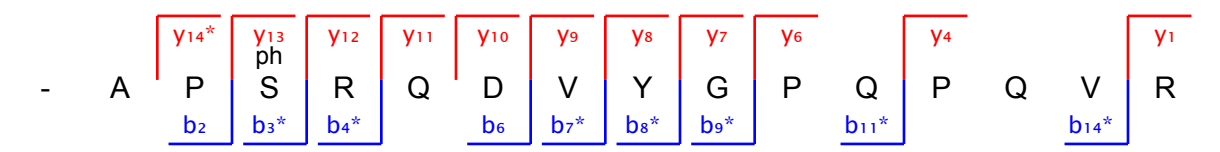
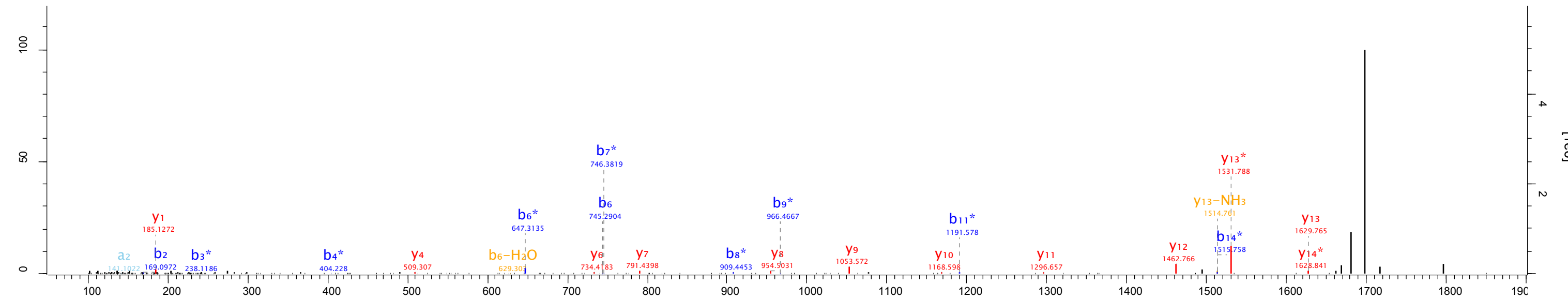


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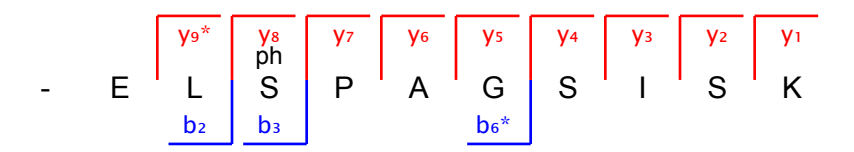
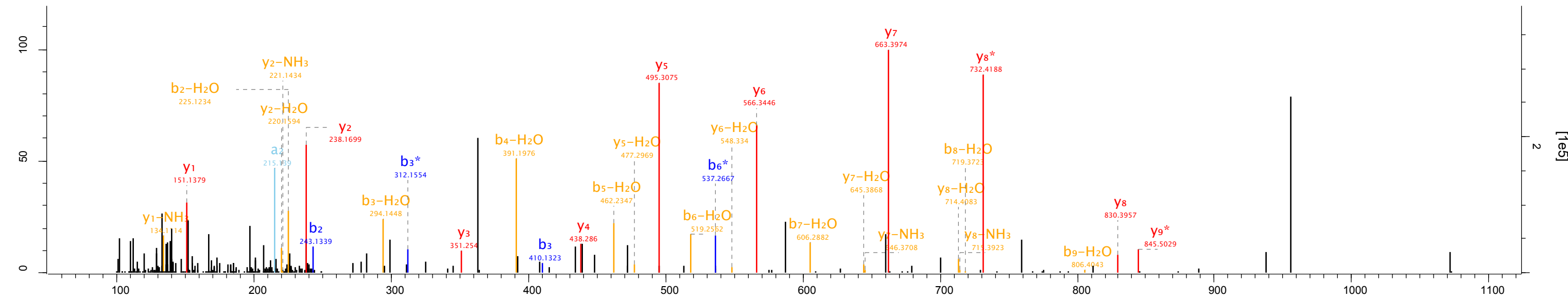




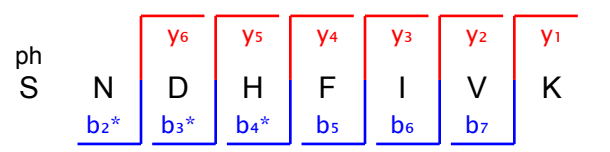
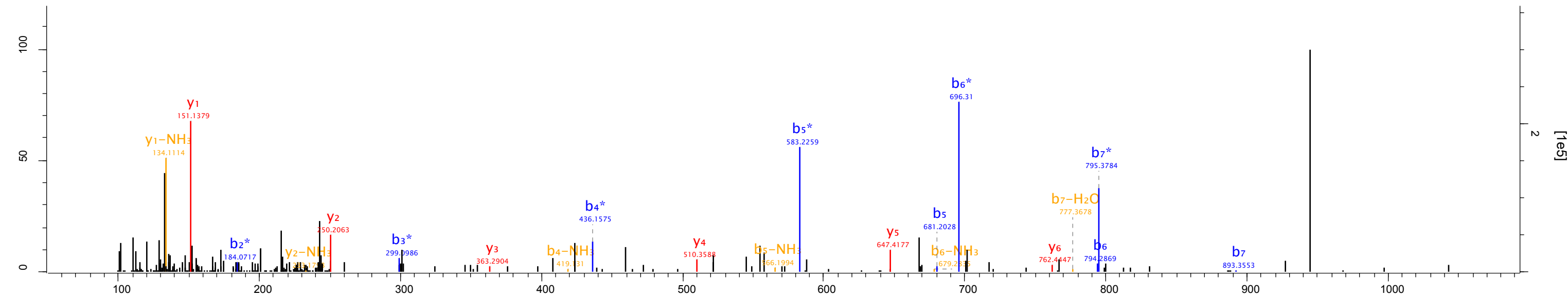
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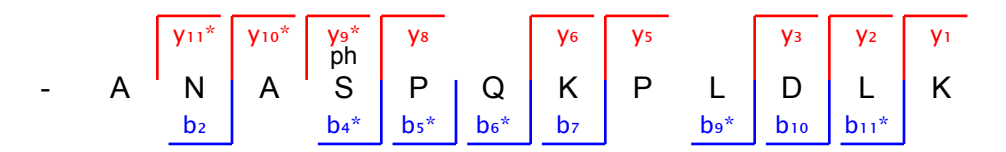
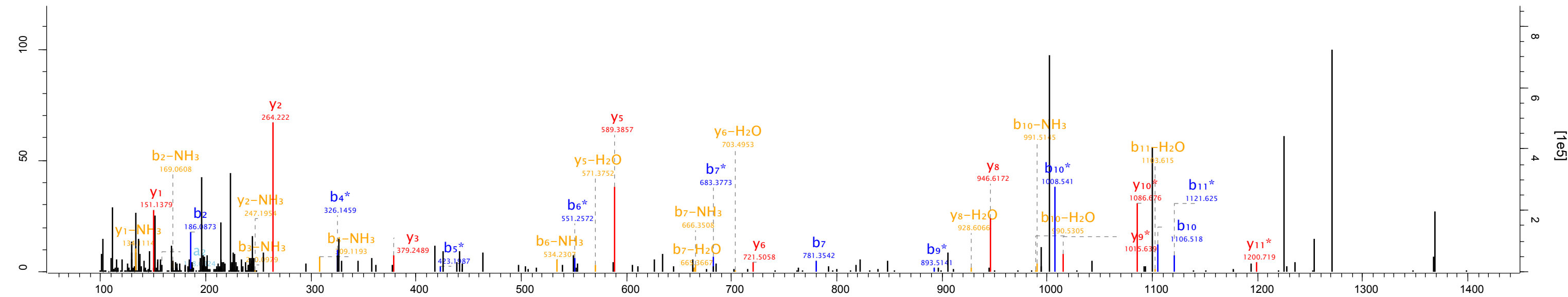
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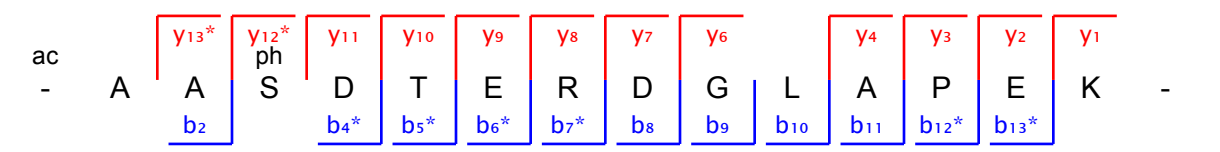
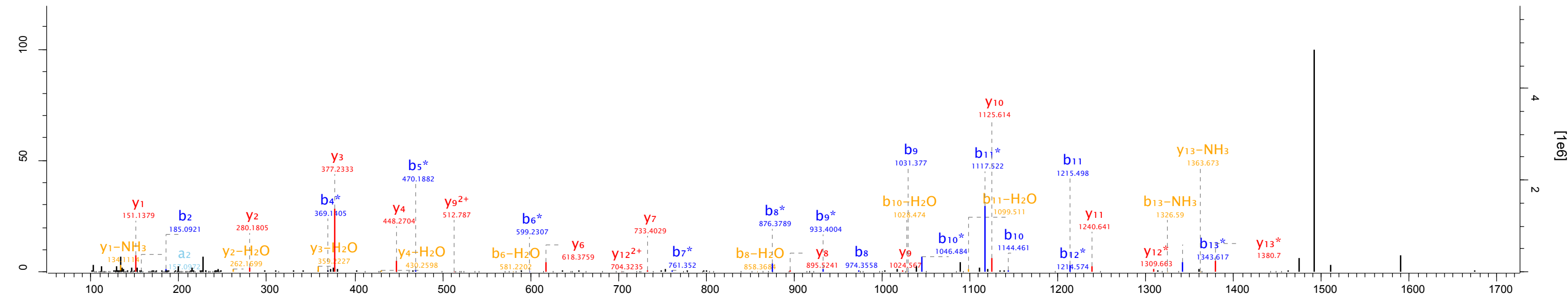
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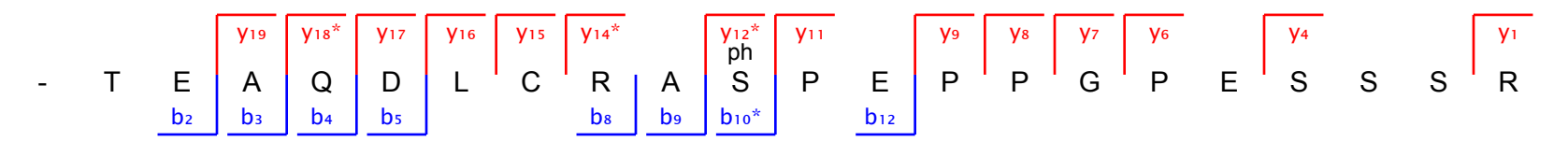
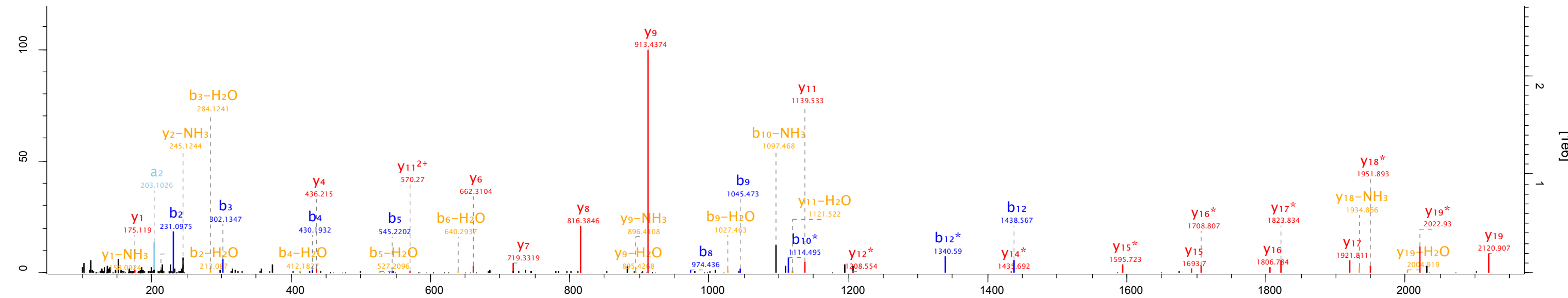
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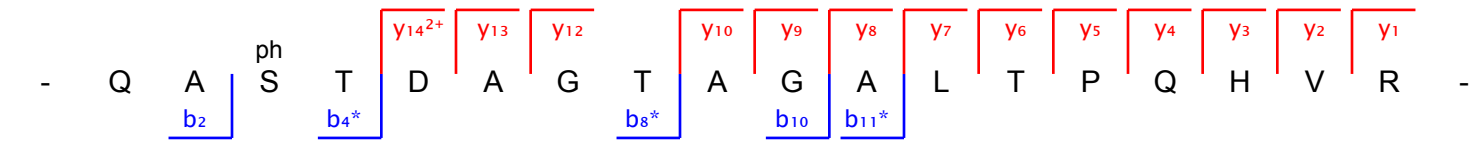
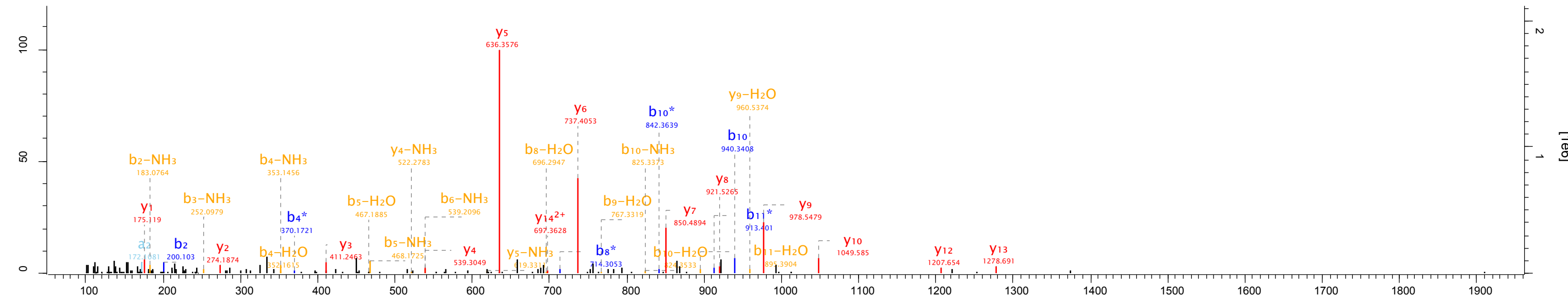


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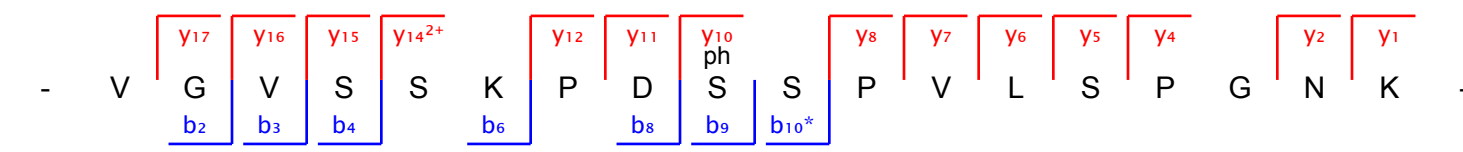
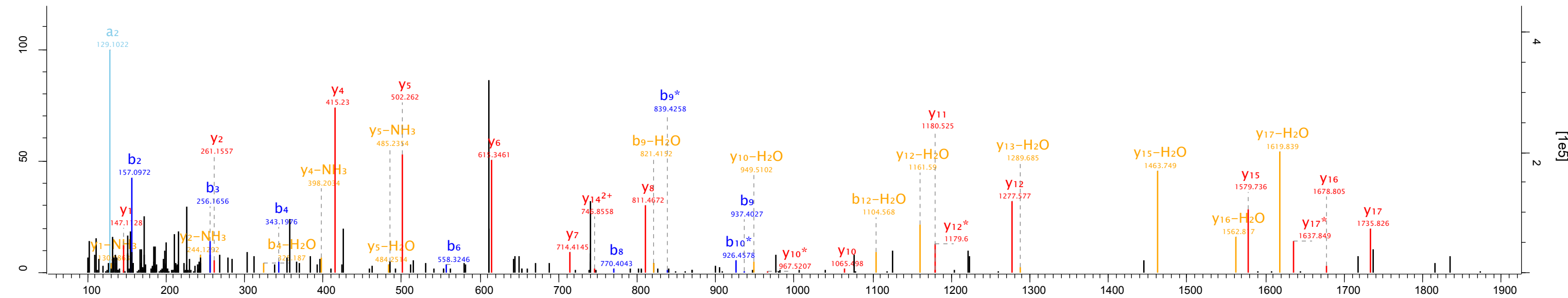


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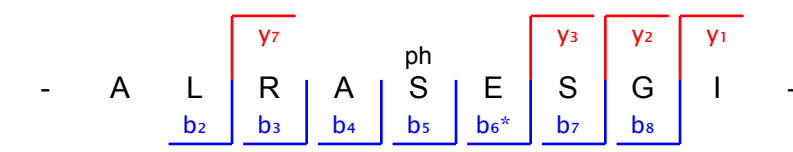
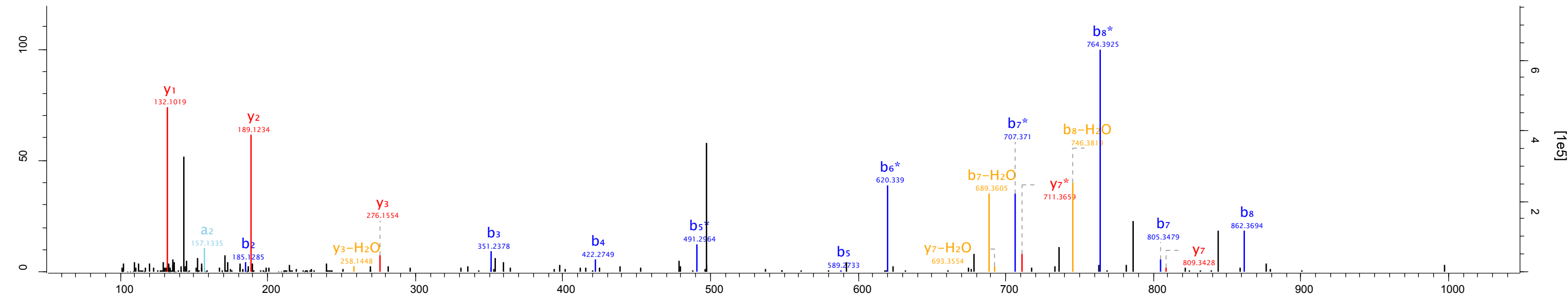




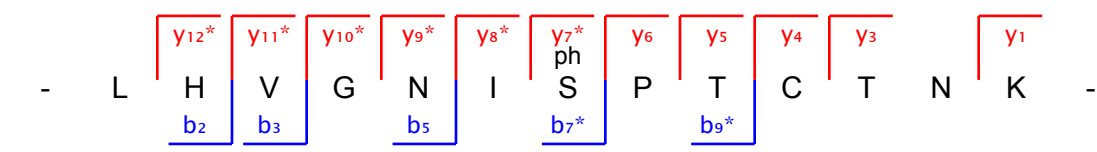
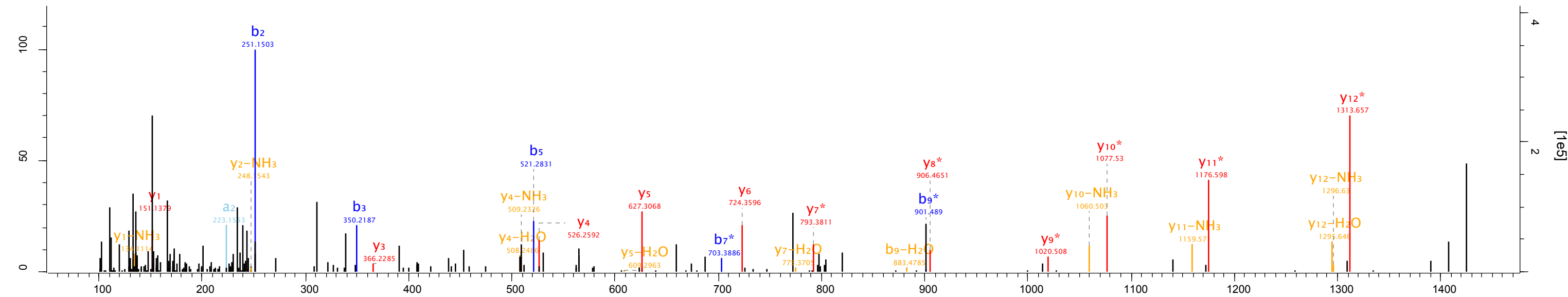
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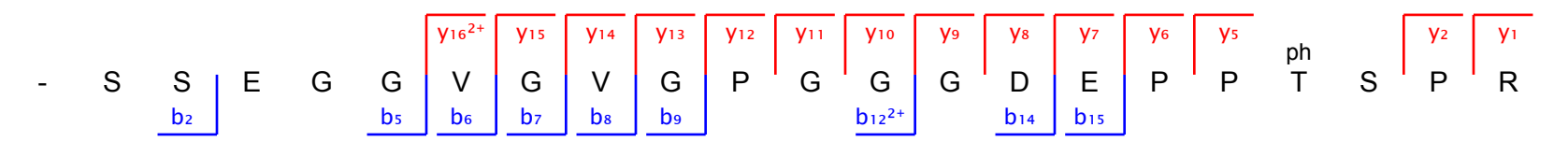
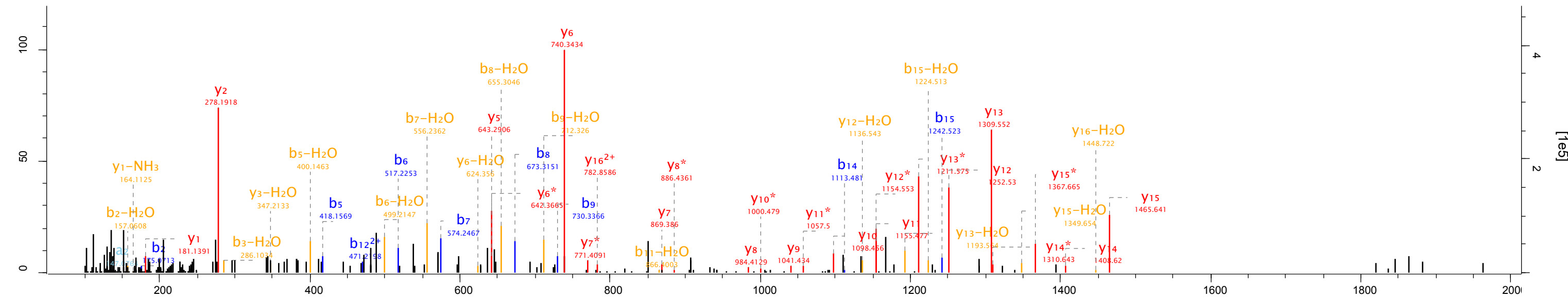
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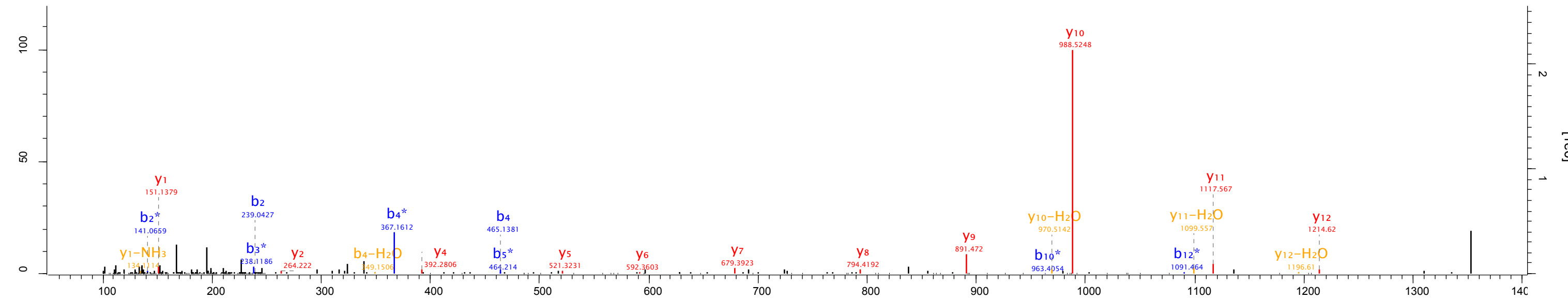
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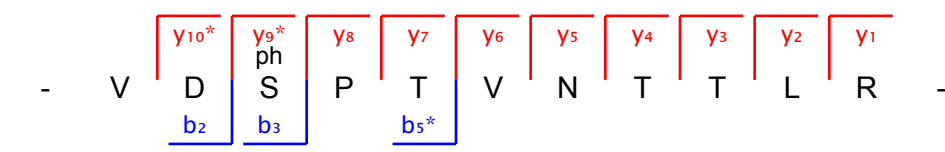
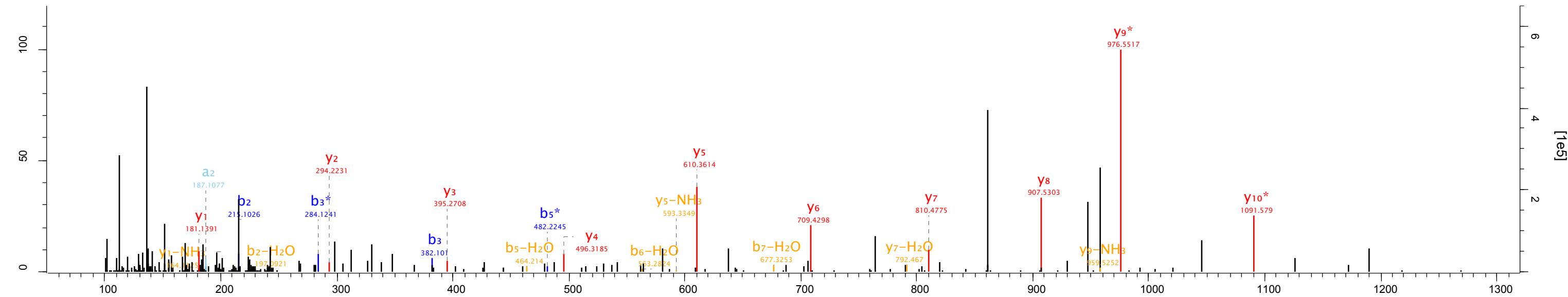
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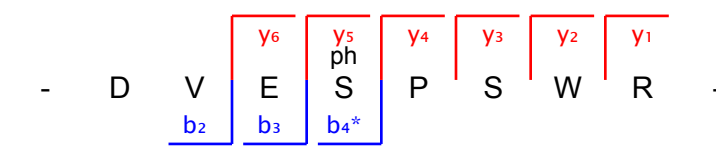
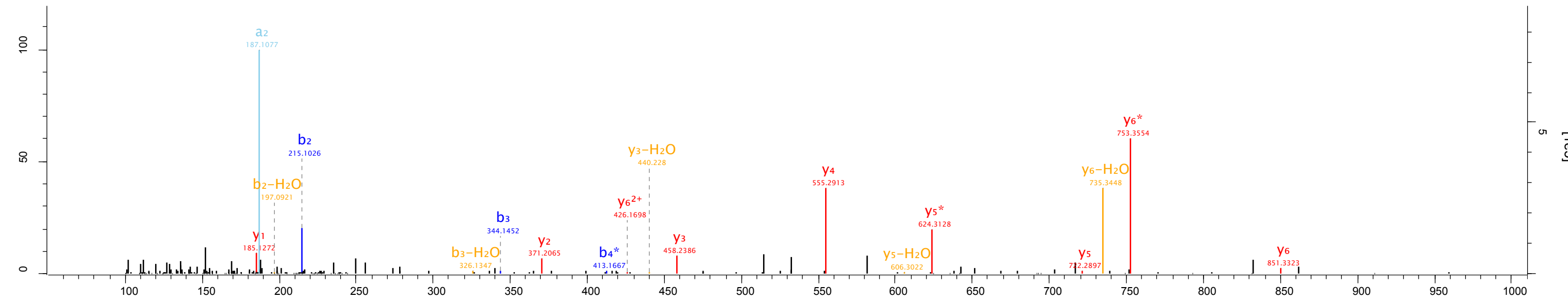
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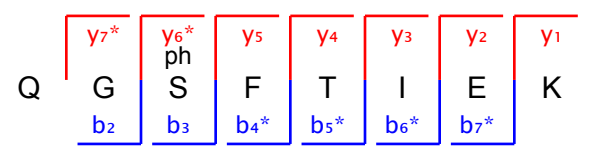
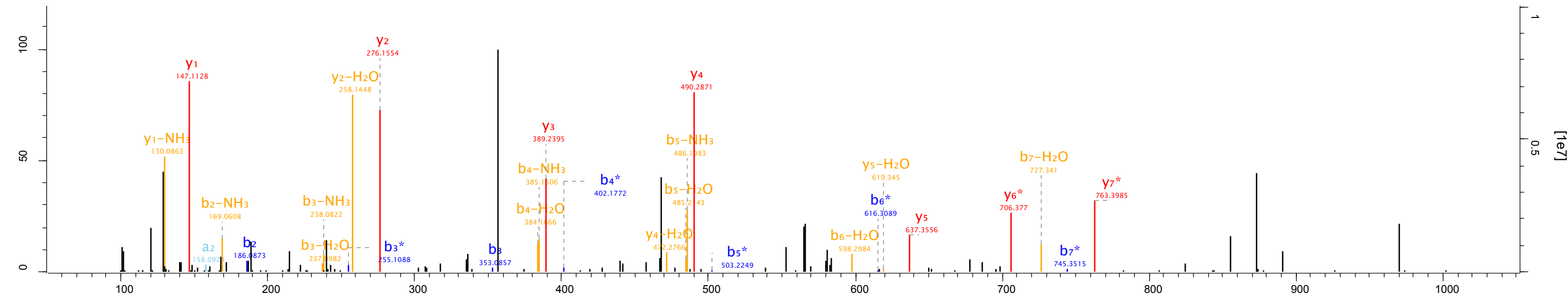
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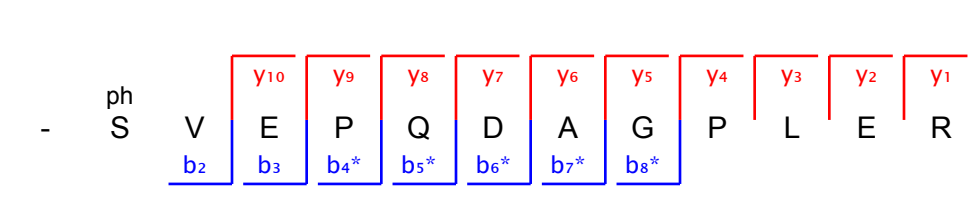
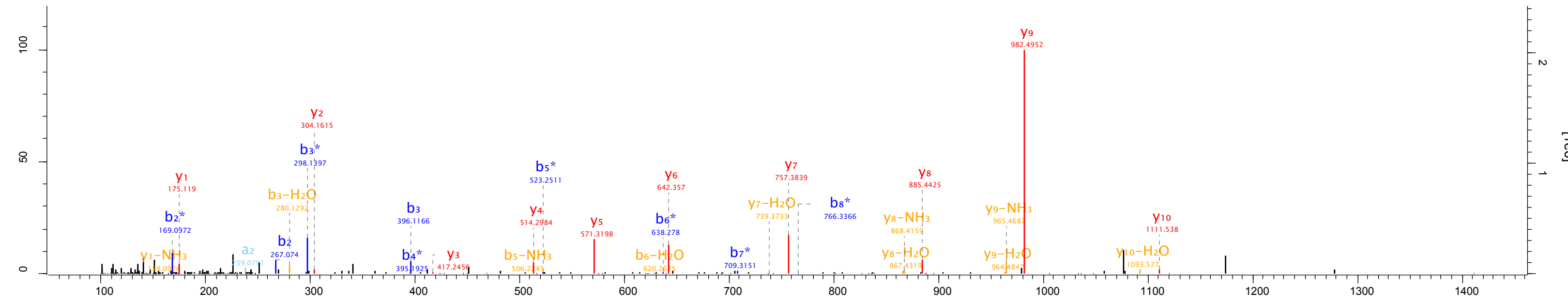
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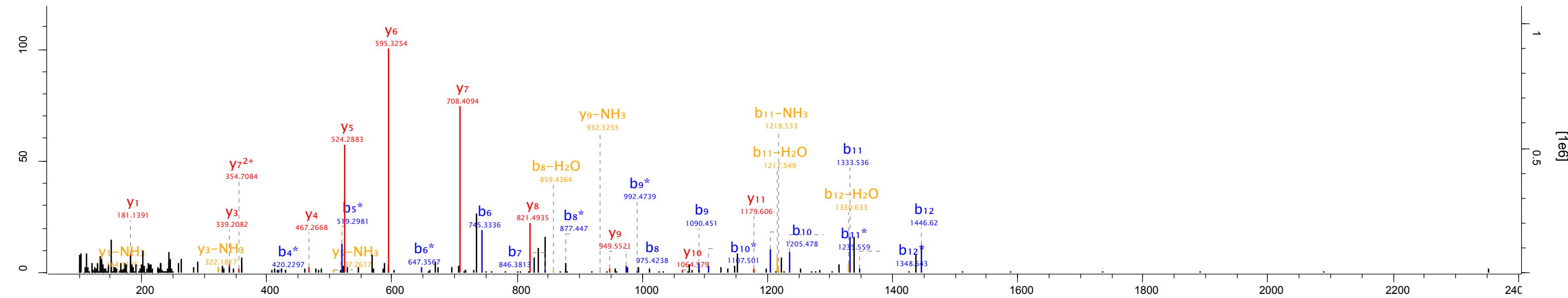
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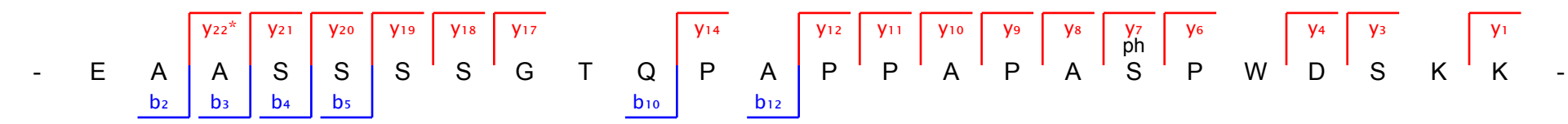
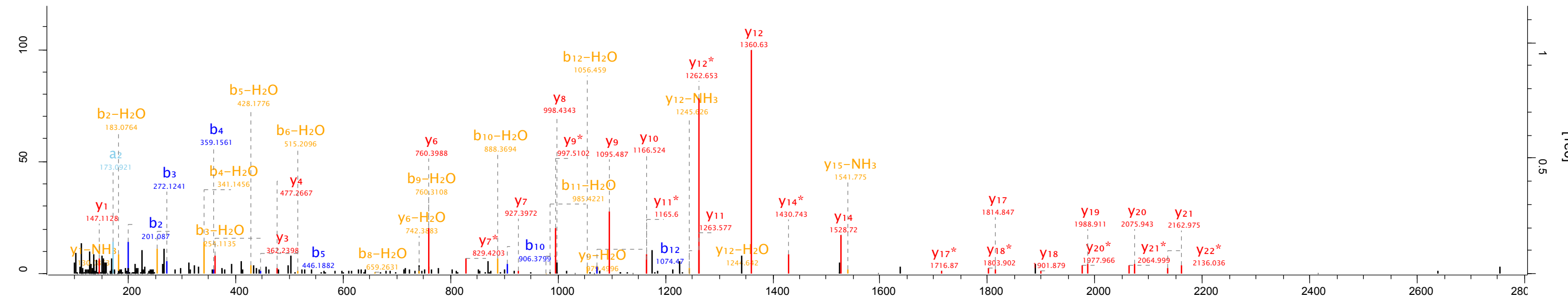


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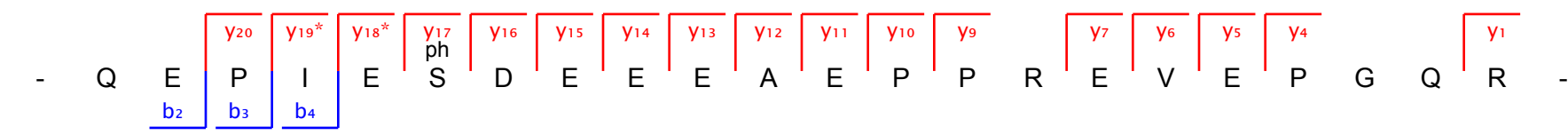
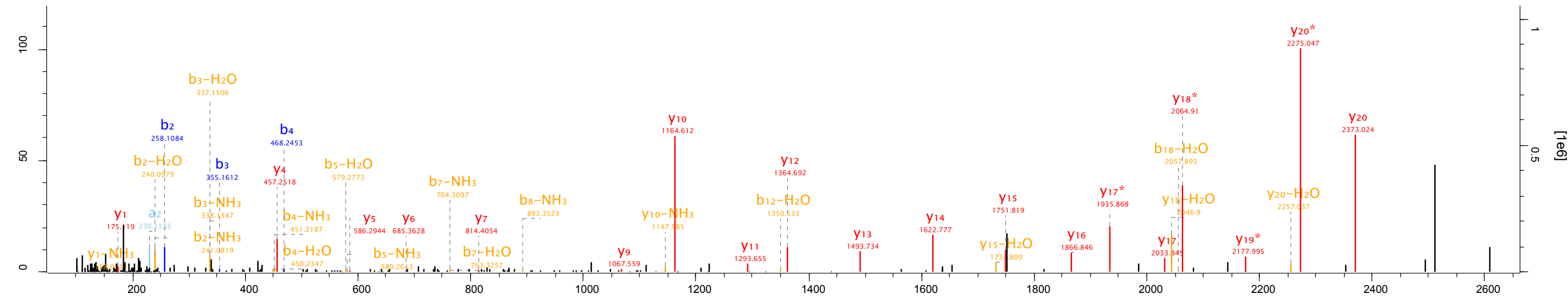


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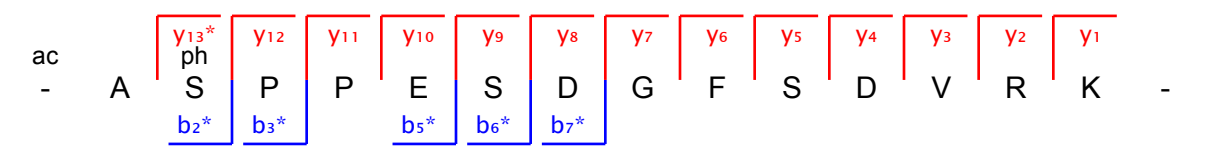
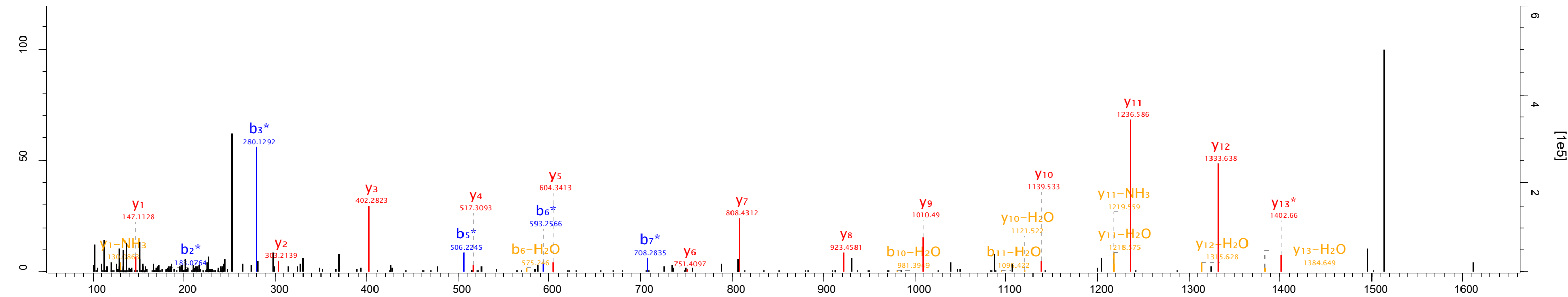
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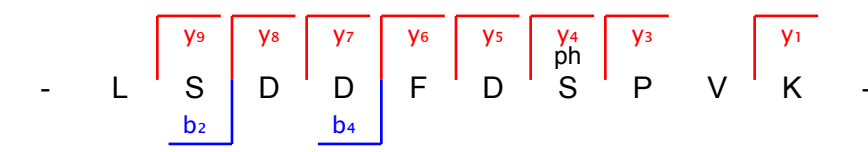
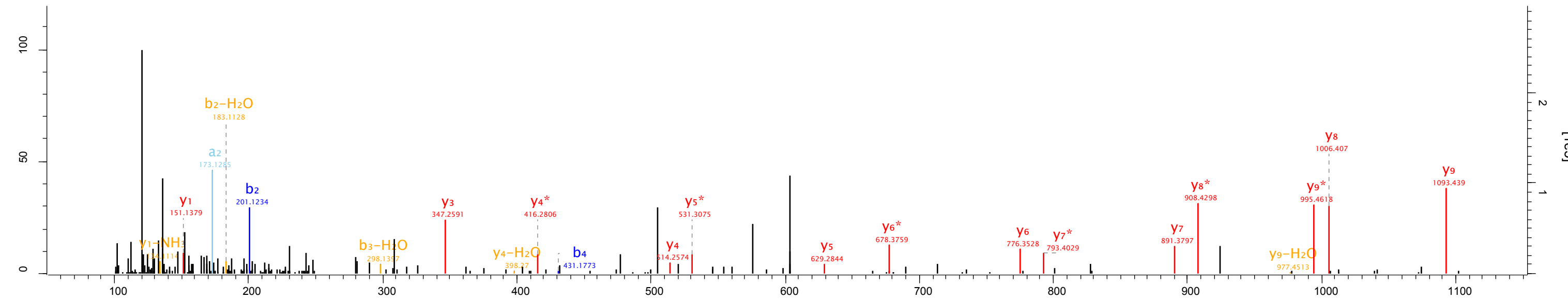
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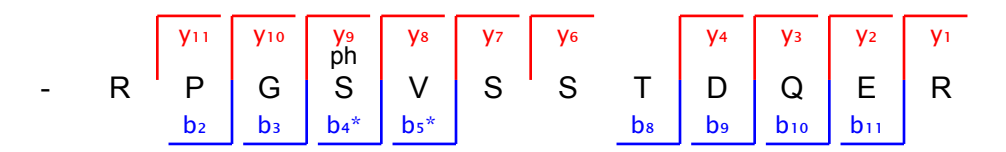
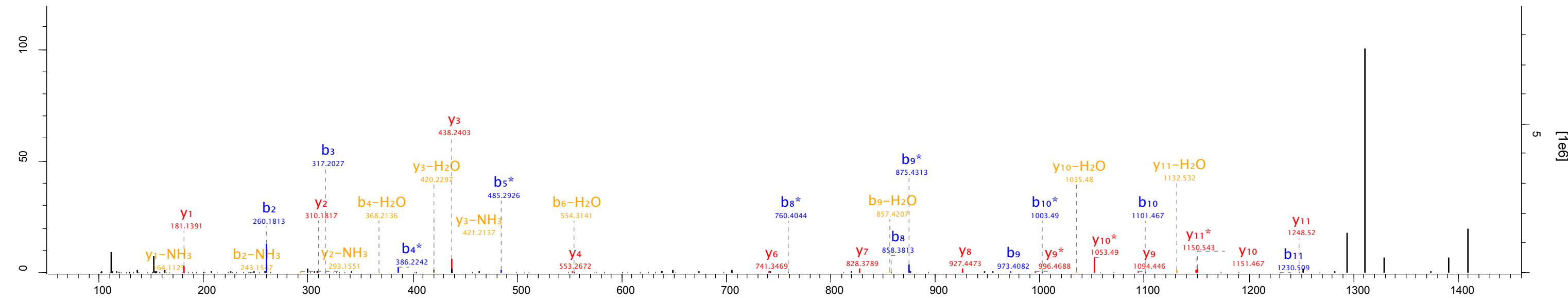
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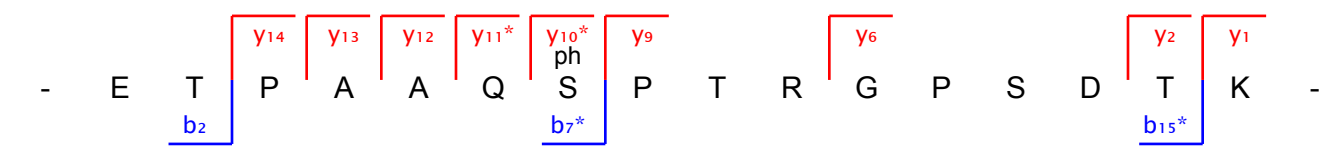
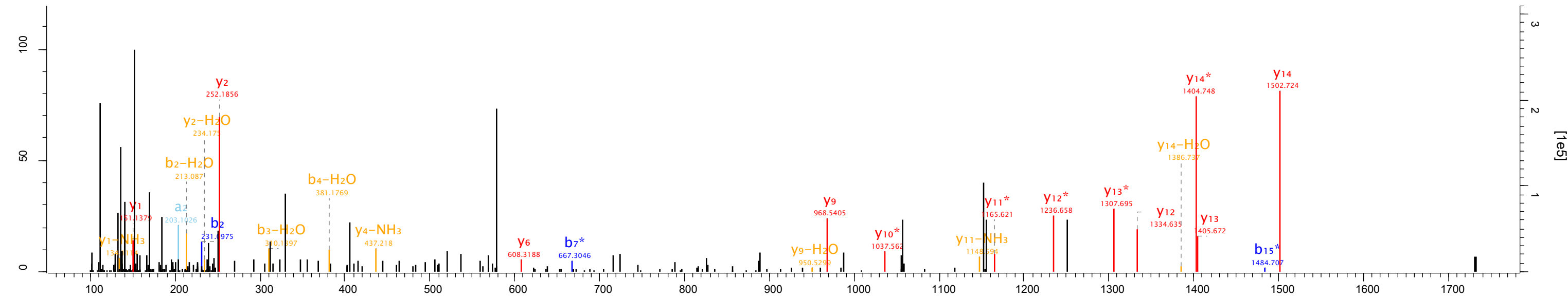
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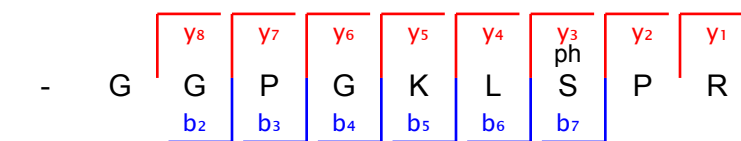
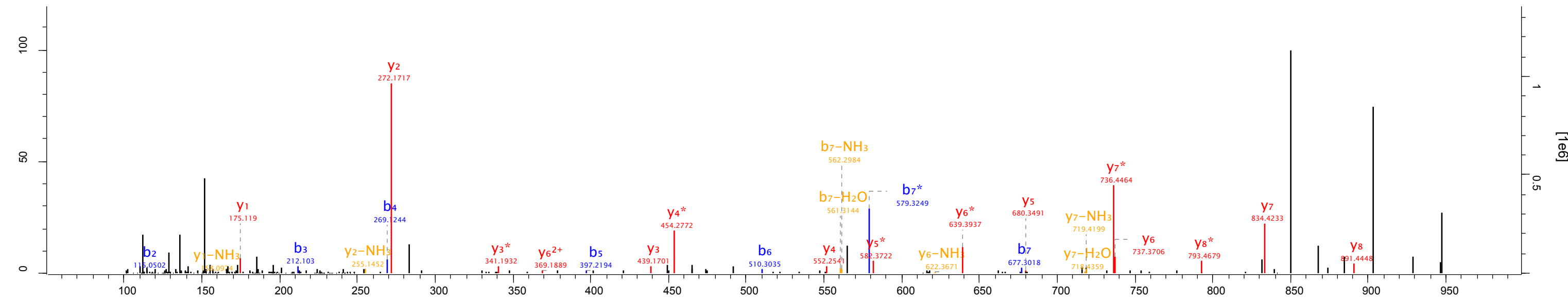


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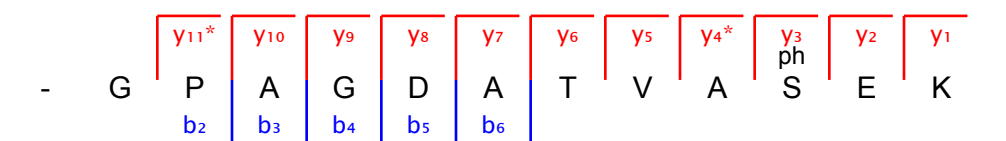
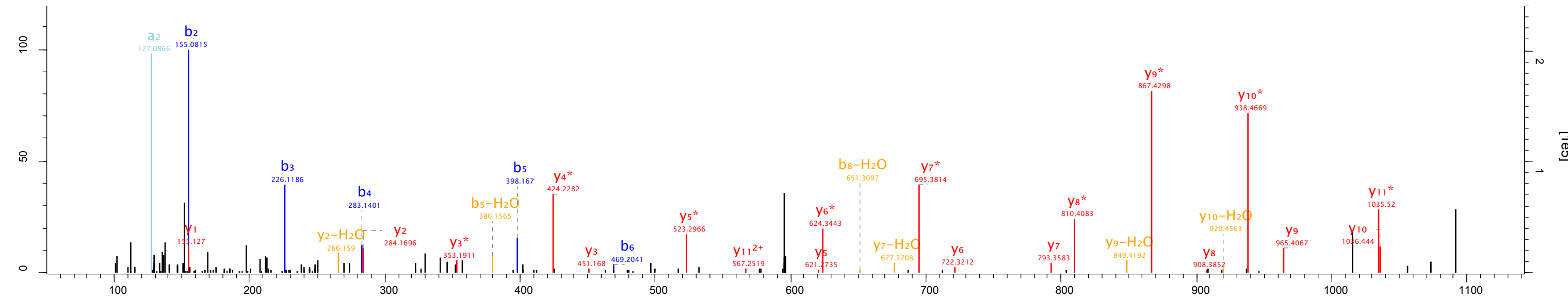


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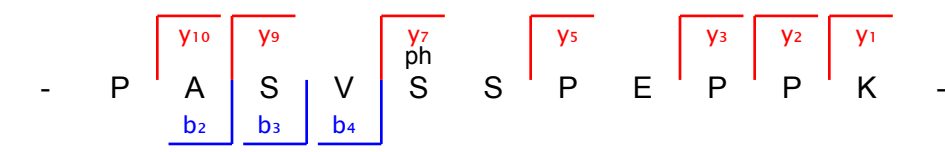
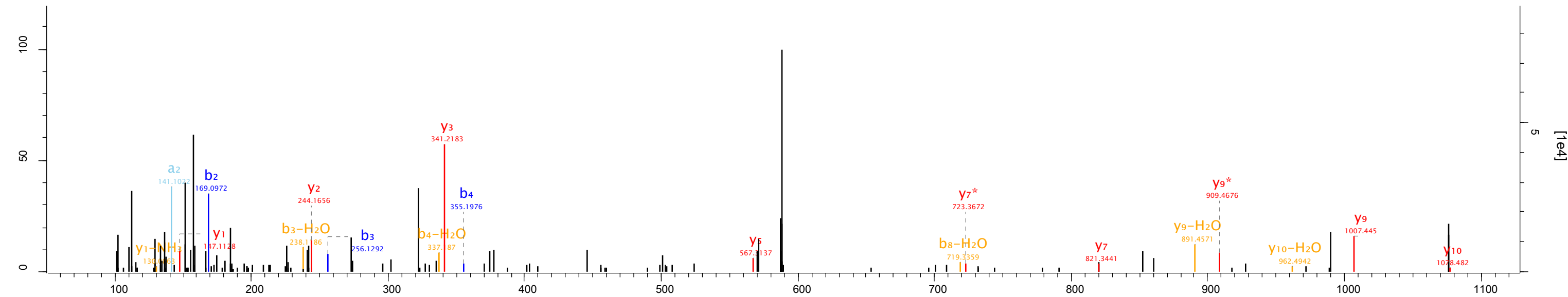




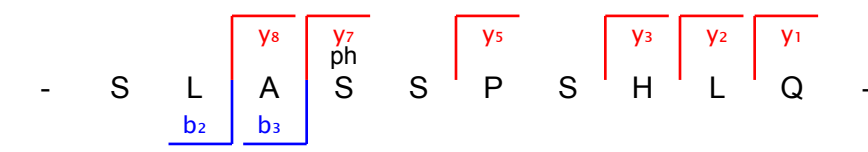
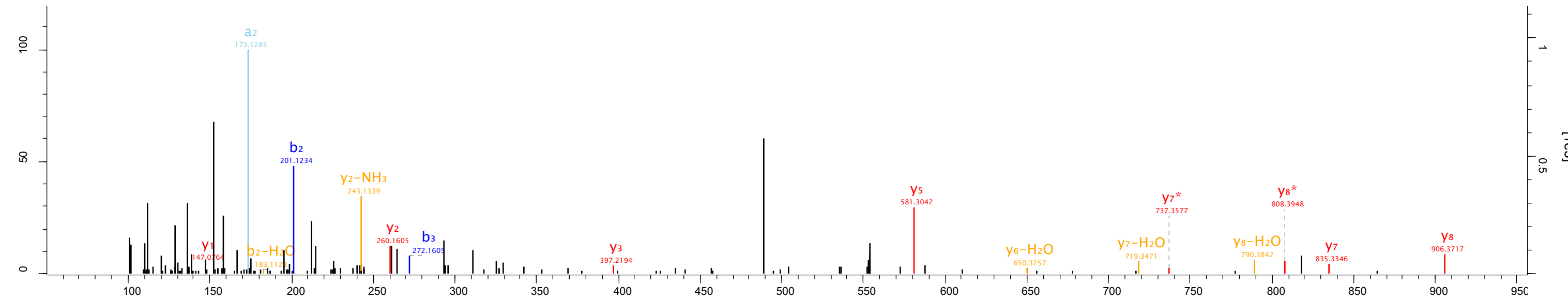
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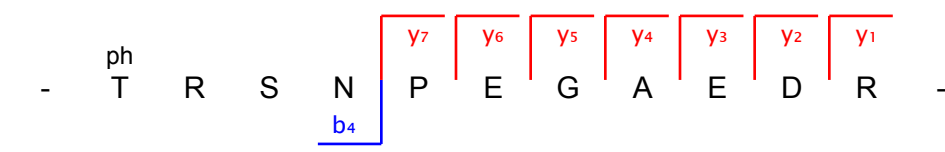
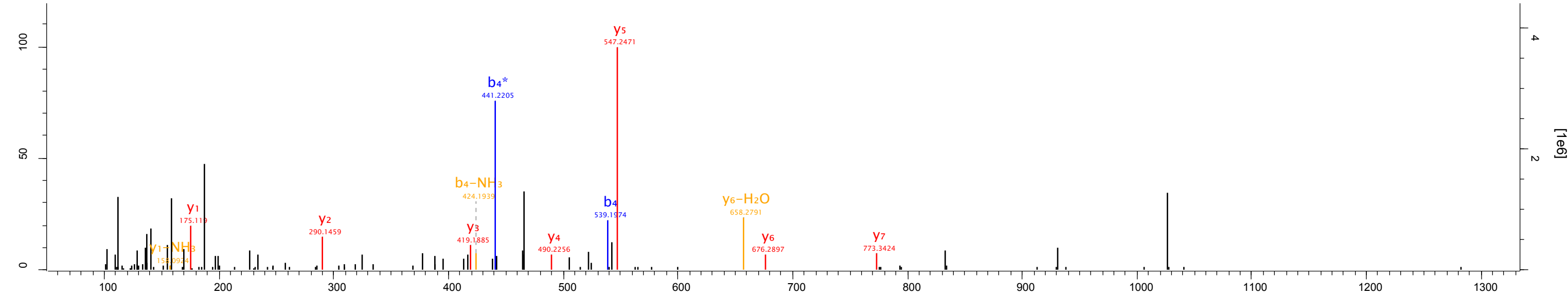
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Raw file

20171215_MaS_33SR_LMH_phospho_08

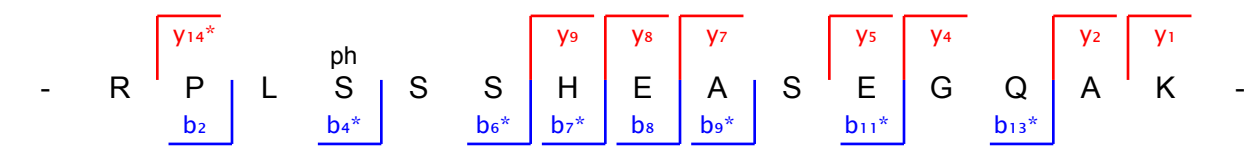
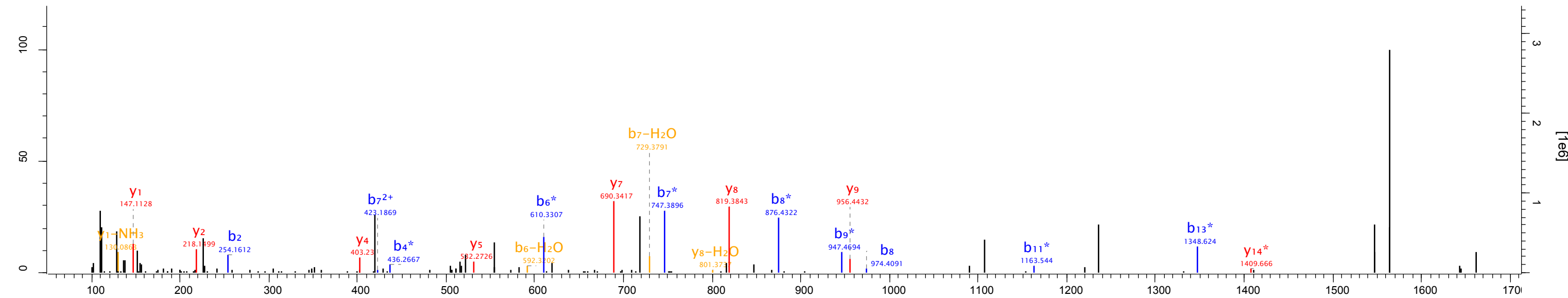
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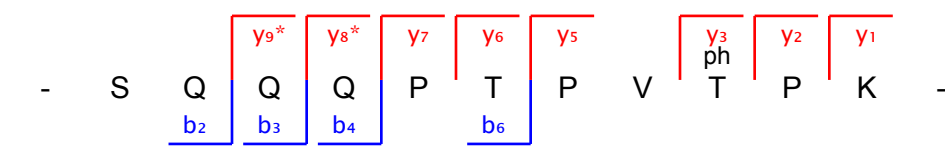
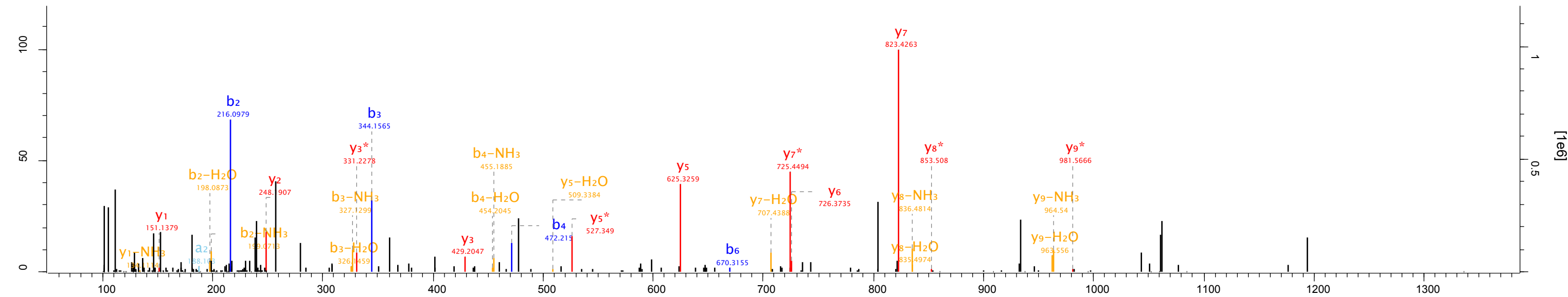
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20171215_MaS_33SR_LMH_phospho_08

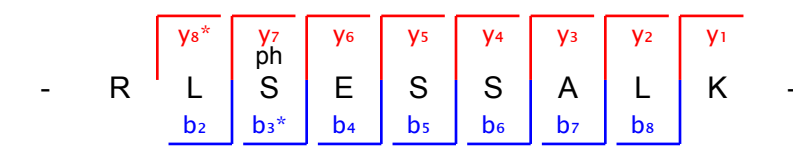
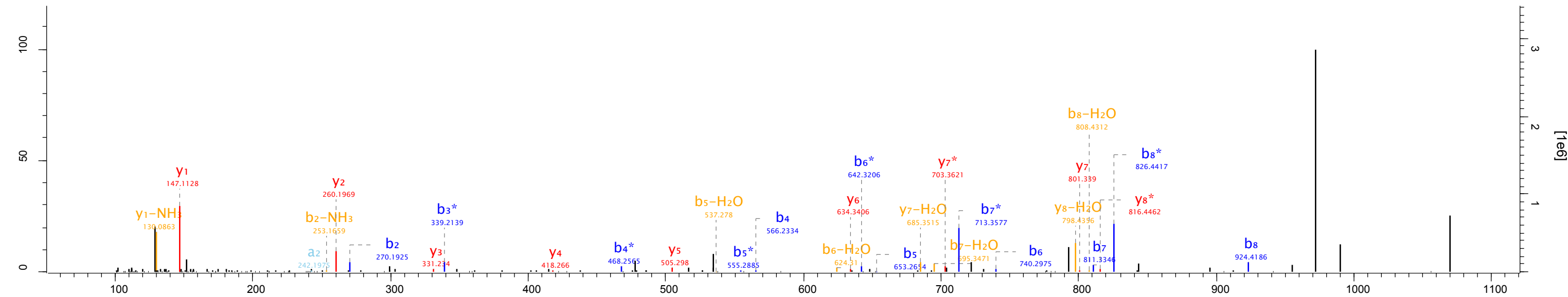
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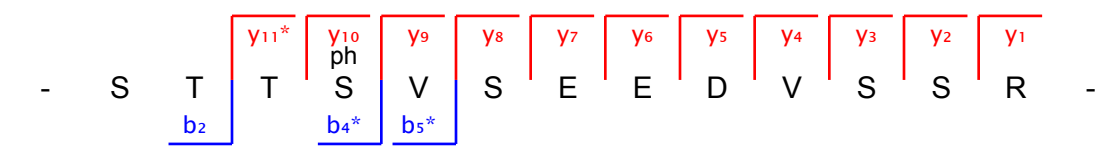
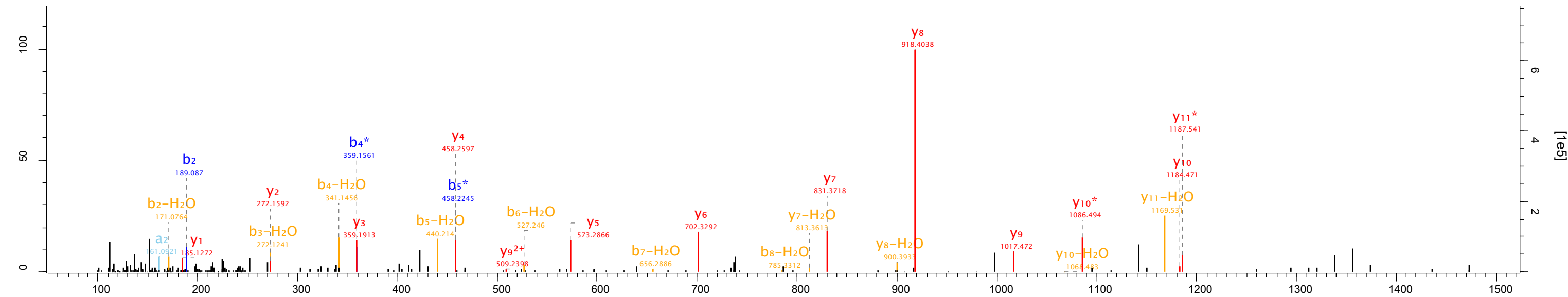
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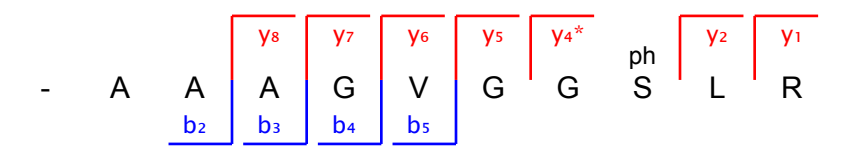
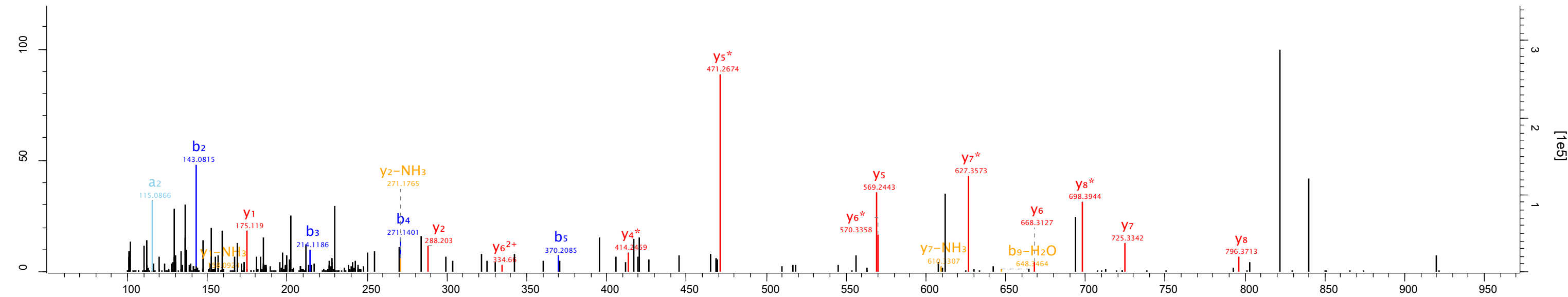
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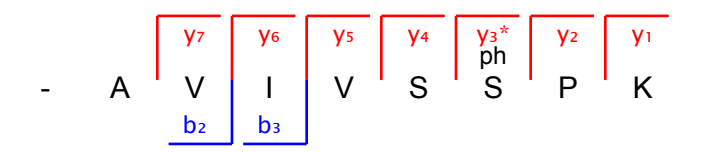
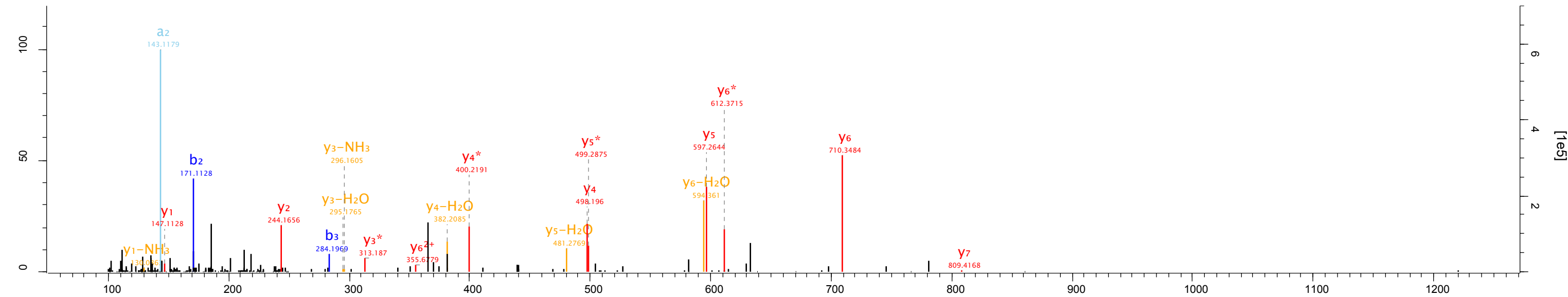
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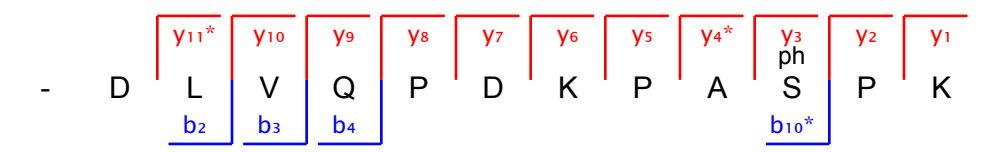
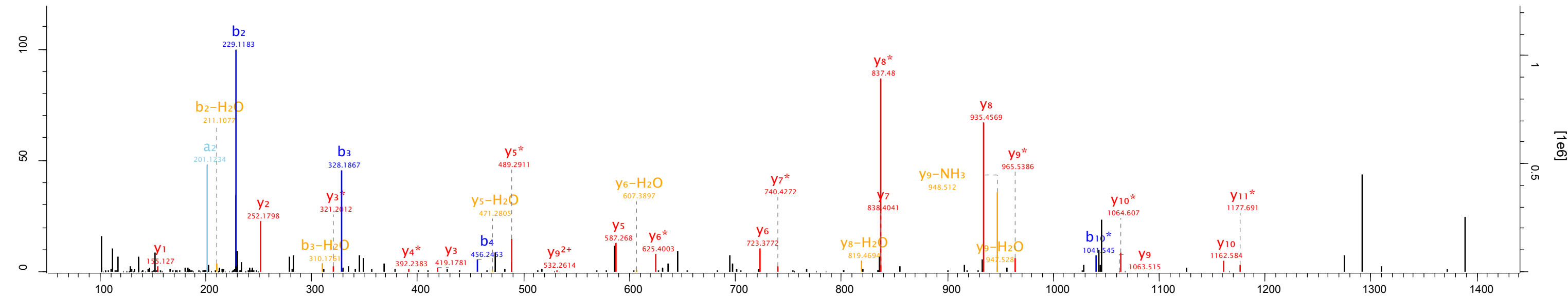
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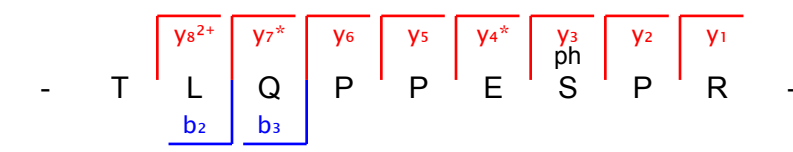
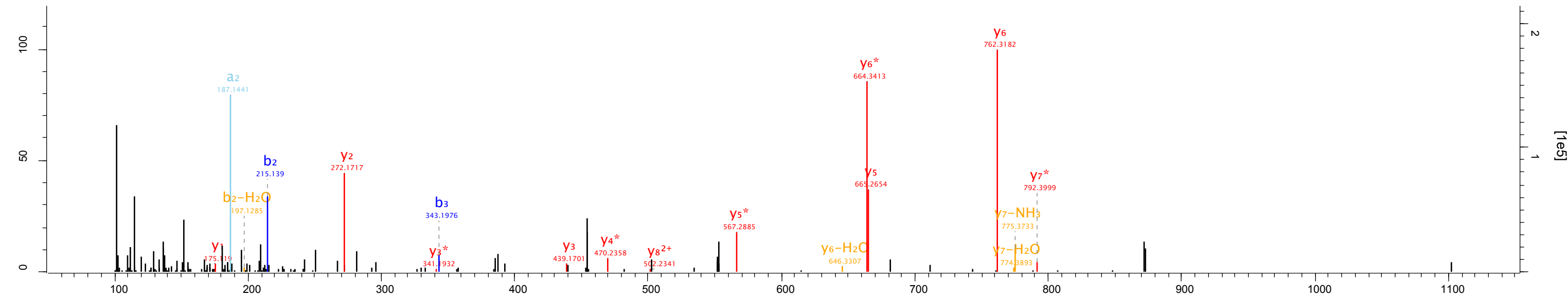
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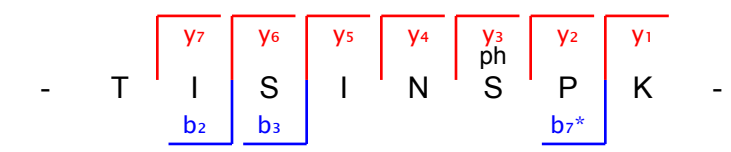
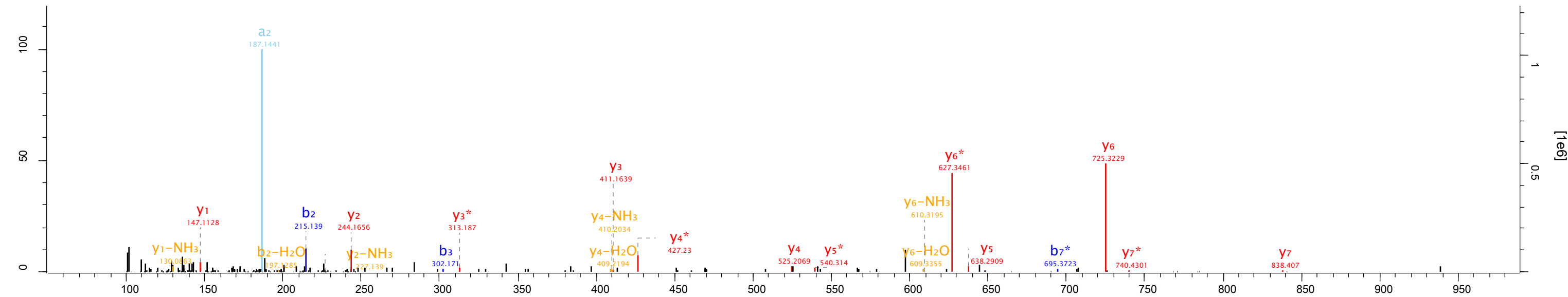
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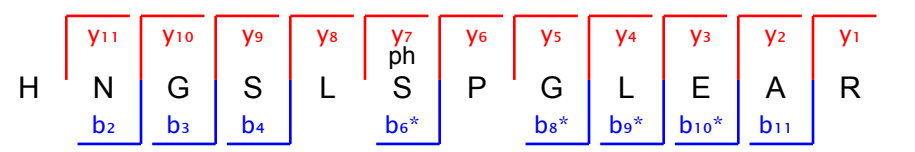
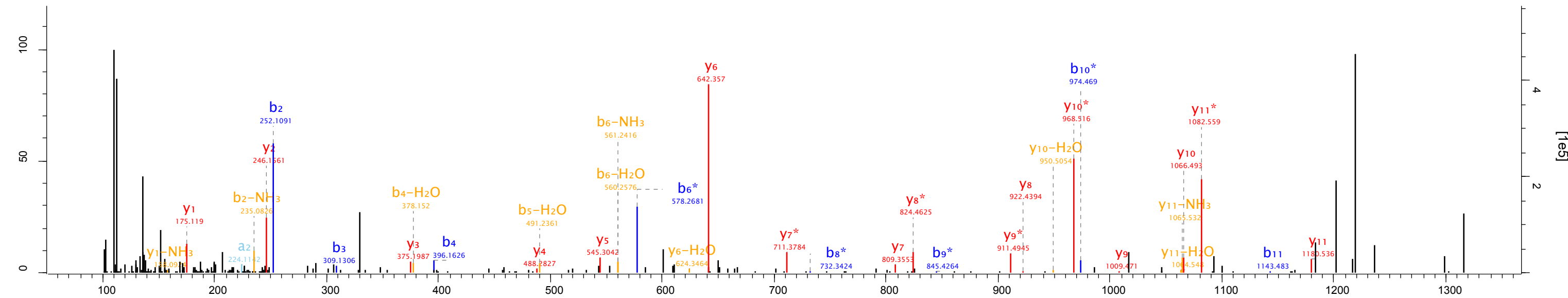
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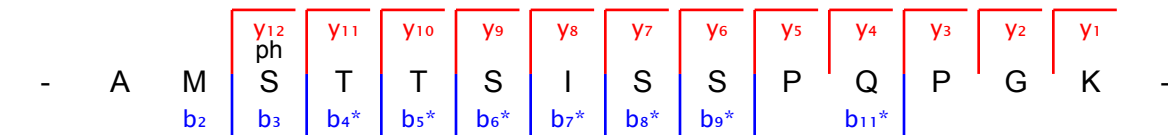
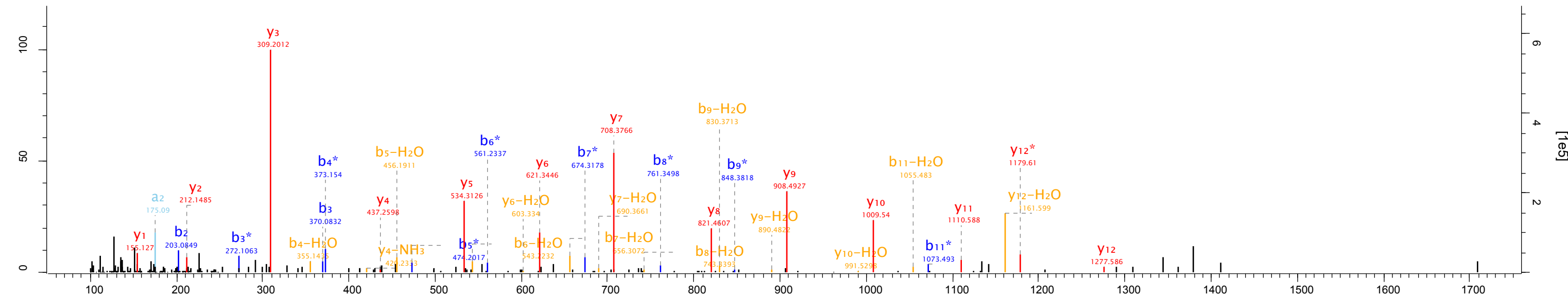


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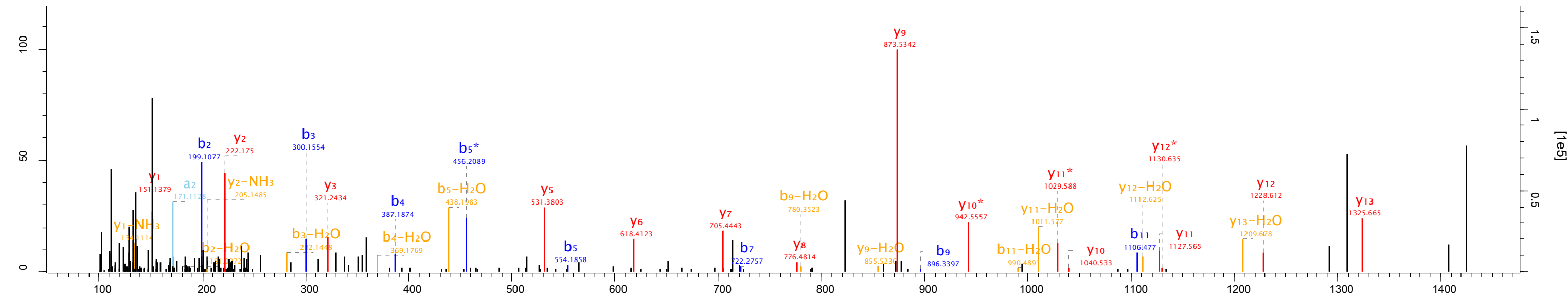


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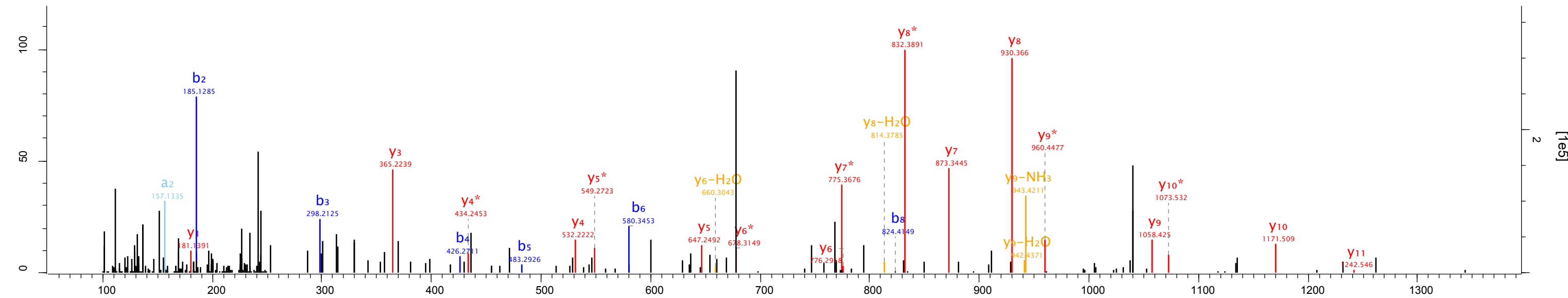




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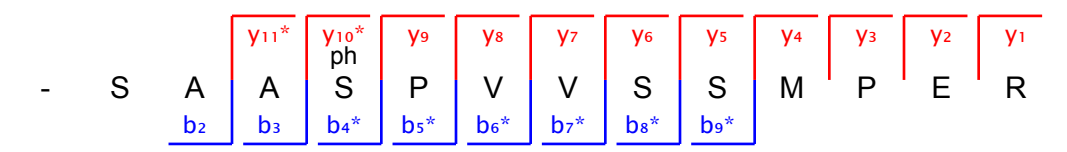
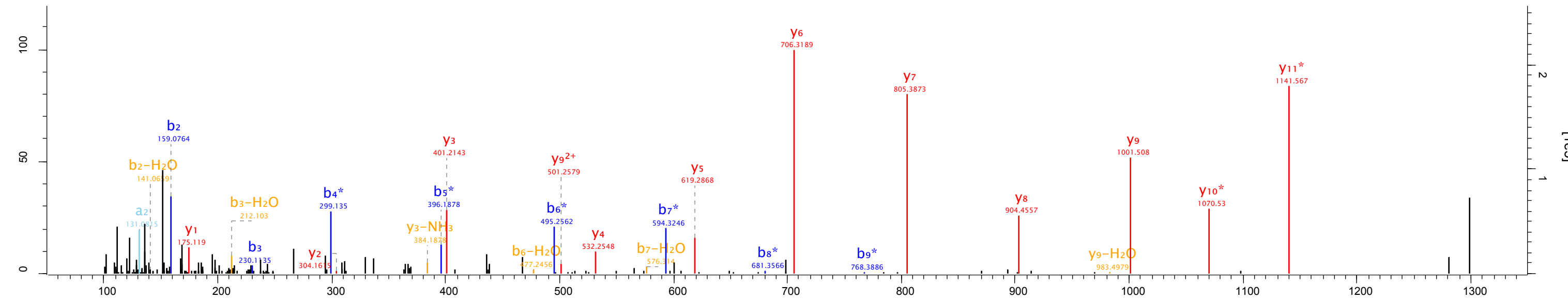
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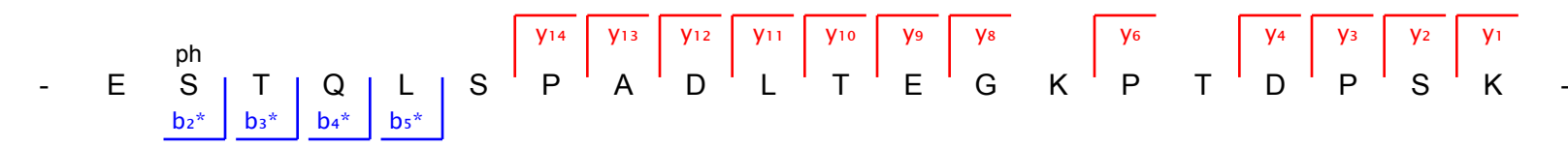
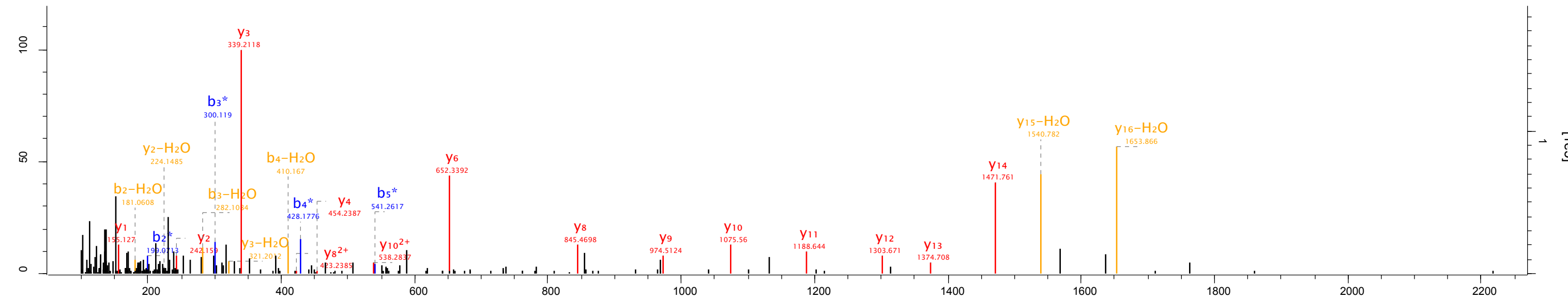
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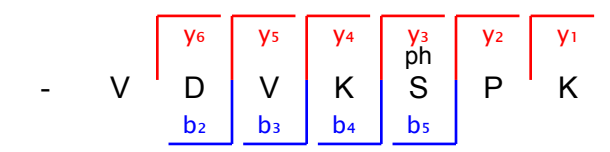
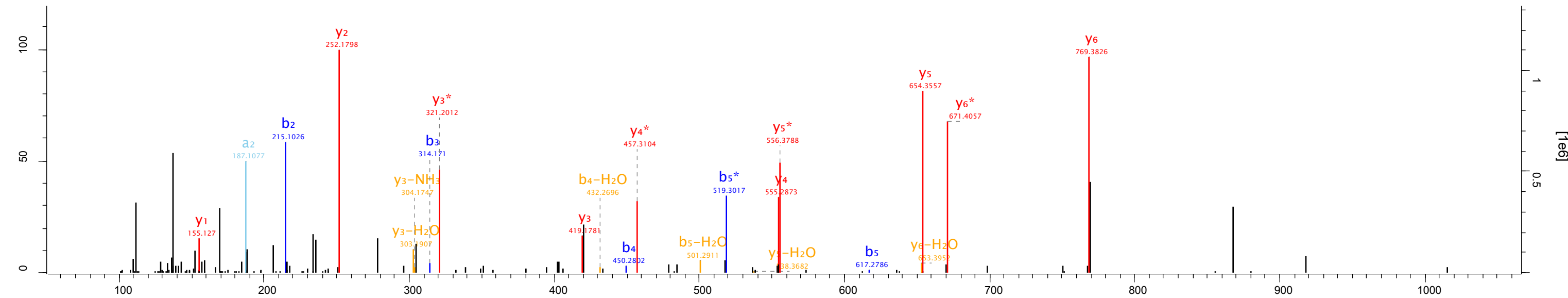
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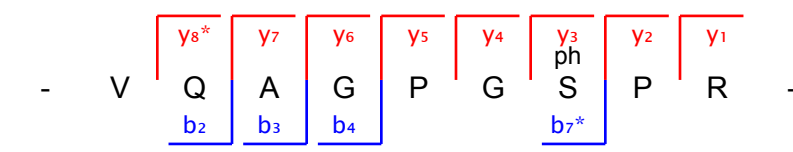
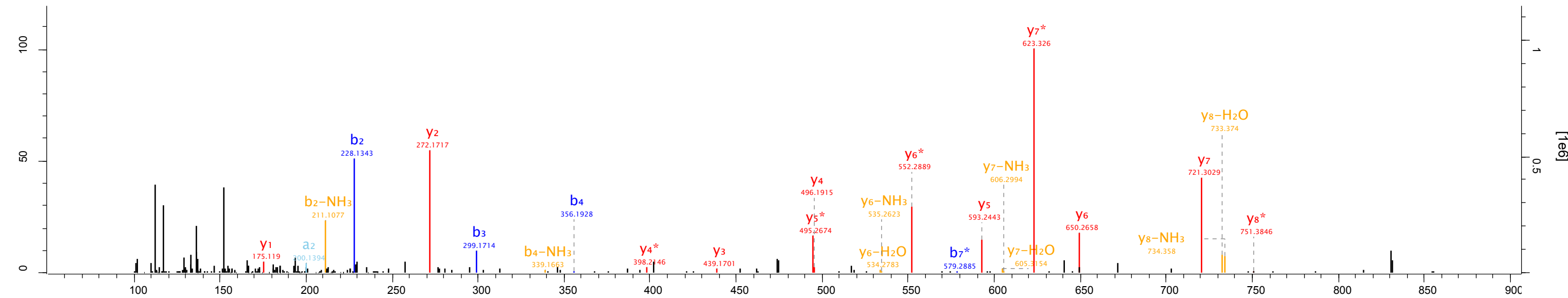
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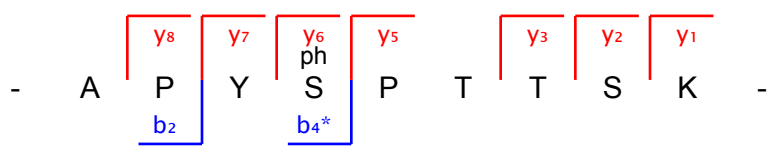
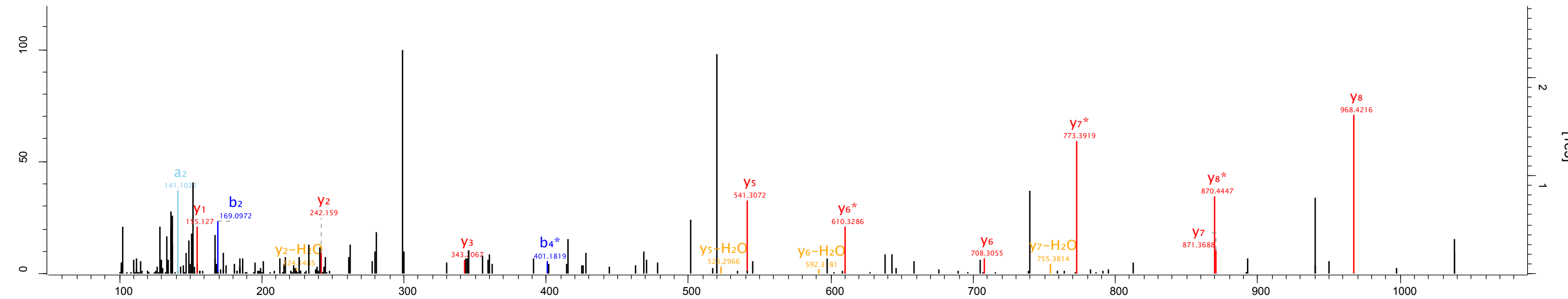
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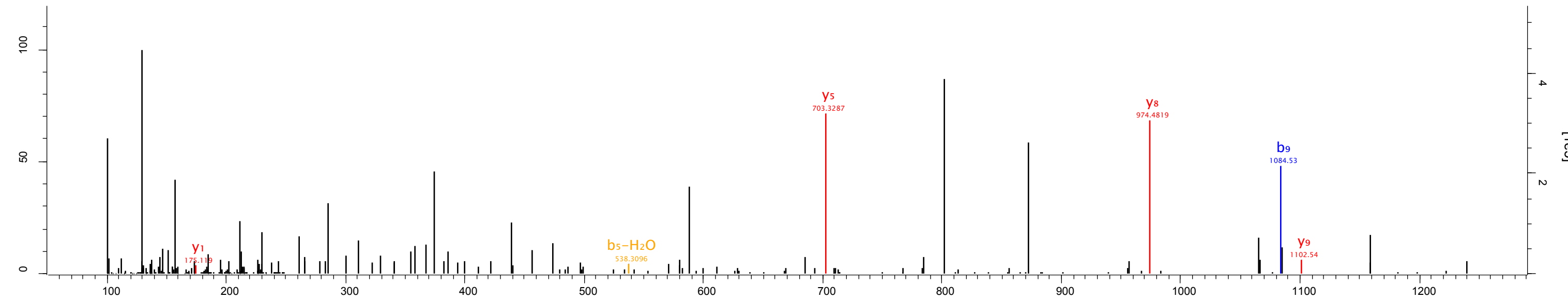
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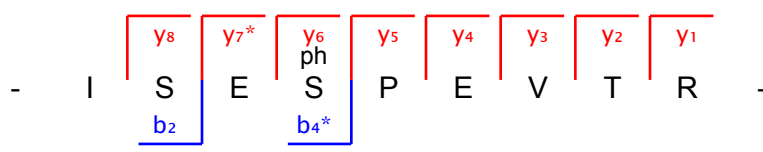
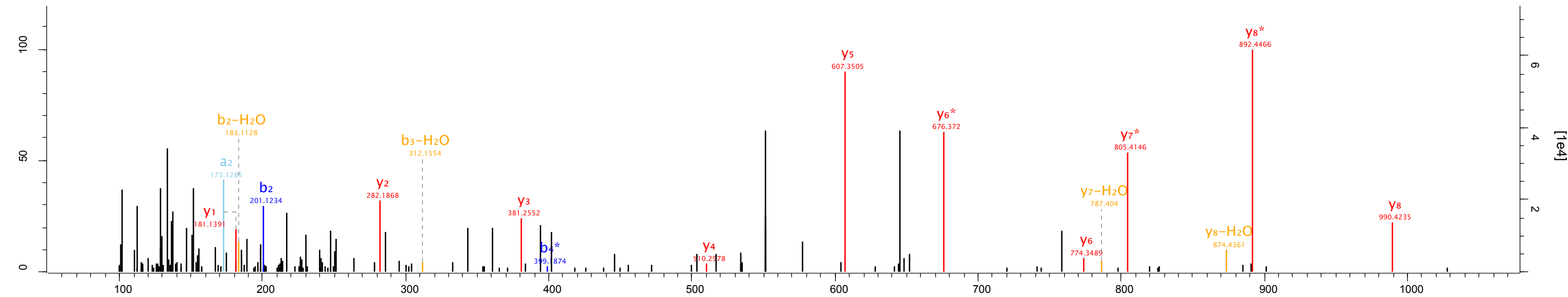
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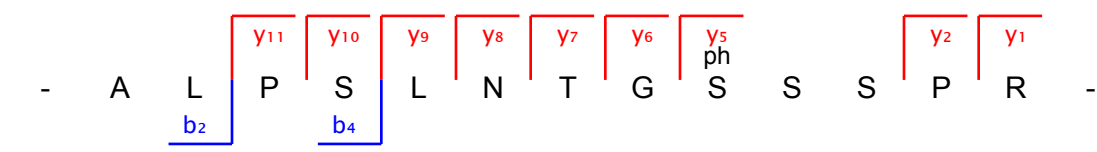
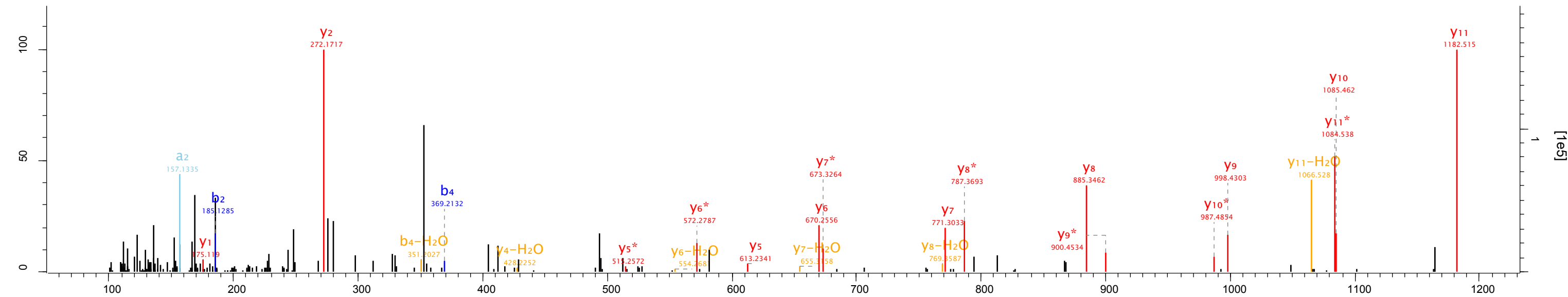
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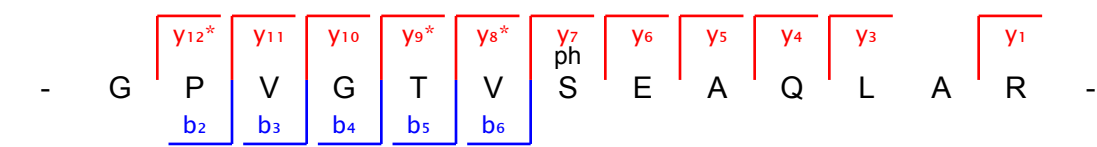
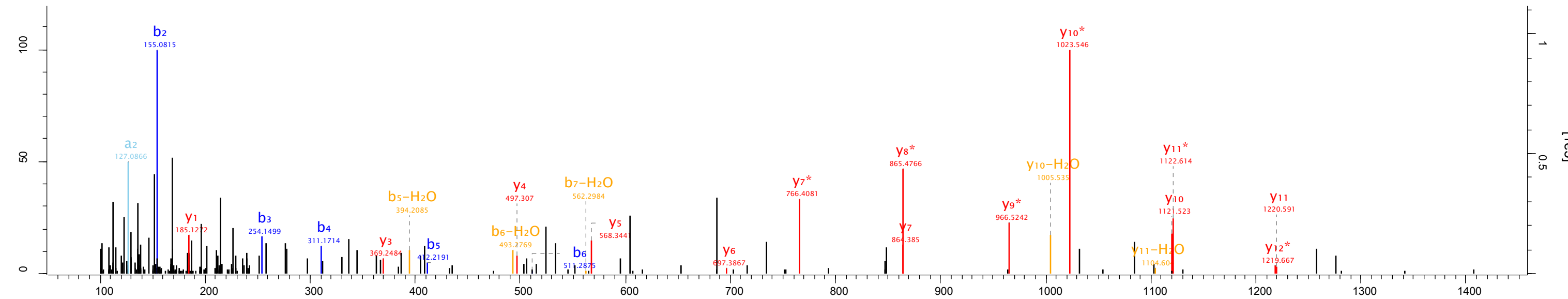
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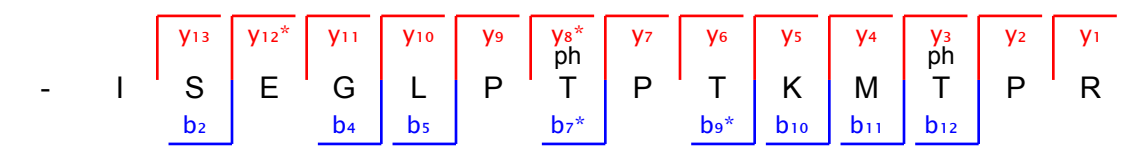
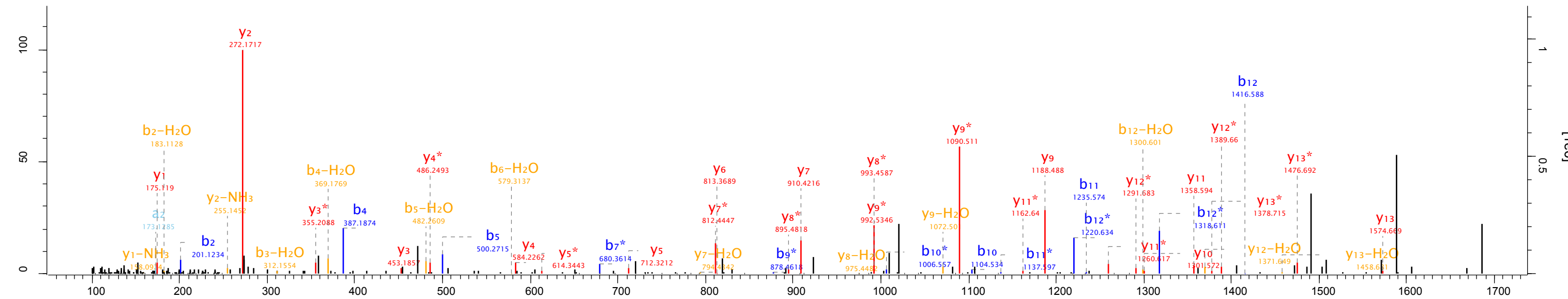
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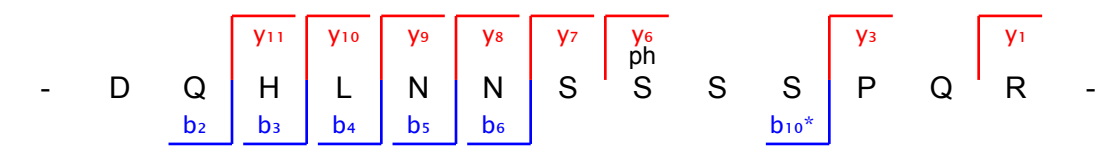
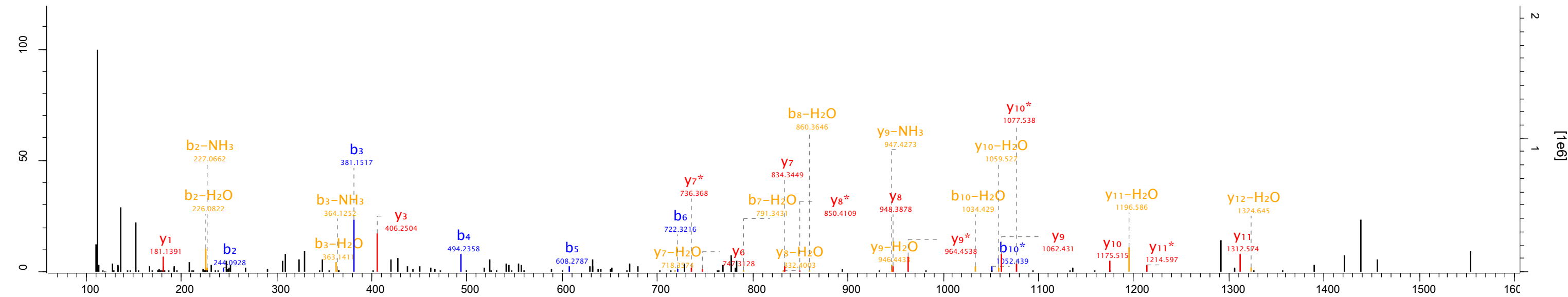
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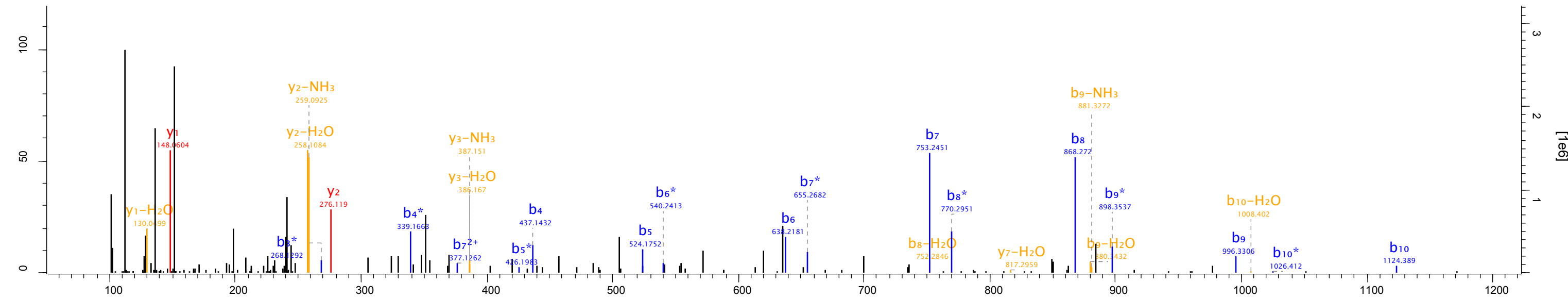


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 Scan: 10284 Method: FTMS; HCD Score: 189.98 m/z: 844.38 Gene names: RB1



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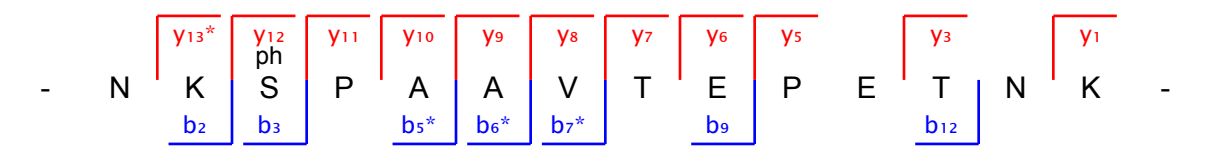
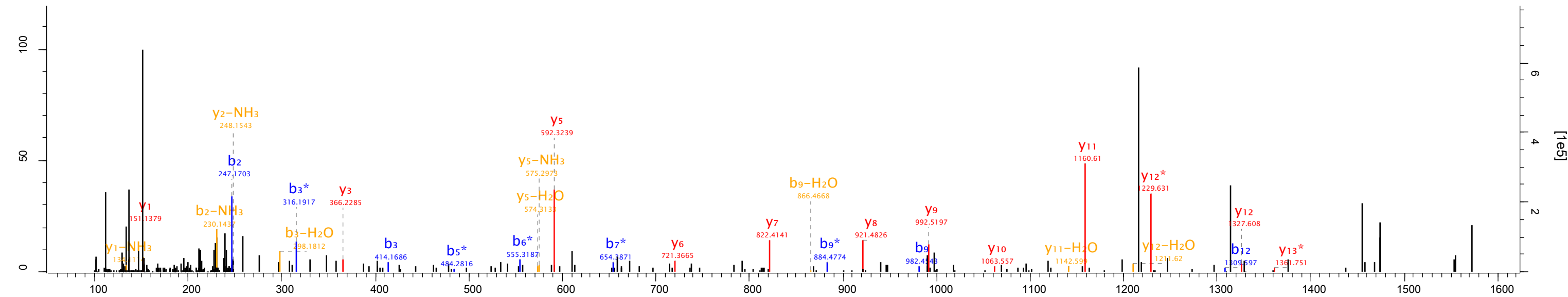




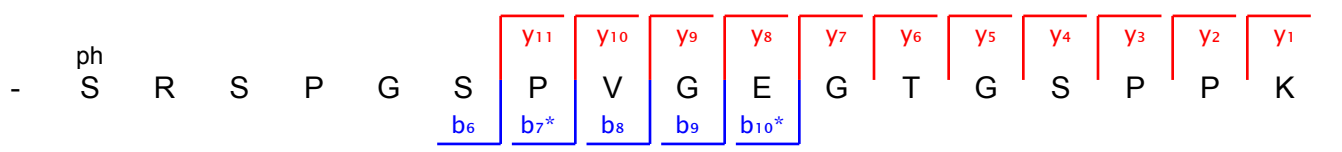
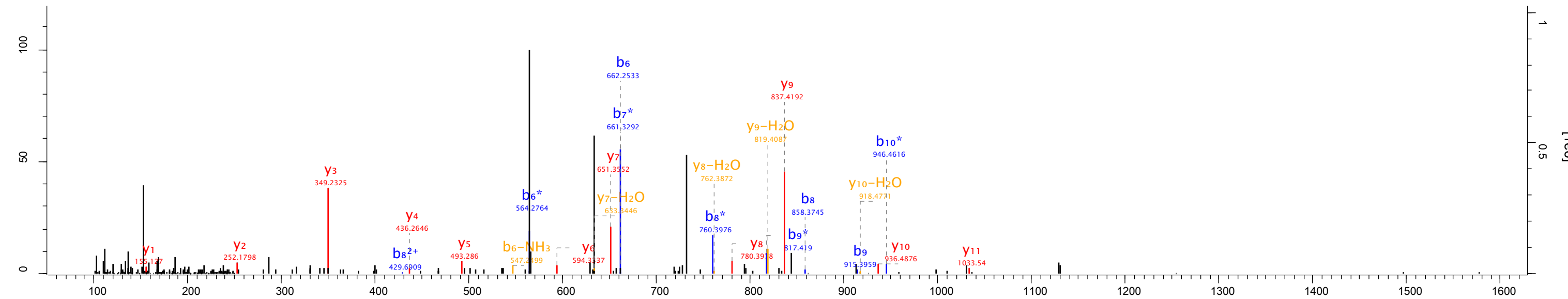
ph
T P S A S N D D Q Q E -
b3* b4 b5 b6 b7 b8 b9 b10

Red boxes highlight the sequence **Q Q E** and the label **y1** above the second **Q**. Blue boxes highlight the labels **b3*** through **b10** below the amino acid sequence.

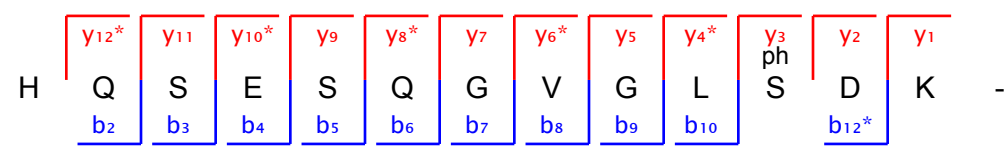
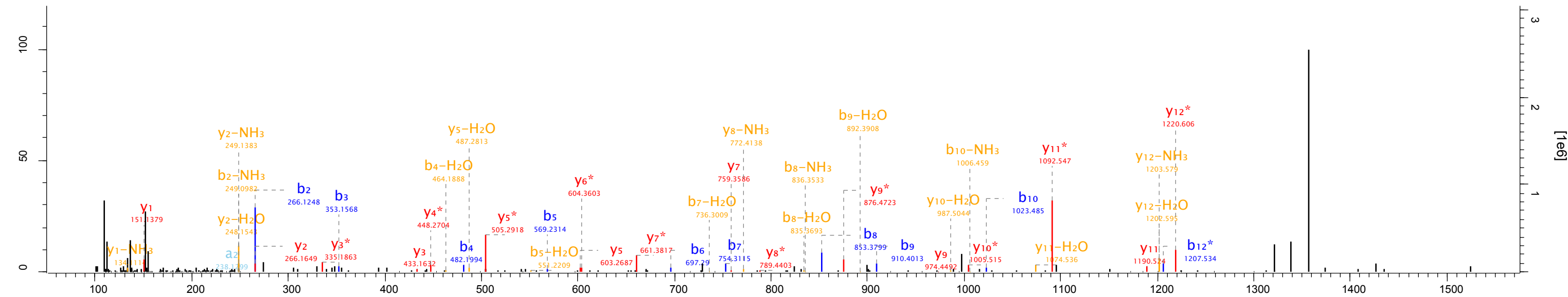
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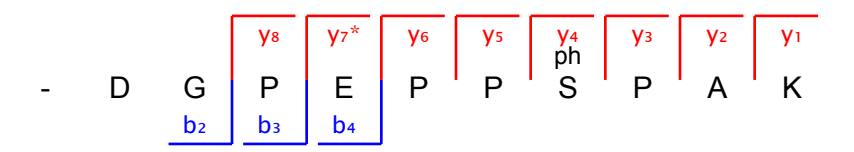
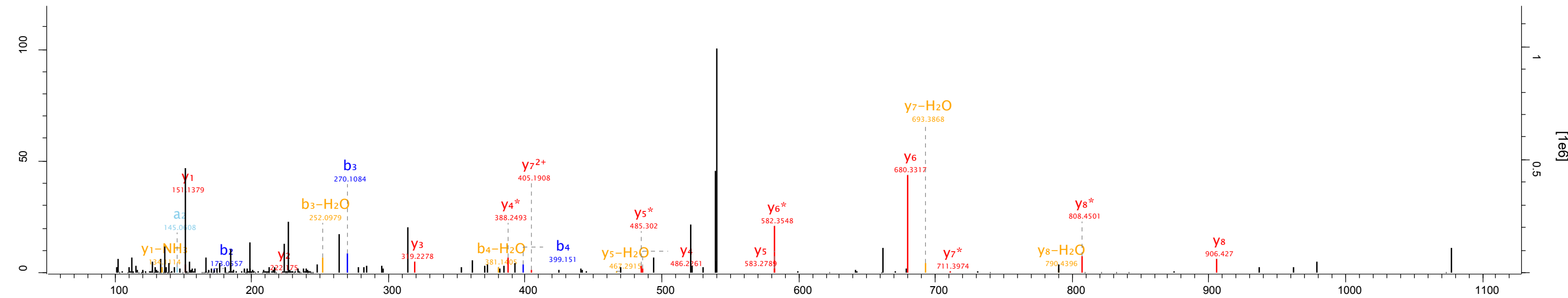
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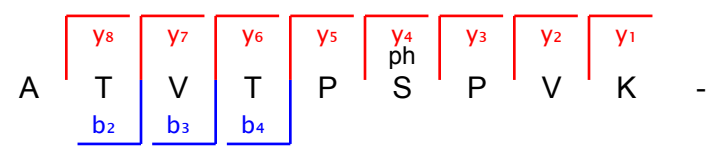
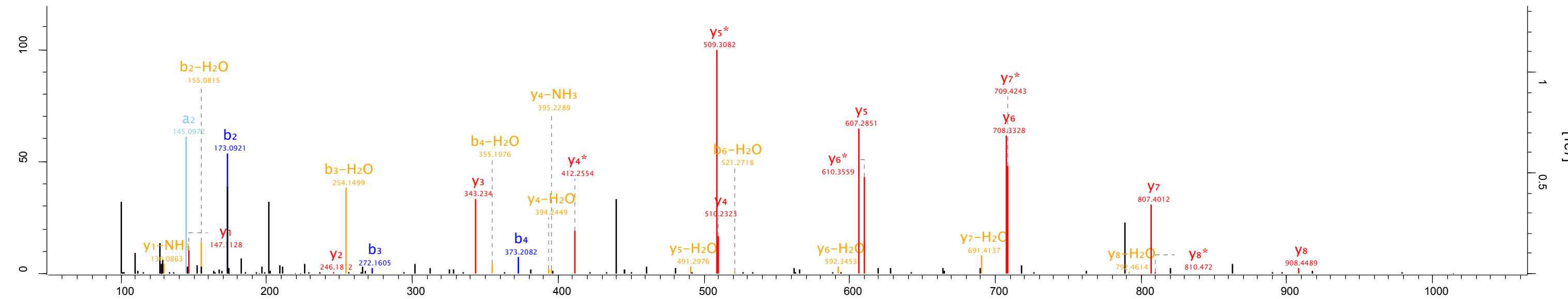
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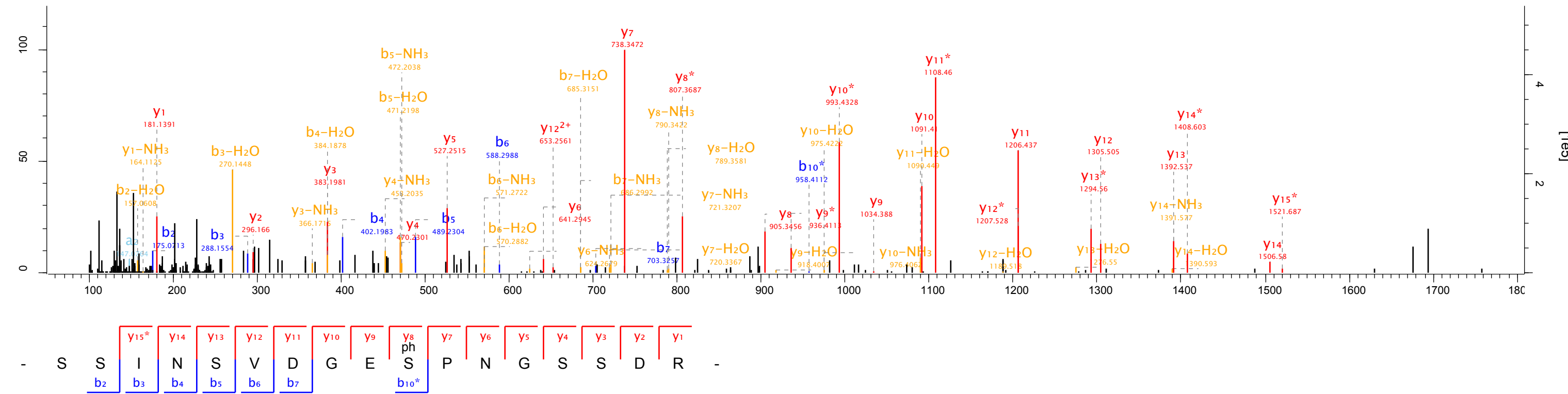


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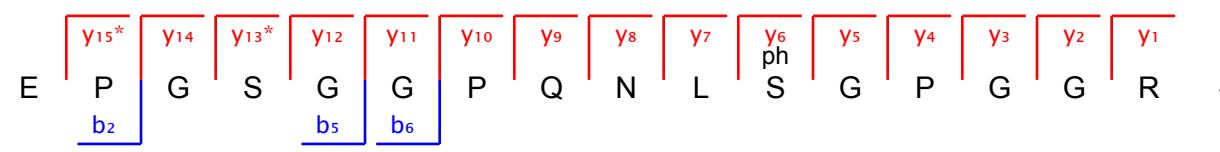
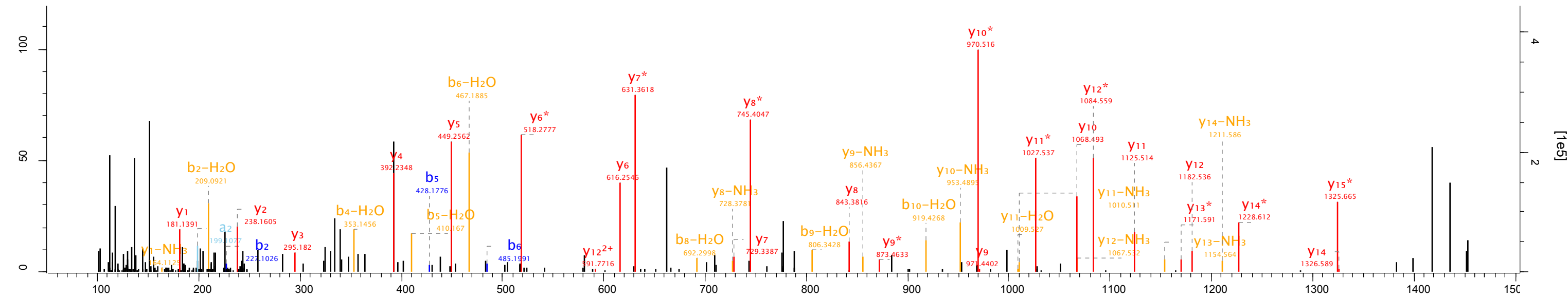


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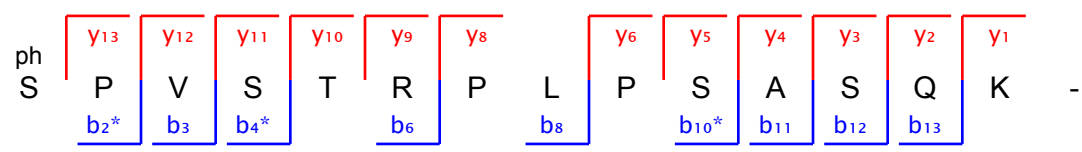
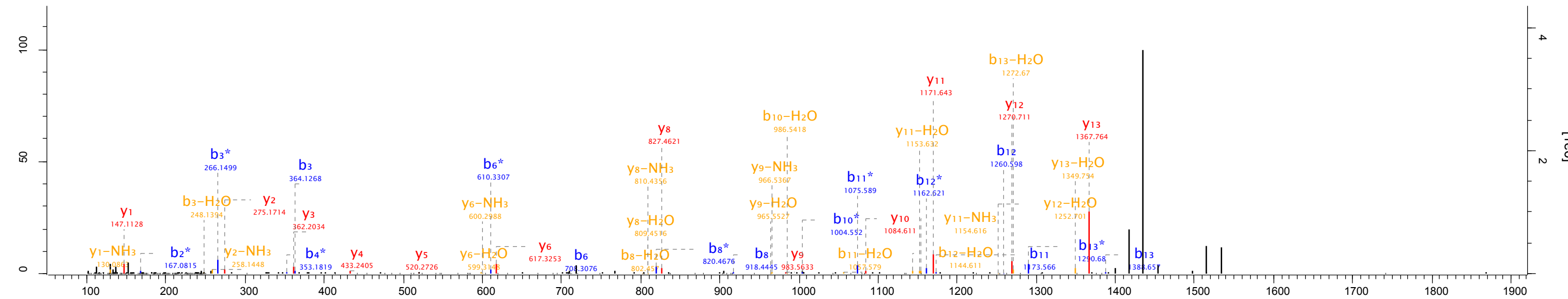




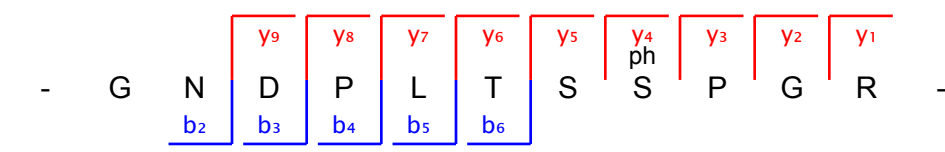
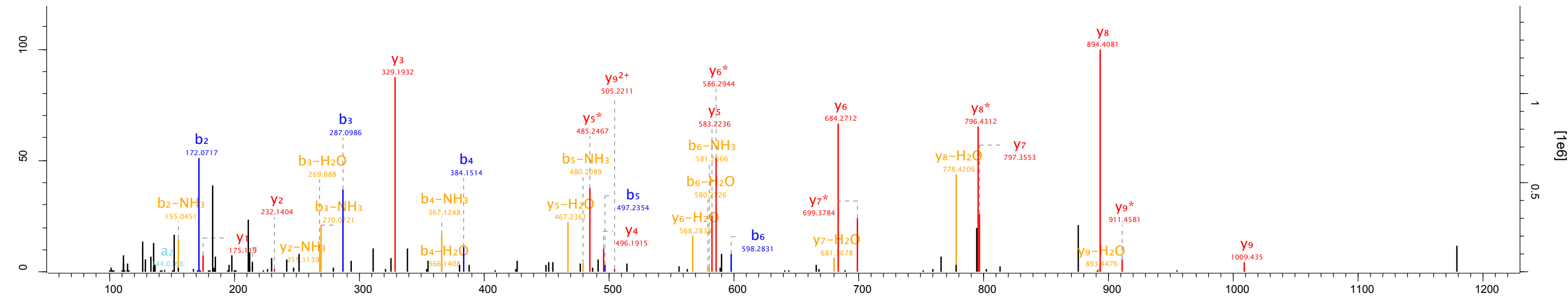
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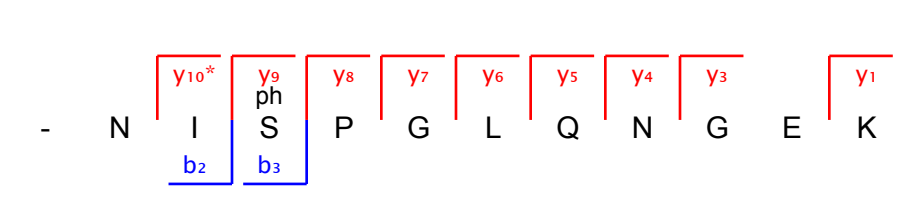
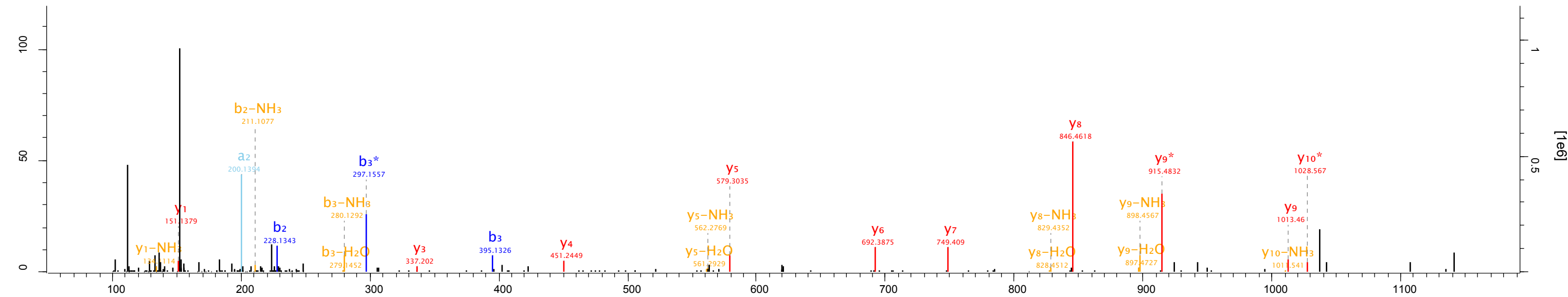
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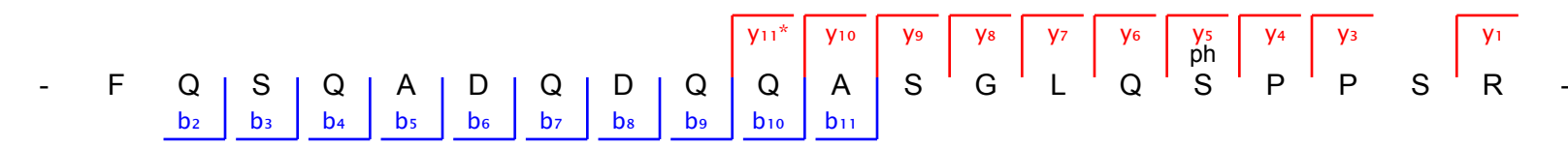
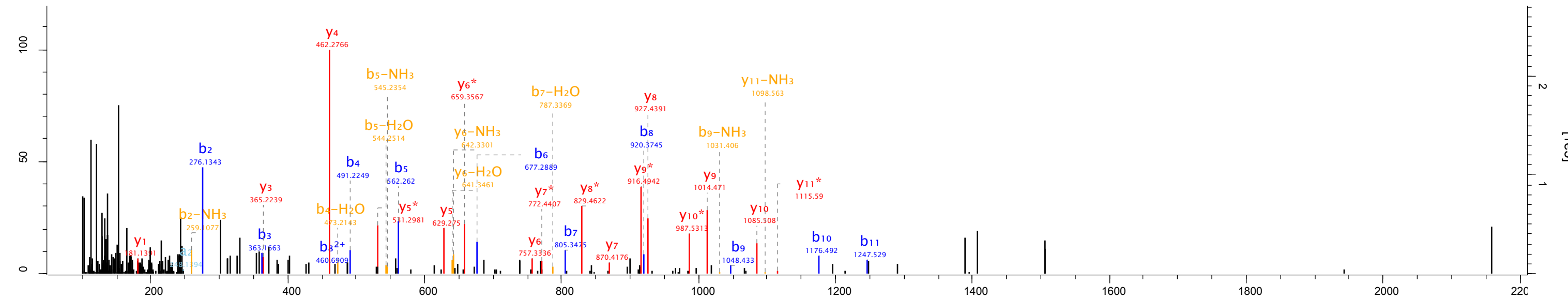
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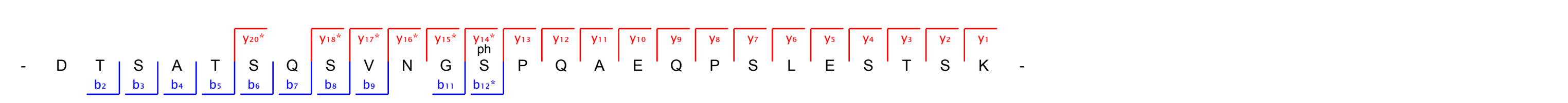
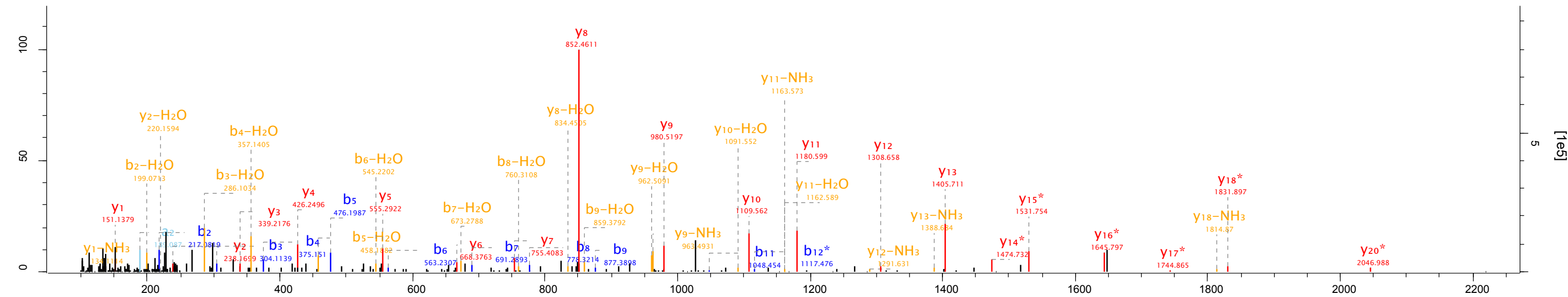
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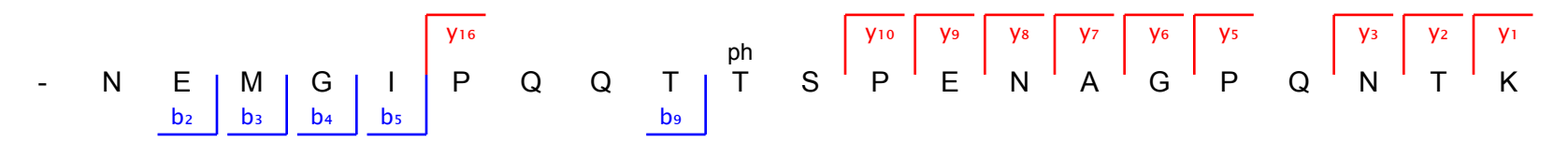
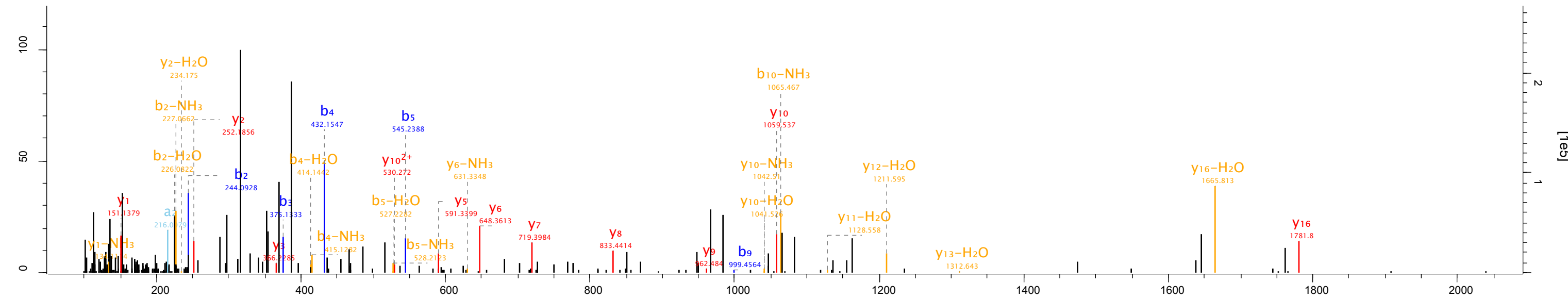


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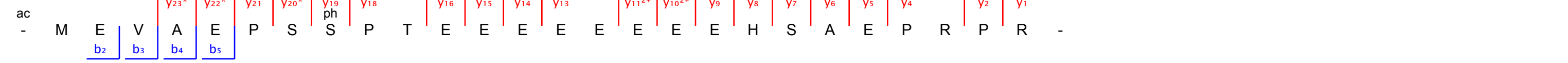
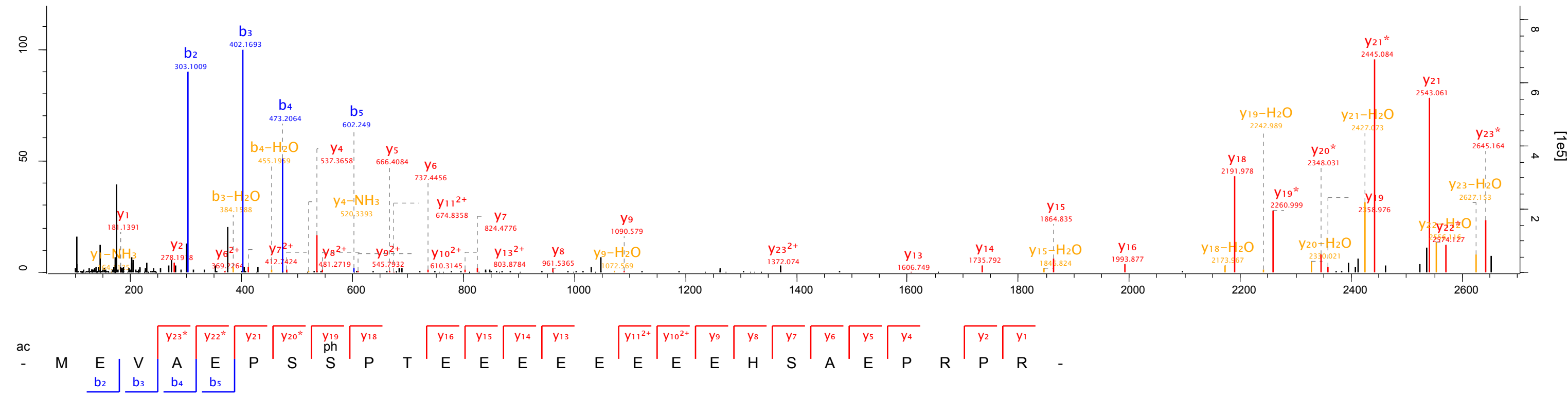


Raw file
20171215_MaS_33SR_LMH_phospho2_01

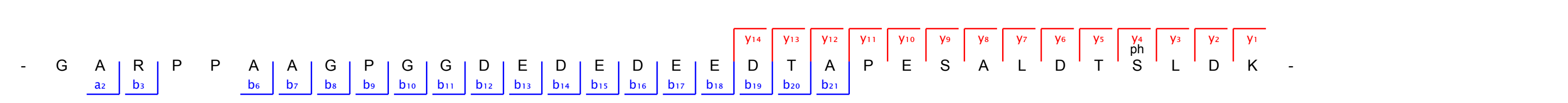
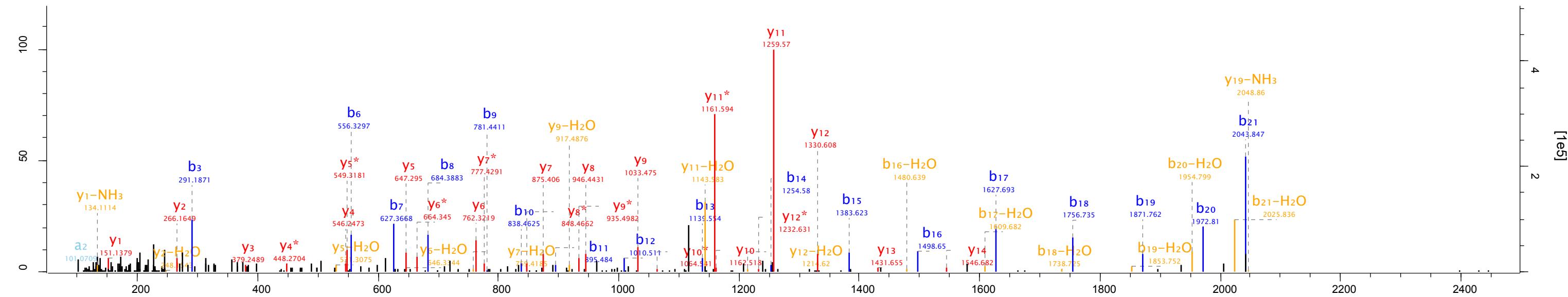
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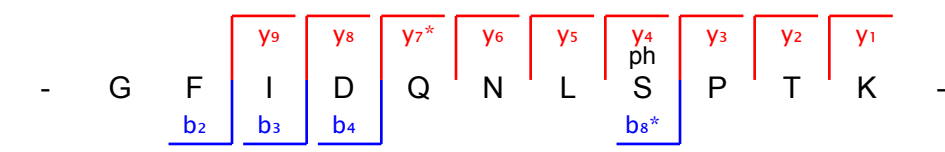
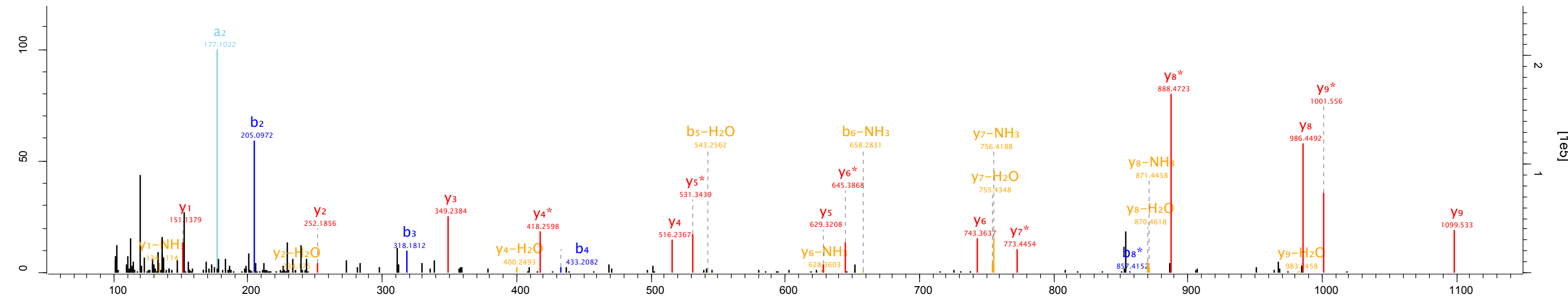
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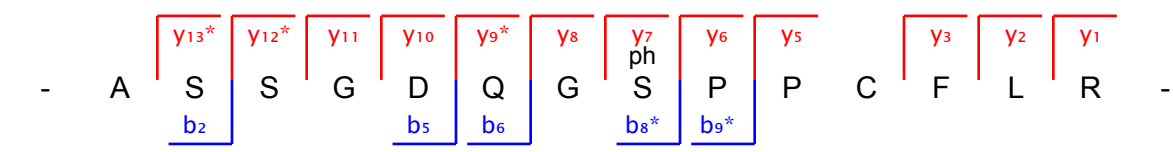
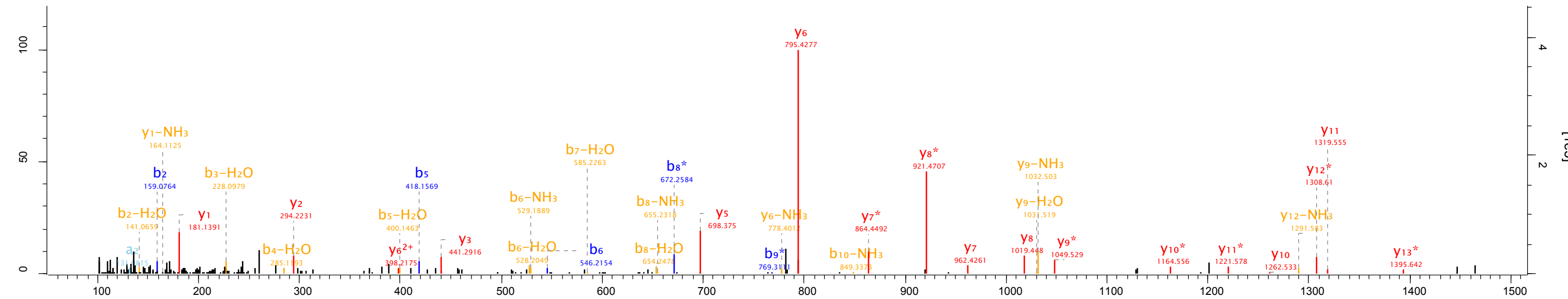
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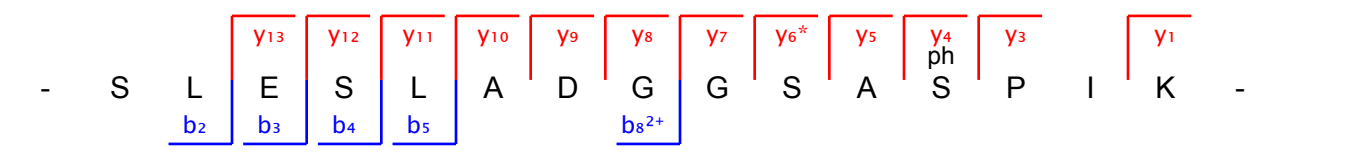
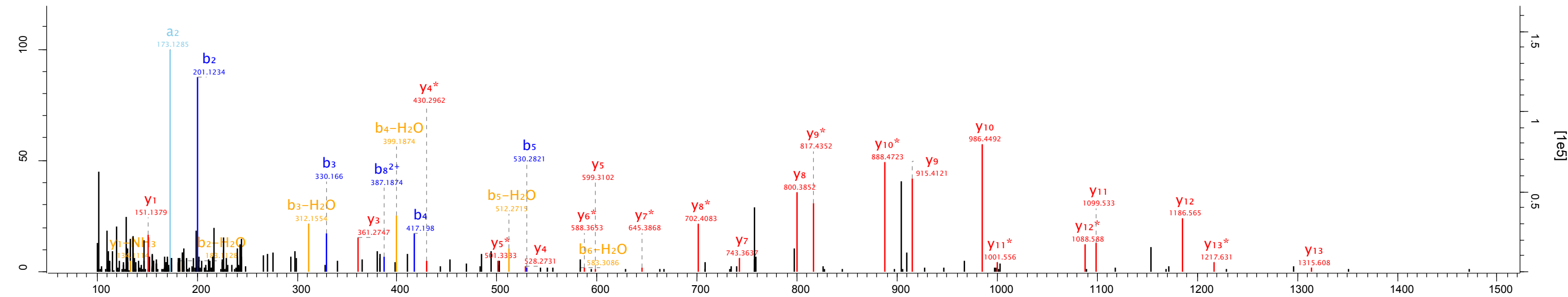
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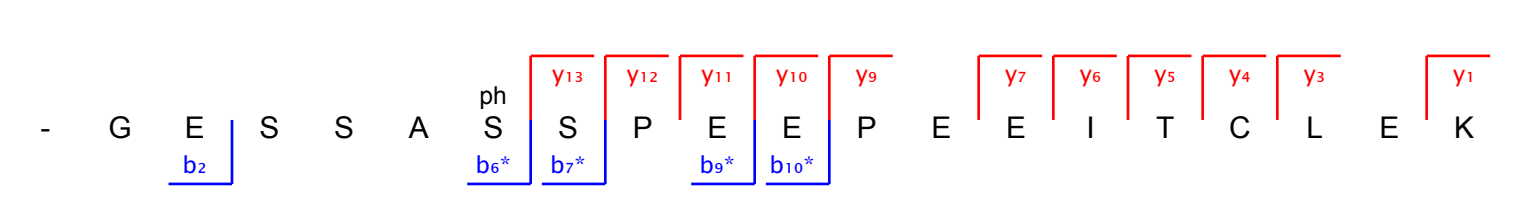
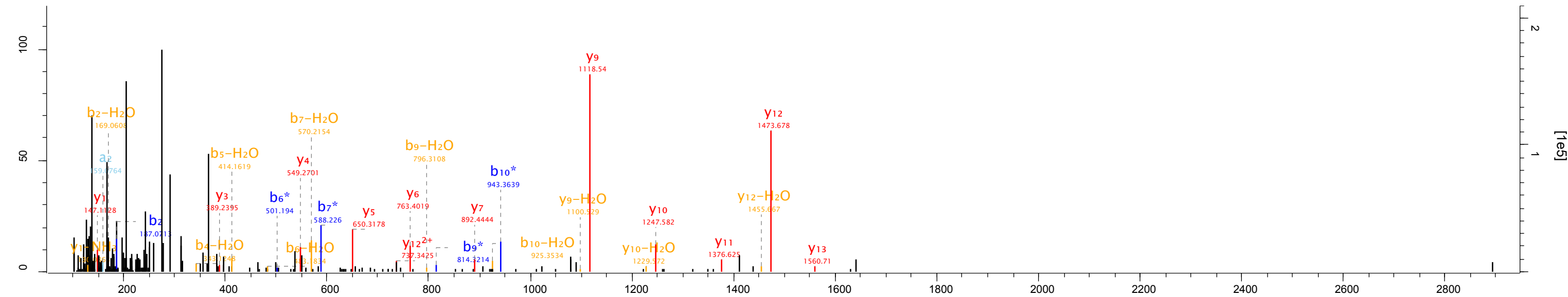
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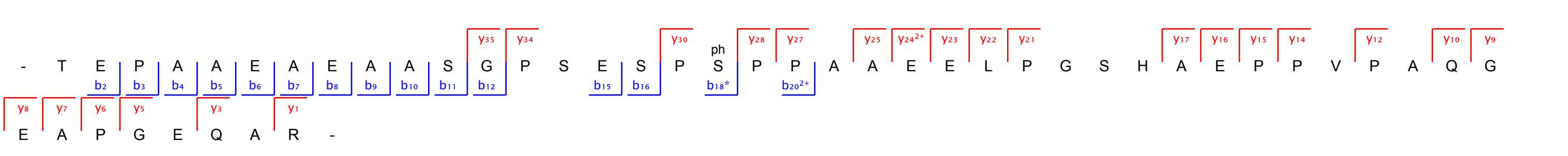
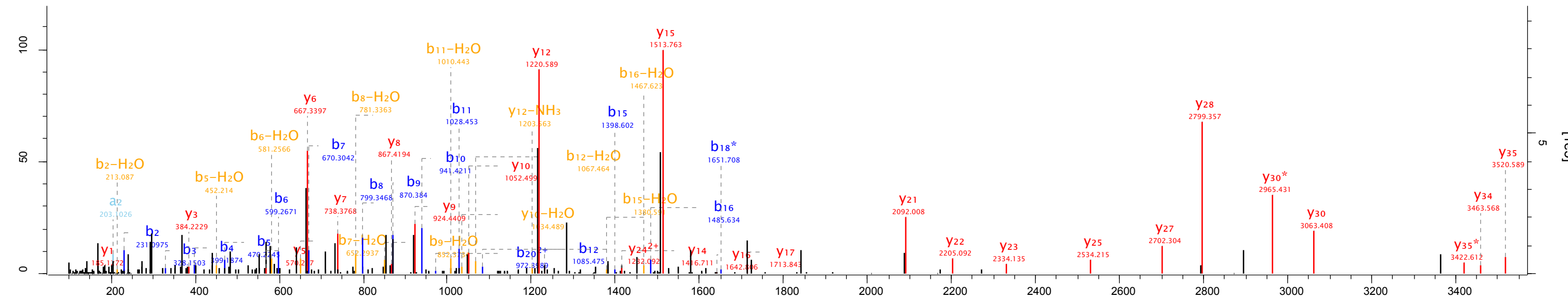
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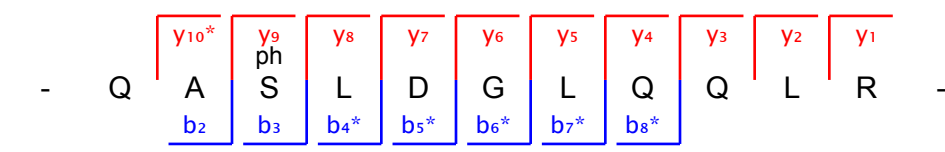
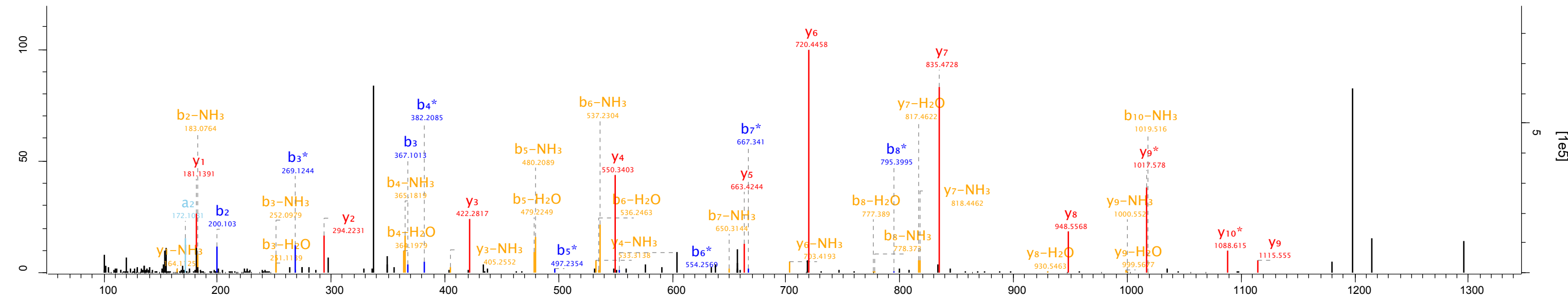
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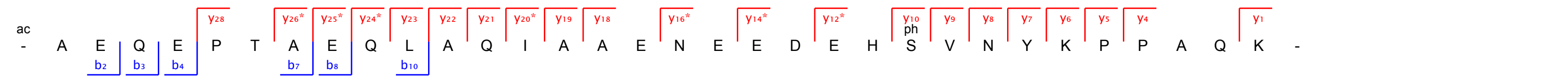
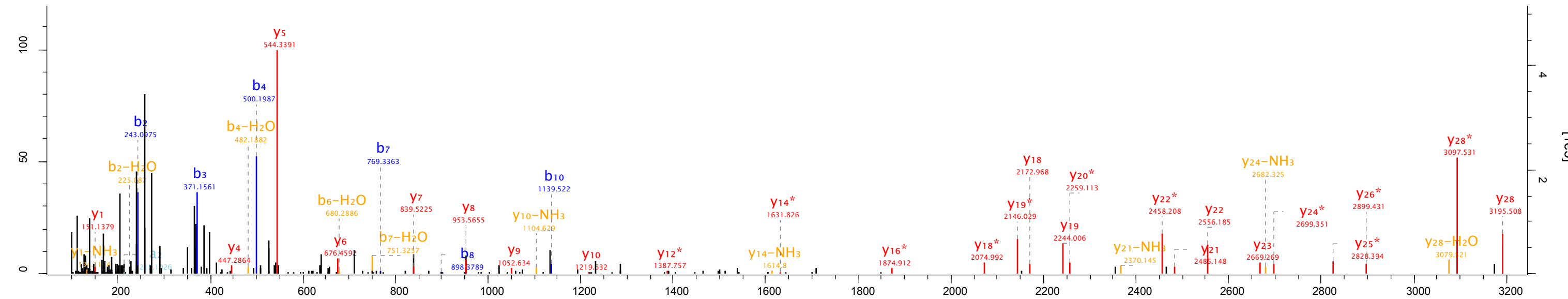
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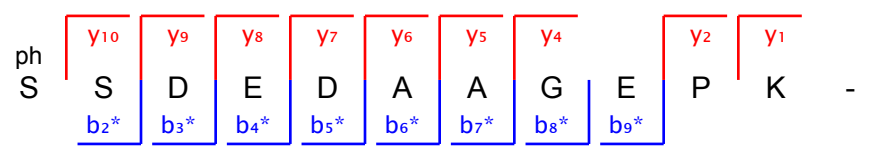
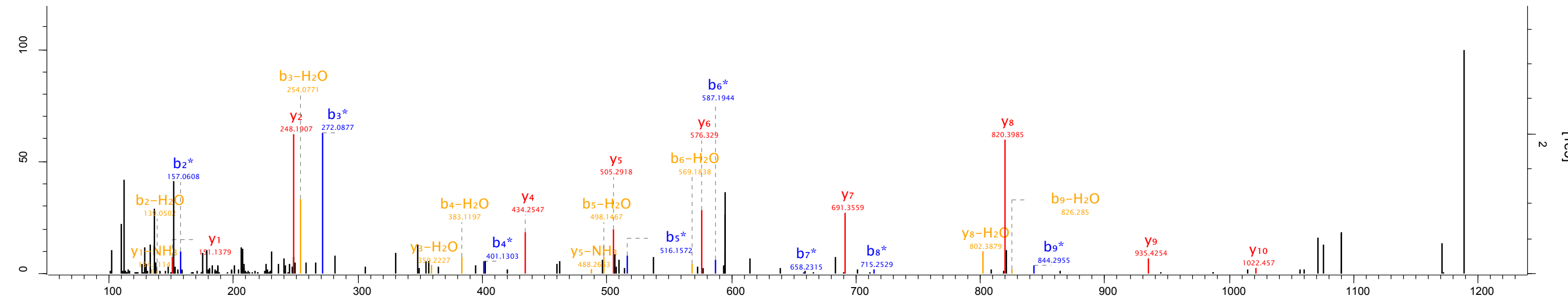
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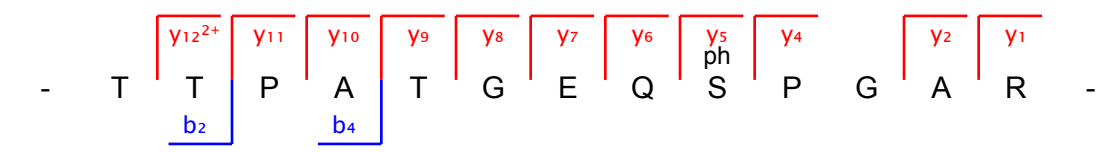
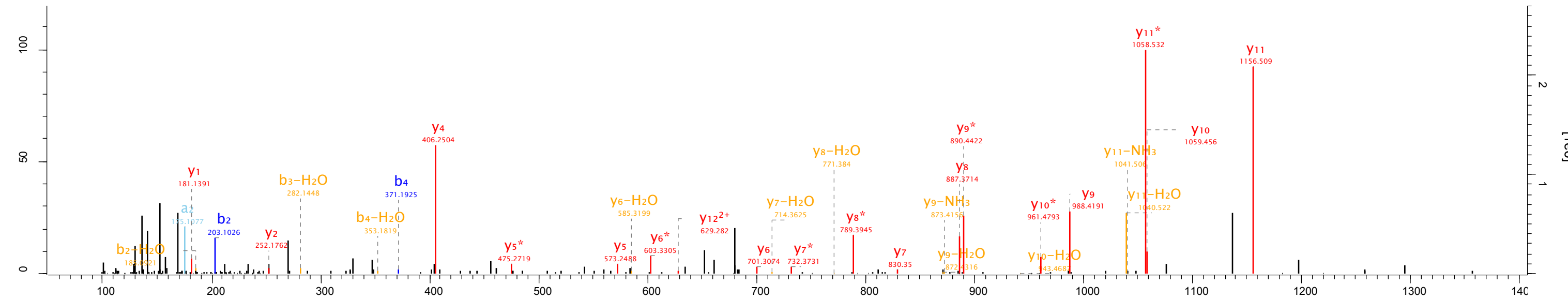
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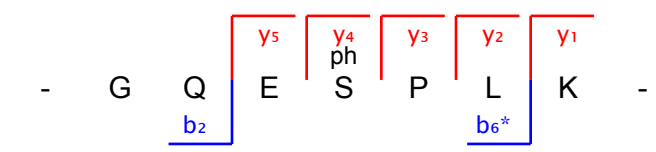
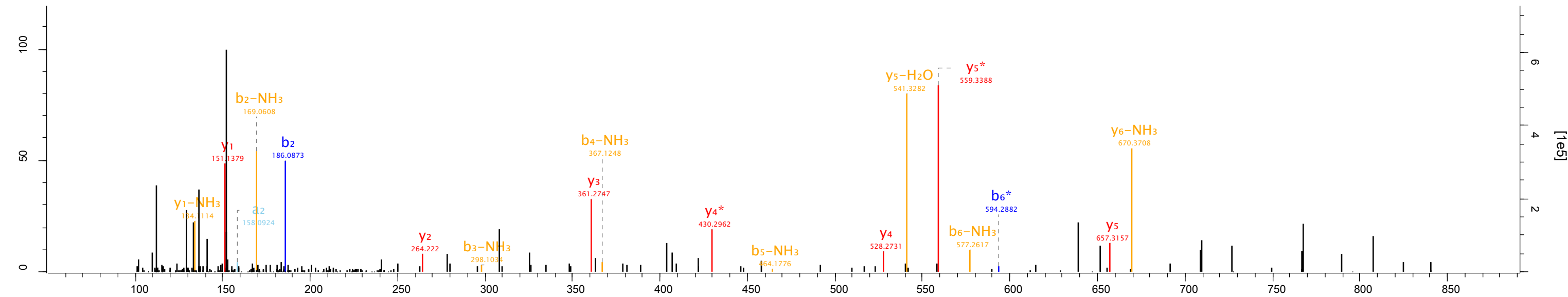
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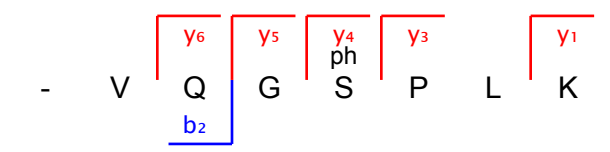
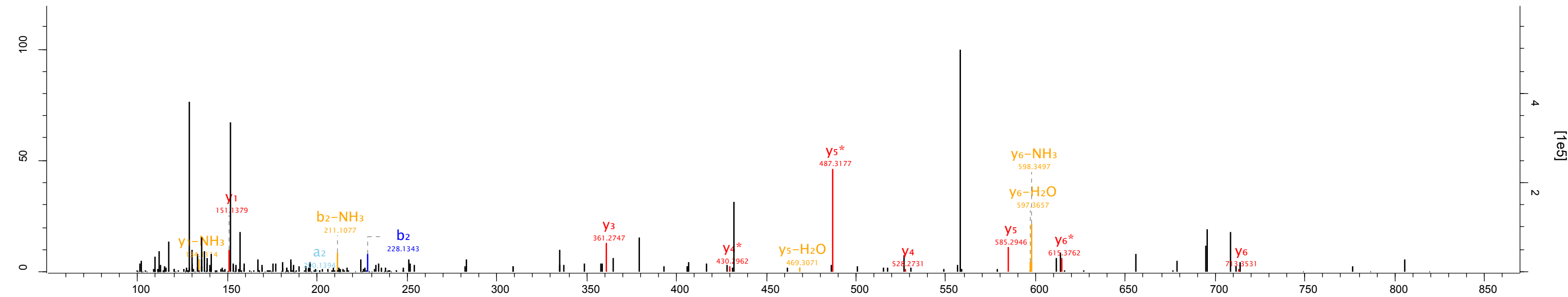
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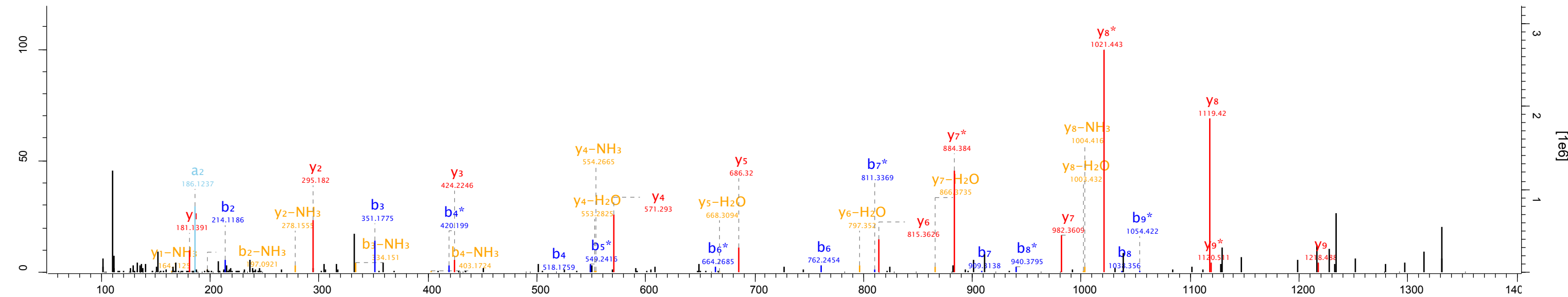


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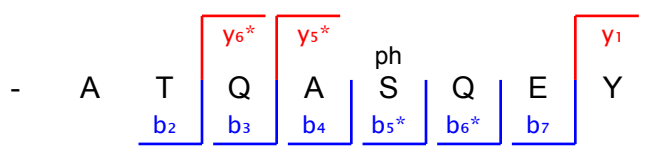
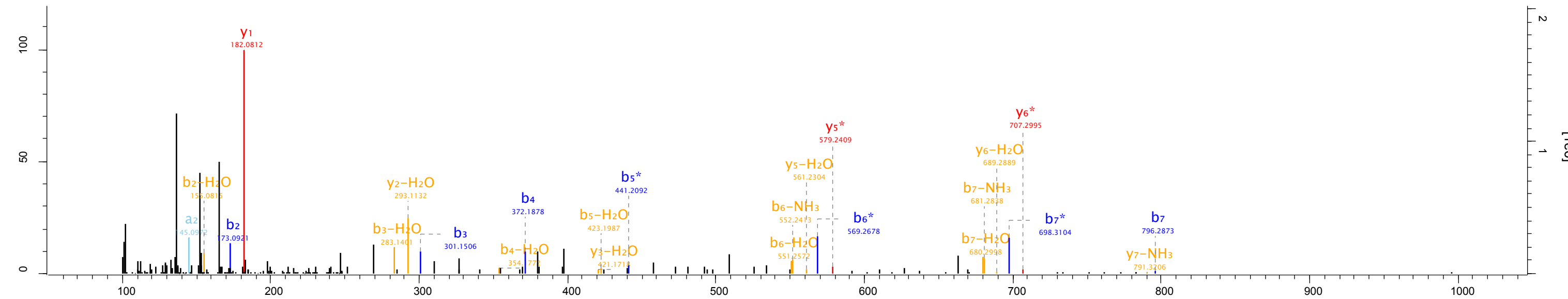
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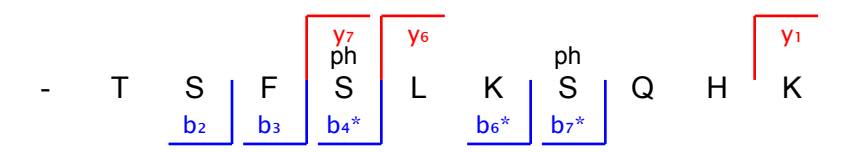
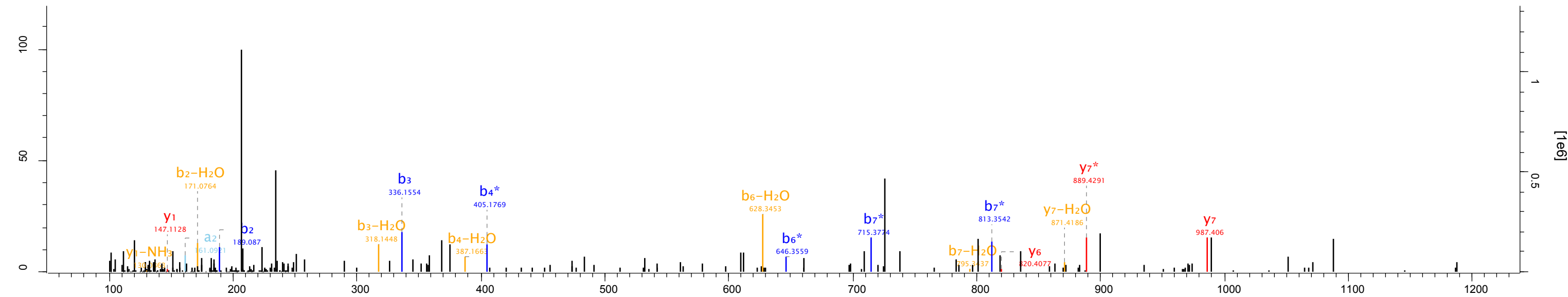


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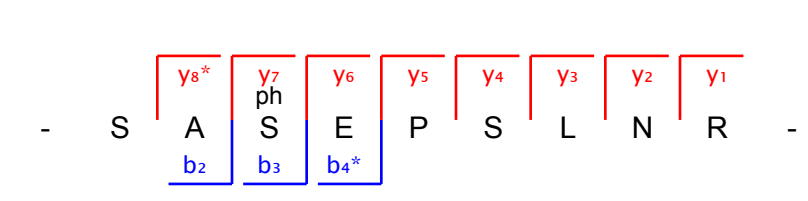
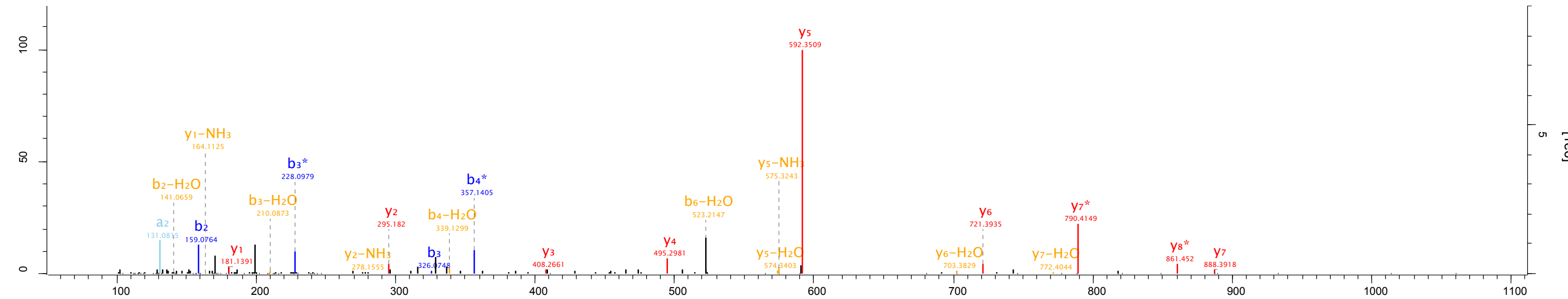
Scan 3994 Method FTMS; HCD Score 101.82 m/z 489.18 Gene names H2AFX



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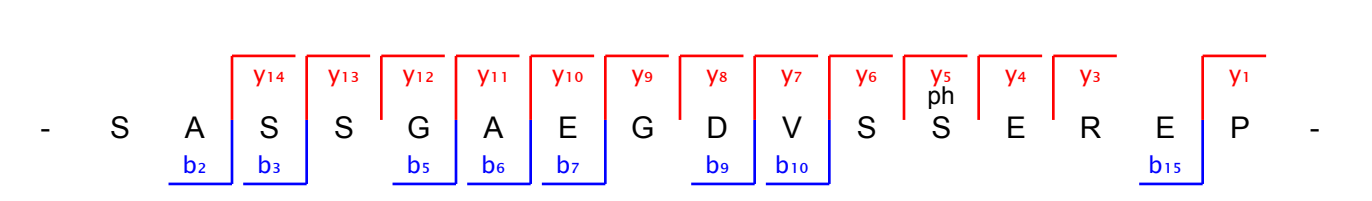
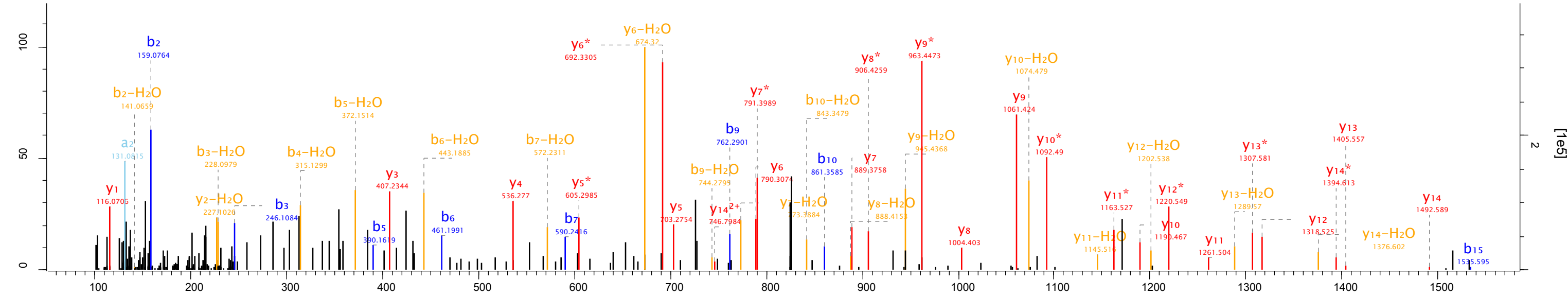


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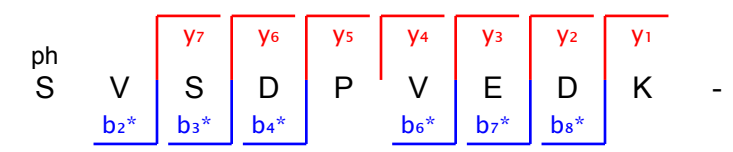
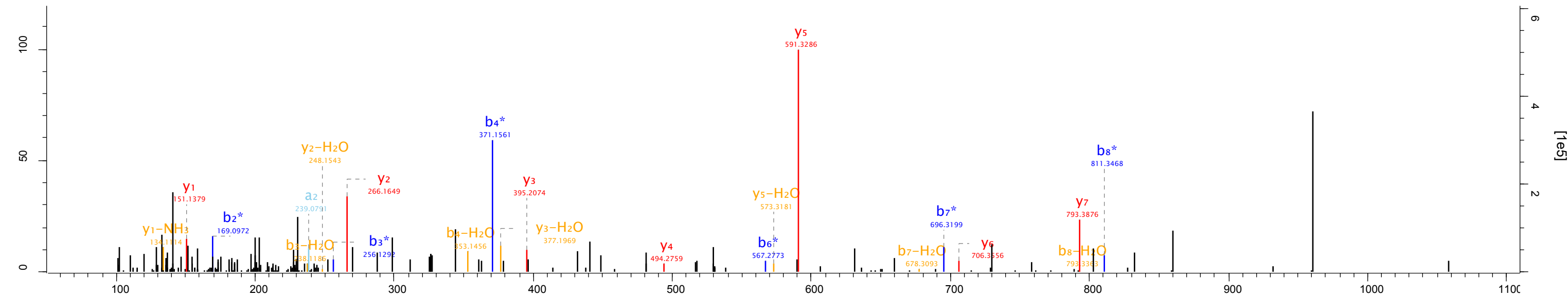
20171215_MaS_33SR_LMH_phospho2_02

4144 FTMS; HCD 250.79 825.83 DTD1



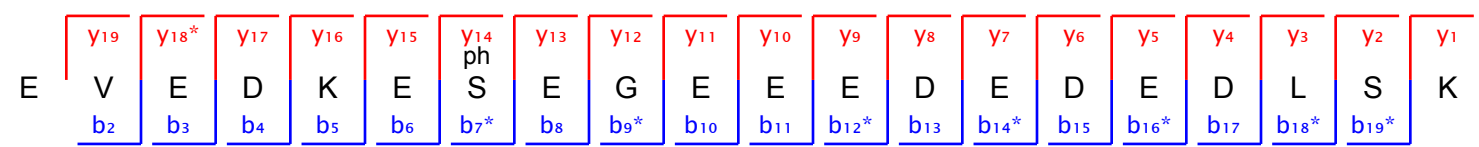
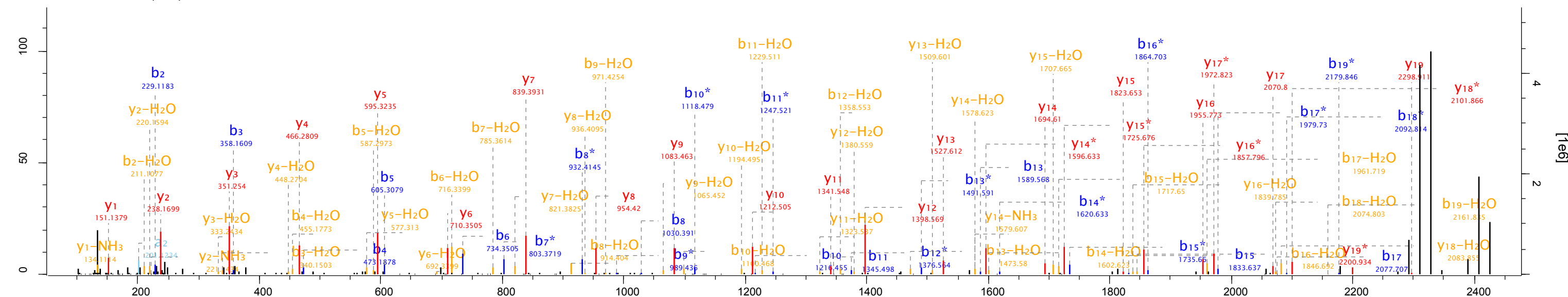
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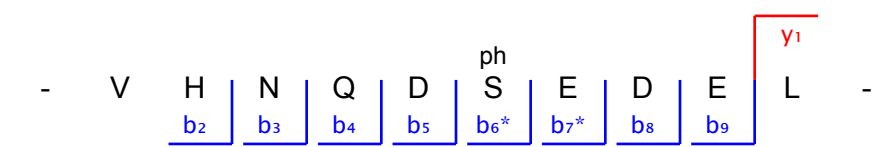
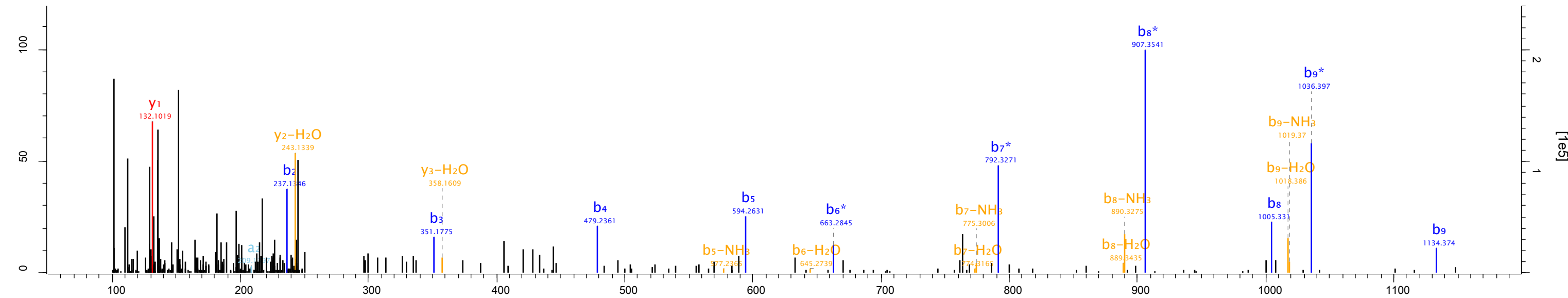
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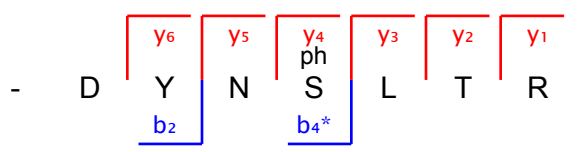
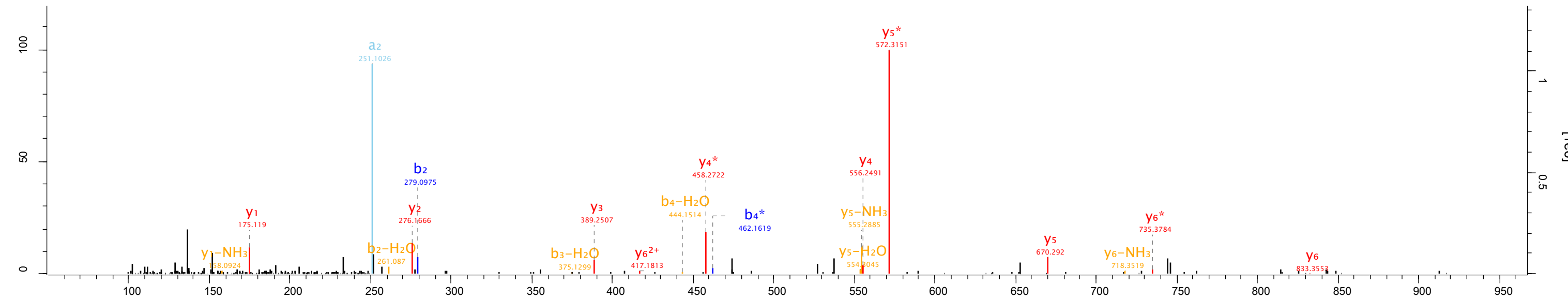
Scan Method Score m/z Gene names
4864 FTMS; HCD 508.58 1214.98 ZRANB2



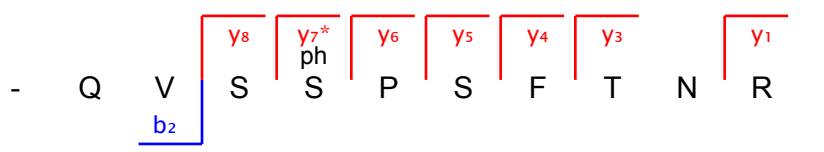
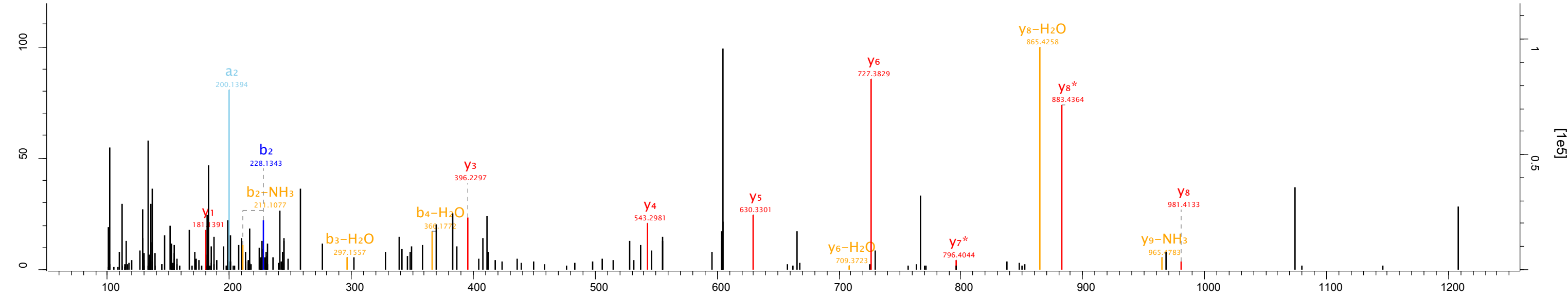


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20171215_MaS_33SR_LMH_phospho2_02

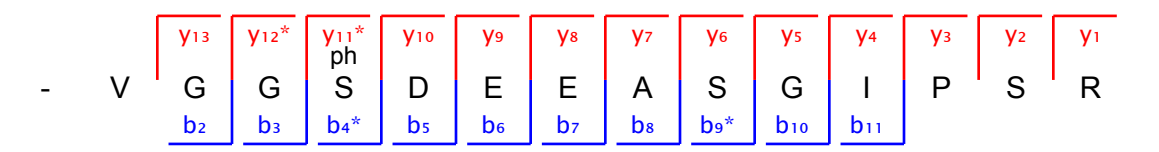
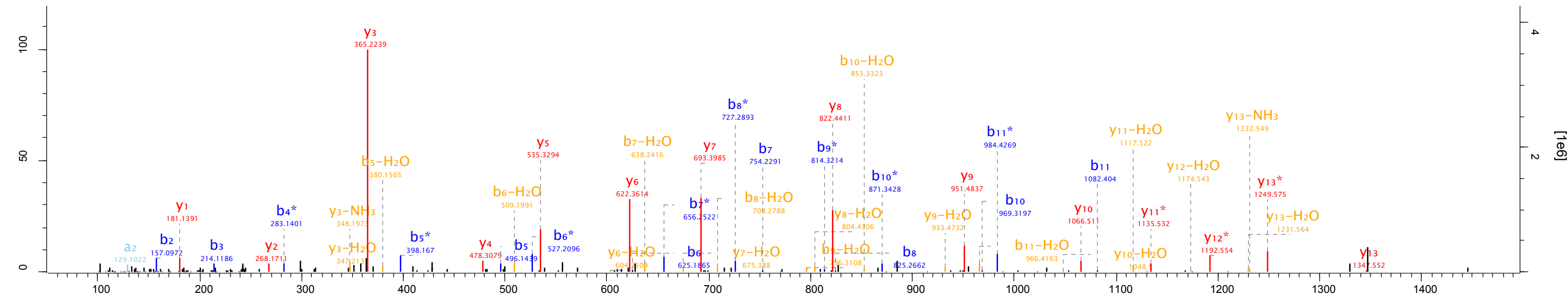
Scan 5424 Method FTMS; HCD Score 115.82 m/z 474.69 Gene names ITGB4



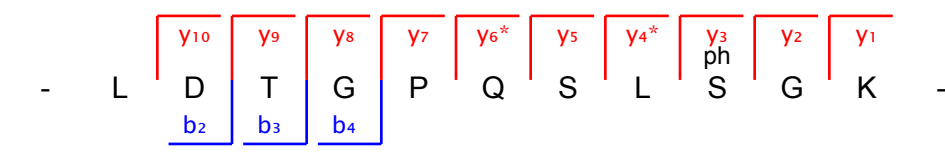
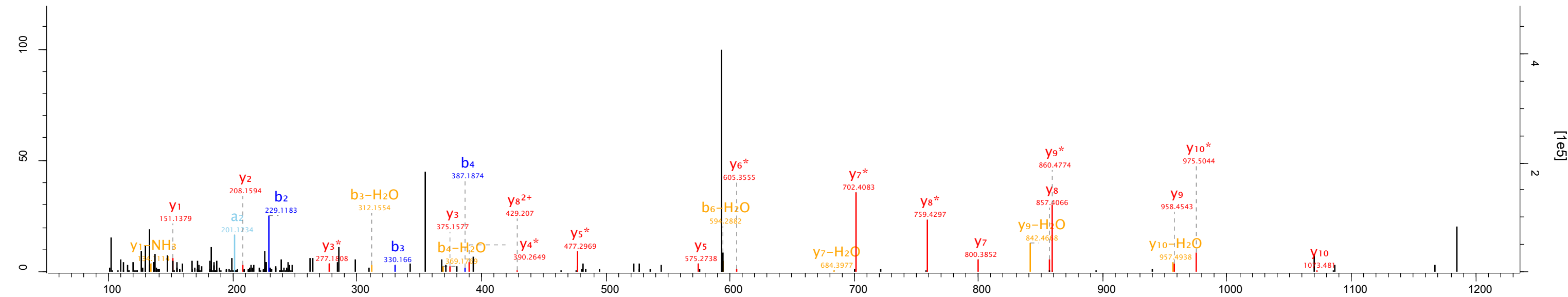
20171215_MaS_33SR_LMH_phospho2_02 5594 FTMS; HCD 45.28 604.77 LUZP1



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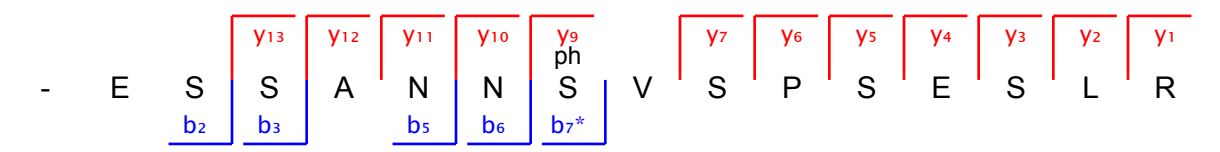
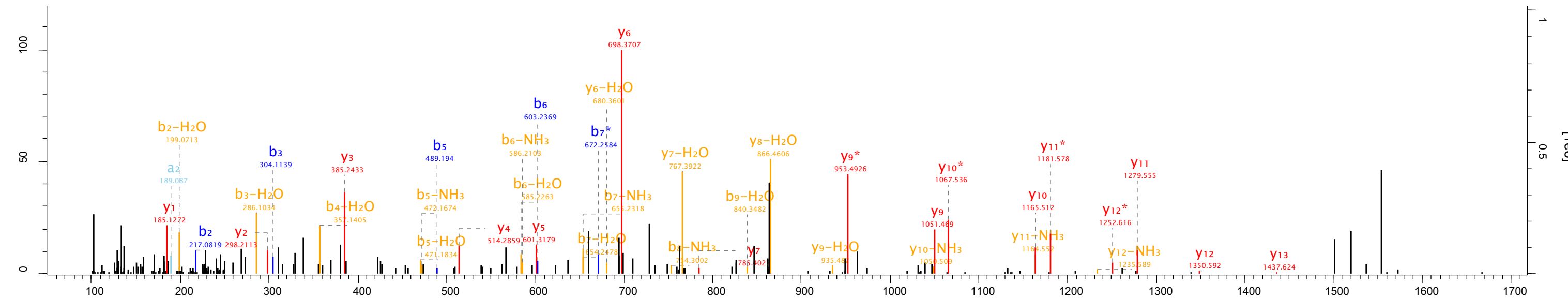
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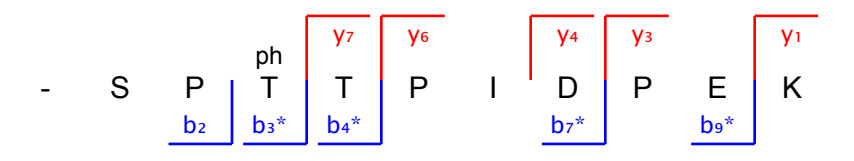
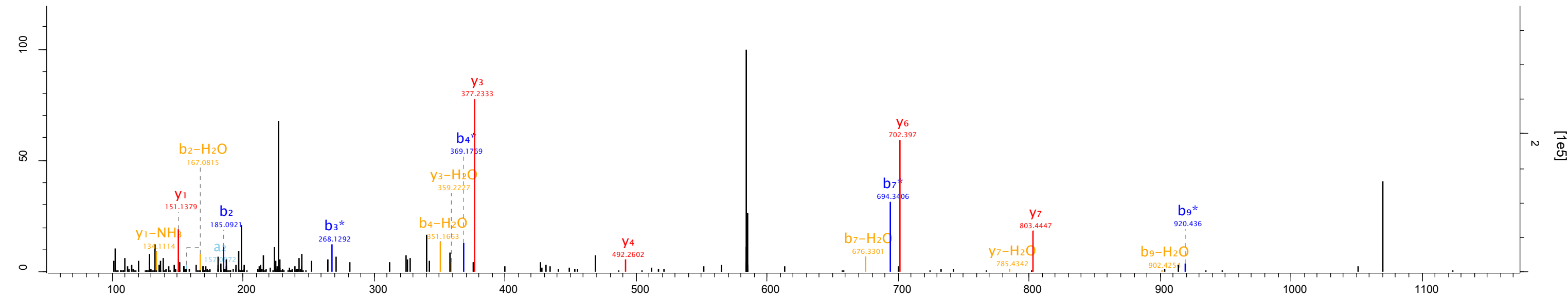
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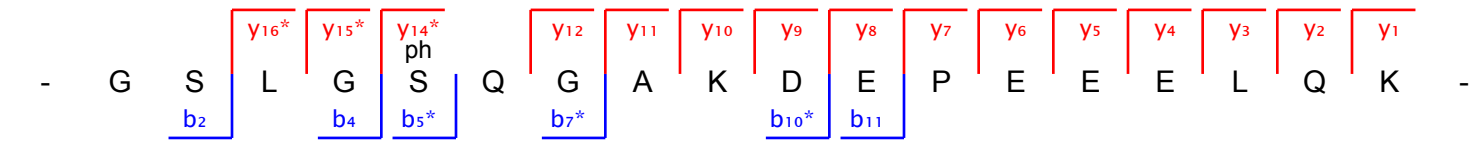
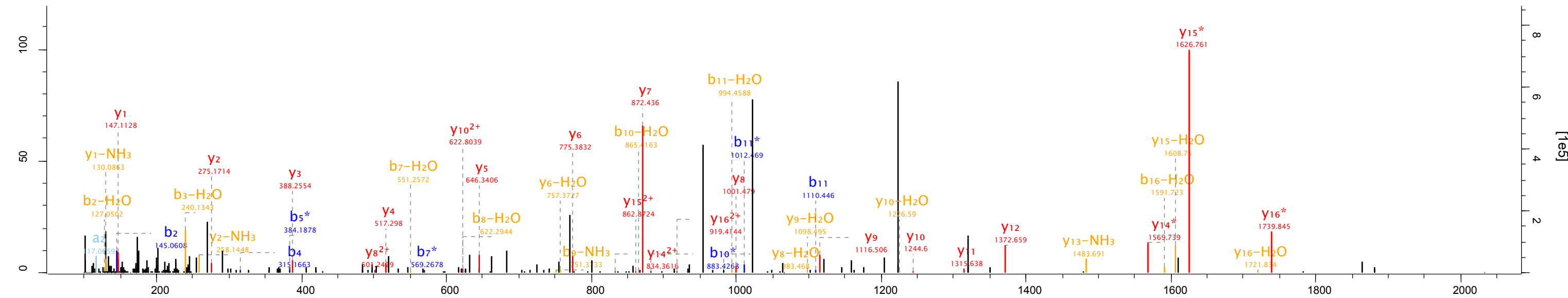
20171215_MaS_33SR_LMH_phospho2_02

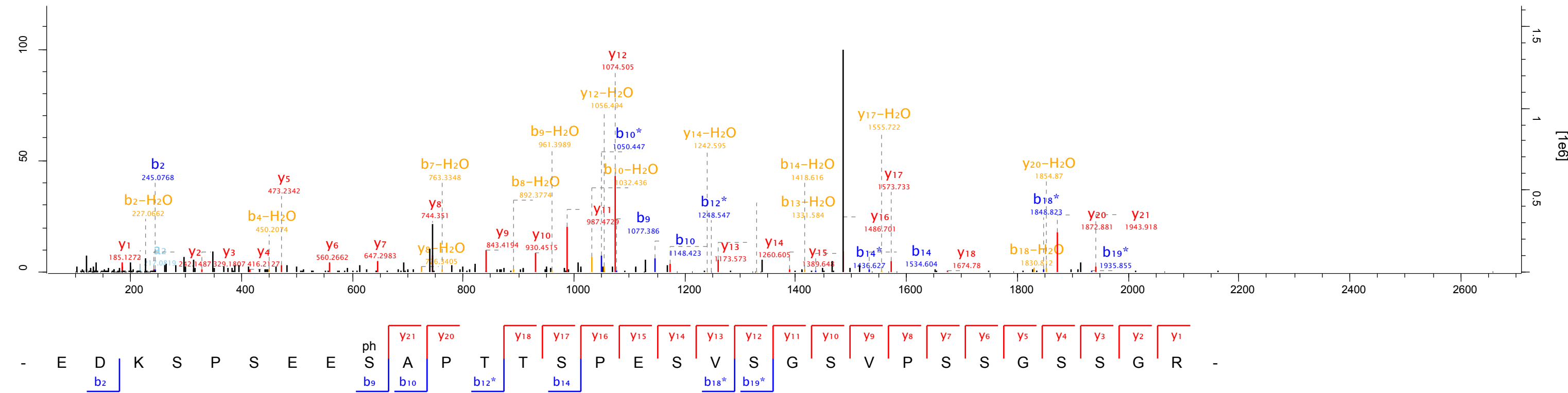
Scan	Method	Score	m/z	Gene names
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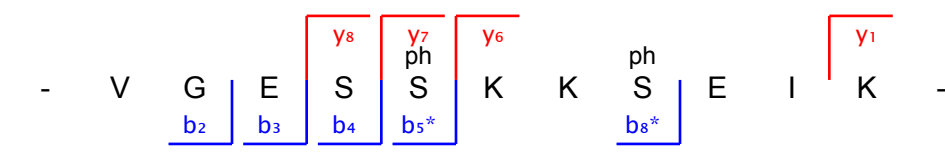
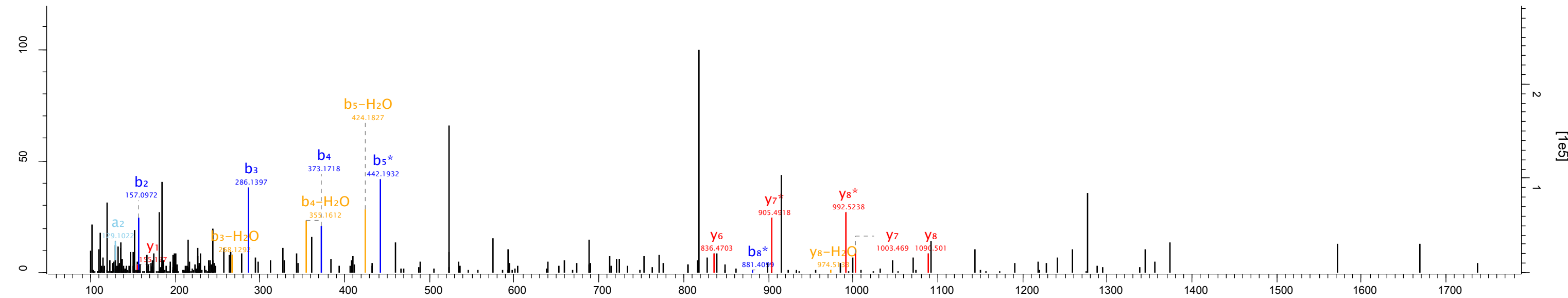


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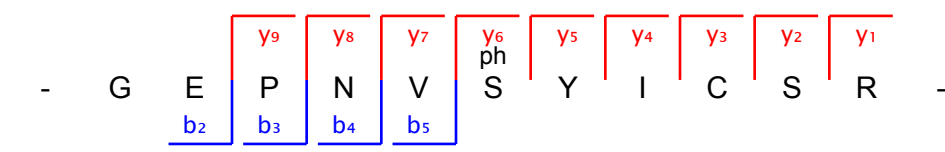
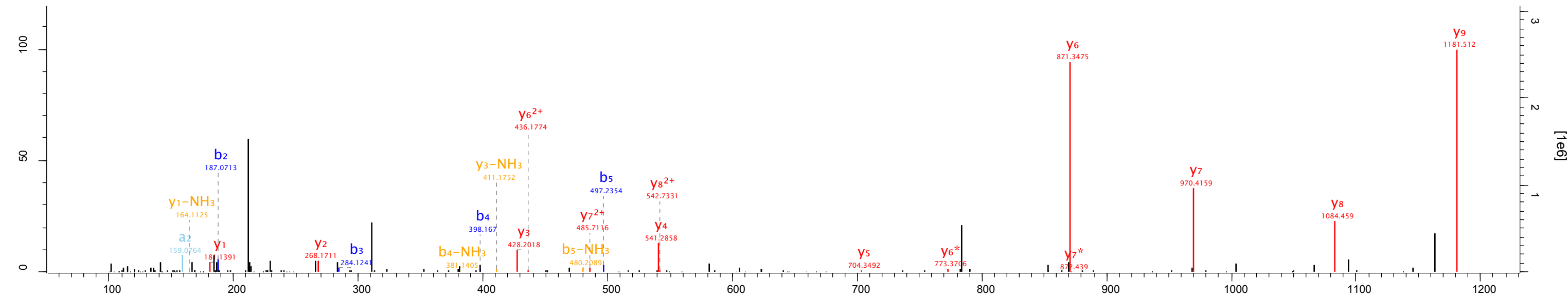




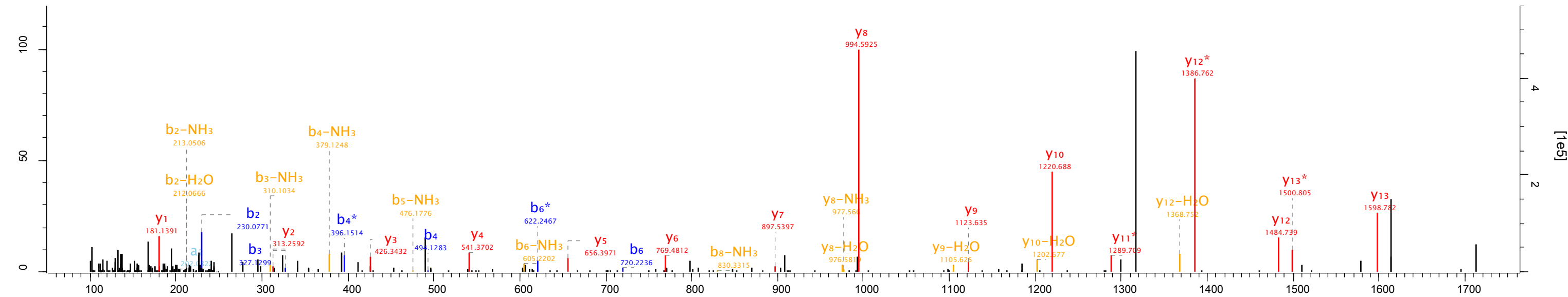




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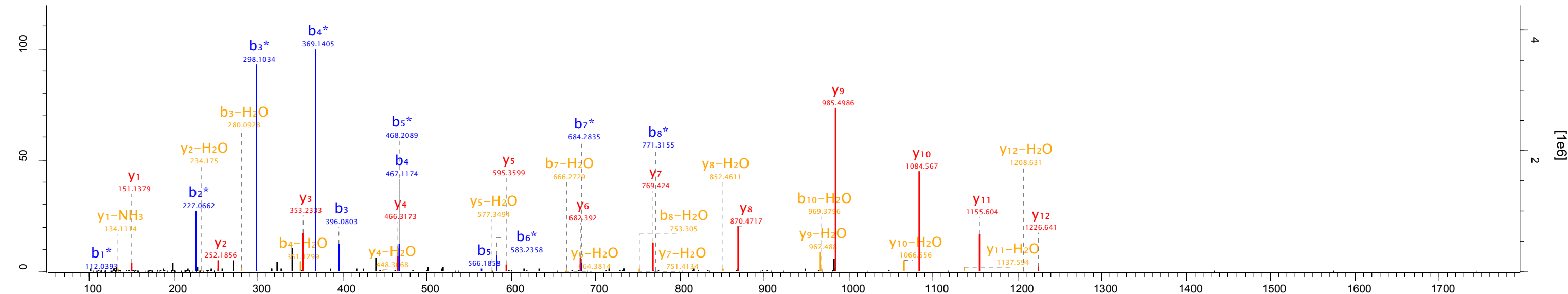


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 Scan: 8574 Method: FTMS; HCD Score: 135.09 m/z: 857.41 Gene names: EAF1



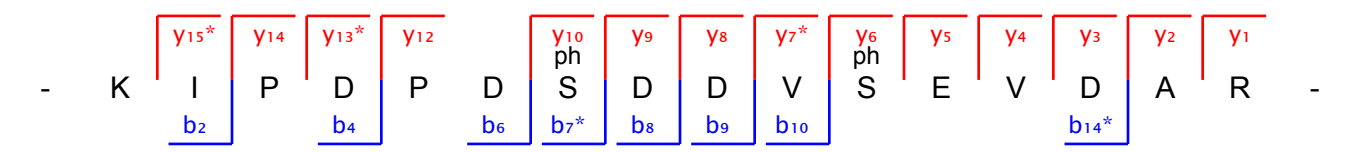
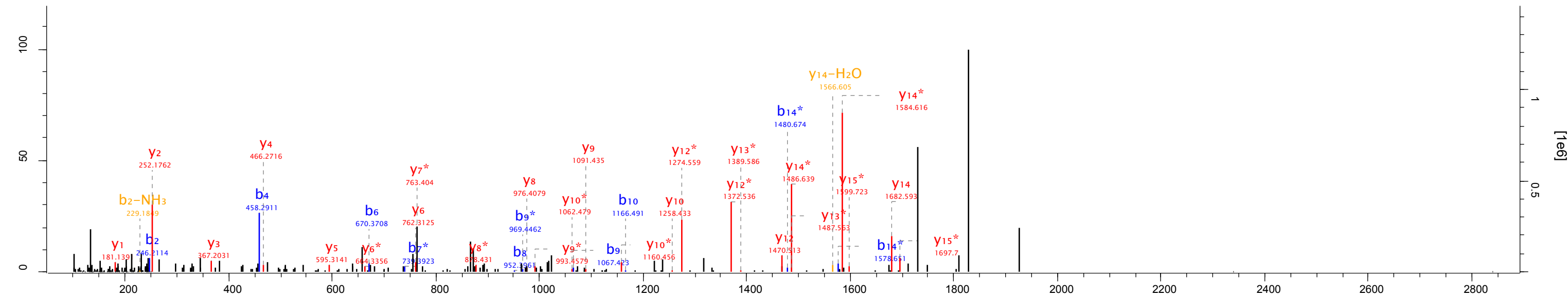
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20171215_MaS_33SR_LMH_phospho2_02

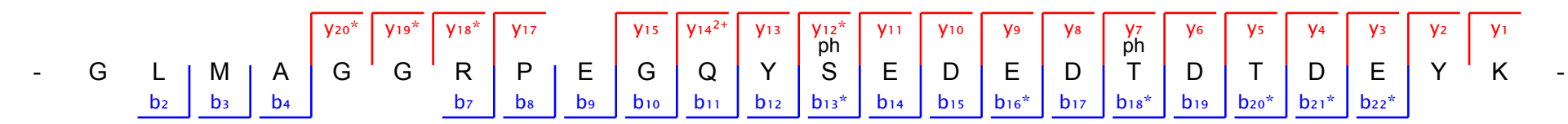
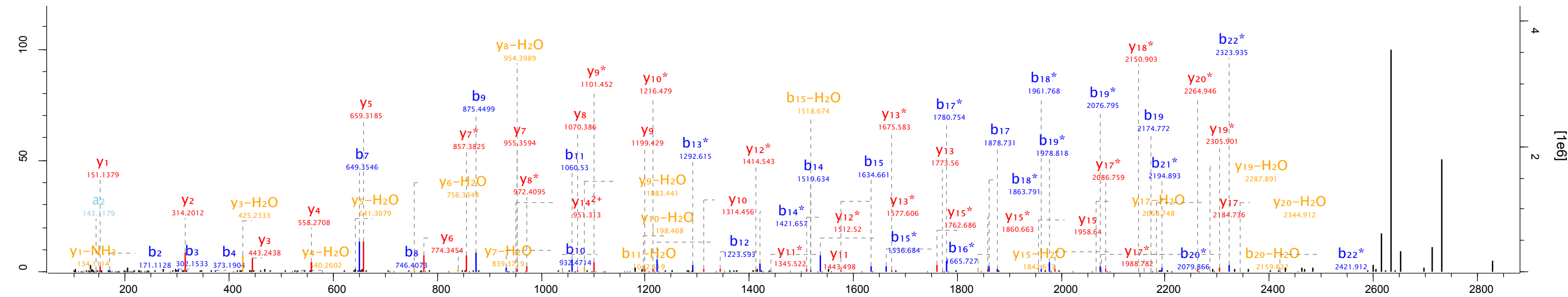
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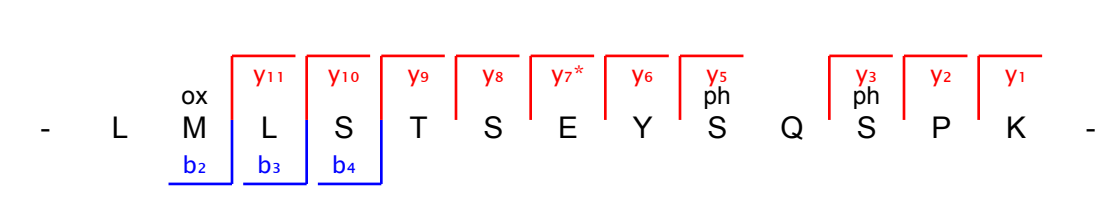
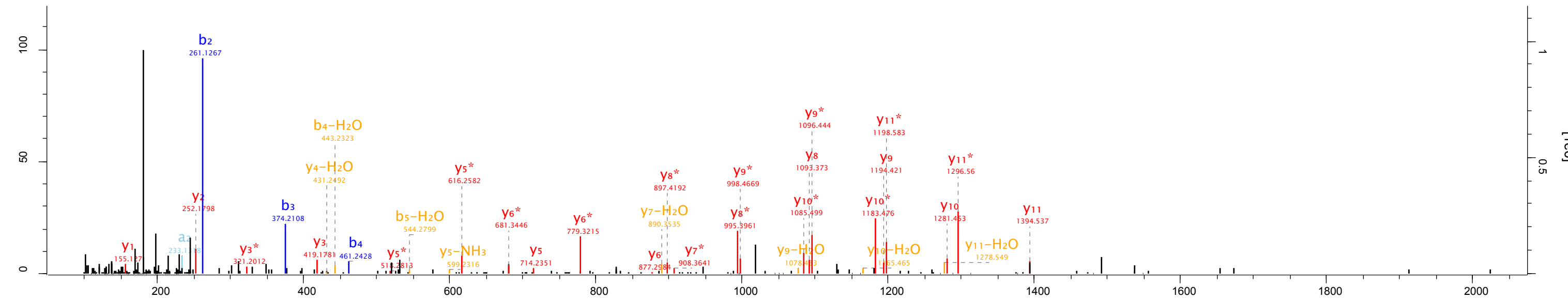
ac - ph S D A A V D T S S E I T T K -
b1* b2* b3 b4 b5 b6* b7* b8*

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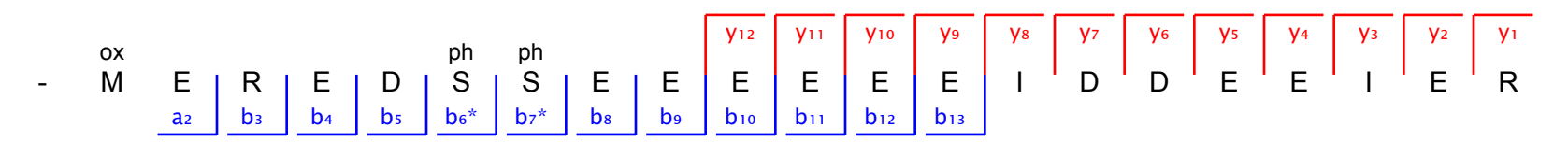
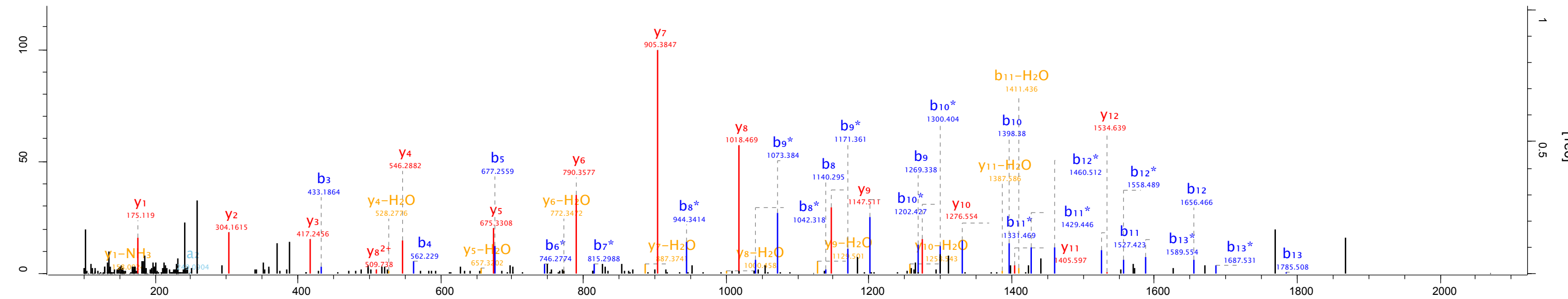


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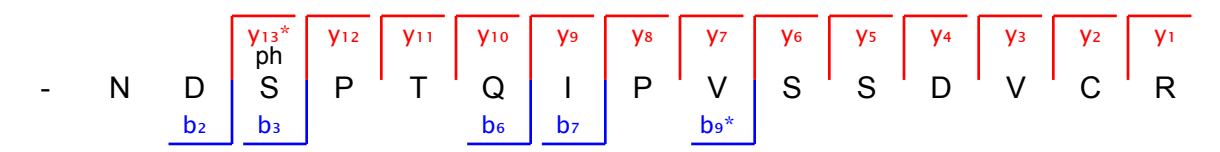
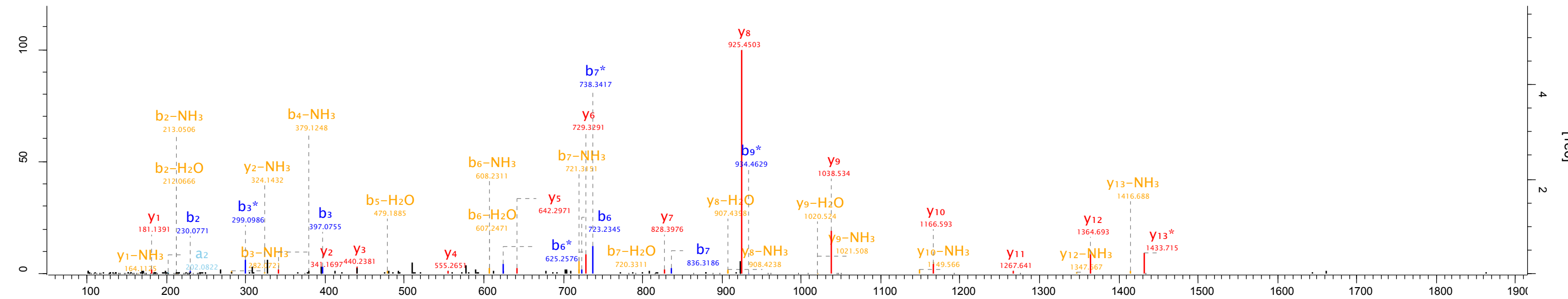
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20171215_MaS_33SR_LMH_phospho2_03

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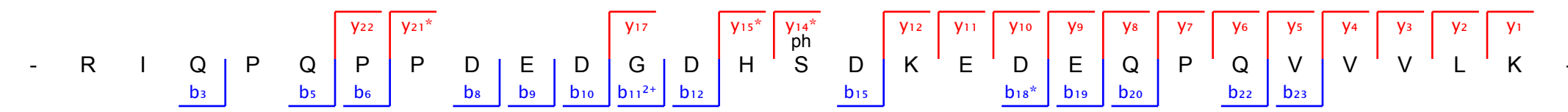
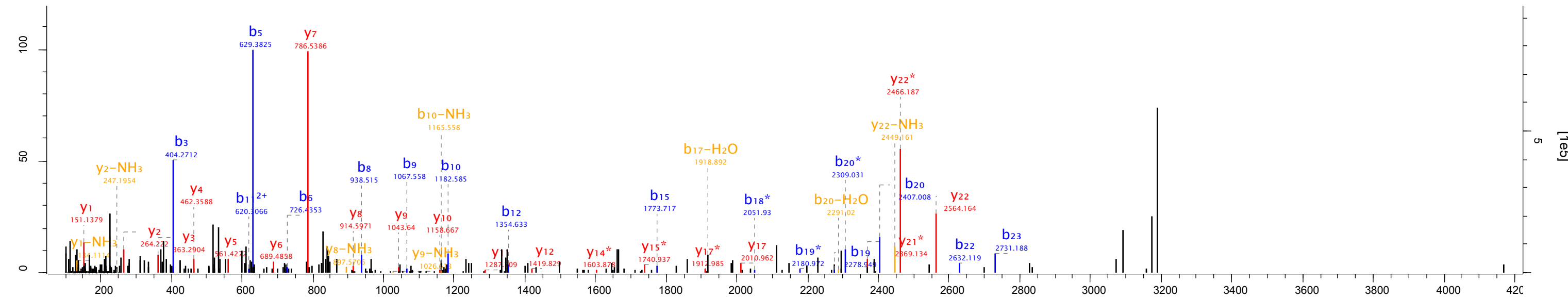


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20171215_MaS_33SR_LMH_phospho2_03

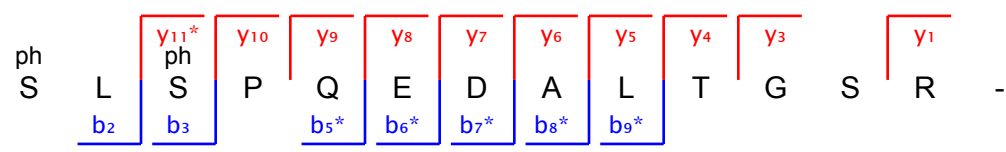
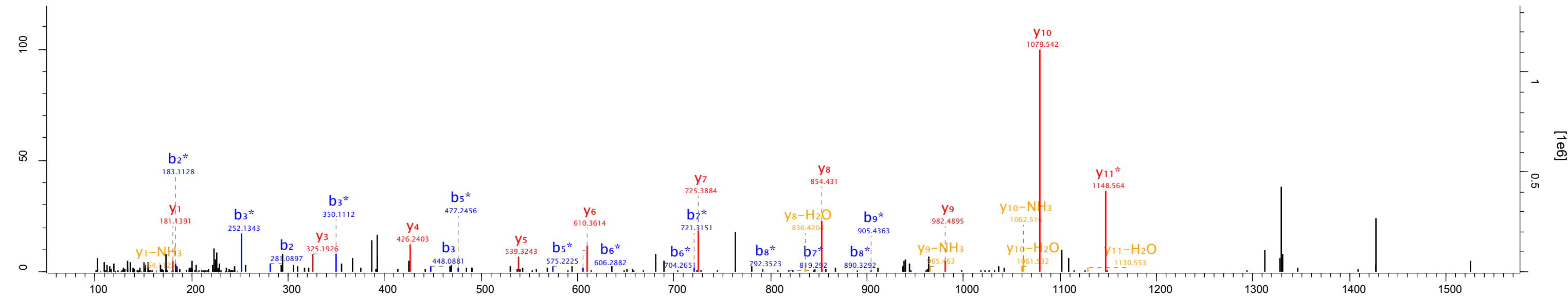
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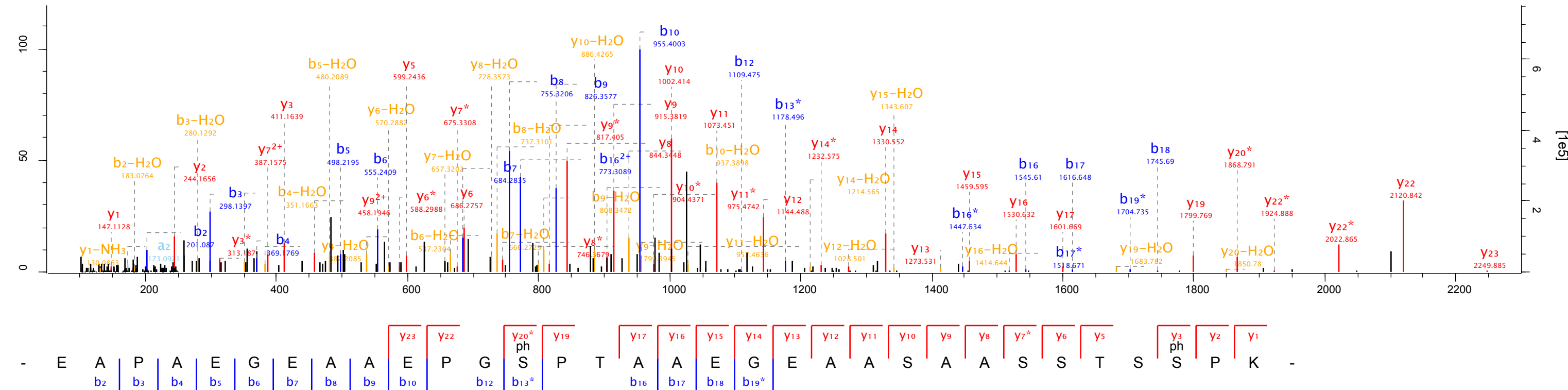


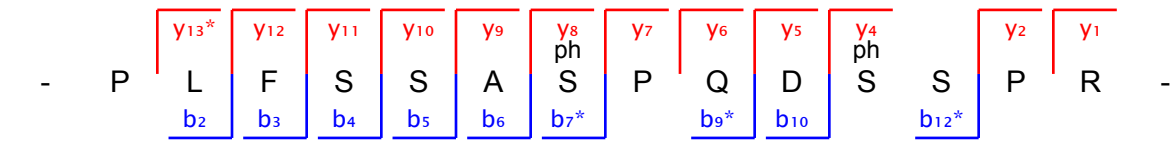
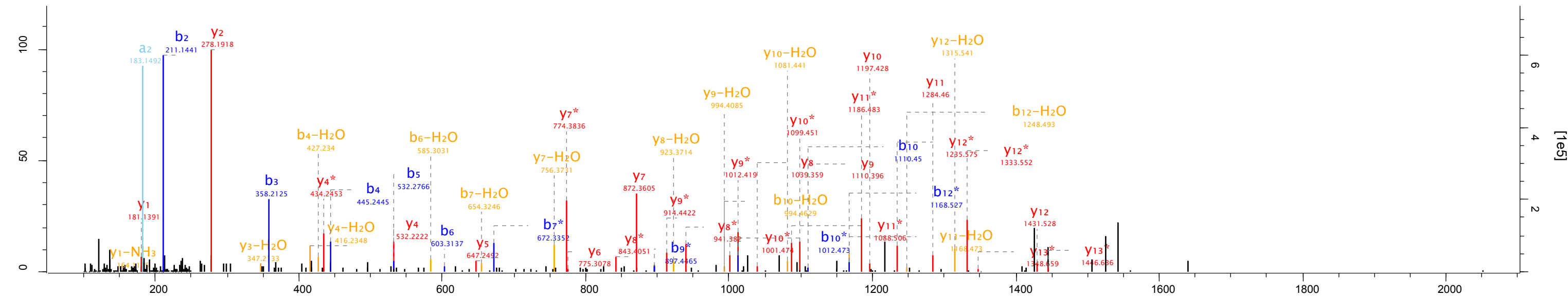
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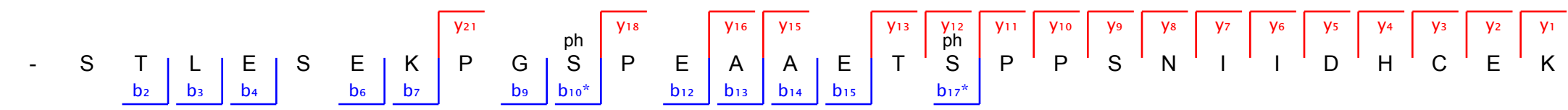
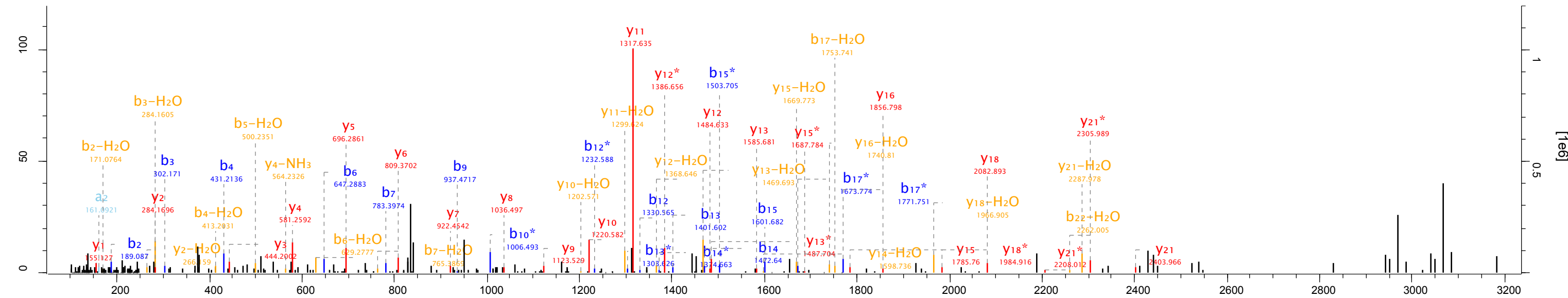
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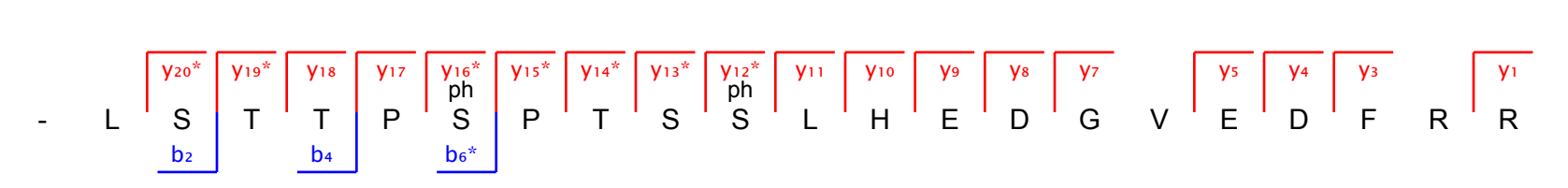
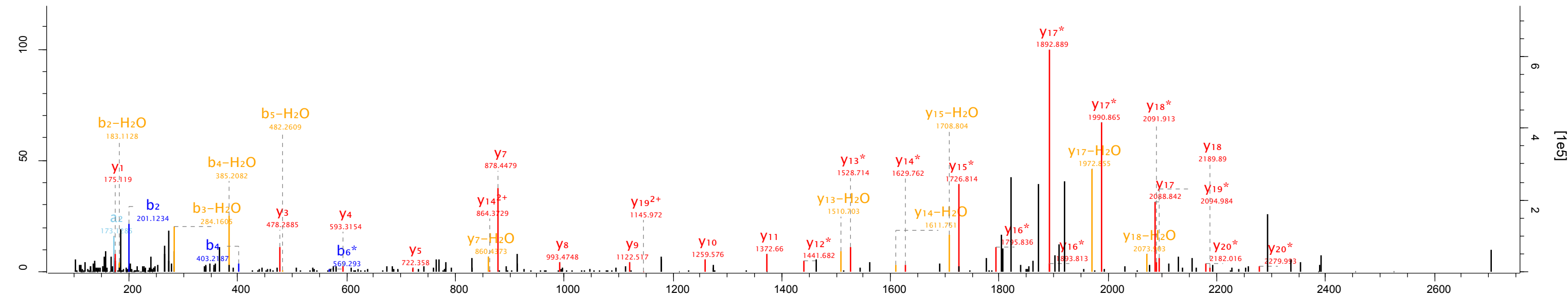




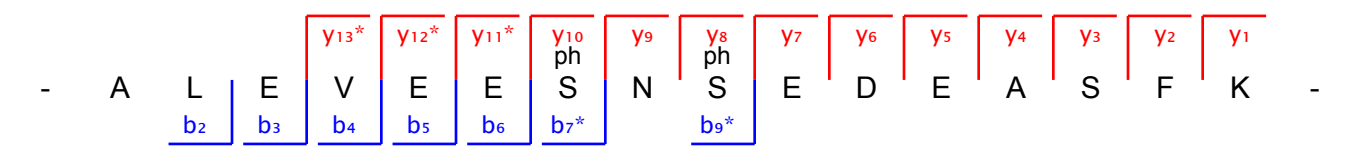
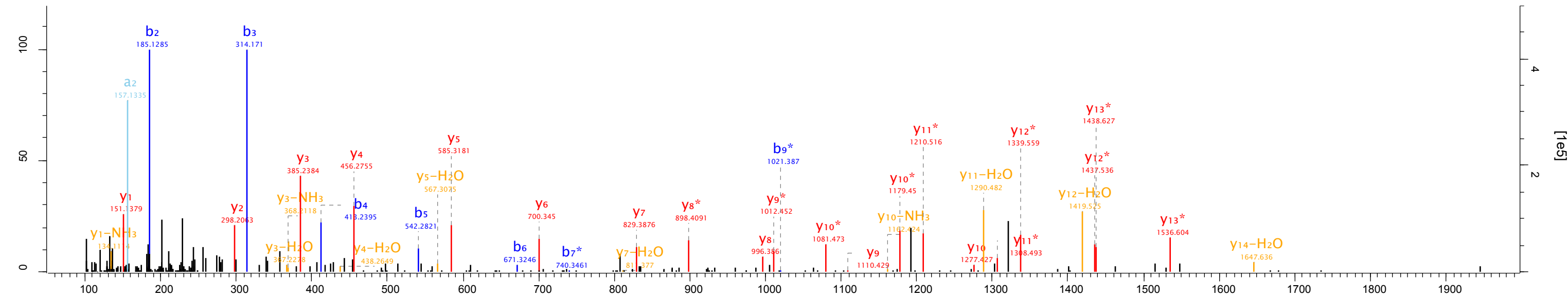
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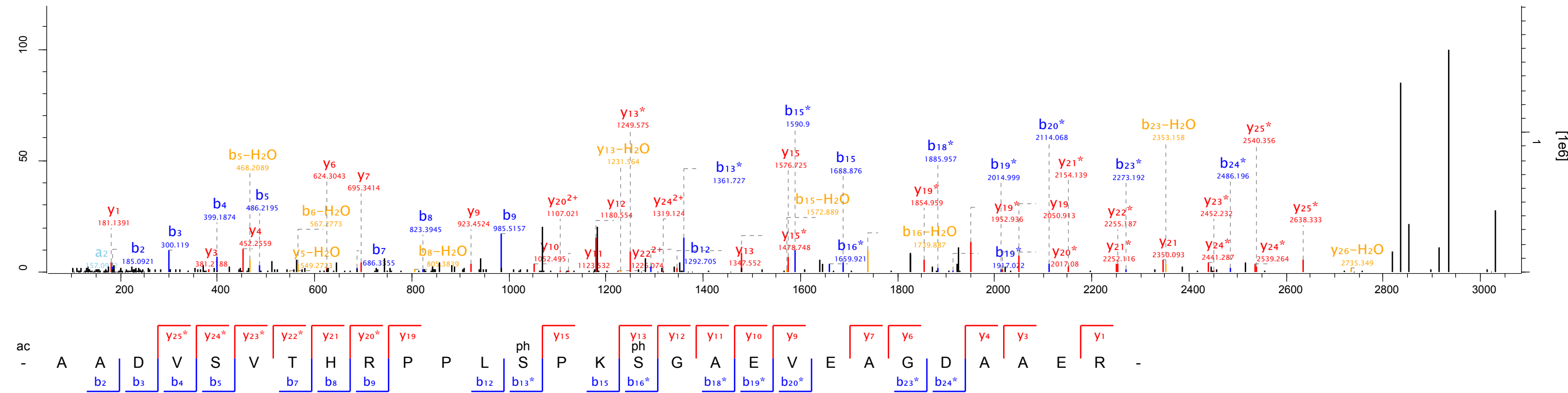
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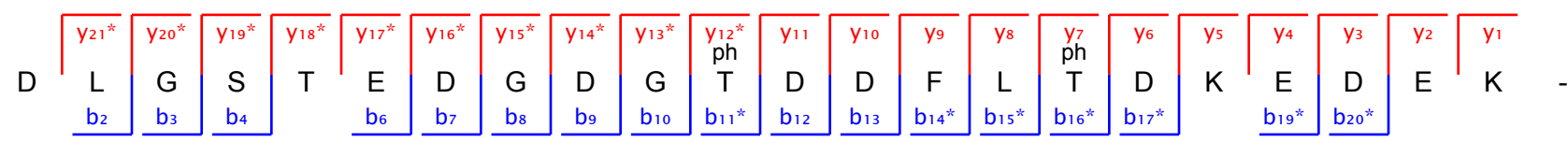
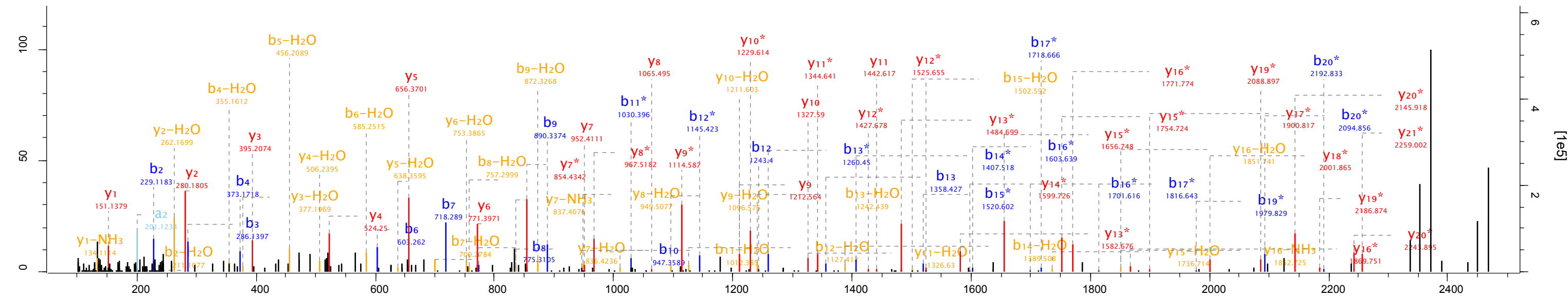
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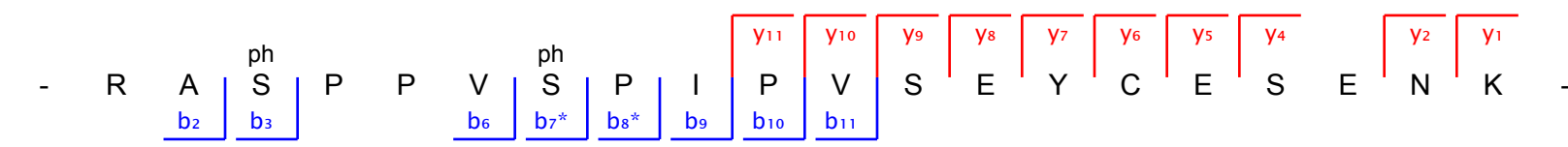
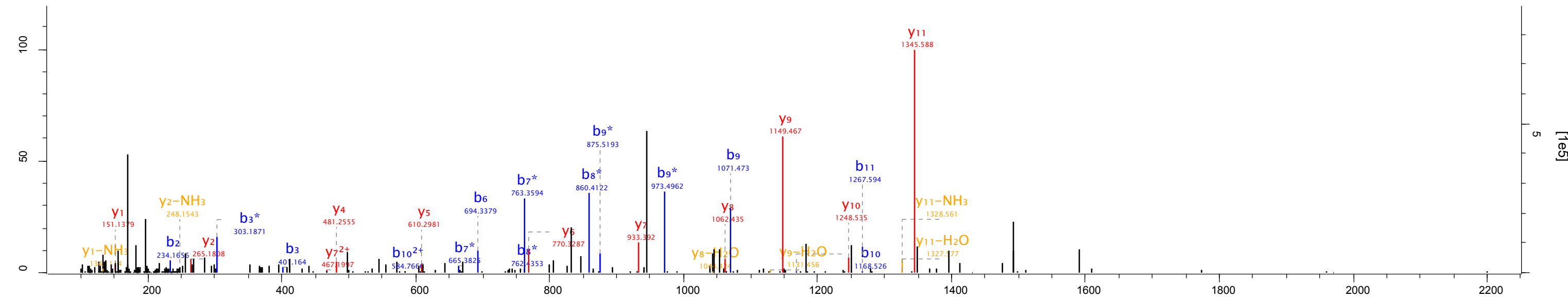
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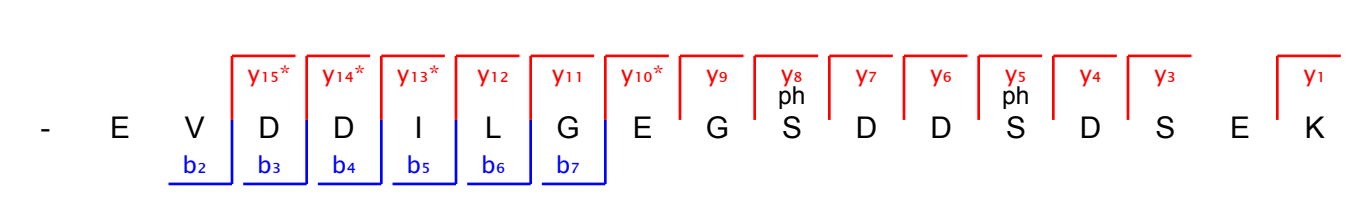
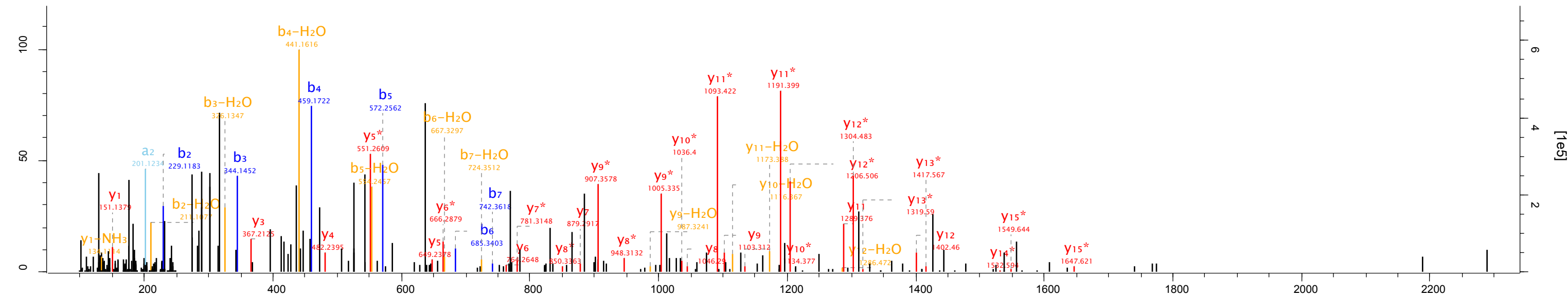
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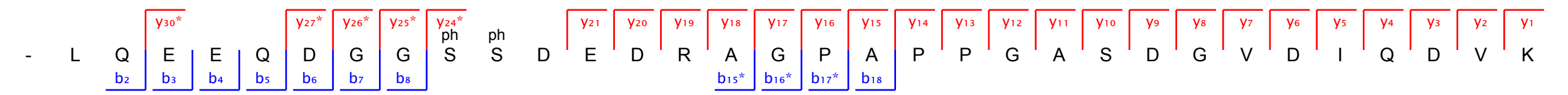
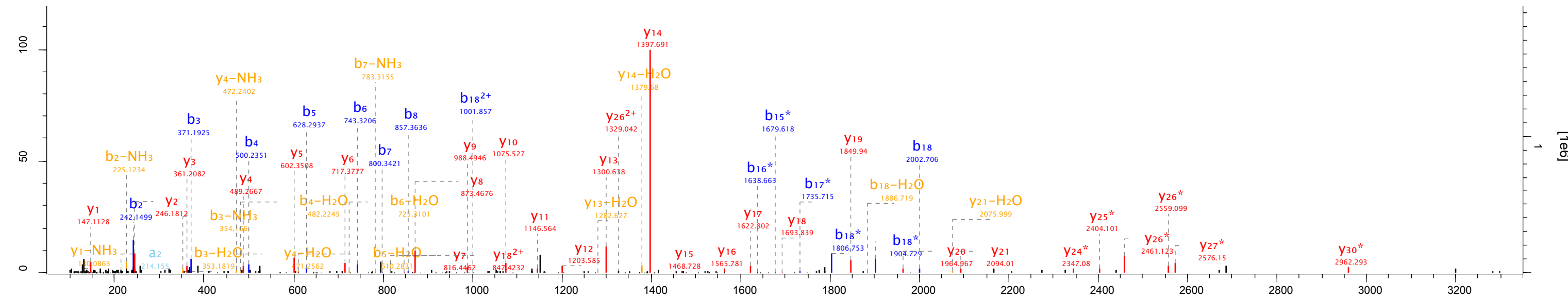
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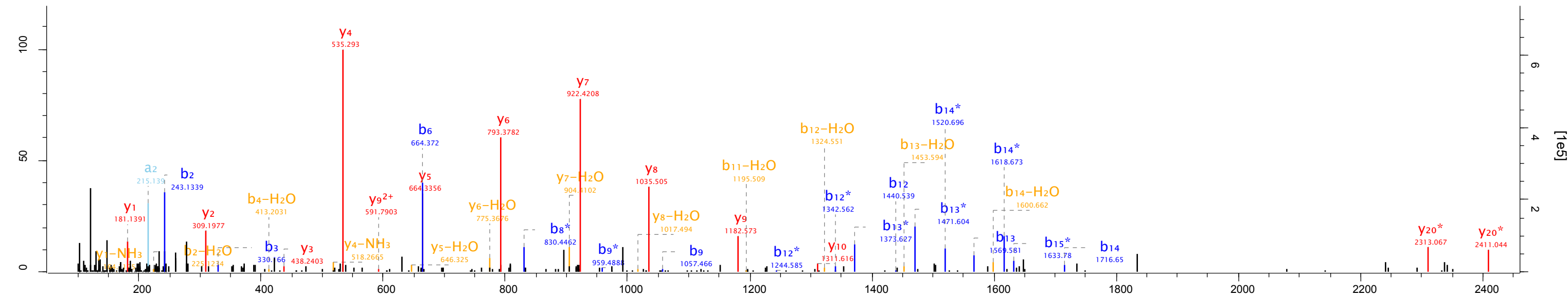
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Raw file Scan Method Score m/z Gene names
 20171215_MaS_33SR_LMH_phospho2_03 12574 FTMS; HCD 158.94 1134.13 DHX34



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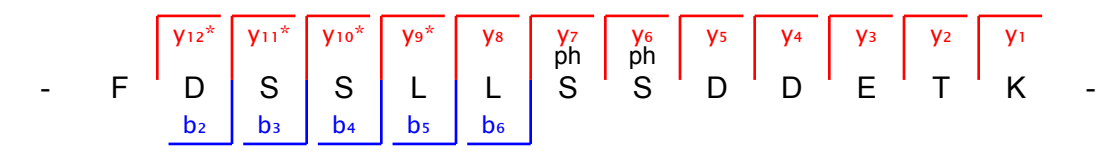
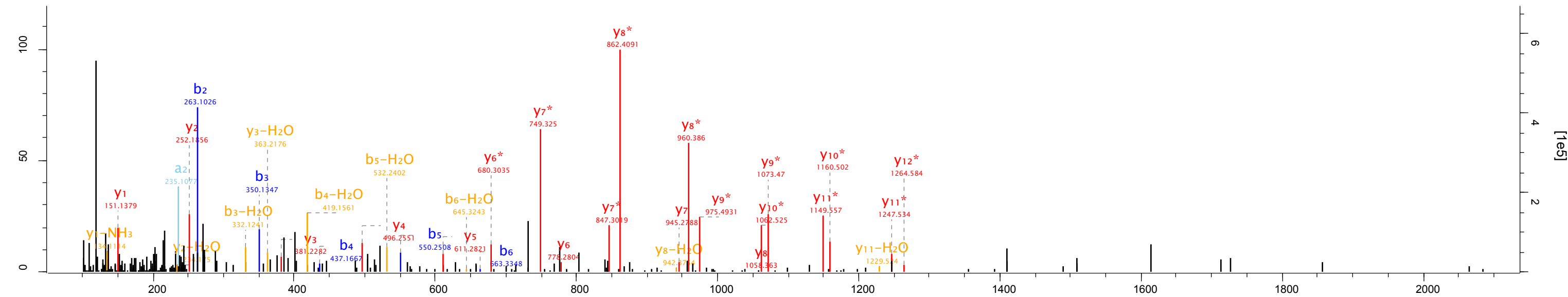


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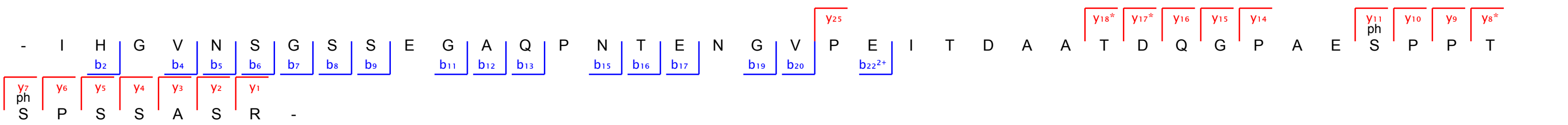
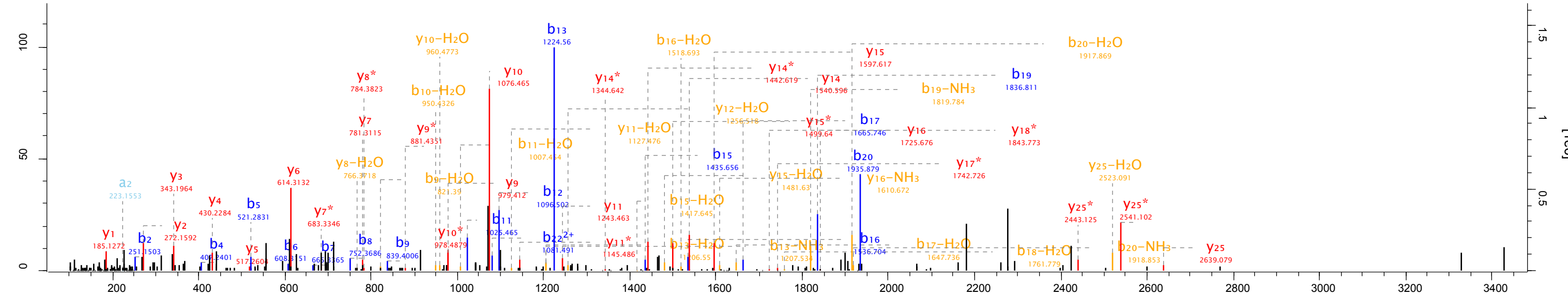
Fragmentation sites (b-ions in blue, y-ions in red):

- b₂ (L-E)
- b₃ (L-E-S)
- b₆ (A-R)
- b₈* (S-E)
- b₉ (S-E-S)
- b₁₂ (S-E-E)
- b₁₃ (S-E-E-F)
- b₁₄ (S-E-E-F-L)
- b₁₅* (S-E-E-F-L-E)
- y₁ (R)
- y₂ (R-E)
- y₃ (R-E-E)
- y₄ (R-E-E-P)
- y₅ (R-E-E-P-E)
- y₆ (R-E-E-P-E-E)
- y₇ (R-E-E-P-E-E-E)
- y₈ (R-E-E-P-E-E-E-F)
- y₉ (R-E-E-P-E-E-E-F-L)
- y₁₀ (R-E-E-P-E-E-E-F-L-E)
- y₂₀* (R-E-E-P-E-E-E-F-L-E-E)
- y₂₀* (R-E-E-P-E-E-E-F-L-E-E-Q)

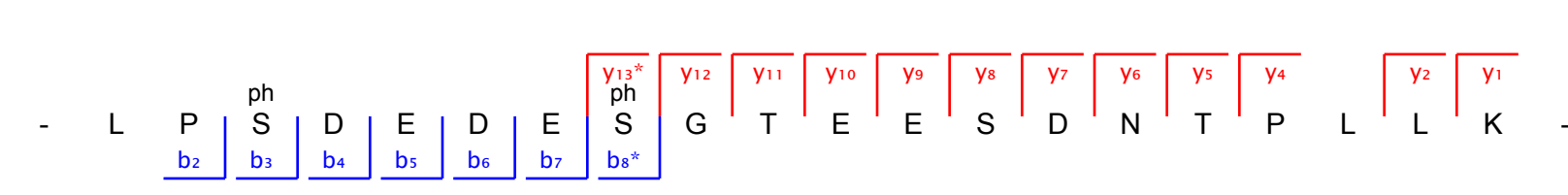
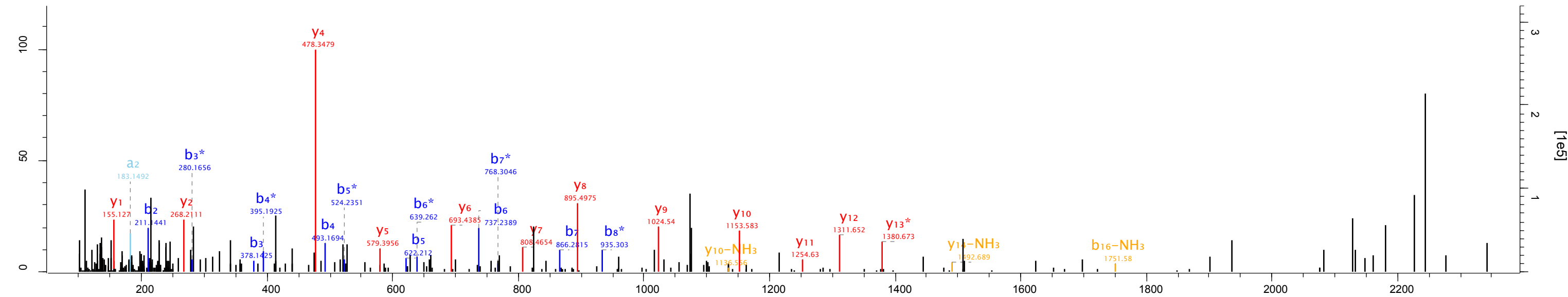
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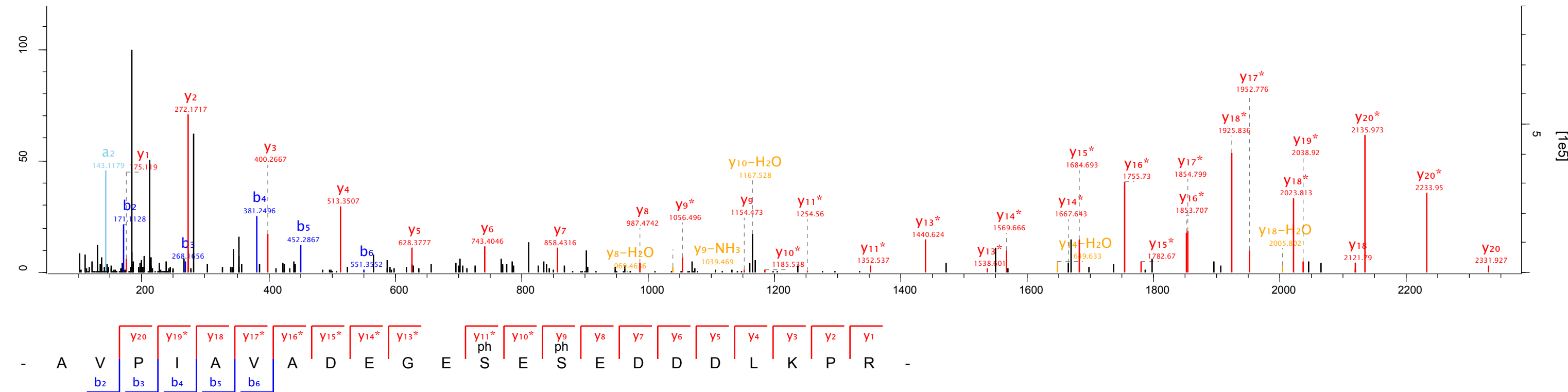
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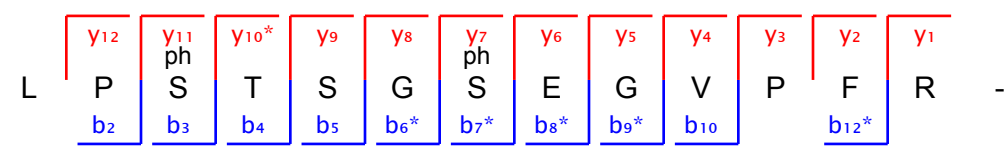
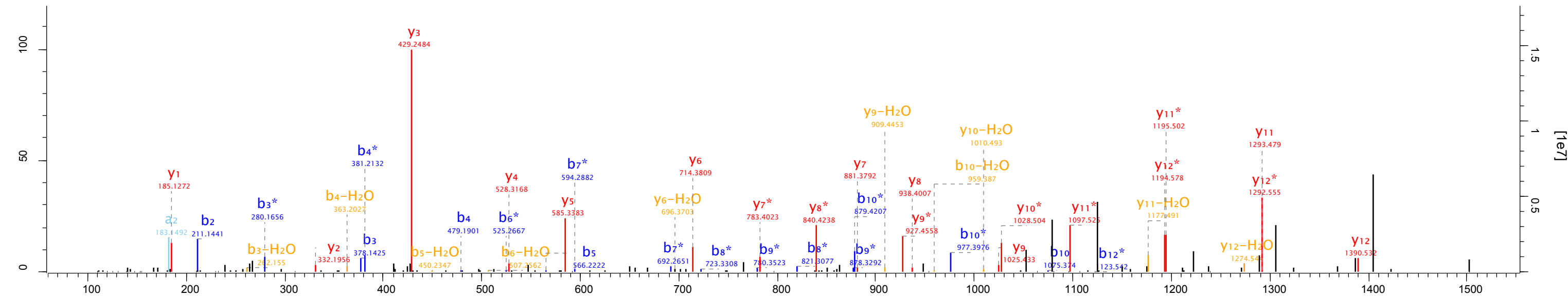
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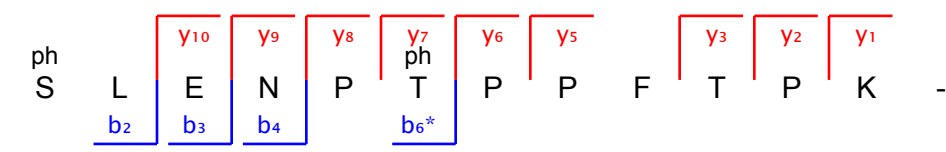
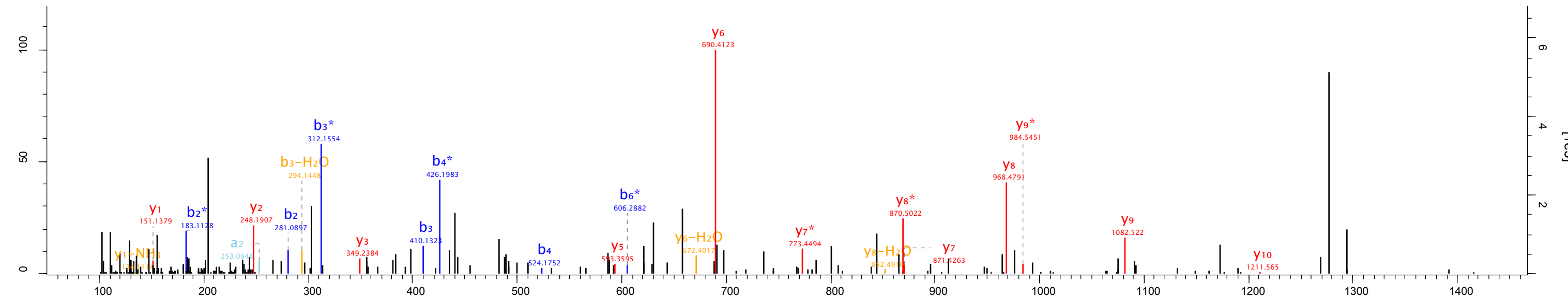
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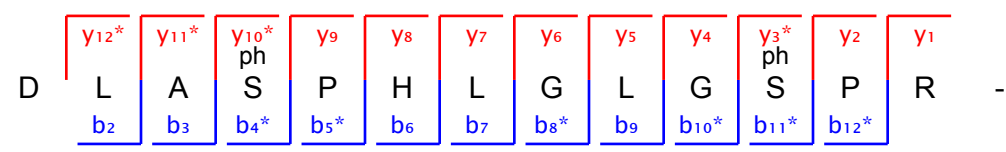
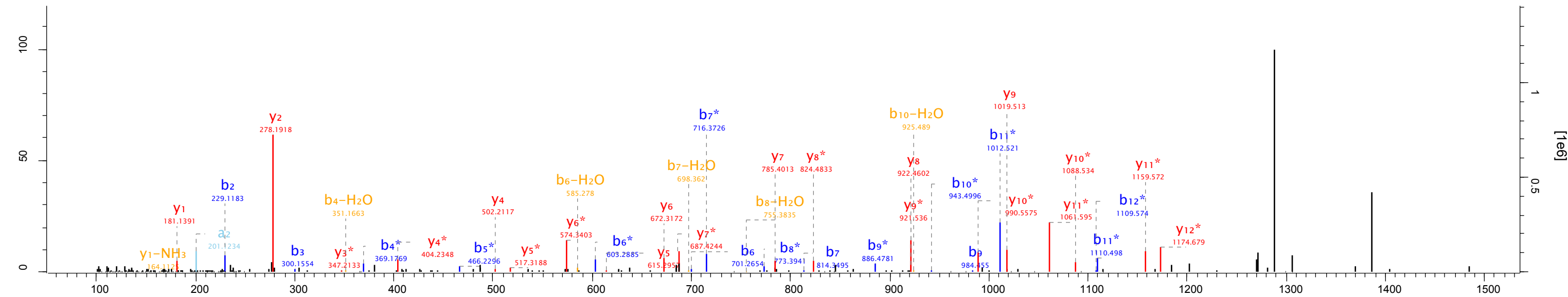
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20171215_MaS_33SR_LMH_phospho2_03

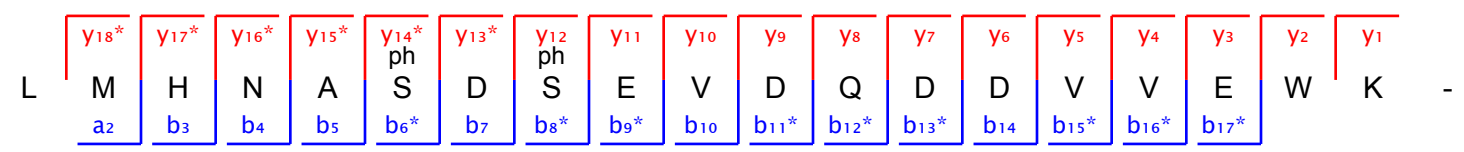
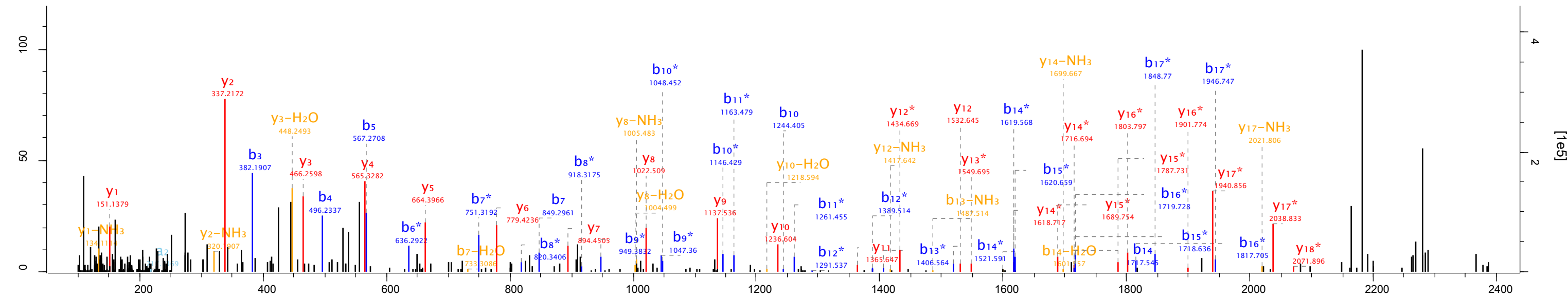
Scan	Method	Score	m/z	Gene names
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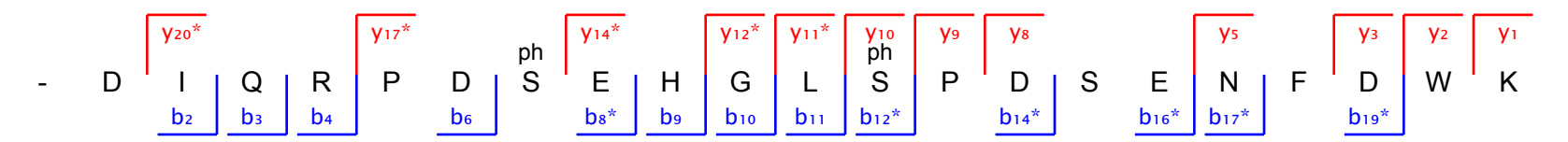
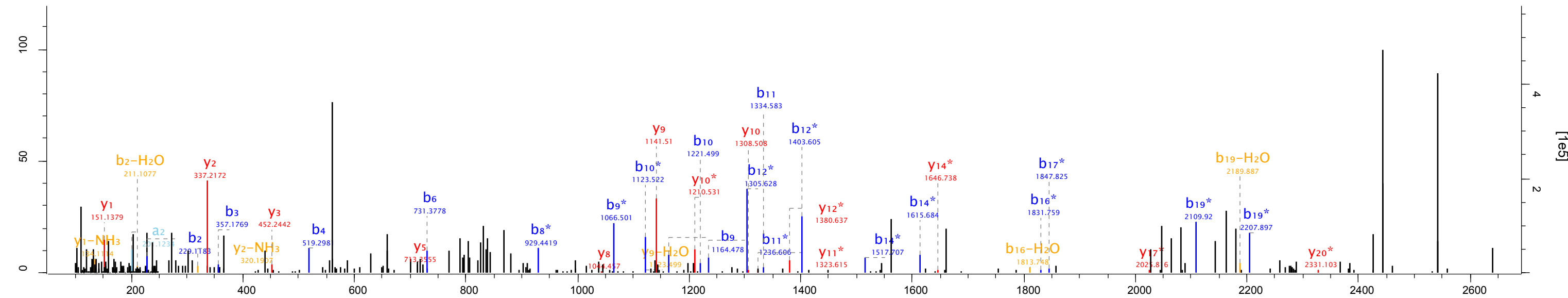
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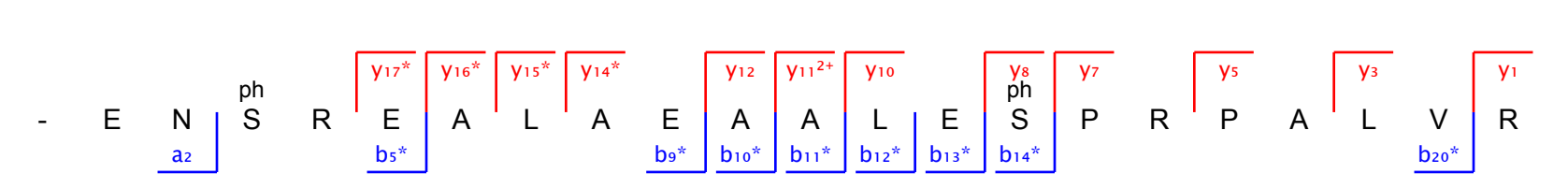
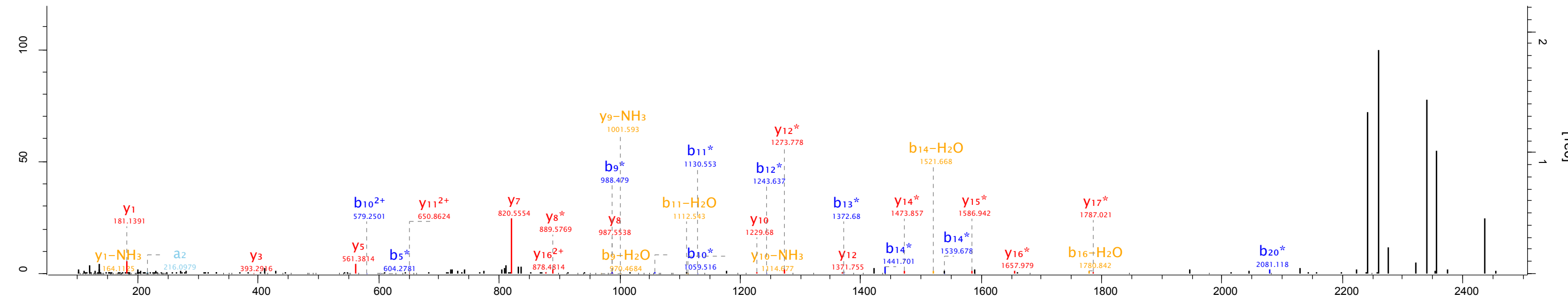
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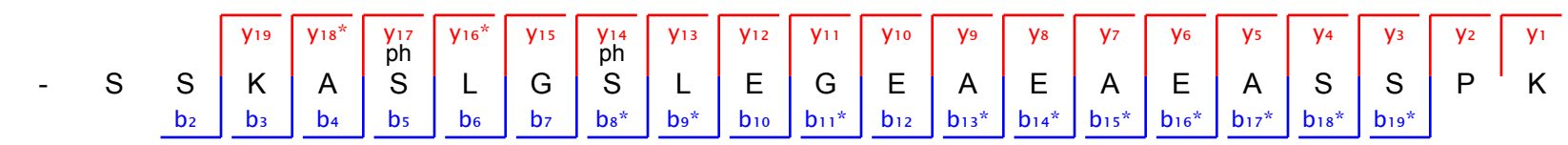
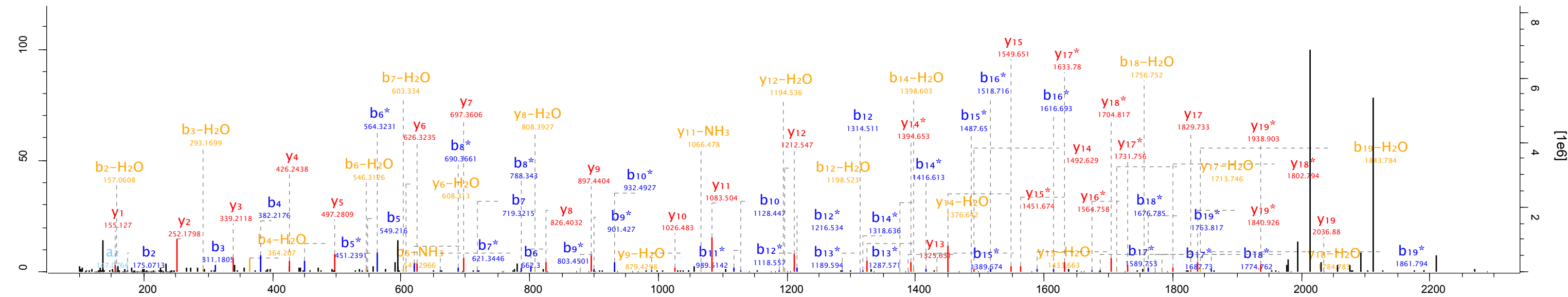
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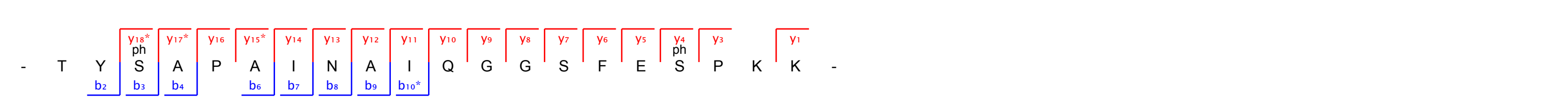
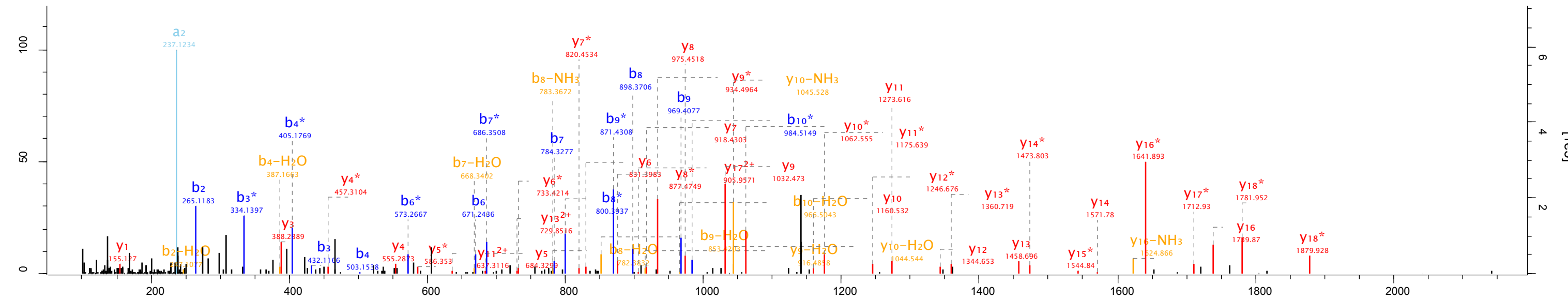
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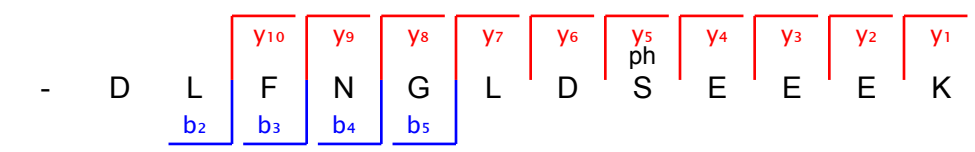
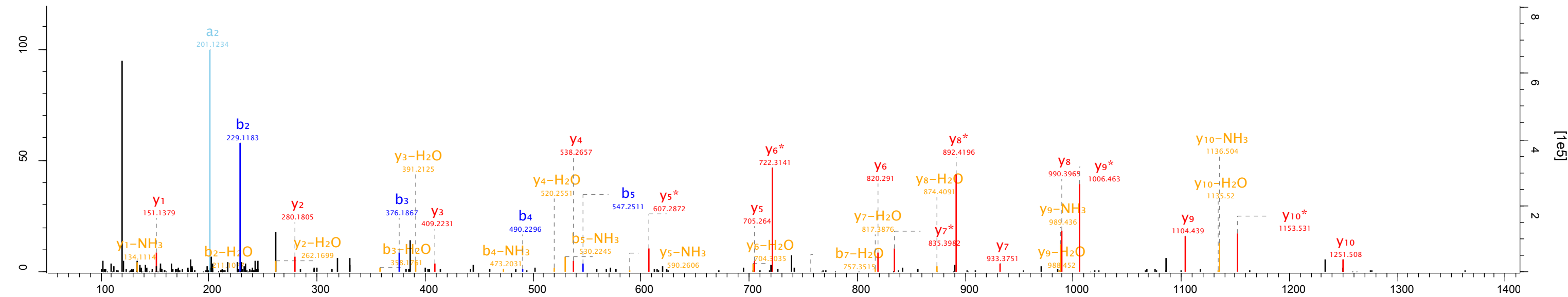
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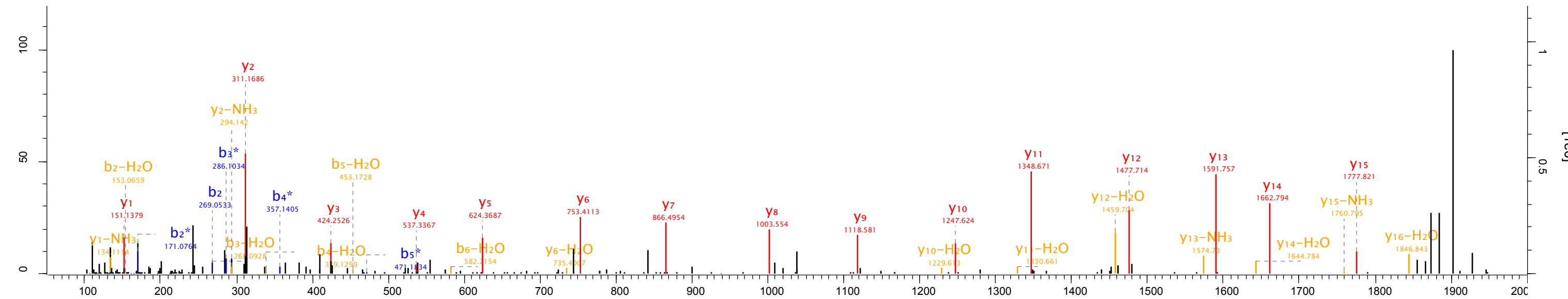
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15424 Method FTMS; HCD Score 166.52 m/z 740.31 Gene names LYSMD1



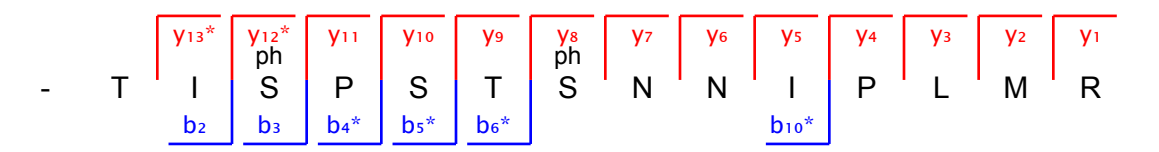
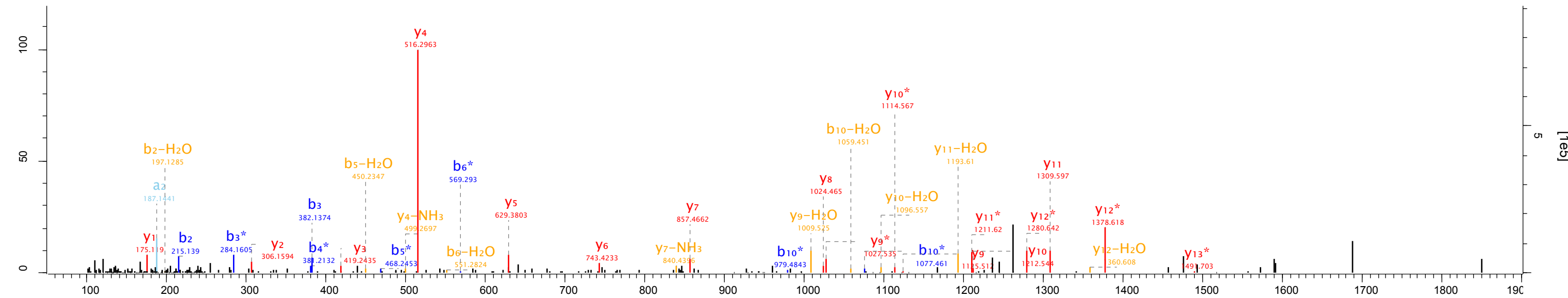
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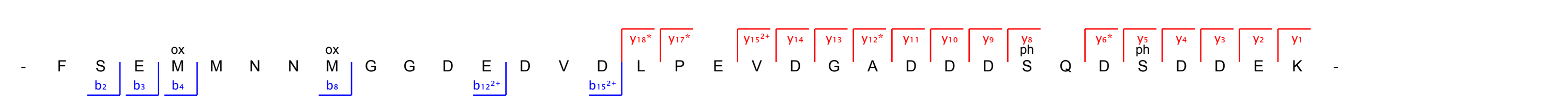
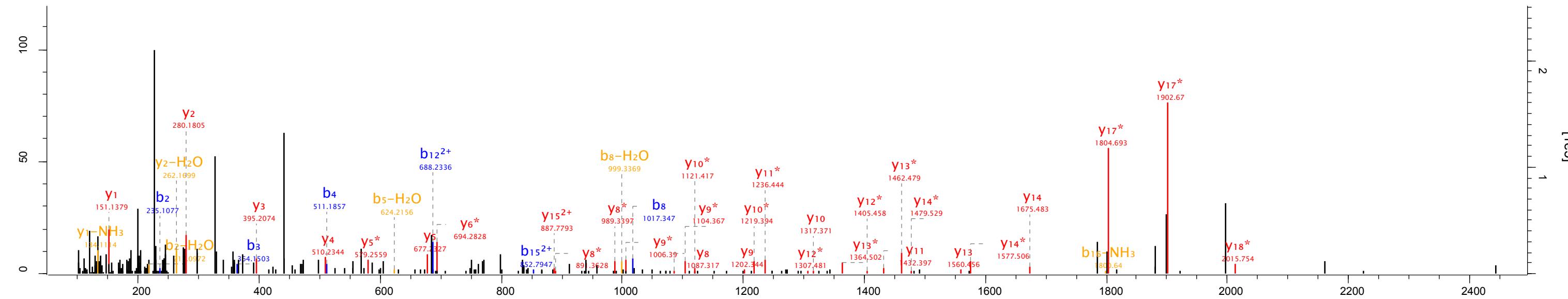
ph T S D A N E T E D H L E S L I C K -

Fragmentation mapping: b2 (S), b3* (D), b4* (A), b5* (N). y-ions (y1 to y16) are mapped to the corresponding amino acids in the sequence above.

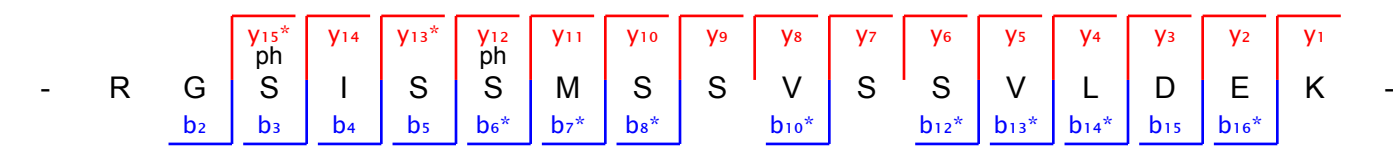
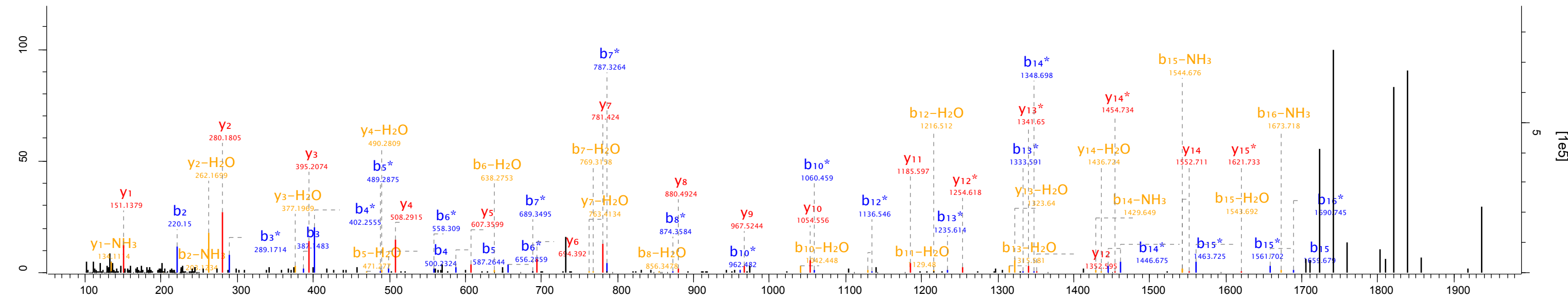
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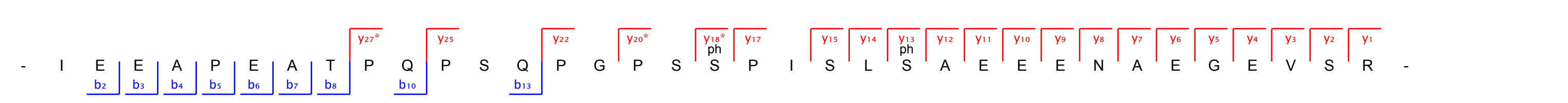
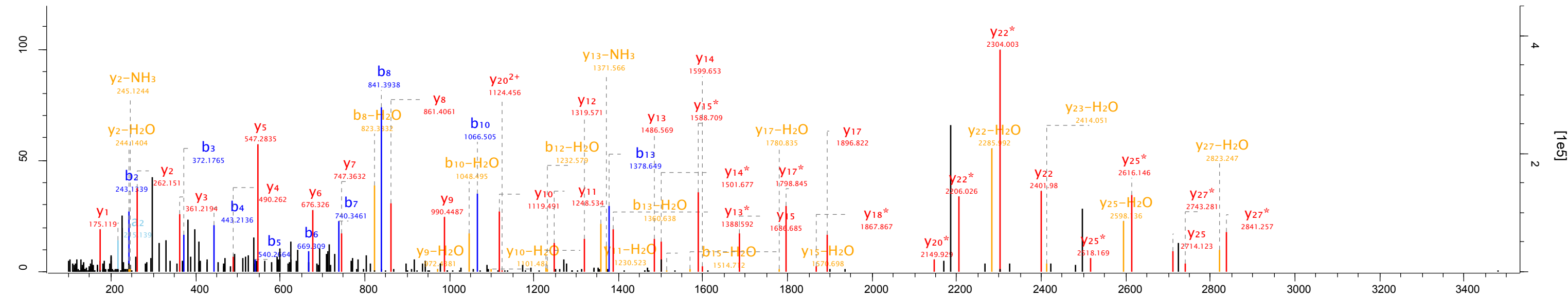
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15984 Method FTMS; HCD Score 53.55 m/z 1273.44 Gene names PTGES3



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 16174 Method: FTMS; HCD Score: 205.24 m/z: 970.43 Gene names: ZFYVE20

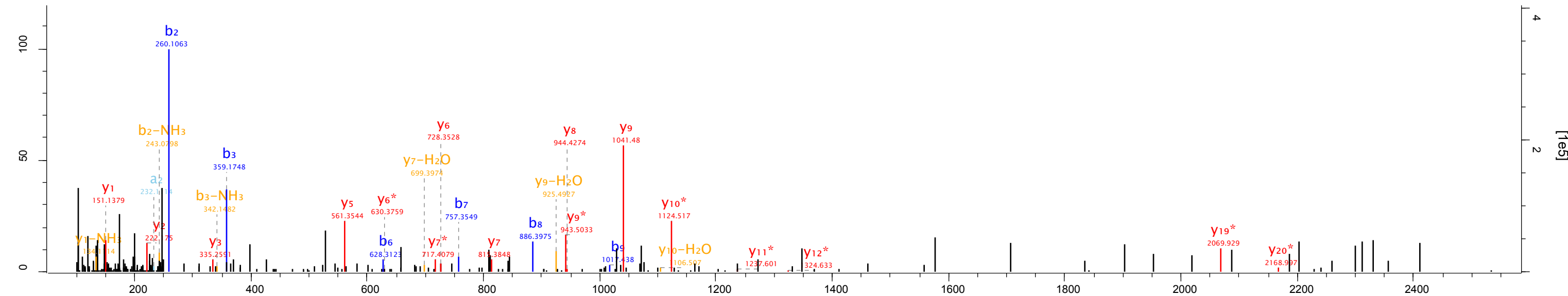


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20171215_MaS_33SR_LMH_phospho2_03

16544 FTMS; HCD 49.52 843.37 BRSK1

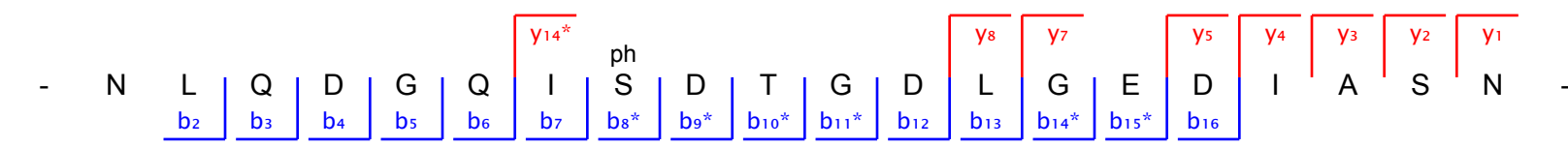
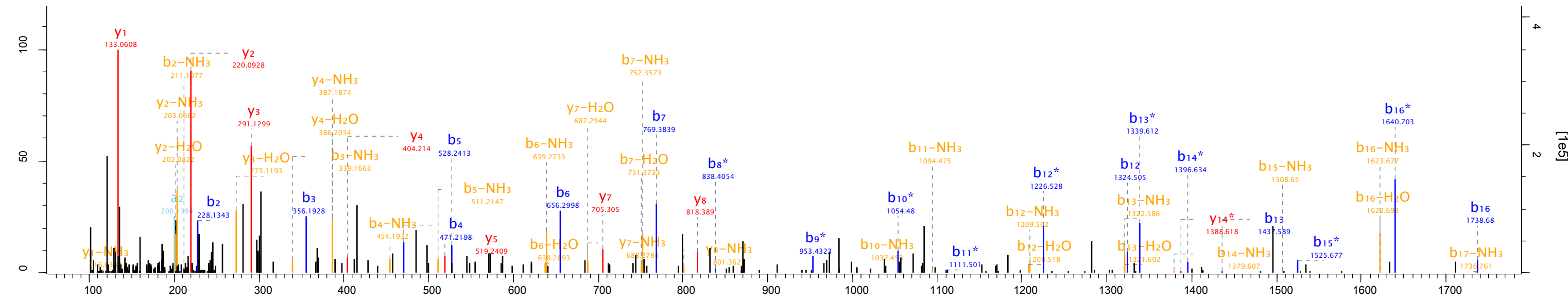


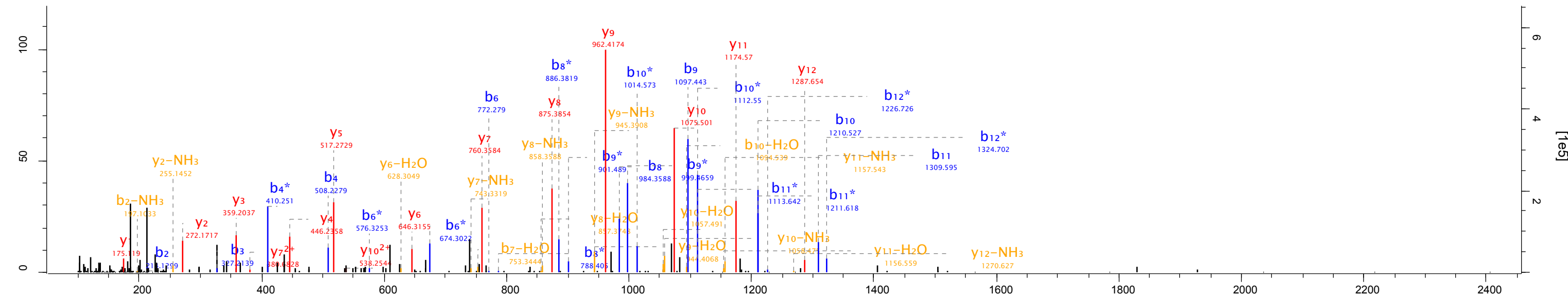
- M Q V P T A E E M S S L T P E S S P E L A K -

Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets (b-ions): M-Q, Q-V, V-P, T-A, A-E, E-E, E-M, M-S.
- Red brackets (y-ions): V-P, P-T, T-S, S-L, L-T, T-P, P-E, E-S, S-S, S-P, P-E, E-L, L-A, A-K.

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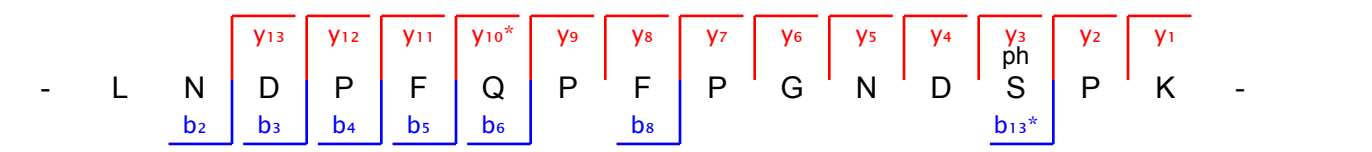
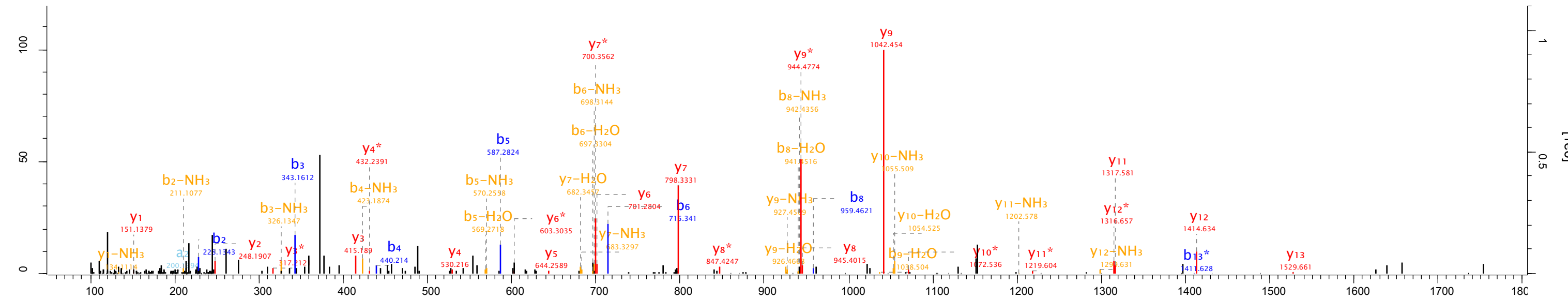
- G R L T P S P D I I V L S D N E A S S P R -

ph ph

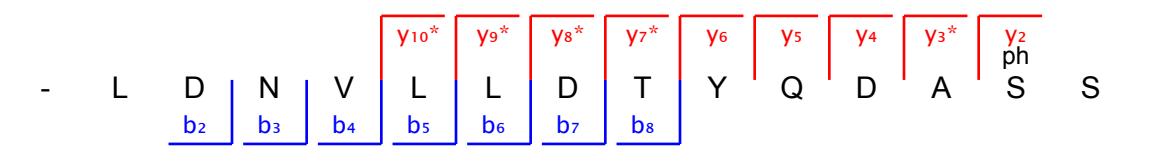
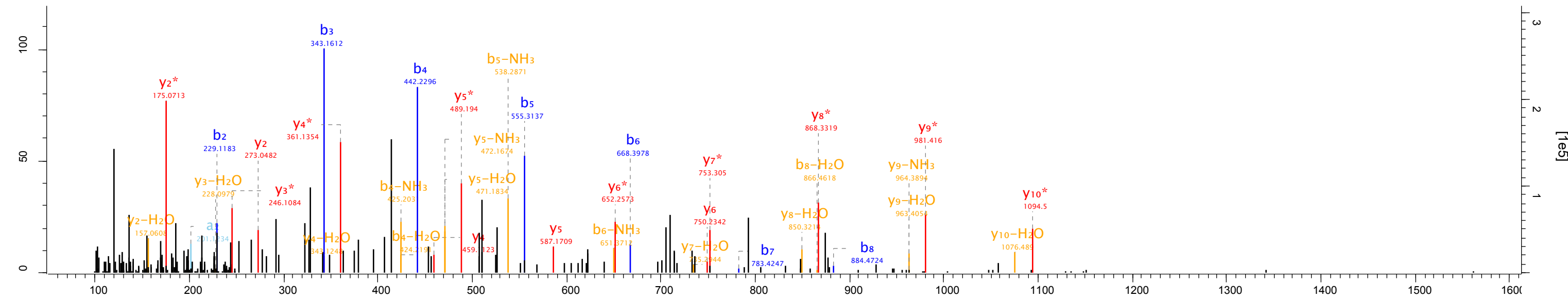
b₂ b₃ b₄ b₆ b₈ b₉ b₁₀ b₁₁ b₁₂*

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

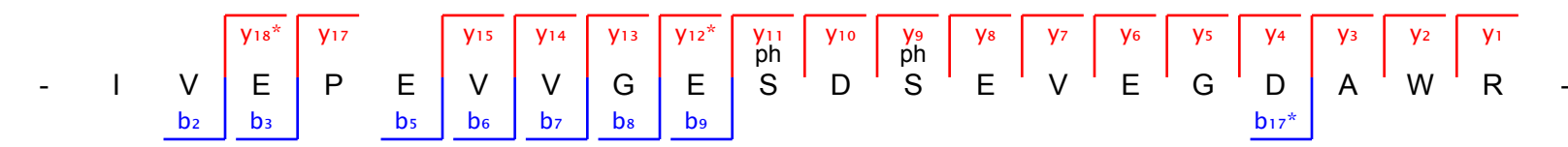
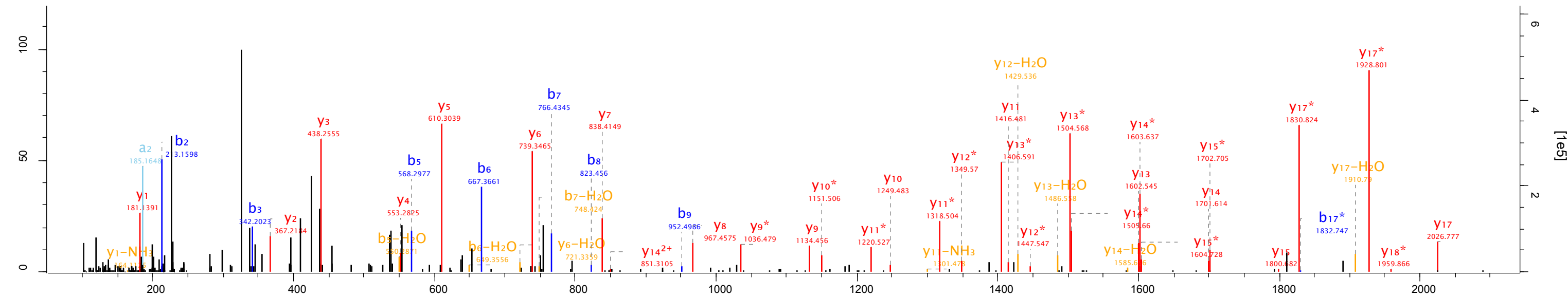
20171215_MaS_33SR_LMH_phospho2_03 17184 FTMS; HCD 177.48 878.9 EPS15



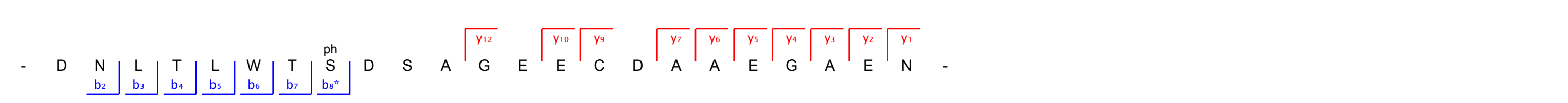
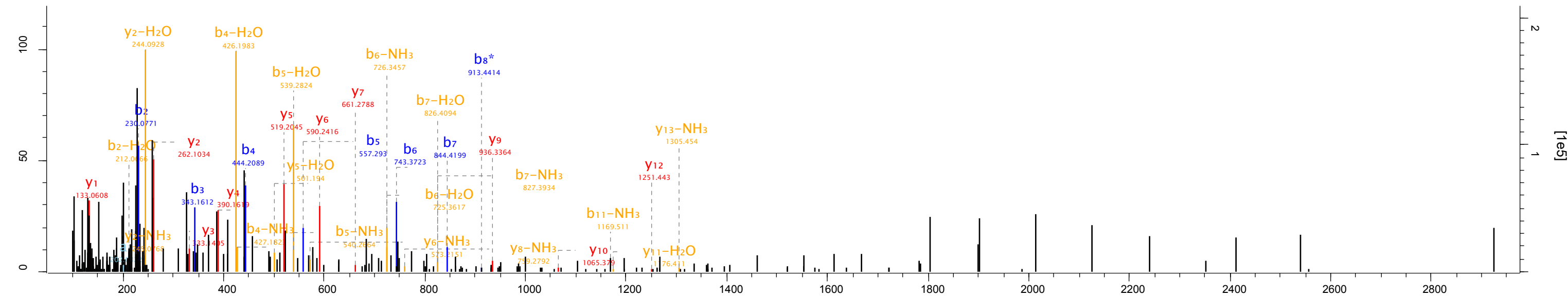
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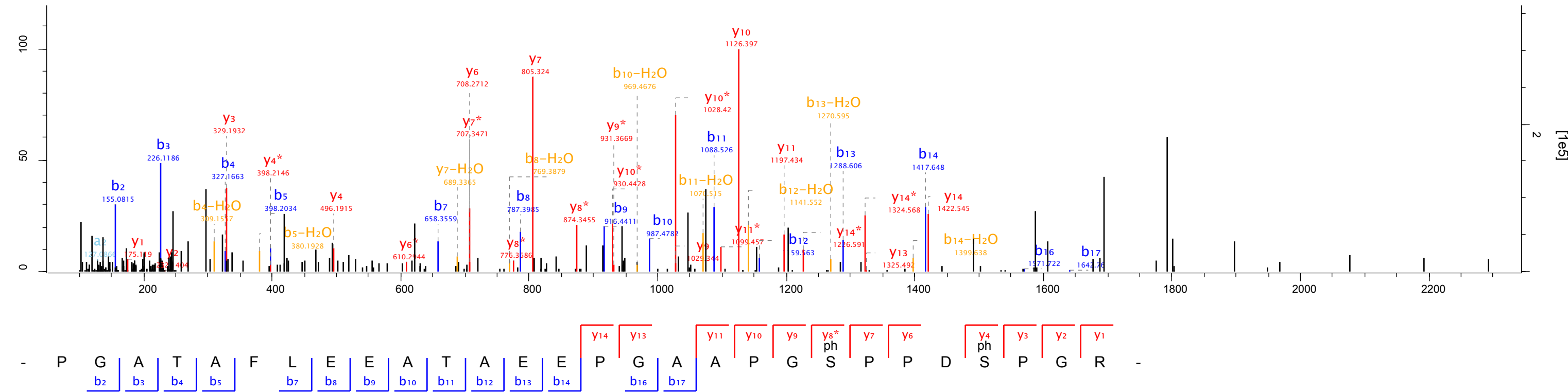


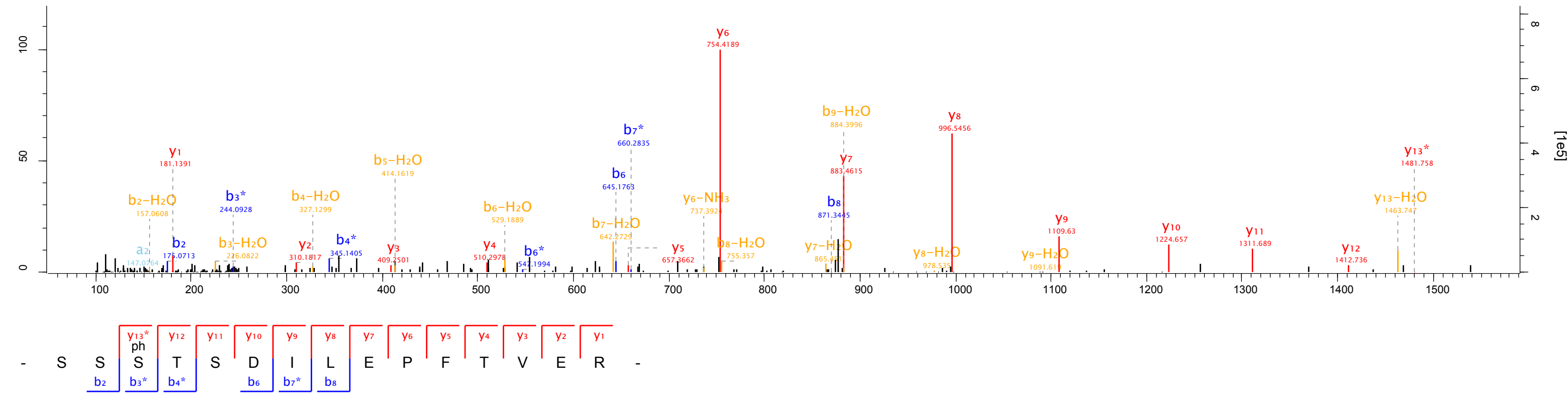
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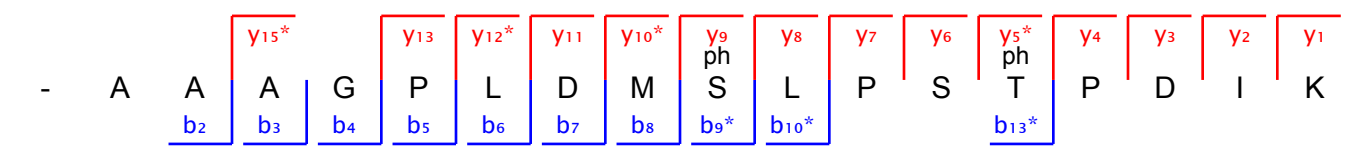
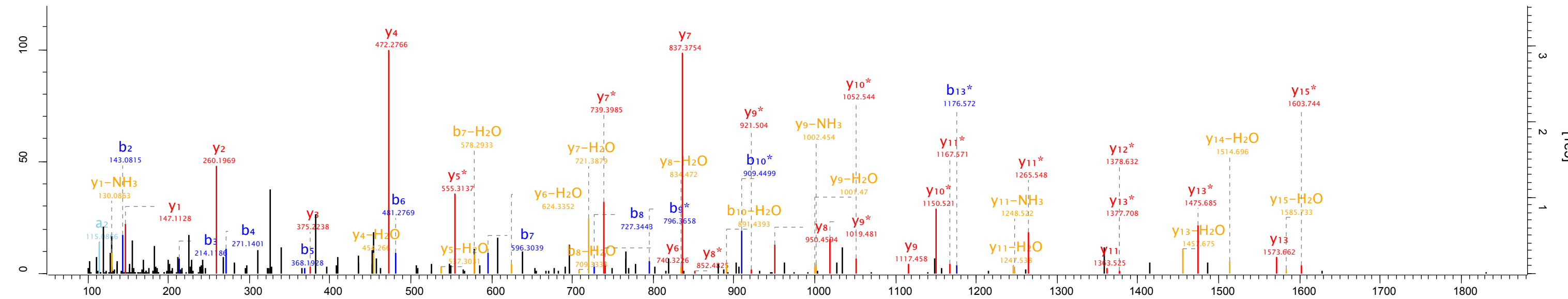
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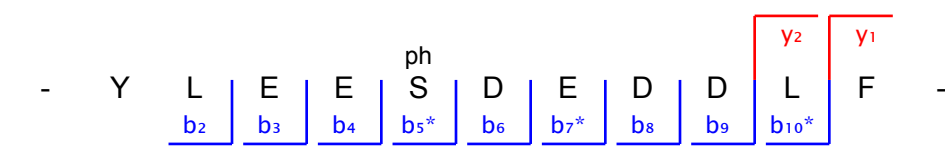
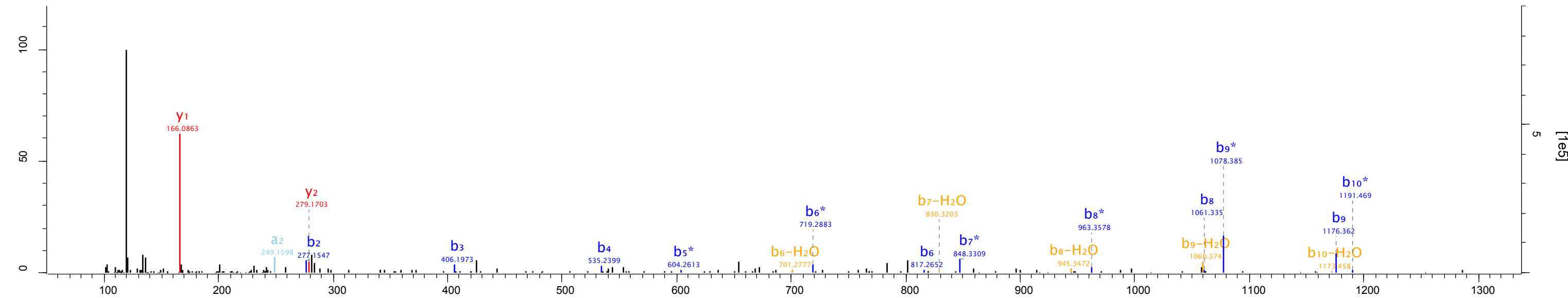




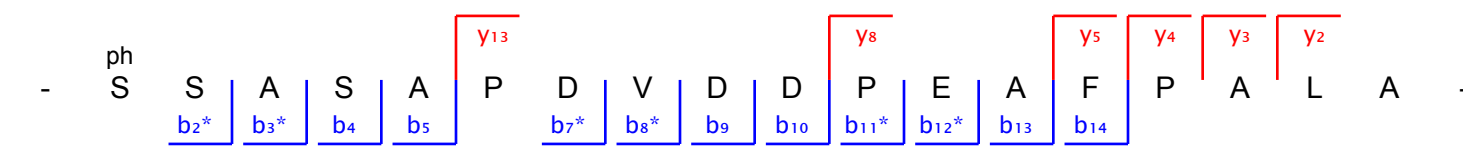
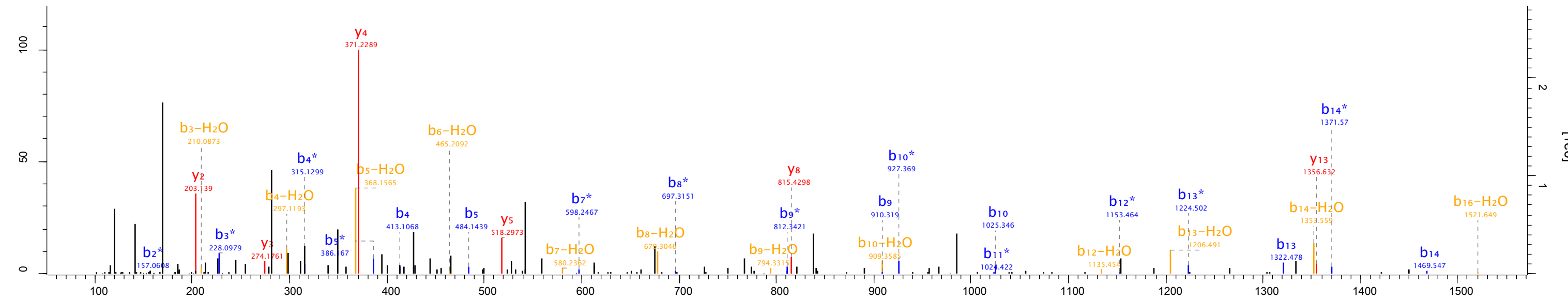
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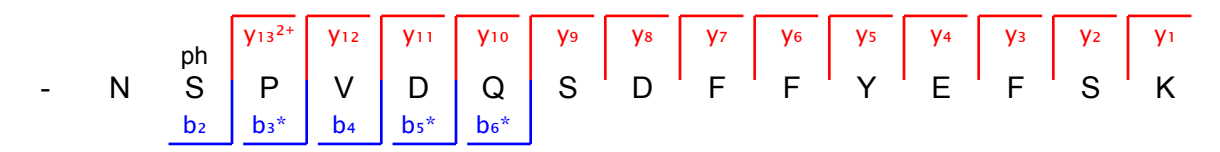
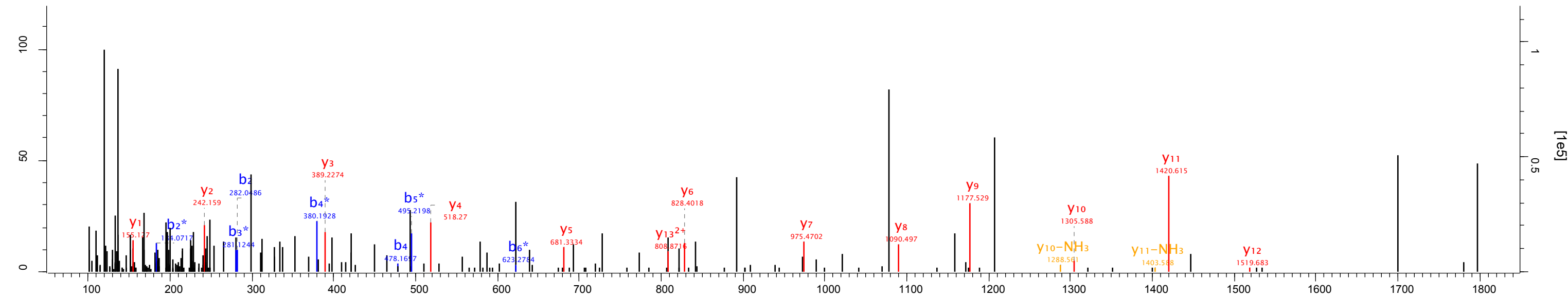
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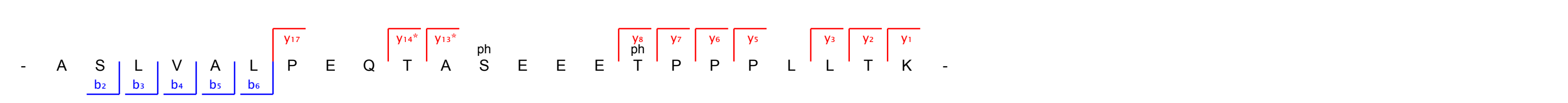
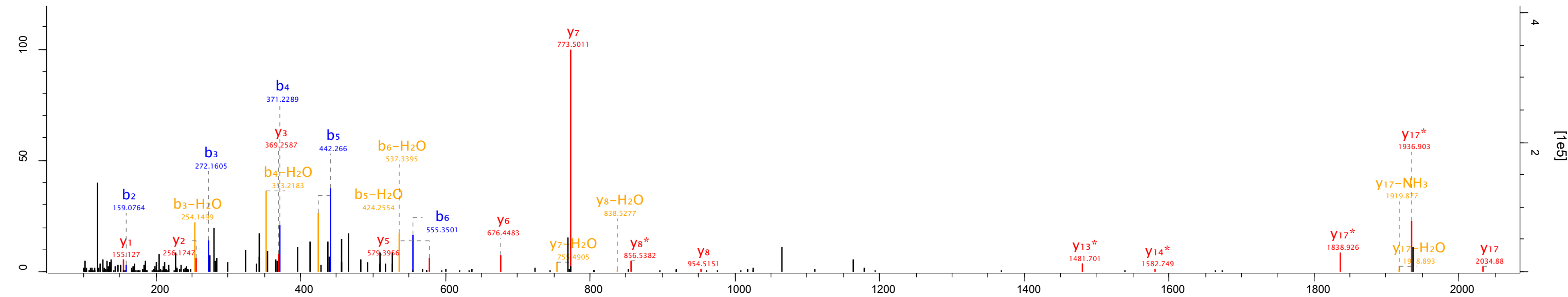
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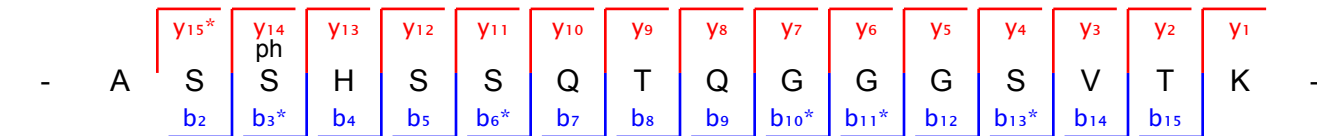
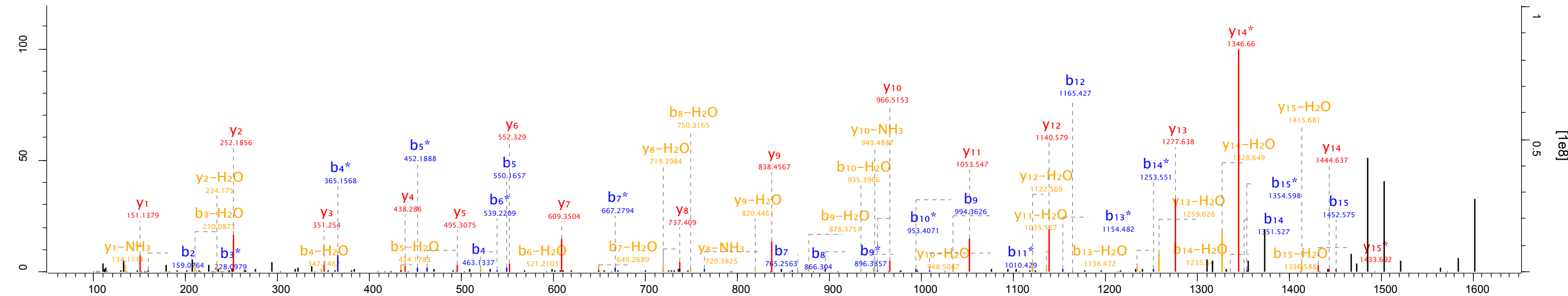


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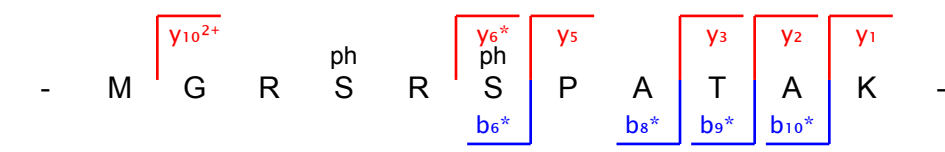
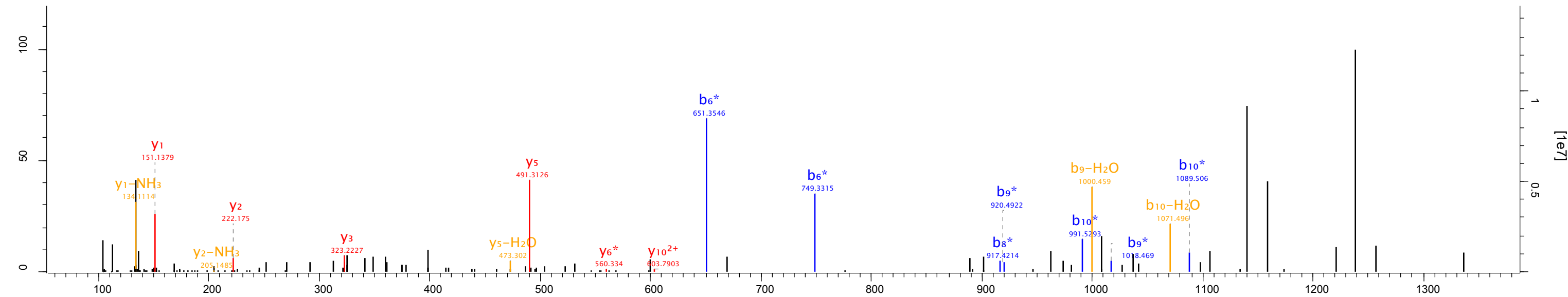


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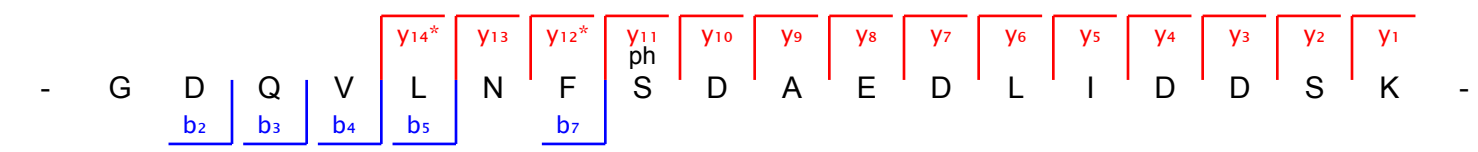
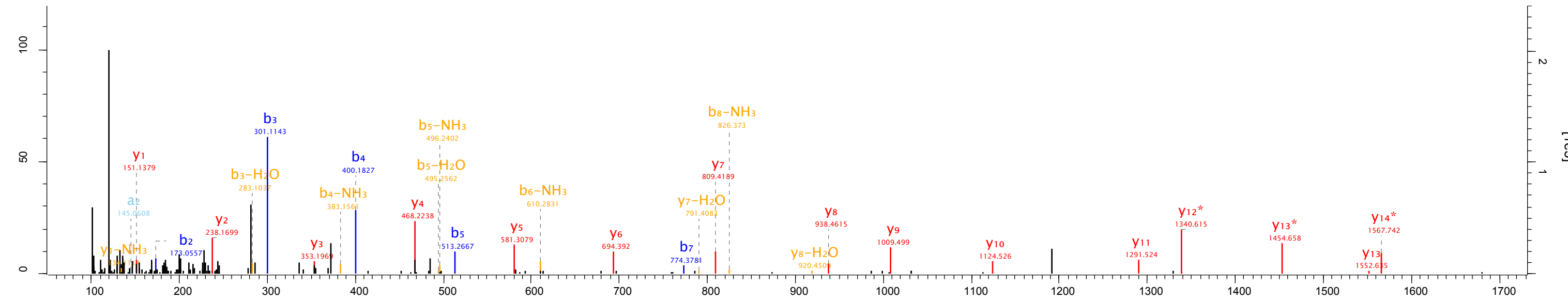




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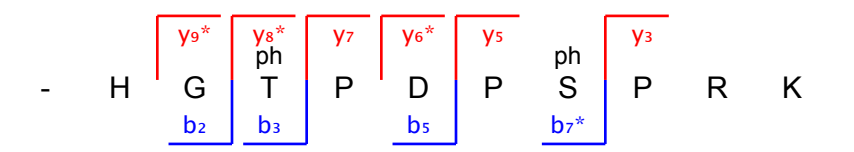
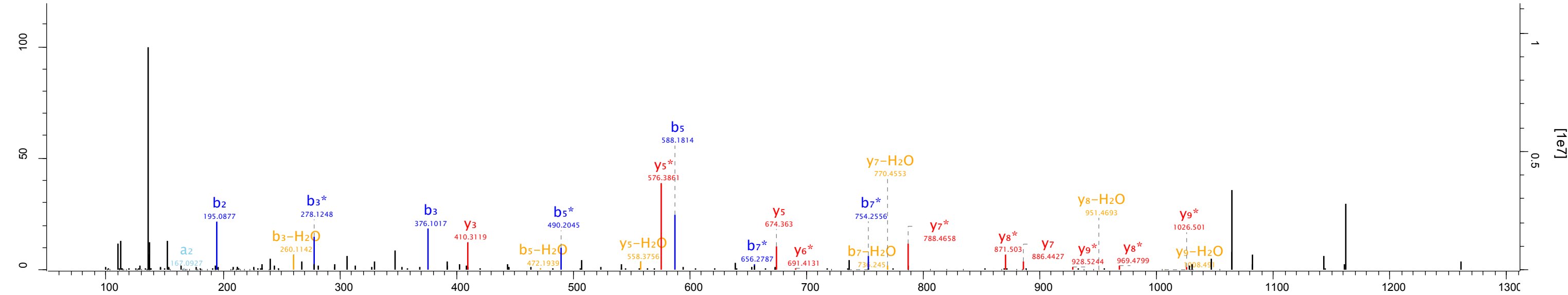


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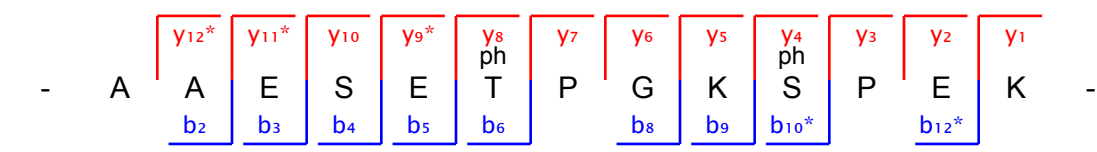
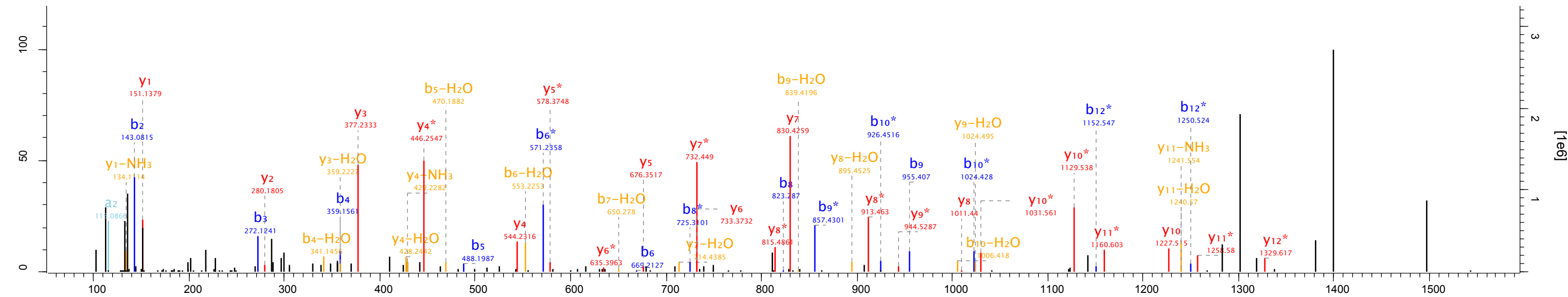


Raw file Scan Method Score m/z Gene names

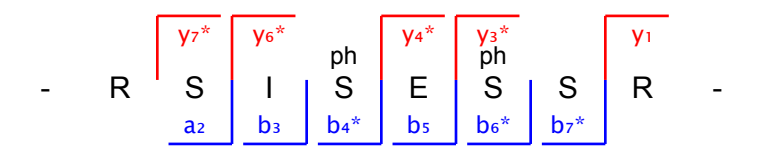
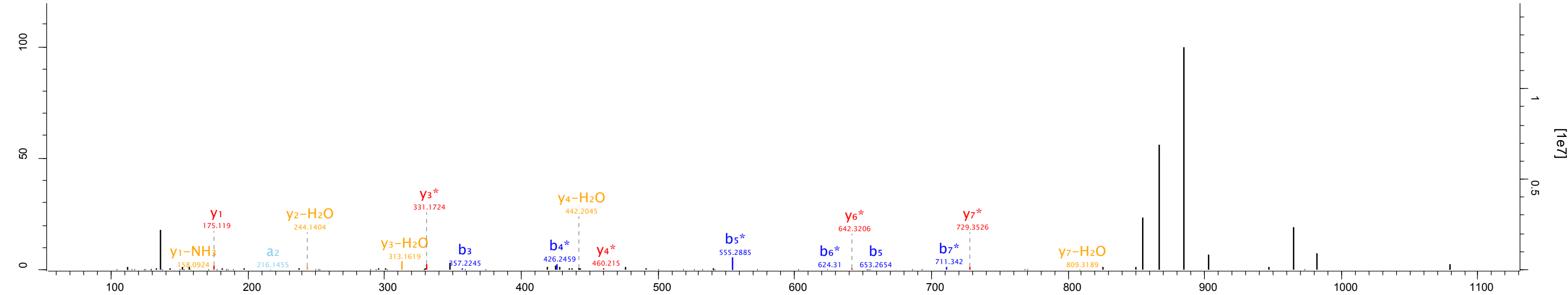
20171215_MaS_33SR_LMH_phospho2_03 2254 FTMS; HCD 94.09 631.27 BUD13



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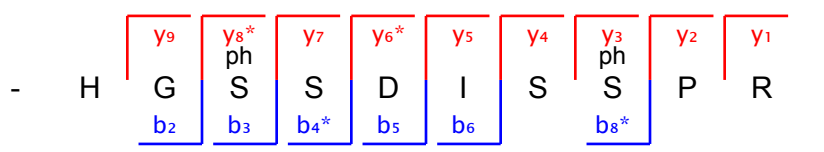
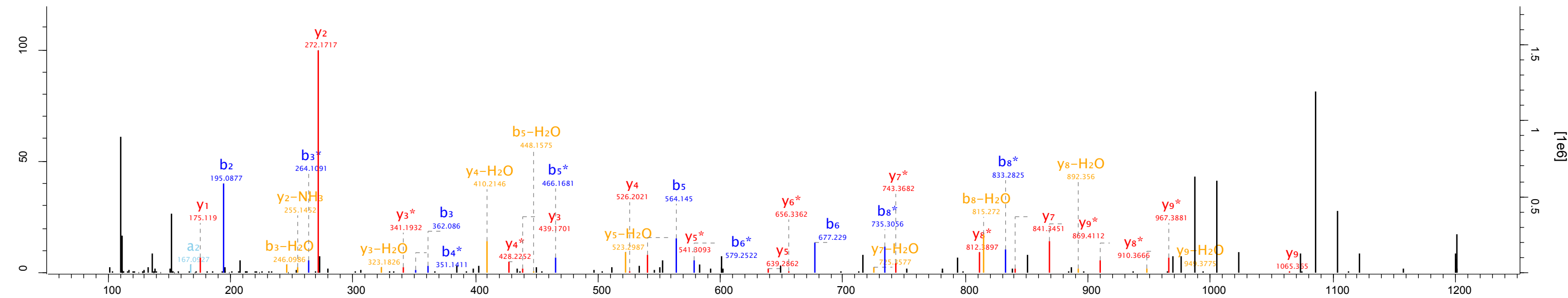


20171215_MaS_33SR_LMH_phospho2_03 2324 FTMS; HCD 54.01 541.21 PNN



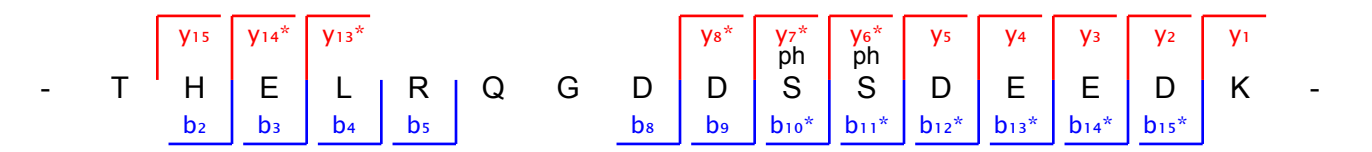
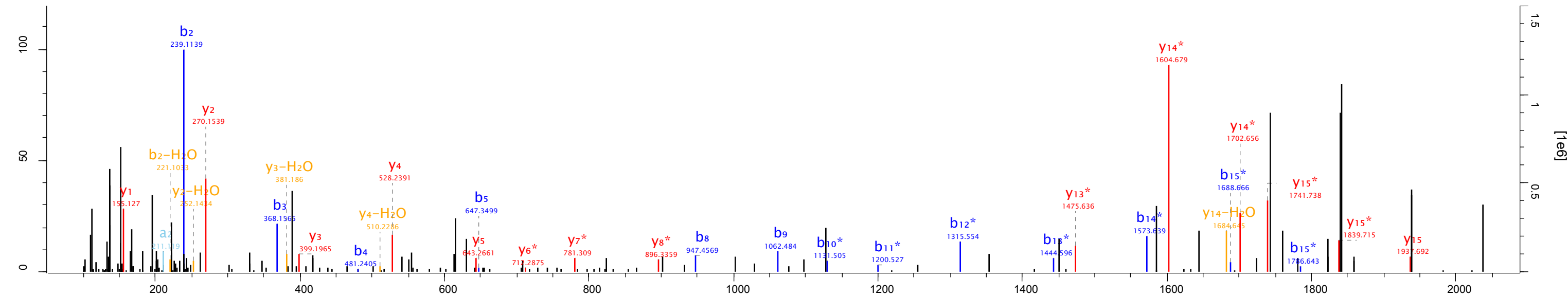
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20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
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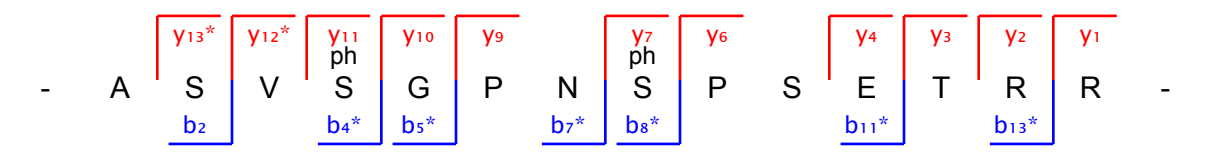
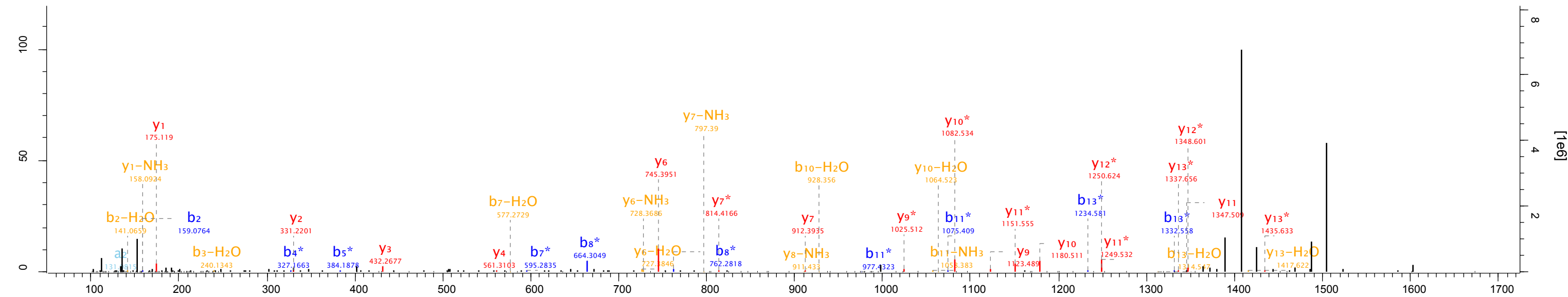


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20171215_MaS_33SR_LMH_phospho2_03

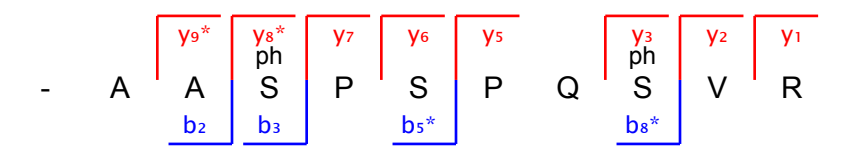
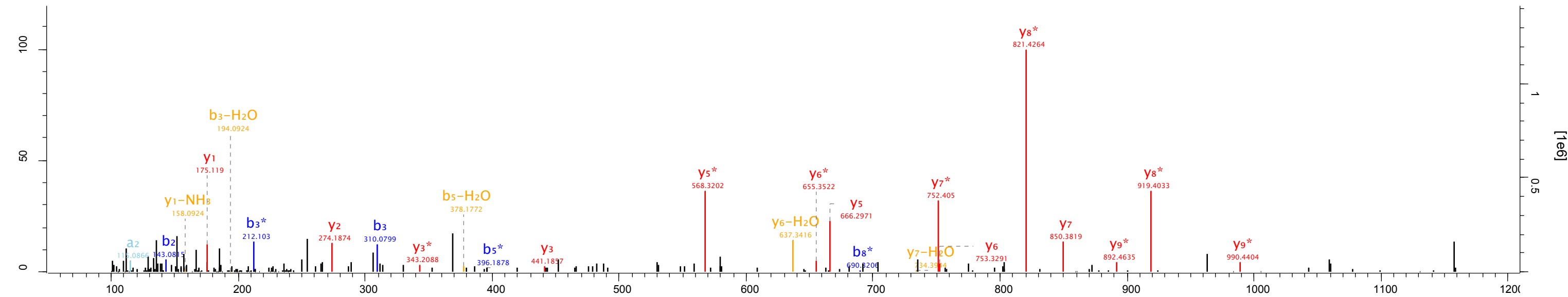
Scan 2774 Method FTMS; HCD Score 103.58 m/z 680.58 Gene names STX4

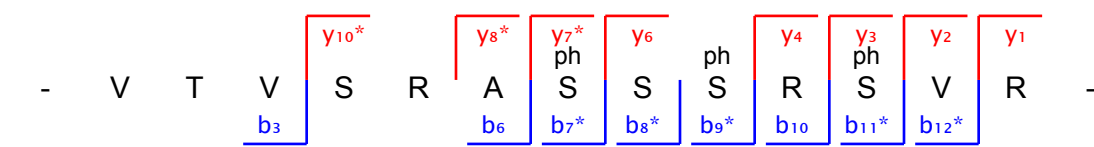
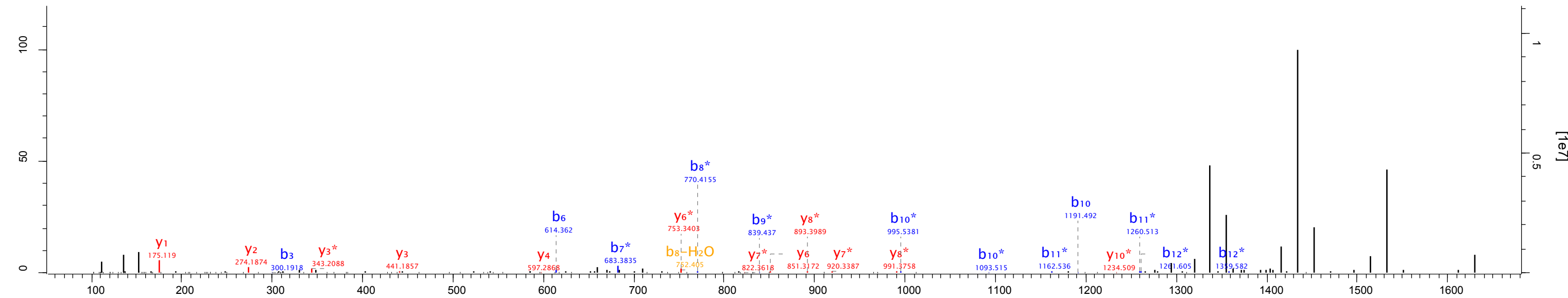


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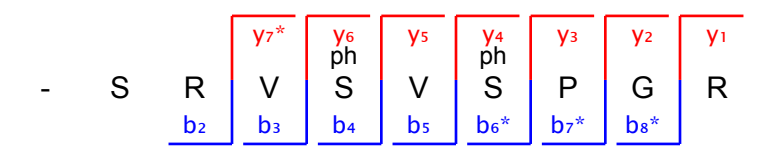
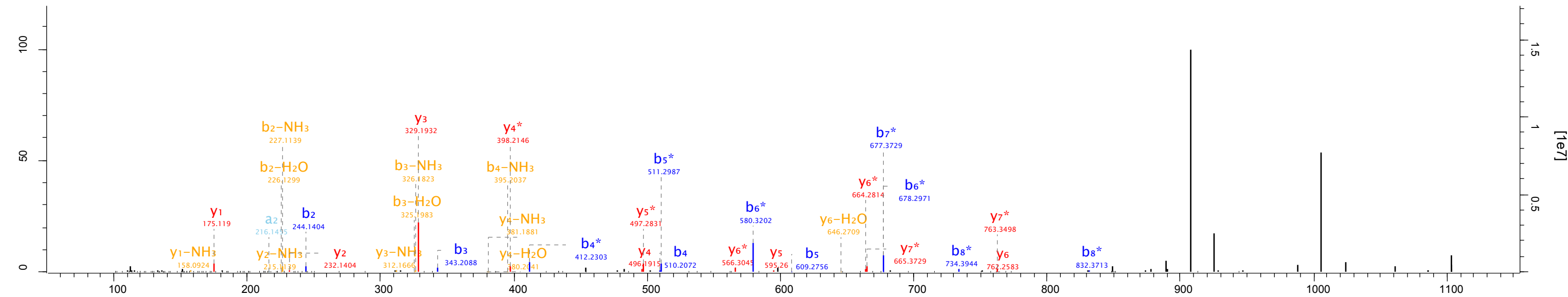


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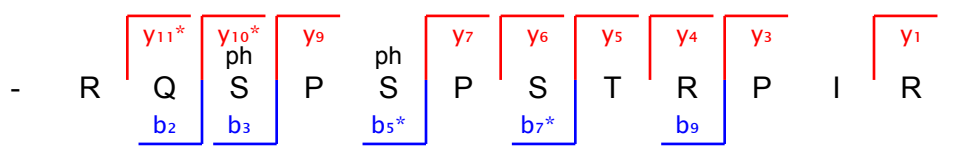
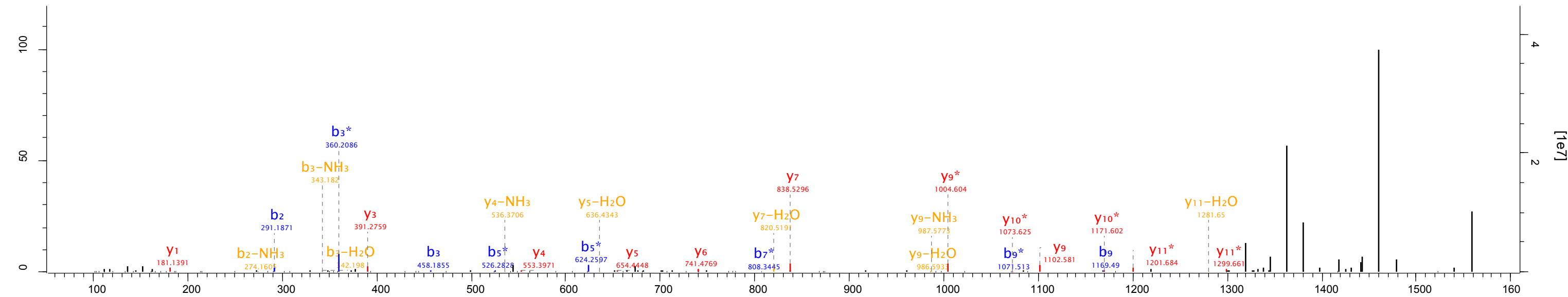


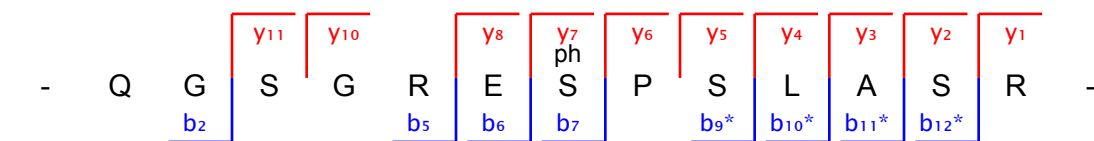
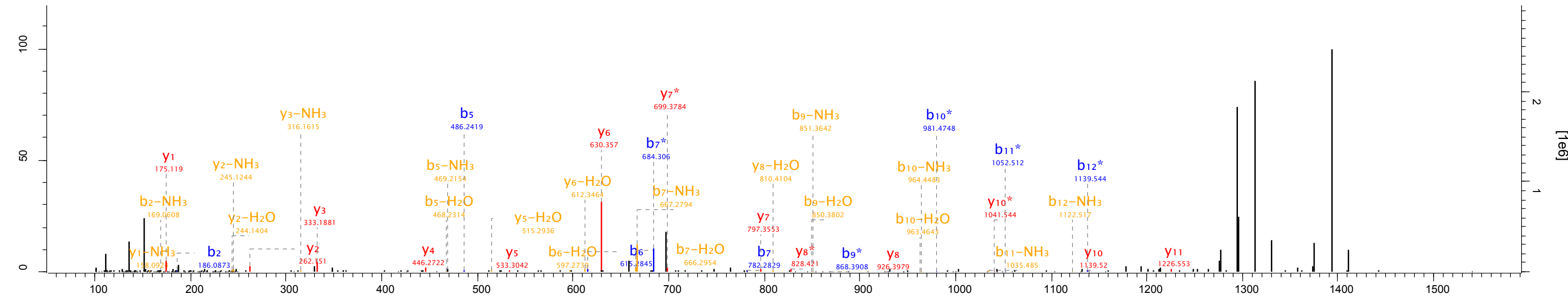


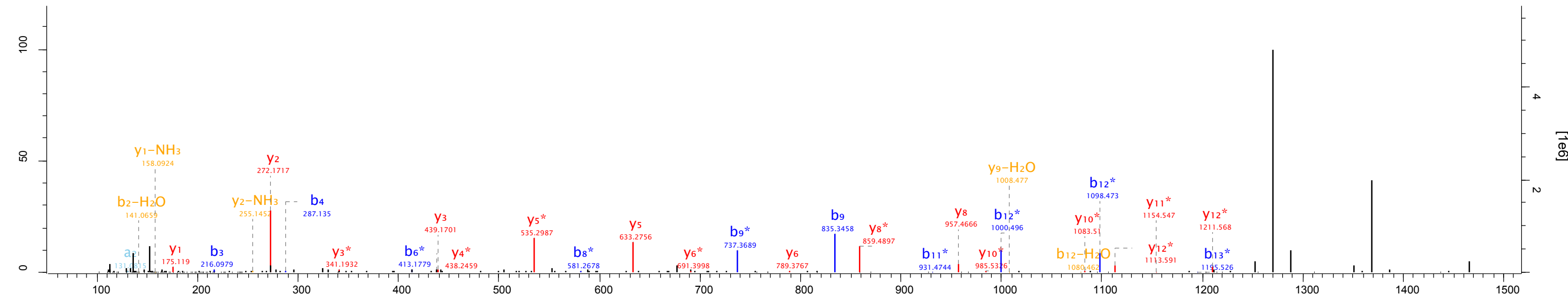
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 Scan: 3254 Method: FTMS; HCD Score: 123.81 m/z: 552.73 Gene names: SRRM1



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 Scan: 3414 Method: FTMS; HCD Score: 112.91 m/z: 780.38 Gene names: SRRM1

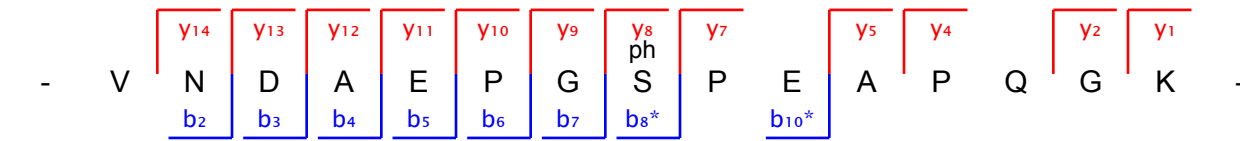
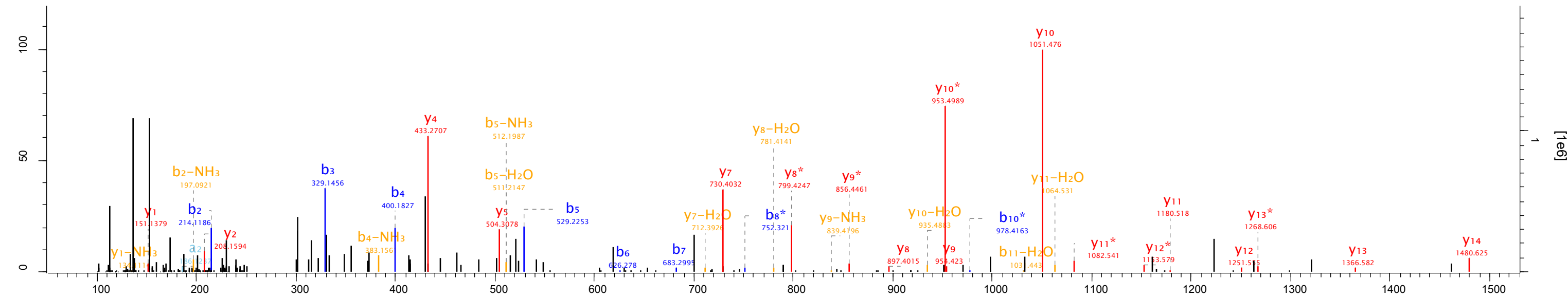


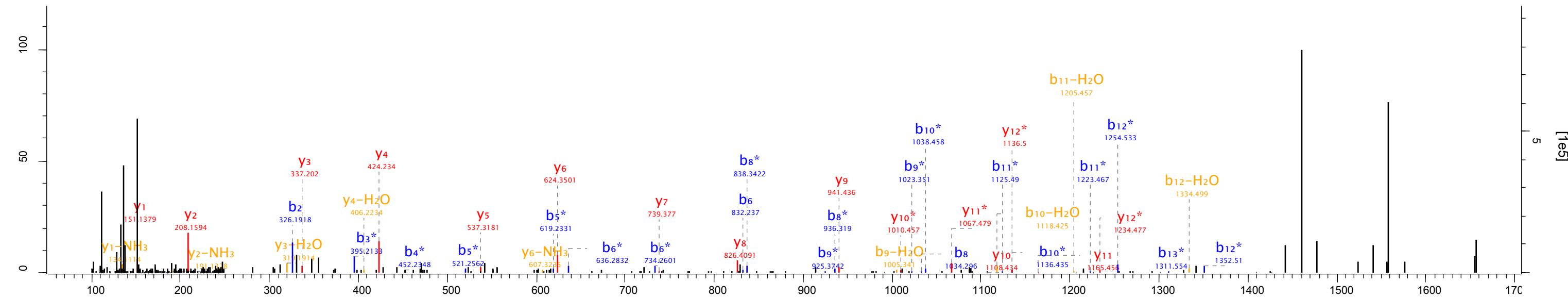




- S A G A G ph S P A R P P S P R -

a₂
b₃
b₄
b₆*
b₈*
b₉
b₁₁*
b₁₂*
b₁₃*
y₁₂*
y₁₁*
y₁₀*
y₈
y₆
y₅
y₄*
y₃ ph
y₂
y₁



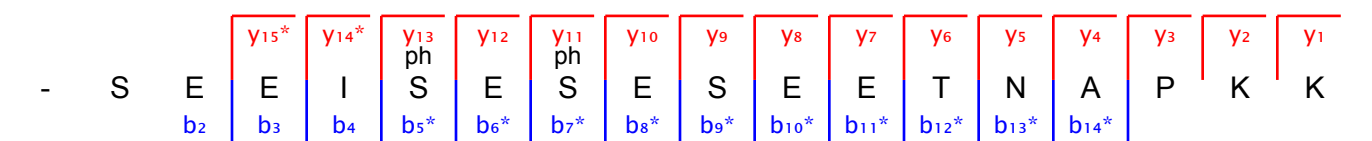
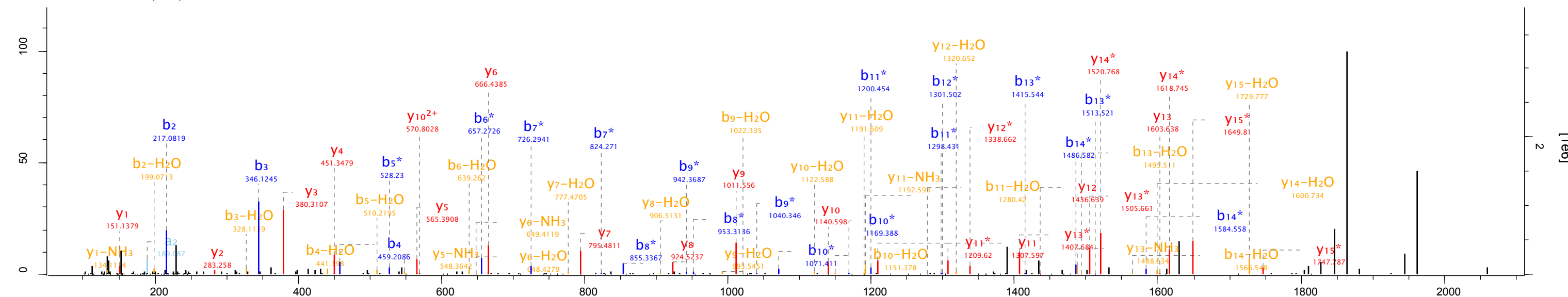


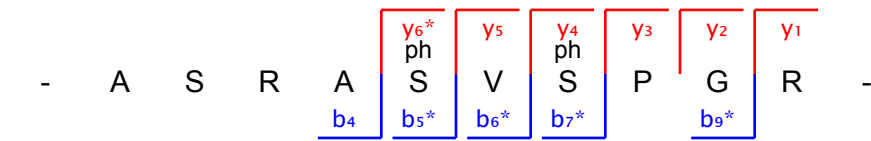
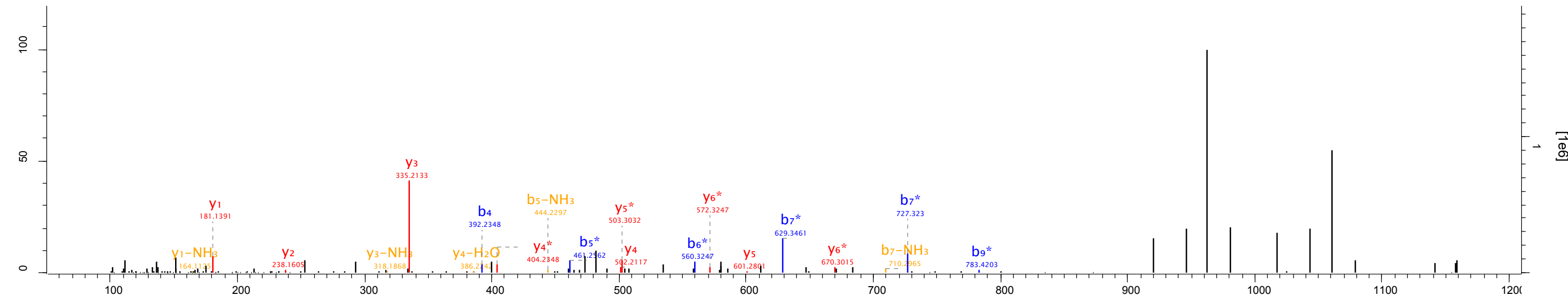
- R Y Y₁₂^{*}
ph
S Y₁₁
G Y₁₀
ph
S Y₉
D S Y₈
D Y₇
D Y₆
S Y₅
I Y₄
S Y₃
E Y₂
G Y₁
K -

b₂ b₃^{*} b₄^{*} b₅^{*} b₆
b₈ b₉^{*} b₁₀^{*} b₁₁^{*} b₁₂^{*} b₁₃^{*}

Raw file
20171215_MaS_33SR_LMH_phospho2_03

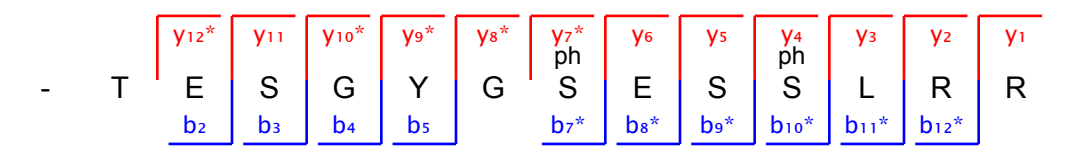
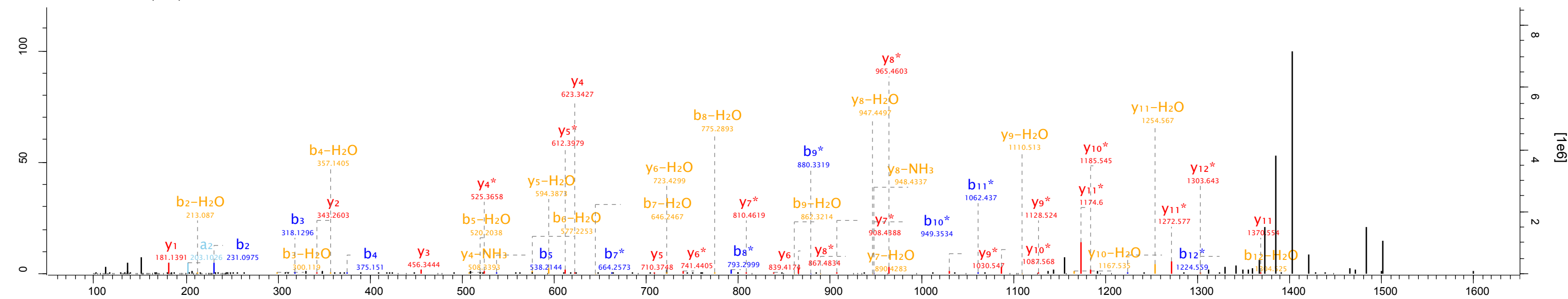
Scan 4084 Method FTMS; HCD Score 302.61 m/z 1031.92 Gene names ATN1





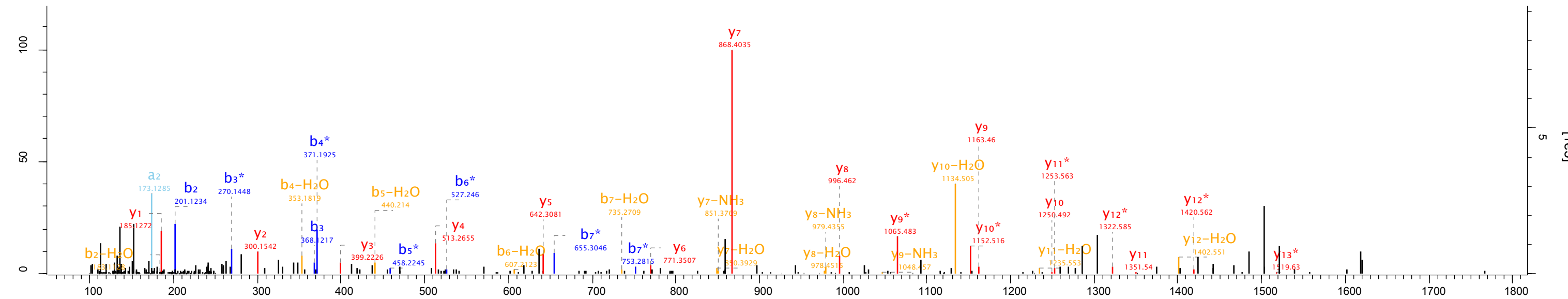
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 4454 Method FTMS; HCD Score 177.79 m/z 800.83 Gene names COL4A3BP



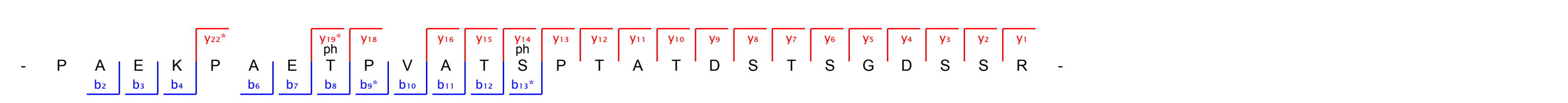
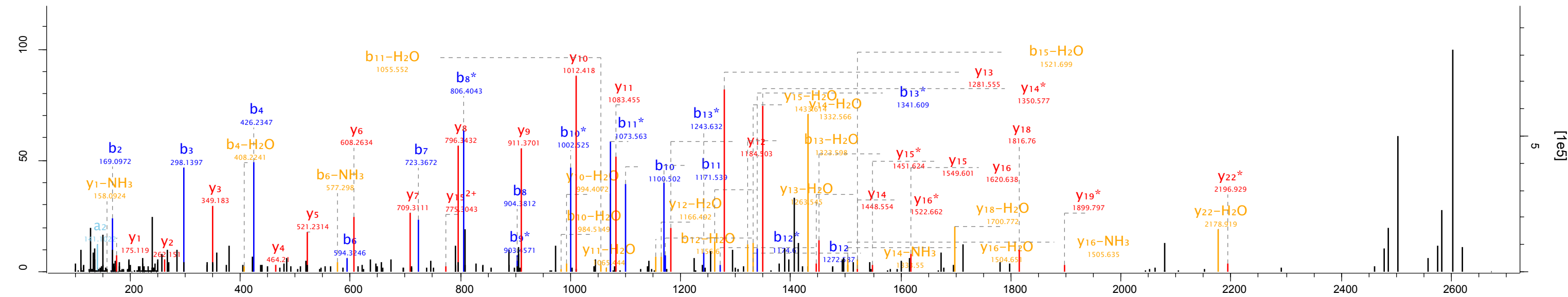
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20171215_MaS_33SR_LMH_phospho2_03



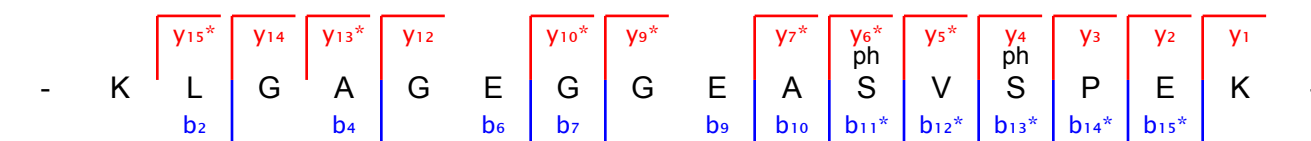
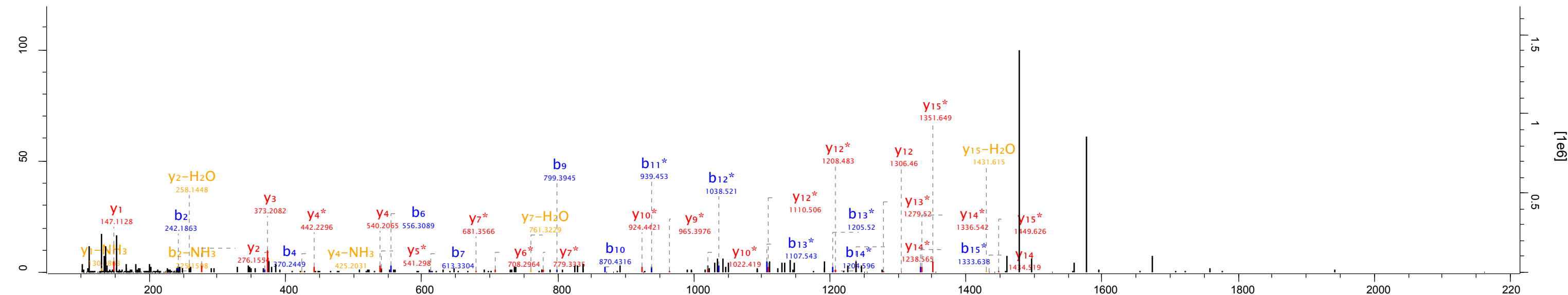
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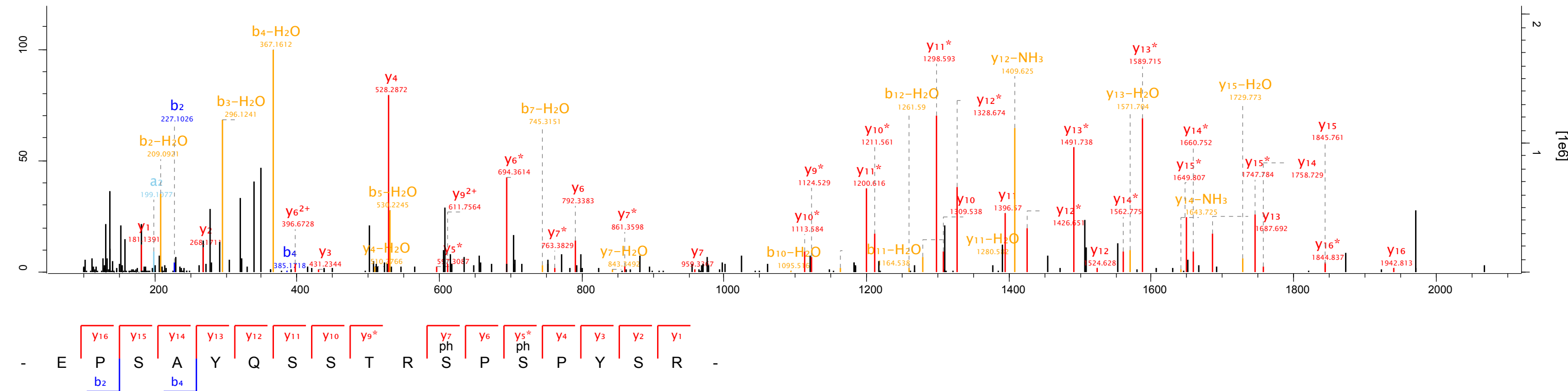
Scan 4934 Method FTMS; HCD Score 134.24 m/z 907.38 Gene names RAD23B



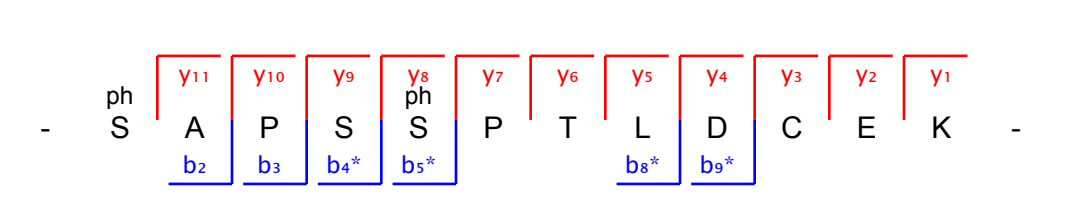
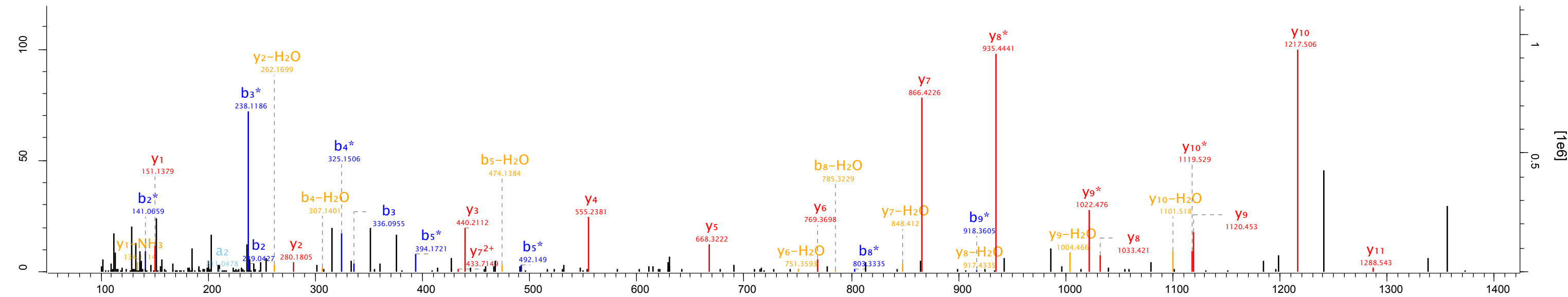
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20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
4954 FTMS; HCD 64.97 838.35 TCOF1

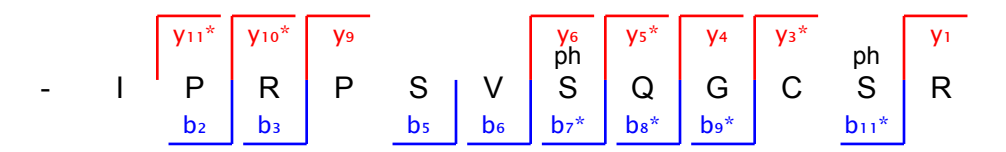
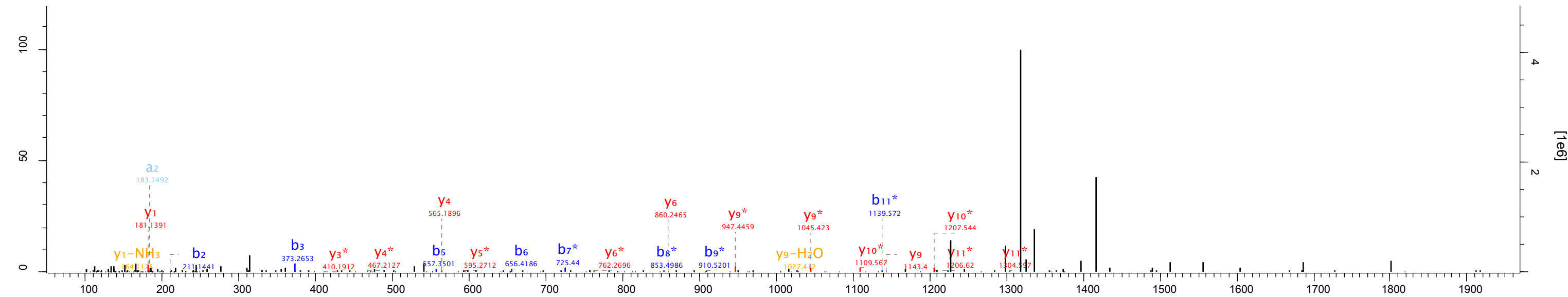




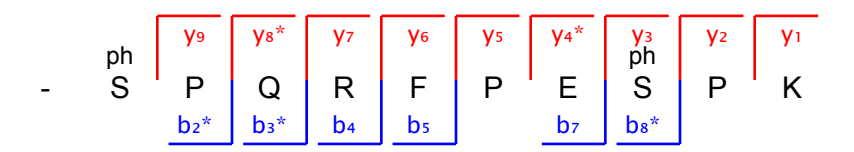
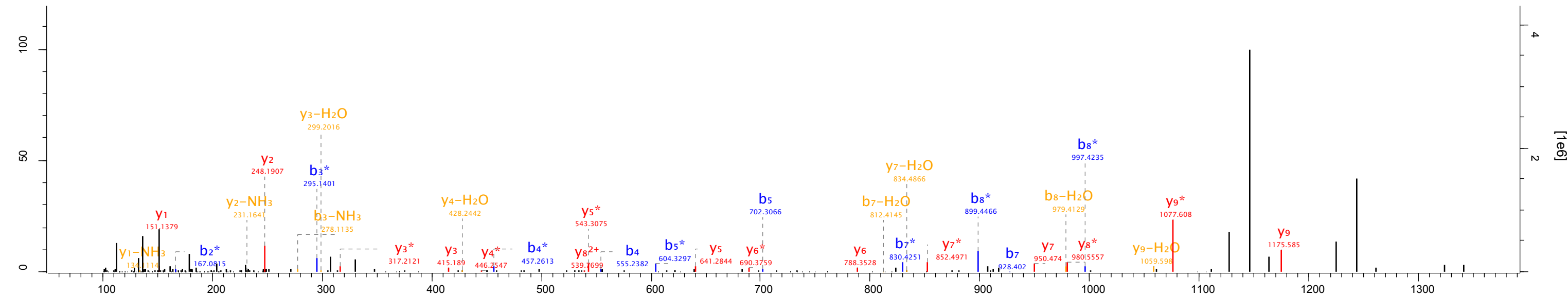
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 5554 Method: FTMS; HCD Score: 123.28 m/z: 728.28 Gene names: NDEL1



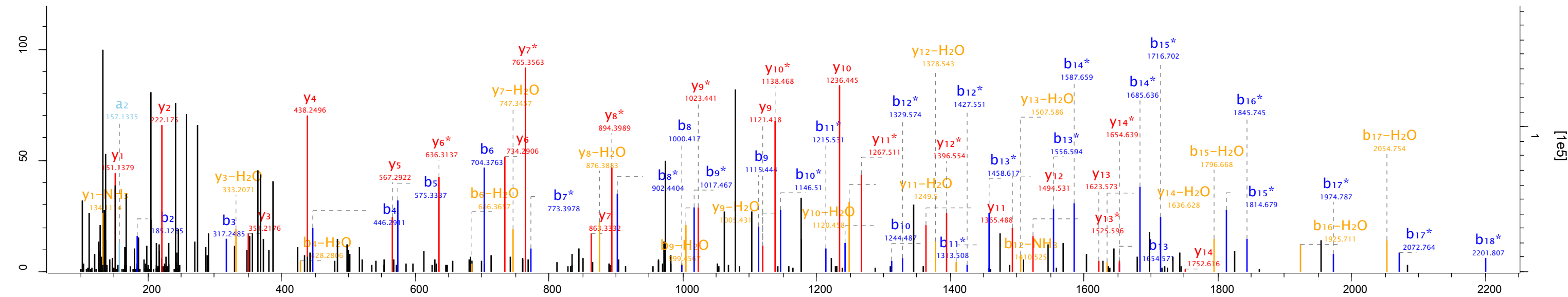
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5594 Method FTMS; HCD Score 47.69 m/z 758.34 Gene names CLASP2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5654 Method FTMS; HCD Score 133.86 m/z 671.8 Gene names ANKRD11



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5674 Method FTMS; HCD Score 171.99 m/z 1179.08 Gene names SMARCA2

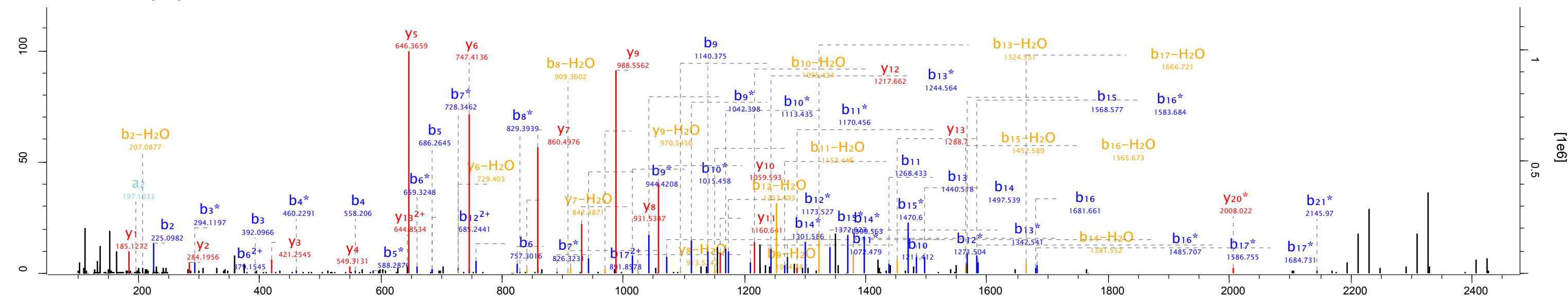


- I A K E E E S E D E S N E E E E D E E E S E S E A K -

b₂
b₃
b₄
b₅
b₆
b₇^{*}
b₈
b₉
b₁₀
b₁₁^{*}
b₁₂^{*}
b₁₃
b₁₄^{*}
b₁₅^{*}
b₁₆^{*}
b₁₇^{*}
b₁₈^{*}
y₁₄
y₁₃
y₁₂
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y₇
y₆
y₅
y₄
y₃
y₂
y₁

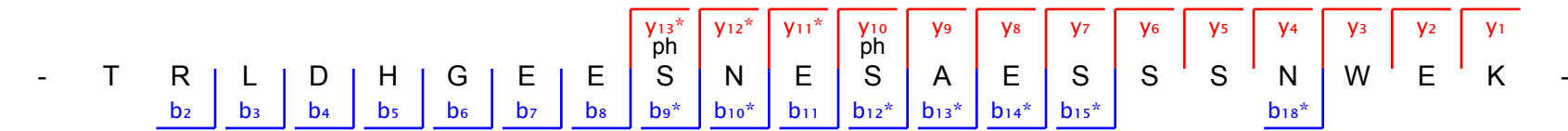
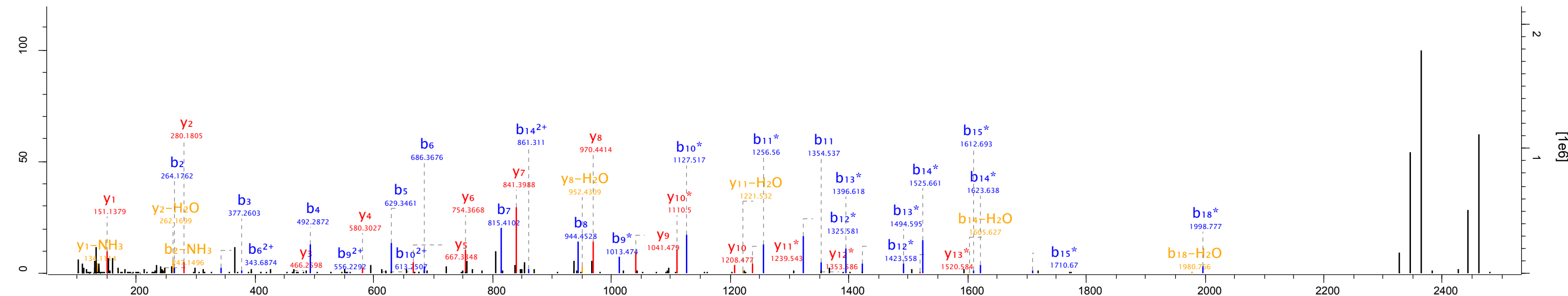
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20171215_MaS_33SR_LMH_phospho2_03

Scan 5734 Method FTMS; HCD Score 233.3 m/z 810.36 Gene names YAP1

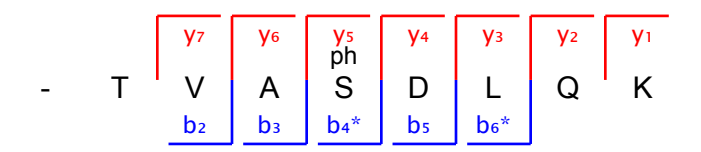
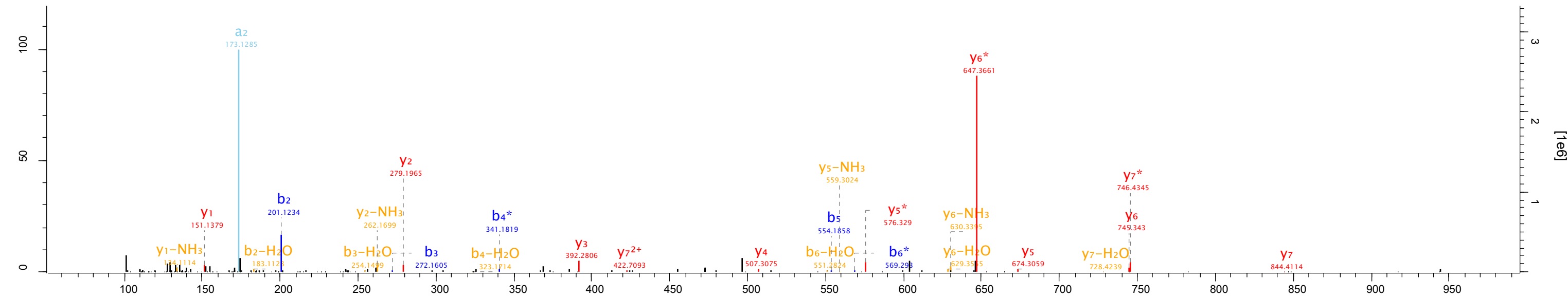


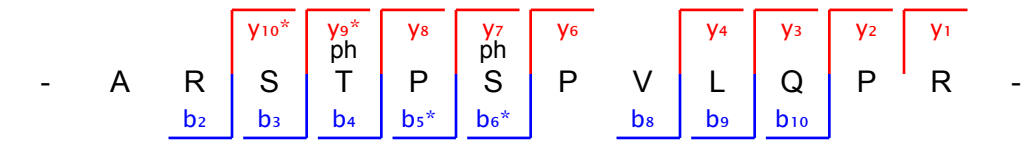
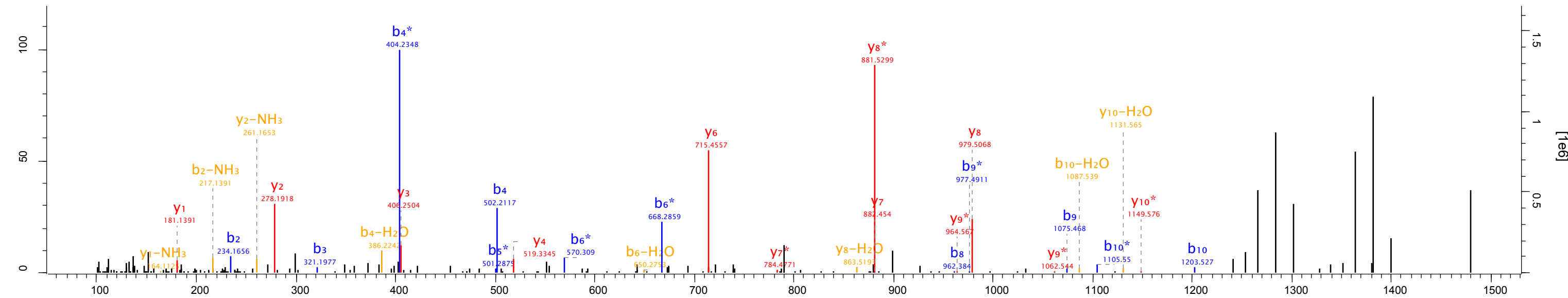
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20171215_MaS_33SR_LMH_phospho2_03

Scan 6114 Method FTMS; HCD Score 128.22 m/z 854.67 Gene names SMARCD1

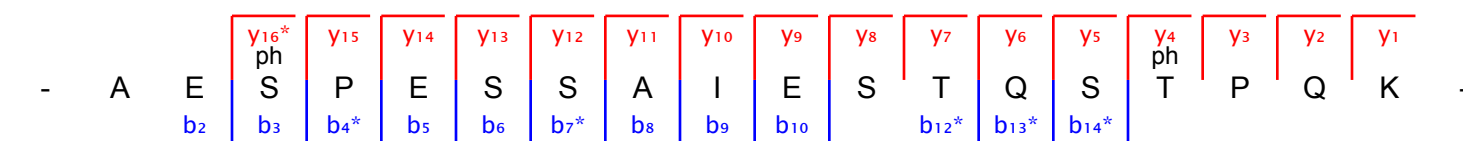
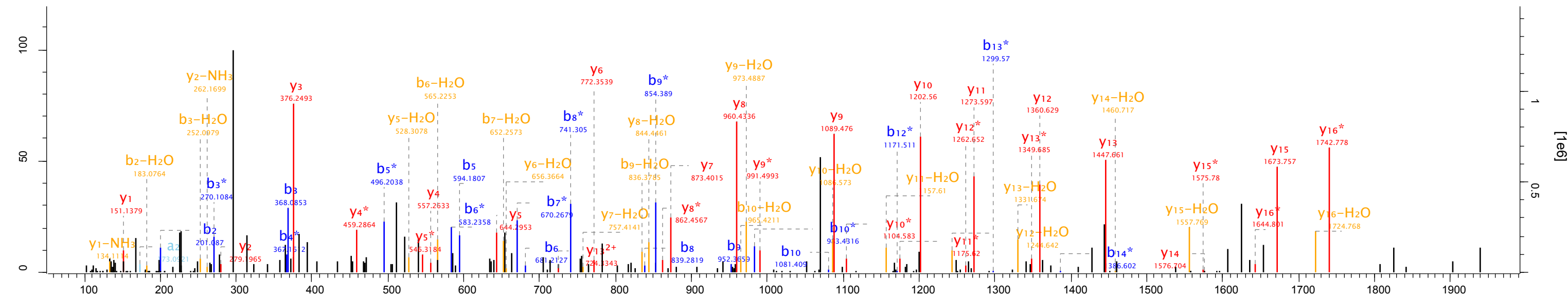


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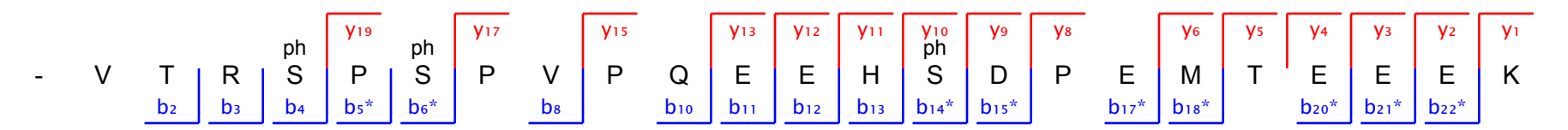
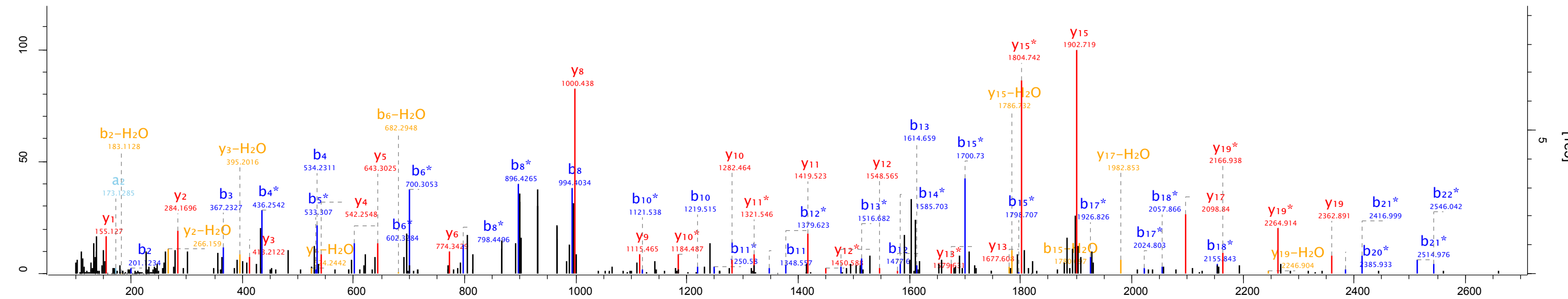


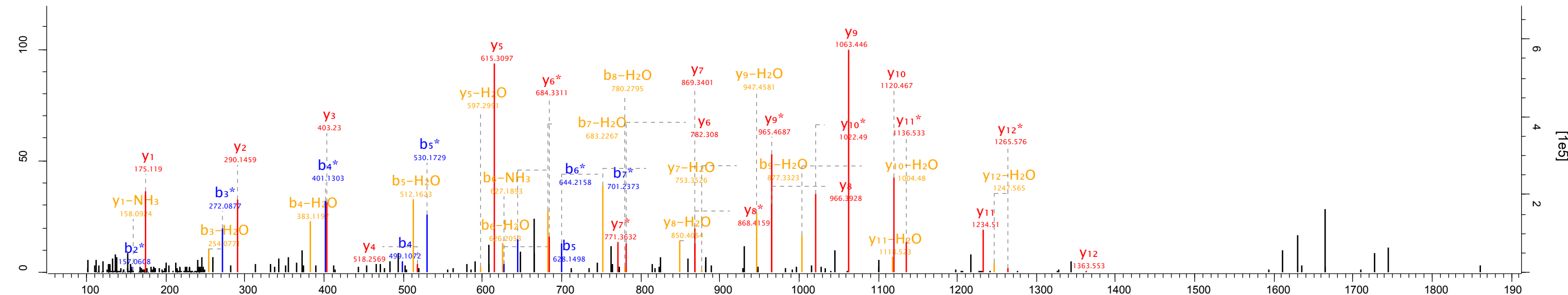
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Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 6774 Method FTMS; HCD Score 166.66 m/z 966.04 Gene names PNISR





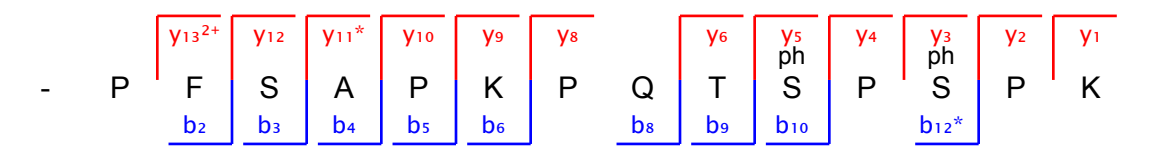
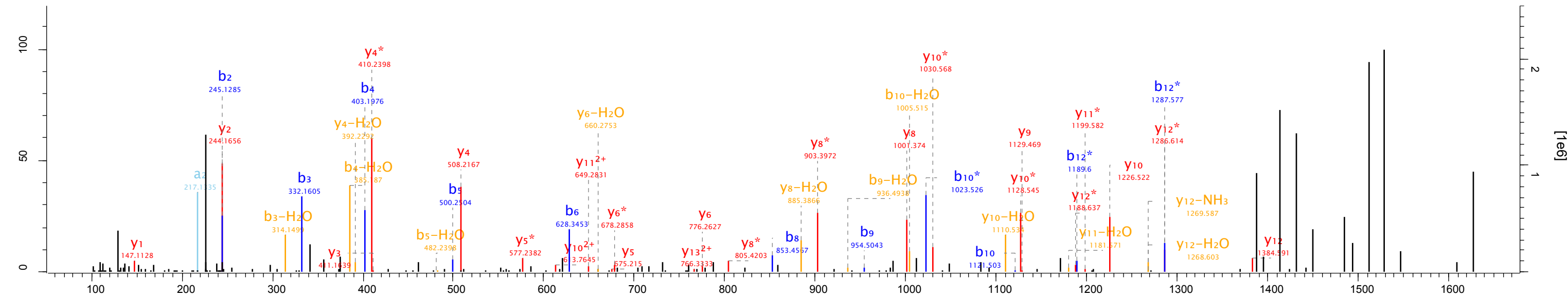
- S ph S D E E N G P P S S P D L D R -

b2* b3* b4 b5 b6* b7*

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

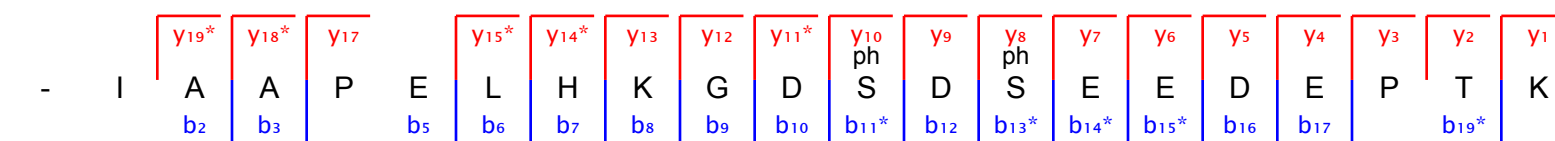
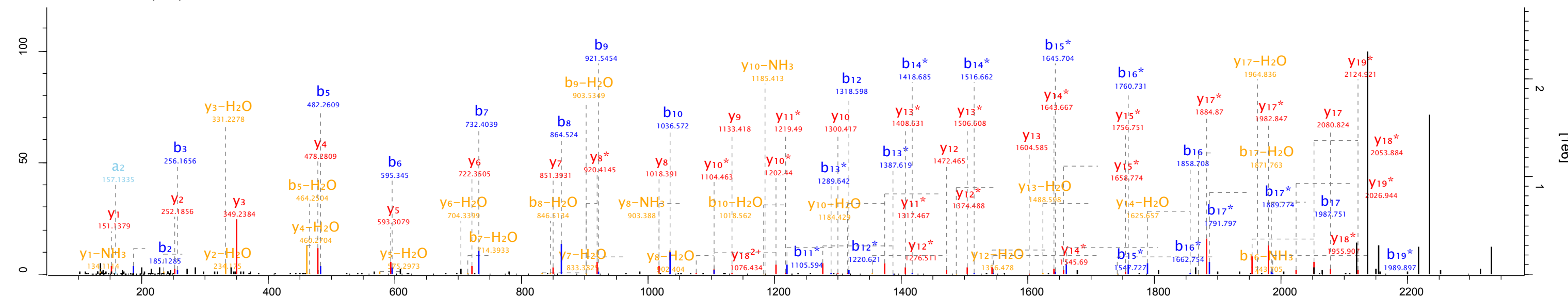
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20171215_MaS_33SR_LMH_phospho2_03

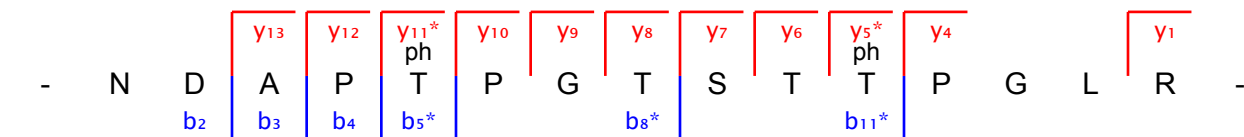
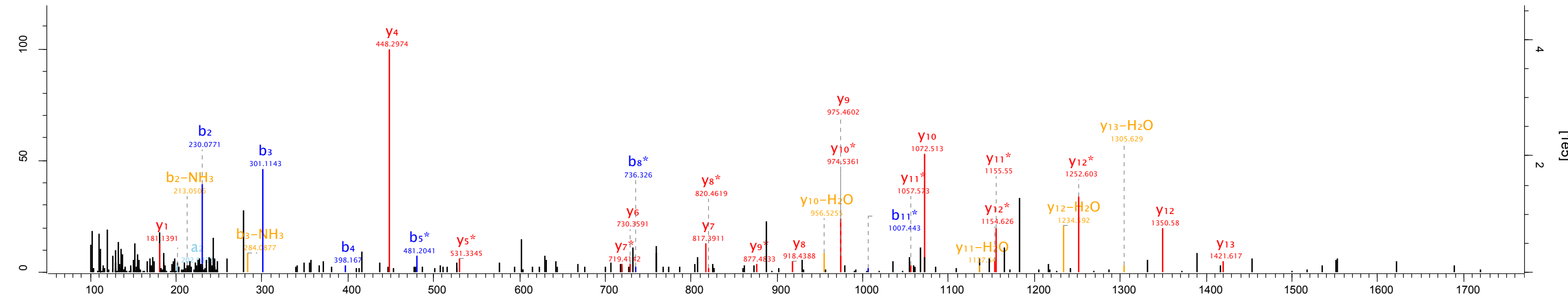
Scan 7004 Method FTMS; HCD Score 192.12 m/z 814.86 Gene names CAPI



Raw file
20171215_MaS_33SR_LMH_phospho2_03

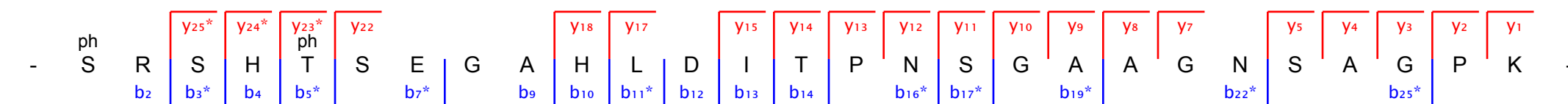
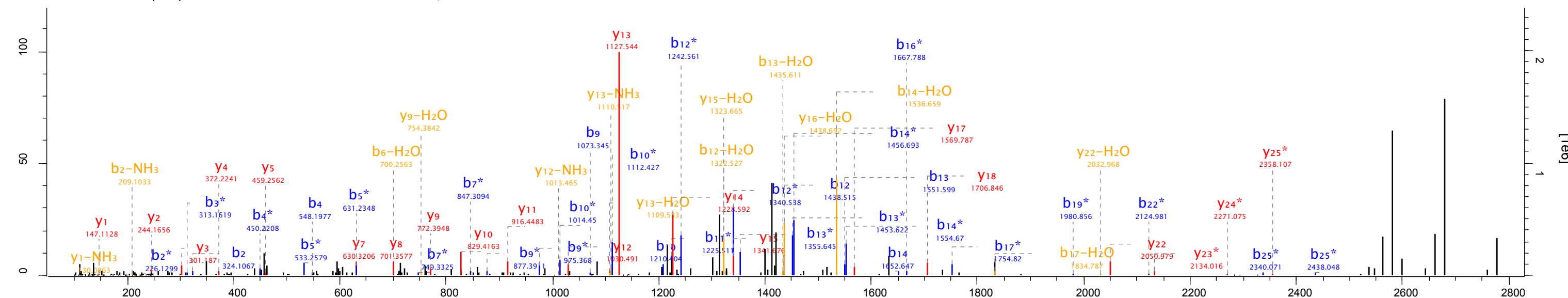
Scan 7114 Method FTMS; HCD Score 294.99 m/z 1168.99 Gene names PRCC





Raw file
20171215_MaS_33SR_LMH_phospho2_03

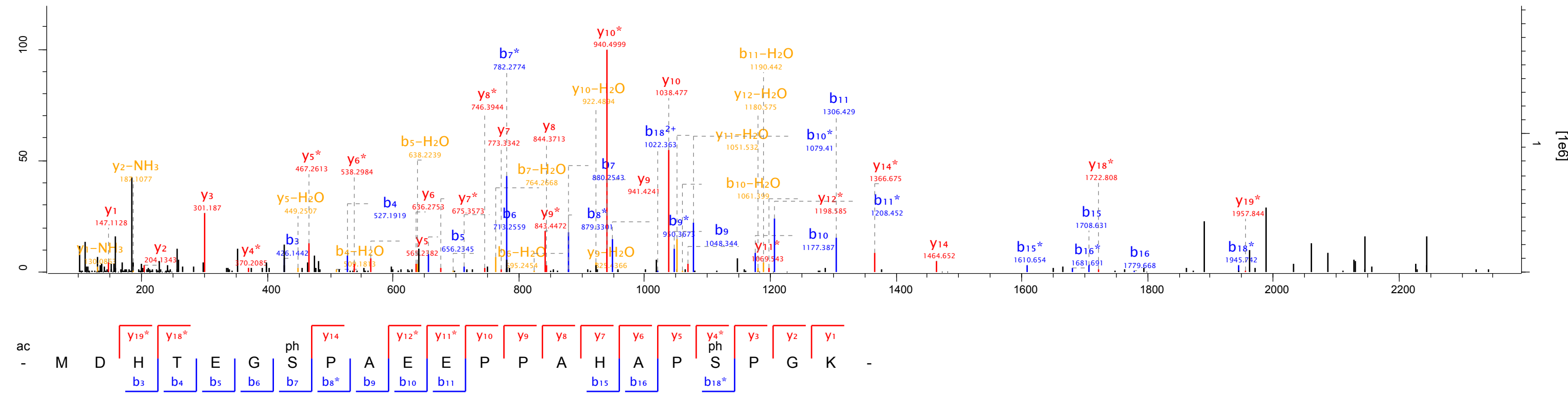
Scan 7414 Method FTMS; HCD Score 152.05 m/z 927.4 Gene names NDRG1

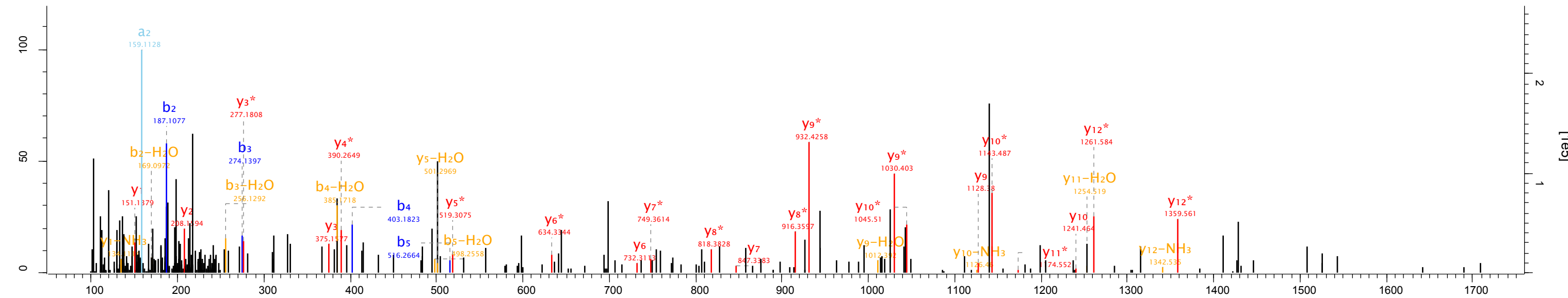


Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
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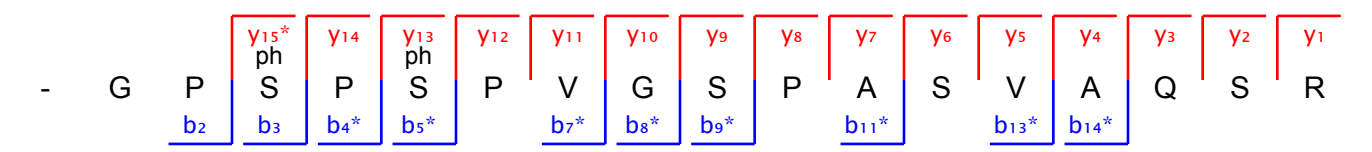
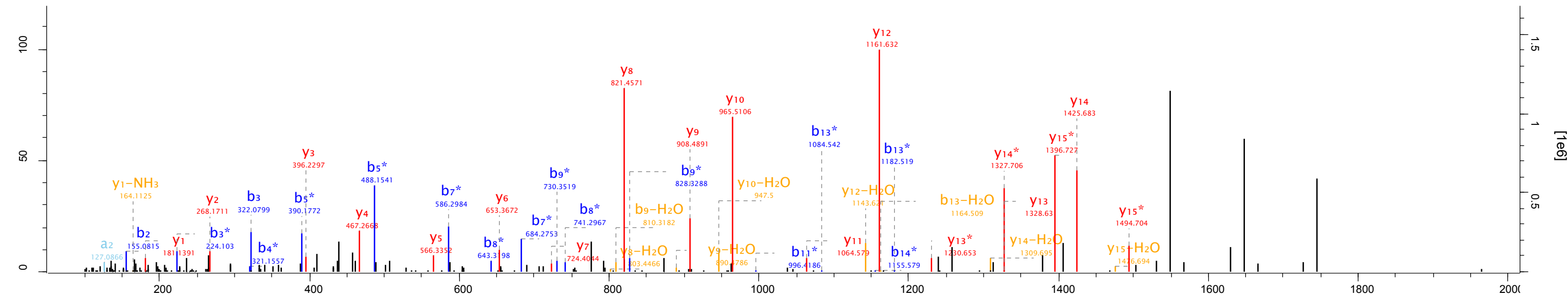


- S V S E I N S D D E L S G K -

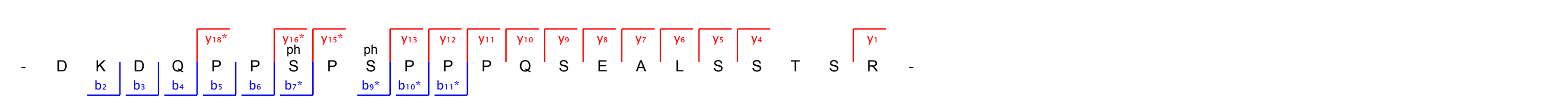
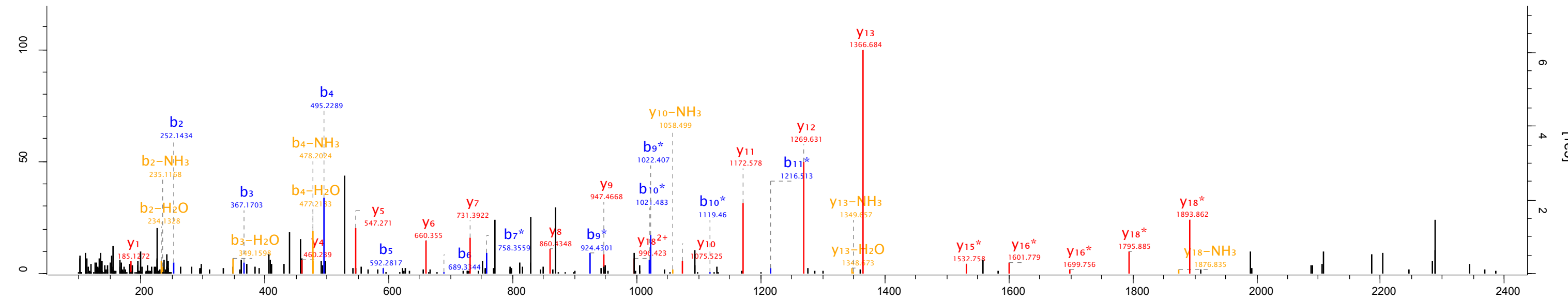
Fragmentation mapping (b and y ions):

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

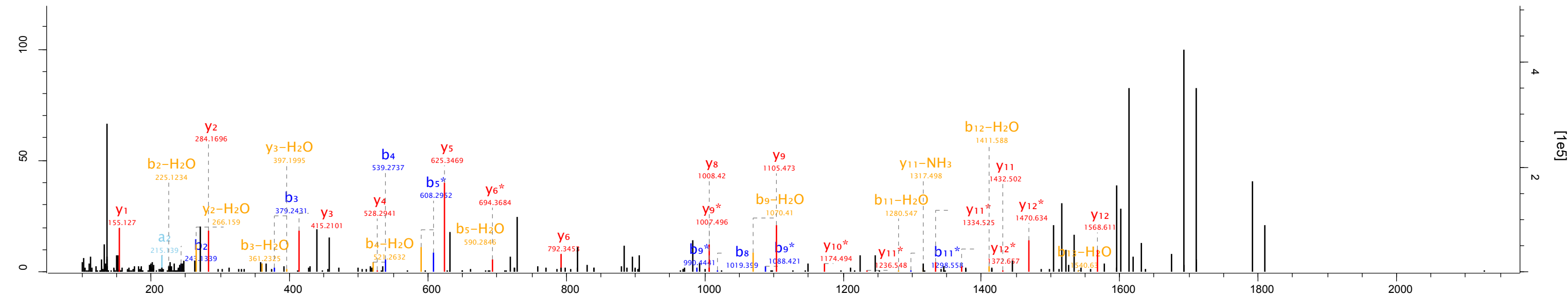
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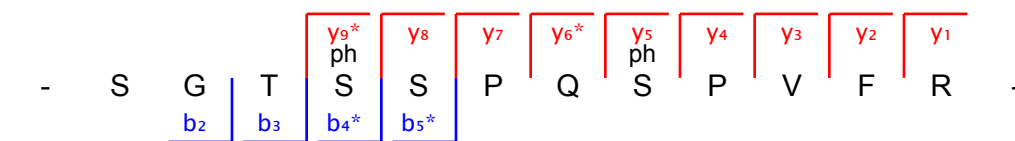
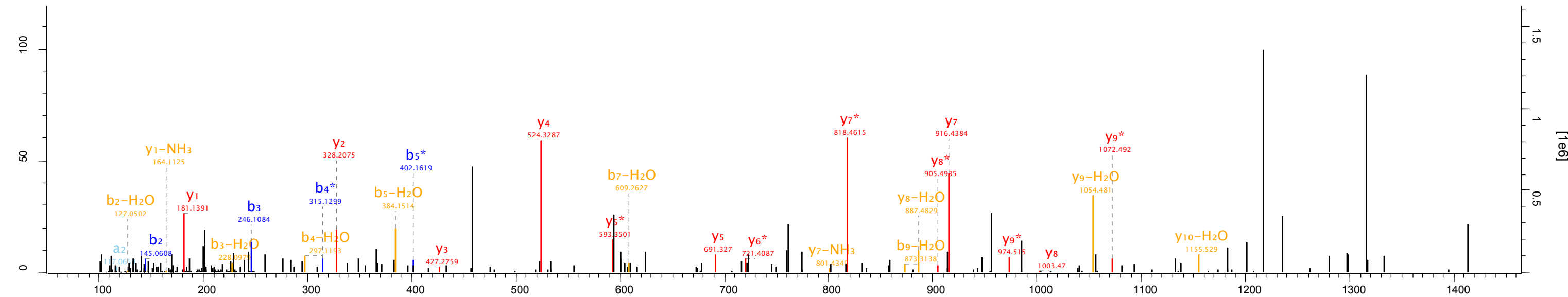


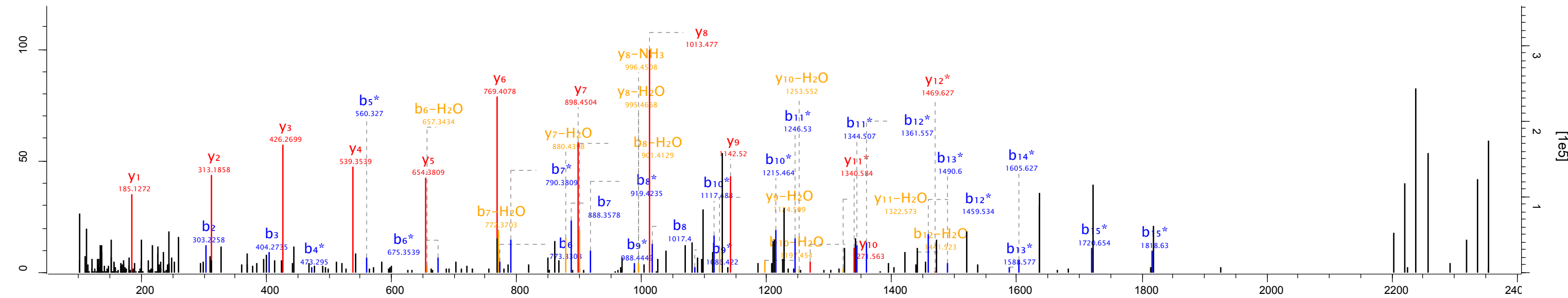
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8394 Method FTMS; HCD Score 81.28 m/z 829.69 Gene names MON1B



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 8434 Method: FTMS; HCD Score: 116.04 m/z: 906.37 Gene names: SLC20A1







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

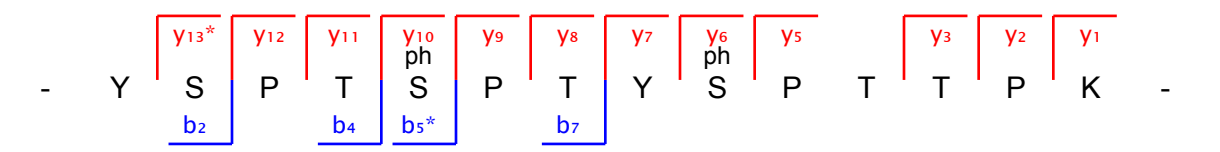
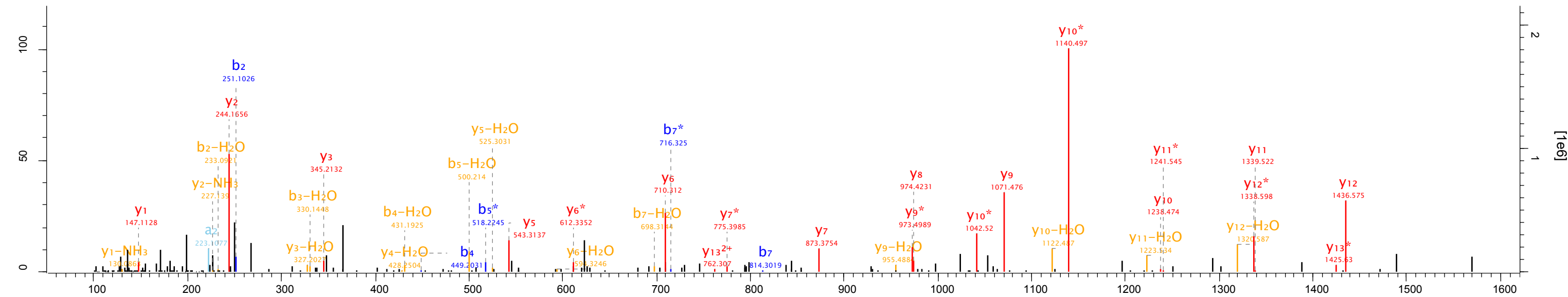
ph
ph

b₂ b₃ b₄* b₅* b₆ b₇ b₈ b₉* b₁₀* b₁₁* b₁₂* b₁₃* b₁₄* b₁₅*

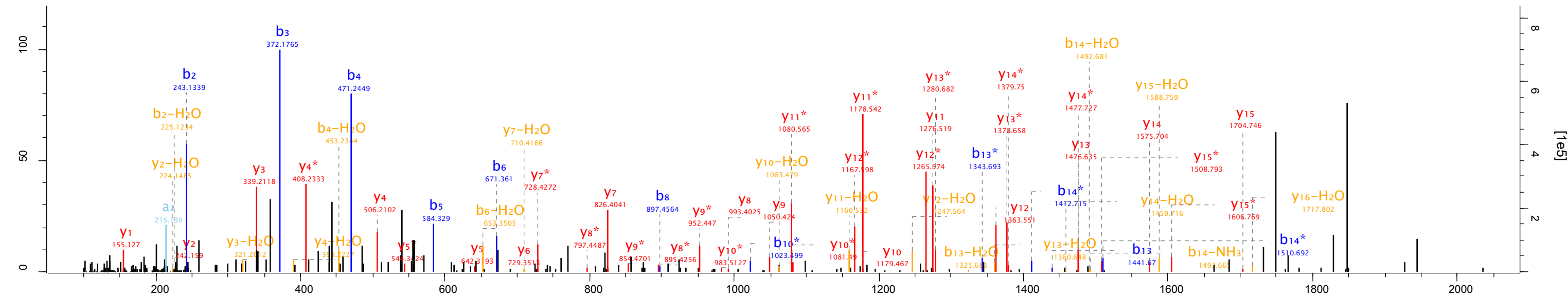
y₁₂* y₁₁* y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file
20171215_MaS_33SR_LMH_phospho2_03

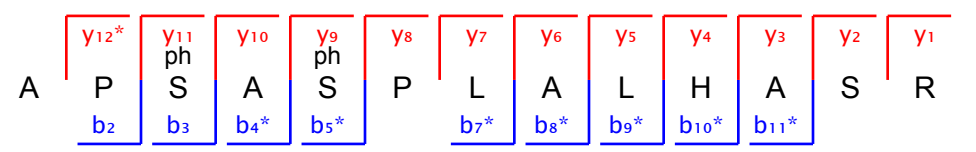
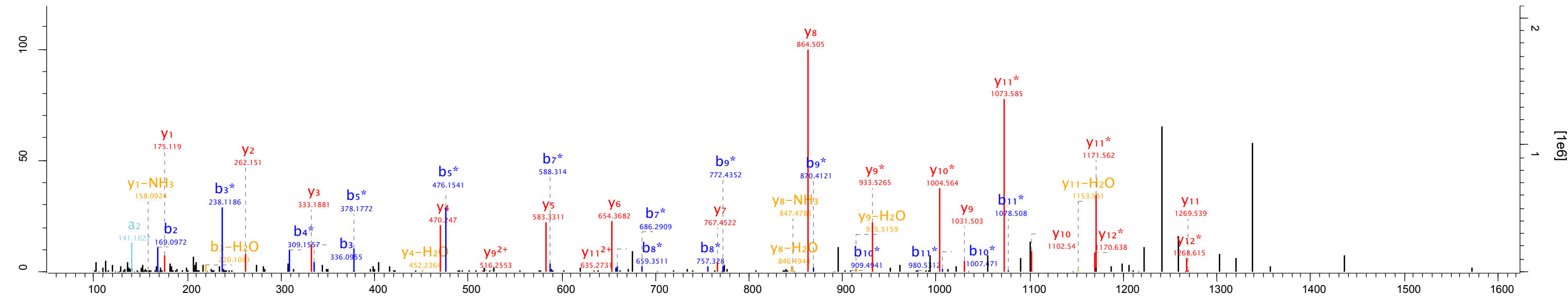
Scan 8854 Method FTMS; HCD Score 141.18 m/z 843.84 Gene names POLR2A



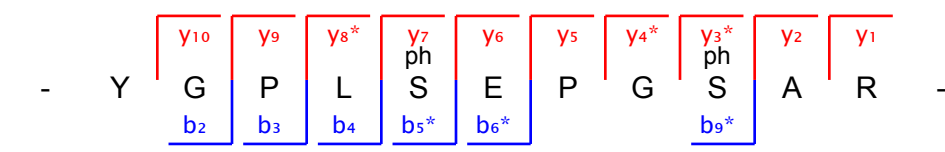
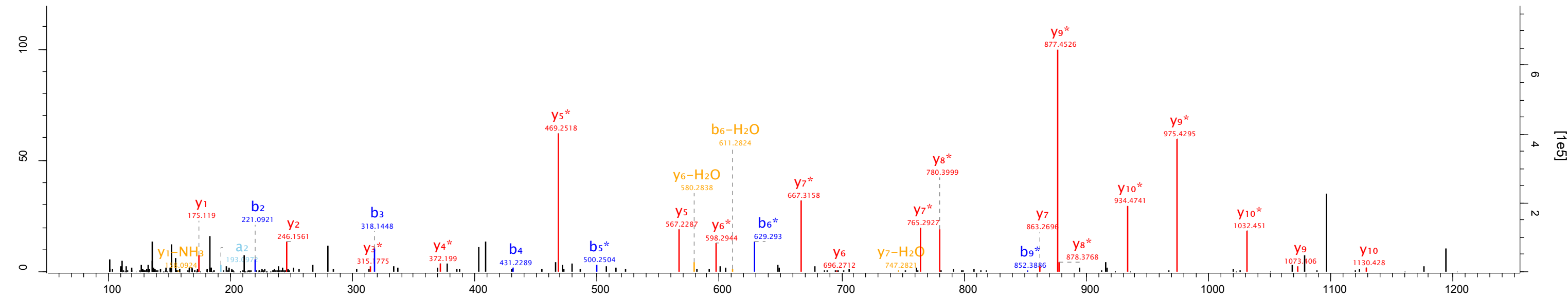
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9034 Method FTMS; HCD Score 236.99 m/z 973.94 Gene names ADD3



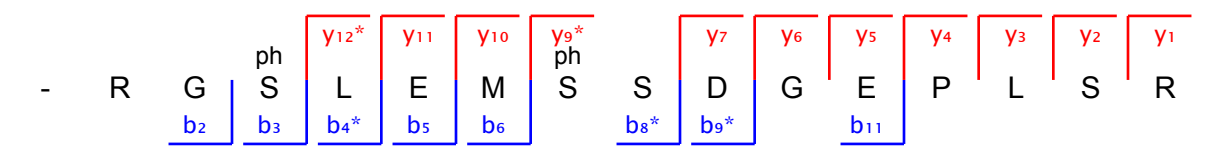
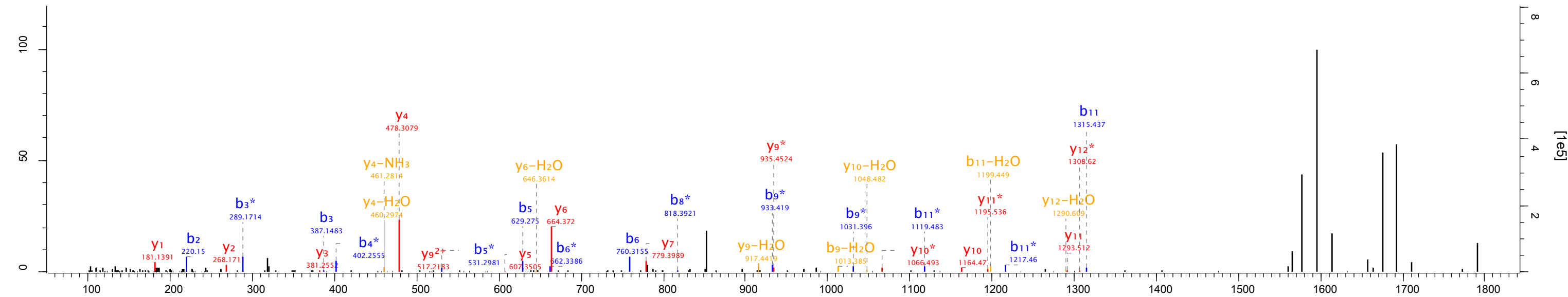
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9444 Method FTMS; HCD Score 155.94 m/z 719.32 Gene names MICALL1



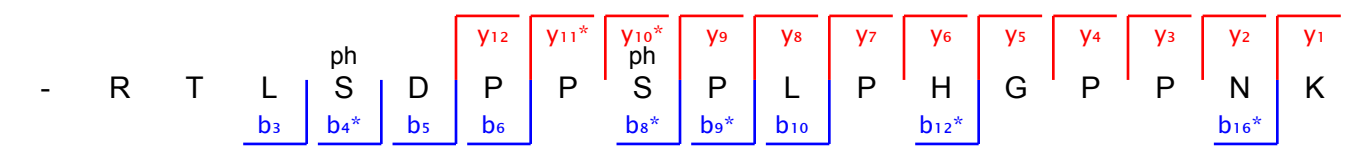
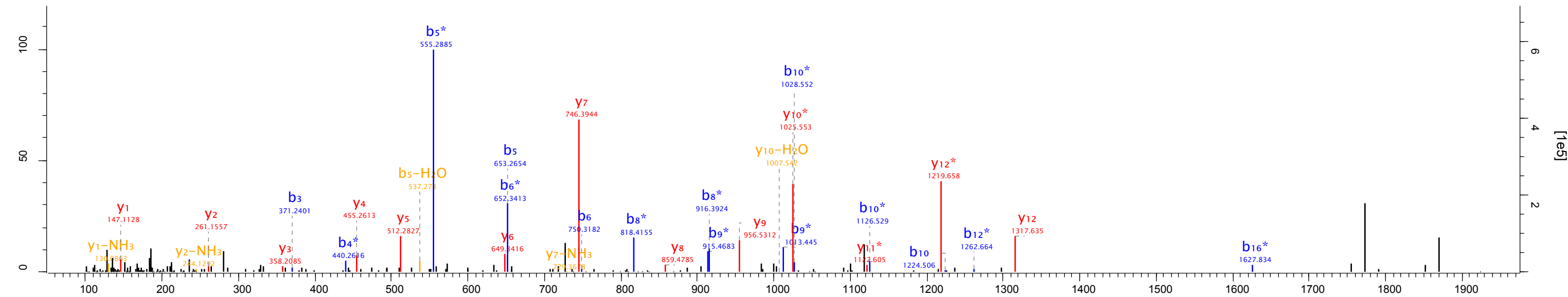
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9534 Method FTMS; HCD Score 104.21 m/z 647.75 Gene names WDR13



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 9614 Method: FTMS; HCD Score: 117.62 m/z: 897.37 Gene names: AEBP2

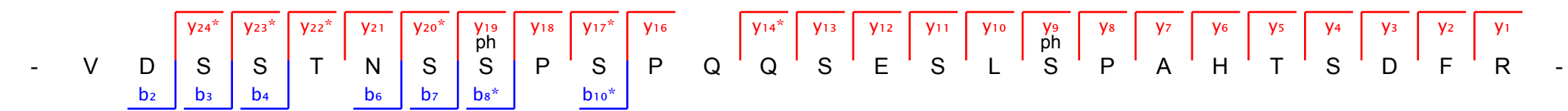
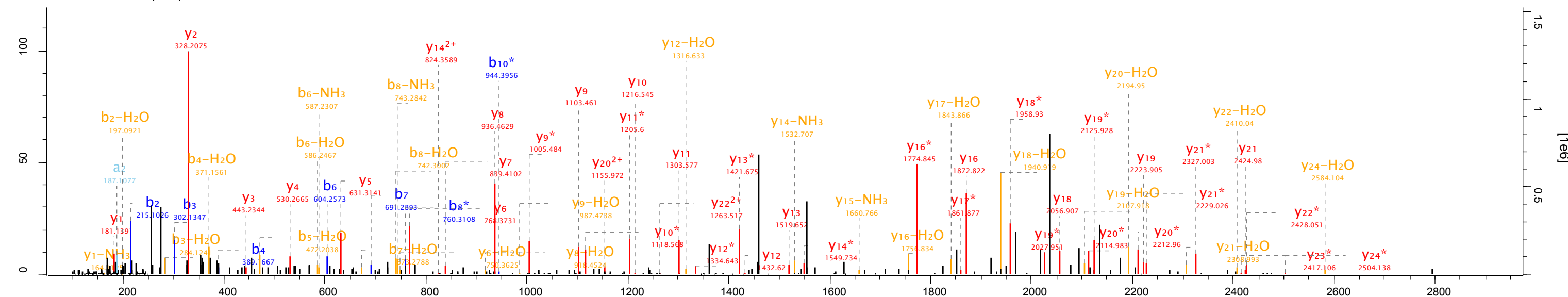


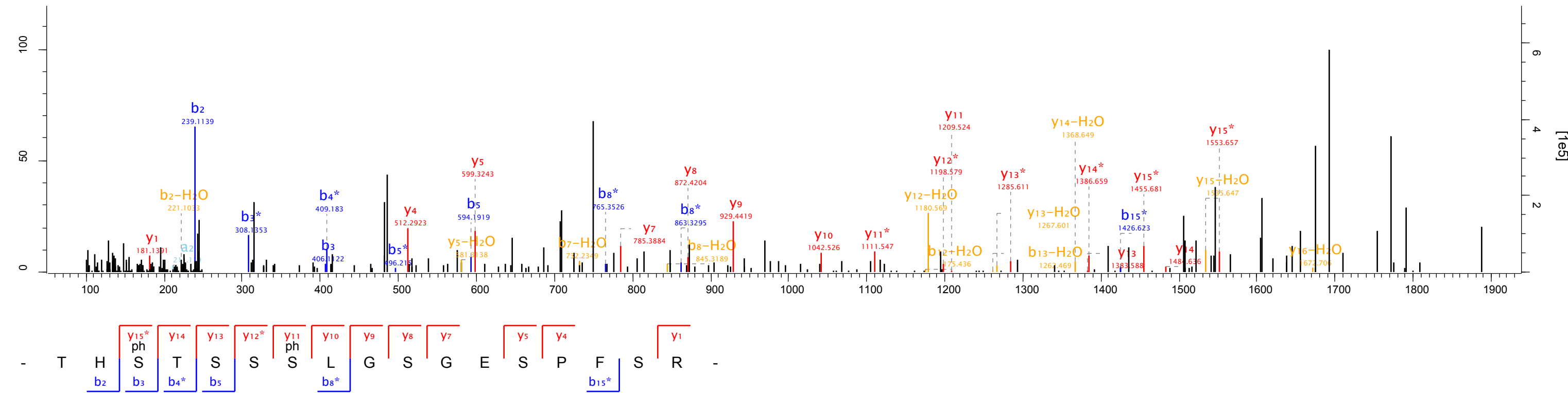
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9704 Method FTMS; HCD Score 104.66 m/z 657.64 Gene names ASAP1

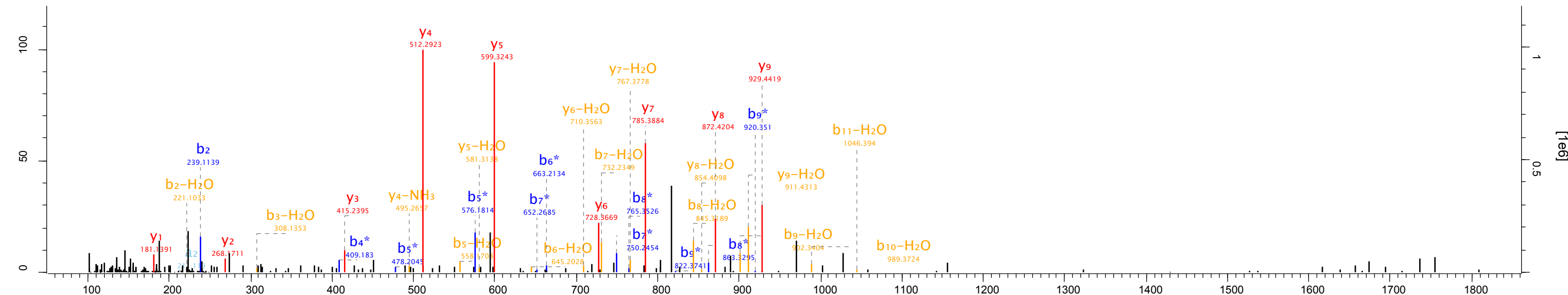


Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 9724 Method FTMS; HCD Score 224.53 m/z 972.41 Gene names BCL7B





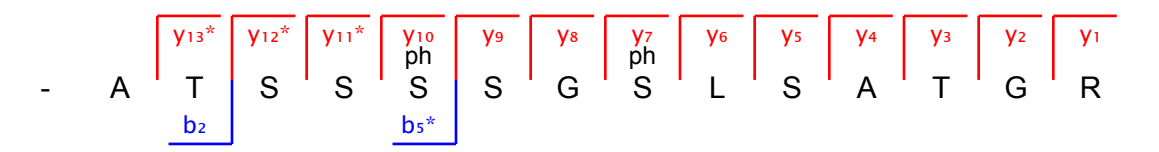
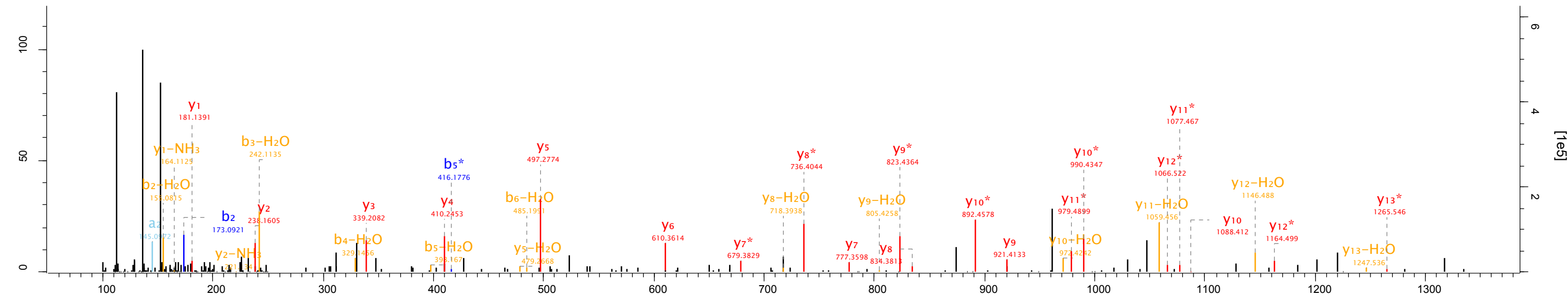


- T H S ph T ph S S S L G S G E S P F S R -

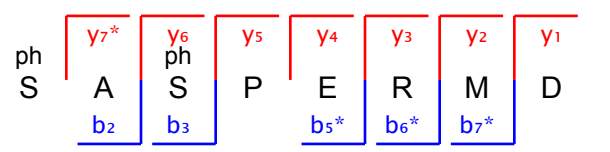
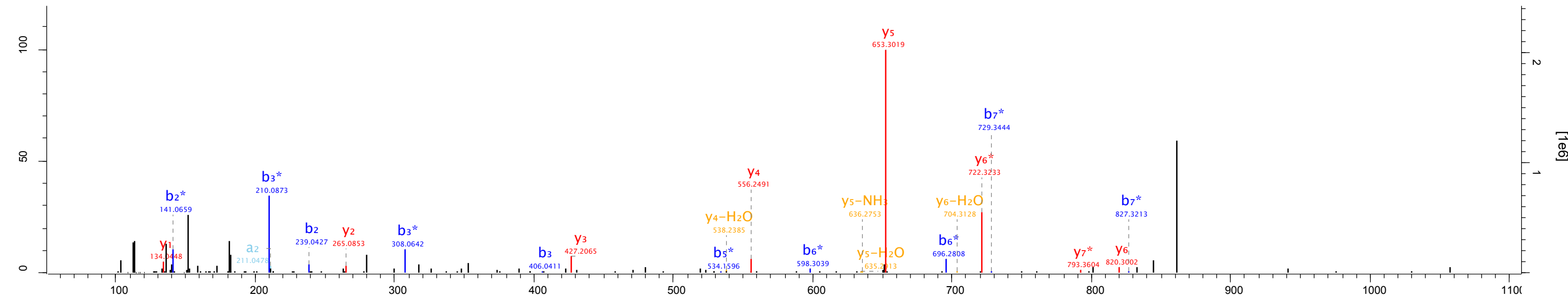
Fragmentation labels (b and y ions) are shown below the corresponding amino acids:

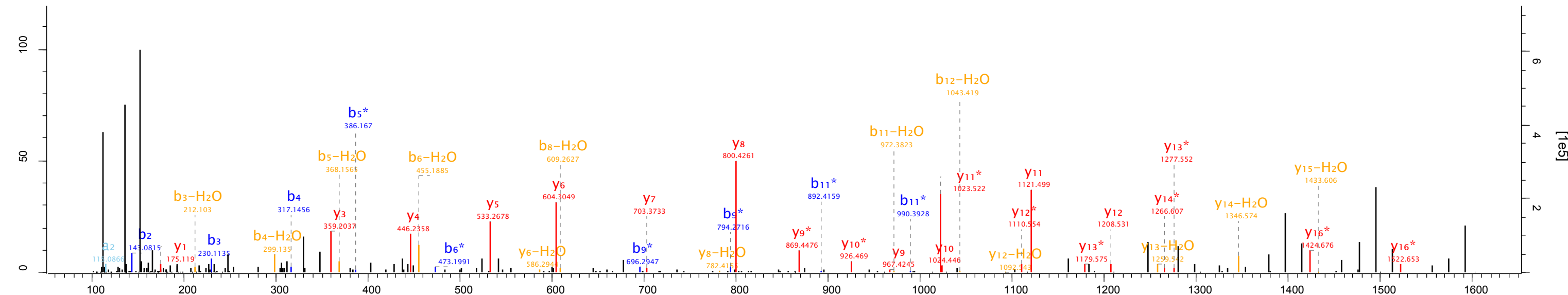
- H: b₂
- T: b₄*
- S: b₅*
- S: b₆*
- S: b₇*
- L: b₈*
- G: b₉*
- S: y₉
- G: y₈
- E: y₇
- S: y₆
- P: y₅
- F: y₄
- S: y₃
- R: y₂

Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 3254 Method FTMS; HCD Score 103.45 m/z 717.78 Gene names LMNB2



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 3434 Method FTMS; HCD Score 92.79 m/z 529.67 Gene names SRSF7



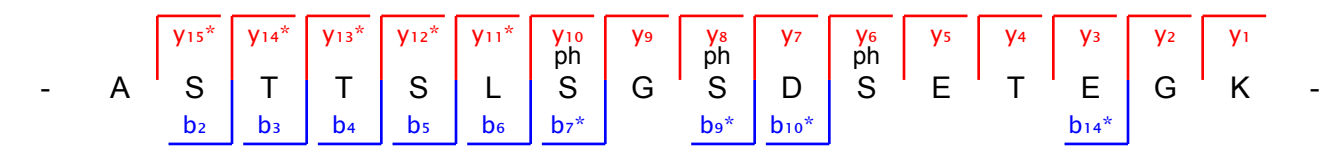
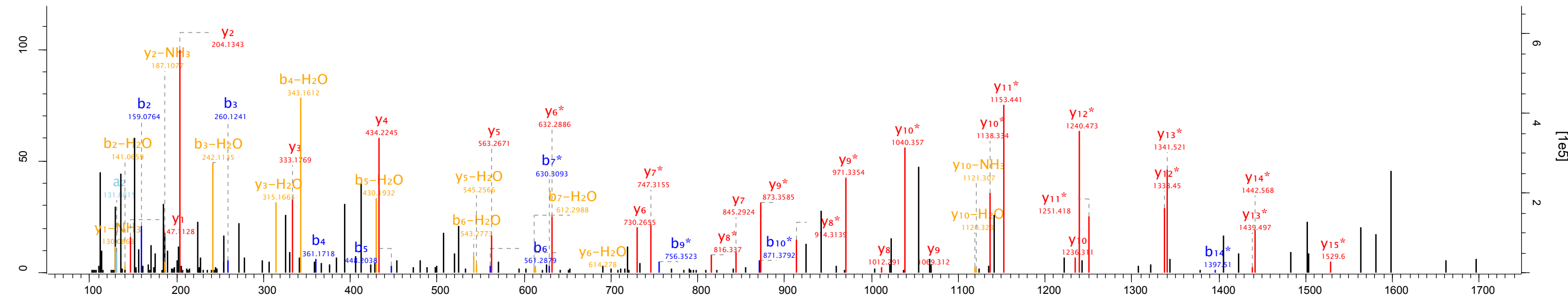


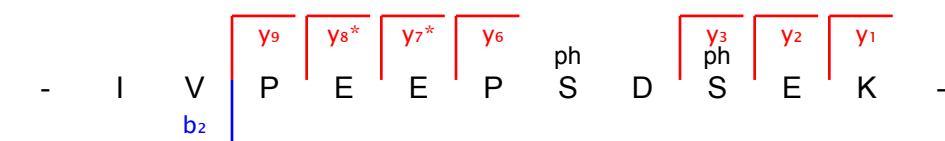
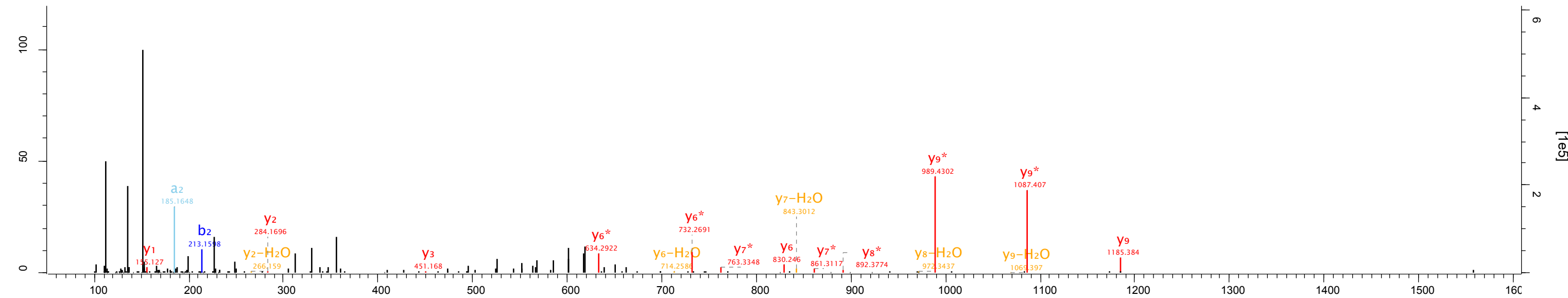
- A A S S S P G S P V A S S P S R -

y₁₆*
y₁₄*
y₁₃*
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₁

b₂
b₃
b₄
b₅*
b₆*
b₉*
b₁₁*

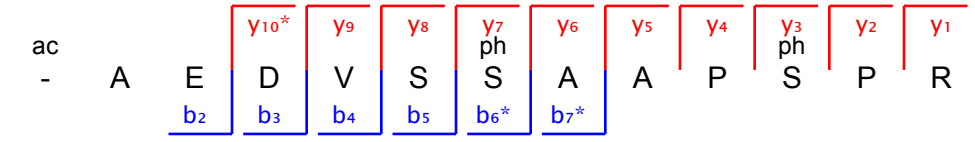
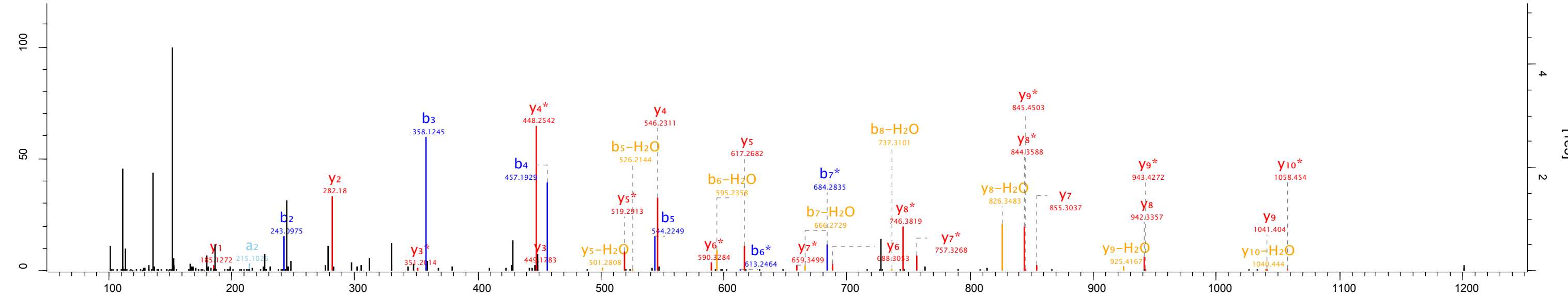
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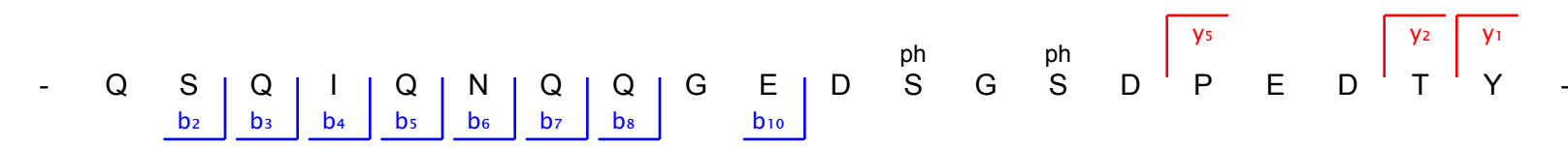
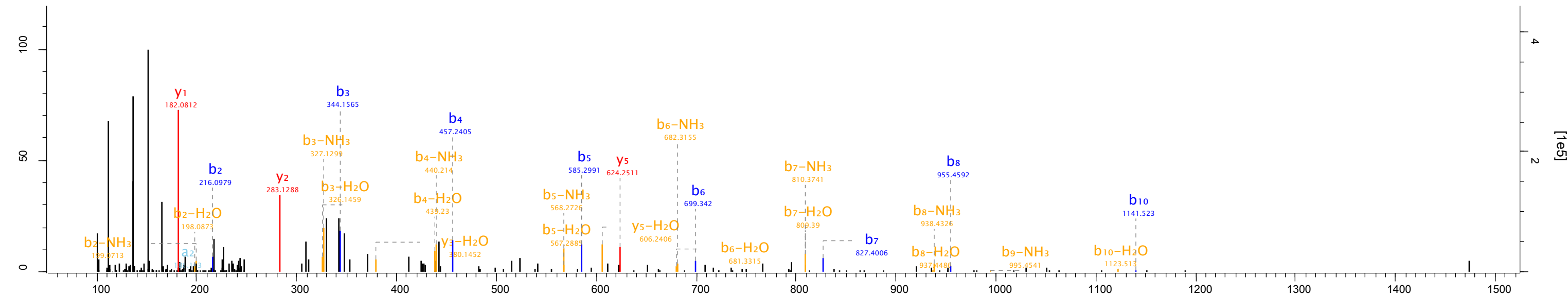
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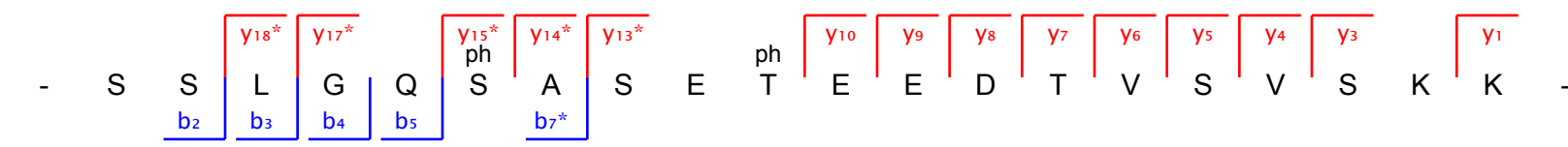
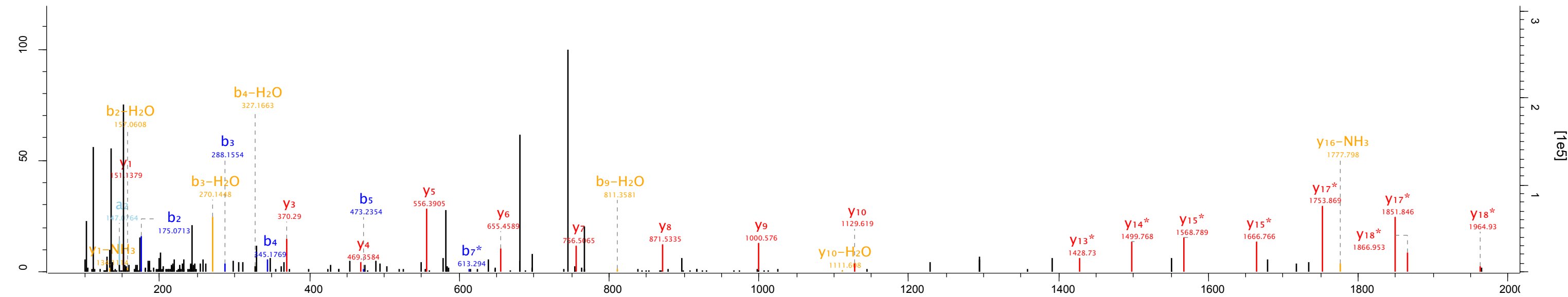


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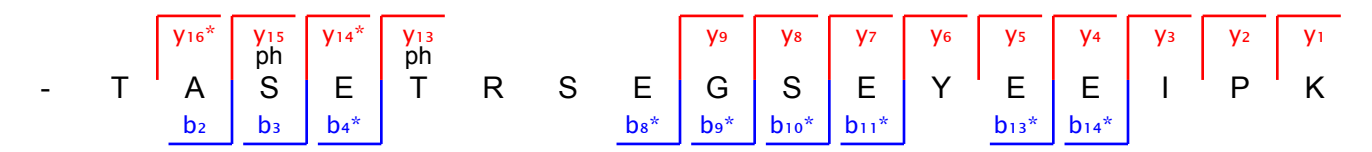
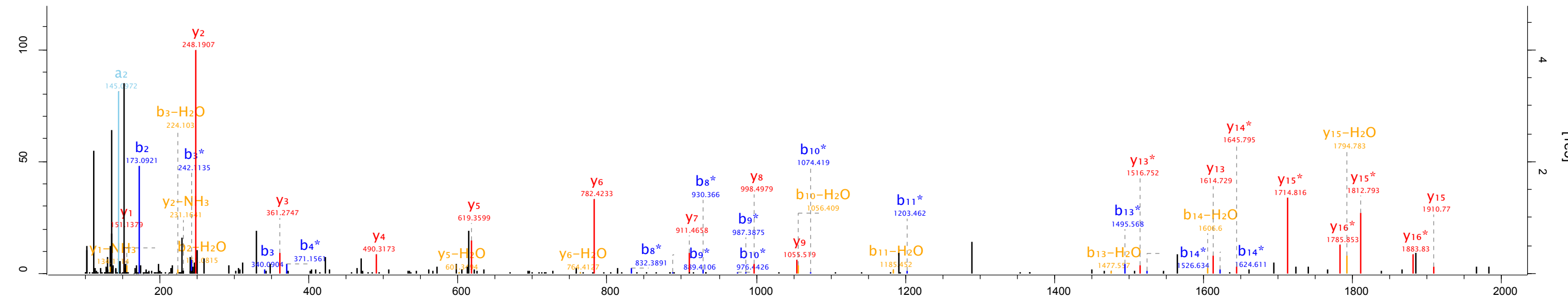
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LIG1



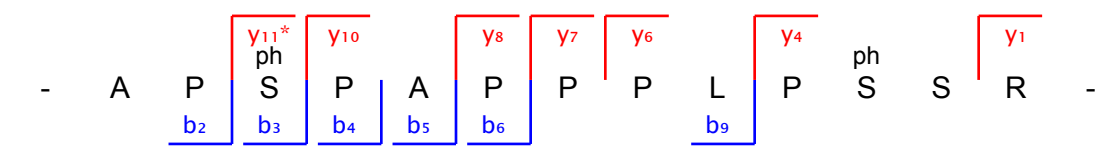
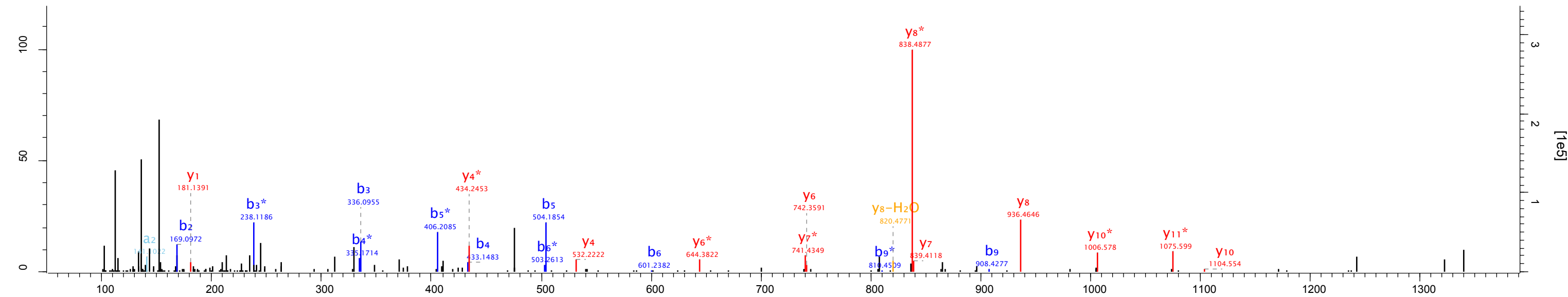
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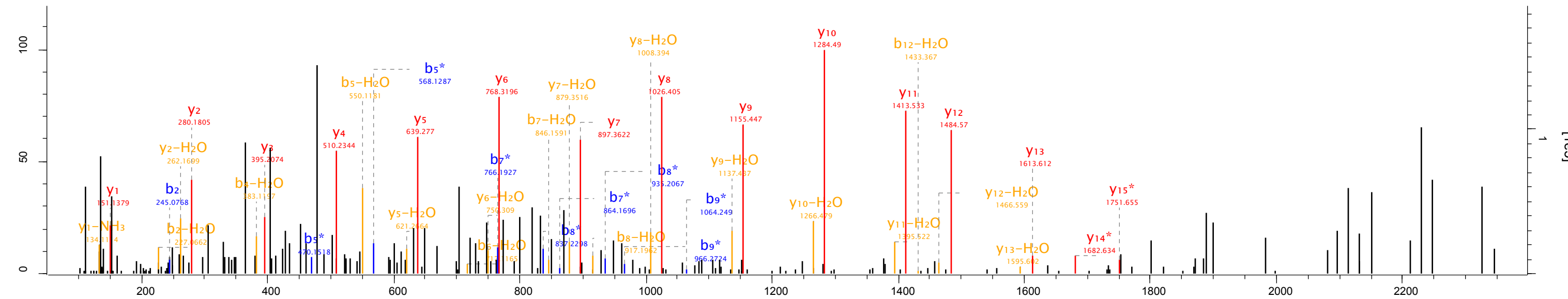
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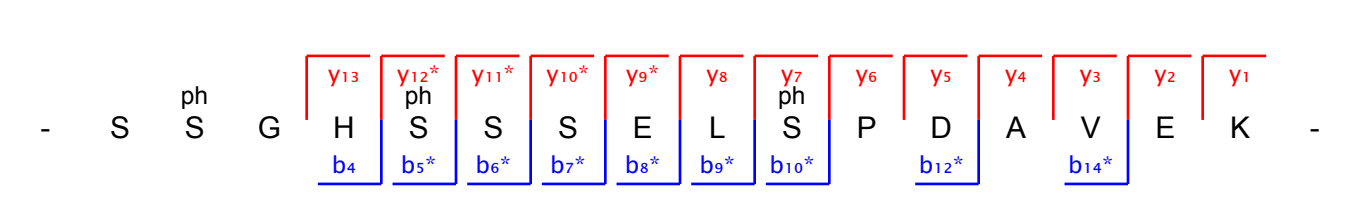
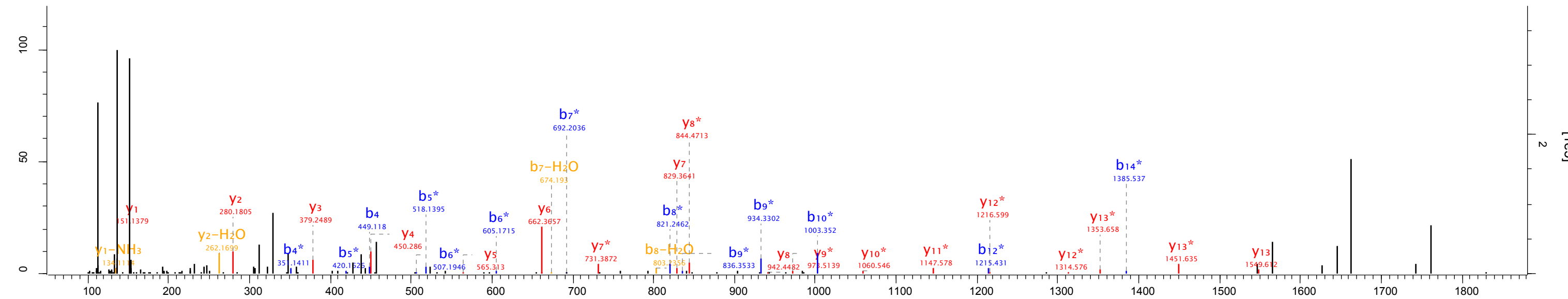
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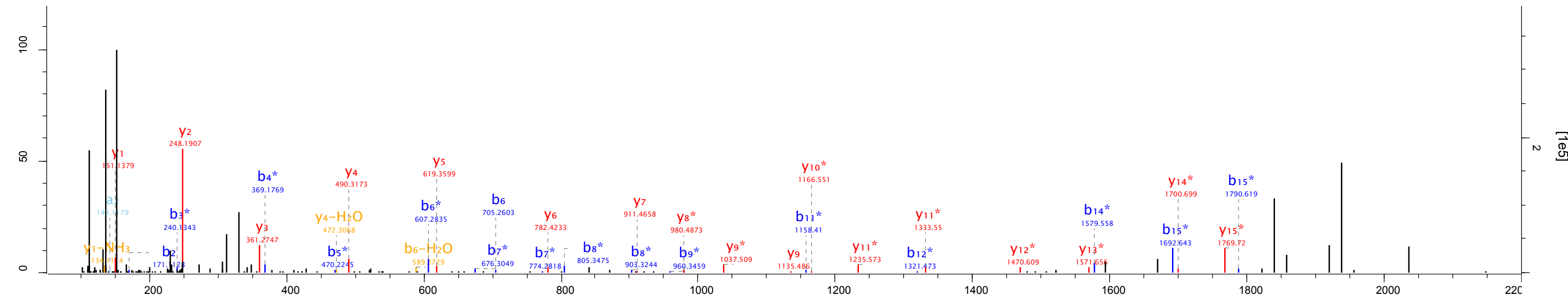
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b₂ b₅* b₇* b₈* b₉*

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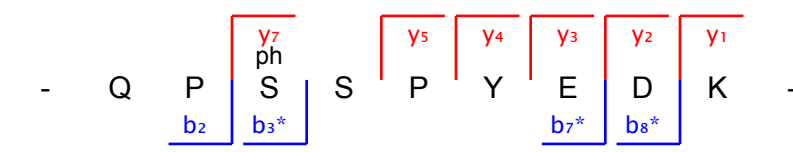
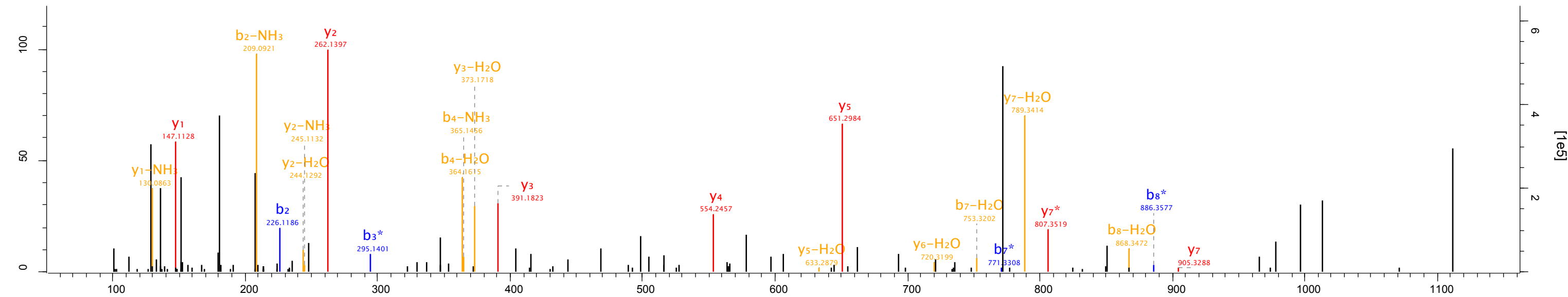


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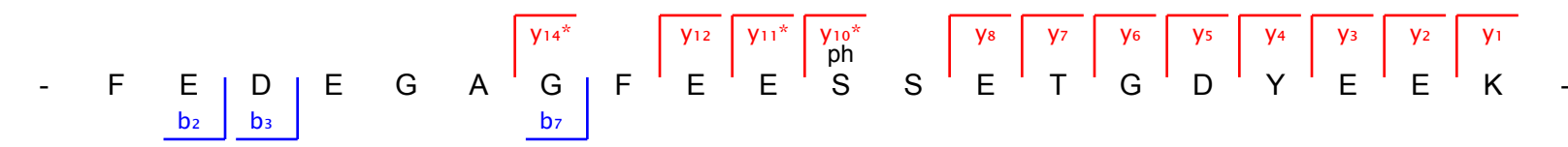
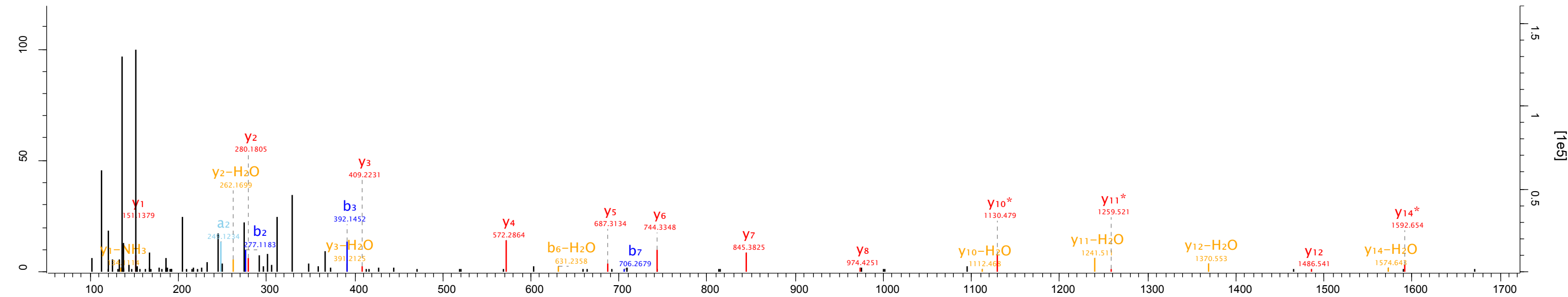
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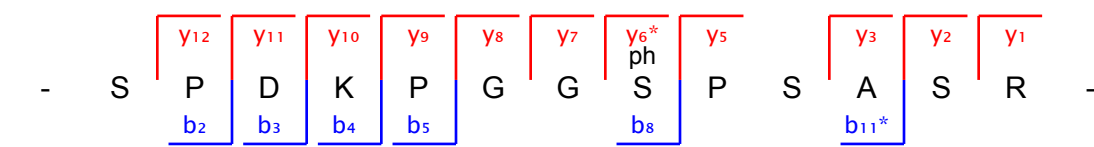
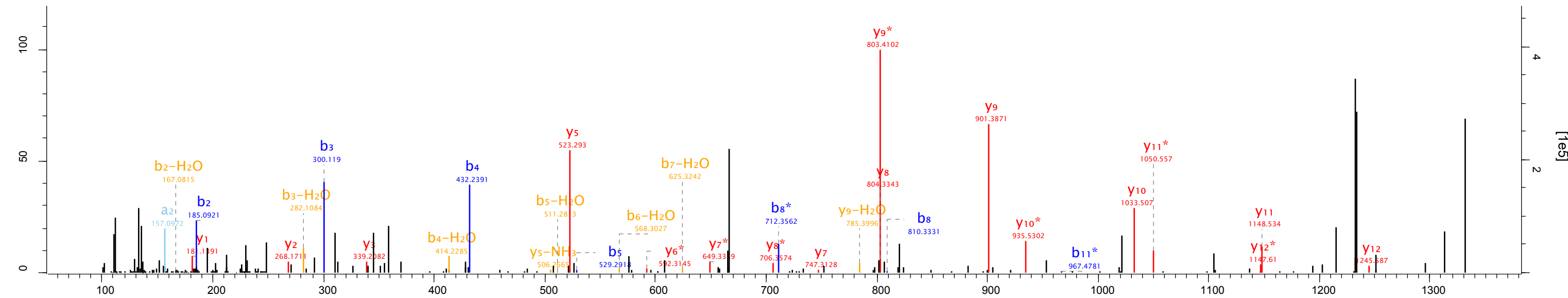
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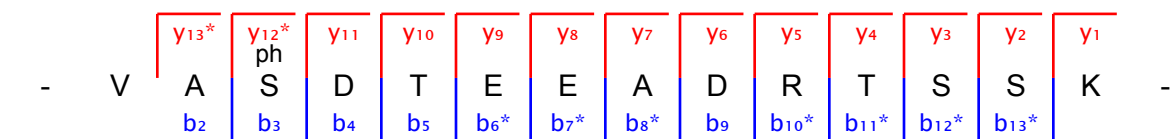
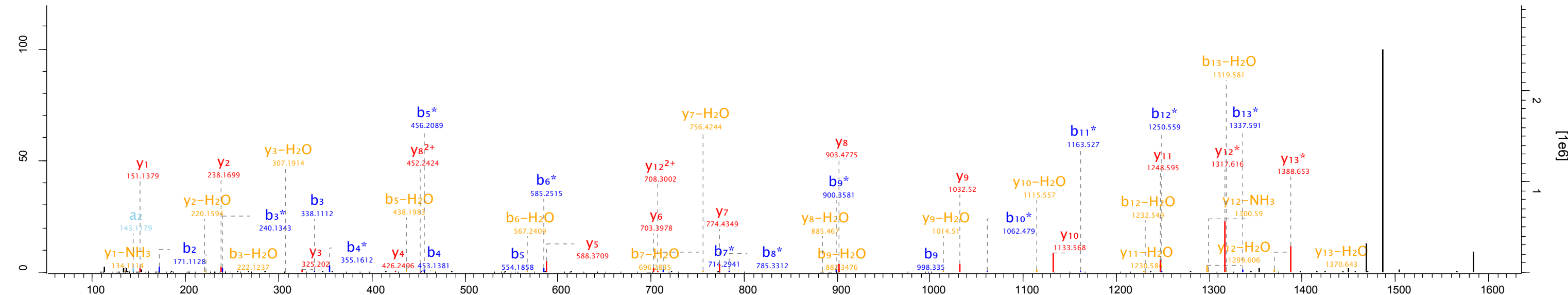


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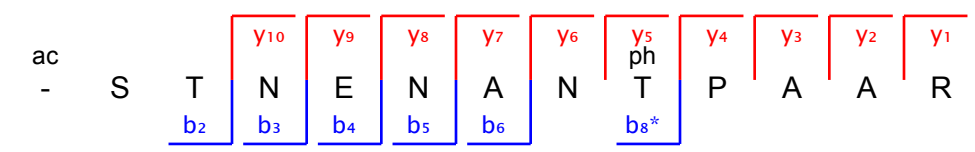
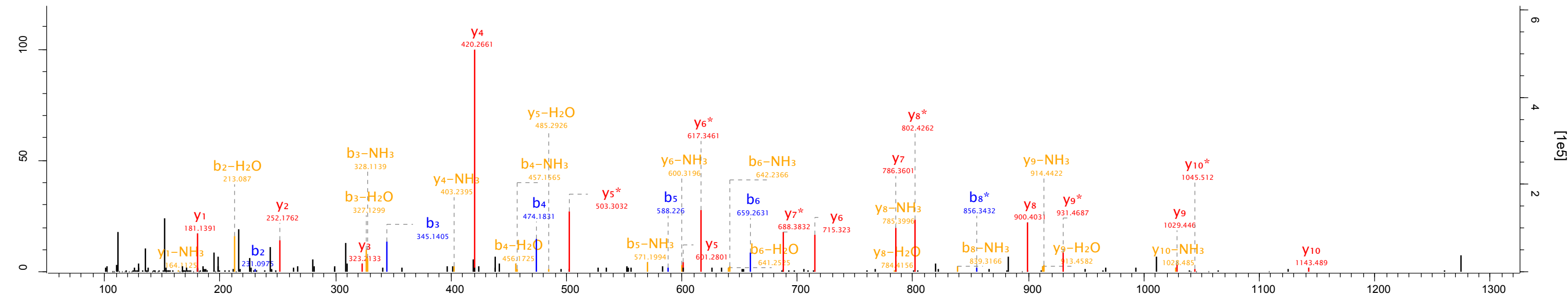
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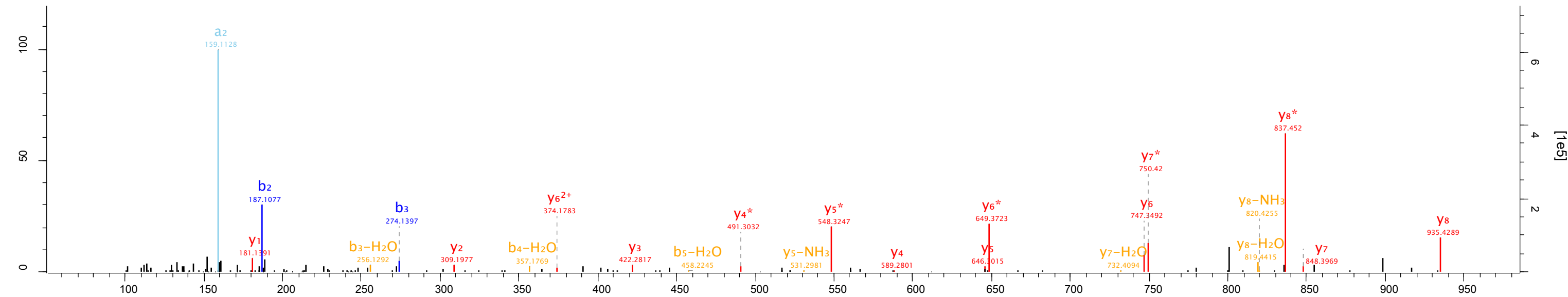




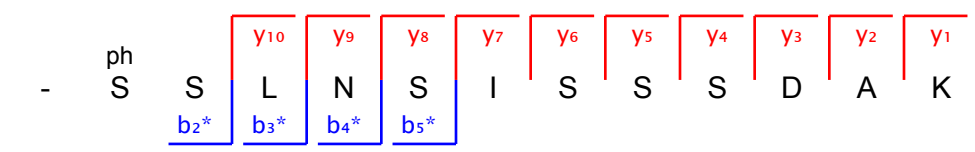
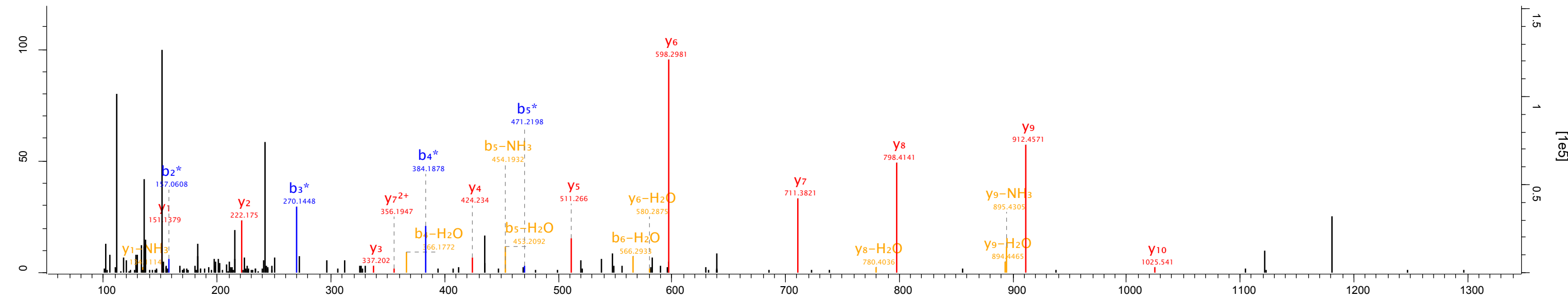
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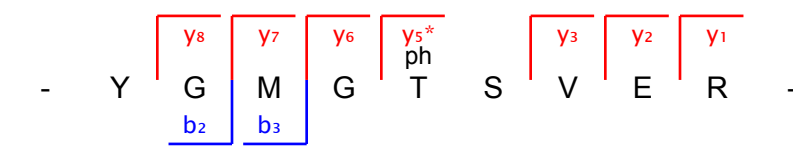
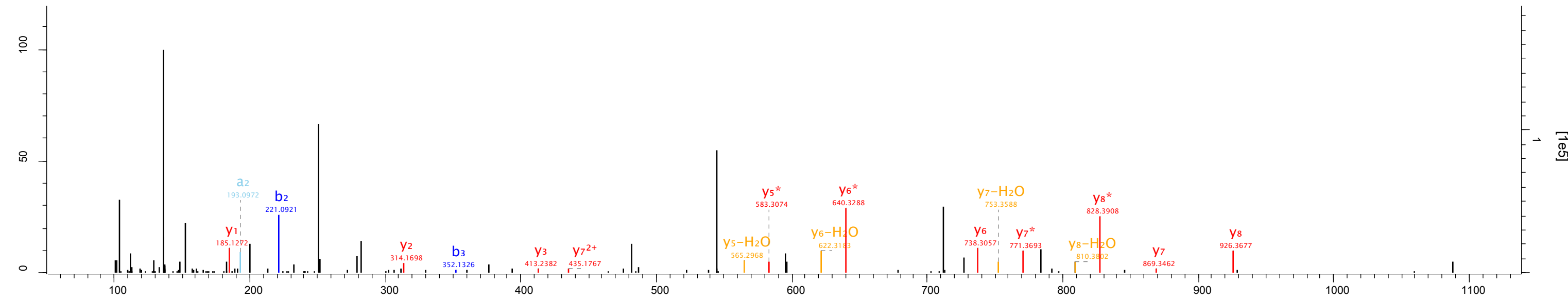
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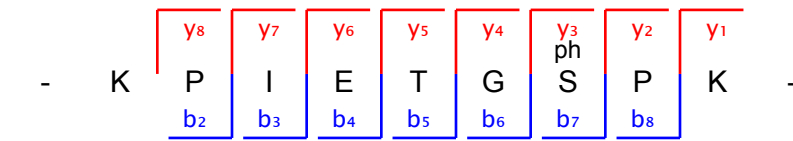
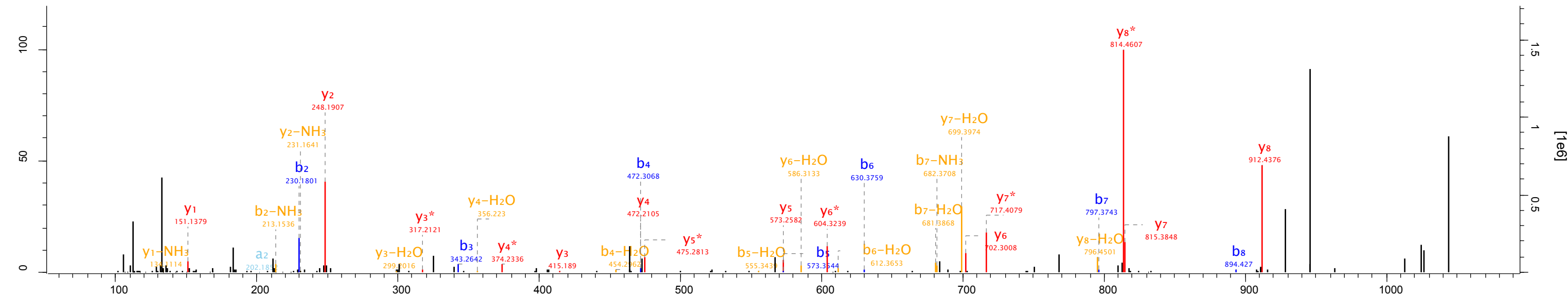


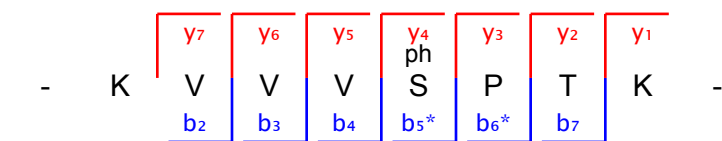
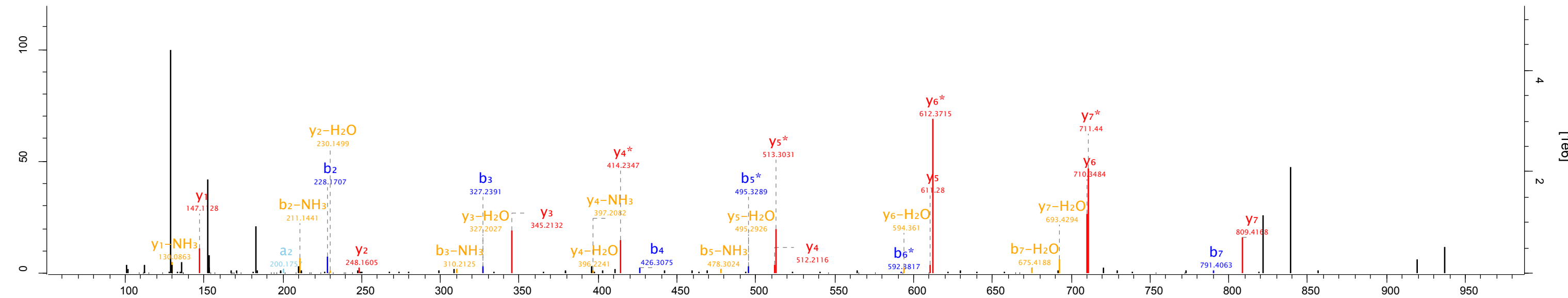
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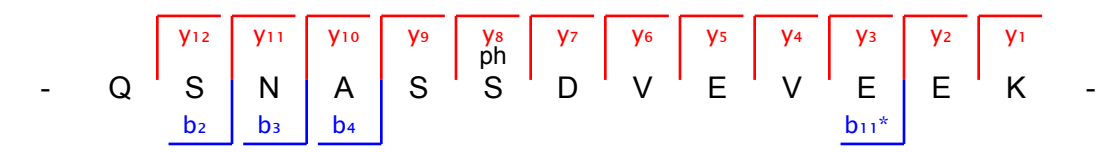
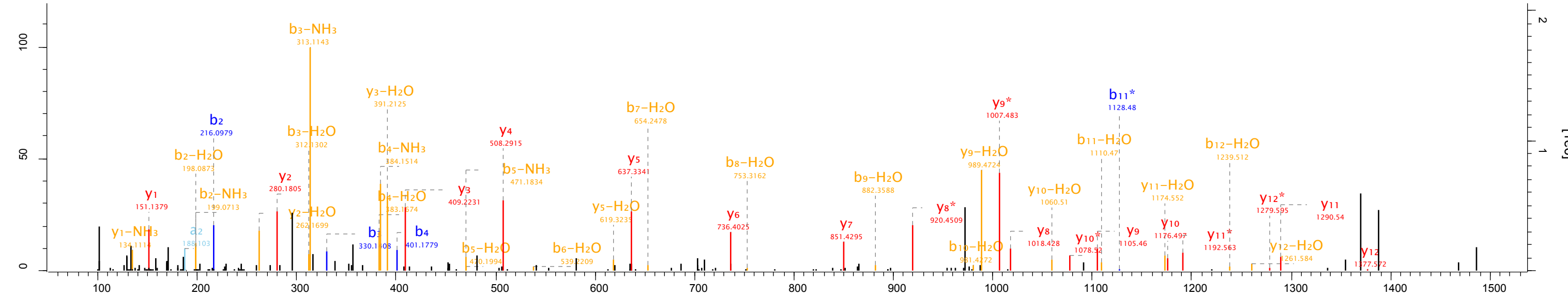
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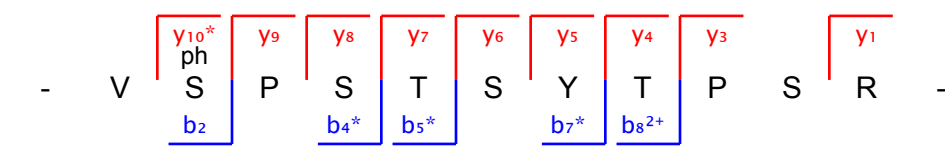
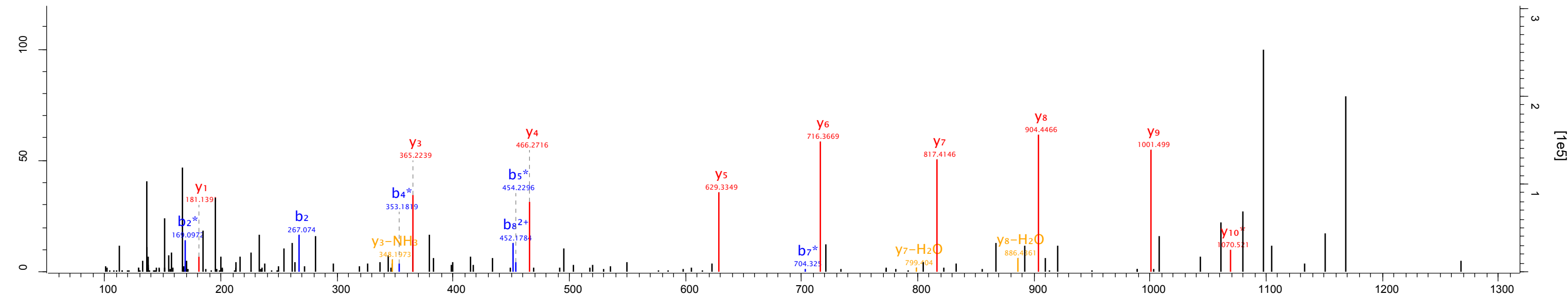




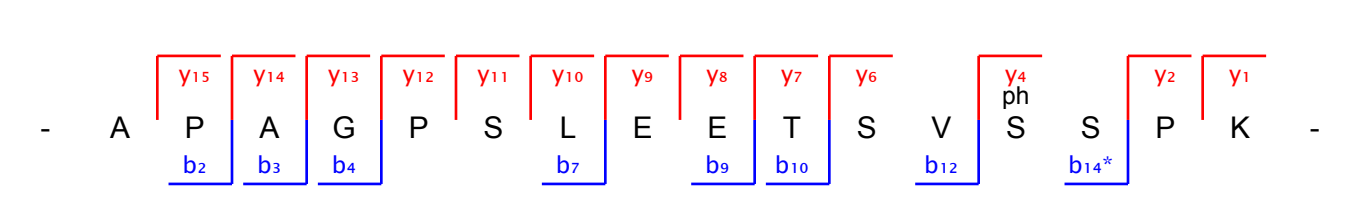
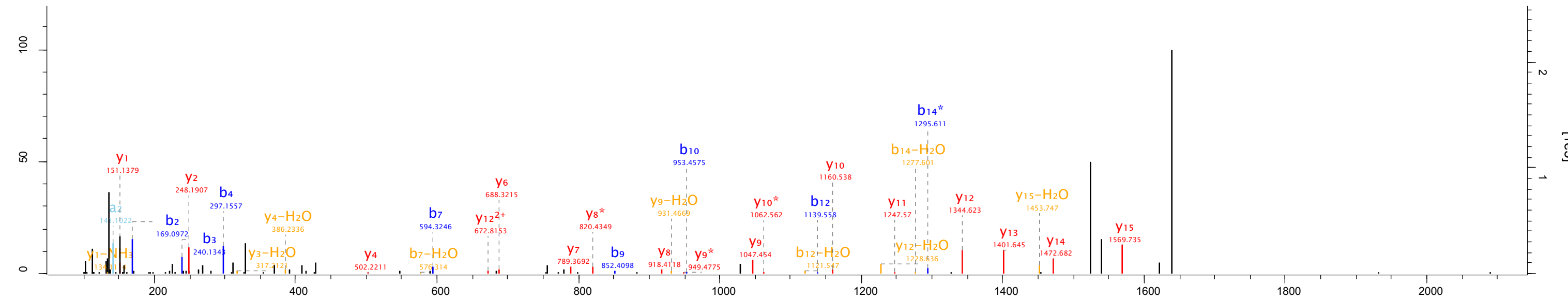
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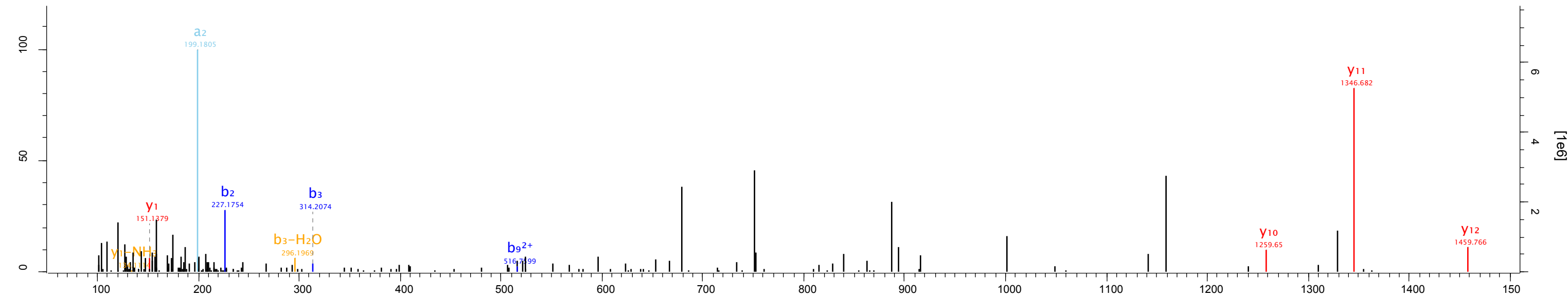
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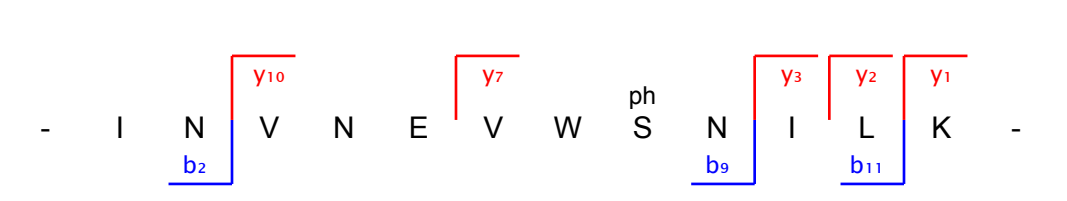
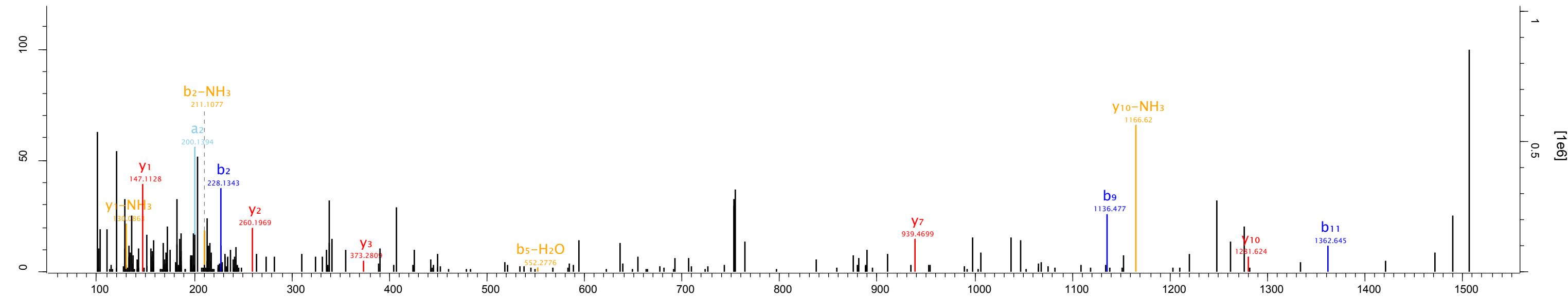
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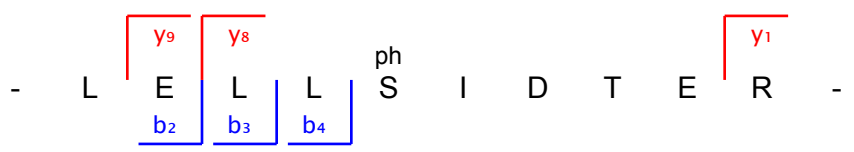
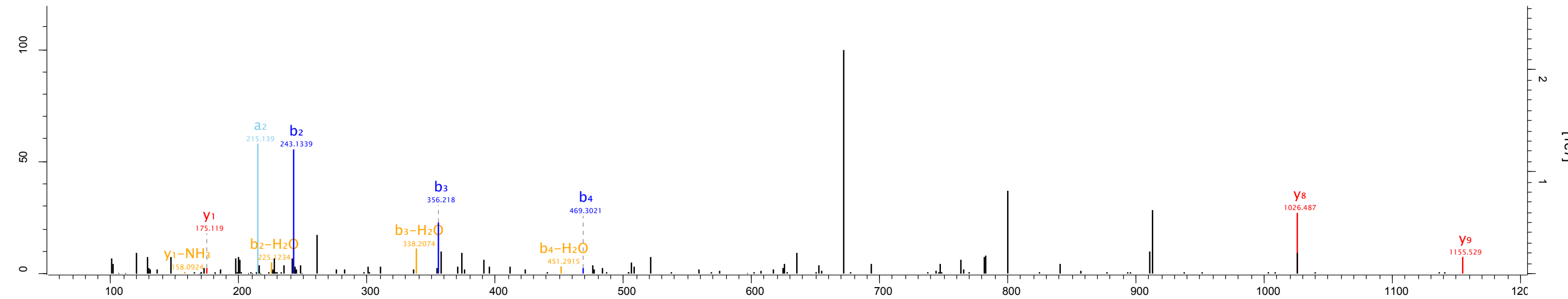
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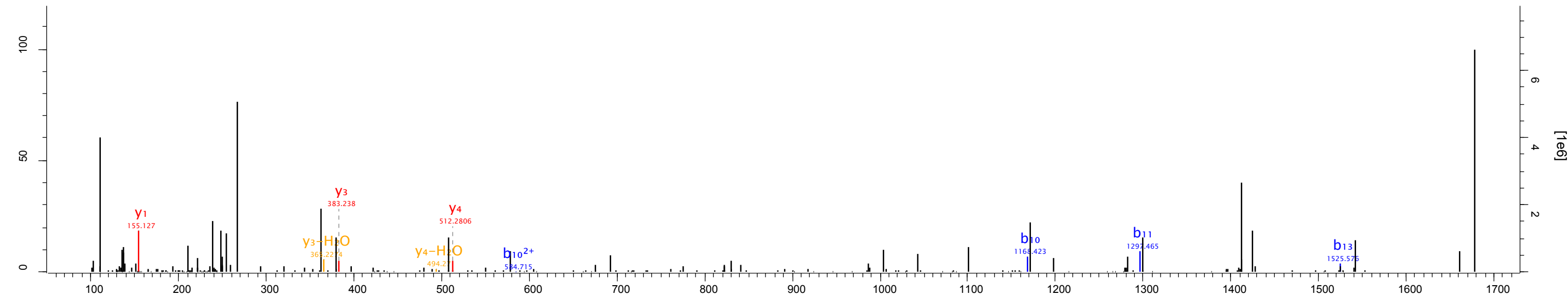
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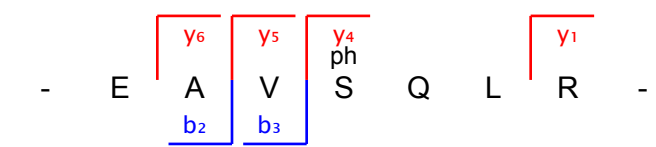
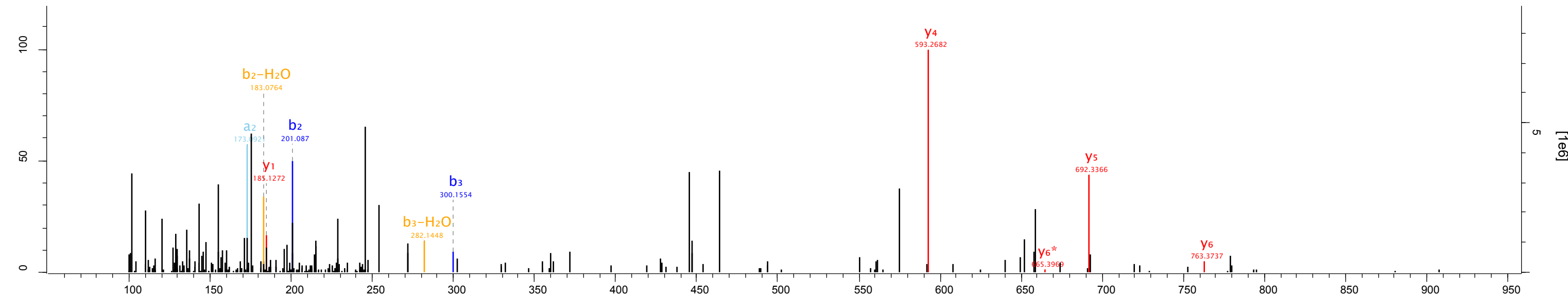
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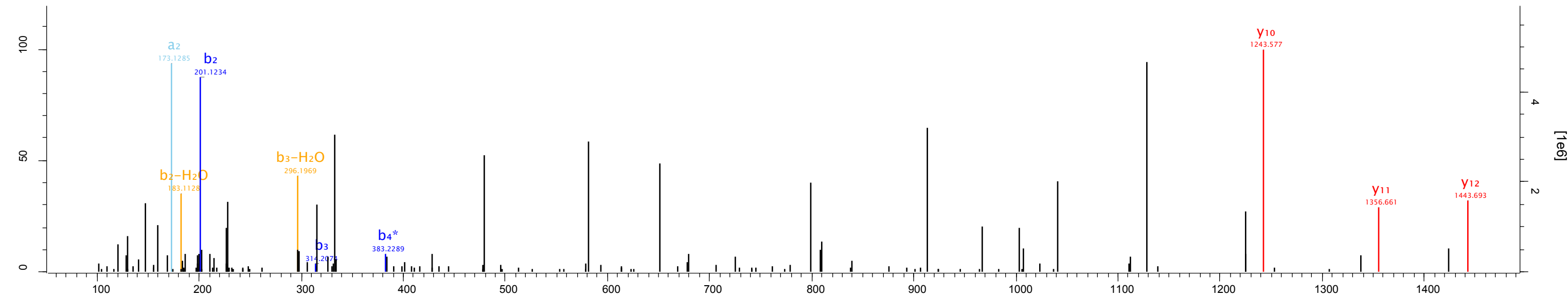
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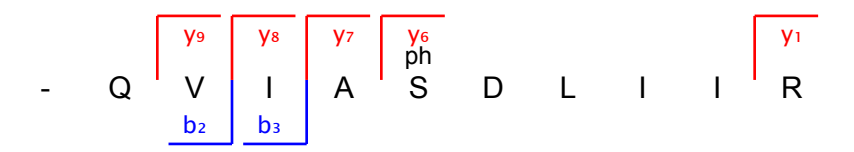
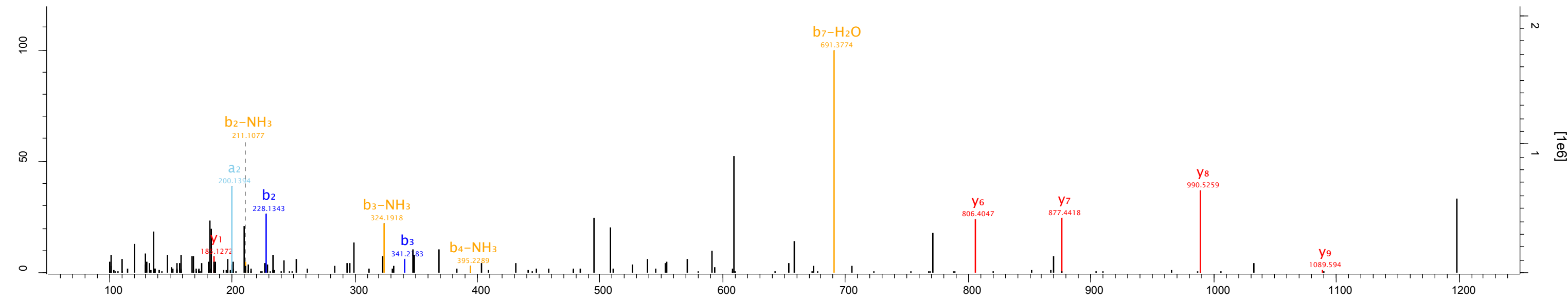


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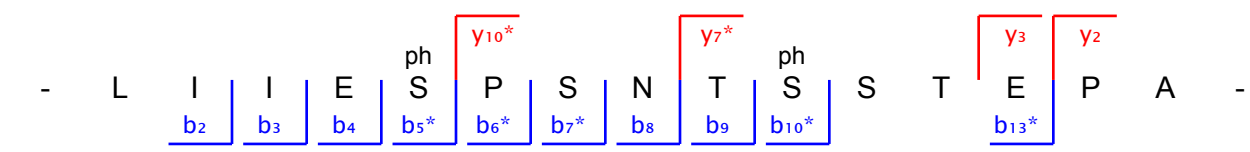
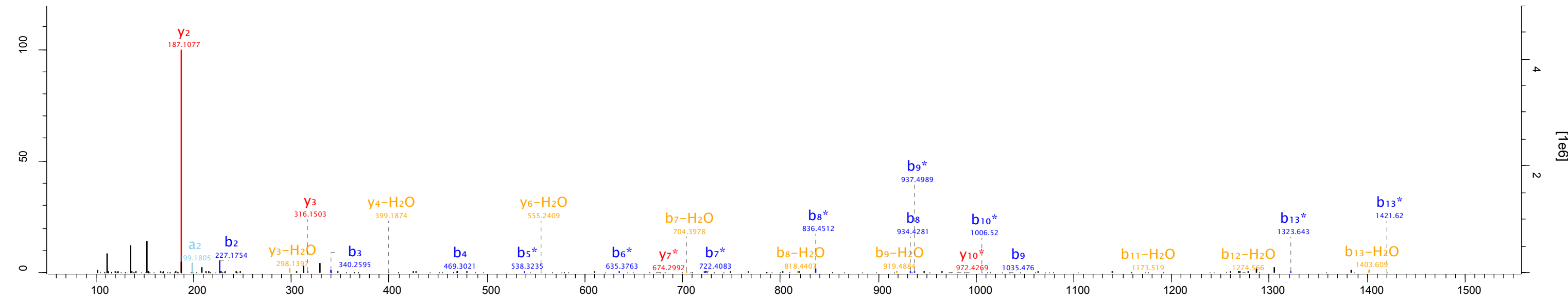
b₂
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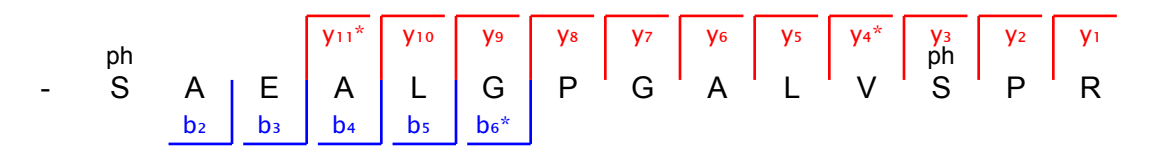
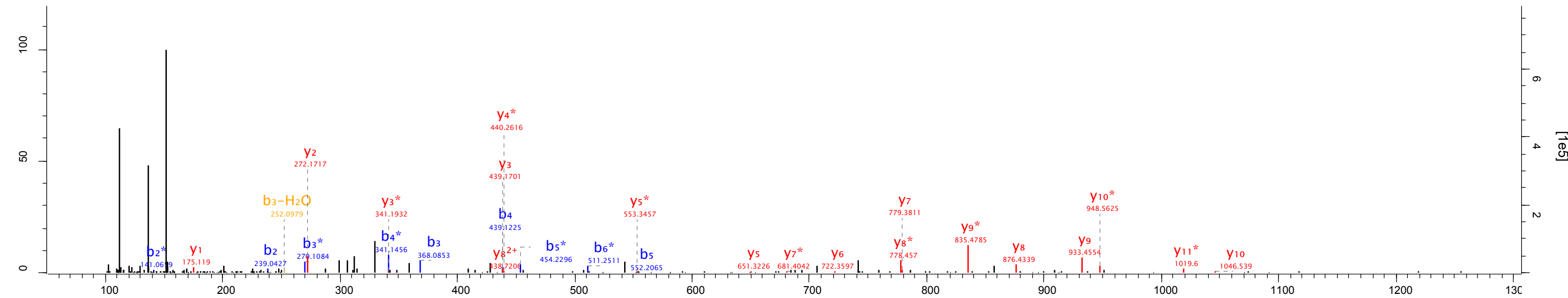
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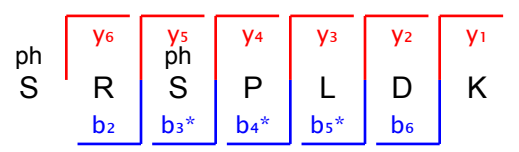
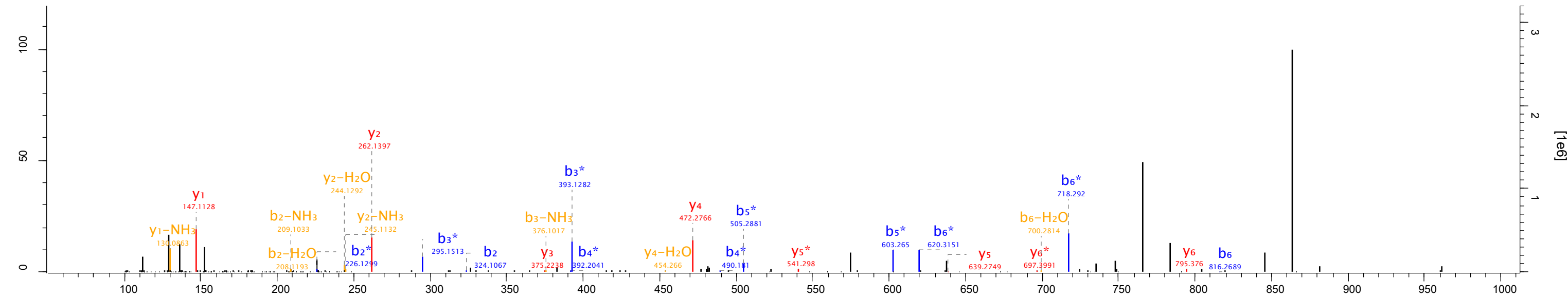
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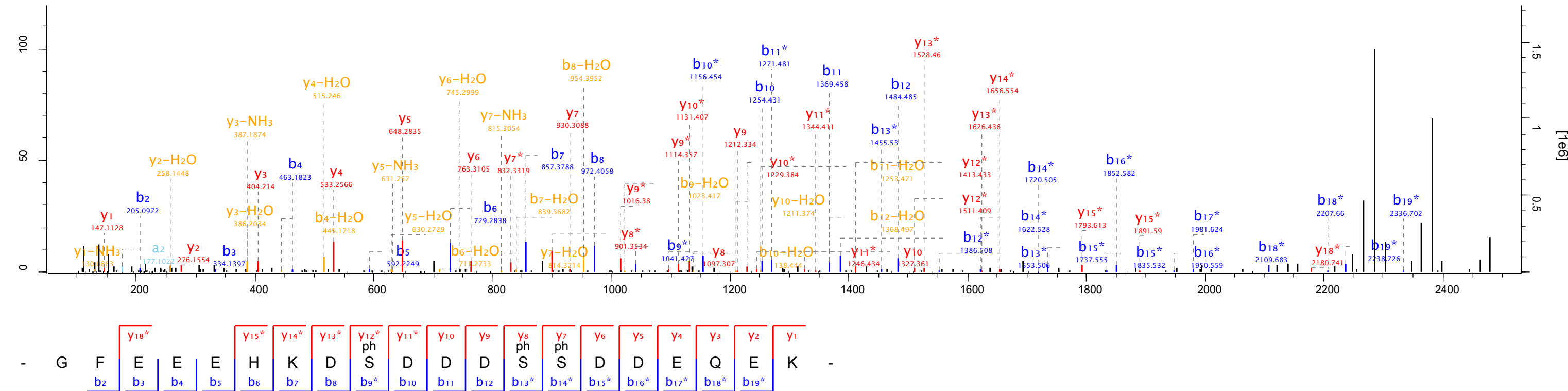


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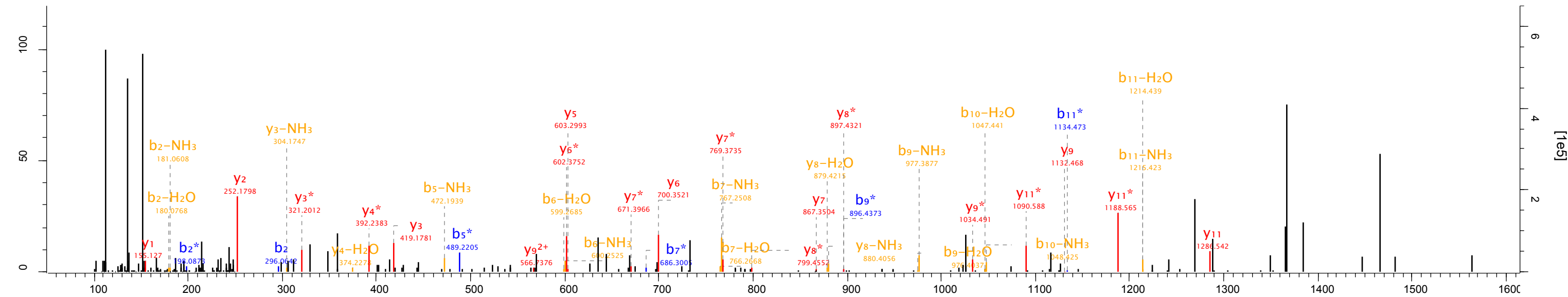


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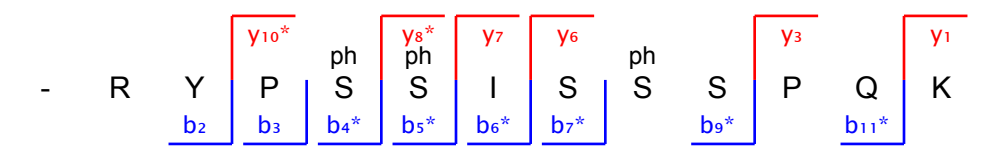
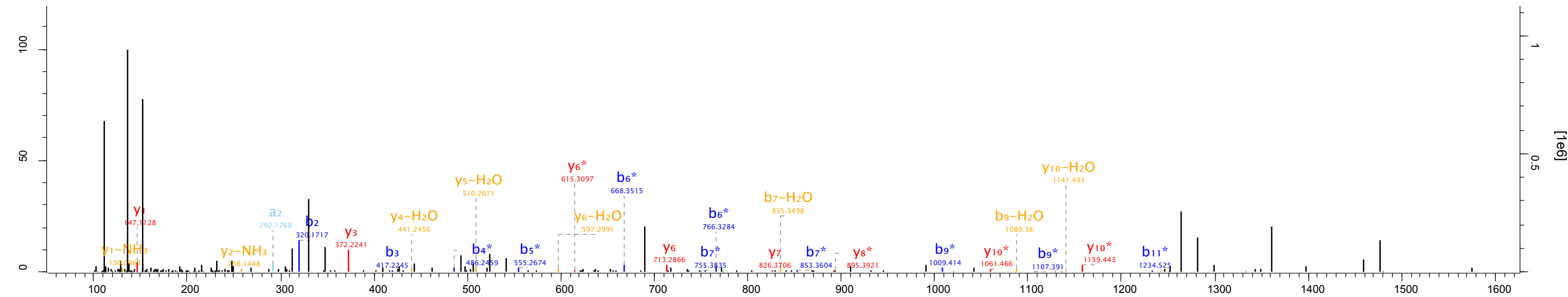




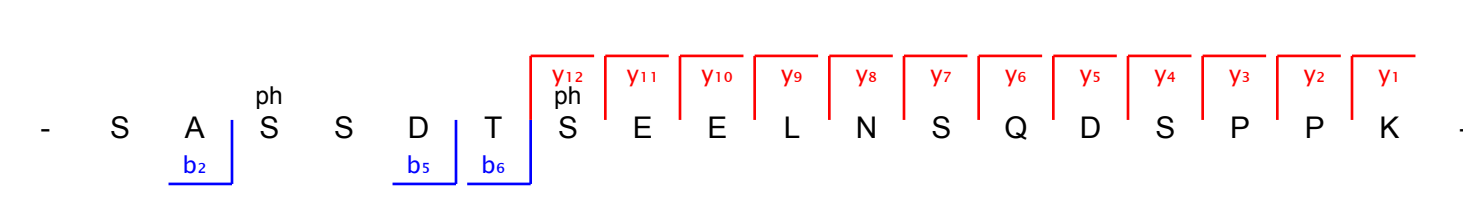
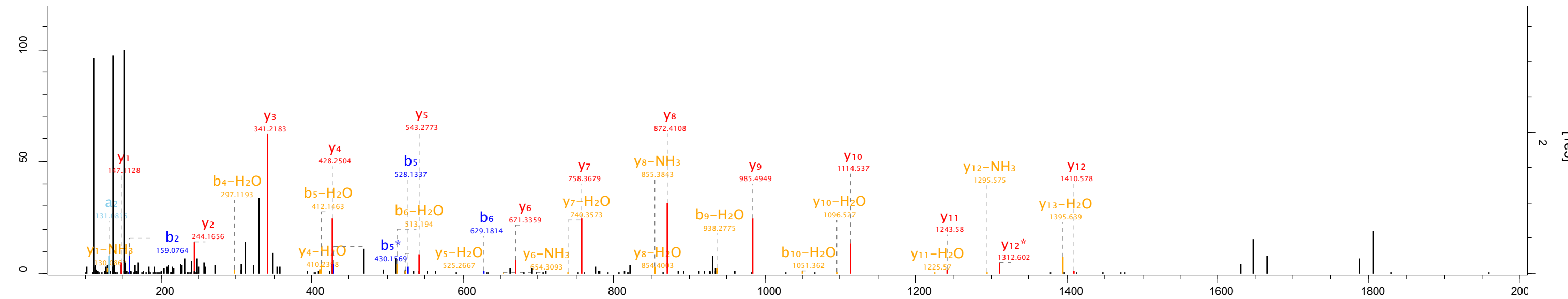
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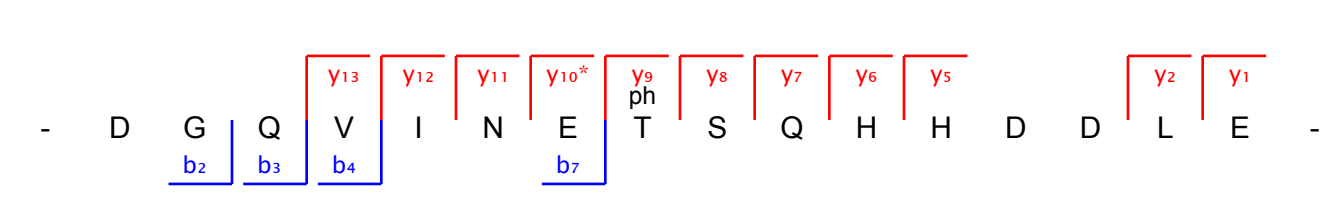
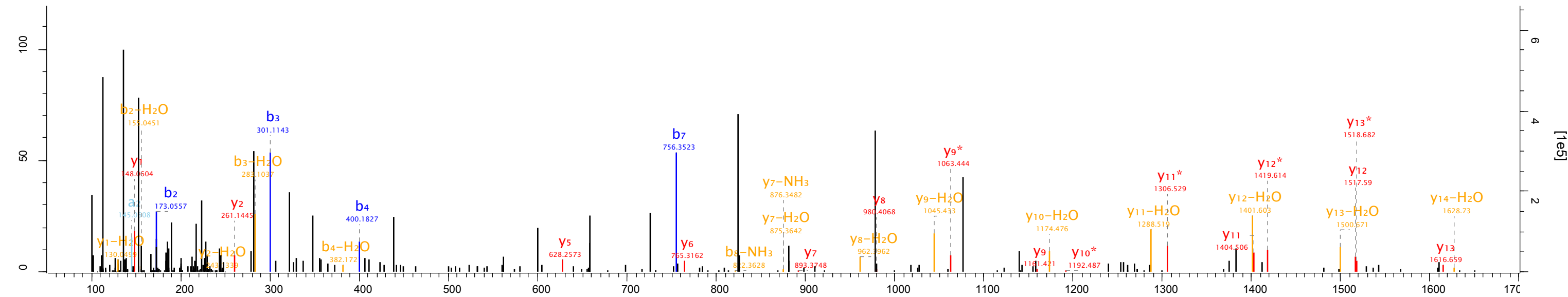
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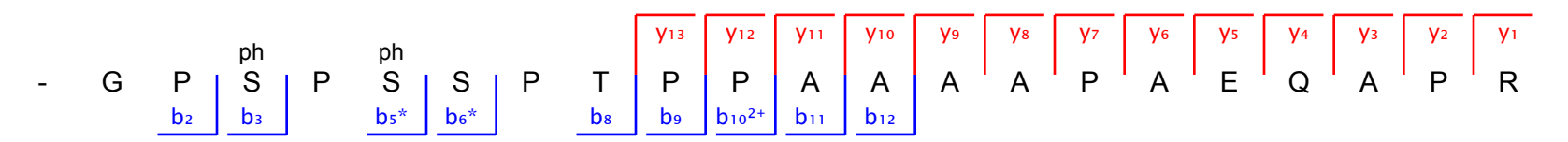
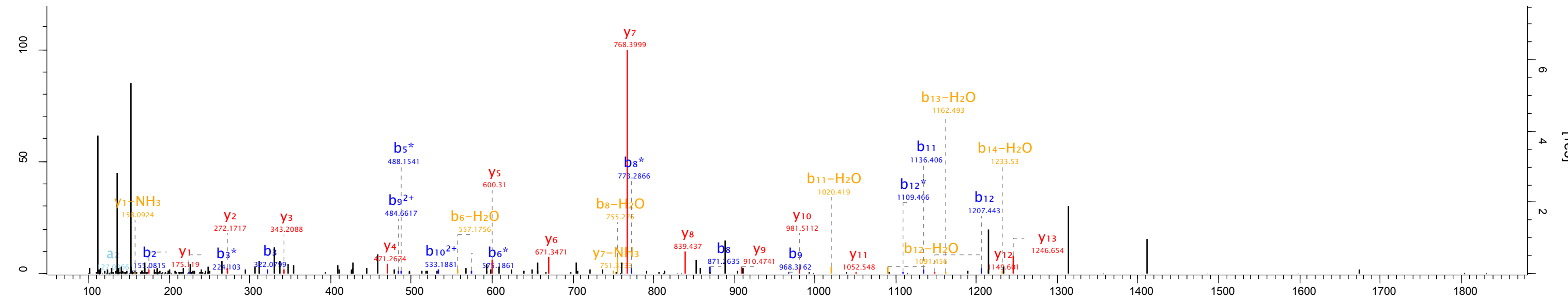


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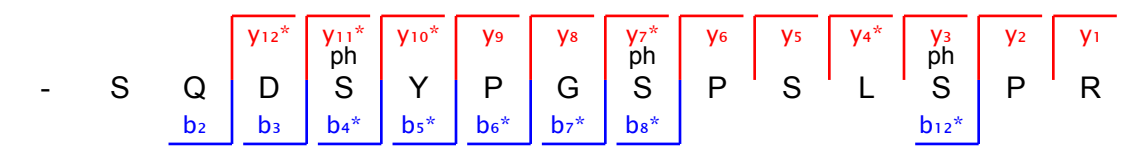
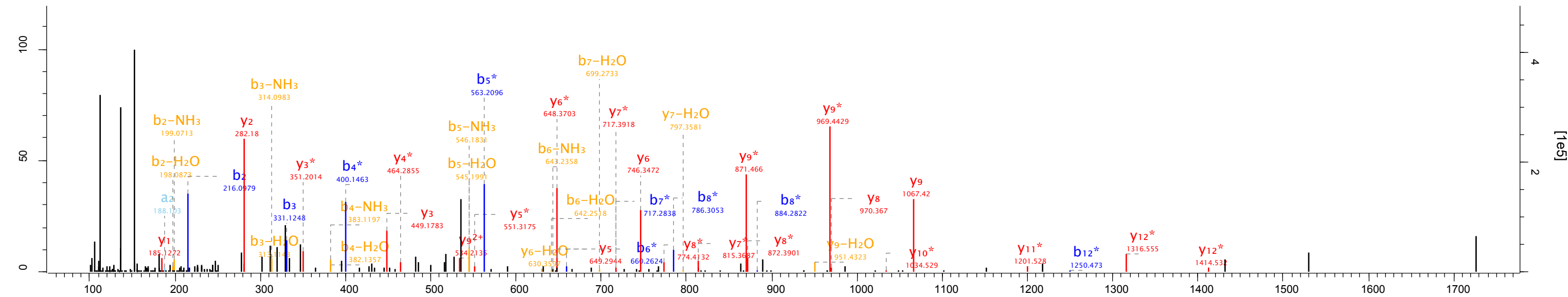


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20171215_MaS_33SR_LMH_phospho_01

Scan Method Score m/z Gene names
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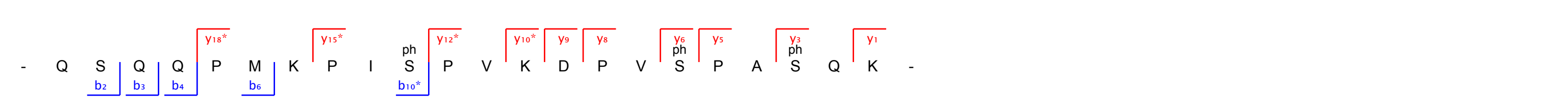
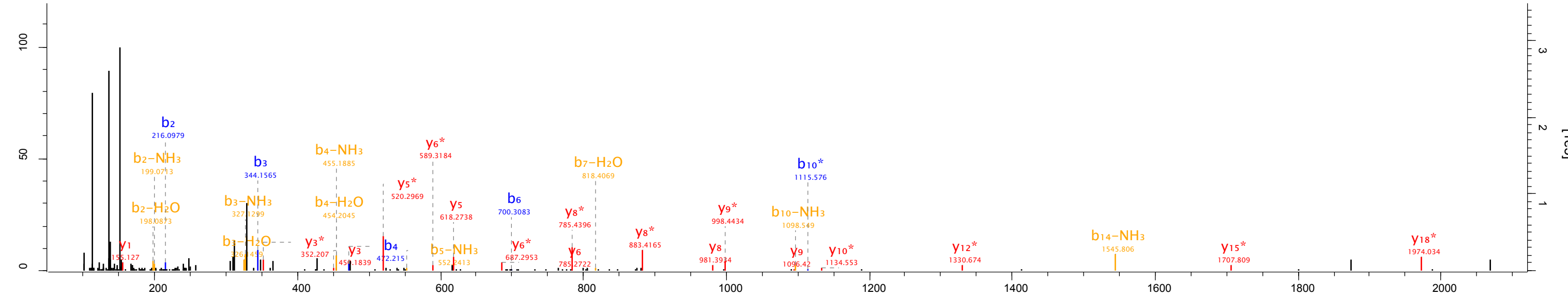


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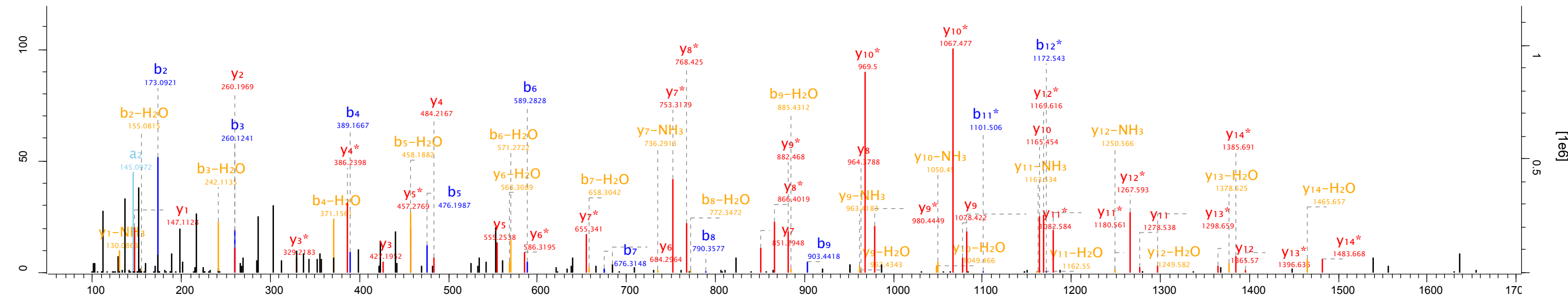


Raw file Scan Method Score m/z Gene names

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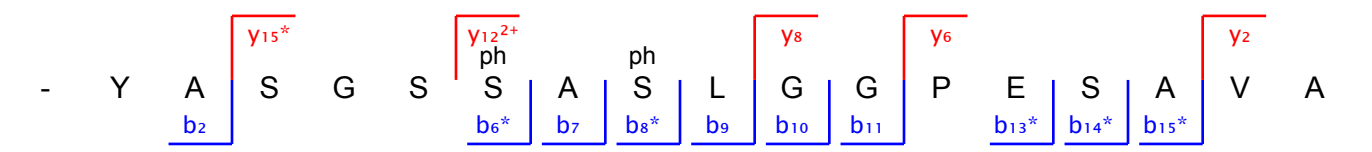
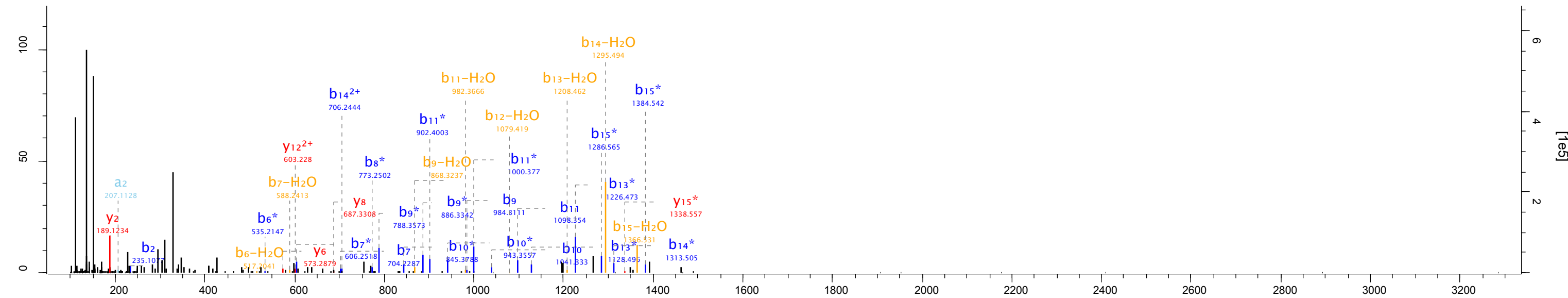
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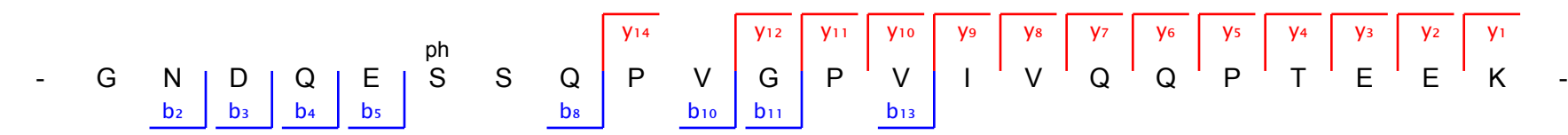
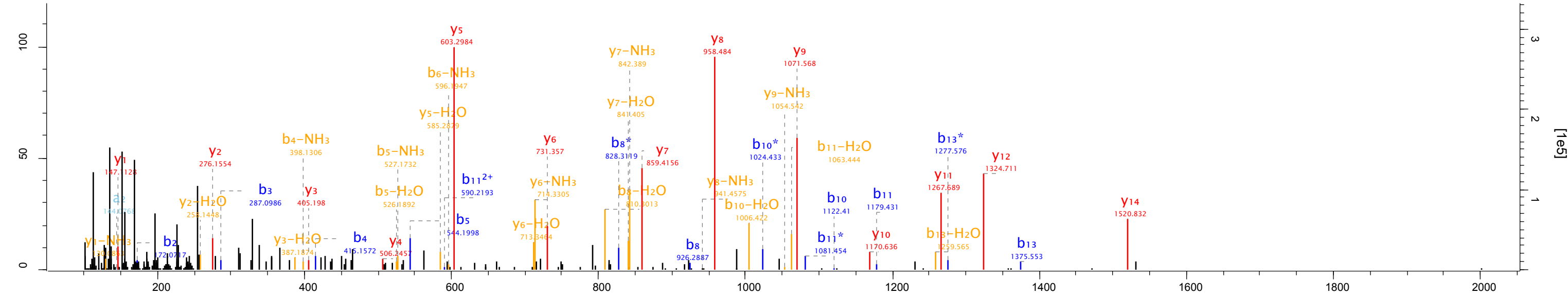
- T A S E S I S N L S E A G S I K -

b2
b3
b4
b5
b6
b7
b8
b9
b11*
b12*
y14*
y13*
y12
y11
y10
y9
y8
y7^{ph}
y6
y5
y4
y3^{ph}
y2
y1

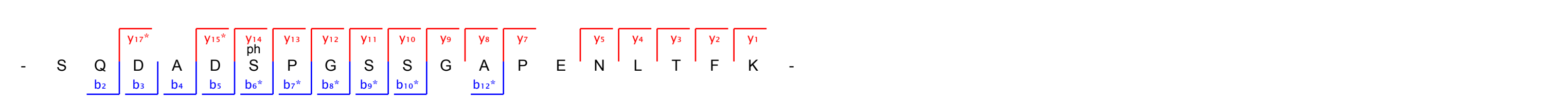
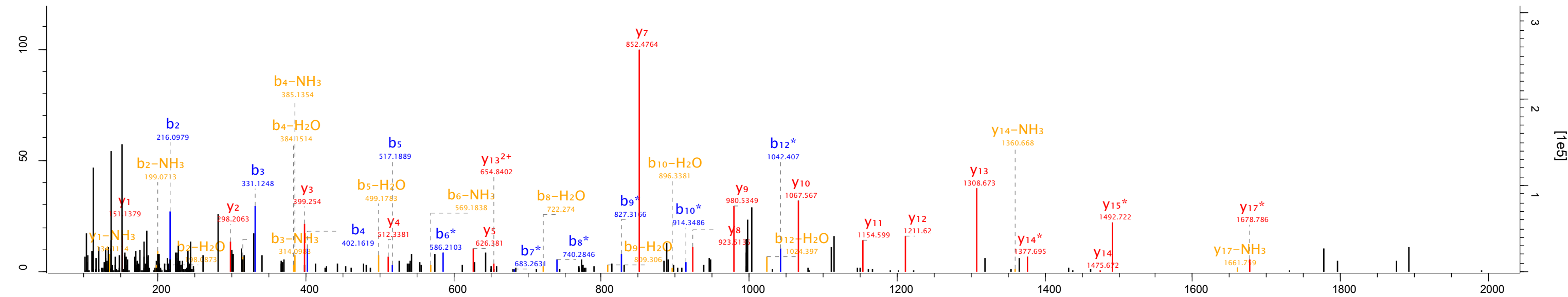
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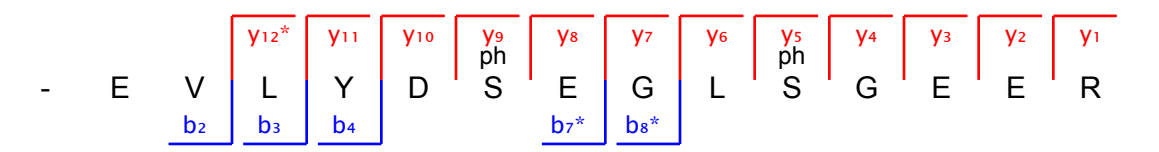
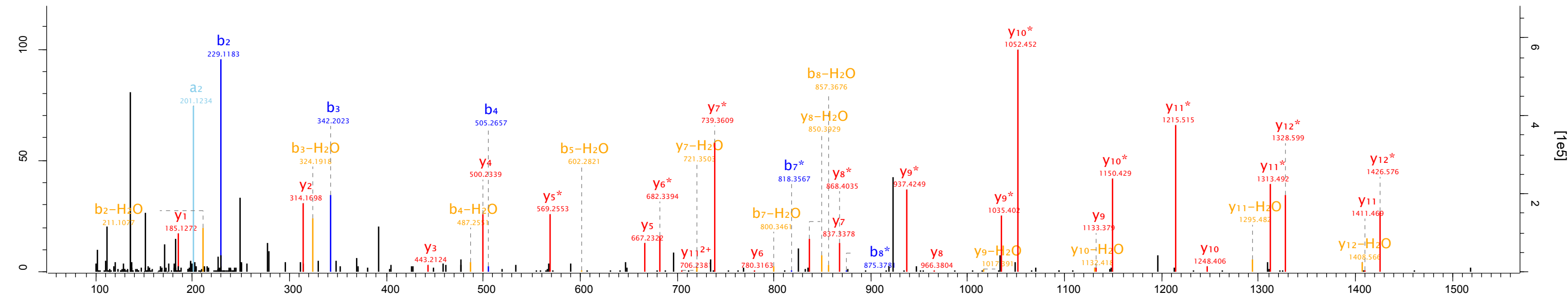
20171215_MaS_33SR_LMH_phospho_02 10725 FTMS; HCD 106.43 816.04 PAGE5



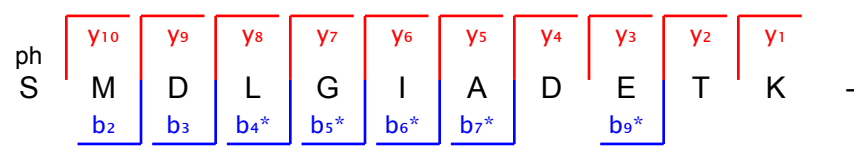
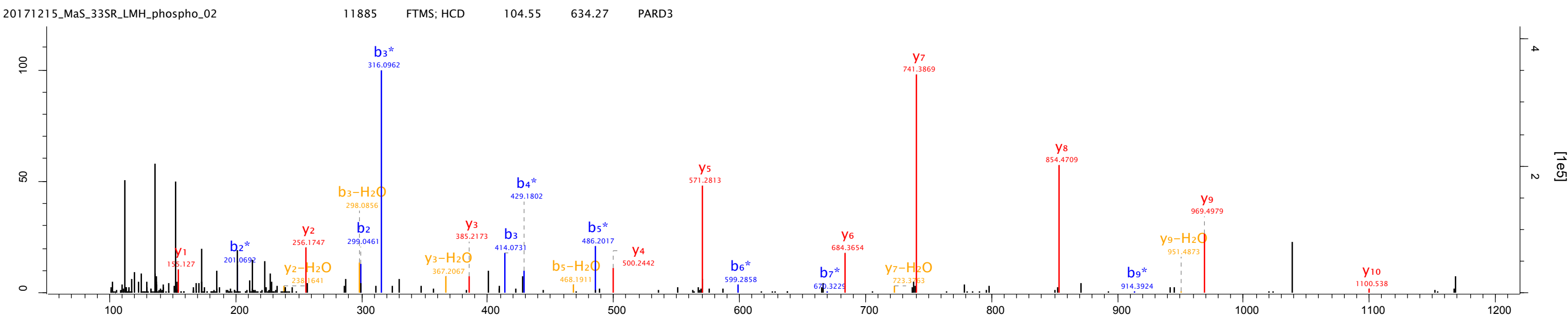
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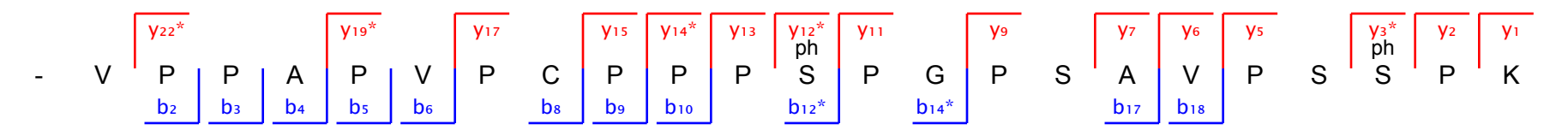
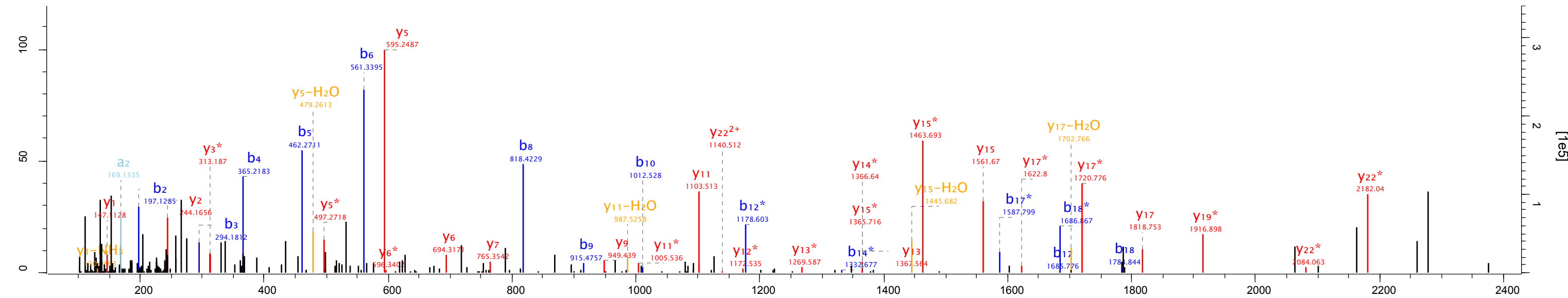
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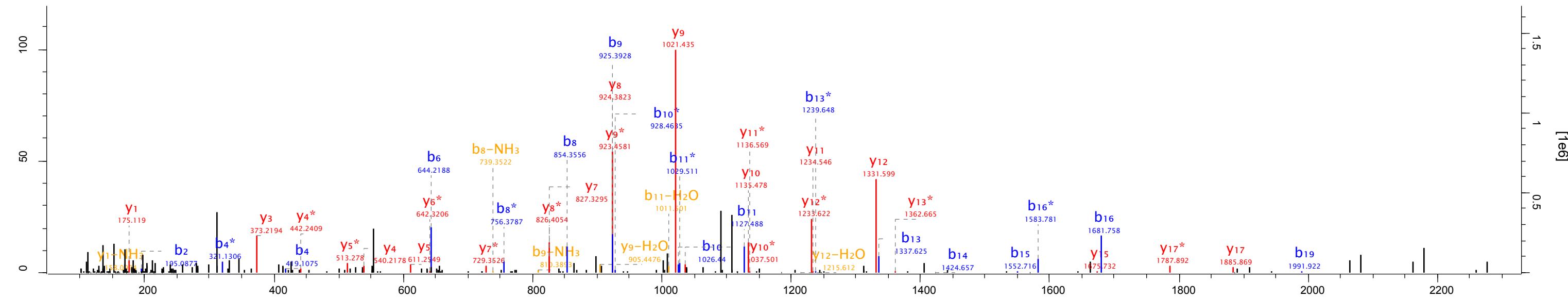


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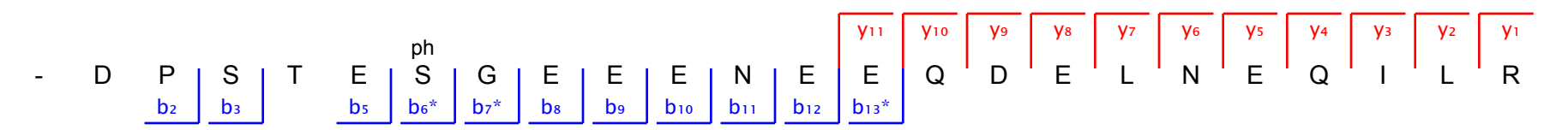
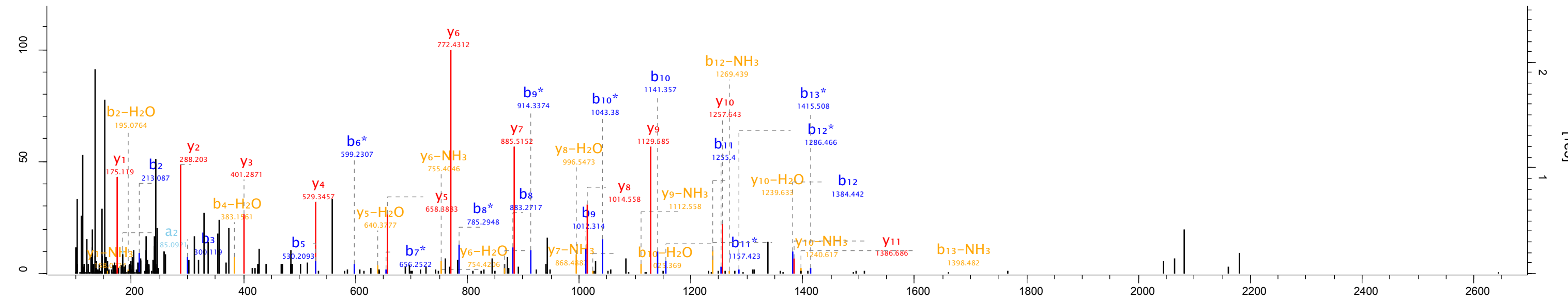
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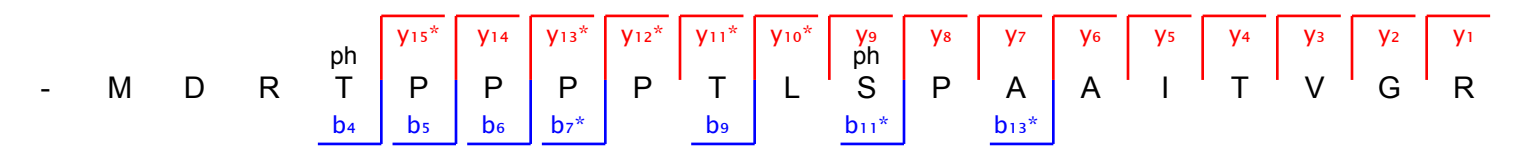
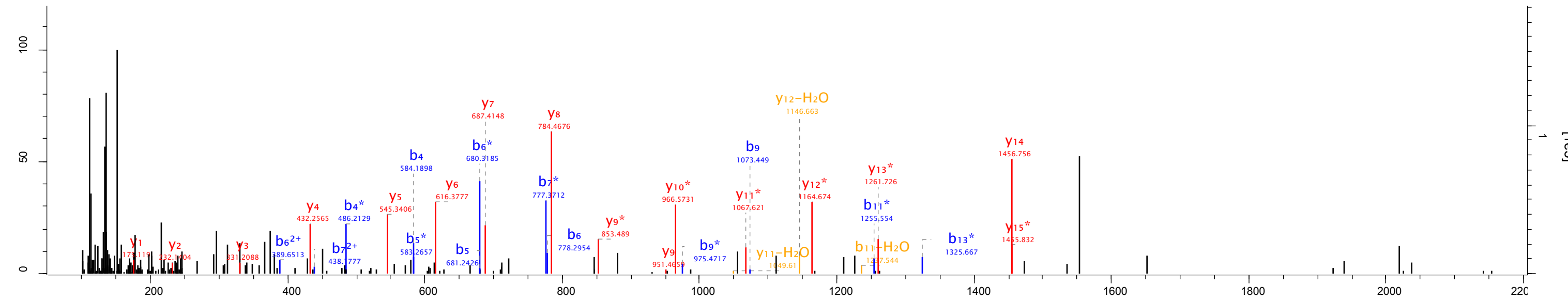
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20171215_MaS_33SR_LMH_phospho_02

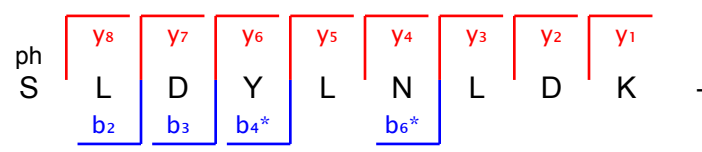
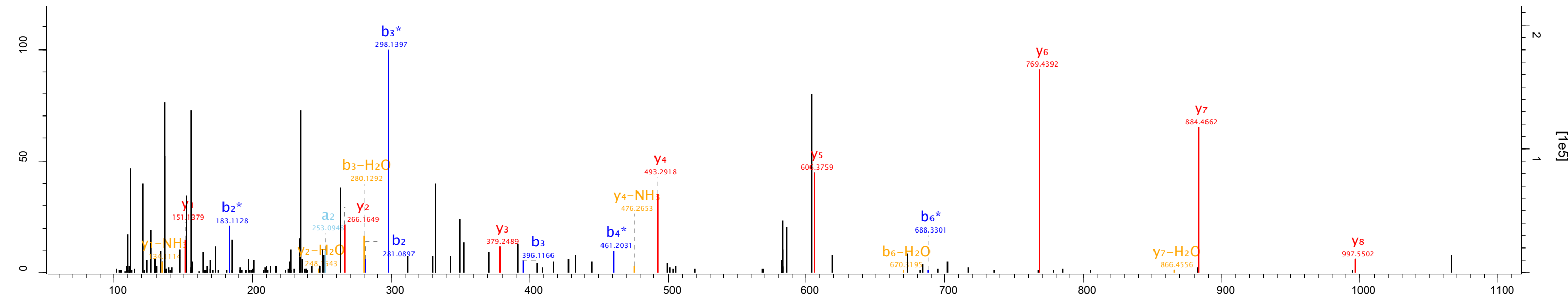
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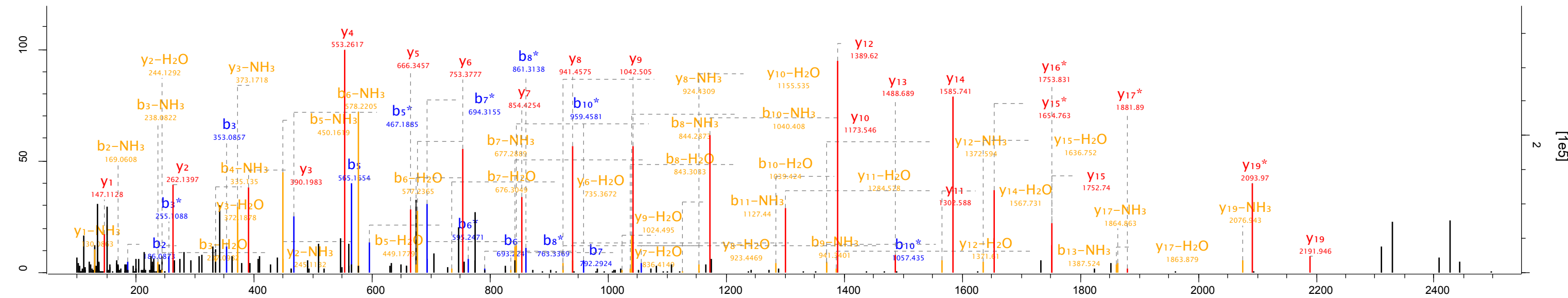


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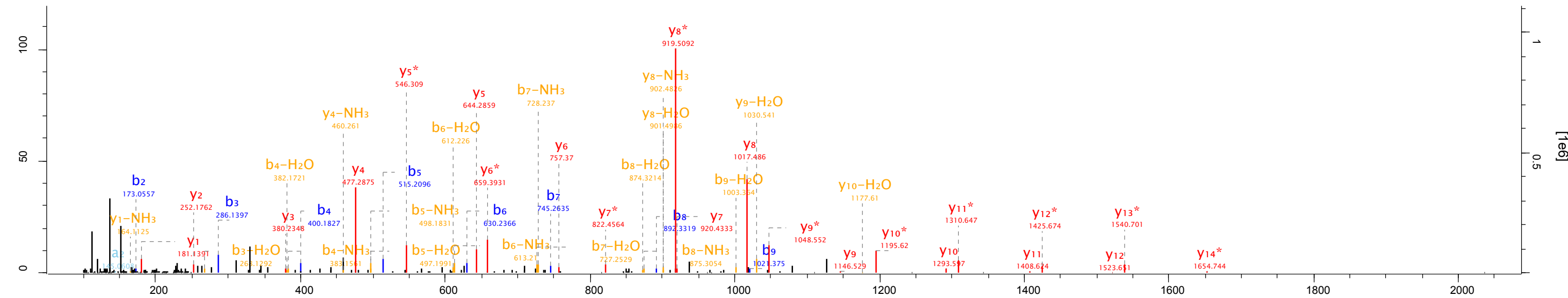




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 b₂ b₃ b₅ b₆ b₇ b₈^{*} b₁₀^{*}

y₁₉ y₁₇^{*} y₁₆^{*} y₁₅ ph y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

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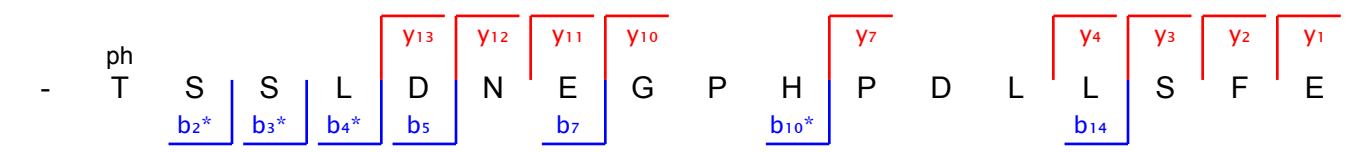
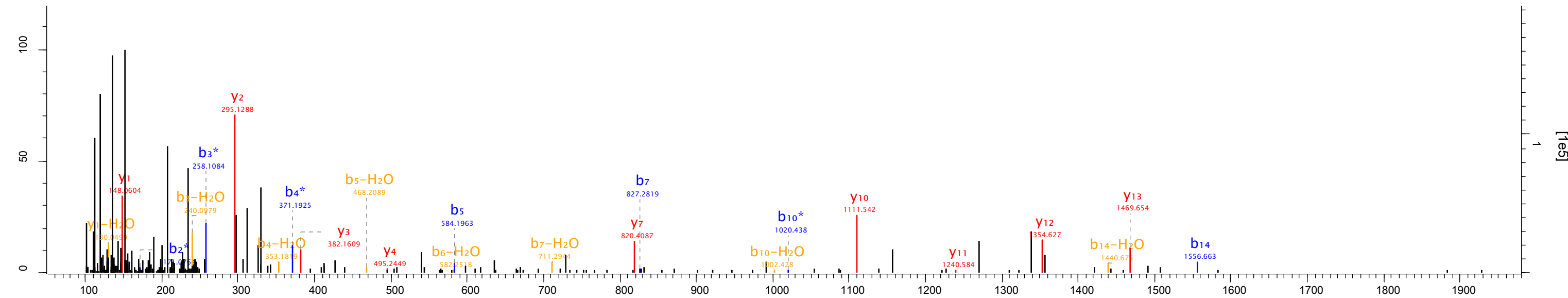


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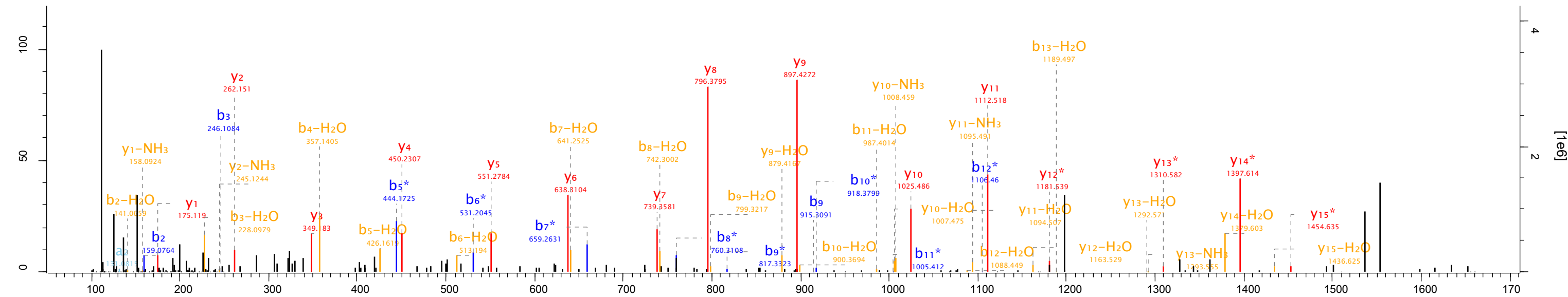
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y₁₄*
y₁₃*
y₁₂
y₁₁
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y₉
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y₆
y₅_{ph}
y₄
y₃
y₂
y₁

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉

Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 17915 Method FTMS; HCD Score 45.71 m/z 969.91 Gene names C1orf226



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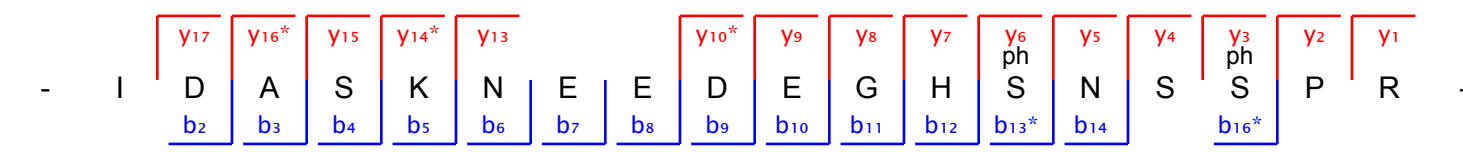
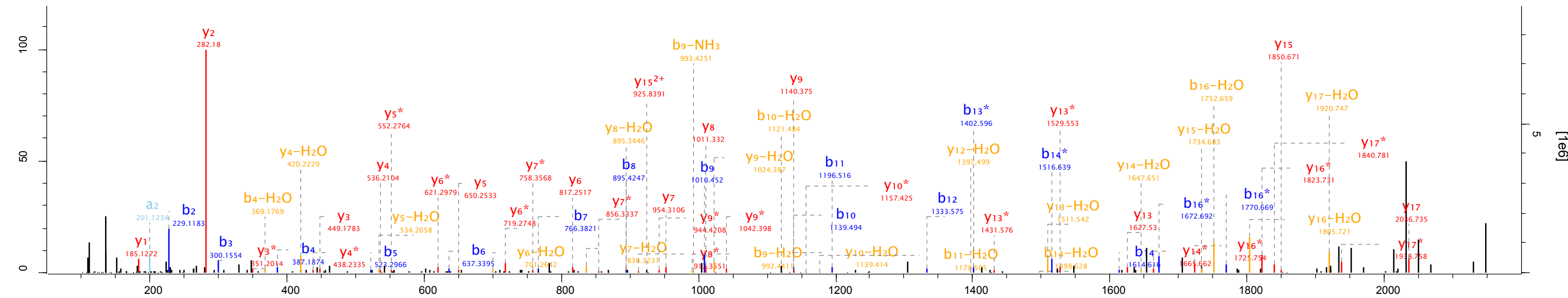


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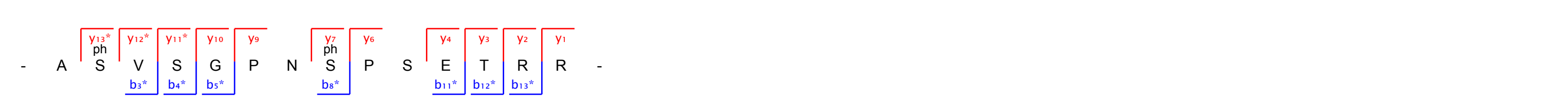
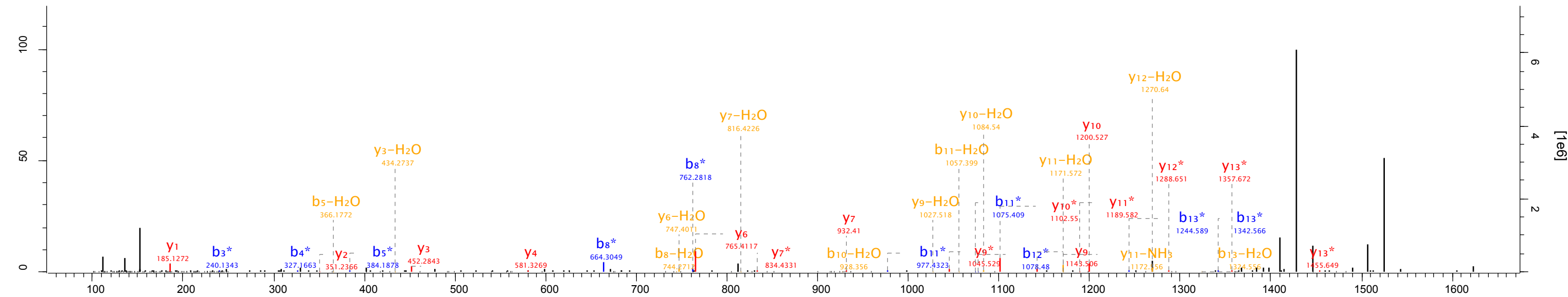
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y12*
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y11
y10
y9
y8
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y6
y5
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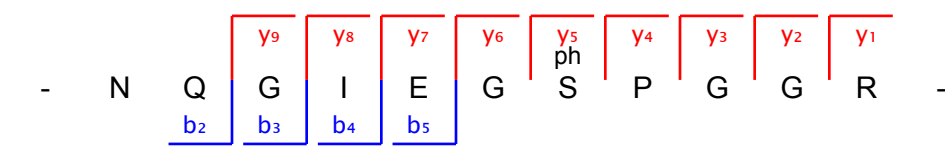
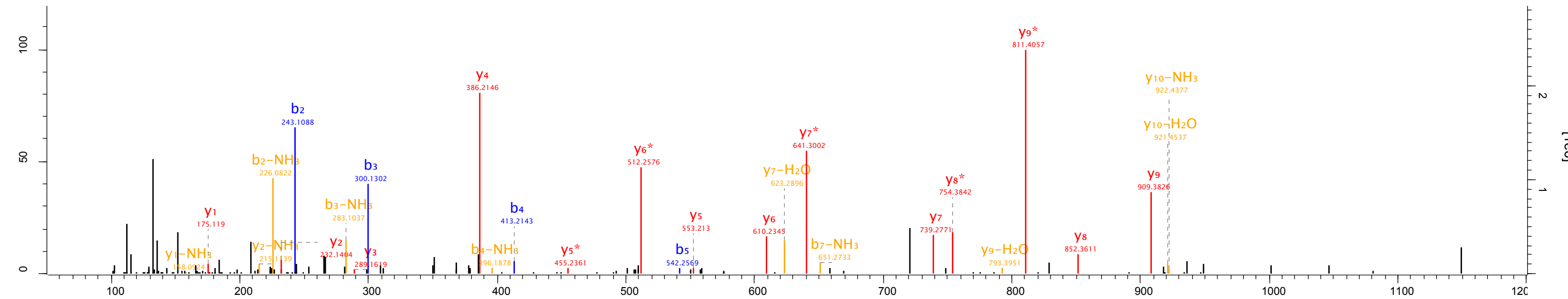
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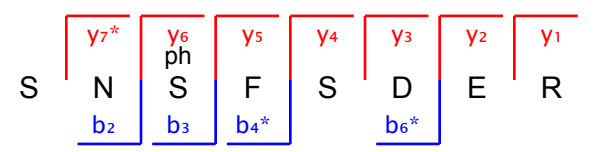
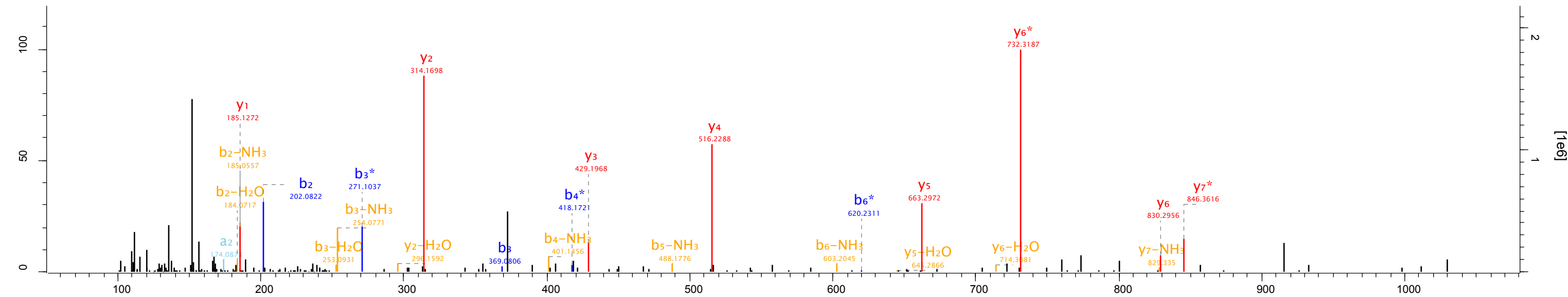
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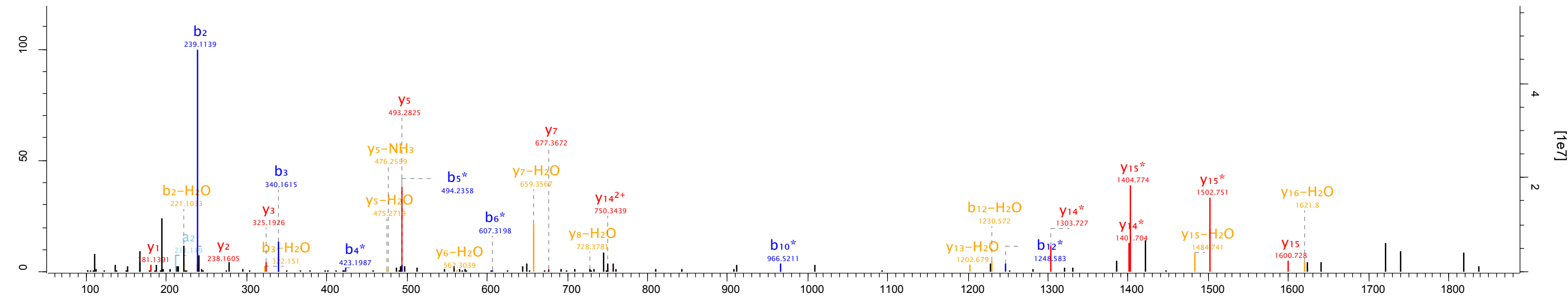
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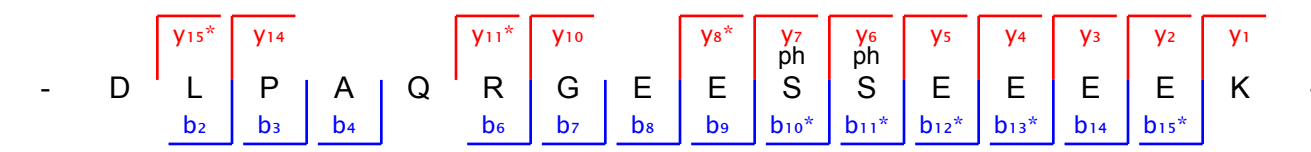
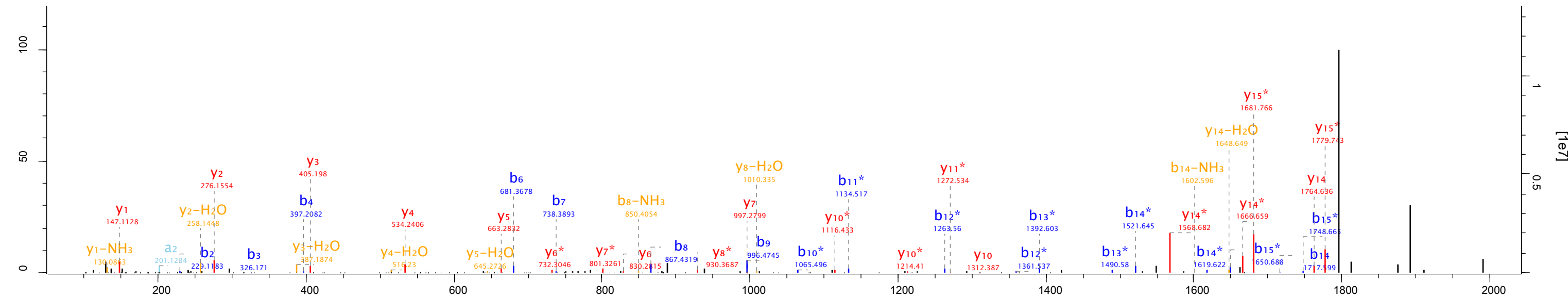
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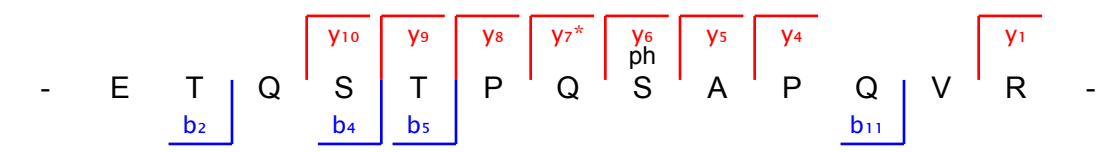
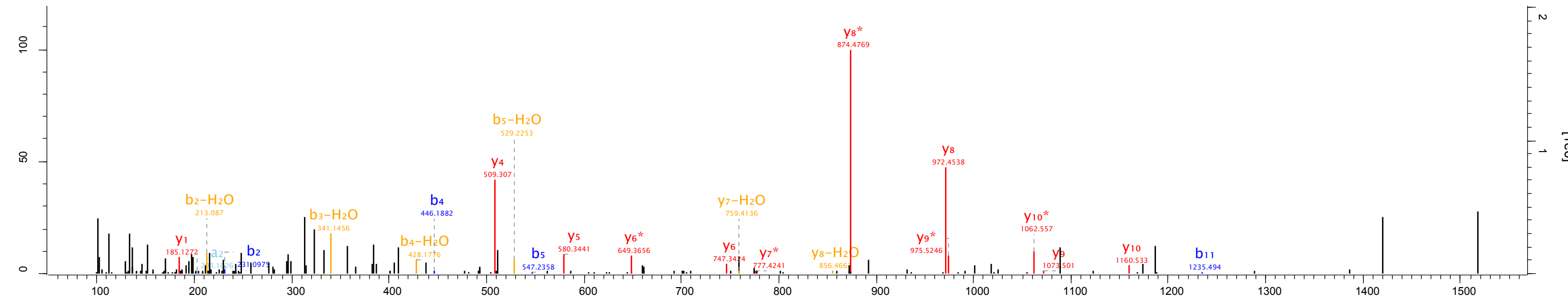
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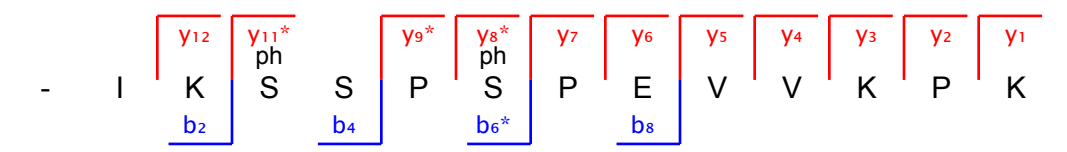
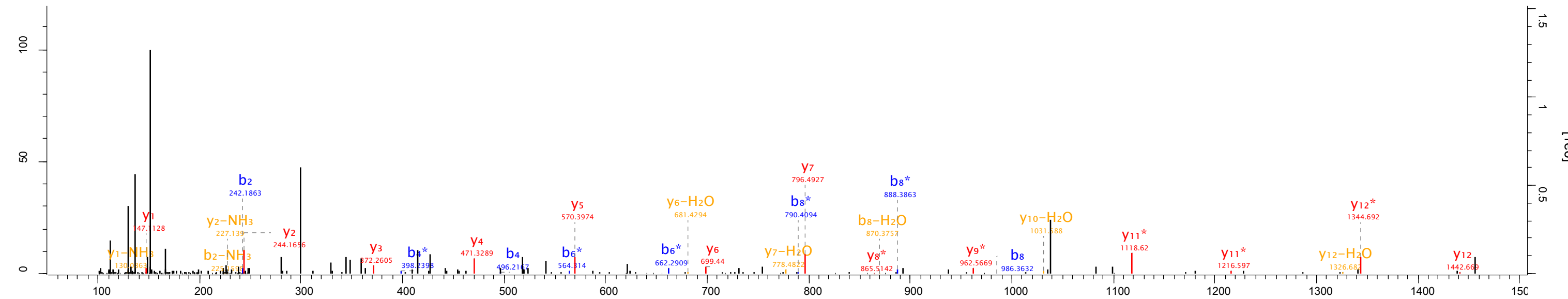
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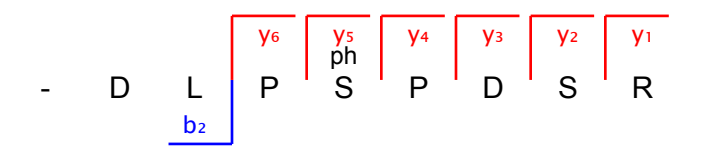
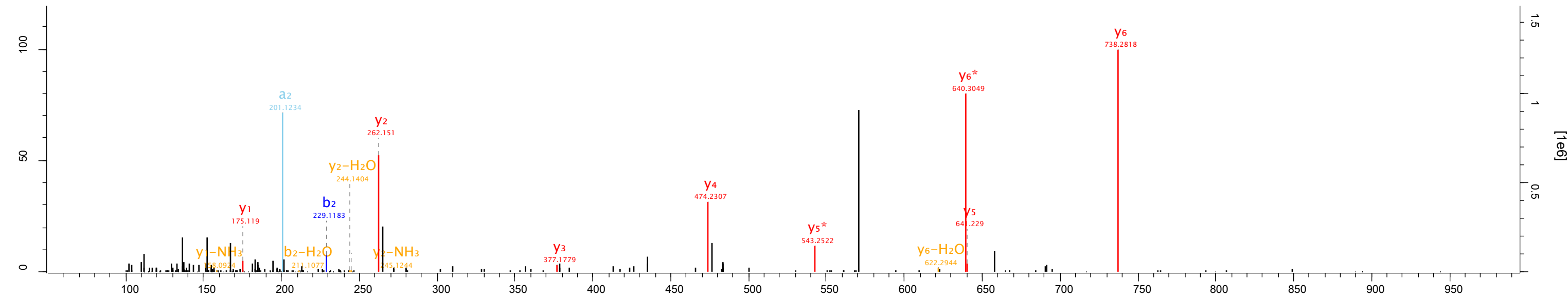
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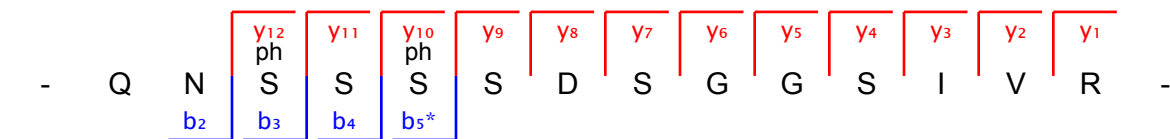
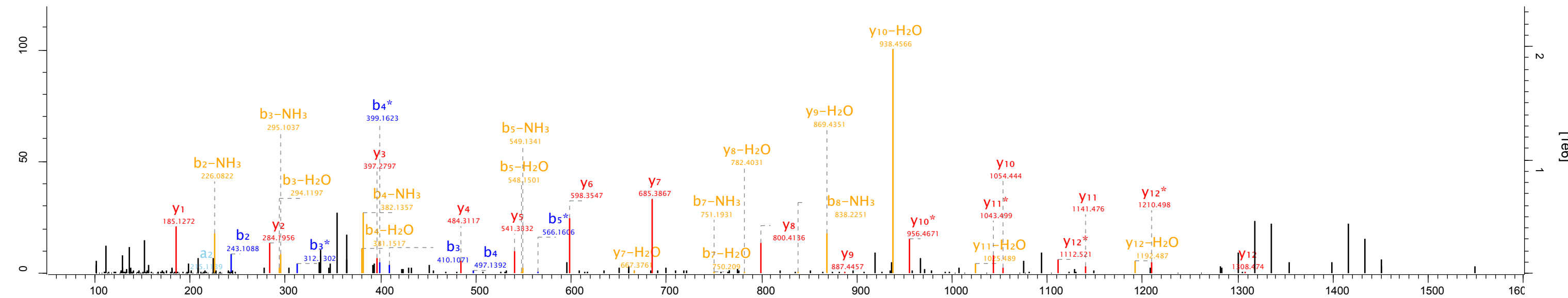


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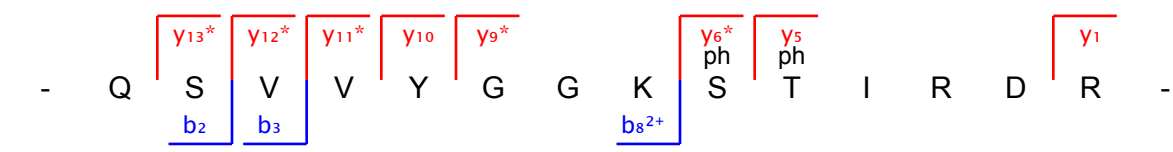
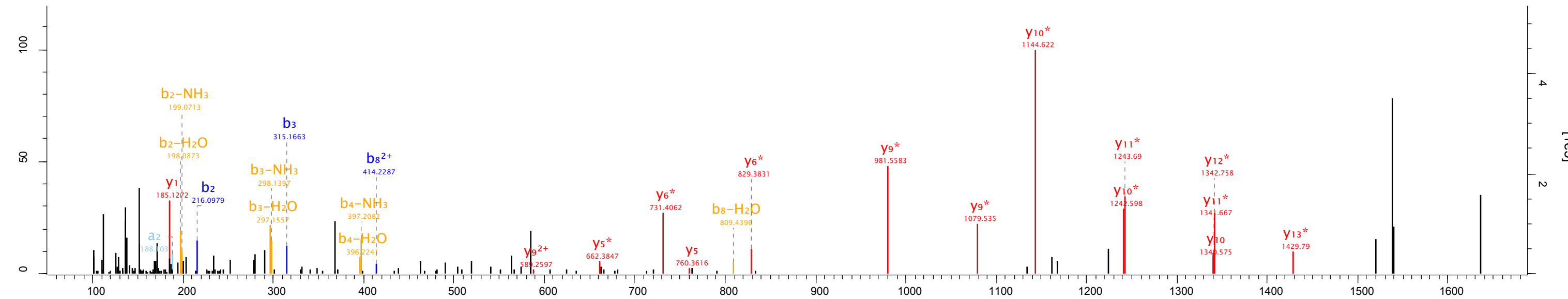


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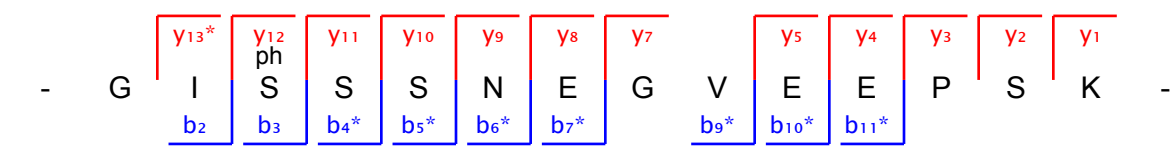
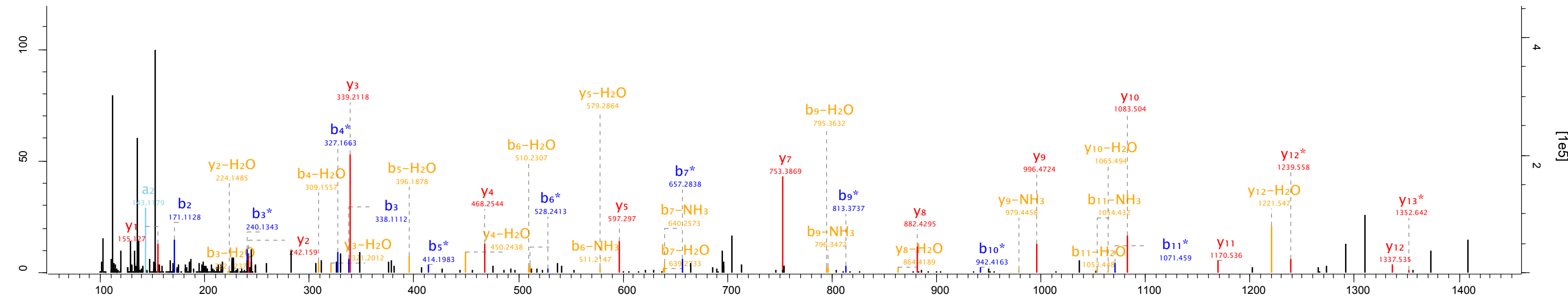




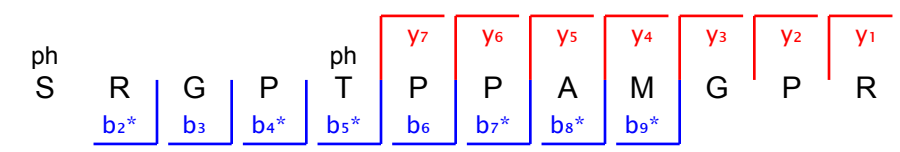
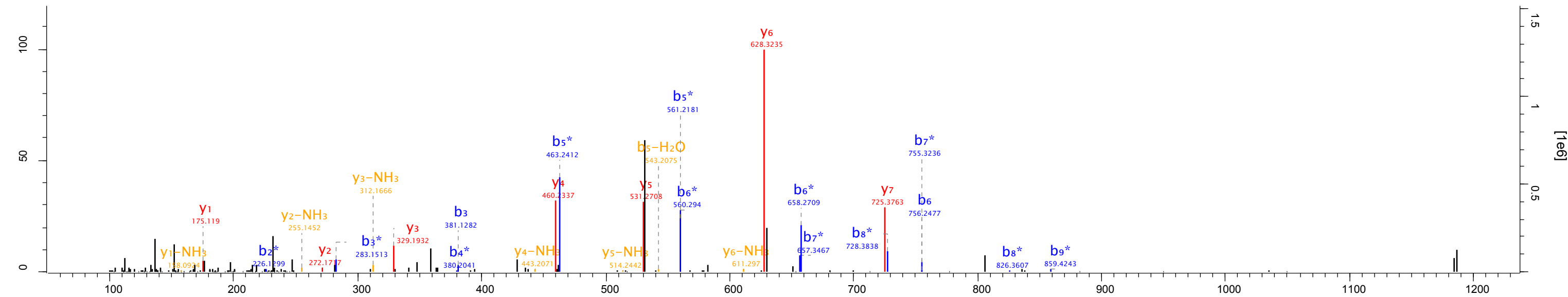
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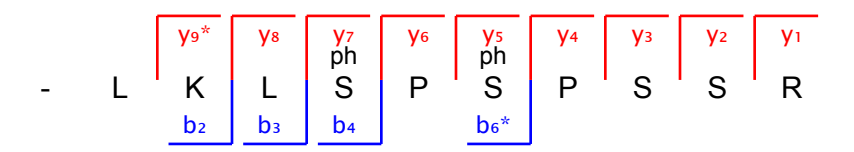
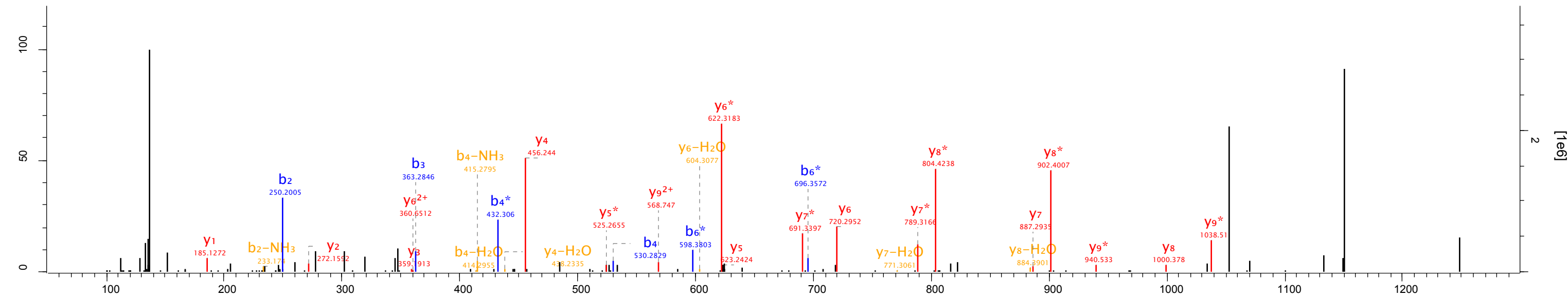
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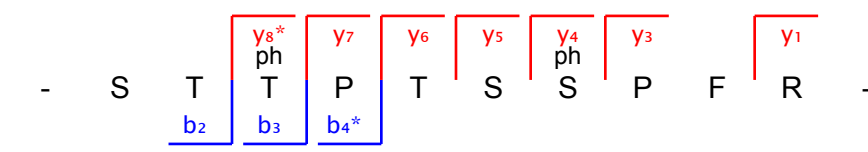
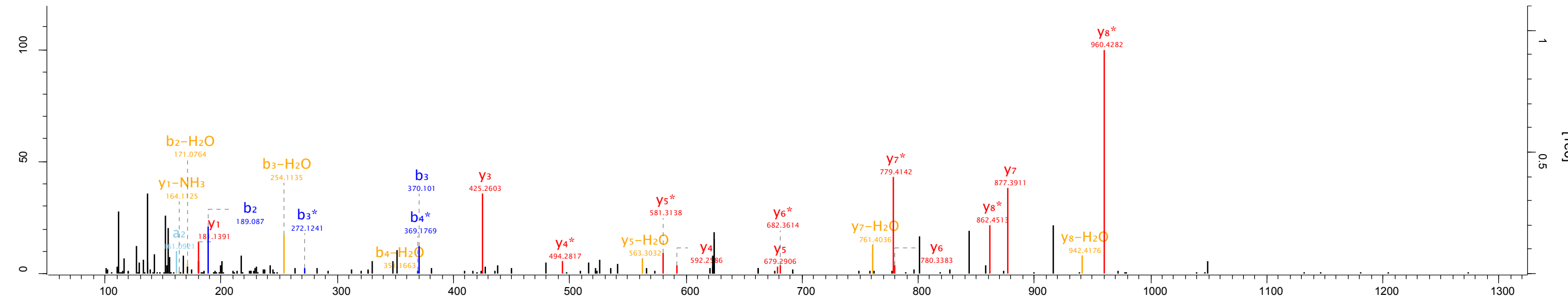
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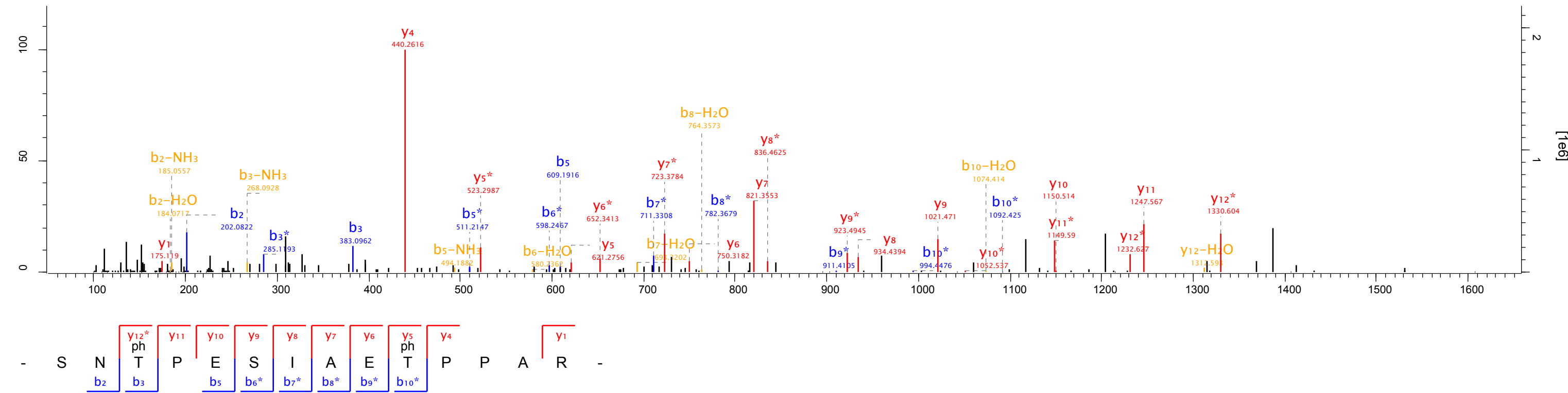


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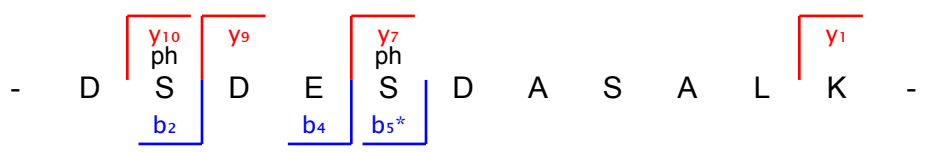
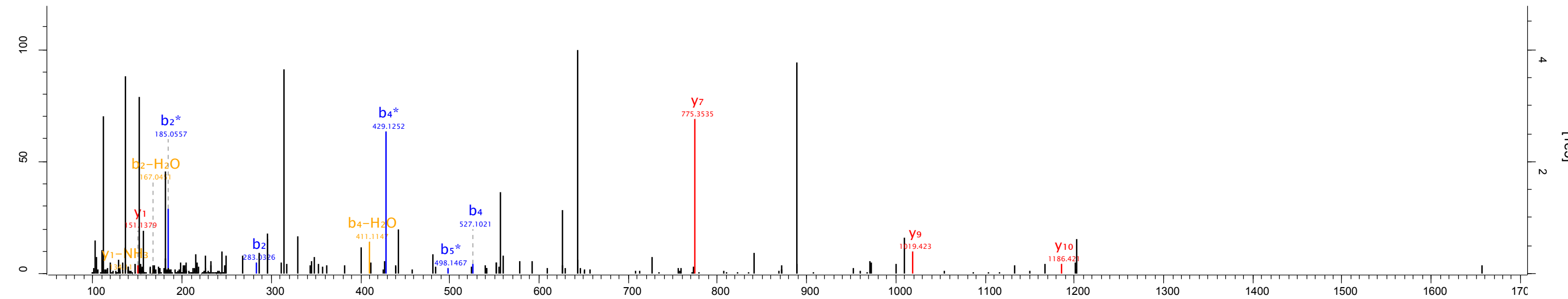


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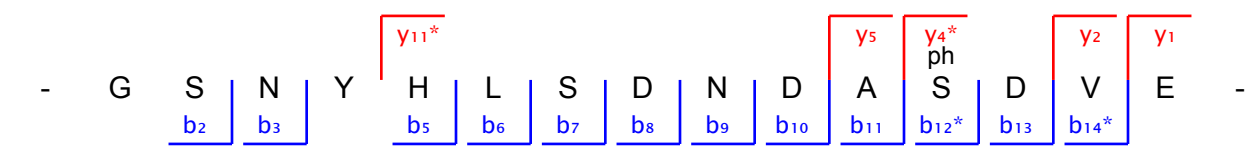
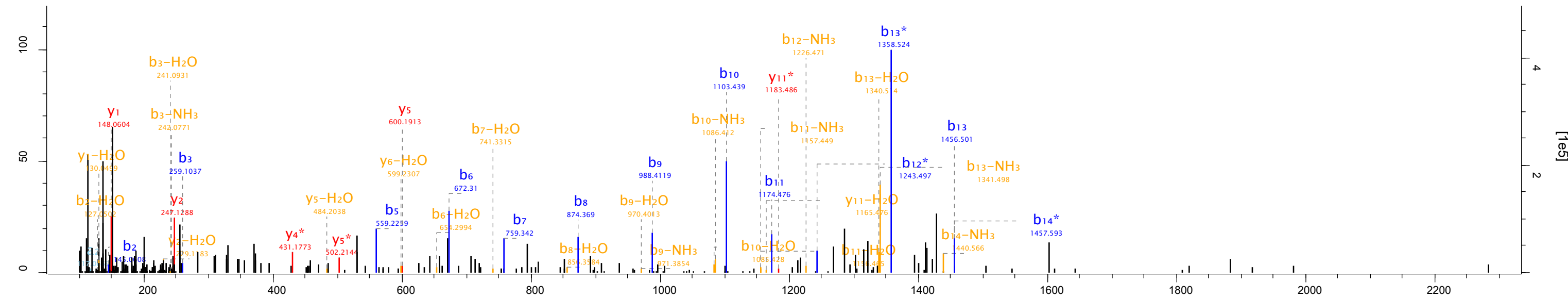




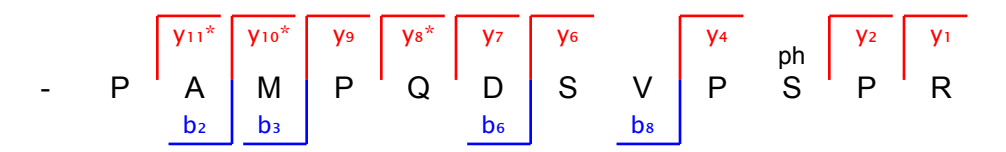
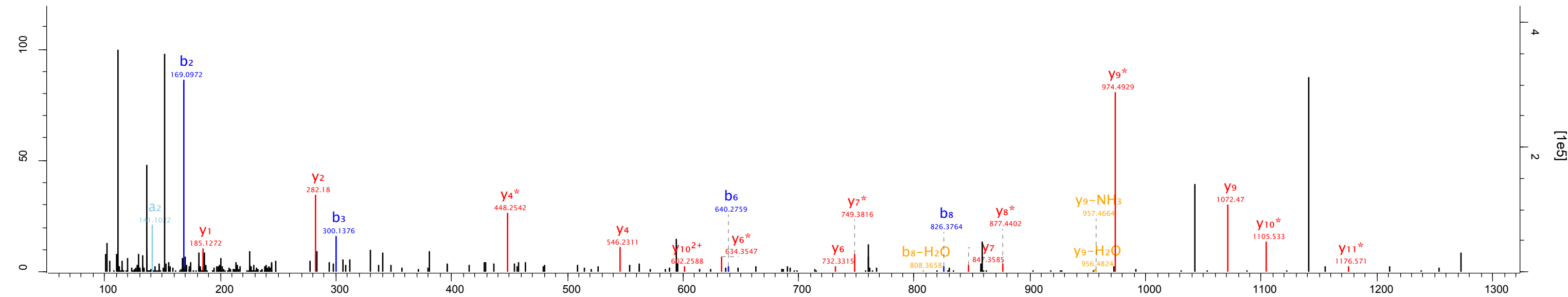
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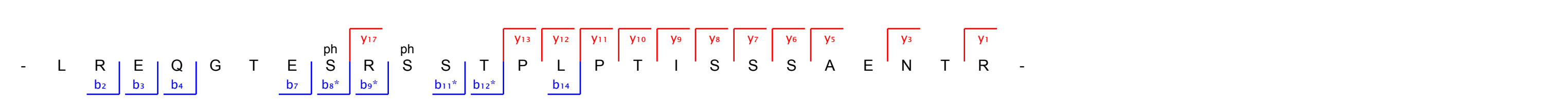
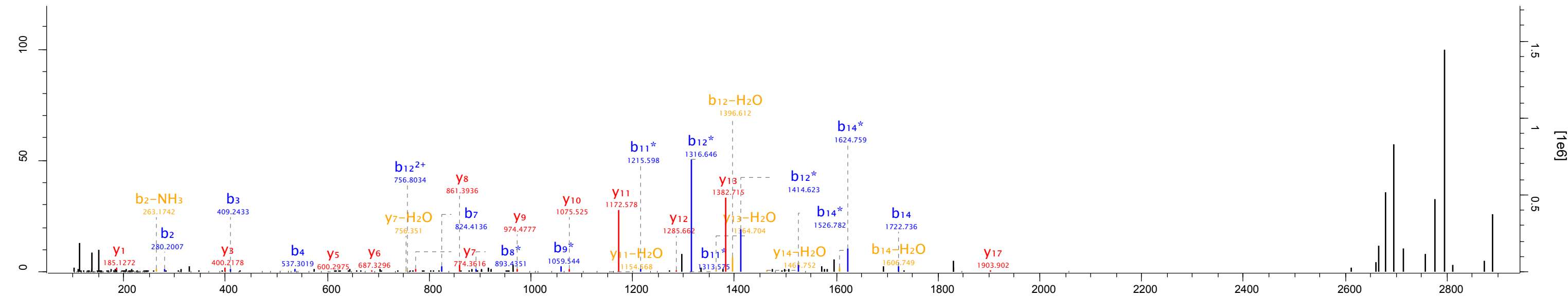
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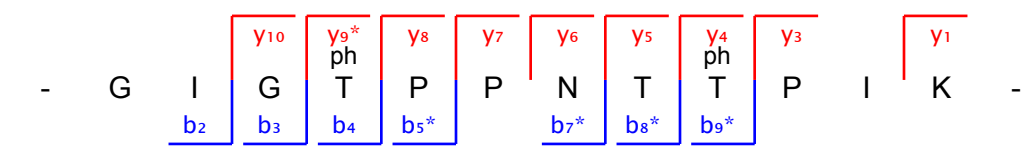
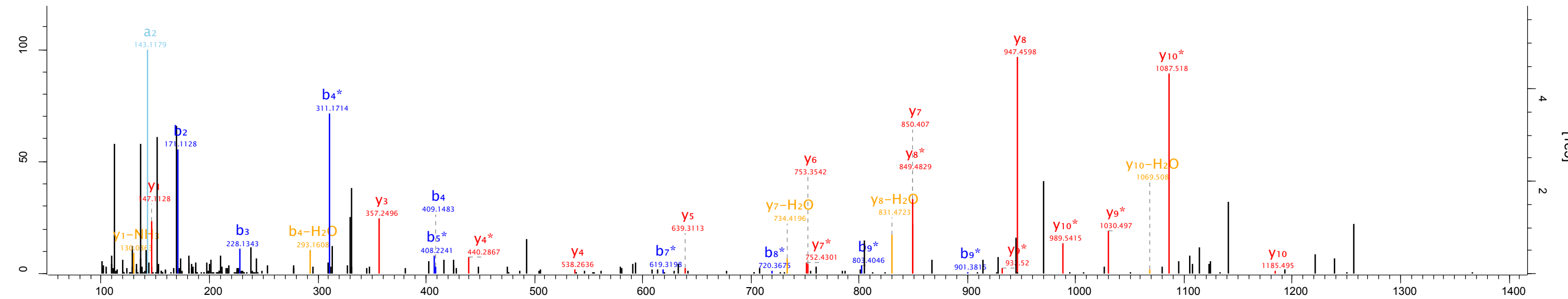
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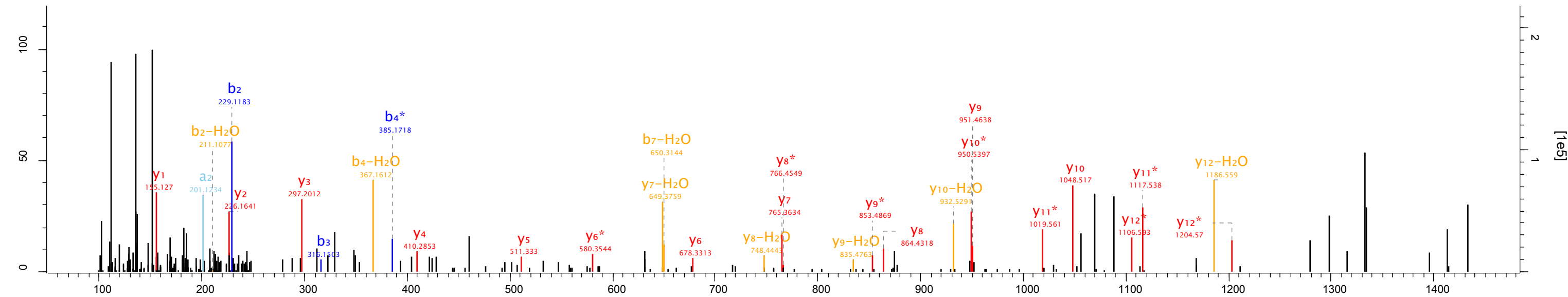
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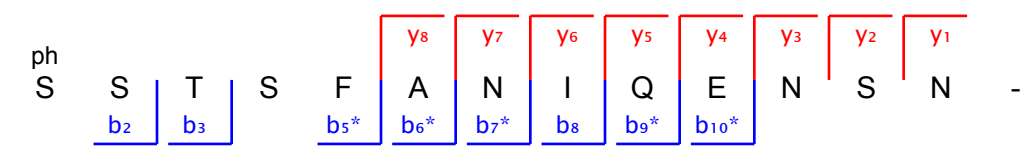
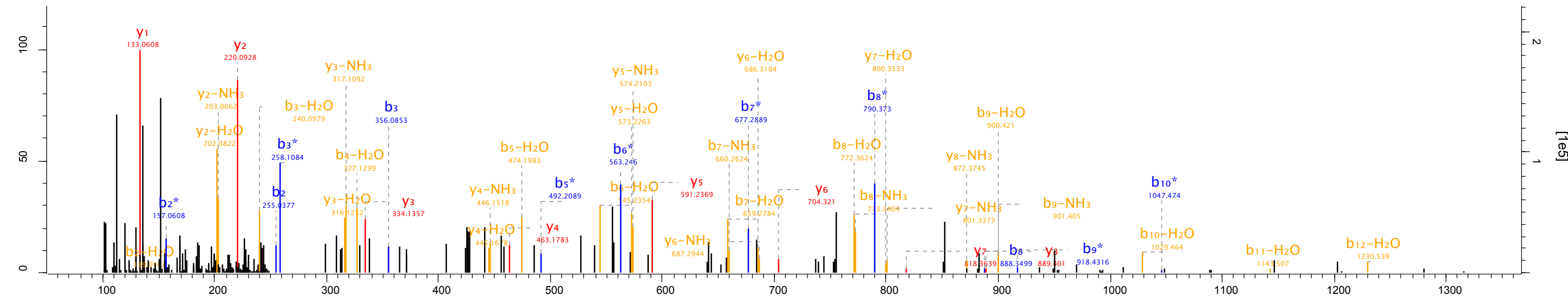
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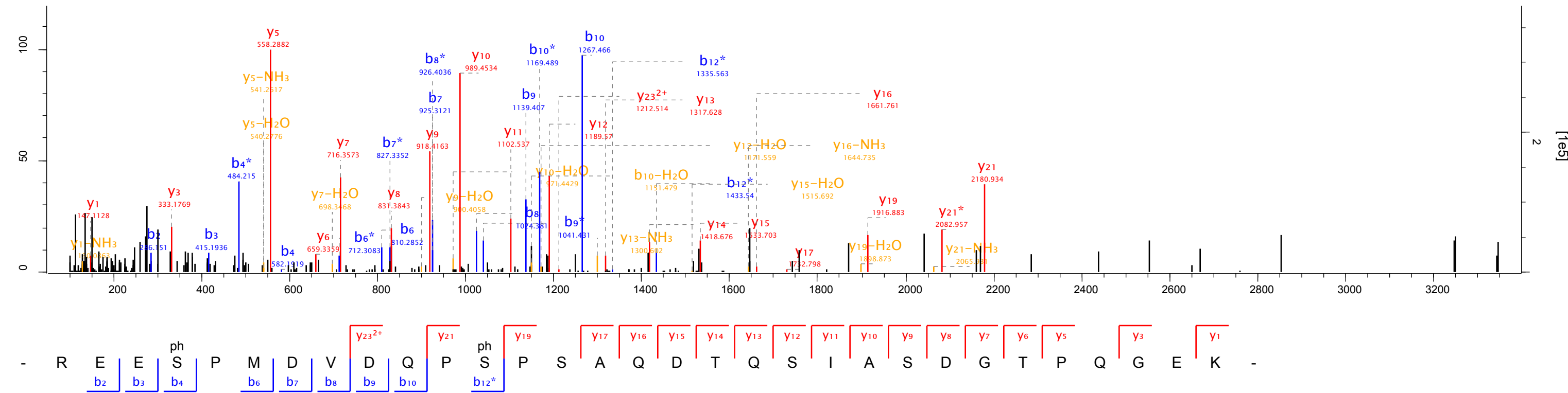


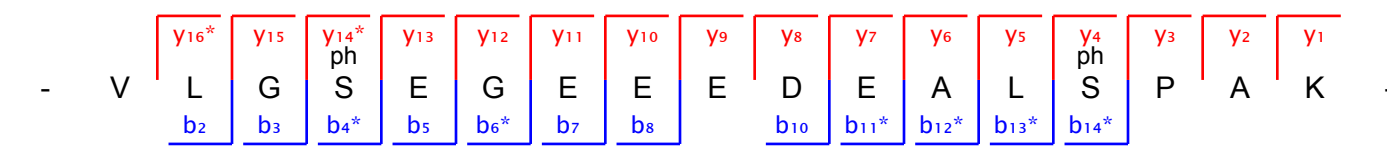
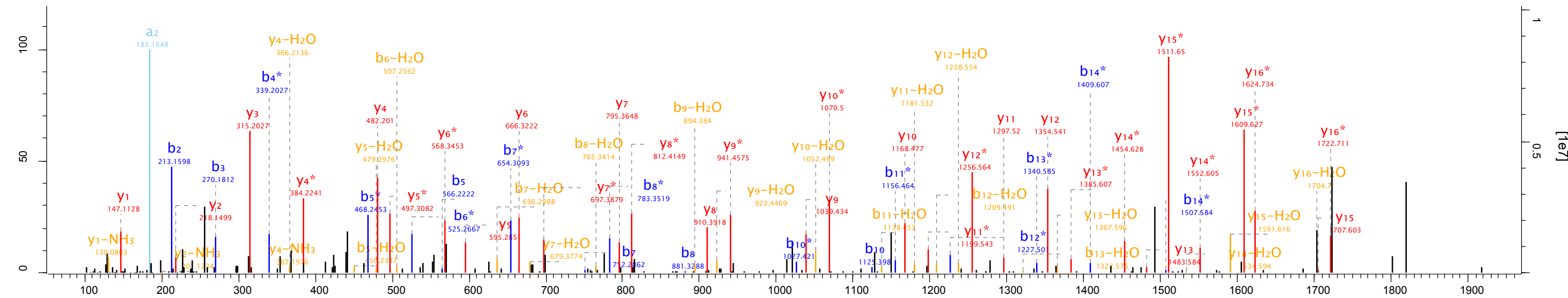
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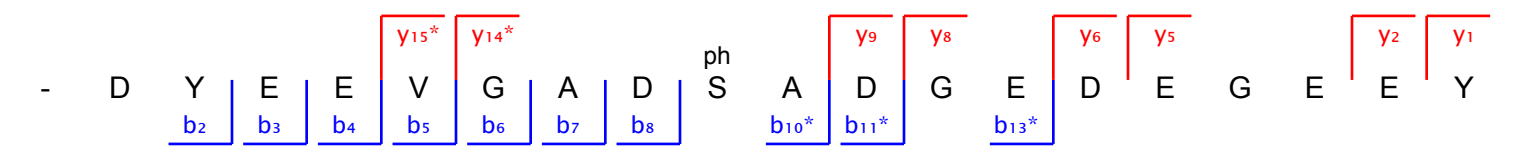
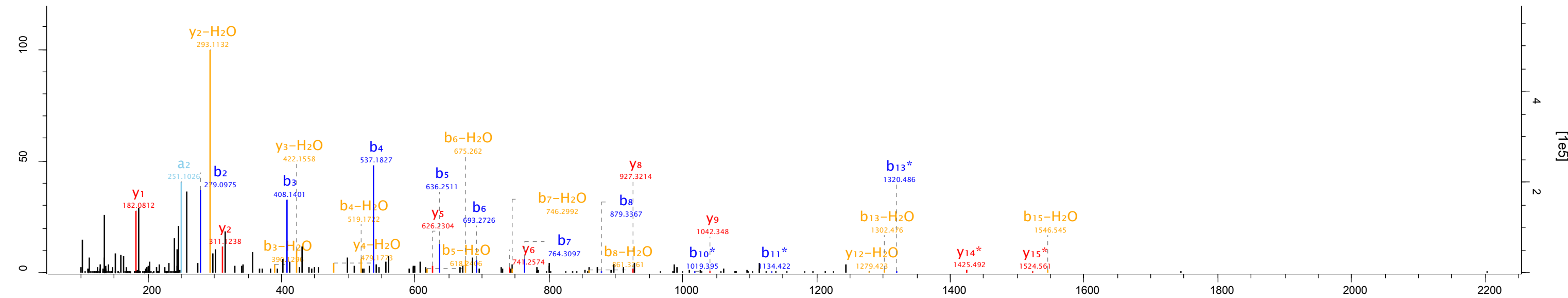
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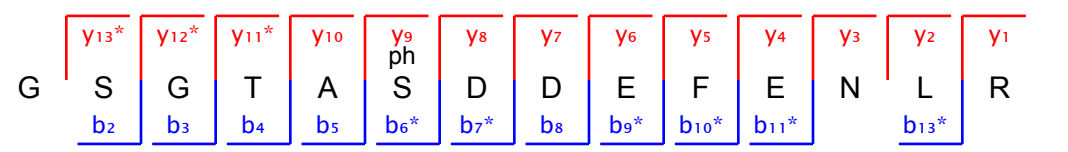
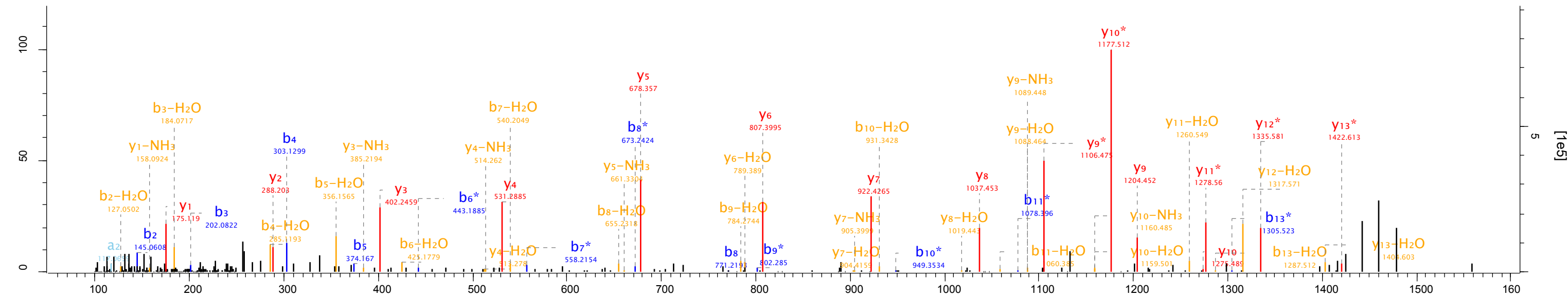




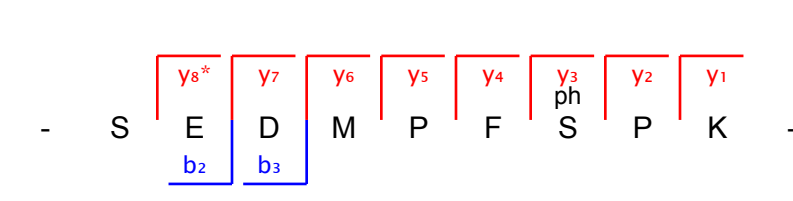
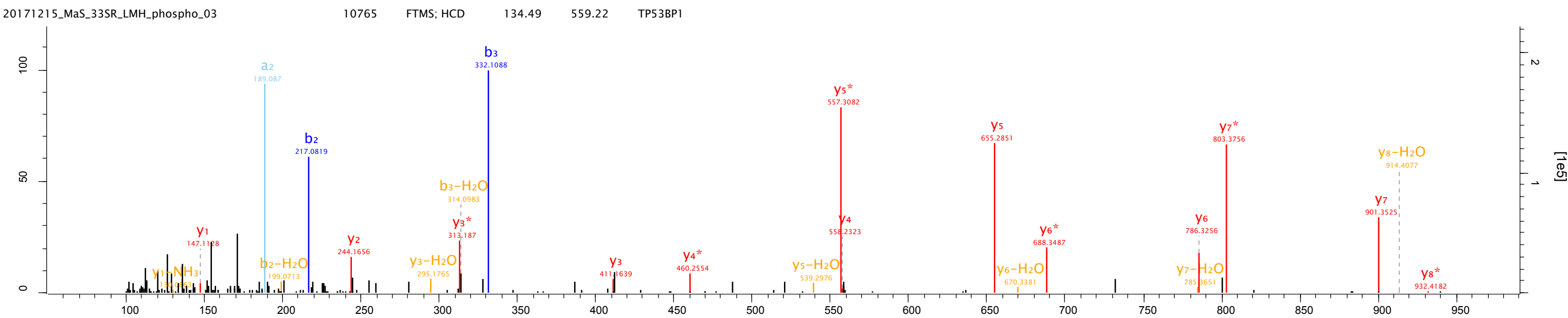
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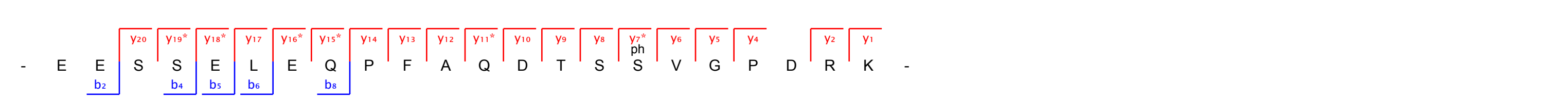
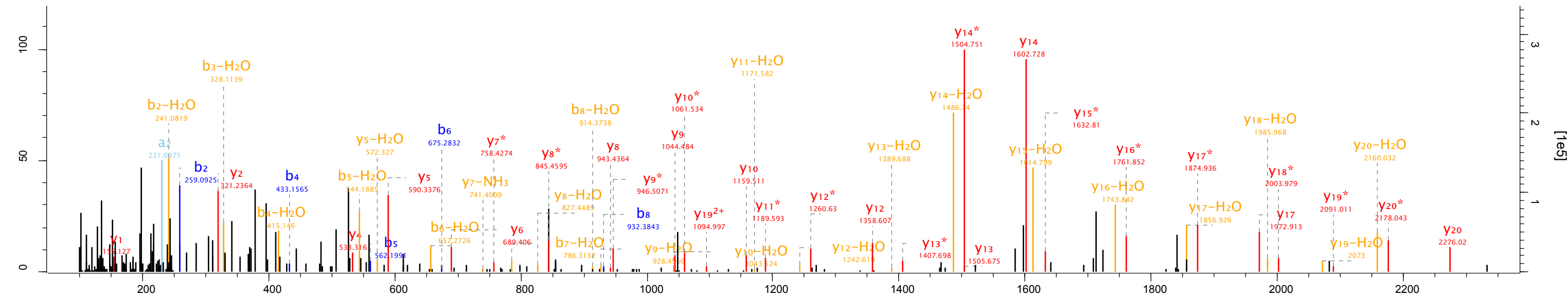
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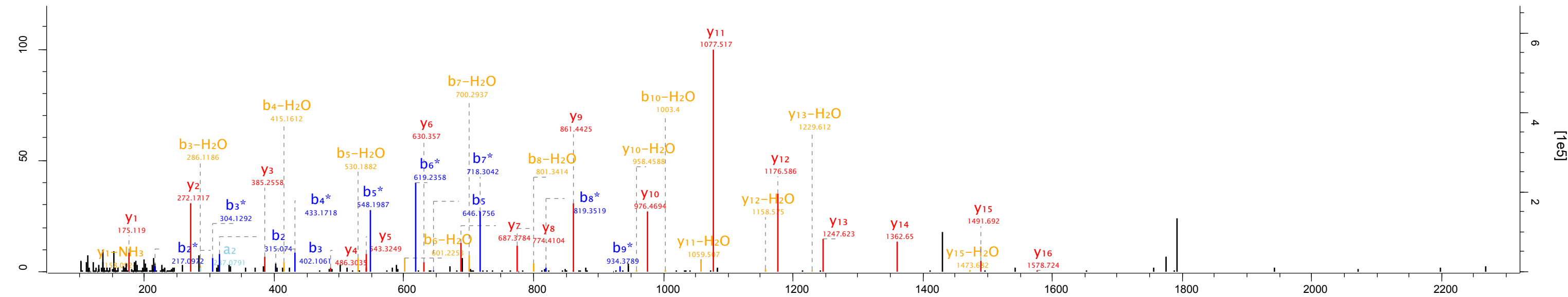
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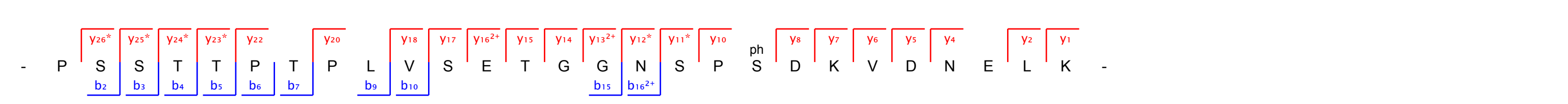
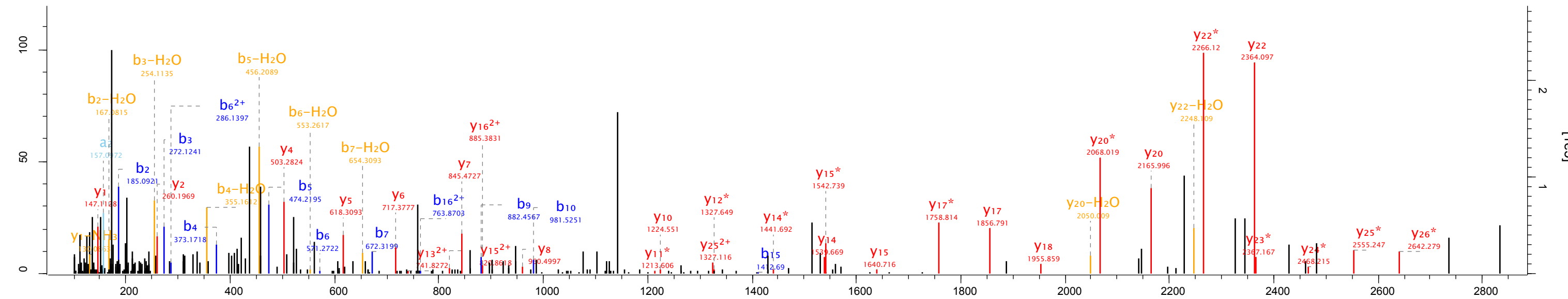


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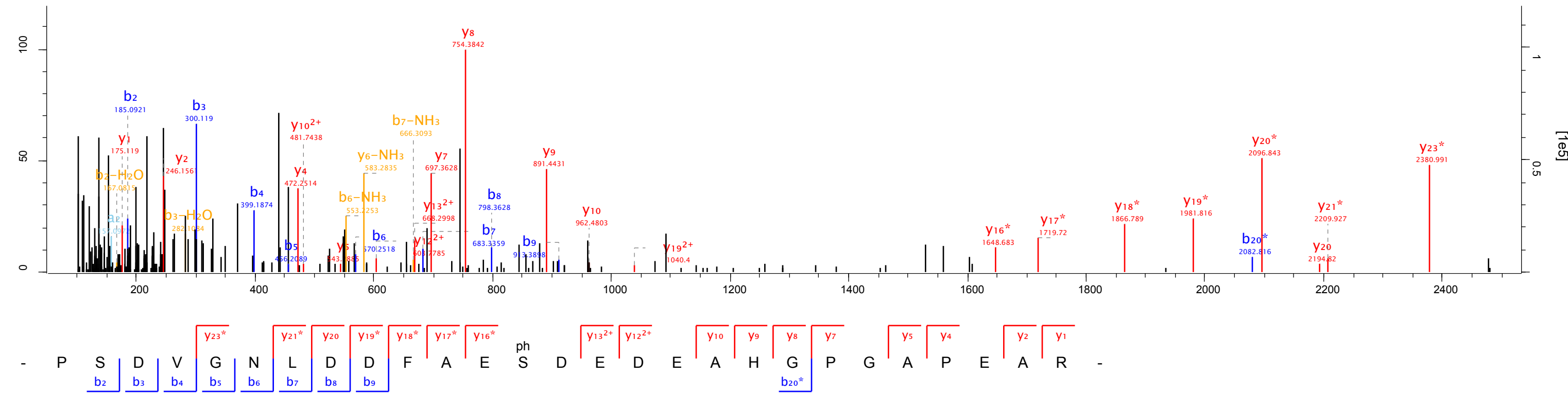


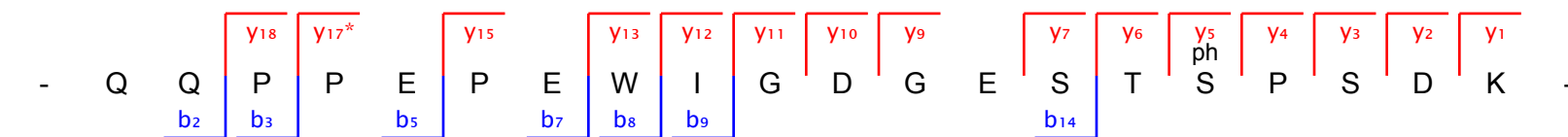
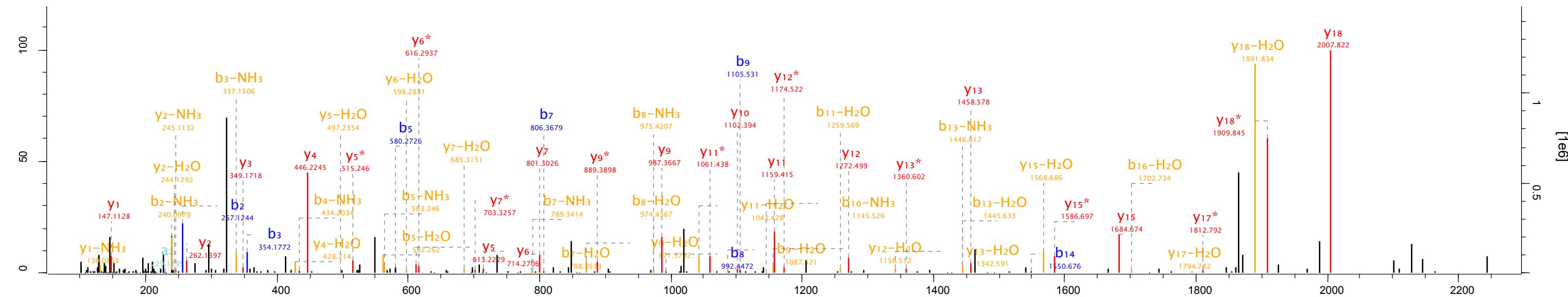
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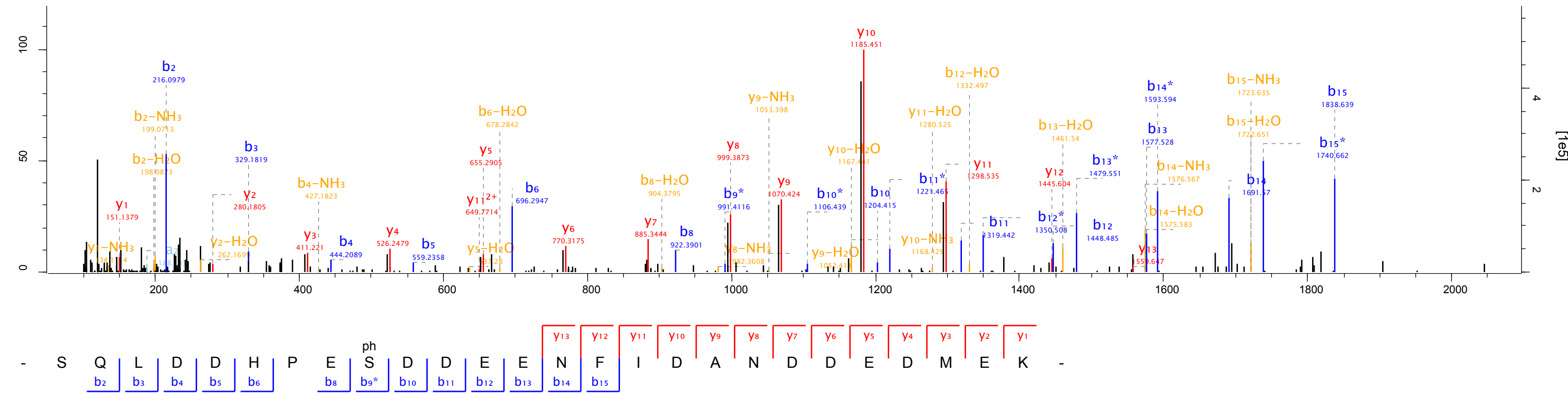
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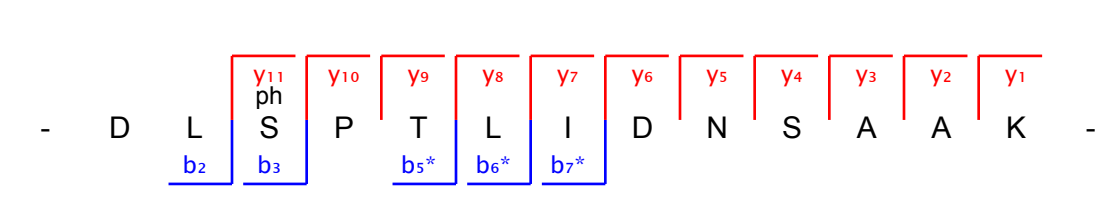
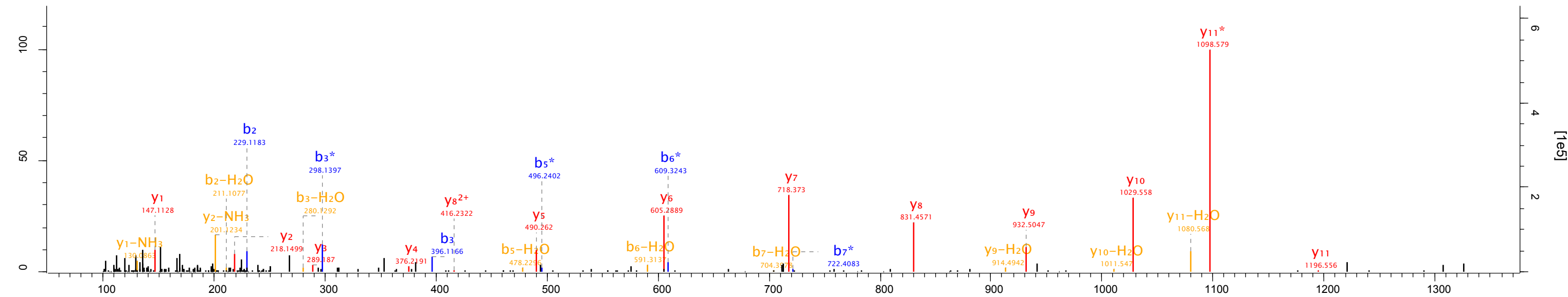
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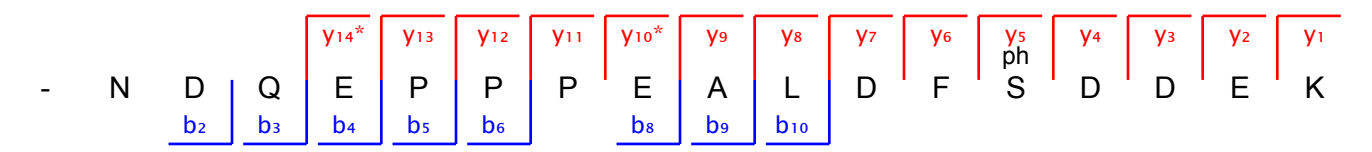
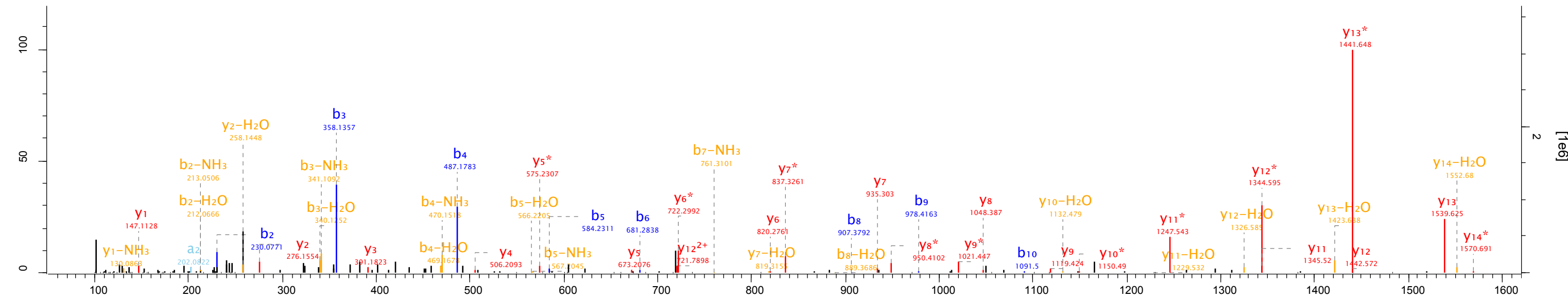




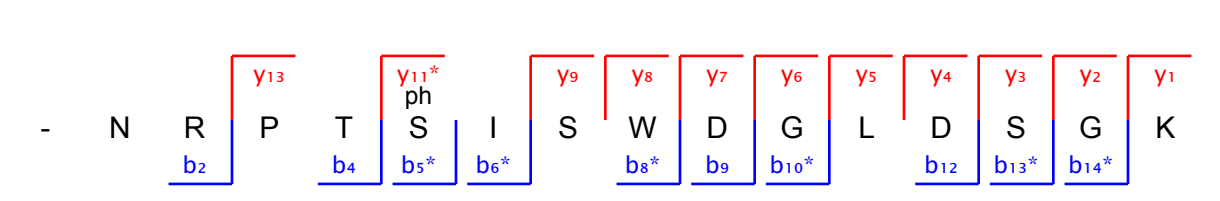
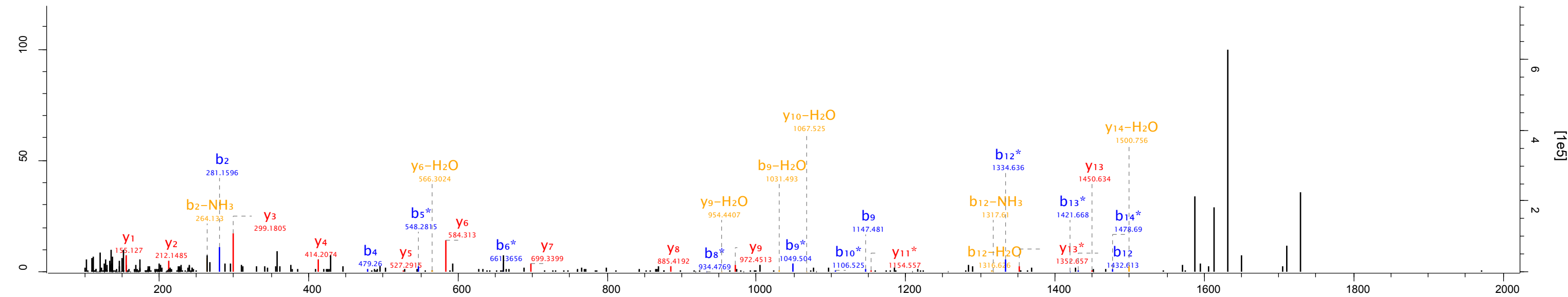
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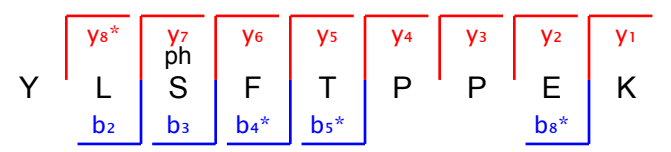
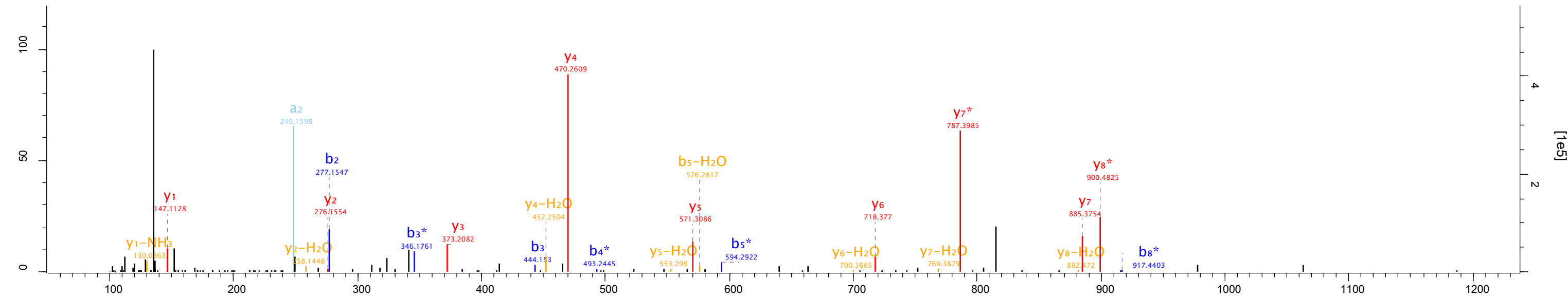
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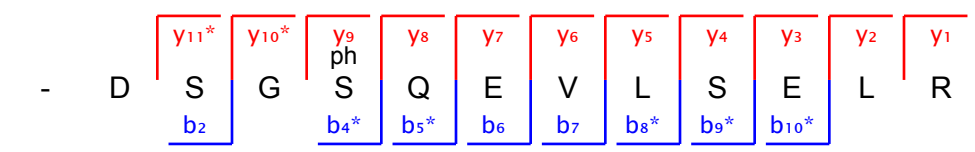
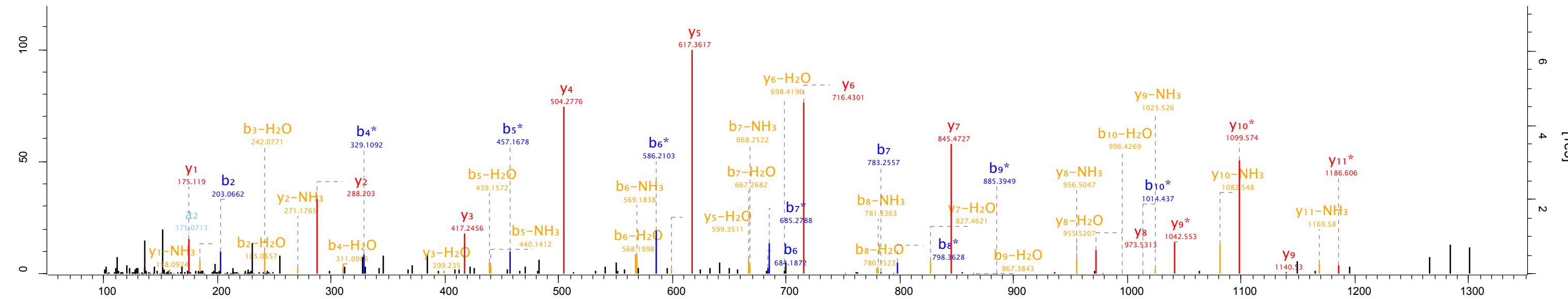
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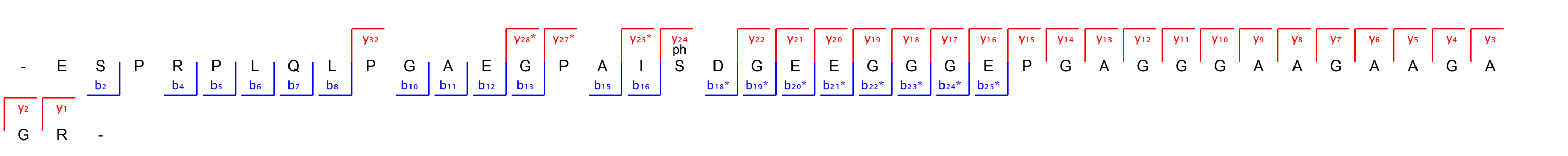
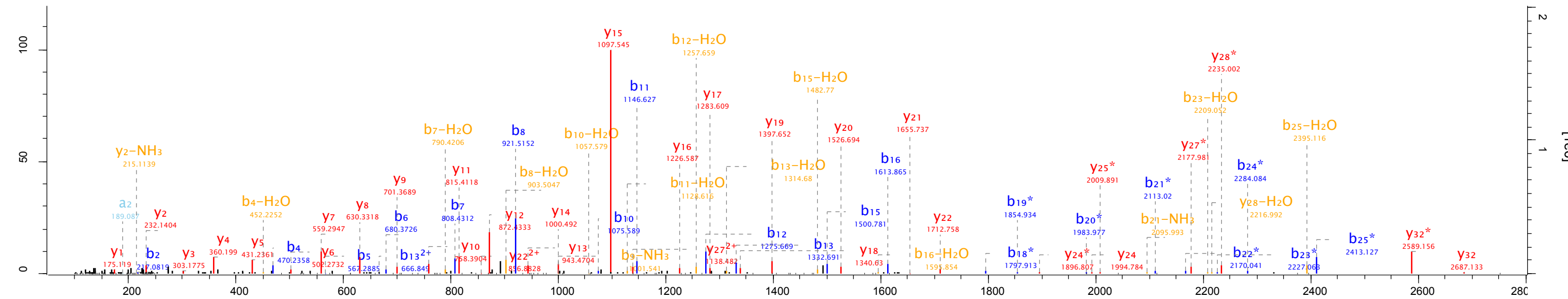
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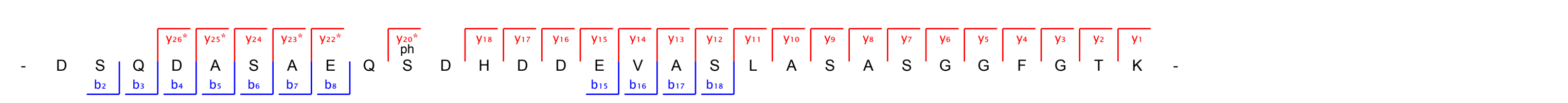
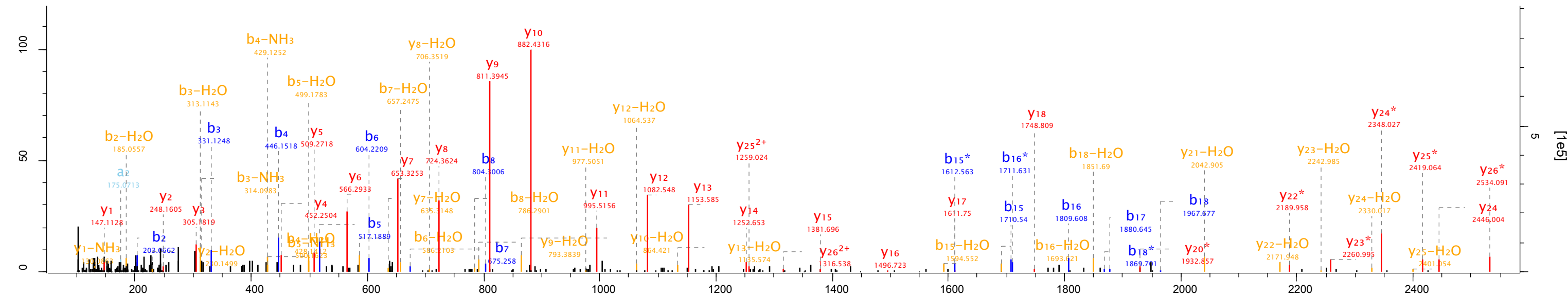
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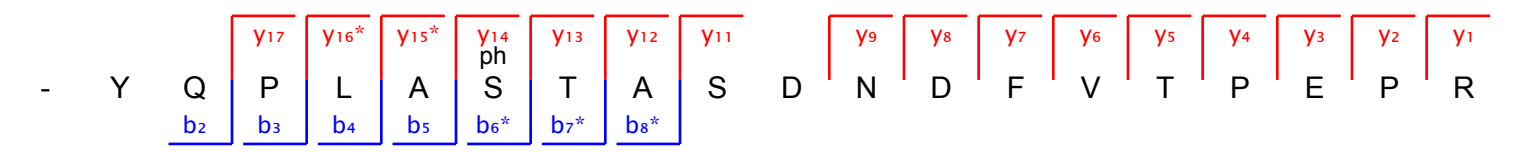
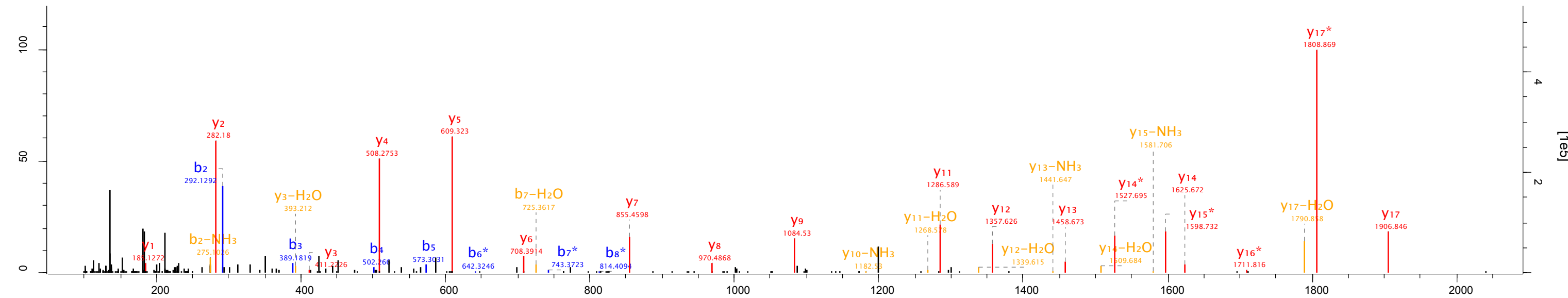
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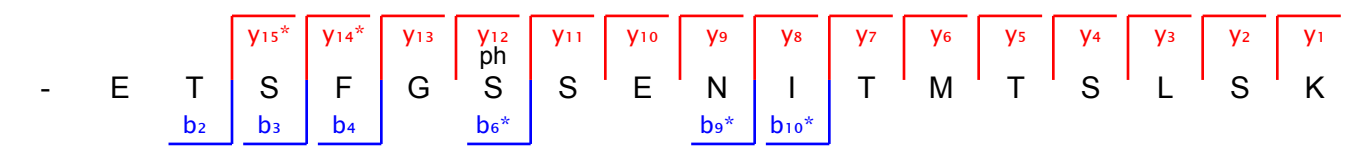
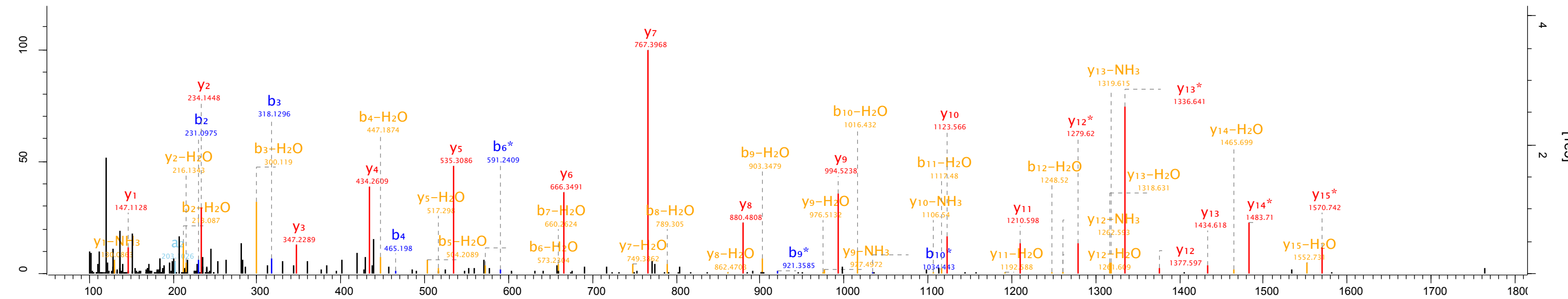
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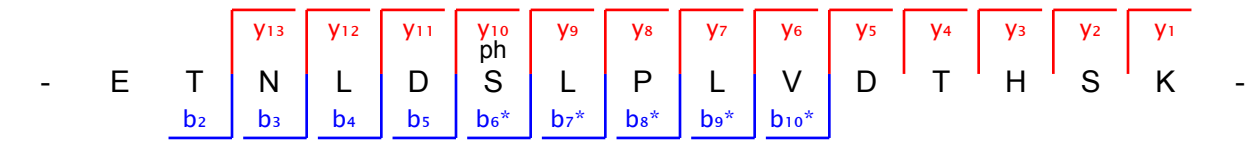
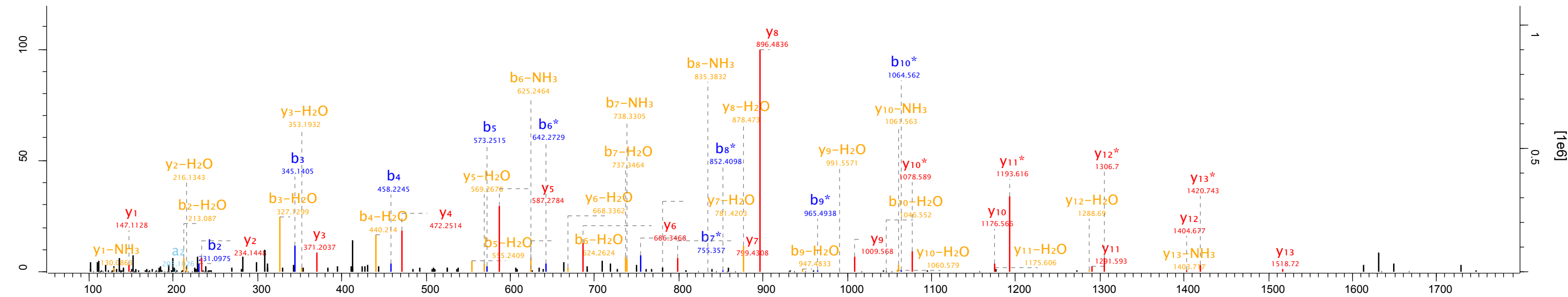


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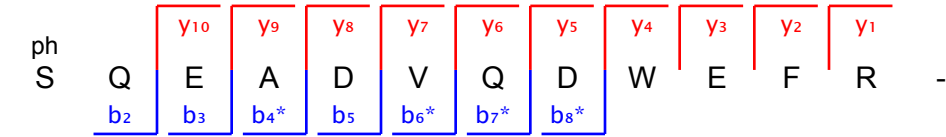
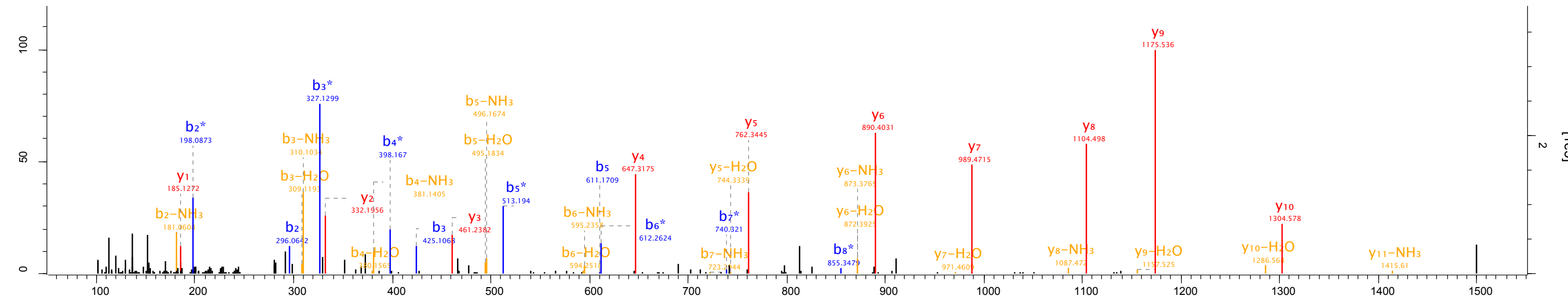


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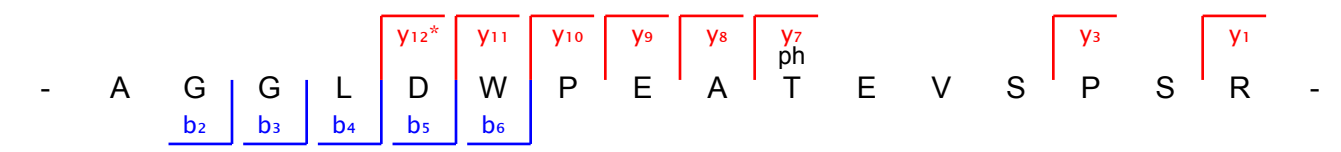
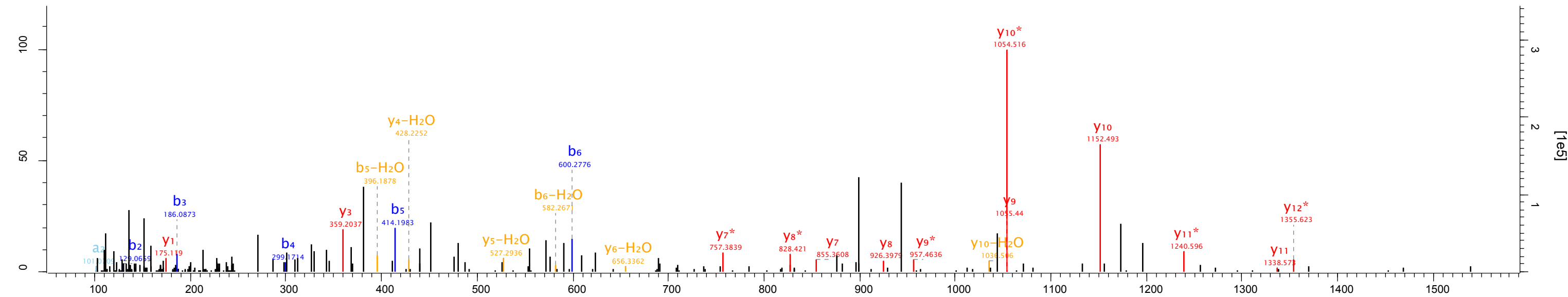




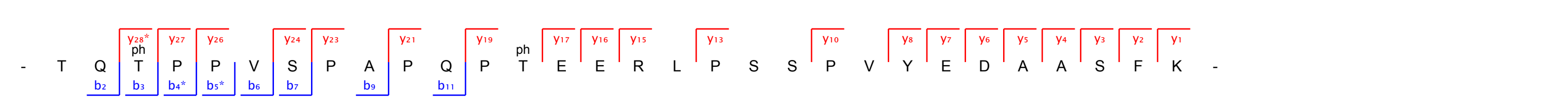
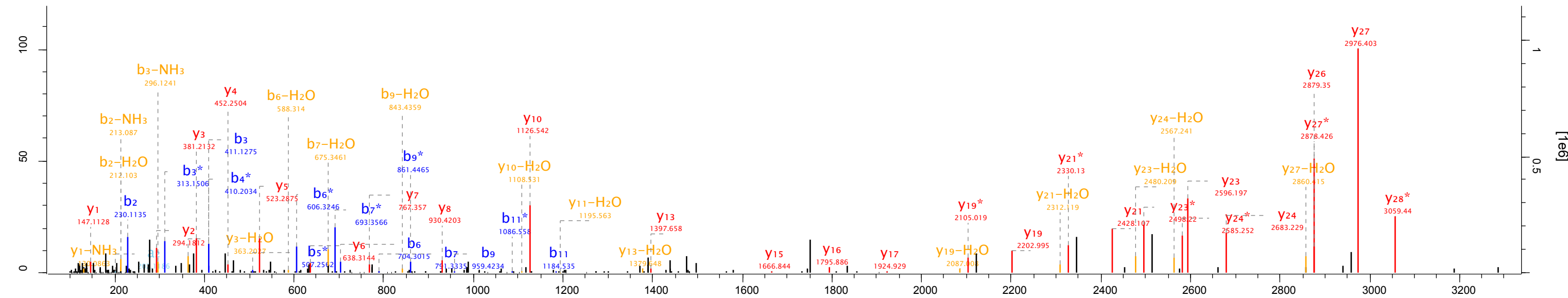
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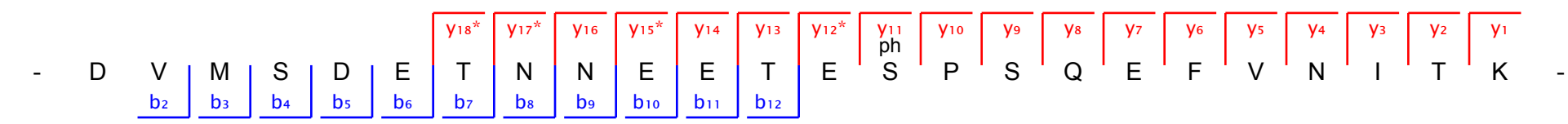
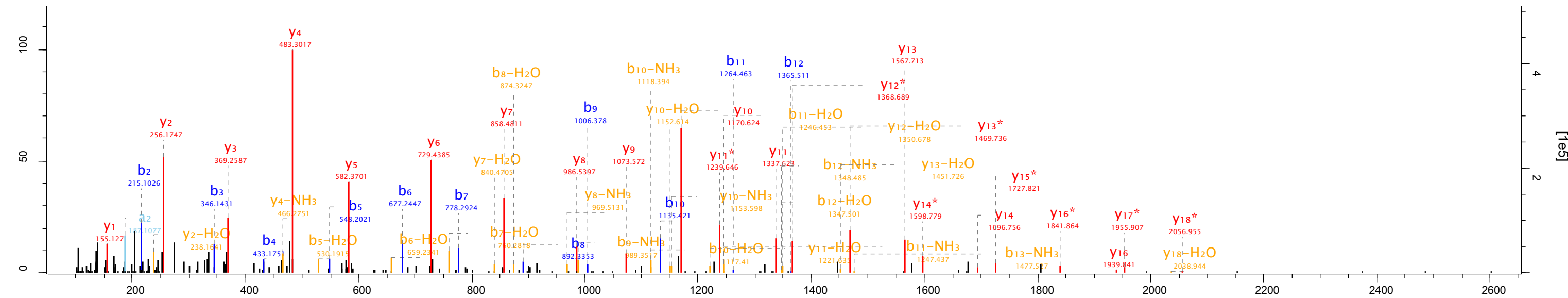
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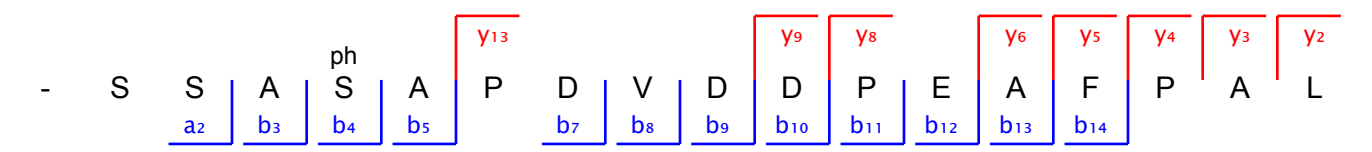
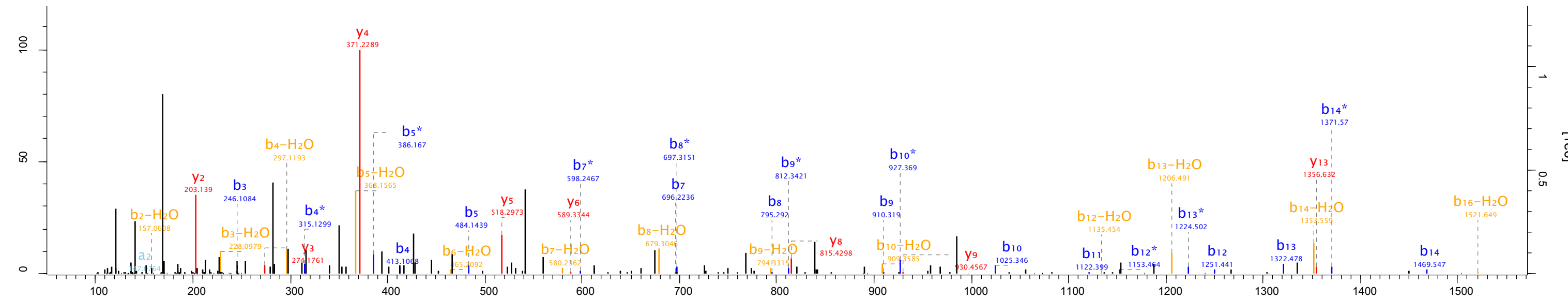
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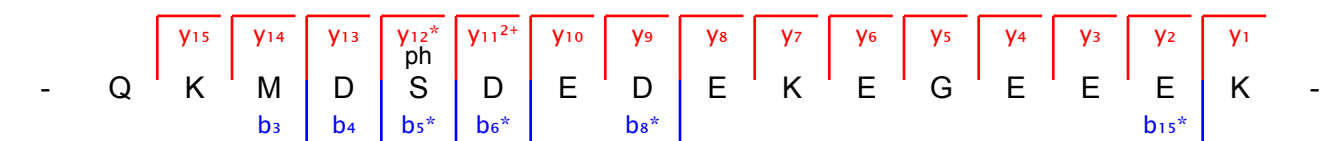
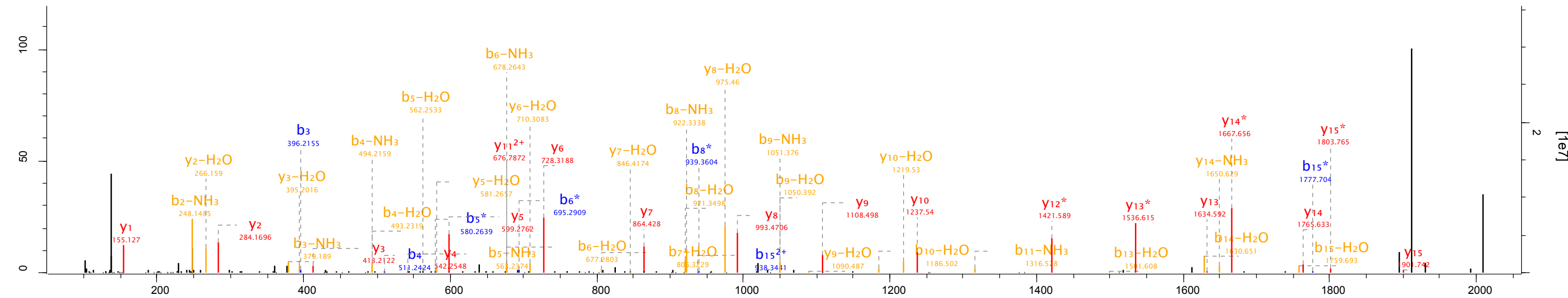
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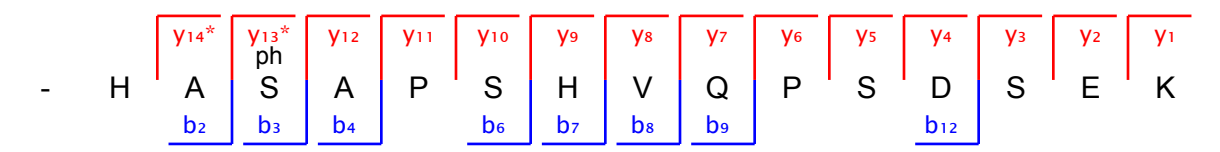
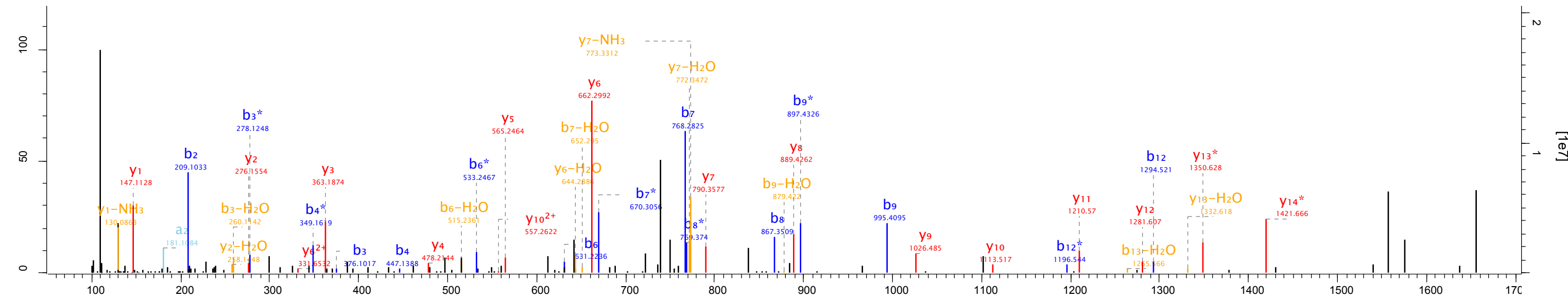
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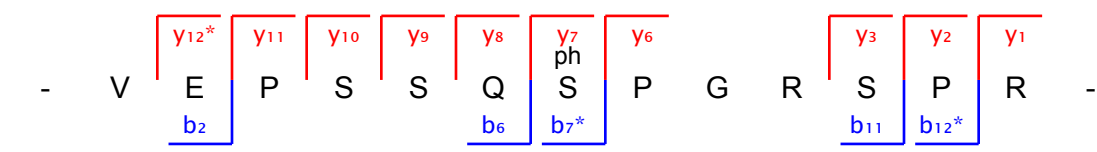
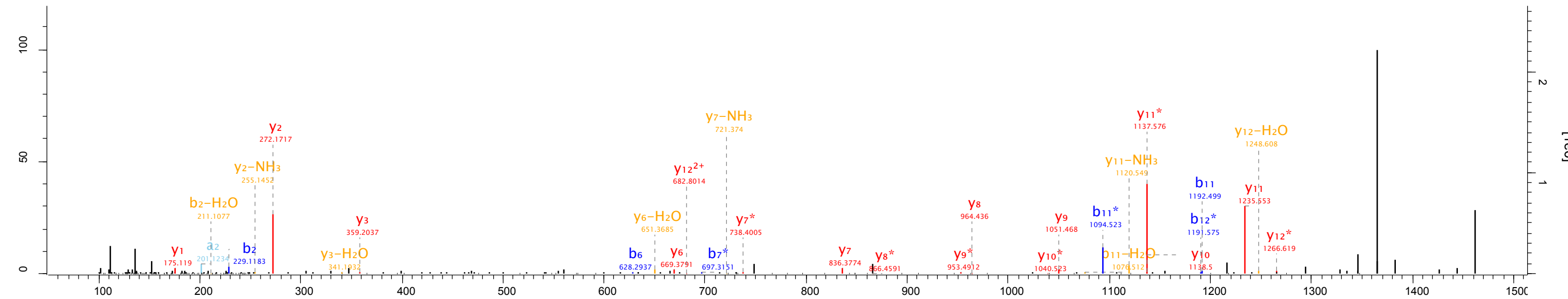
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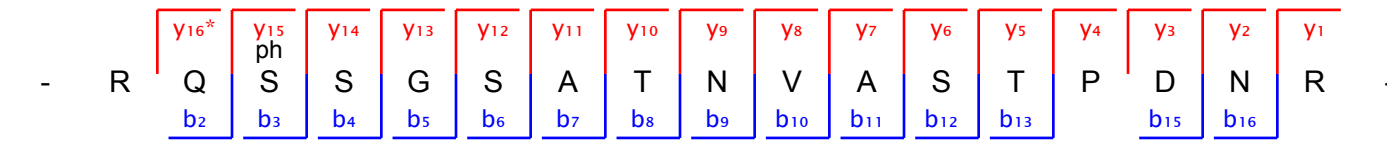
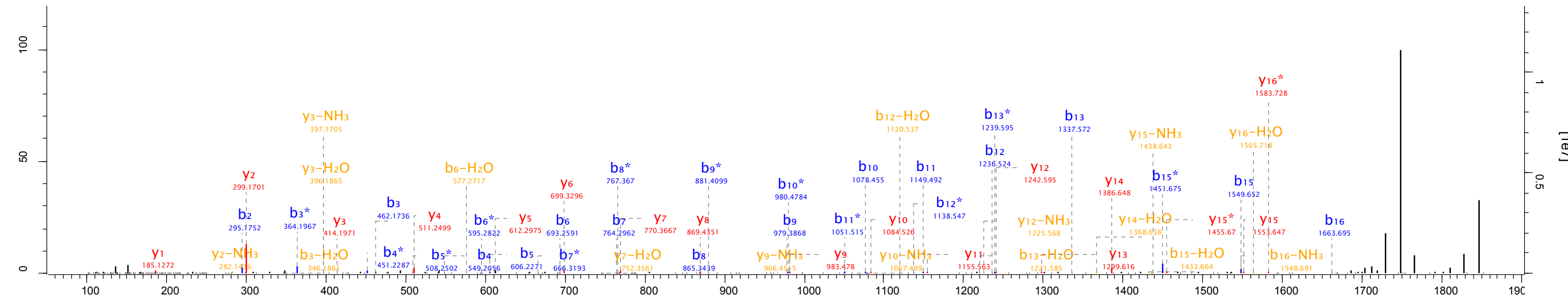
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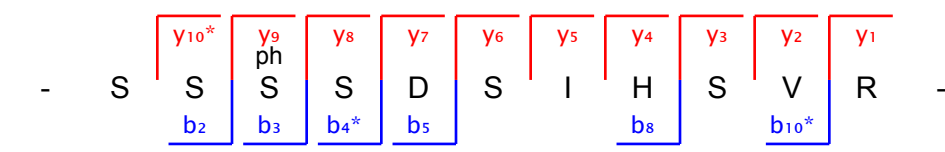
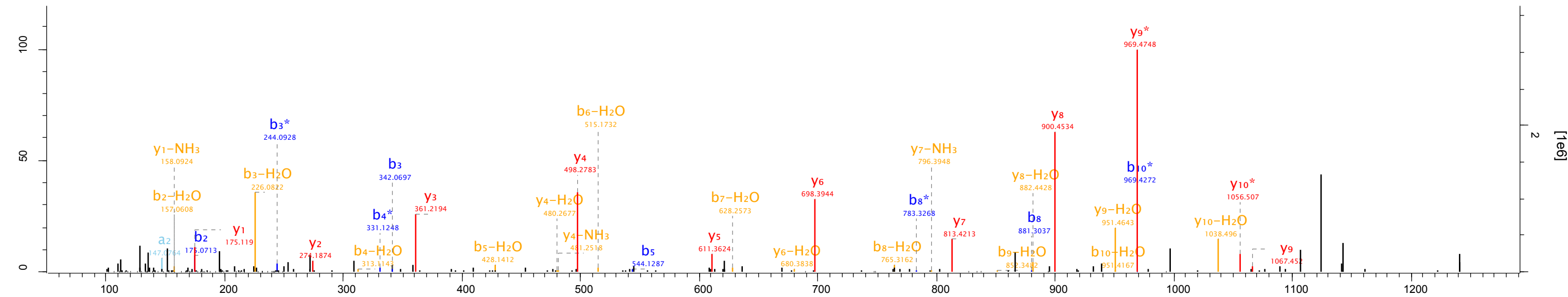
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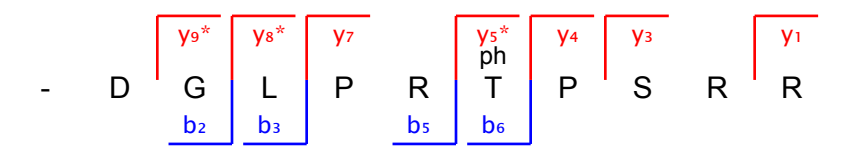
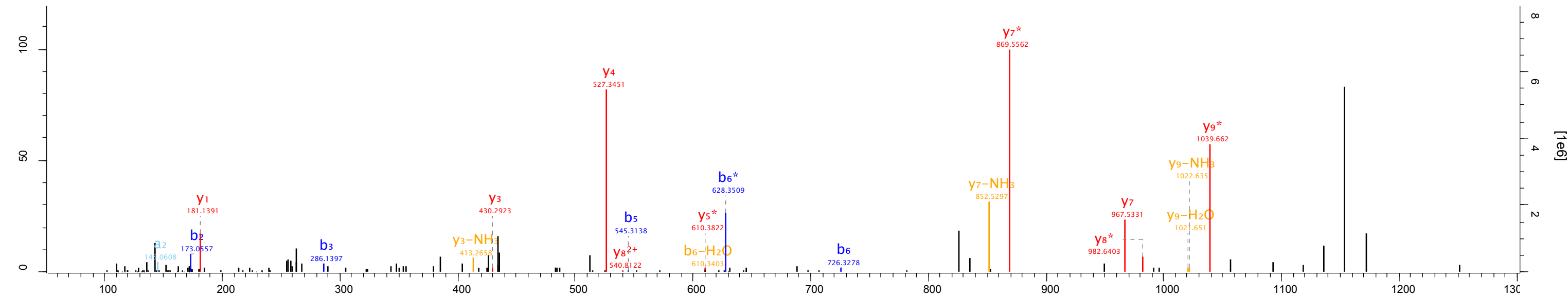
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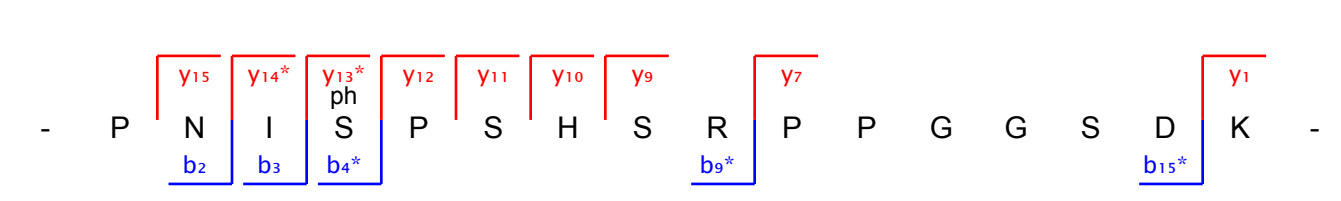
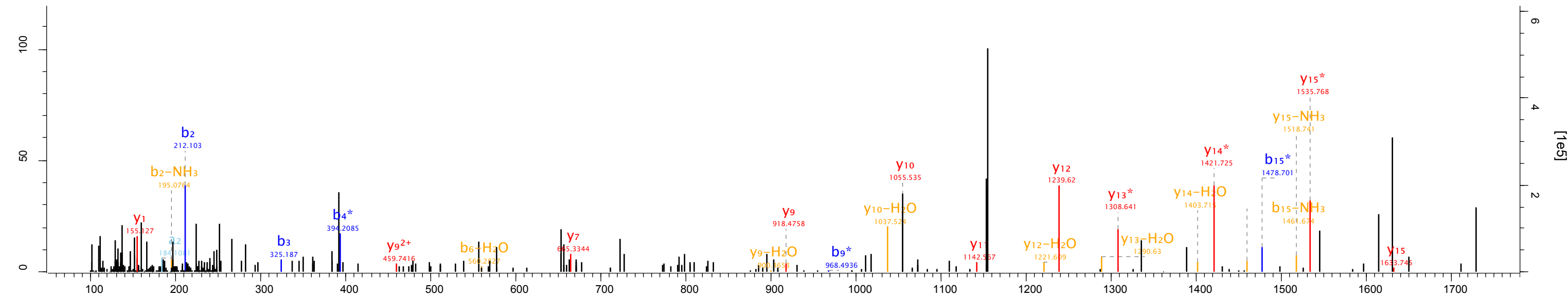
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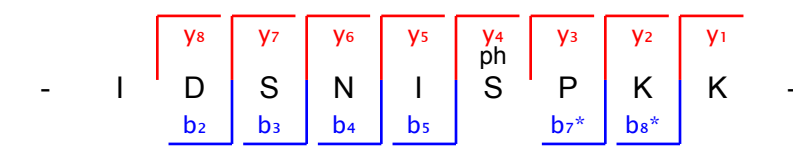
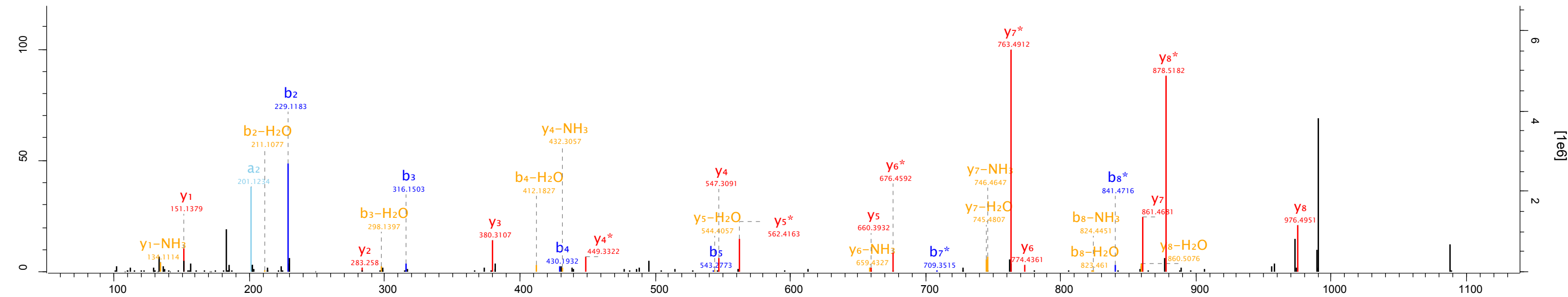
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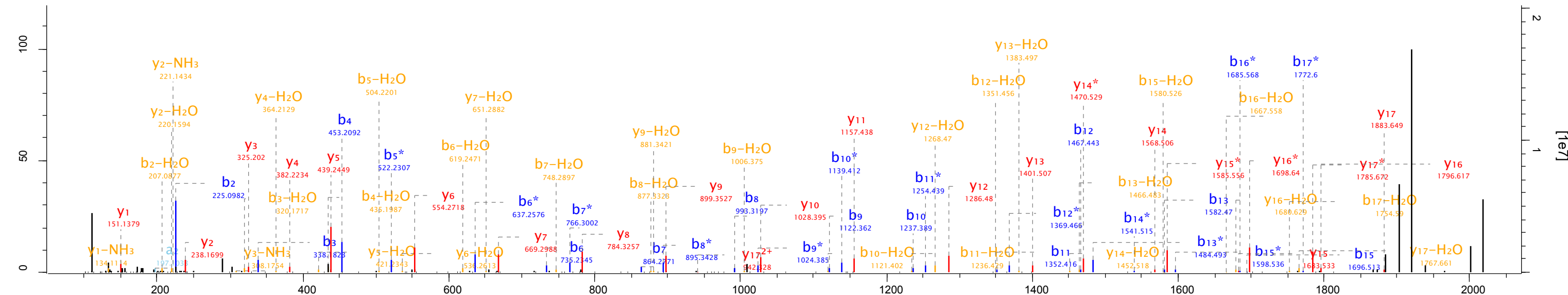


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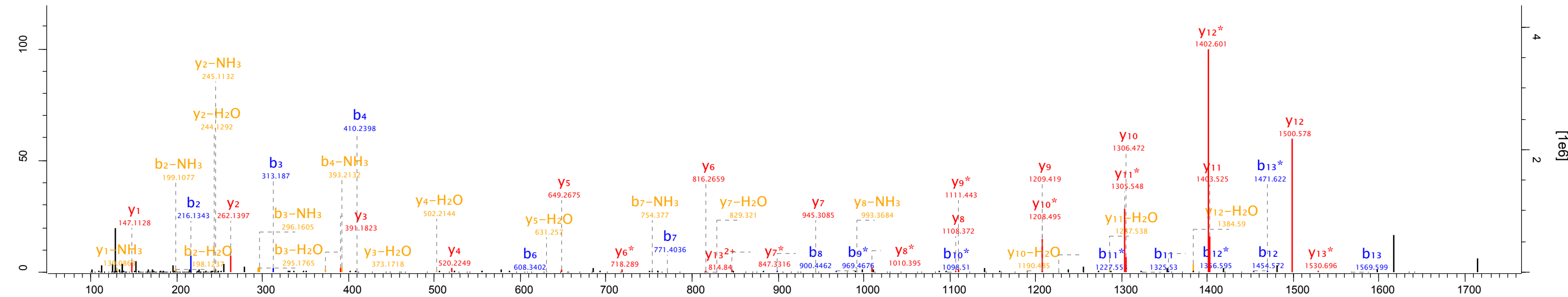




- H

y17	y16	y15	y14 ph	y13	y12	y11	y10	y9	y8	y7	y6	y5	y4	y3	y2	y1
S	L	D	S	D	E	E	E	D	D	D	D	G	G	S	S	K
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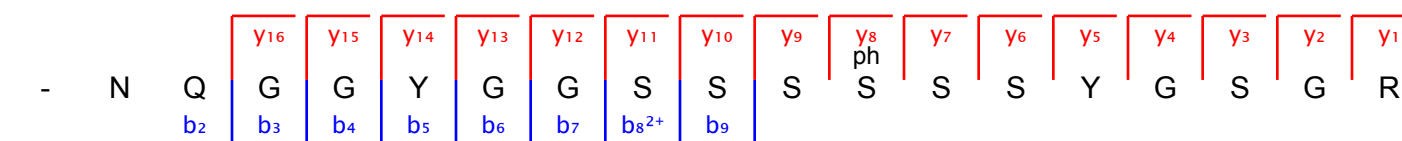
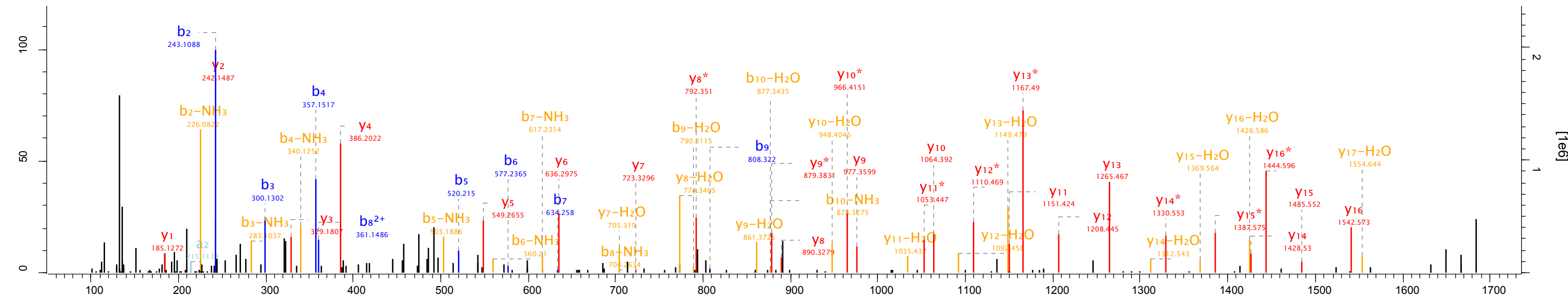
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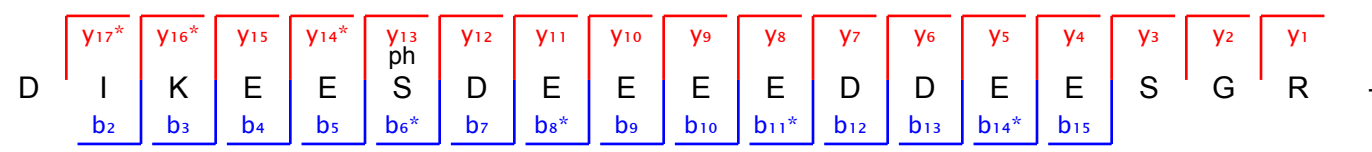
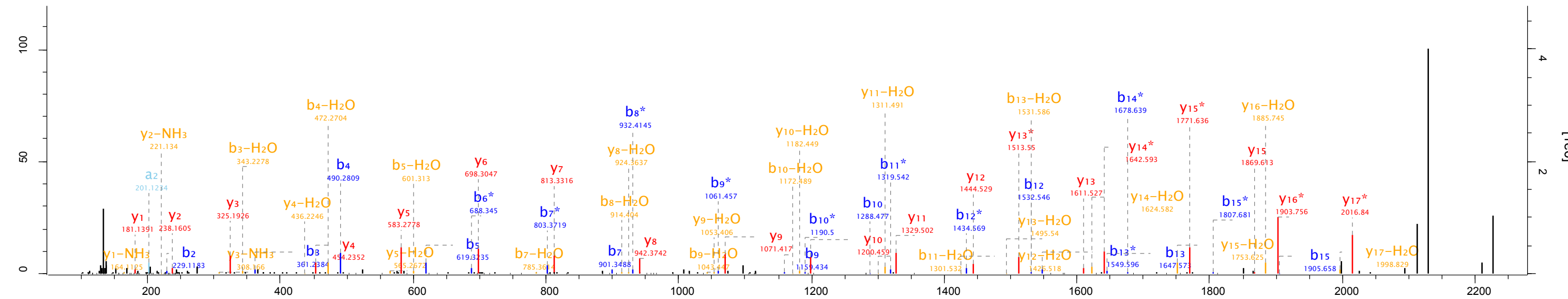
- S -

y13*	y12	y11	y10	y9	y8	y7	y6 _{ph}	y5	y4	y3	y2	y1
K	P	P	P	T	Y	E	S	E	E	E	D	K
b2	b3	b4	b6	b7	b8	b9*	b10*	b11	b12	b13		

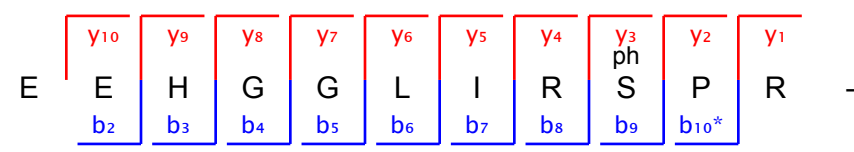
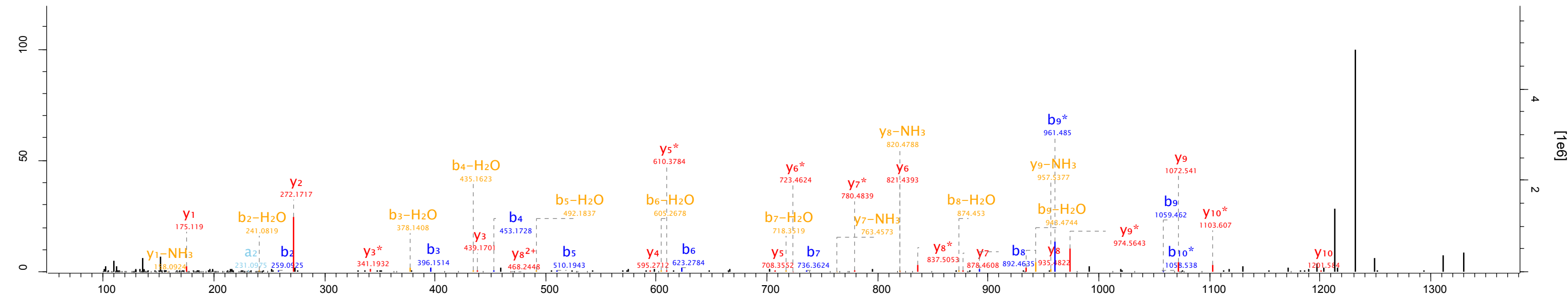
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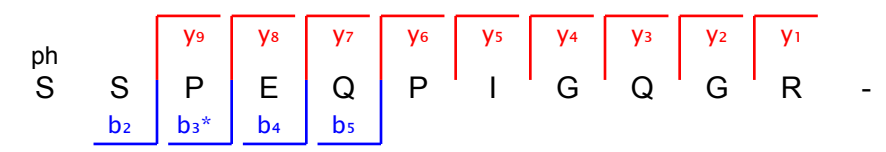
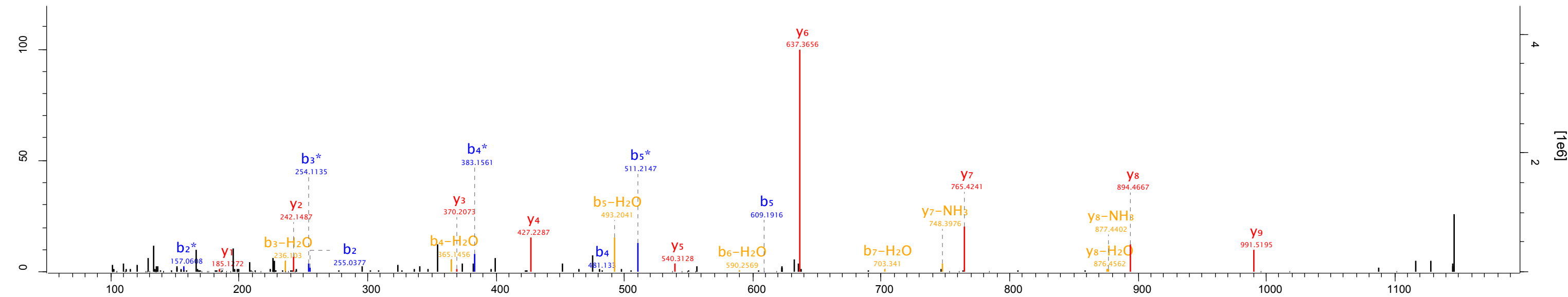
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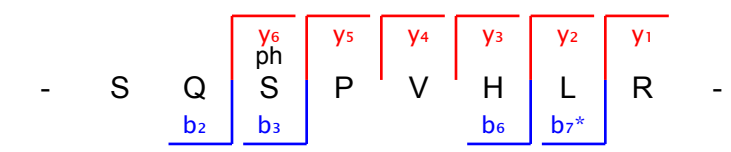
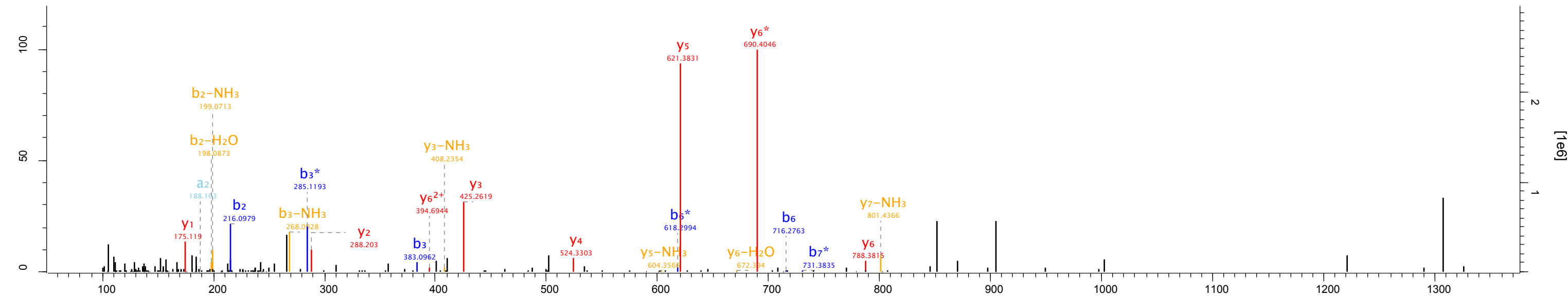
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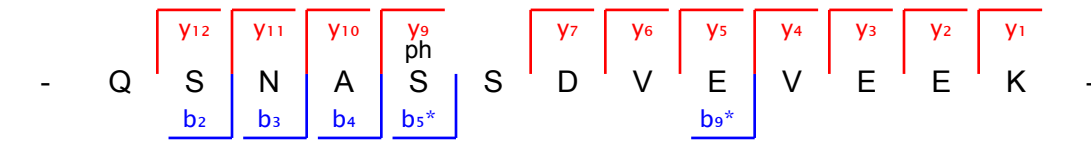
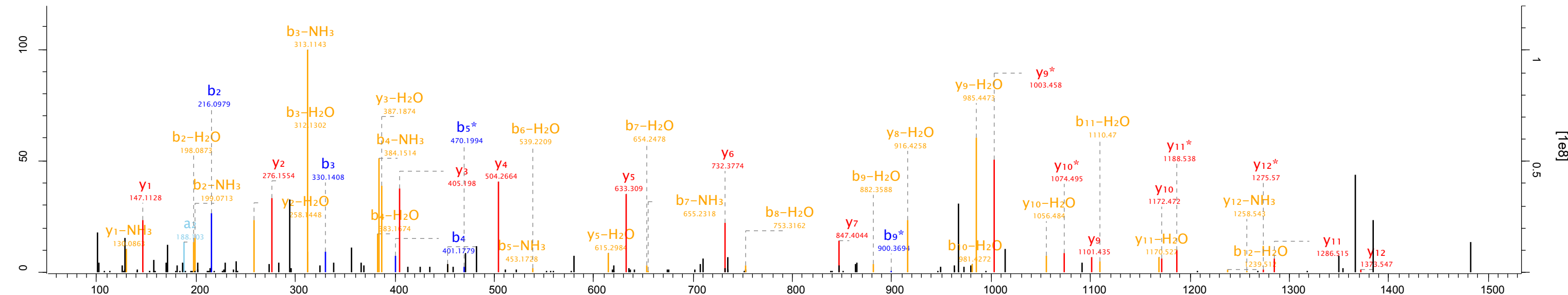


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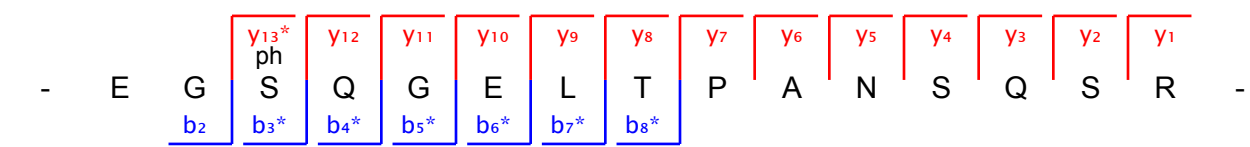
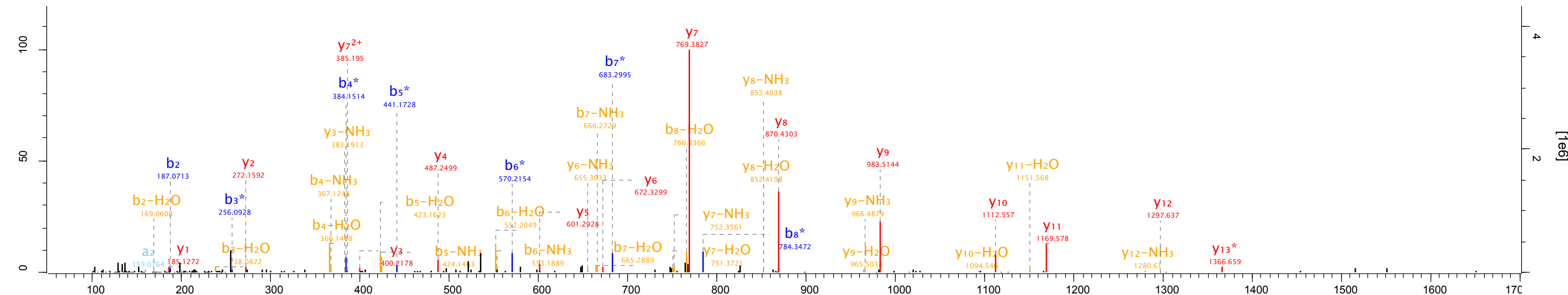


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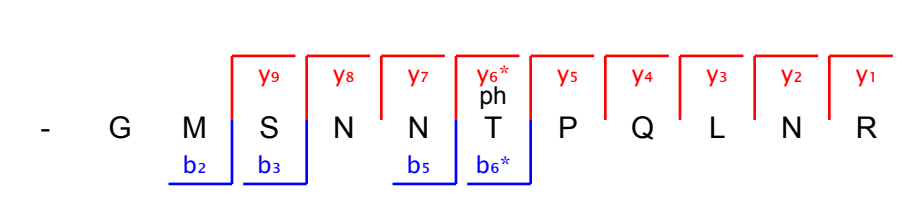
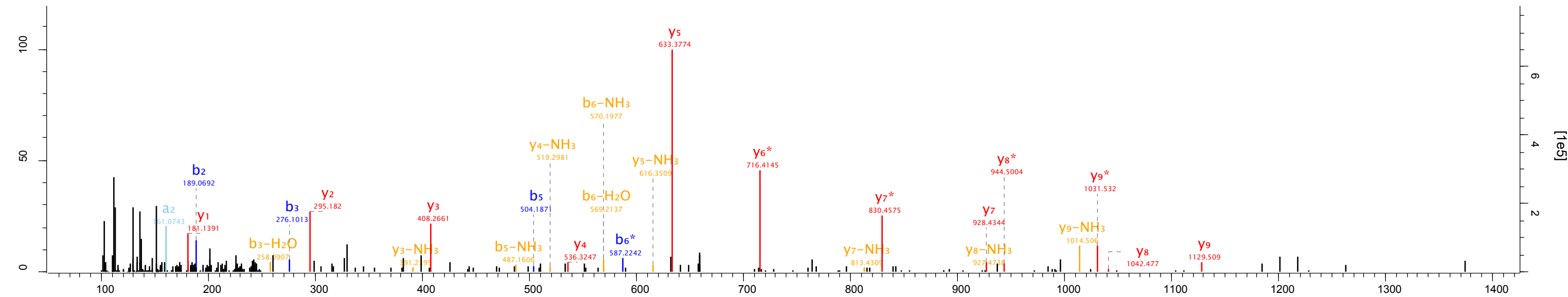




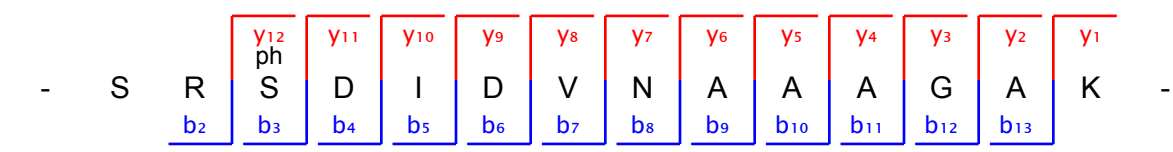
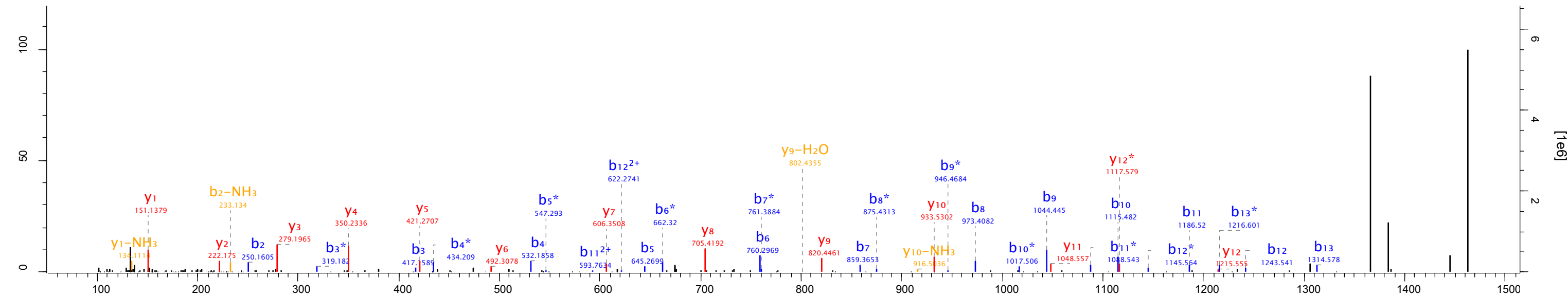
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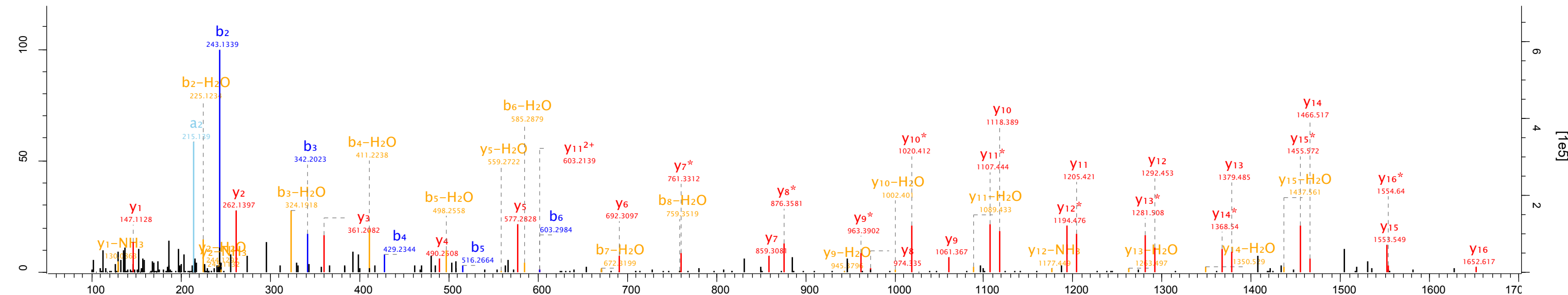


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Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan Method Score m/z Gene names
 4725 FTMS; HCD 199.7 732.86 CLASP2





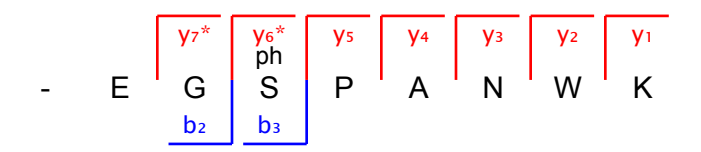
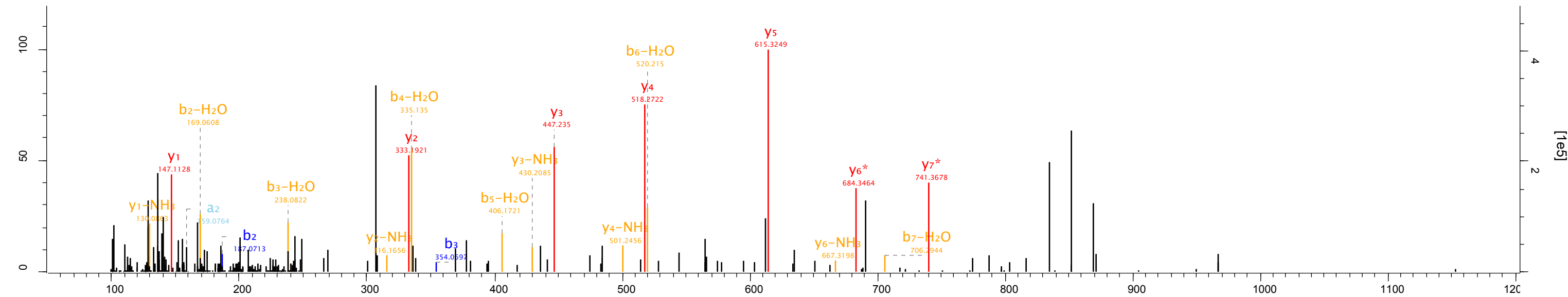
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b₂ b₃ b₄ b₅ b₆

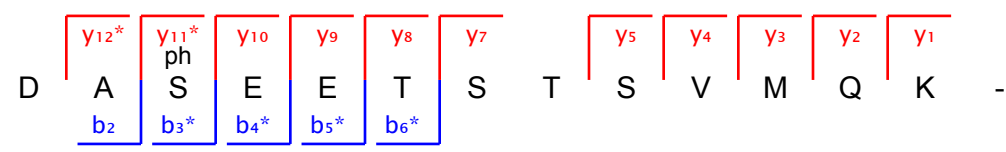
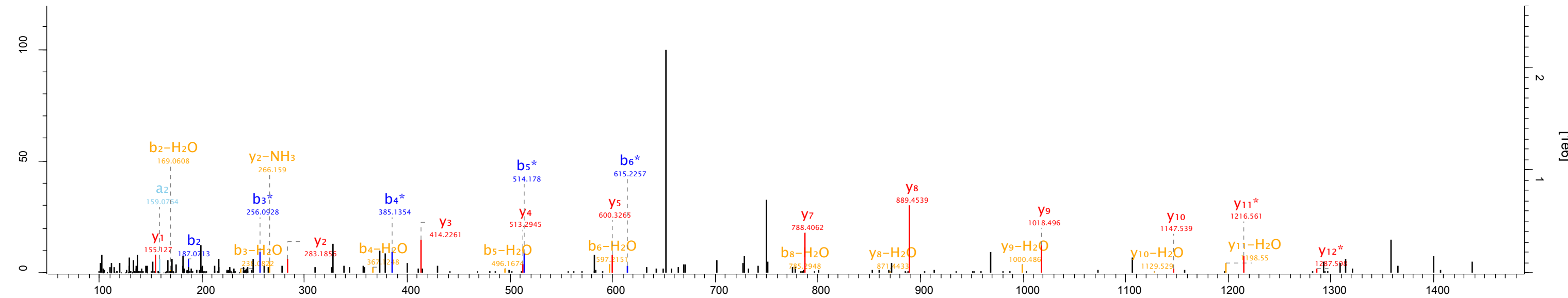
y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

y₇^{ph}

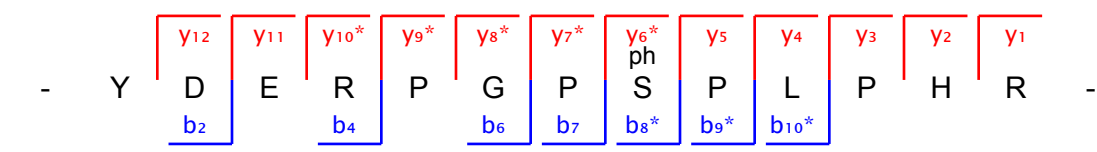
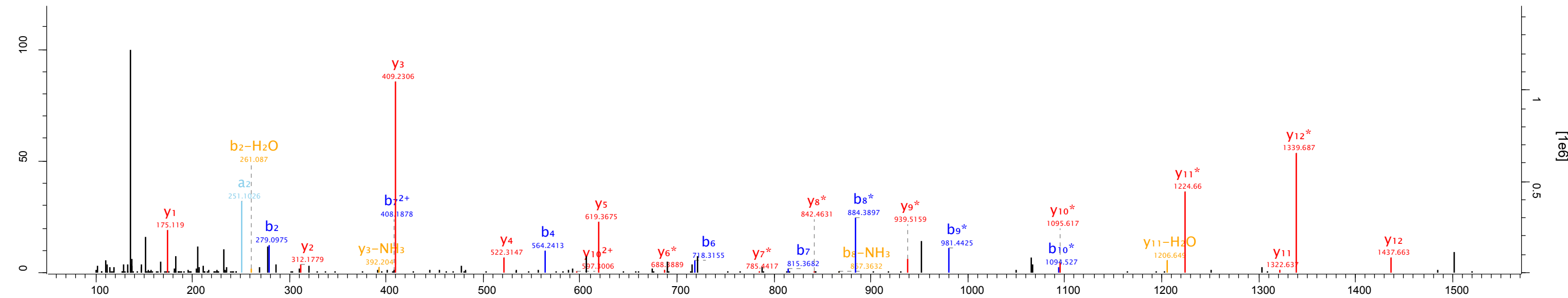
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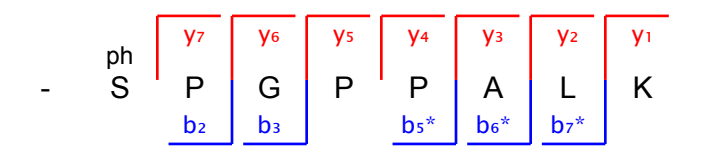
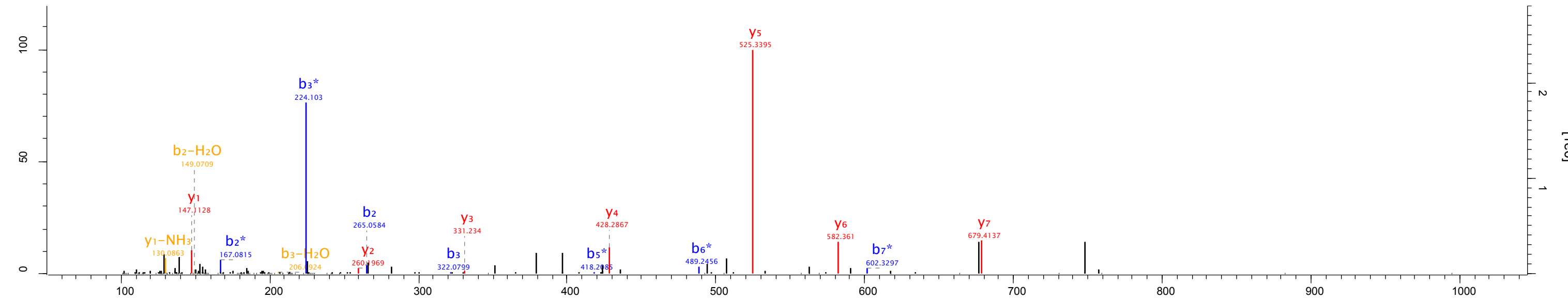
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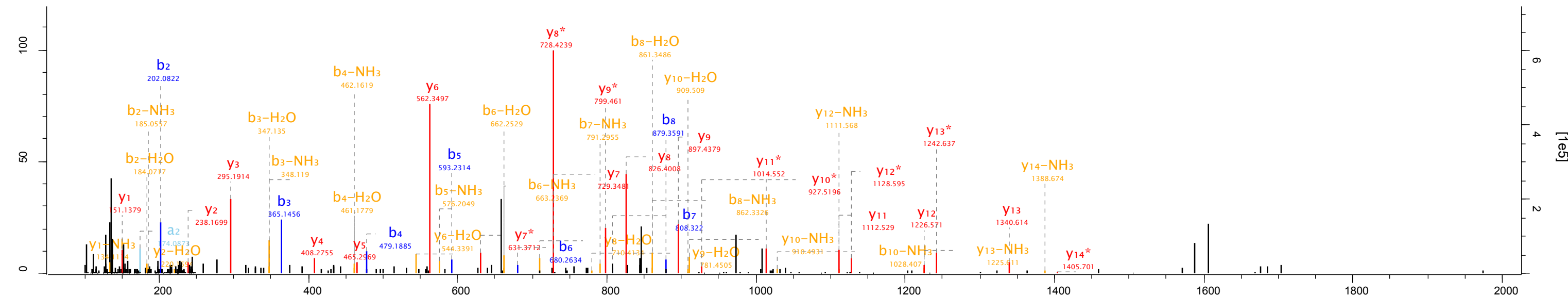
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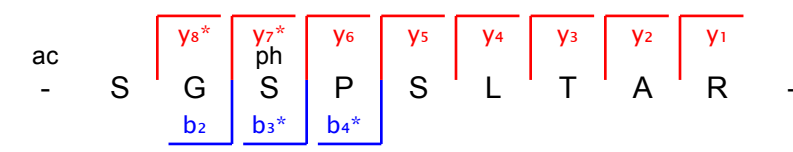
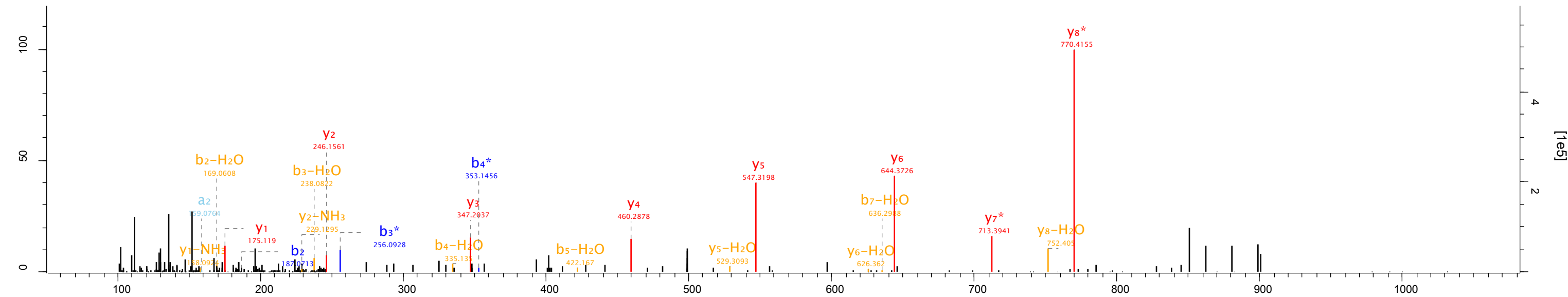
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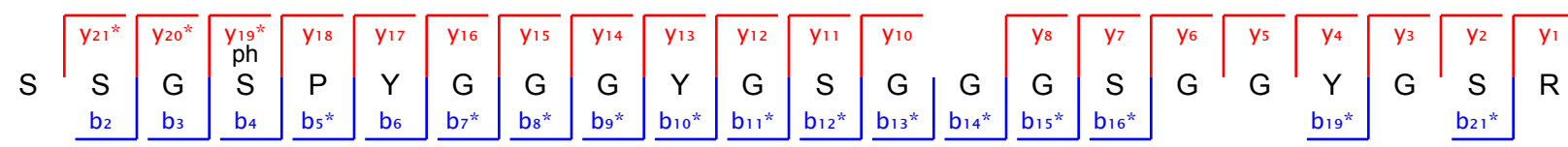
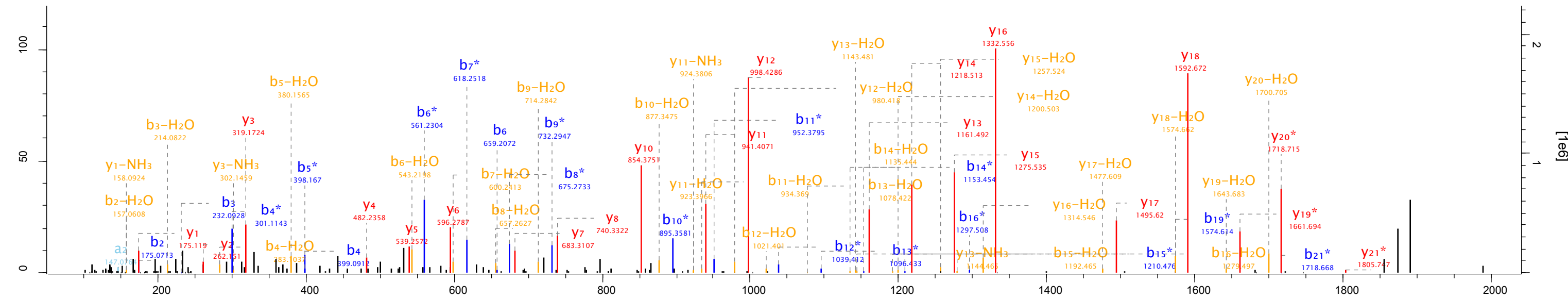
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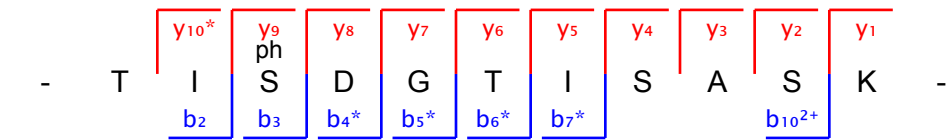
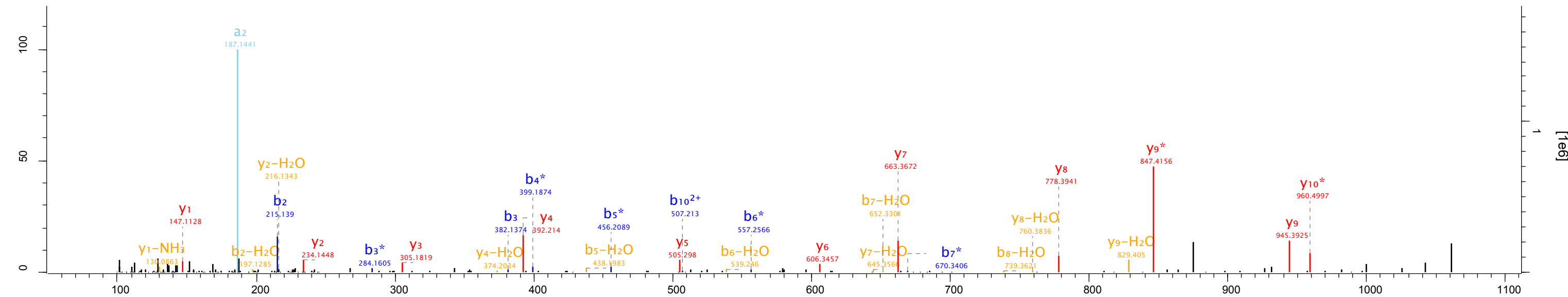
b₂
b₃
b₄
b₅
b₆
b₇
b₈
y₁₄*
y₁₃
y₁₂
y₁₁
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y₈
y₇^{ph}
y₆
y₅
y₄
y₃
y₂
y₁

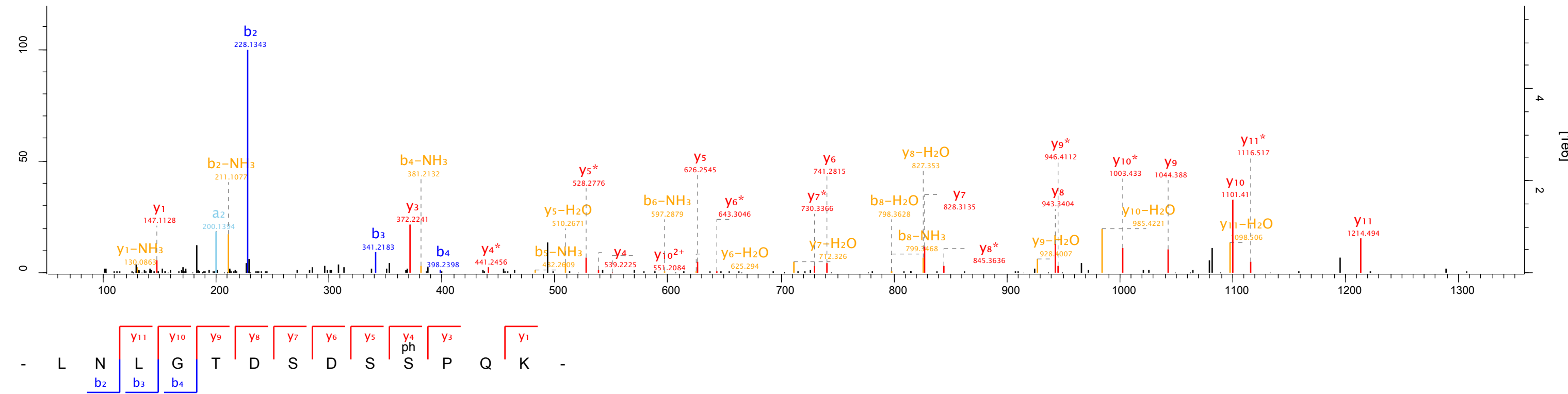
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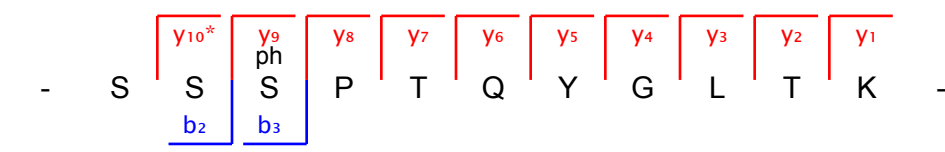
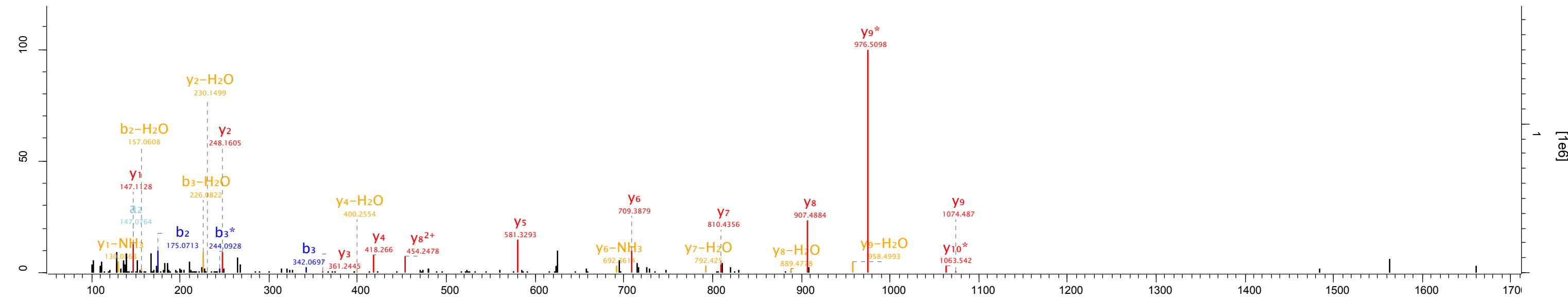
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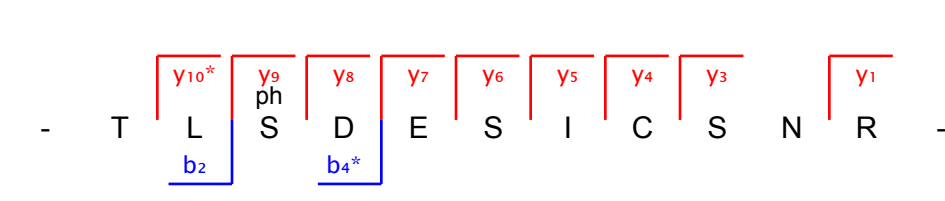
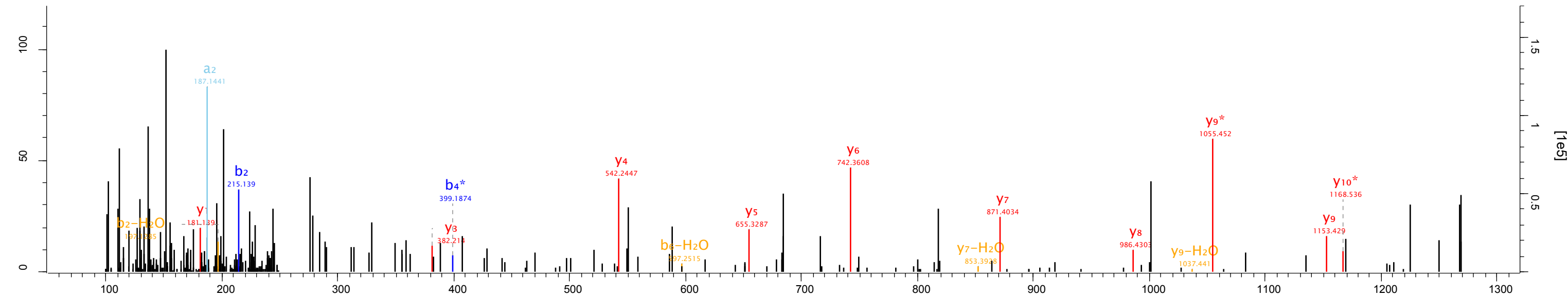




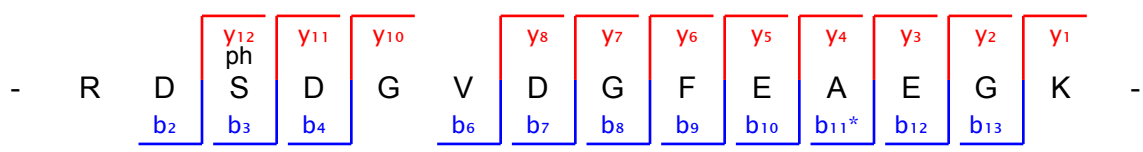
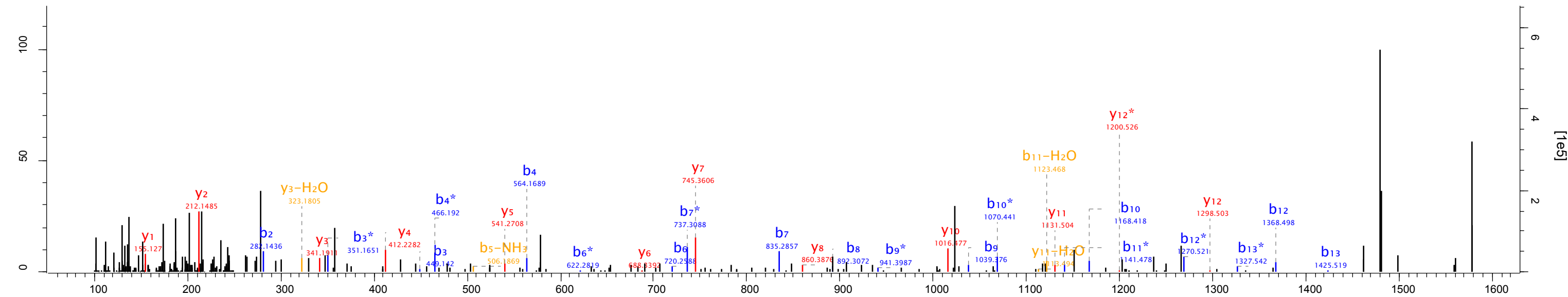
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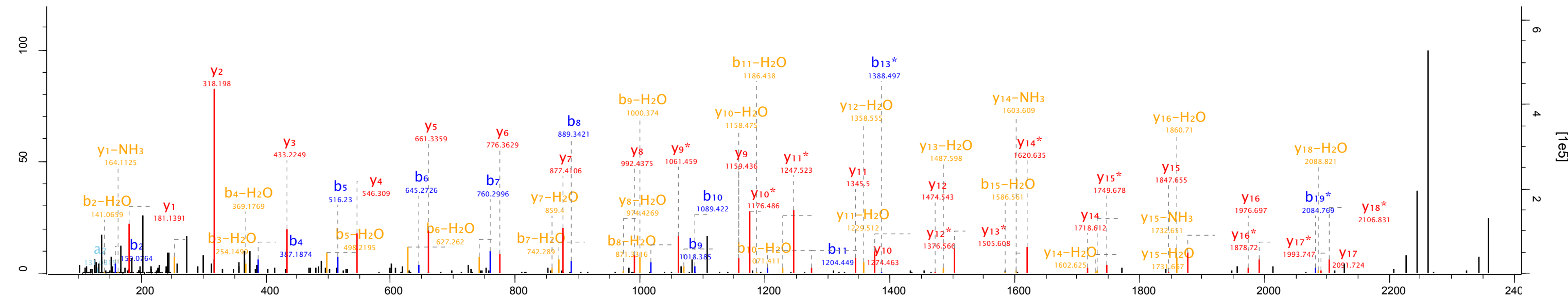


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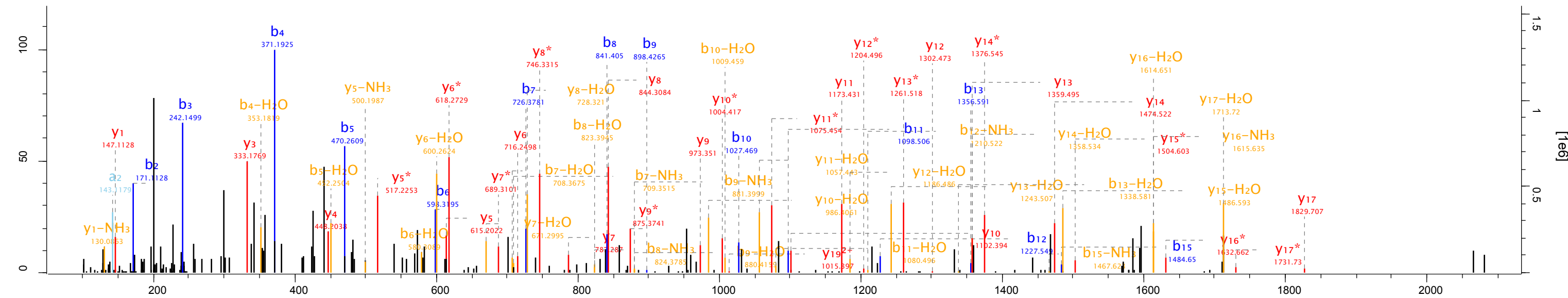
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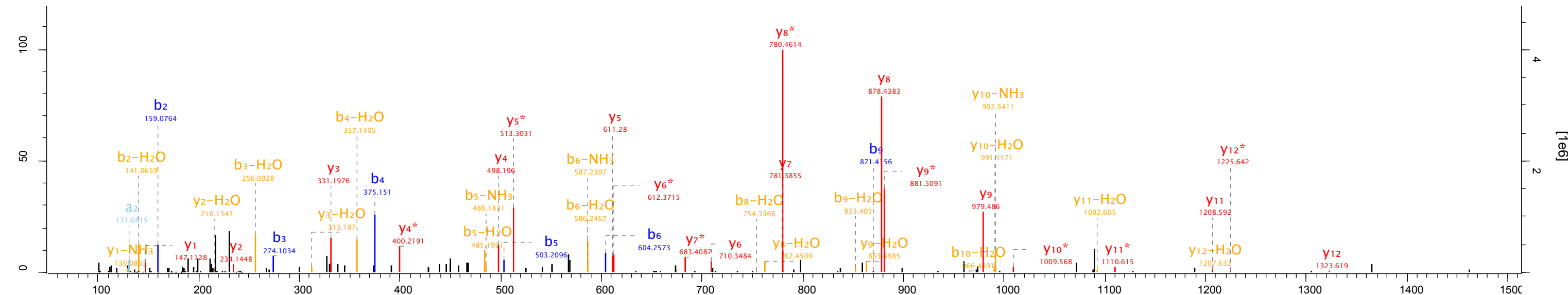
- G T L D E E D E E A D S D T D D I D H R -

b₂ b₄ b₅ b₆ b₇ b₈ b₉ b₁₀ b₁₁ y_{ph} b₁₃* b₁₉*



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

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃
b₁₅
y₁₉²⁺
y₁₇
y₁₆^{*}
y₁₅^{*}
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅_{ph}
y₄
y₃
y₁

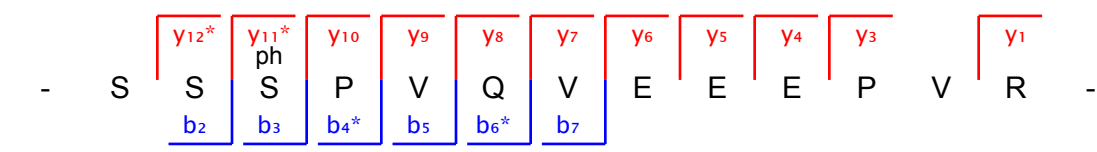
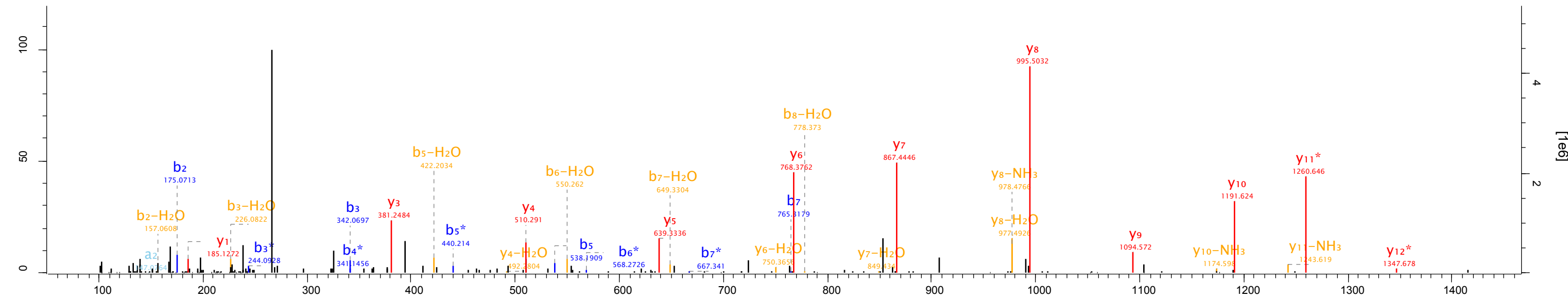


- G T D T Q T P A V L S P S K -

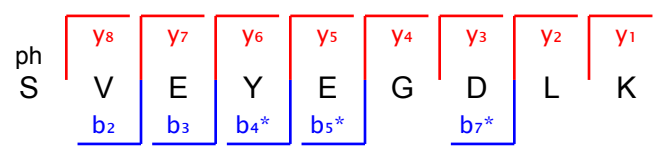
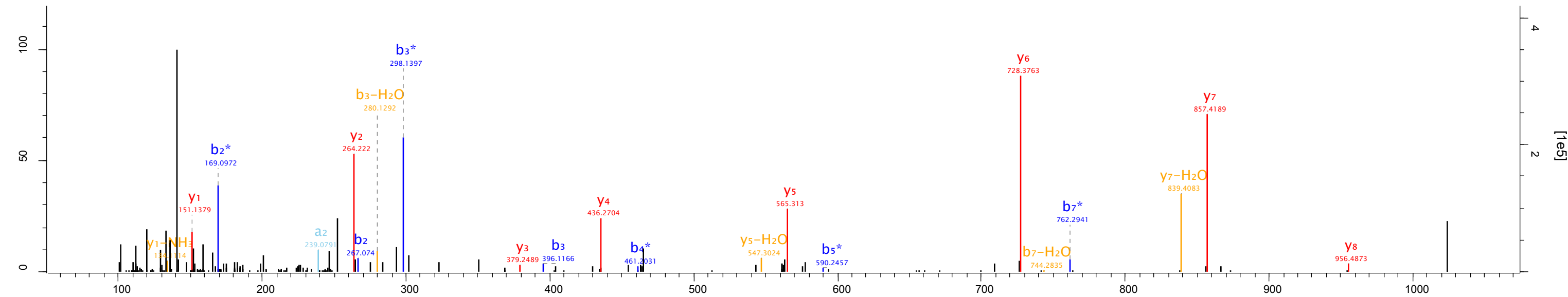
Fragmentation labels (b and y ions) are shown below the corresponding amino acids:

- b₂ (under T)
- b₃ (under D)
- b₄ (under T)
- b₅ (under Q)
- b₆ (under T)
- b₉ (under V)
- y₁ (under K)
- y₂ (under S)
- y₃ (under P)
- y₄ (under S)
- y₄ph (under L)
- y₅ (under L)
- y₆ (under V)
- y₇ (under A)
- y₈ (under P)
- y₉ (under T)
- y₁₀* (under Q)
- y₁₁ (under T)
- y₁₂ (under D)

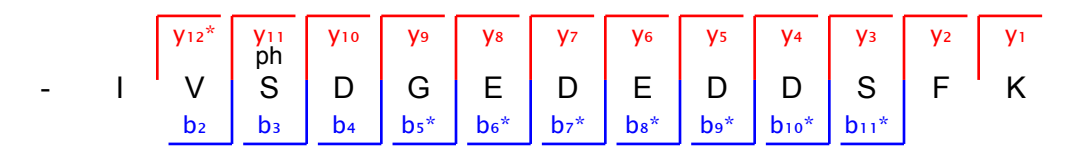
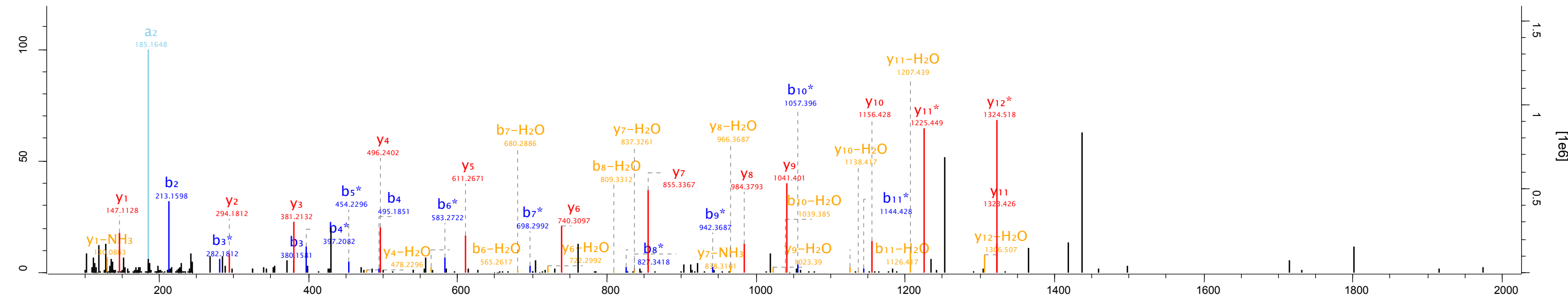
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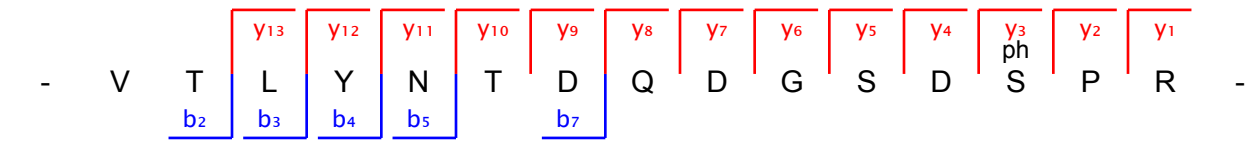
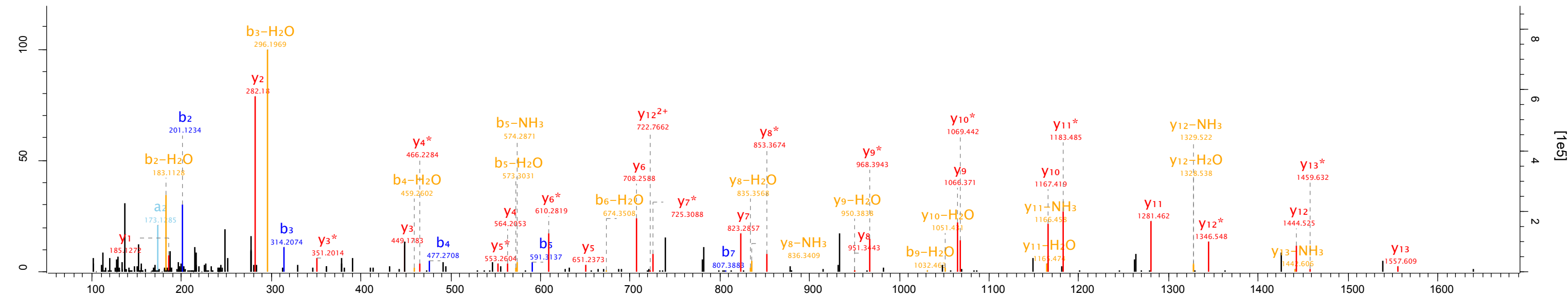


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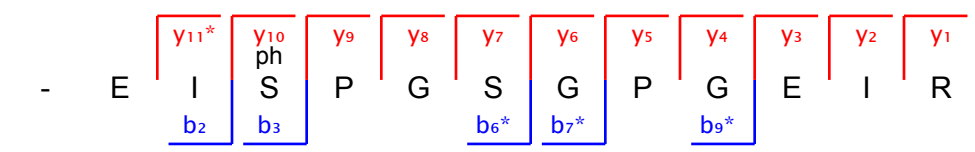
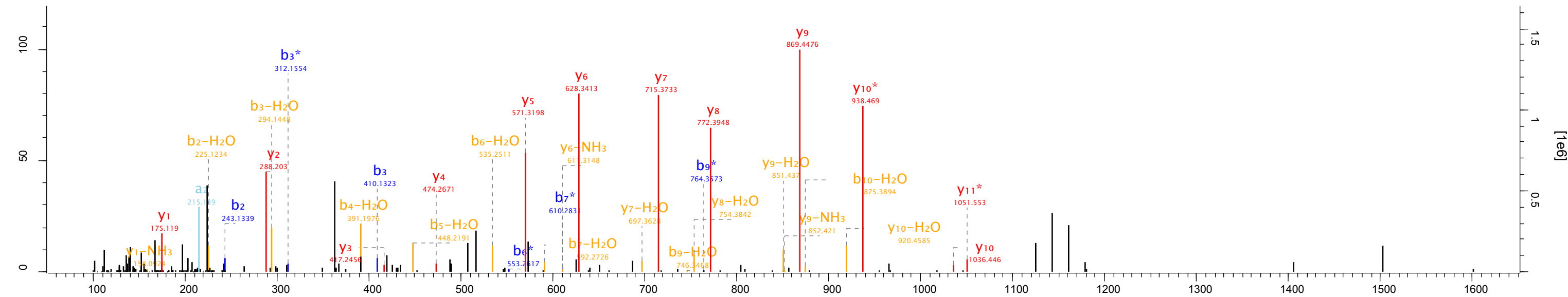


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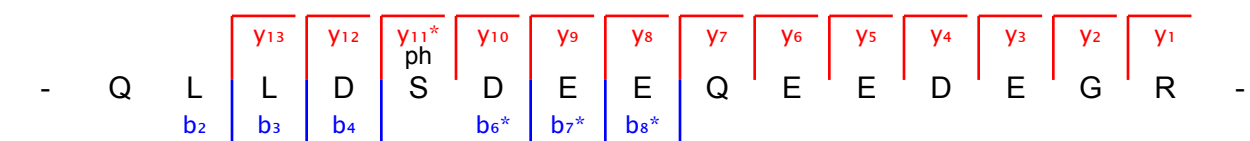
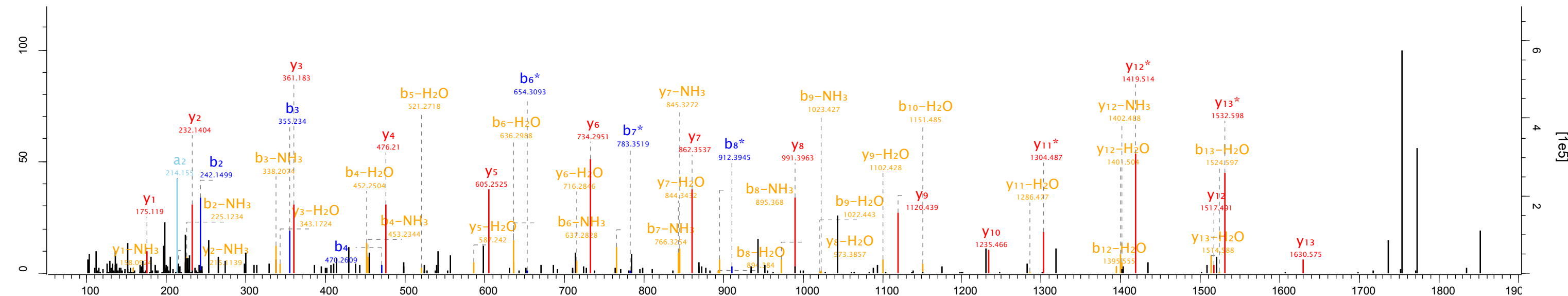




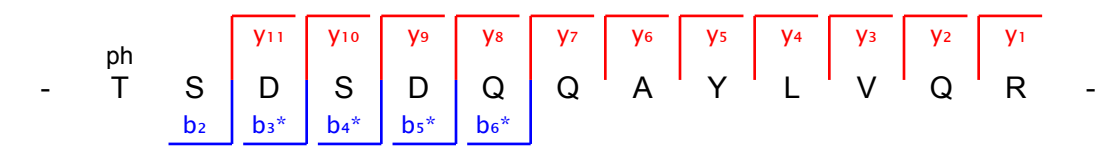
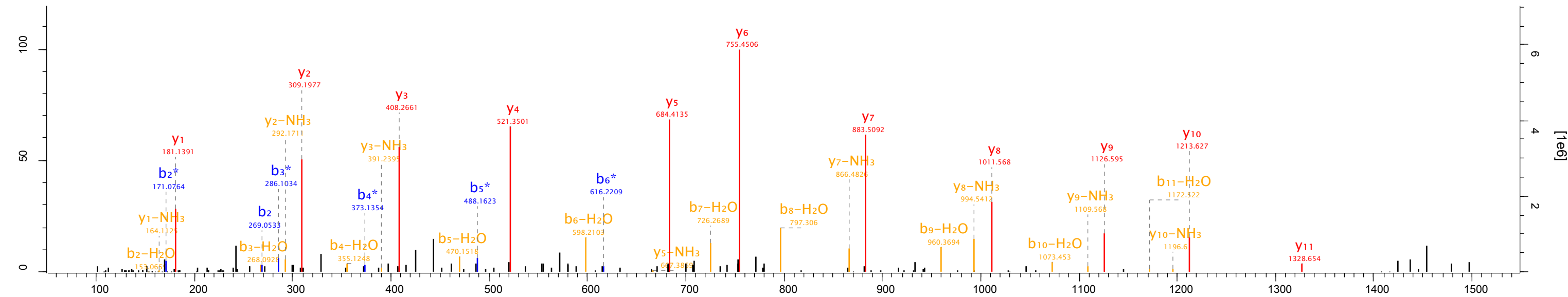
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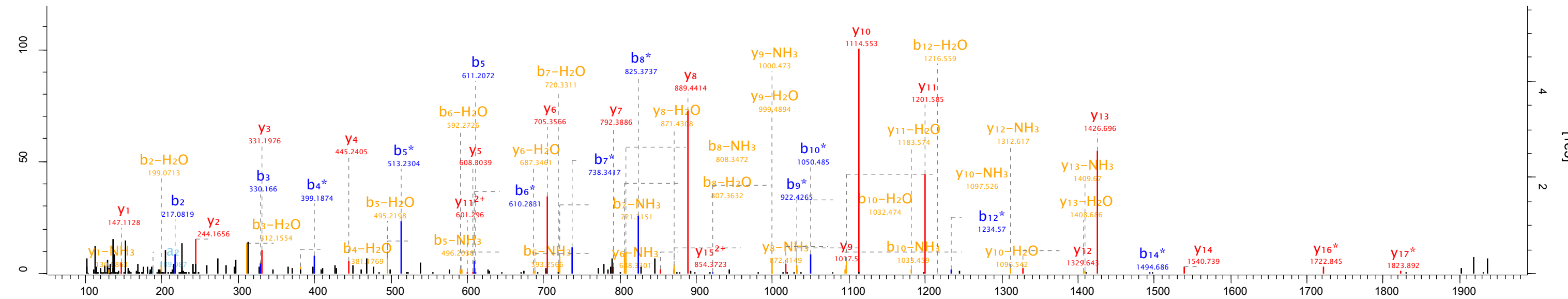
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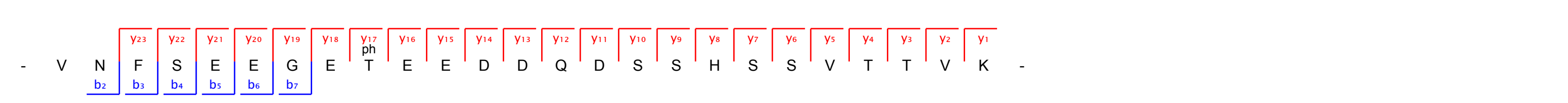
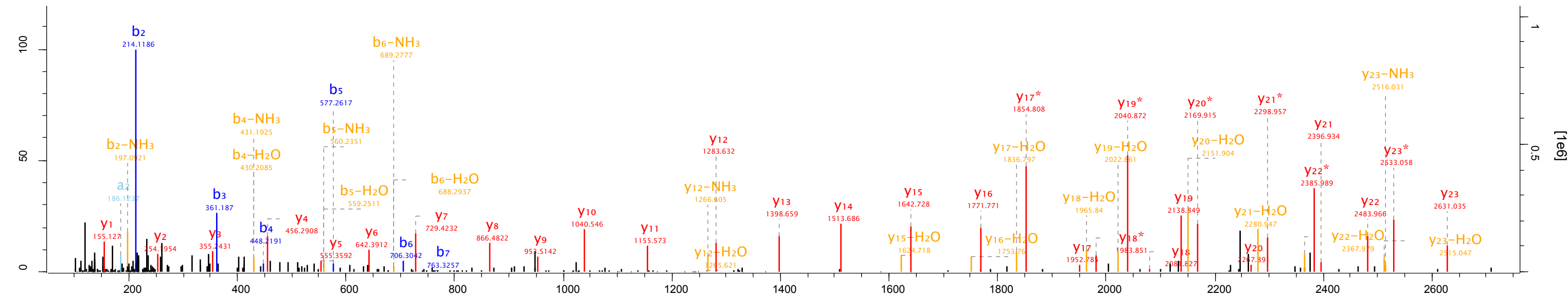
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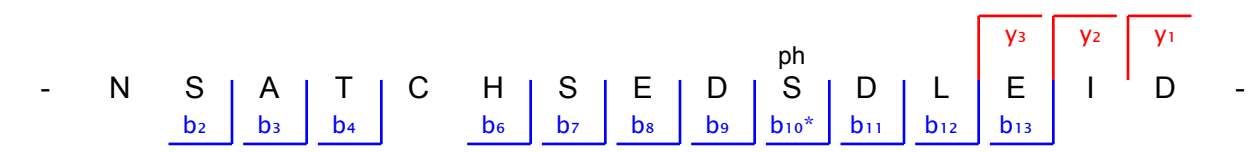
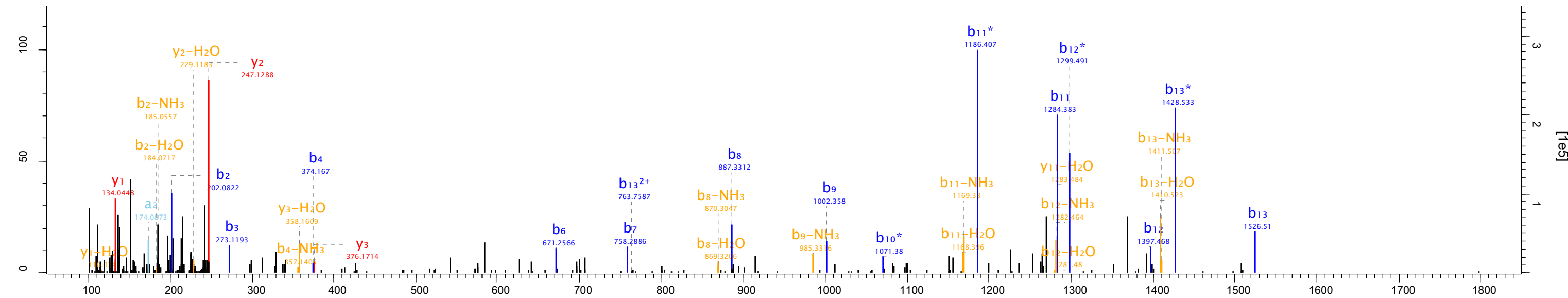
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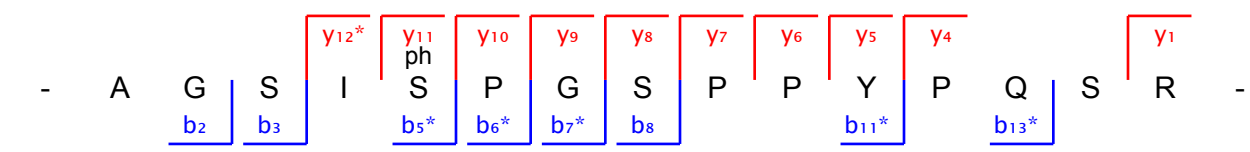
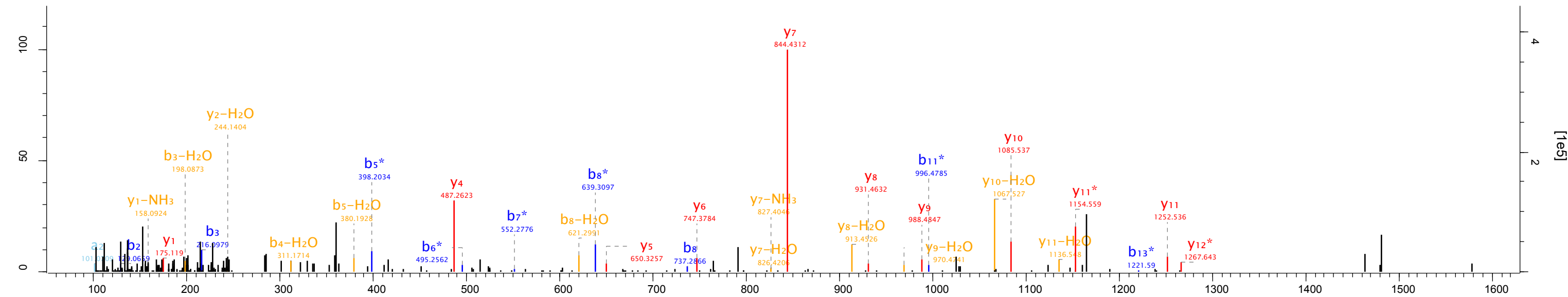
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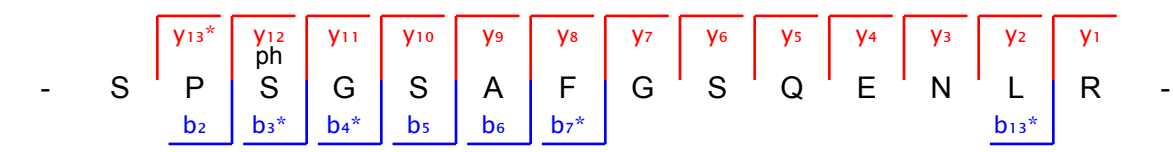
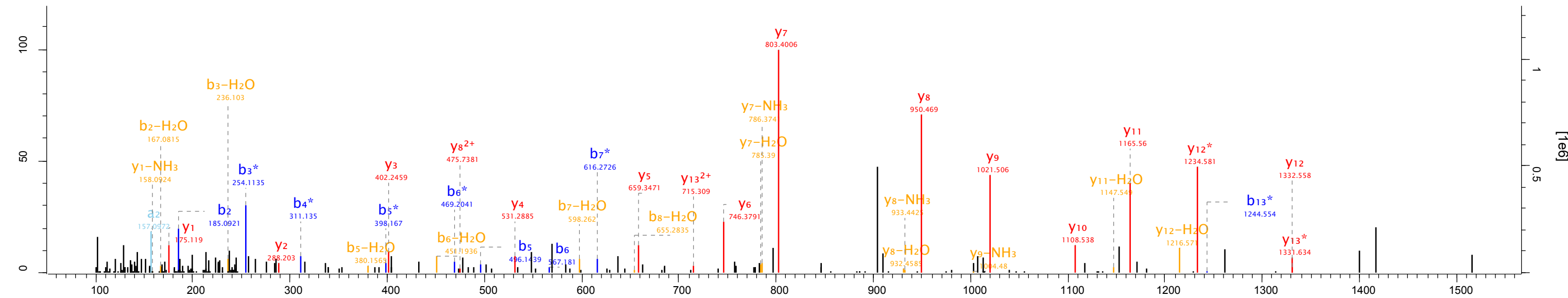
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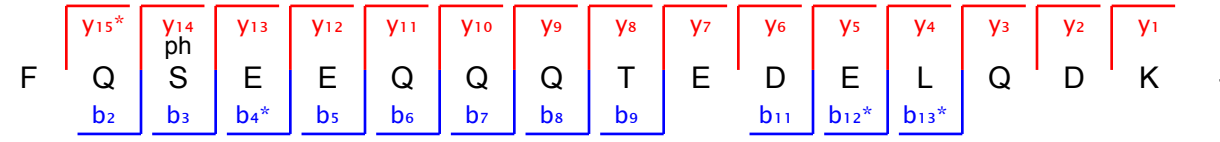
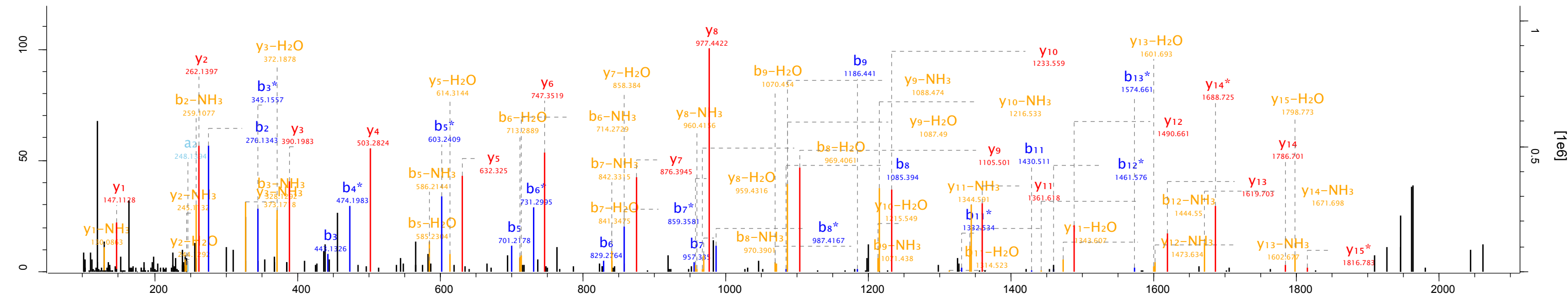
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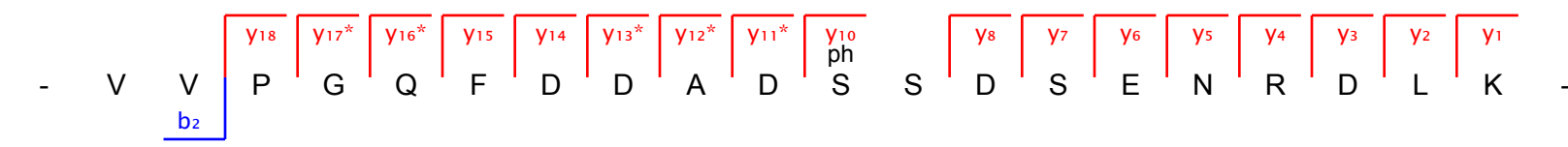
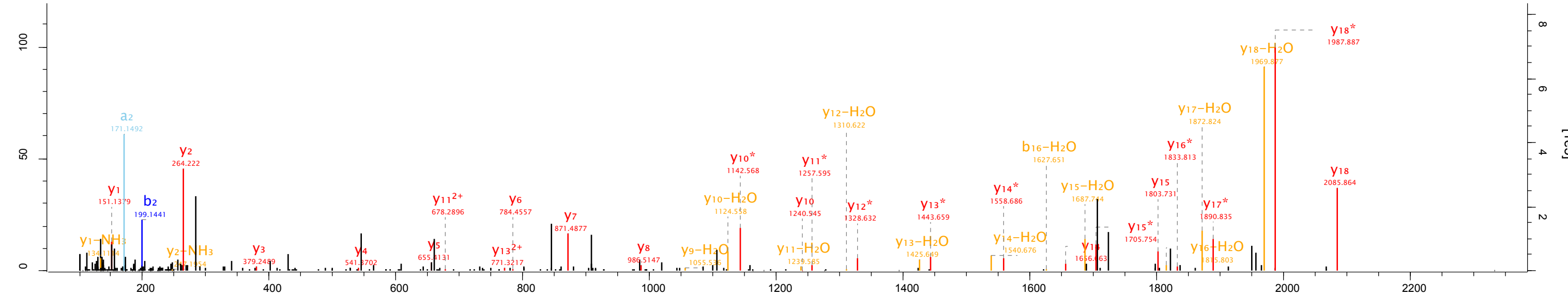
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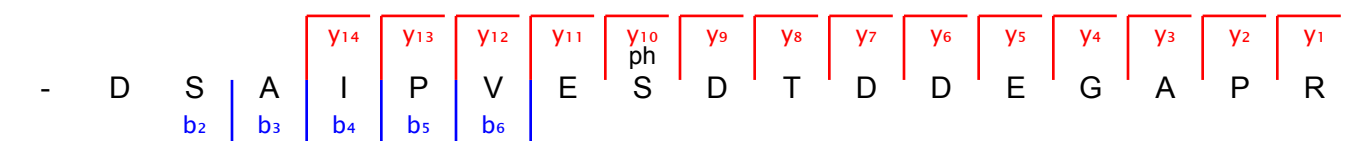
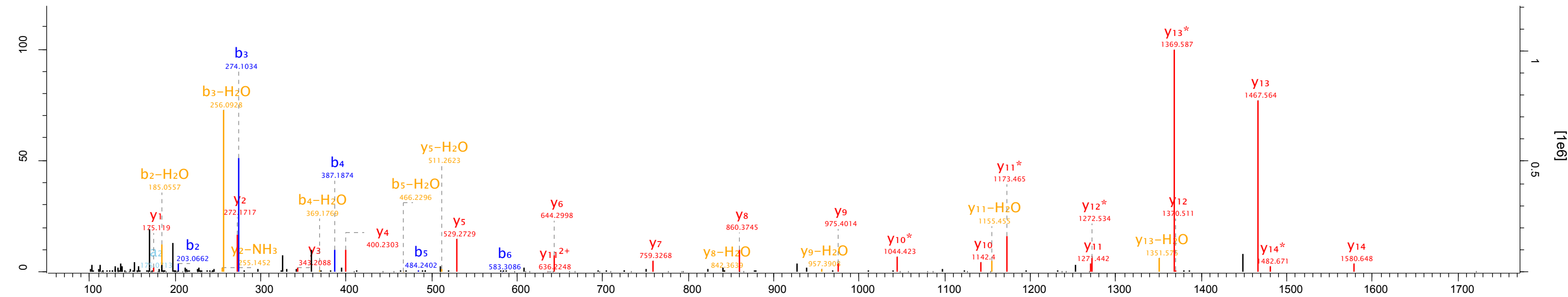
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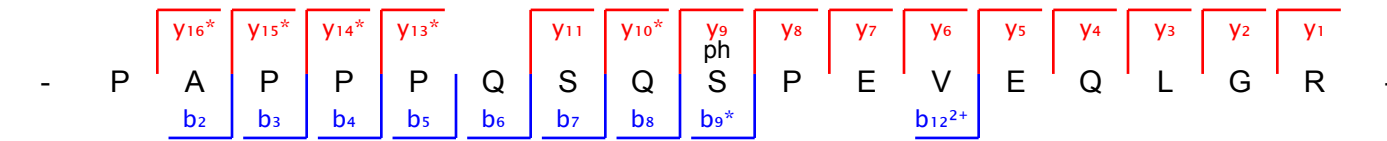
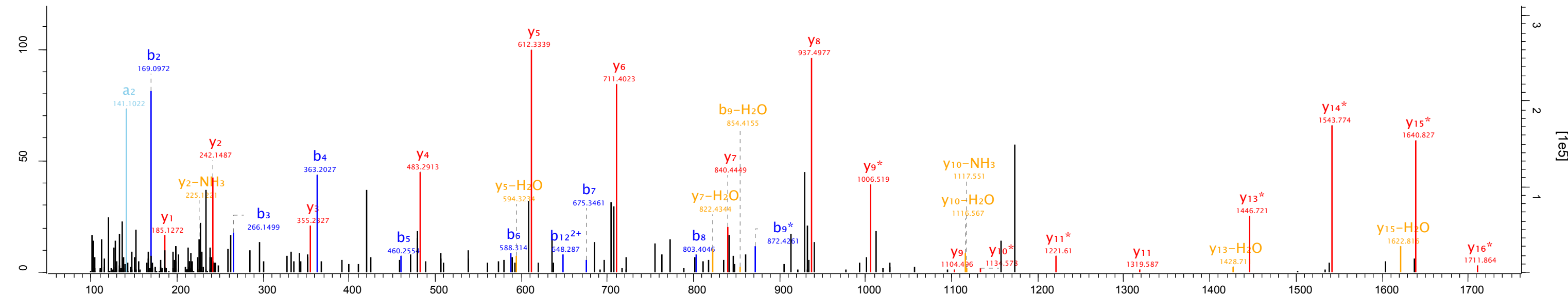
20171215_MaS_33SR_LMH_phospho_03 8945 FTMS; HCD 124.7 762.34 RIOK1



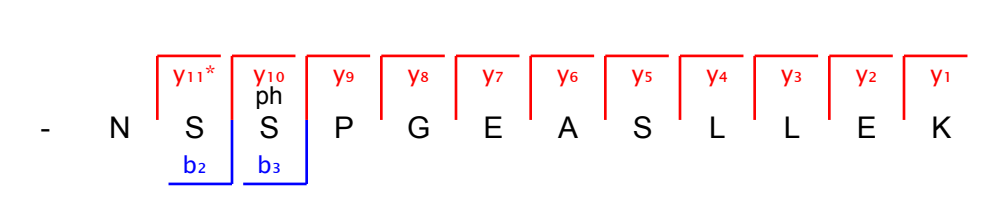
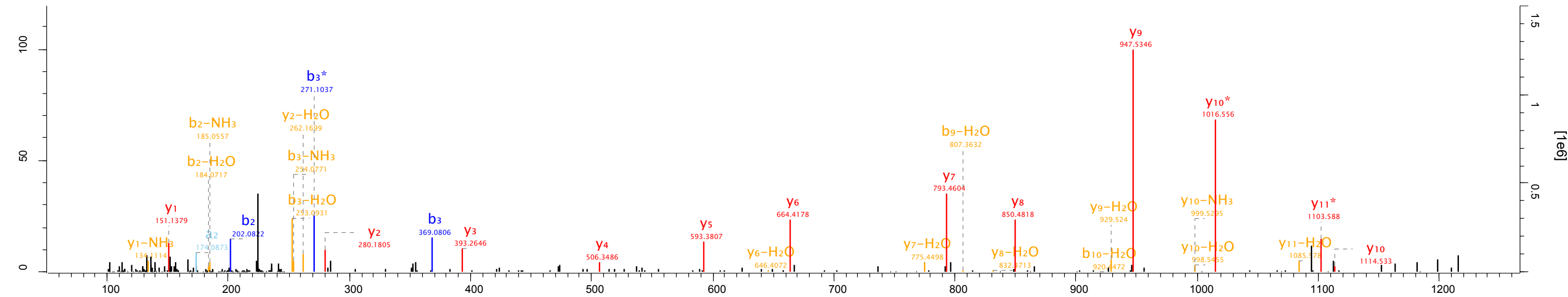
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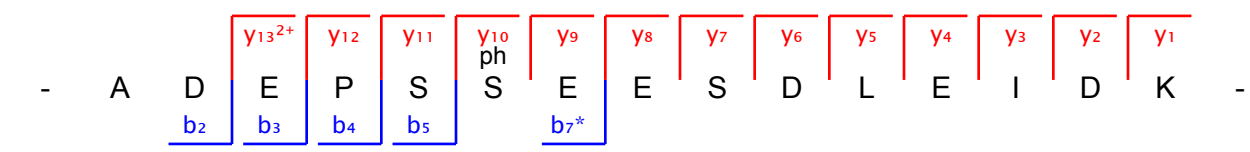
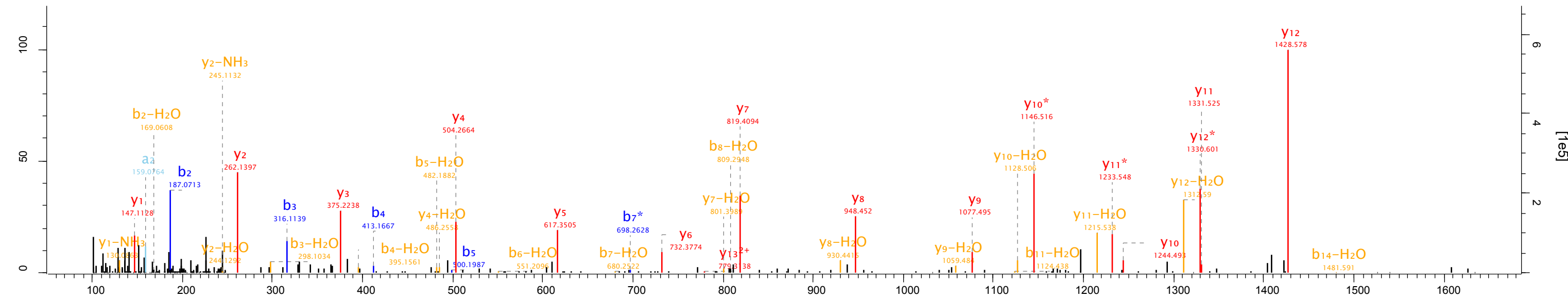
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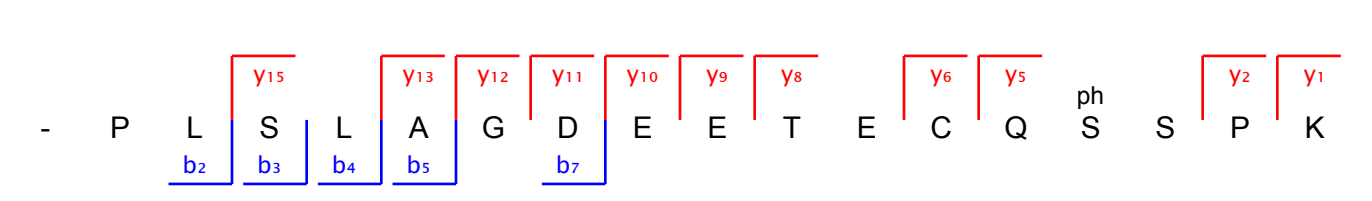
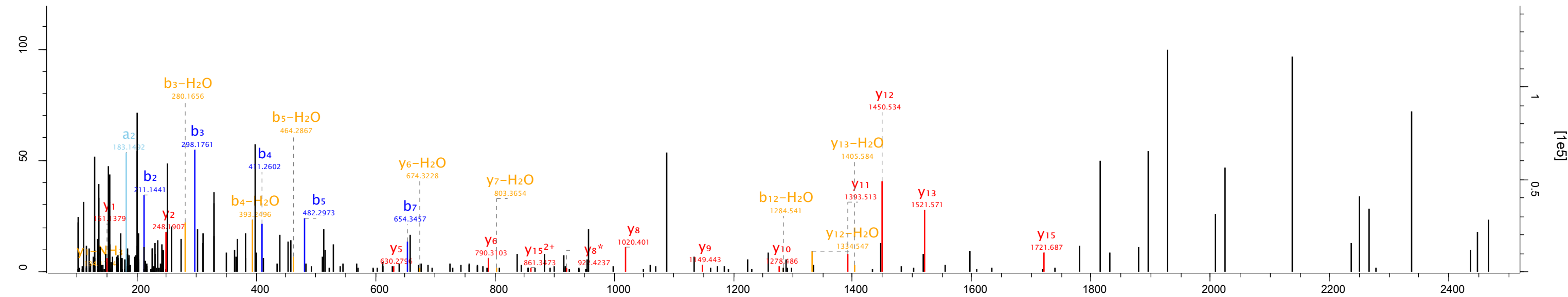
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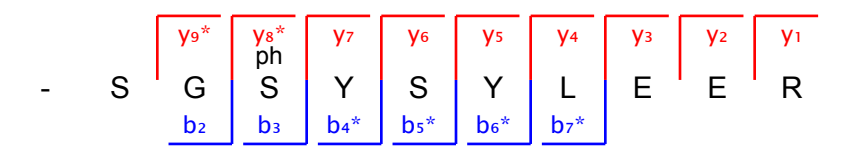
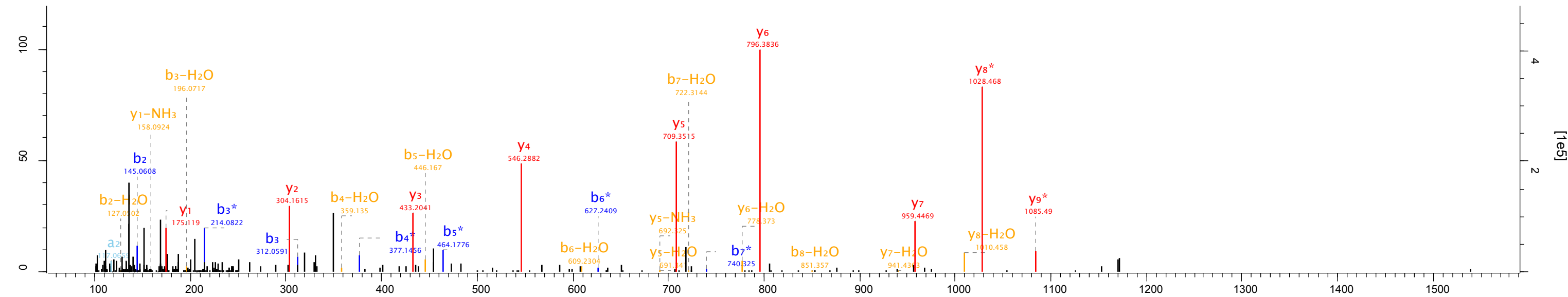
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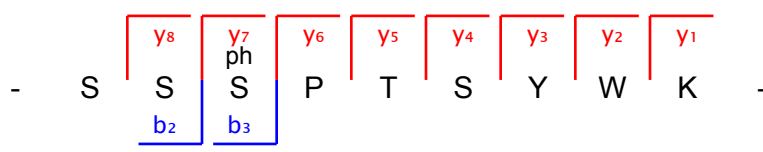
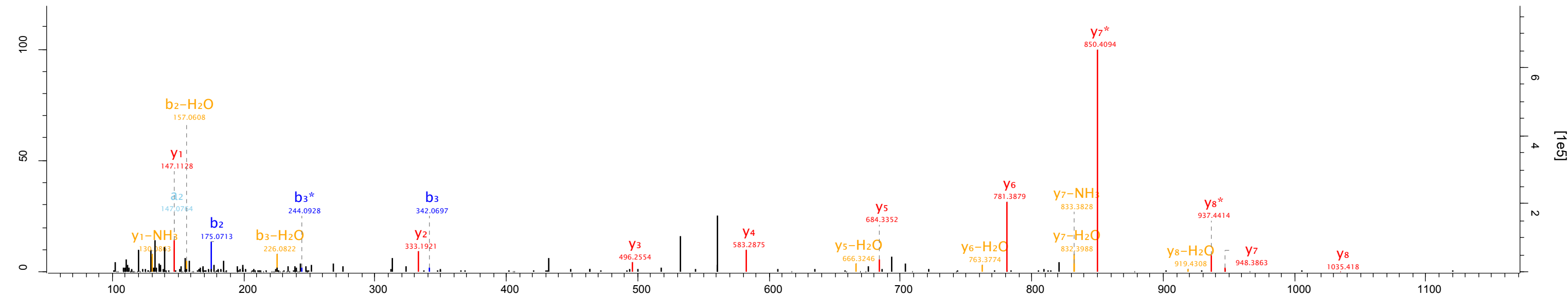
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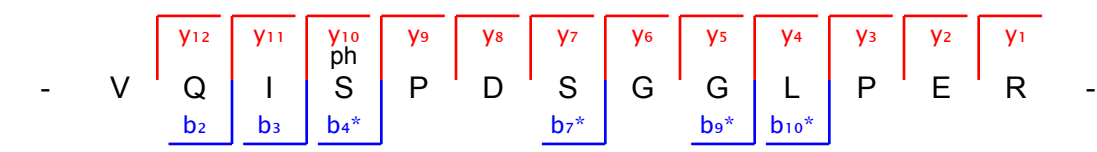
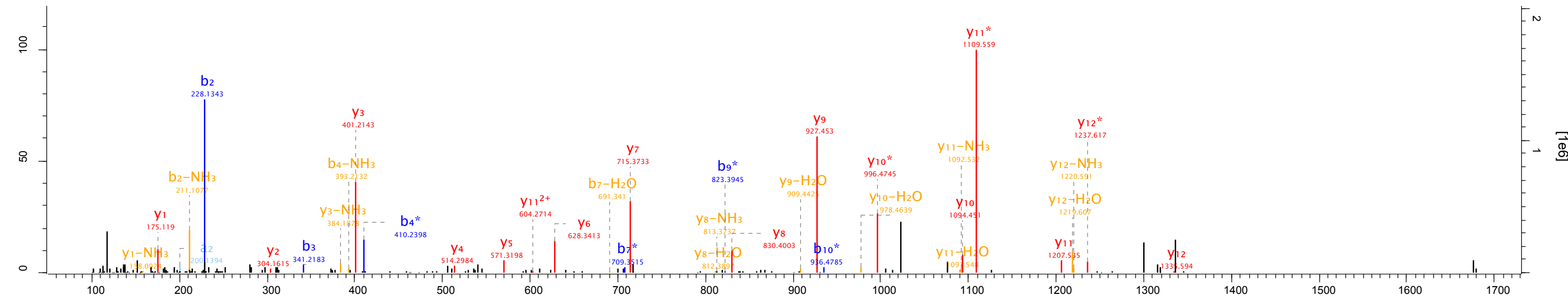
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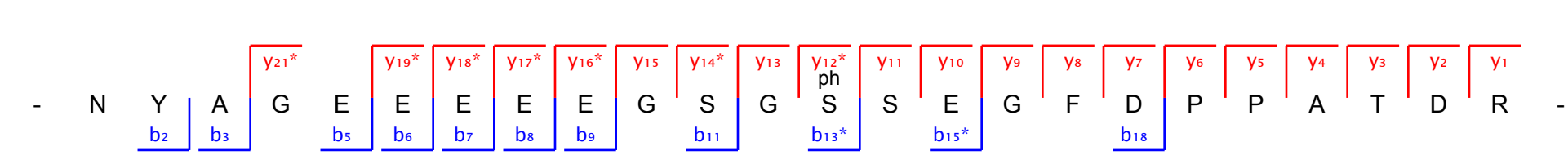
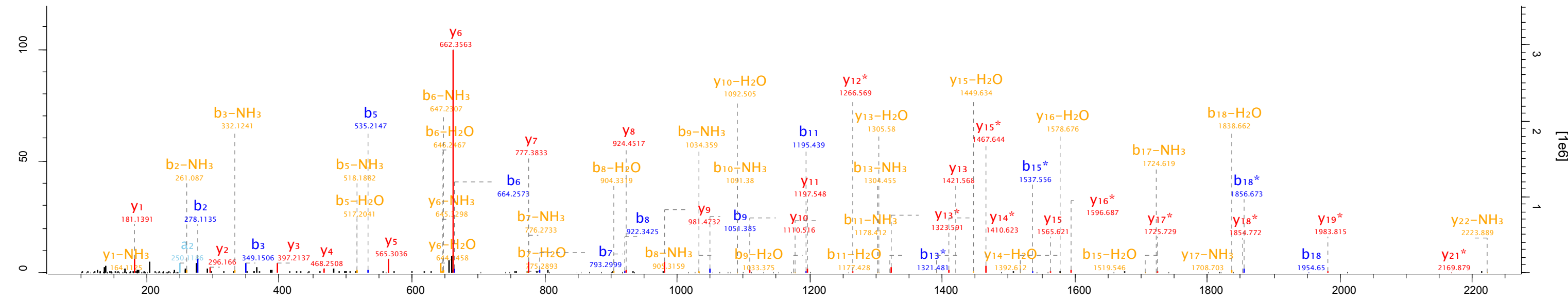
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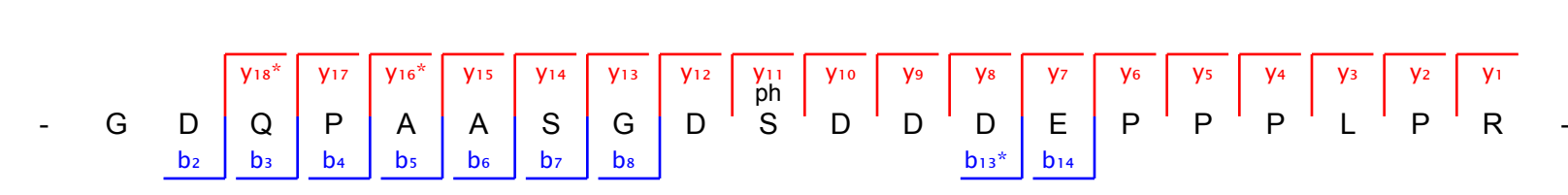
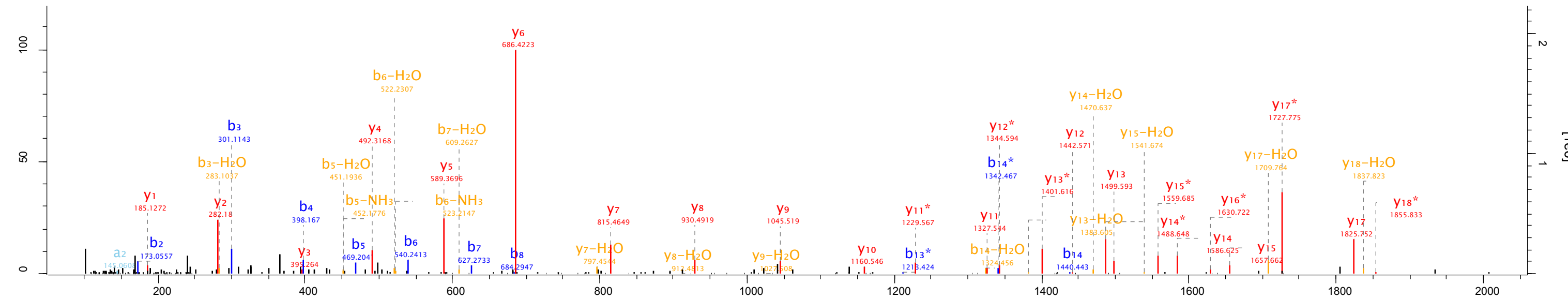
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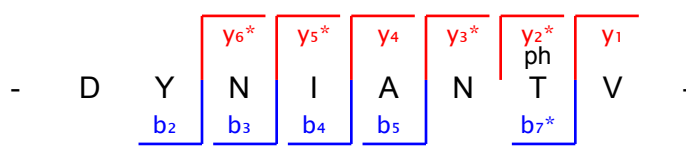
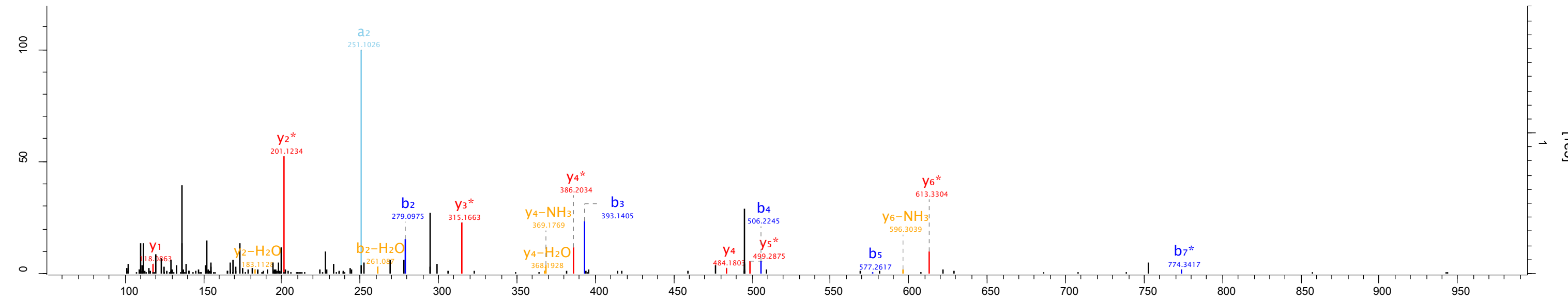
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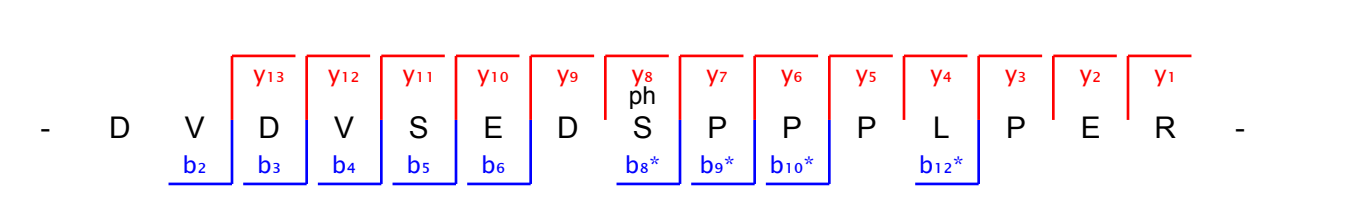
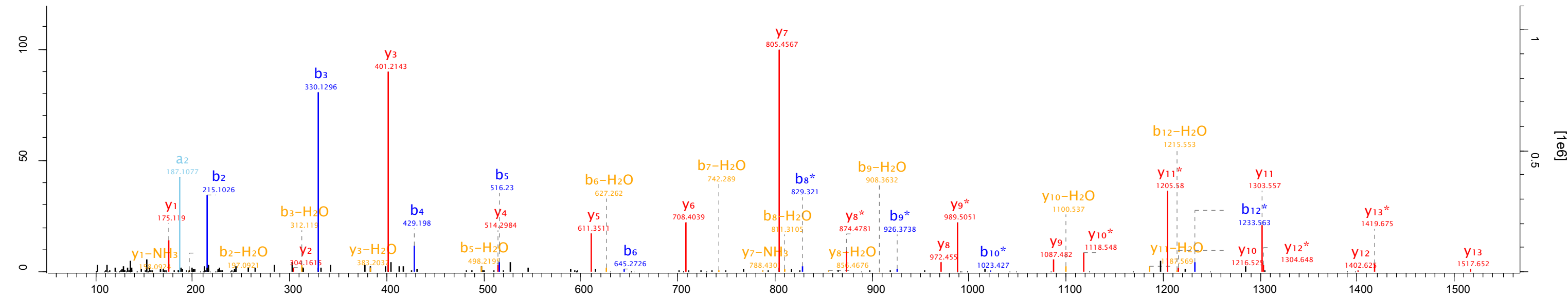
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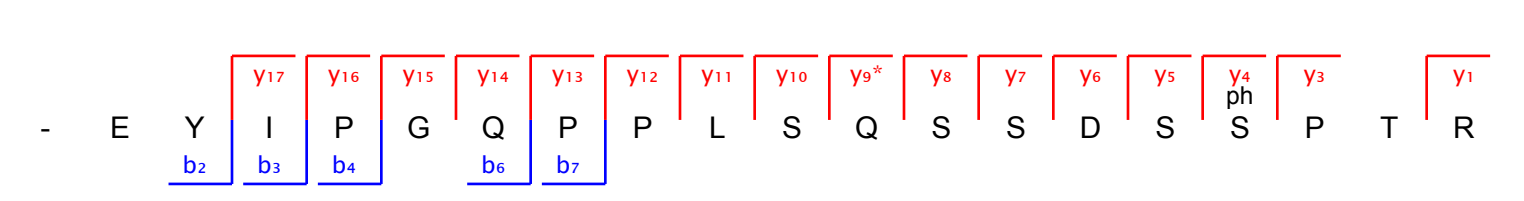
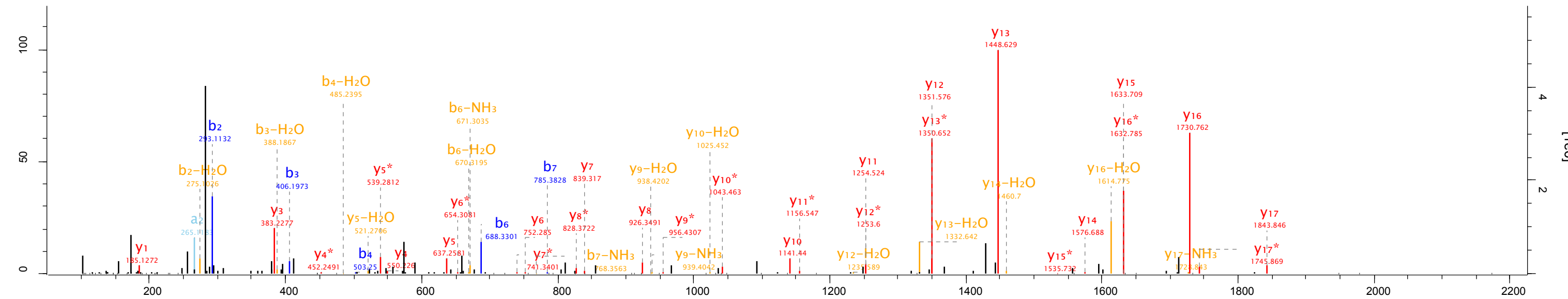
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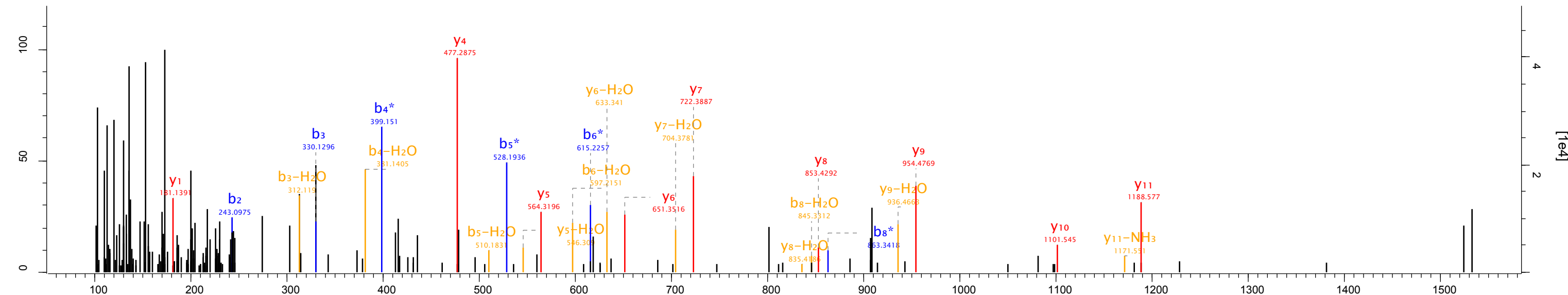


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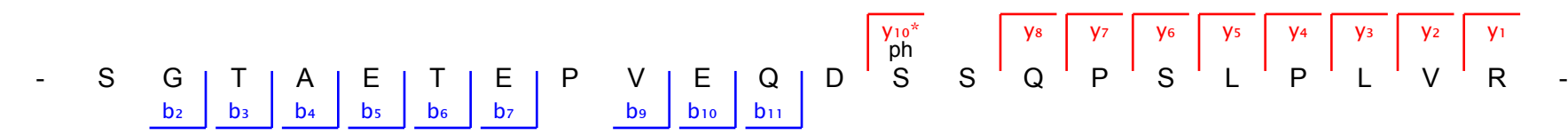
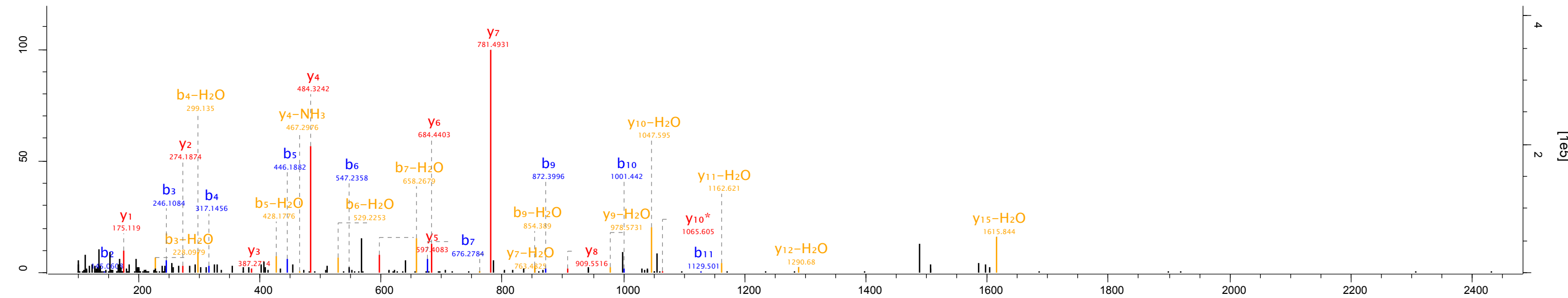
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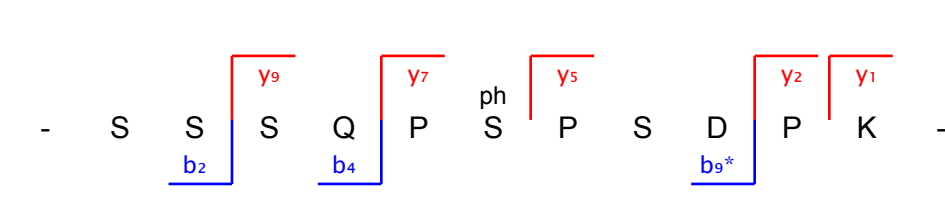
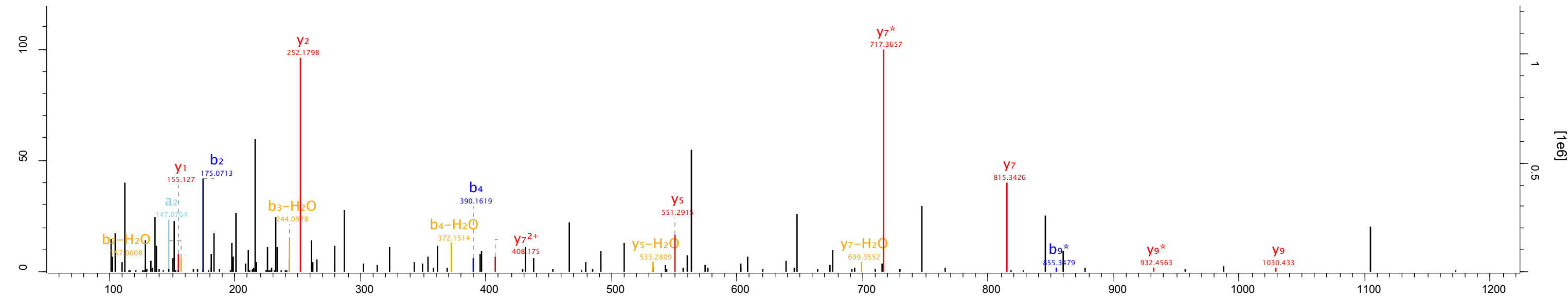
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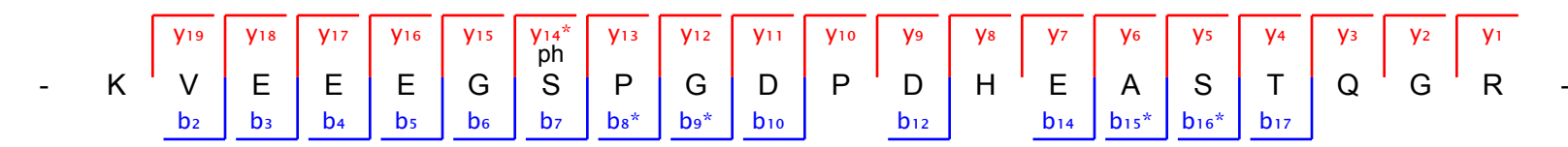
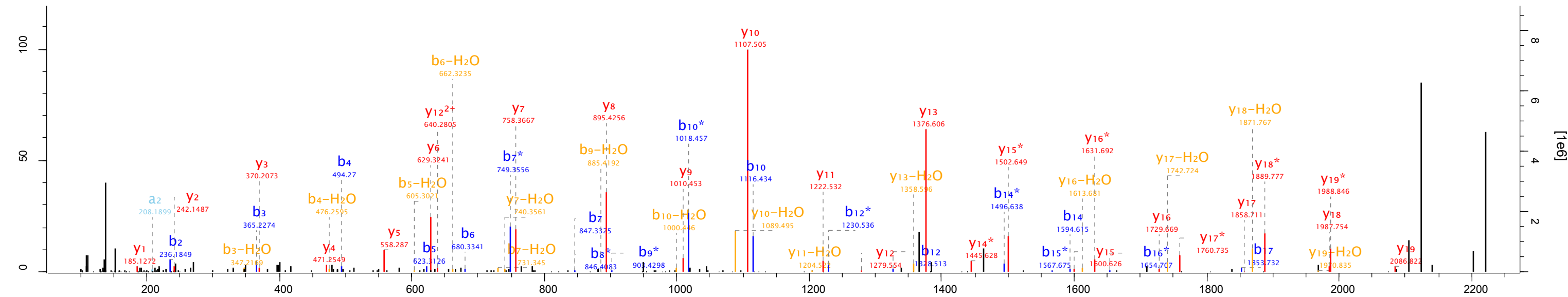
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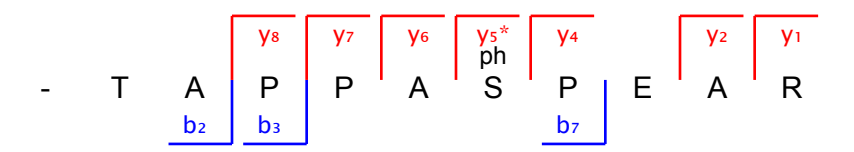
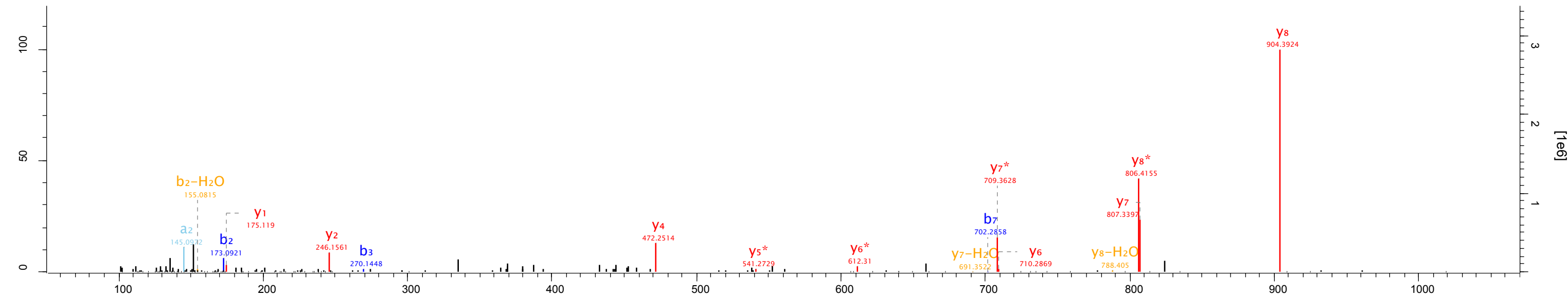
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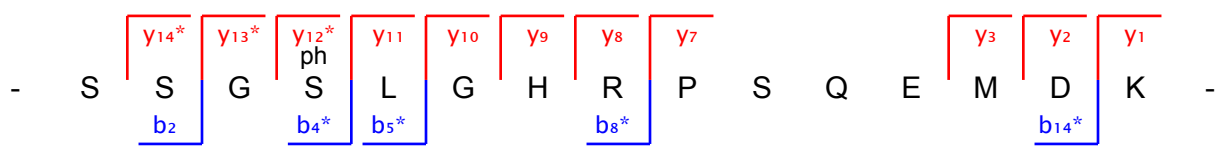
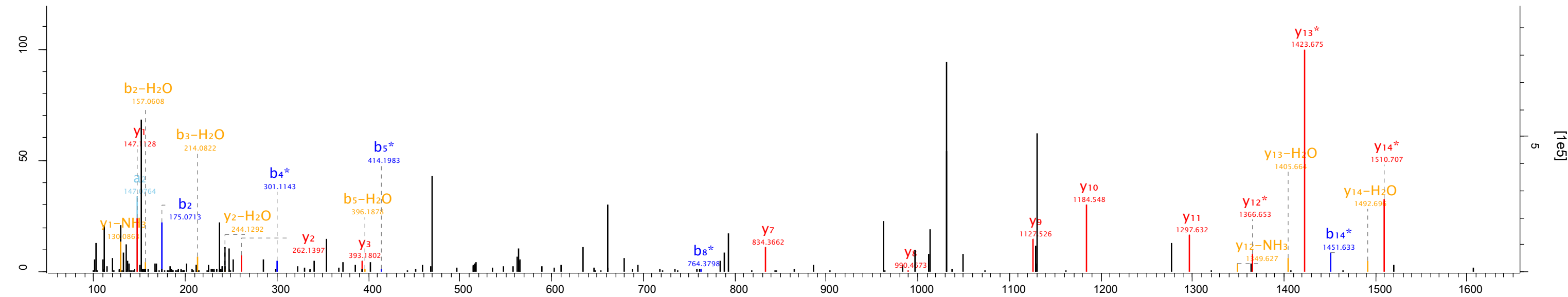
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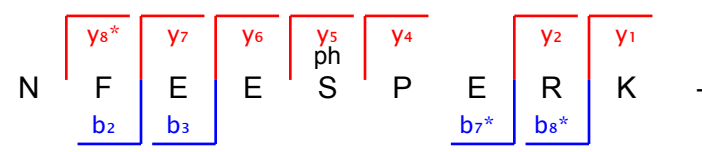
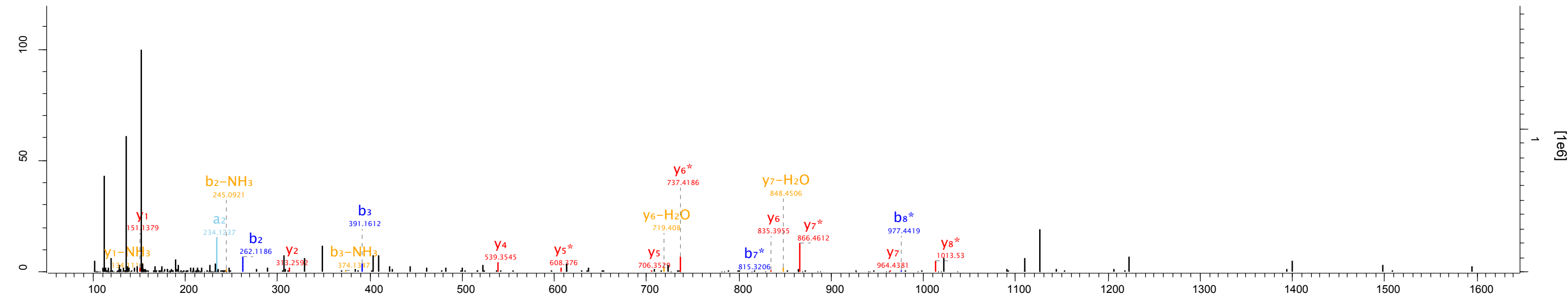
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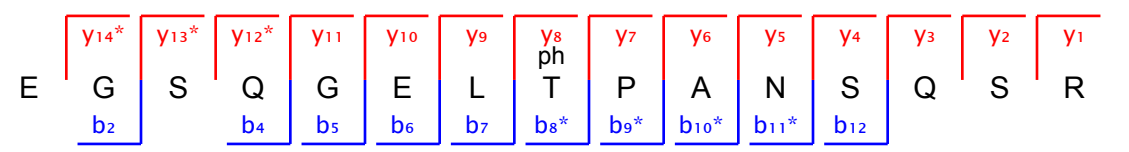
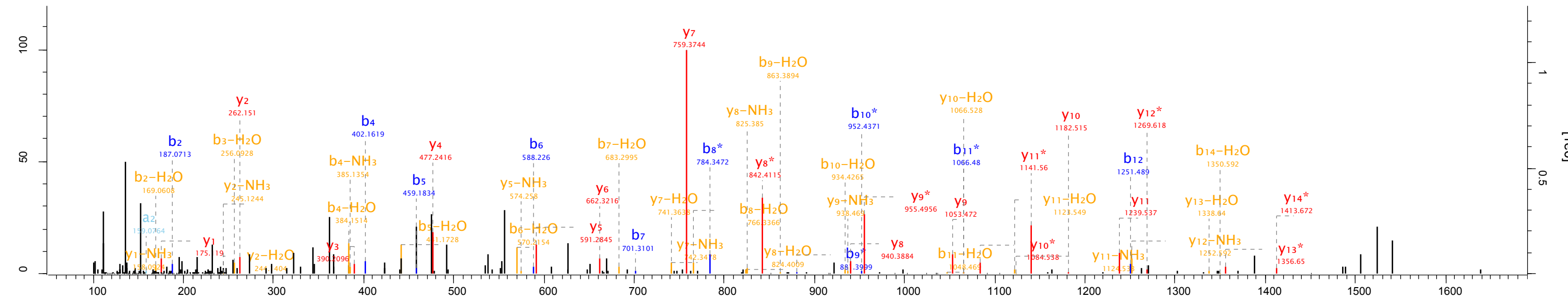
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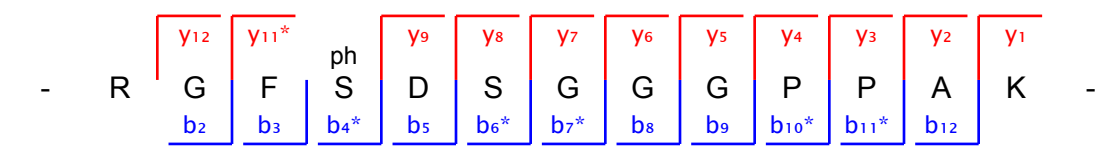
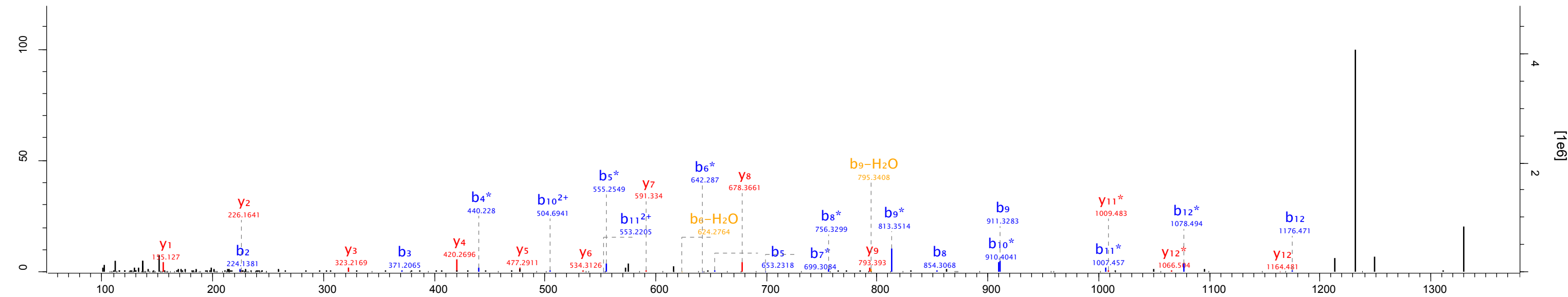
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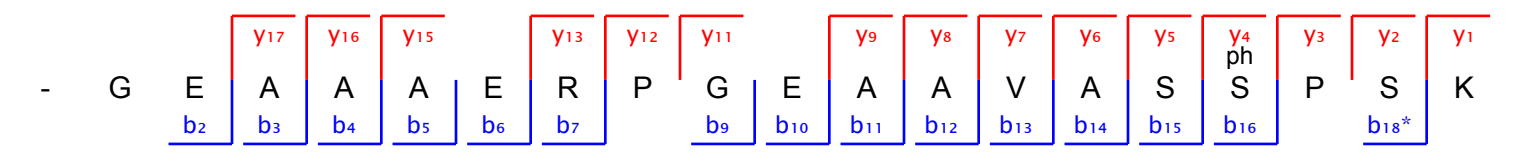
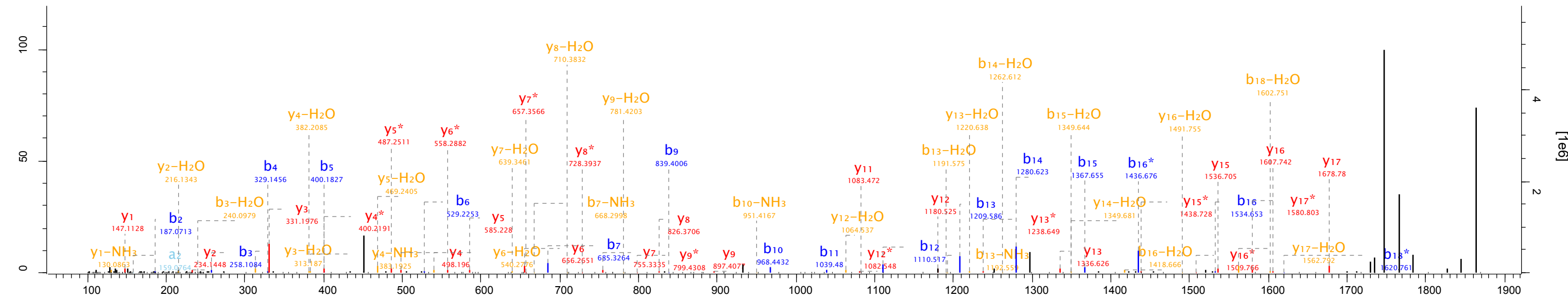
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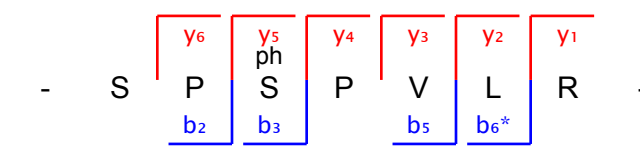
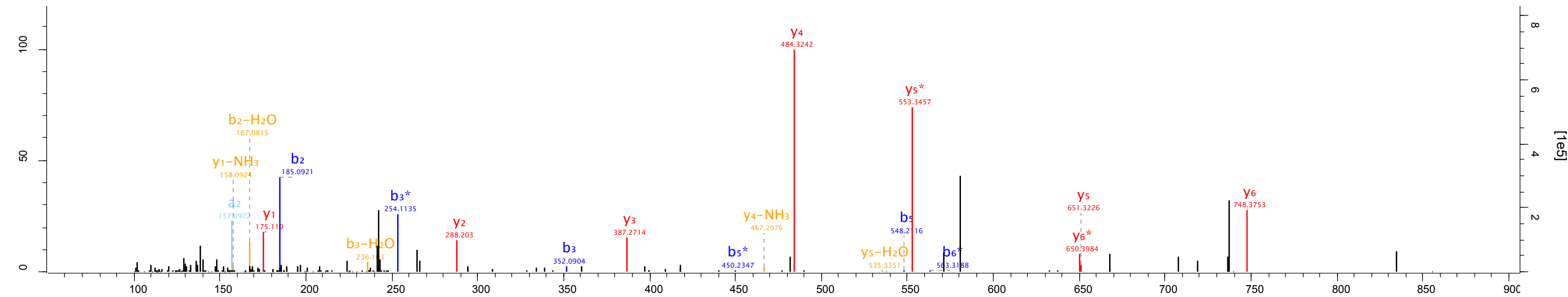
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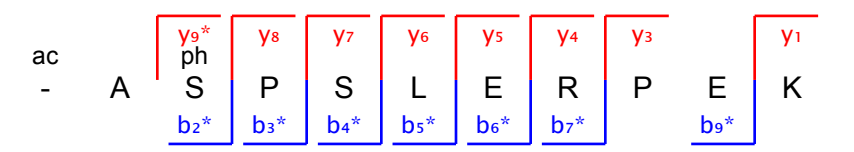
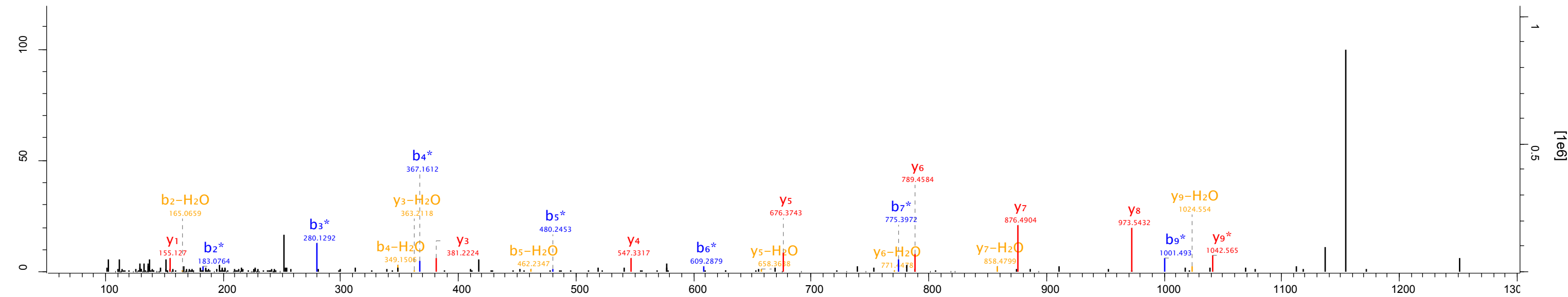
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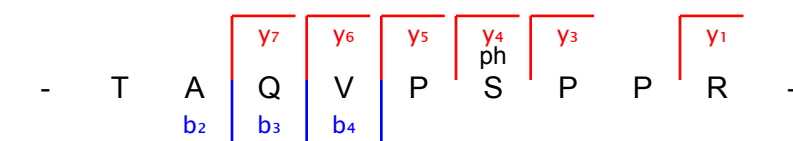
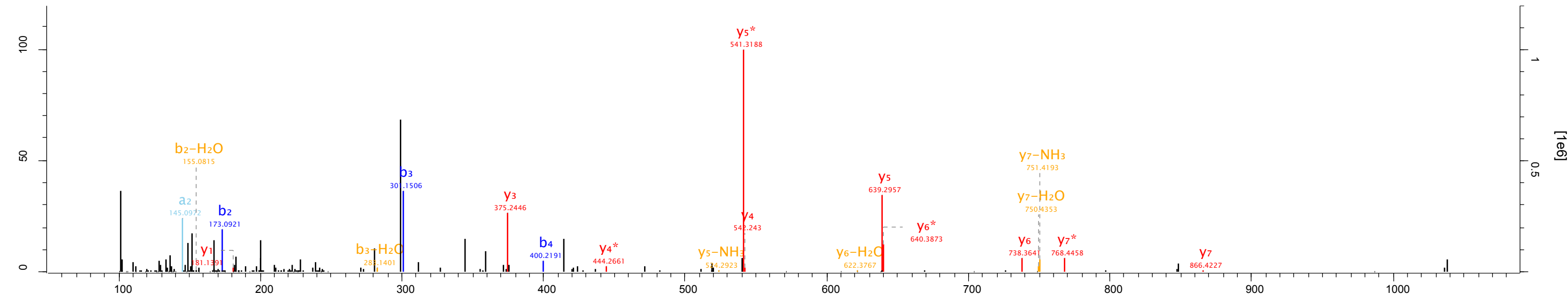


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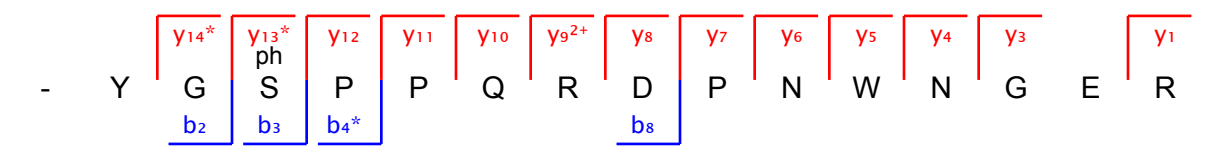
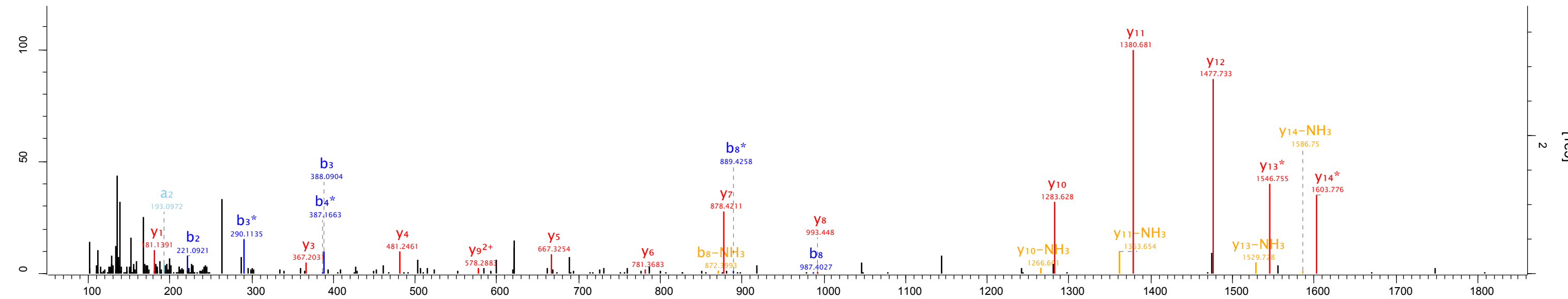


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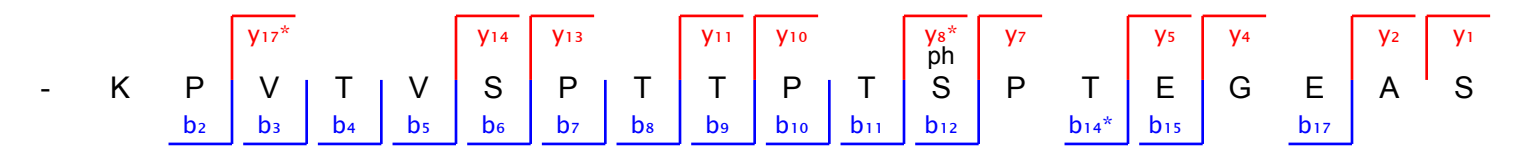
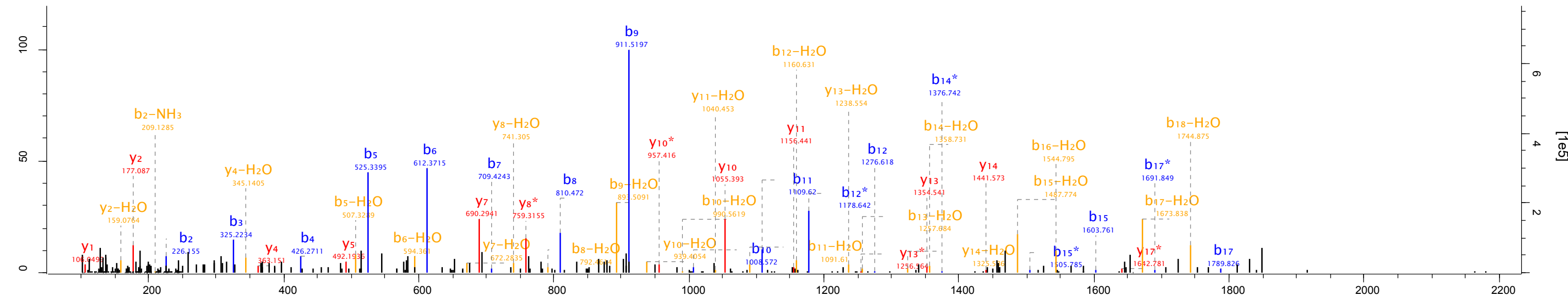


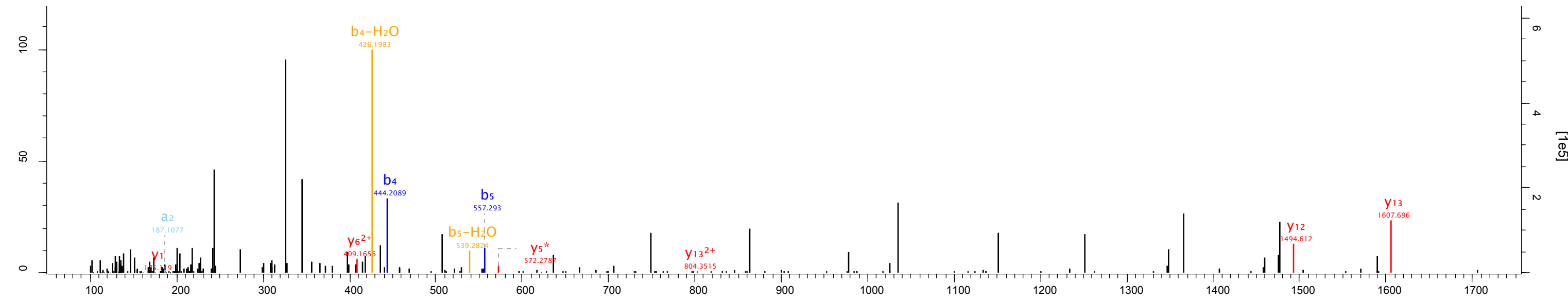


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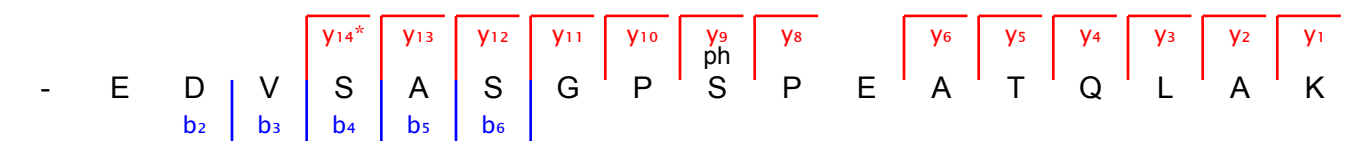
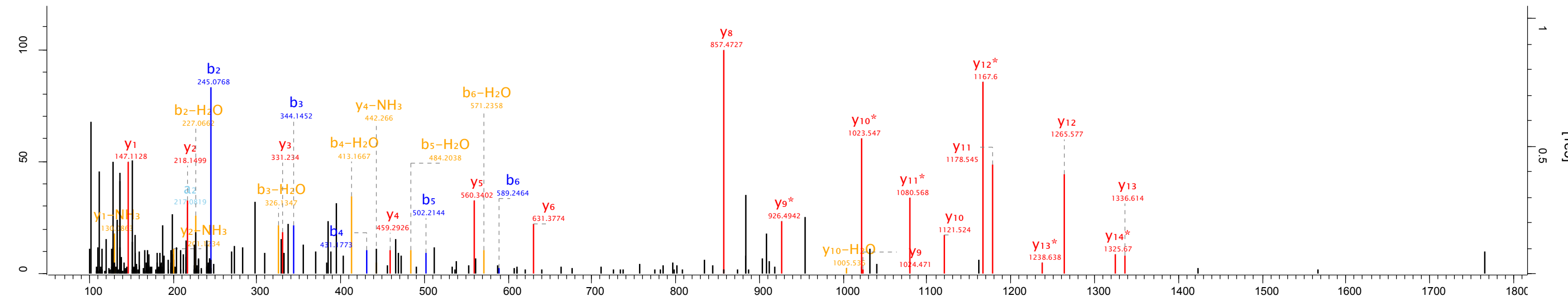


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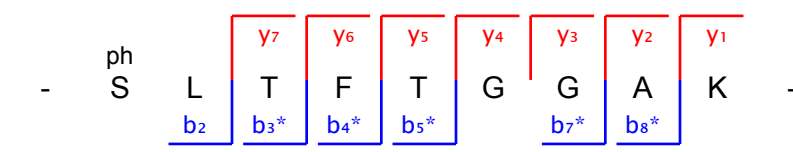
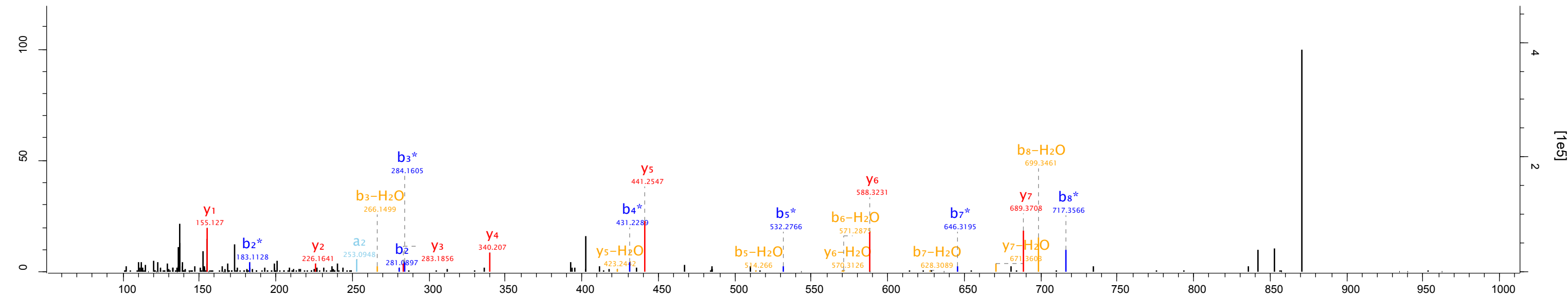
Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets: a₂ (V), b₄ (T), b₅ (L)
- Red brackets: y₁₃ (L), y₁₂ (A), y₆²⁺ (F), y₅^{*} (E), y₁ (R)

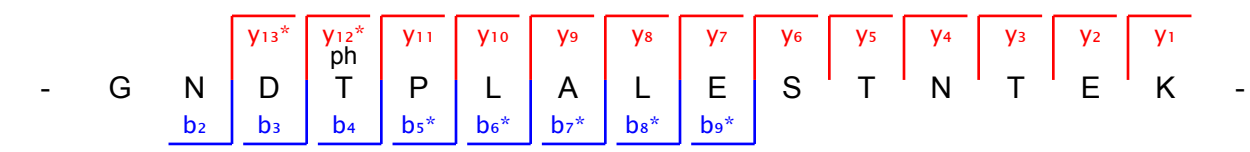
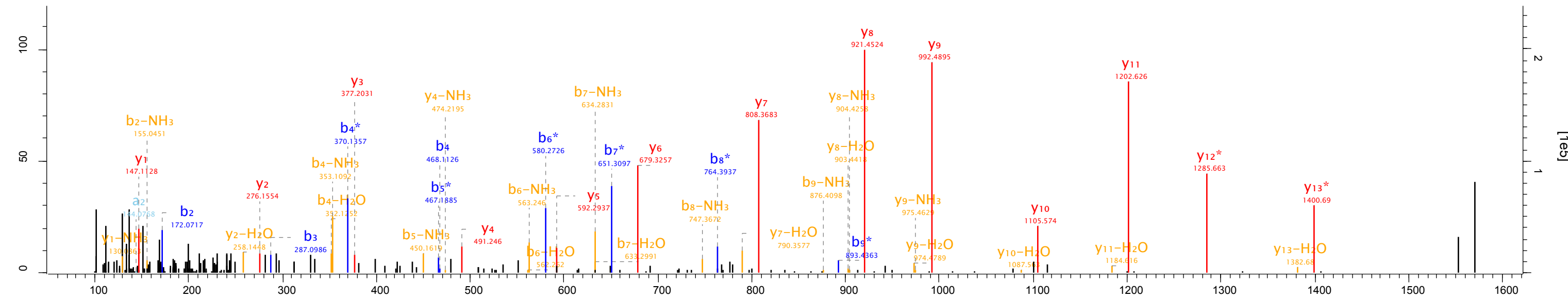
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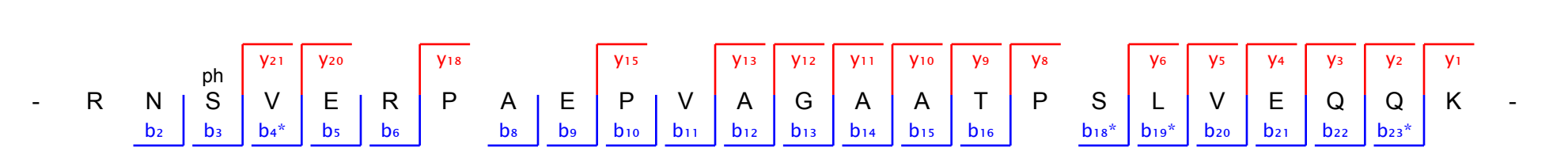
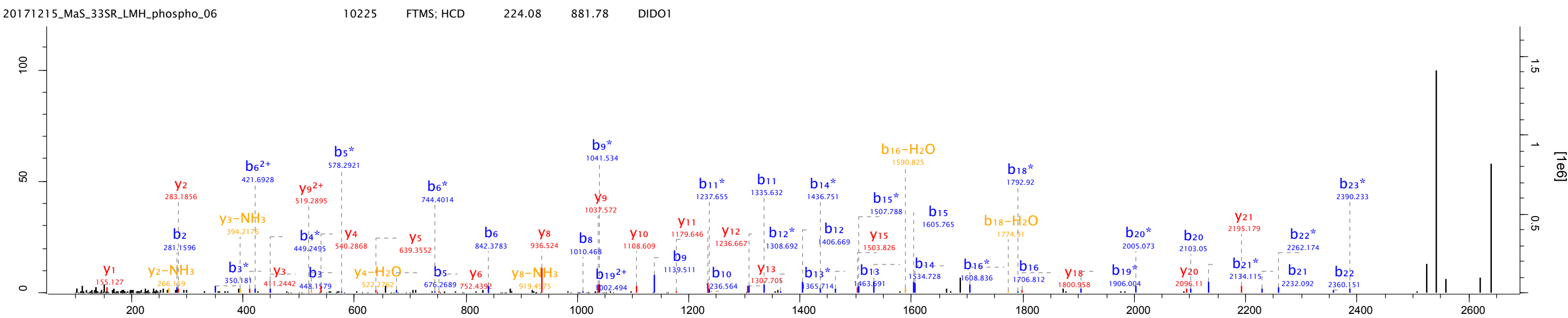
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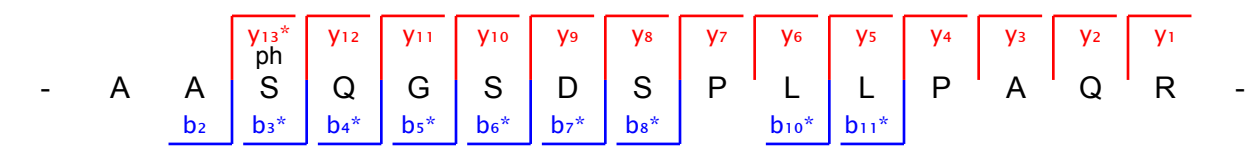
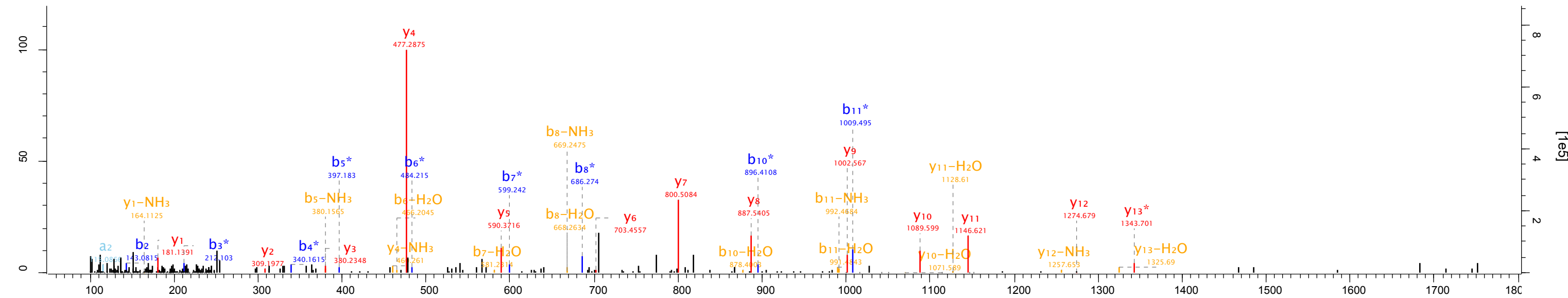
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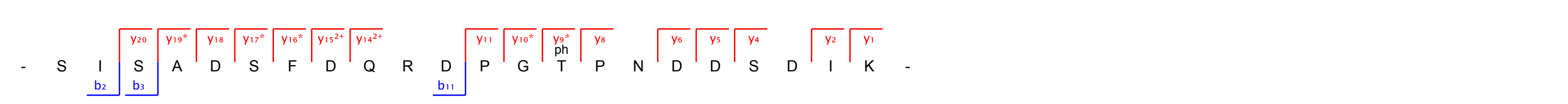
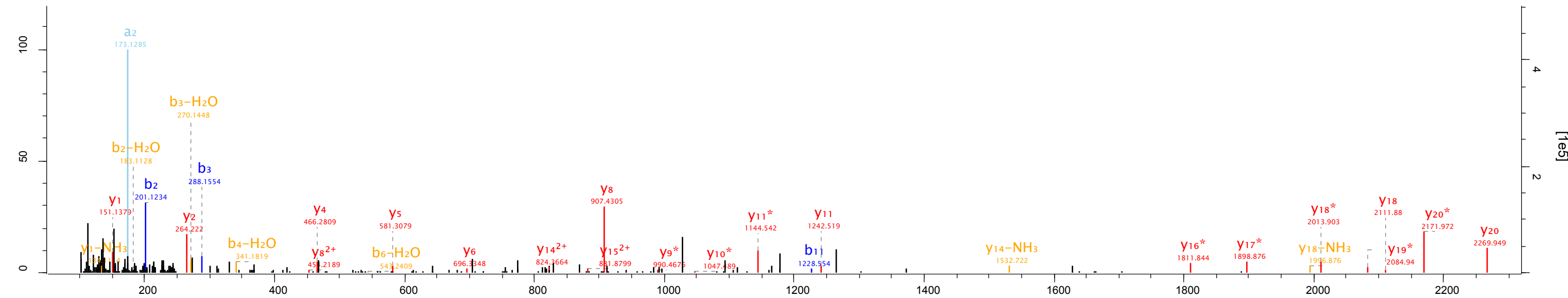
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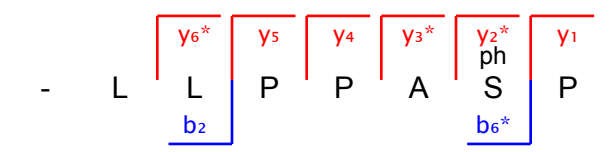
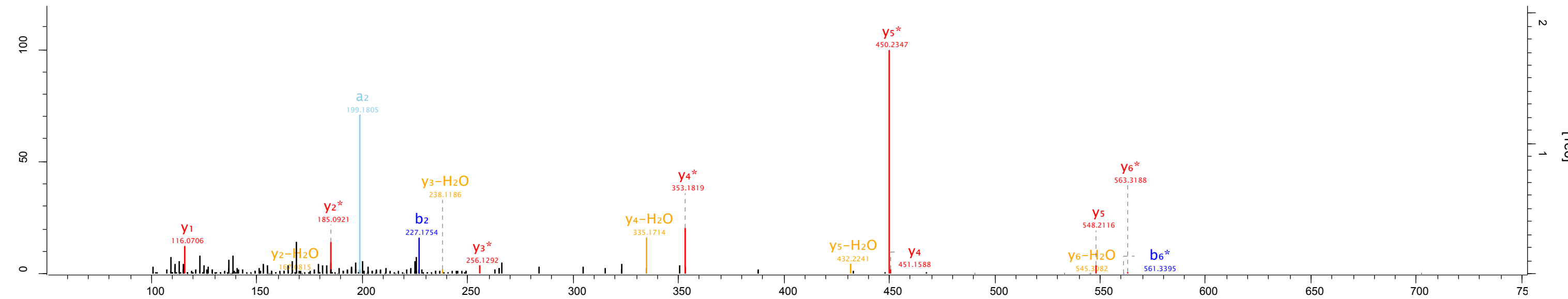
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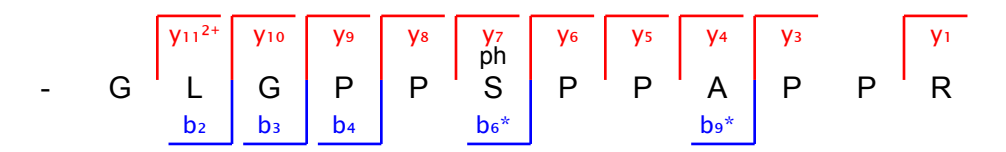
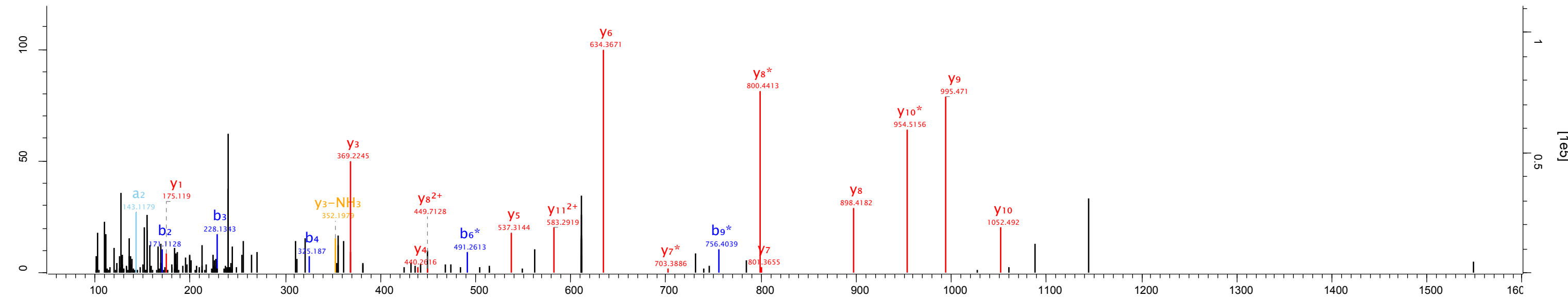
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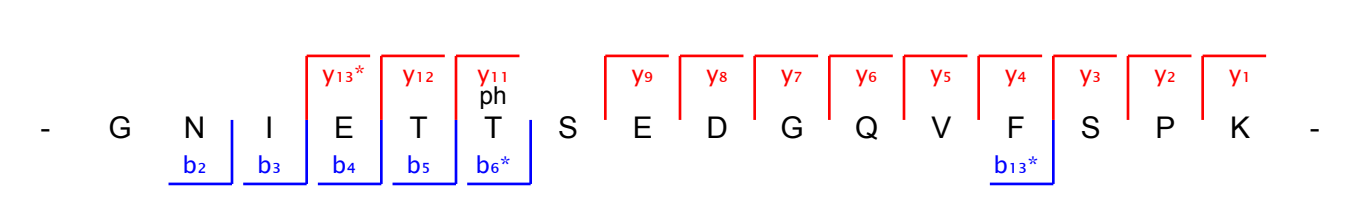
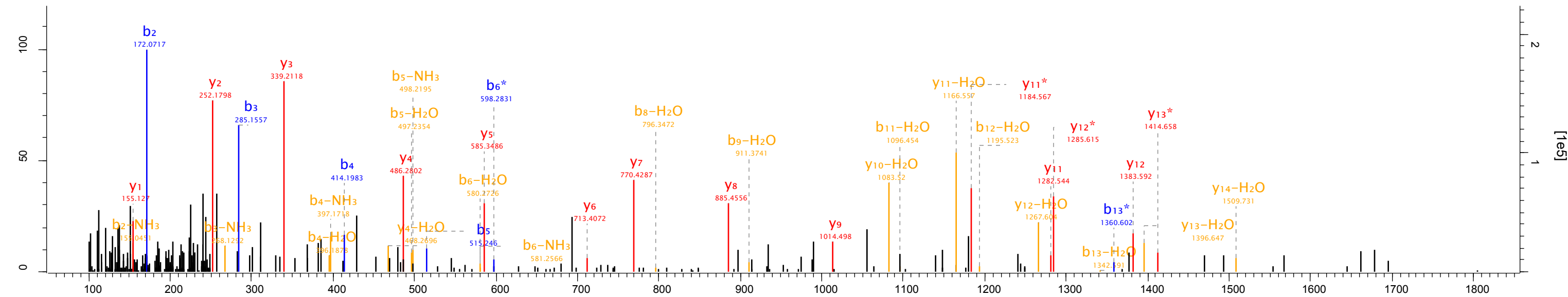
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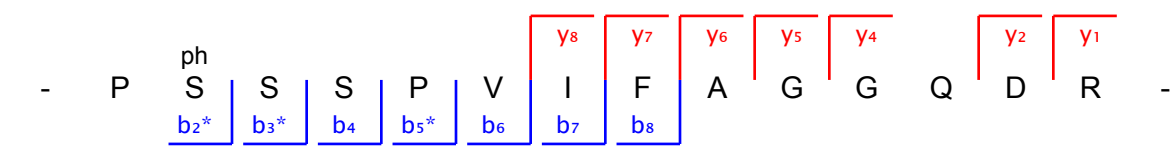
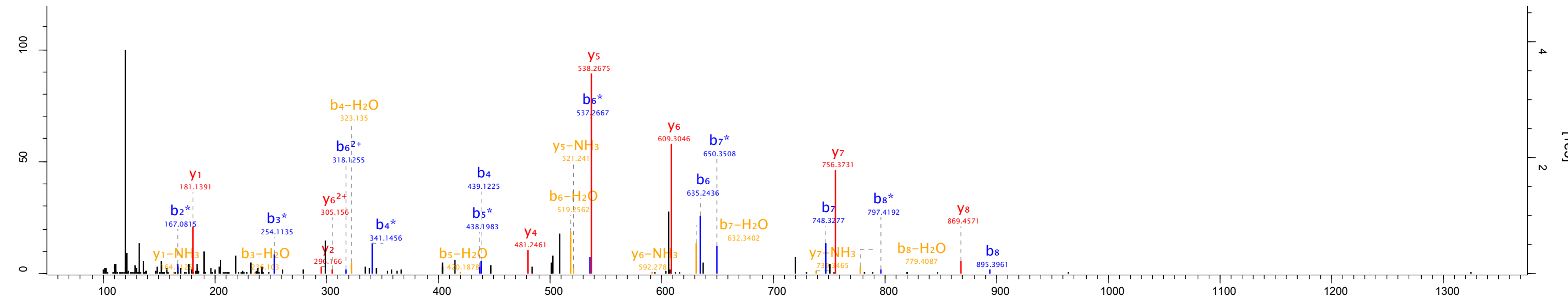
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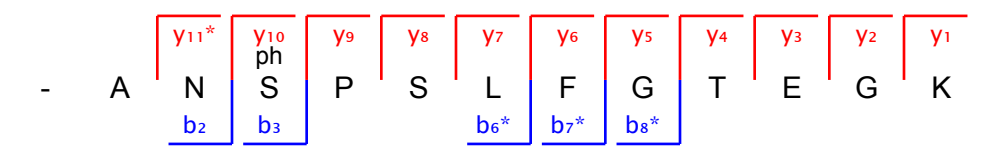
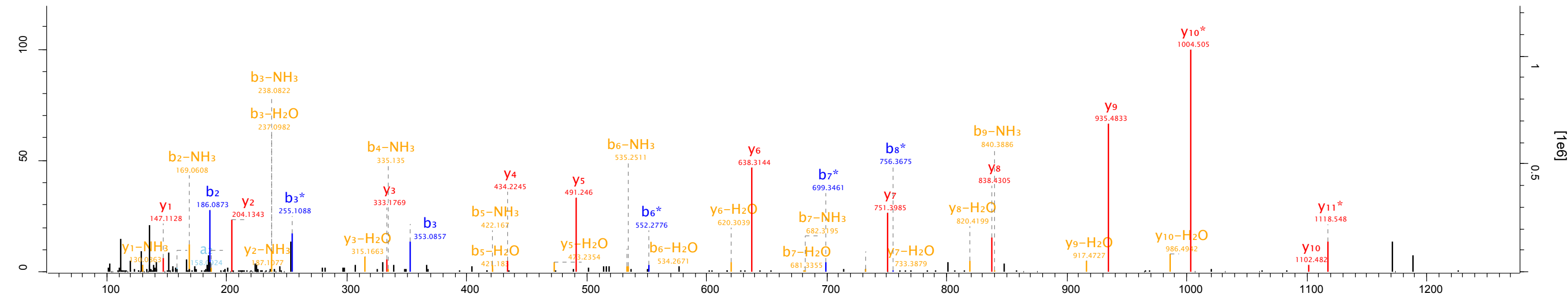
Raw file

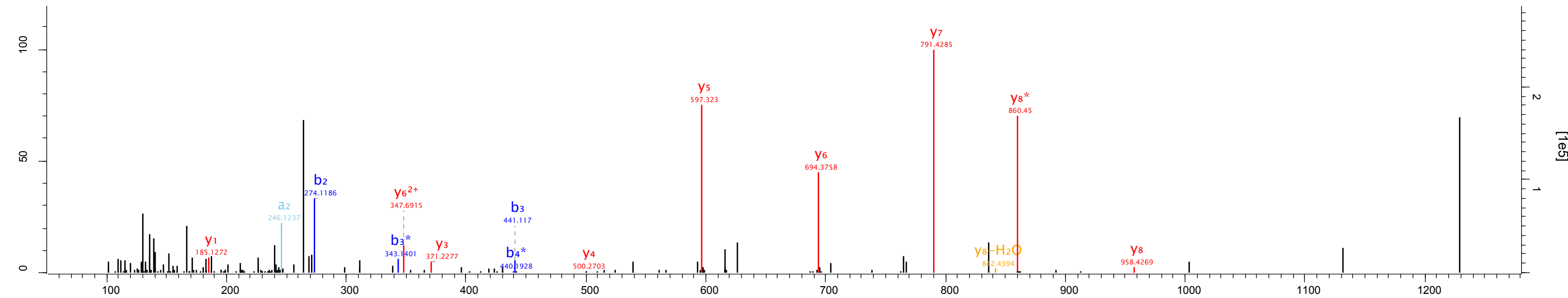
20171215_MaS_33SR_LMH_phospho_06

Scan	Method	Score	m/z	Gene names
10855	FTMS; HCD	78.23	502.24	PCBP2



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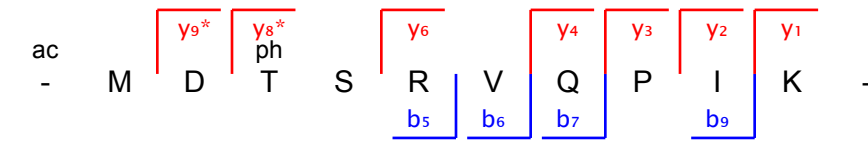
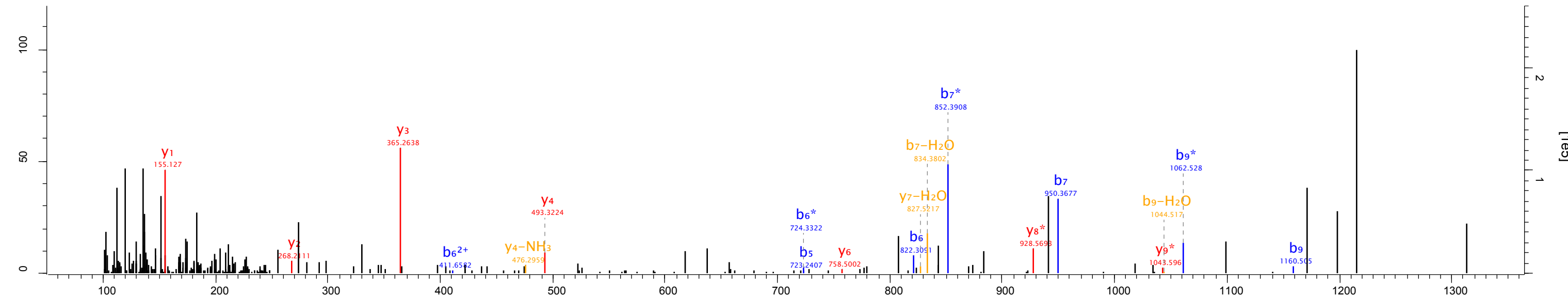


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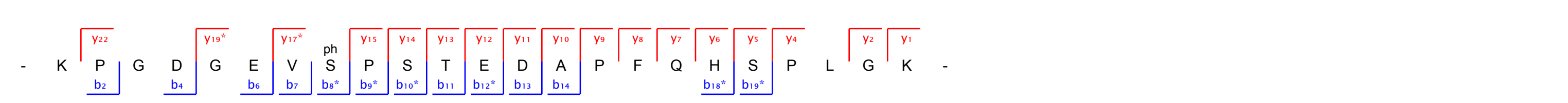
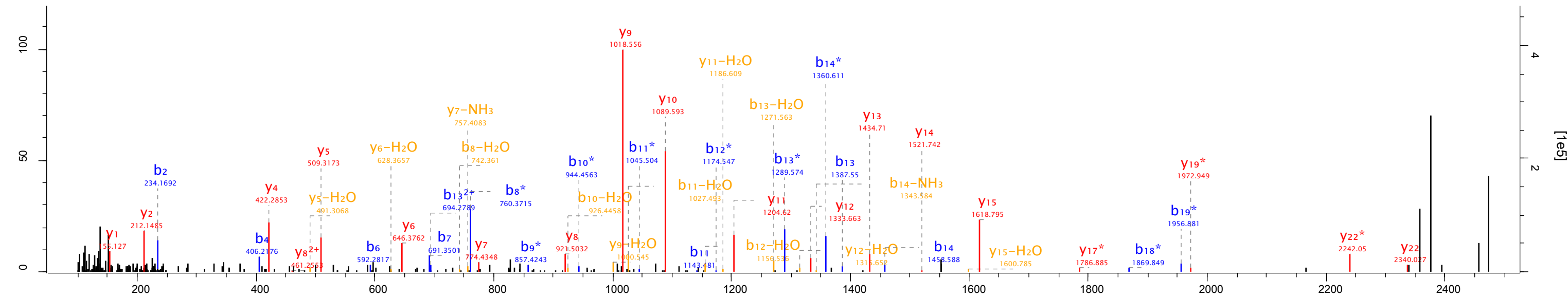
Fragmentation mapping:

- W: b₂
- S: b₃
- P: b₄*
- P: y₈ph
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- V: y₄
- S: y₃
- R: y₁

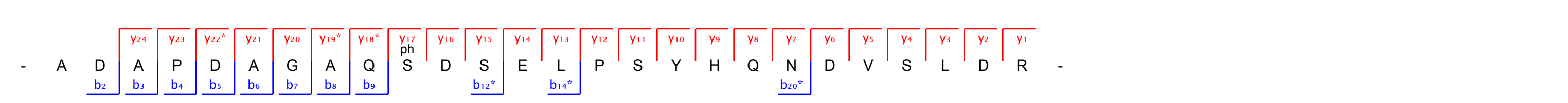
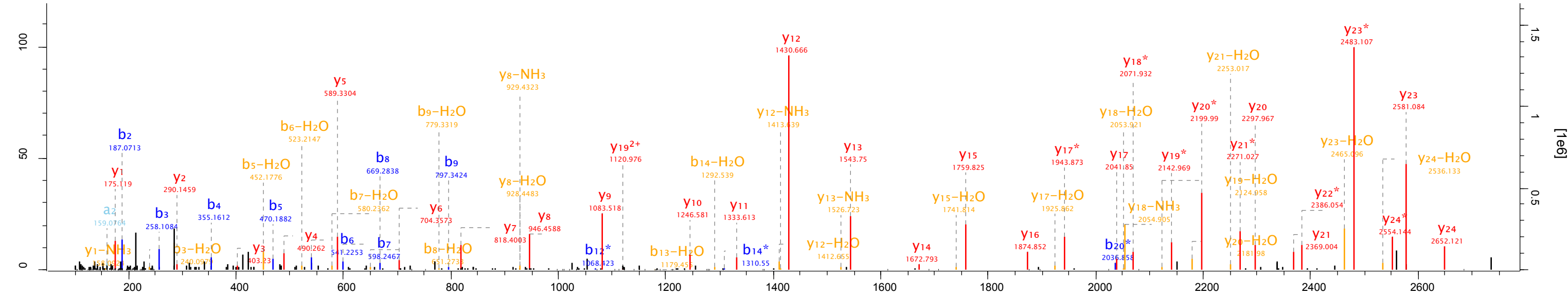
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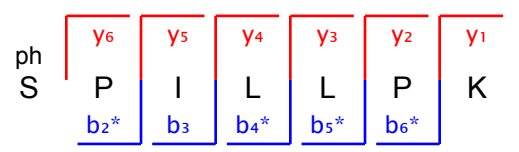
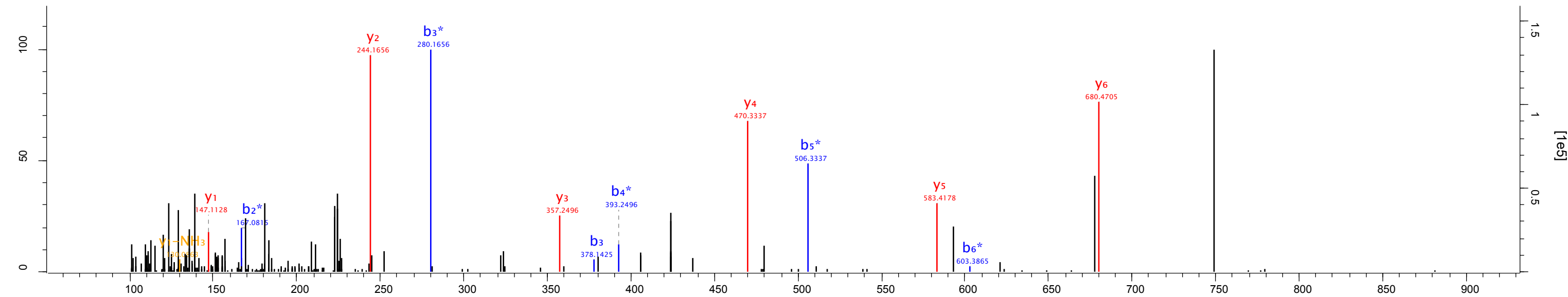
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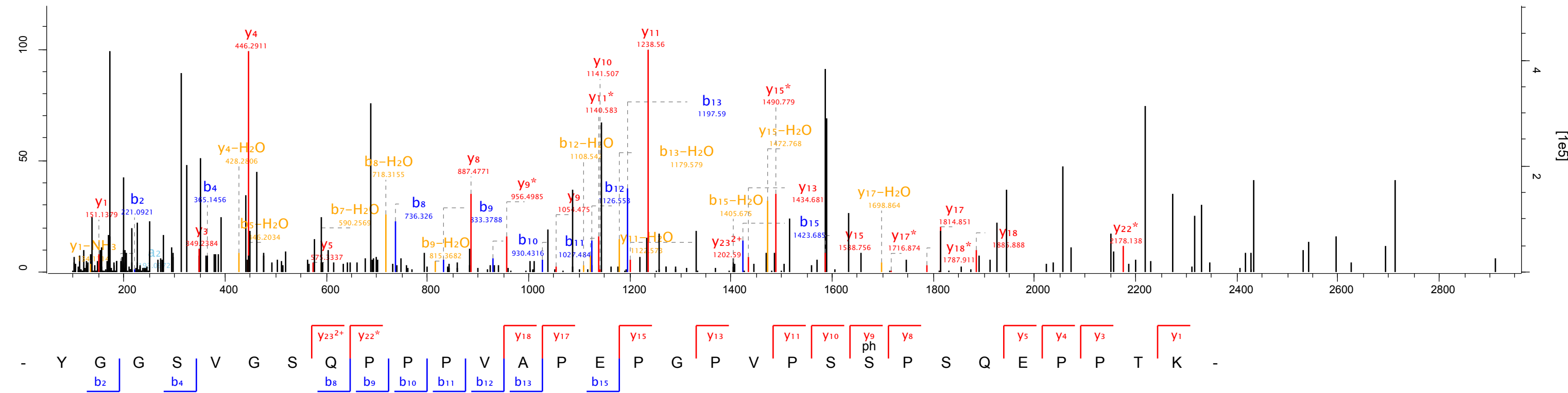
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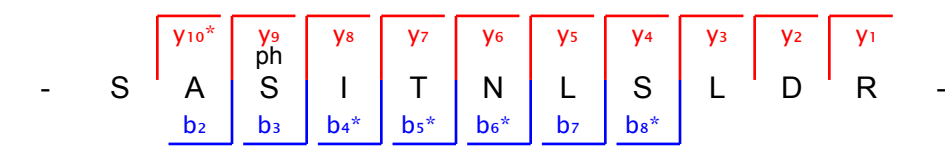
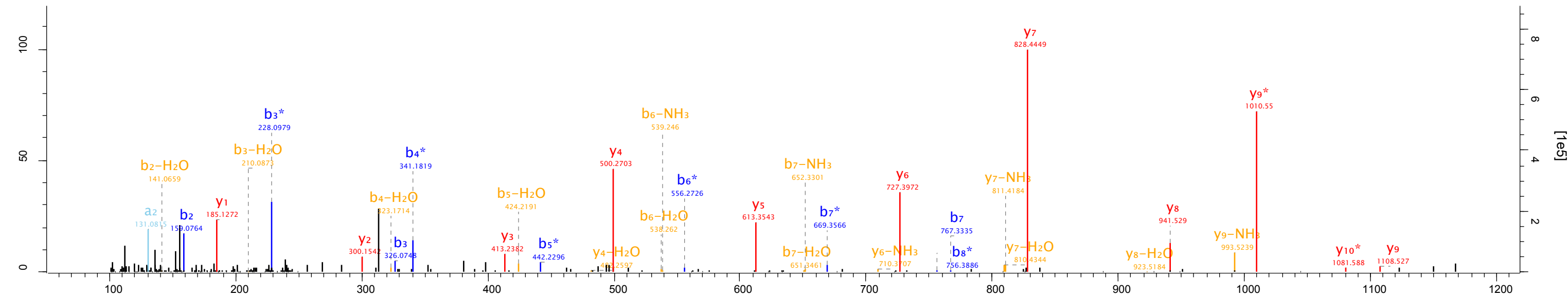
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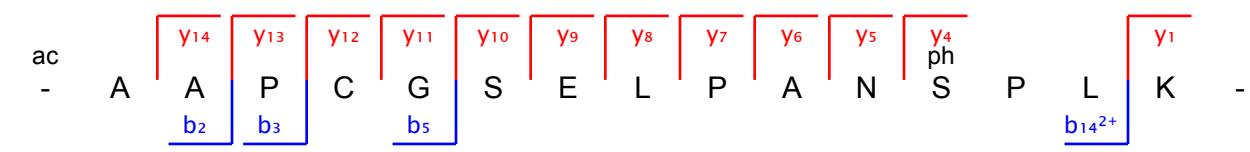
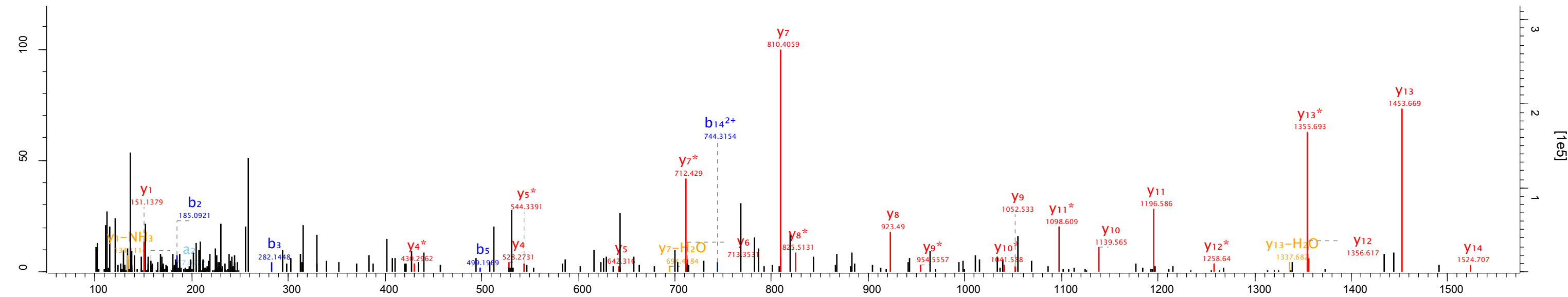
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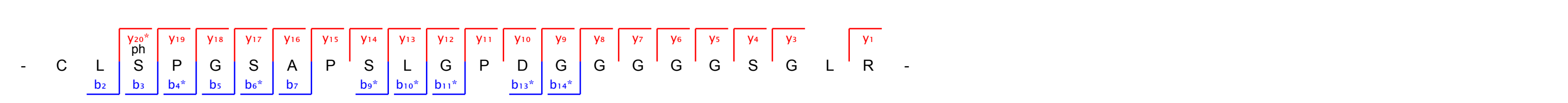
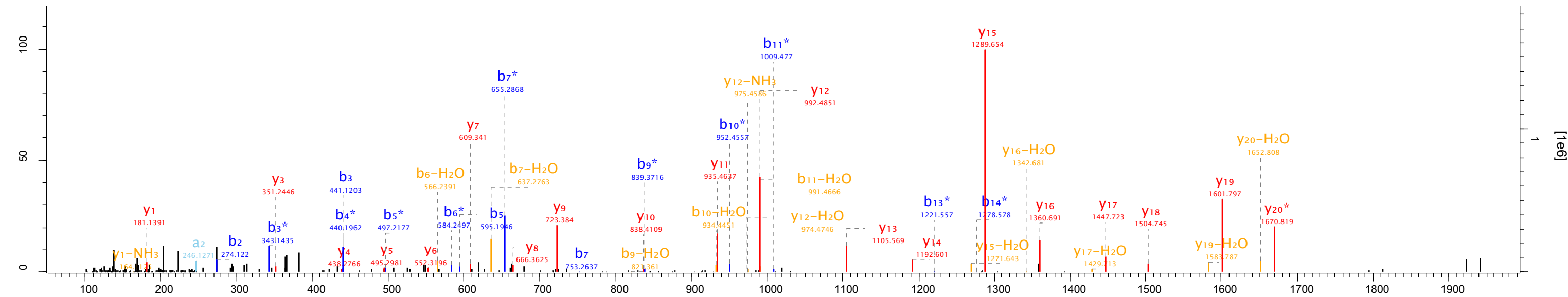
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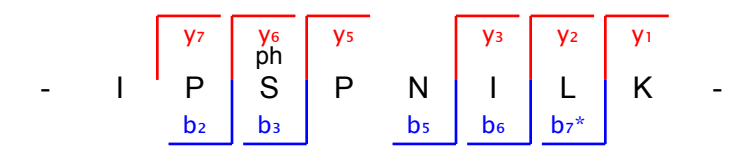
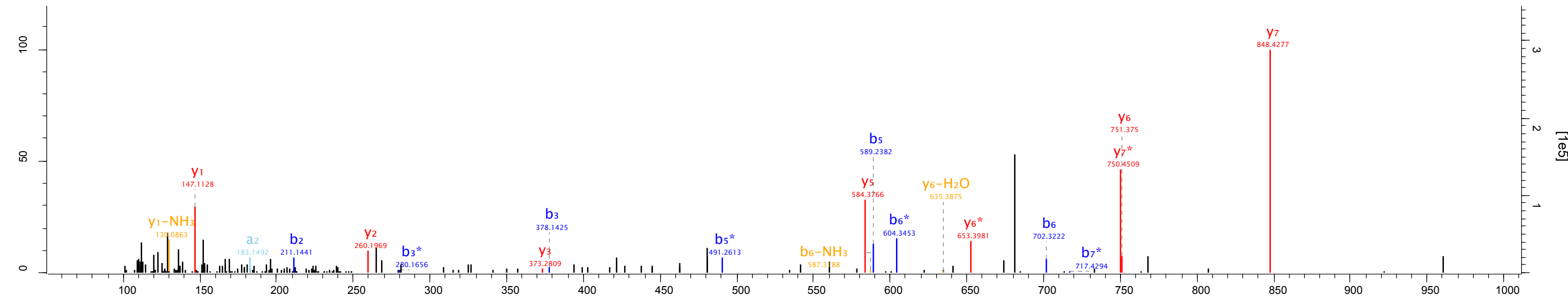
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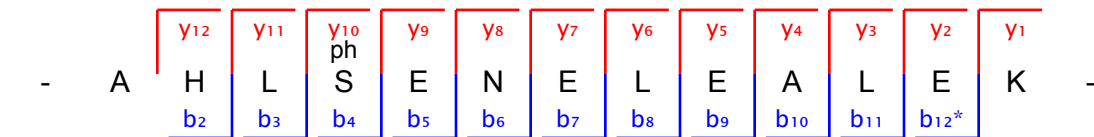
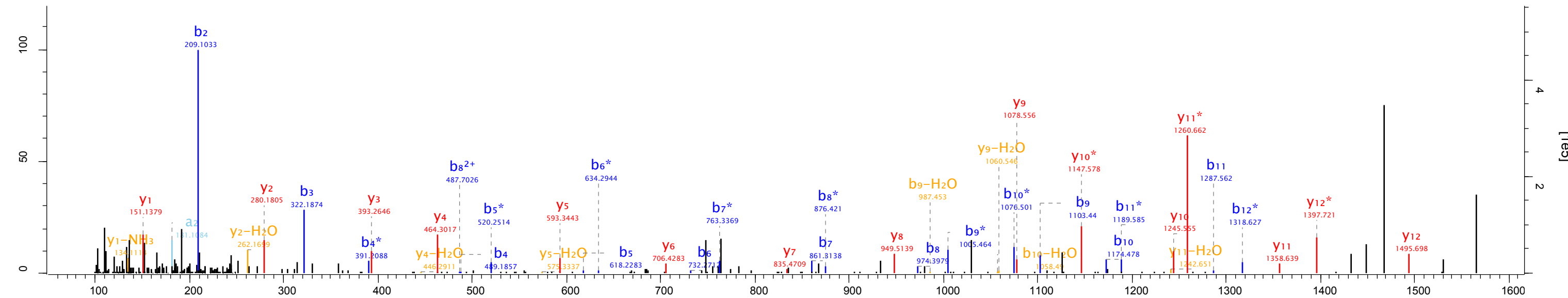


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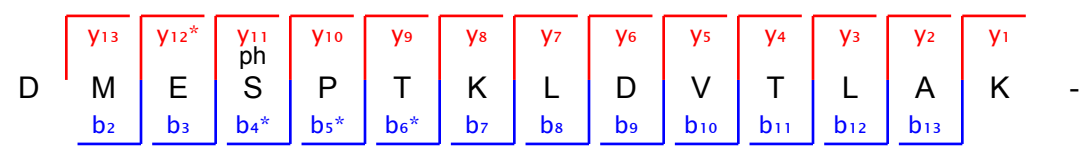
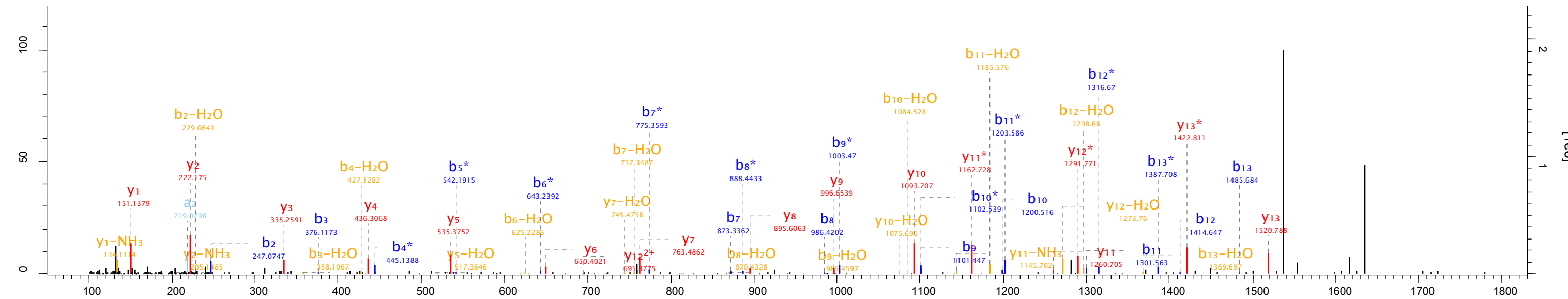


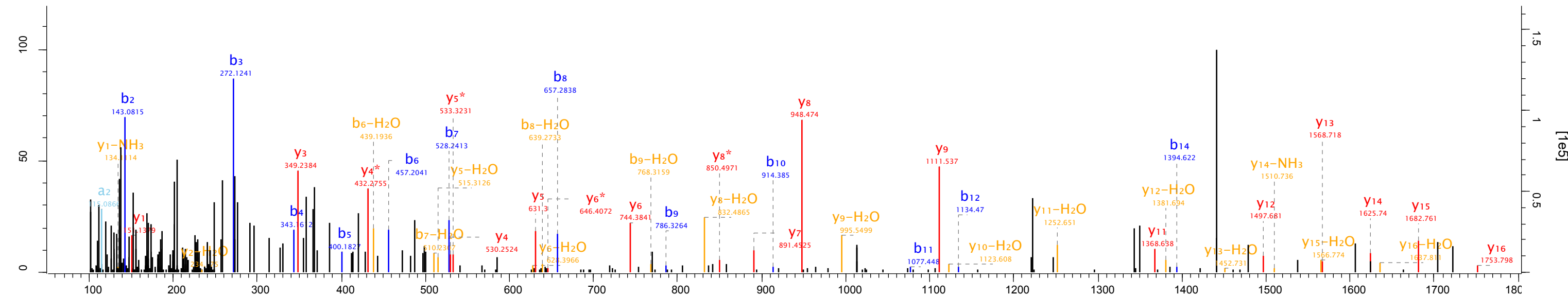
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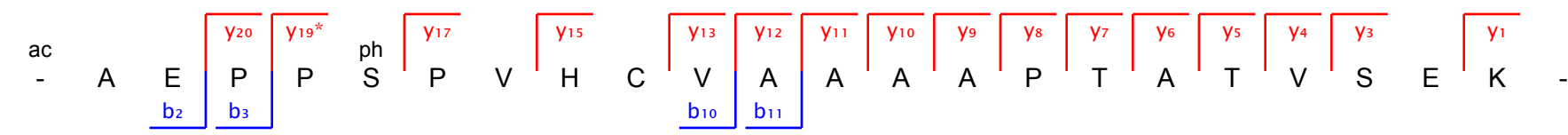
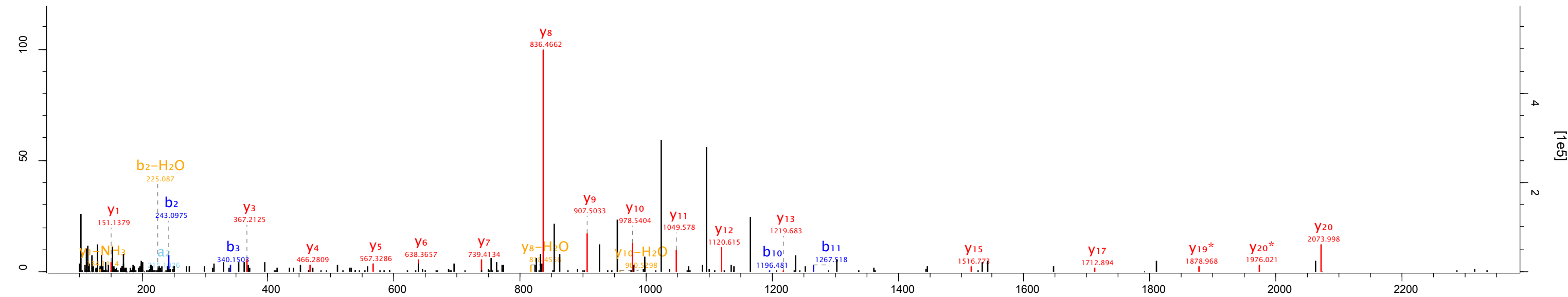




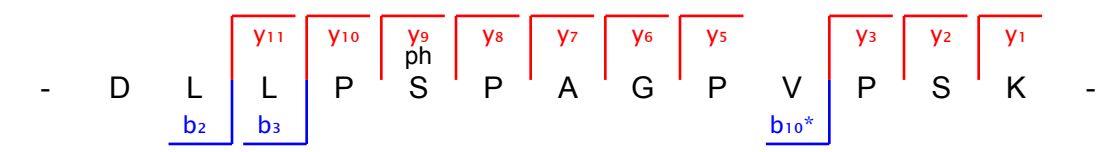
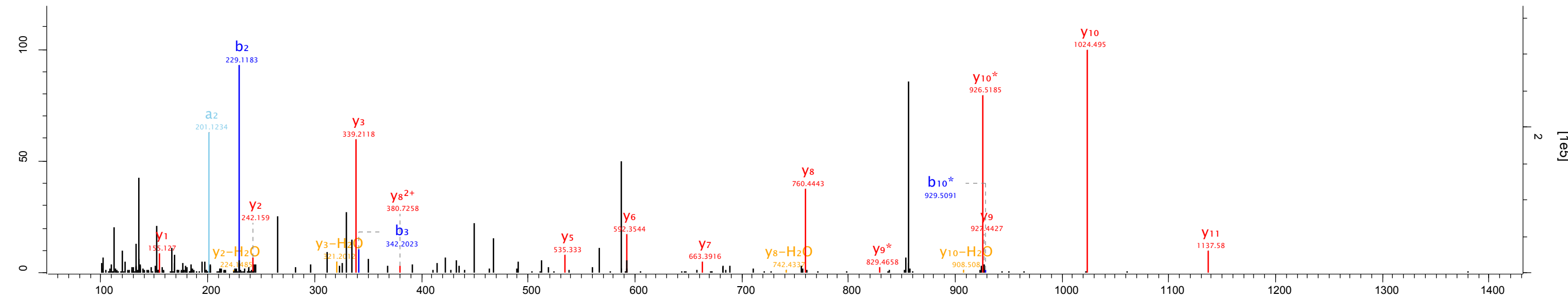
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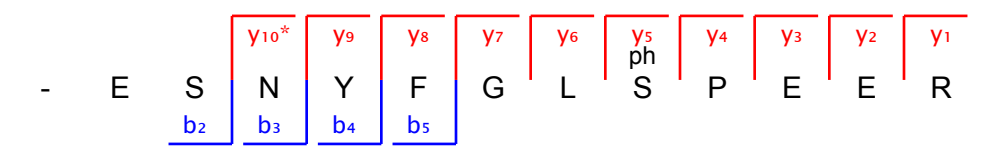
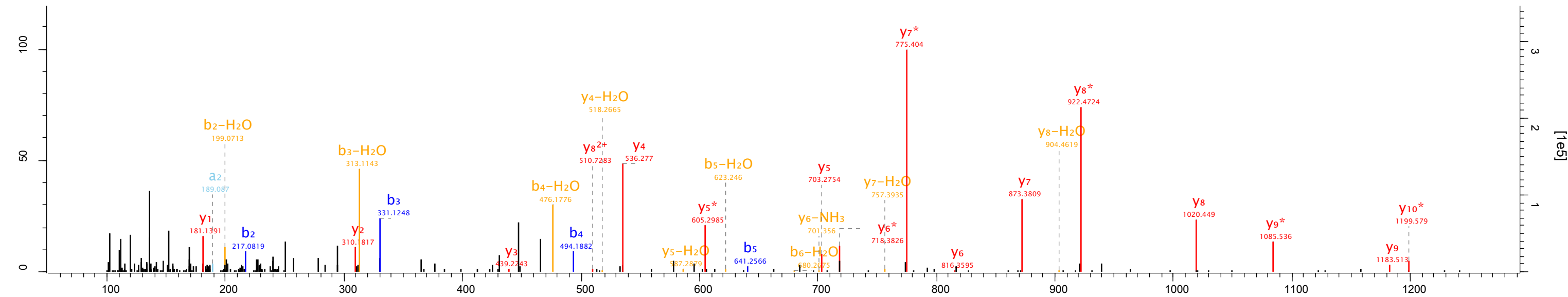
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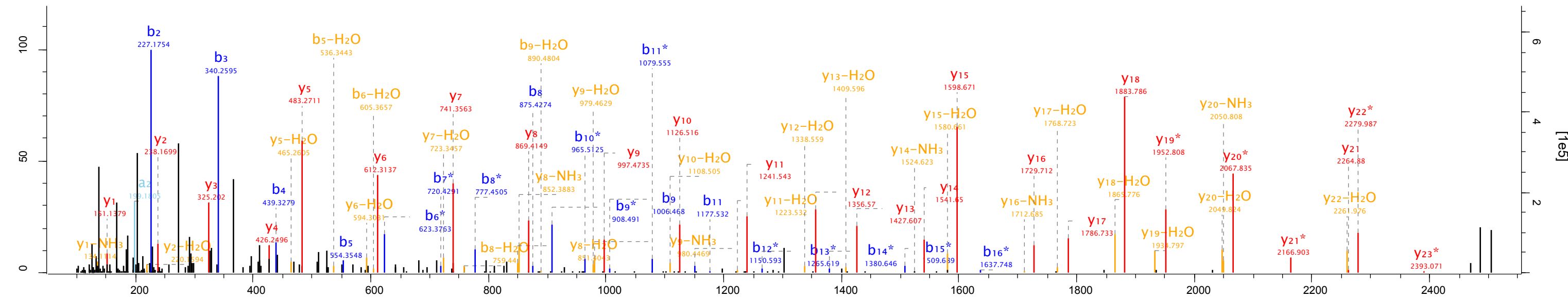
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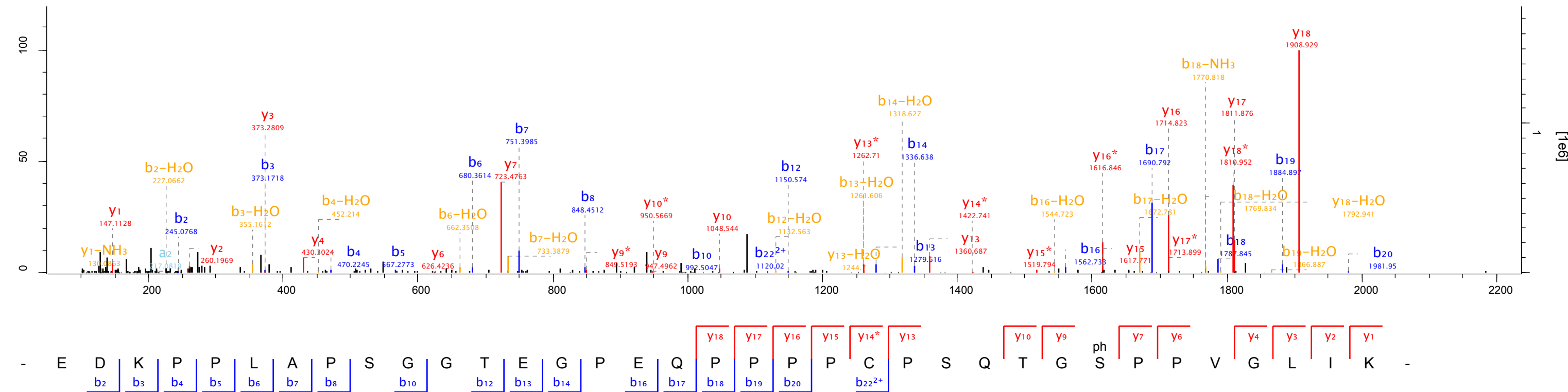


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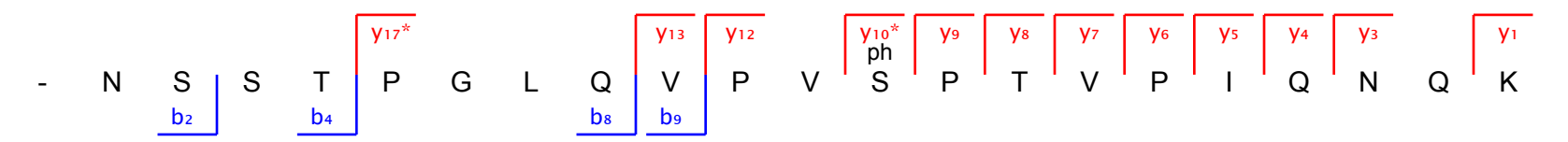
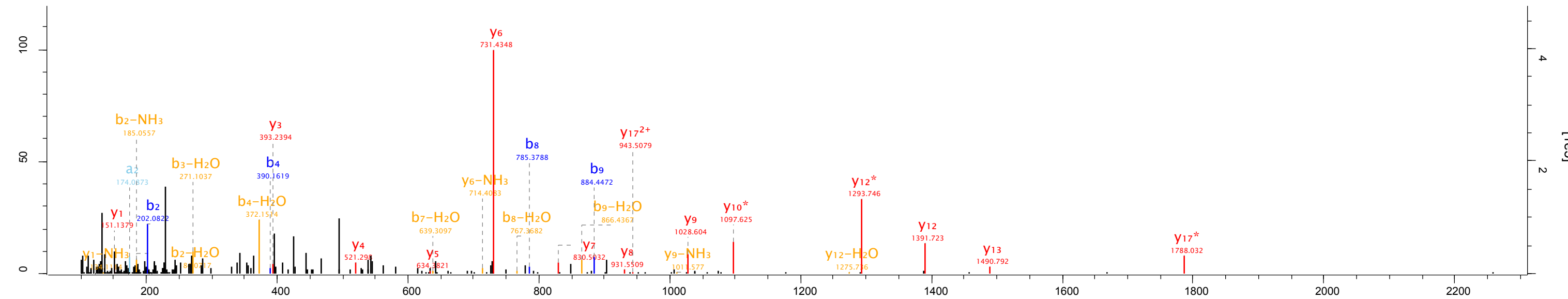
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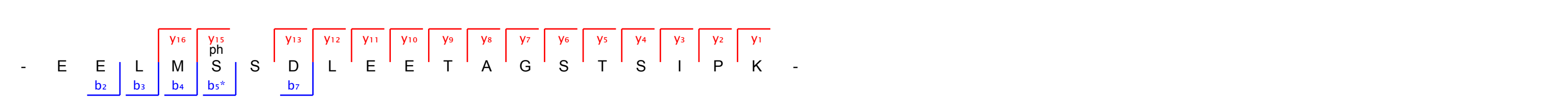
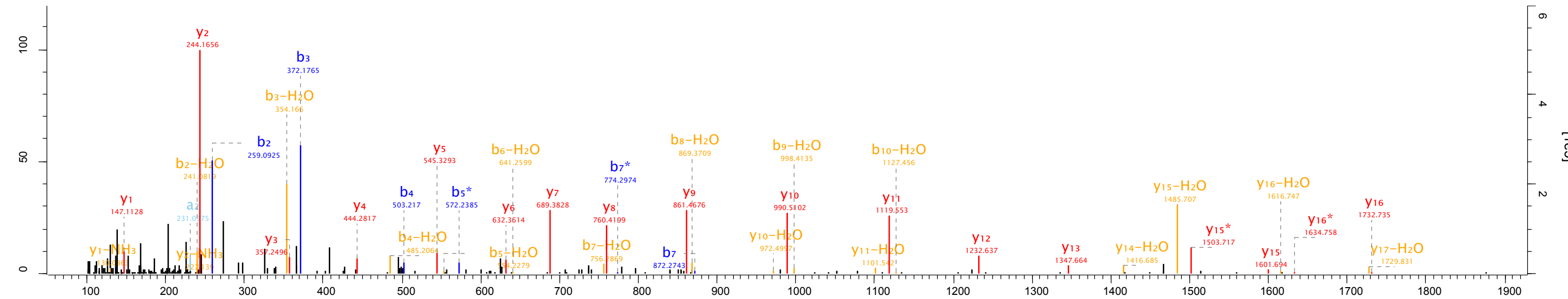
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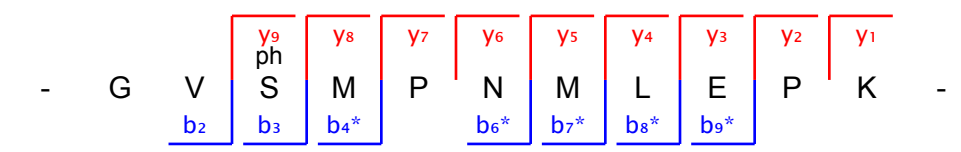
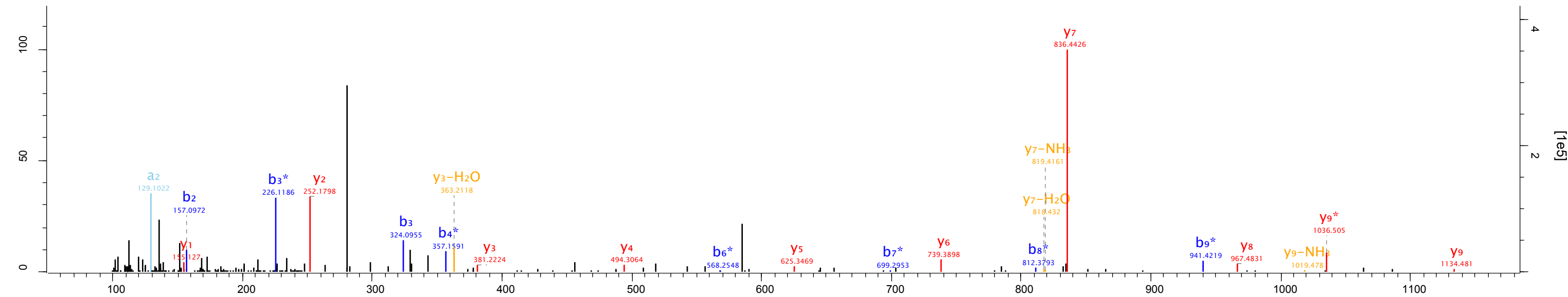
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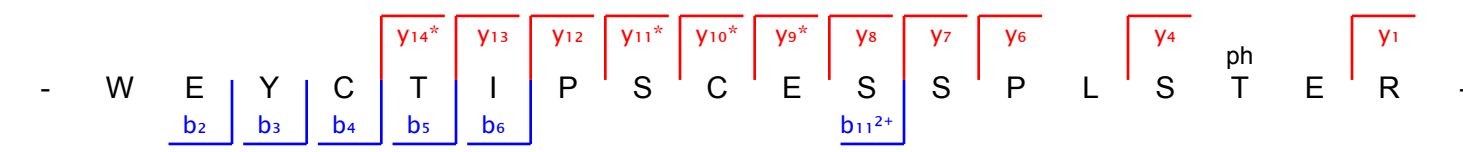
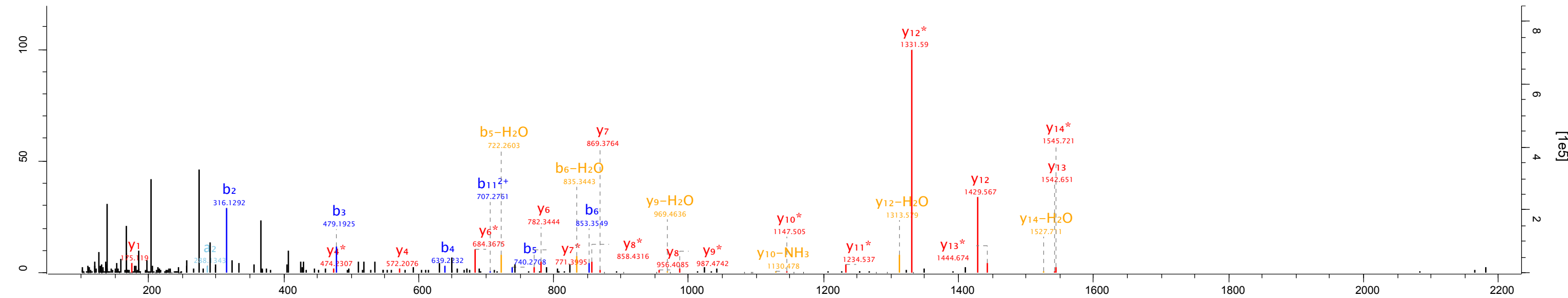
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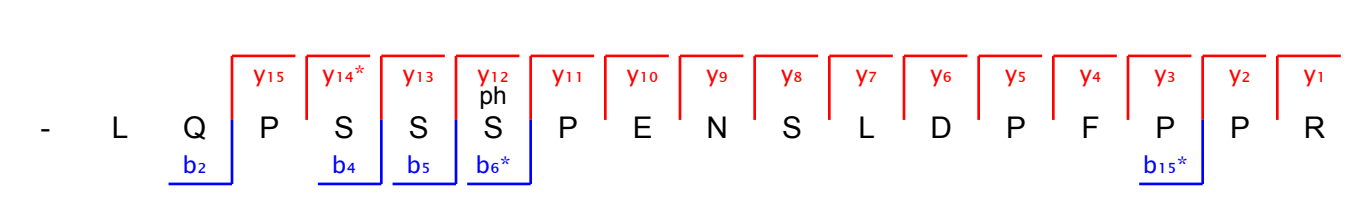
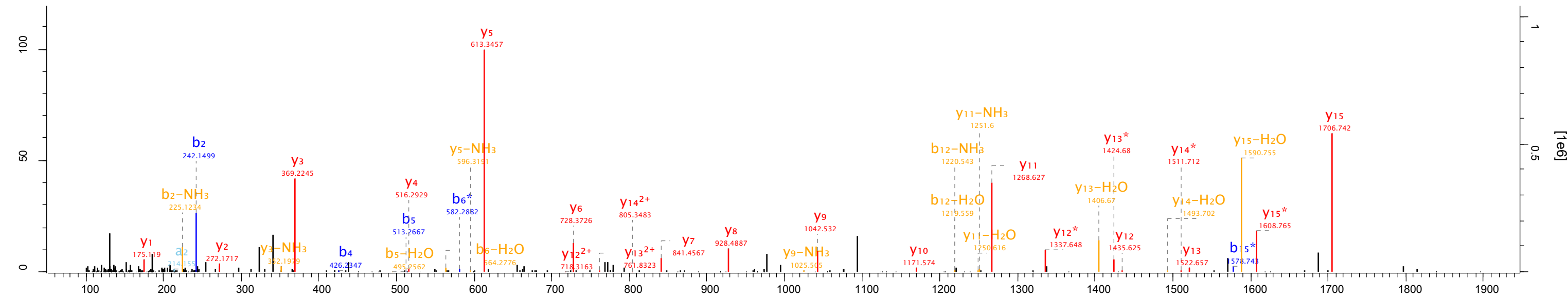
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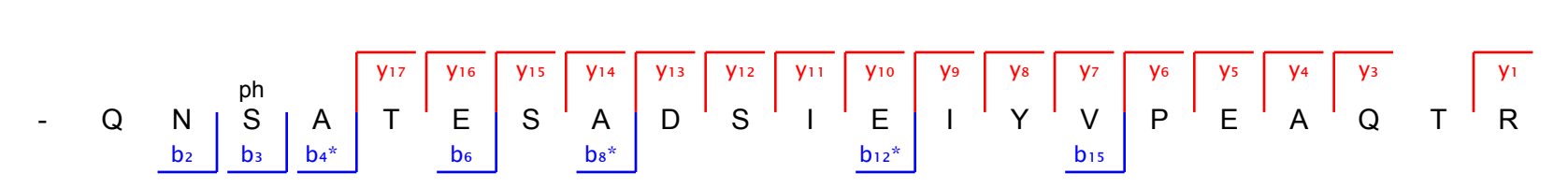
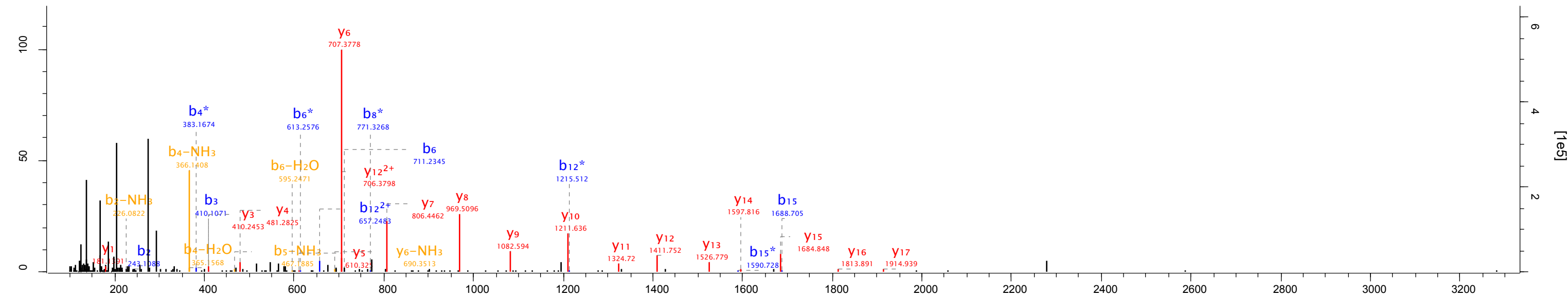
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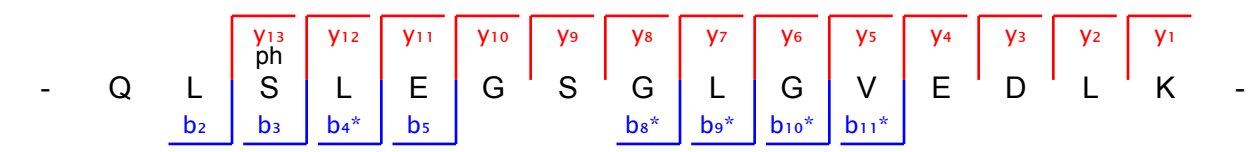
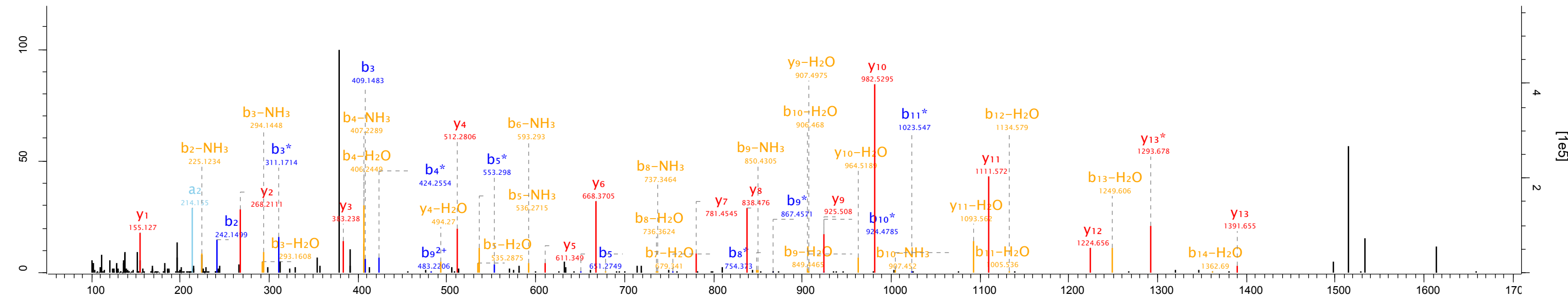
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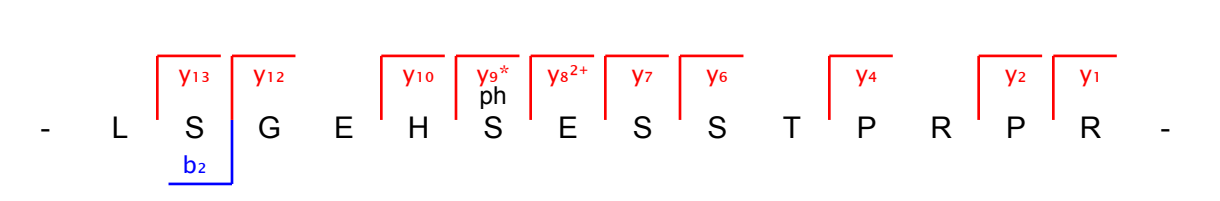
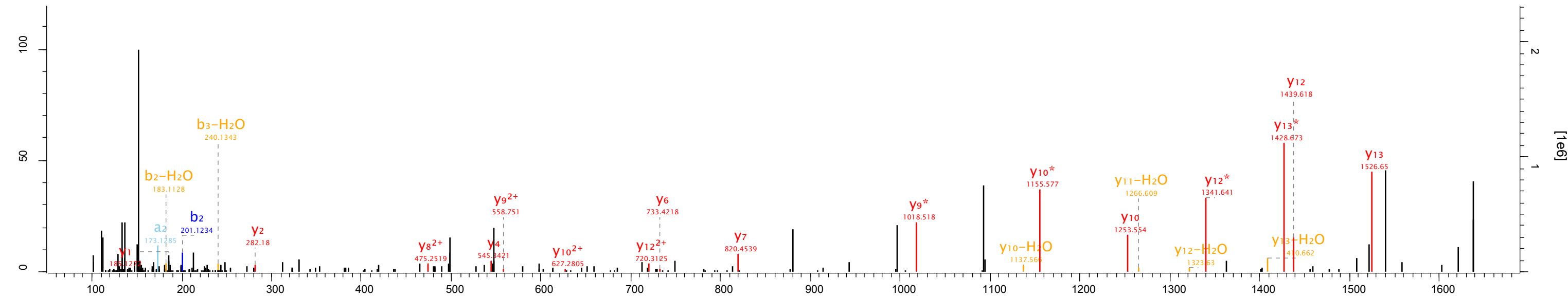
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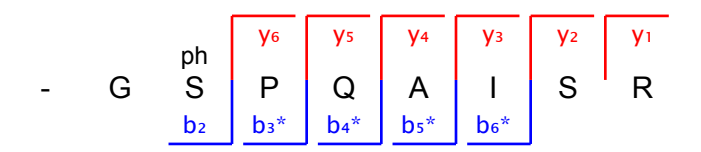
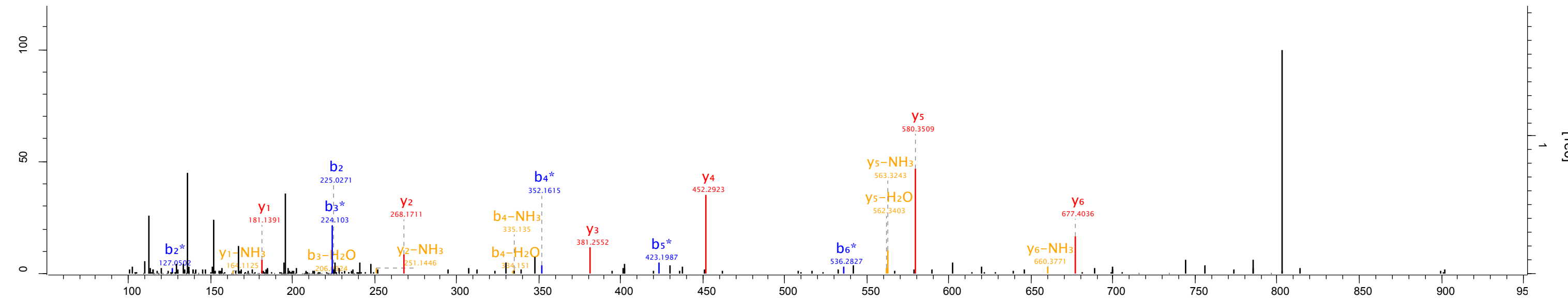
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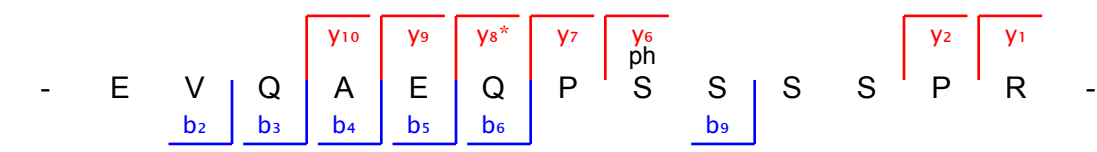
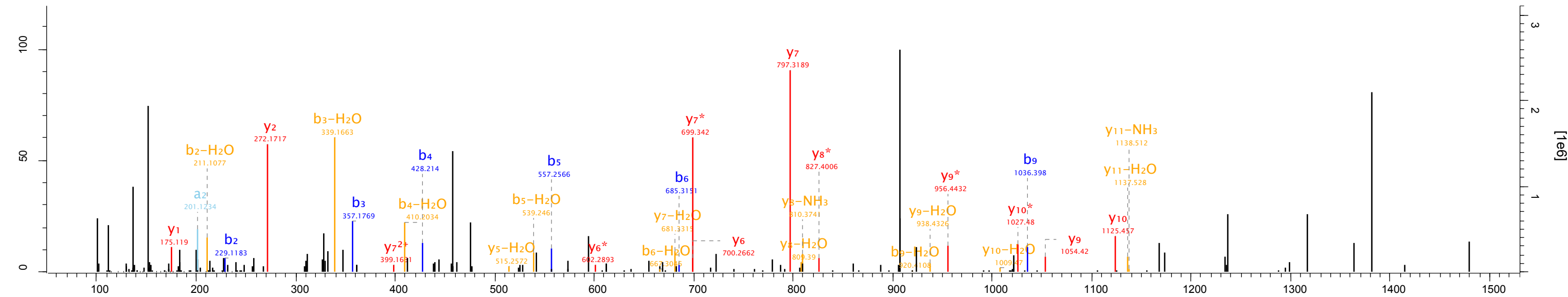
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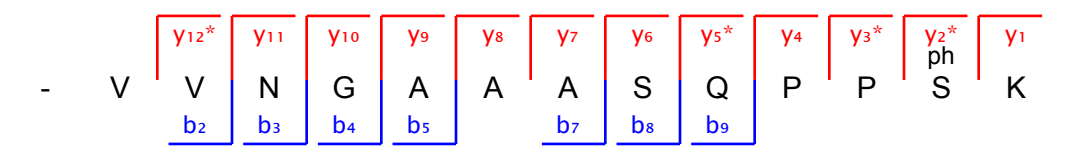
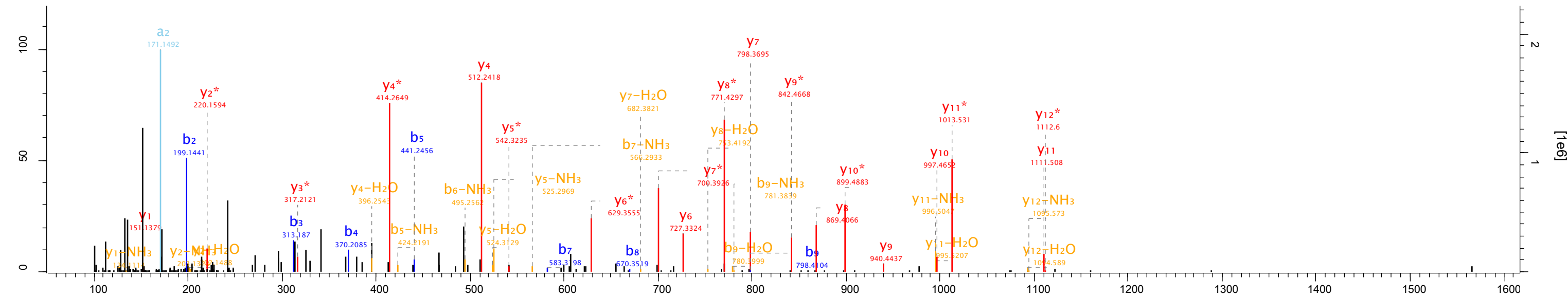


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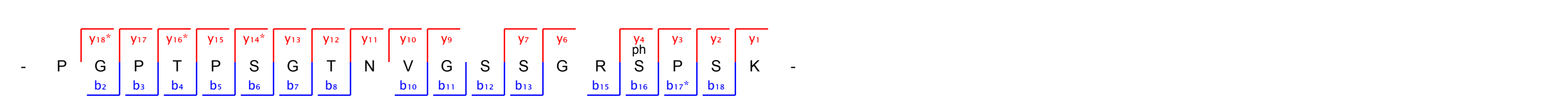
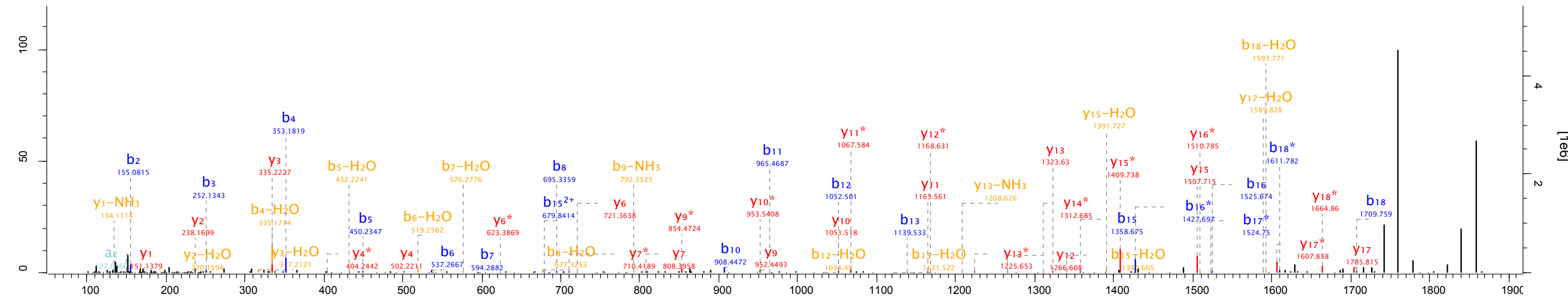


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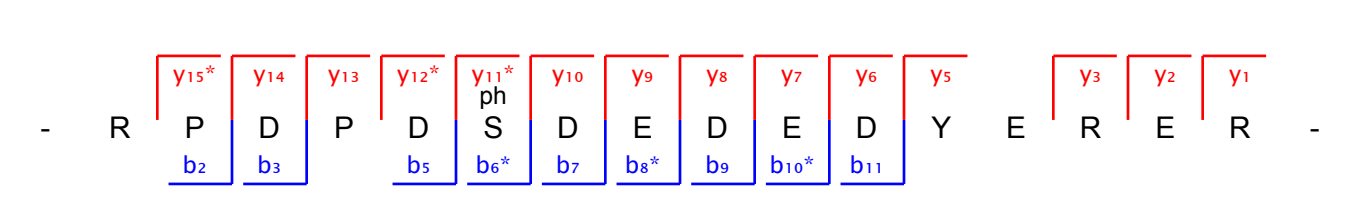
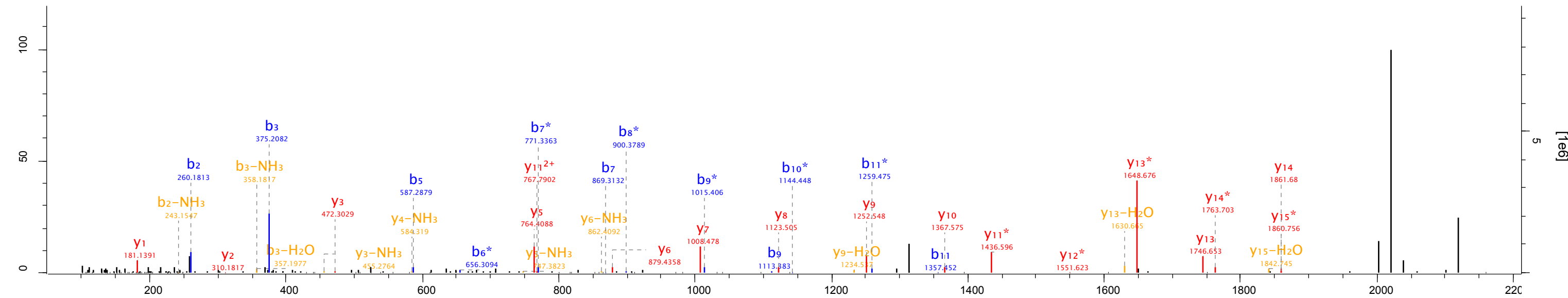
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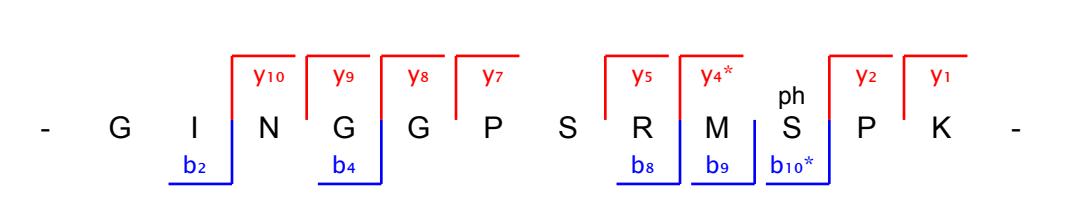
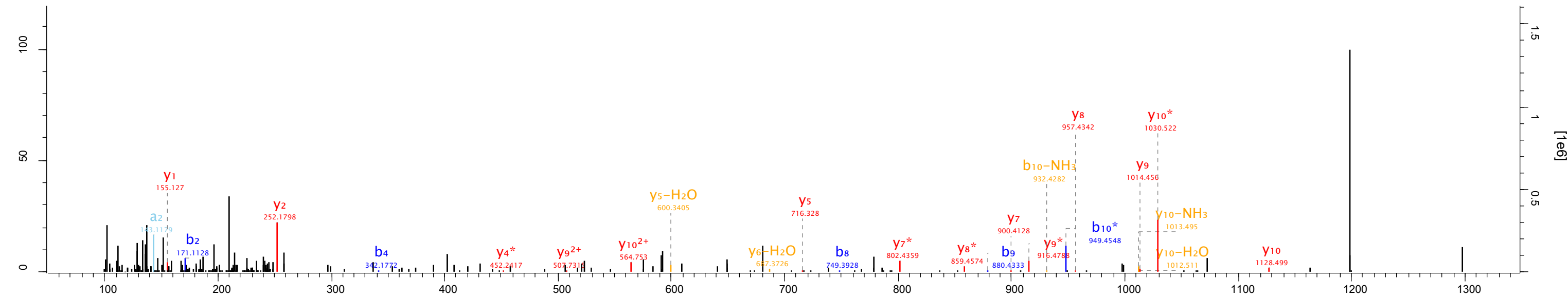
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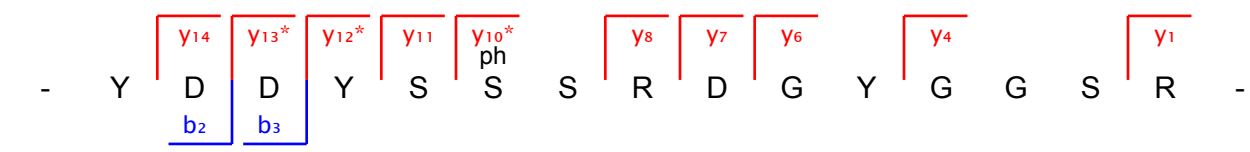
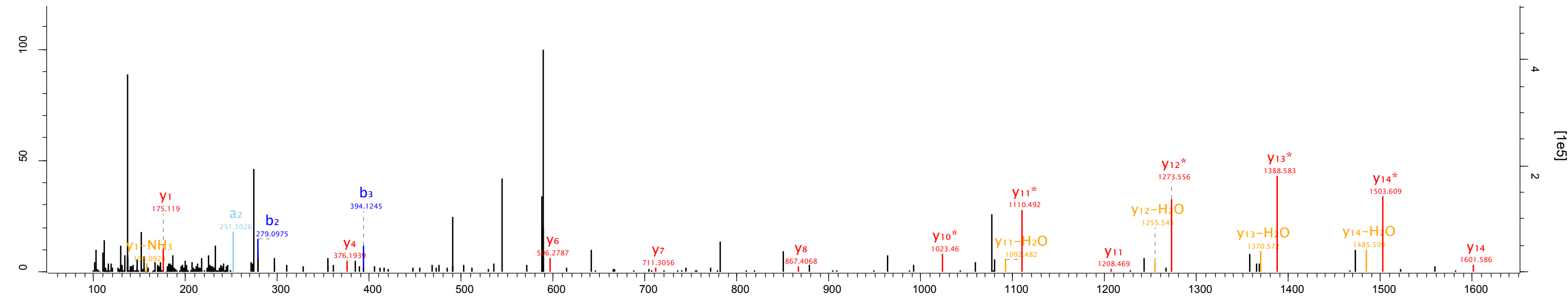
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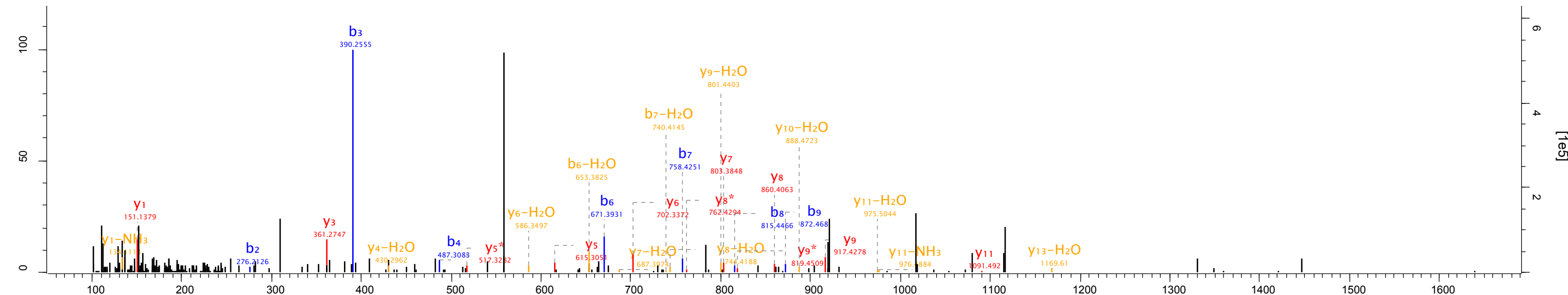


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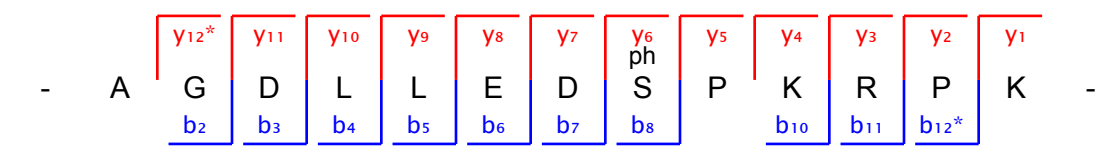
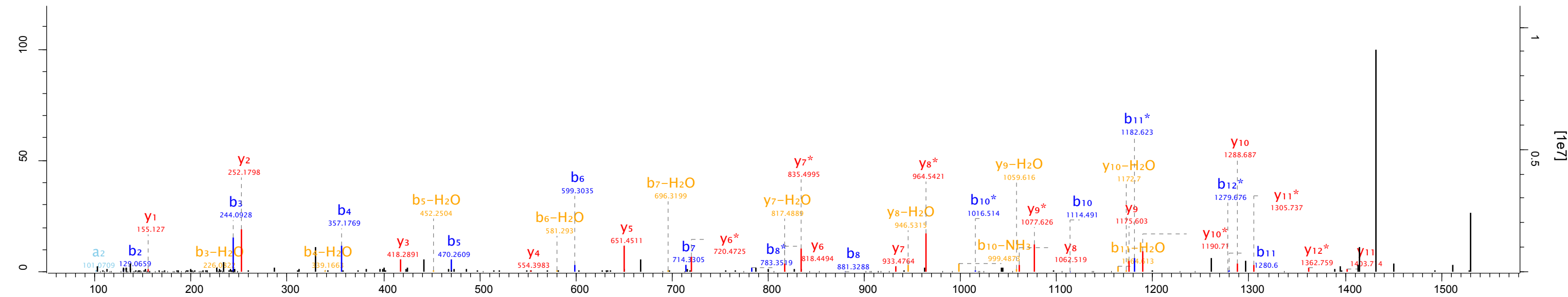




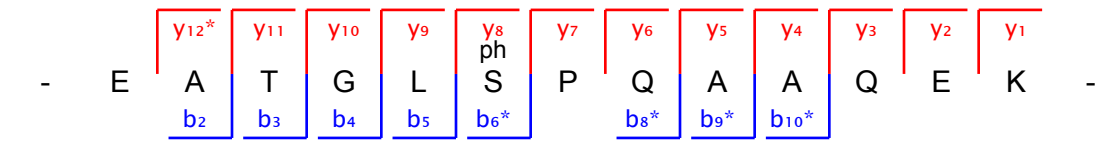
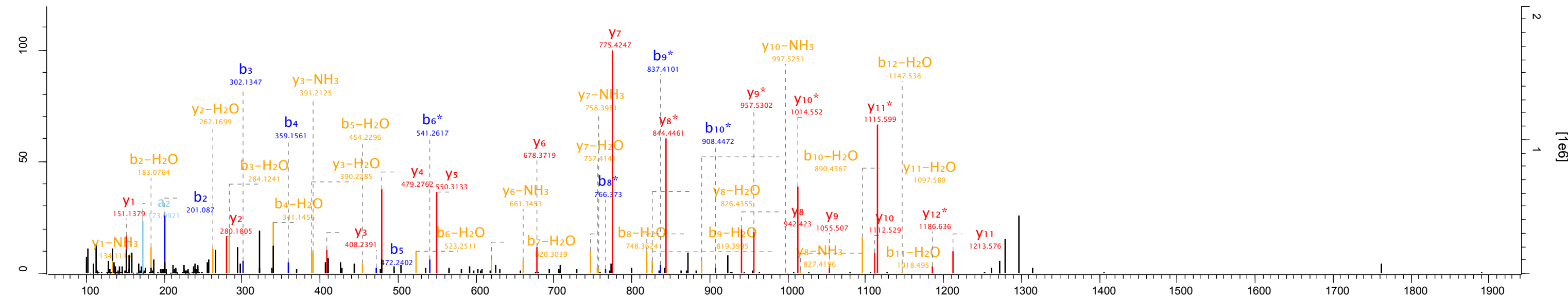
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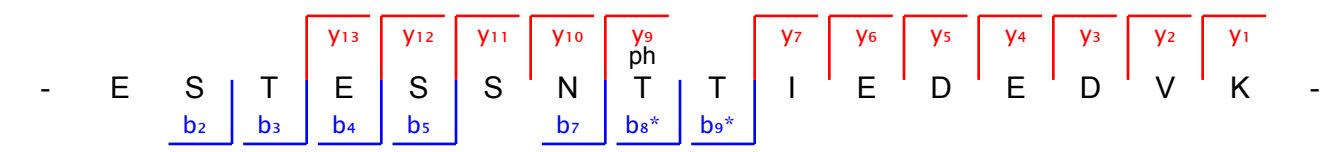
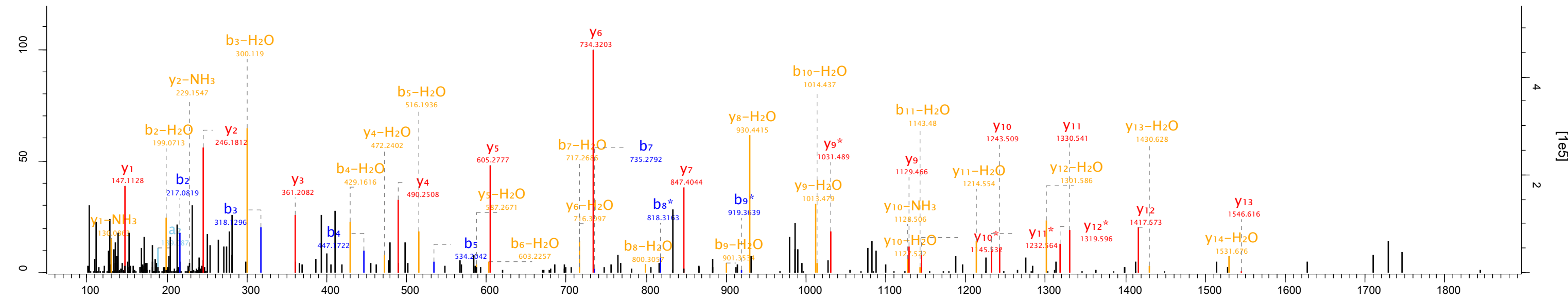
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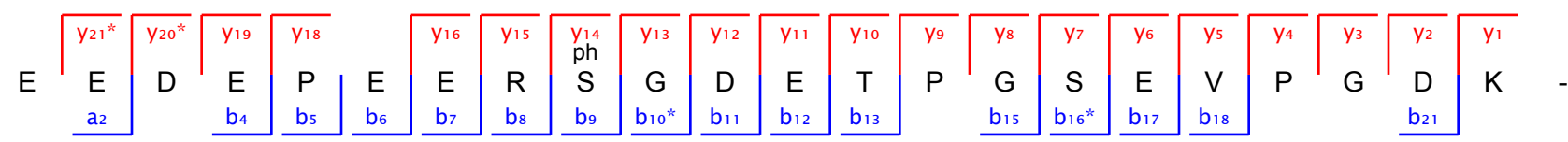
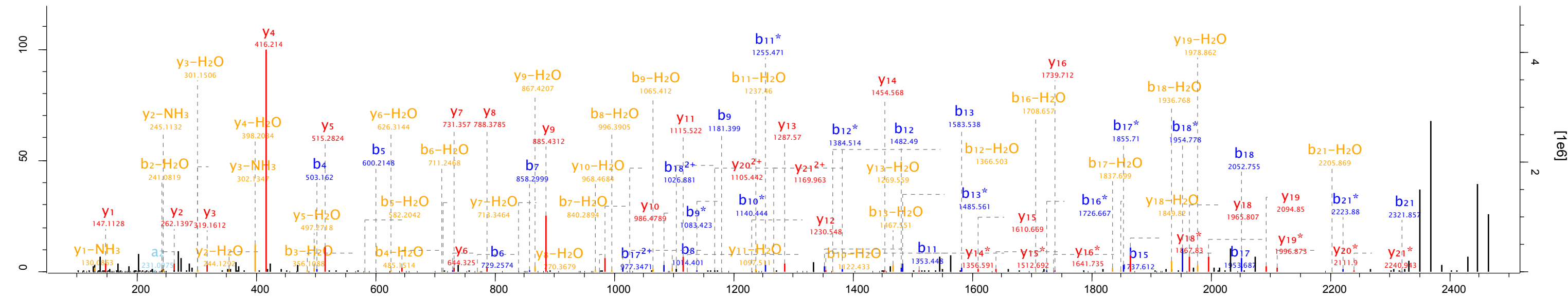
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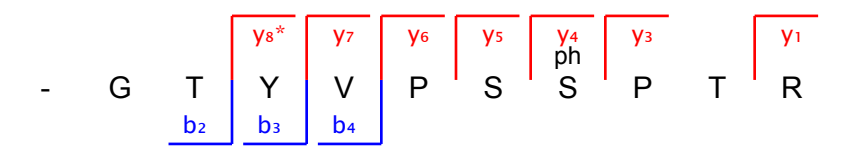
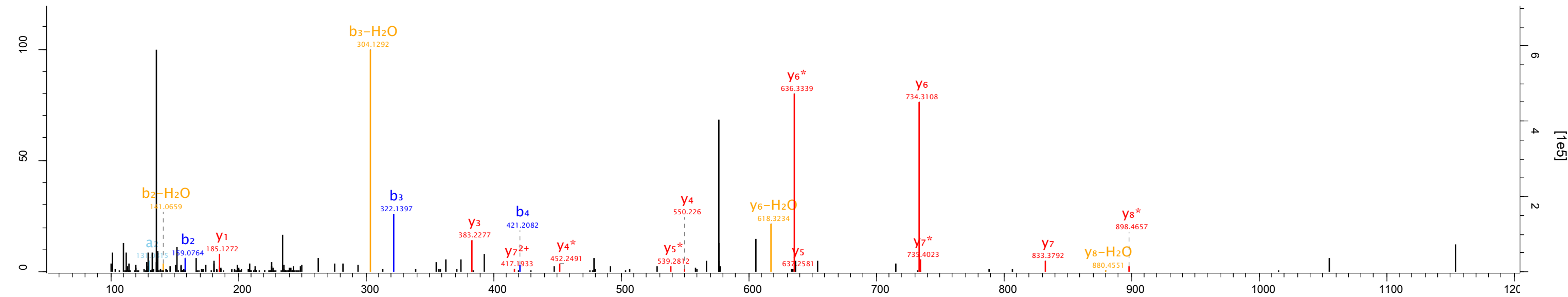
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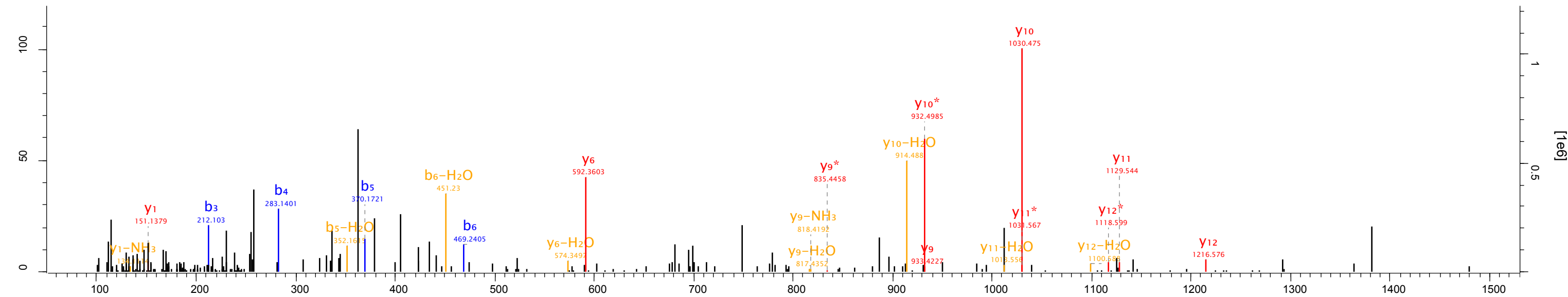
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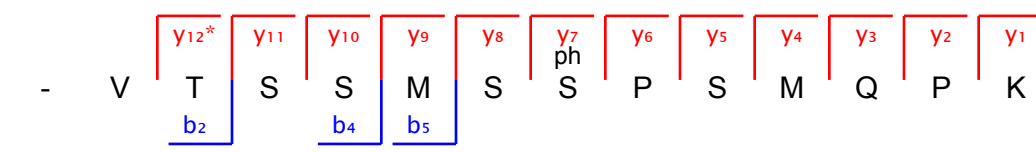
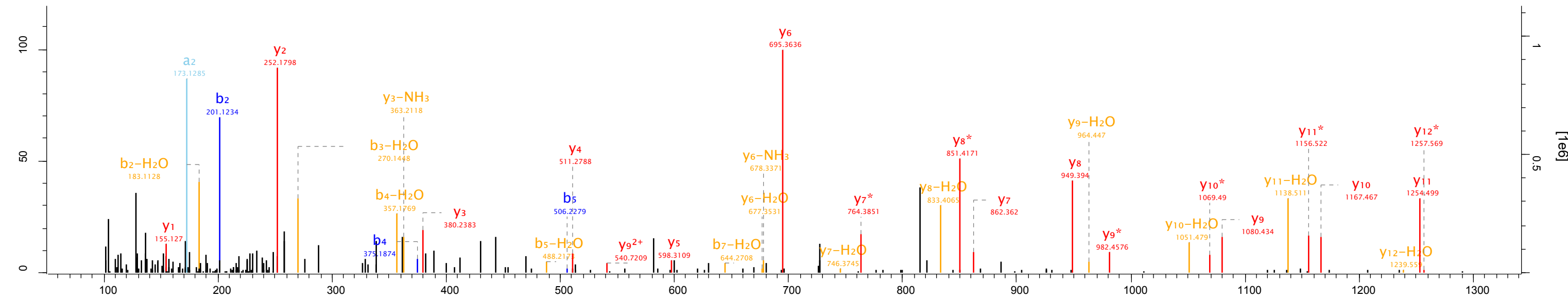


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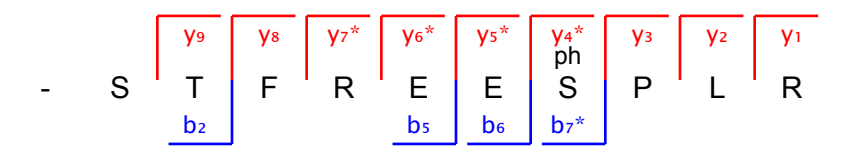
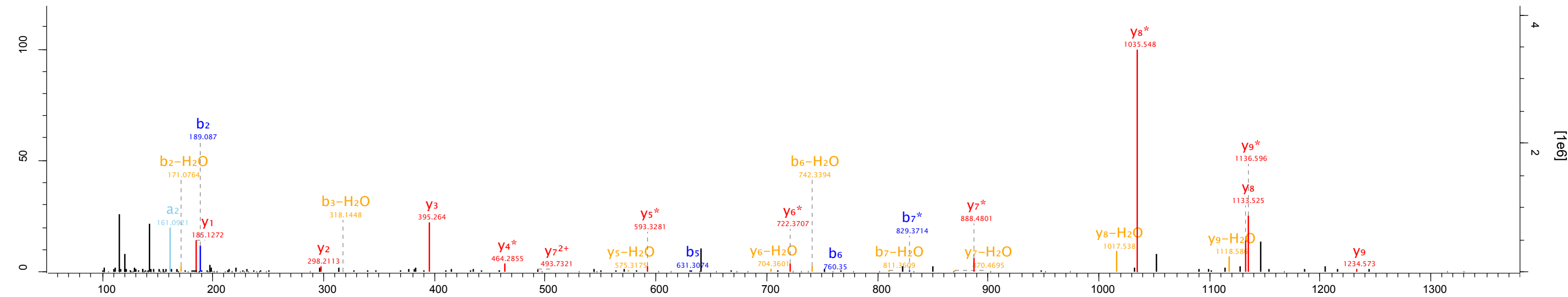
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- b4: A
- b5: S
- b6: V
- y9: S
- y10: P
- y11: V
- y12: S
- y6: P
- y1: K

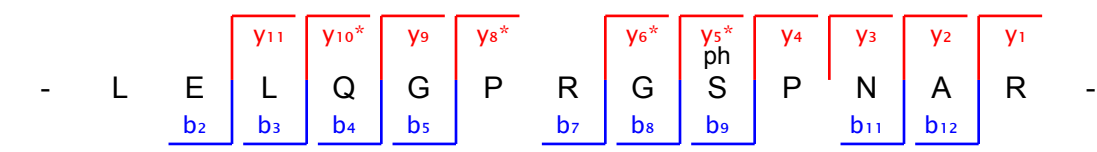
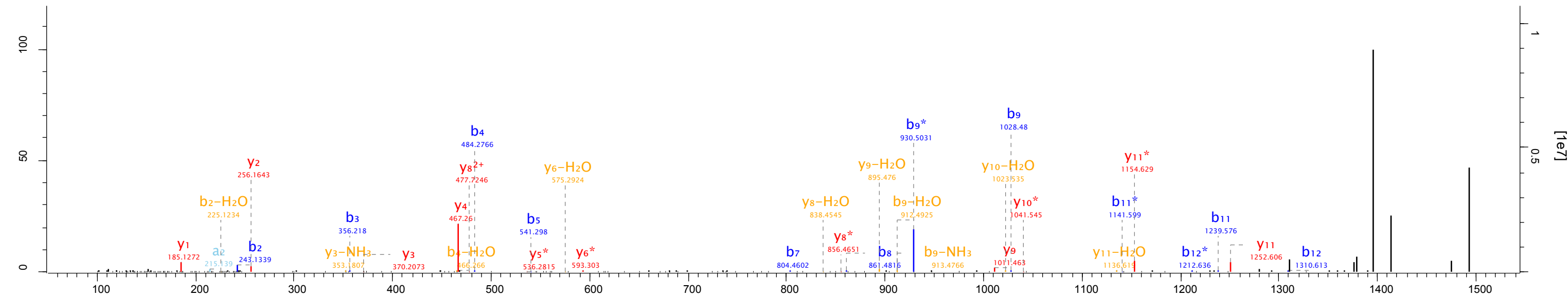
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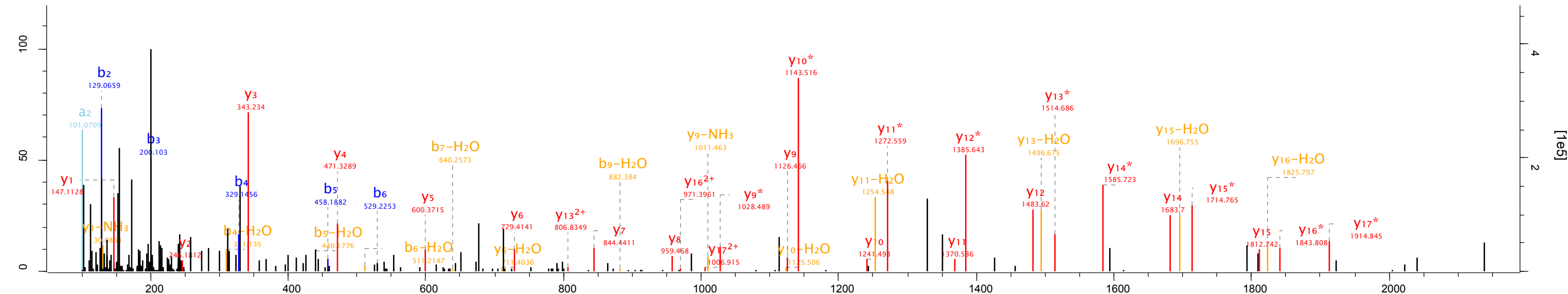


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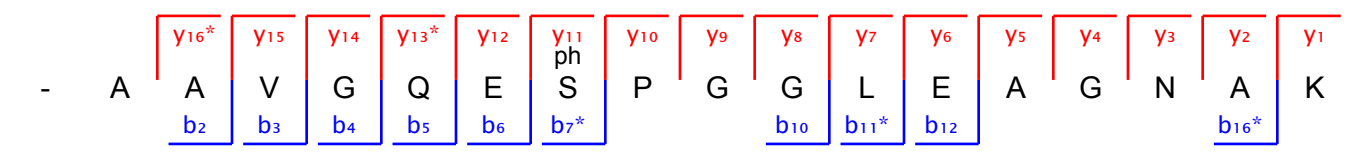
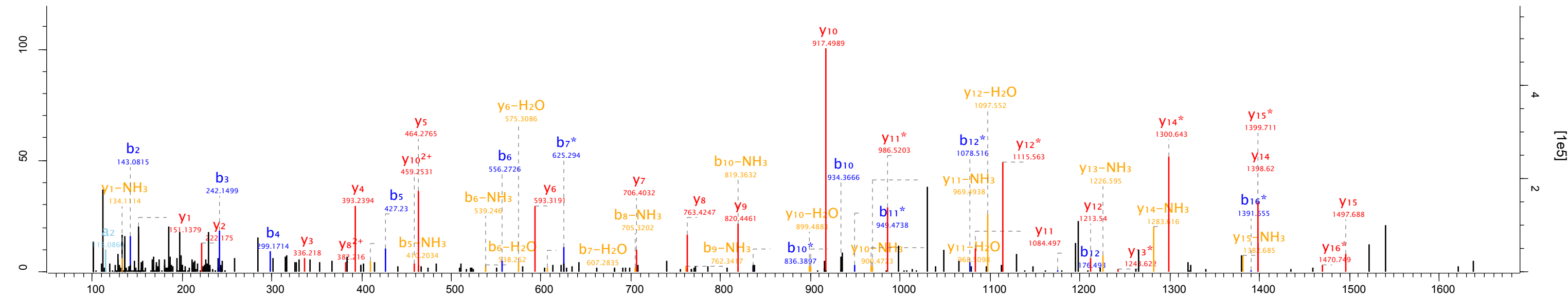




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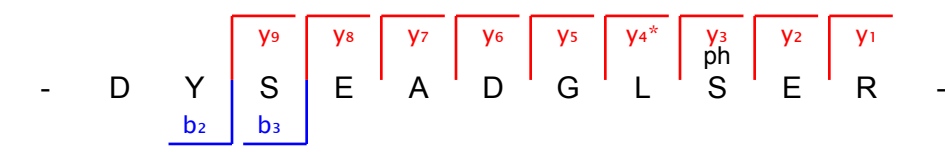
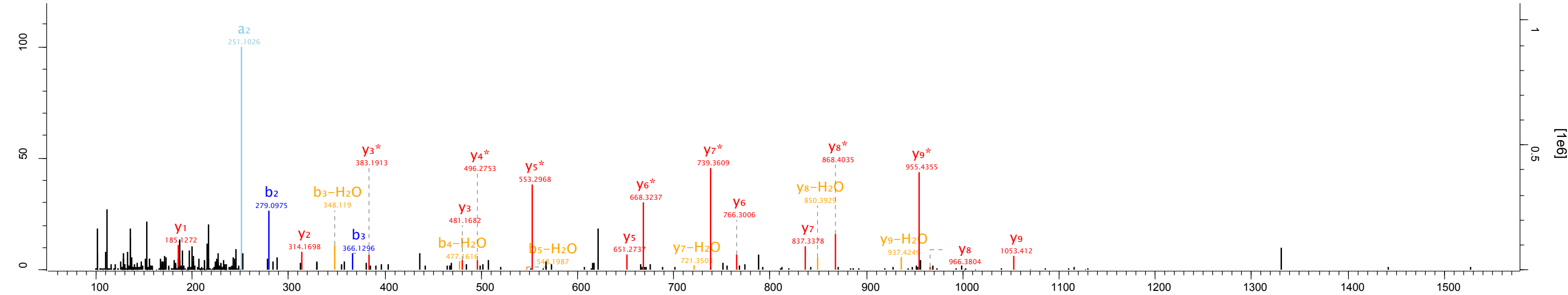
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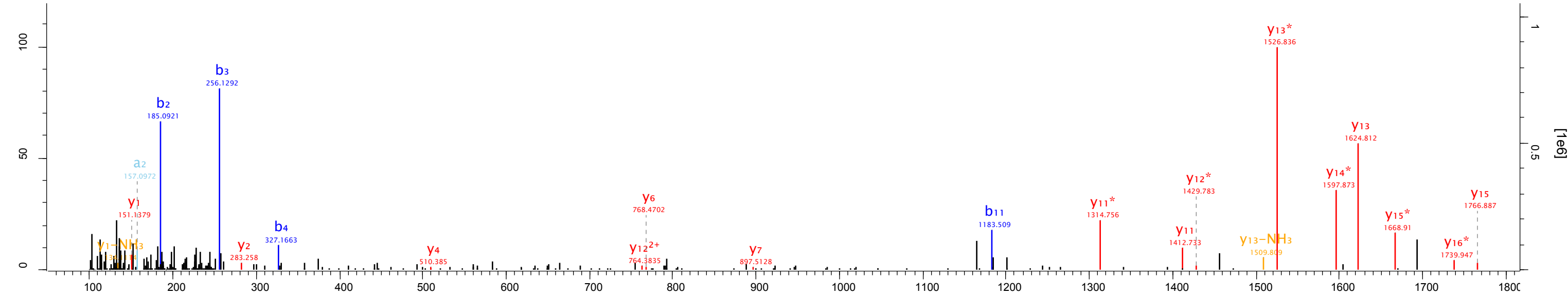


20171215_MaS_33SR_LMH_phospho_06

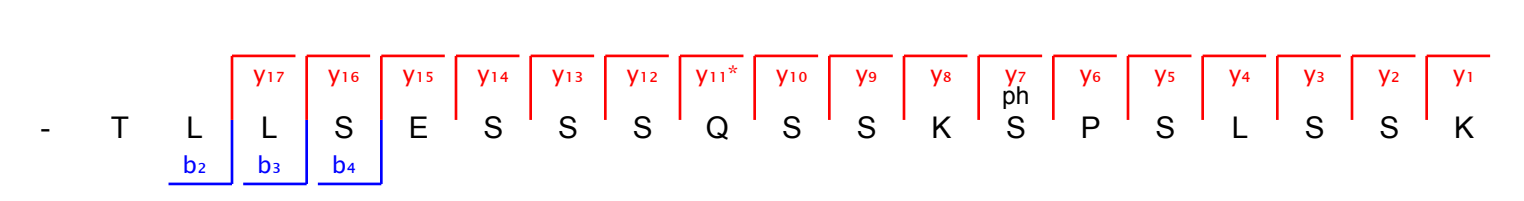
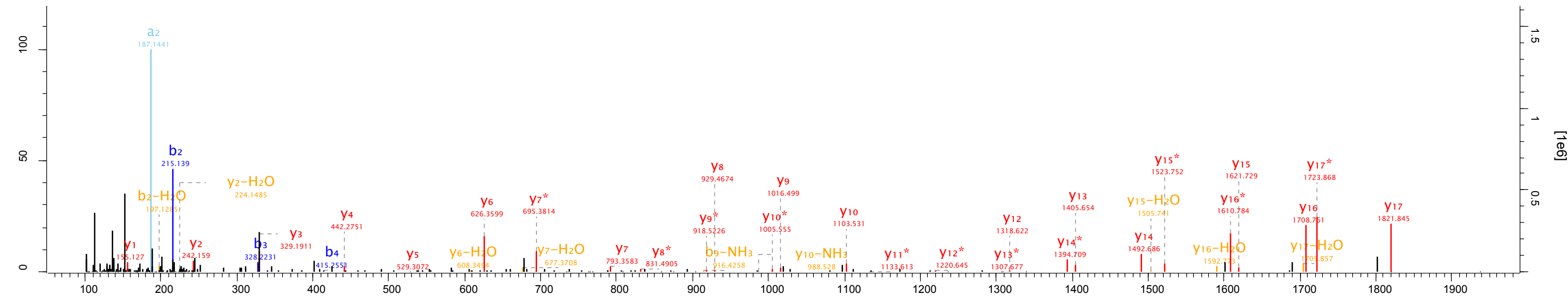
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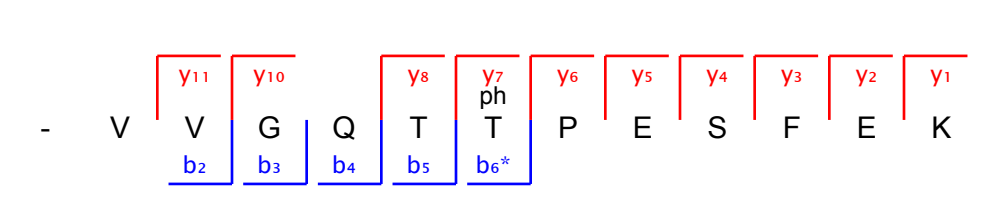
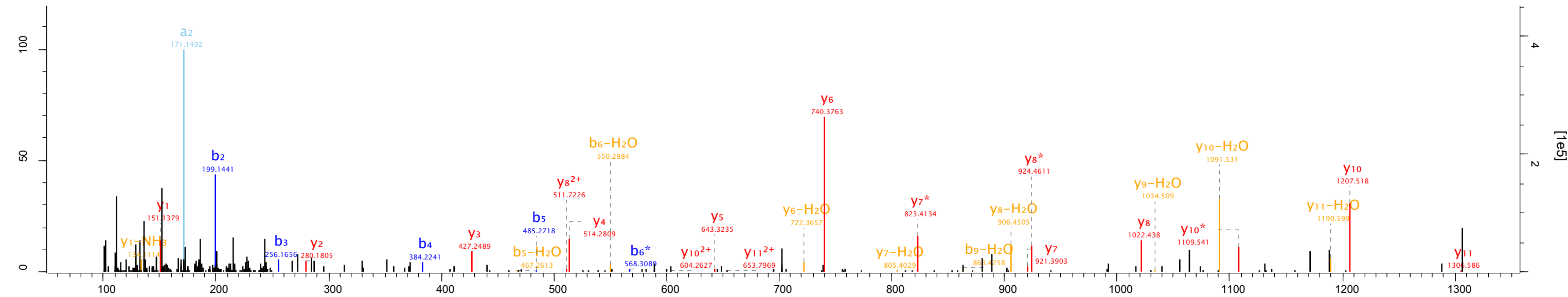
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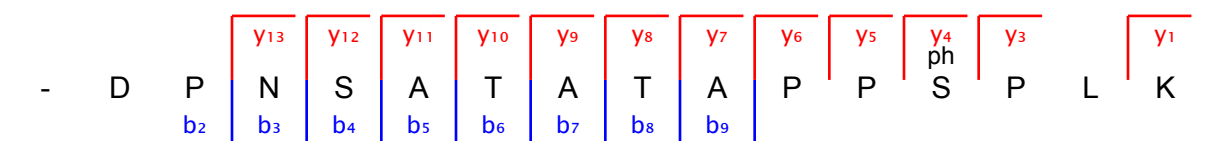
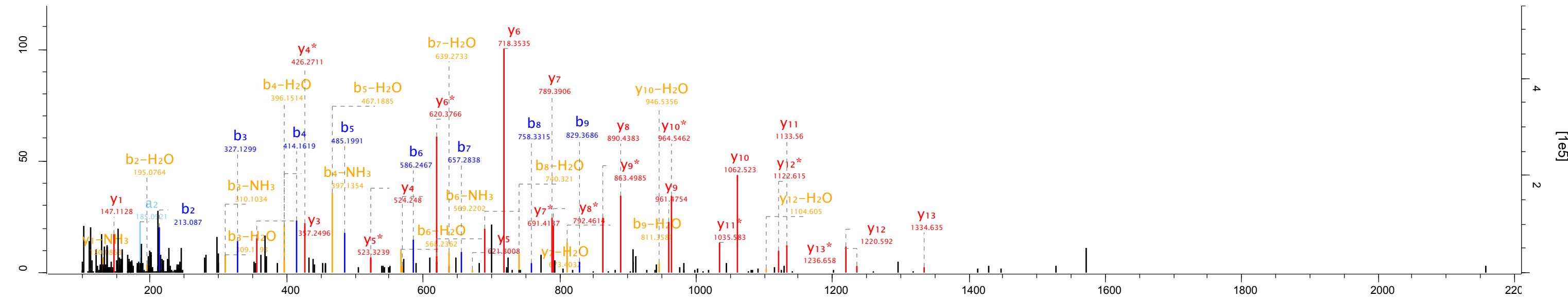
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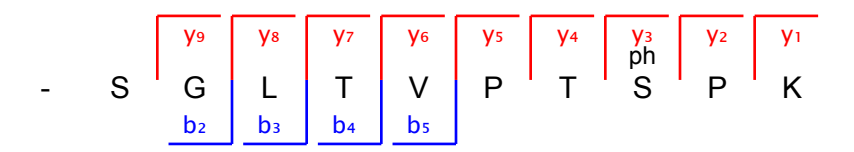
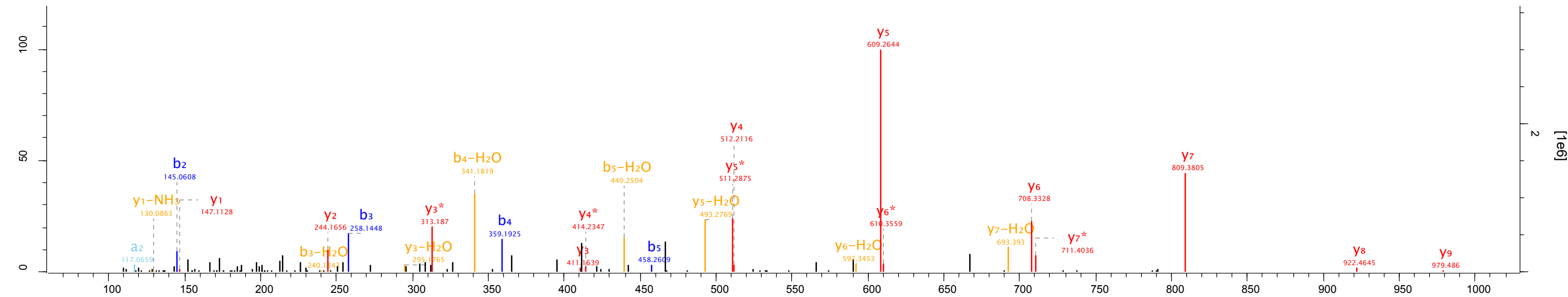
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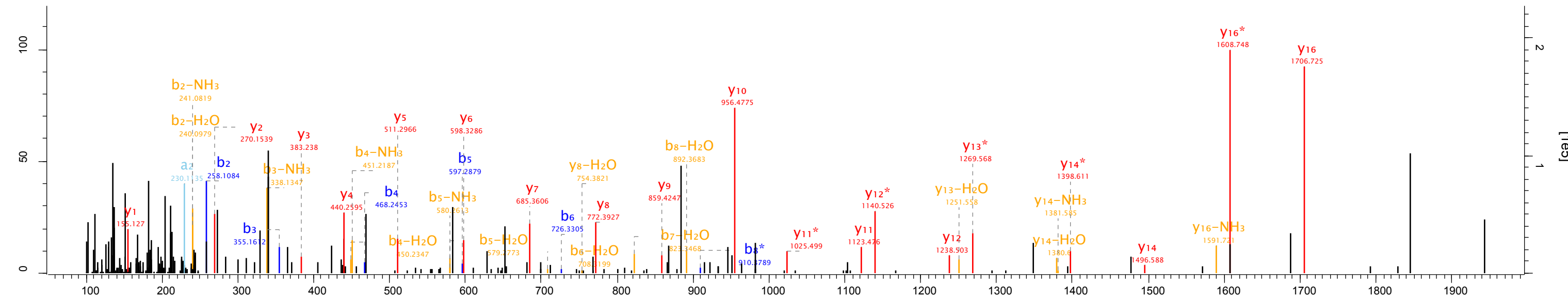


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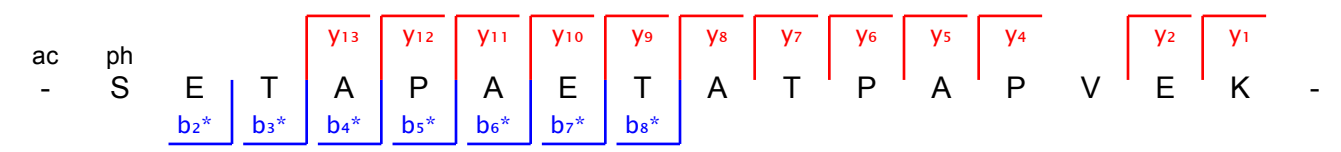
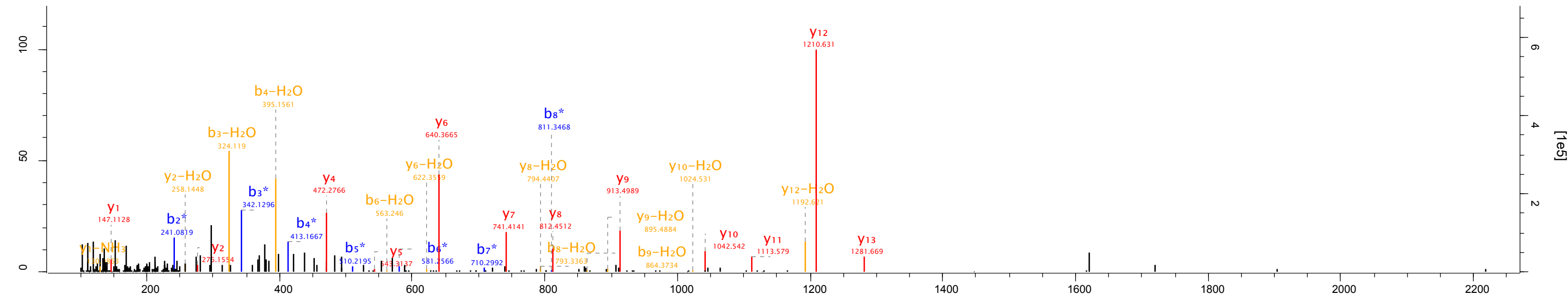
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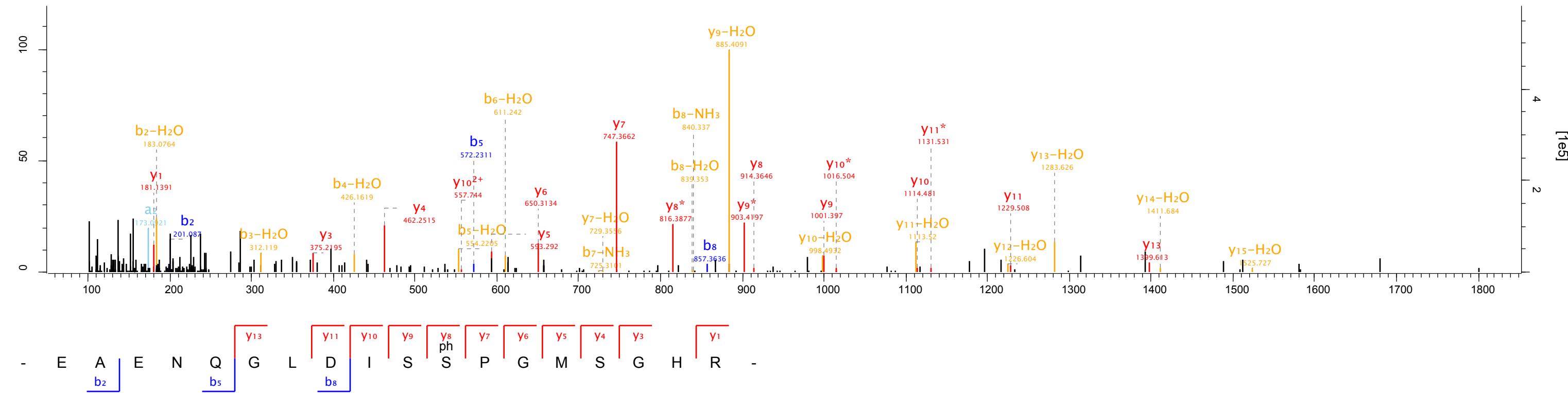




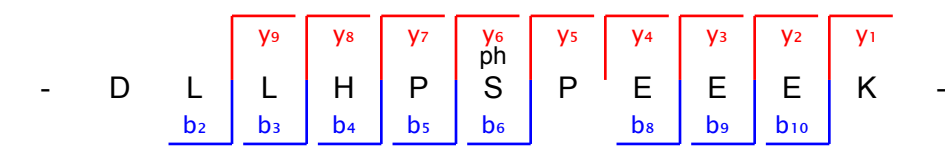
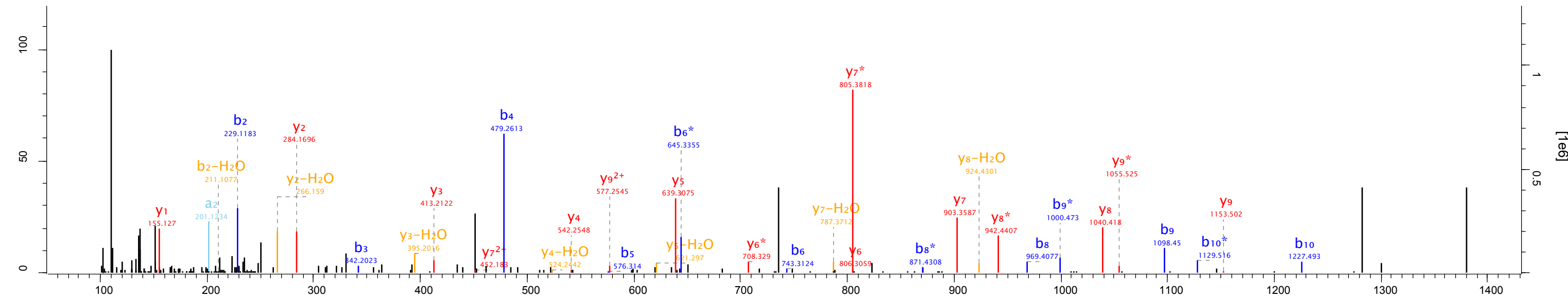
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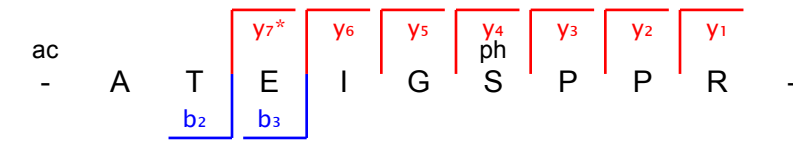
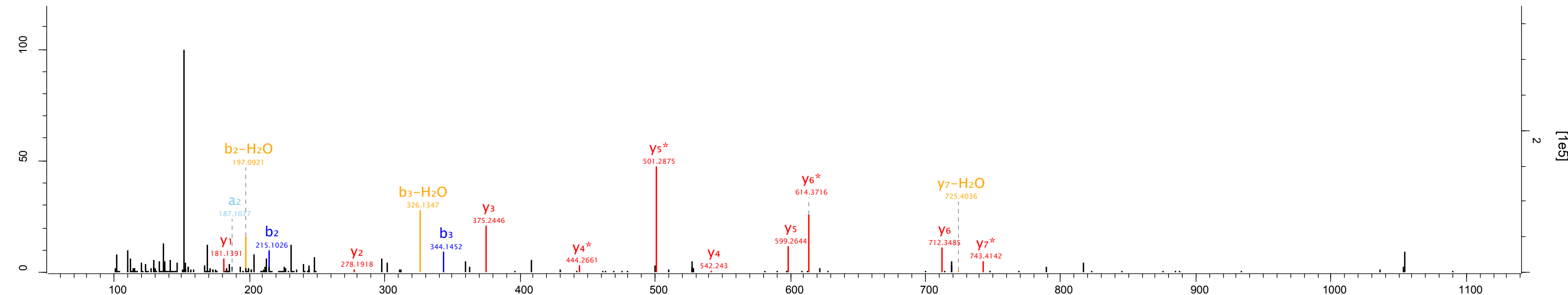




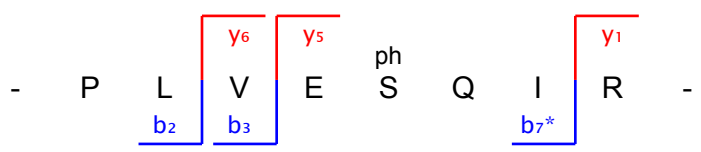
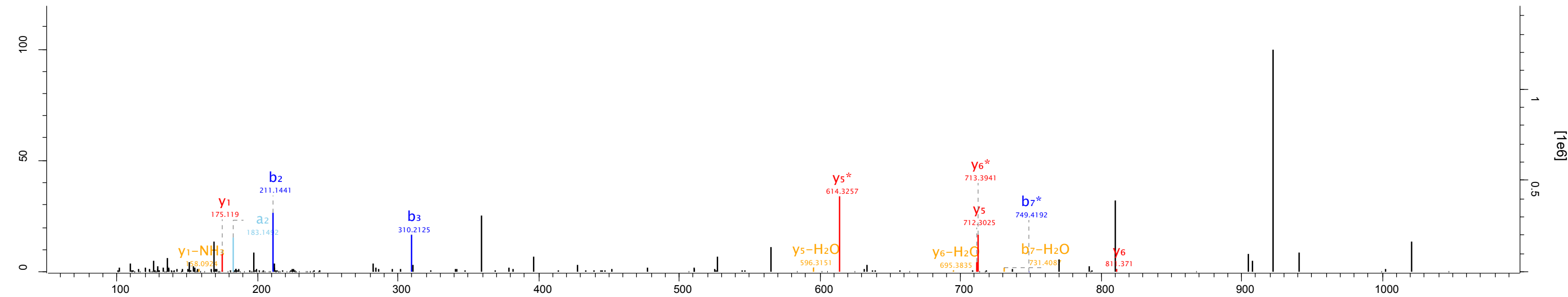
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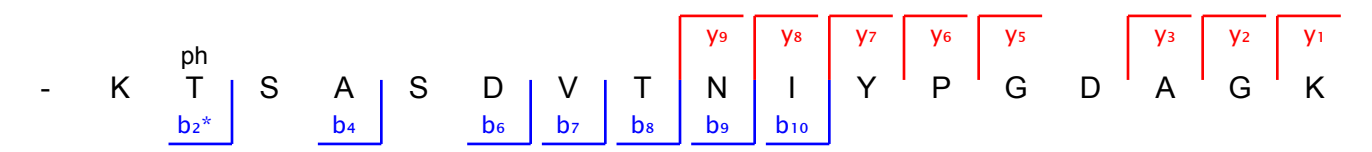
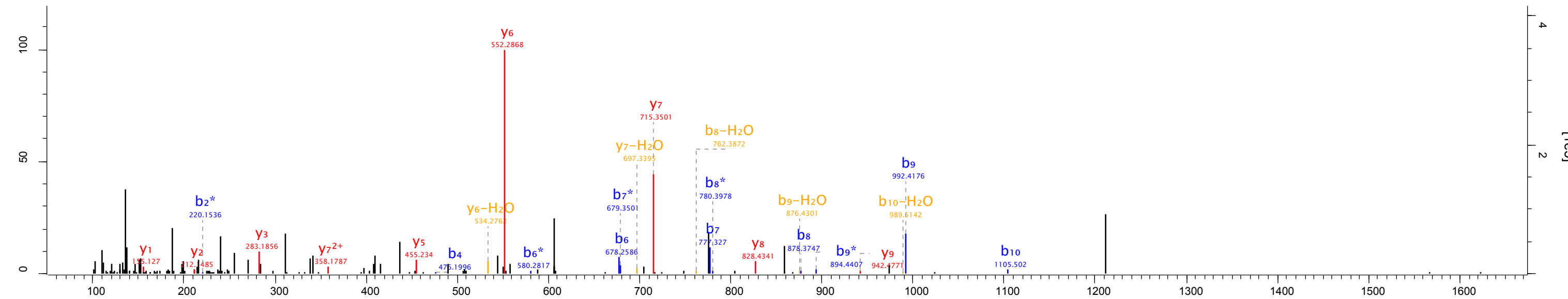
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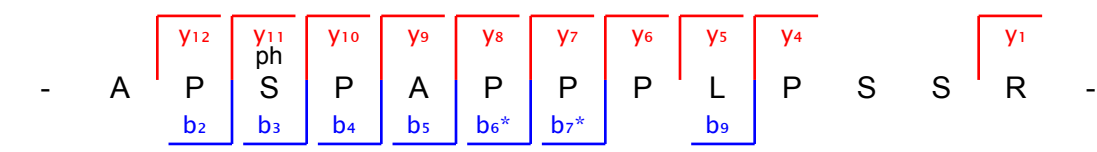
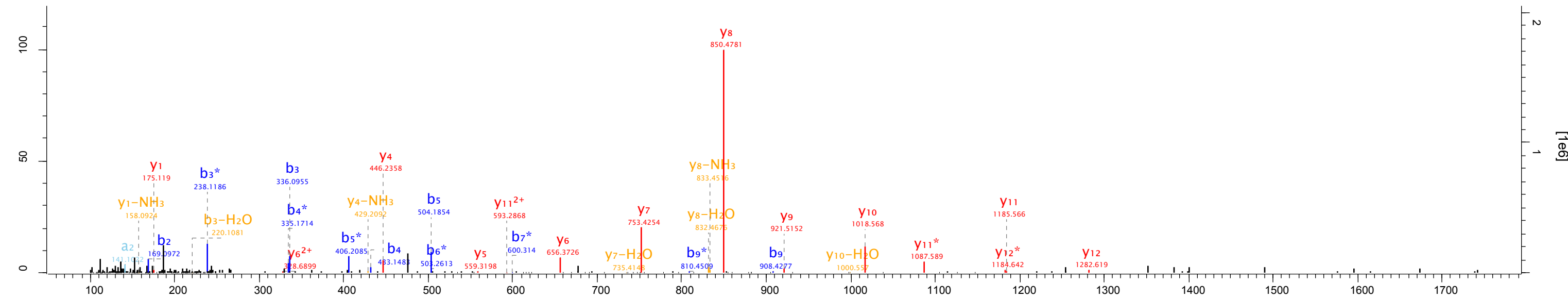
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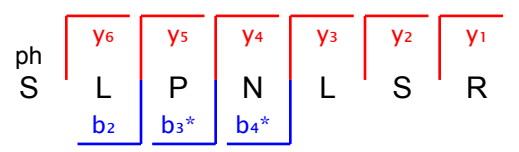
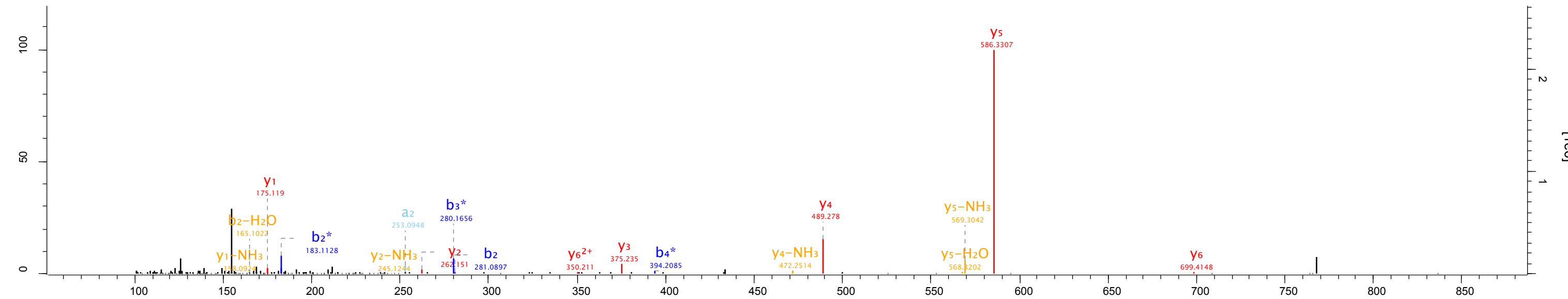
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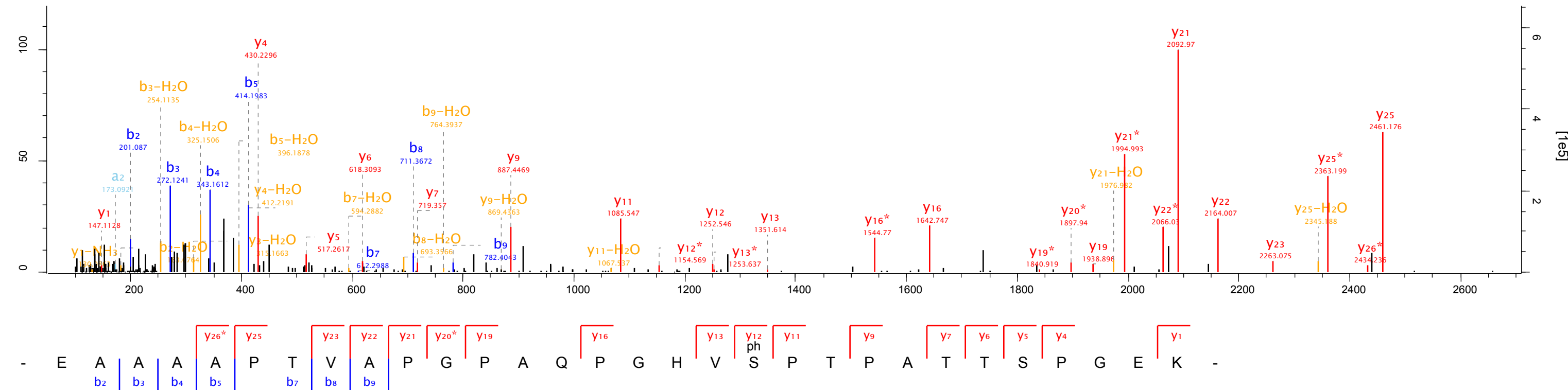


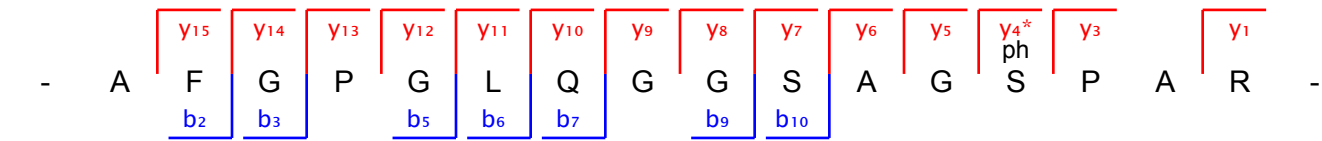
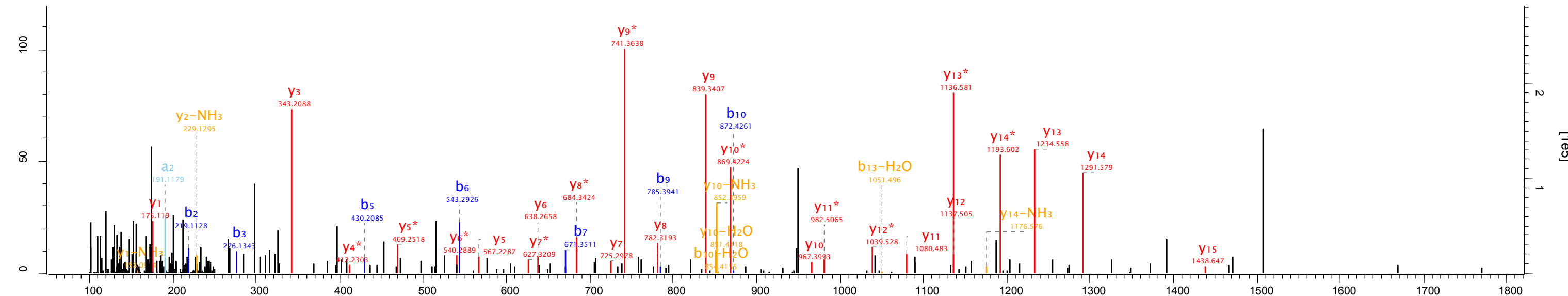
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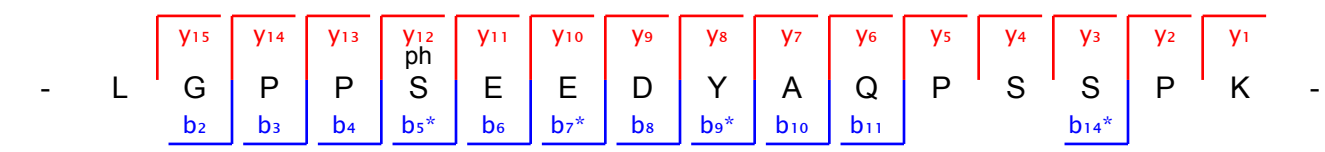
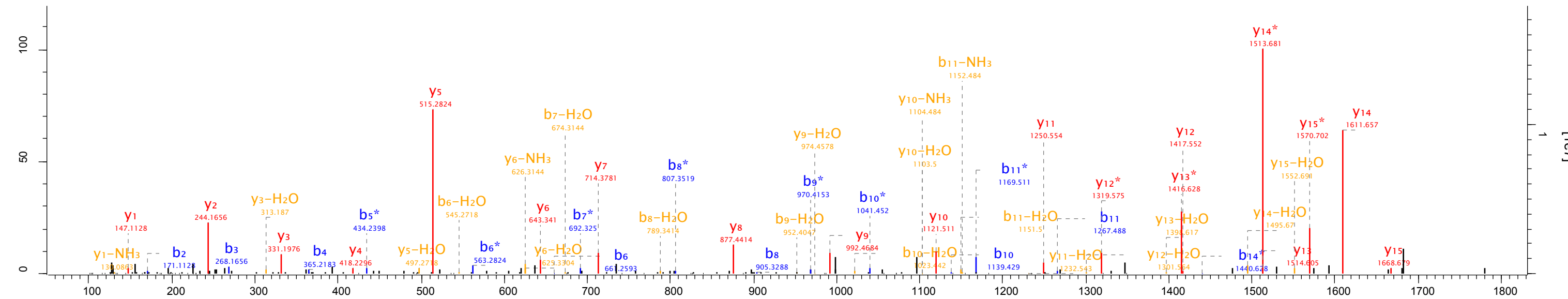
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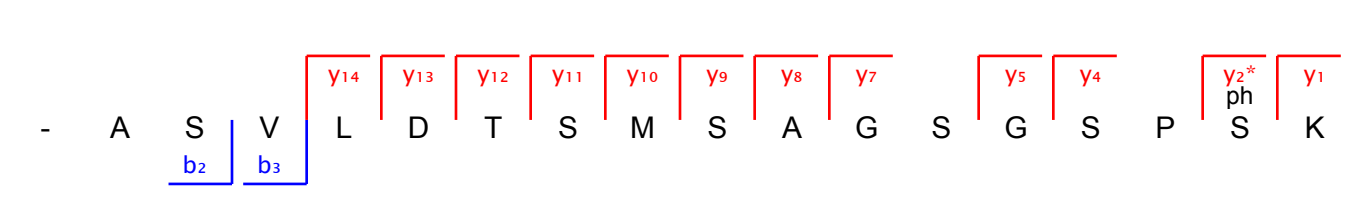
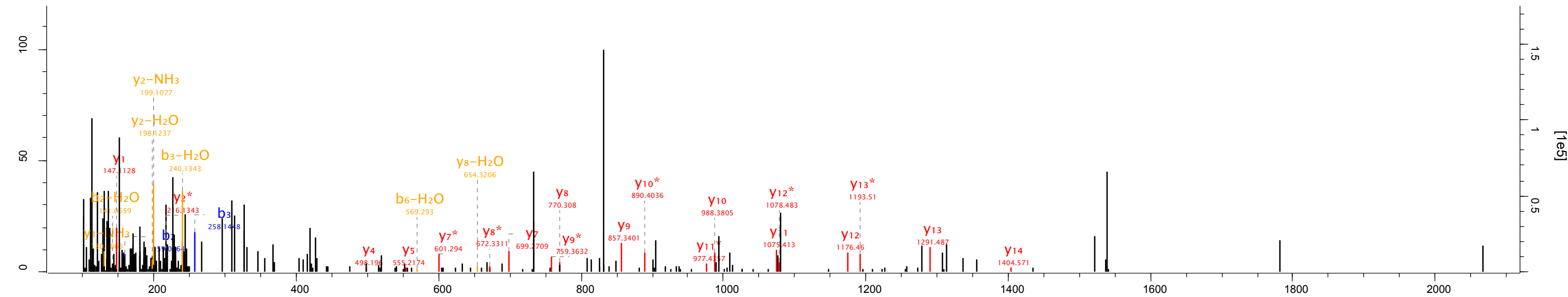




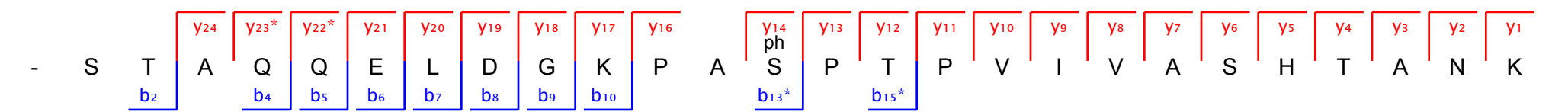
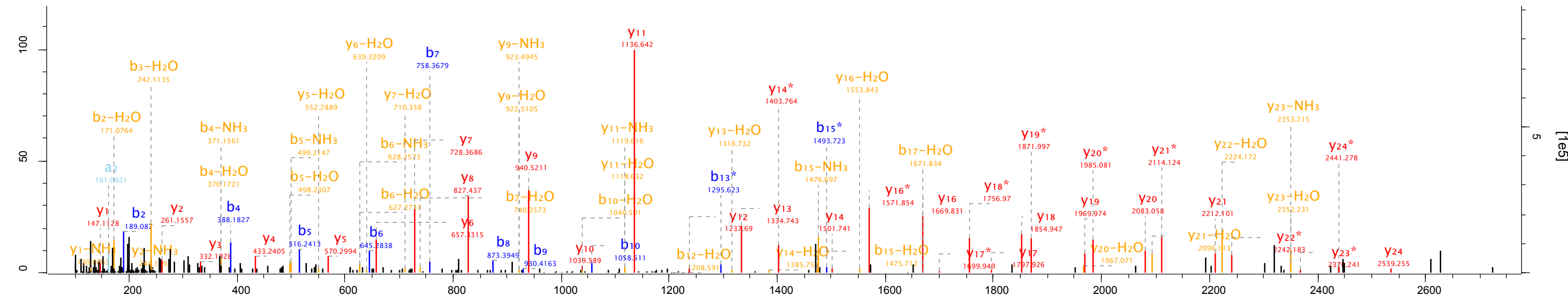
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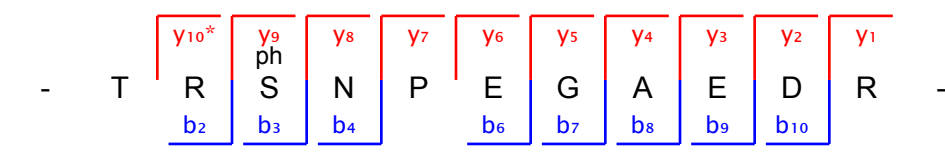
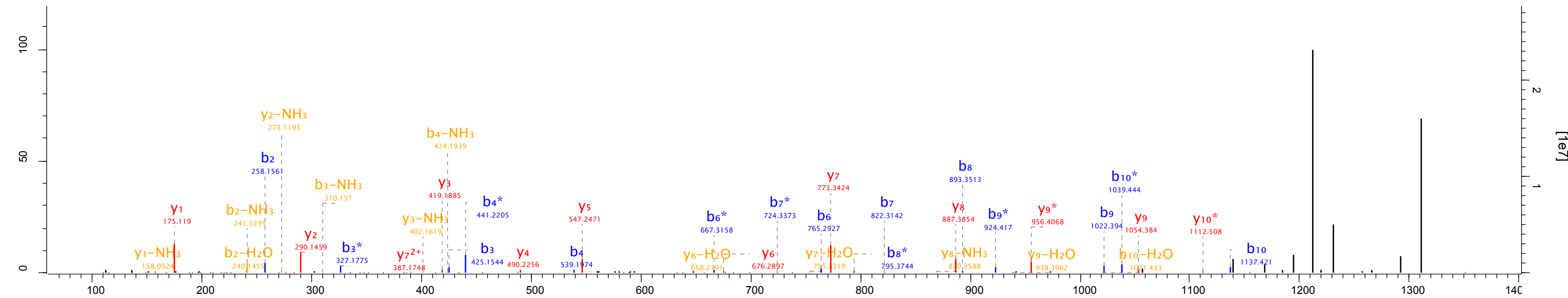
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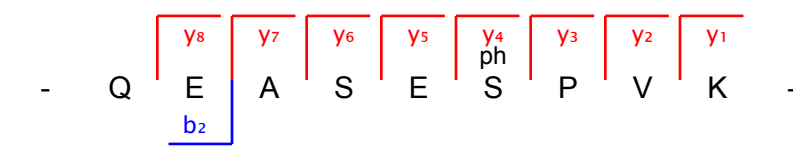
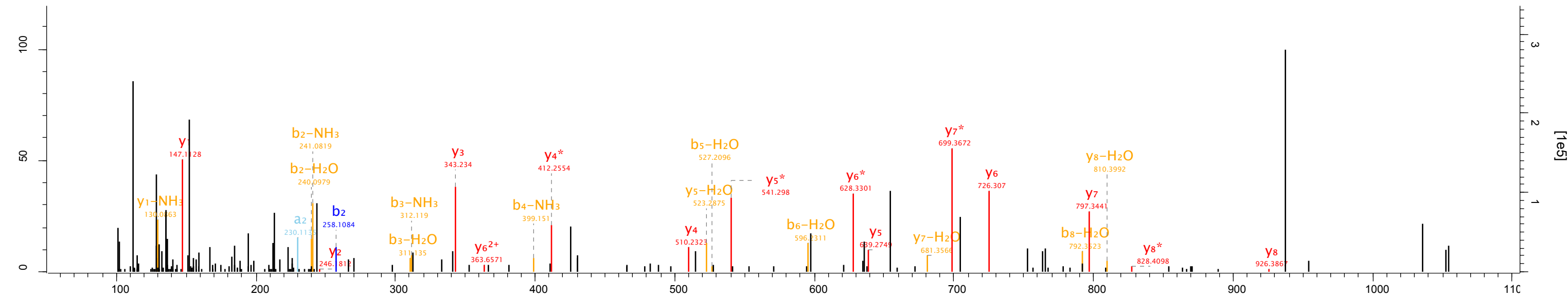
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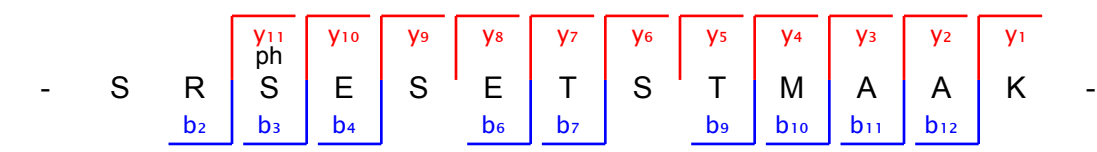
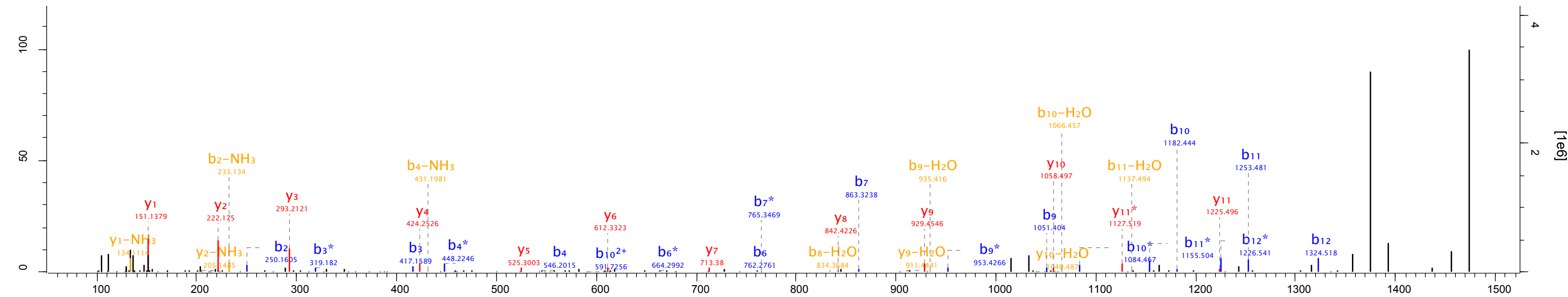
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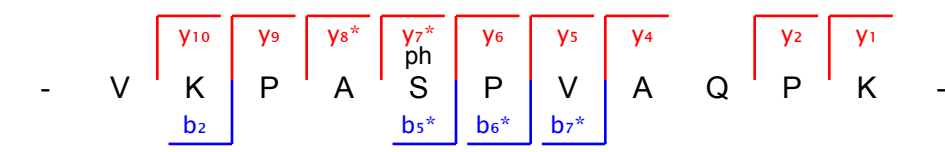
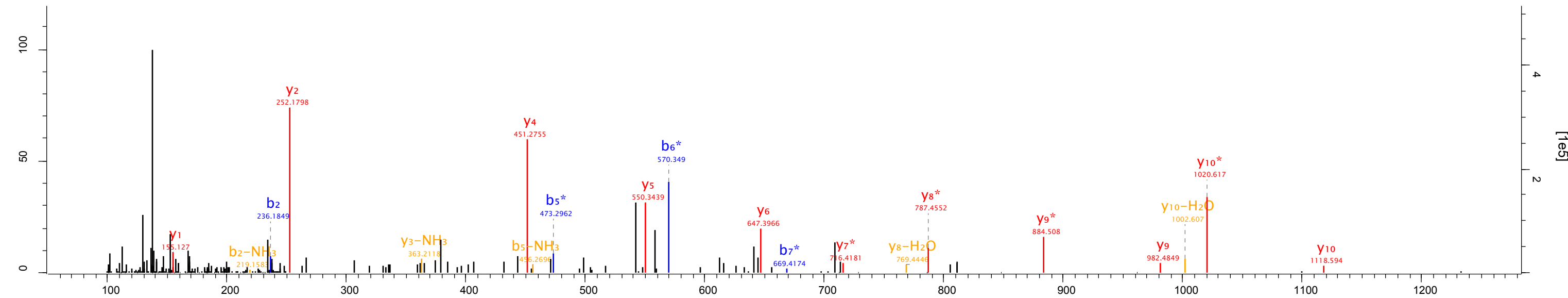
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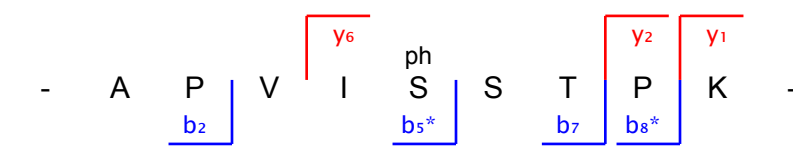
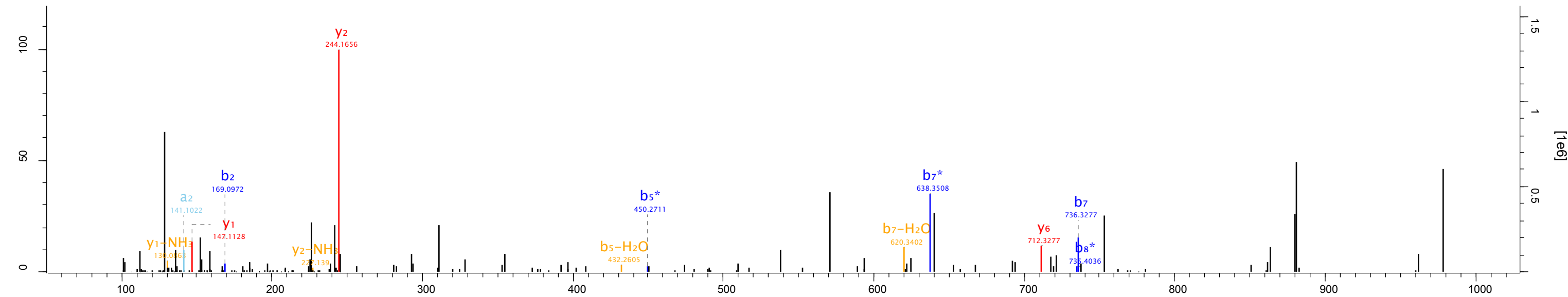
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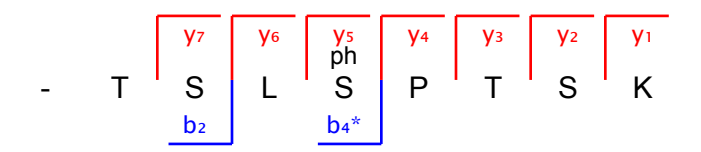
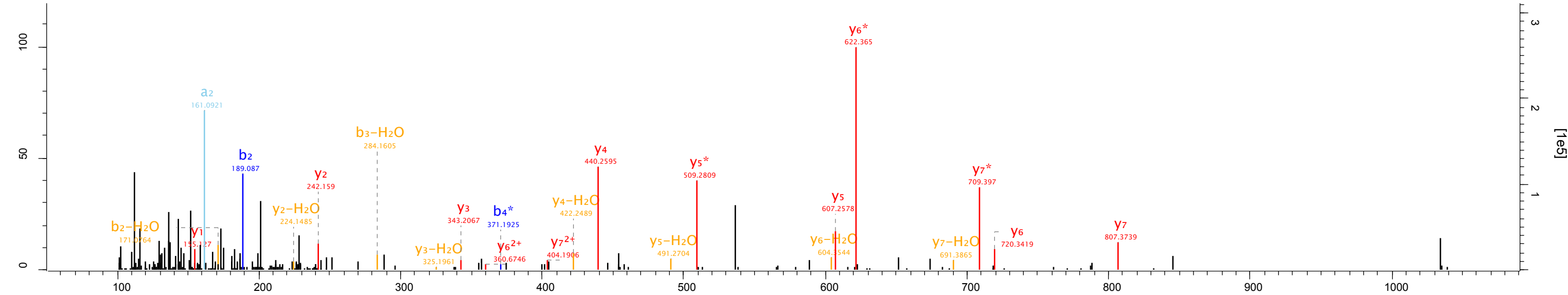
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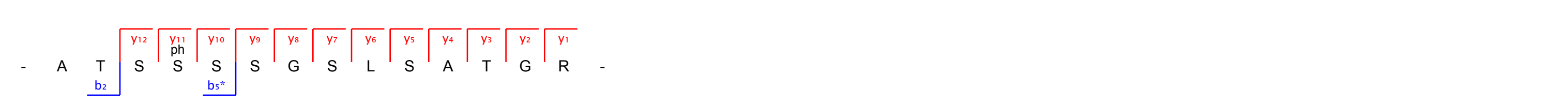
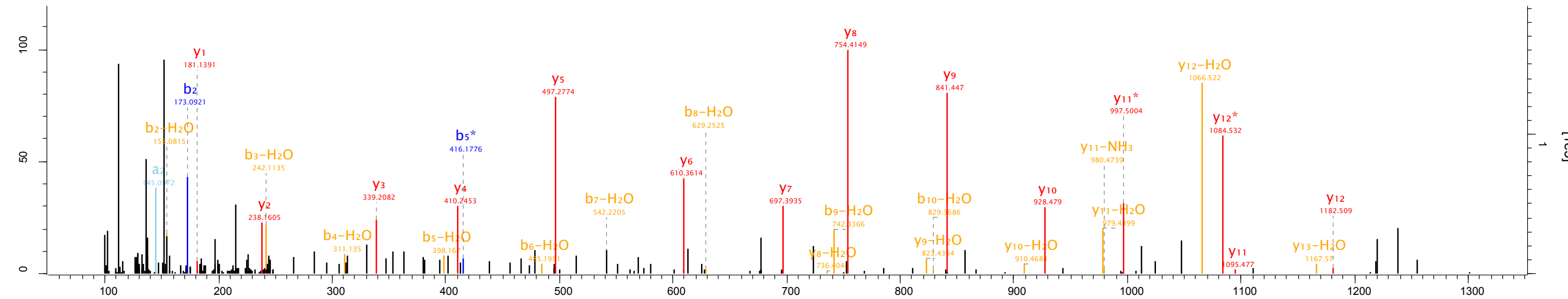
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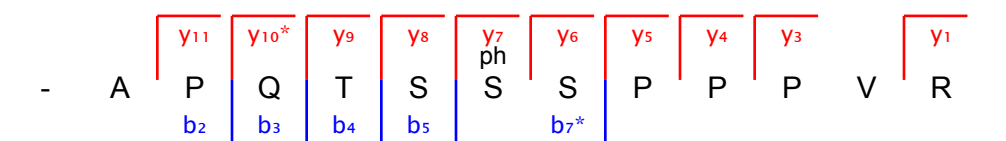
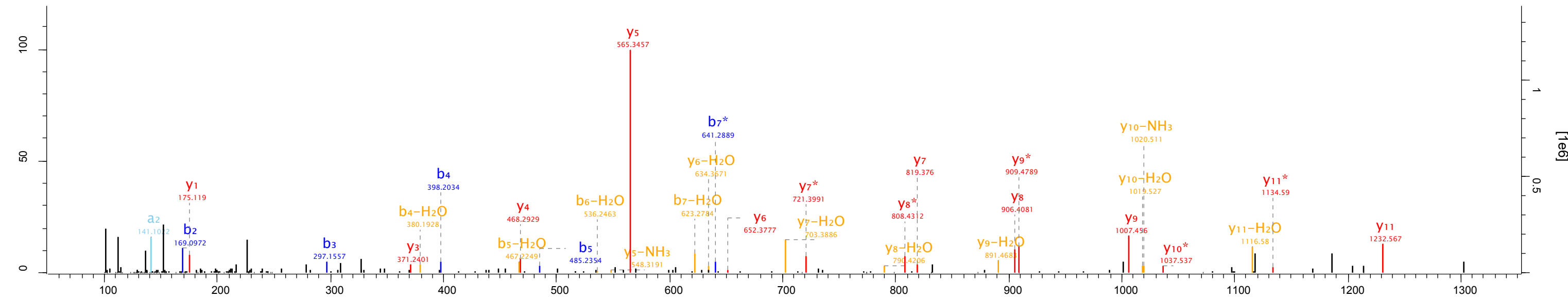
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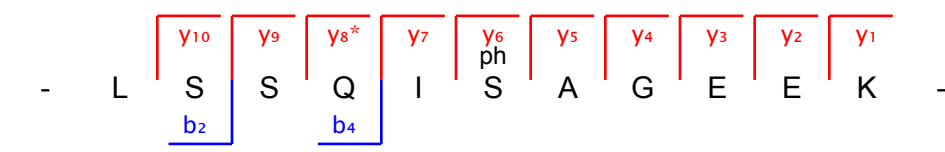
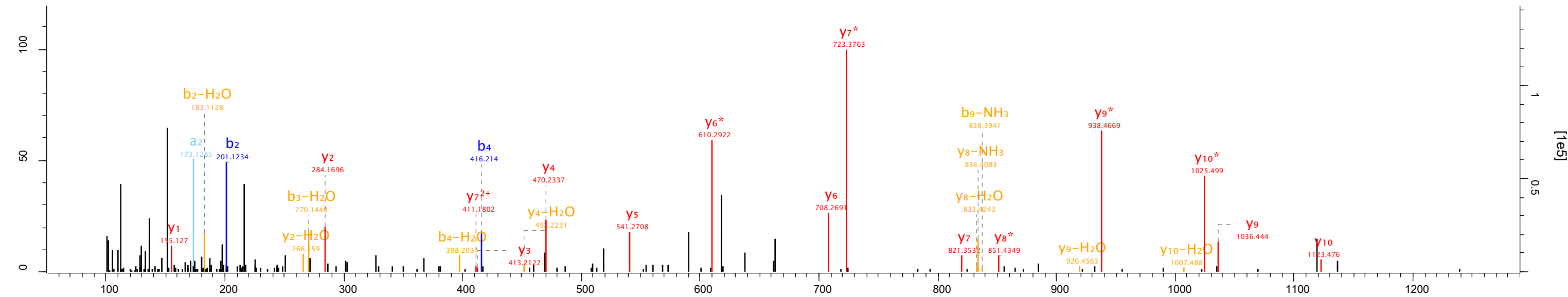
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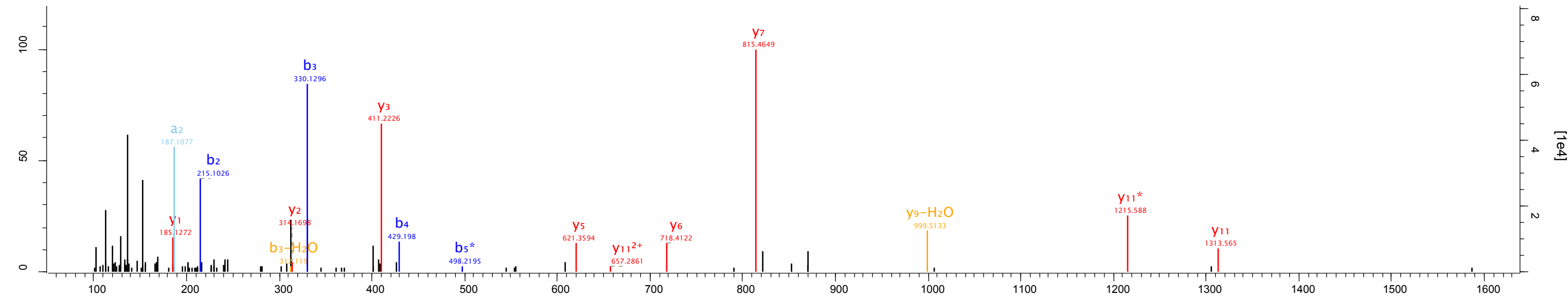
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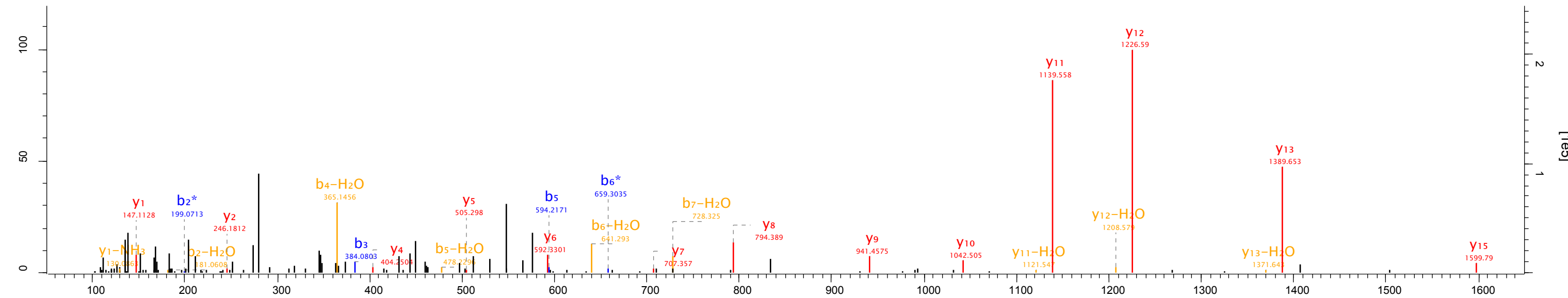
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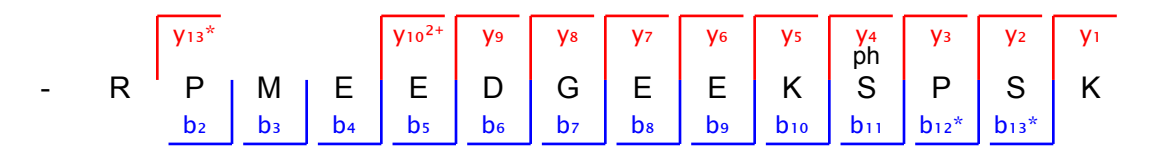
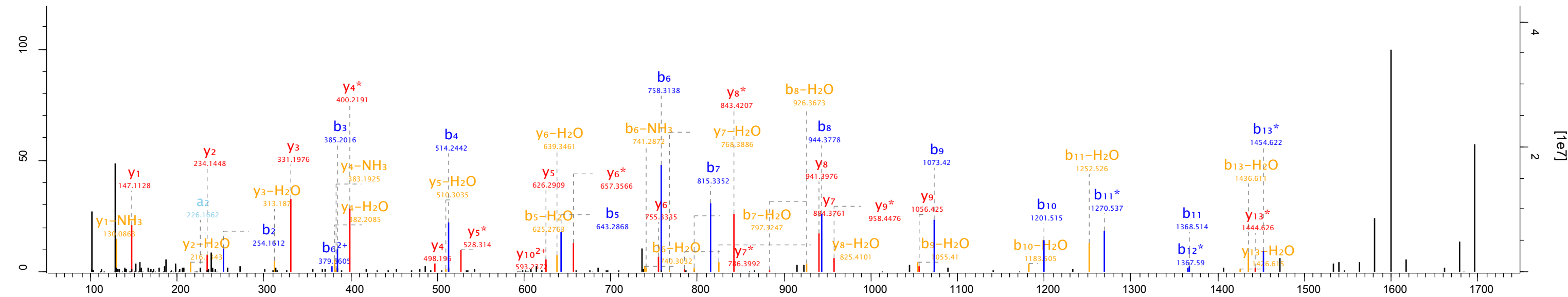
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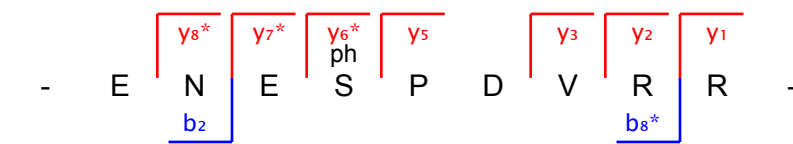
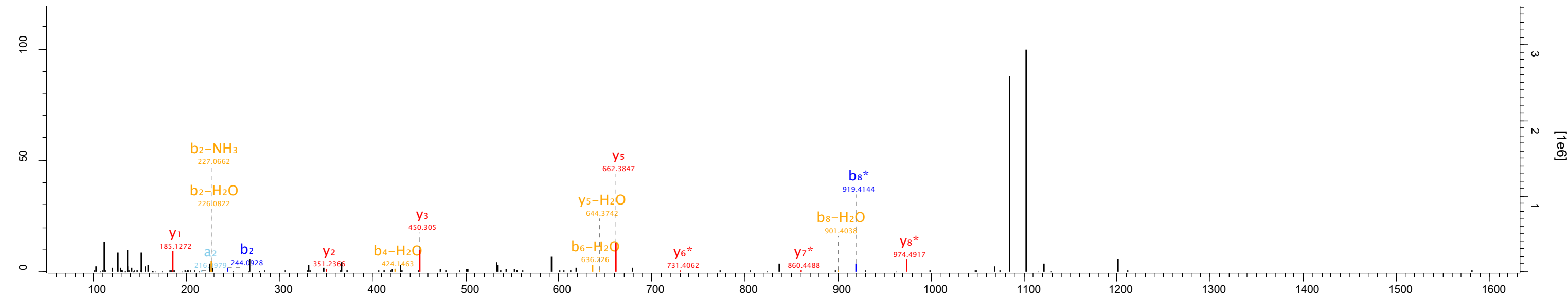


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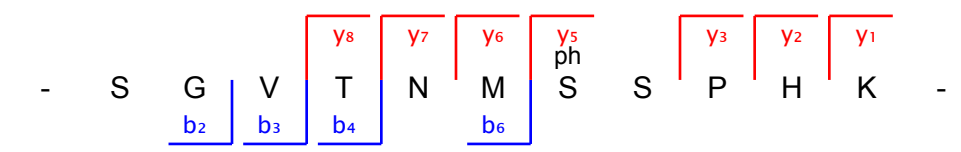
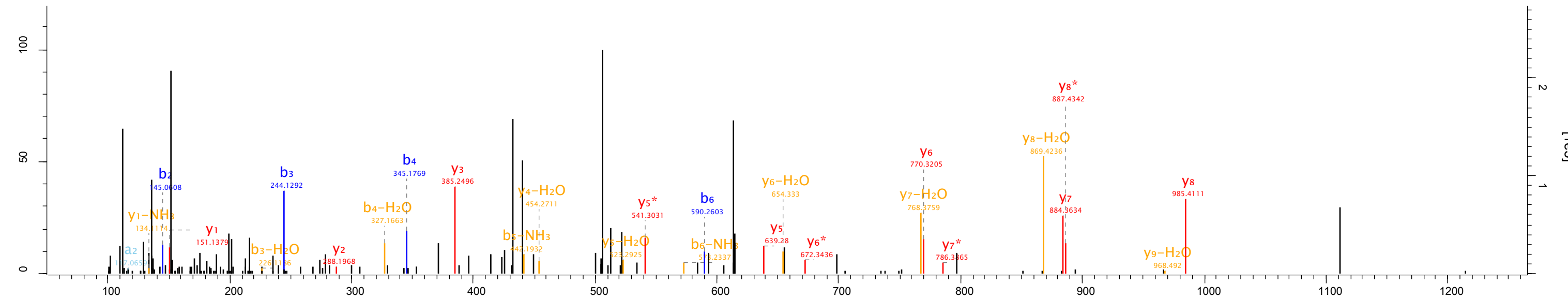


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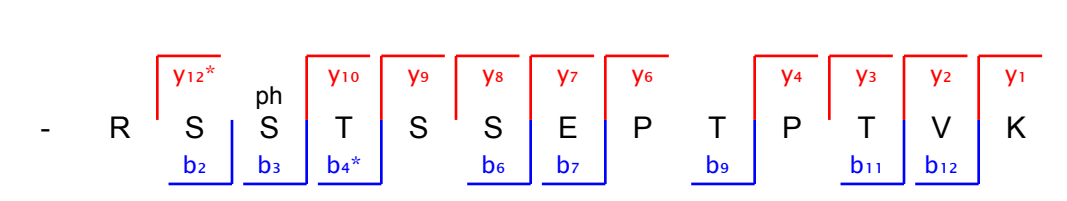
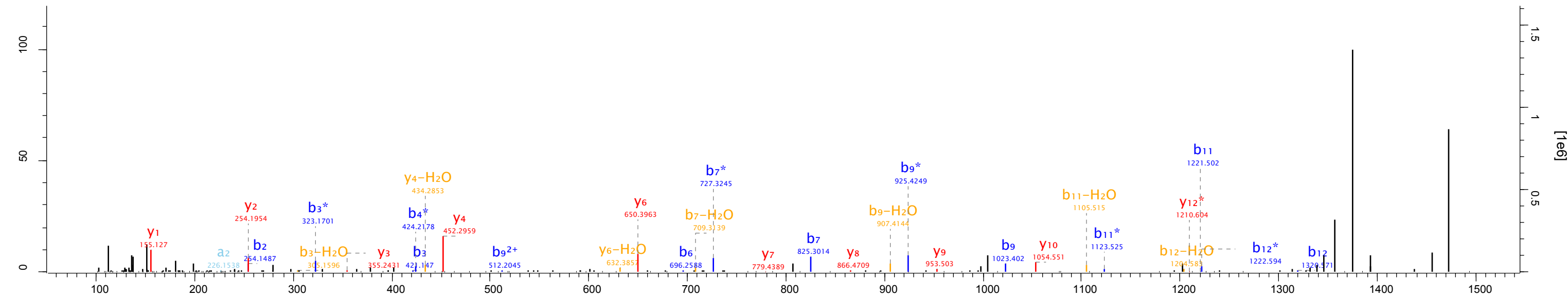




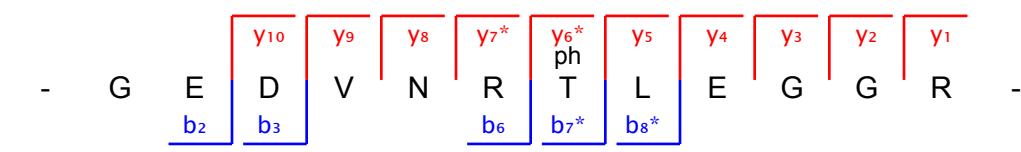
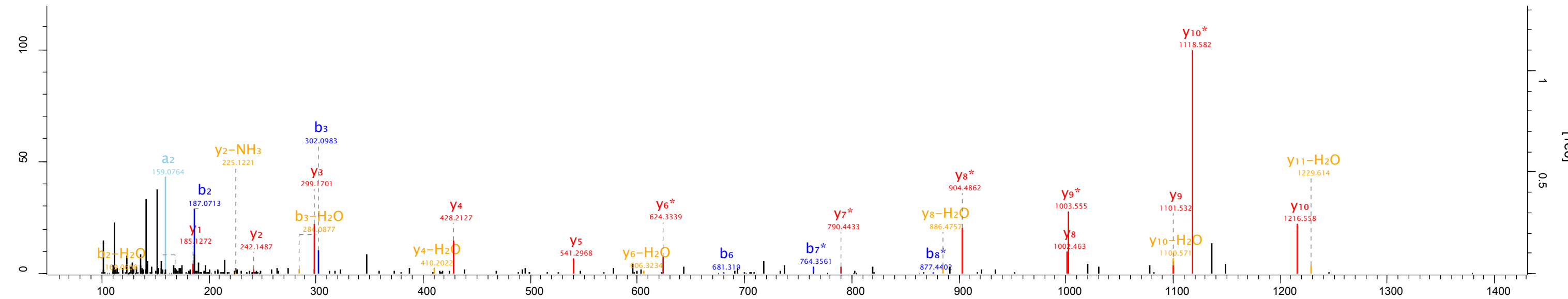
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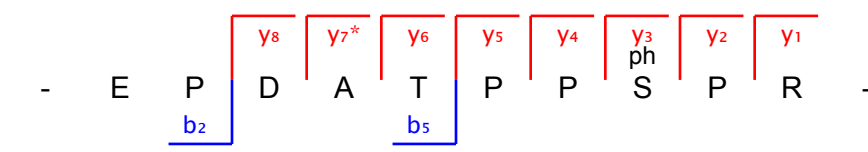
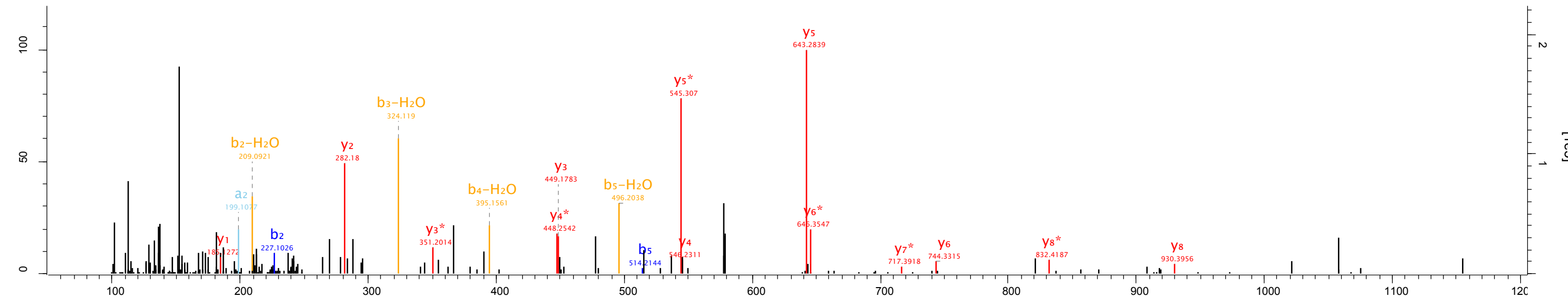
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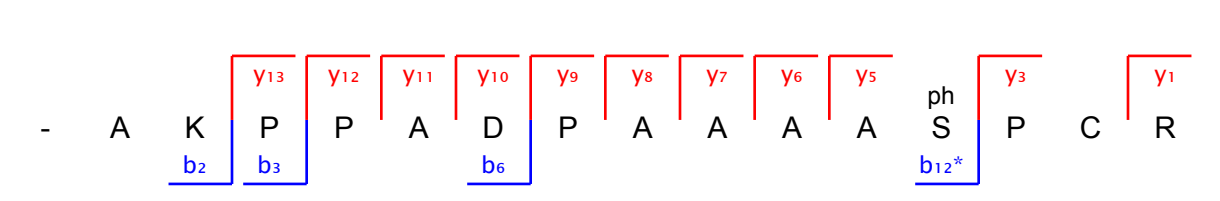
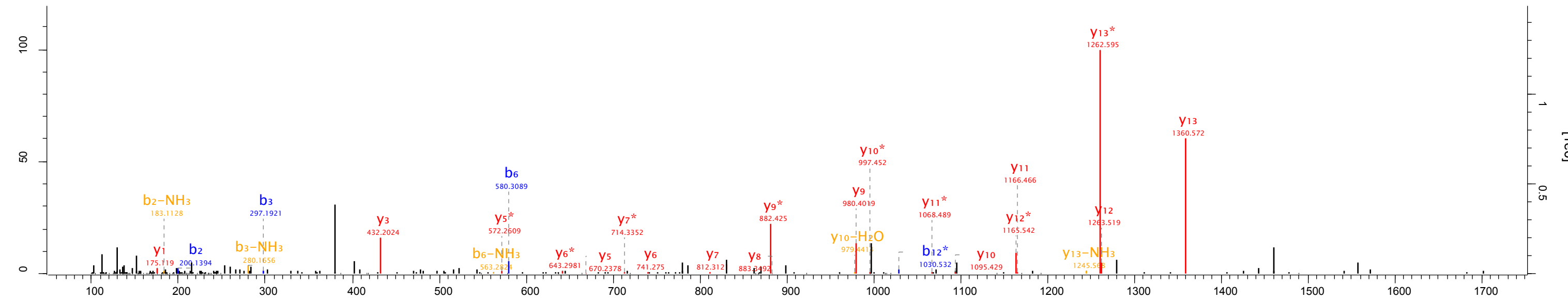
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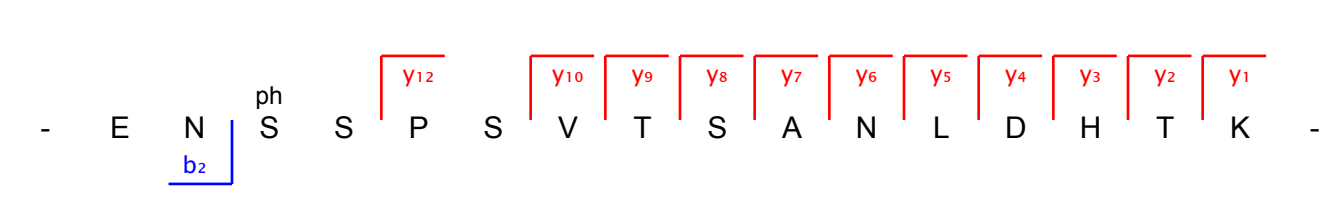
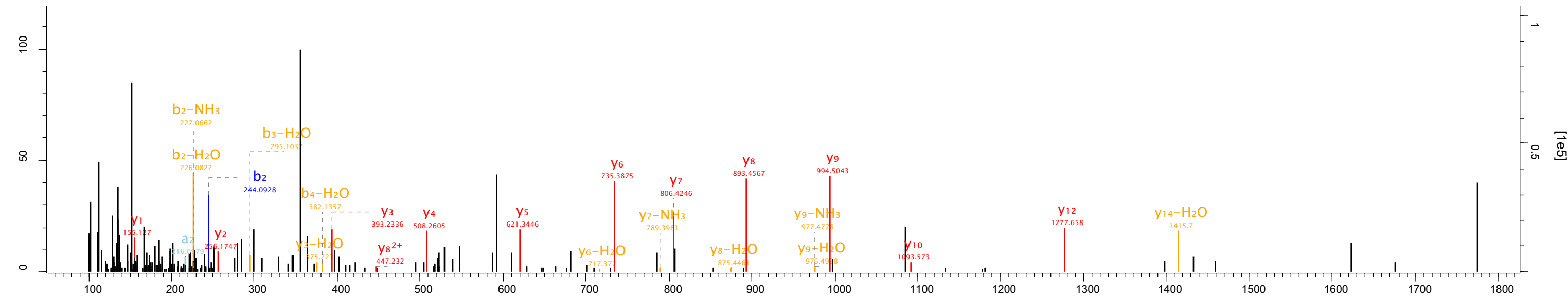
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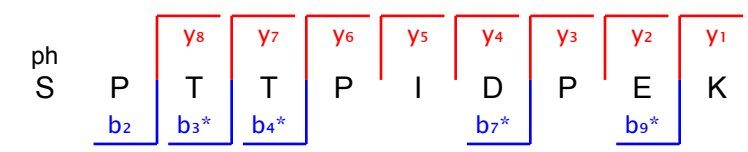
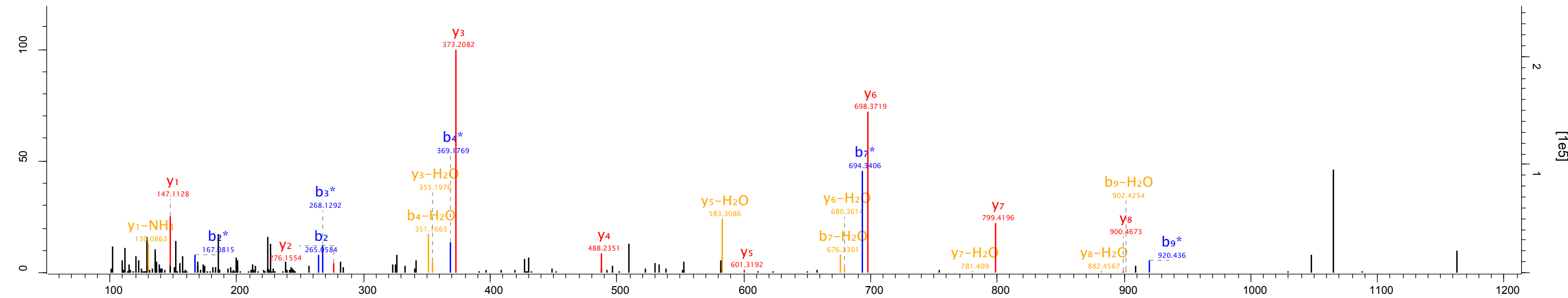
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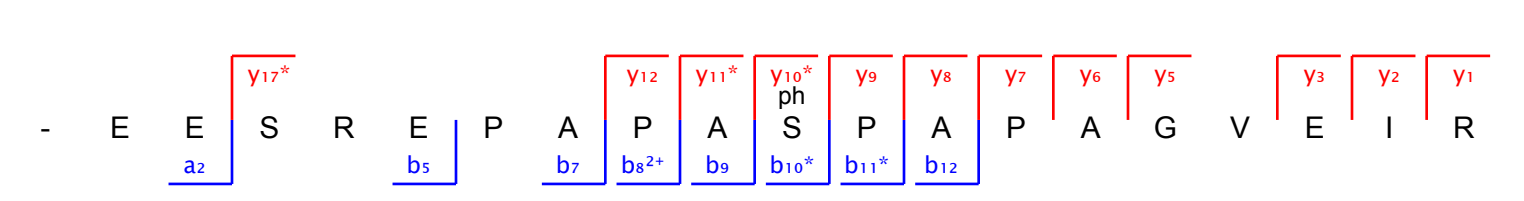
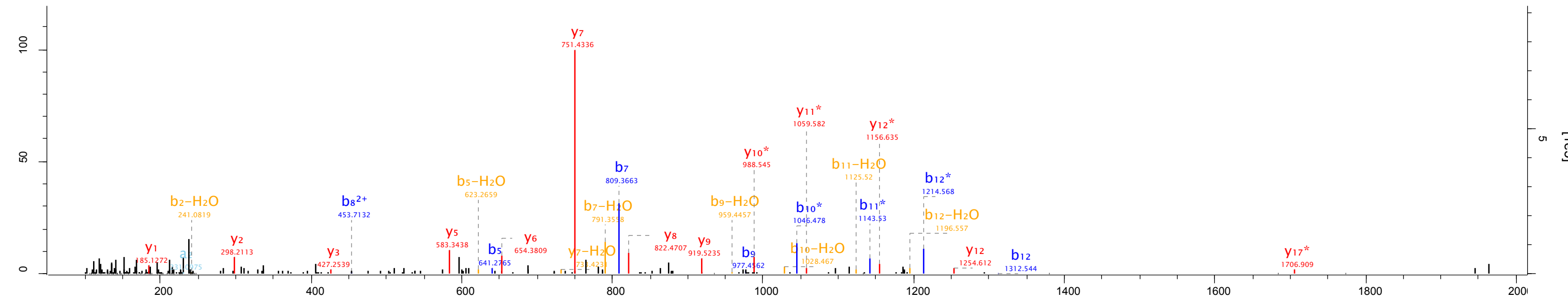


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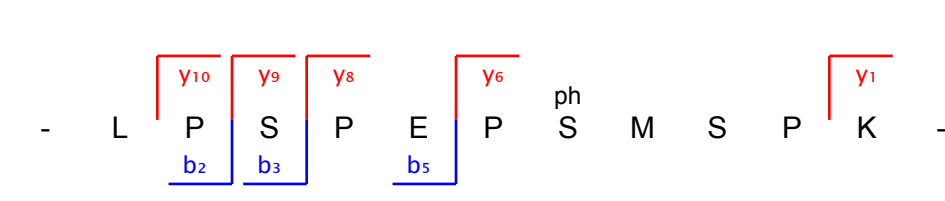
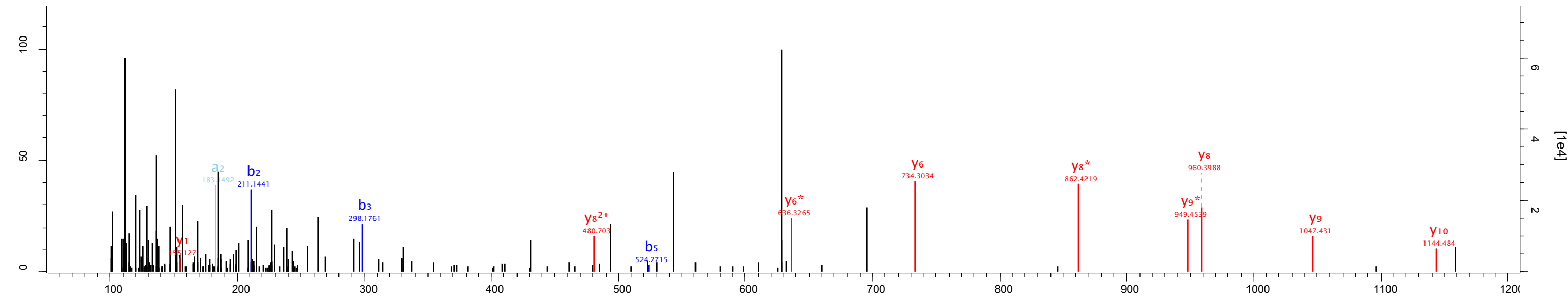


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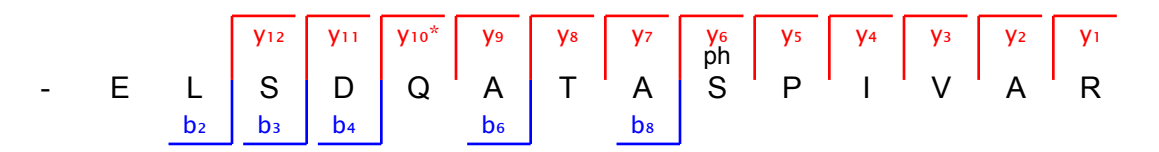
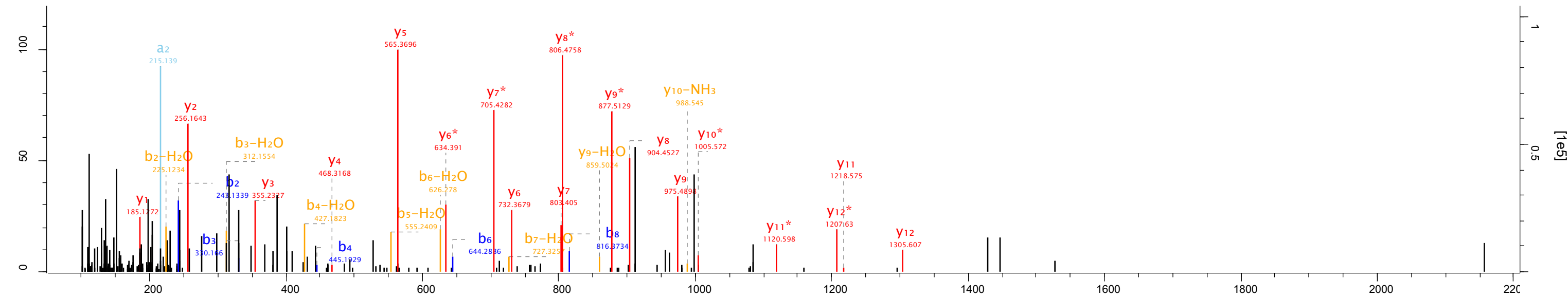
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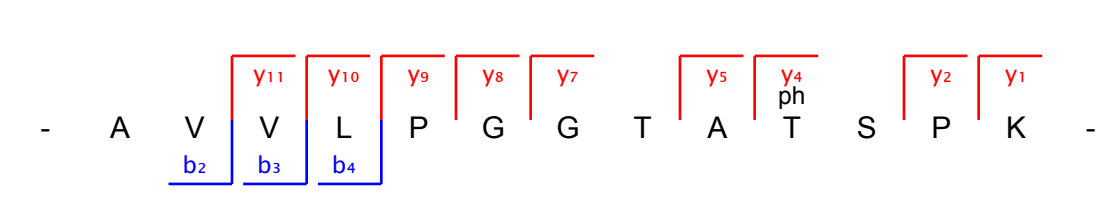
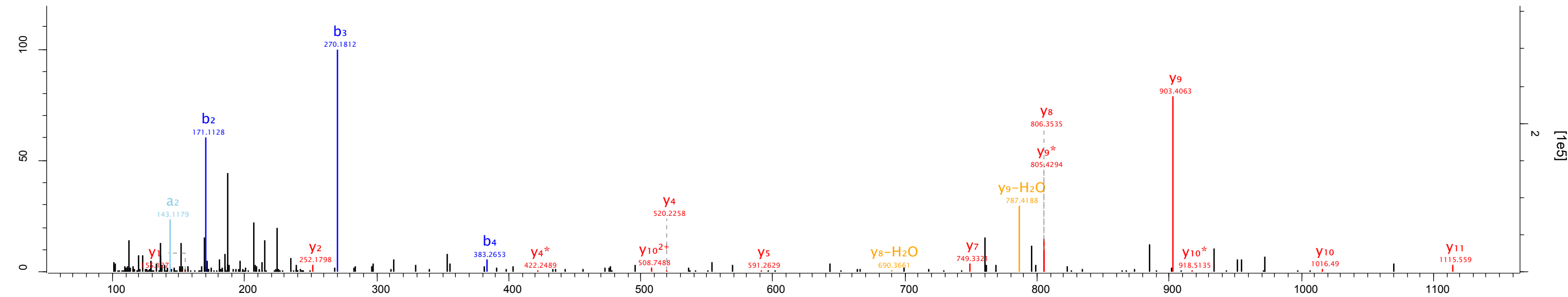
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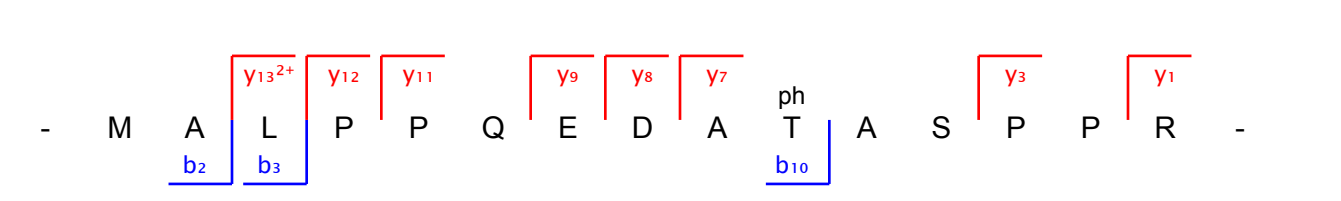
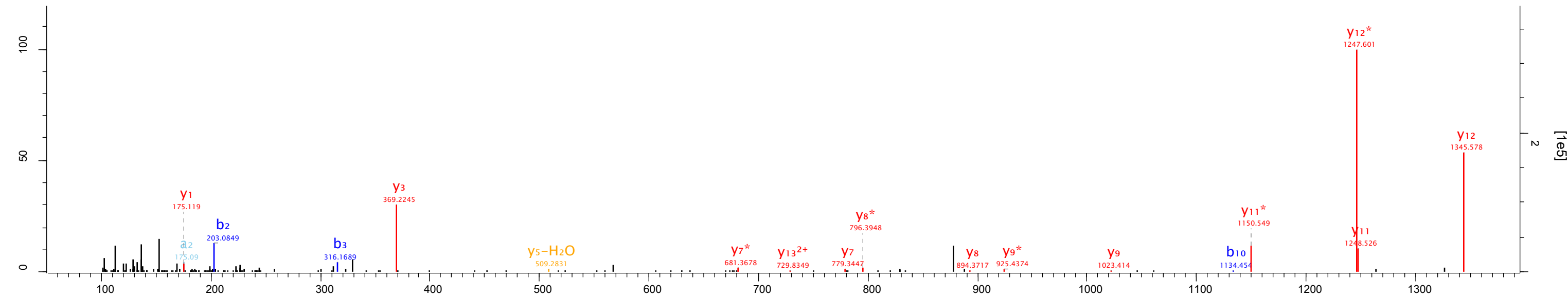
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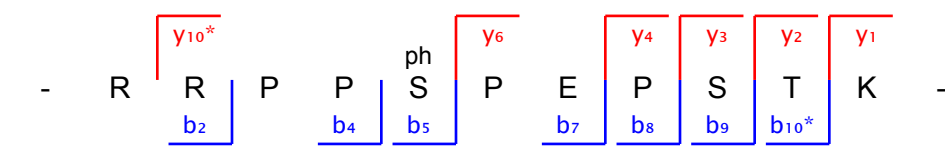
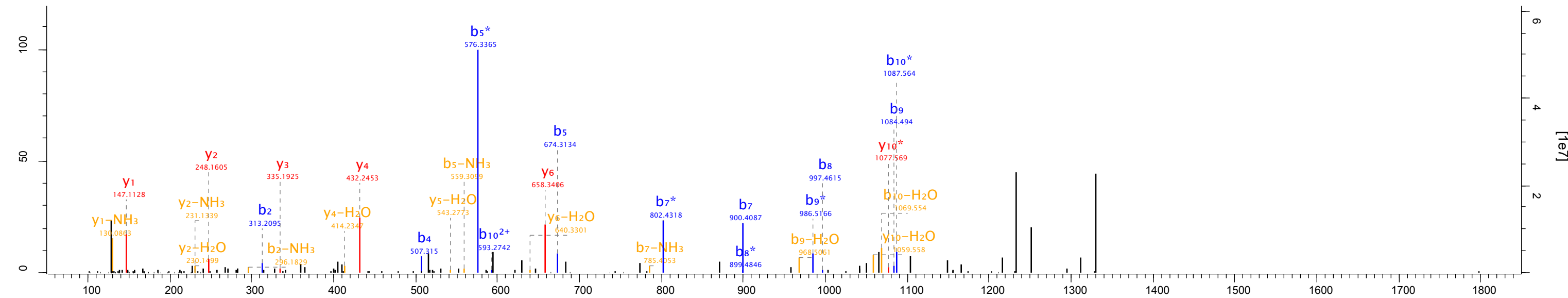
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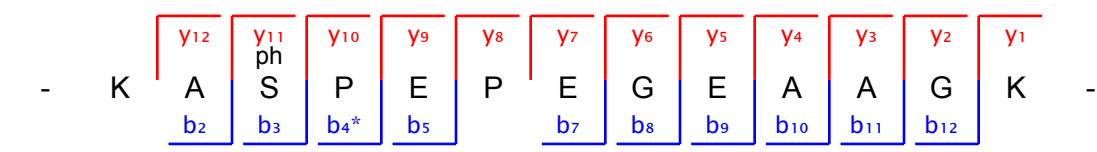
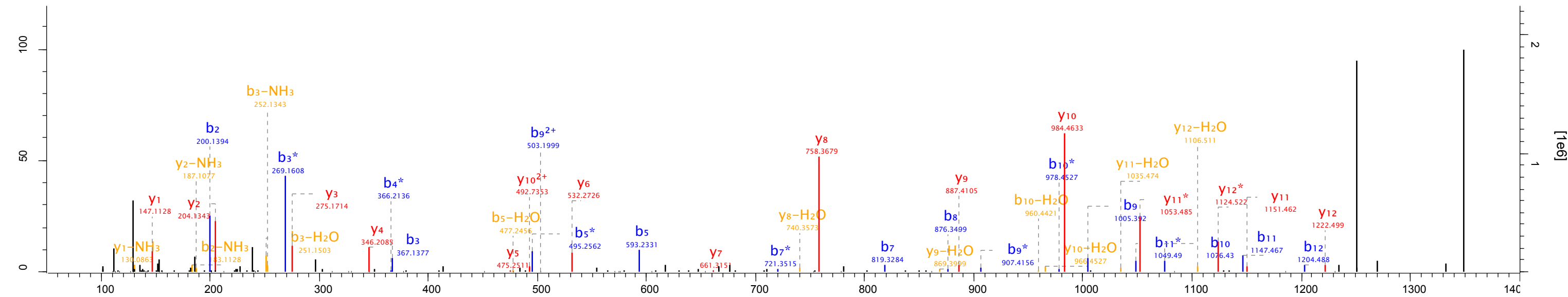
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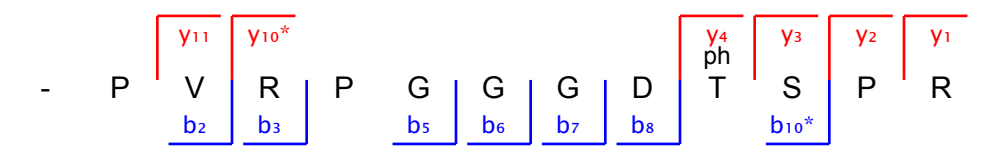
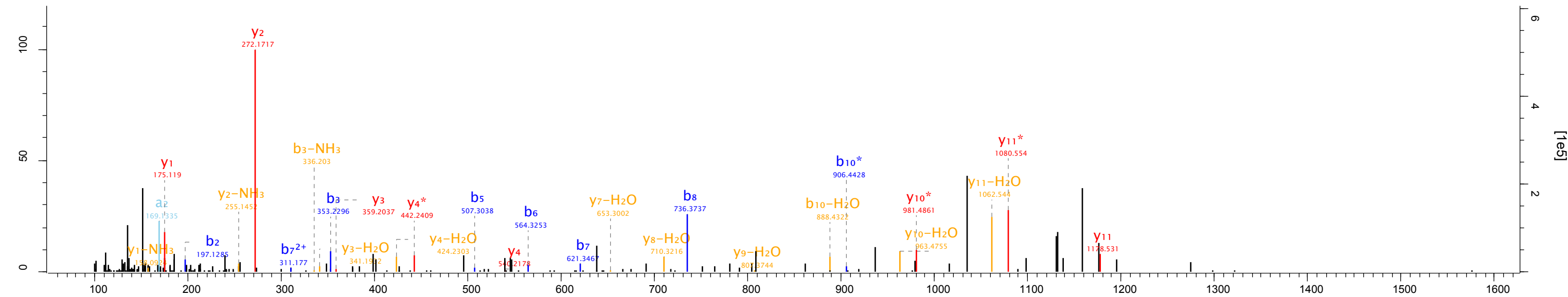
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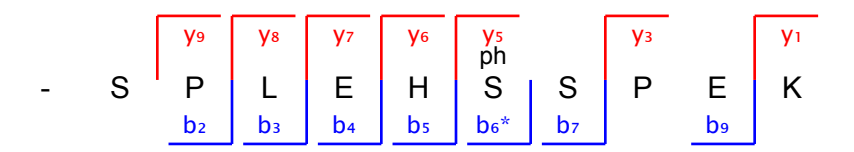
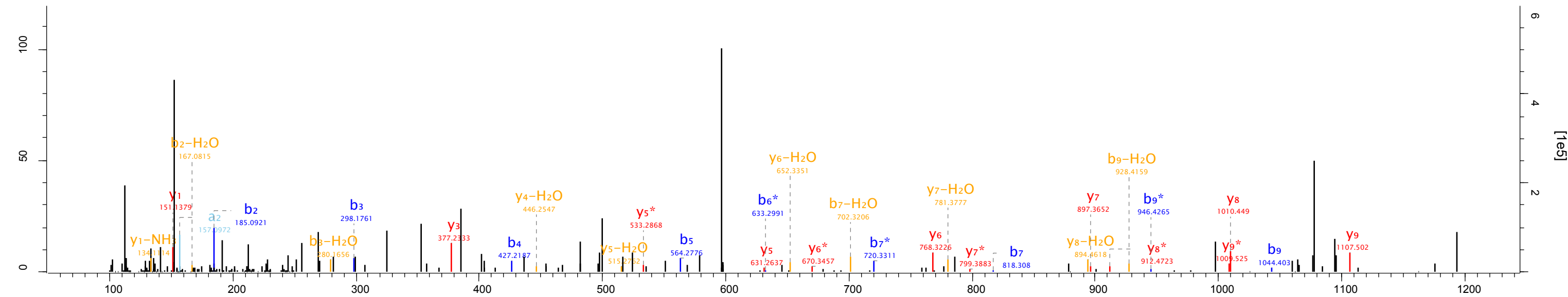
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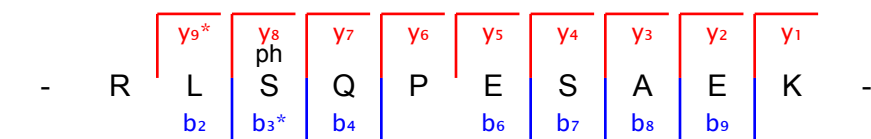
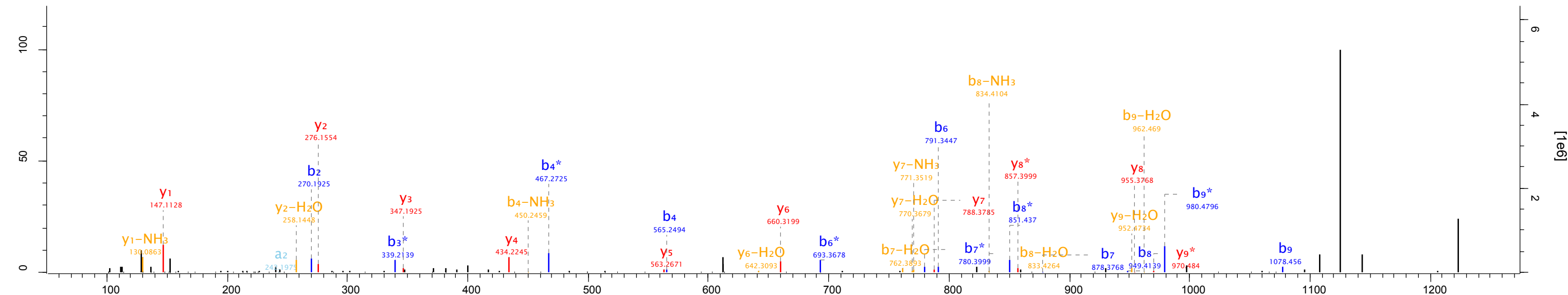


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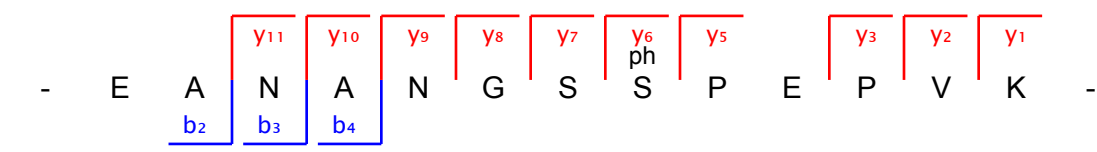
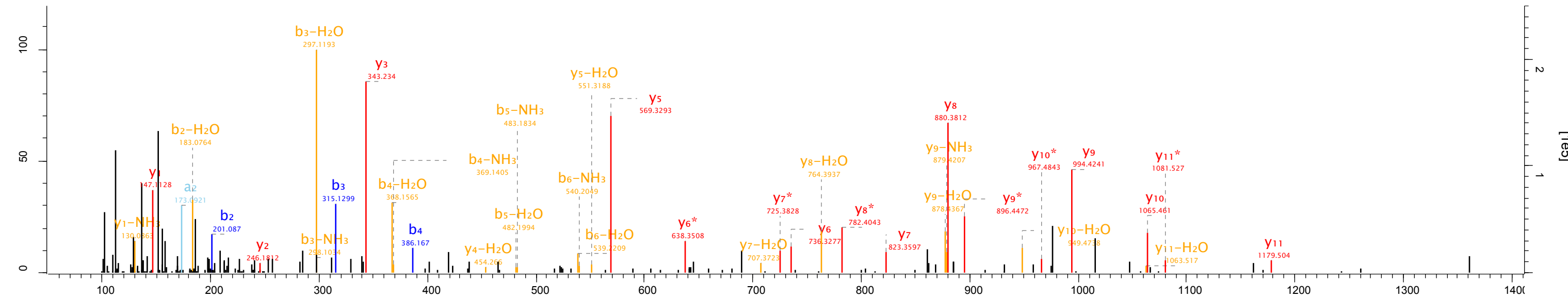


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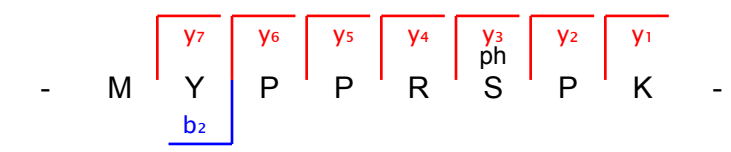
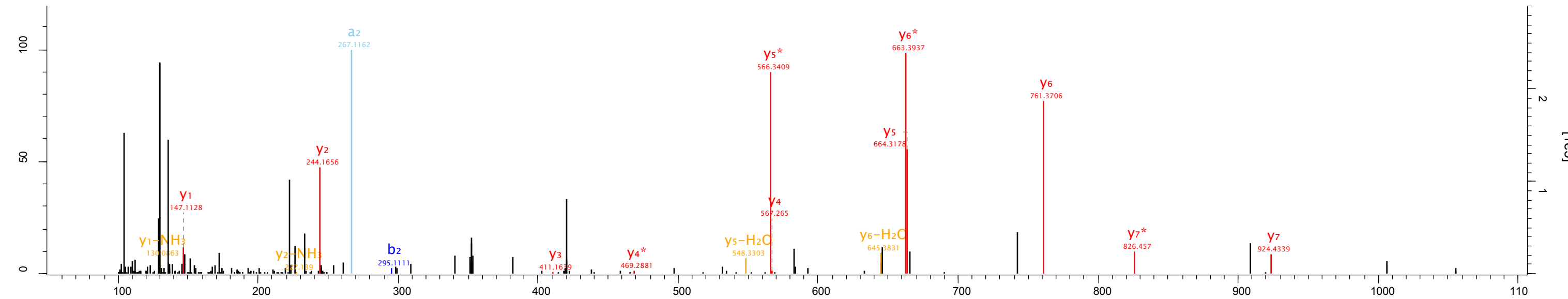




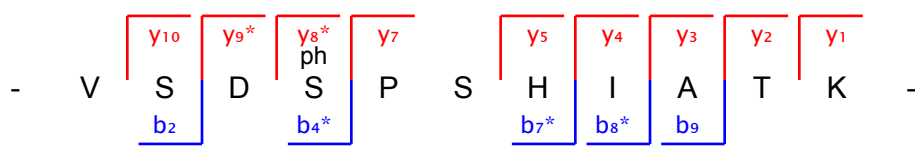
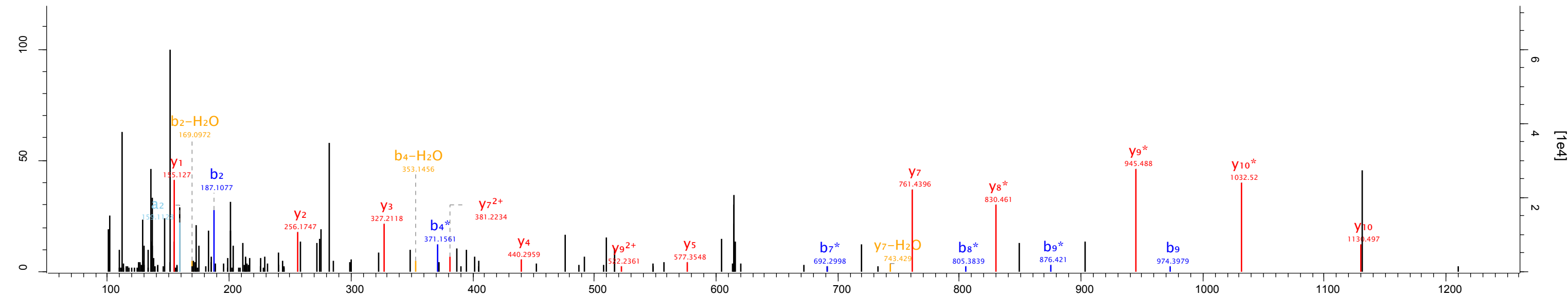
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 20171215_MaS_33SR_LMH_phospho_09
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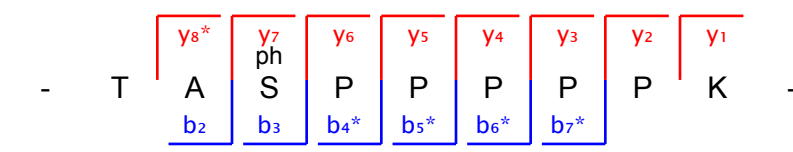
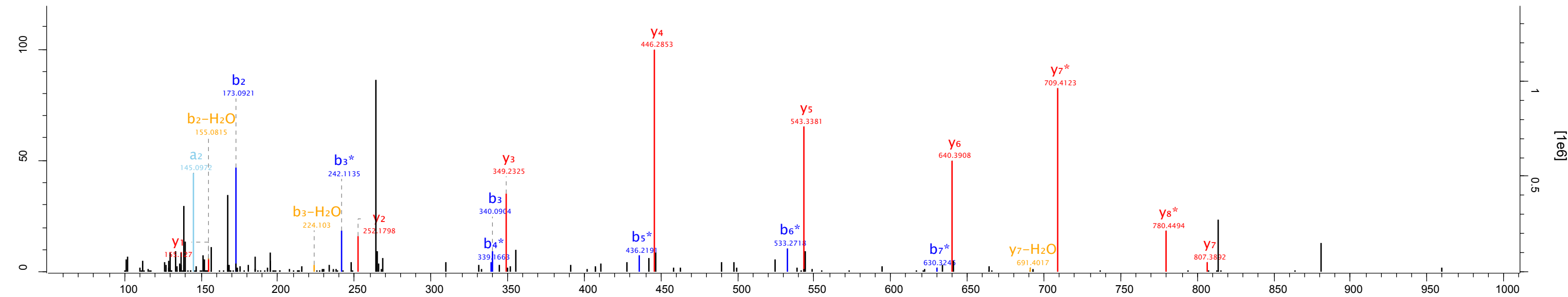
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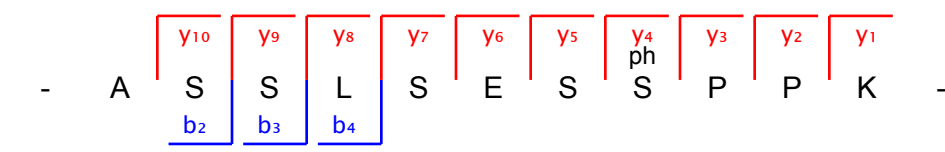
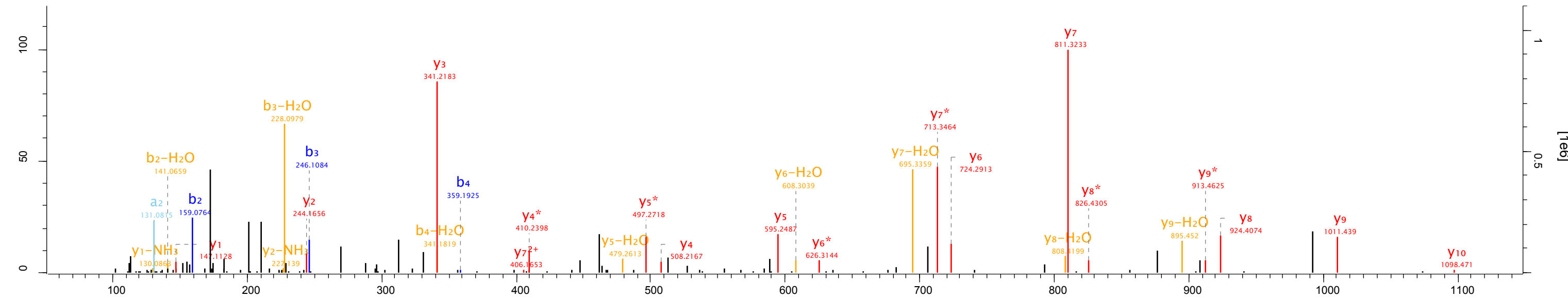
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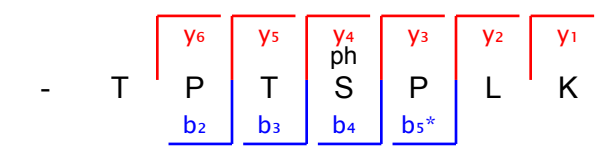
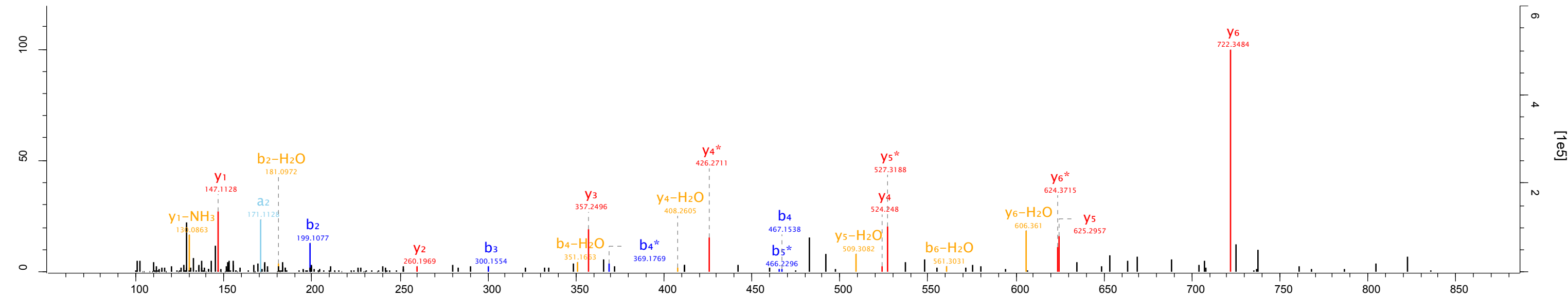
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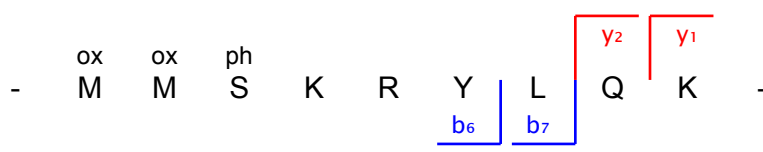
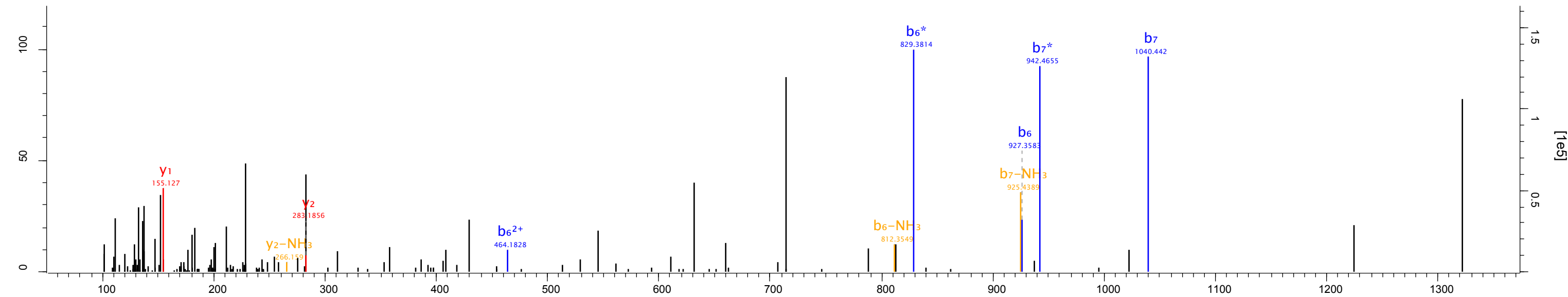
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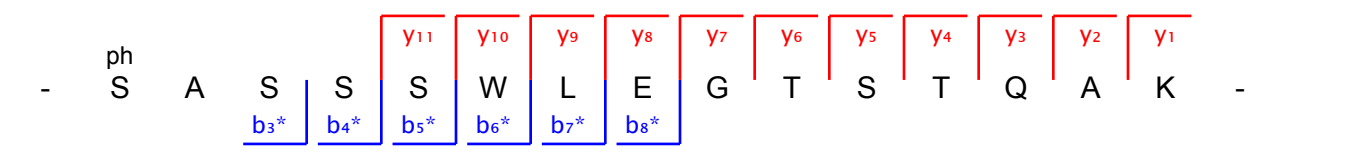
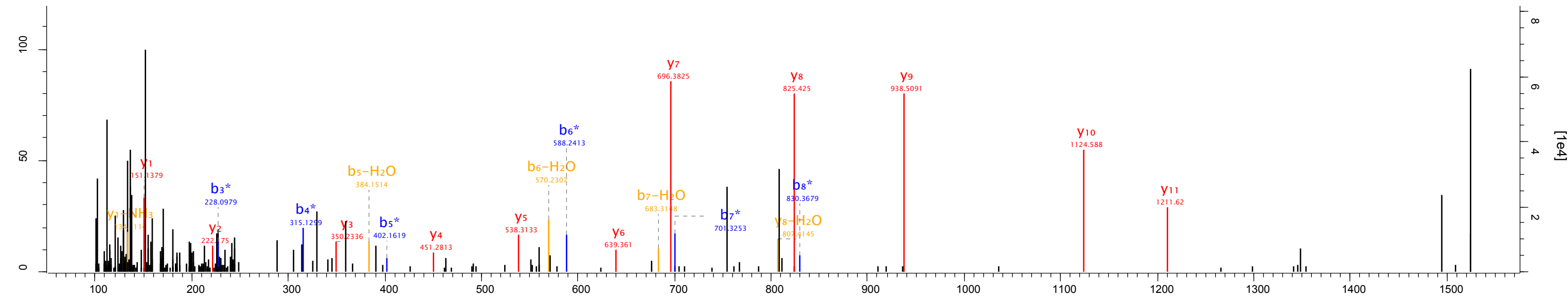
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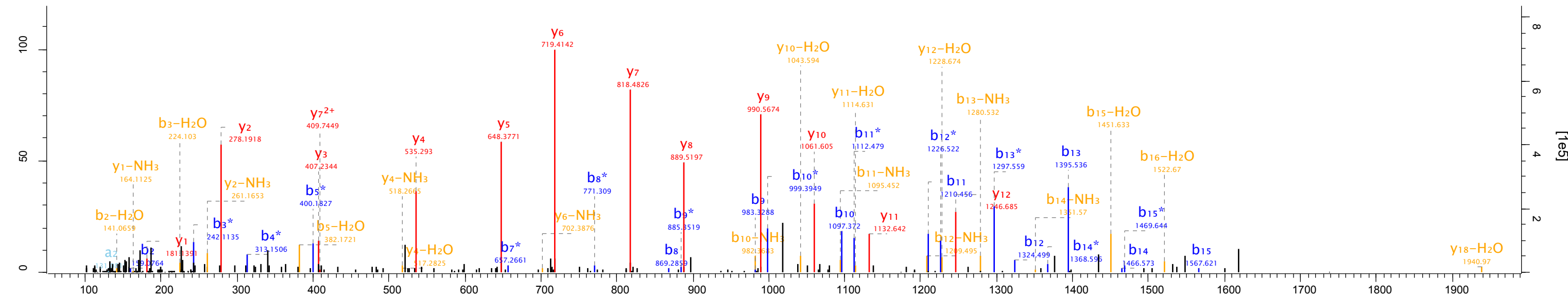


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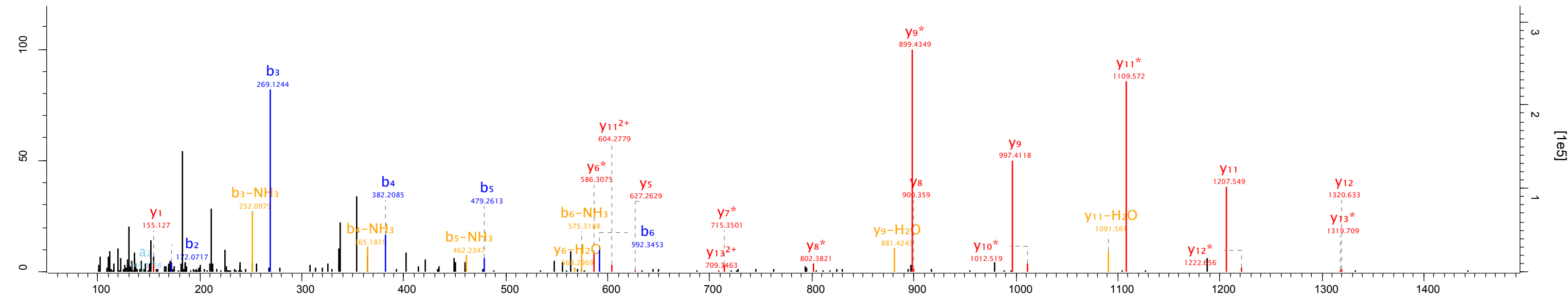


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ph

b₂ b₃^{*} b₄^{*} b₅^{*} b₇^{*} b₈ b₉ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄ b₁₅ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

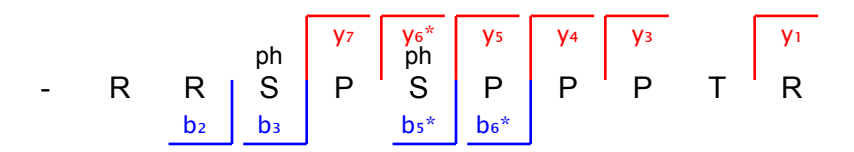
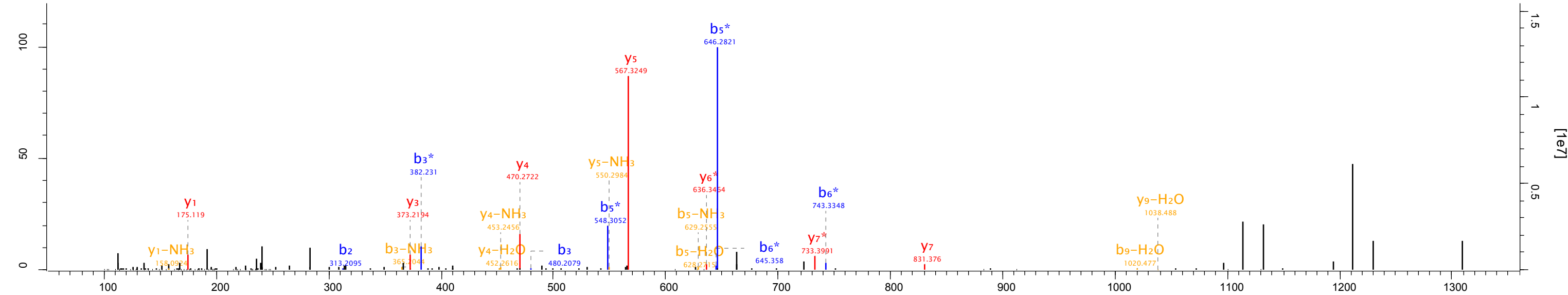
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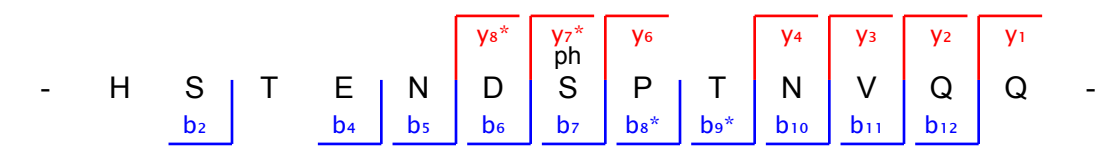
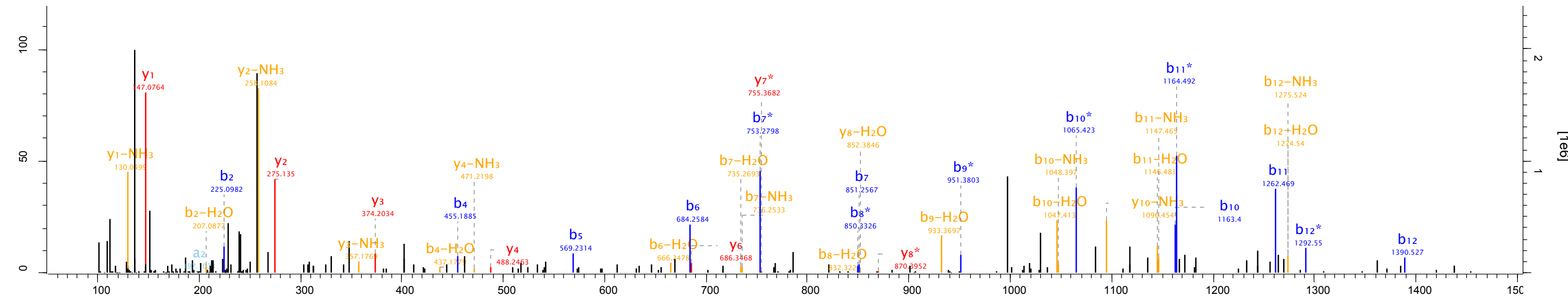
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20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
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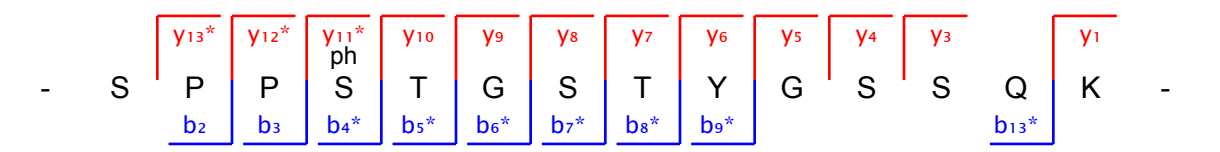
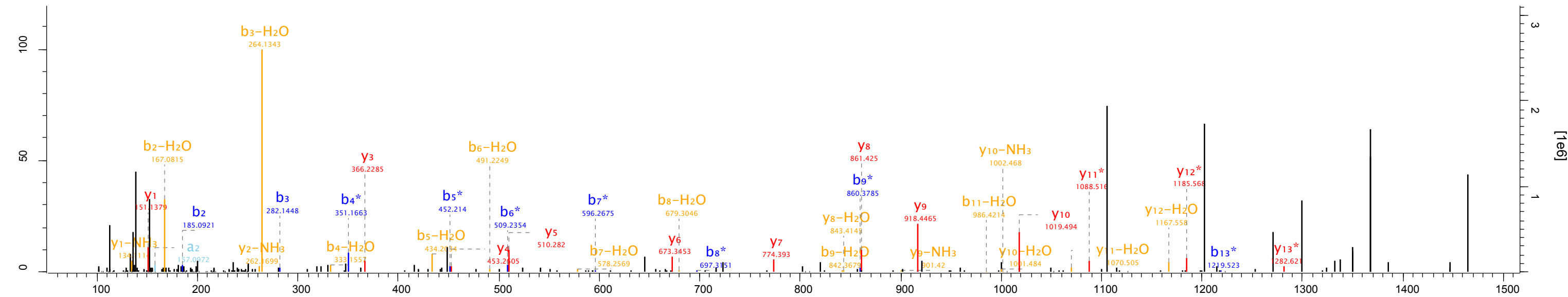


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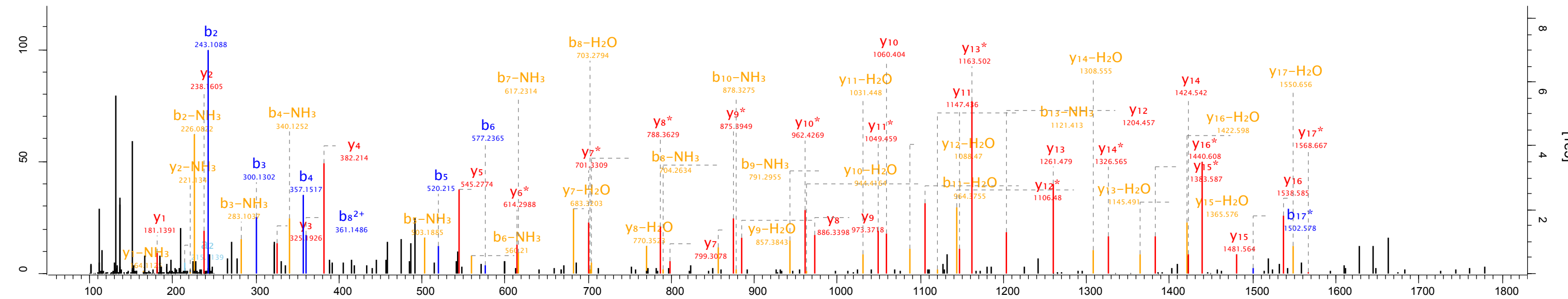


Raw file
20171215_MaS_33SR_LMH_phospho2_01

Scan 3175 Method FTMS; HCD Score 119.55 m/z 734.32 Gene names THRAP3

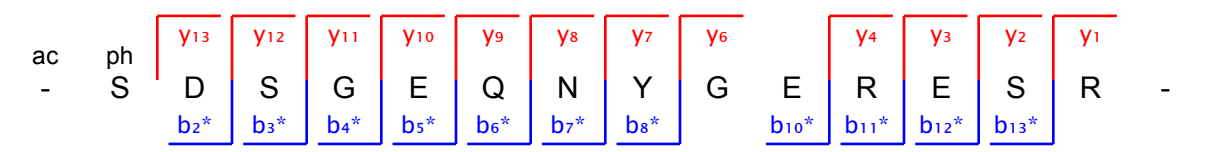
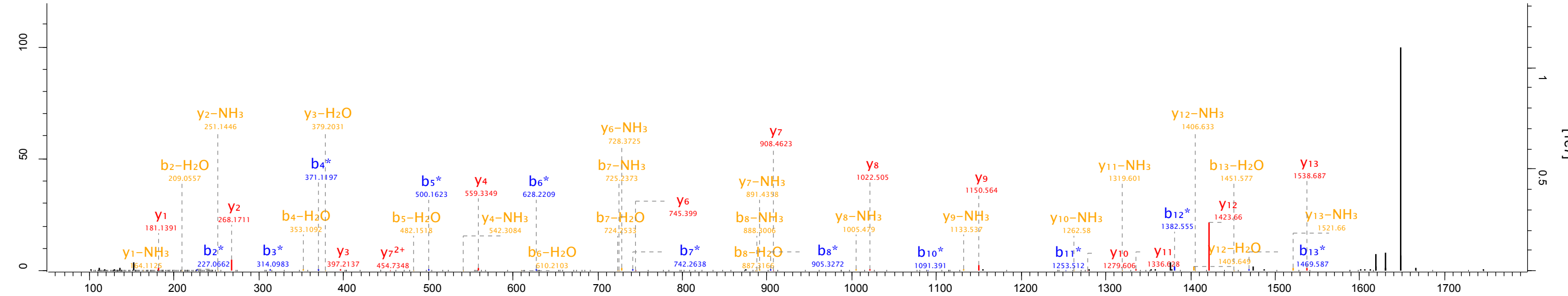


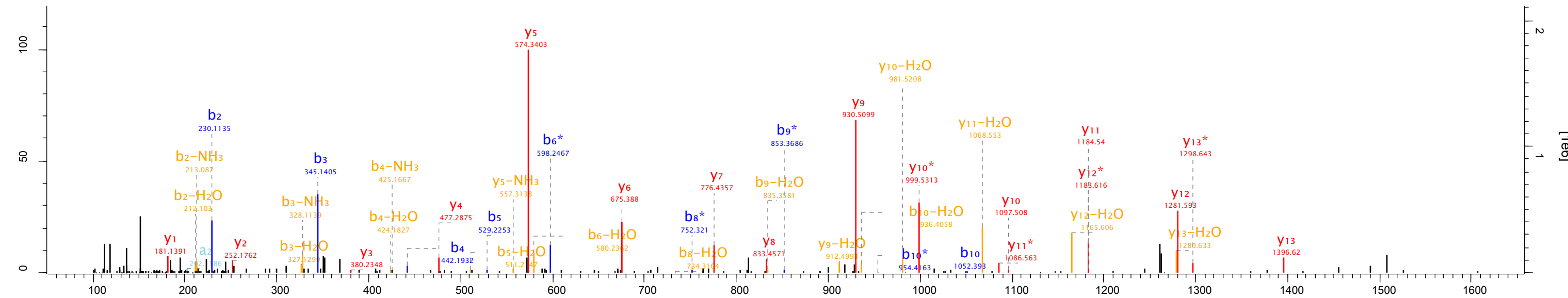
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Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_01 3415 FTMS; HCD 214.54 874.85 TRA2B



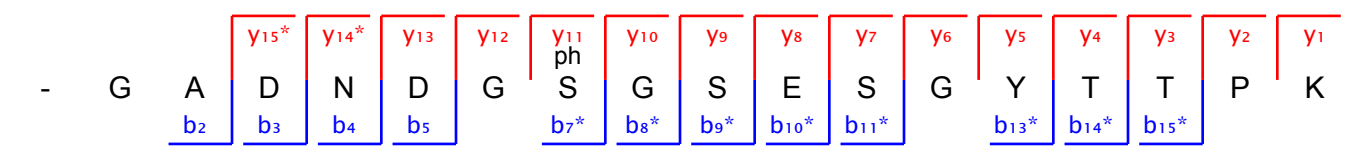
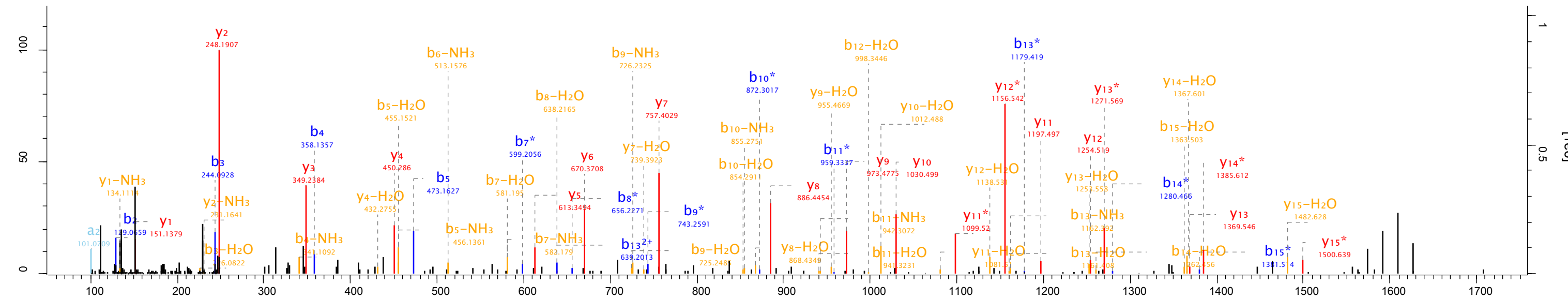


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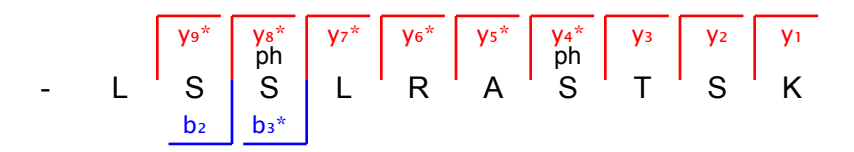
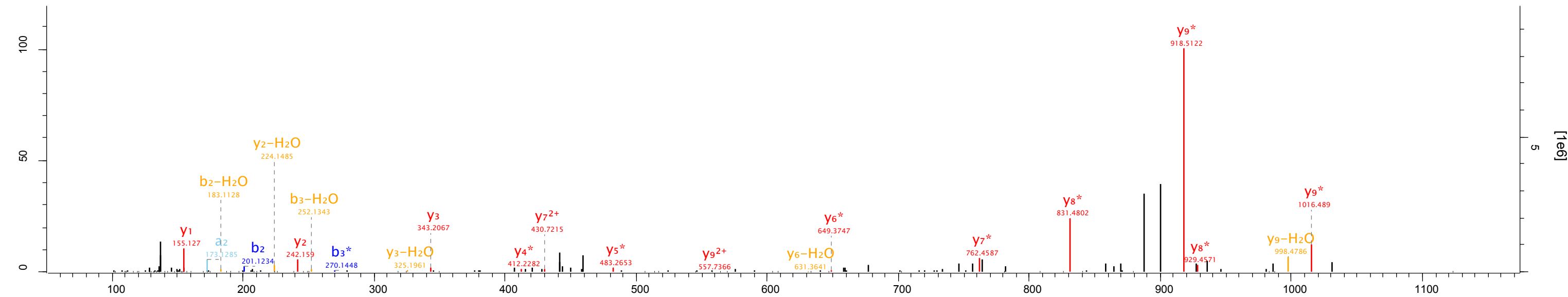
b₂
b₃
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b₈*
b₉*
b₁₀

y₁₃
y₁₂
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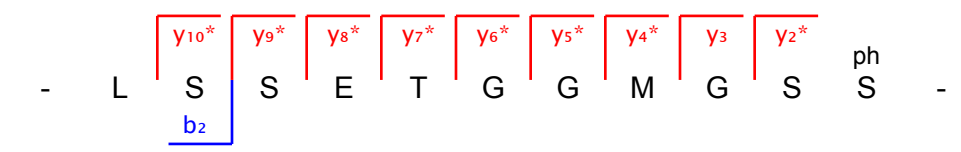
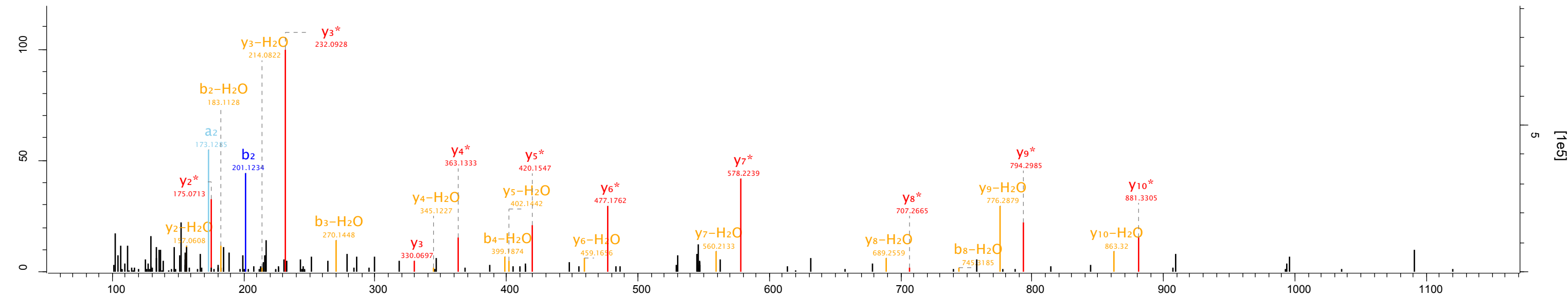
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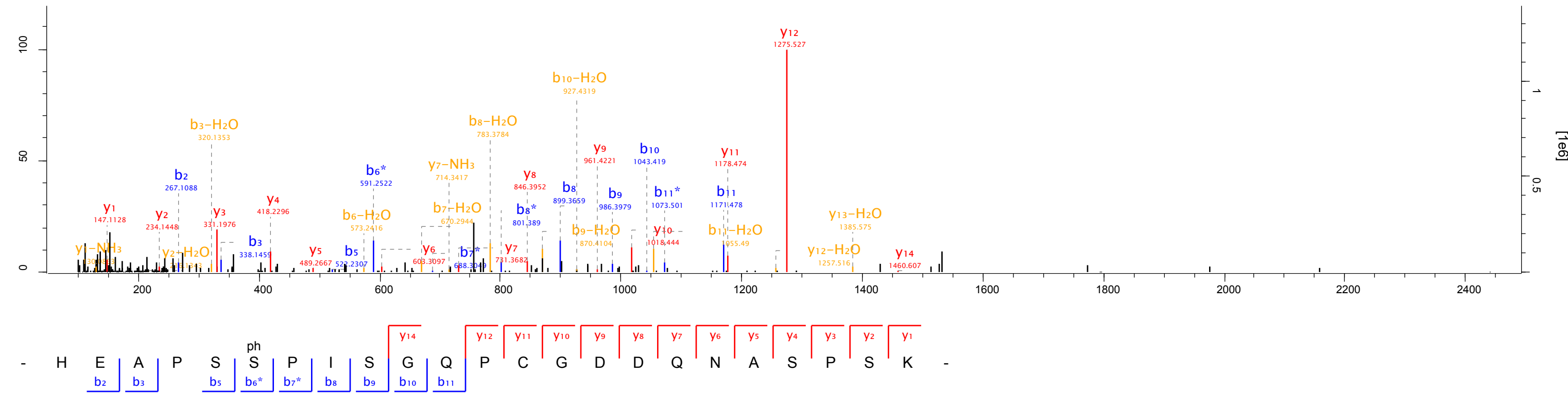


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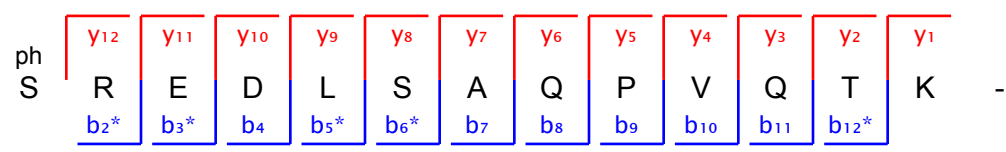
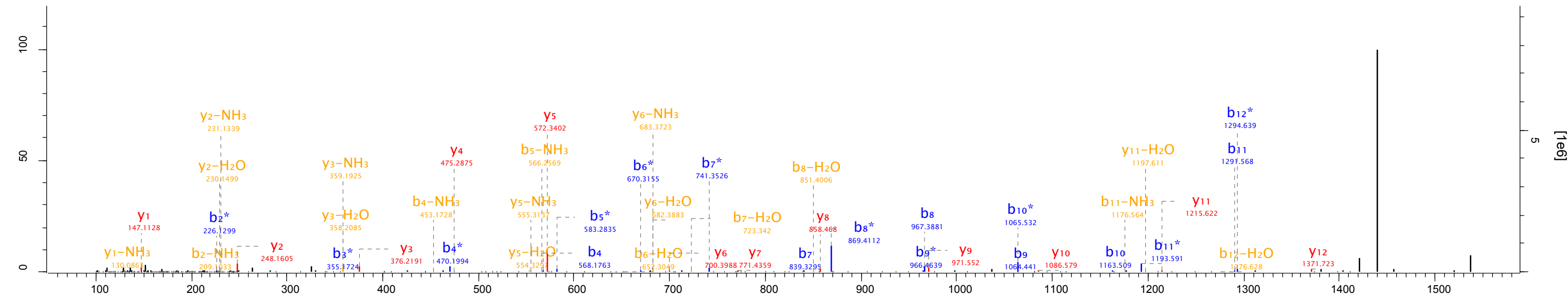


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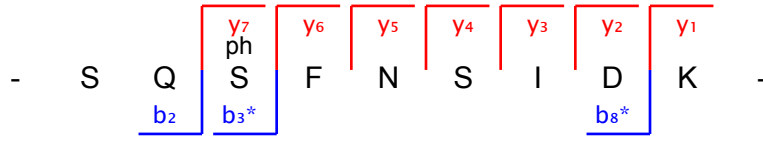
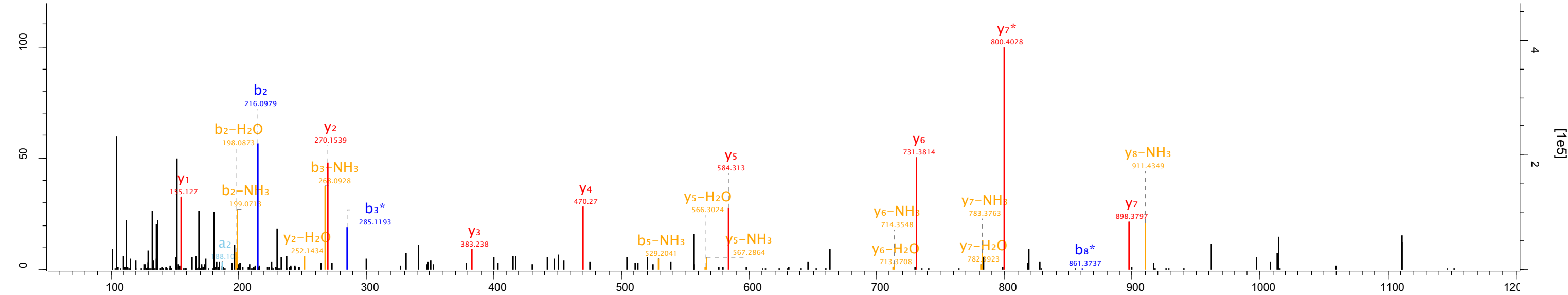
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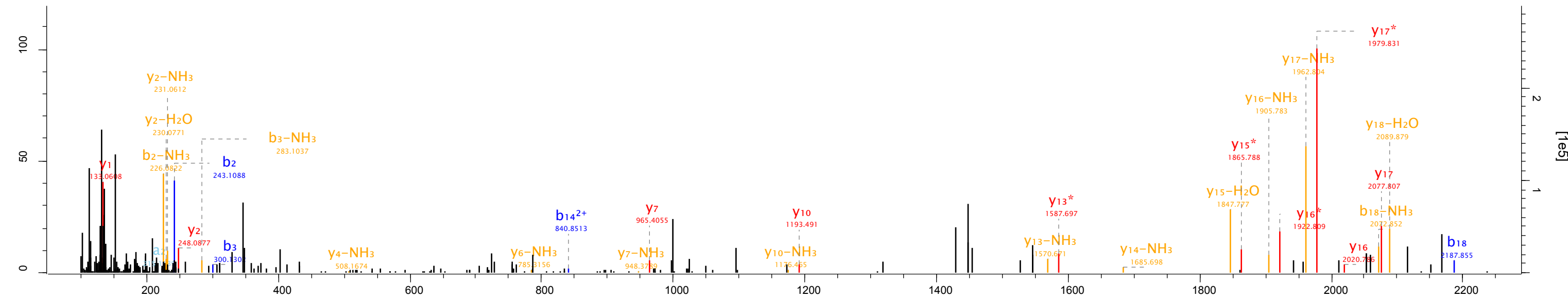
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20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
5865	FTMS; HCD	100.93	557.24	NAV3



Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 6225 Method FTMS; HCD Score 83.87 m/z 774.31 Gene names RBM3

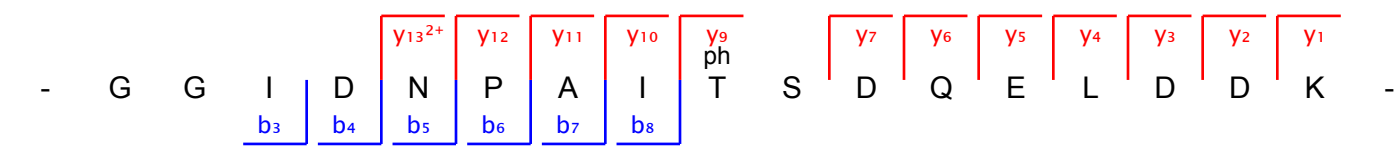
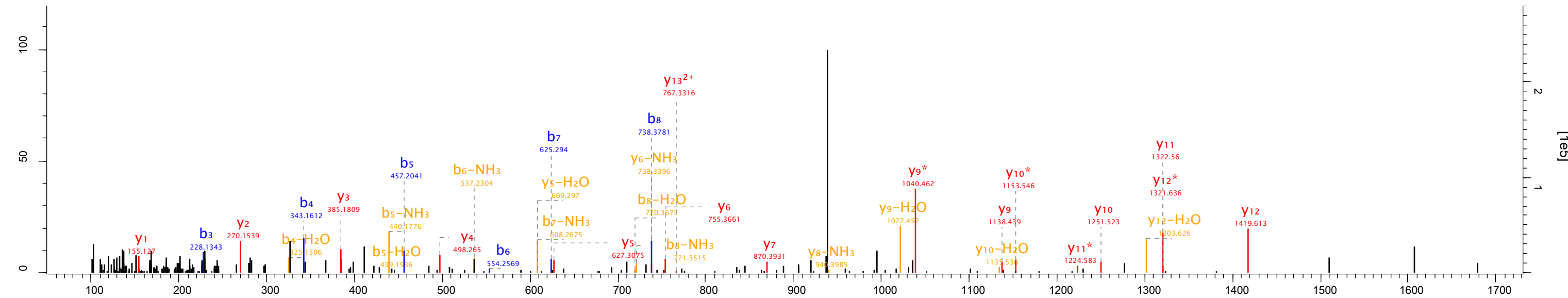


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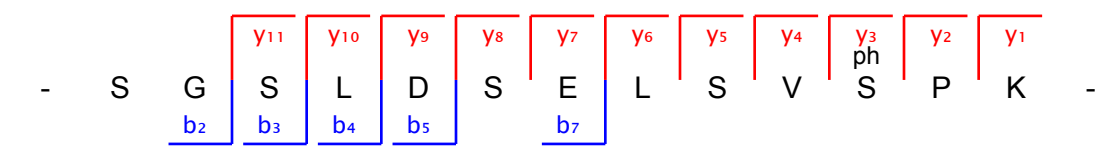
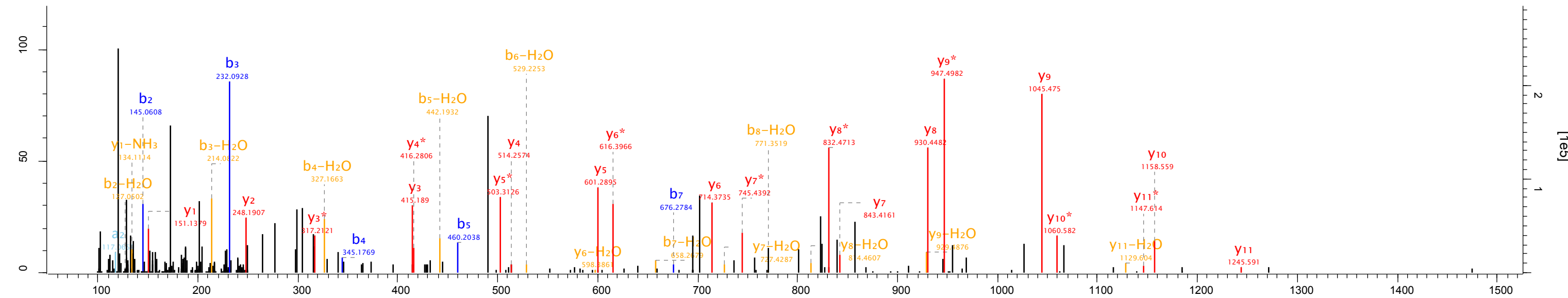
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- b2: N-Q
- b3: Q-G
- y1: G-G
- y2: G-Y
- y7: Y-R
- y10: S-G
- y13*: R-D
- y15*: Y-D
- y16: G-G
- y17: G-G
- b14²⁺: R-D
- b18: Y-D
- y1: D-N

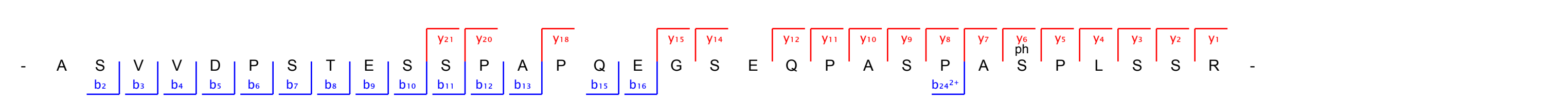
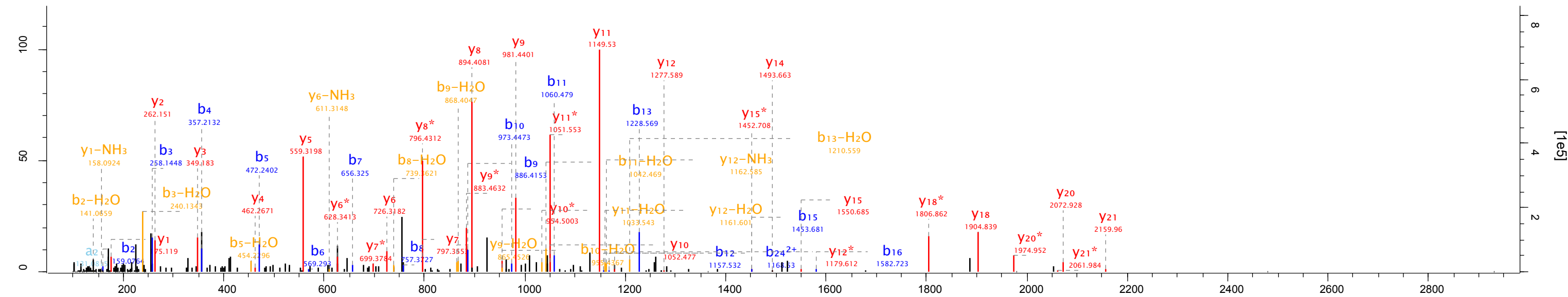
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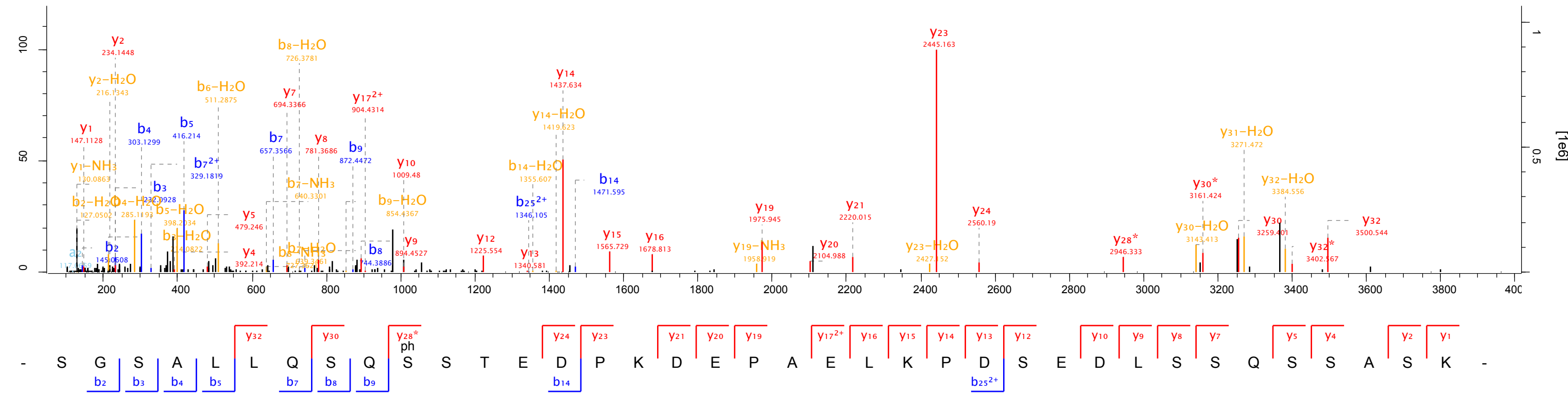
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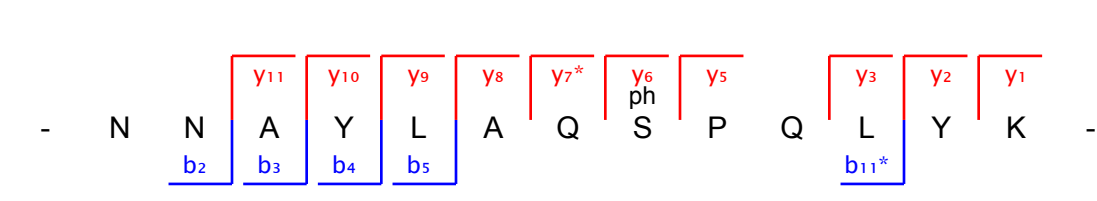
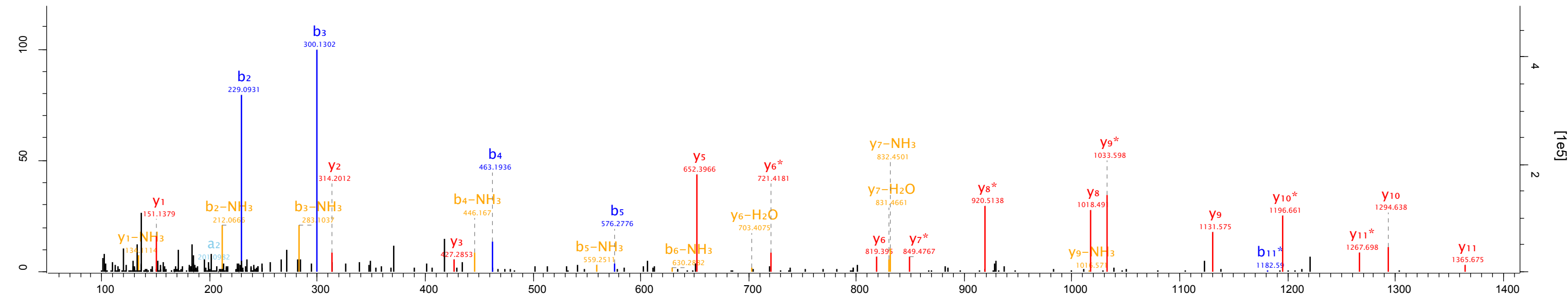
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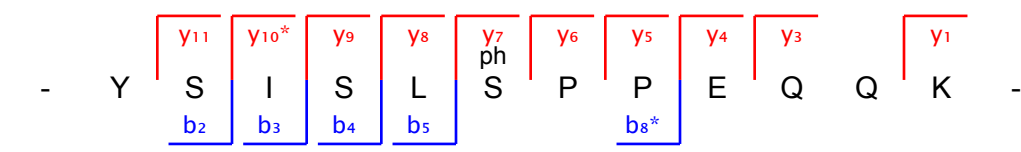
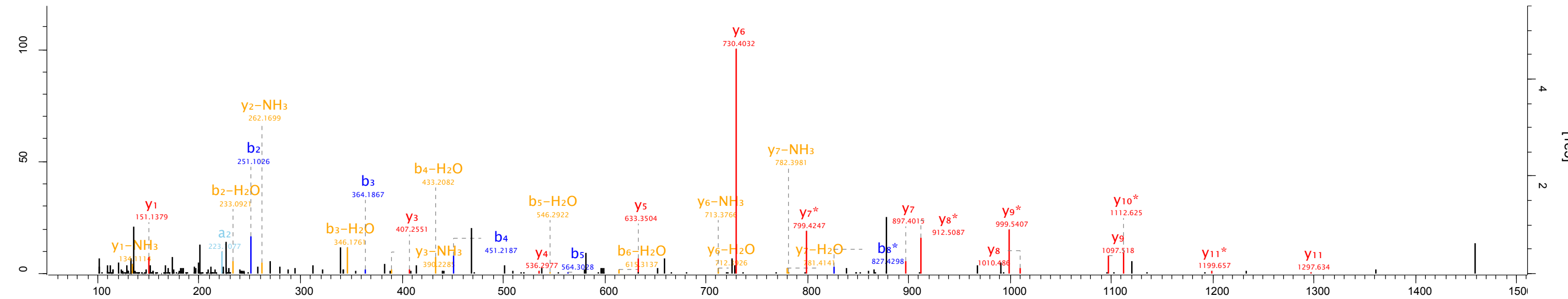
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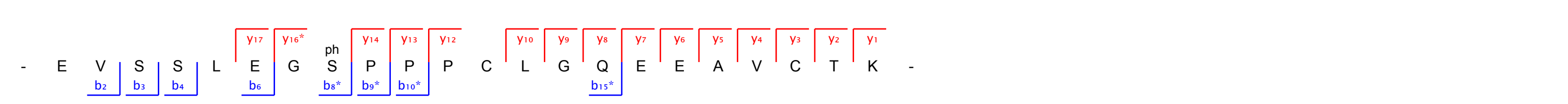
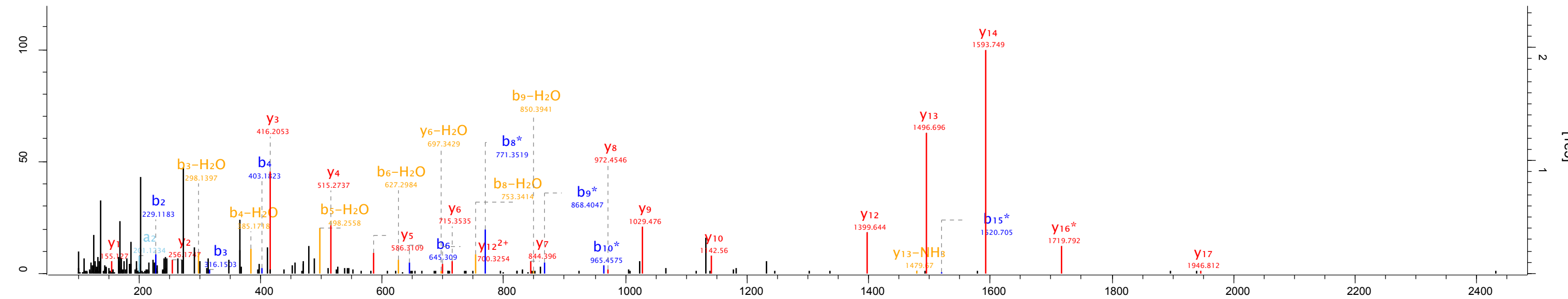
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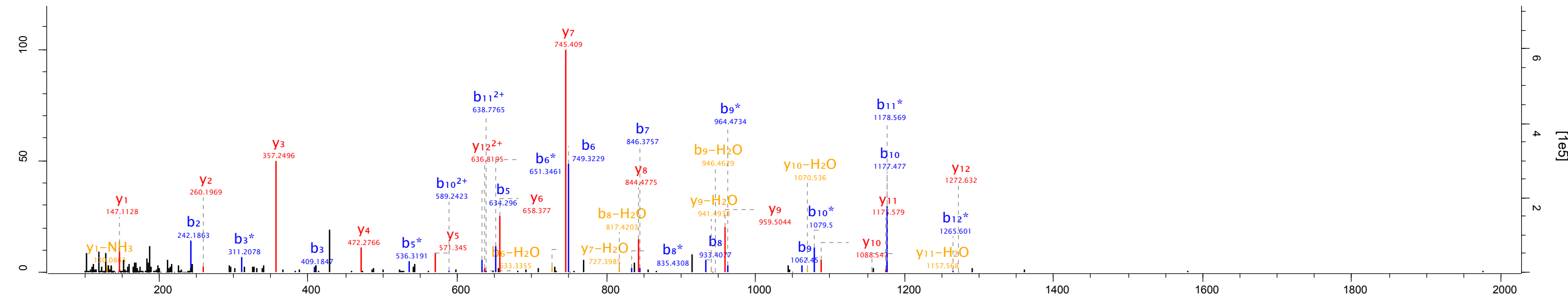


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11825 Method FTMS; HCD Score 110.84 m/z 730.85 Gene names ACAP2



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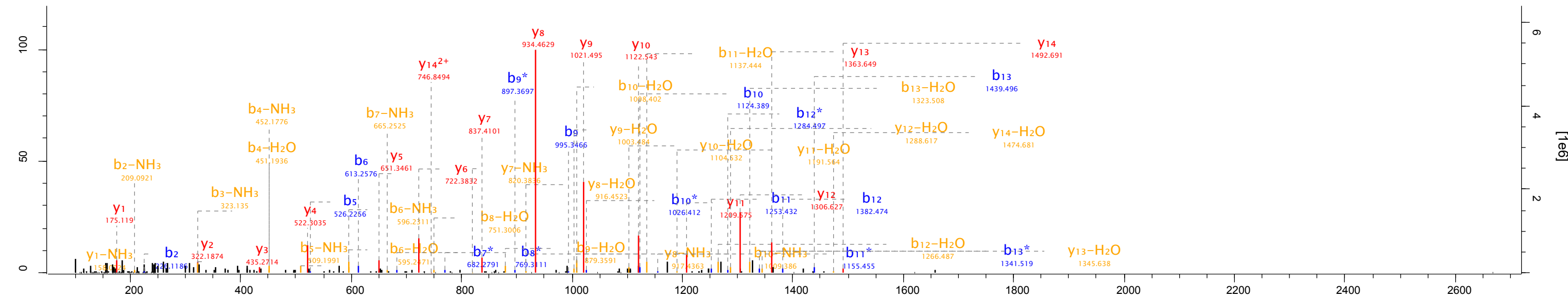
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b₂ b₃ b₅ b₆ b₇ b₈ b₉ b₁₀ b₁₁* b₁₂*

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

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20171215_MaS_33SR_LMH_phospho2_02

Scan 13435 Method FTMS; HCD Score 149.35 m/z 916.04 Gene names MAGEA4



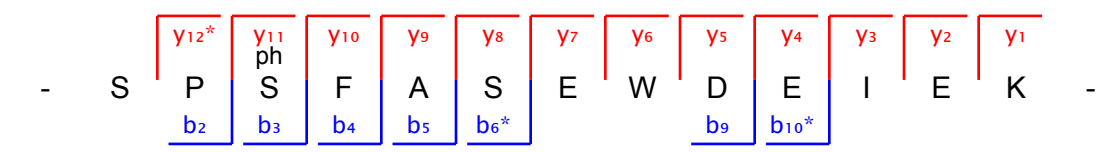
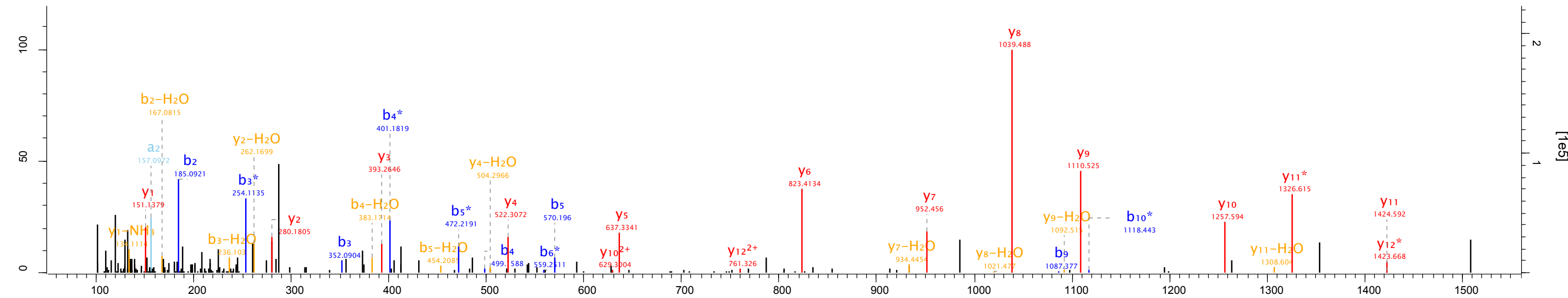
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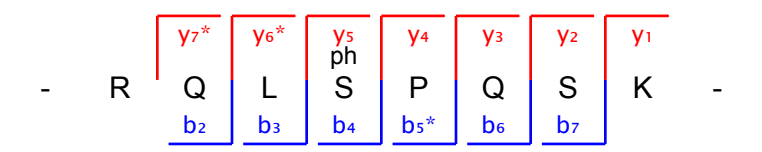
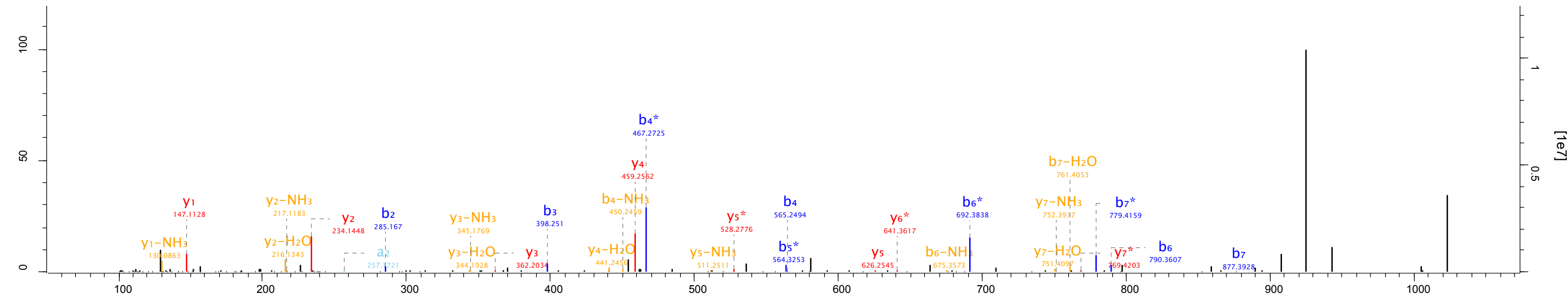
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y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1

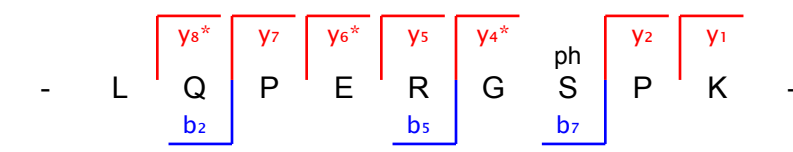
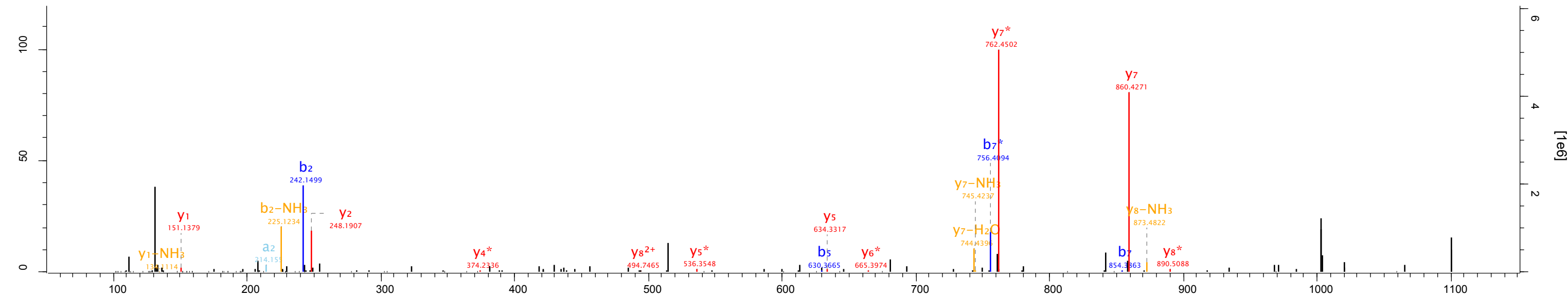
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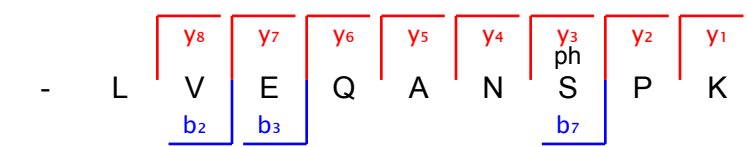
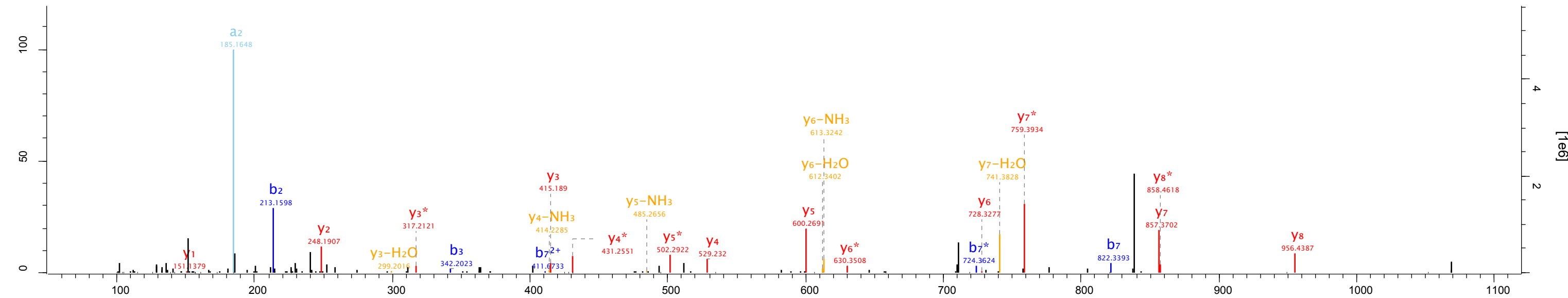
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 20171215_MaS_33SR_LMH_phospho2_02
 Scan 2045 Method FTMS; HCD Score 63.91 m/z 551.29 Gene names ACIN1



Raw file

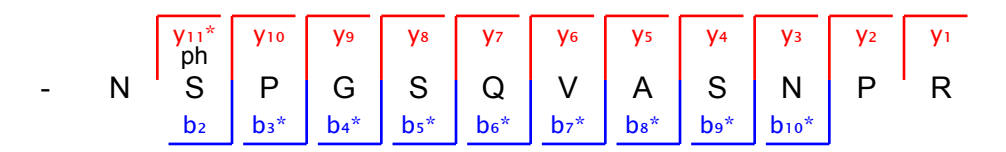
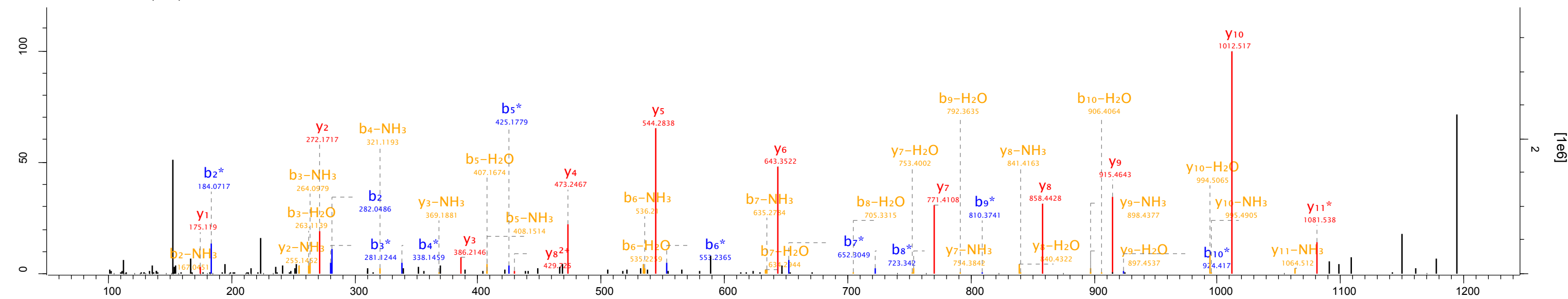
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Scan	Method	Score	m/z	Gene names
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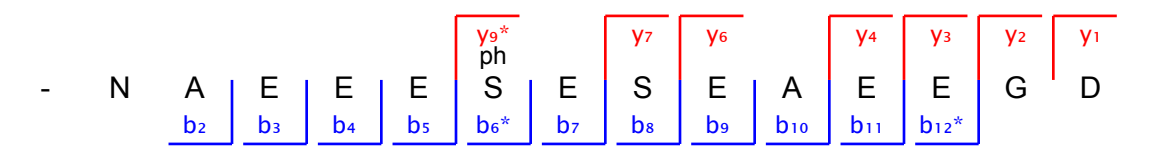
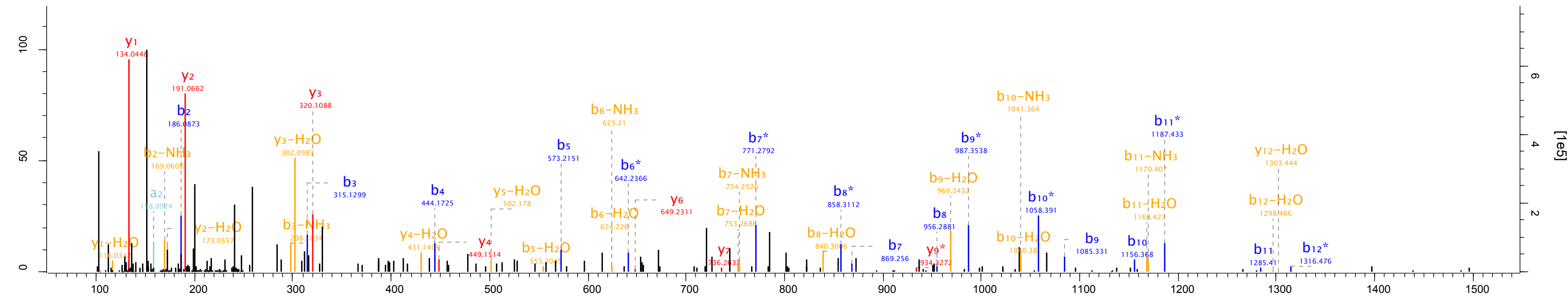
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Scan Method Score m/z Gene names
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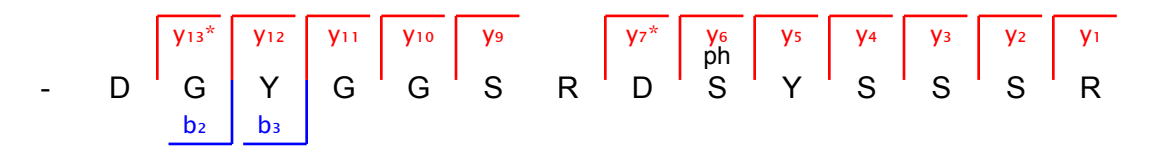
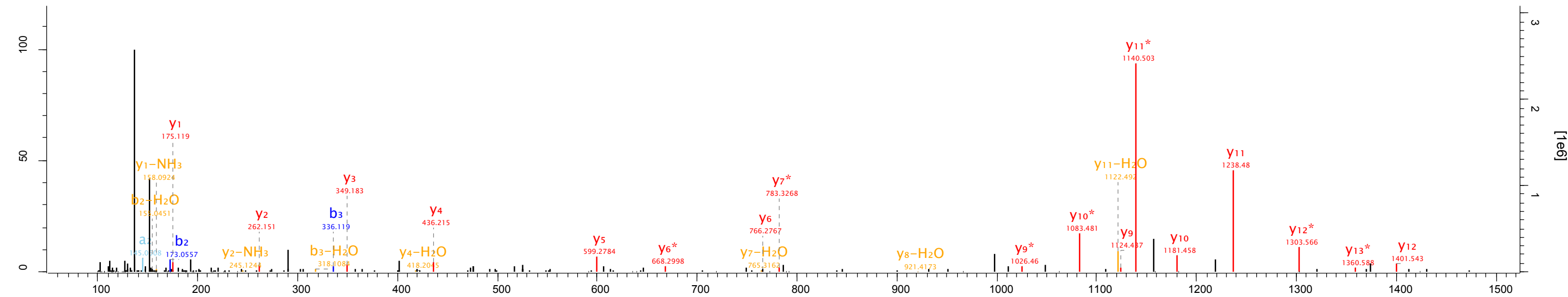


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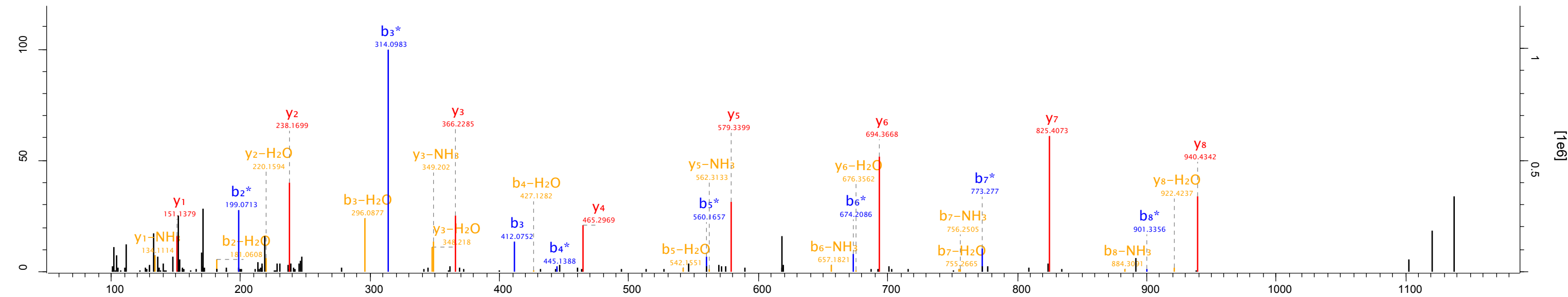
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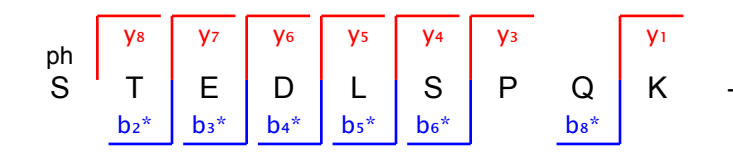
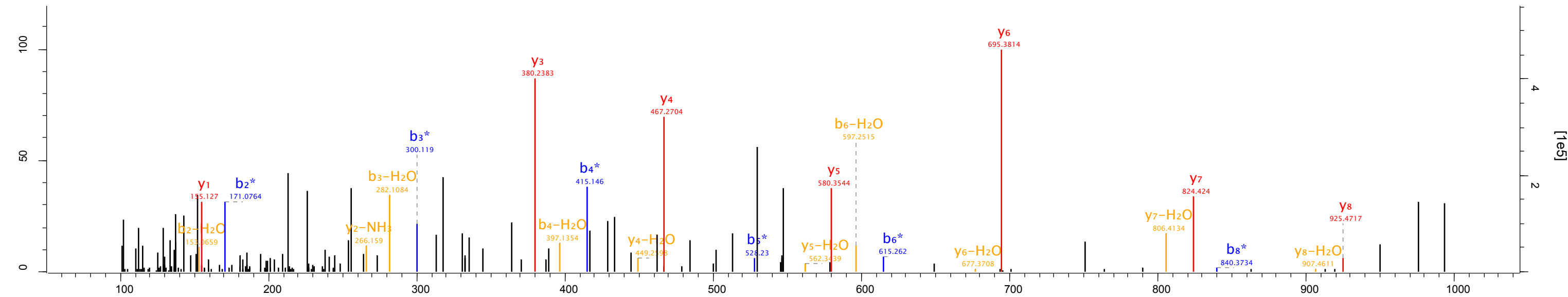
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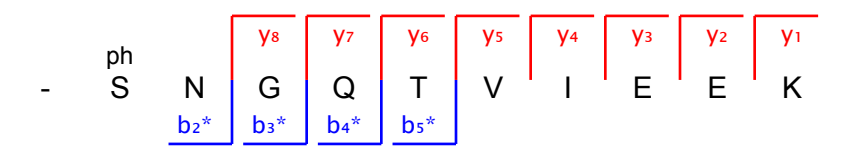
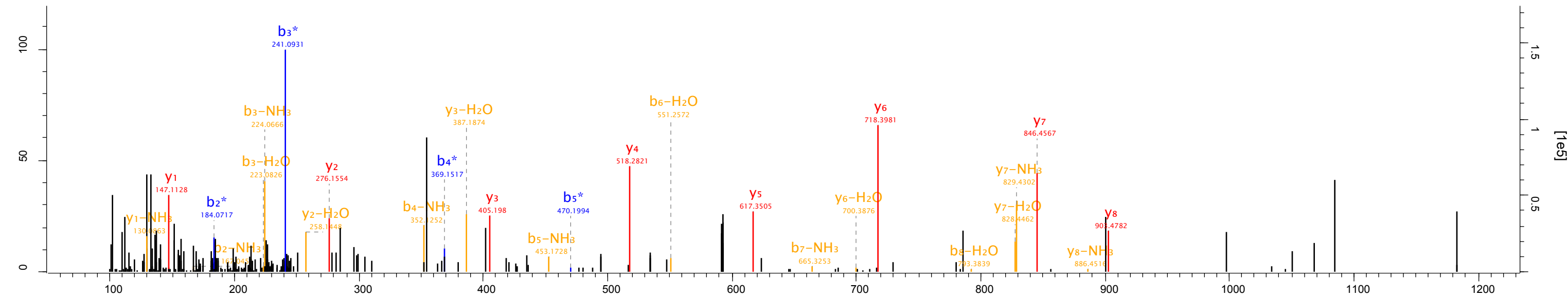
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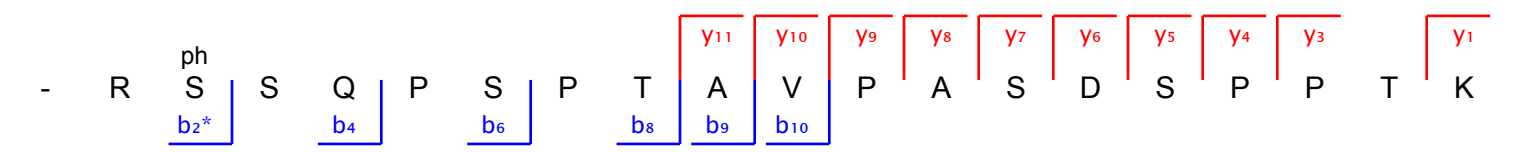
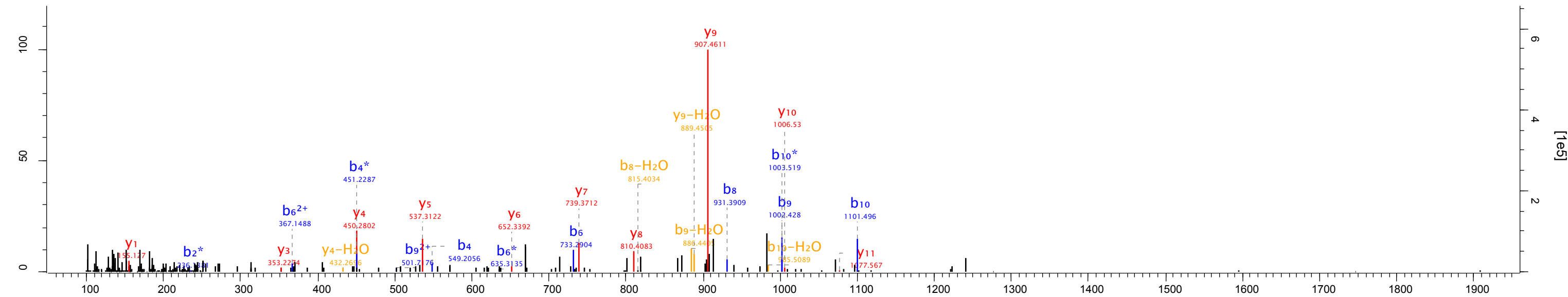
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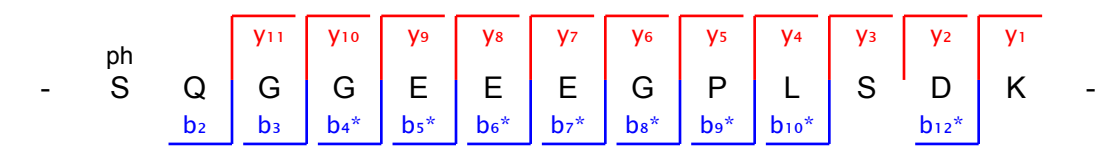
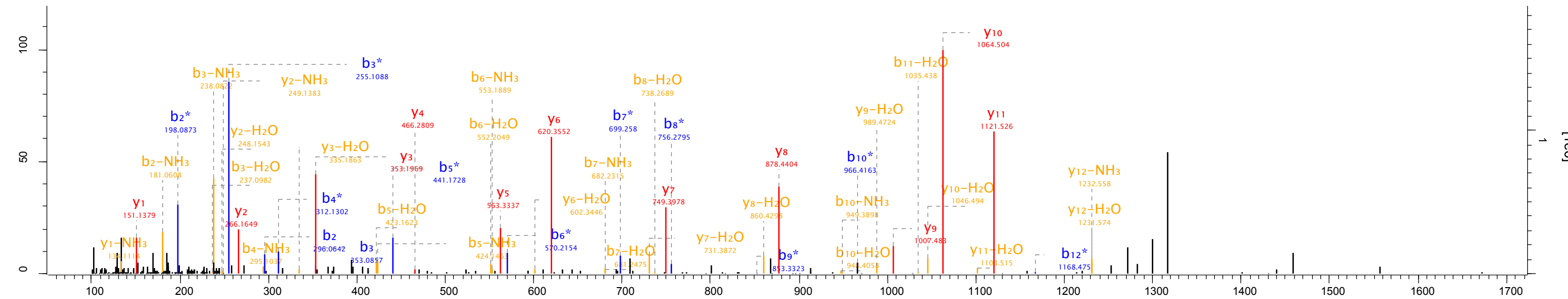
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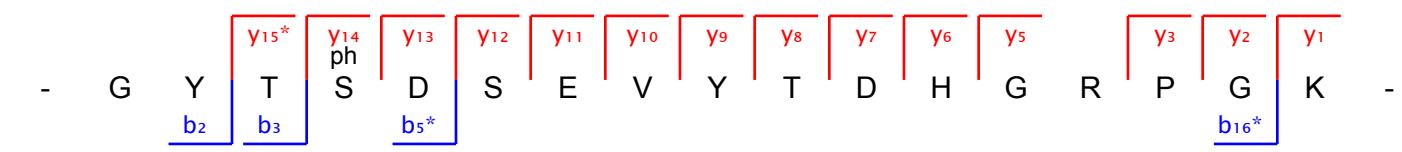
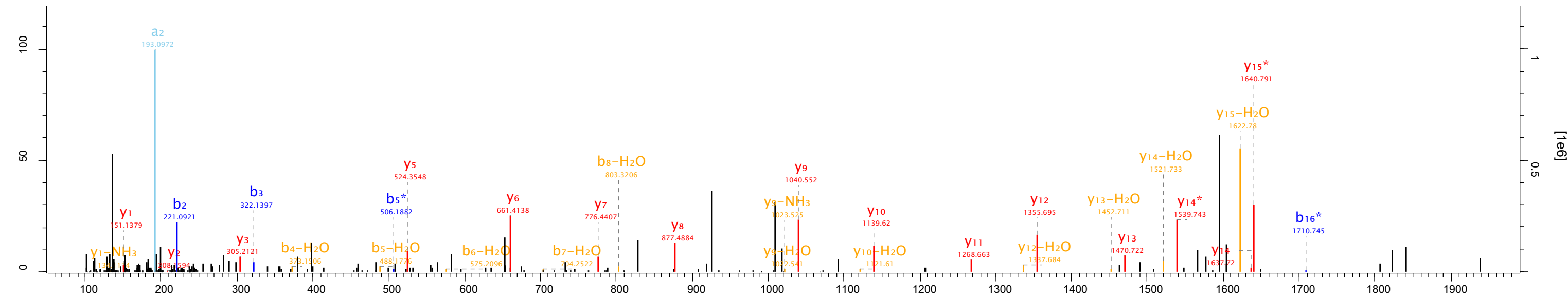
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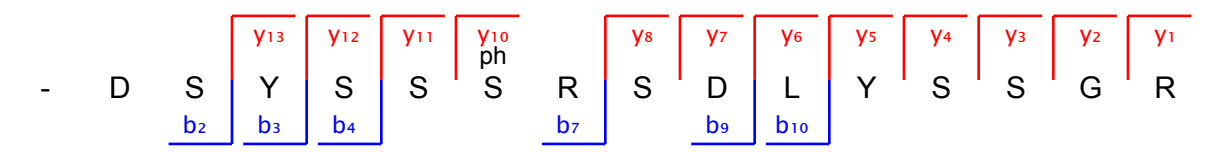
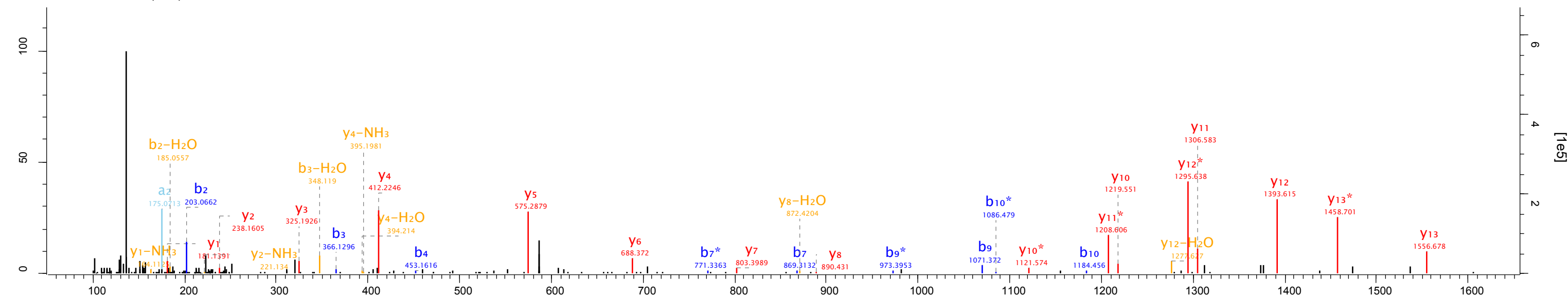


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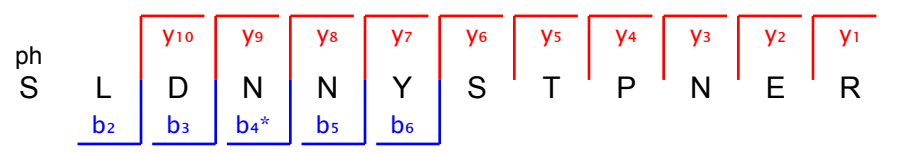
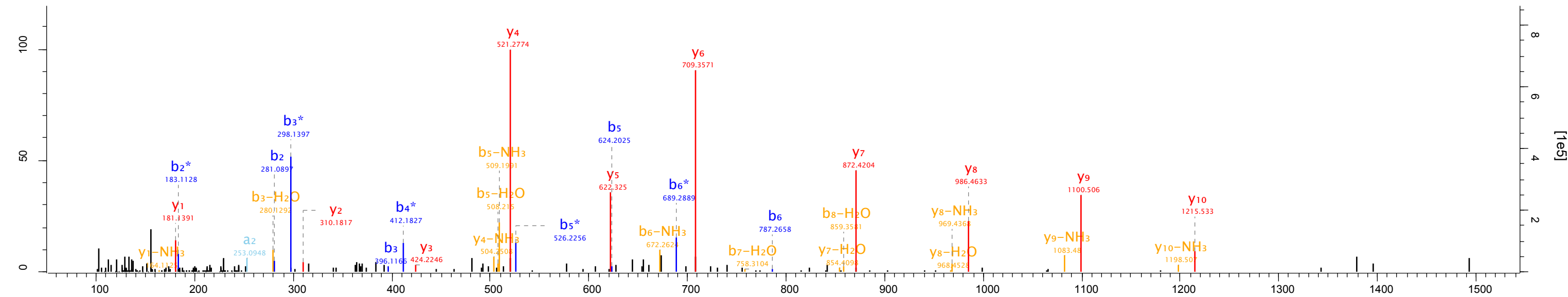


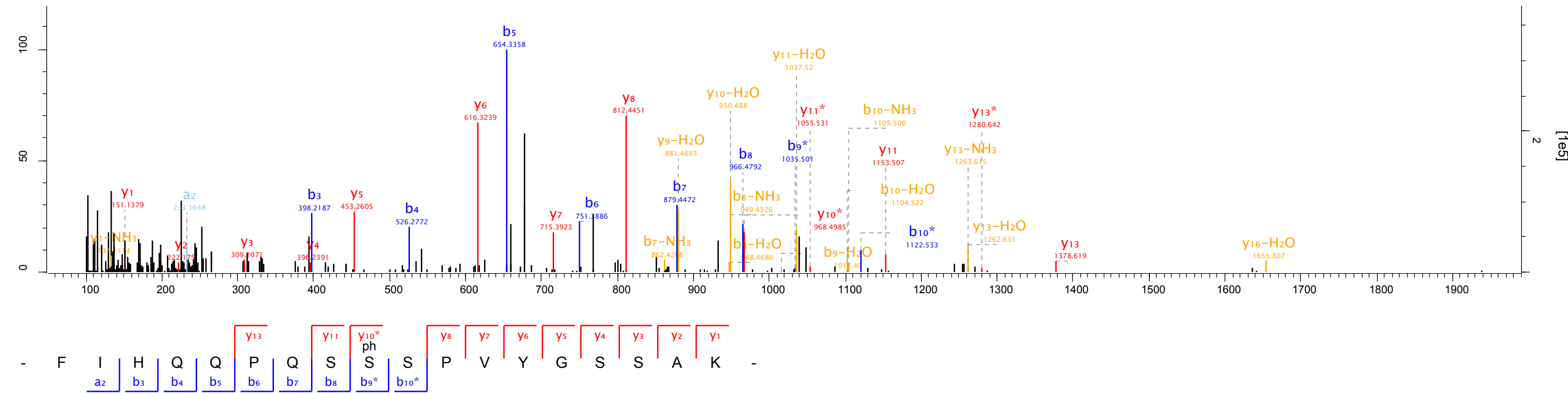
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Scan 5675 Method FTMS; HCD Score 141.31 m/z 587.25 Gene names RBMX

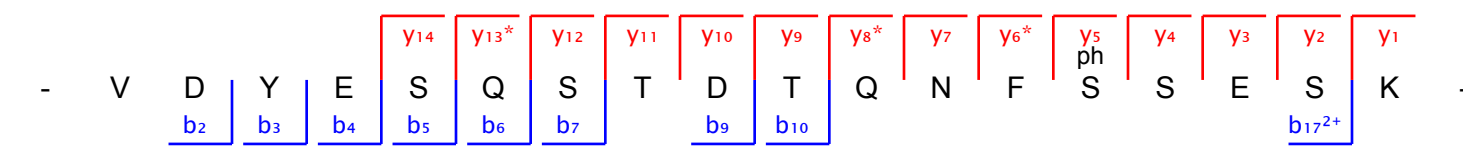
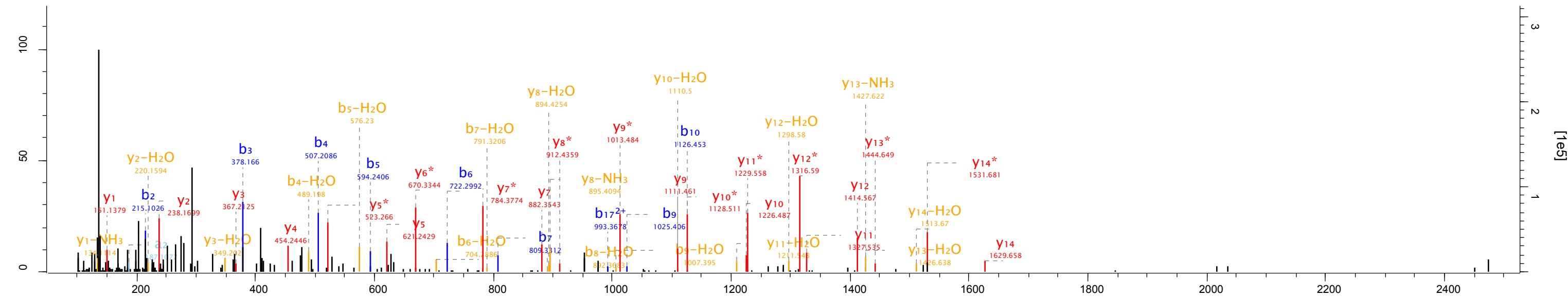


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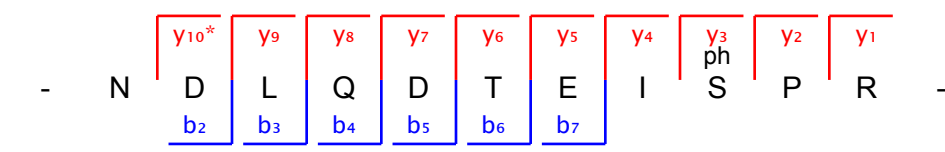
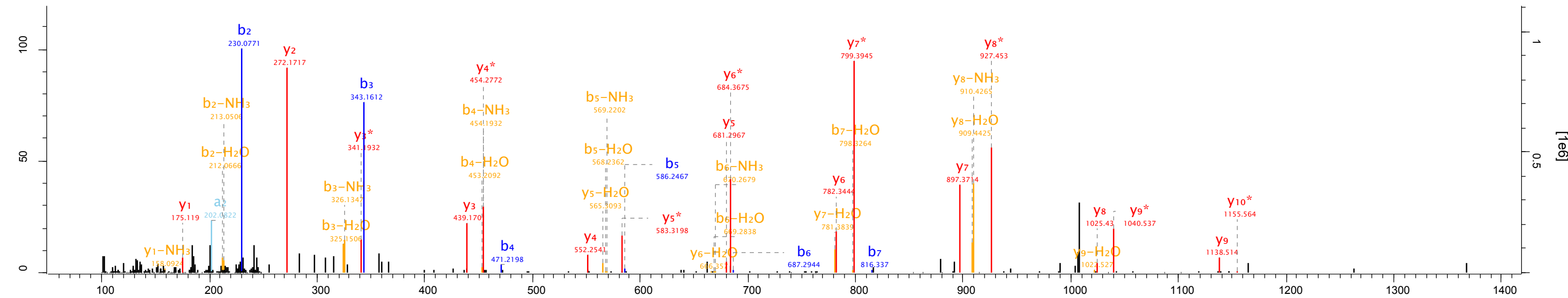




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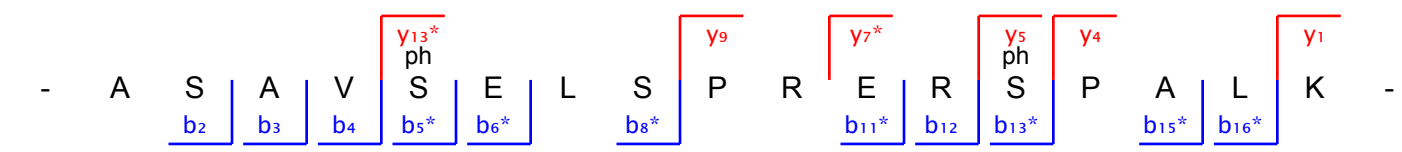
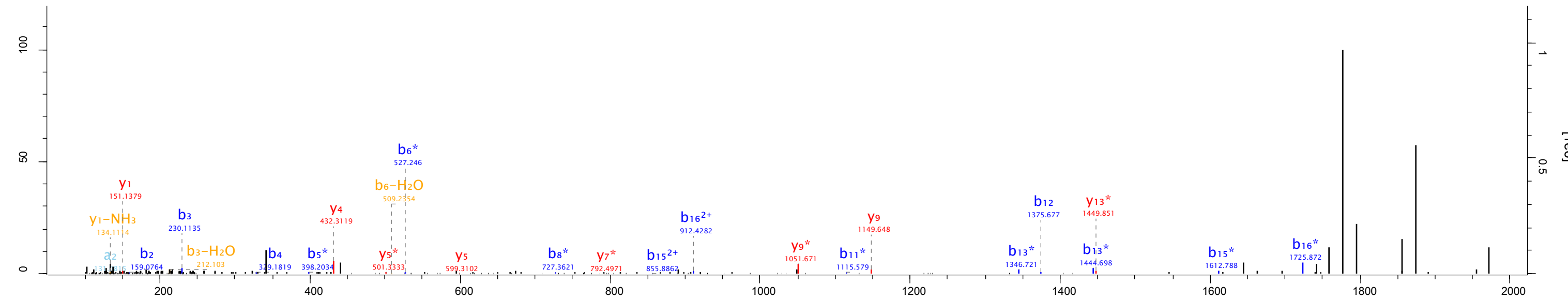


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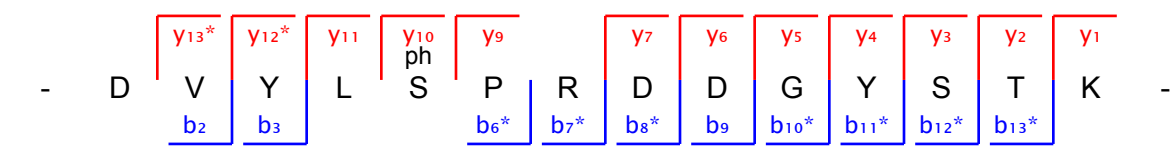
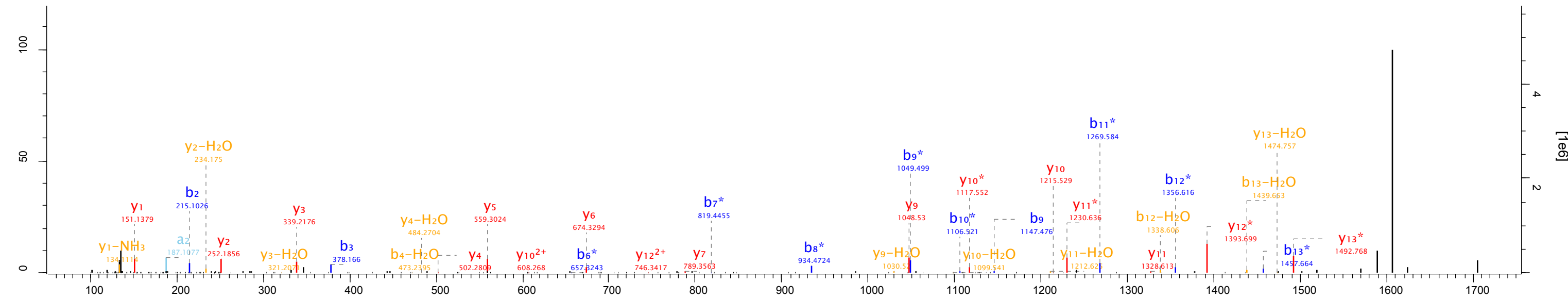


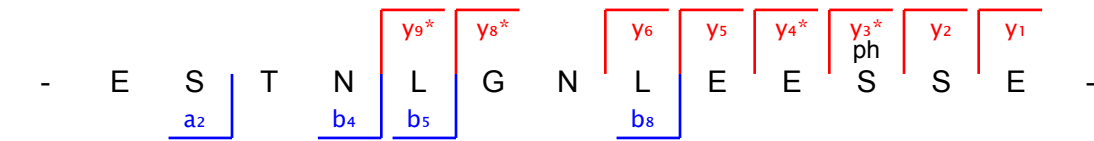
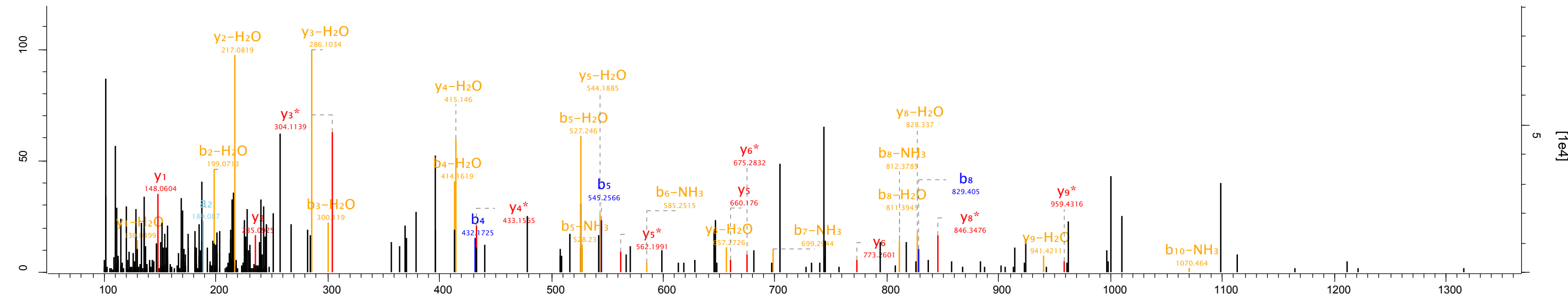
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20171215_MaS_33SR_LMH_phospho2_02

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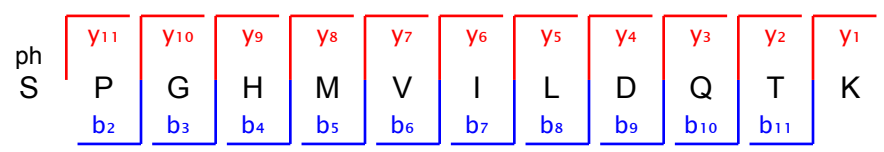
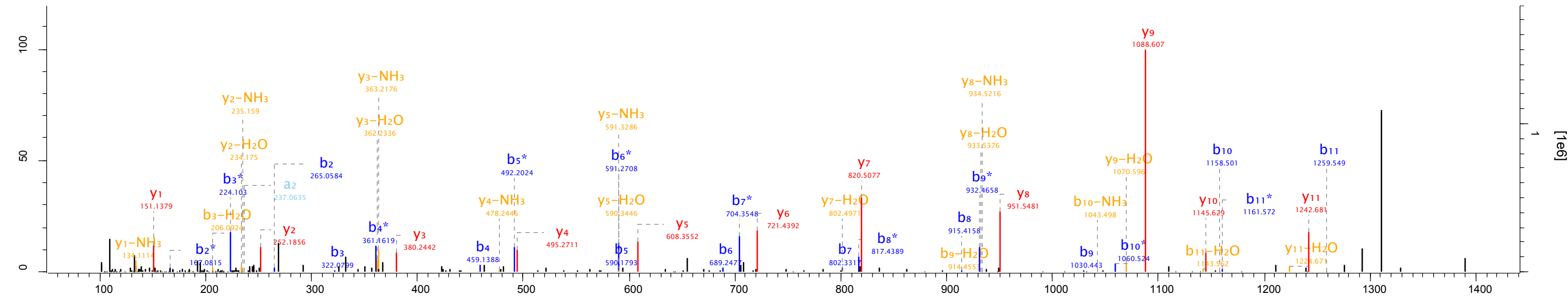


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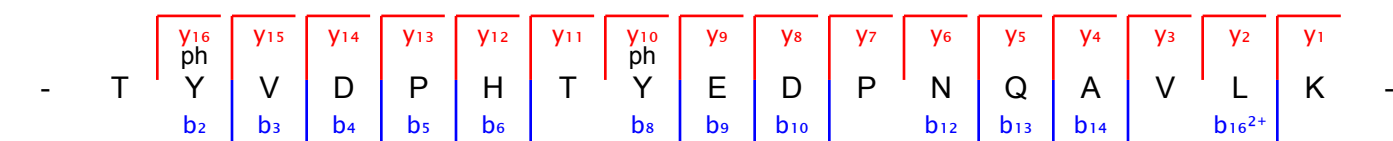
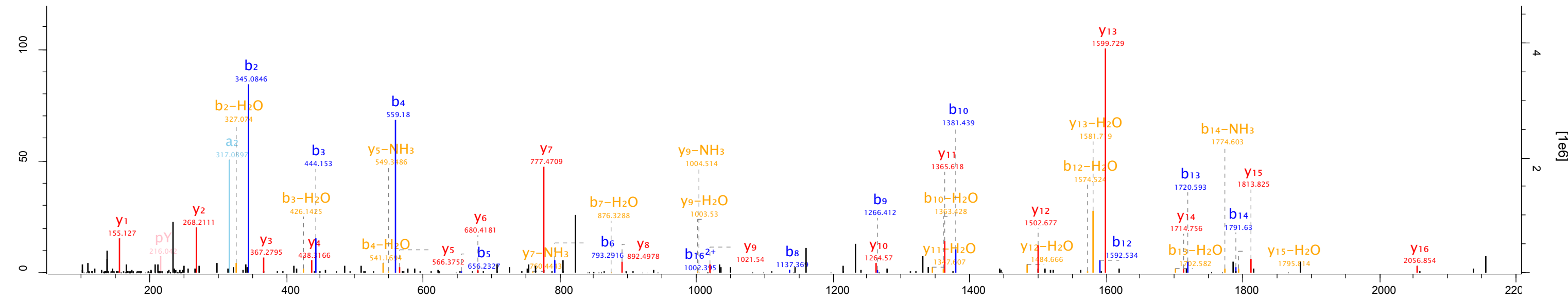


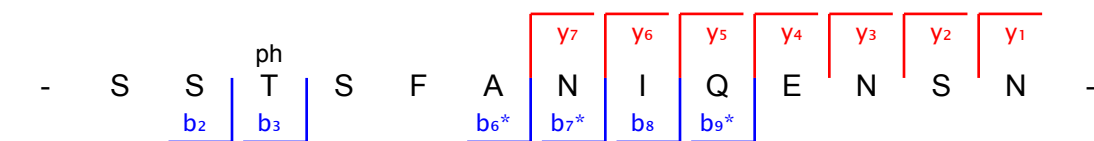
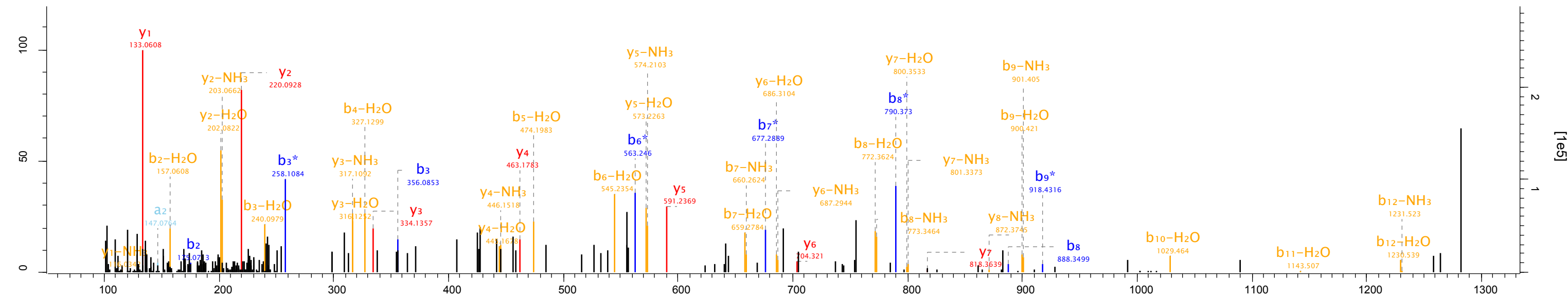


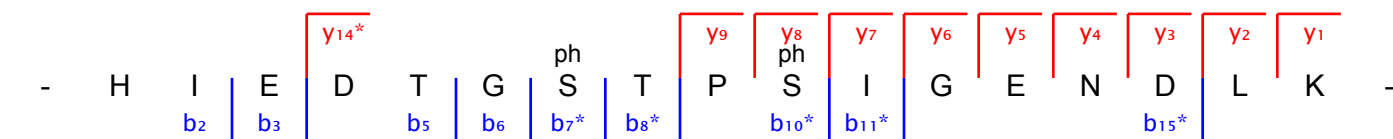
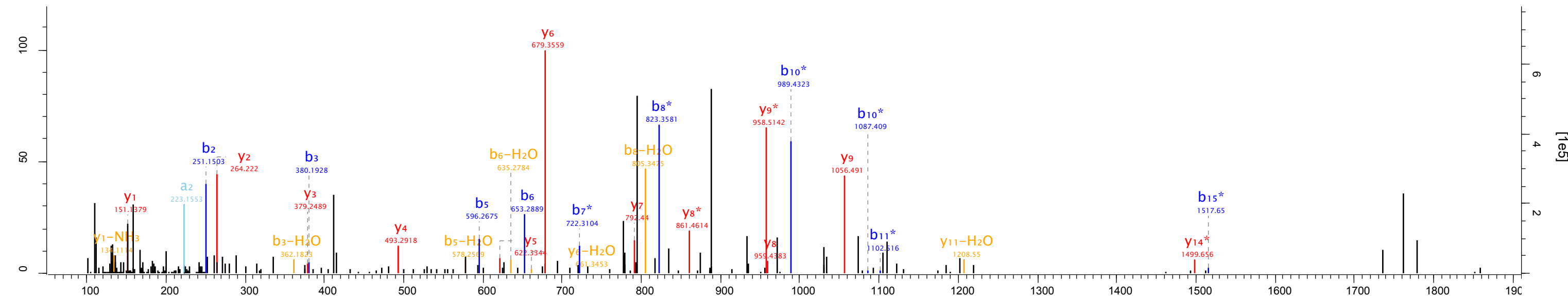
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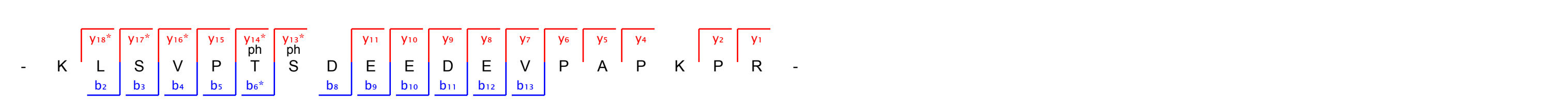
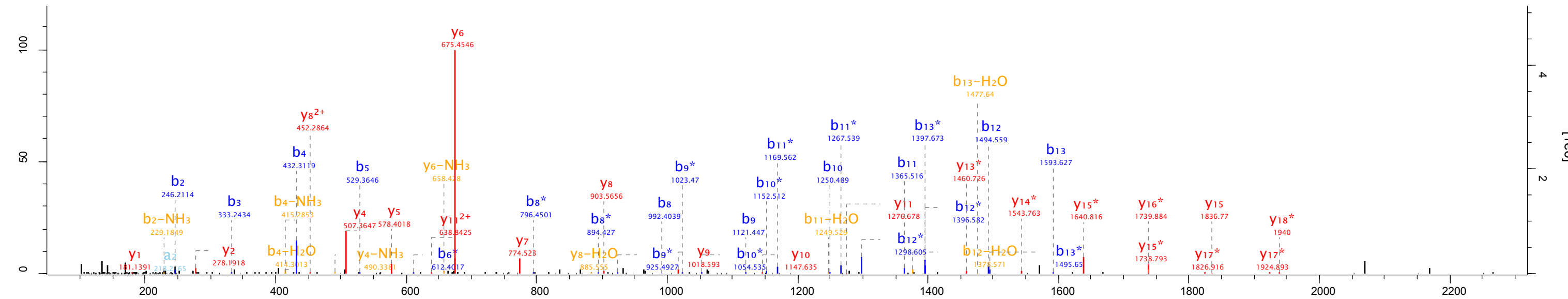
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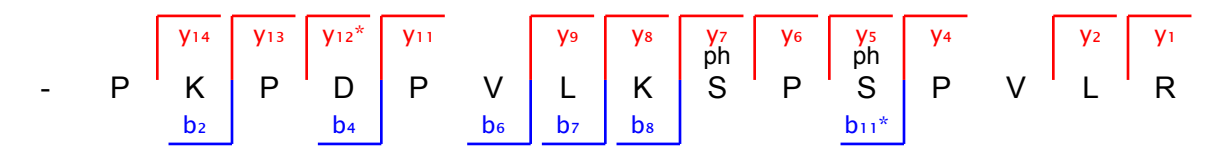
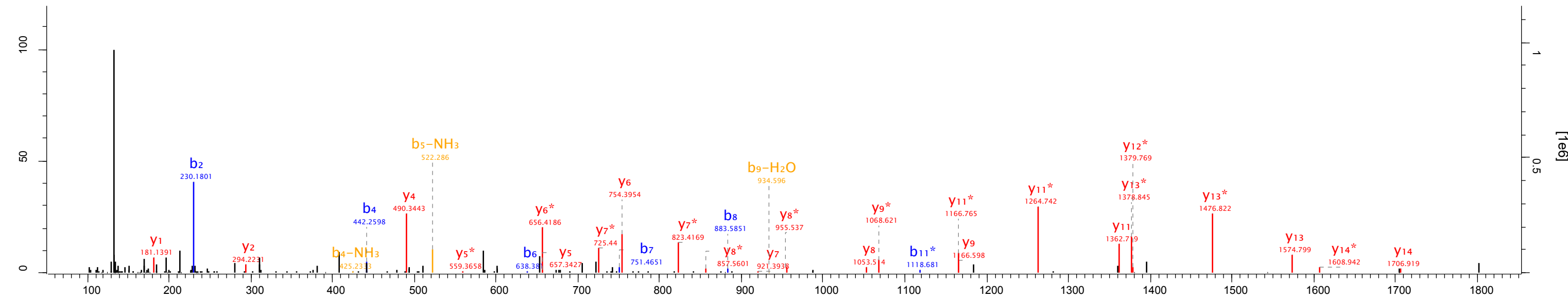




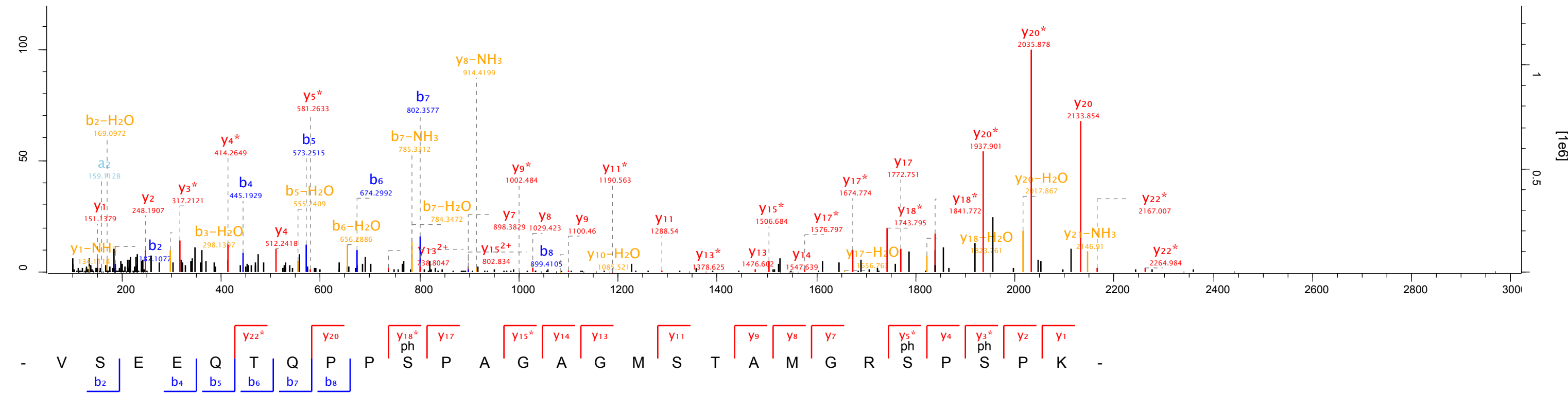
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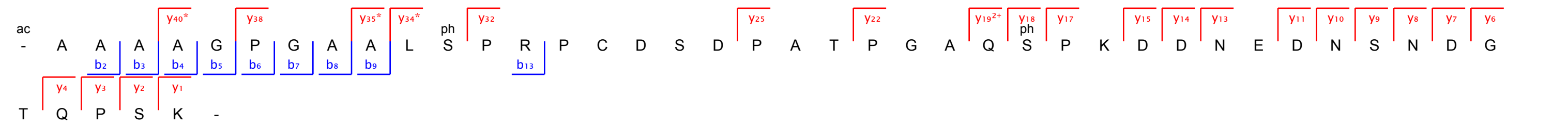
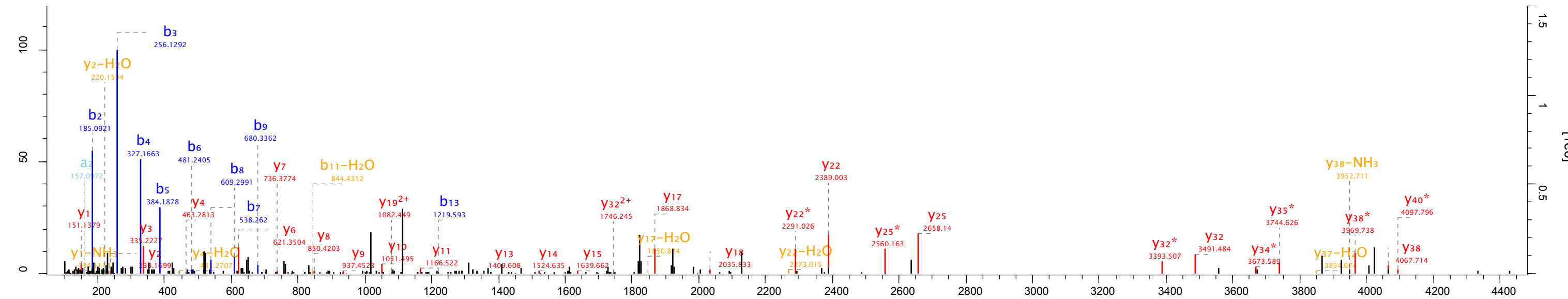
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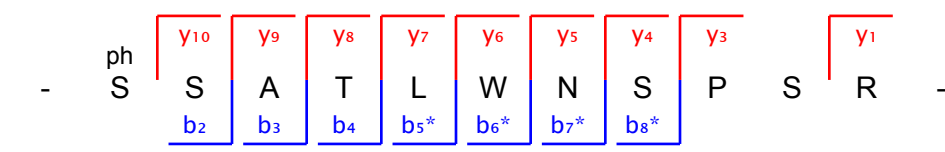
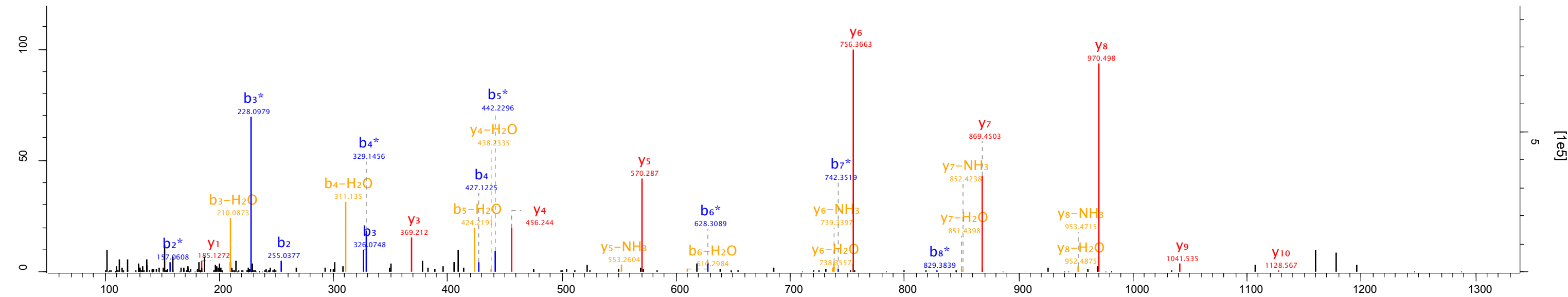
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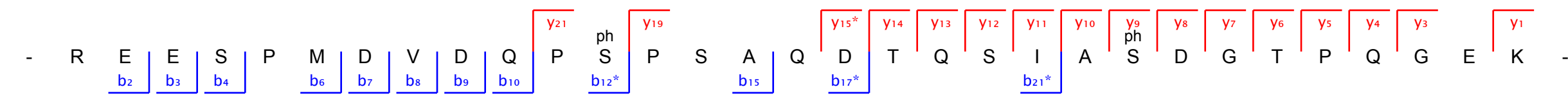
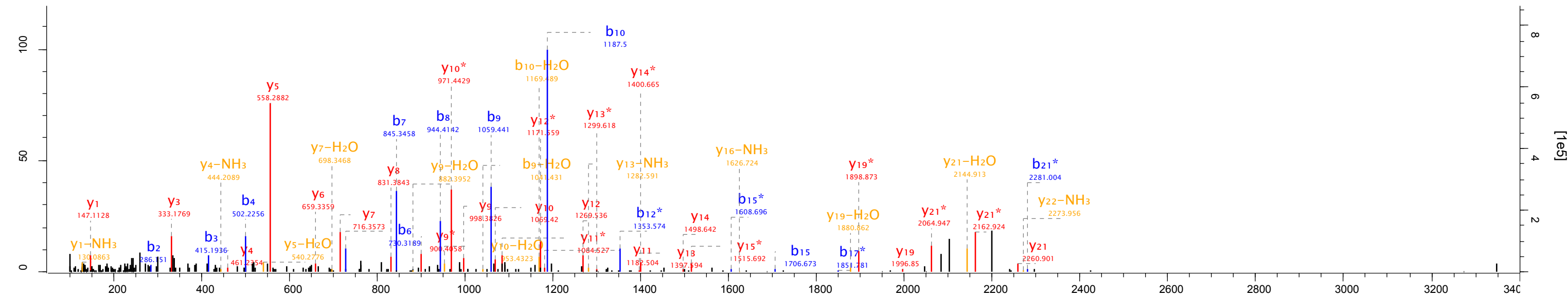
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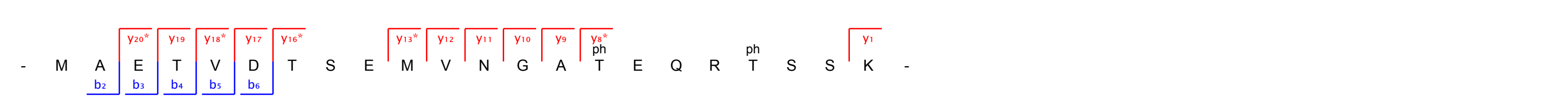
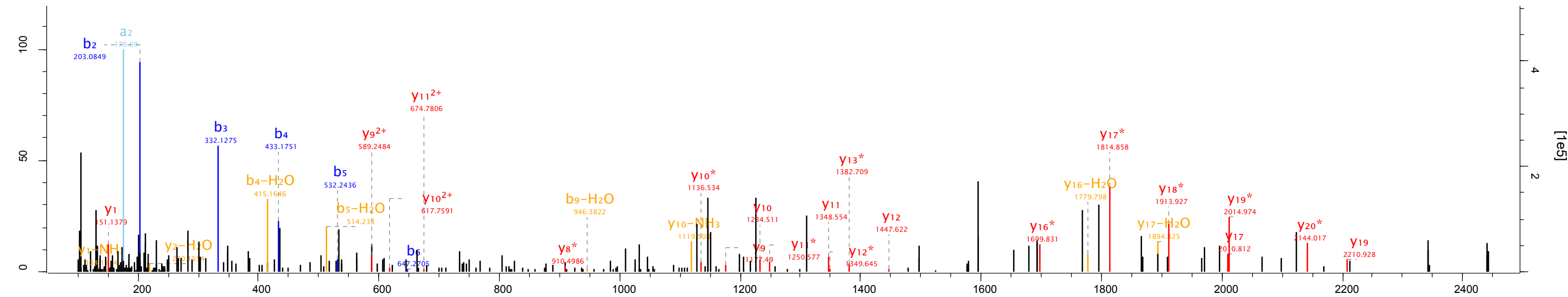
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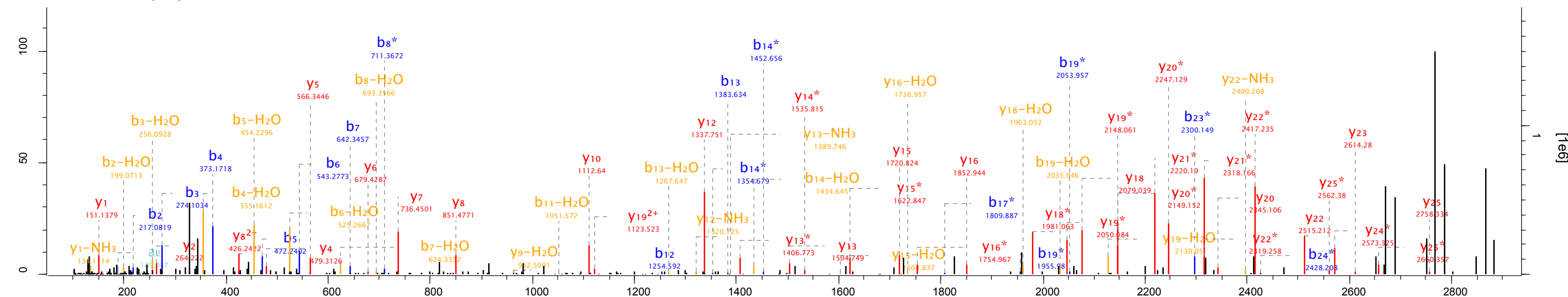


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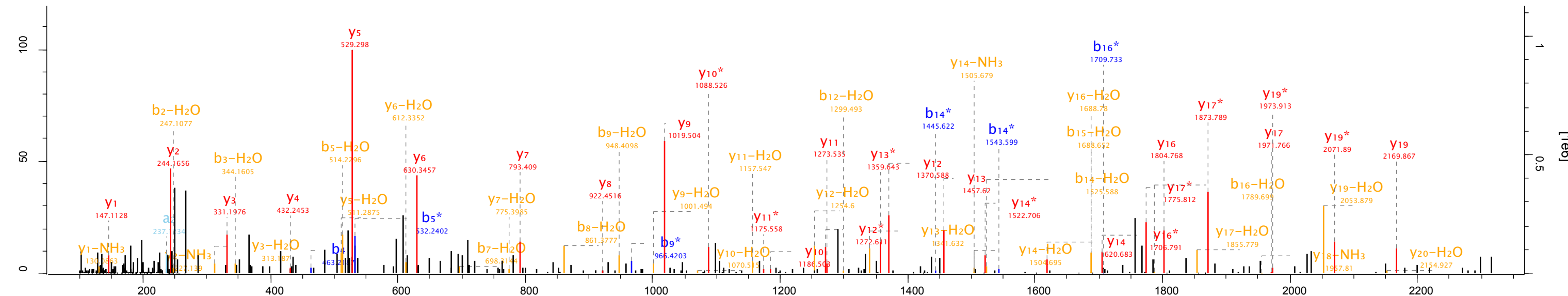




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y25
y24*
y23
y22
y21*
y20
y19*
y18
y16
y15
y14*
y13
y12
y10
y8
y7
y6
y5
y4
y2
y1

b2
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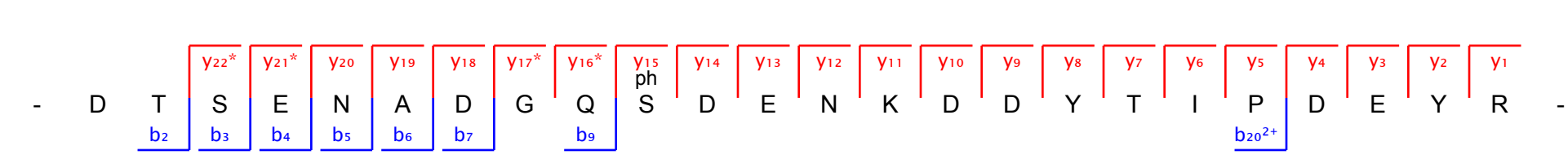
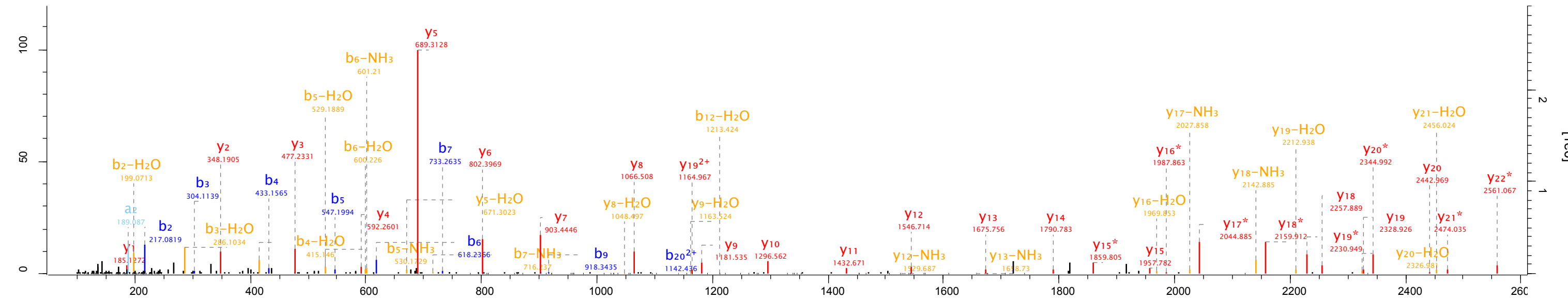


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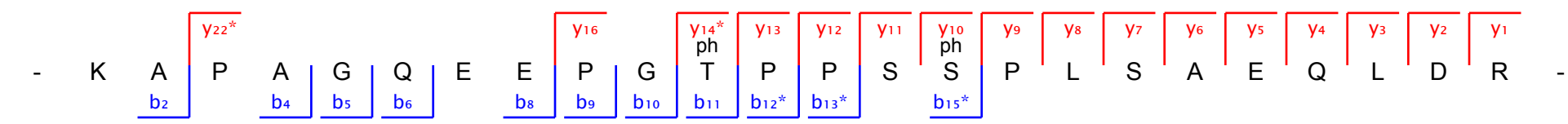
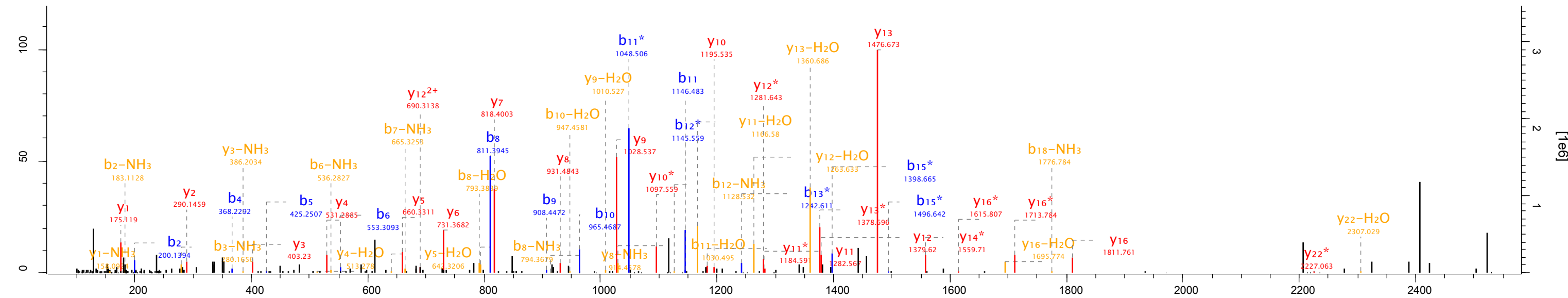
Fragmentation sites are indicated by brackets below the sequence:

- Red brackets: y19 (T-P), y17^{ph} (S), y16 (P-S), y14 (Y-S), y13 (S-P), y12 (P-S), y11 (S-S), y10^{ph} (S-P), y9 (P-E), y8 (E-Y), y7 (Y-T), y6 (T-P), y5 (P-T), y4 (T-S), y3 (S-P), y2 (P-K), y1 (K).
- Blue brackets: a₂ (T), b₄ (T), b₅^{*} (S), b₉^{*} (S), b₁₄^{*} (E), b₁₆^{*} (T).

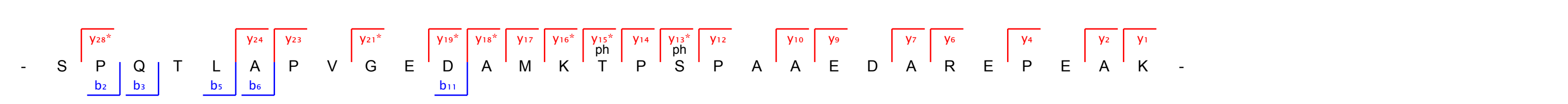
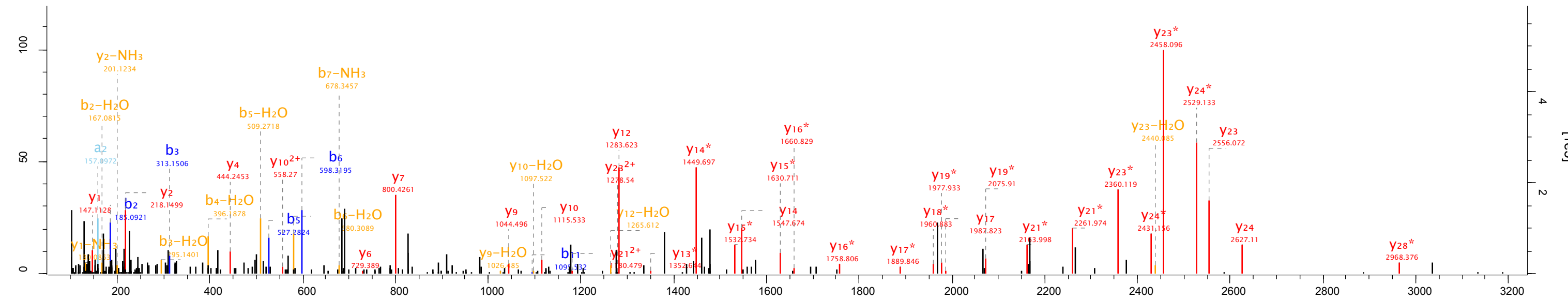
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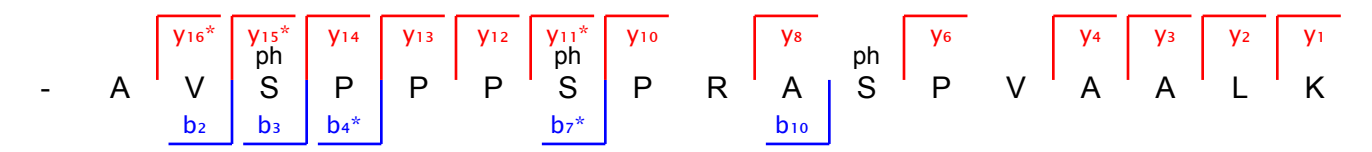
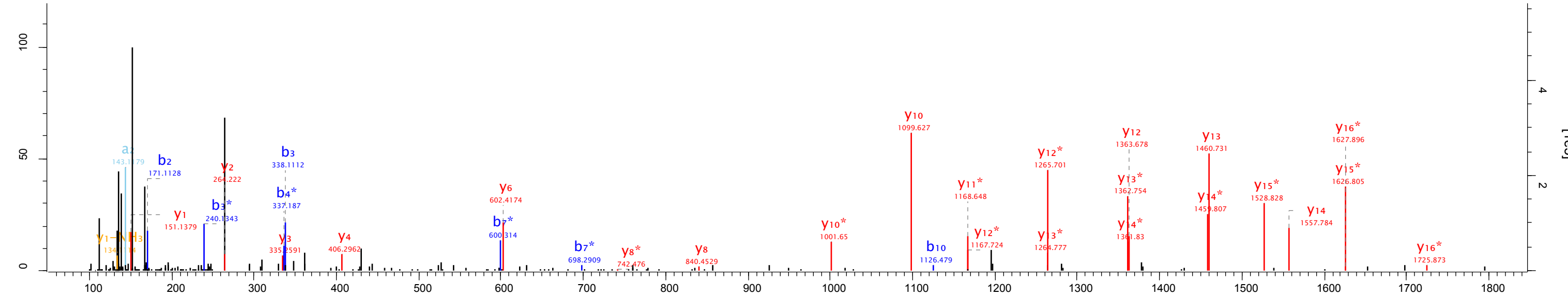
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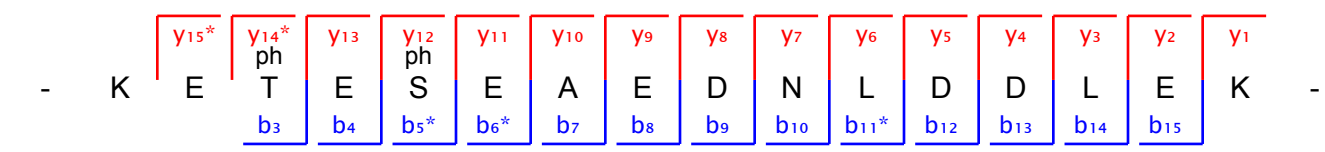
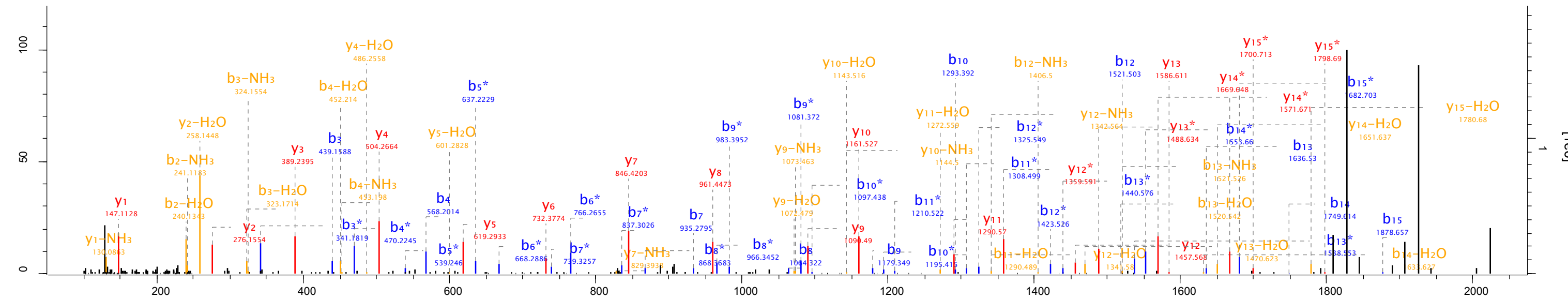
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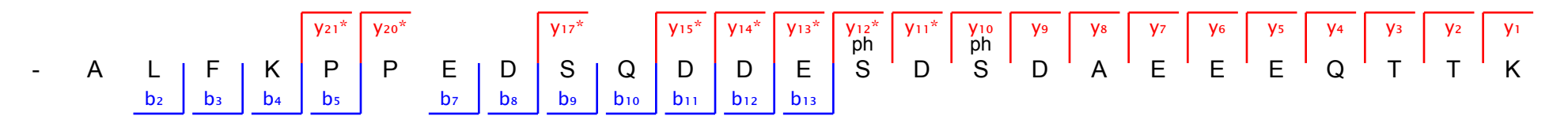
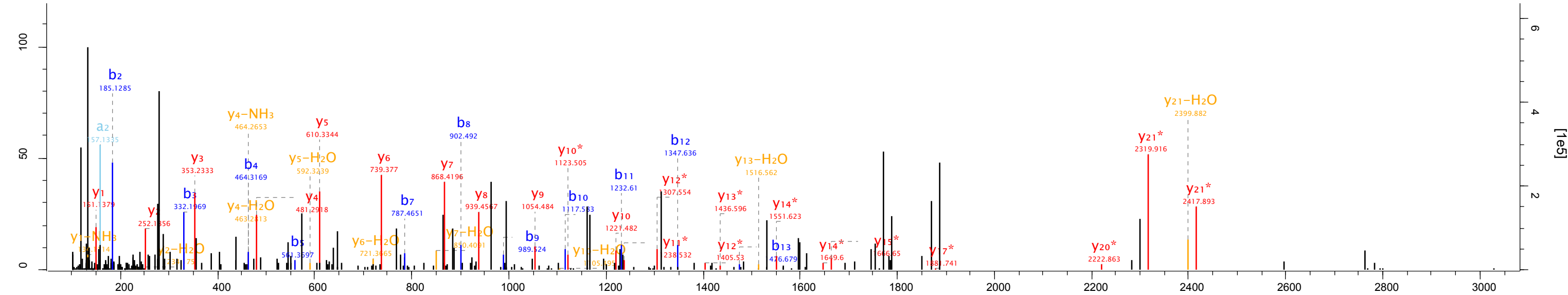
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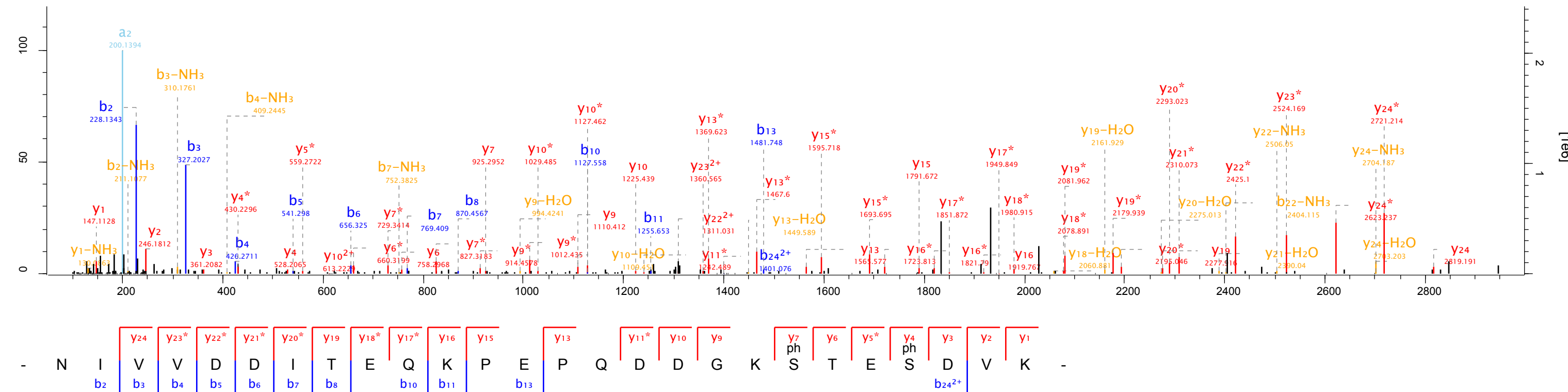
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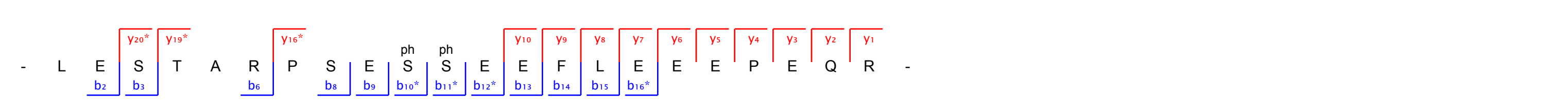
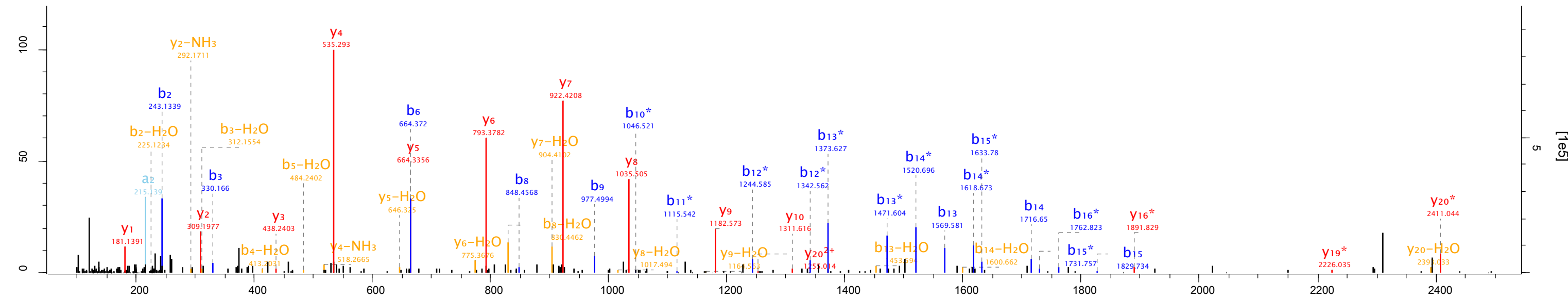
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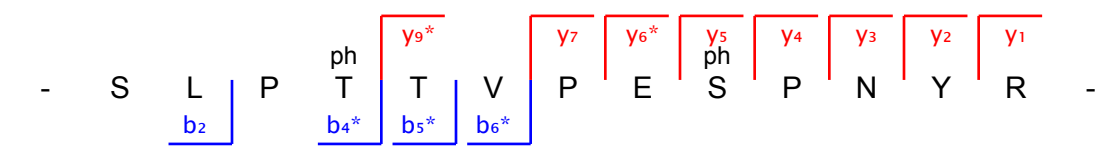
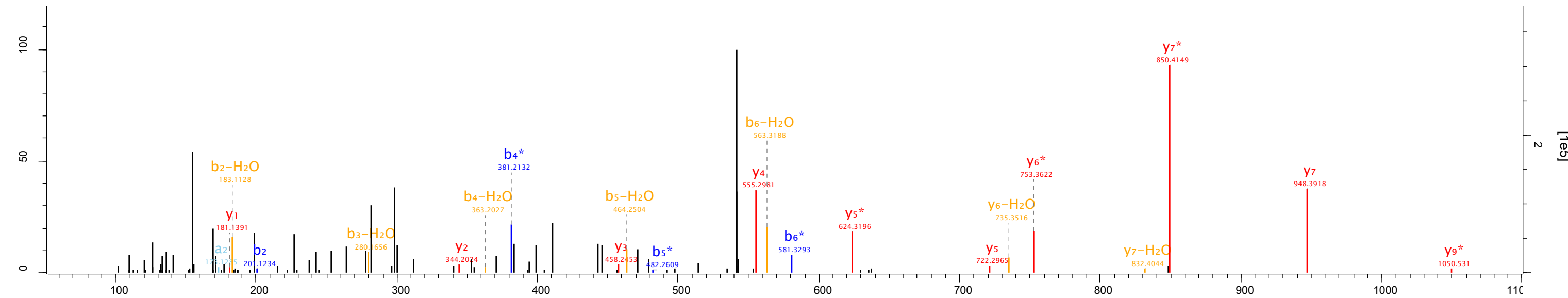
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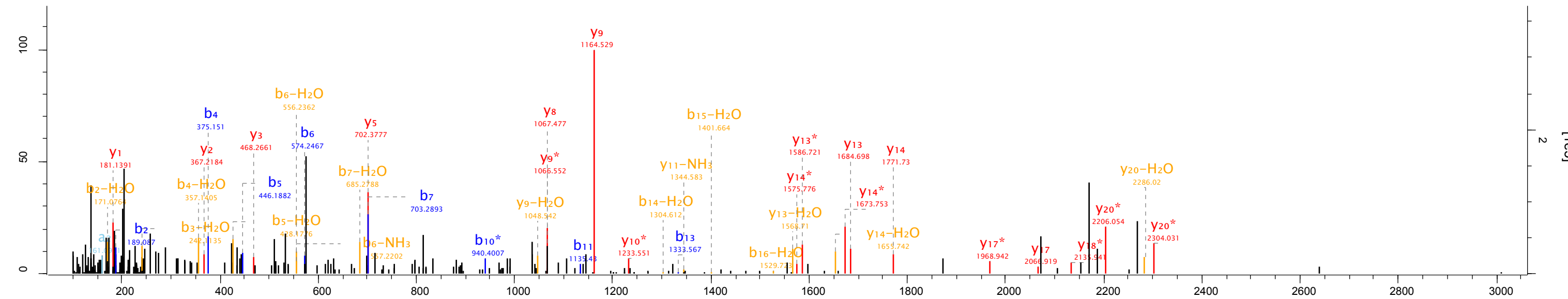
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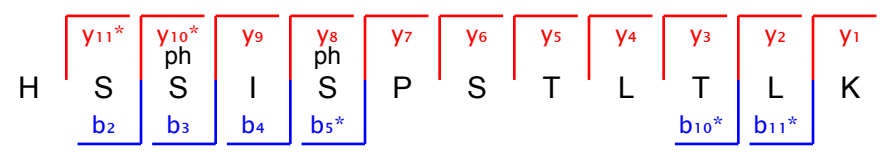
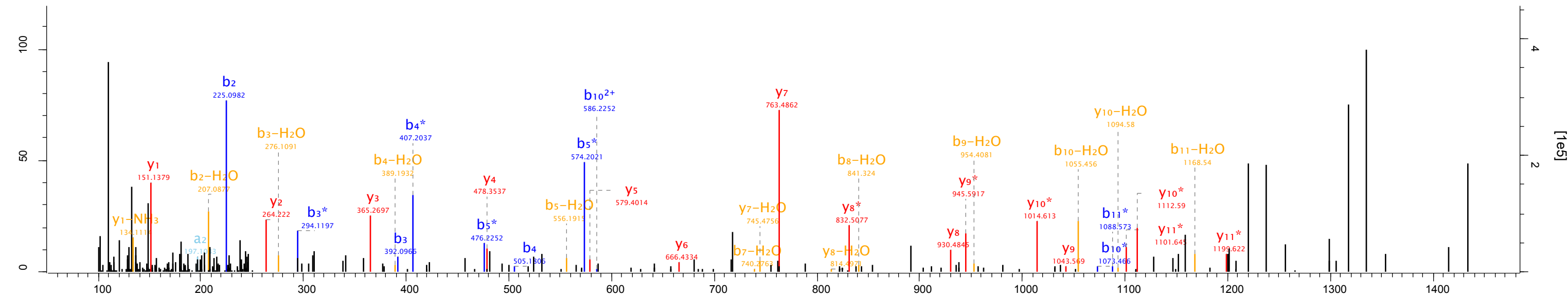
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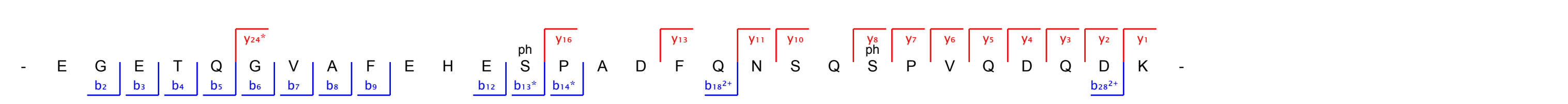
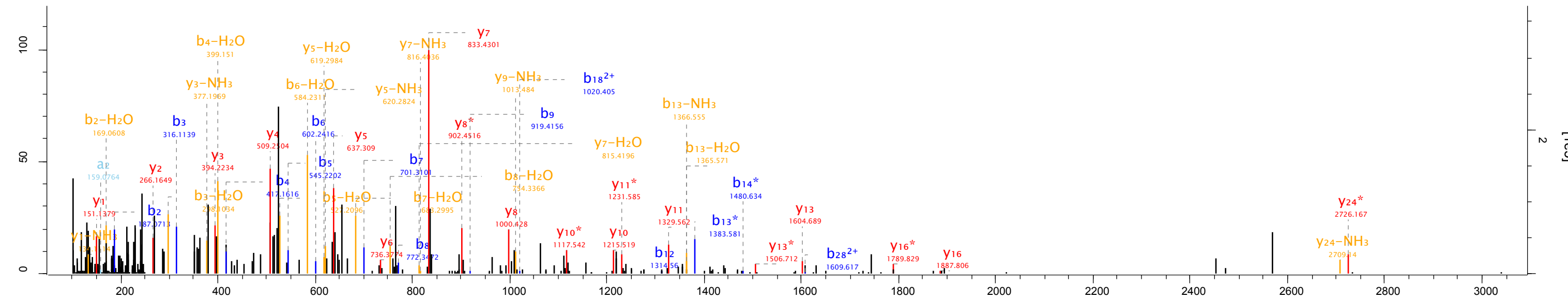
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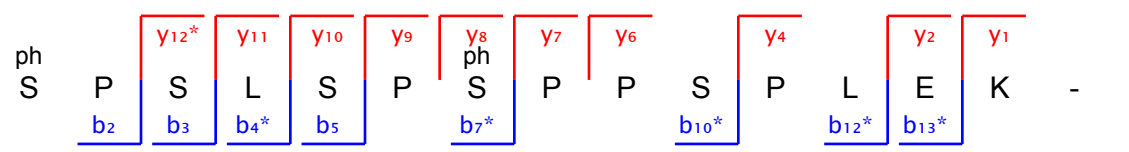
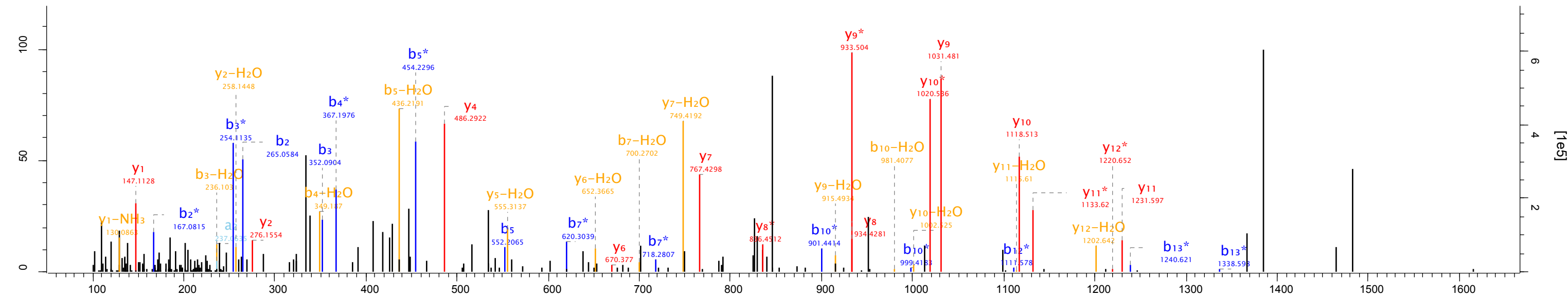
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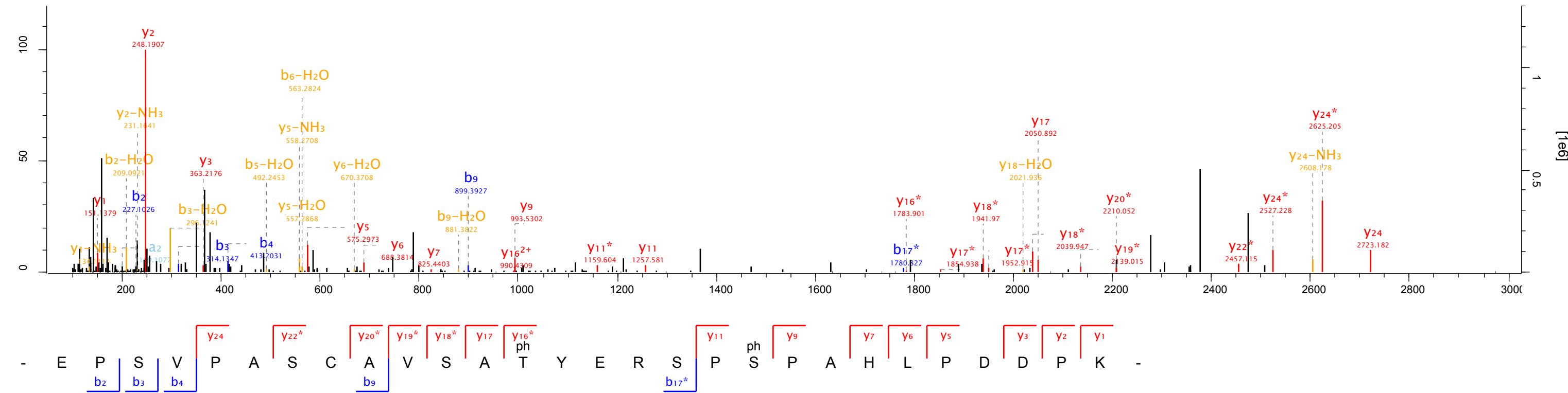
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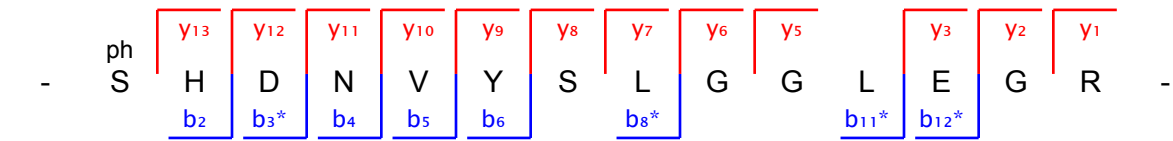
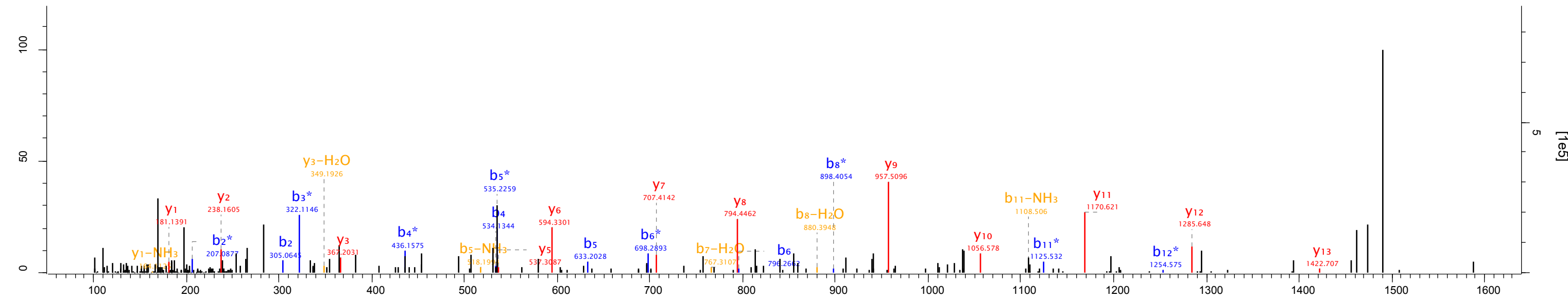


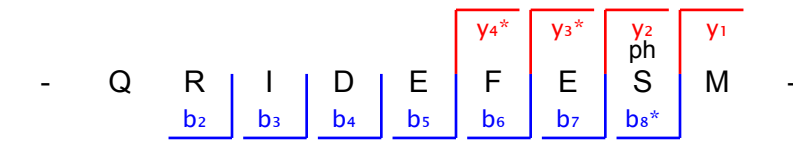
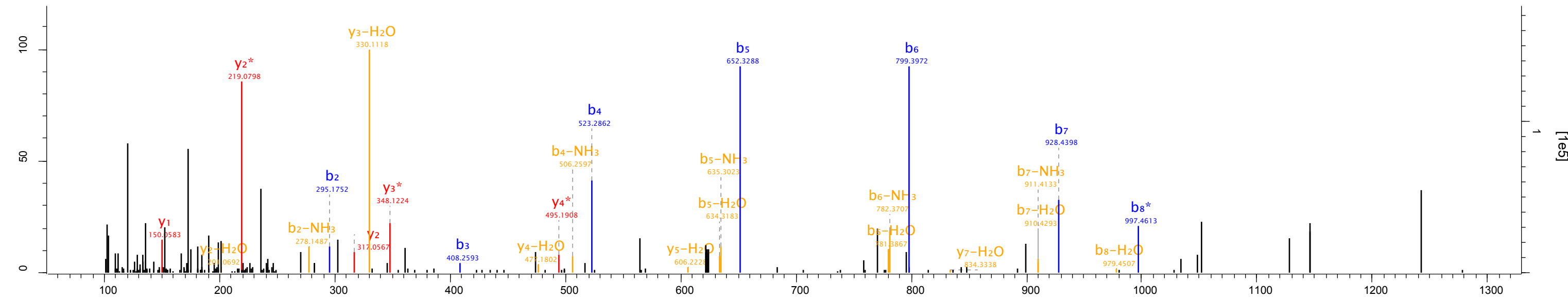
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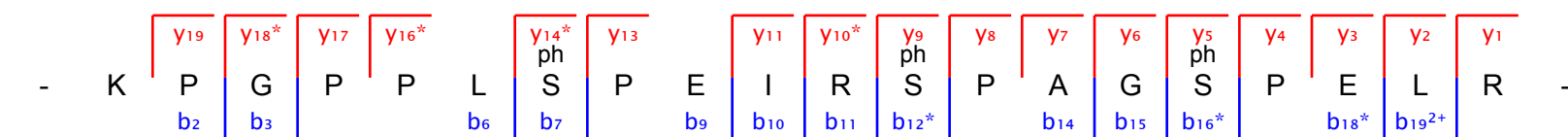
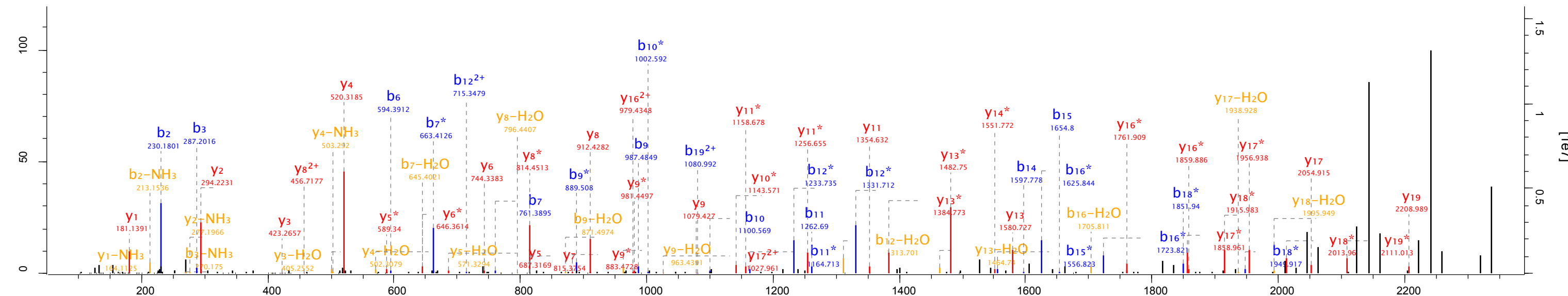
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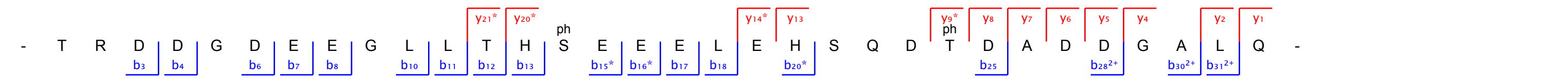
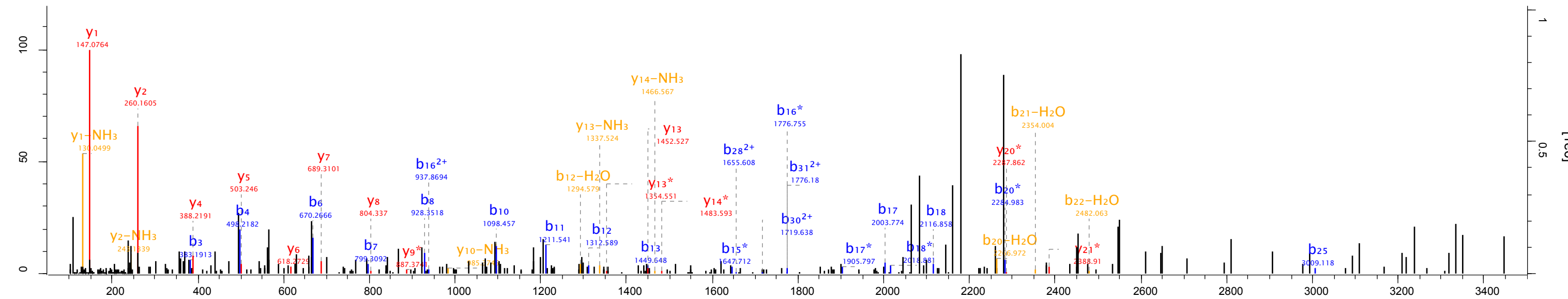




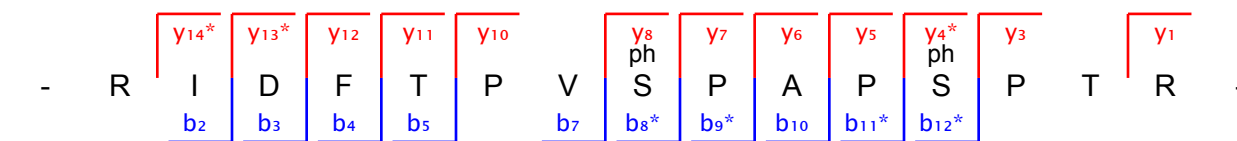
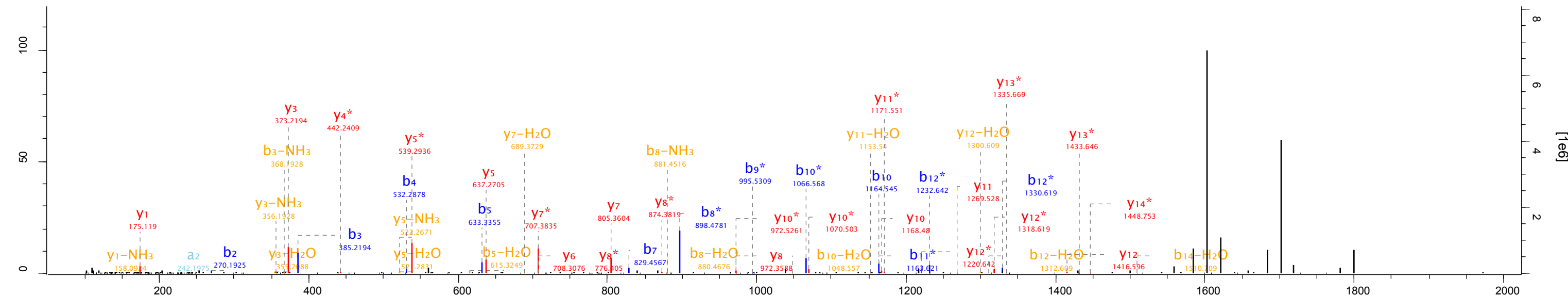
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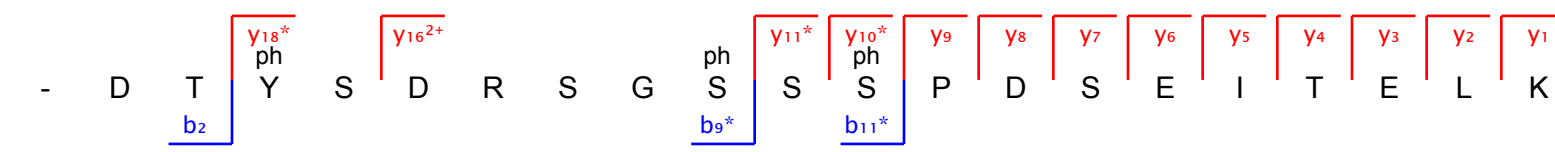
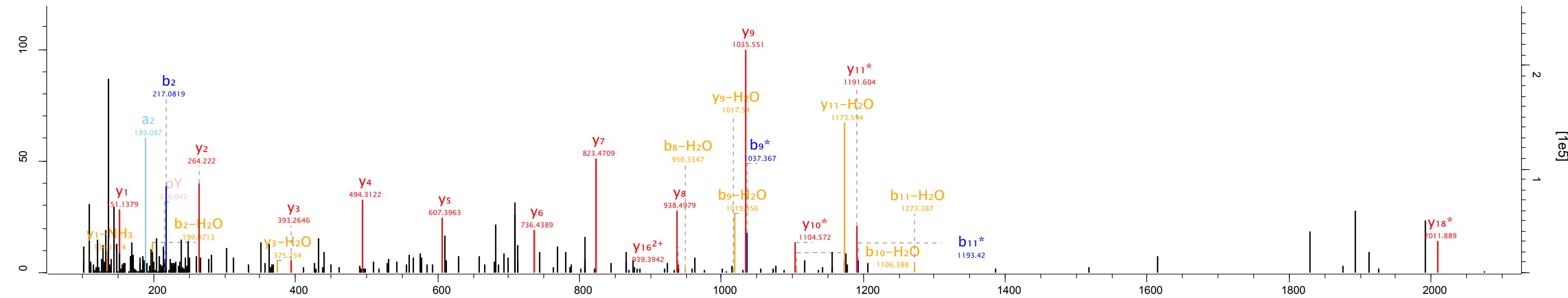
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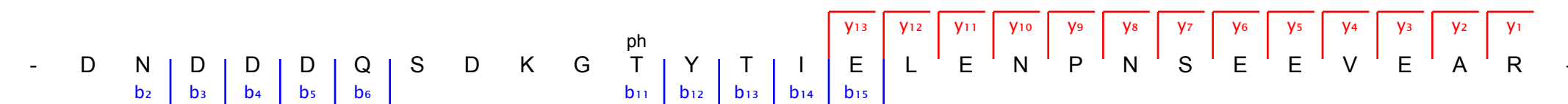
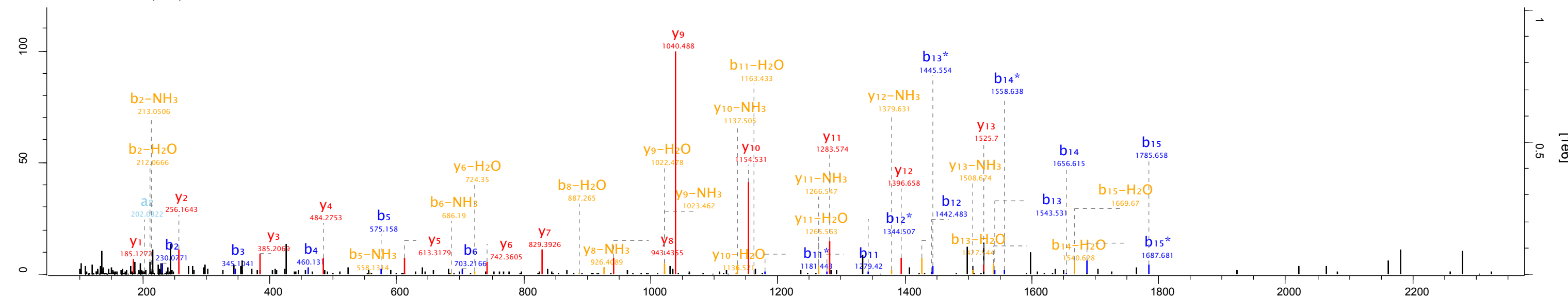


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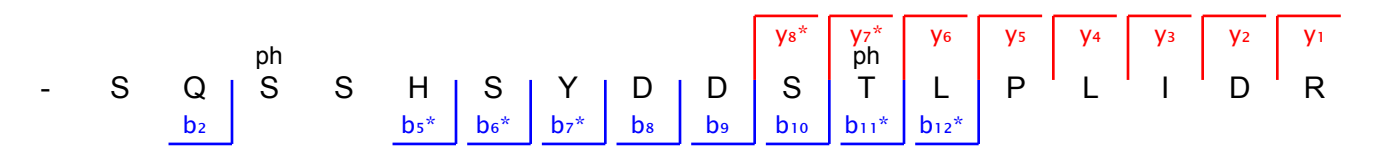
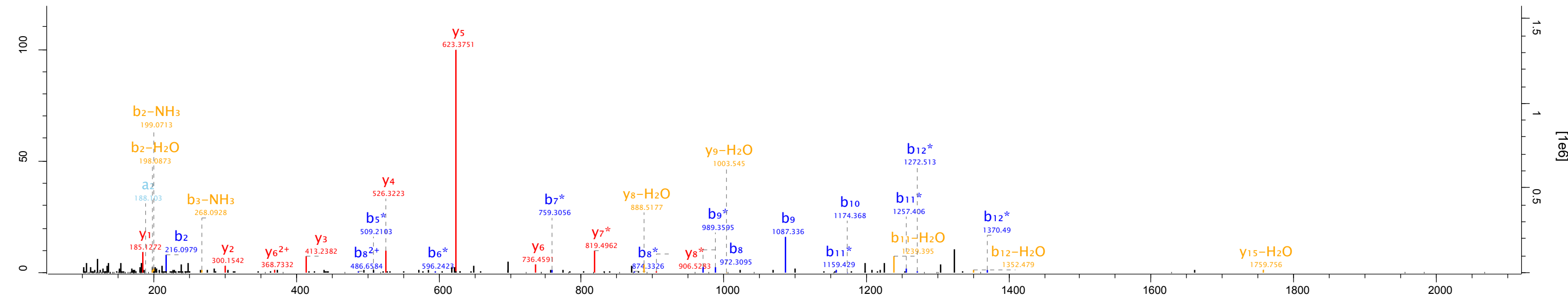


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20171215_MaS_33SR_LMH_phospho2_03

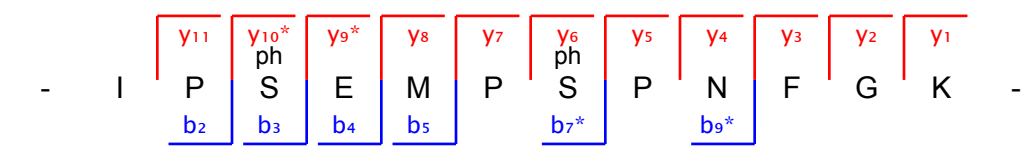
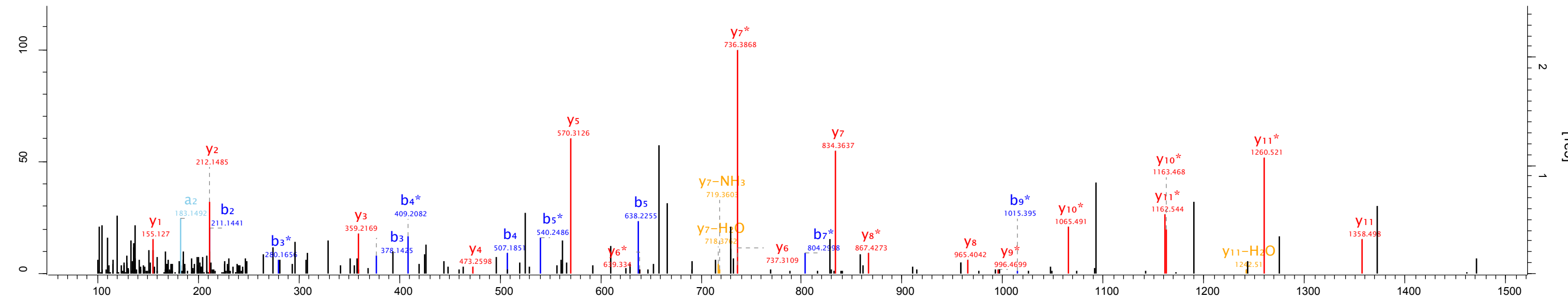
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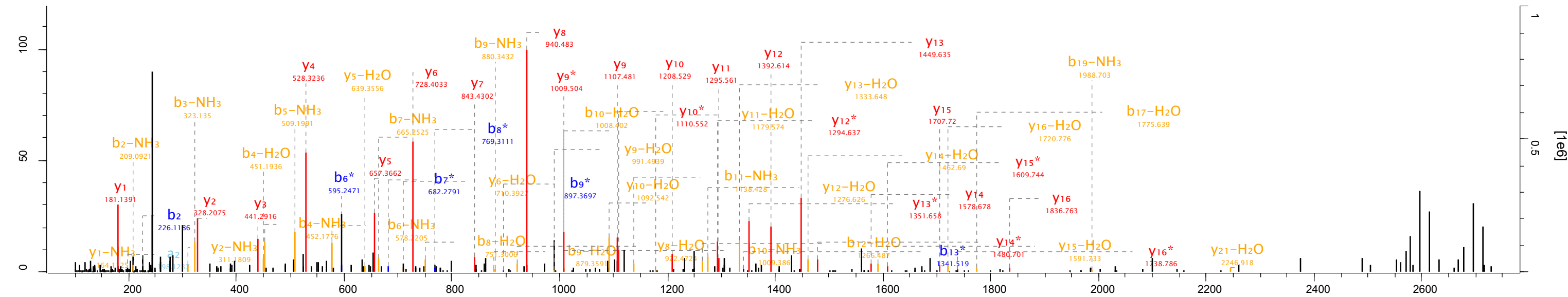
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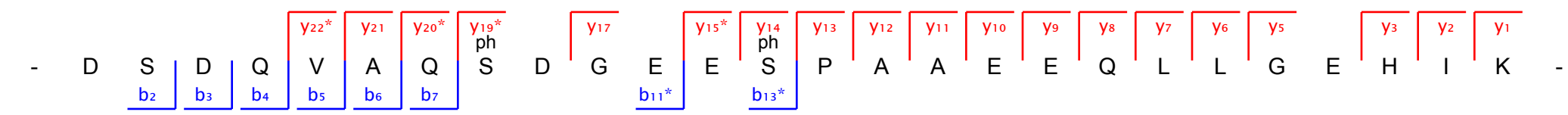
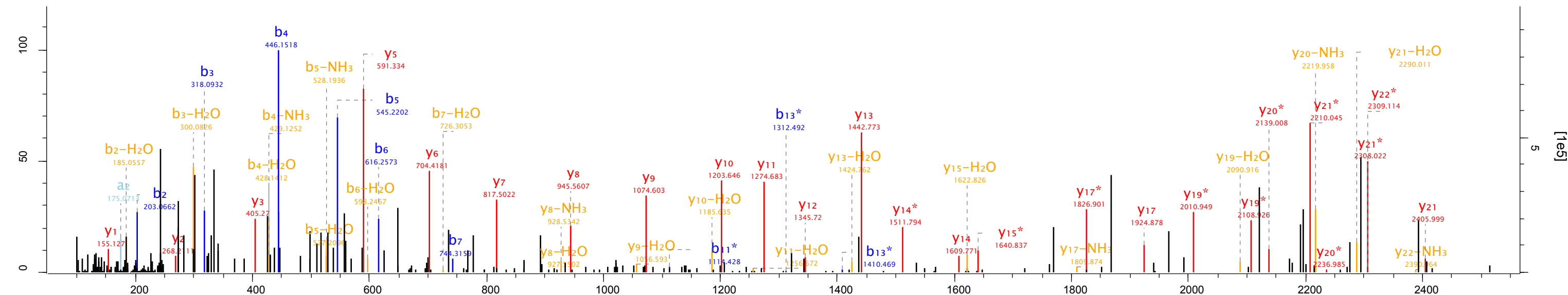
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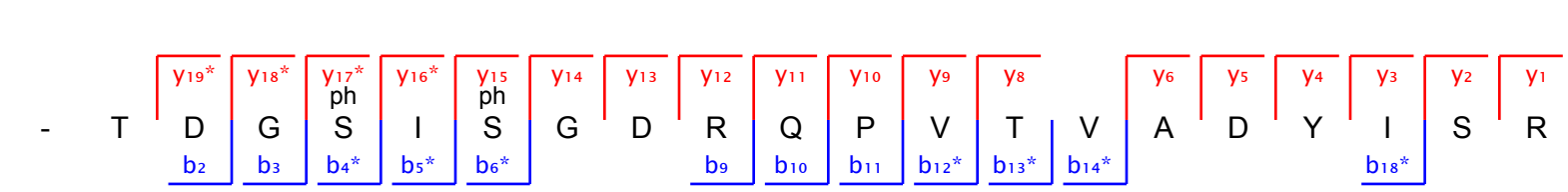
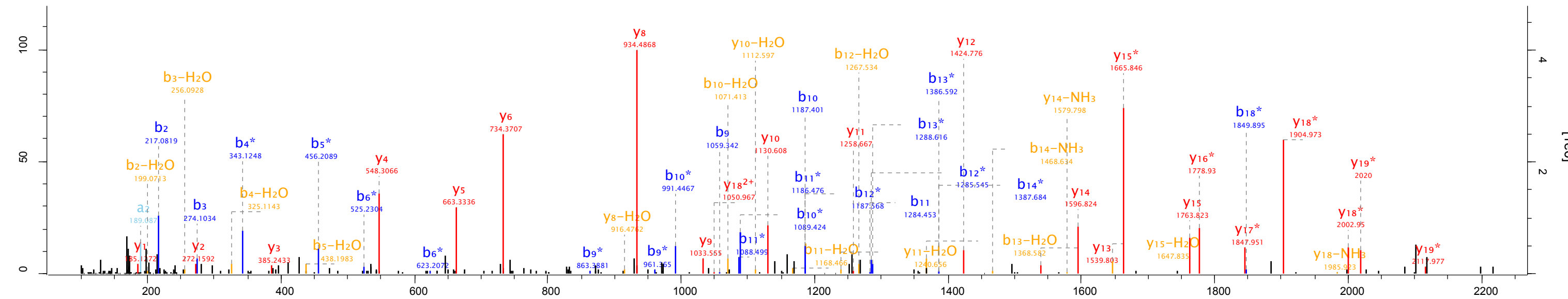
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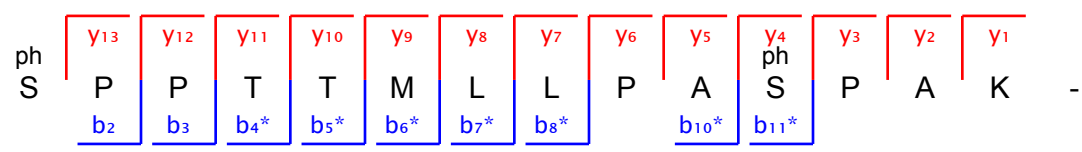
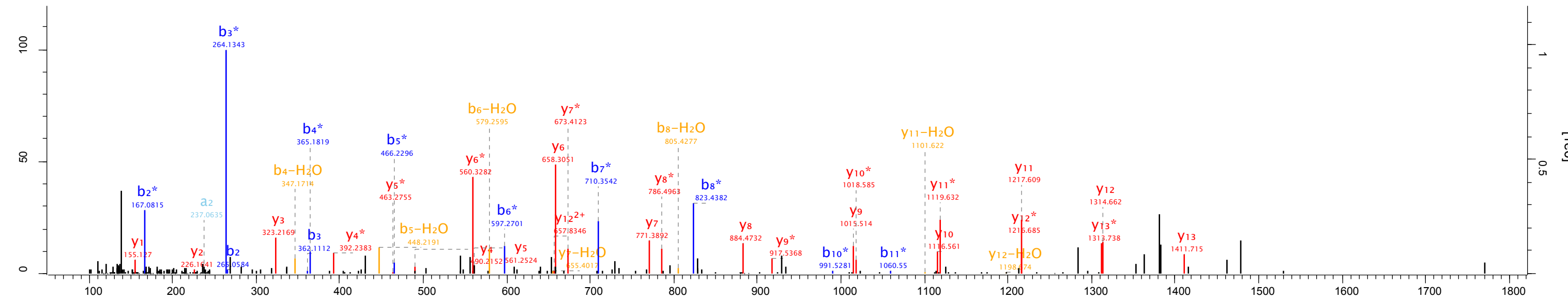
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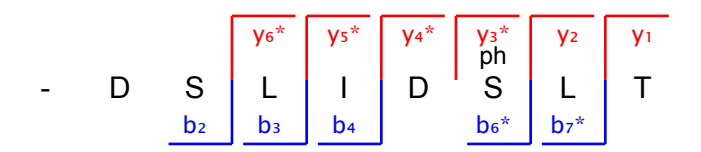
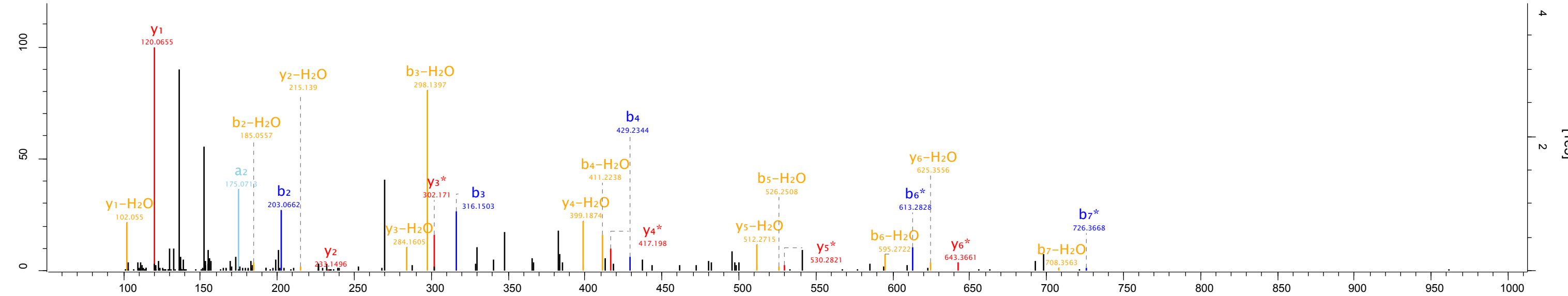


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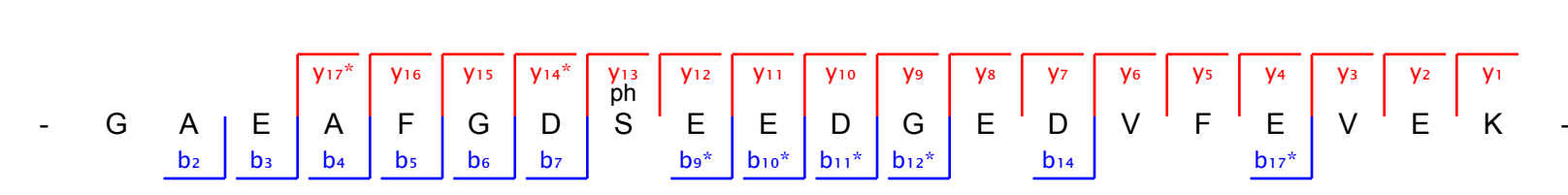
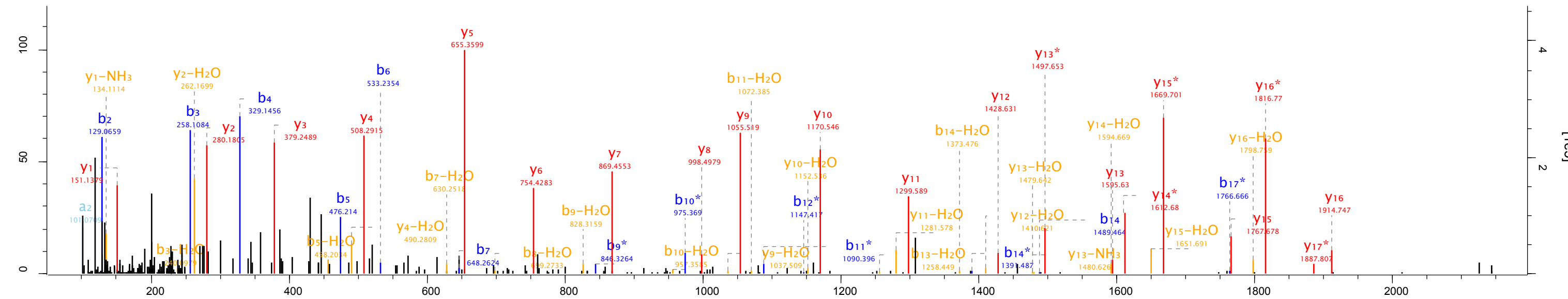


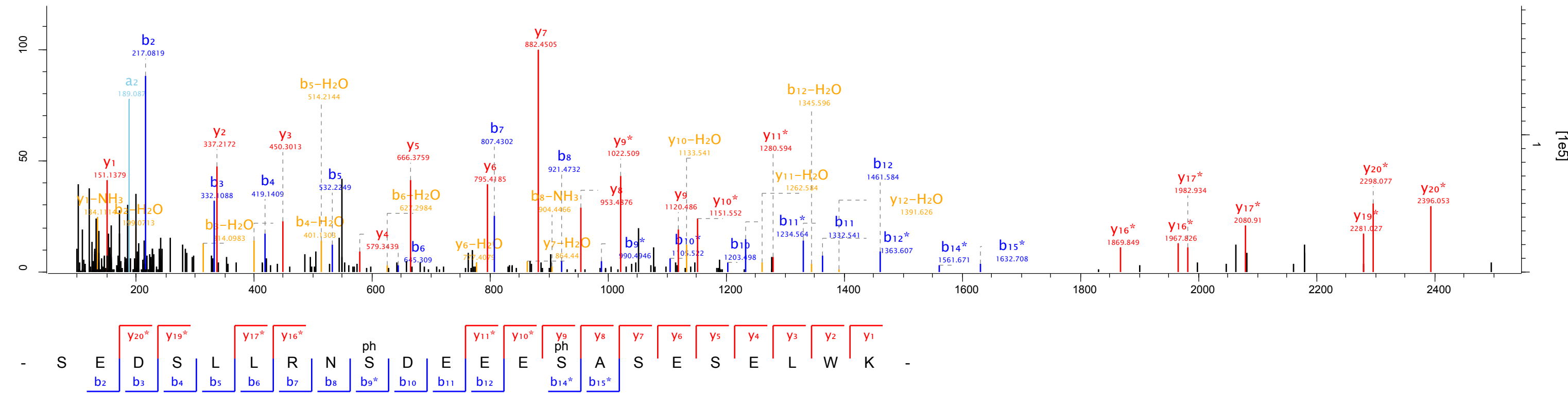
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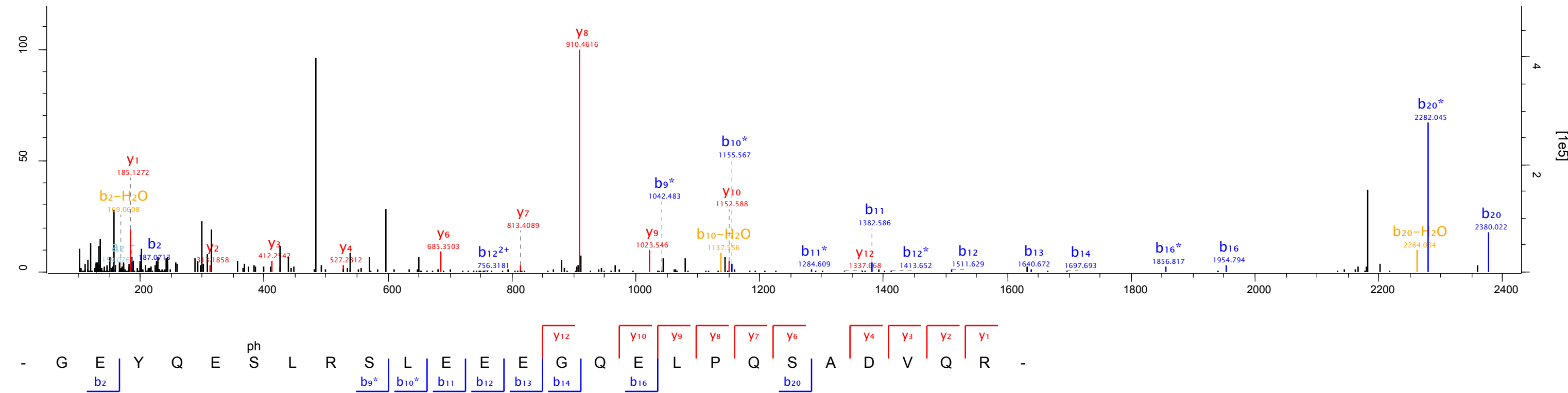




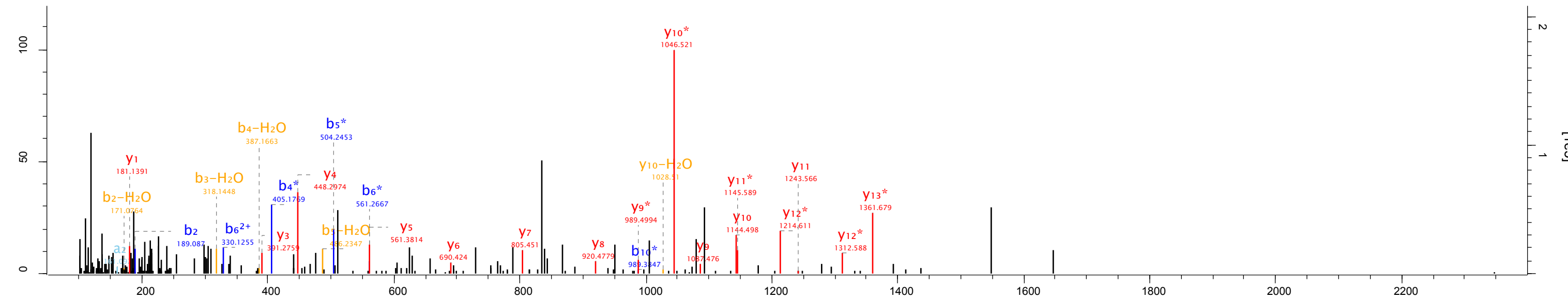
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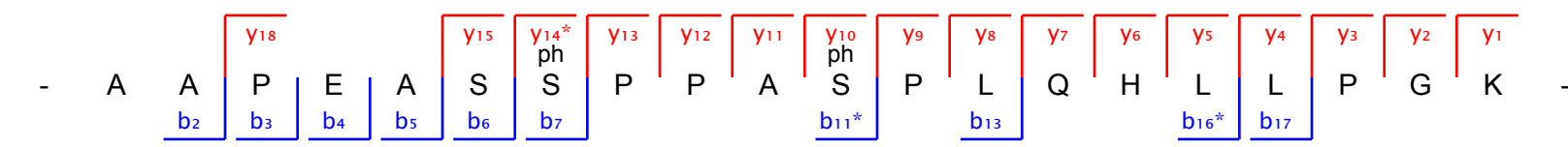
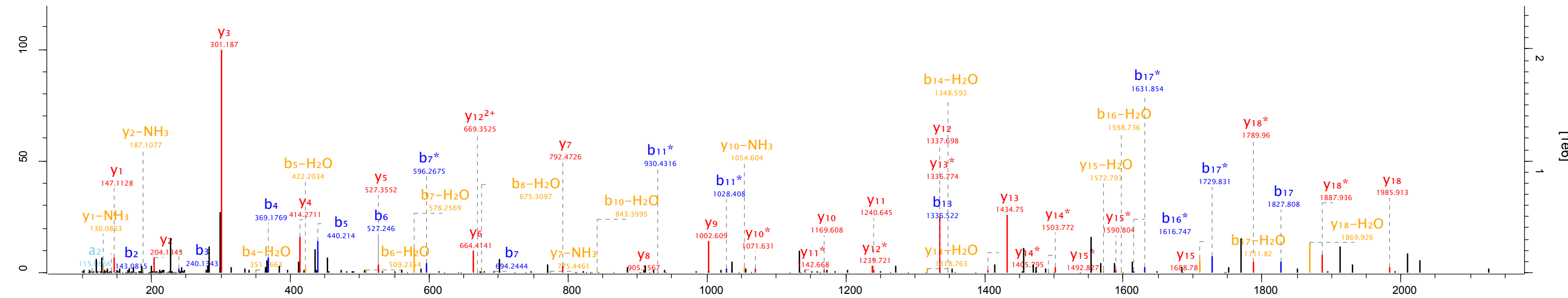




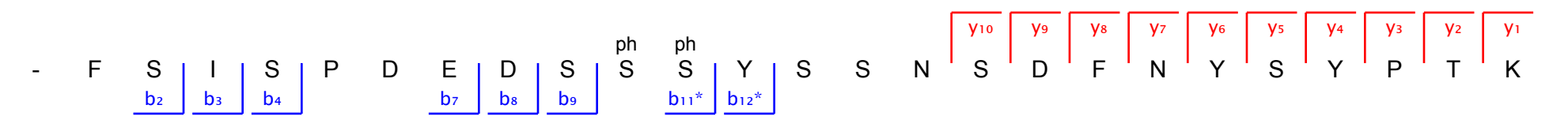
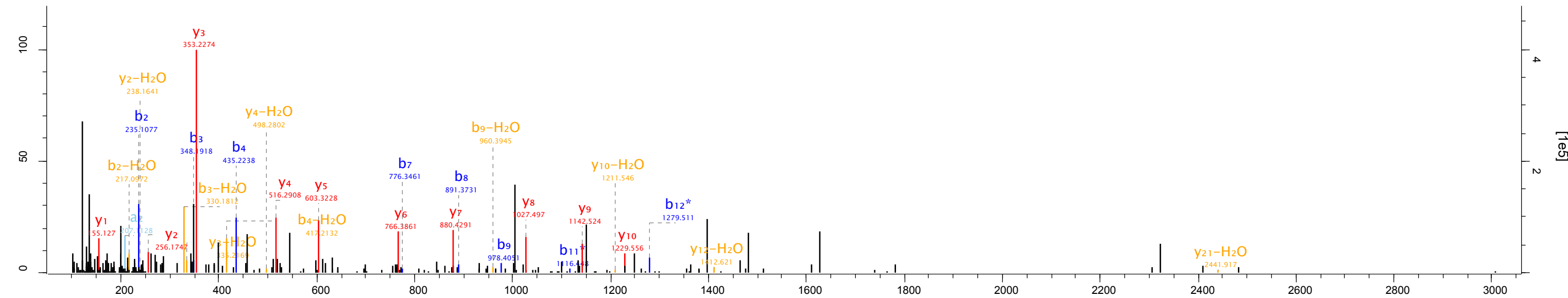
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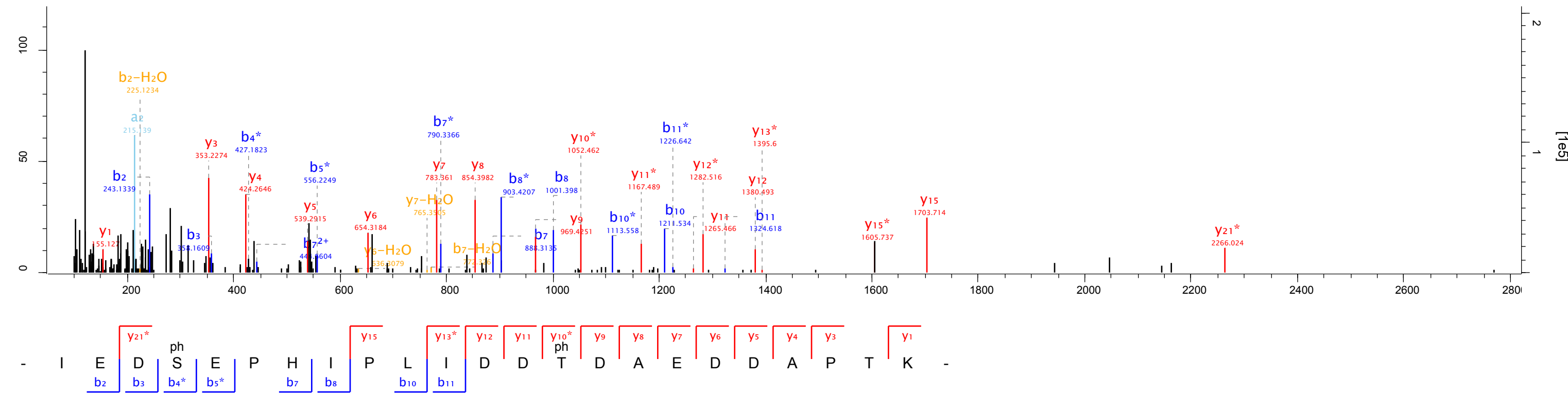


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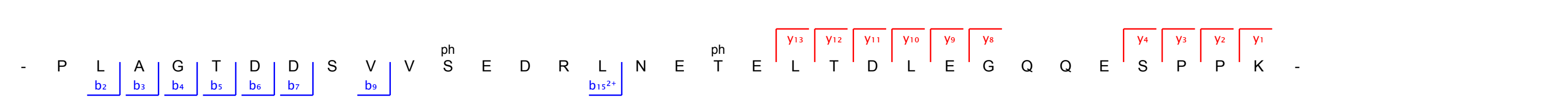
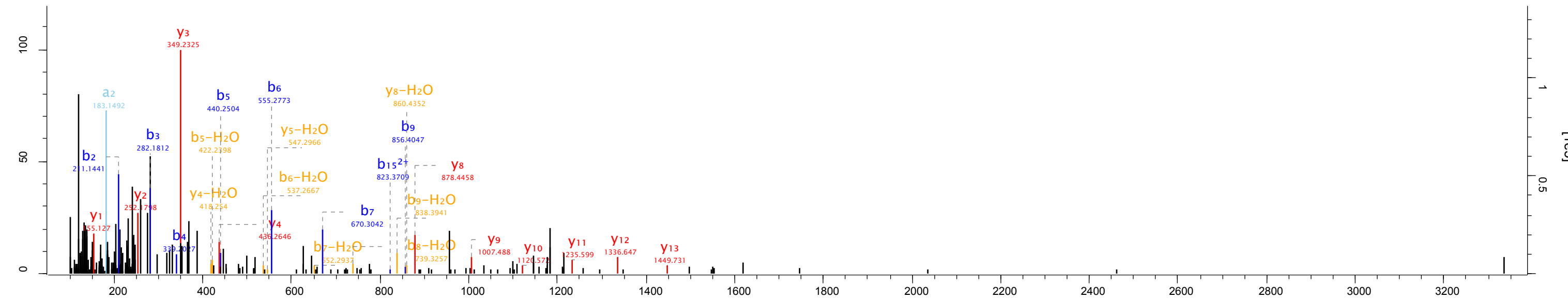


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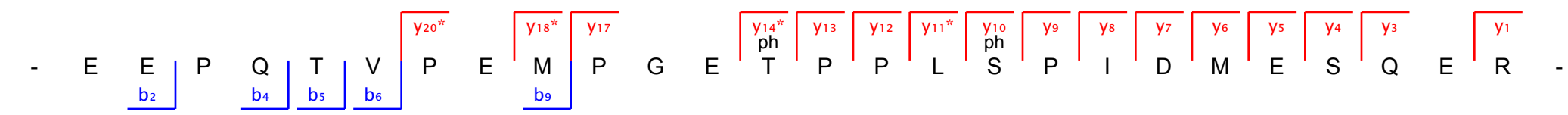
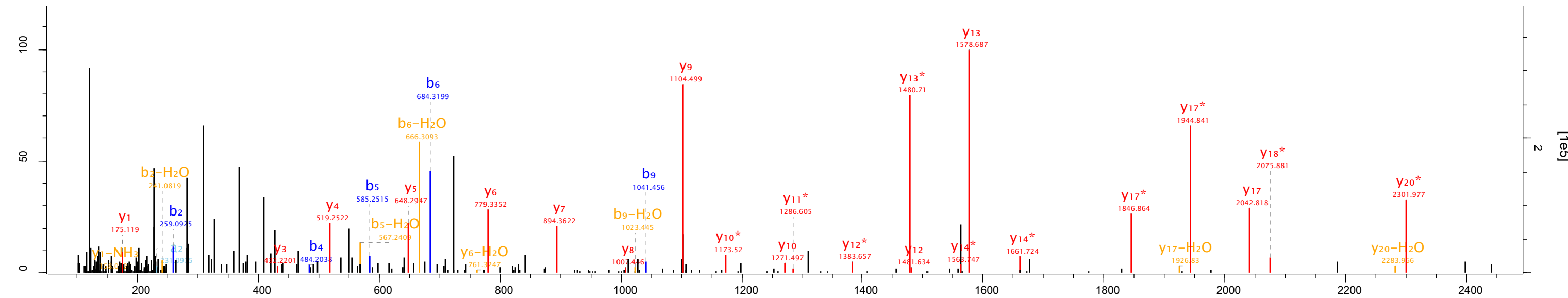


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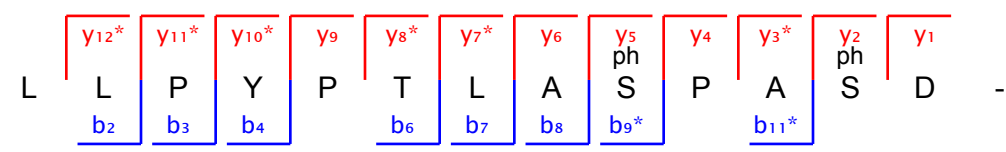
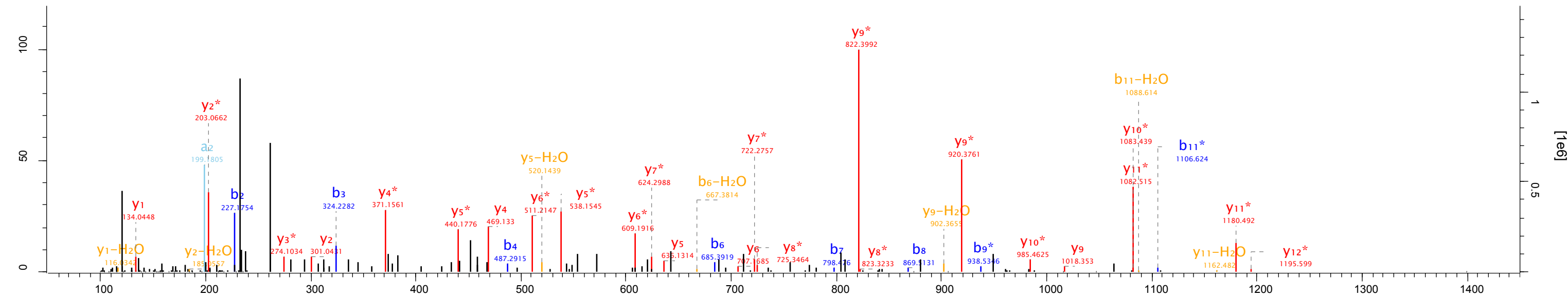


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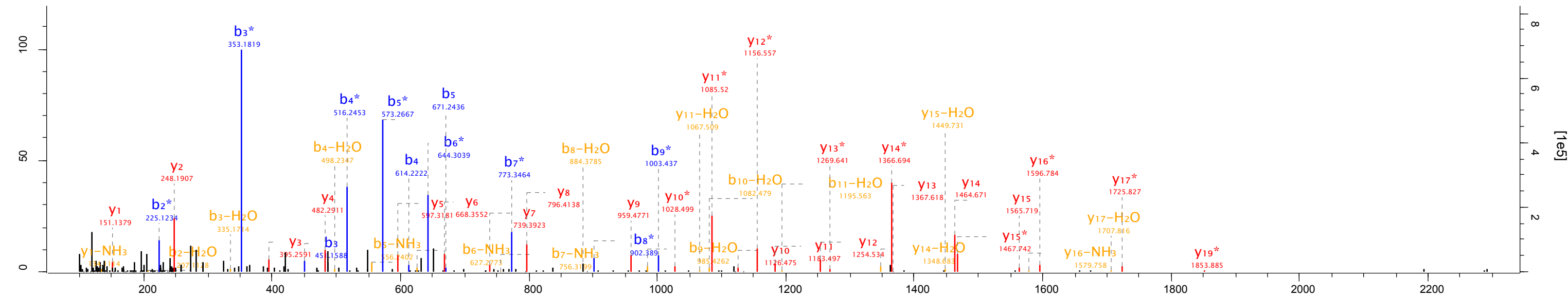
Scan 18025 Method FTMS; HCD Score 92.37 m/z 1029.1 Gene names JUN



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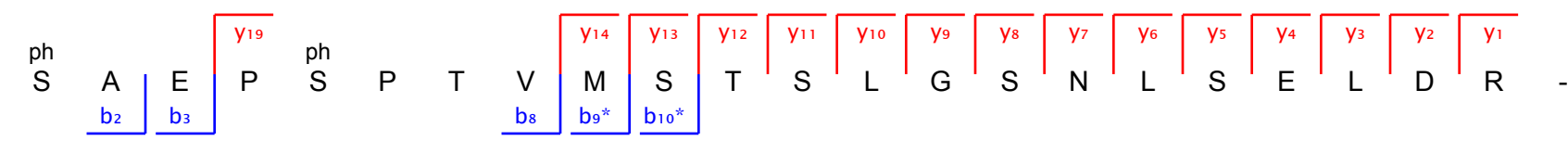
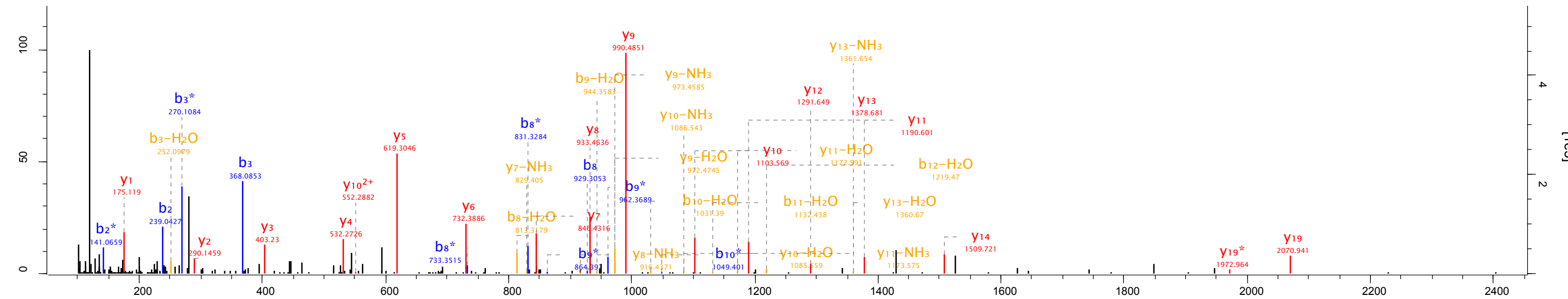
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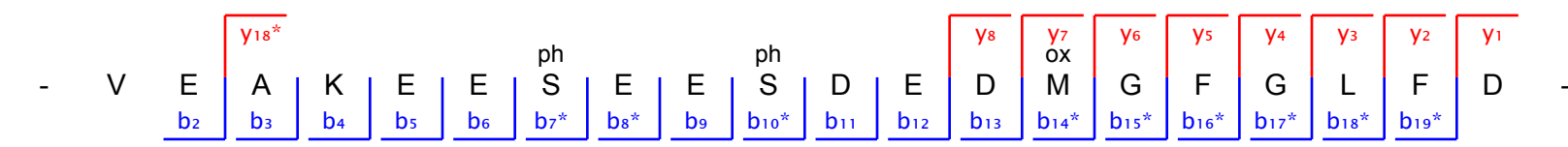
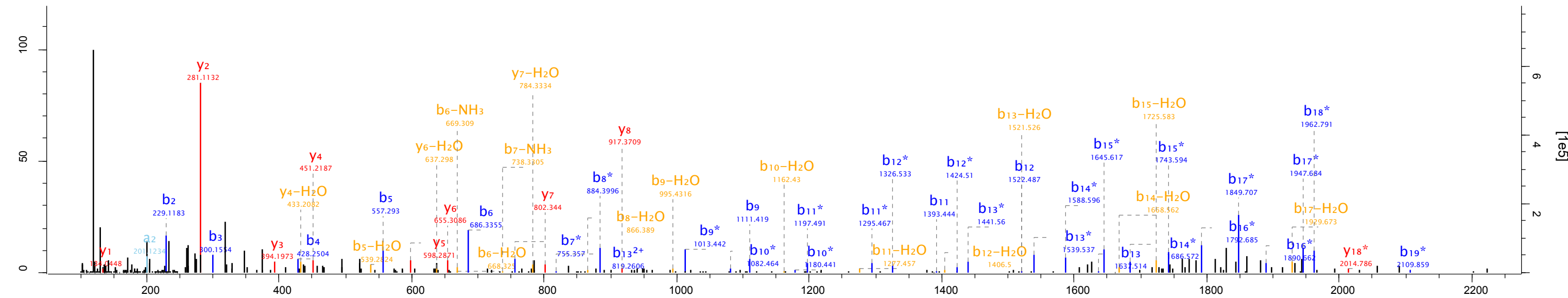
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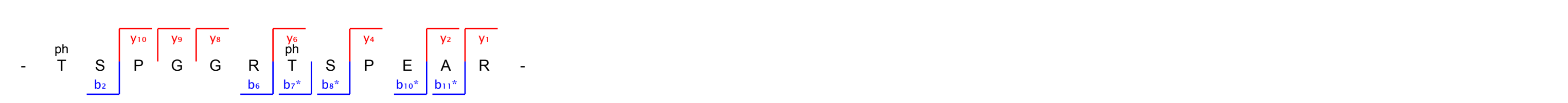
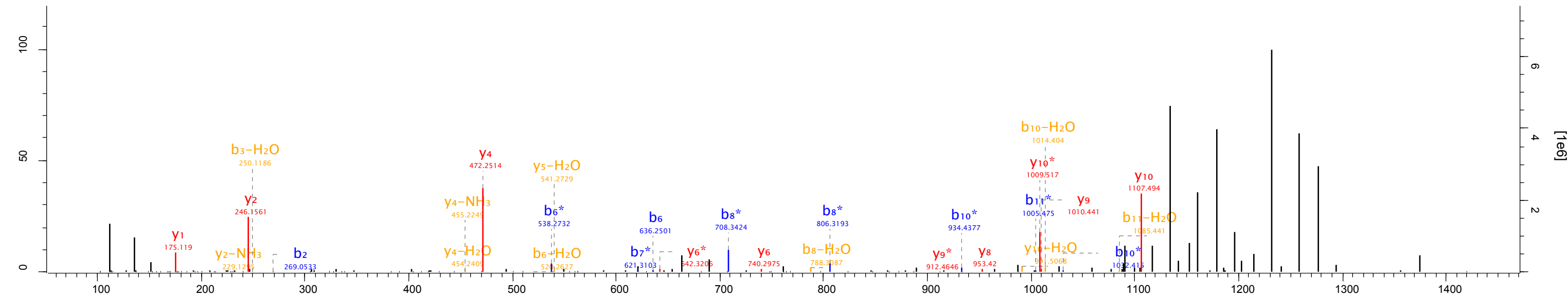
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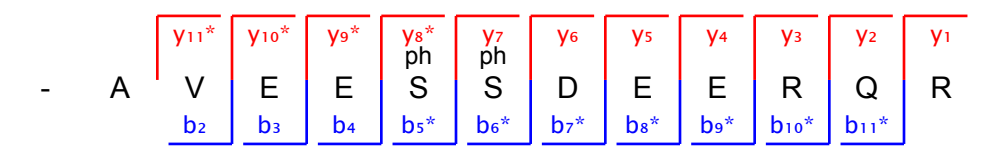
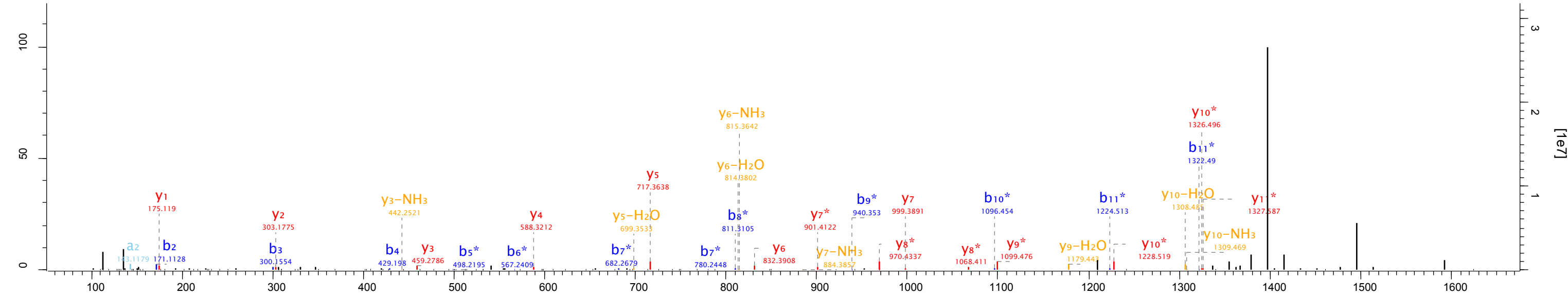
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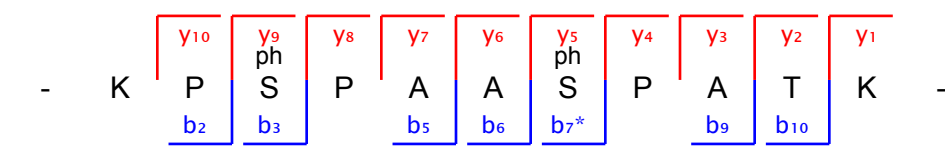
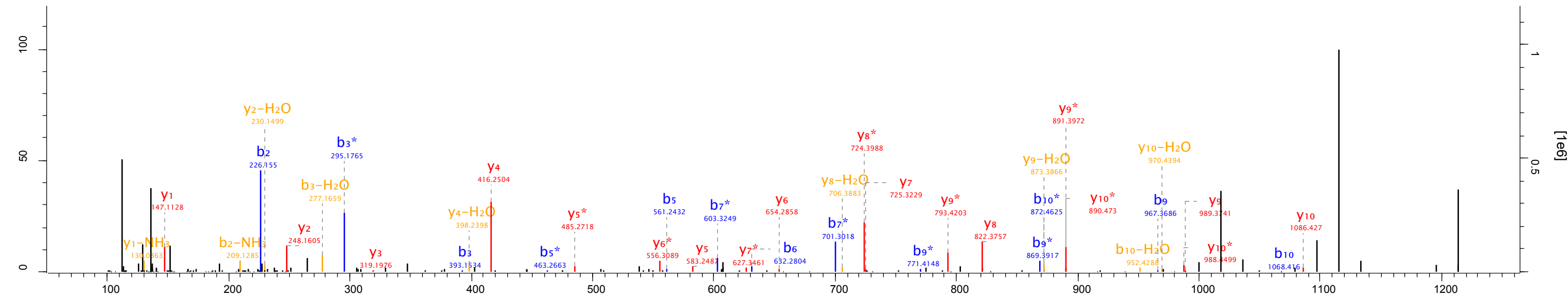
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 2285 Method FTMS; HCD Score 62.97 m/z 688.27 Gene names BICD2



20171215_MaS_33SR_LMH_phospho2_03 2325 FTMS; HCD 162.46 797.79 HIRIP3

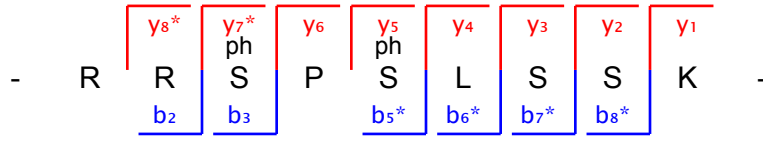
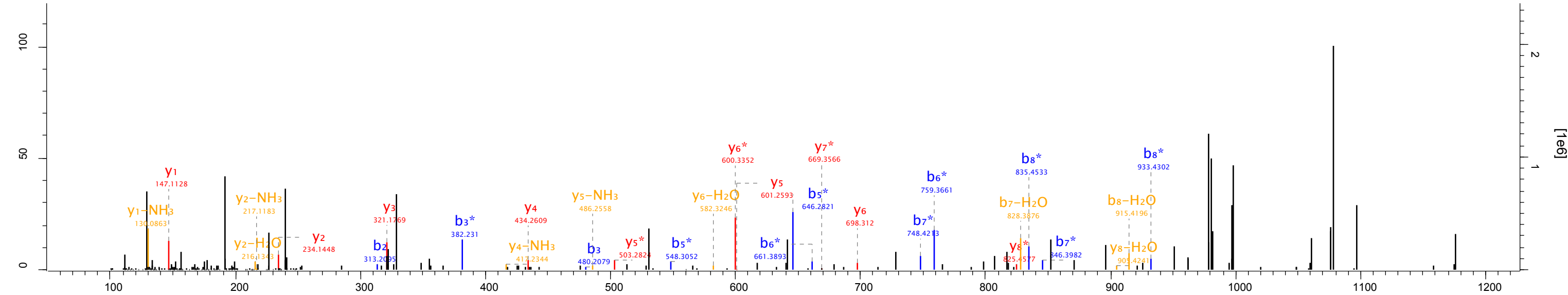


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 Scan: 2345 Method: FTMS; HCD Score: 174.87 m/z: 607.76 Gene names: MICALL1



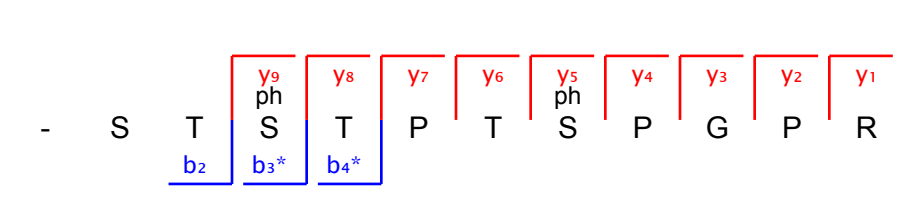
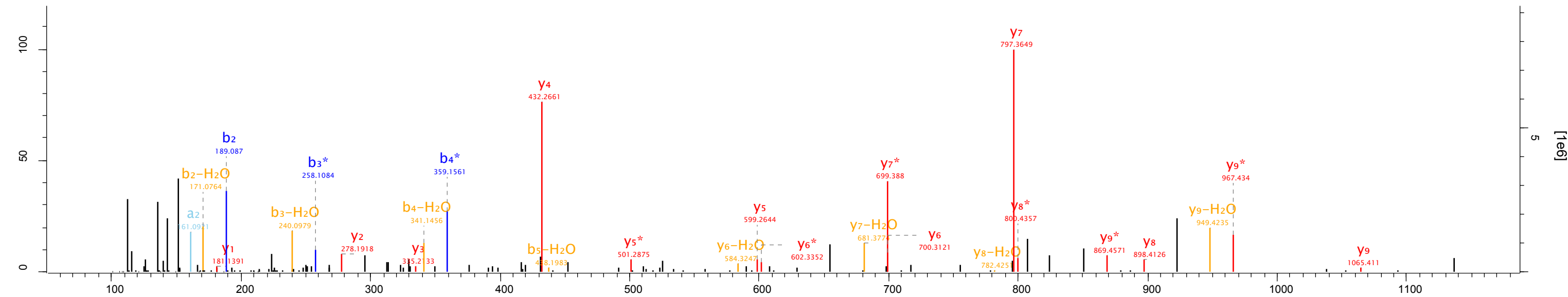
Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 2445 FTMS; HCD 101.55 393.18 SRRM1

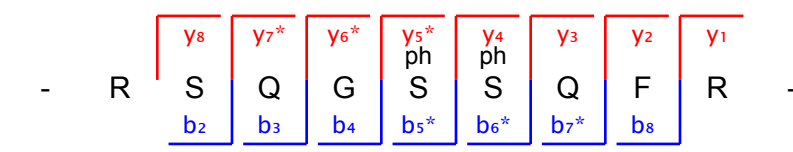
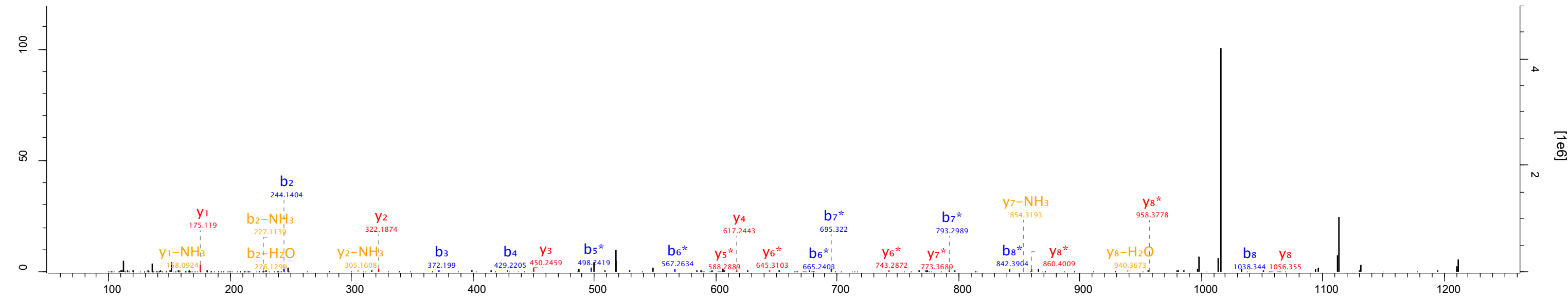


[1e6]

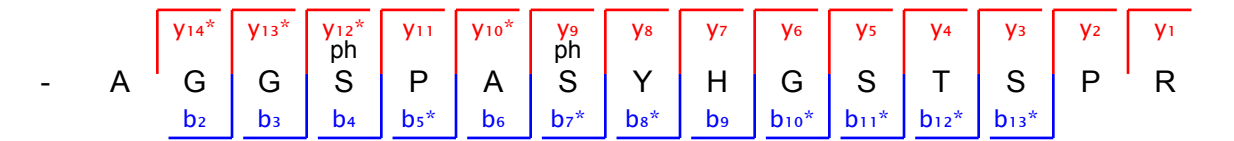
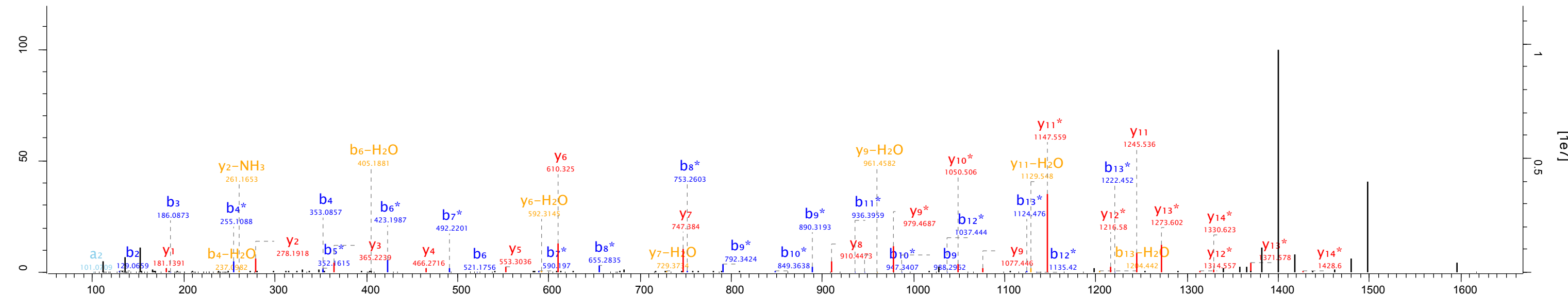
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 2915 Method: FTMS; HCD Score: 104.95 m/z: 627.25 Gene names: ATXN2L



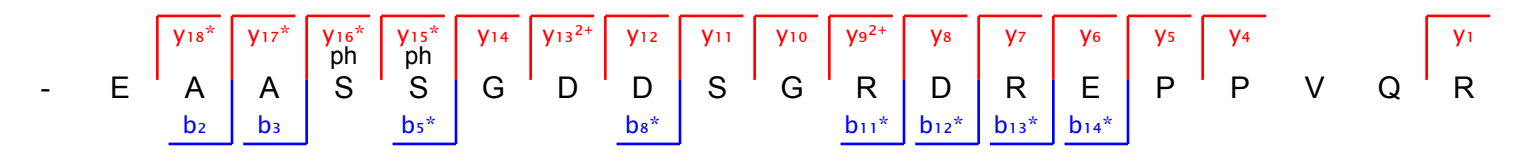
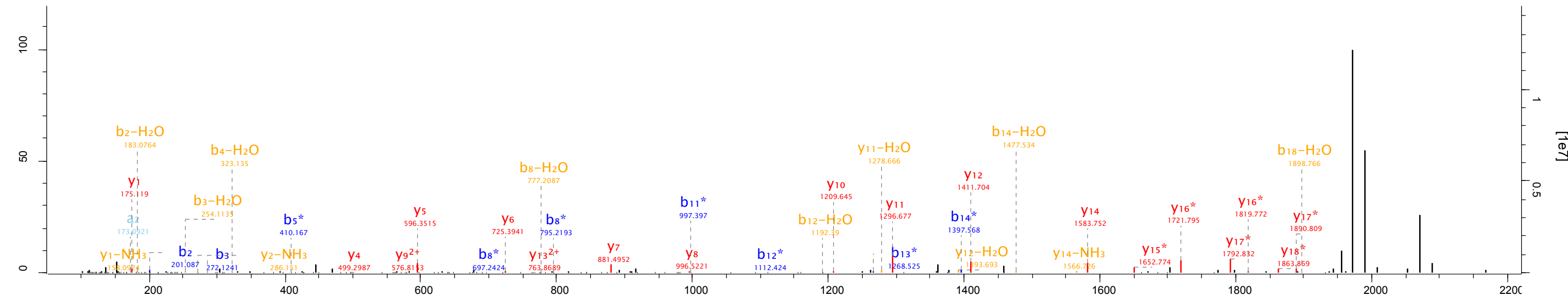
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3215 Method FTMS; HCD Score 58.08 m/z 606.73 Gene names PPP2R5A



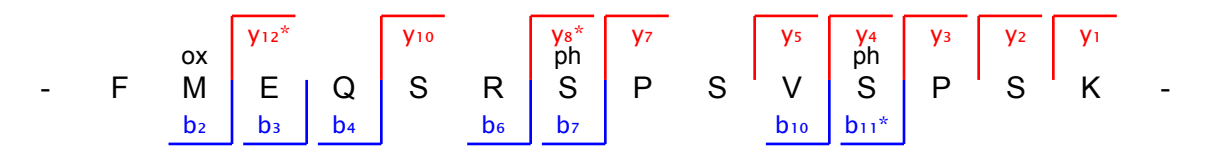
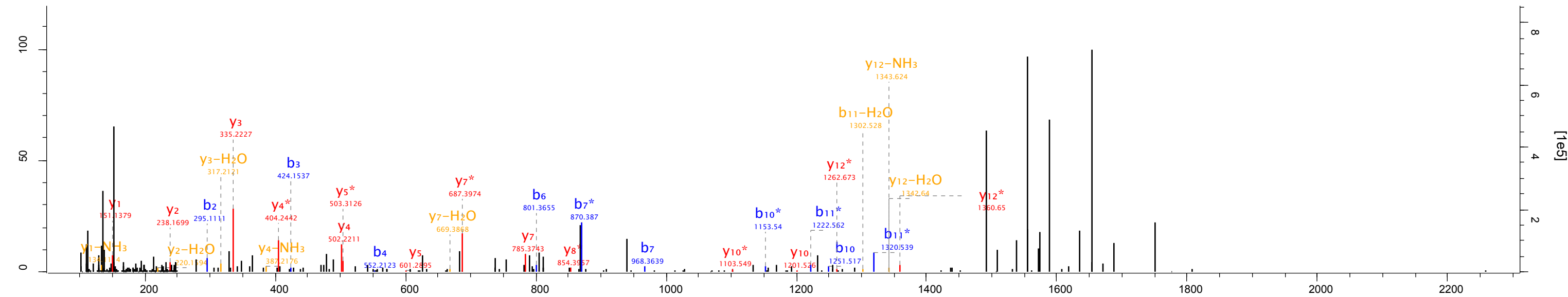
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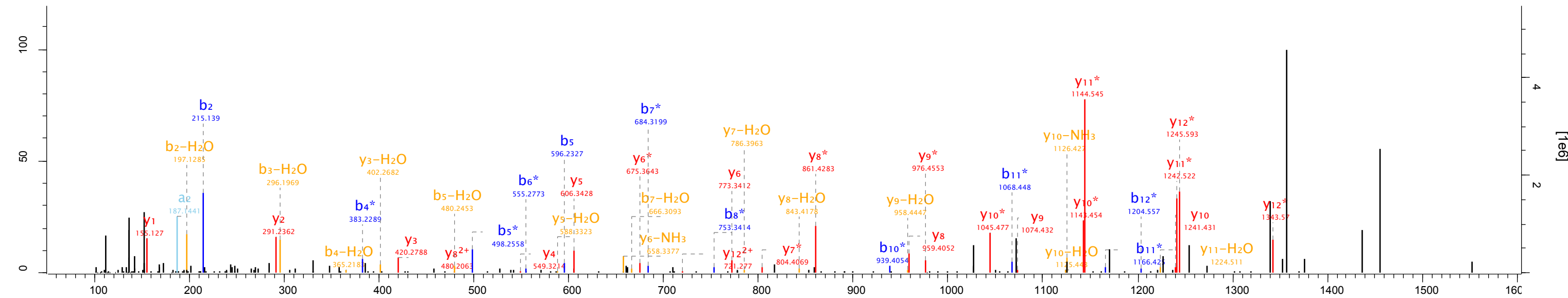


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3475 Method FTMS; HCD Score 89.92 m/z 730.63 Gene names HIRIP3



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4135 Method FTMS; HCD Score 73.45 m/z 877.37 Gene names CCDC132



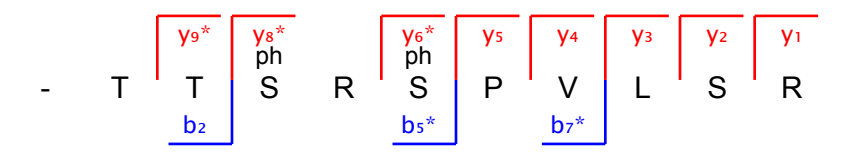
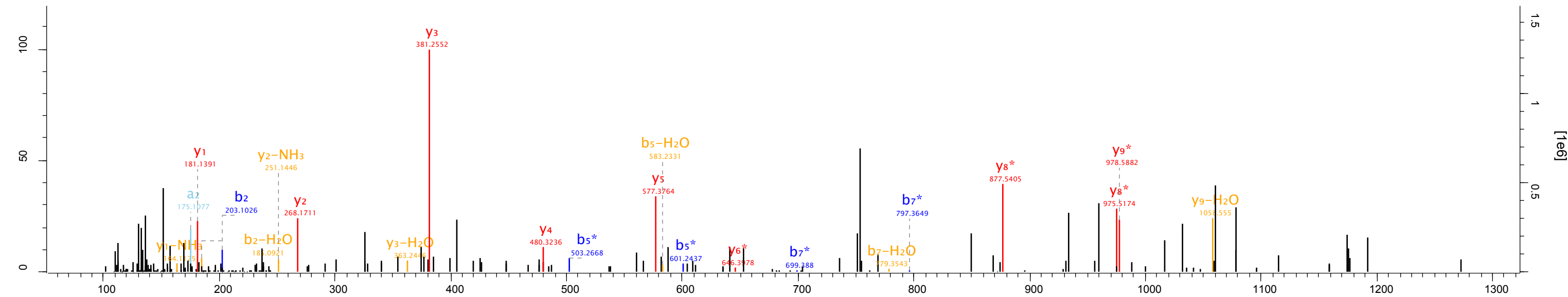


- L T V S D G E S G E E K K -

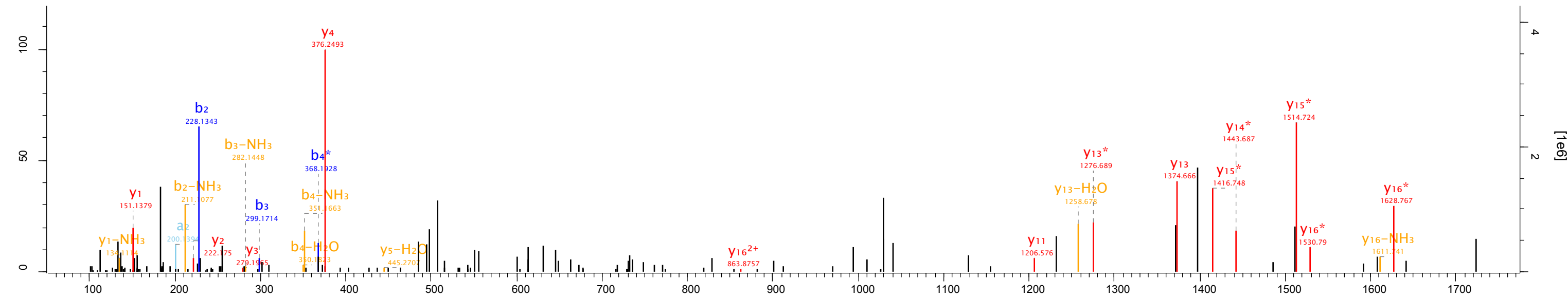
Fragmentation mapping:

- b₂** (blue box) covers T and V.
- b₄*** (blue box) covers S.
- b₅** (blue box) covers D.
- b₆*** (blue box) covers G.
- b₇*** (blue box) covers E.
- b₈*** (blue box) covers S.
- b₁₀*** (blue box) covers G.
- b₁₁*** (blue box) covers E.
- b₁₂*** (blue box) covers E.
- y₁** (red box) covers K.
- y₂** (red box) covers K.
- y₃** (red box) covers E.
- y₄** (red box) covers E.
- y₅** (red box) covers G.
- y₆** (red box) covers S.
- y₇*** (red box) covers E.
- y₈** (red box) covers G.
- y₉** (red box) covers D.
- y₁₀ ph** (red box) covers S.
- y₁₁*** (red box) covers V.
- y₁₂*** (red box) covers T.

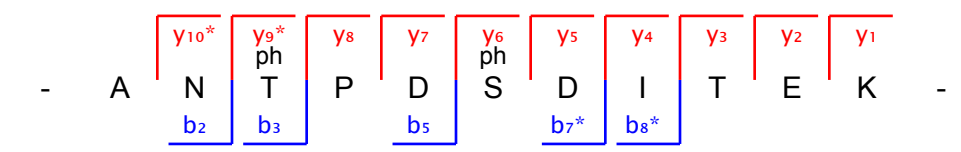
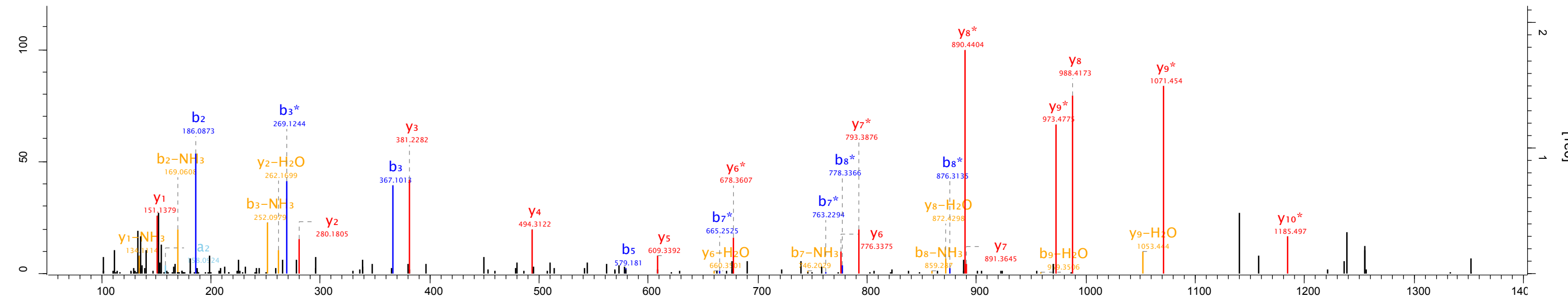
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4205 Method FTMS; HCD Score 44.93 m/z 425.87 Gene names MAP4K4

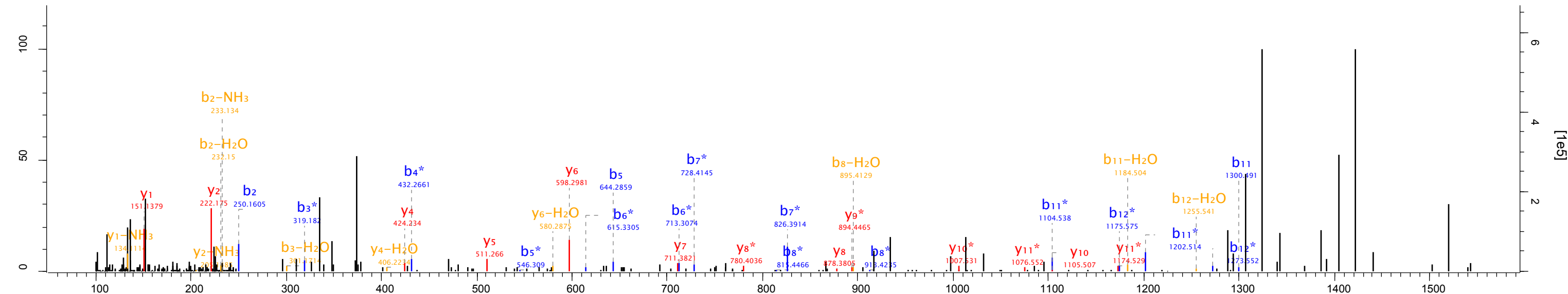


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4595 Method FTMS; HCD Score 59.54 m/z 613.95 Gene names TCF20



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4675 Method FTMS; HCD Score 135.09 m/z 677.76 Gene names SMARCD1

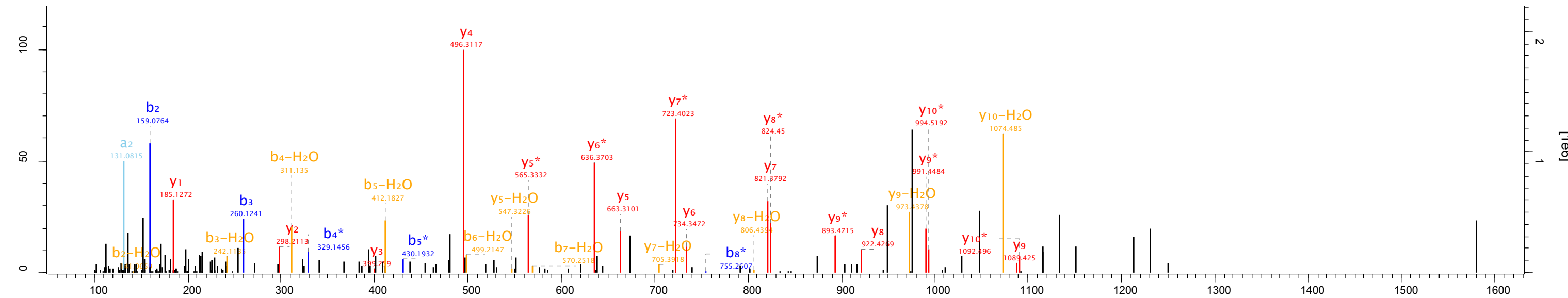




- R S S Y₁₁* Y₁₀ Y₉* Y₈ Y₇ Y₆ Y₅ Y₄ D Y₂ Y₁ -

ph S L N S I S S A K

b₂ b₃* b₄* b₅ b₆* b₇* b₈* b₁₁ b₁₂*



- S A T S A S P T L R -

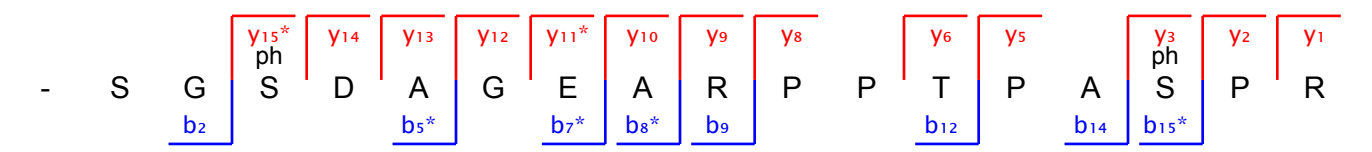
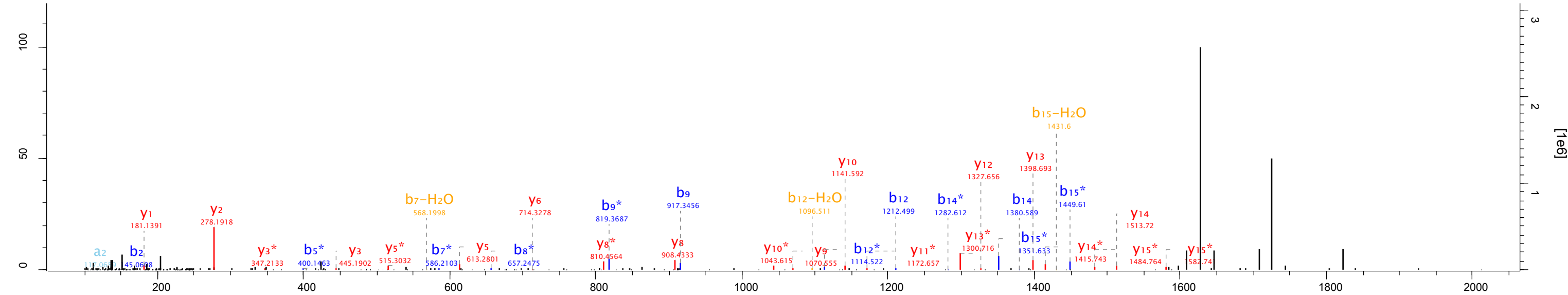
Fragmentation mapping (b and y ions):

- b2: A
- b3: AT
- b4*: ATS
- b5*: AT
- b8*: AS
- y1: R
- y2: L
- y3: T
- y4: P
- y5: SP
- y6: AS
- y7: S
- y8: TS
- y9: ST
- y10*: AT

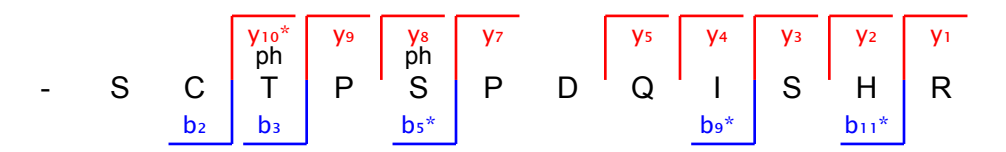
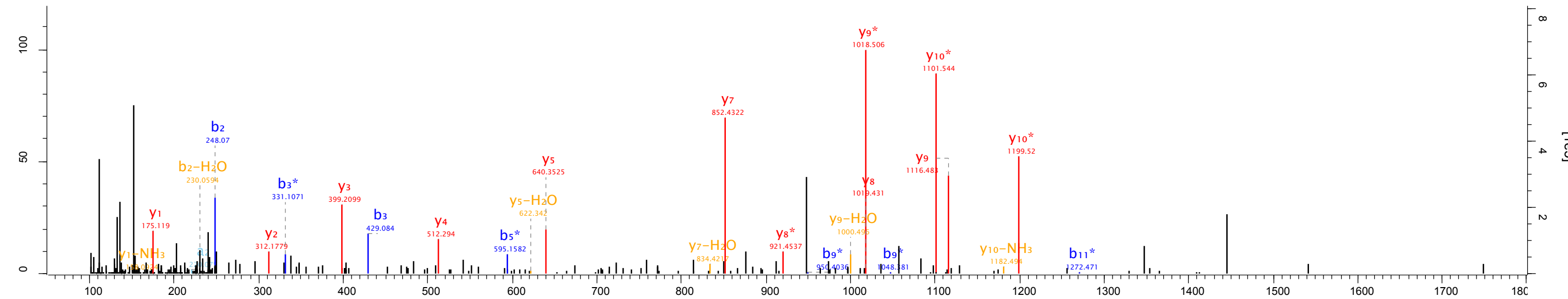
Raw file

20171215_MaS_33SR_LMH_phospho2_03

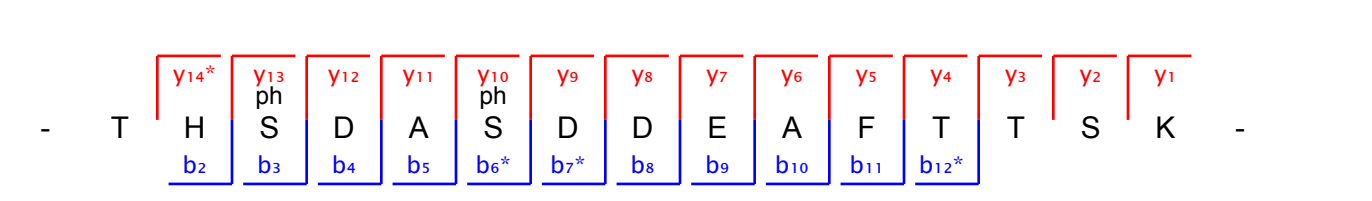
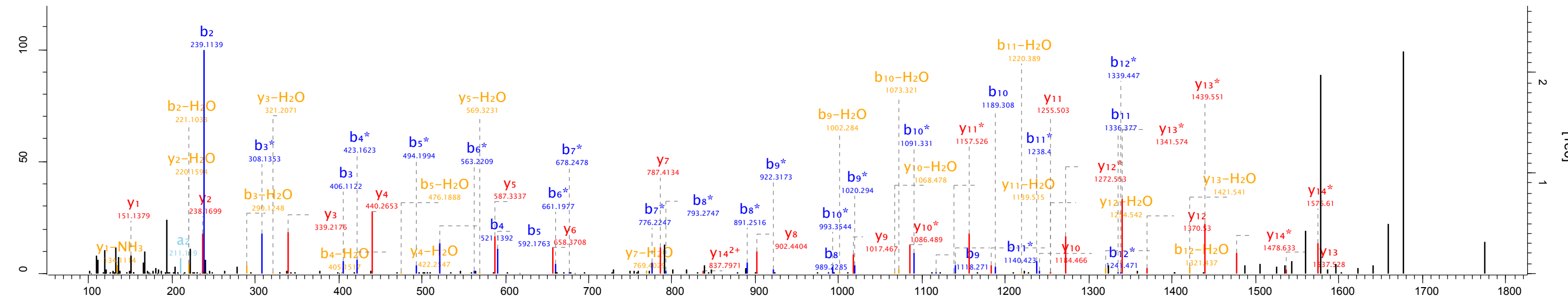
Scan 5135 Method FTMS; HCD Score 84.03 m/z 912.89 Gene names SIPA1



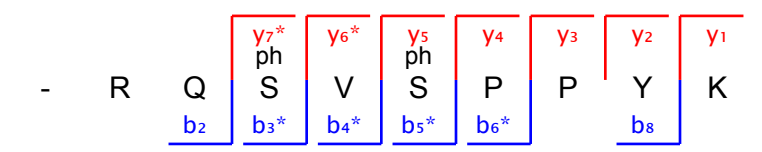
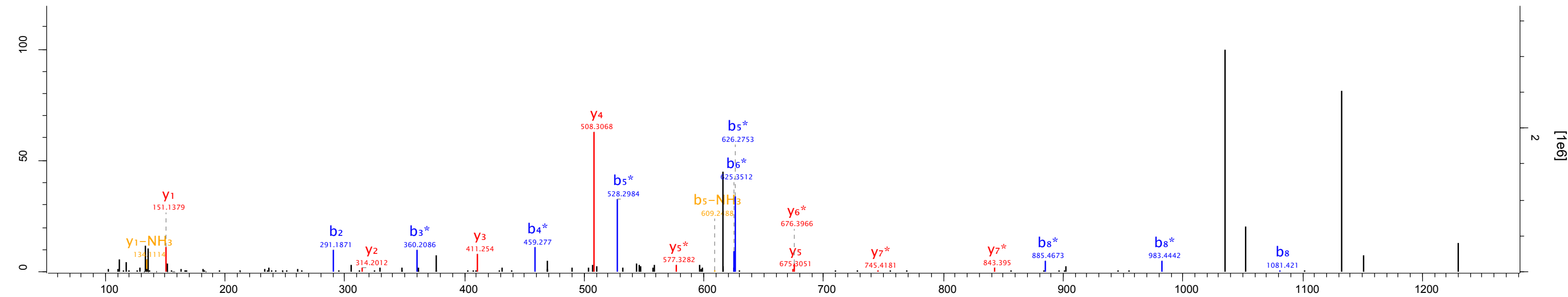
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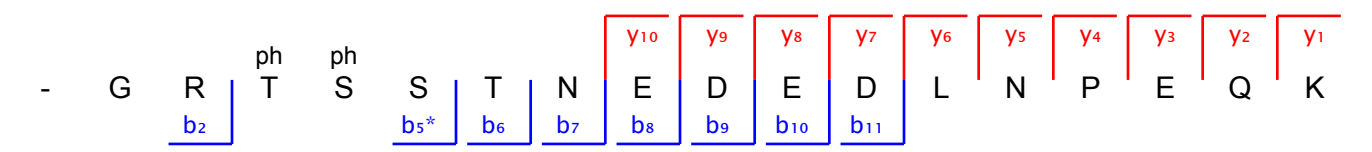
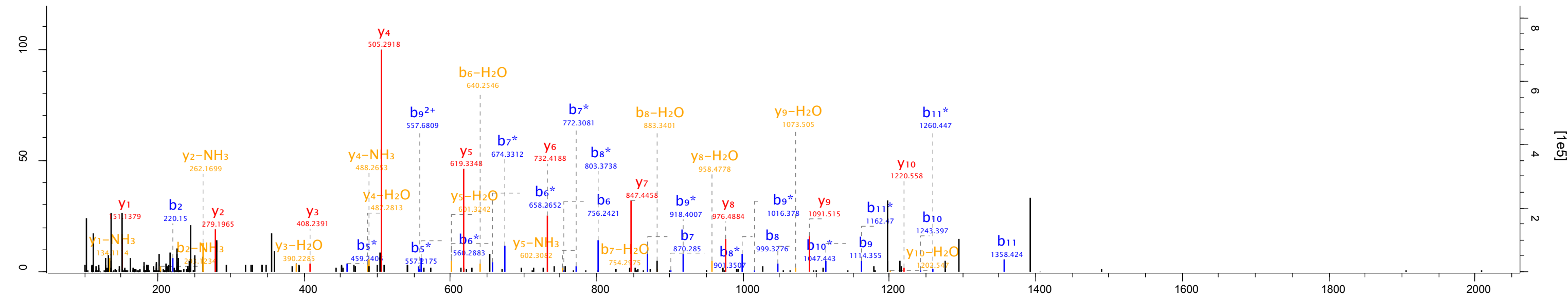
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 Scan: 5365 Method: FTMS; HCD Score: 294.09 m/z: 888.32 Gene names: ARHGAP5



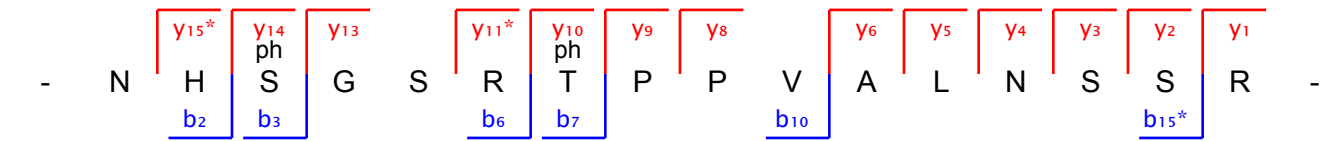
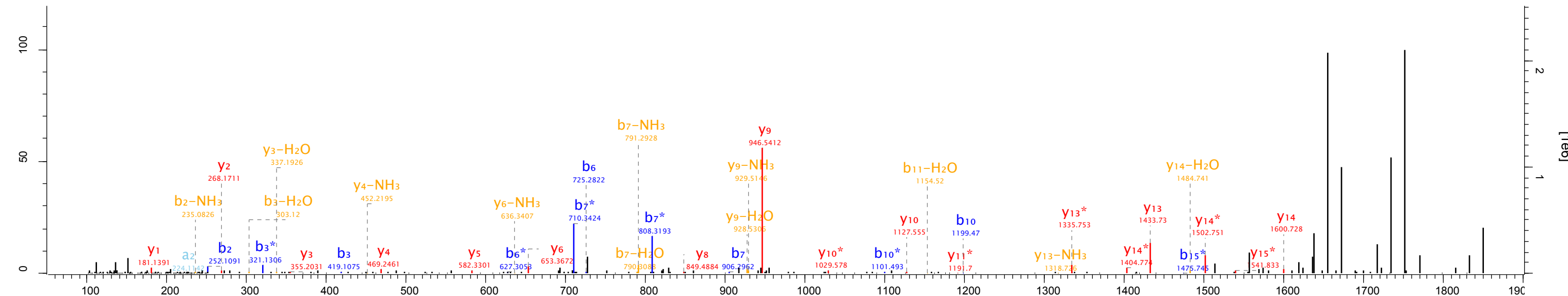
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5395 Method FTMS; HCD Score 88.08 m/z 616.28 Gene names CDK12



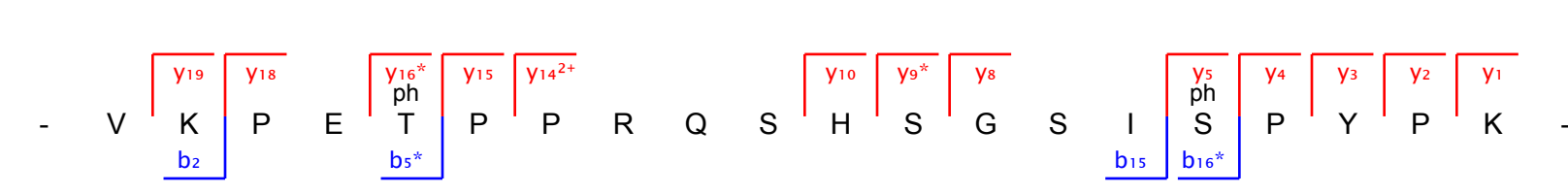
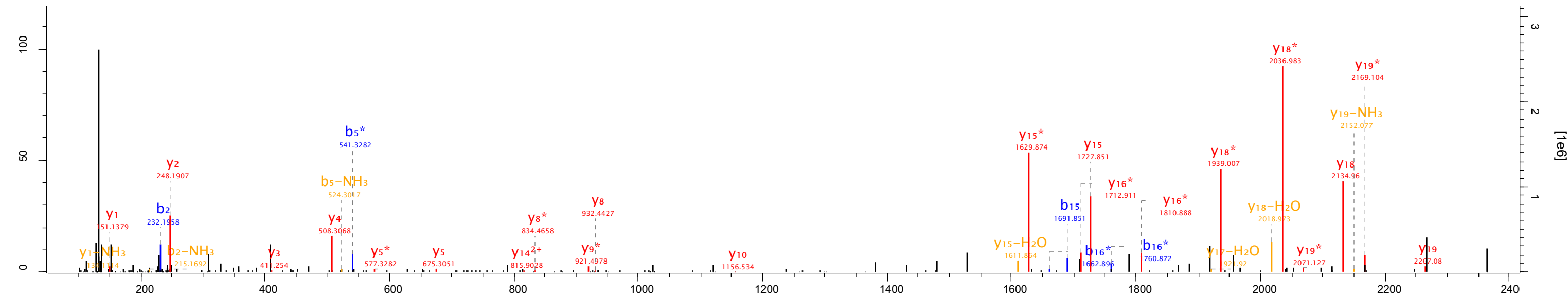
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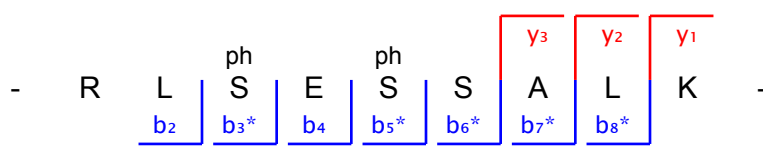
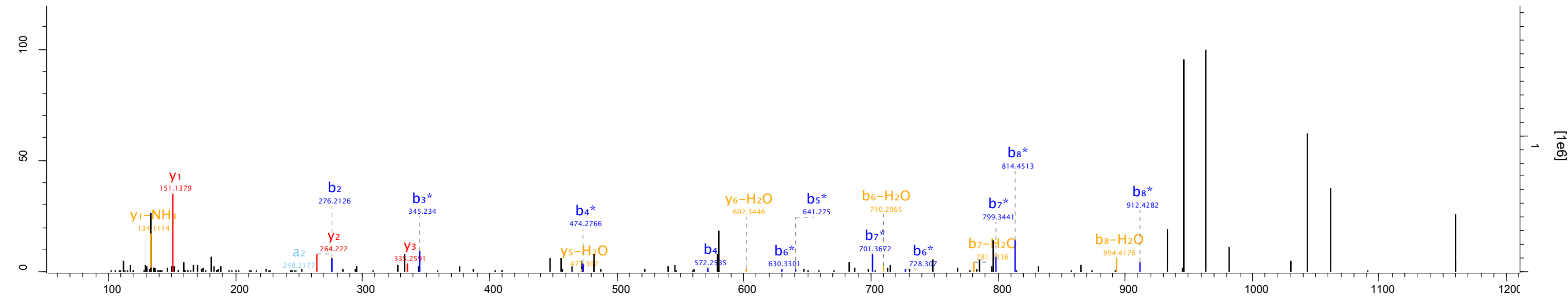
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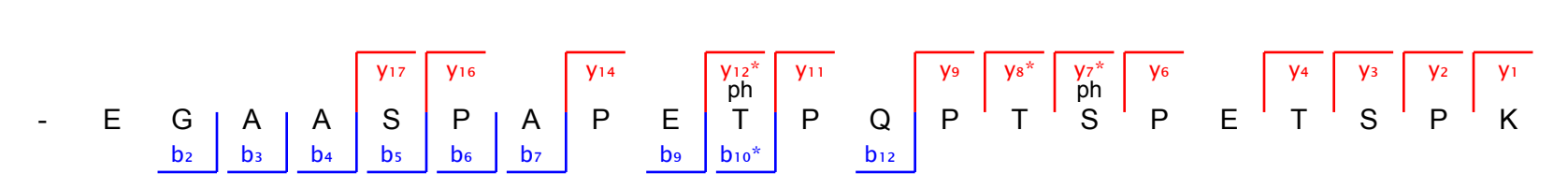
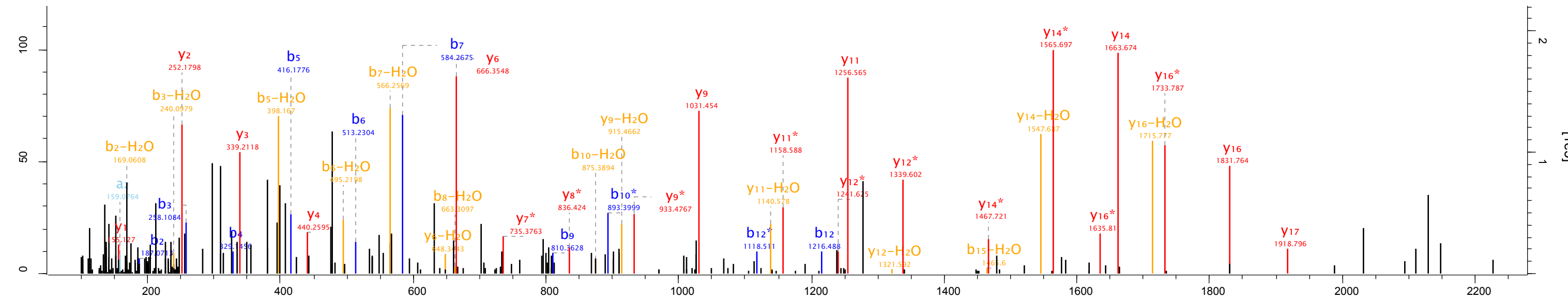
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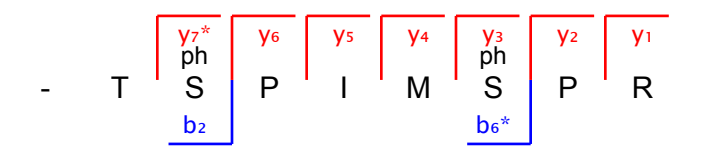
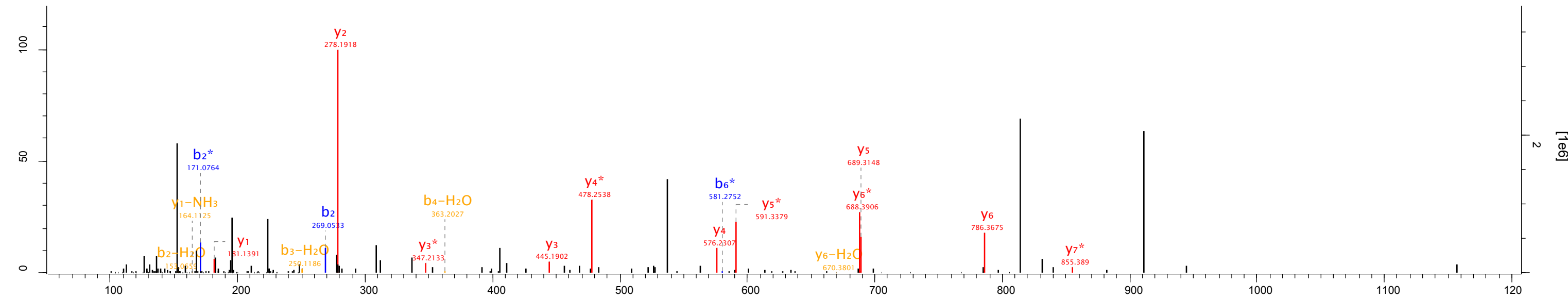
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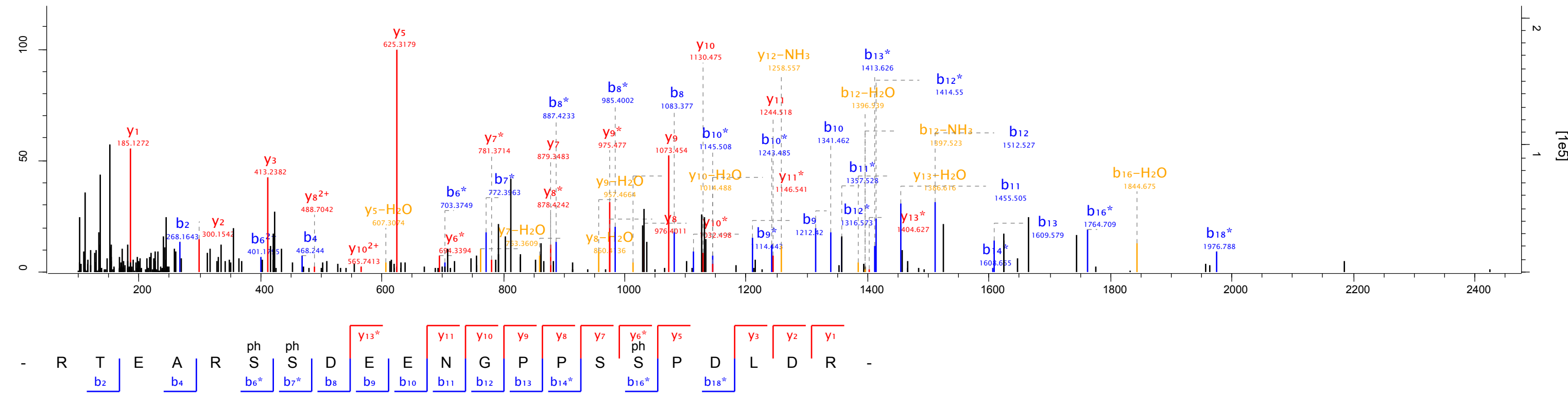


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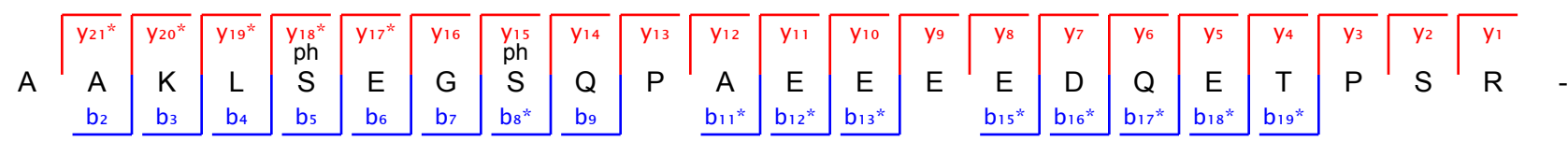
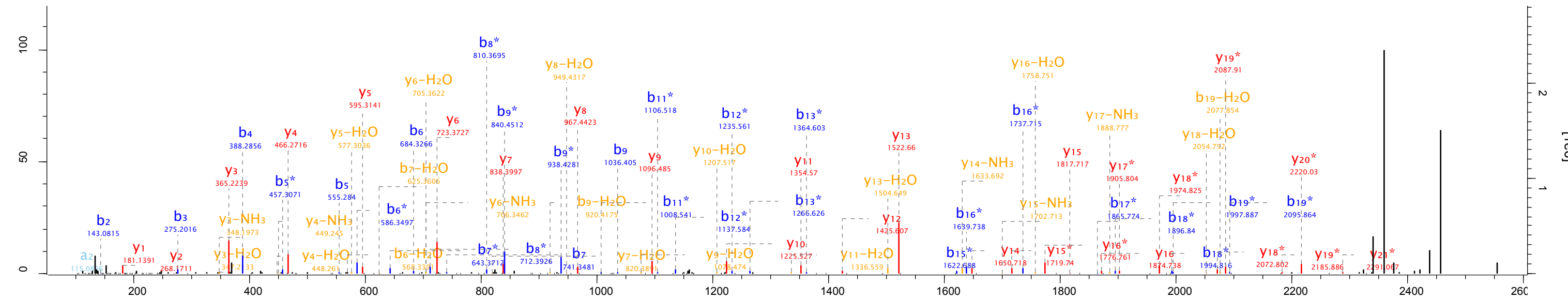


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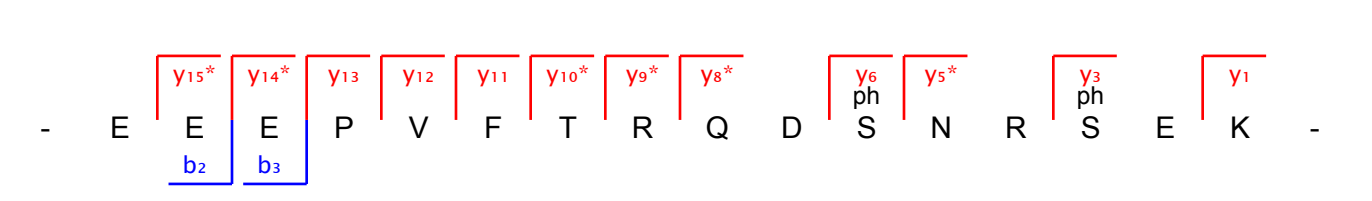
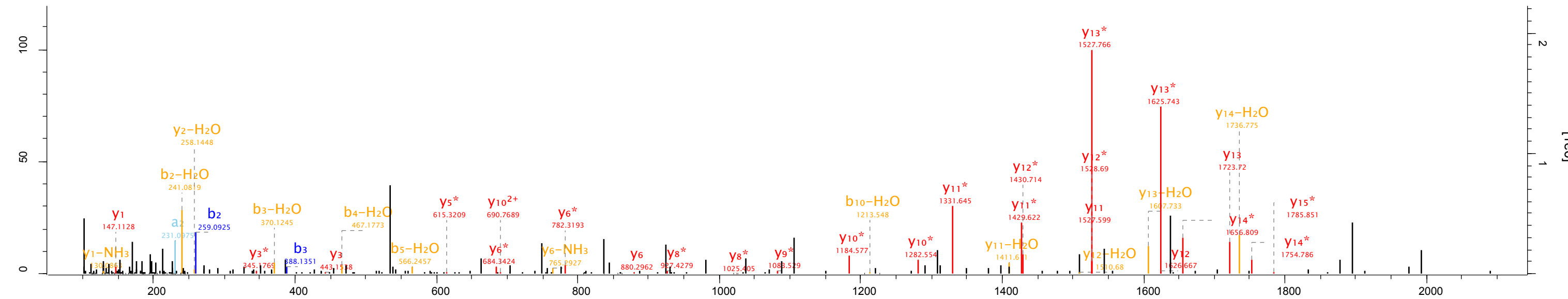




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 Scan: 6055 Method: FTMS; HCD Score: 302.29 m/z: 1280.04 Gene names: ACIN1

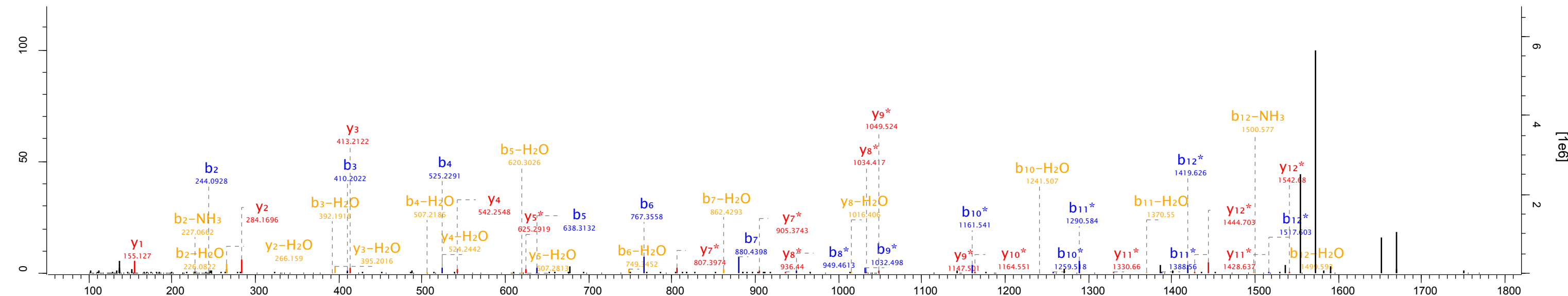


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 6095 Method: FTMS; HCD Score: 108.96 m/z: 704.29 Gene names: PRRC2C



Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 6285 Method FTMS; HCD Score 177.6 m/z 885.35 Gene names LARP7



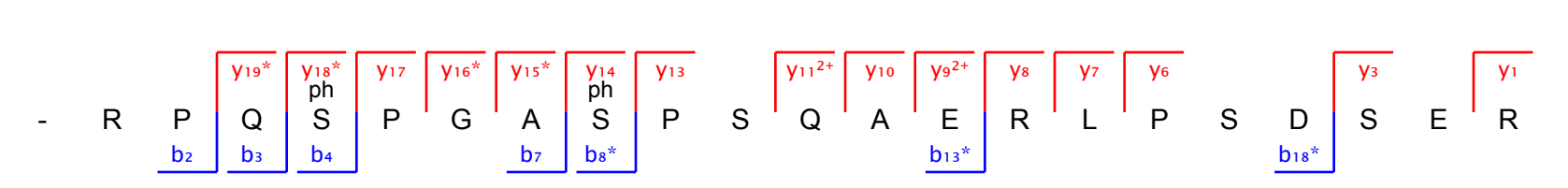
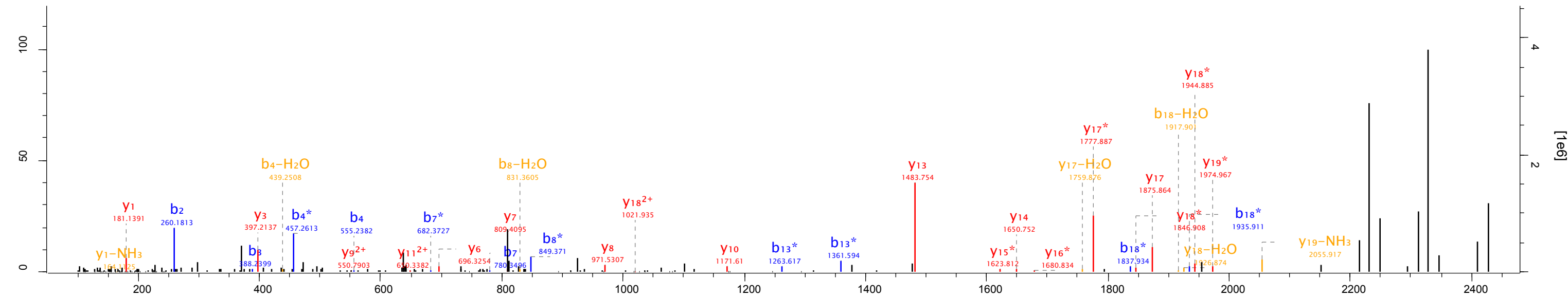
- E N R D I E I S P T E E E K -

Peptide sequence: E N R D I E I S P T E E E K

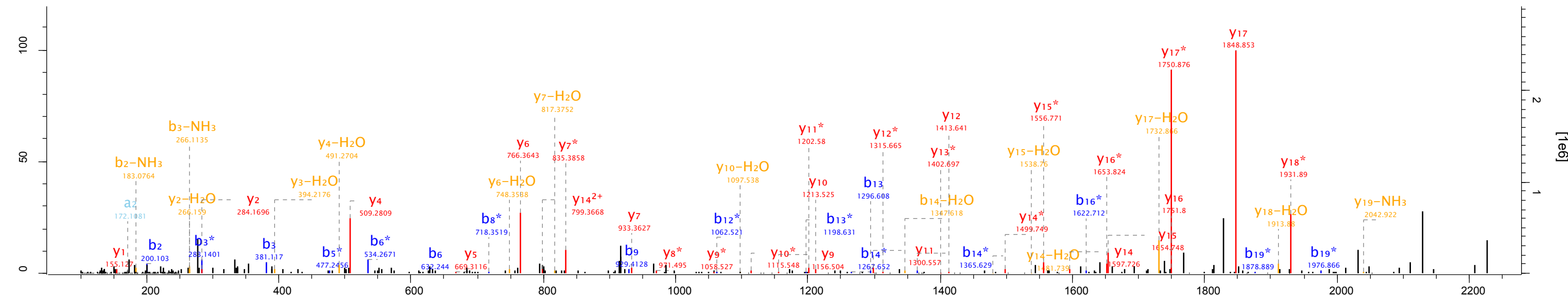
Fragmentation sites (b and y ions) are indicated by boxes below the sequence:

- b2: N
- b3: NR
- b4: NRD
- b5: NRDI
- b6: NRDE
- b7: NRDEI
- b8*: NRS
- b9*: NRSP
- b10*: NRSPTE
- b11*: NRSPTEE
- b12*: NRSPTEEE

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 6565 Method: FTMS; HCD Score: 61.24 m/z: 810.7 Gene names: SPEN

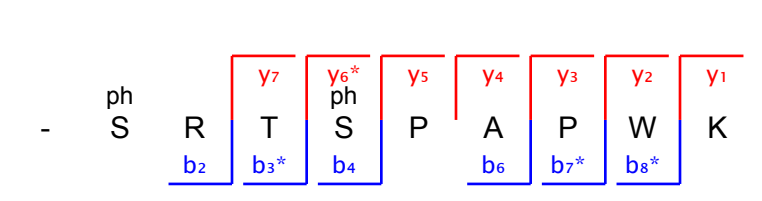
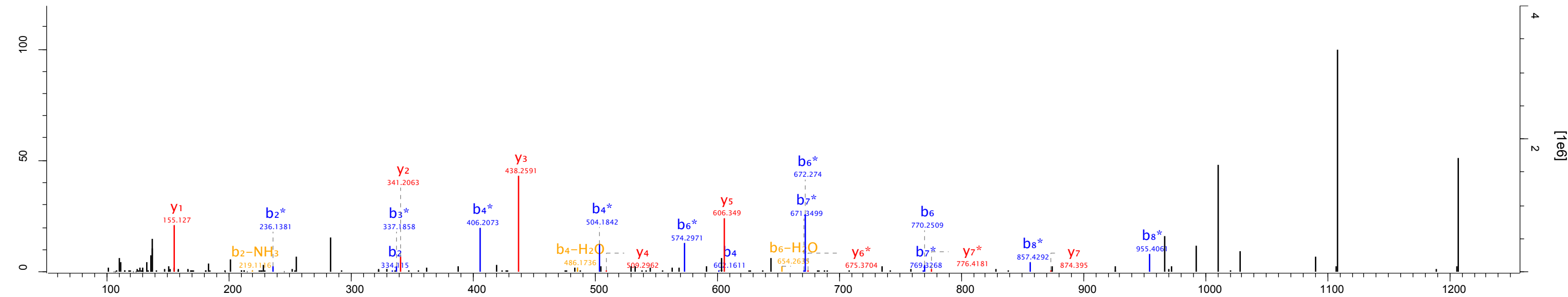


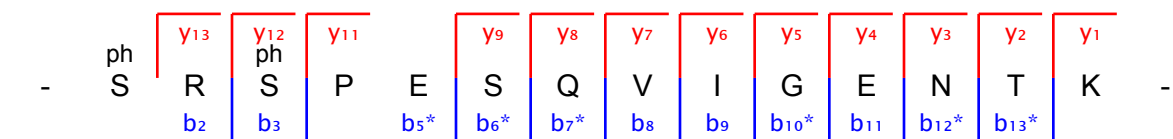
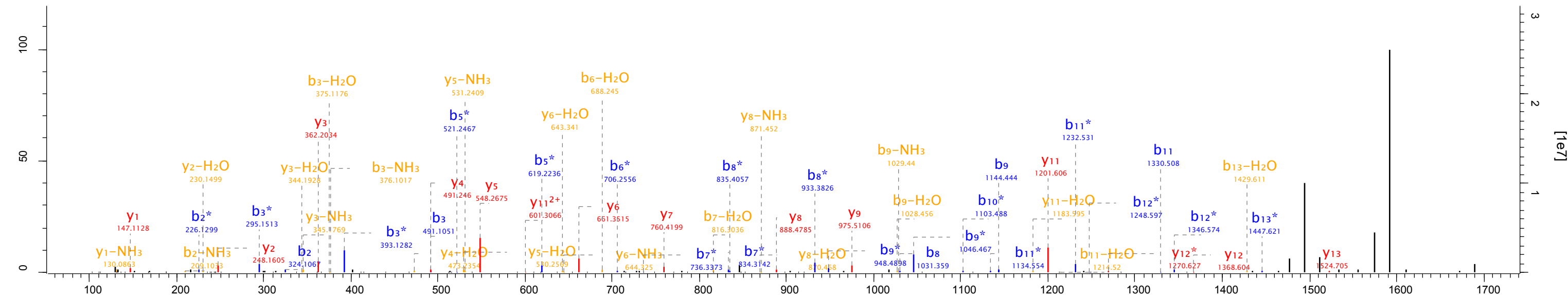
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6675 Method FTMS; HCD Score 134.74 m/z 1115.49 Gene names SRRM2



- A Q Y18* Y17 Y16 Y15 Y14 Y13* Y12 Y11 Y10 Y9 Y8* Y7 Y6 Y5 Y4 Y2 Y1 -
 - A Q b2 b3 P b5* b6 P b8* b9 S G b12* b13 b14* P b16* Q b19* K -
 - A Q b2 b3 P b5* b6 P b8* b9 S G b12* b13 b14* P b16* Q b19* K -

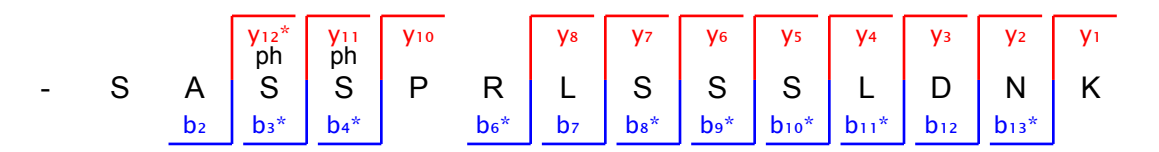
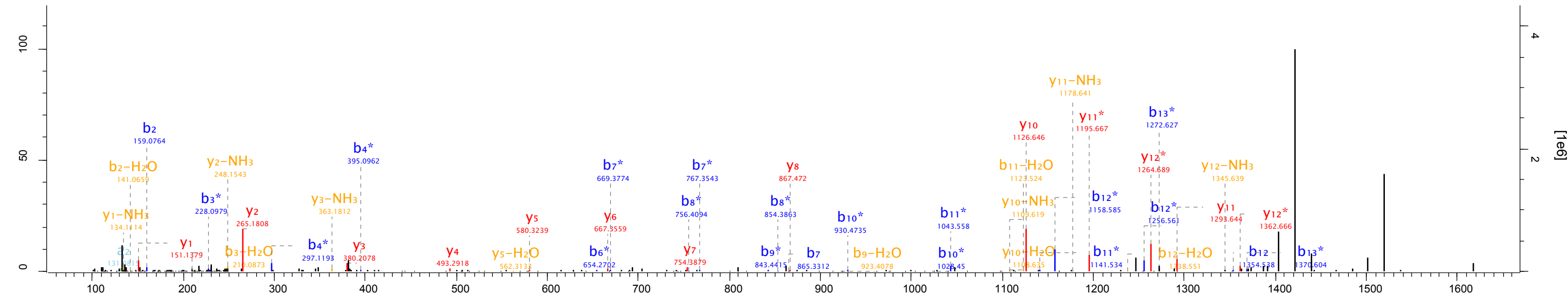
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6725 Method FTMS; HCD Score 77.37 m/z 604.25 Gene names SRRM2

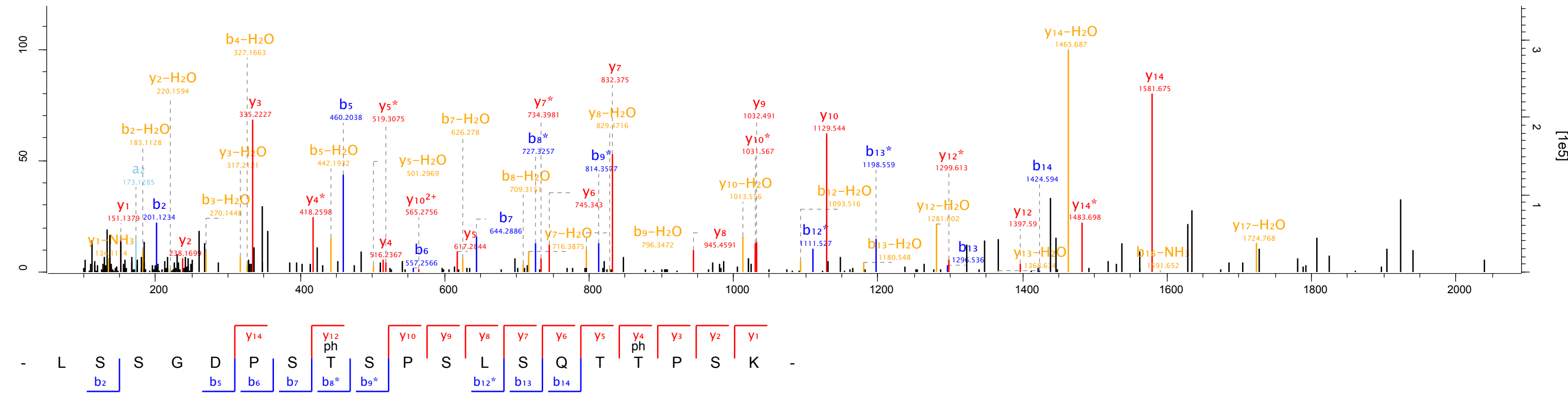




Raw file
20171215_MaS_33SR_LMH_phospho2_03

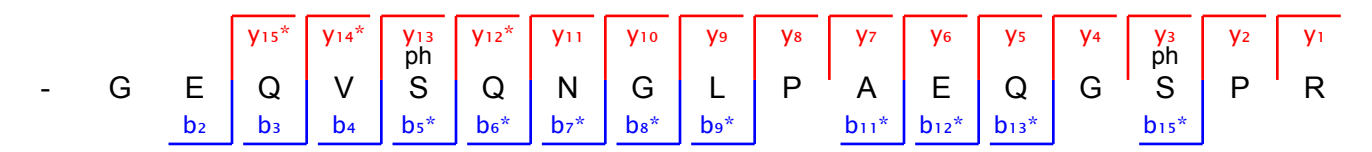
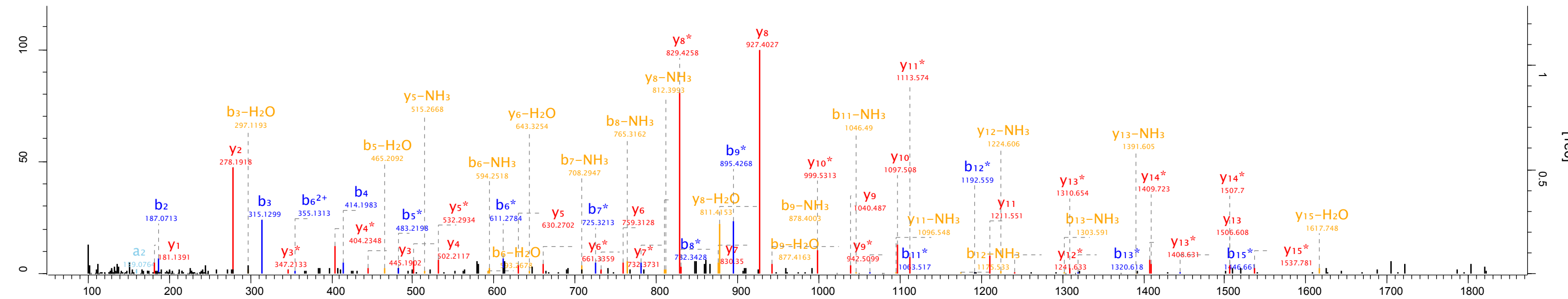
Scan 6895 Method FTMS; HCD Score 114.29 m/z 809.86 Gene names PPP1R12A



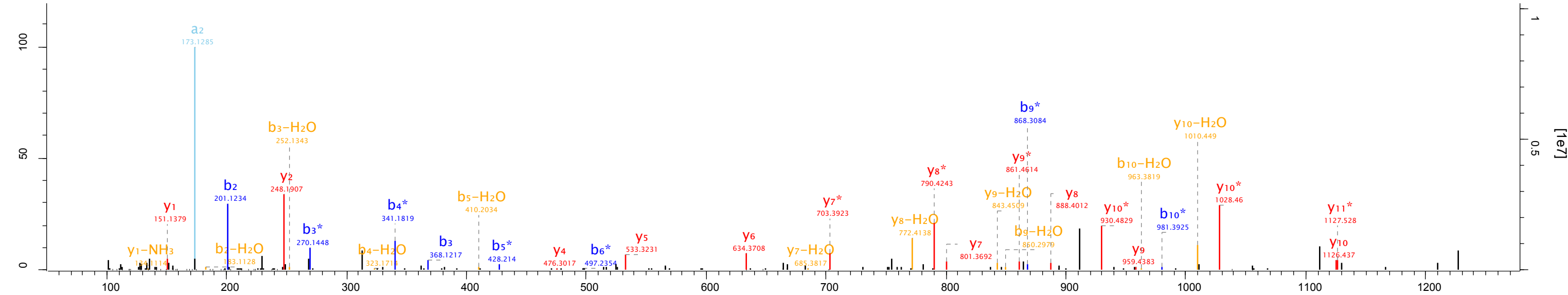


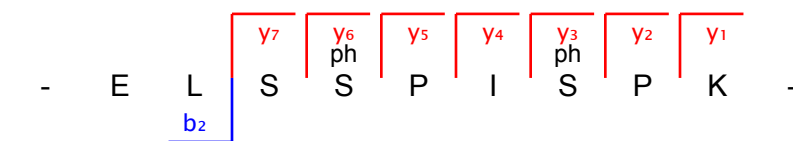
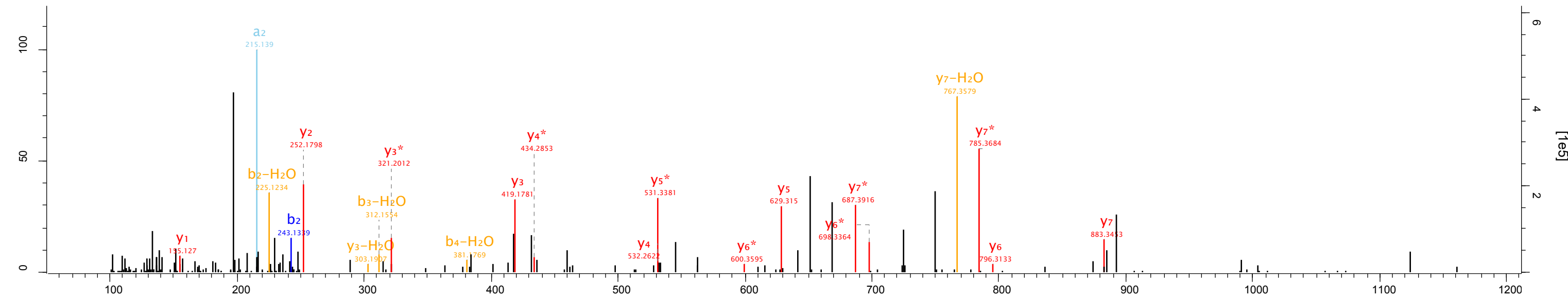
Raw file
20171215_MaS_33SR_LMH_phospho2_03

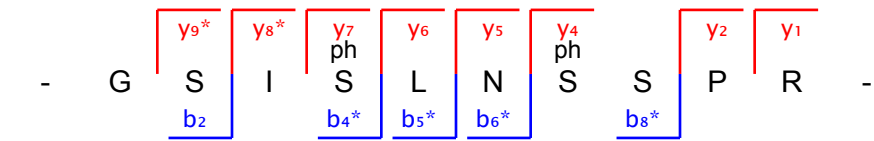
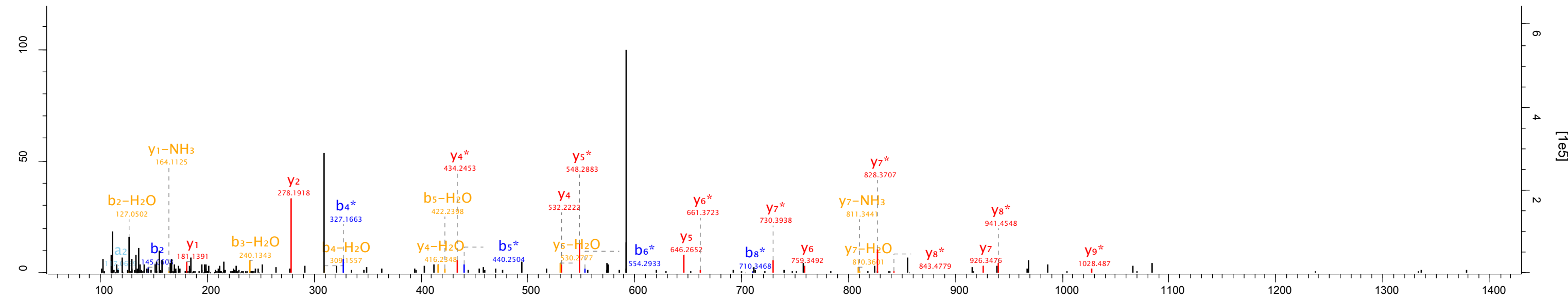
Scan 7035 Method FTMS; HCD Score 225.95 m/z 960.91 Gene names SPTBN1

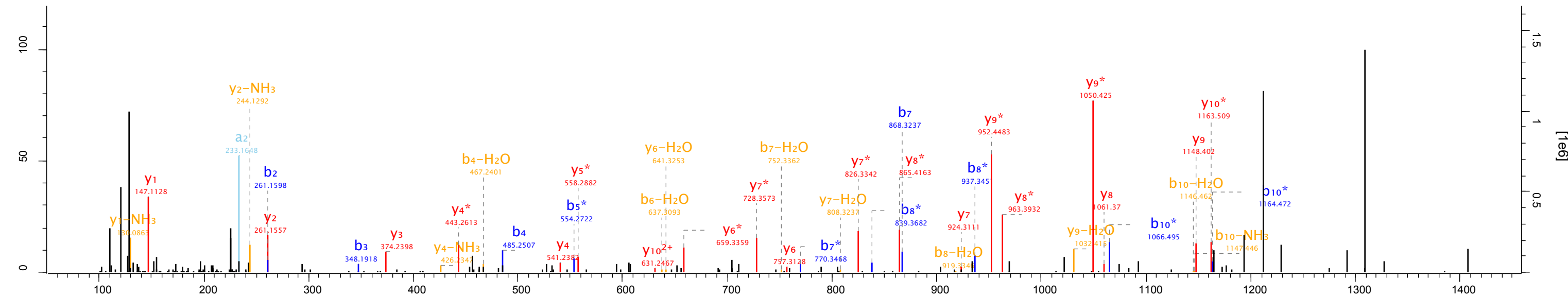


20171215_MaS_33SR_LMH_phospho2_03 7045 FTMS; HCD 112.36 663.78 SRPK2





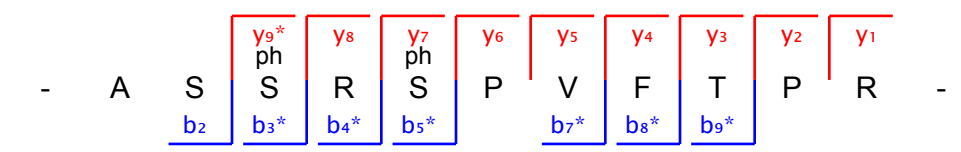
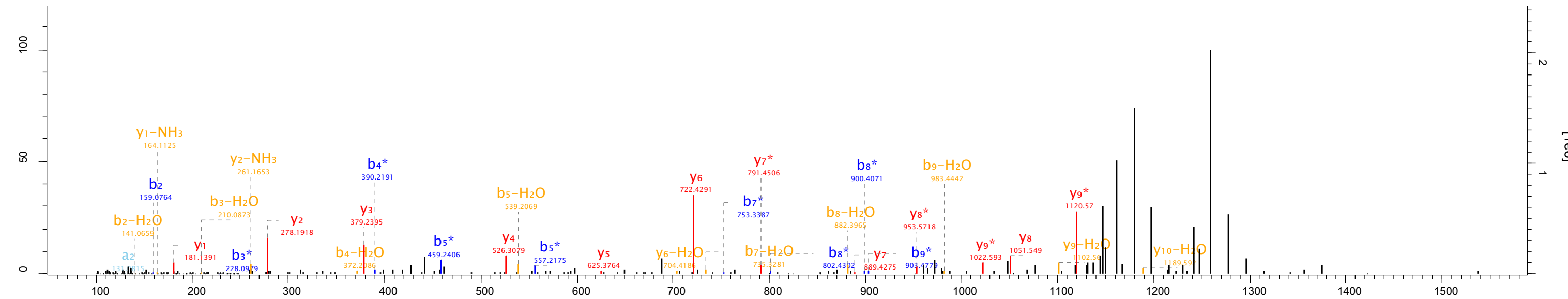


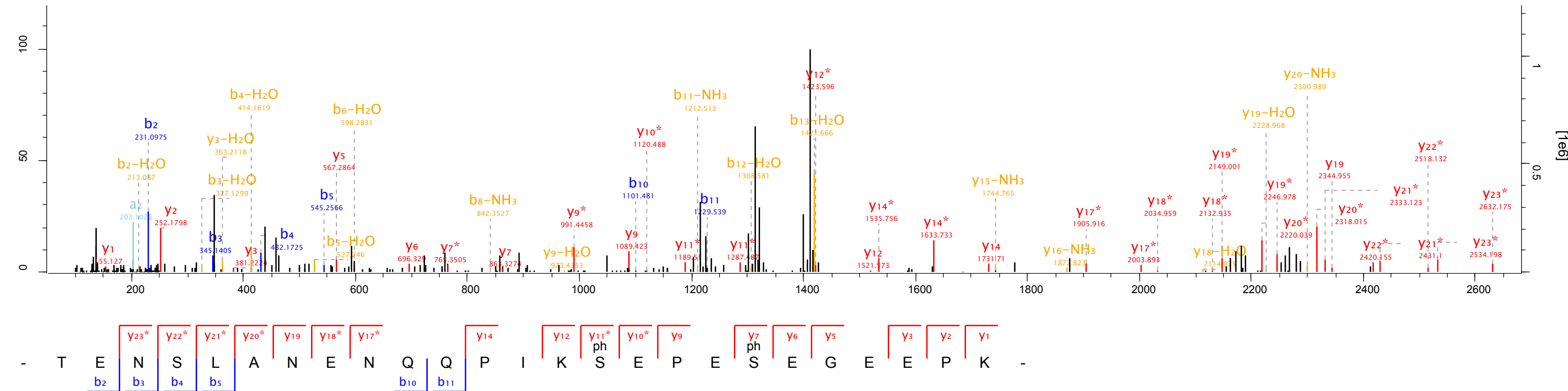


- F y10* y9 y8 y7
ph y6 y5* y4
ph y3 y2 y1 -

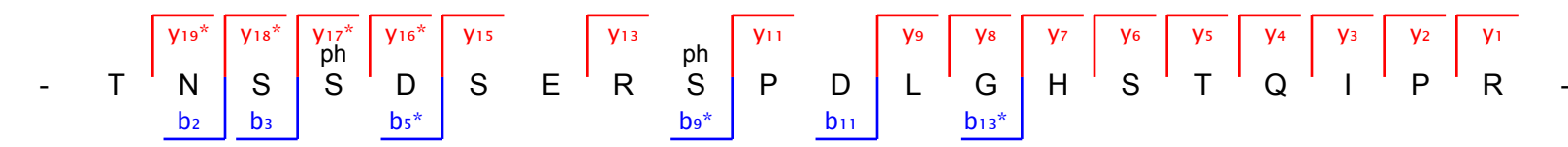
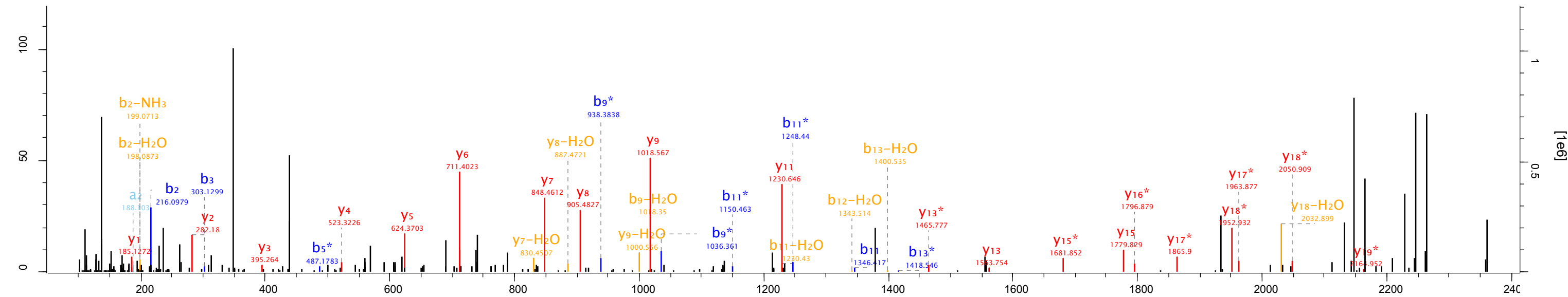
b2 b3 b4 b5* b7 b8* b10*

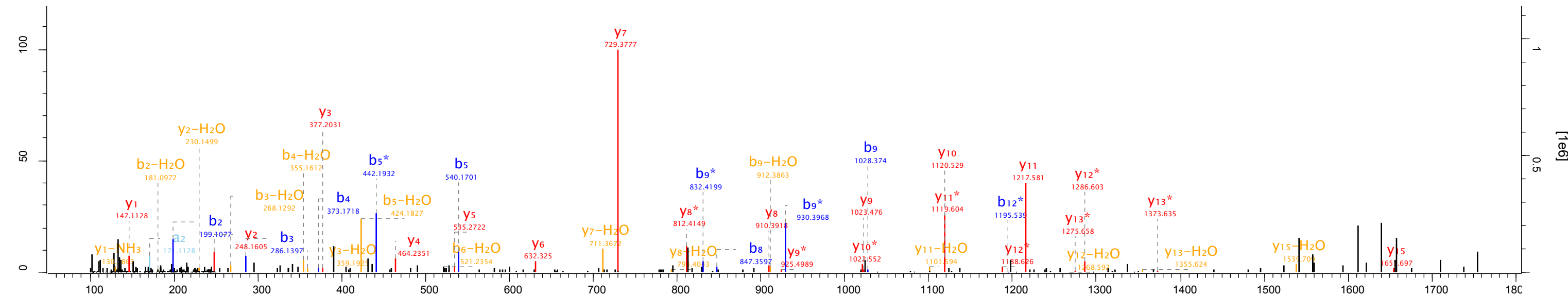
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 7465 Method FTMS; HCD Score 84.4 m/z 688.81





Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 7685 Method FTMS; HCD Score 109.44 m/z 788.66 Gene names PACS1



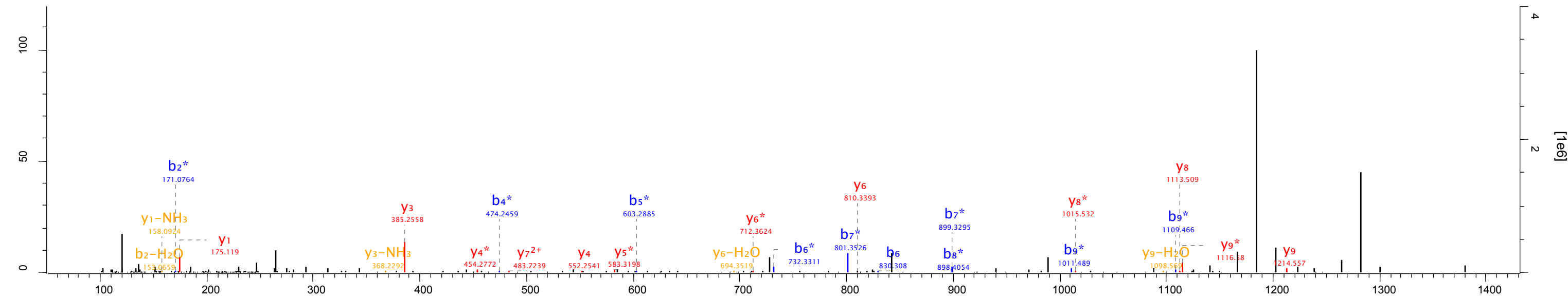


- T P S S P P I T P P A S E T K -

b₂ b₃ b₄ b₅ b₈ b₉ b₁₂*

y₁₅ y₁₃* y₁₂* y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

ph

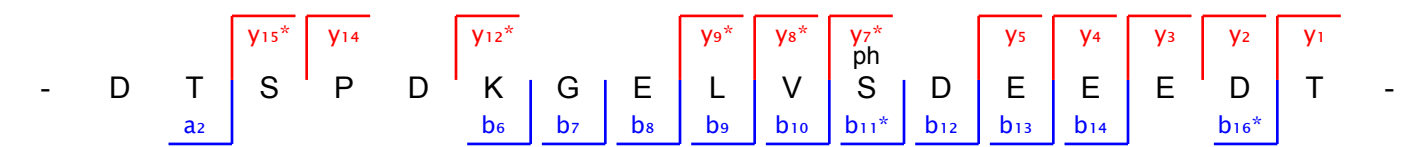
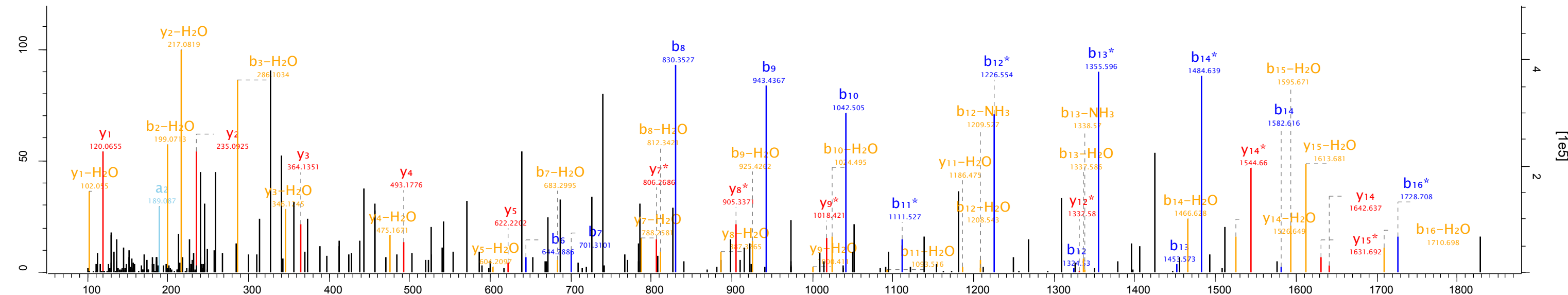


ph S -

y ₉	y ₈	y ₇ ²⁺	y ₆	y ₅ *	y ₄ ph	y ₃	y ₁
T	F	R	E	E	S	P	R
b ₂ *		b ₄ *	b ₅ *	b ₆	b ₇ *	b ₈ *	b ₉ *

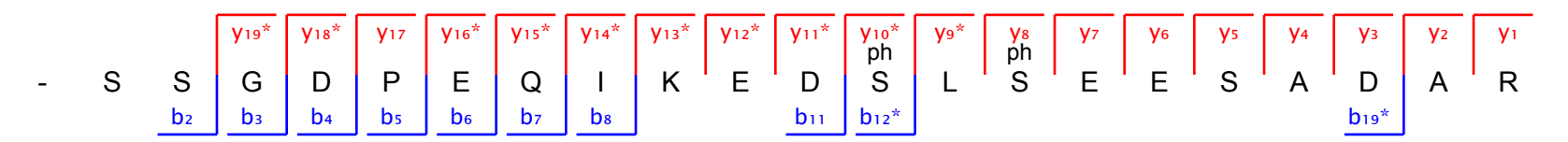
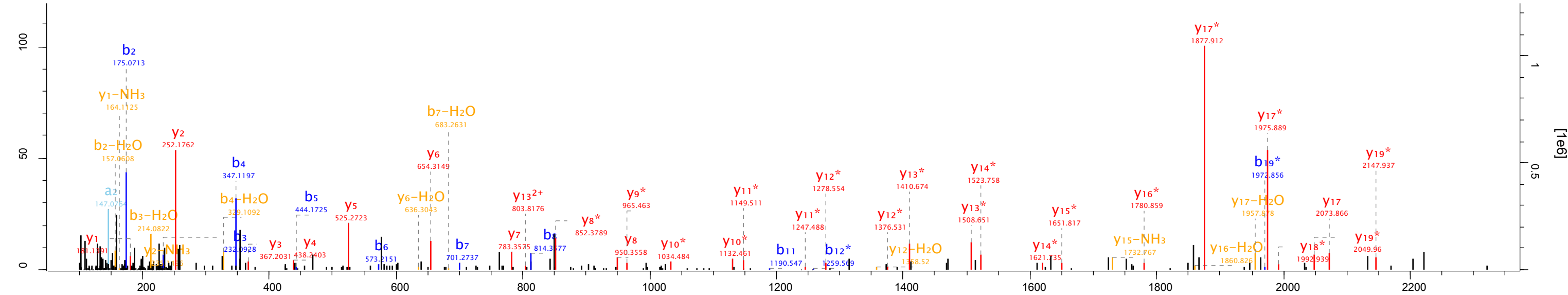
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8055 Method FTMS; HCD Score 178.1 m/z 973.88 Gene names TBC1D2B



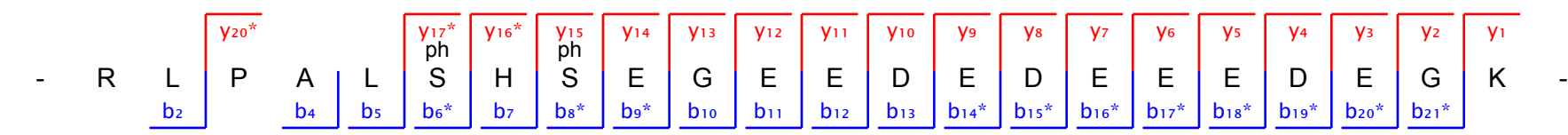
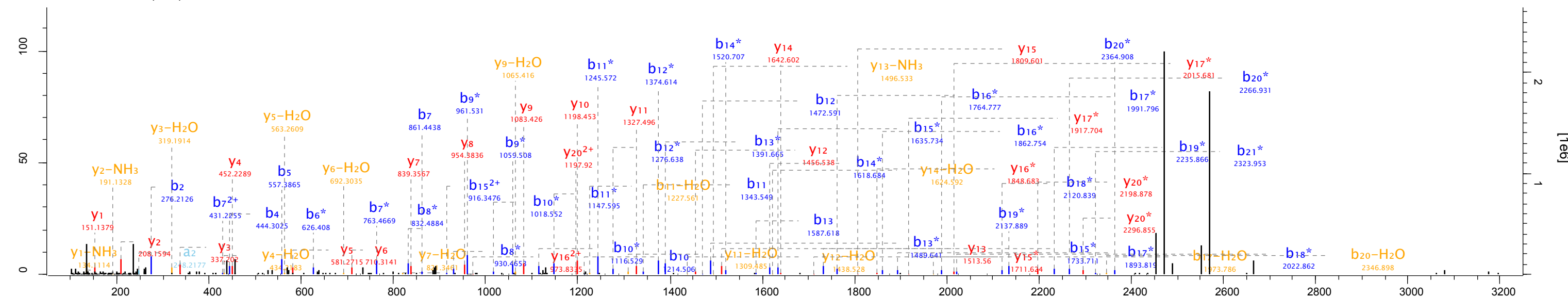
Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 8095 FTMS; HCD 151.28 807.33 RIOK2

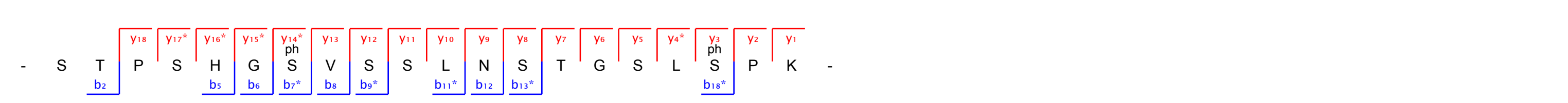
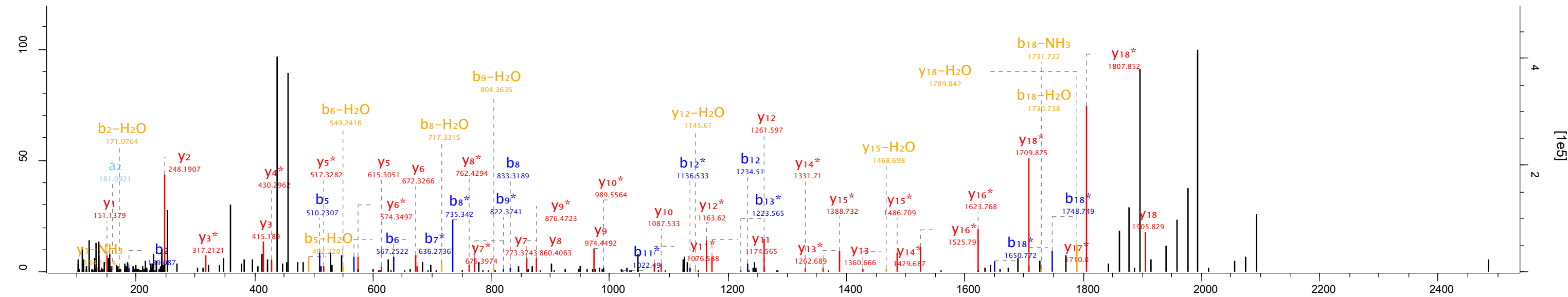


Raw file
20171215_MaS_33SR_LMH_phospho2_03

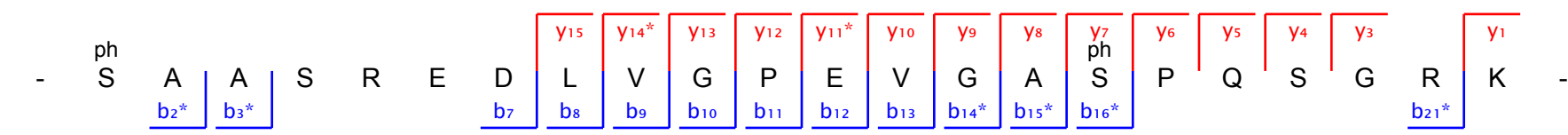
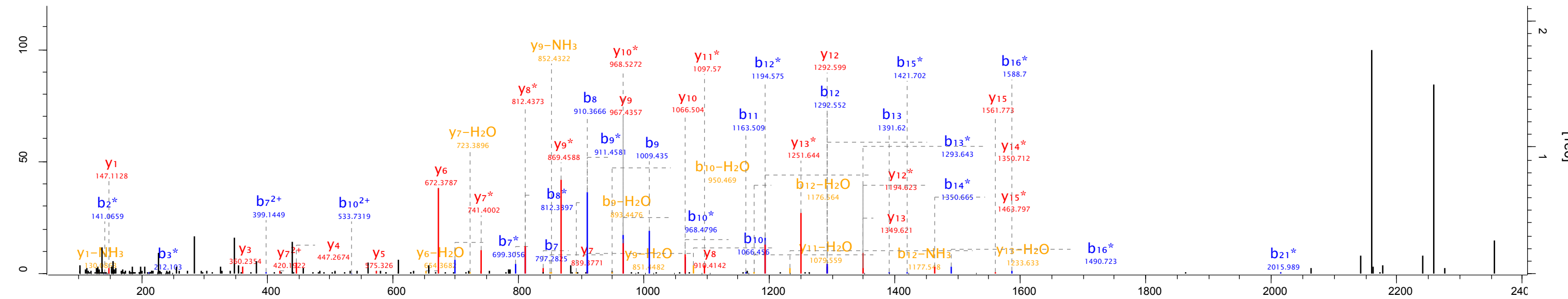
Scan 8255 Method FTMS; HCD Score 291.68 m/z 890.68 Gene names BRPF1



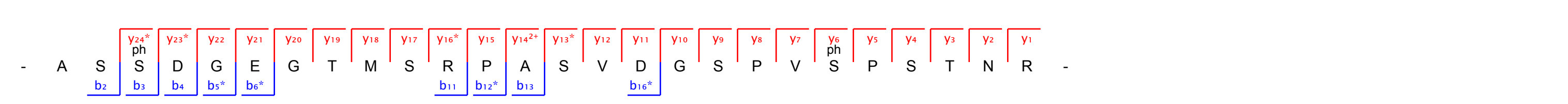
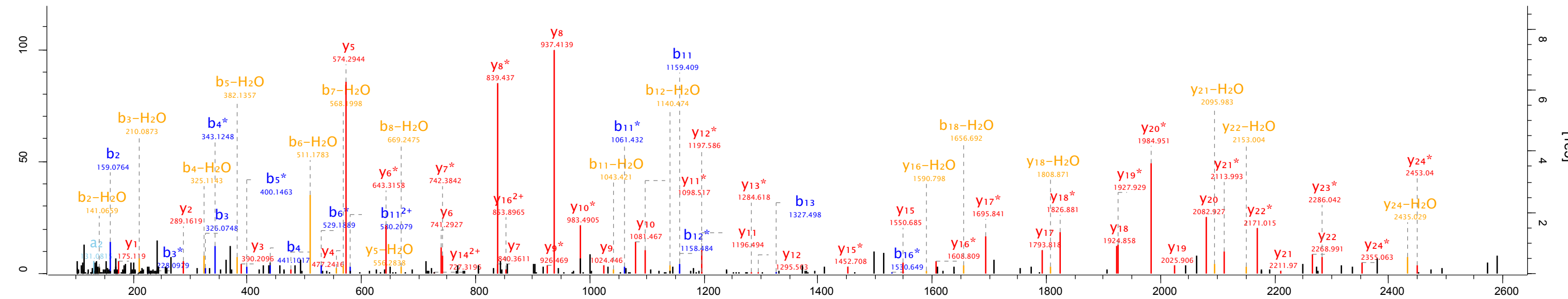
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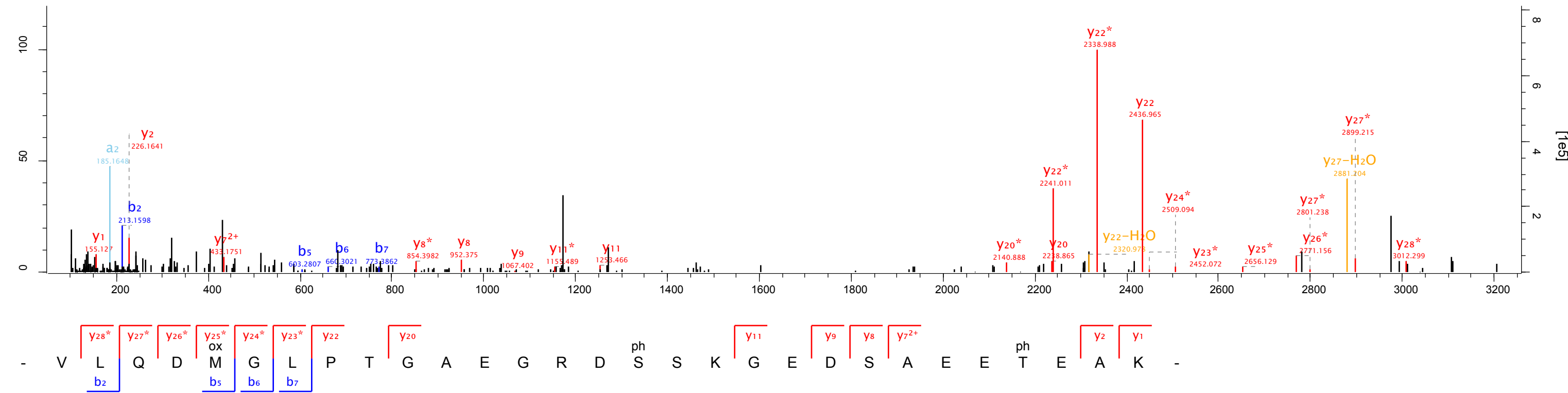


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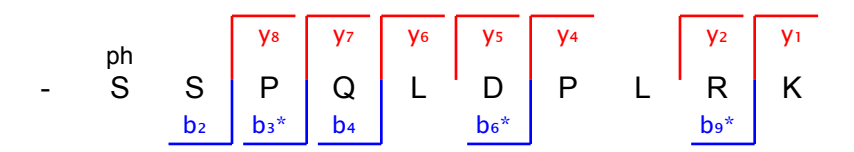
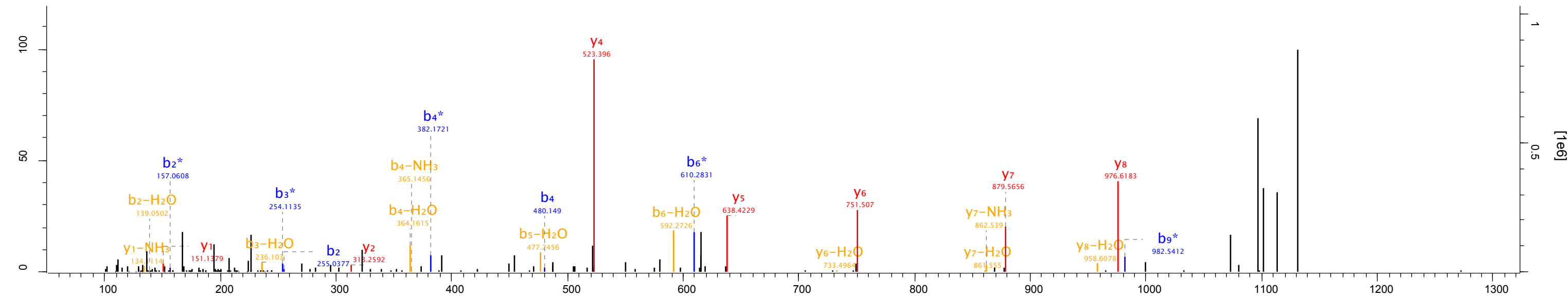


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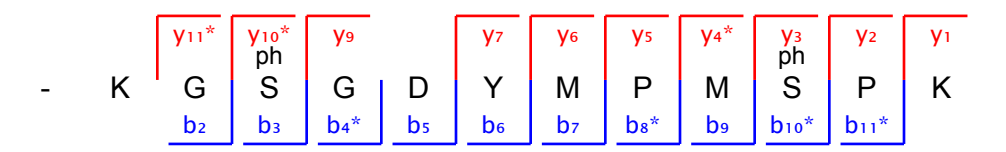
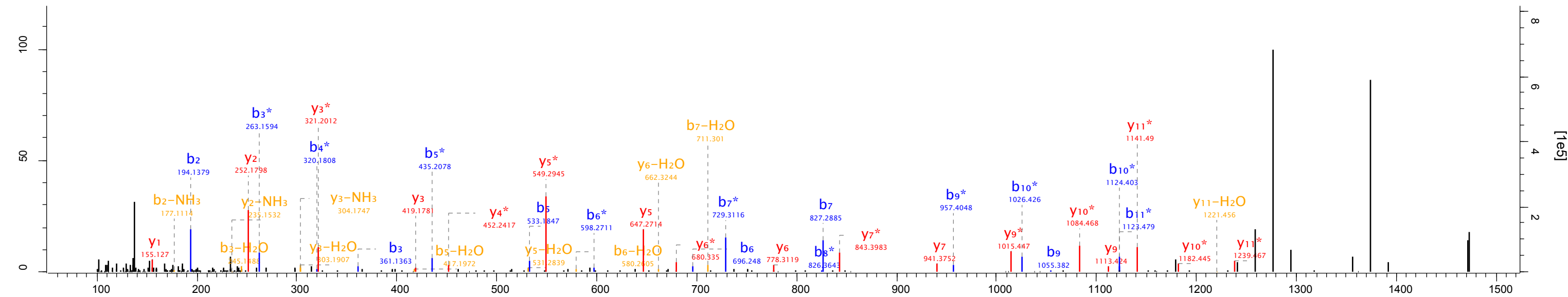


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 Scan: 8605 Method: FTMS; HCD Score: 97.46 m/z: 615.83 Gene names: LSM14A

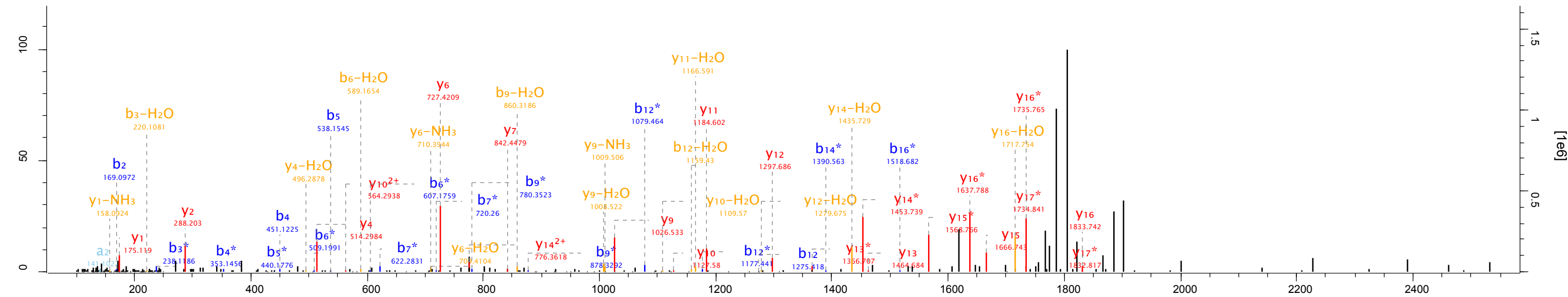


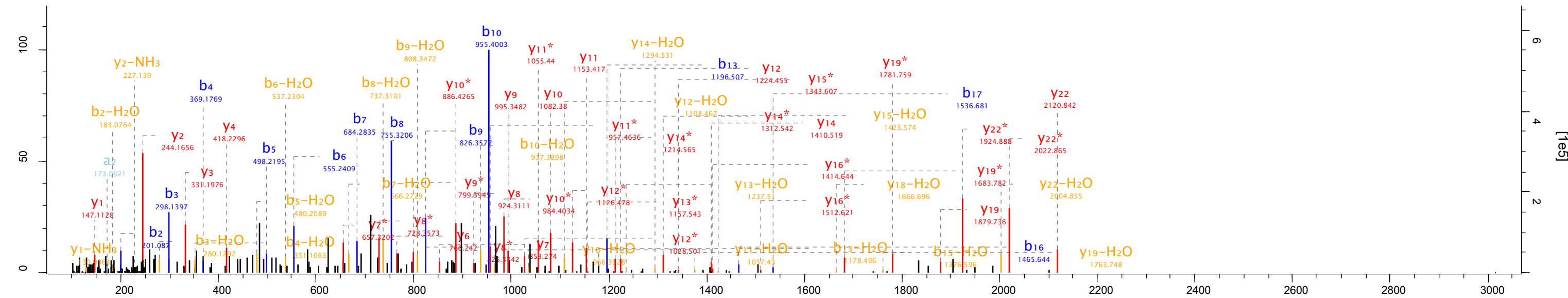
Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 8735 FTMS; HCD 190.67 737.78 IRS1



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 8845 Method: FTMS; HCD Score: 184.14 m/z: 1001.42 Gene names: TRIP10





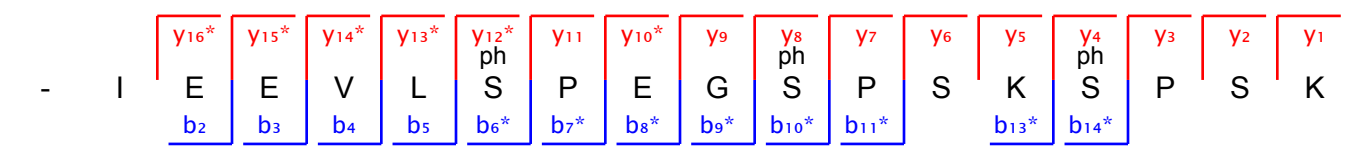
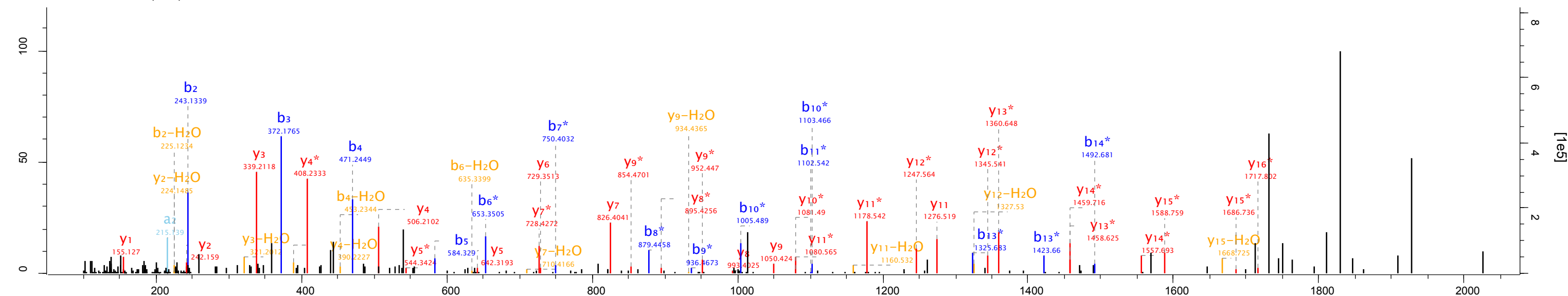
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Fragmentation labels (b and y ions) are shown below the corresponding amino acids in the sequence:

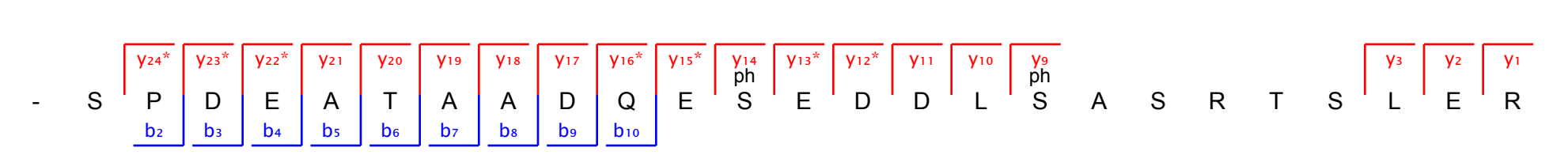
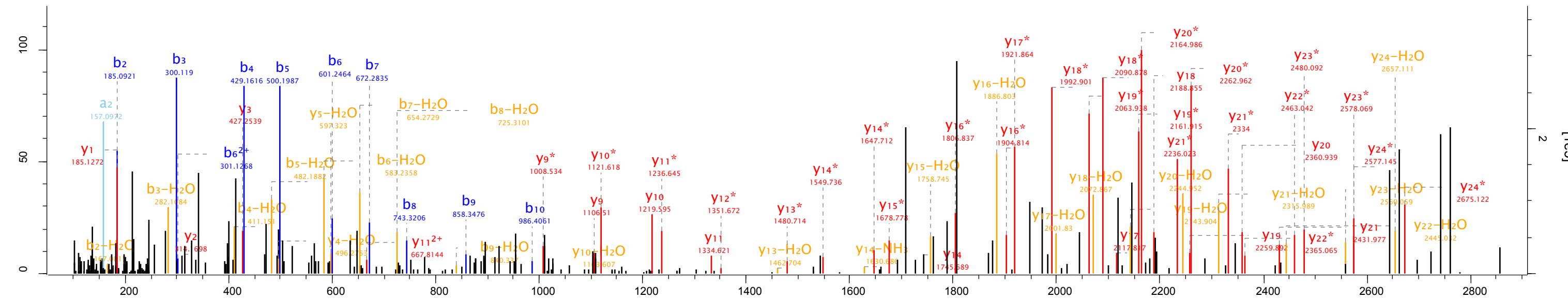
- b₂ (under A), b₃ (under P), b₄ (under A), b₅ (under E), b₆ (under G), b₇ (under E), b₈ (under A), b₉ (under A), b₁₀ (under E)
- b₁₃ (under S), b₁₆ (under A), b₁₇ (under A)
- y₁ (under K), y₂ (under P), y₃ (under S), y₄ (under S), y₆ (under S), y₇ (under S), y₈ (under A), y₉ (under A), y₁₀ (under S), y₁₁ (under A), y₁₂ (under E), y₁₃ (under G), y₁₄ (under E), y₁₅ (under E), y₁₆ (under A), y₁₉ (under P), y₂₂ (under P)

Raw file
20171215_MaS_33SR_LMH_phospho2_03

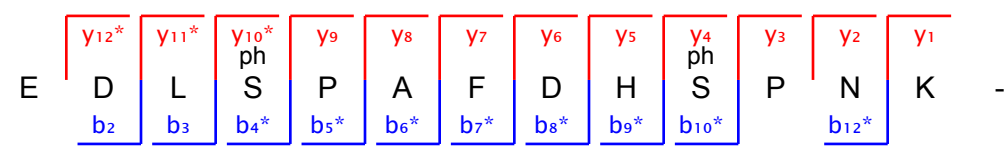
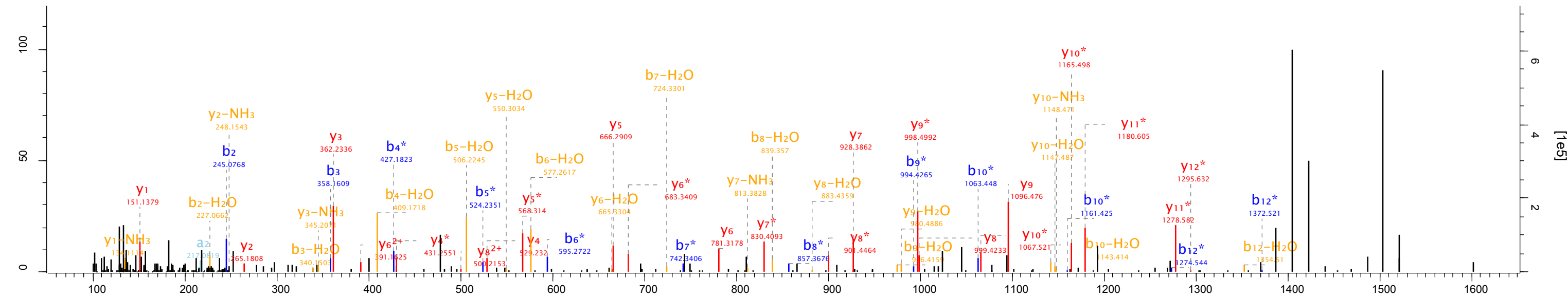
Scan 9045 Method FTMS; HCD Score 216.48 m/z 1014.42 Gene names ADD3



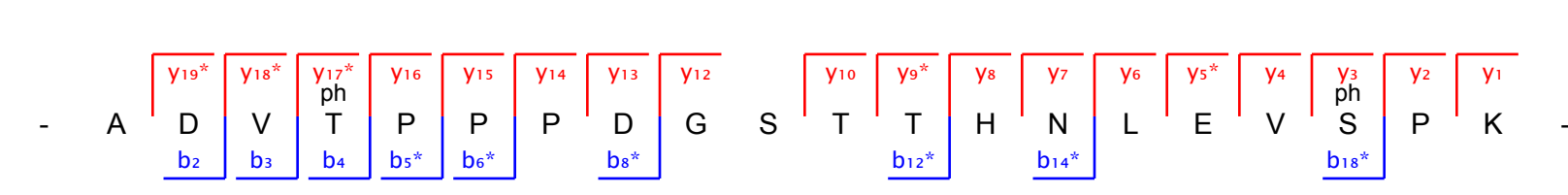
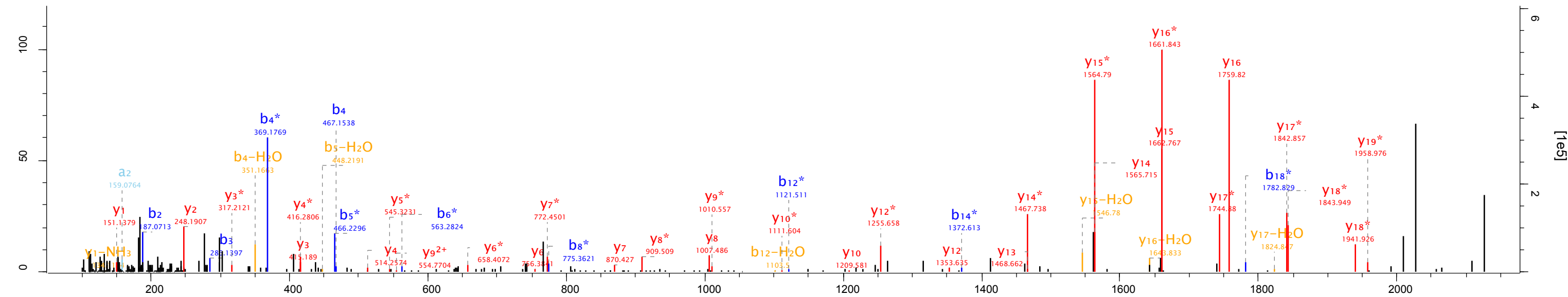
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 Scan: 9125 Method: FTMS; HCD Score: 260.68 m/z: 954.38 Gene names: FARP1



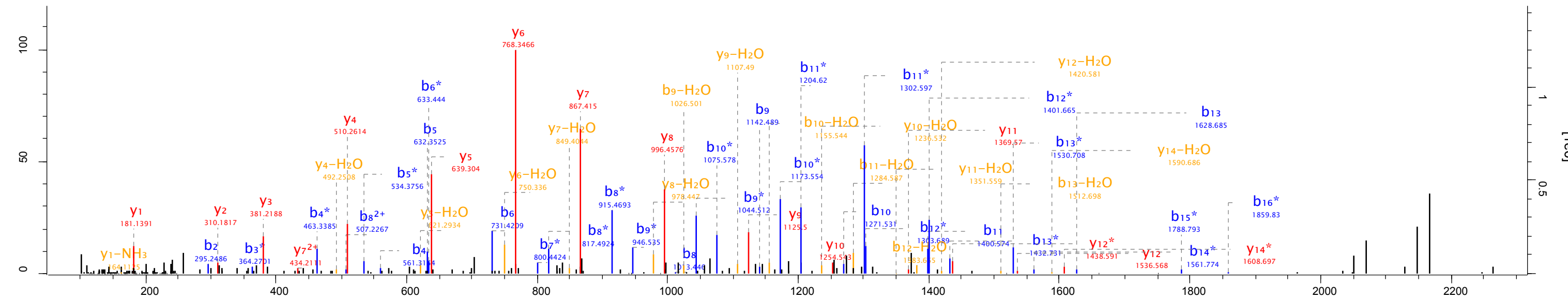
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 9255 Method: FTMS; HCD Score: 250.29 m/z: 810.82 Gene names: PTPN2



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 9485 Method: FTMS; HCD Score: 142.09 m/z: 742.66 Gene names: ZNF217

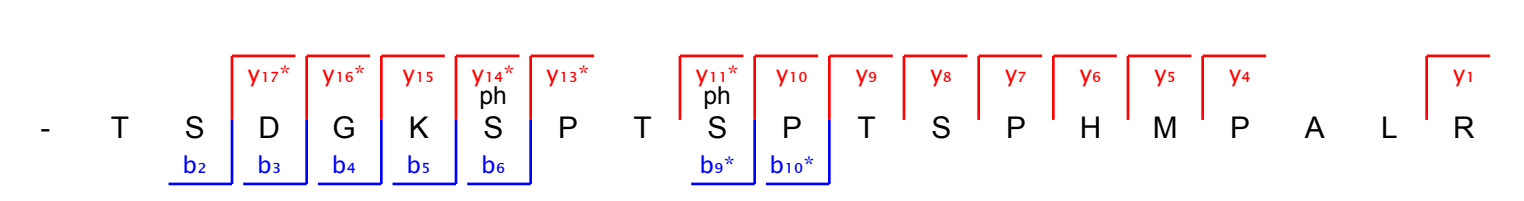
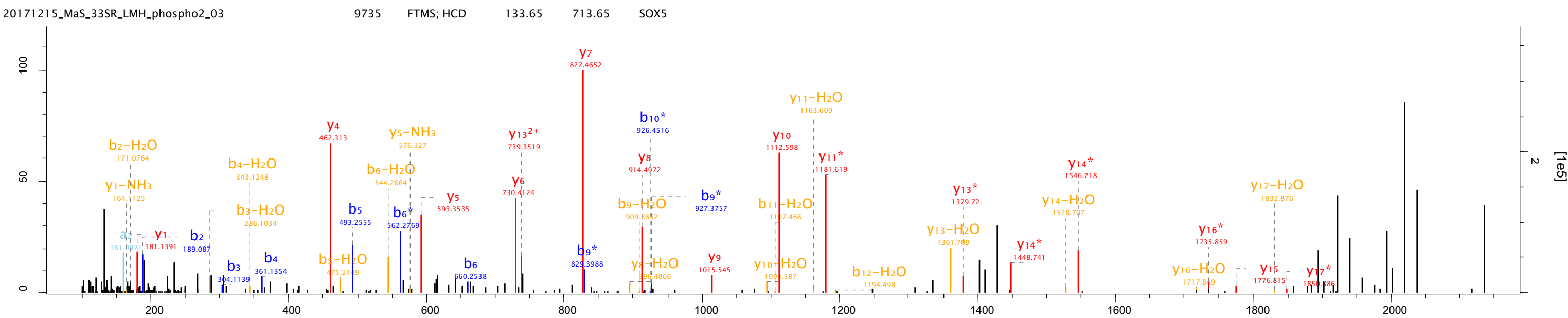


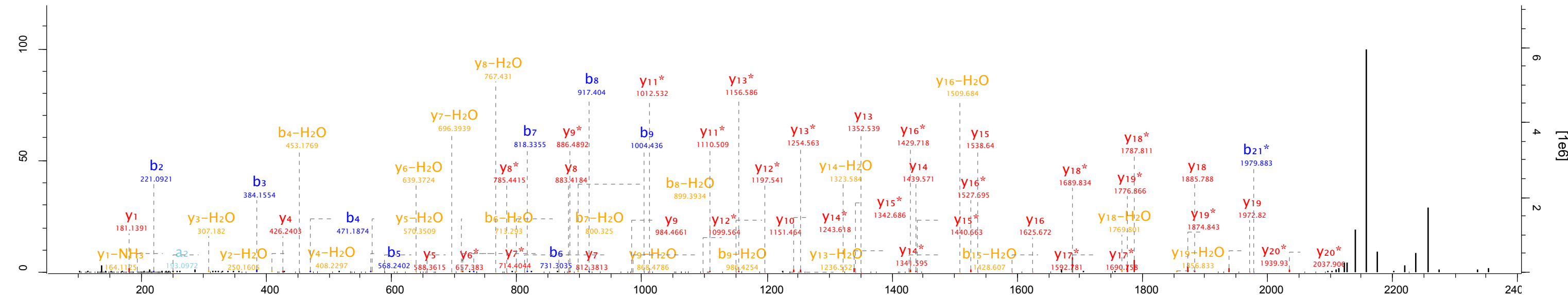
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- K R S V A V S D E E E V E E E A E R -
 b₂ b₃^{*} b₄ b₅ b₆ b₇^{*} b₈ b₉ b₁₀ b₁₁ b₁₂^{*} b₁₃ b₁₄^{*} b₁₅^{*} b₁₆^{*}
 y₁₄^{*} y₁₂ ph y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9735 Method FTMS; HCD Score 133.65 m/z 713.65 Gene names SOX5





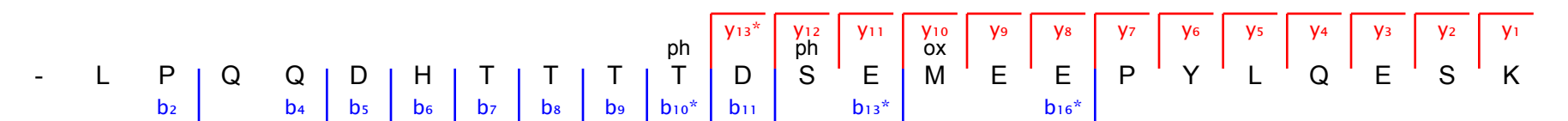
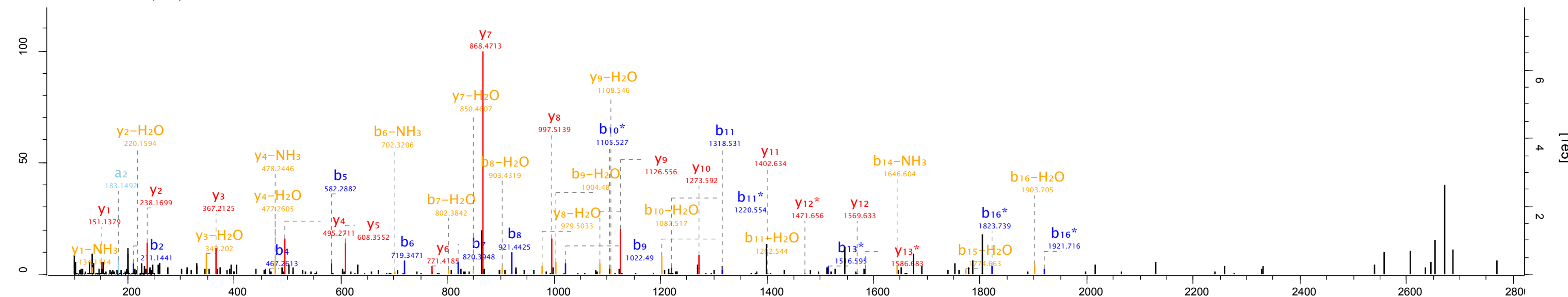
- G Y Y S P Y S V S G S G S T A G S R T G S R -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₂₁*

y₂₀*
y₁₉
y₁₈
y₁₇*
y₁₆
y₁₅
y₁₄
y₁₃
y₁₂*
y₁₁*
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y₉
y₈
y₇
y₆*
y₅
y₄
y₁

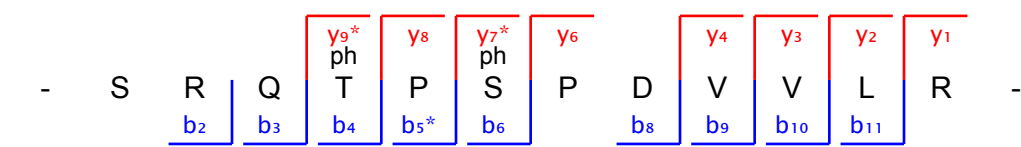
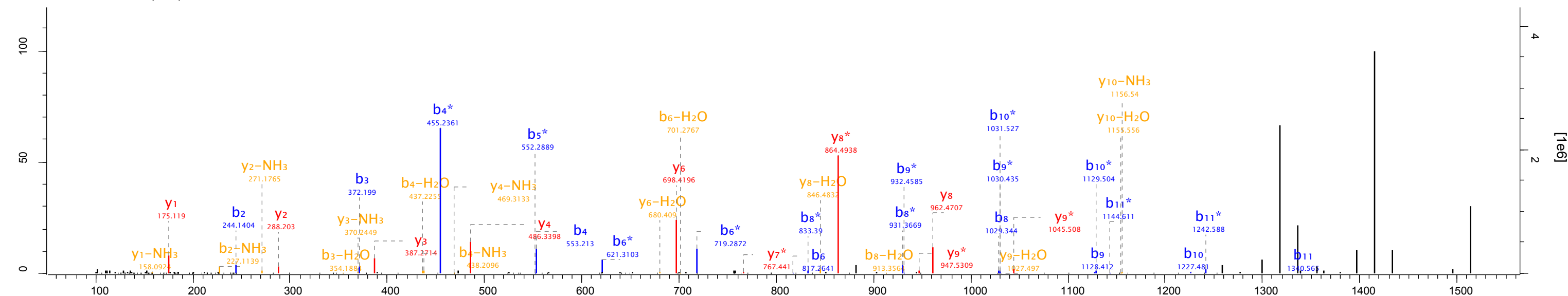
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20171215_MaS_33SR_LMH_phospho2_03

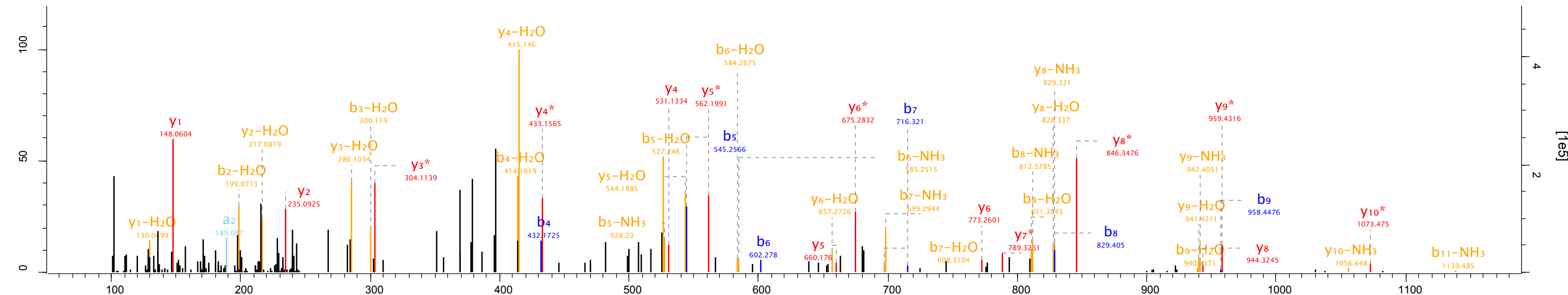
Scan 9835 Method FTMS; HCD Score 129.8 m/z 963.39 Gene names PHC2



Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan Method Score m/z Gene names
9855 FTMS; HCD 186.62 757.84 LIMCH1





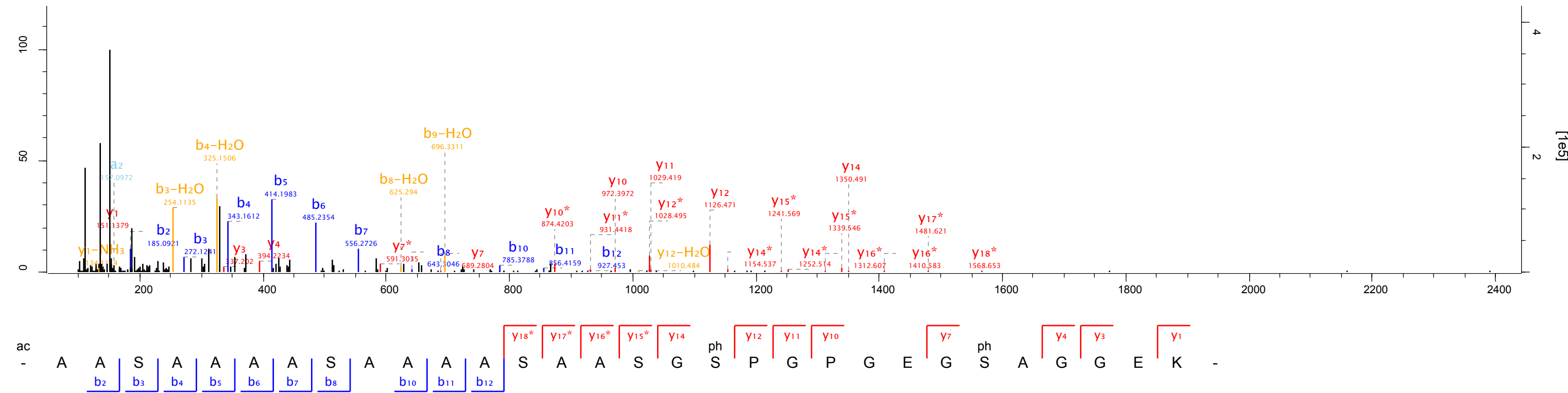
- E S T N L G N L E E S S E -

az
y10*
y9*
y8
y7*
y6
y5
y4
y3*
y2
y1

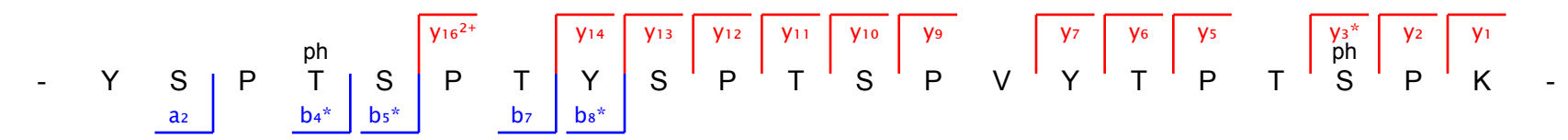
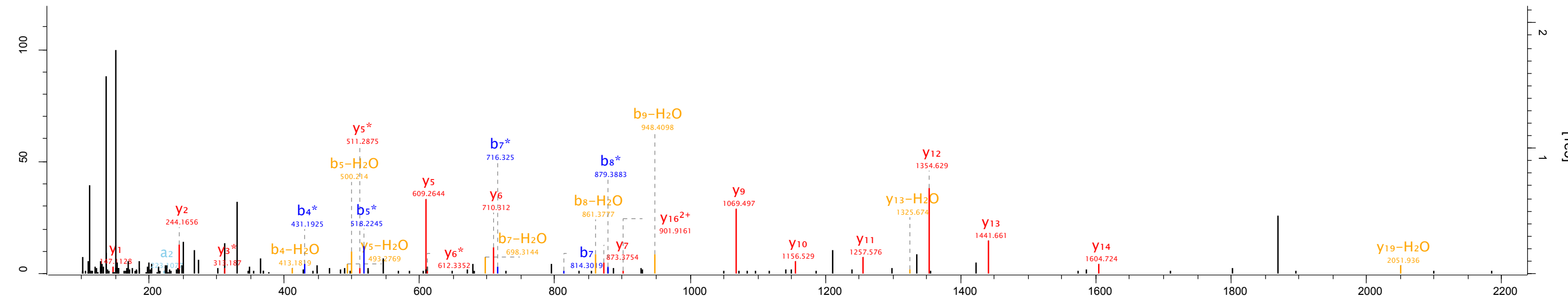
b4
b5
b6
b7
b8
b9
ph

Raw file
20171215_MaS_33SR_LMH_phospho2_04

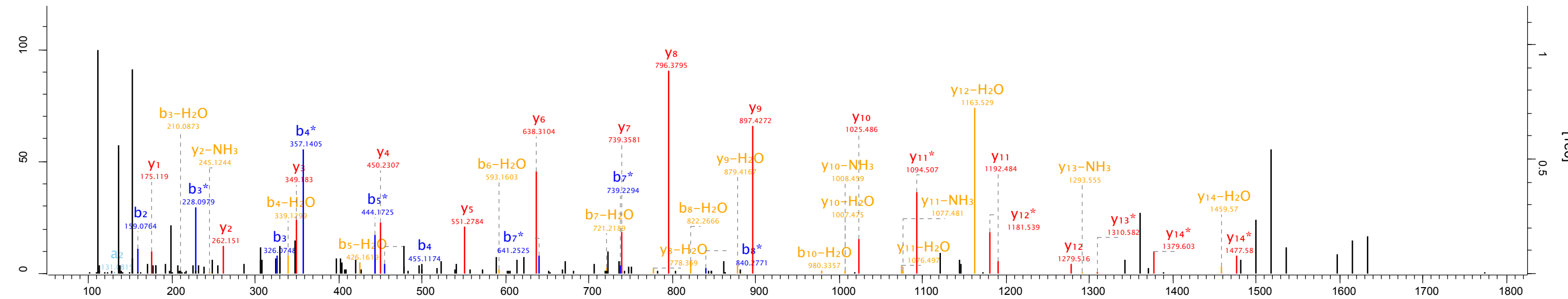
Scan 11235 Method FTMS; HCD Score 58.12 m/z 865.03 Gene names TRIM28



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 12165 Method FTMS; HCD Score 84.17 m/z 1209.51 Gene names POLR2A



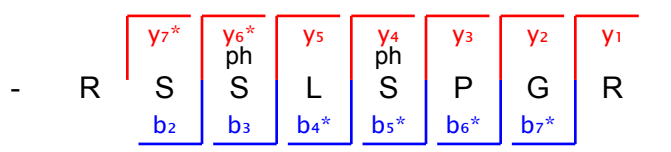
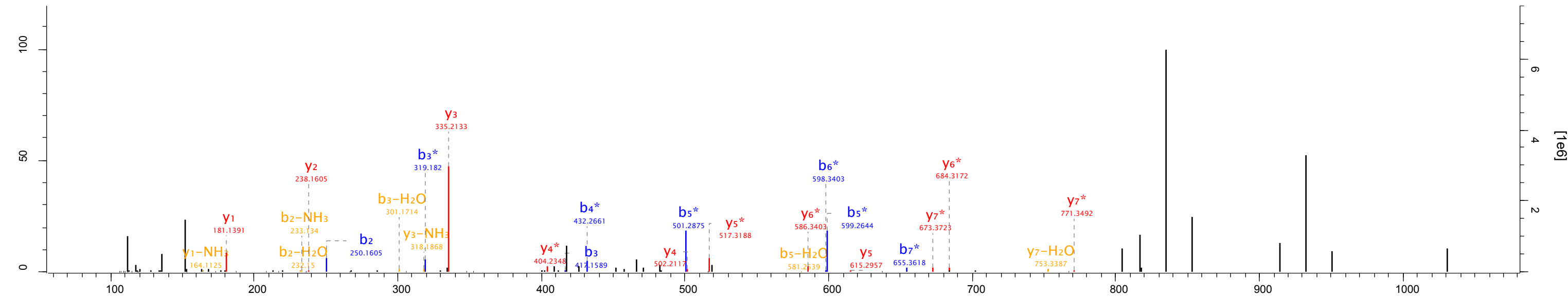
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- T G S E S S Q T G T S T T S S R -

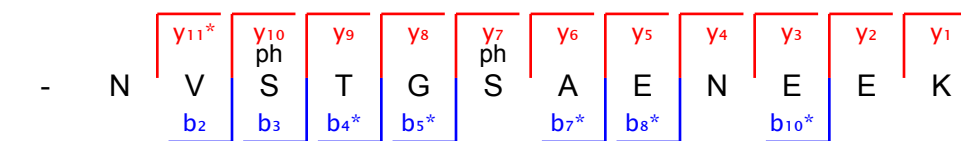
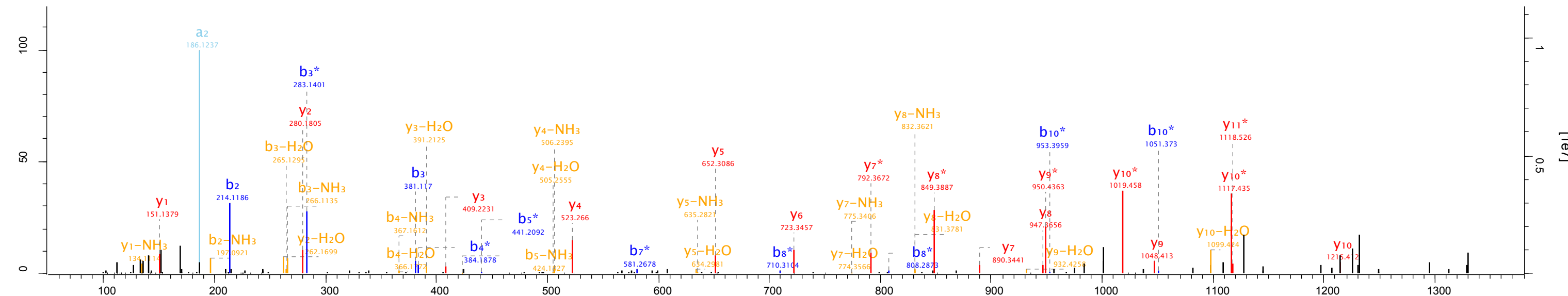
b₂
b₃
b₄
b₅^{*}
b₇^{*}
b₈^{*}
y₁₄^{*}
y₁₃^{*}
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

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 Scan: 2635 Method: FTMS; HCD Score: 105.66 m/z: 516.23 Gene names: DDX23

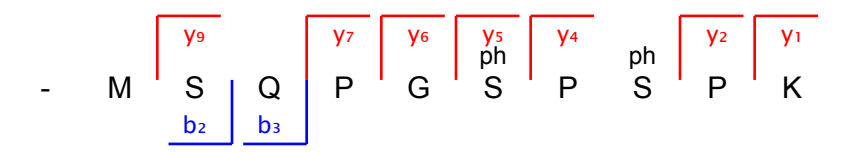
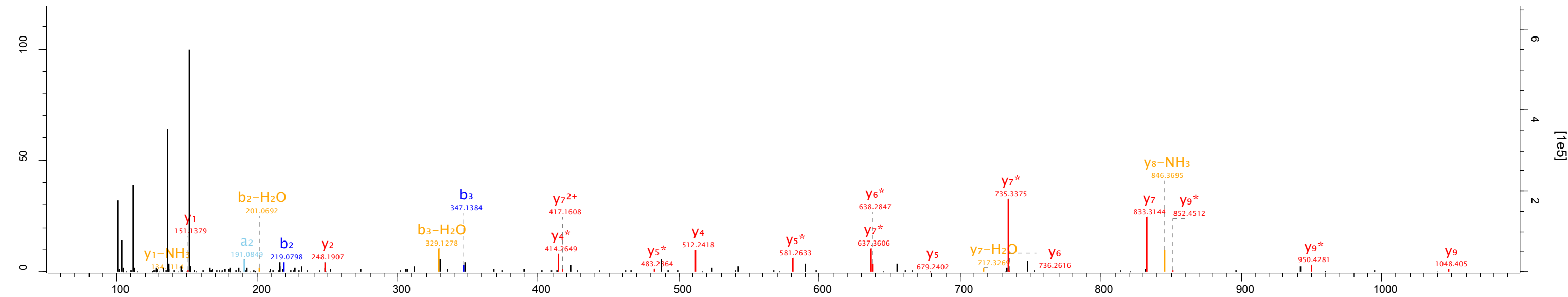


Raw file
20171215_MaS_33SR_LMH_phospho2_04

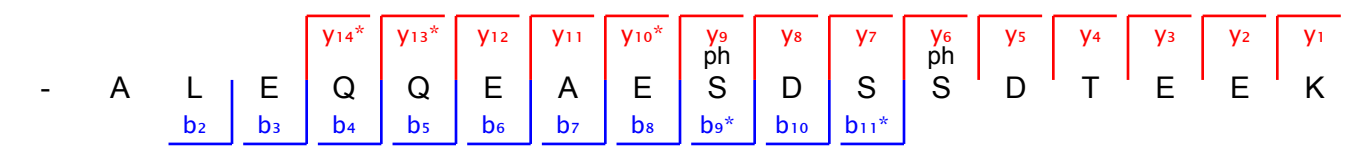
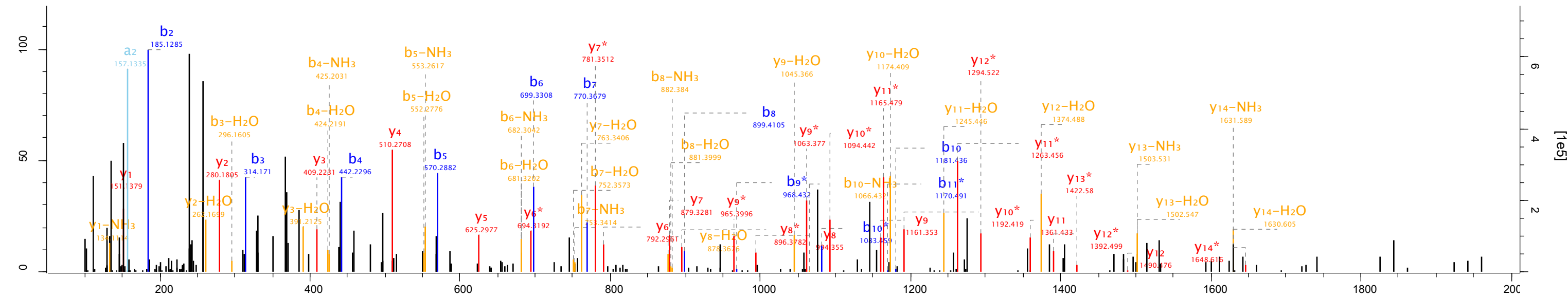
Scan 2745 Method FTMS; HCD Score 190.46 m/z 714.76 Gene names SPAG9



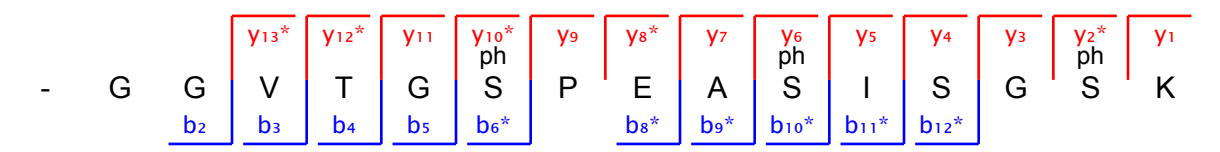
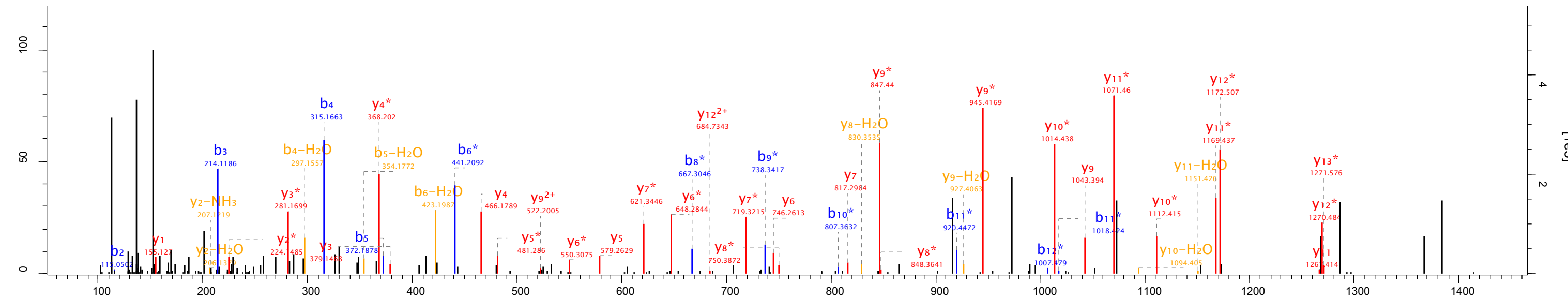
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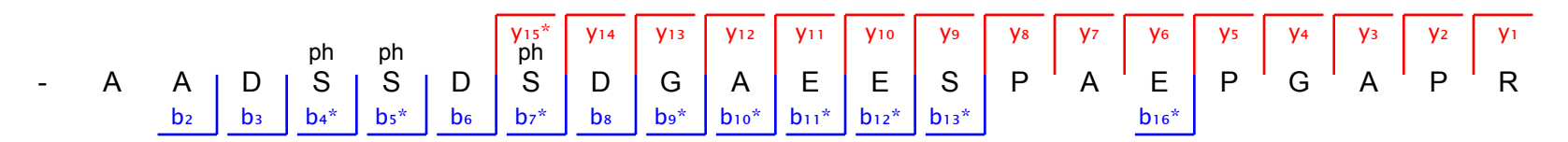
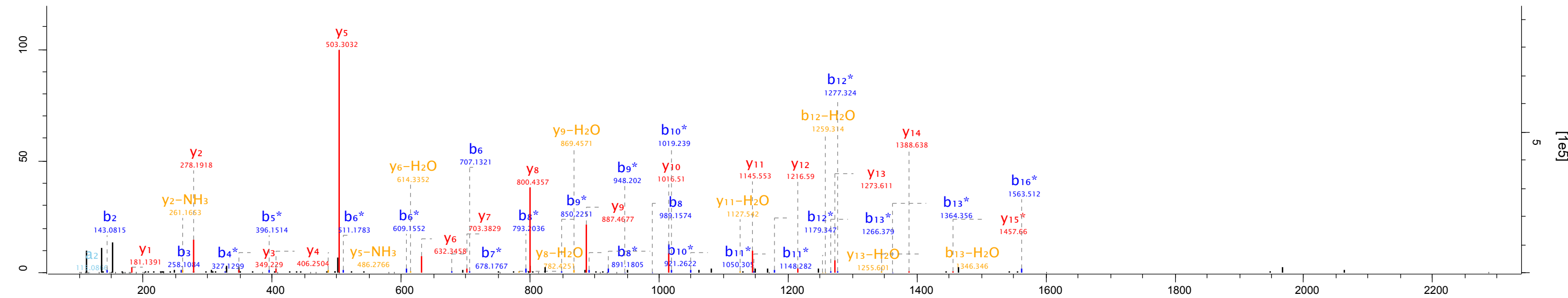
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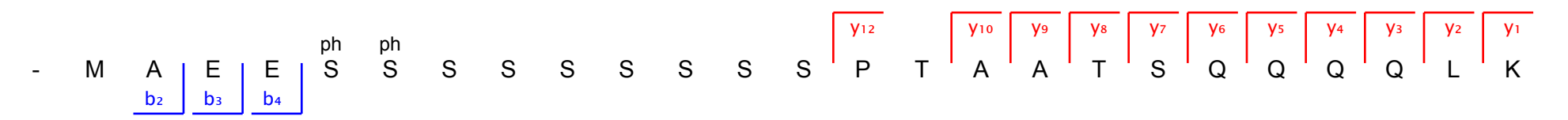
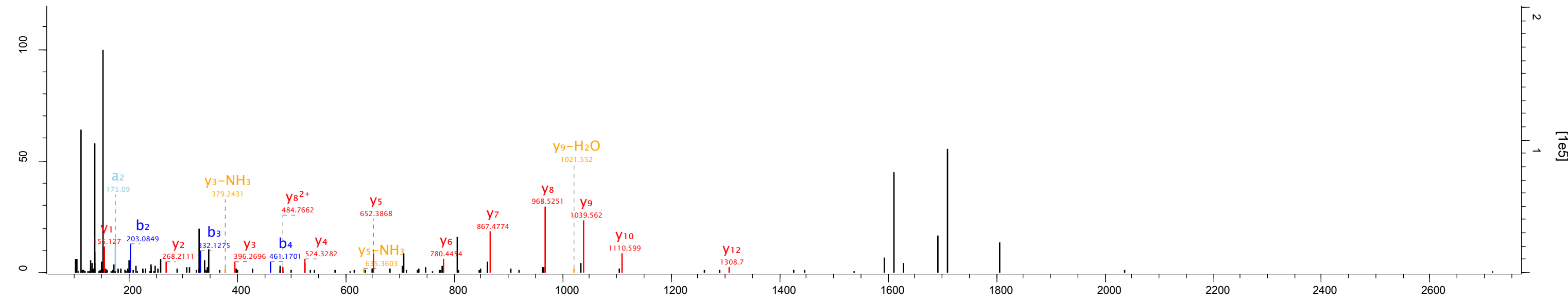
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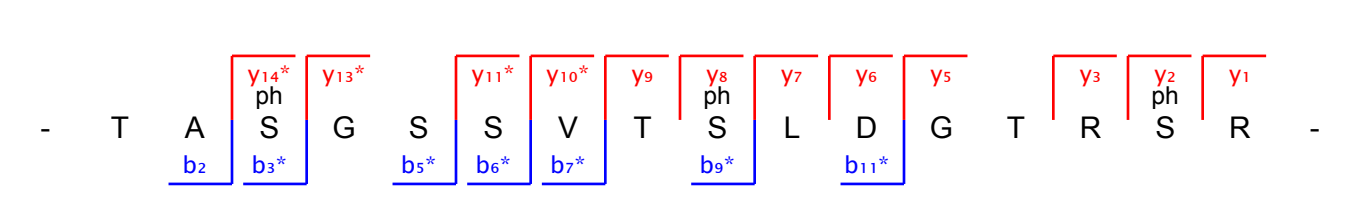
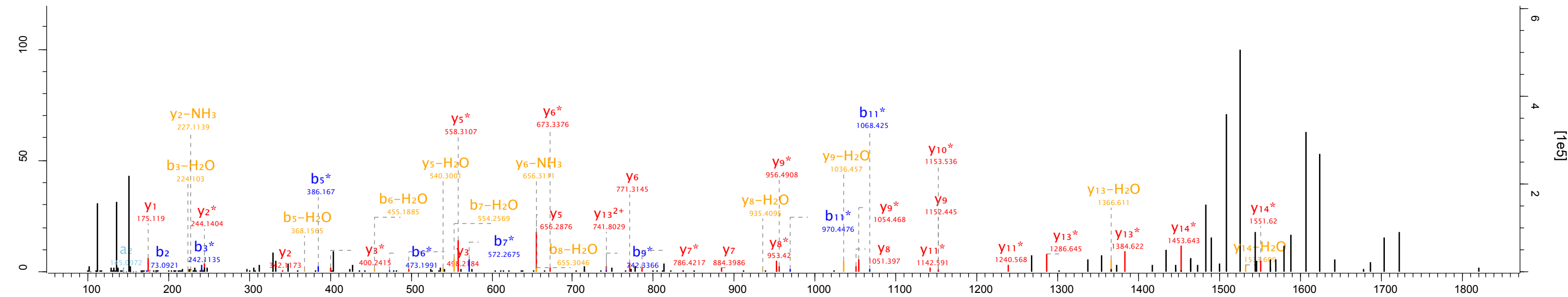
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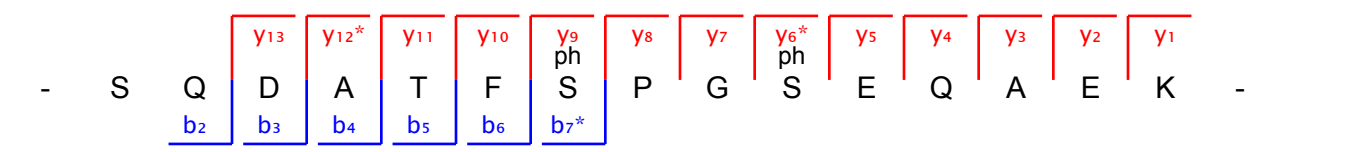
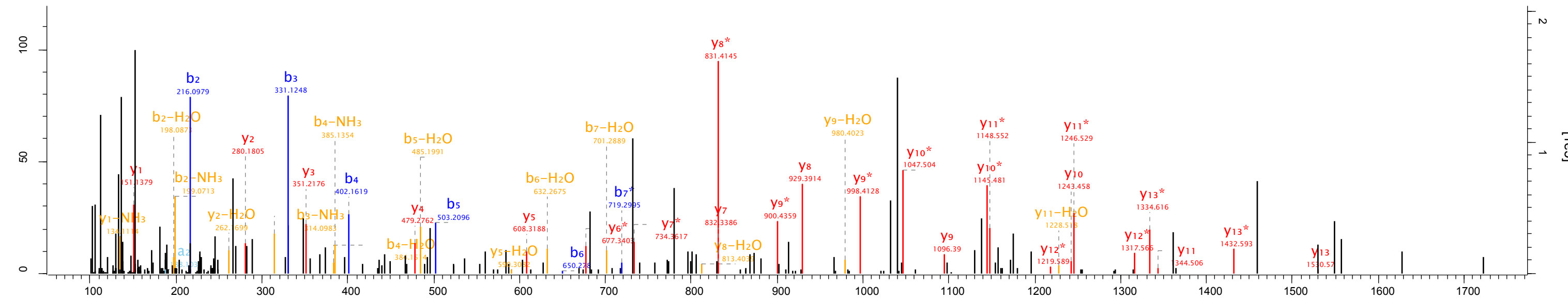
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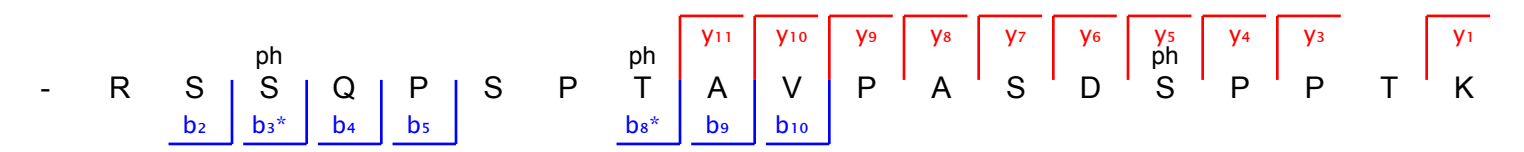
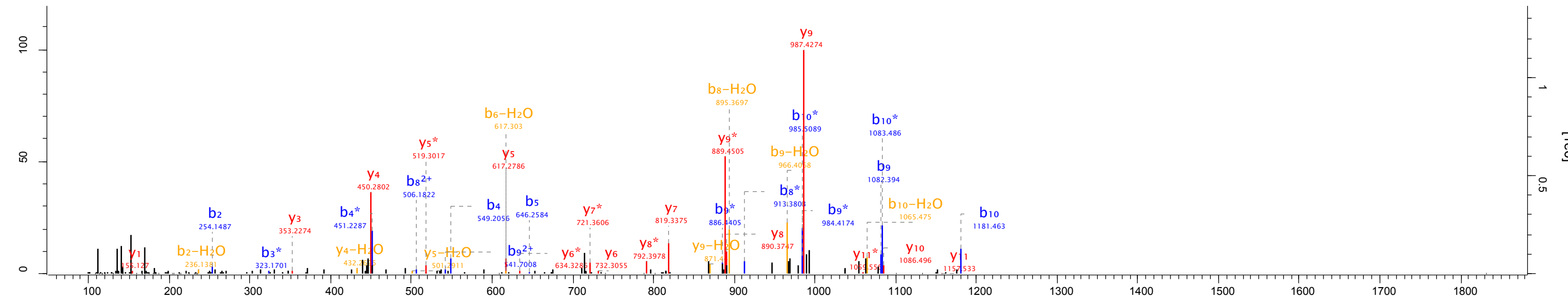
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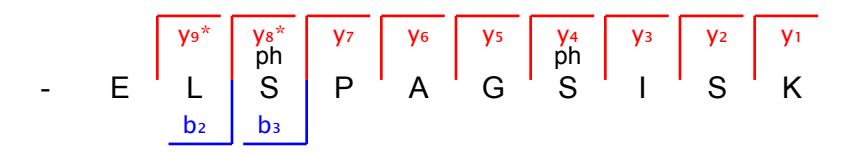
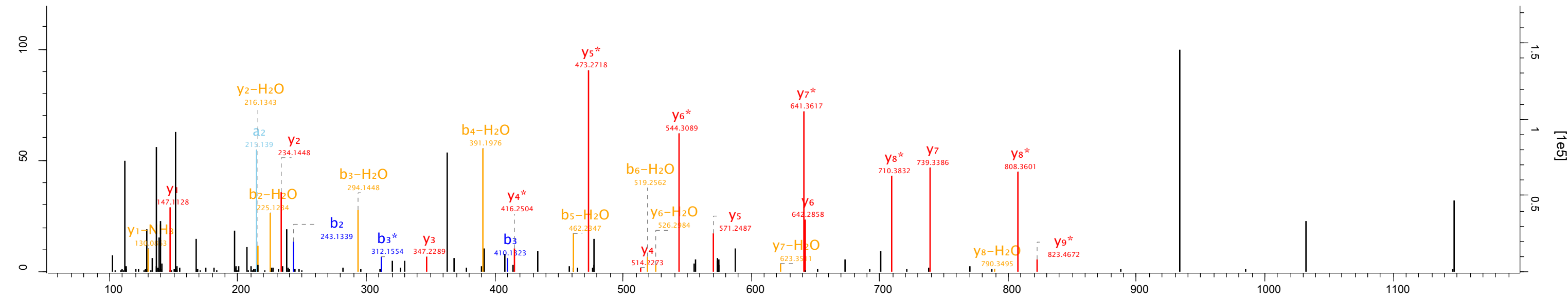
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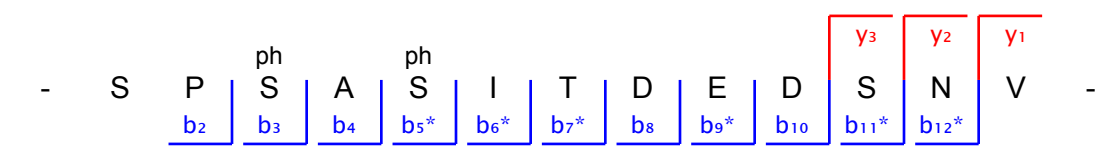
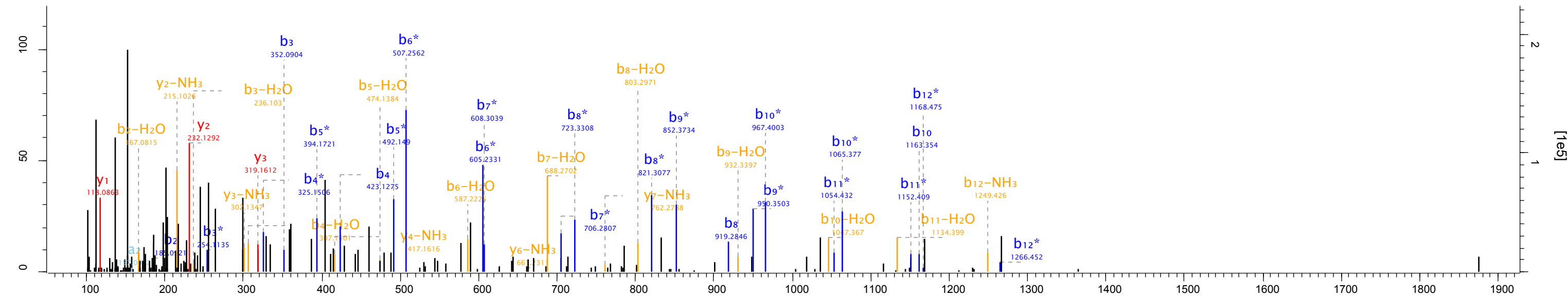
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 Scan: 5745 Method: FTMS; HCD Score: 87.24 m/z: 723.3 Gene names: MAP7D1



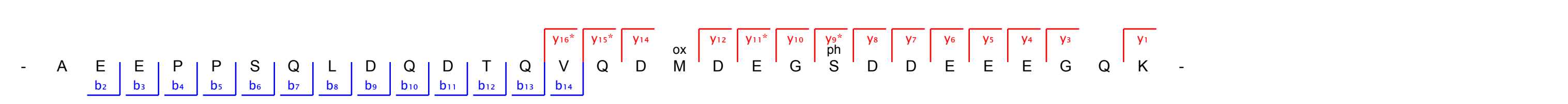
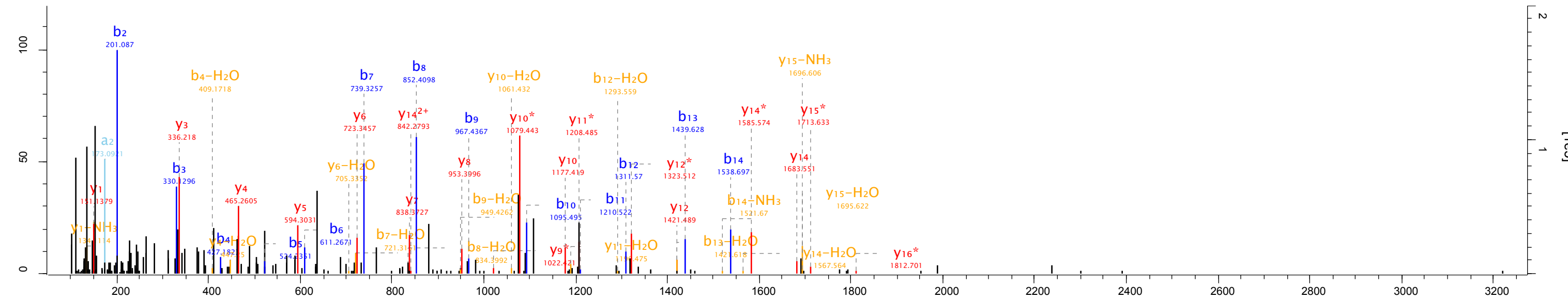
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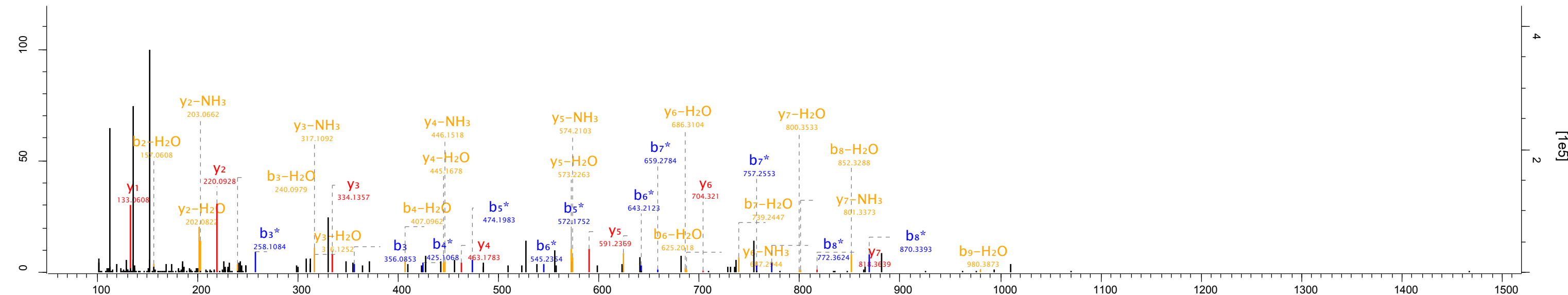


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 Scan: 7695 Method: FTMS; HCD Score: 179.79 m/z: 741.26 Gene names: PPF1BP1



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 7745 Method FTMS; HCD Score 110.67 m/z 1117.1 Gene names SF3A1

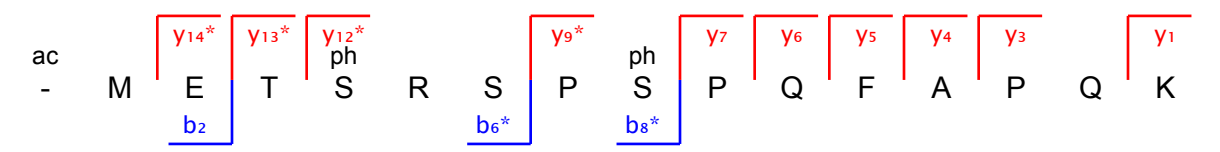
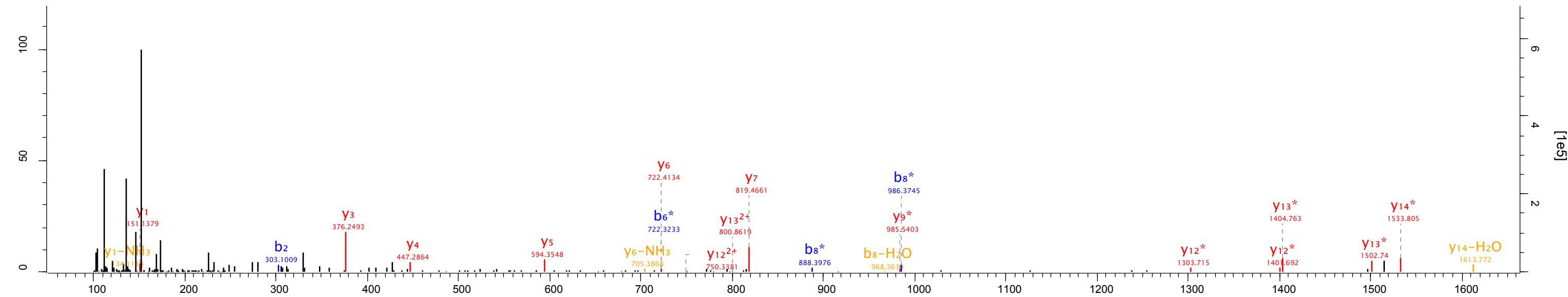




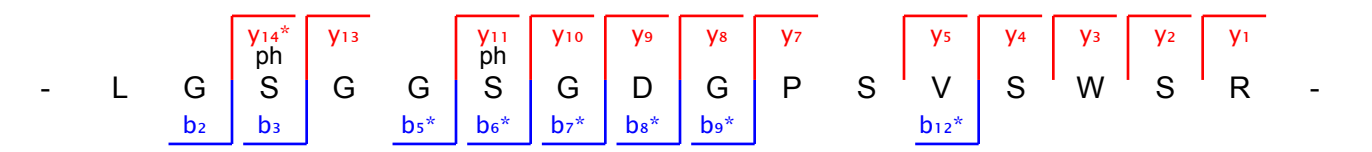
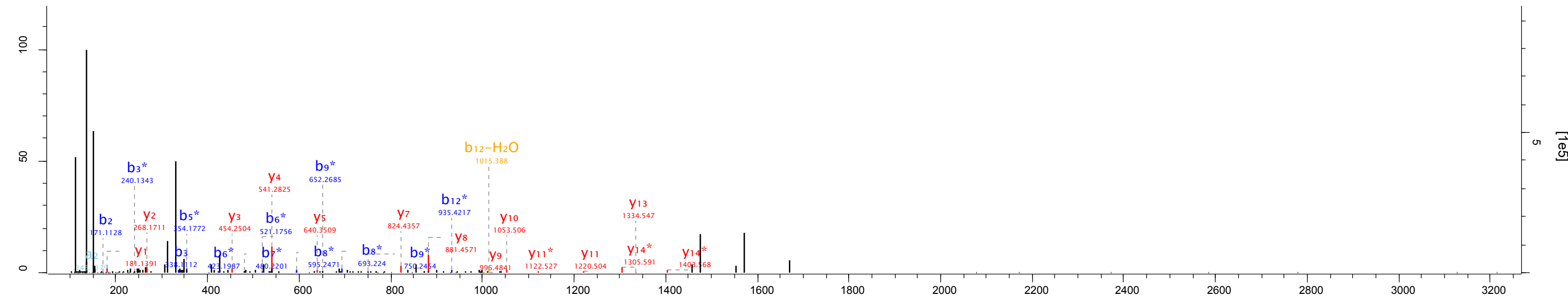
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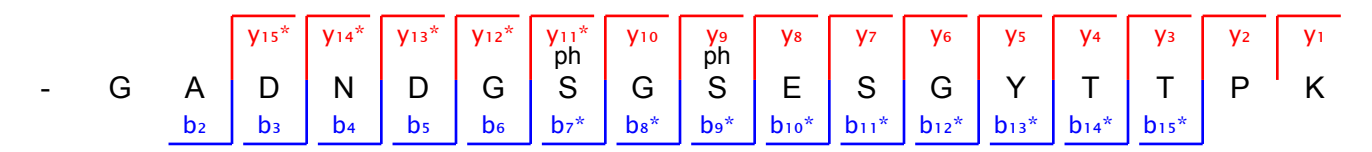
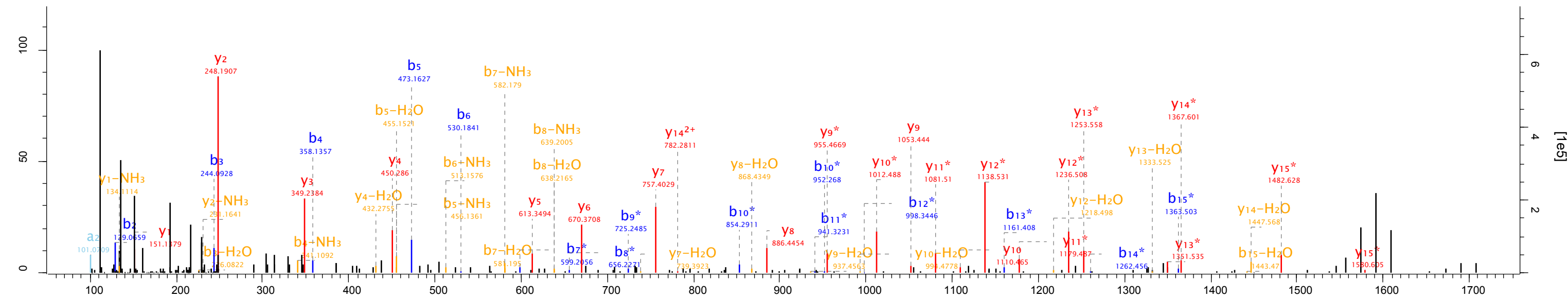


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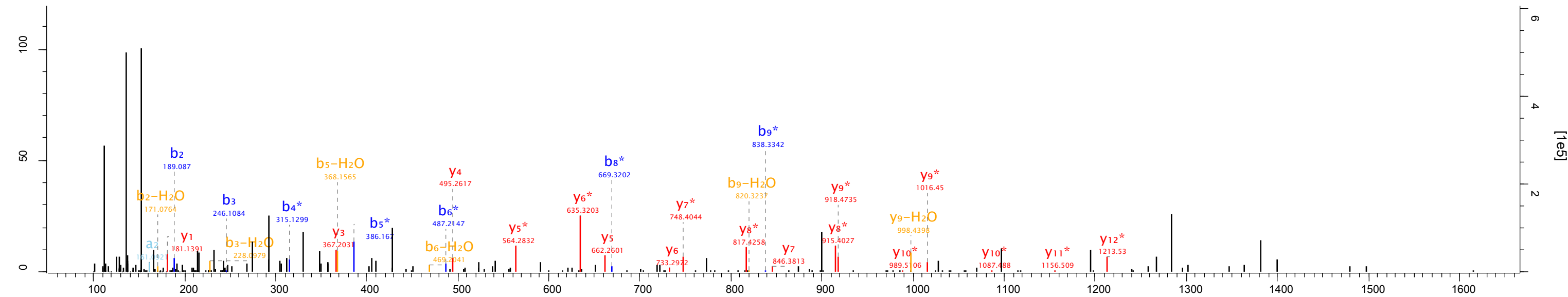


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20171215_MaS_33SR_LMH_phospho2_05

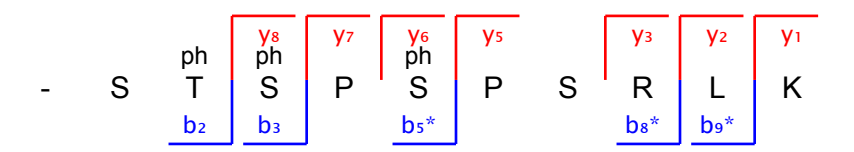
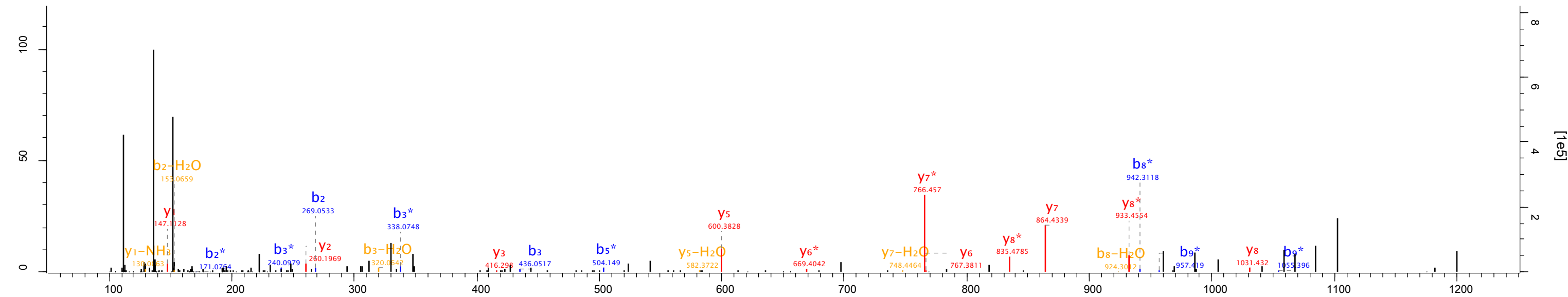
Scan 4045 Method FTMS; HCD Score 160.62 m/z 904.33 Gene names NUFIP2

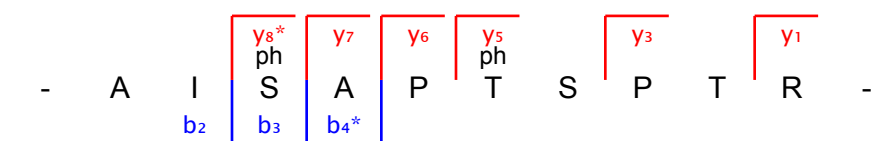
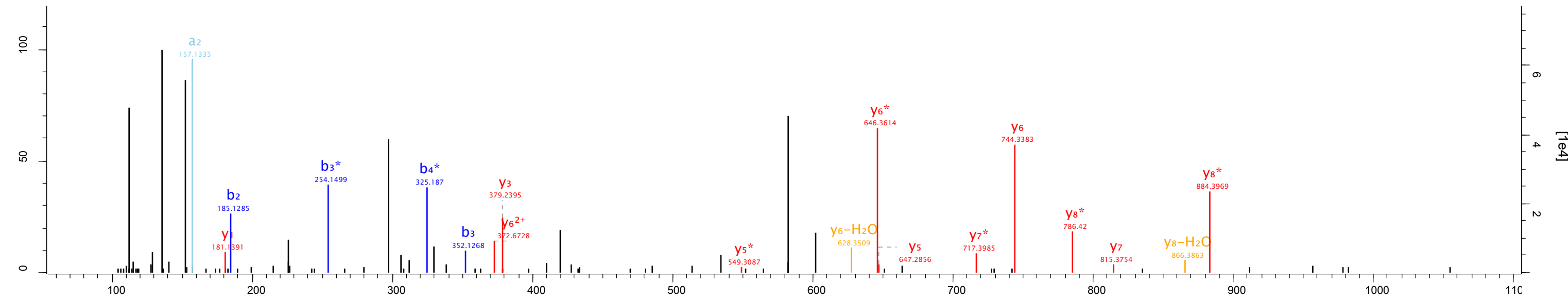


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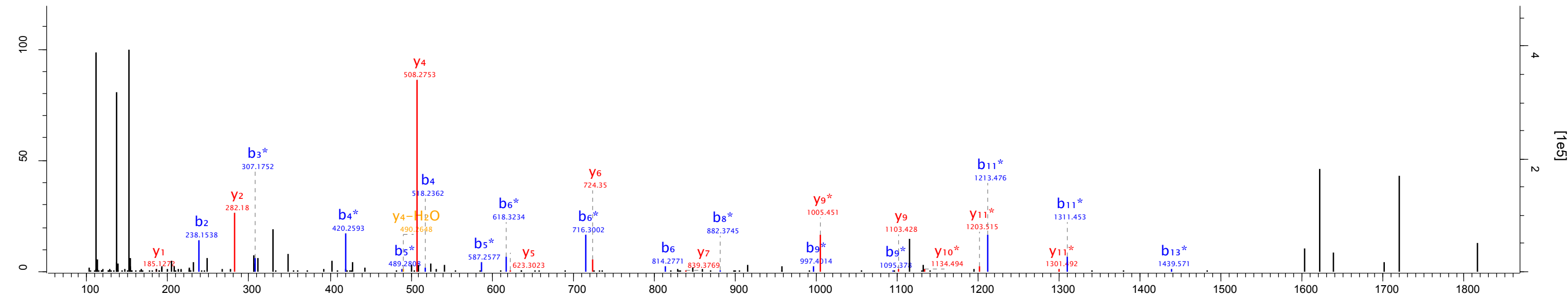


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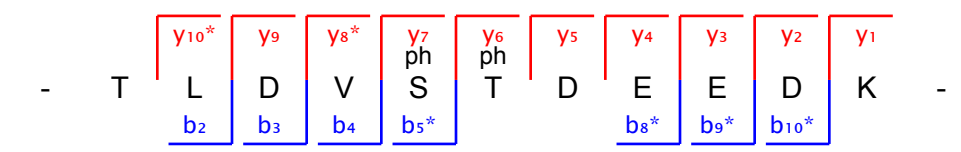
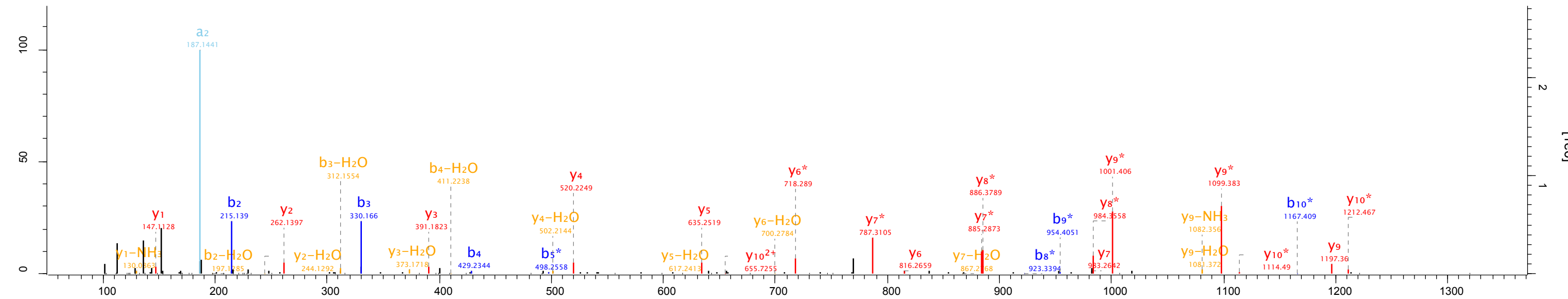


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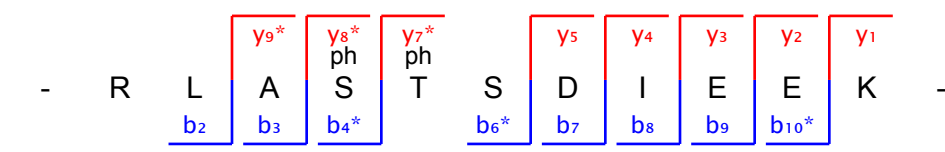
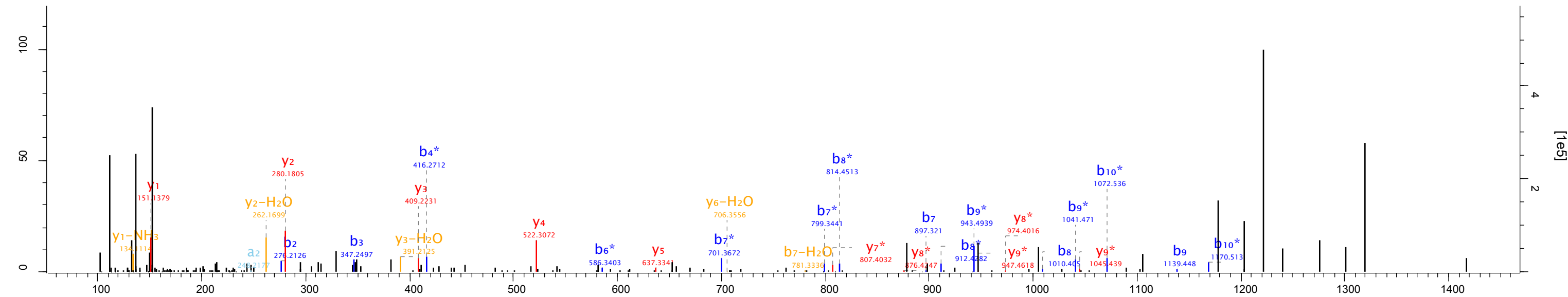


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20171215_MaS_33SR_LMH_phospho2_05

Scan 5435 Method FTMS; HCD Score 140.3 m/z 706.25 Gene names GCFC2



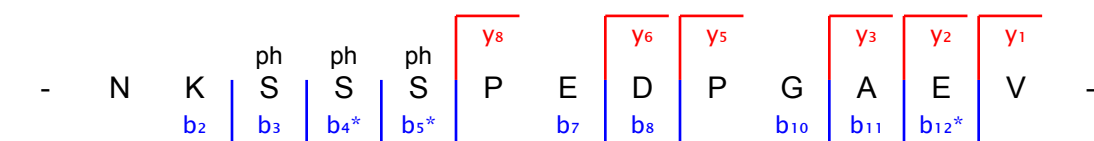
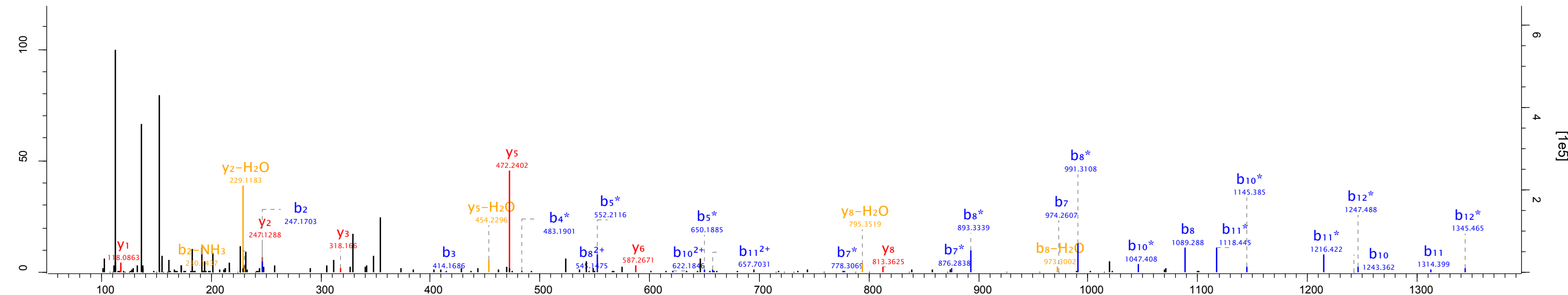
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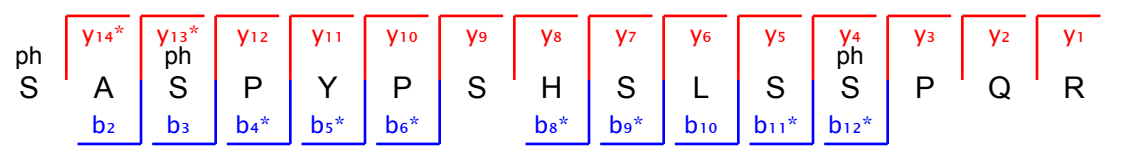
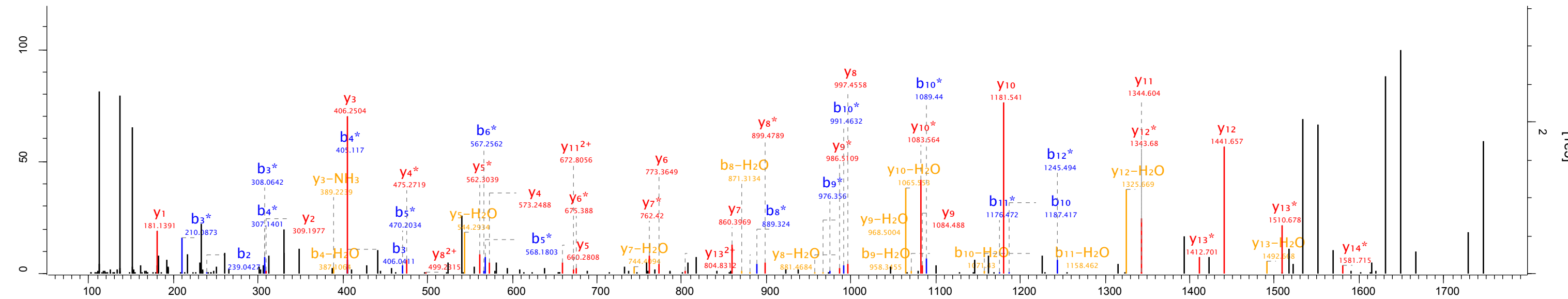
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20171215_MaS_33SR_LMH_phospho2_05

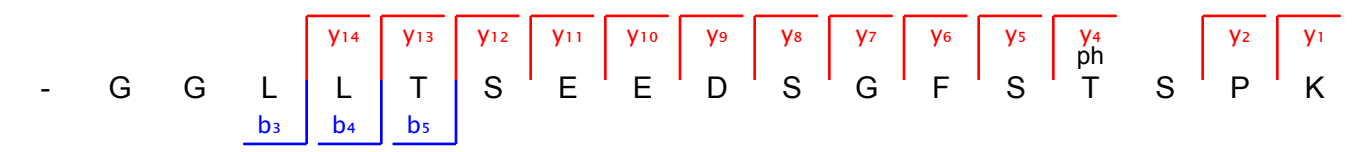
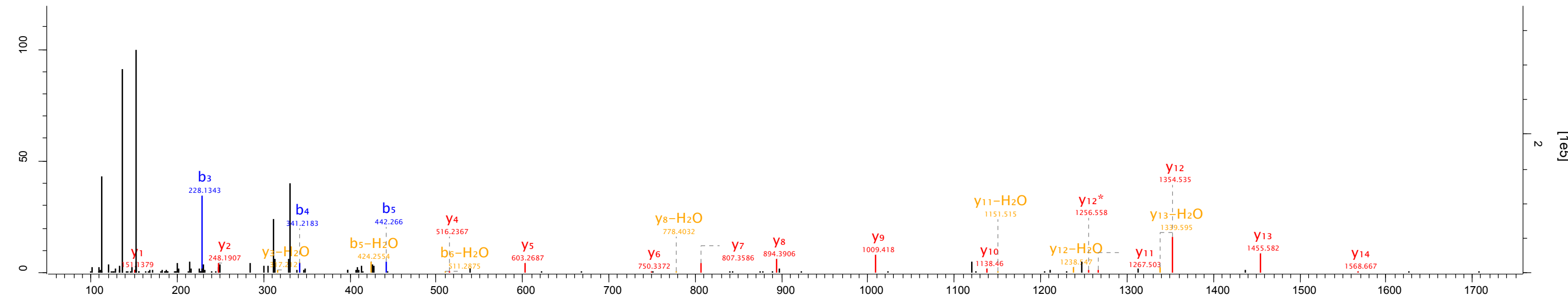
Scan	Method	Score	m/z	Gene names
5845	FTMS; HCD	122.44	780.76	TSSC4

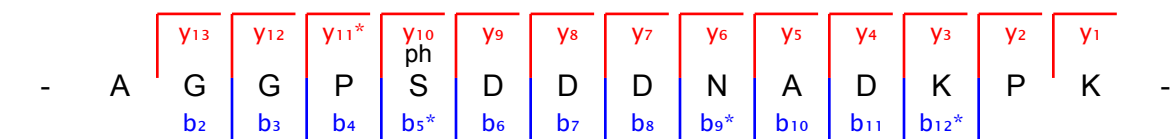
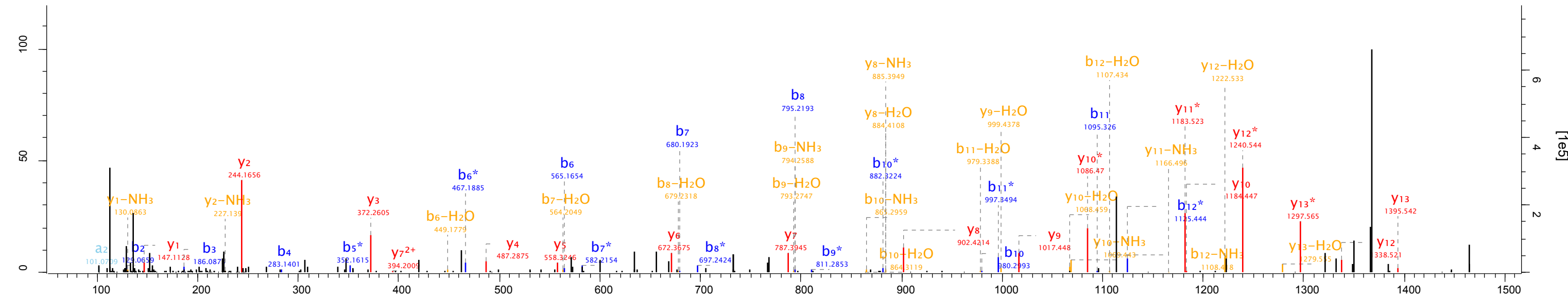


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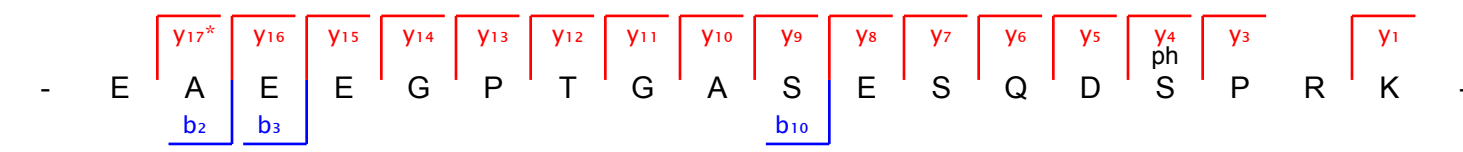
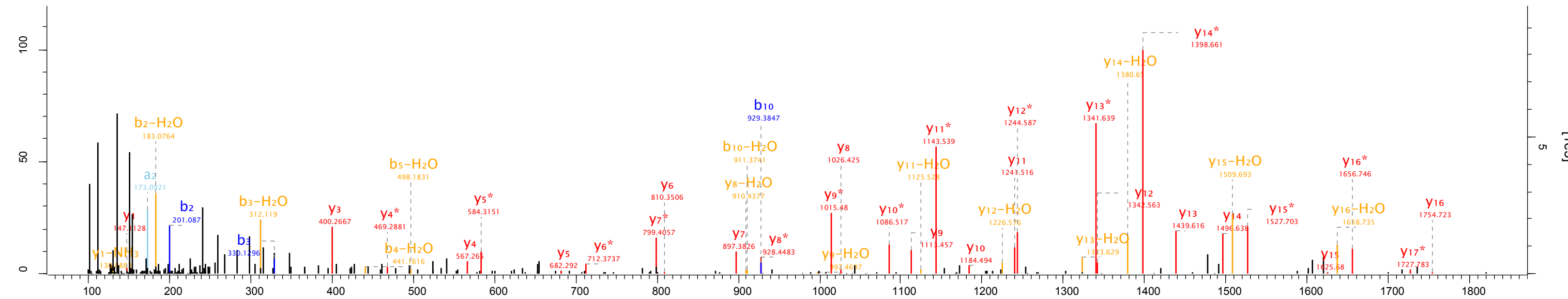


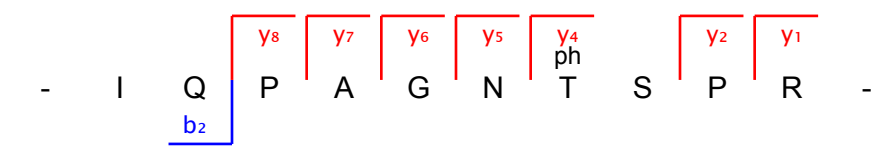
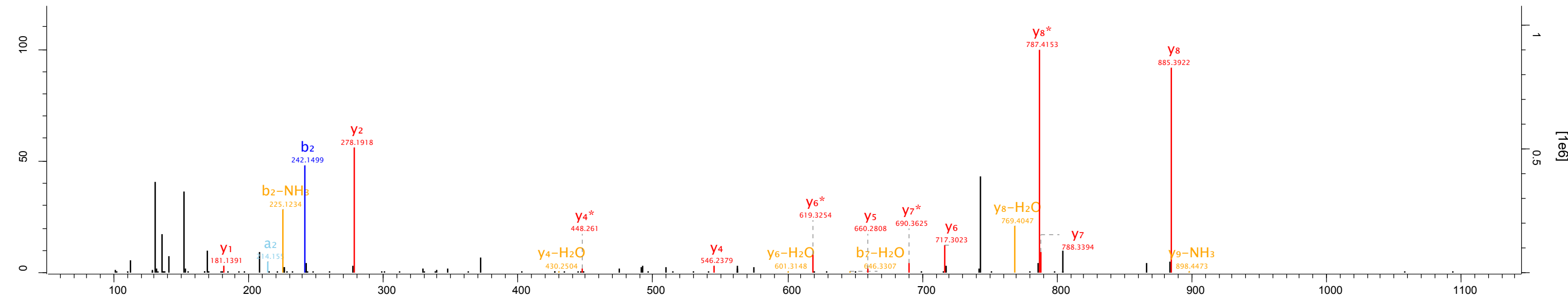
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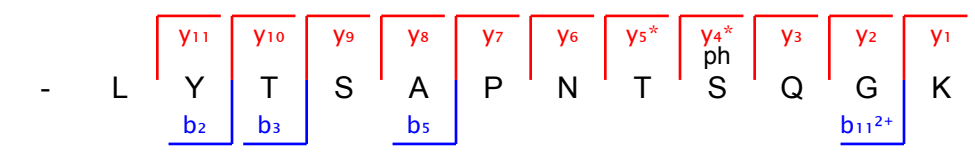
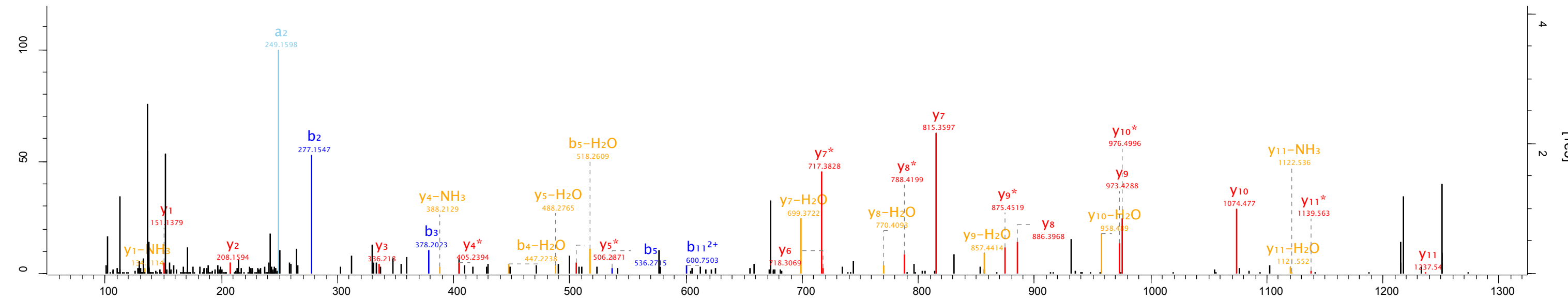


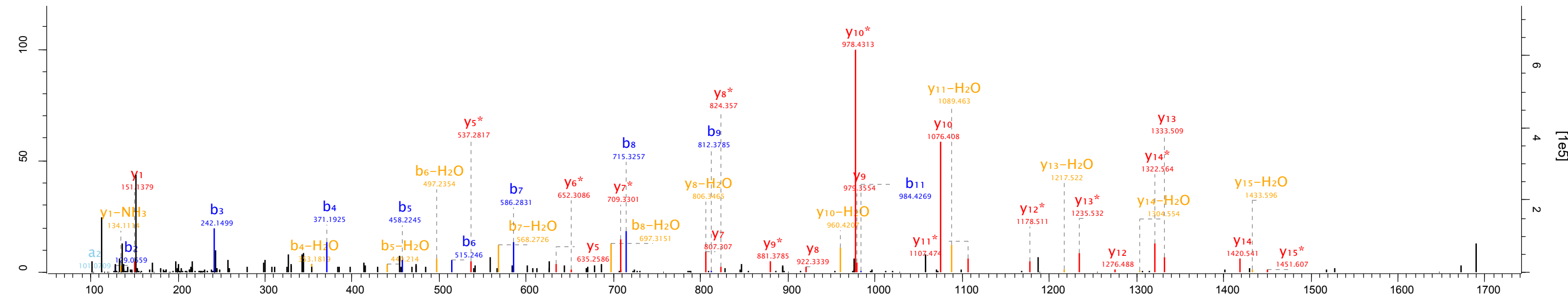
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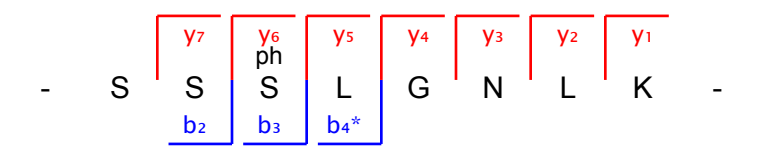
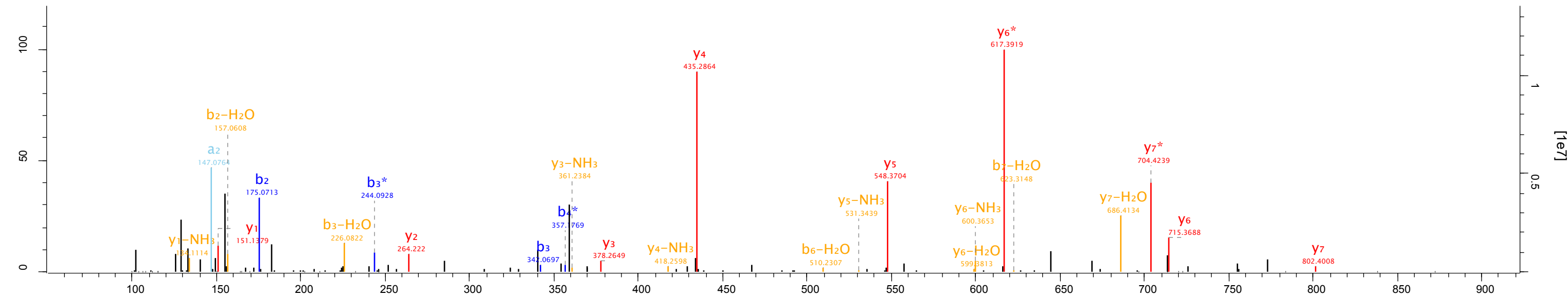


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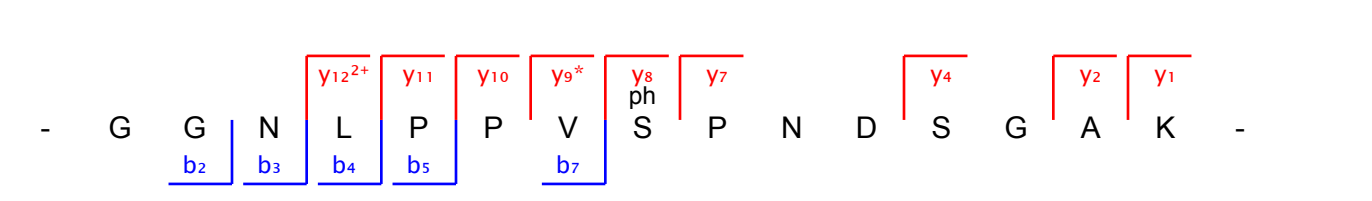
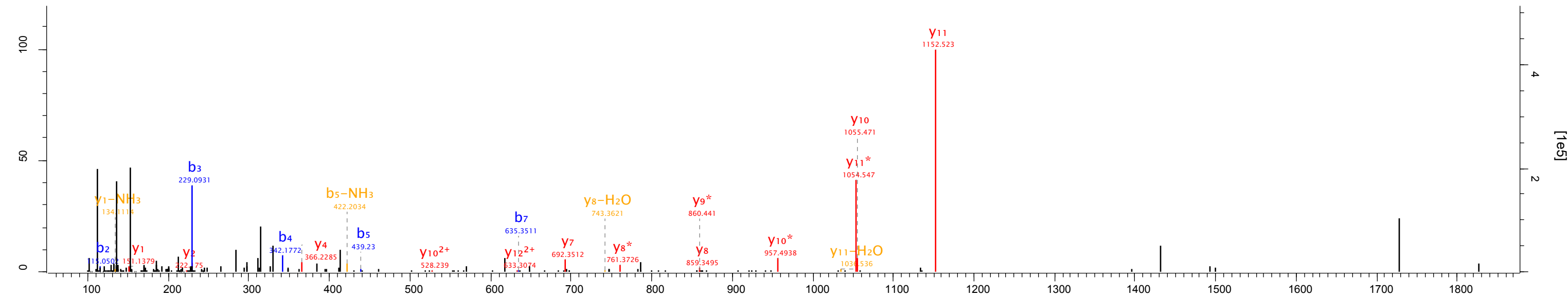
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- b2: G
- b3: L
- b4: E
- b5: S
- b6: G
- b7: A
- b8: E
- b9: P
- b11: D
- y1: K
- y5: S
- y6*: D
- y7: G
- y8: D
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- y10: P
- y11*: E
- y12: A
- y13: G
- y14: S
- y15*: E

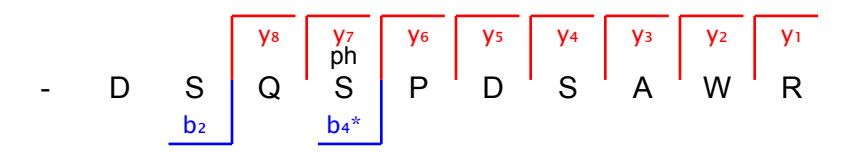
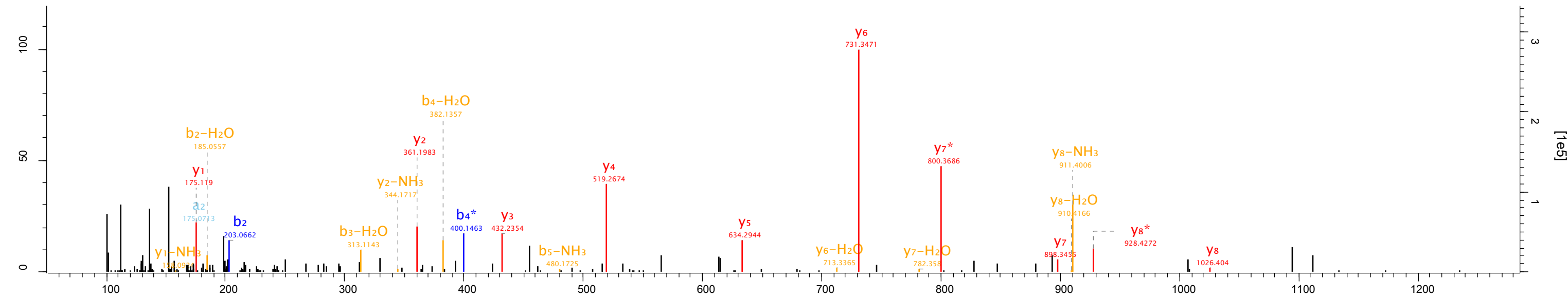
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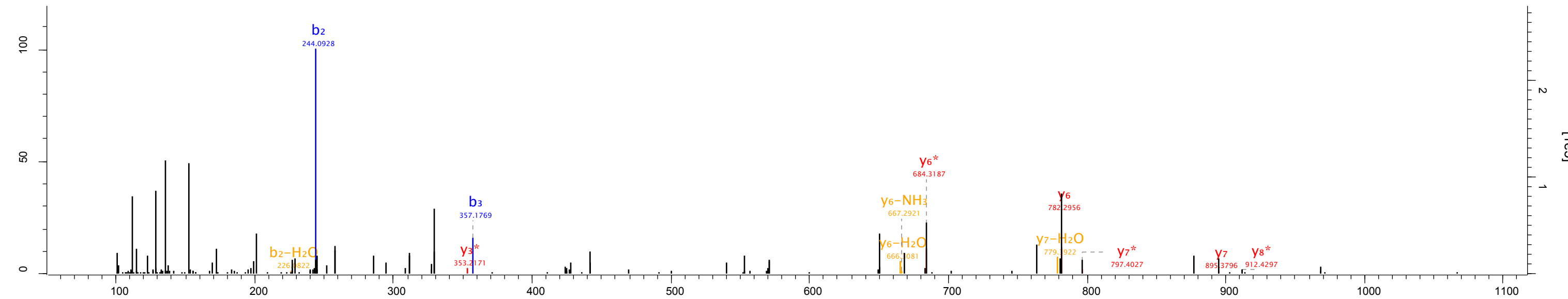
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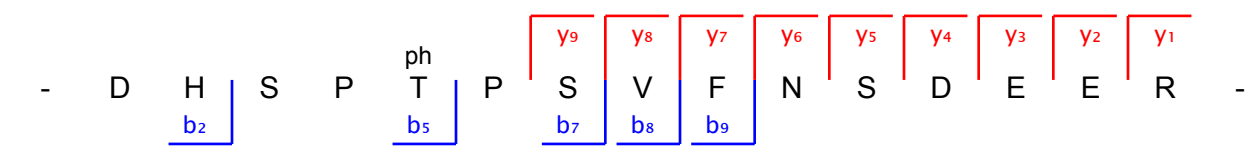
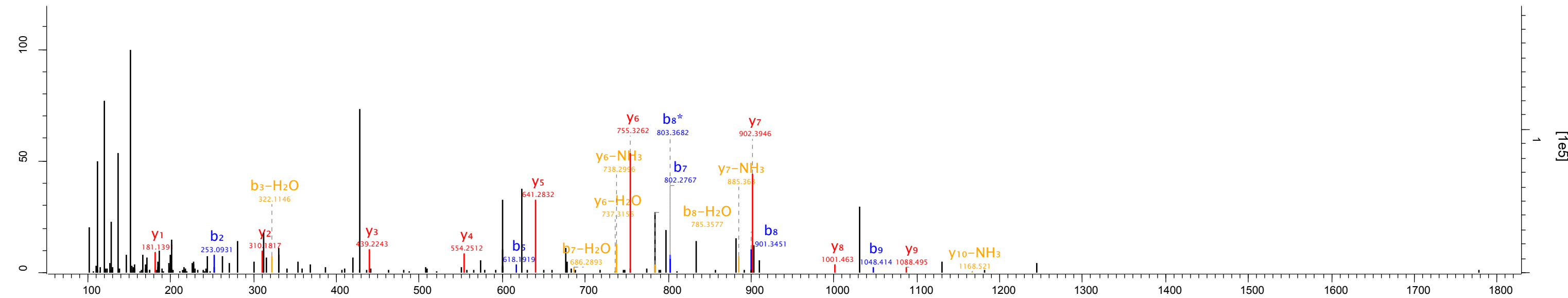


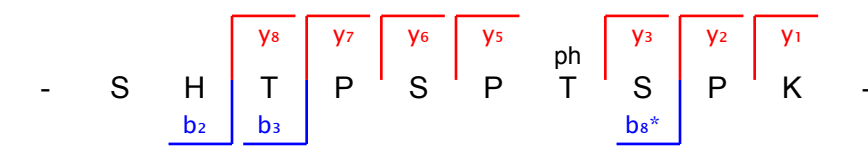
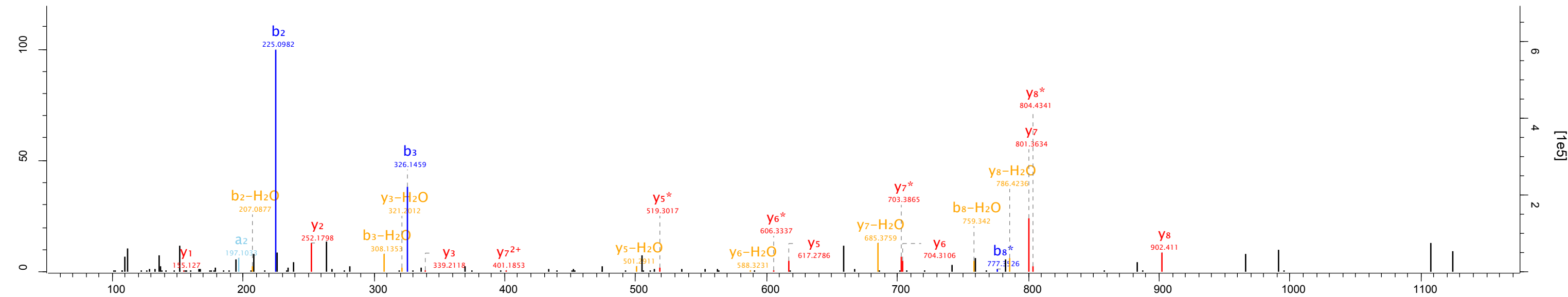
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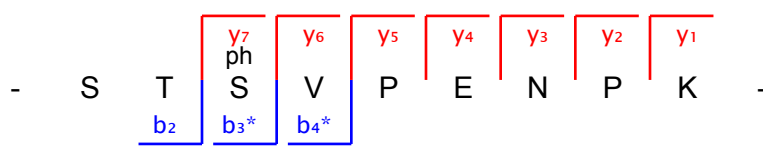
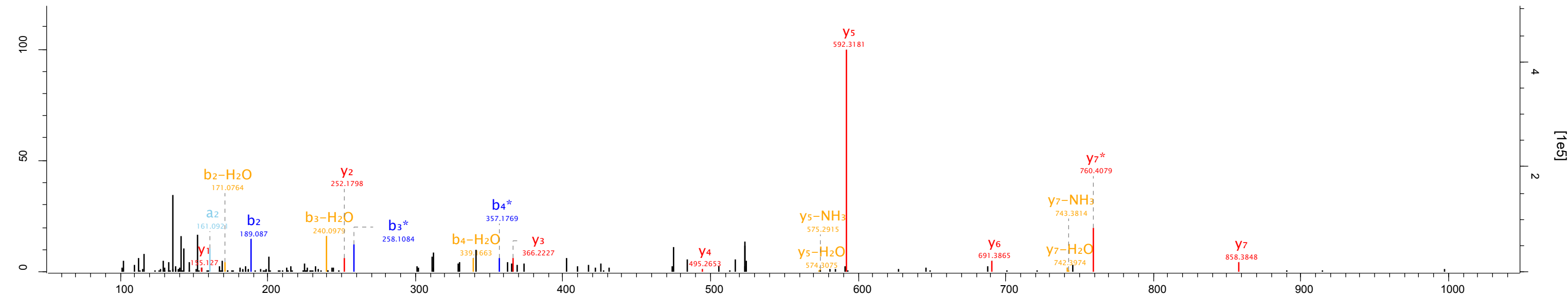
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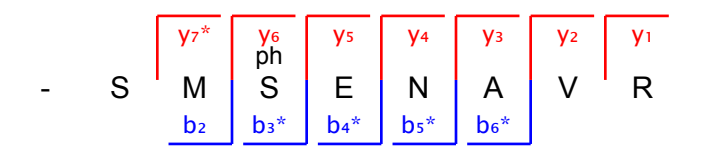
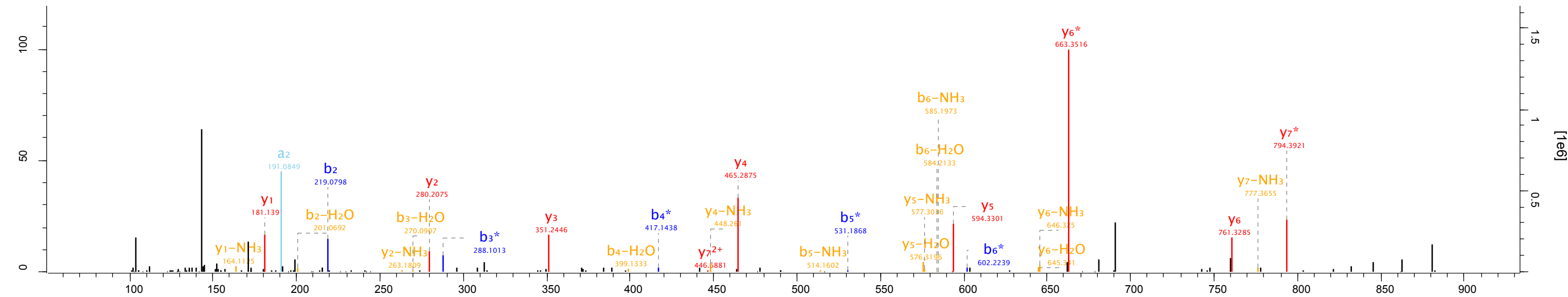




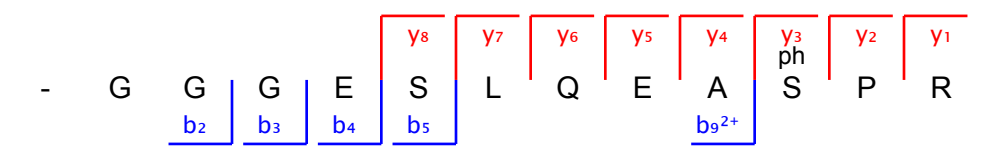
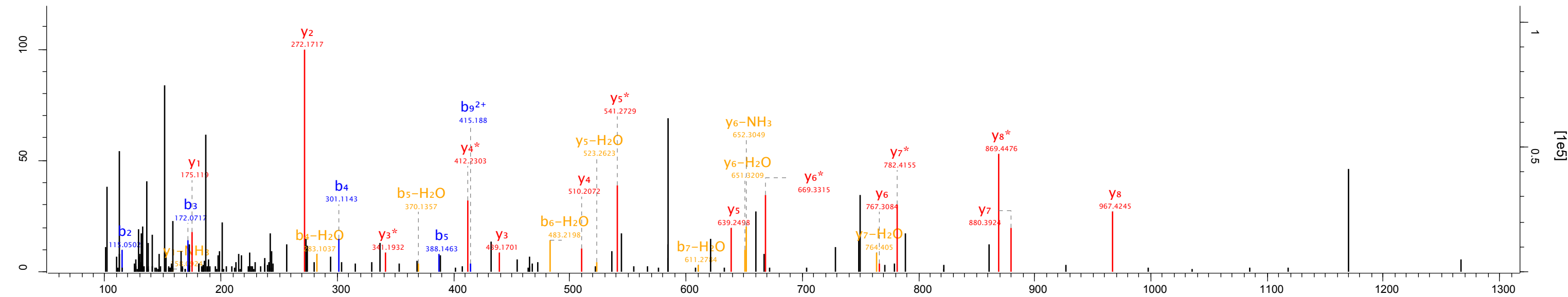
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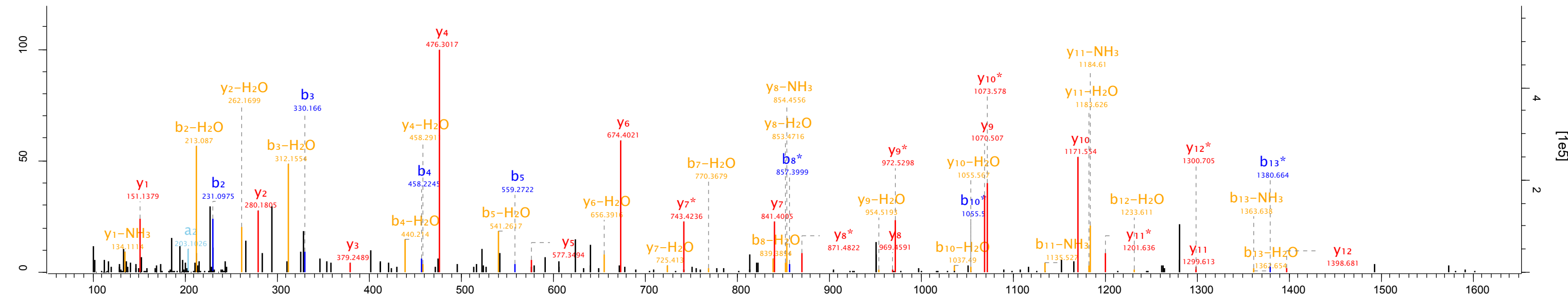


Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 3345 Method FTMS; HCD Score 139.32 m/z 490.2 Gene names MFF



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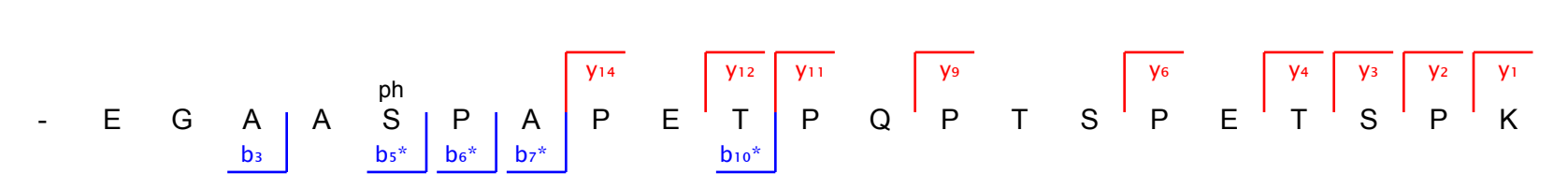
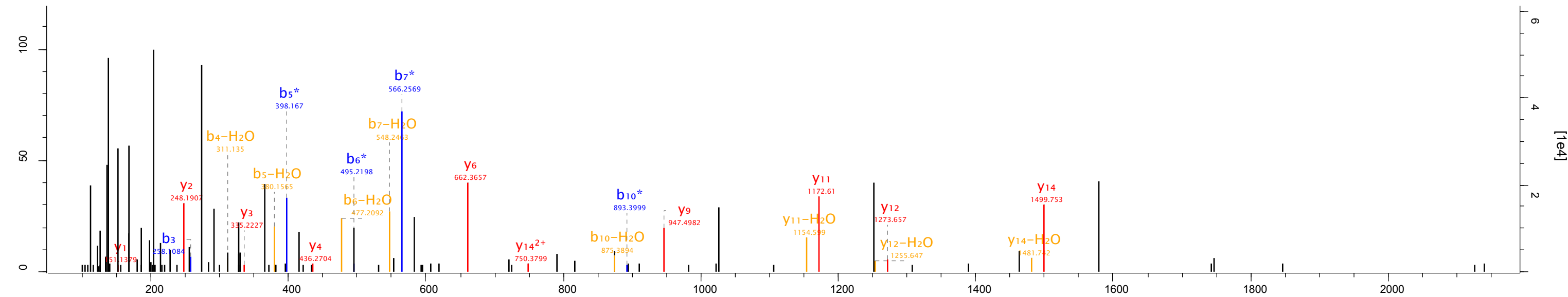


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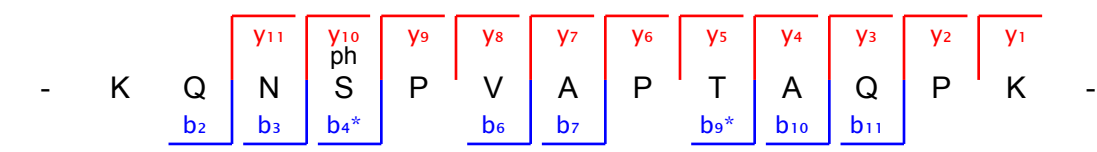
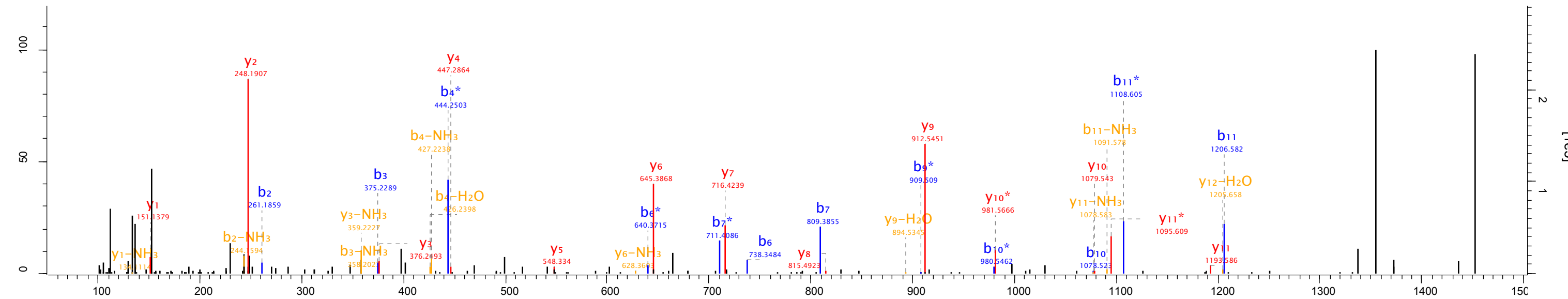
b₂ b₃ b₄ b₅ b₈* b₁₀* b₁₃*

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

Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 5615 Method FTMS; HCD Score 56.68 m/z 1082 Gene names CCDC9

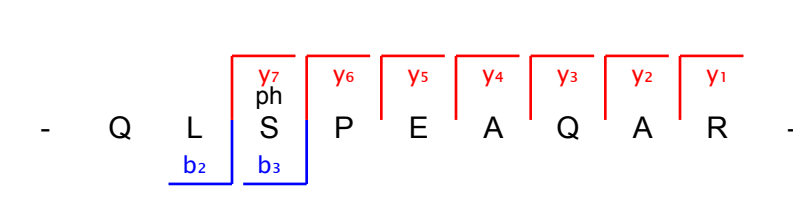
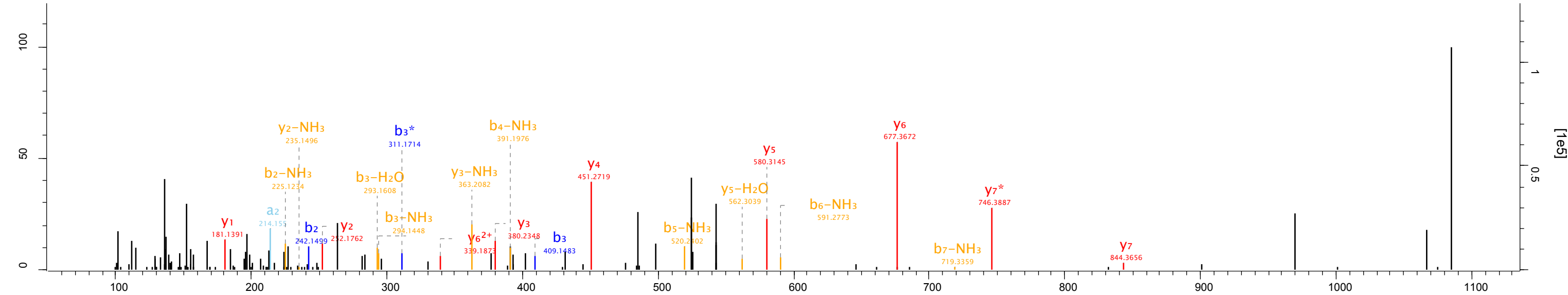


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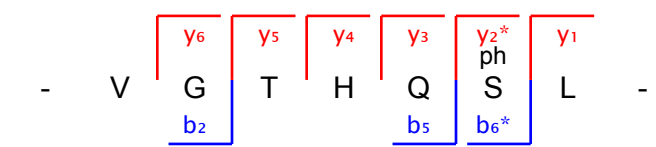
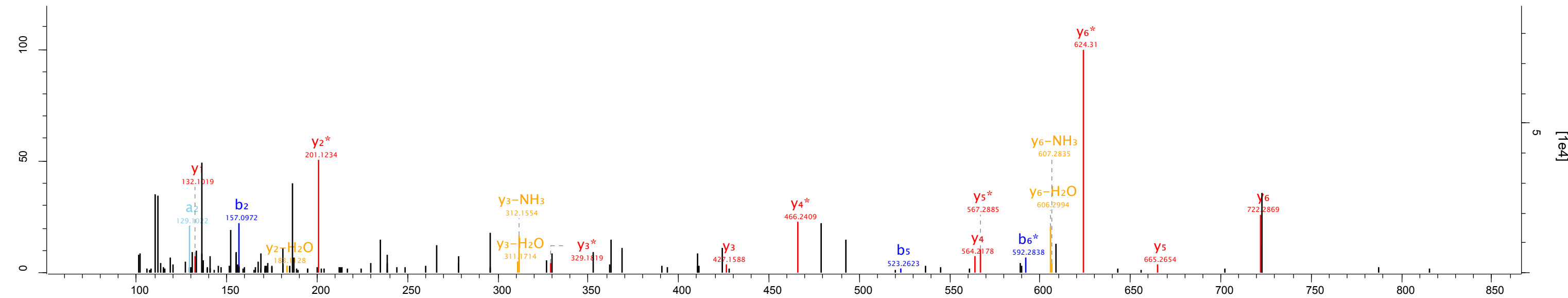


Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 3575 Method FTMS; HCD Score 72.61 m/z 543.26 Gene names PHF14

20171215_MaS_33SR_LMH_phospho2_09

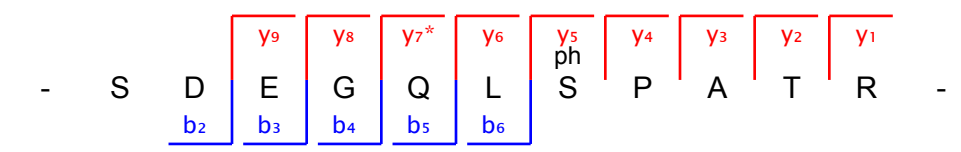
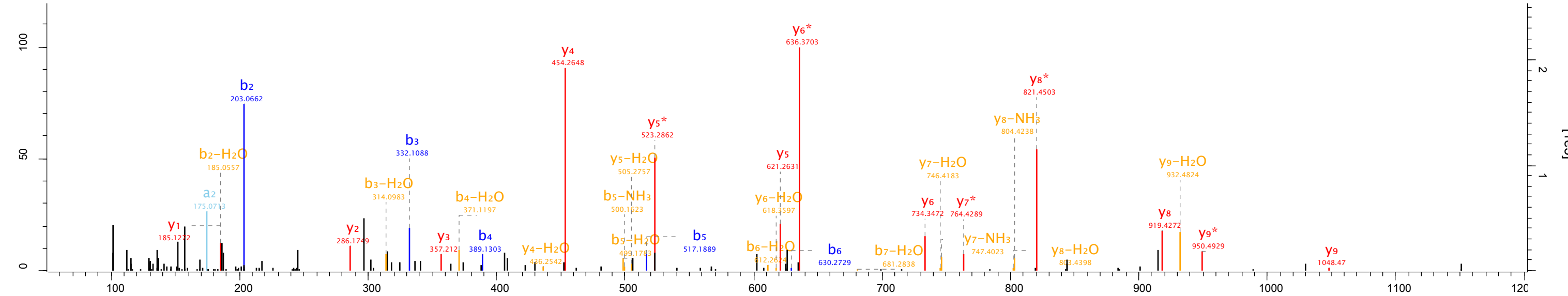


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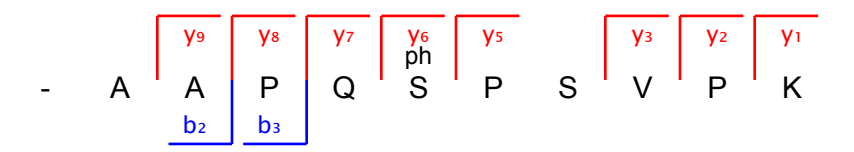
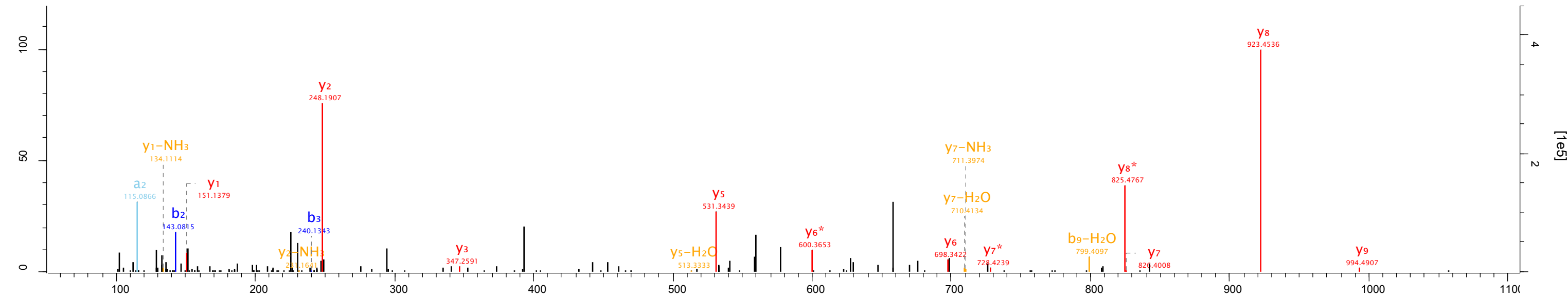


Raw file Scan Method Score m/z Gene names

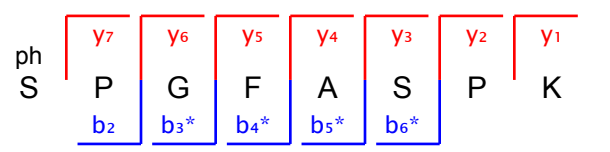
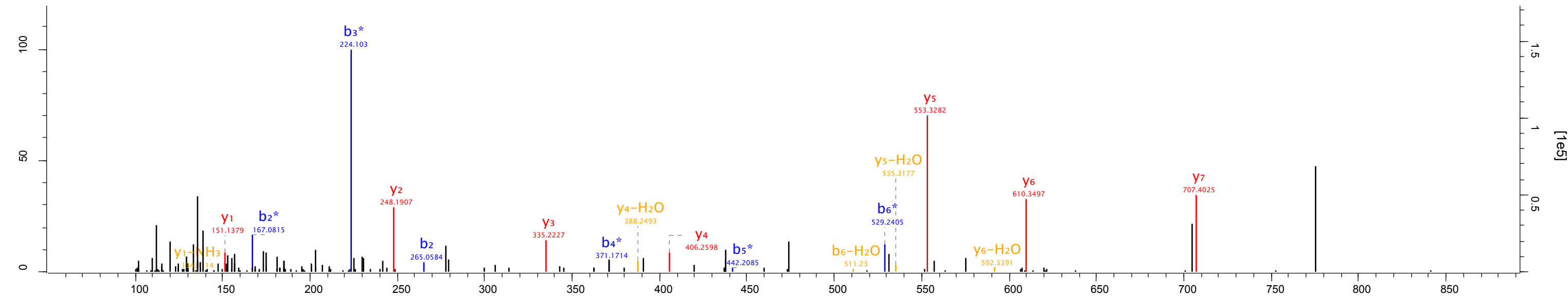
20171215_MaS_33SR_LMH_phospho2_09 3655 FTMS; HCD 167.03 625.77 PLEC



Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 3775 Method FTMS; HCD Score 70.54 m/z 533.27 Gene names NUP155



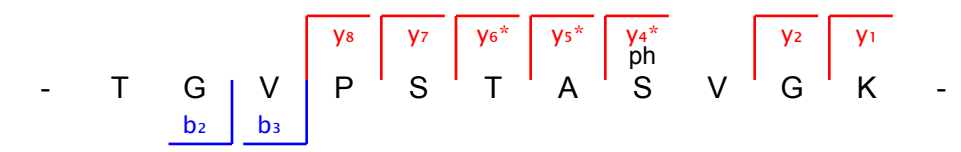
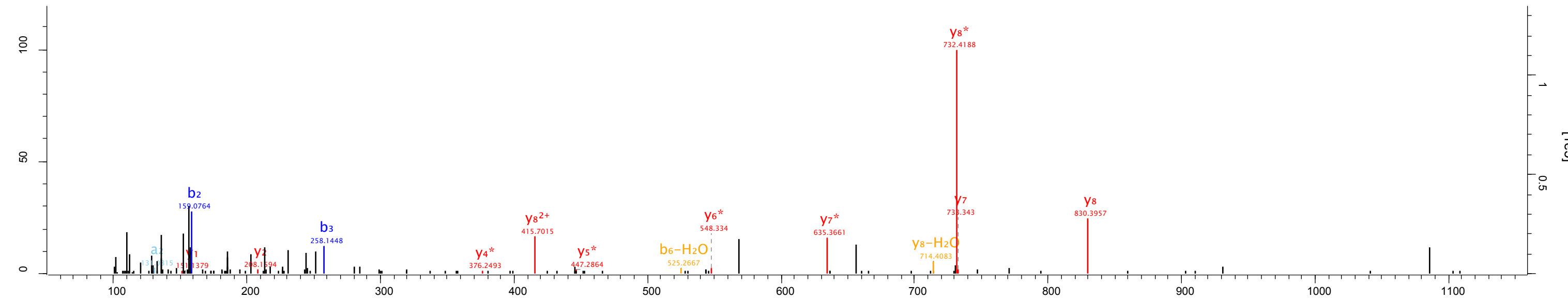
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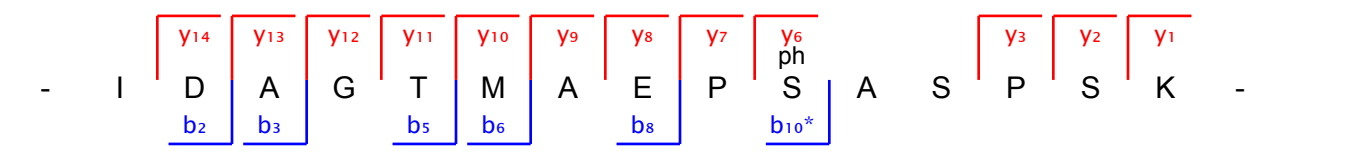
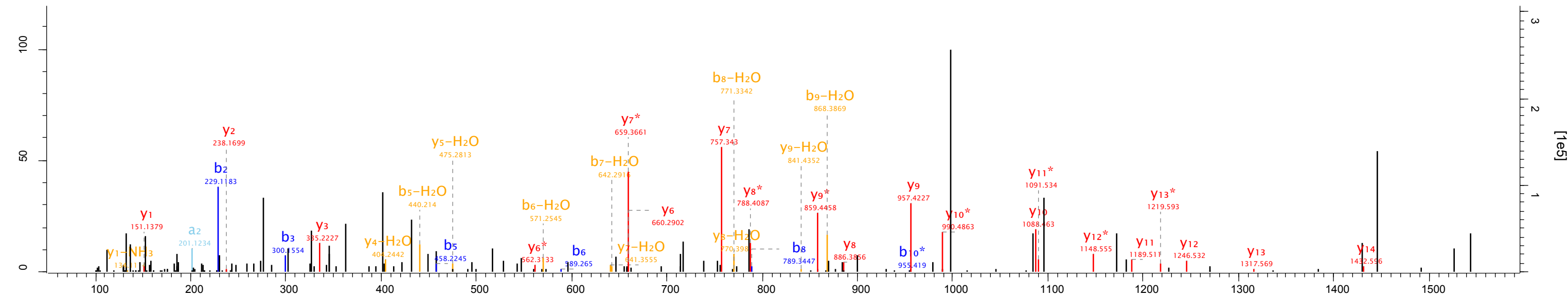
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20171215_MaS_33SR_LMH_phospho2_09

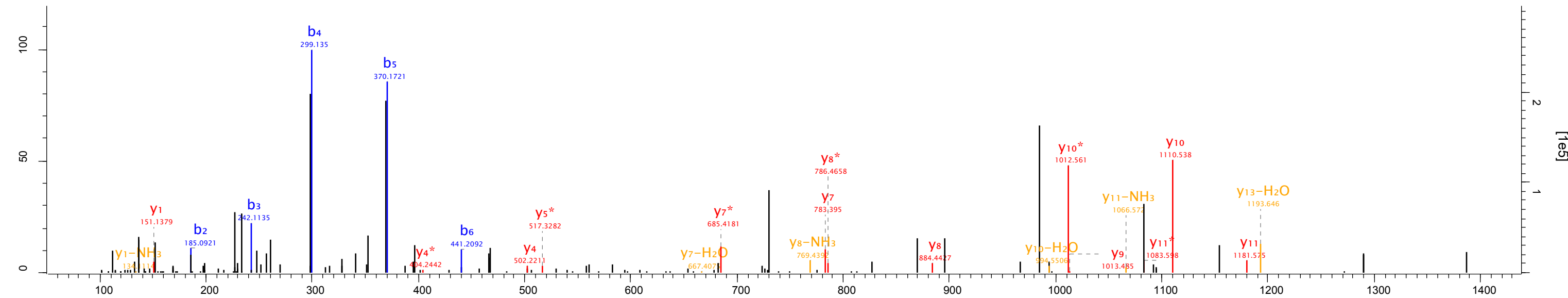
Scan	Method	Score	m/z	Gene names
4465	FTMS; HCD	40.28	544.27	SSFA2



Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 5945 Method FTMS; HCD Score 112.14 m/z 773.34 Gene names C9orf40

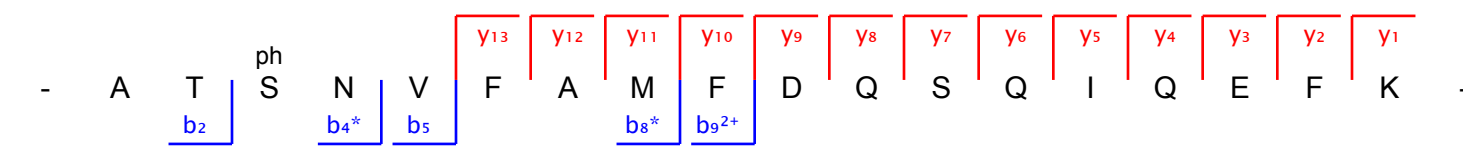
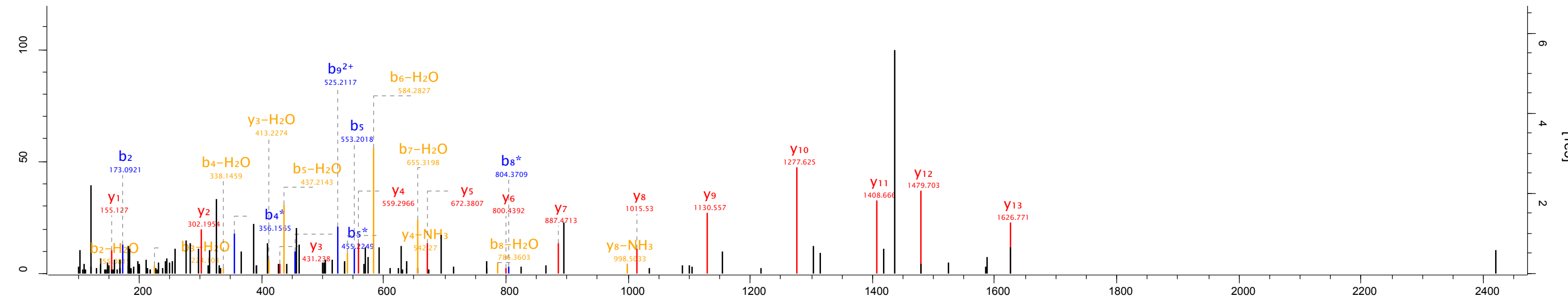


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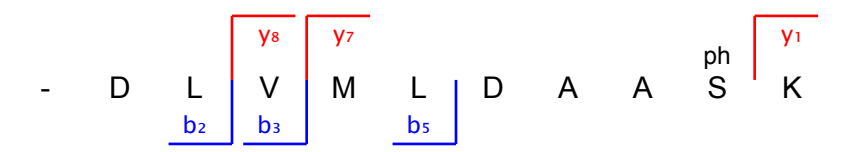
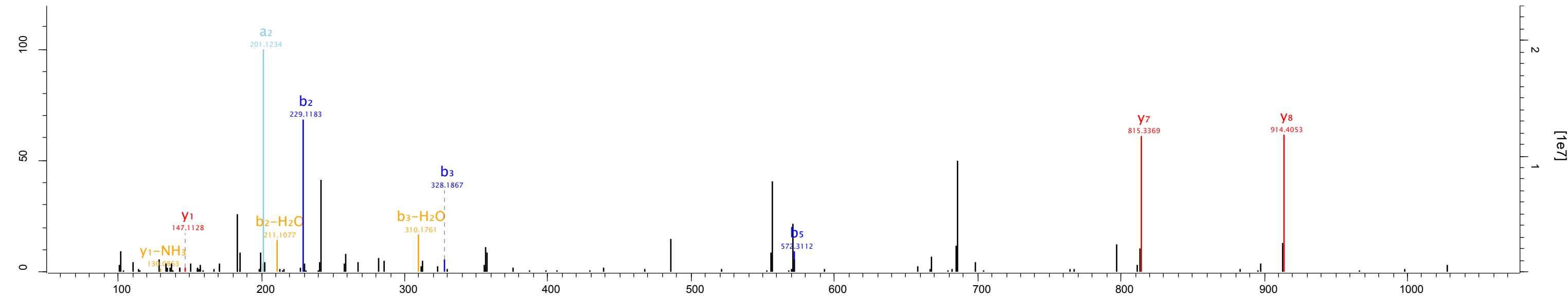


ac
 - A A G G A A P E T P A I S P S K -
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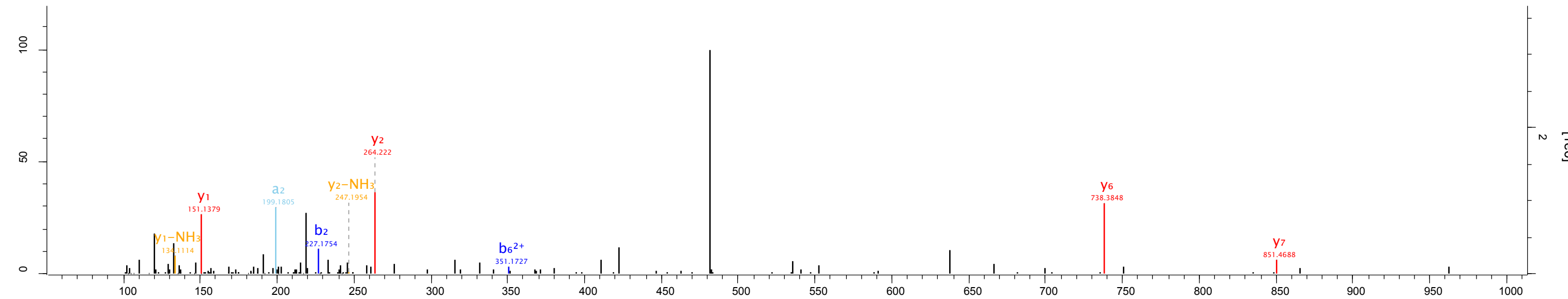
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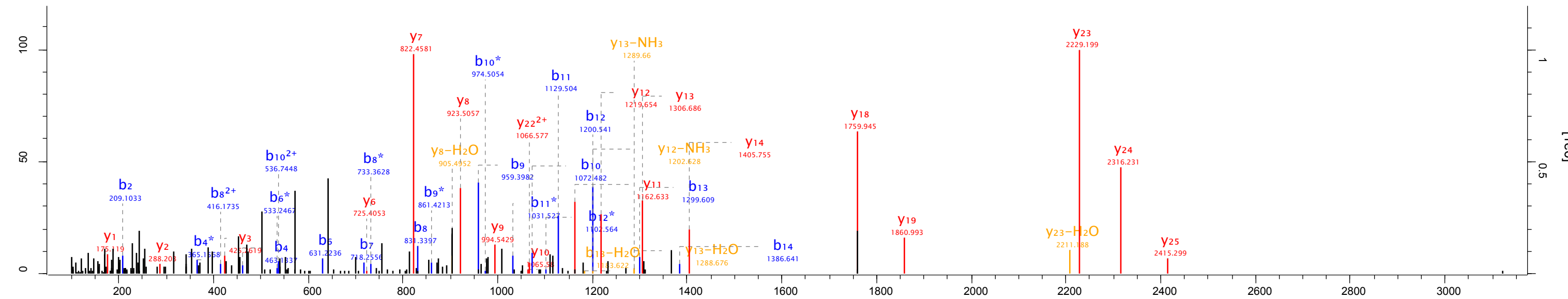
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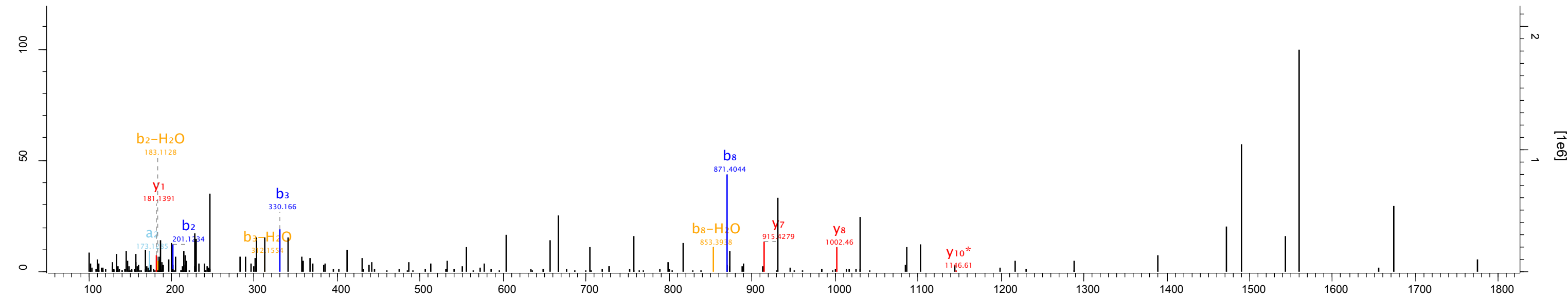
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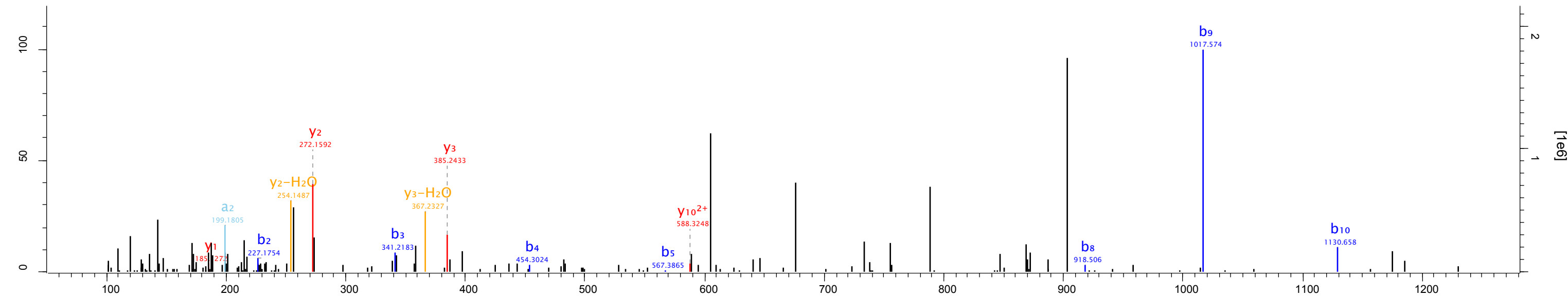
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y₂₄
y₂₃
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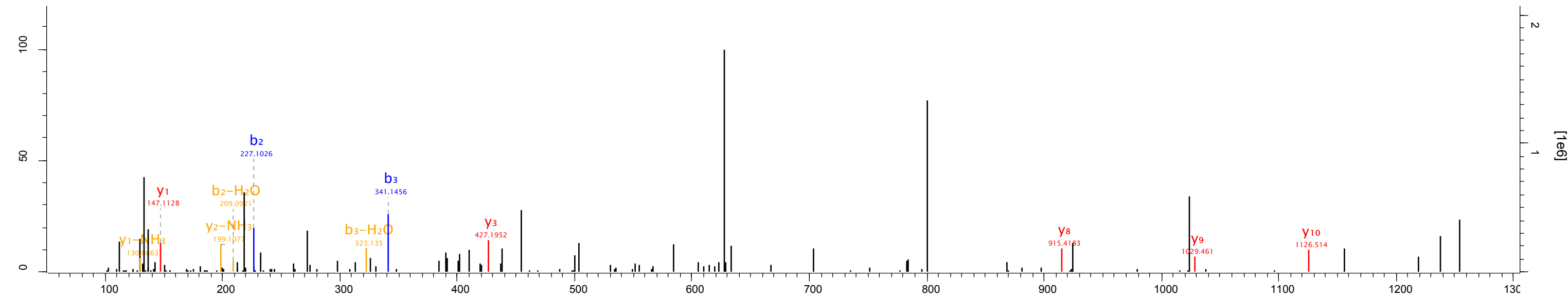
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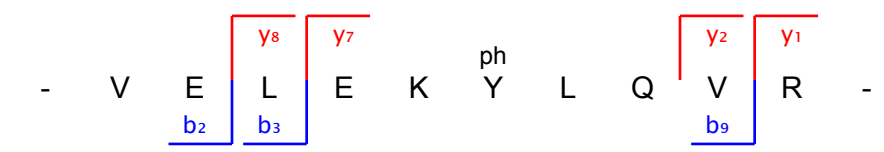
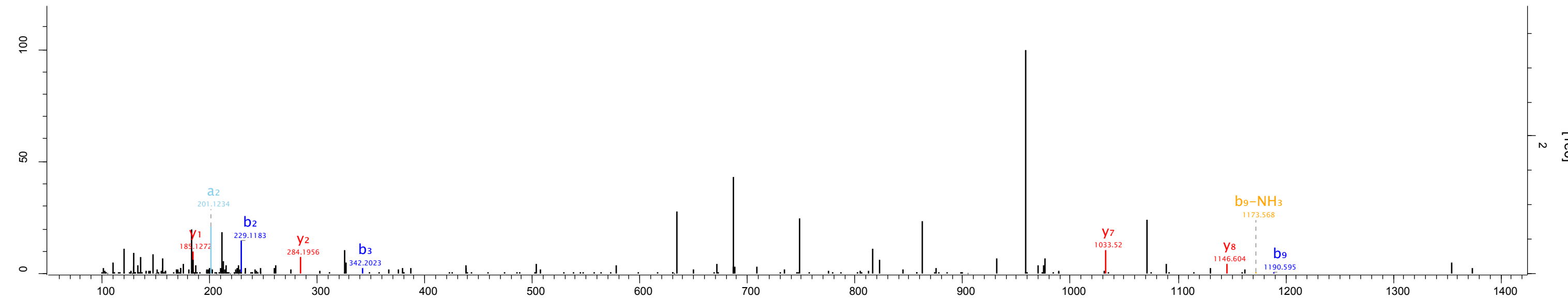
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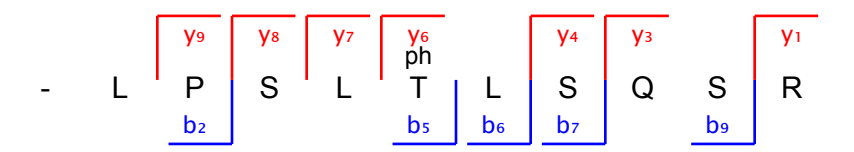
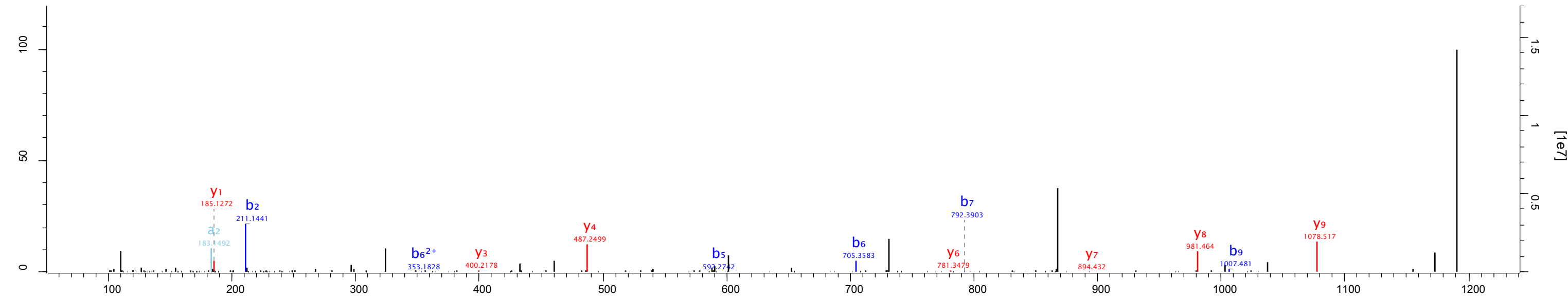
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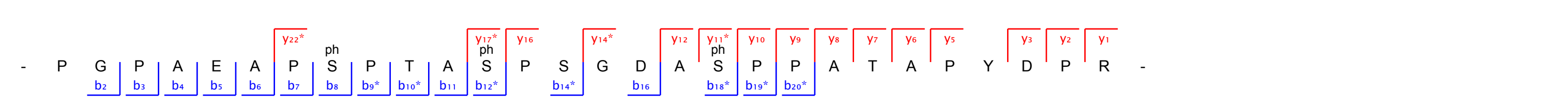
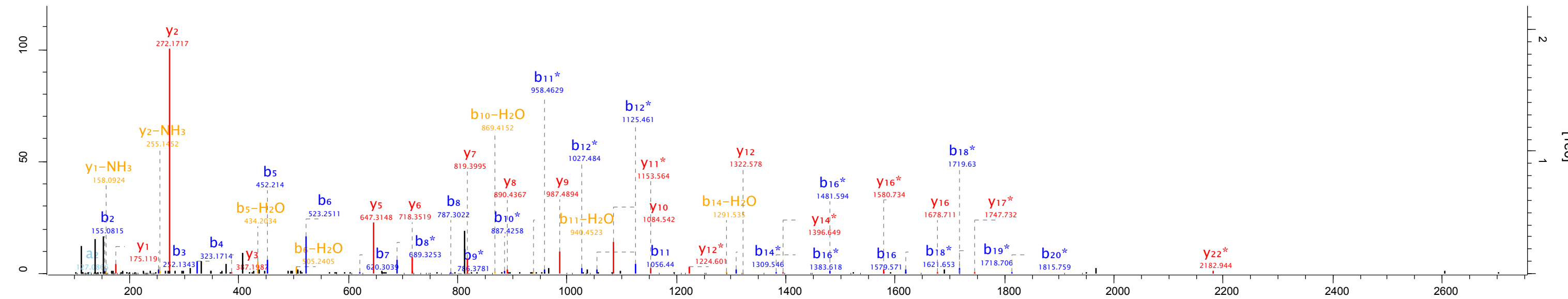
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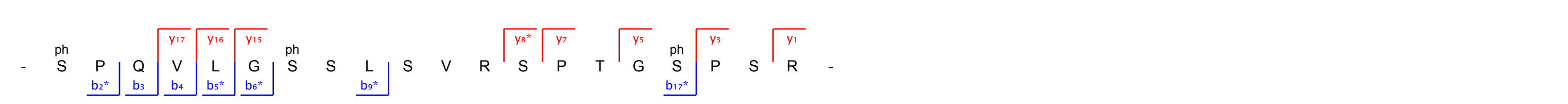
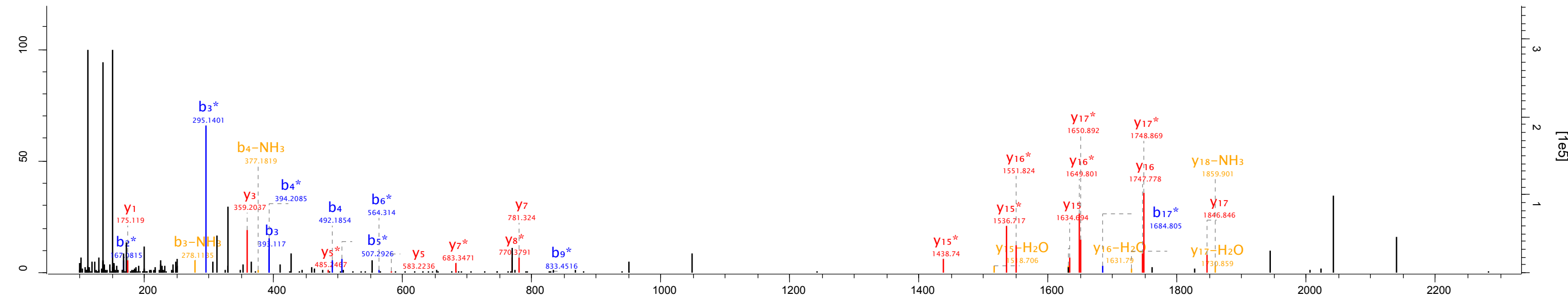
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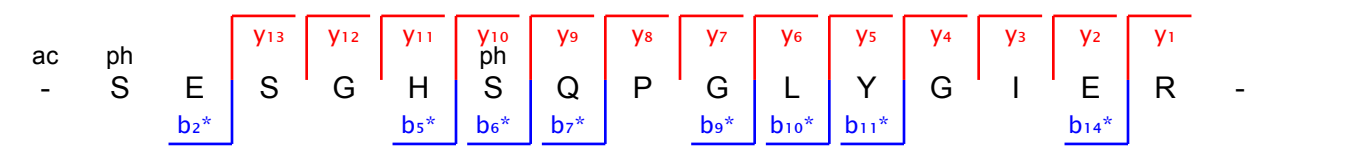
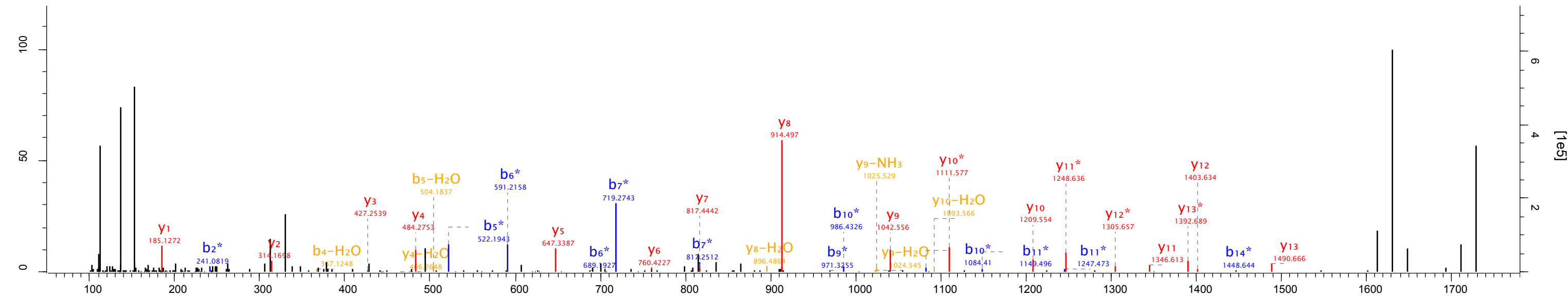
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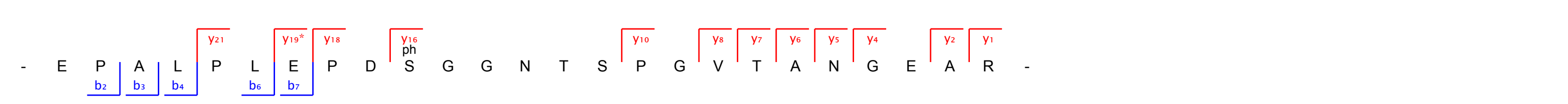
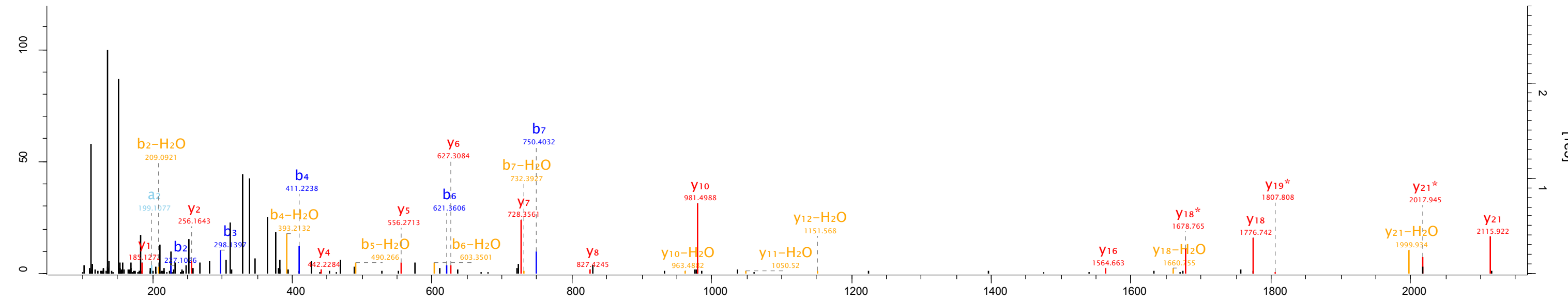
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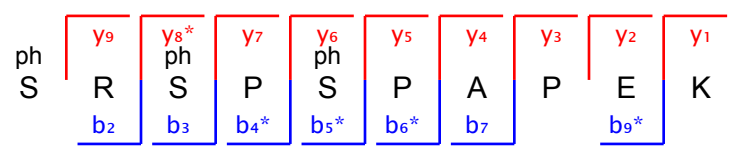
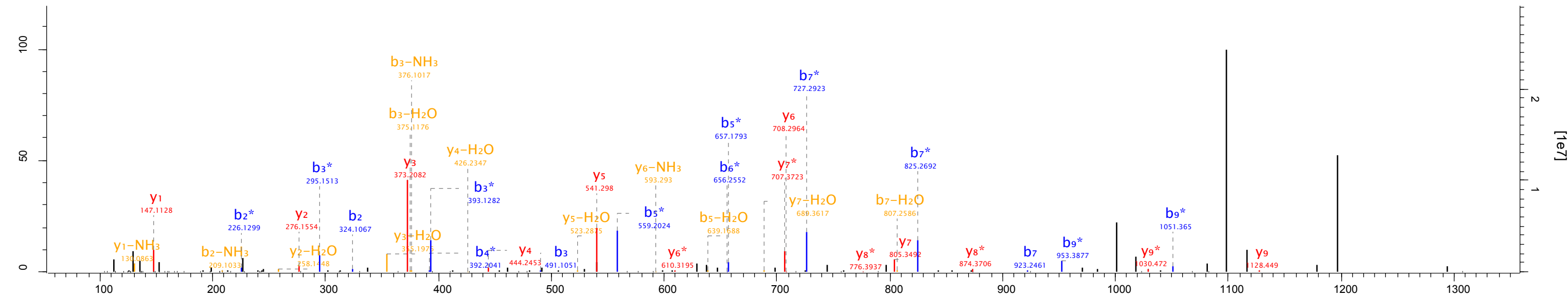
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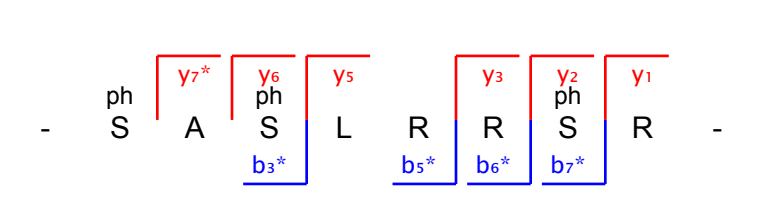
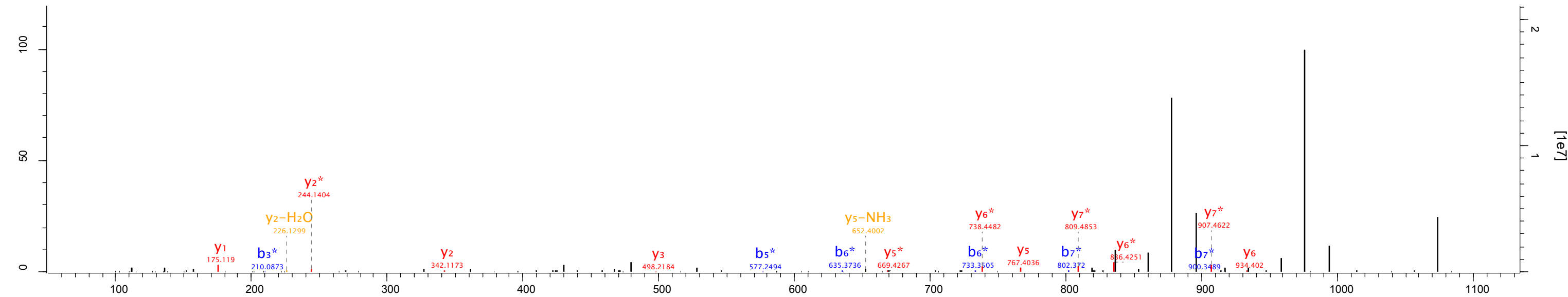
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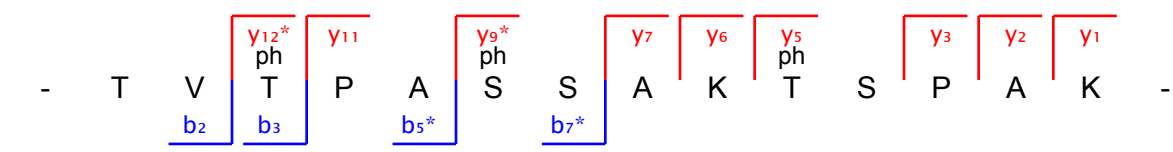
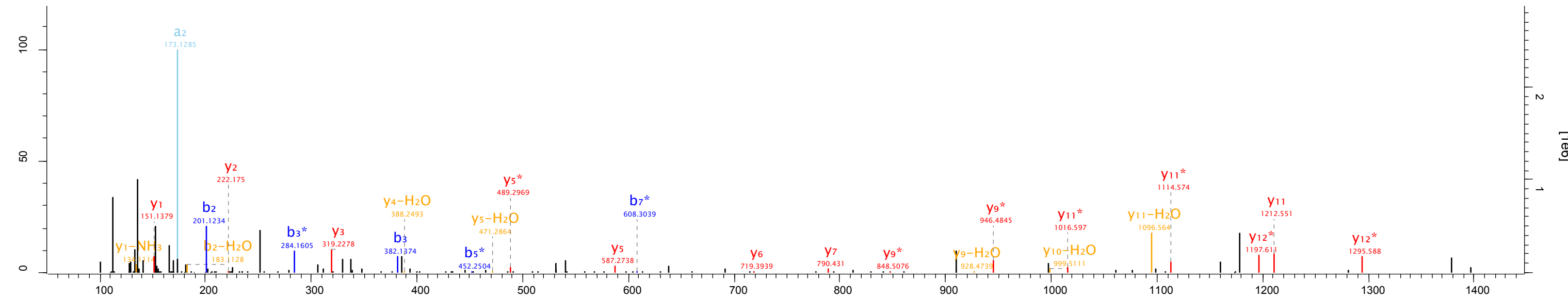
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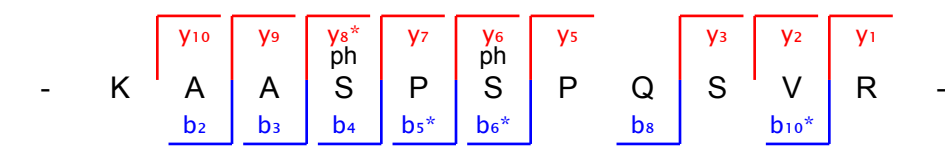
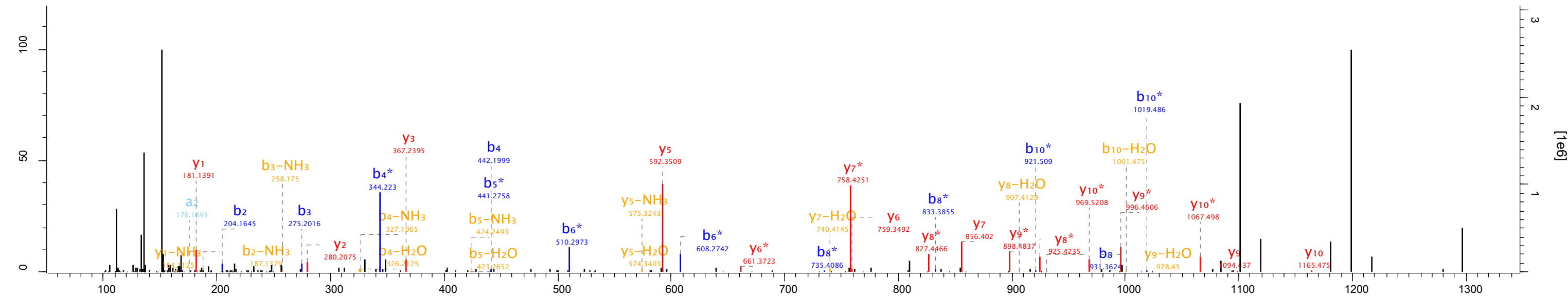
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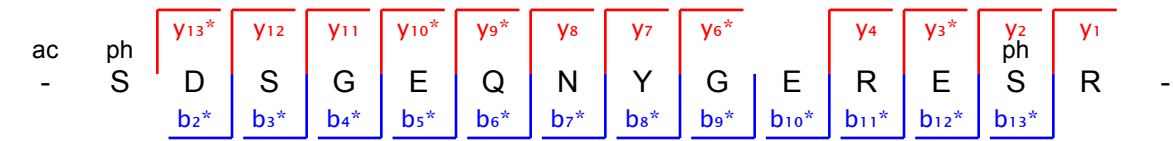
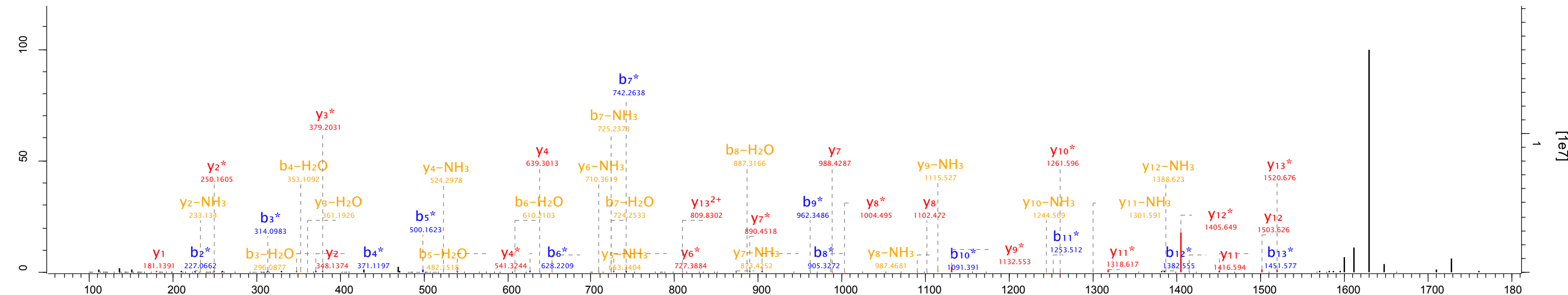
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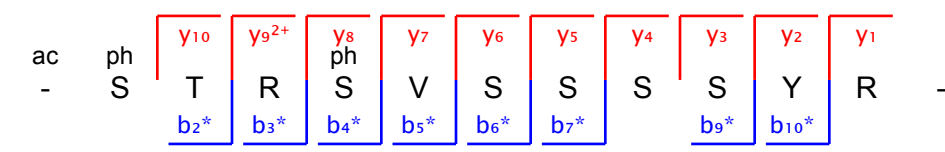
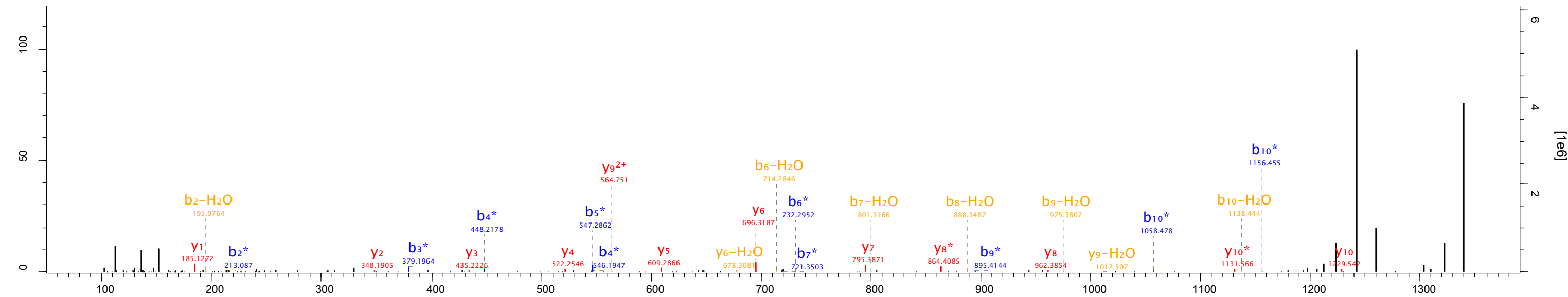
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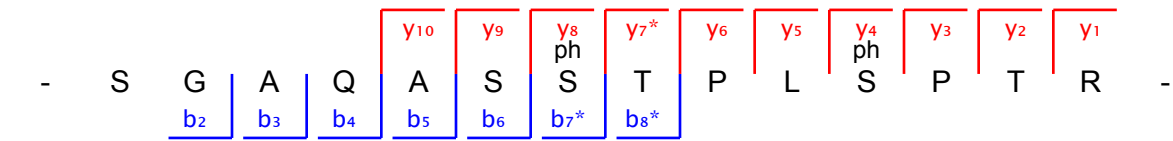
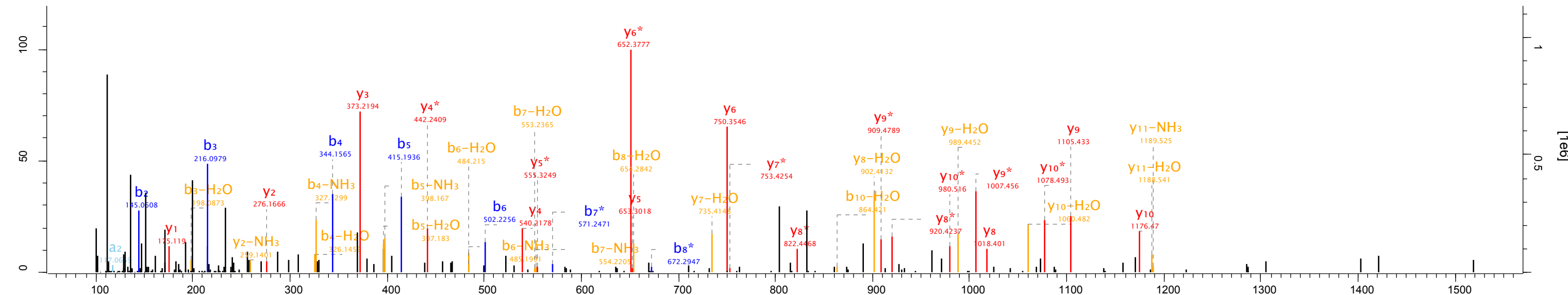
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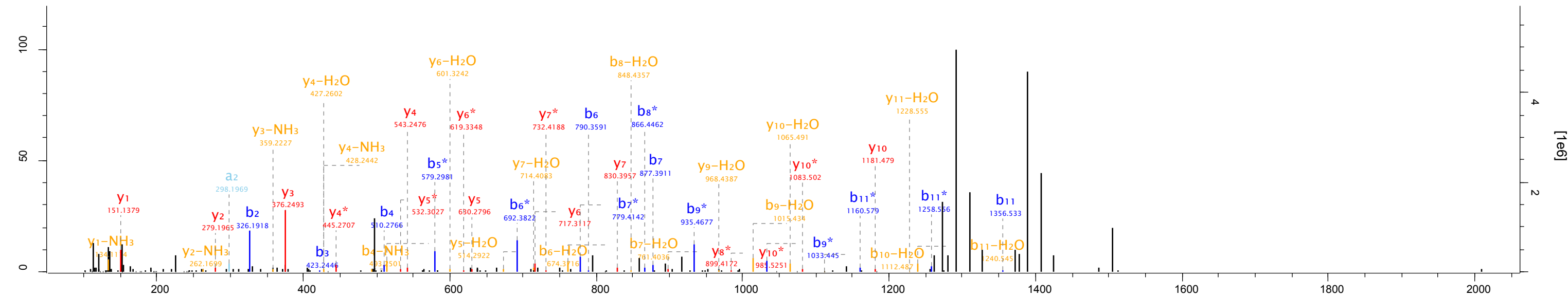
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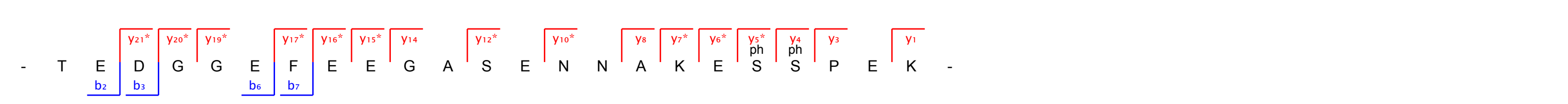
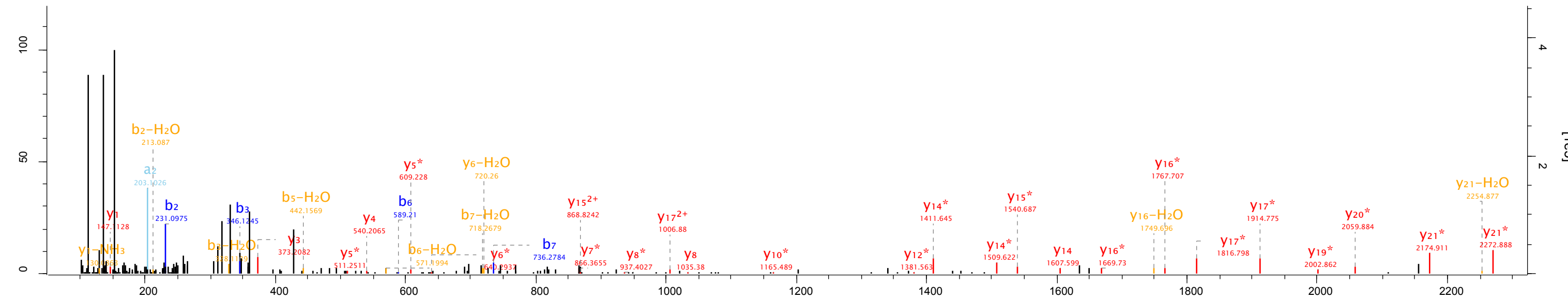
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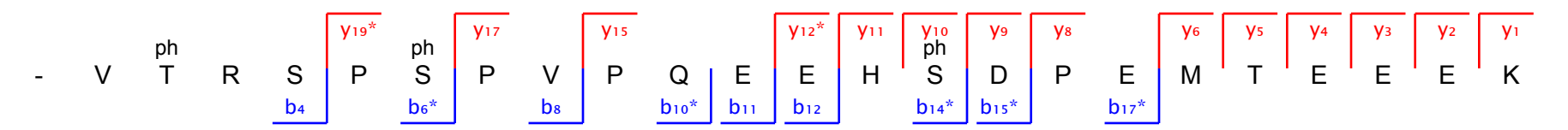
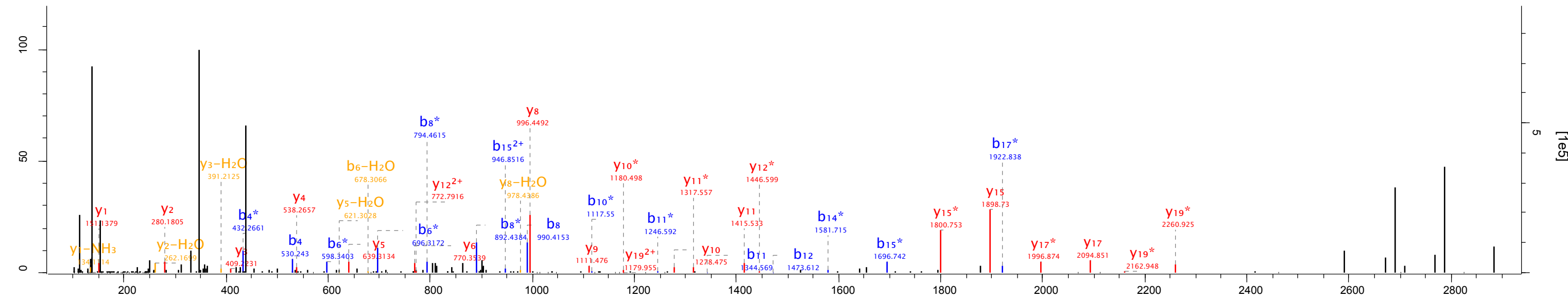
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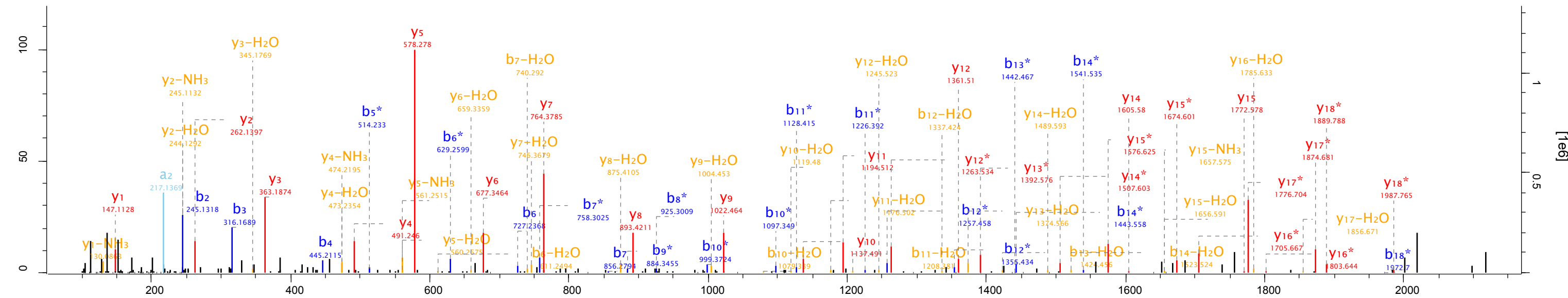
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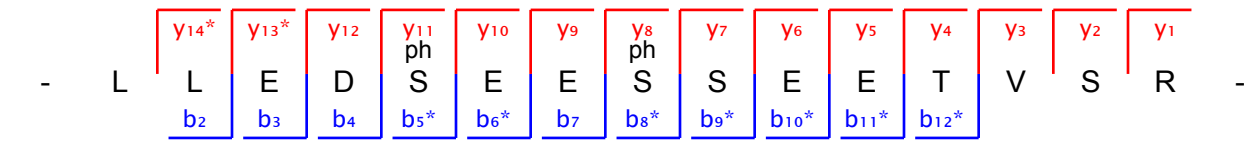
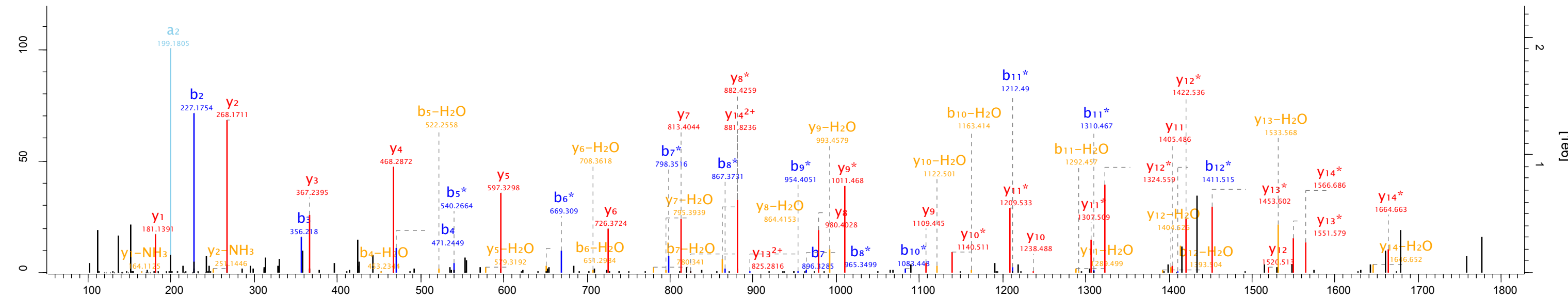
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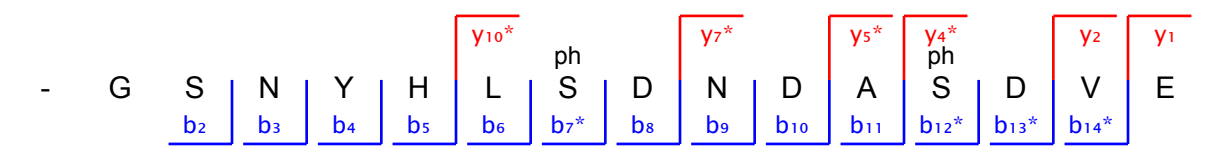
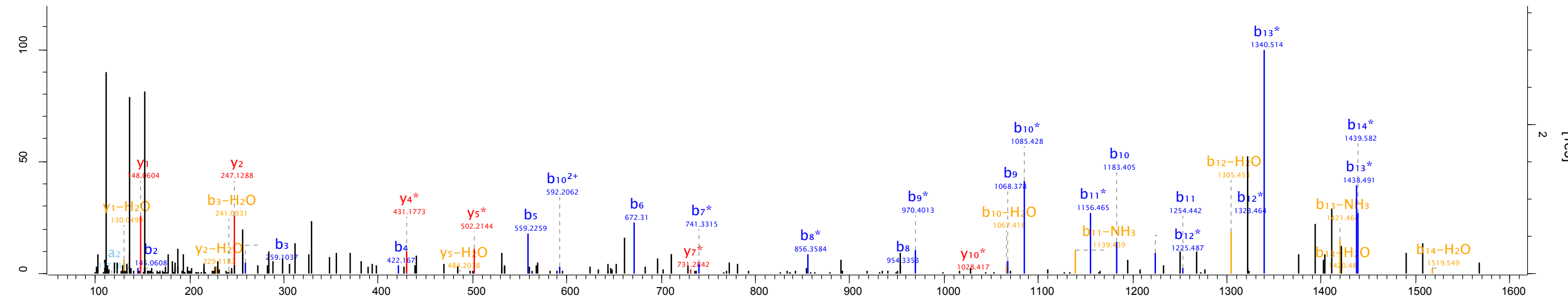
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y18*
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y16*
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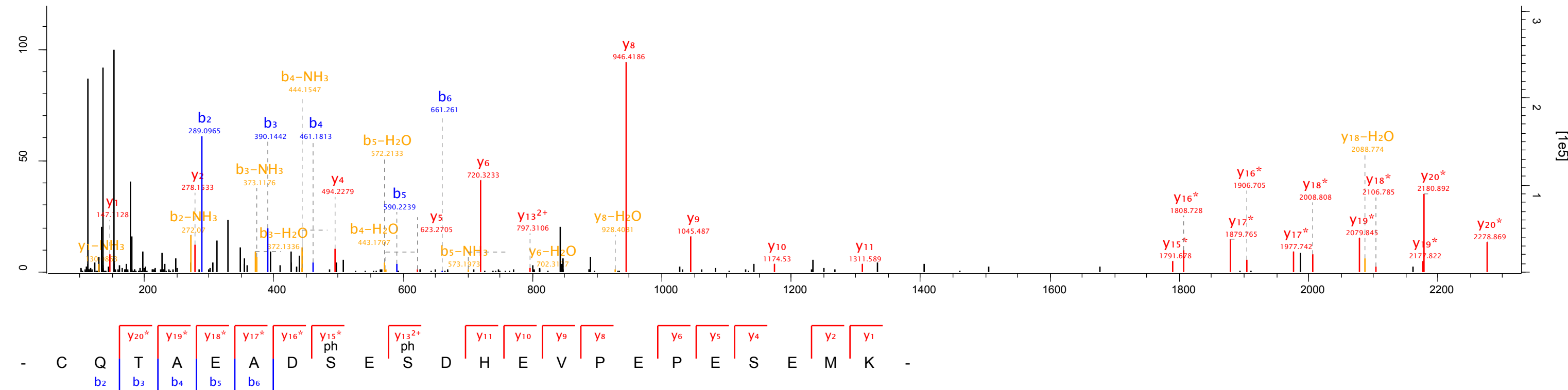
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b11*
b12*
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b14*
b18*



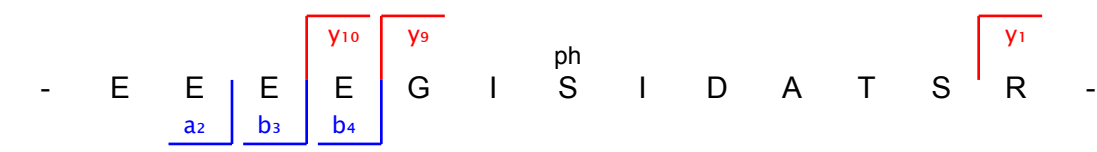
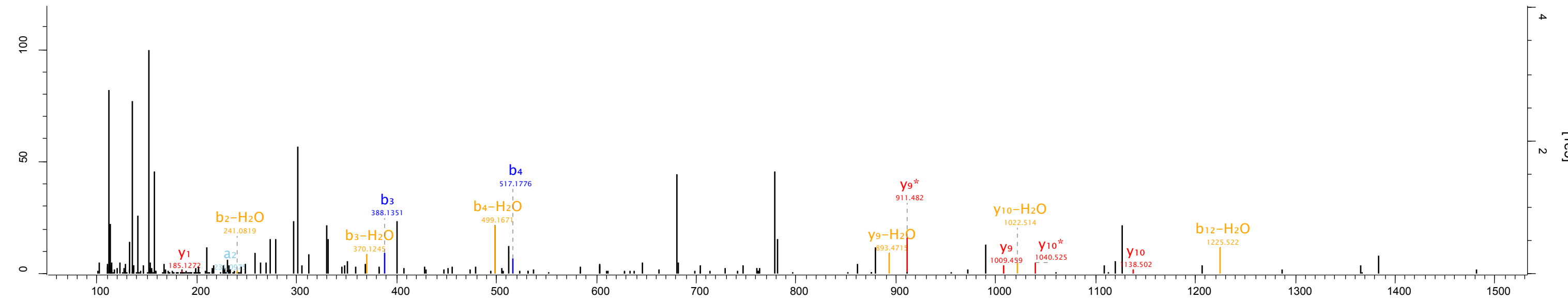
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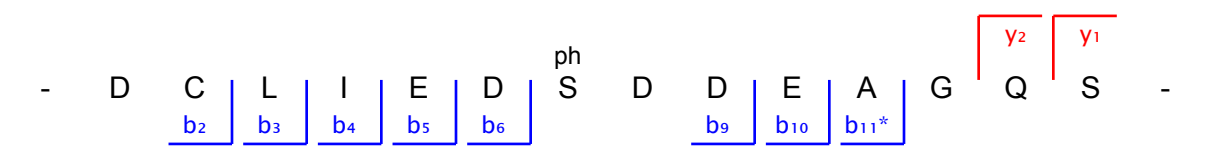
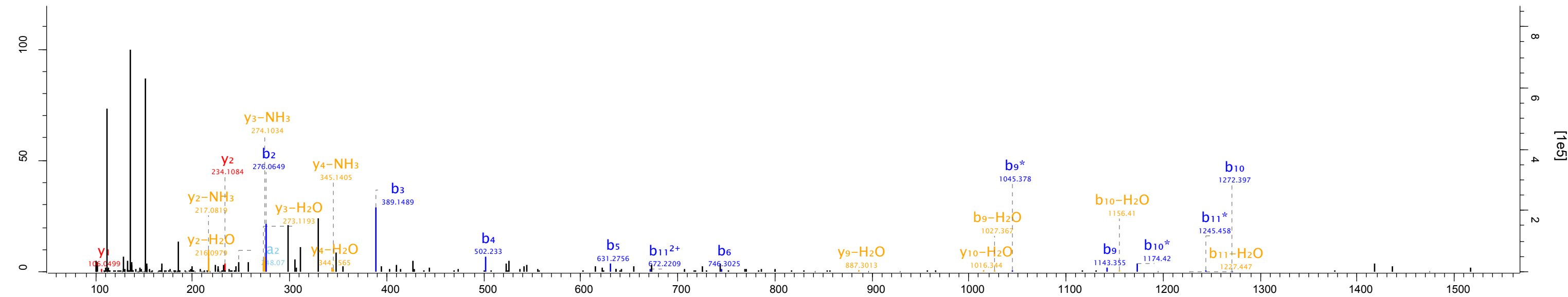
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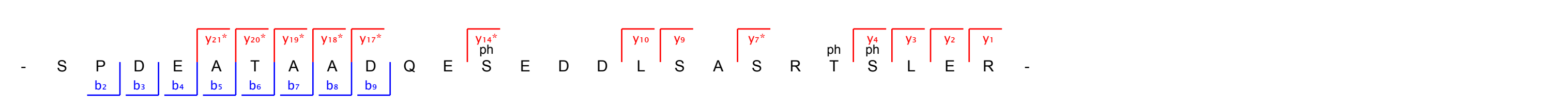
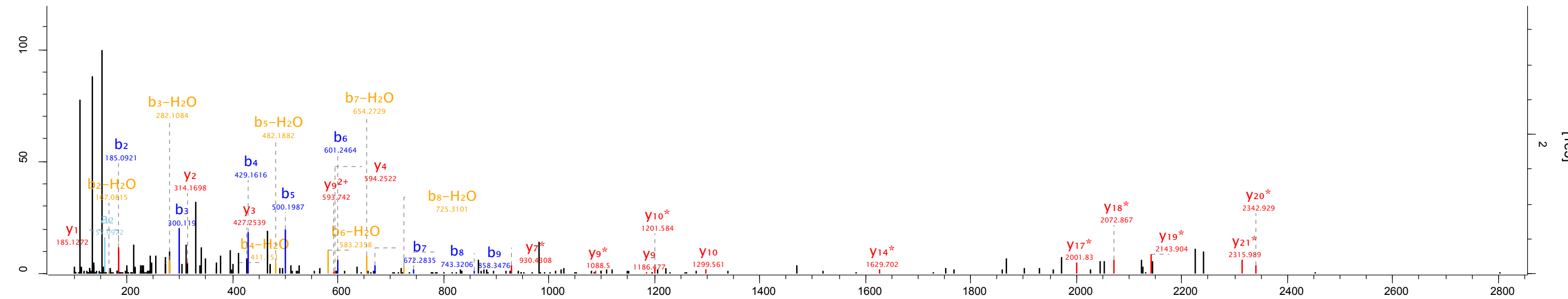
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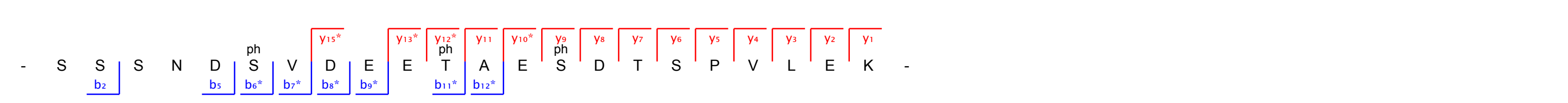
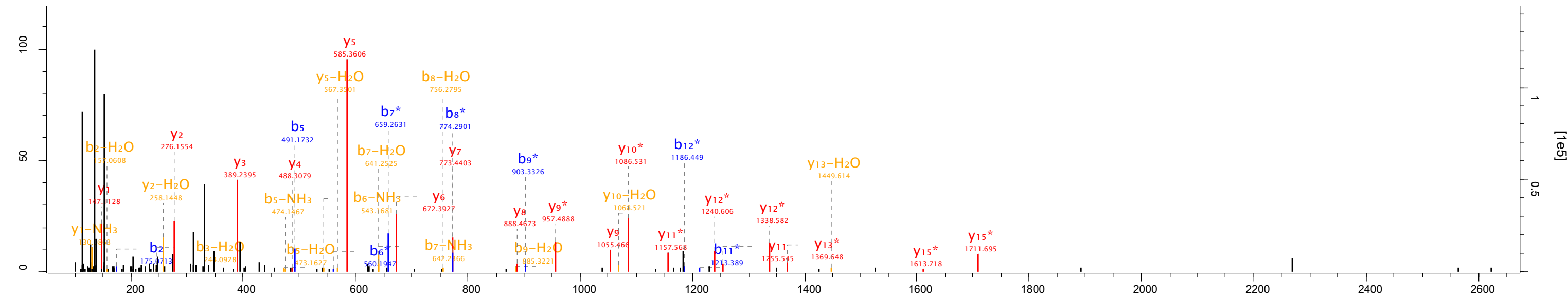
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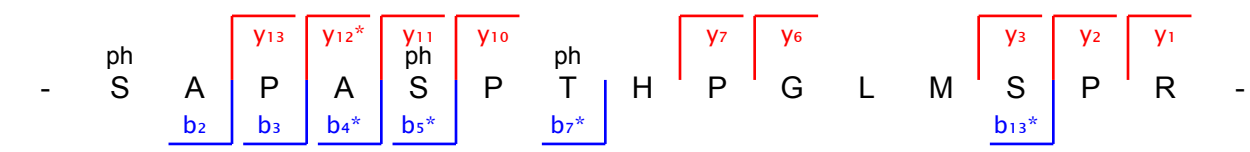
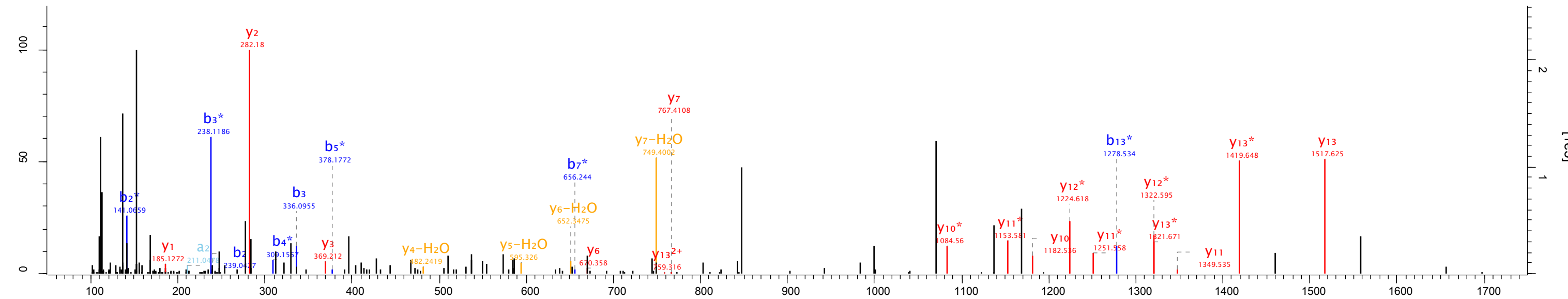
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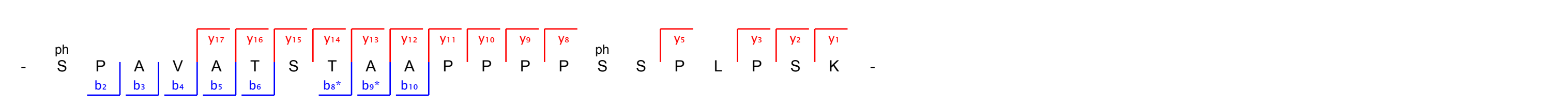
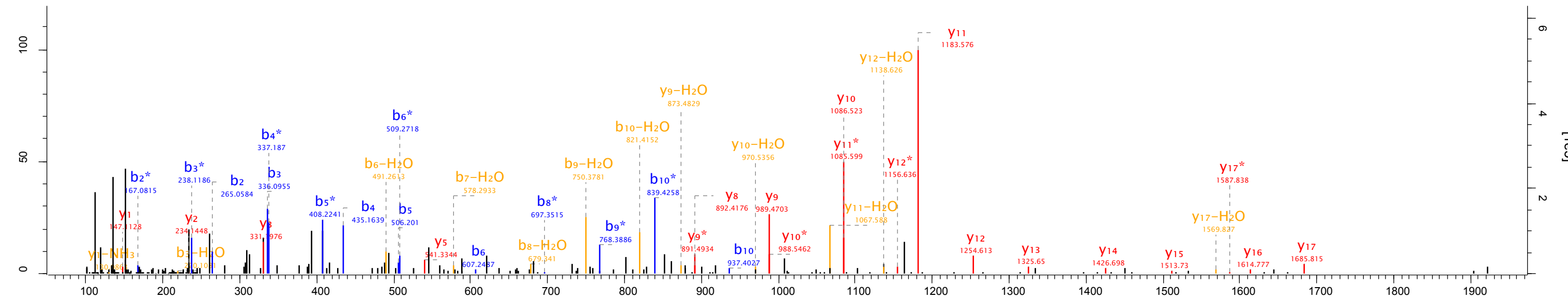
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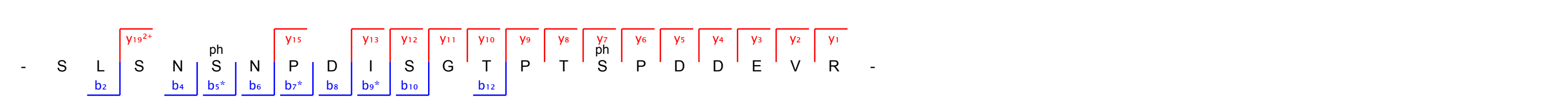
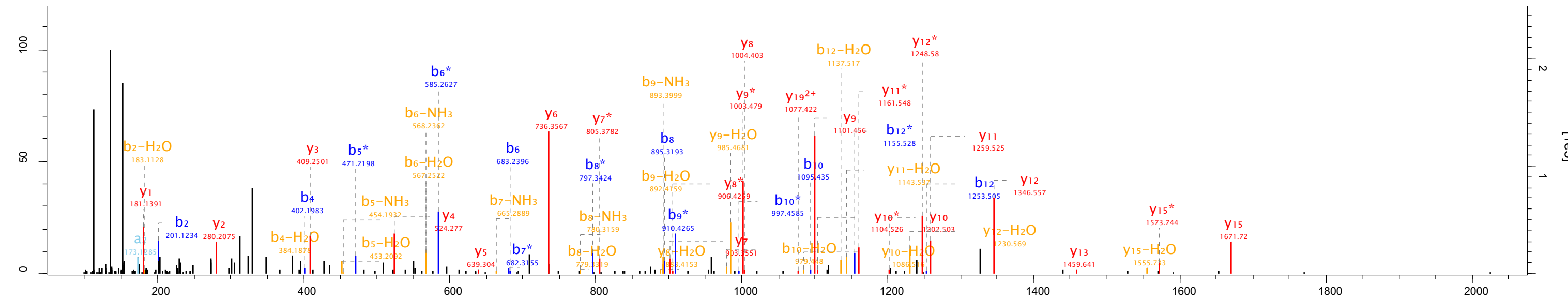
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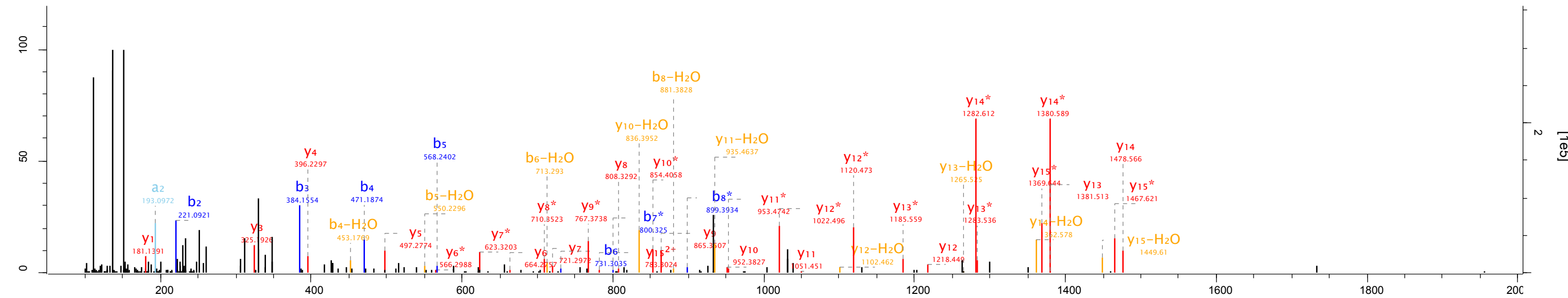
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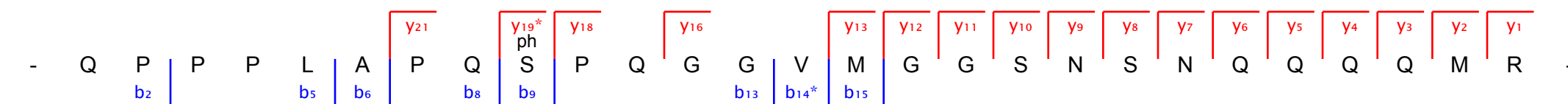
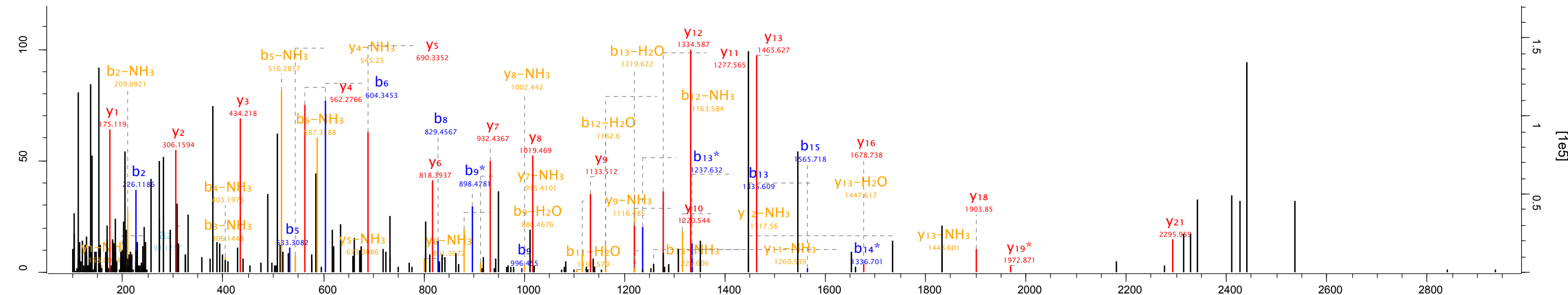


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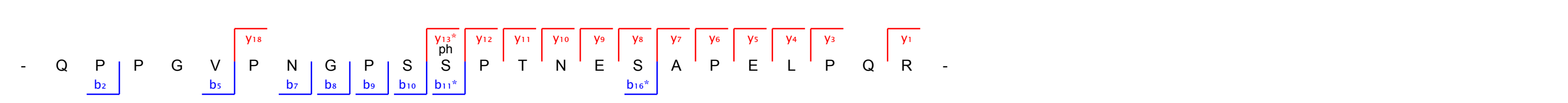
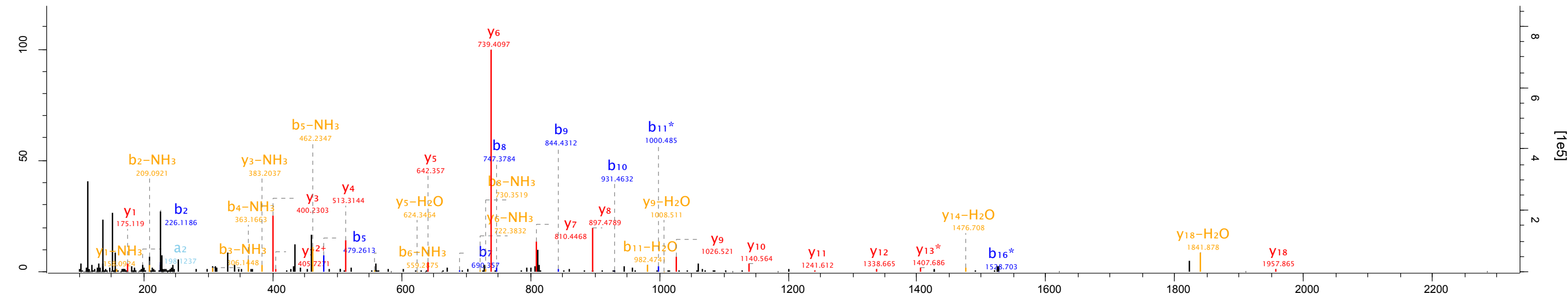


- G Y Y S P Y S V S G S G S T A G S R -

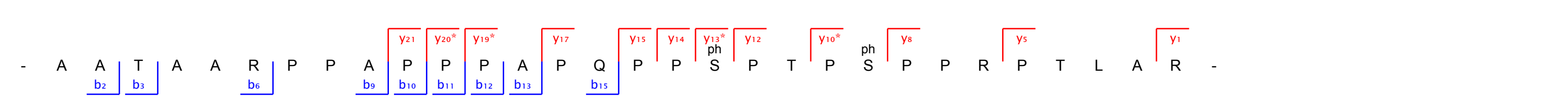
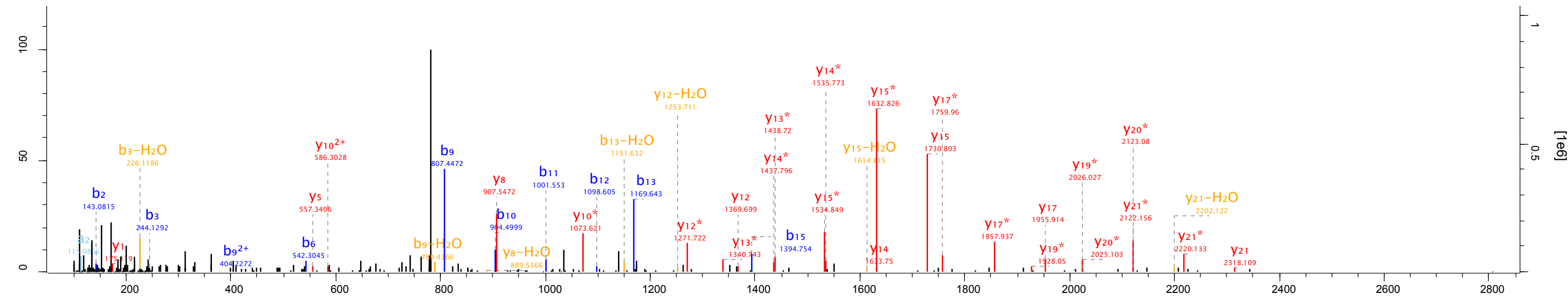
Fragmentation scheme showing amino acid sequence: G Y Y S P Y S V S G S G S T A G S R. Fragmentation sites are indicated by brackets below the sequence, with labels b1-b8 (blue) and y1-y15* (red) corresponding to the peaks in the mass spectrum above.



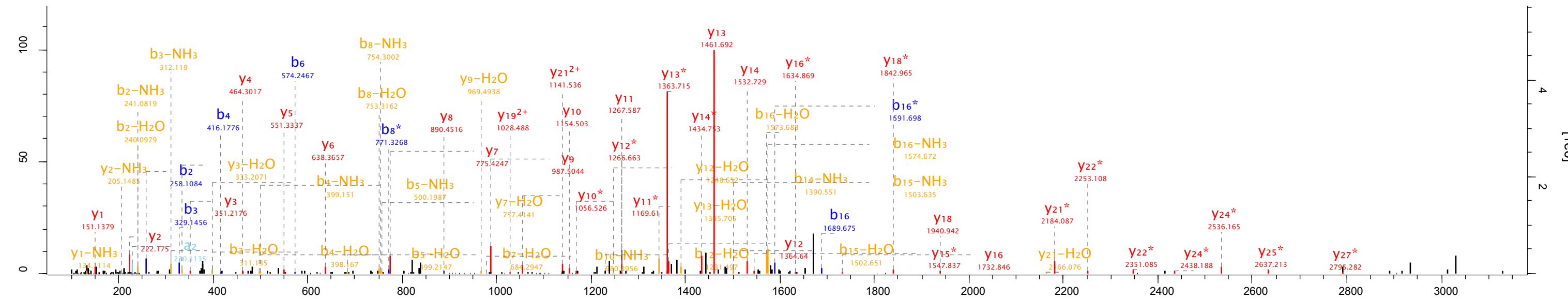
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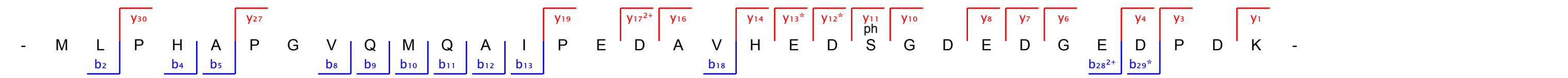
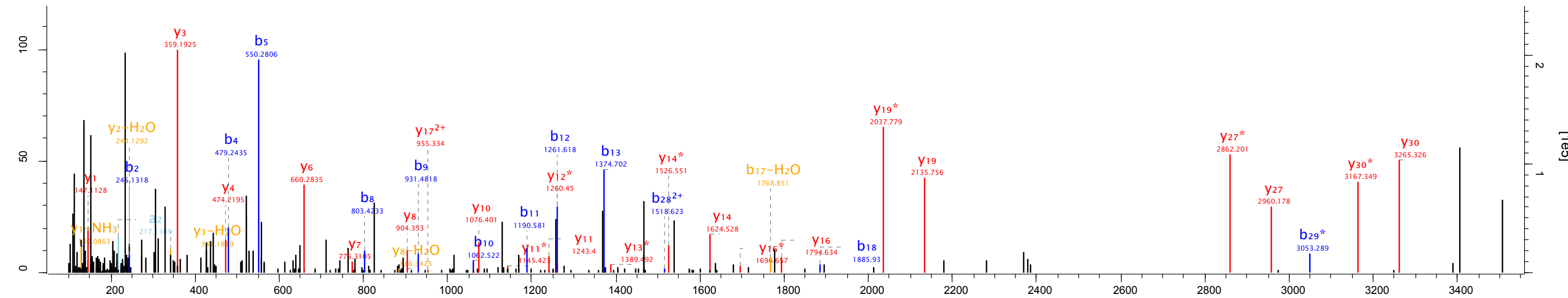


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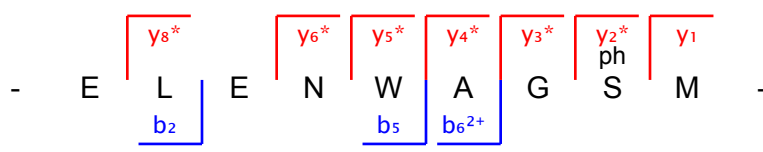
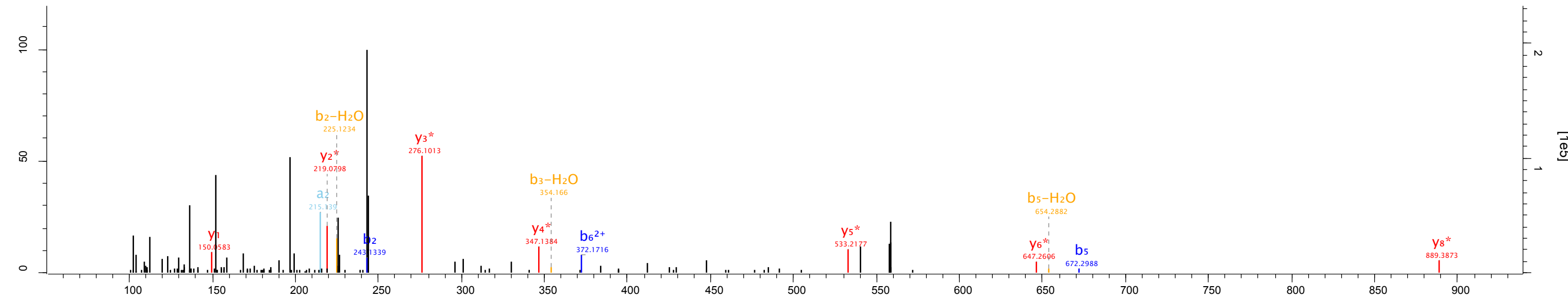
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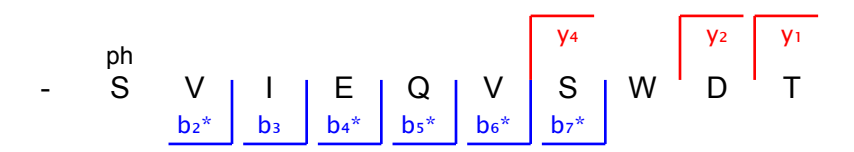
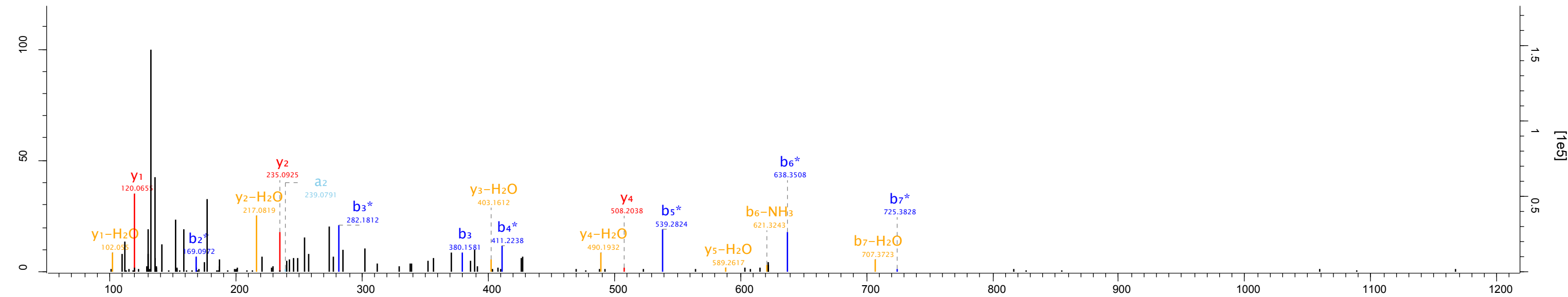
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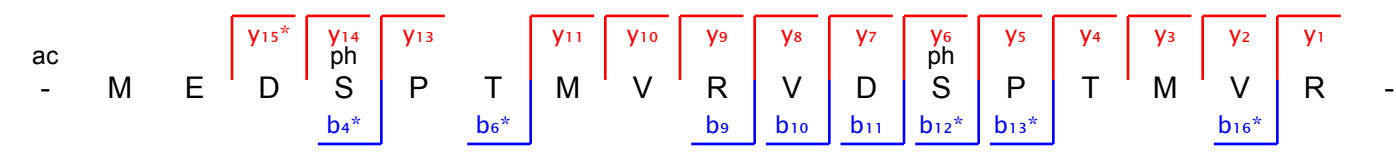
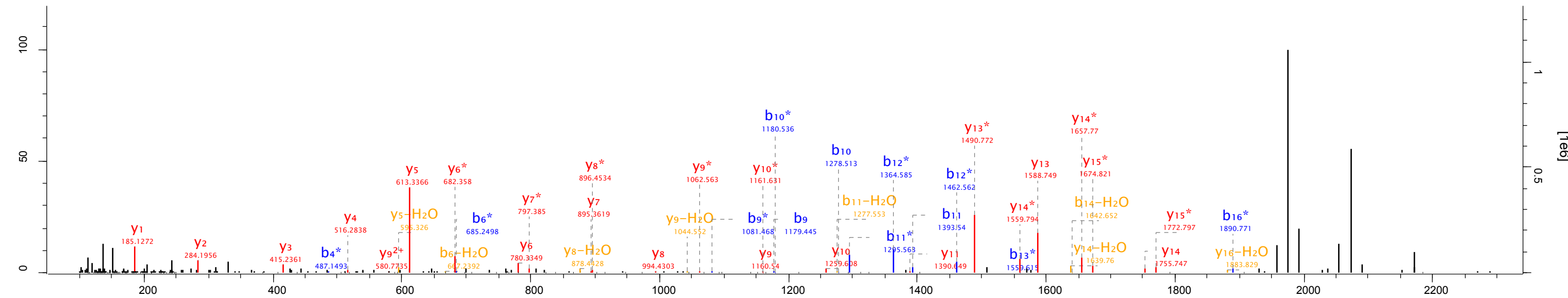
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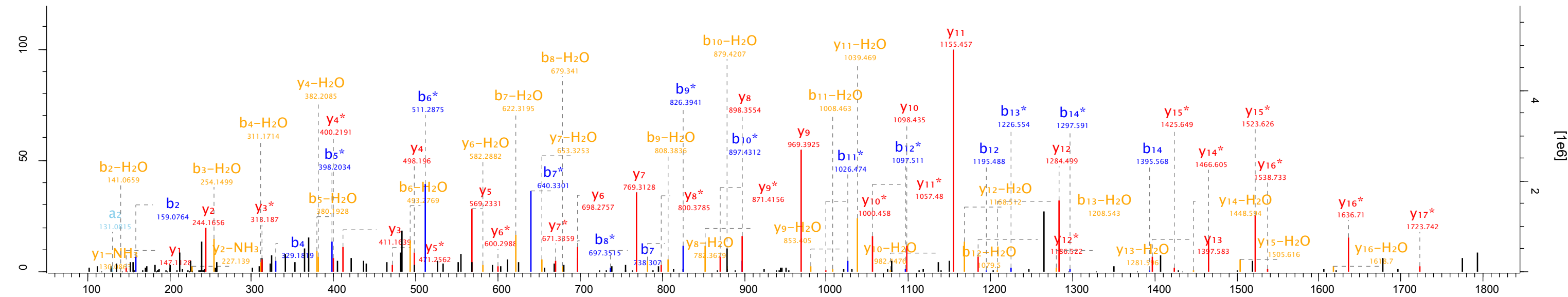
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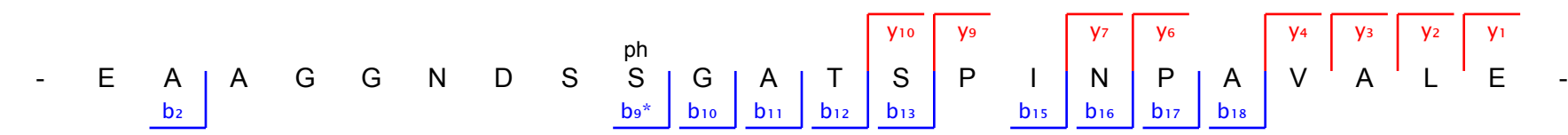
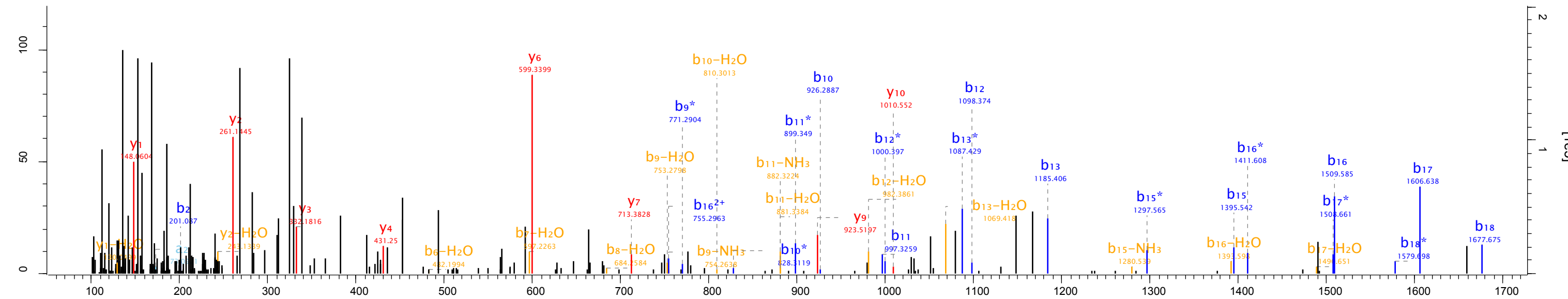
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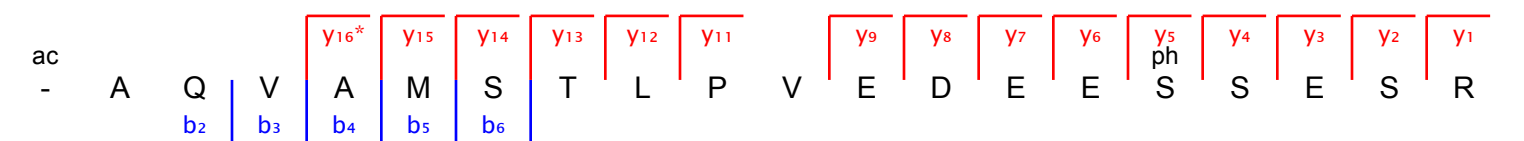
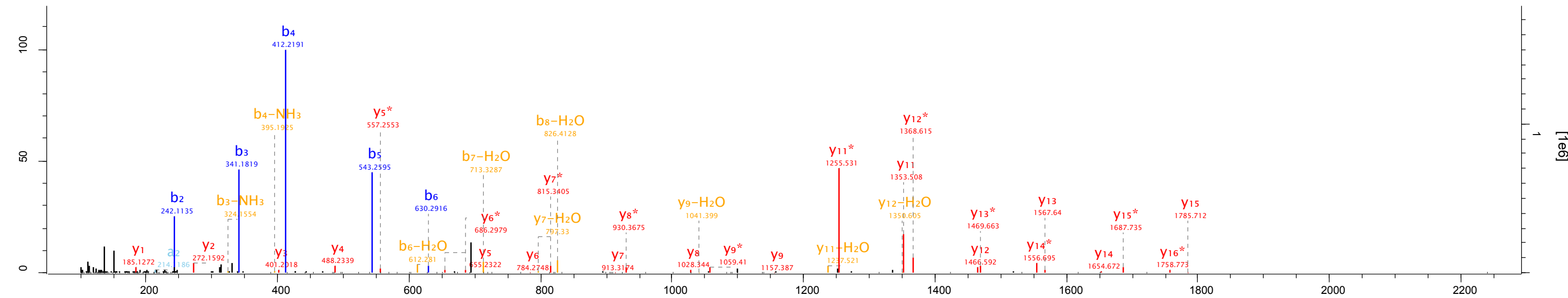
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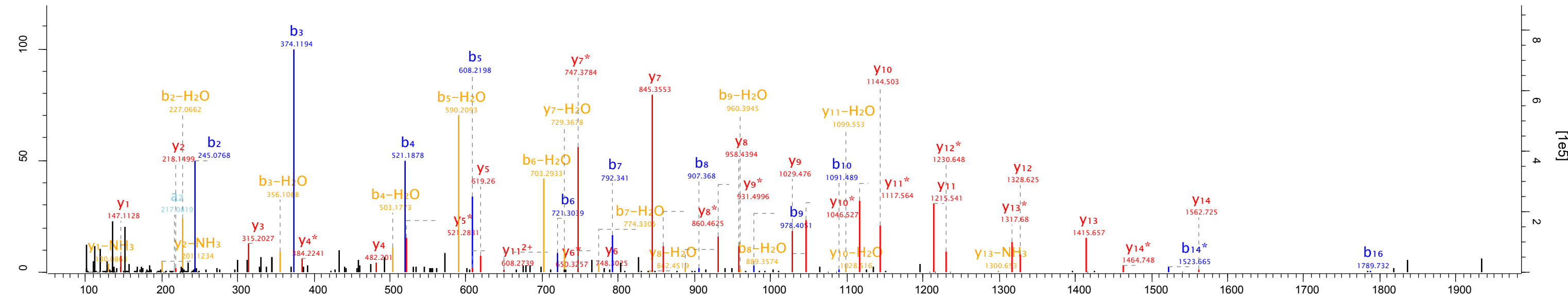


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ac

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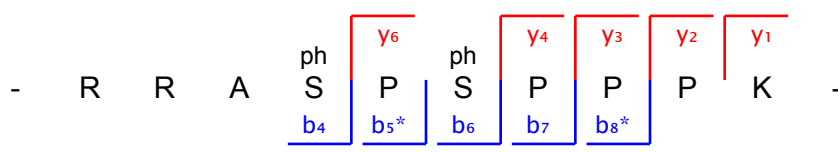
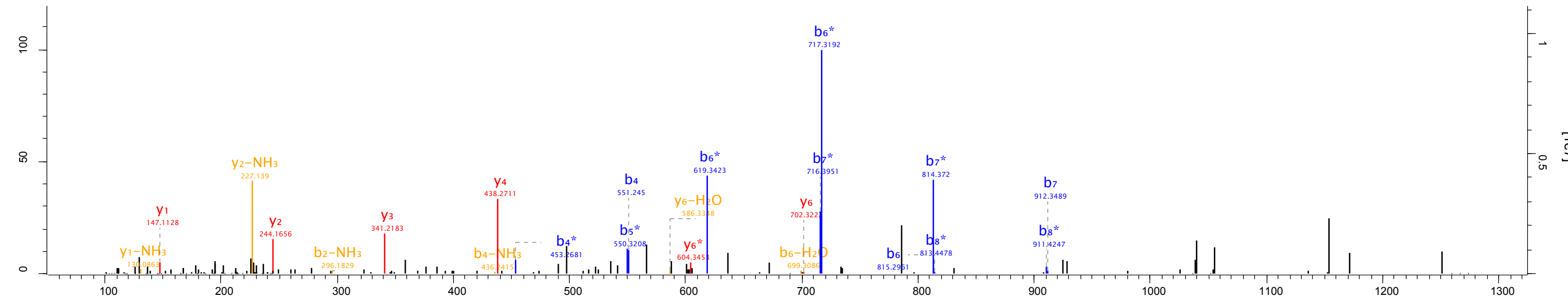
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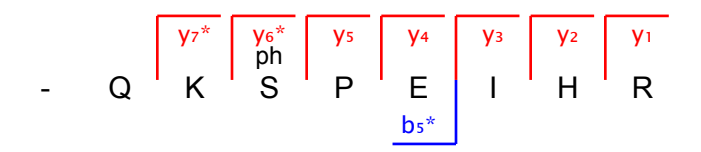
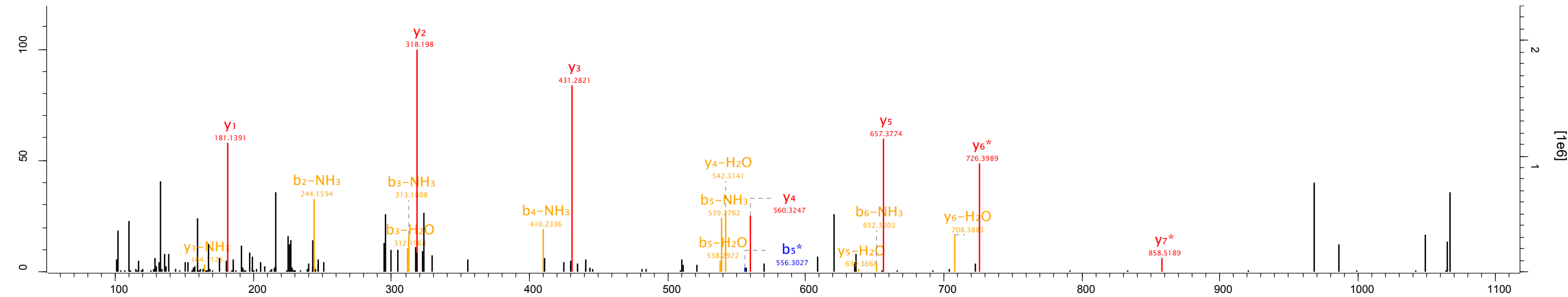
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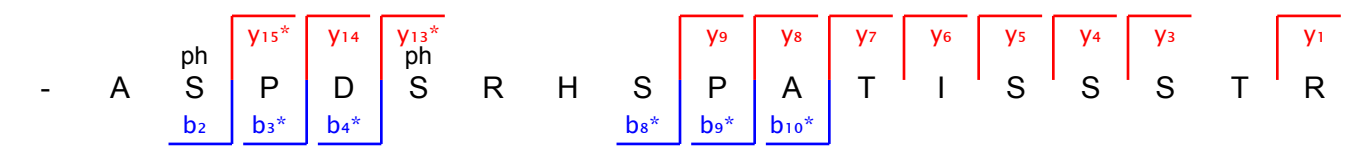
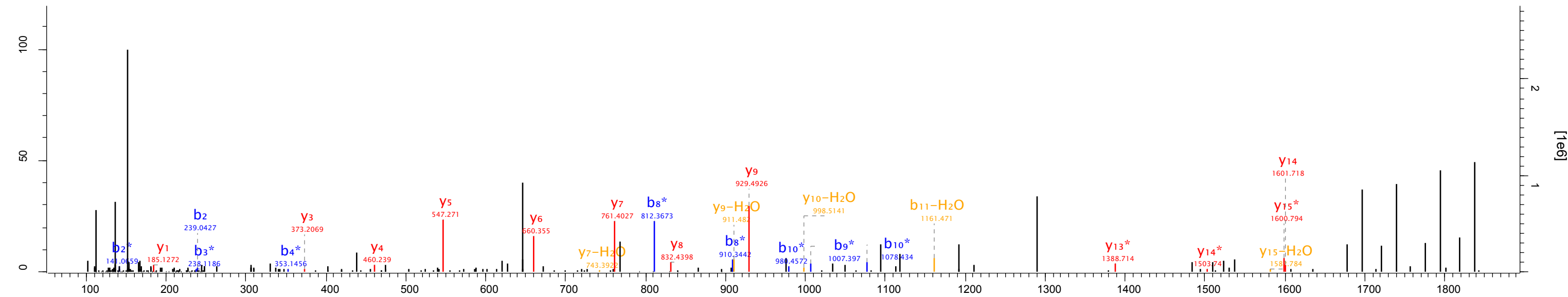
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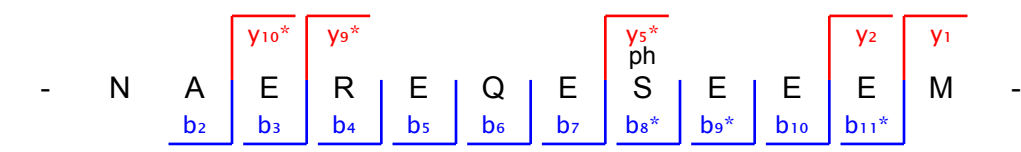
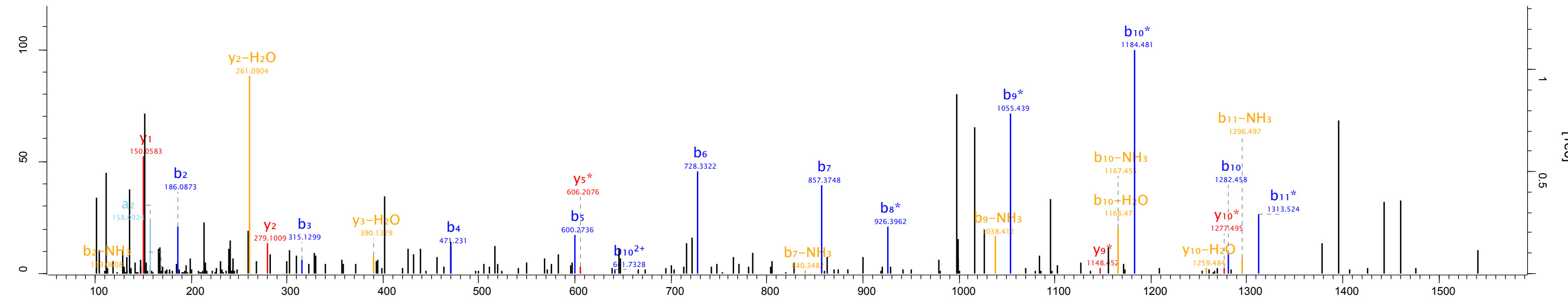
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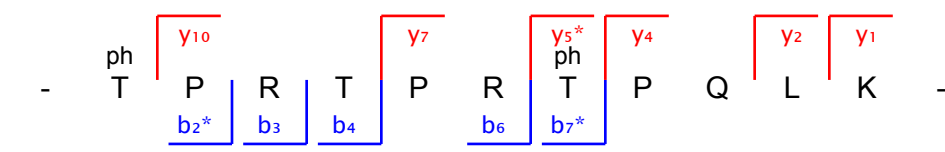
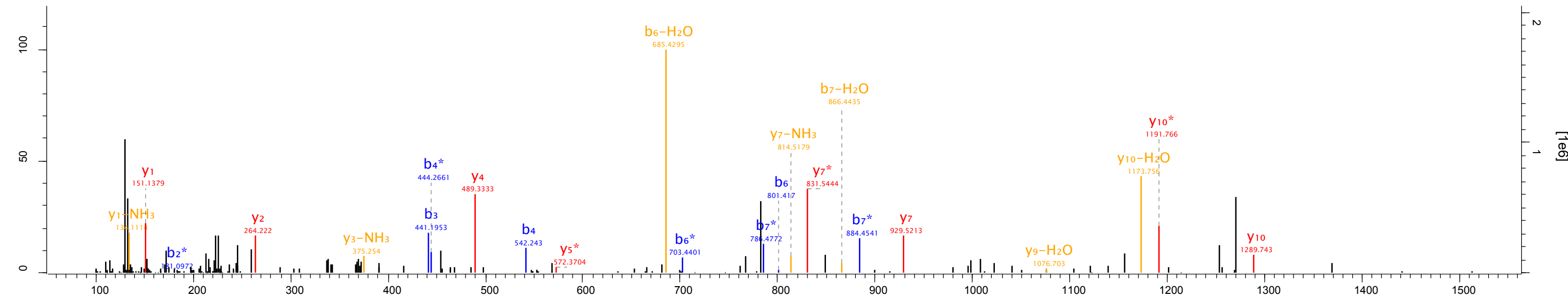
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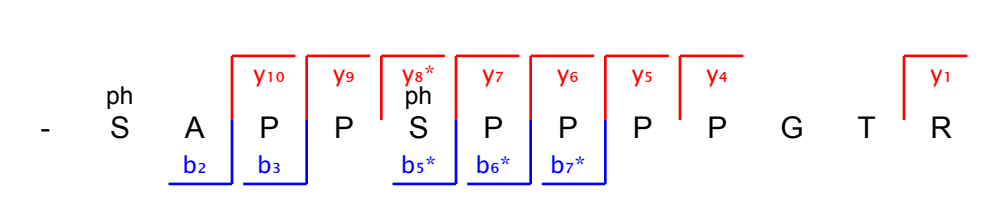
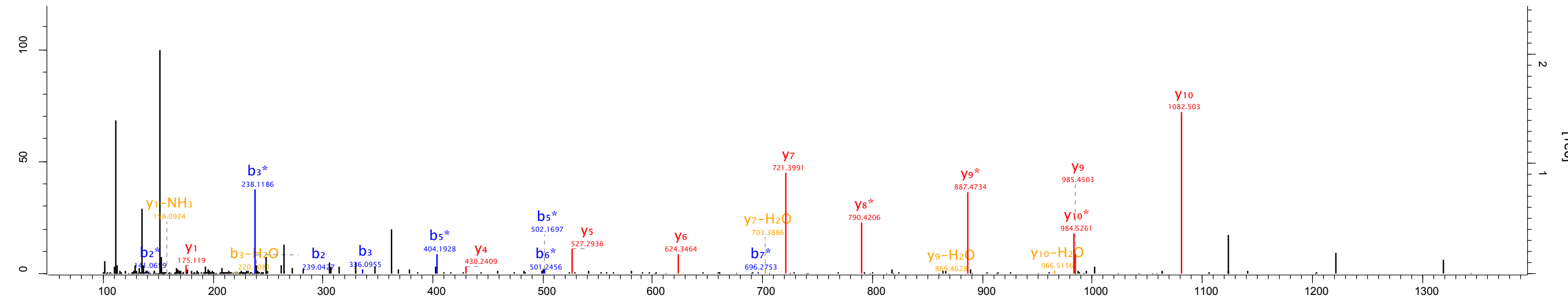
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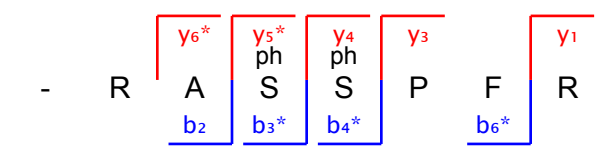
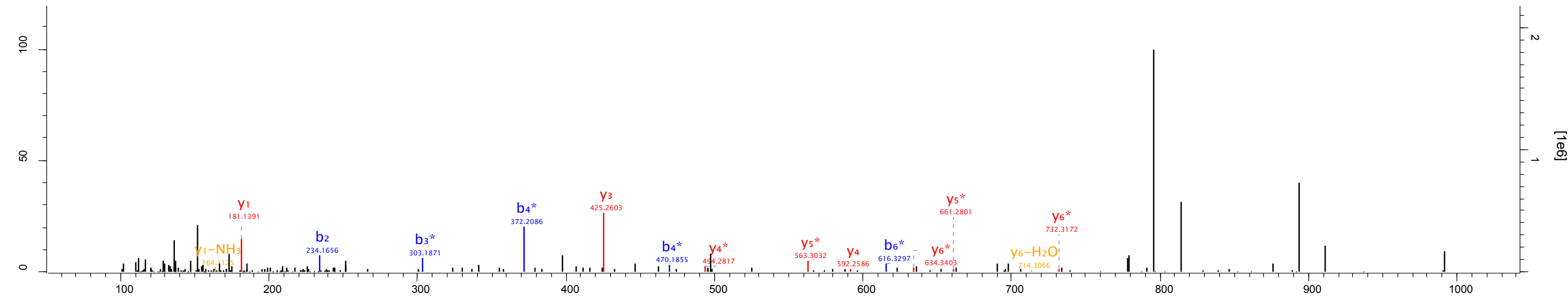
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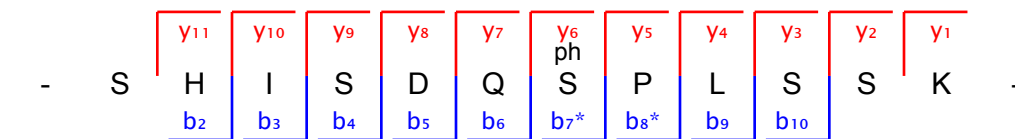
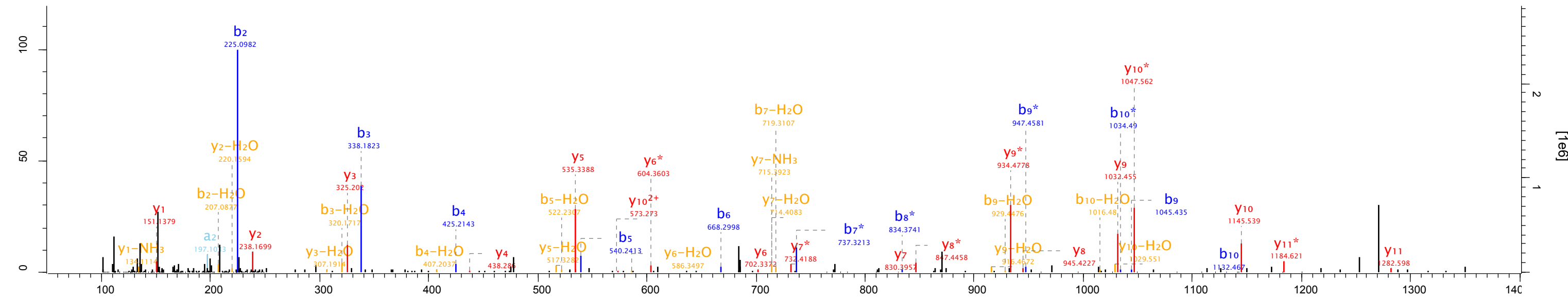


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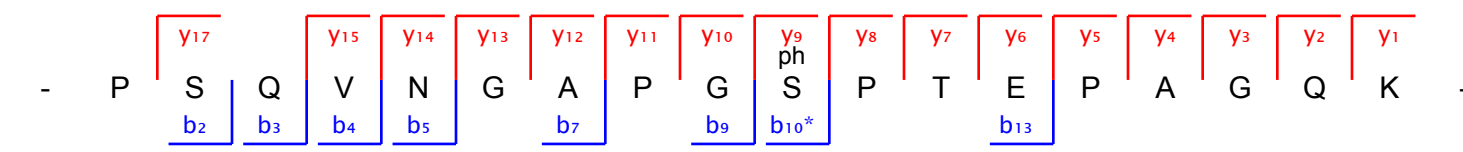
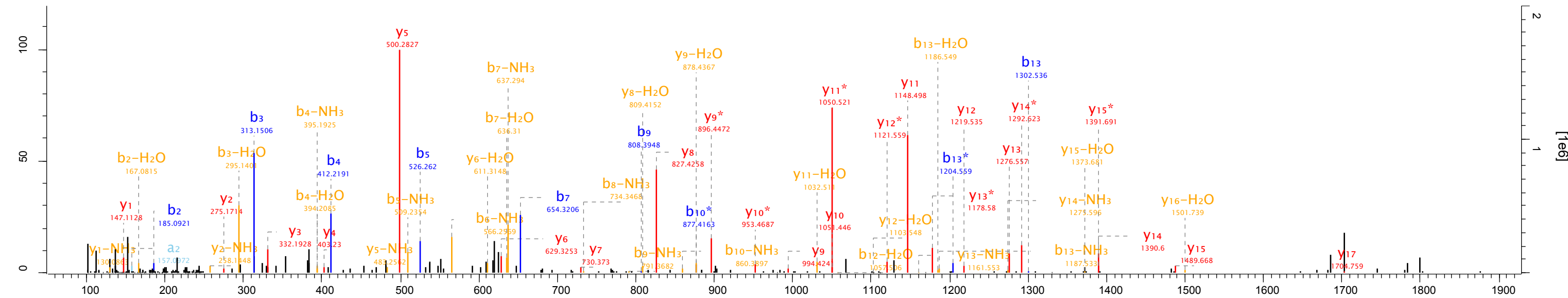


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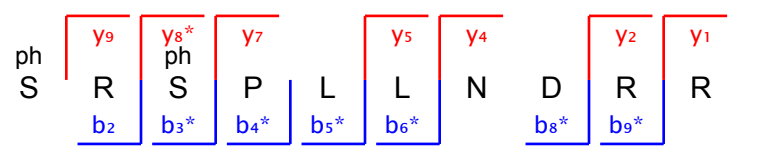
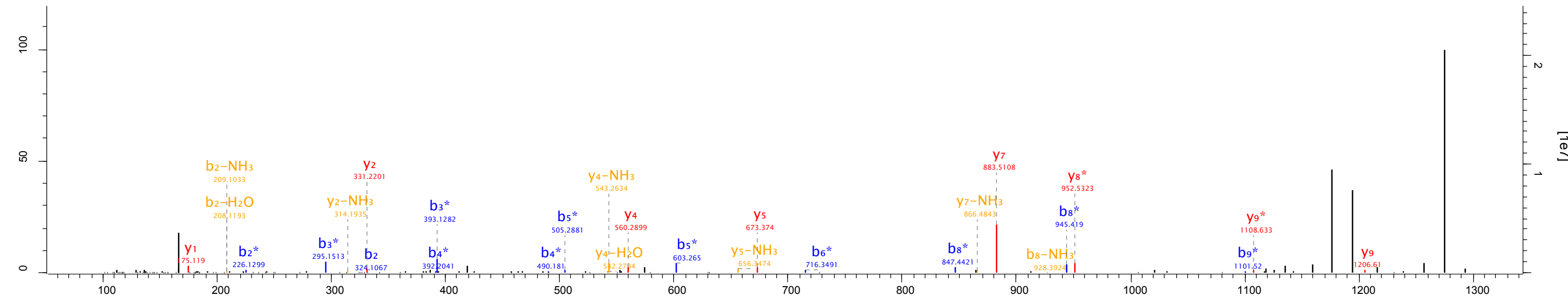




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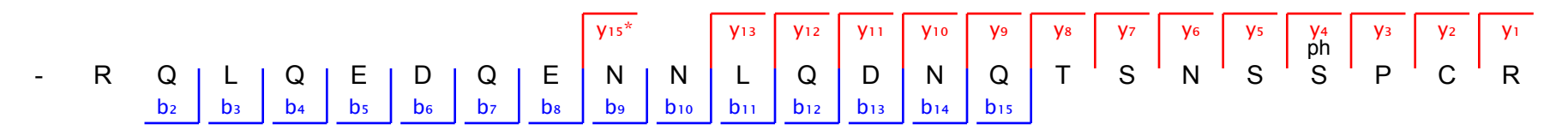
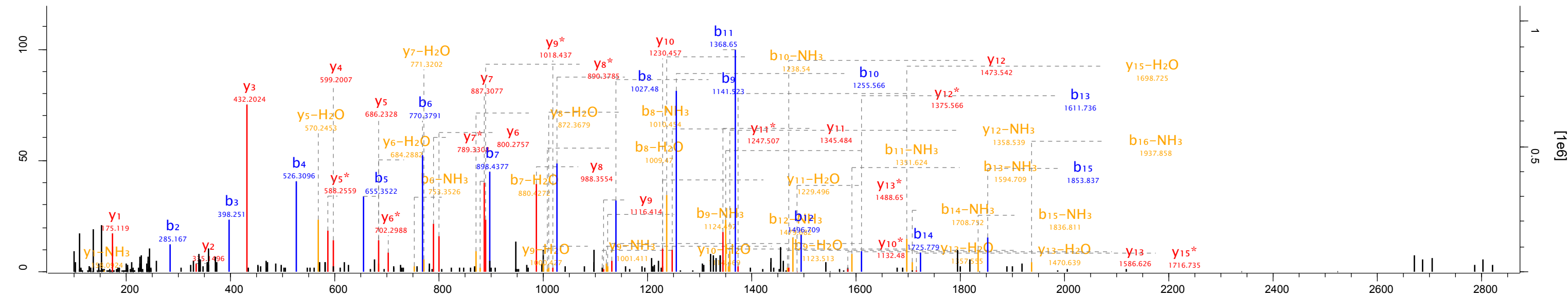


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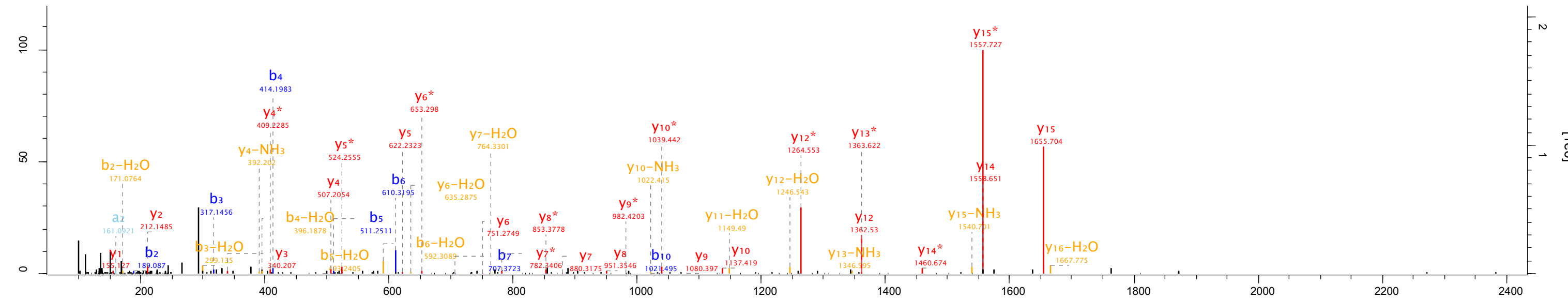


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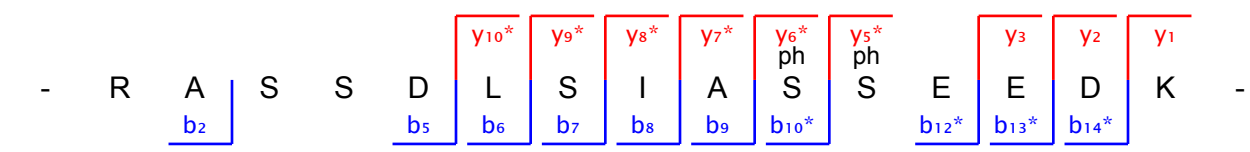
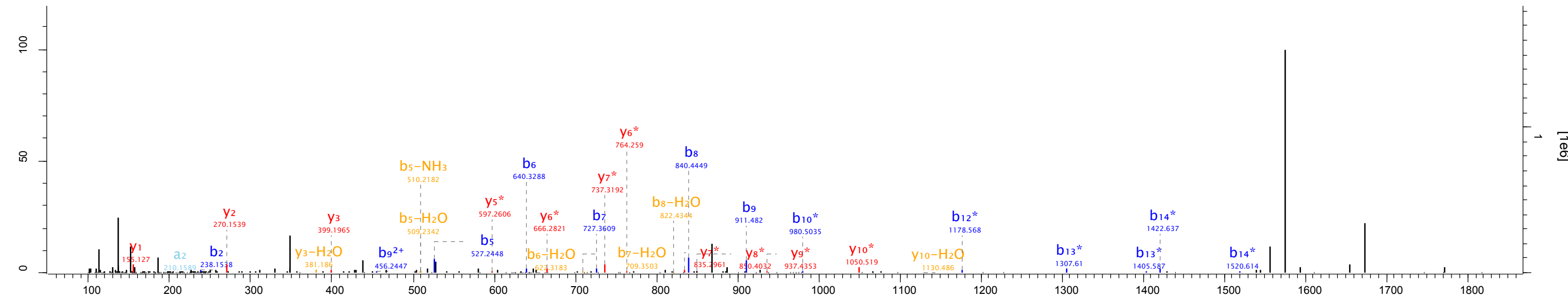
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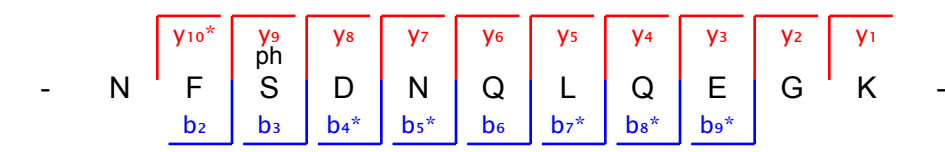
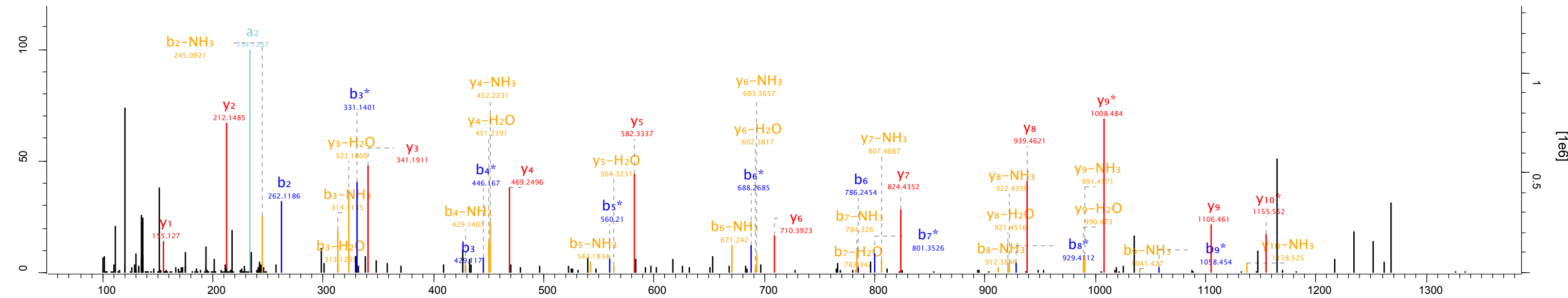
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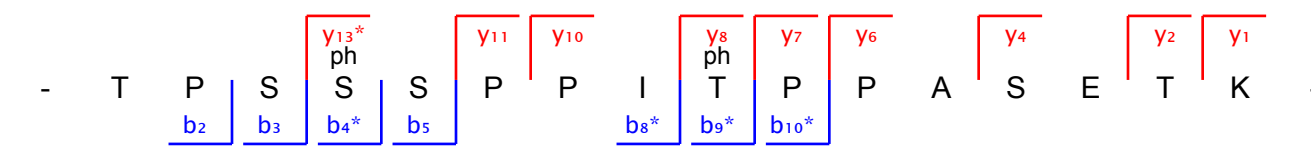
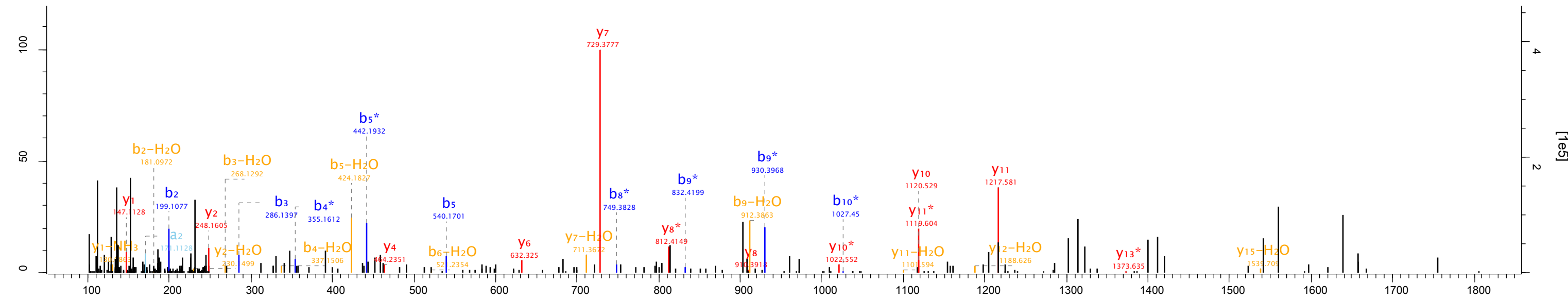
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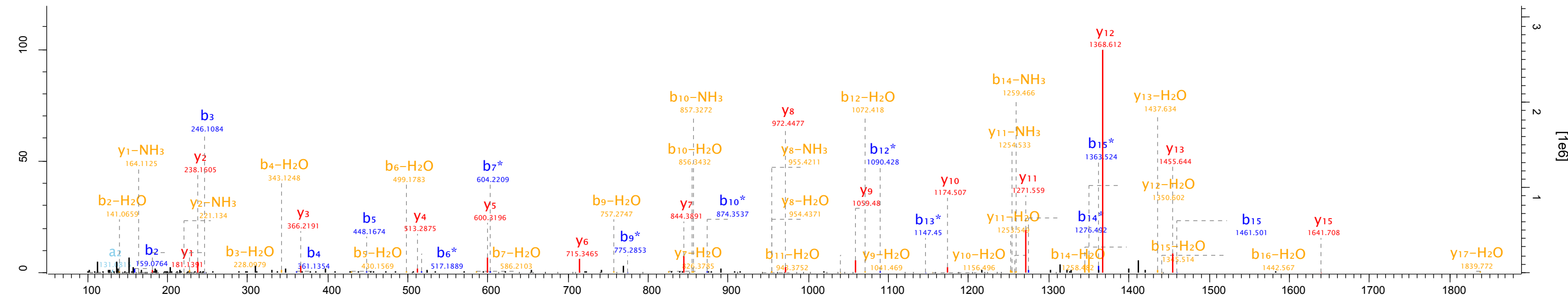
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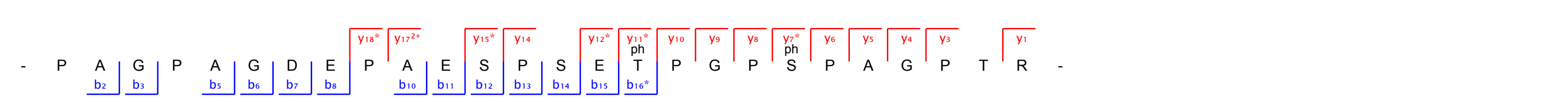
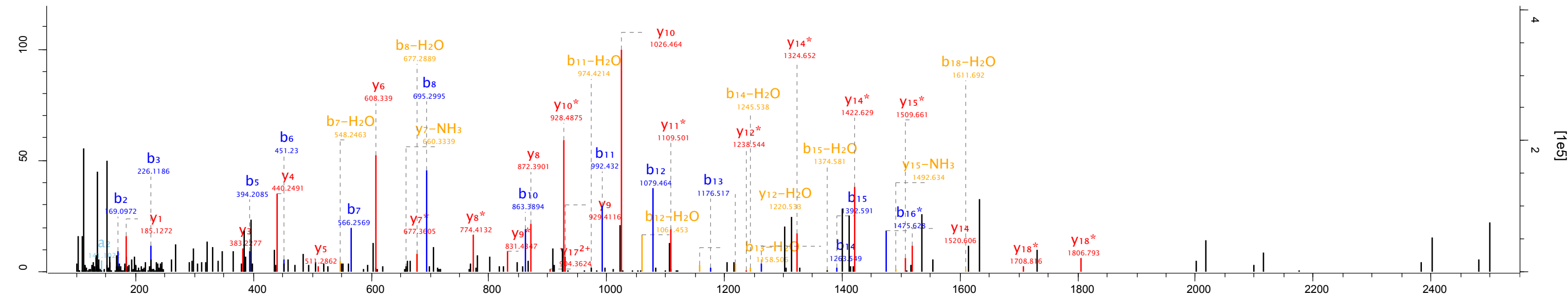
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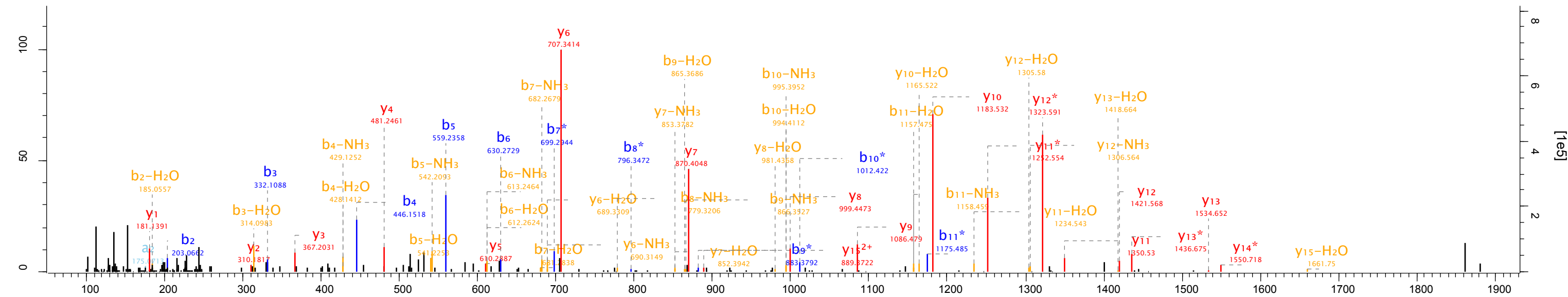
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b₂
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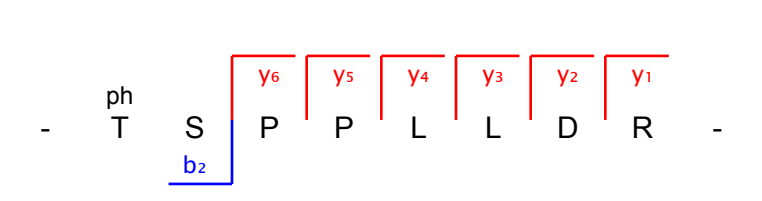
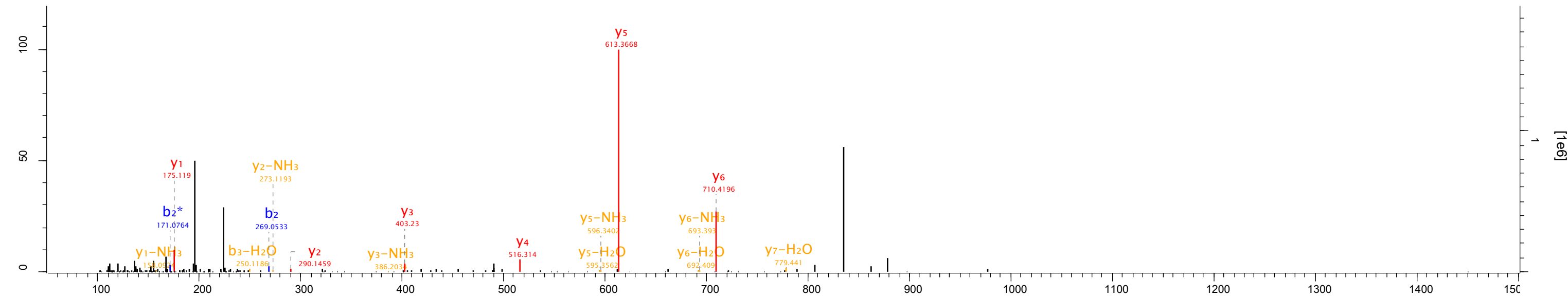
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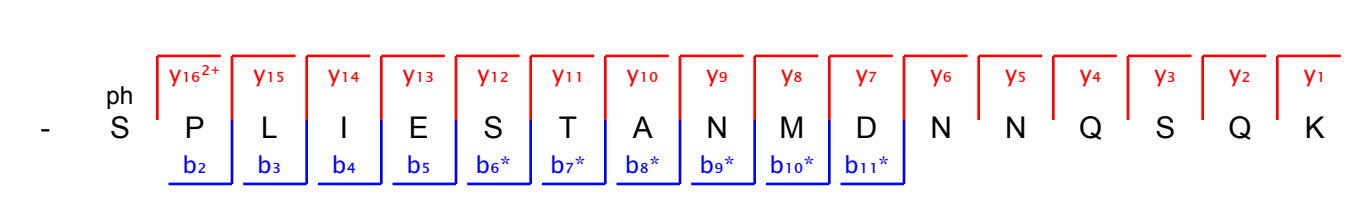
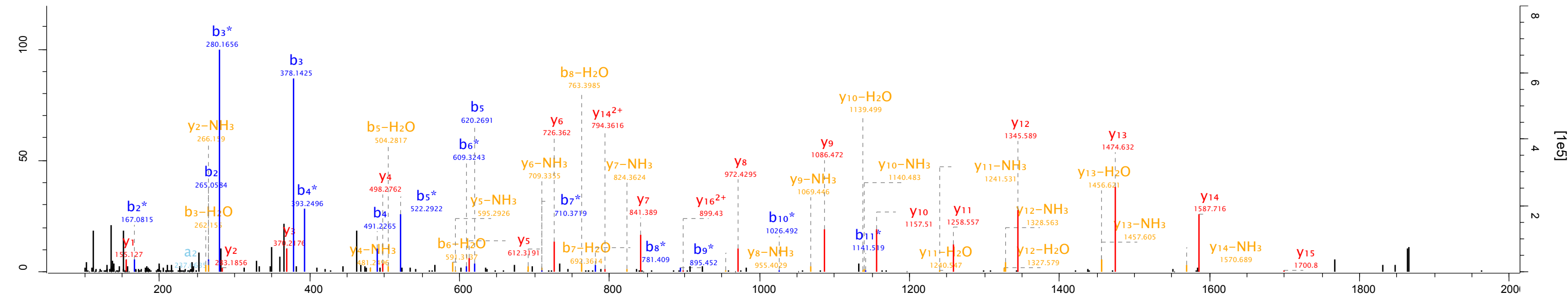
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b₁₀^{*}
b₁₁^{*}
y₁₅²⁺
y₁₄^{*}
y₁₃
y₁₂
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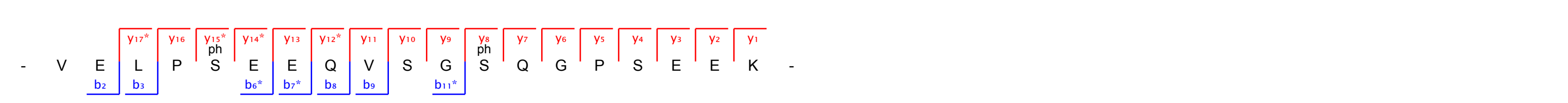
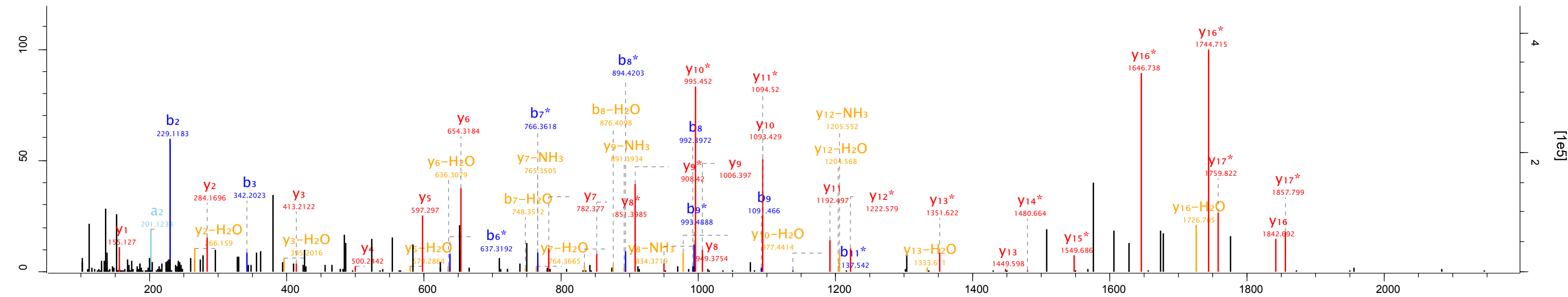
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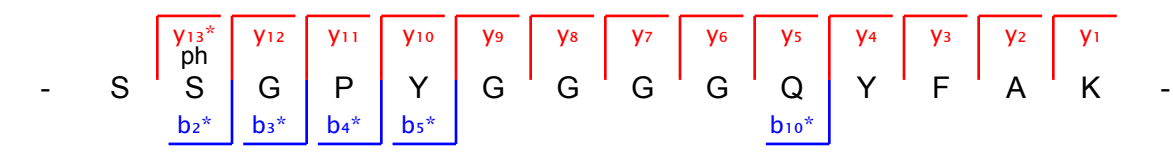
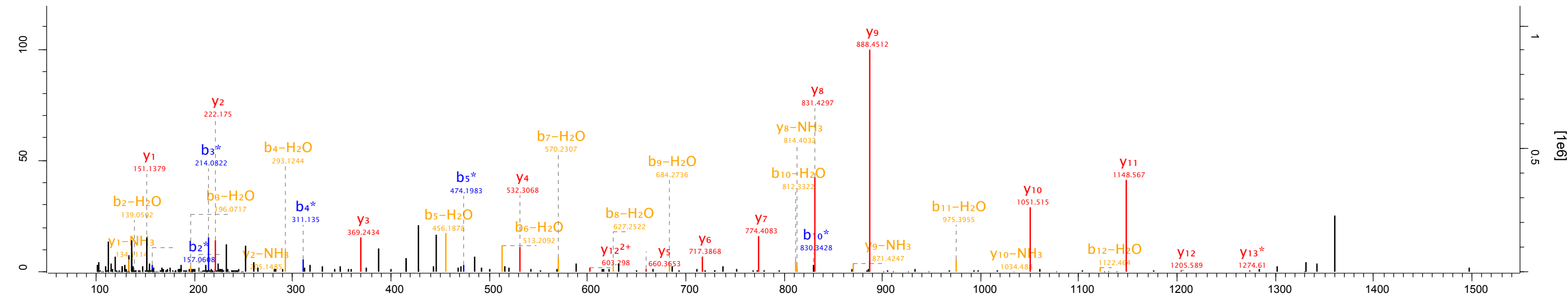
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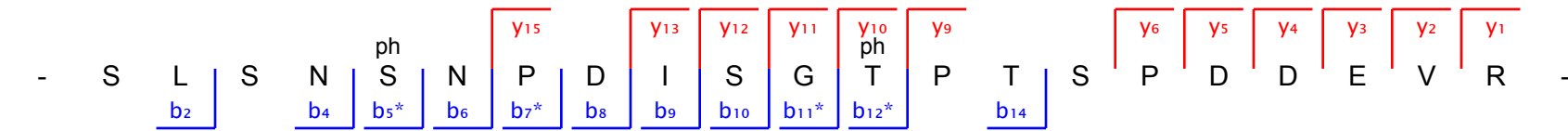
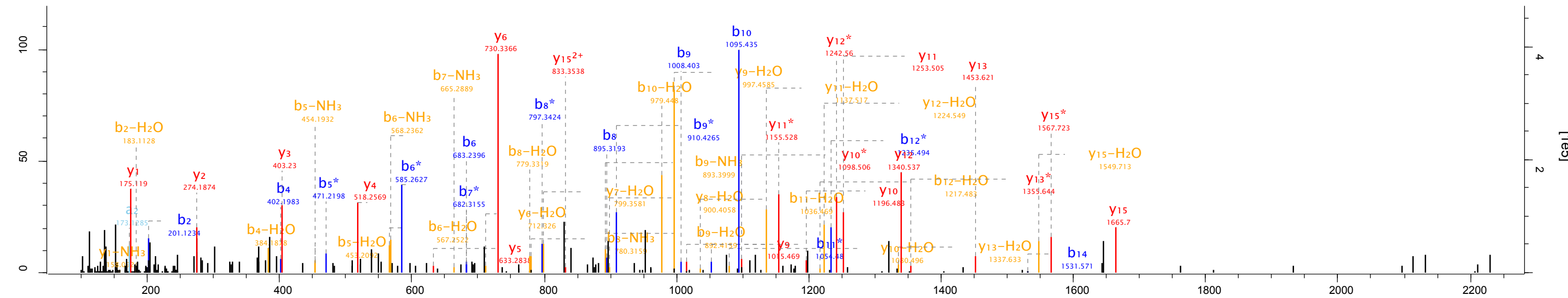


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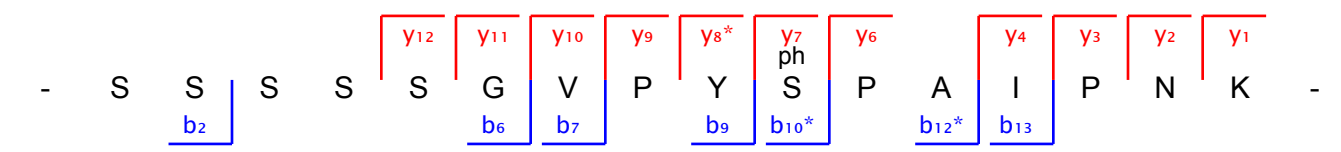
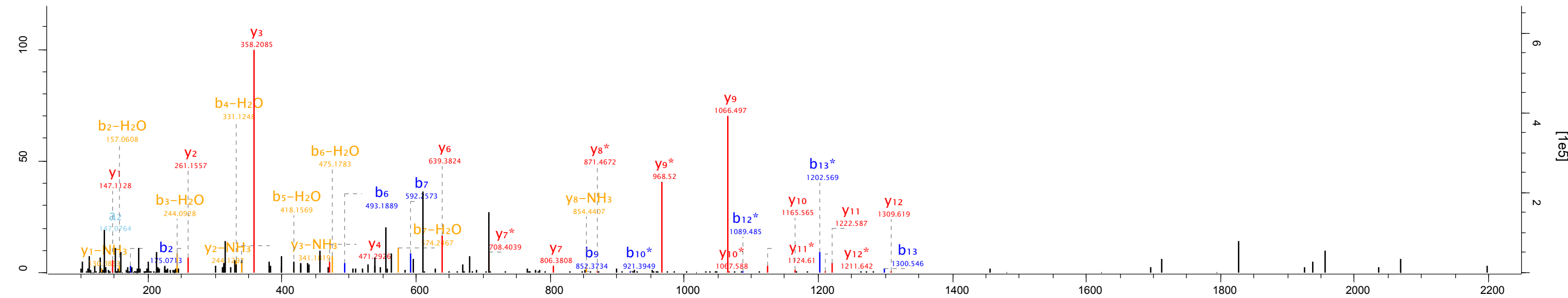


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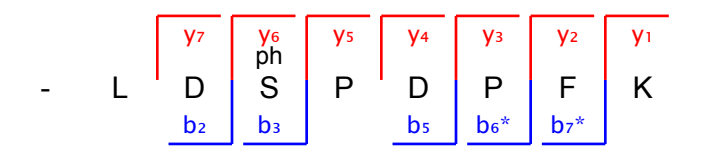
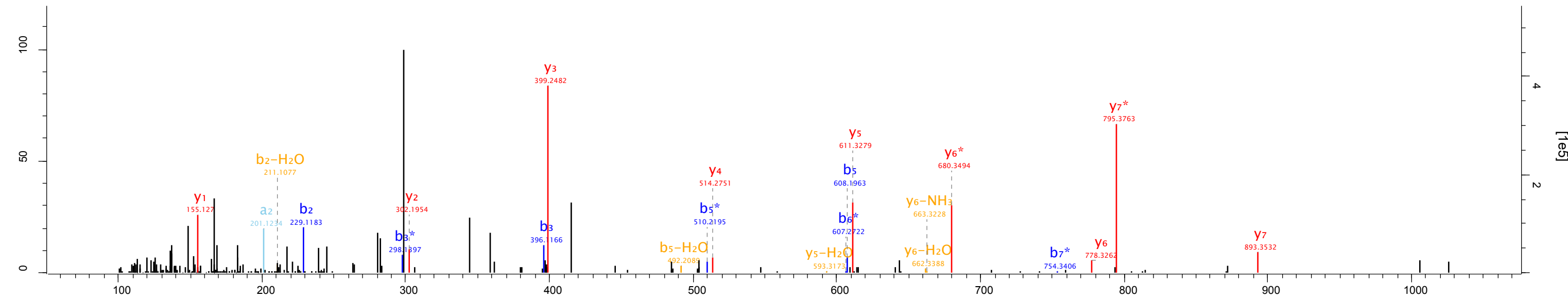




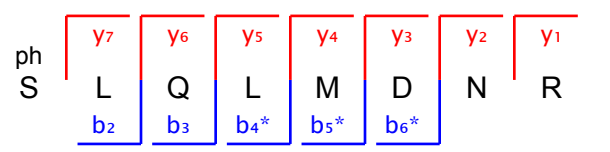
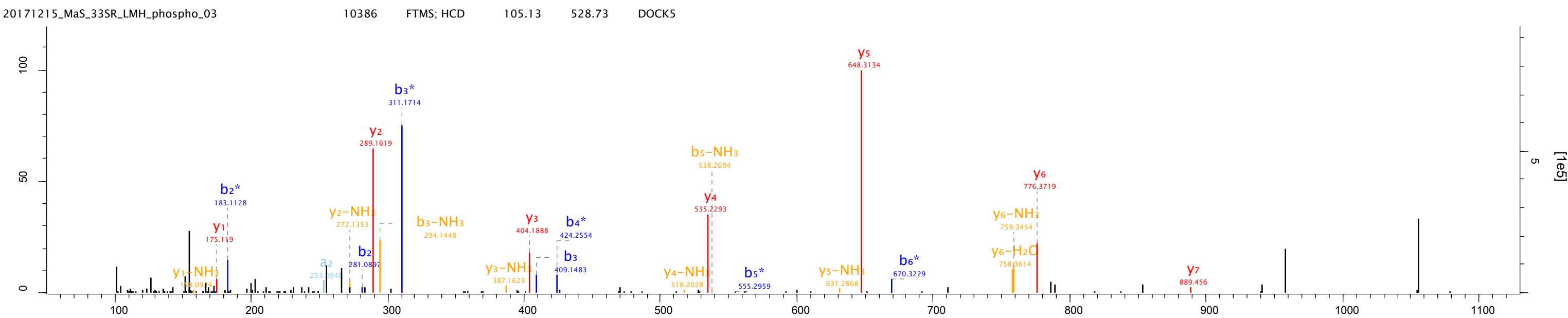
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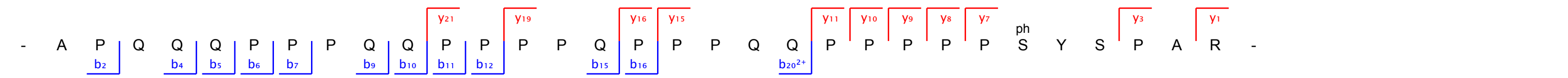
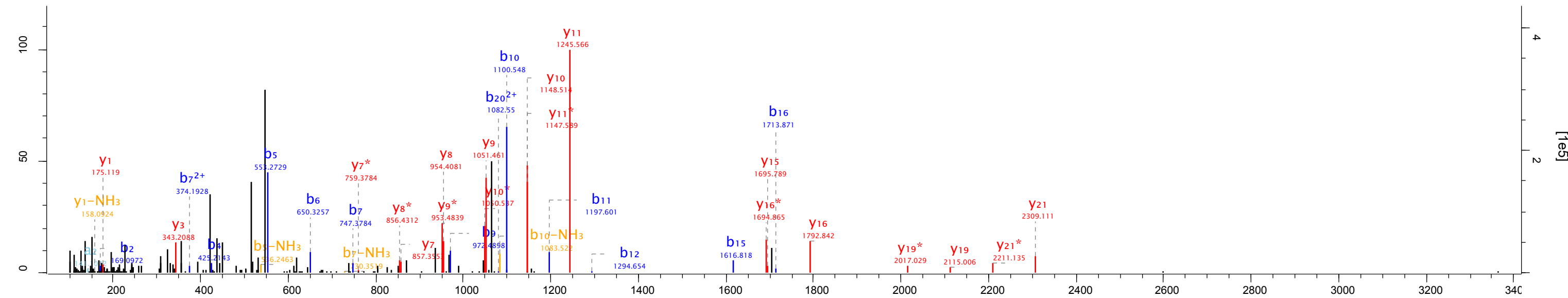
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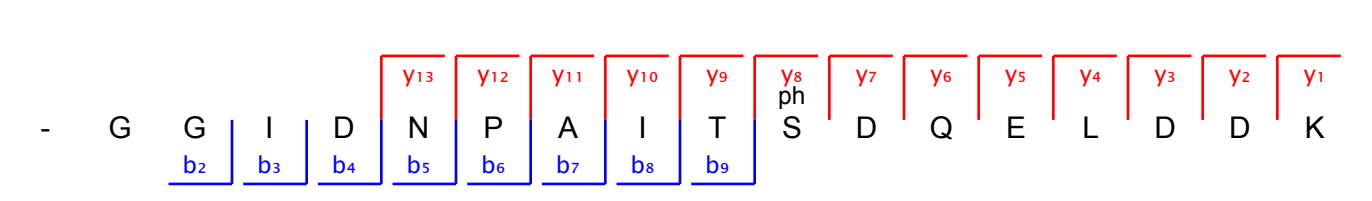
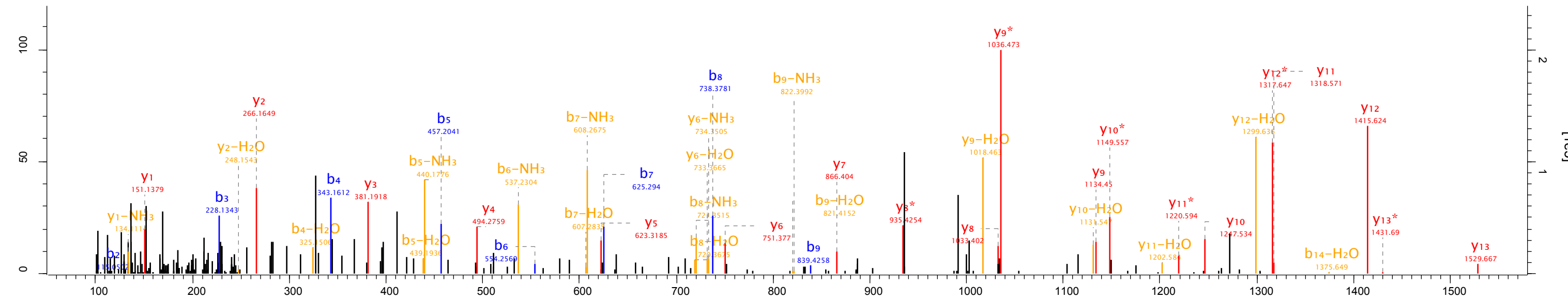
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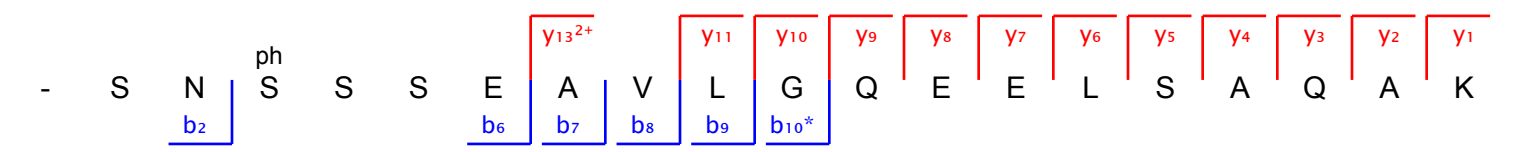
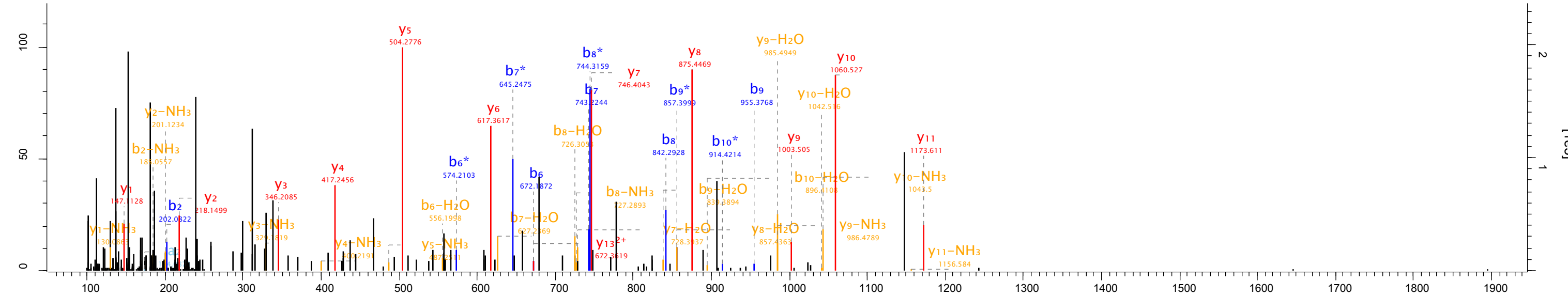


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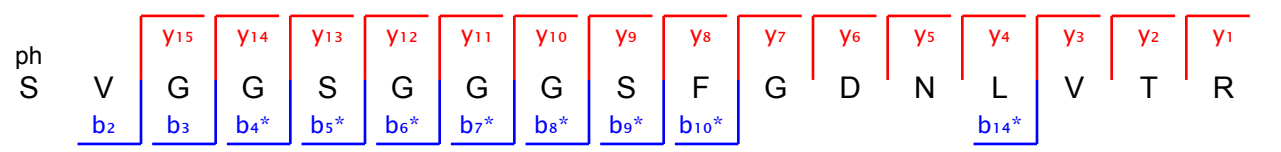
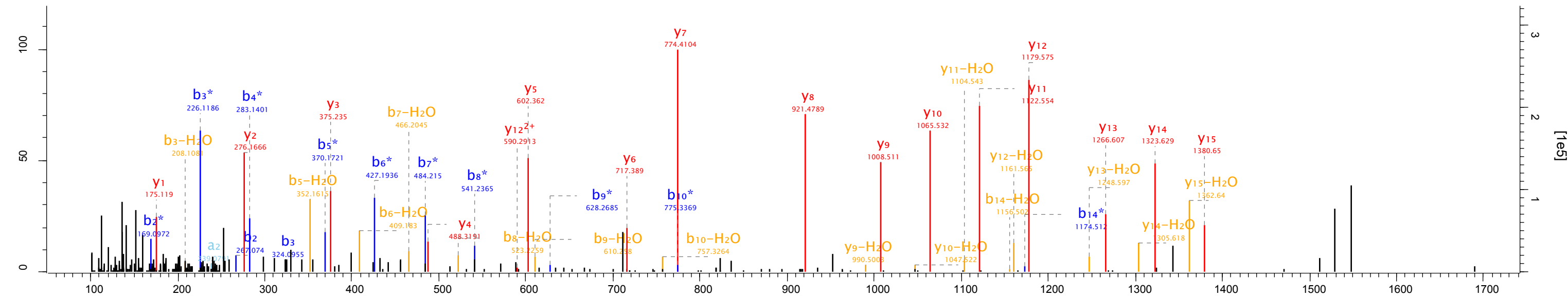


Raw file Scan Method Score m/z Gene names

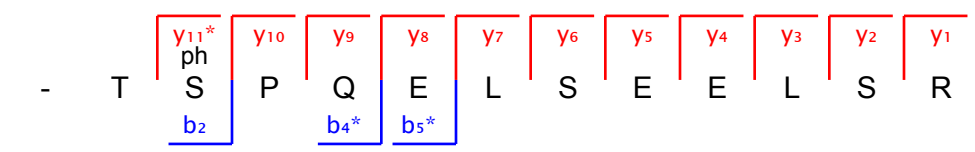
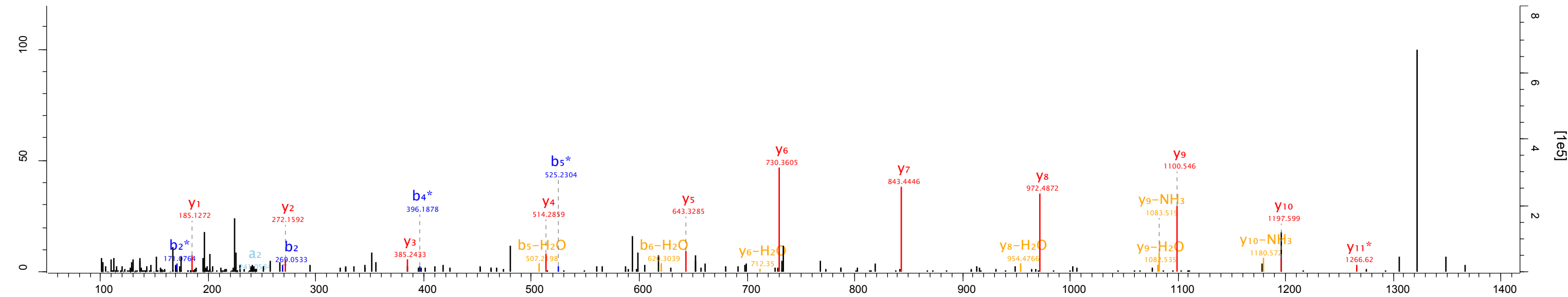
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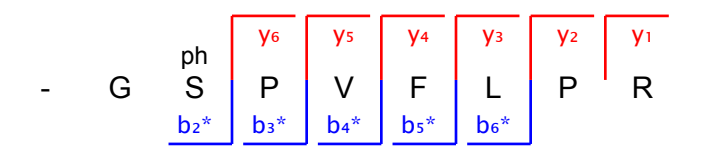
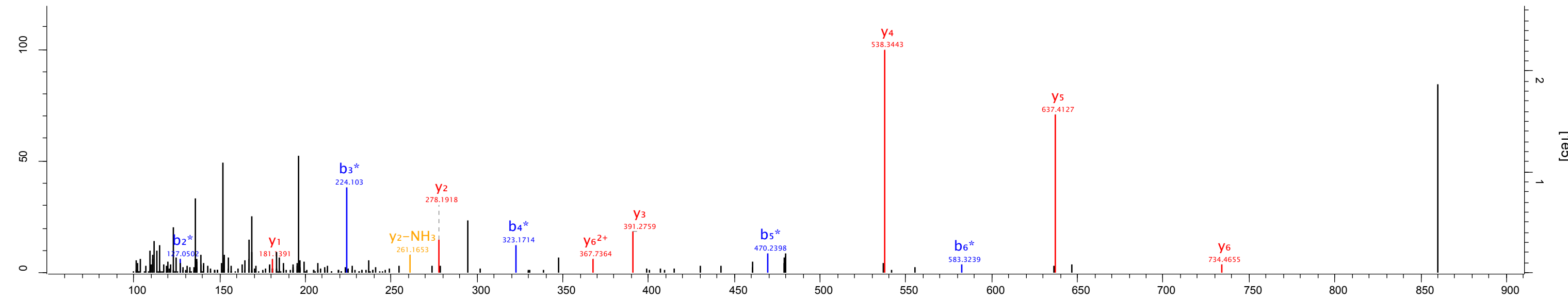
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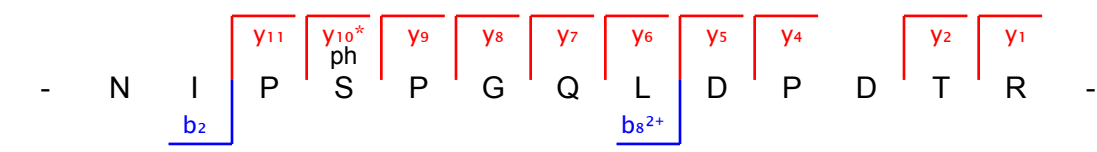
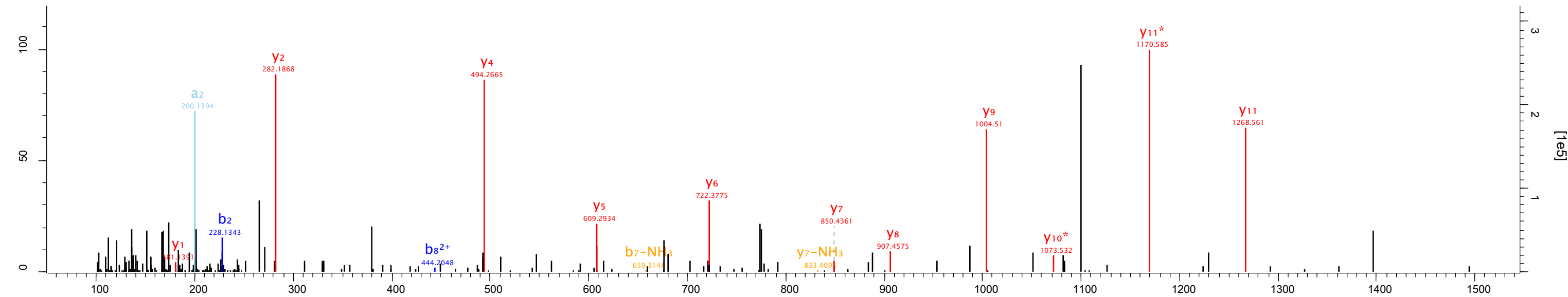
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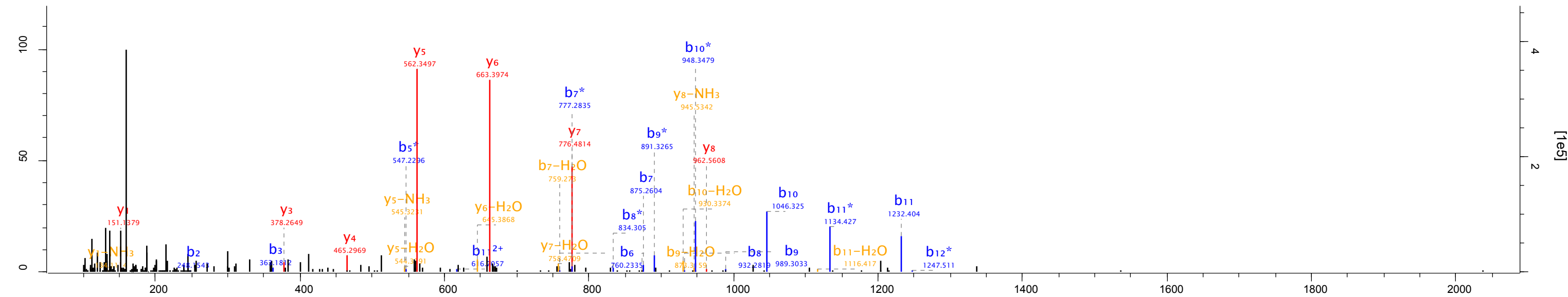
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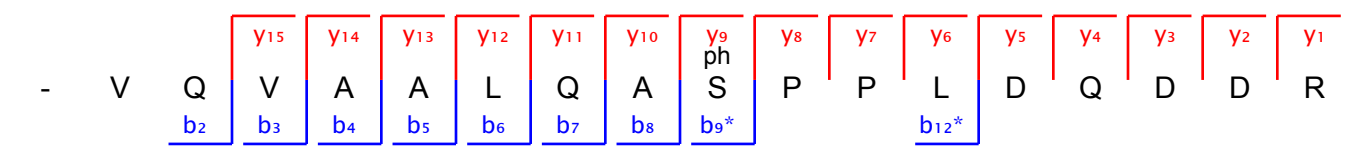
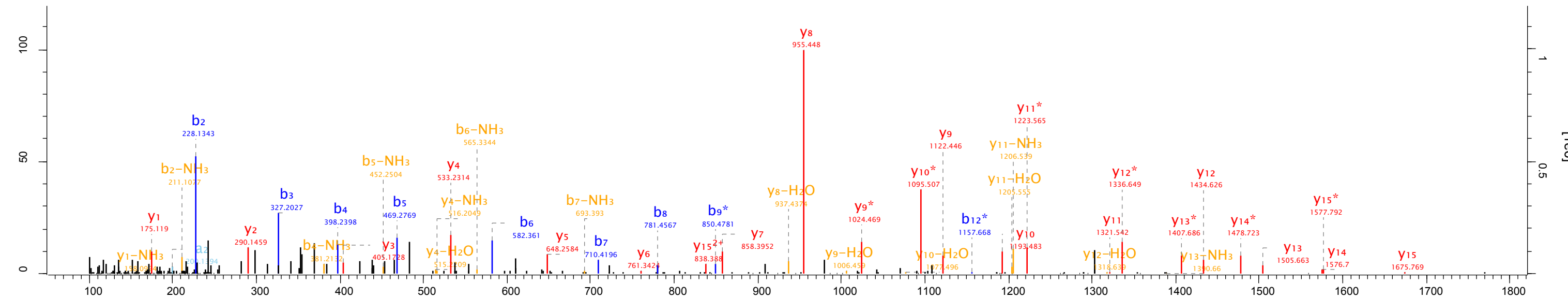
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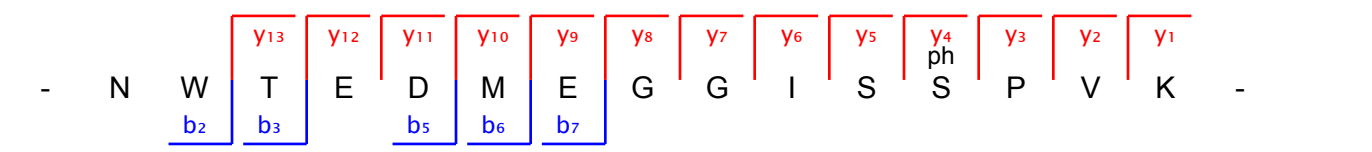
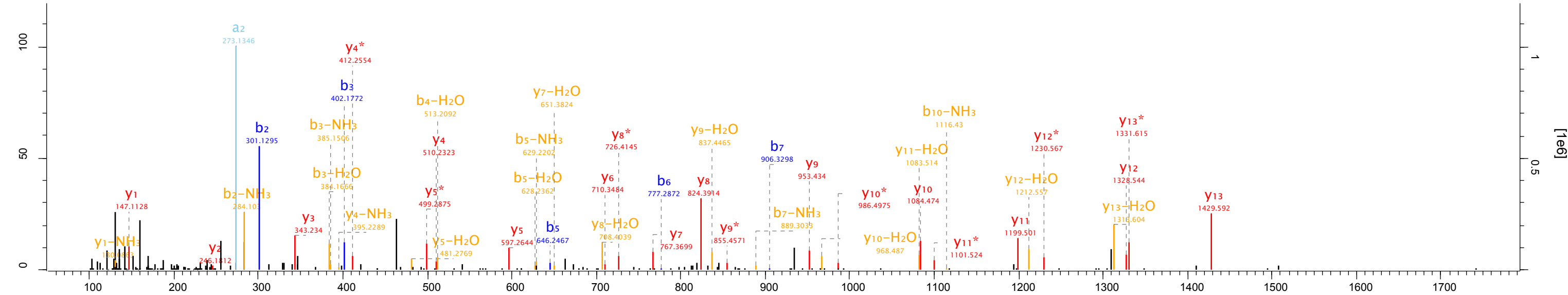
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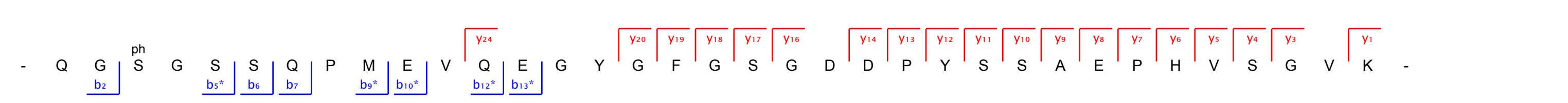
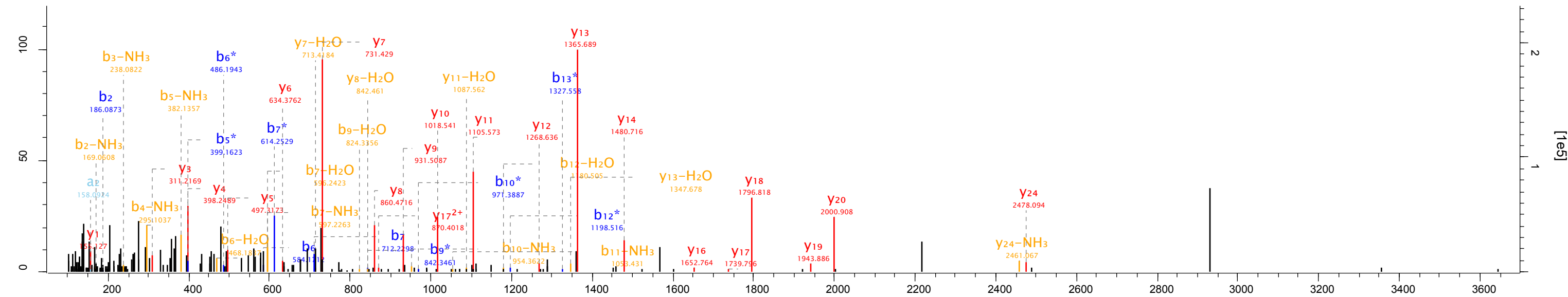
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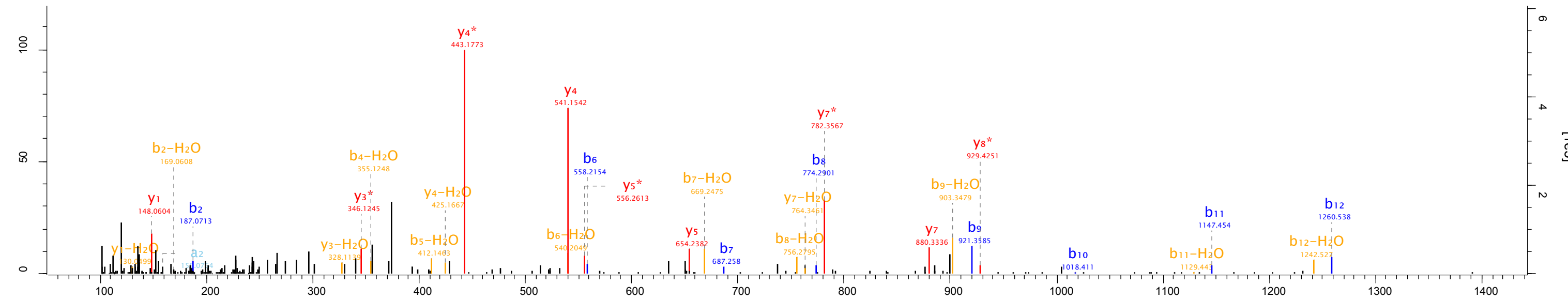
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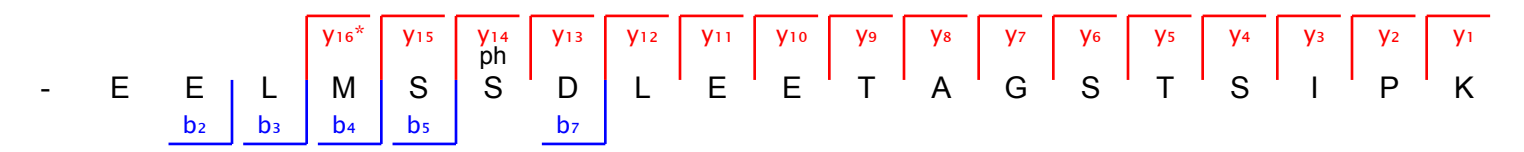
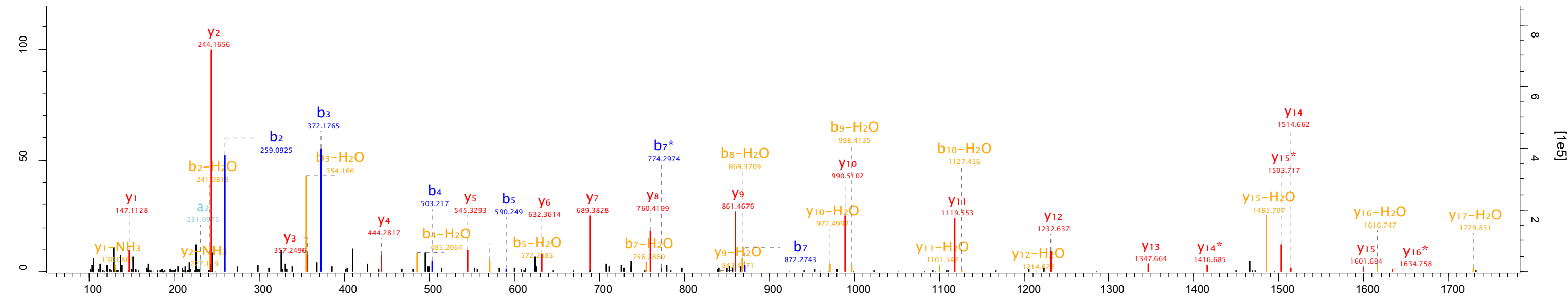
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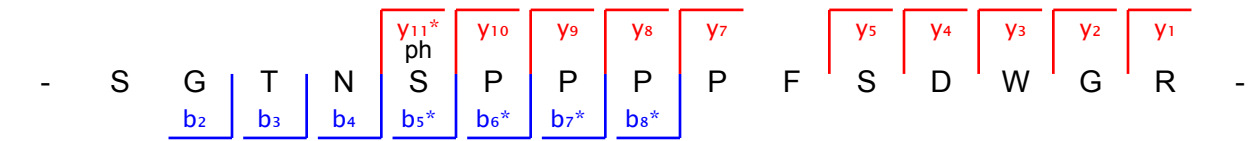
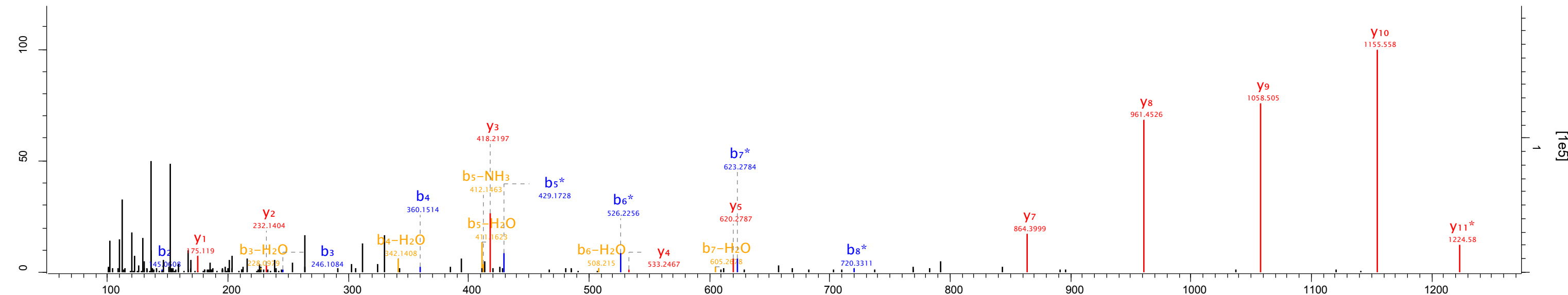
- E G E G G Q E S F P E L P S E E -

Fragmentation mapping: b2 (under G), b6 (under Q), b7 (under E), b8 (under S), b9 (under F), b10 (under P), b11 (under E), b12 (under L), y8* (above F), y7 (above P), y5 (above L), y4 (above P), y3* (above S), y1 (above E).

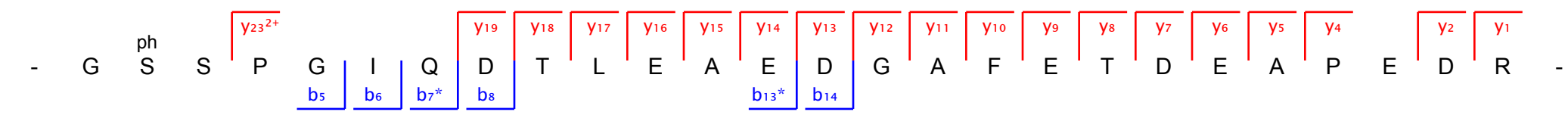
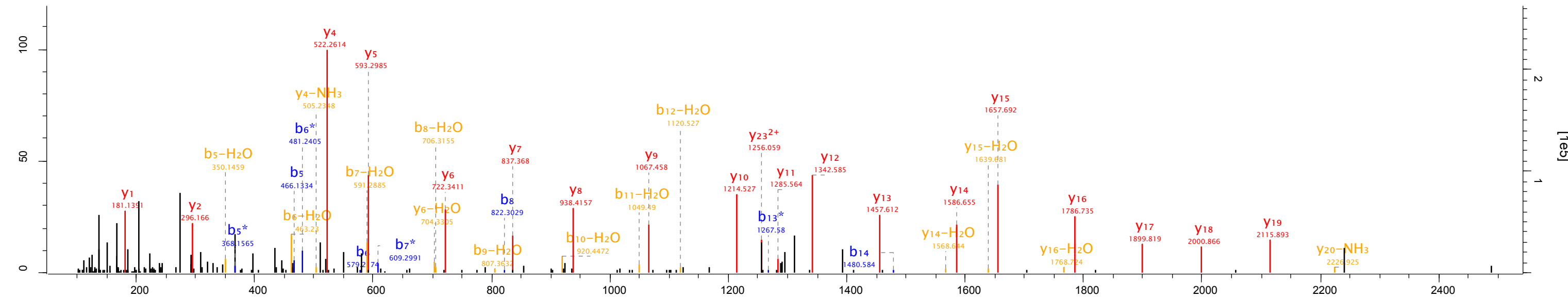
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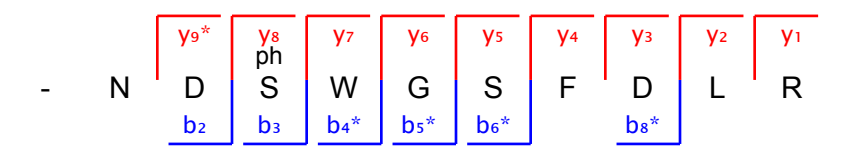
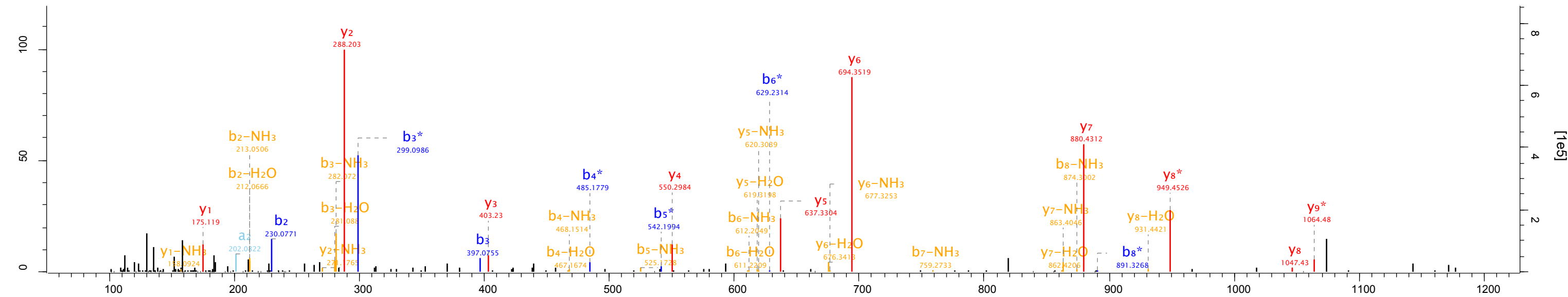
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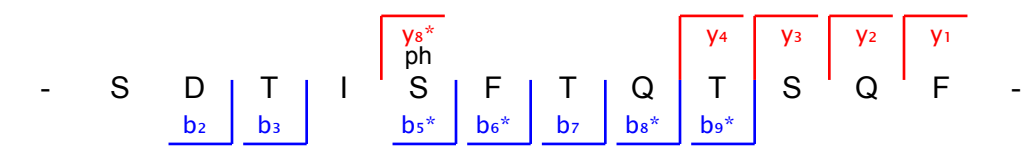
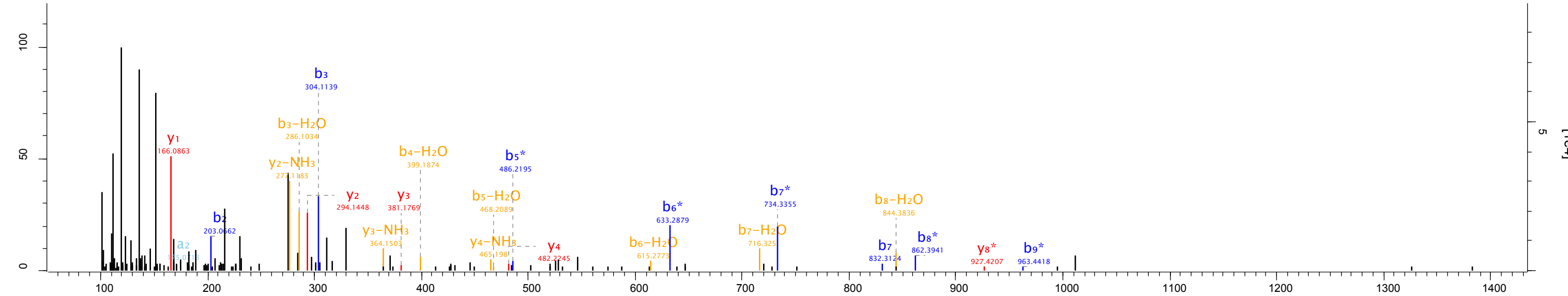


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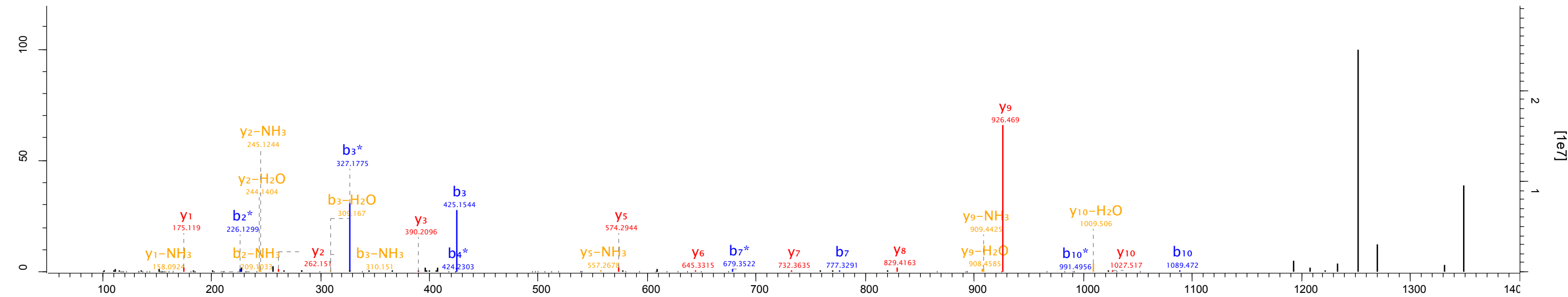
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20171215_MaS_33SR_LMH_phospho_03 16236 FTMS; HCD 78.4 721.3 SLC1A1

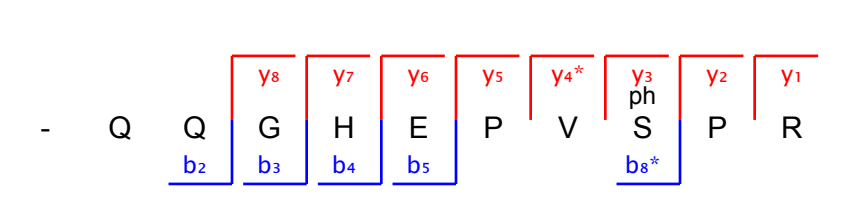
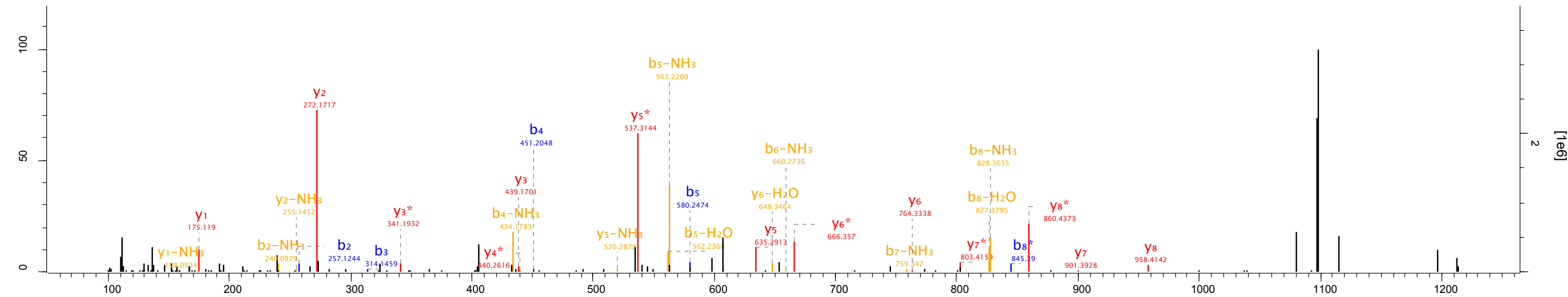


[1e4]

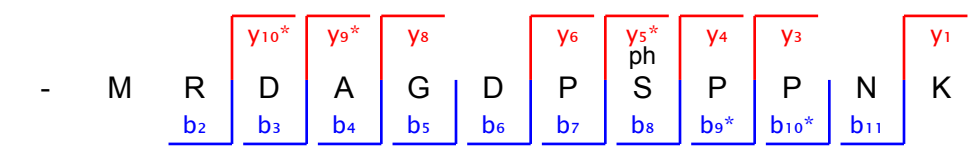
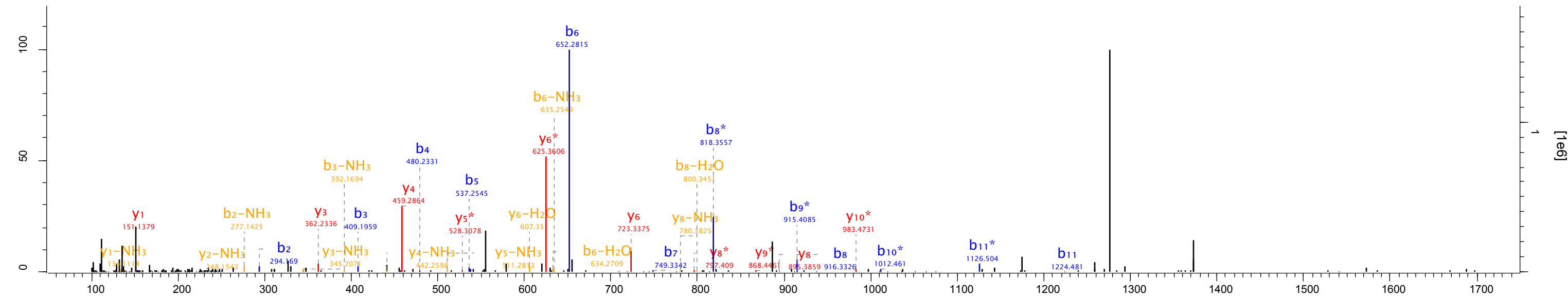
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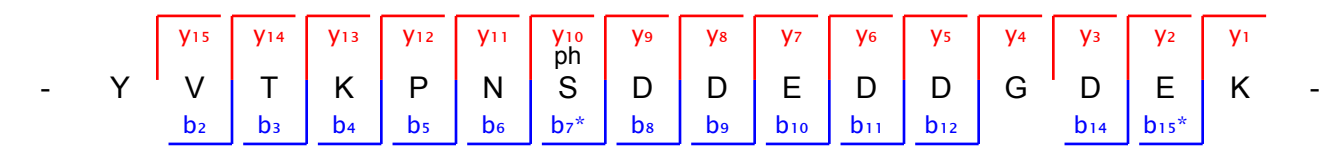
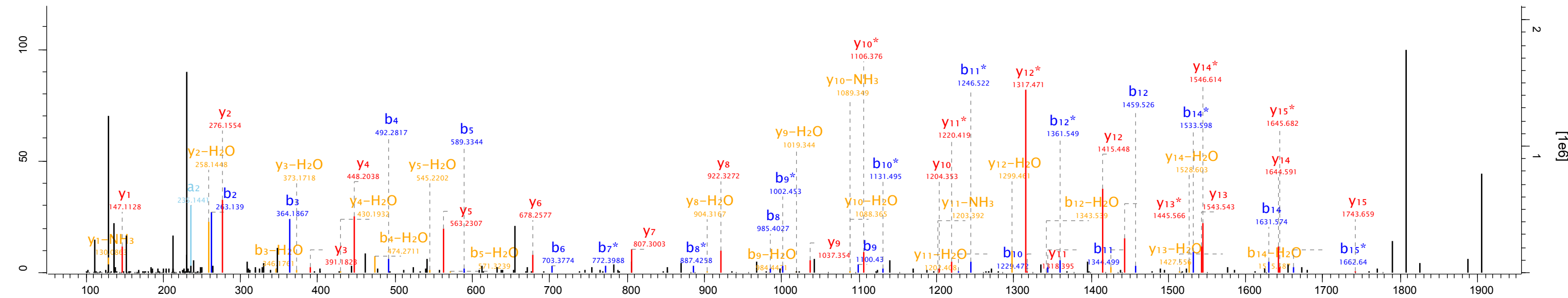
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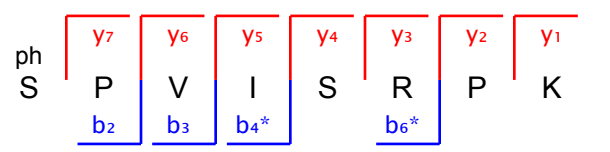
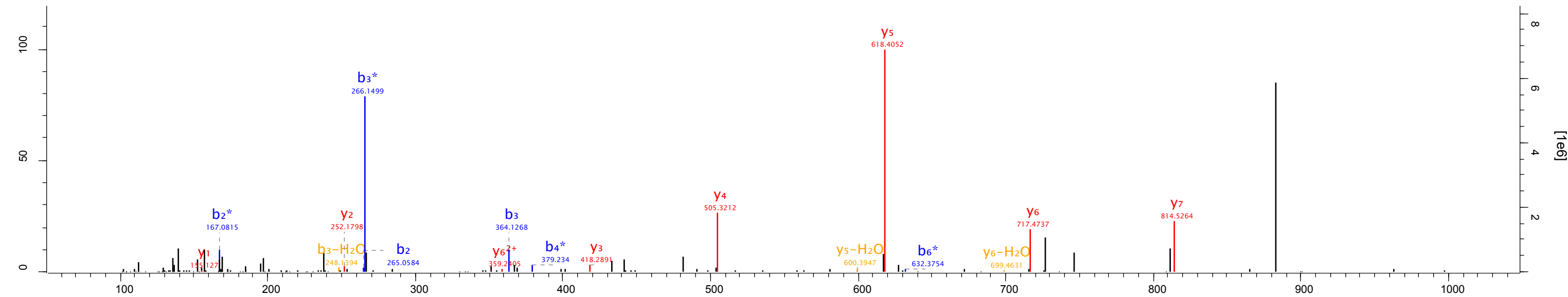


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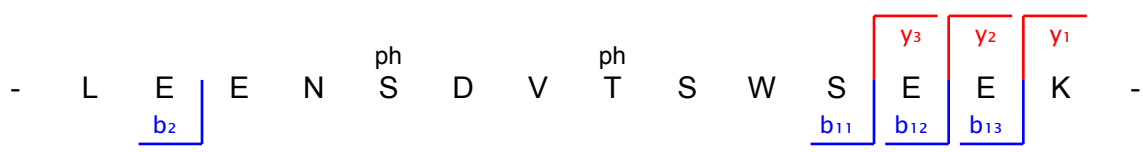
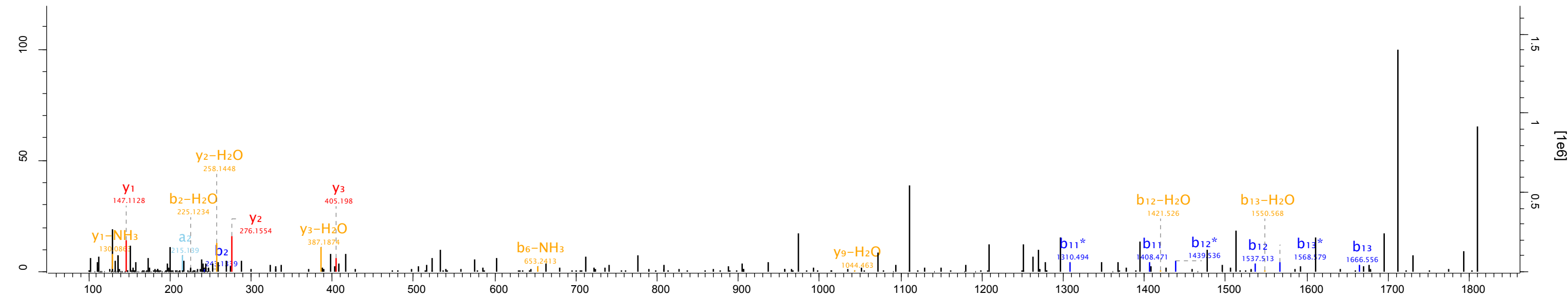


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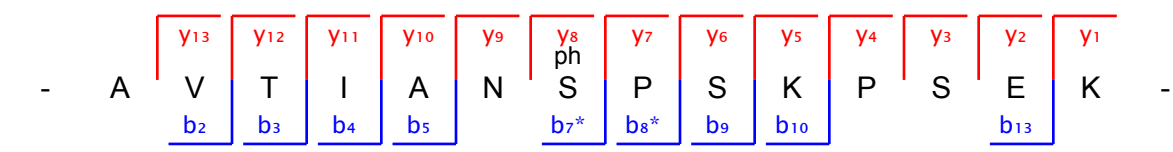
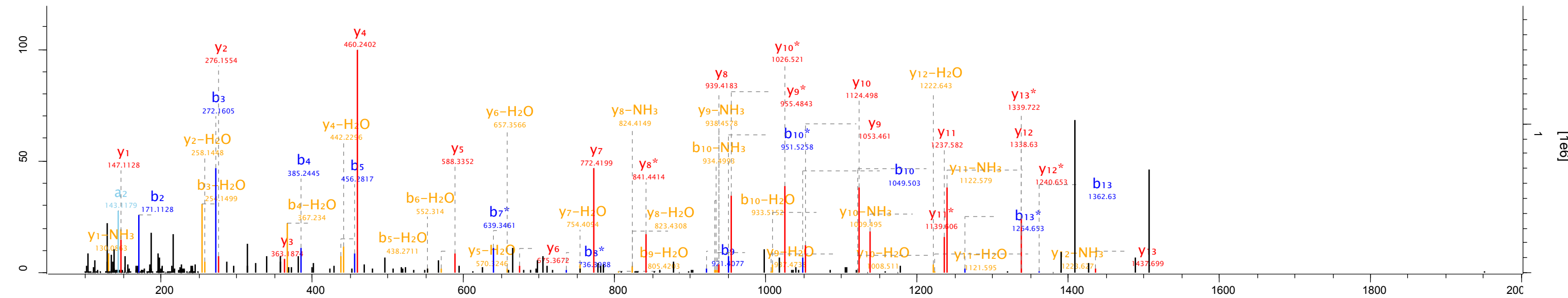
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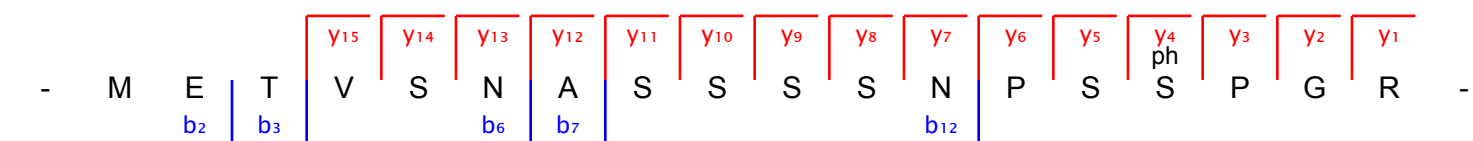
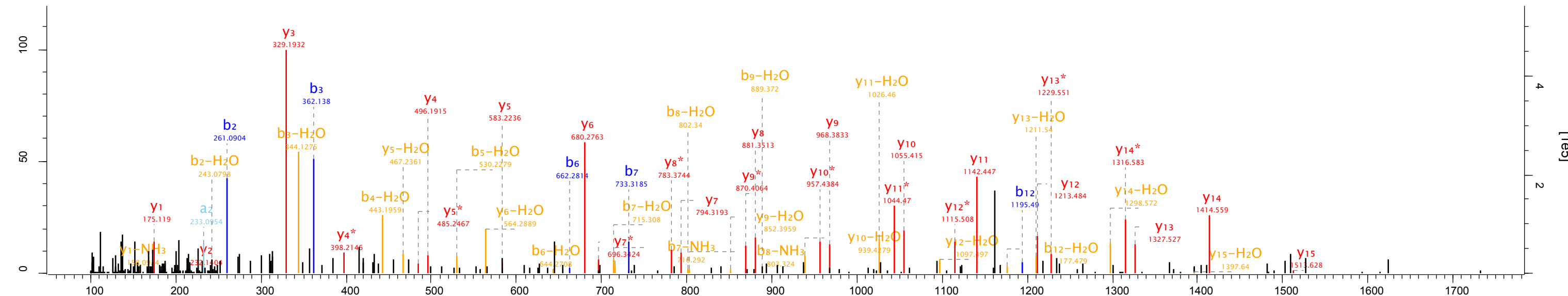


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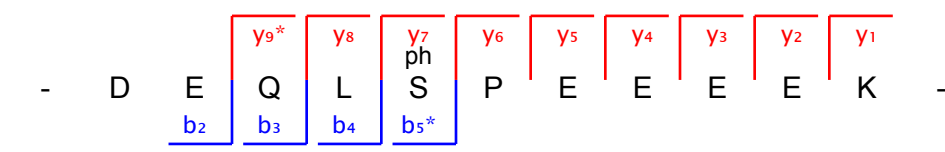
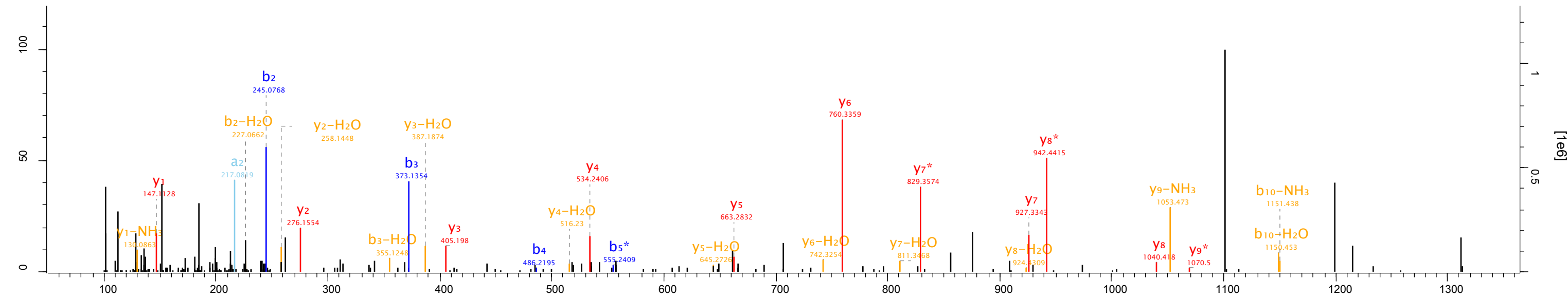


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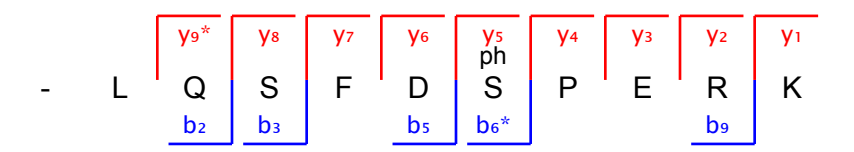
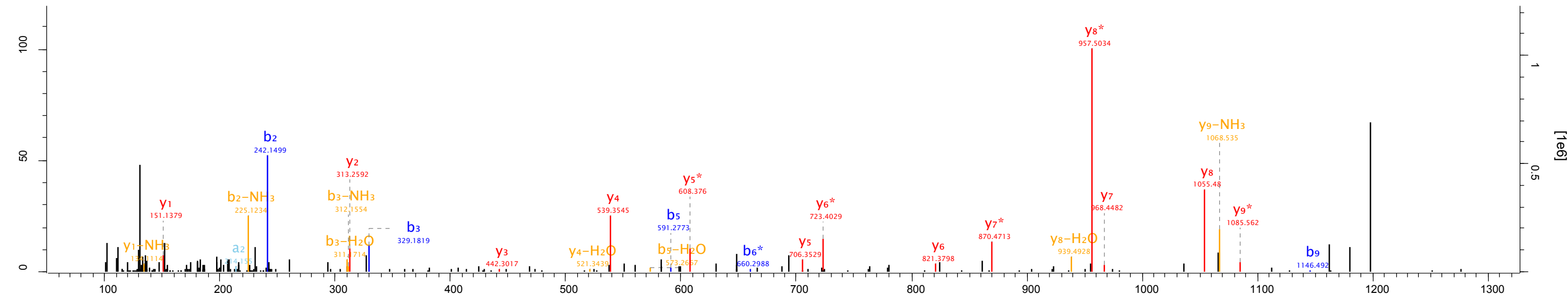




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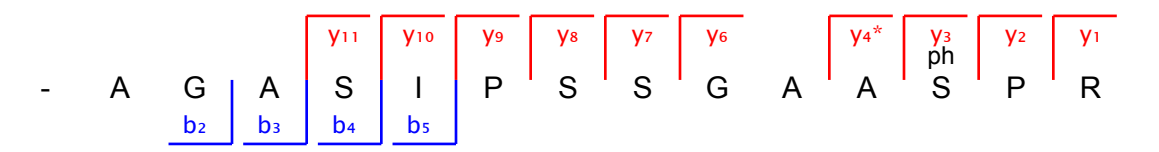
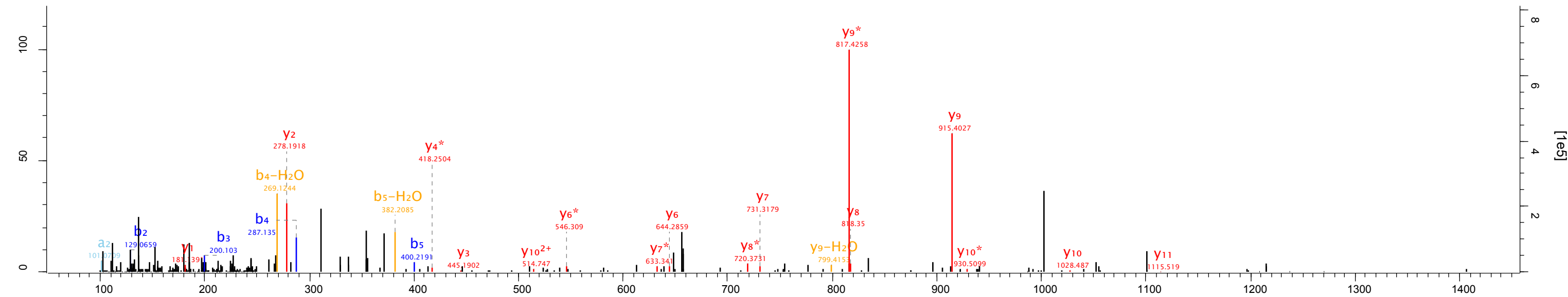


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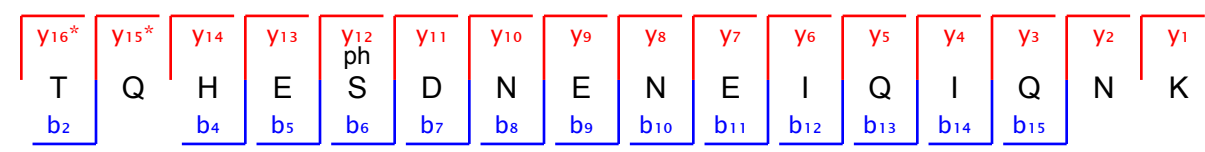
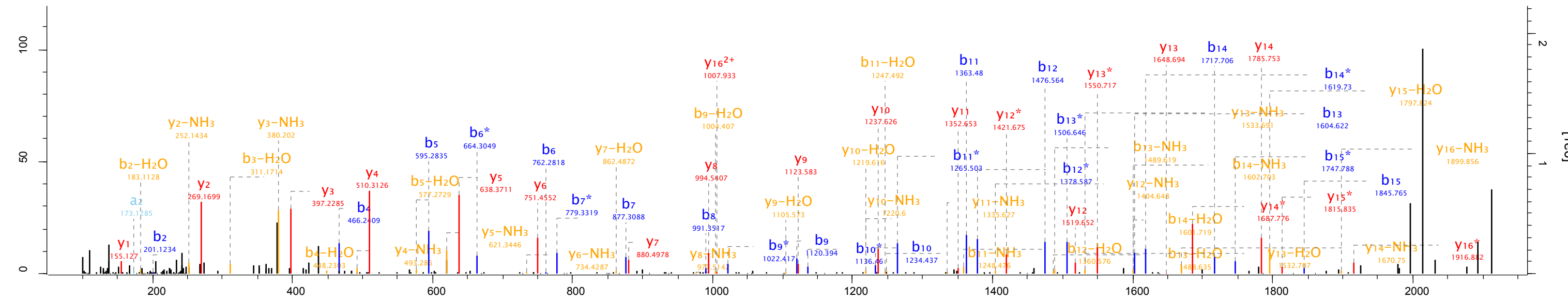


Q S F D S P E R K

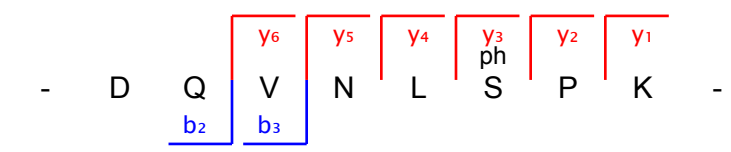
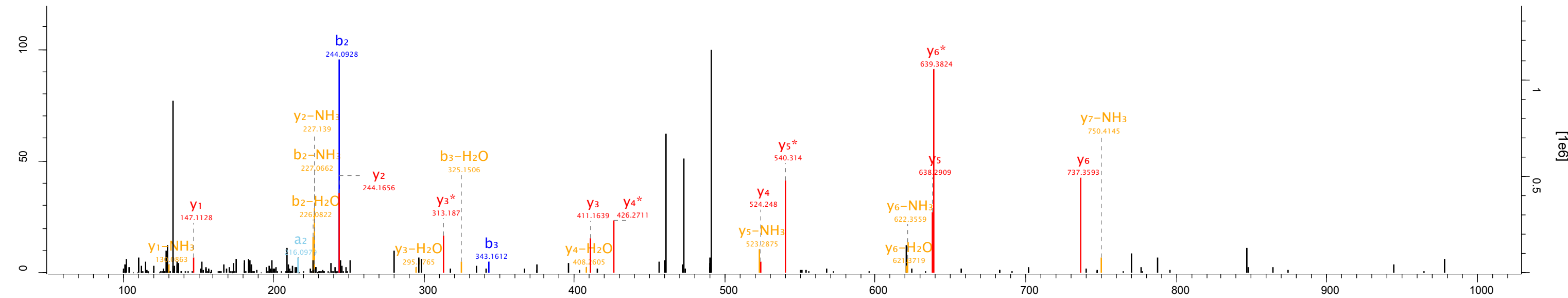
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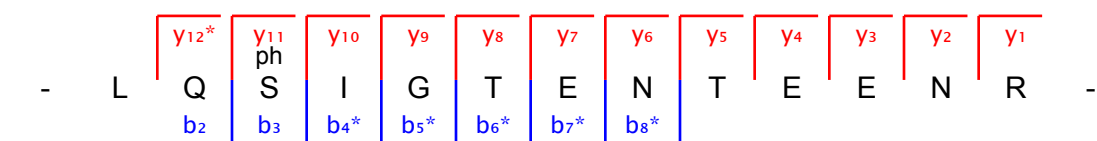
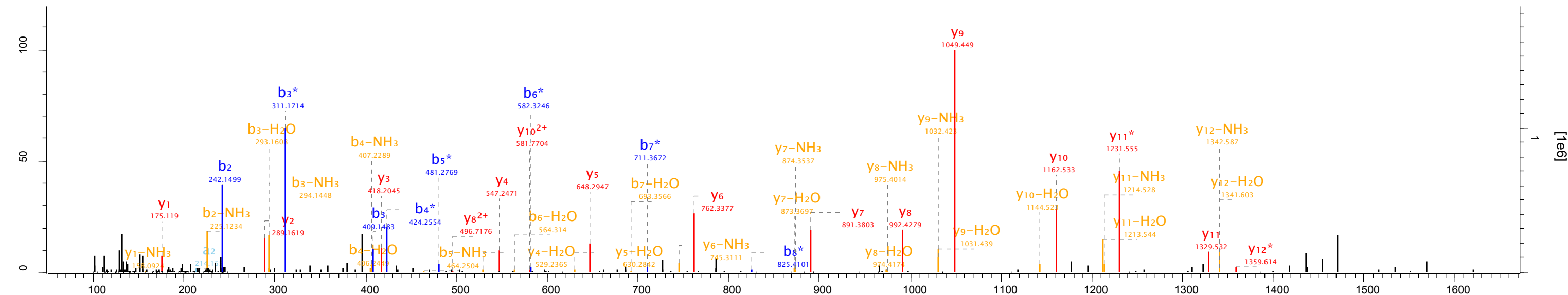
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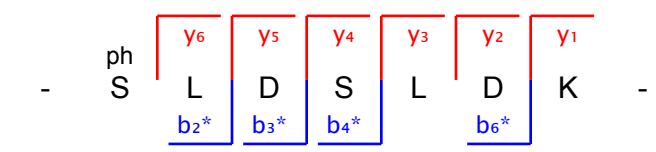
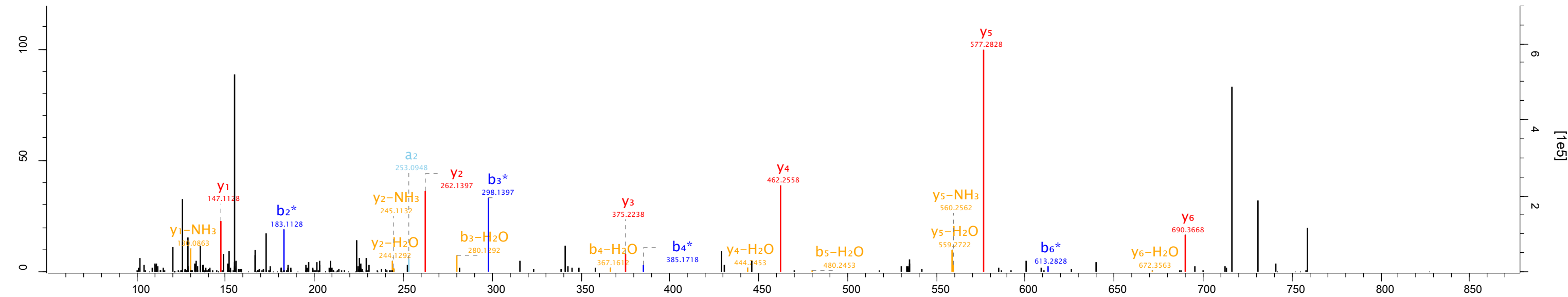
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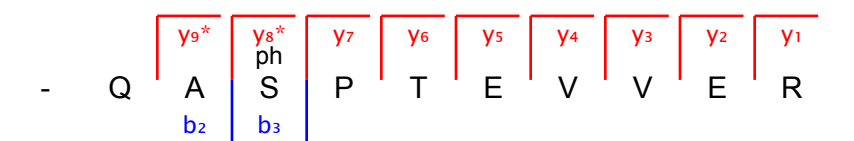
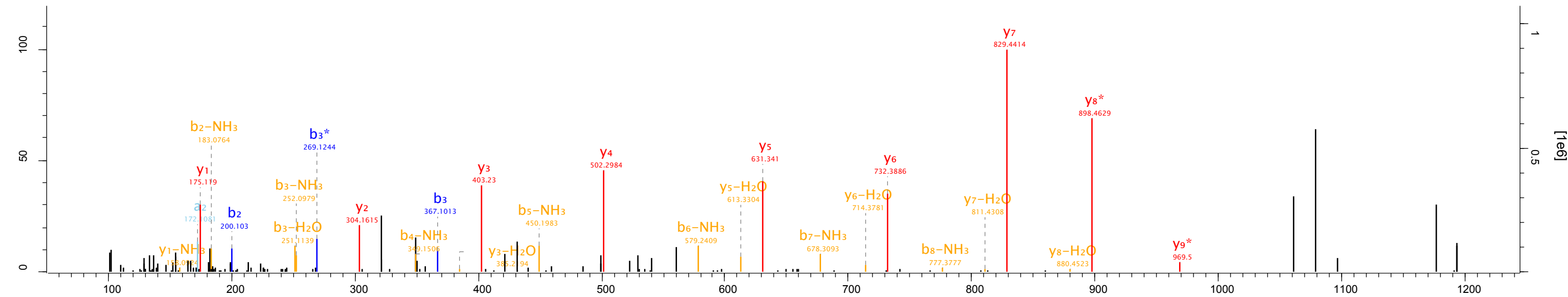
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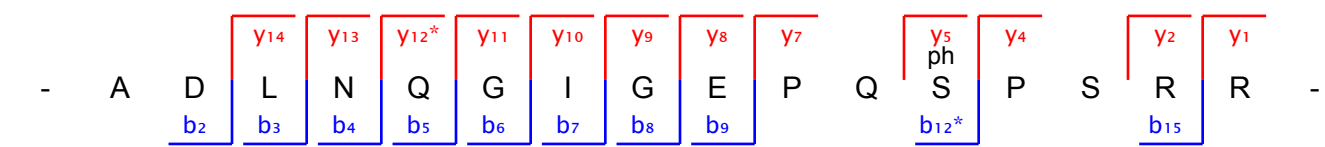
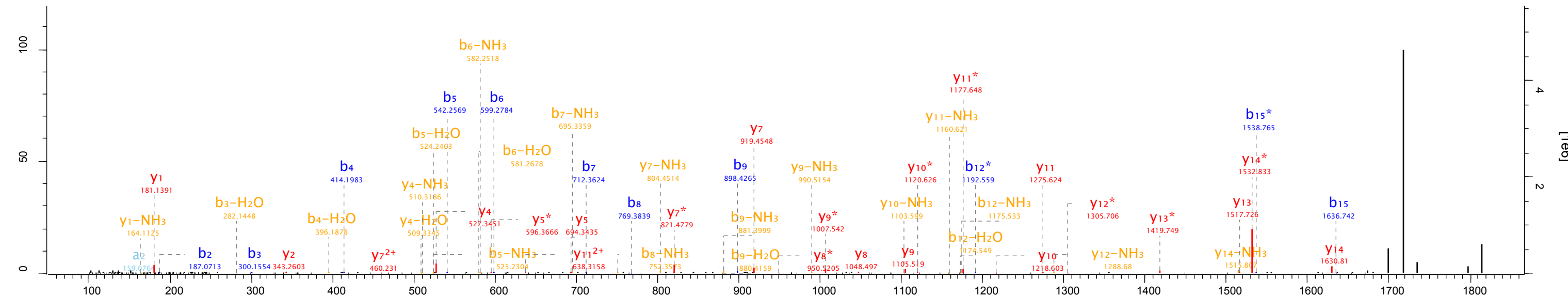
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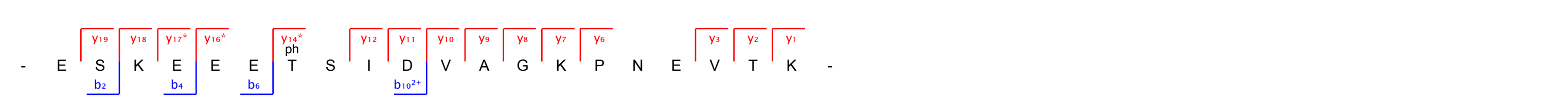
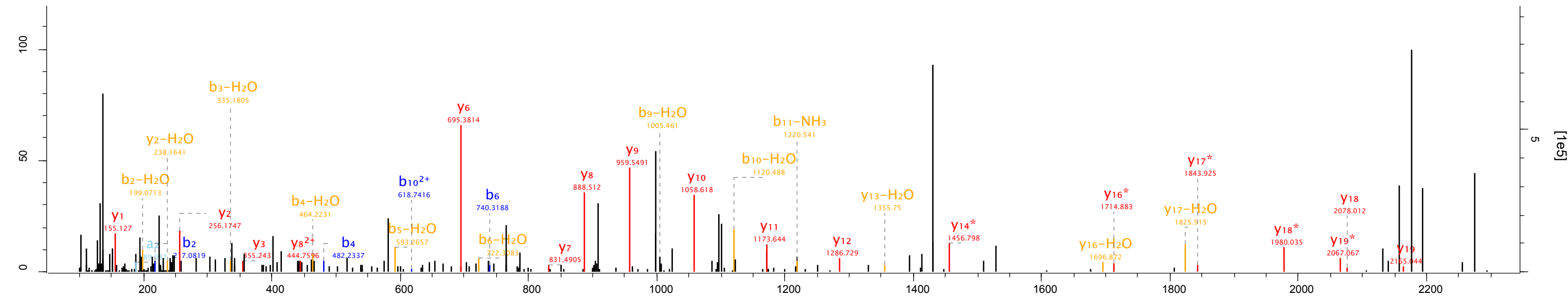
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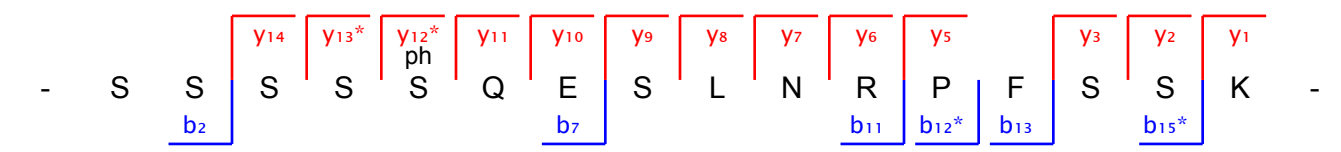
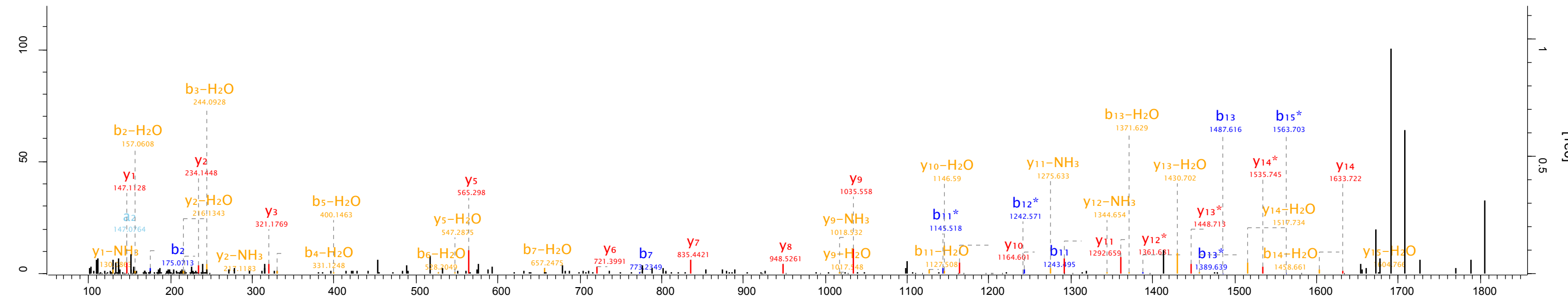
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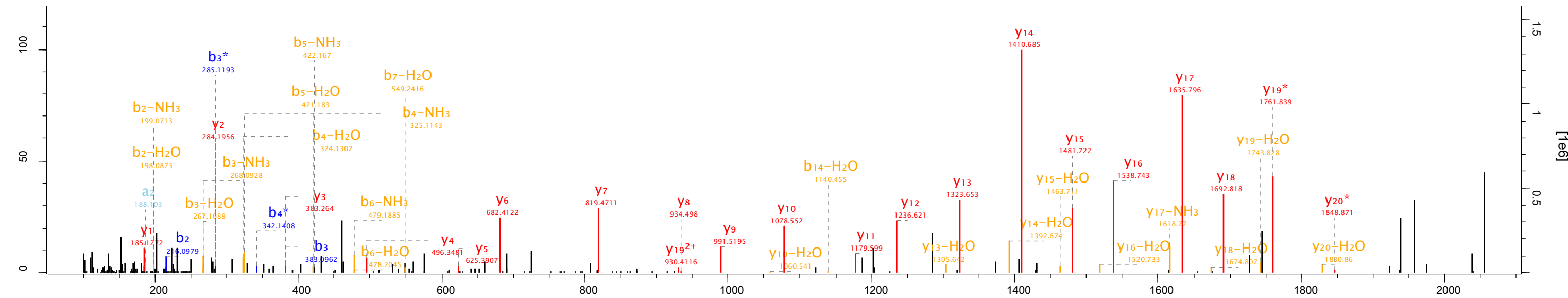
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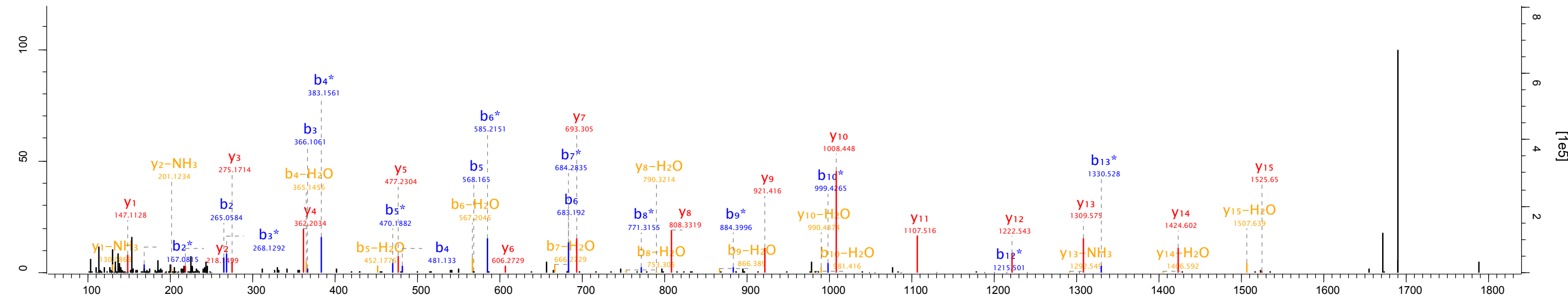
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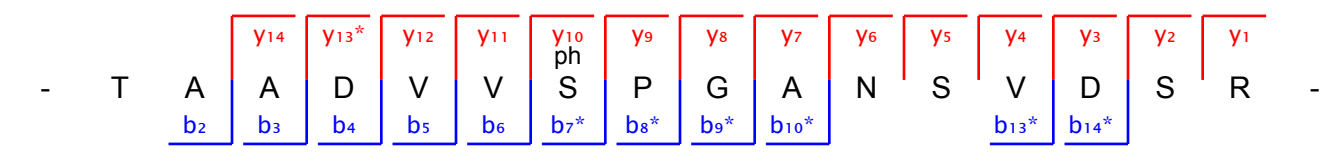
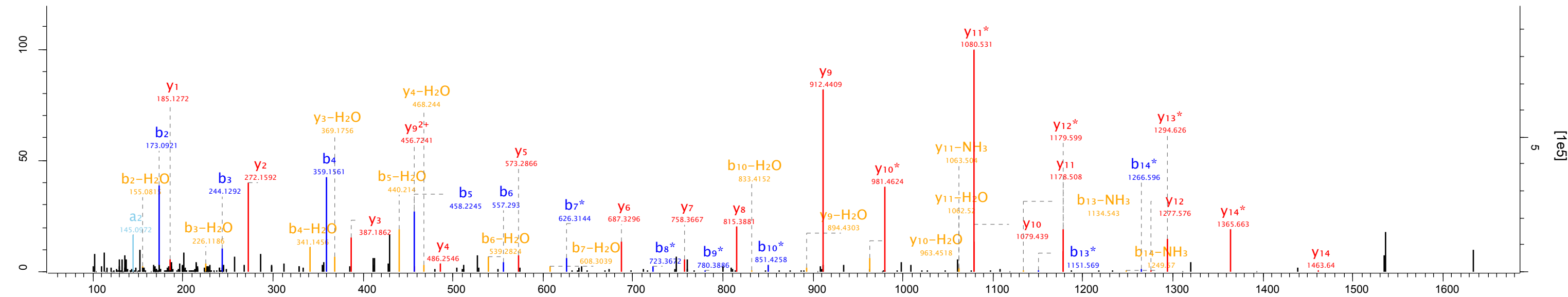
b₂
b₃
b₄*

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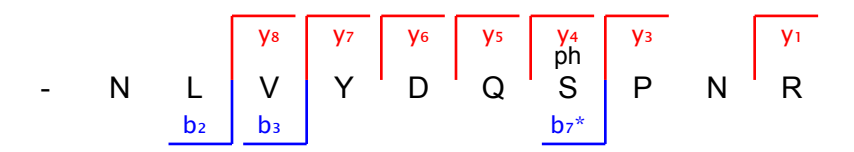
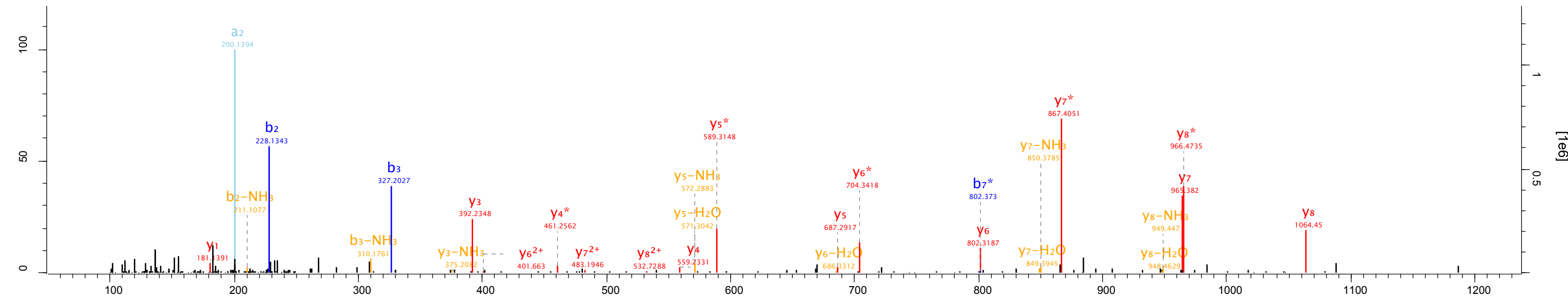


ph S
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 b2 b3 b4 b5 b6 b7* b8* b9* b10* b12* b13*

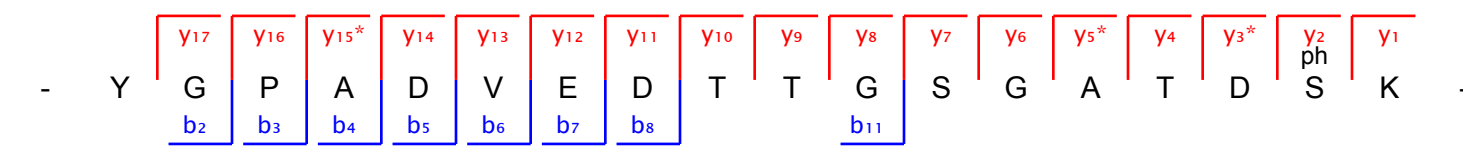
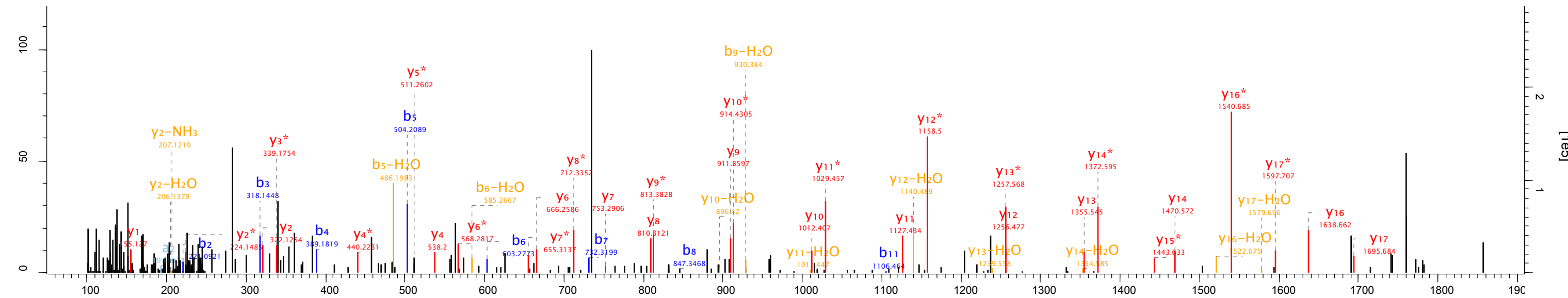
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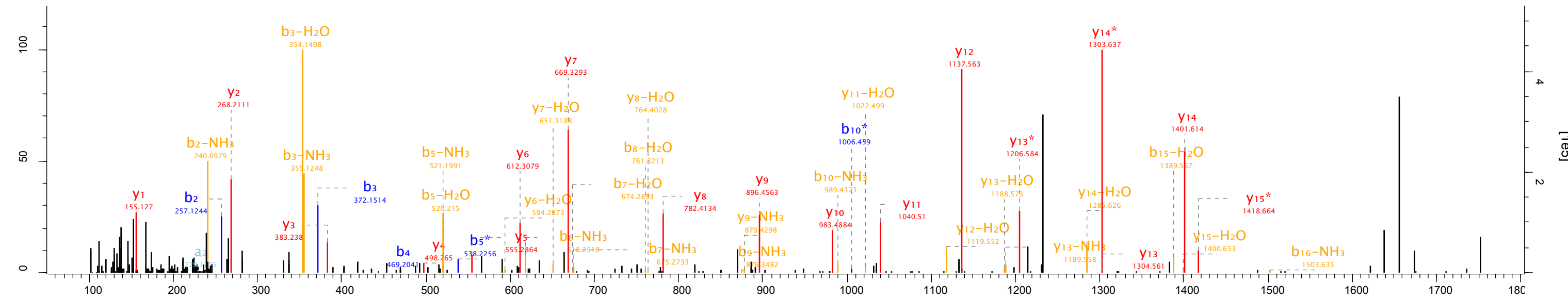


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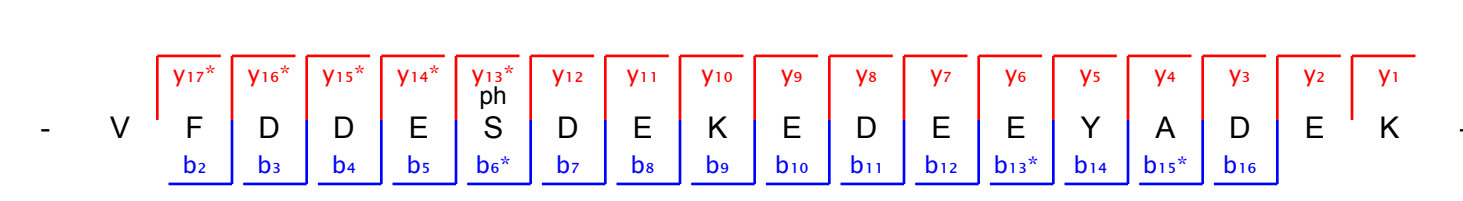
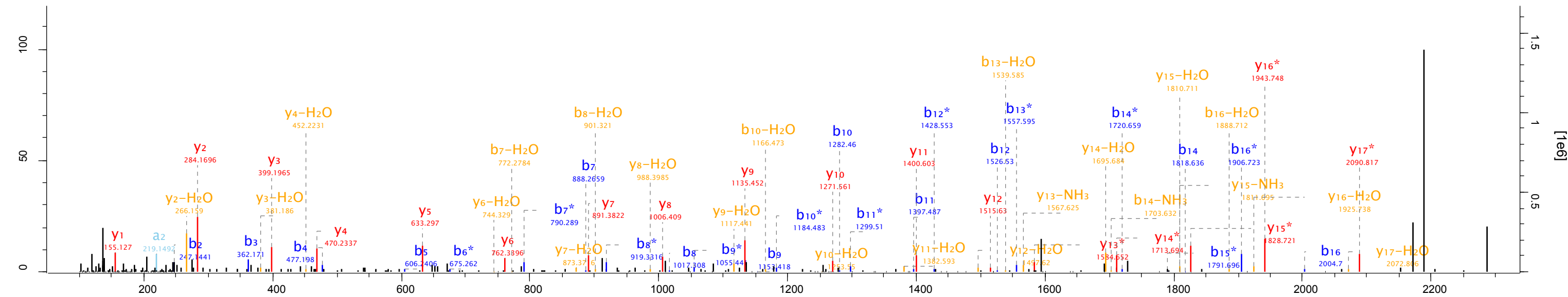
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Fragmentation sites are indicated by brackets below the sequence:

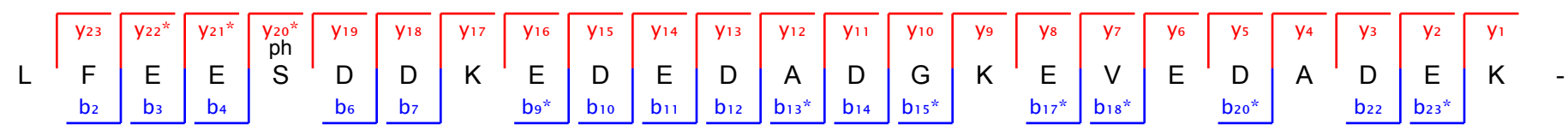
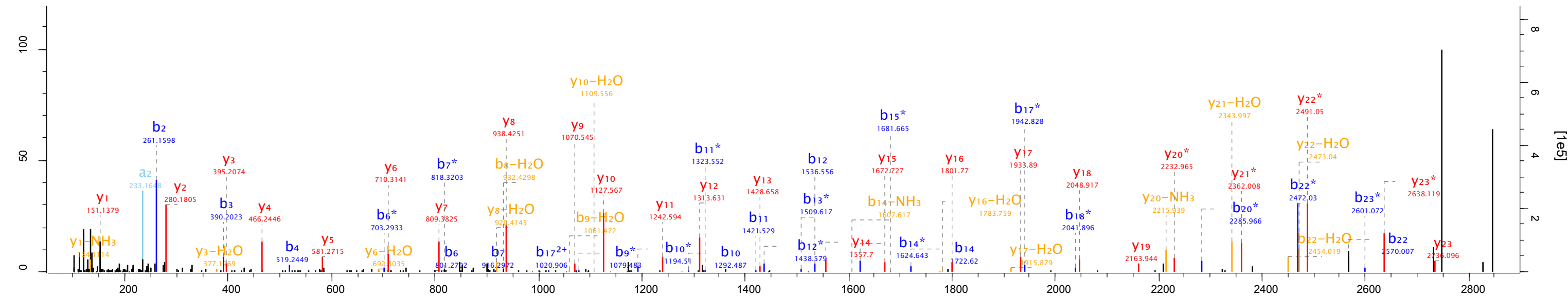
- b2: Q-Q
- b3: Q-D
- b4: D-P
- b5*: P-S
- b10*: N-L

Peptide sequence: Q Q D P S P G S N L G G G D D L K

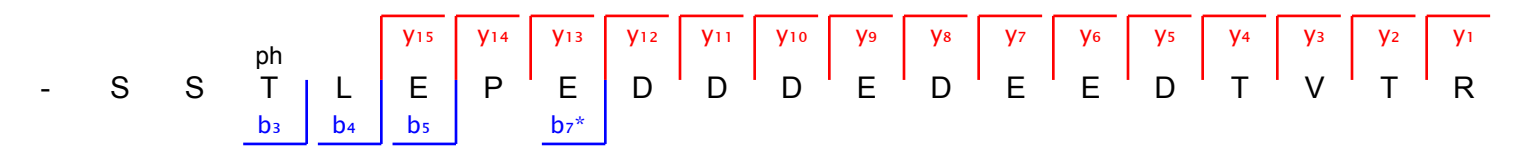
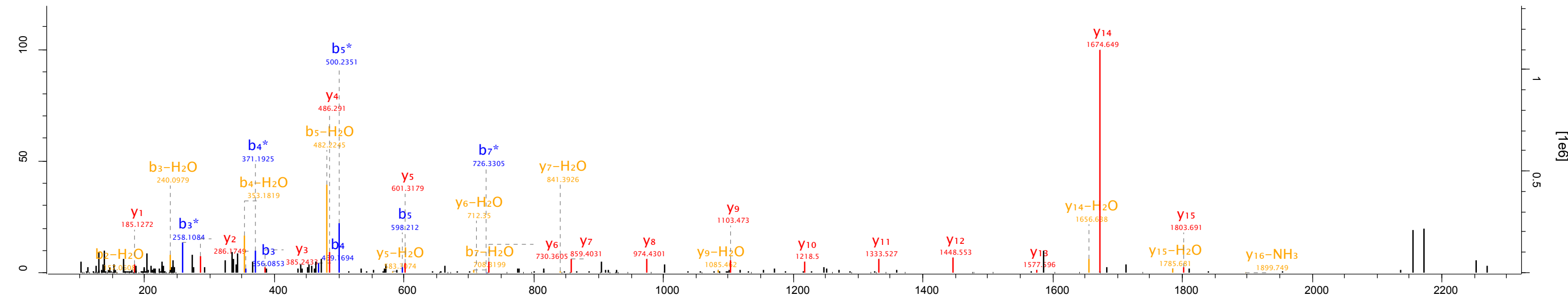
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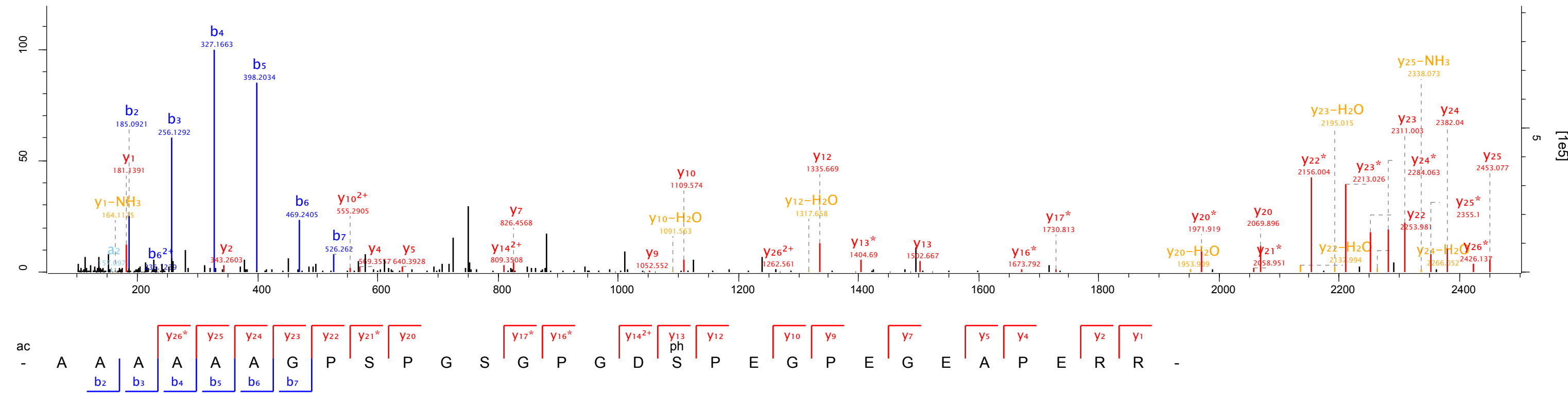
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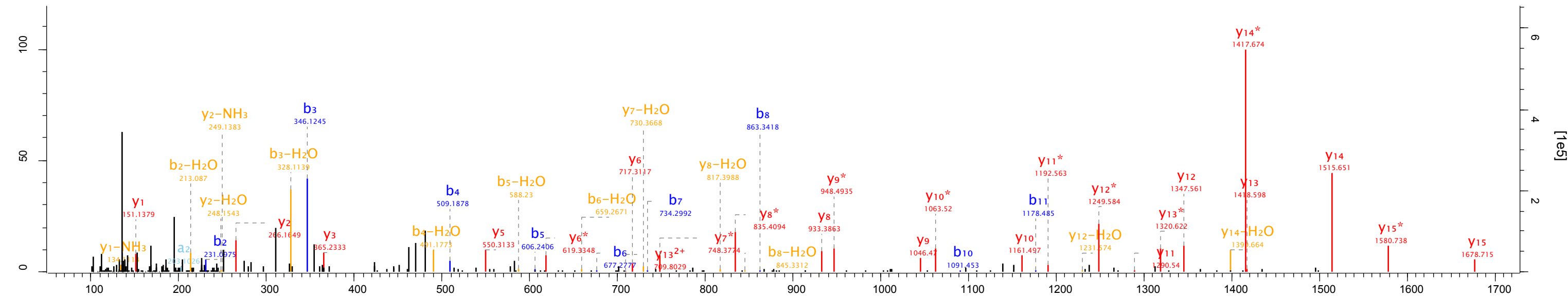
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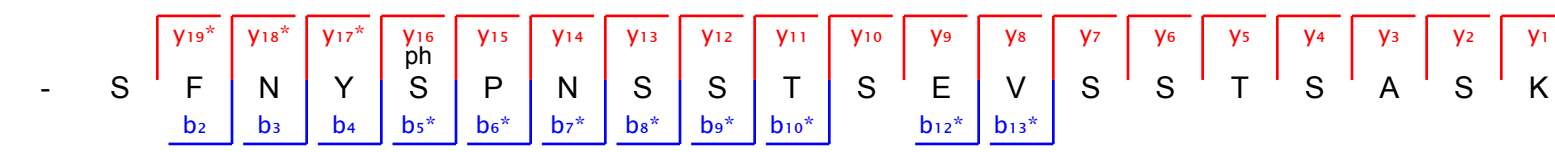
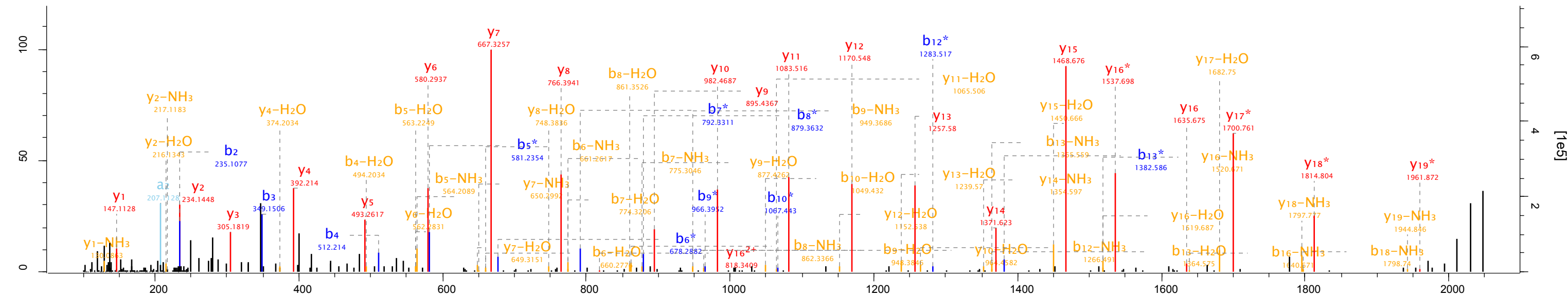


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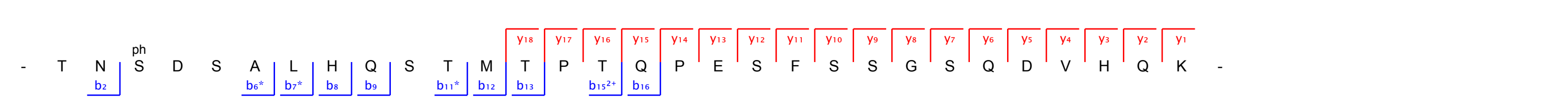
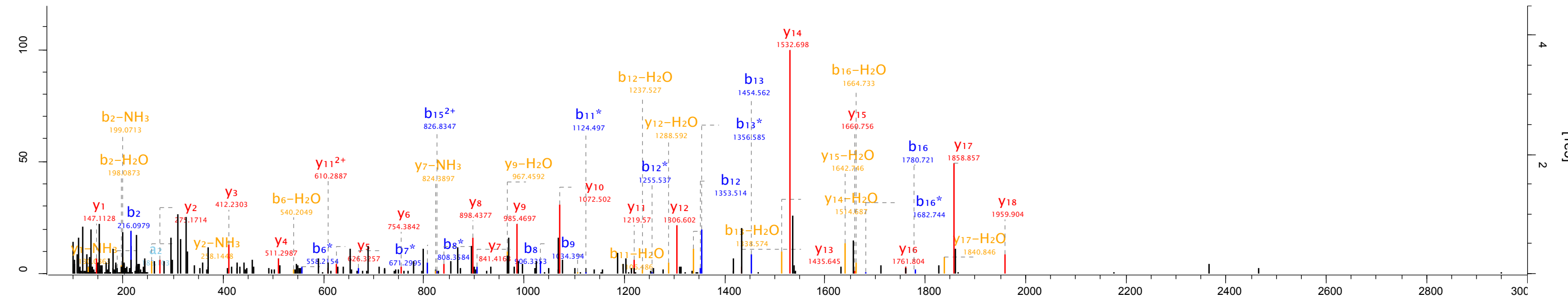


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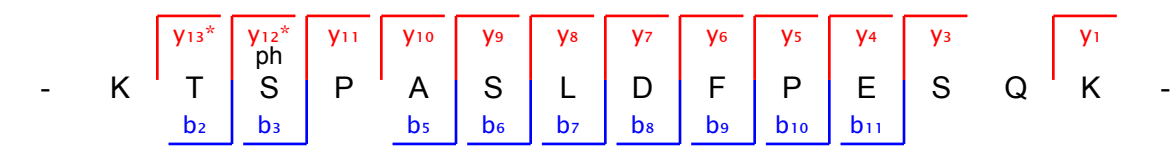
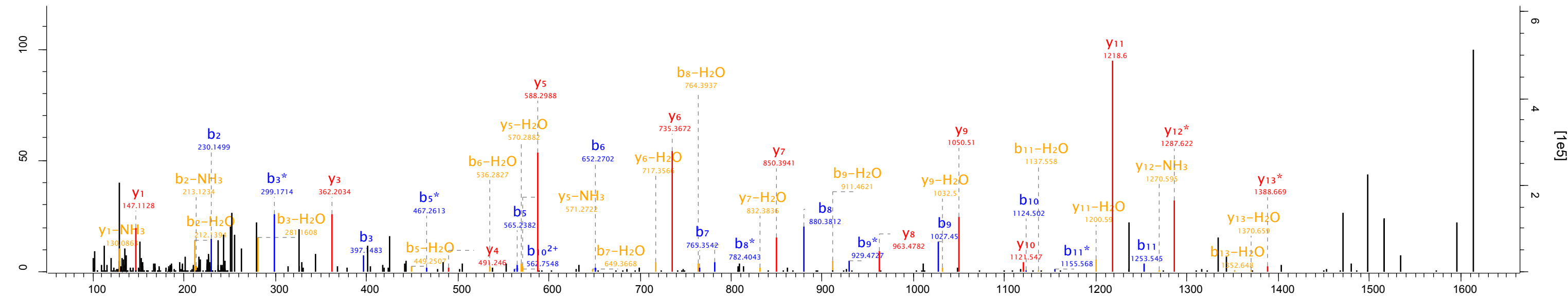
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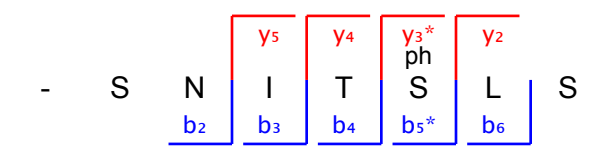
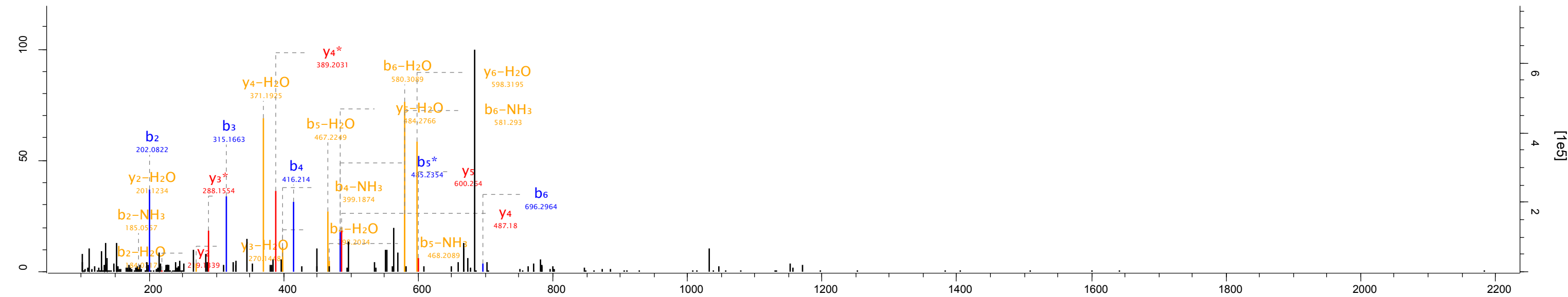
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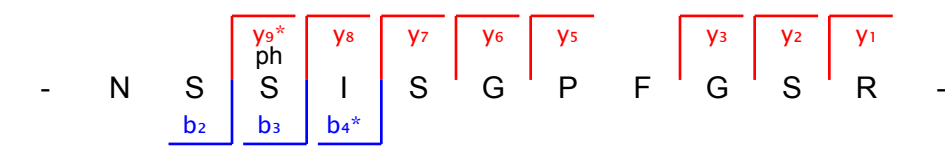
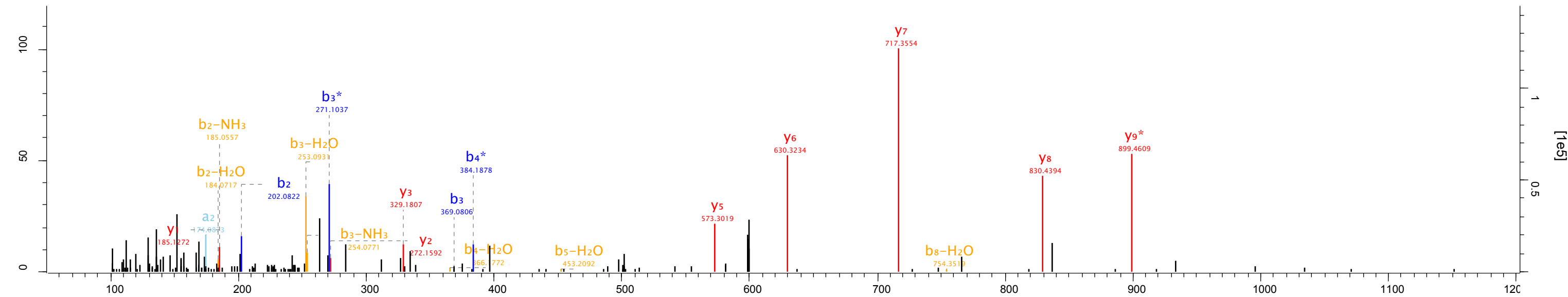
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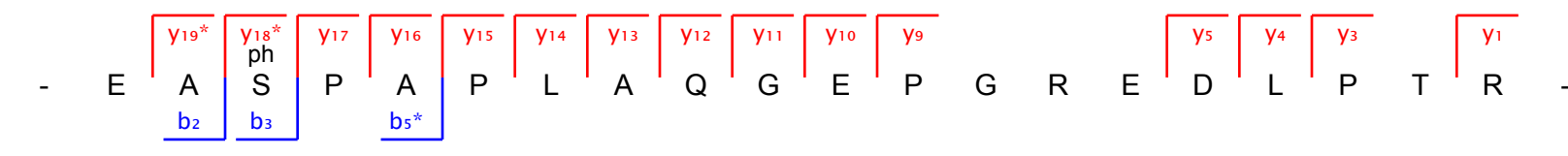
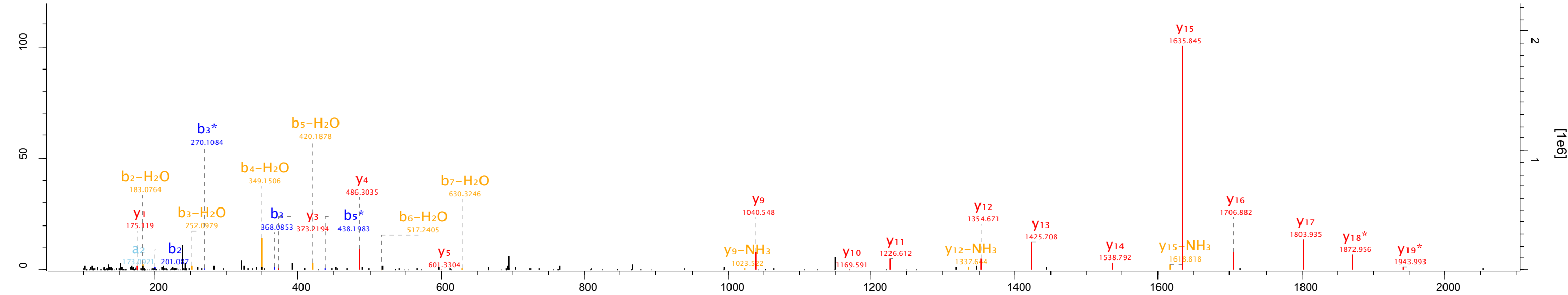
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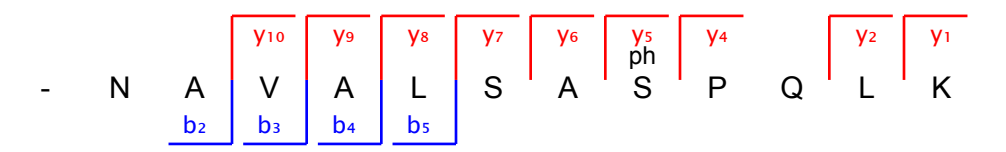
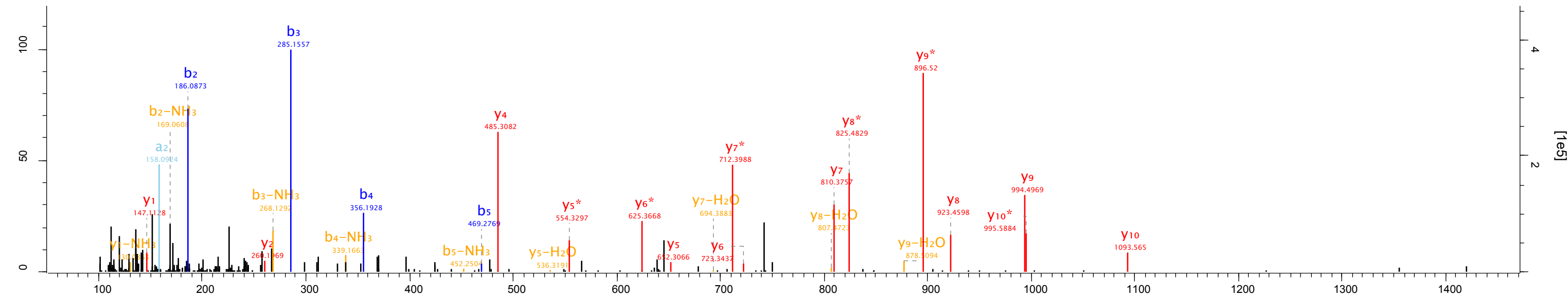
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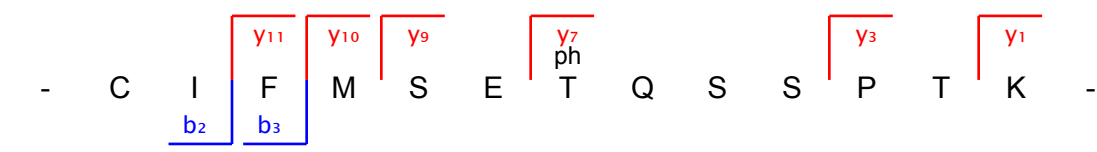
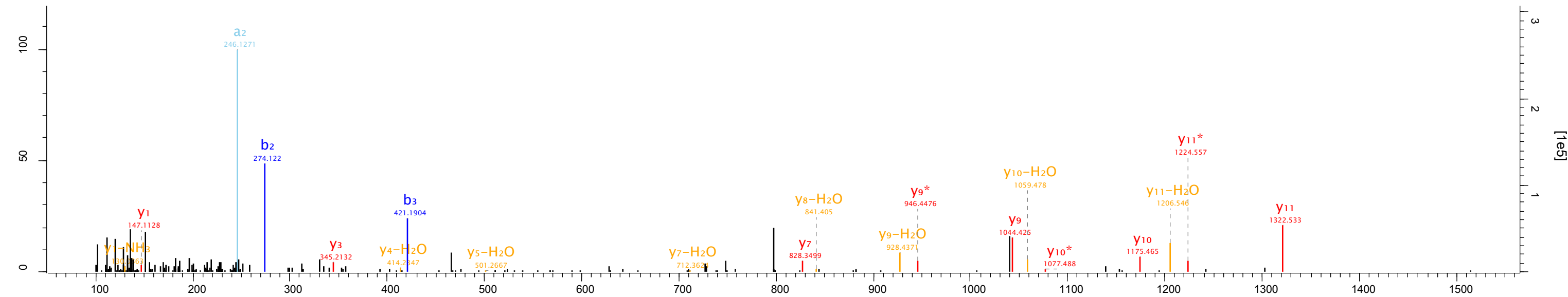


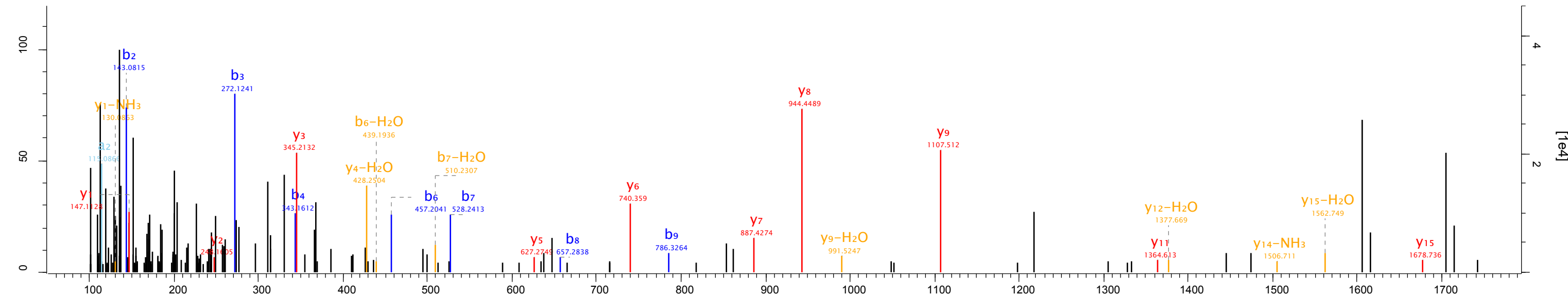
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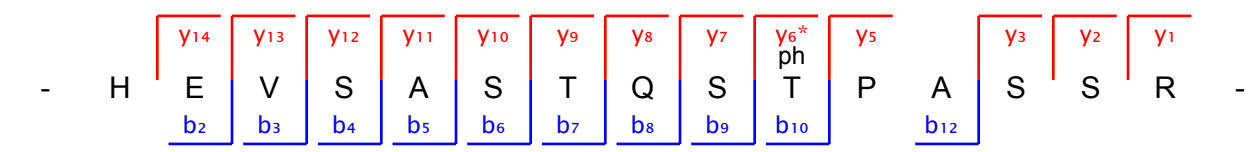
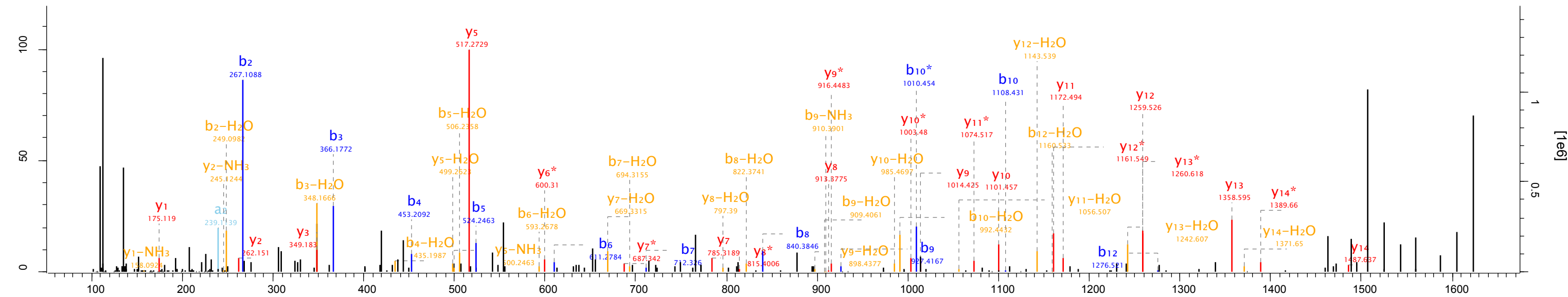




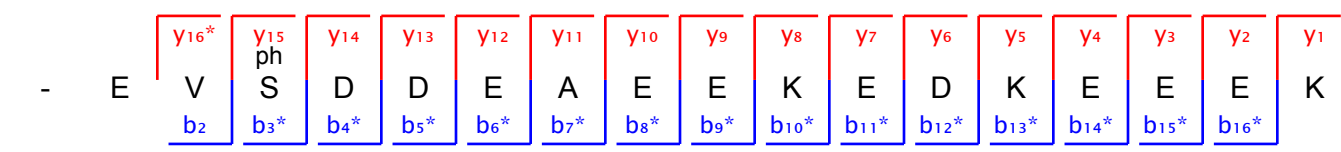
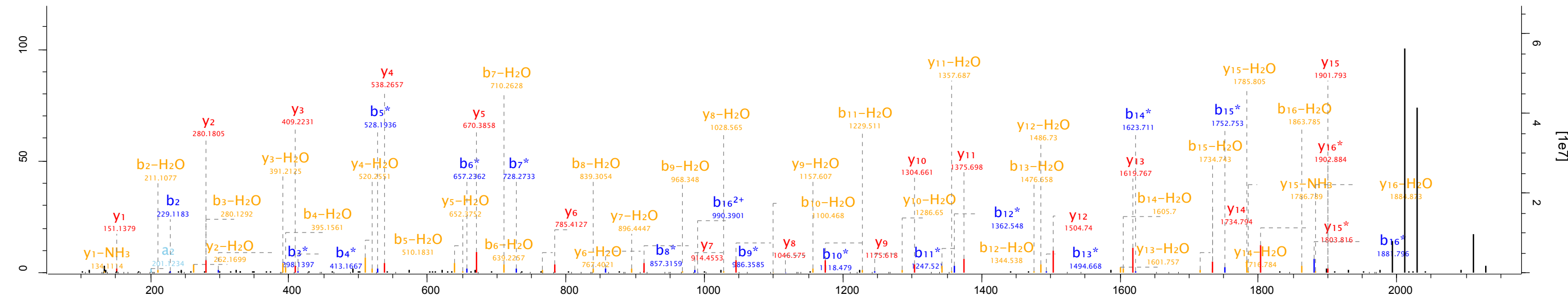
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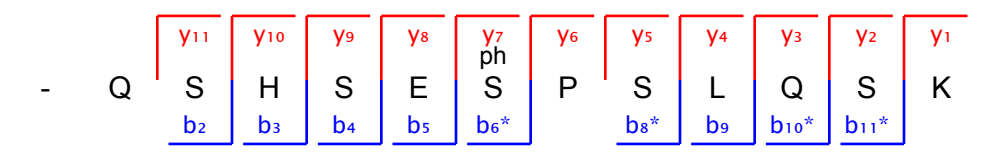
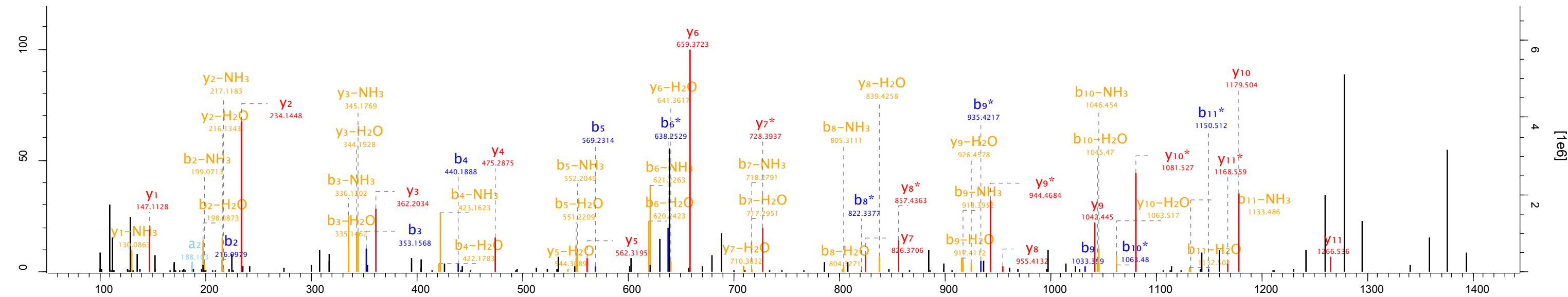
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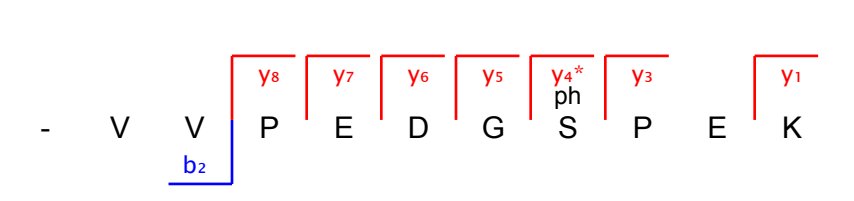
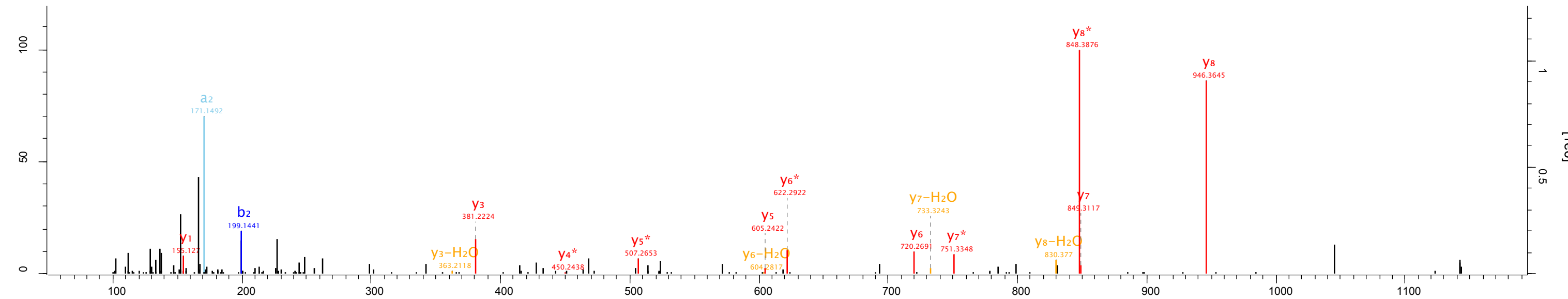
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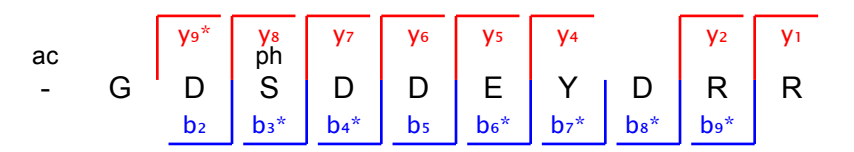
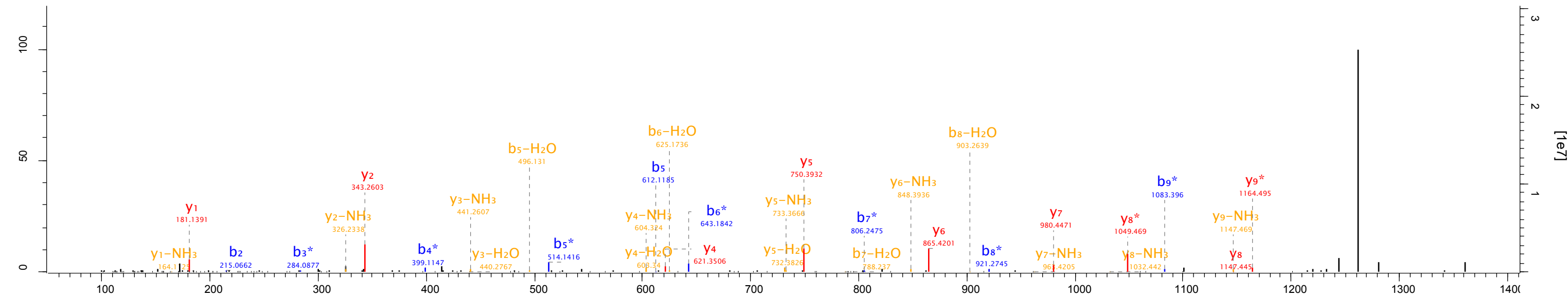
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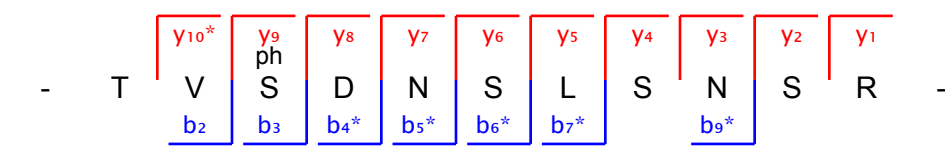
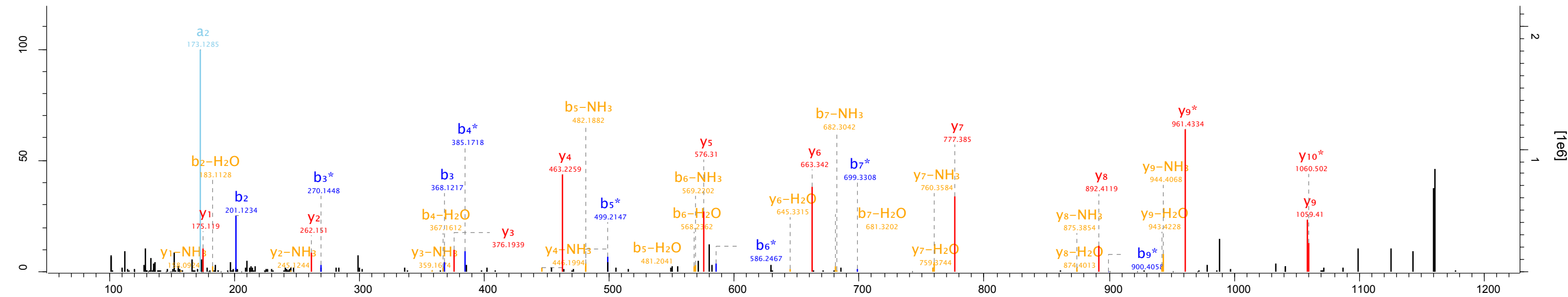
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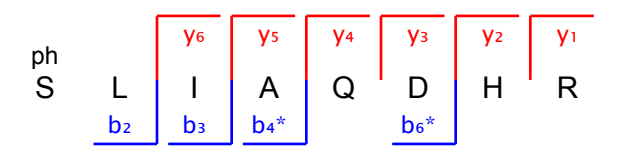
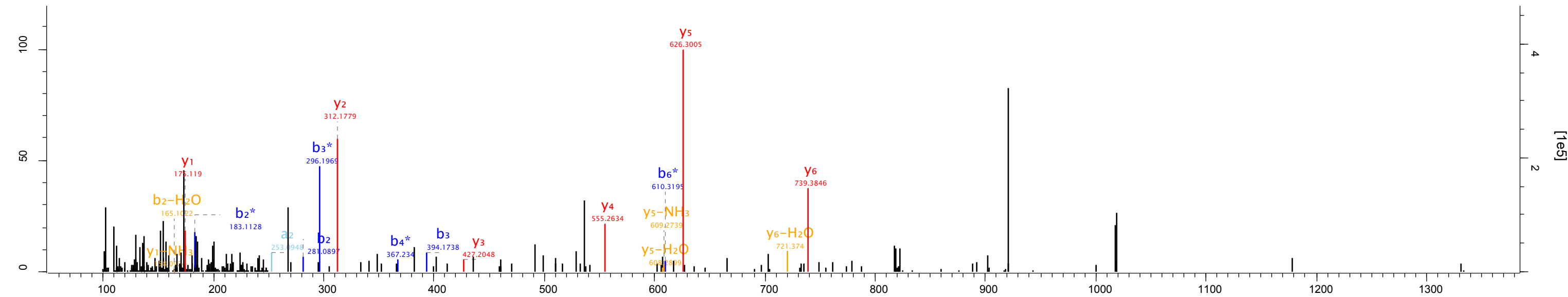
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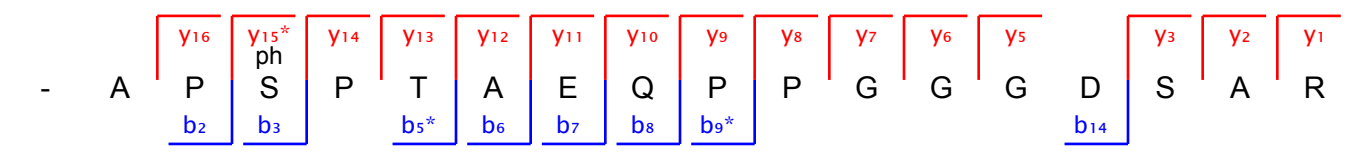
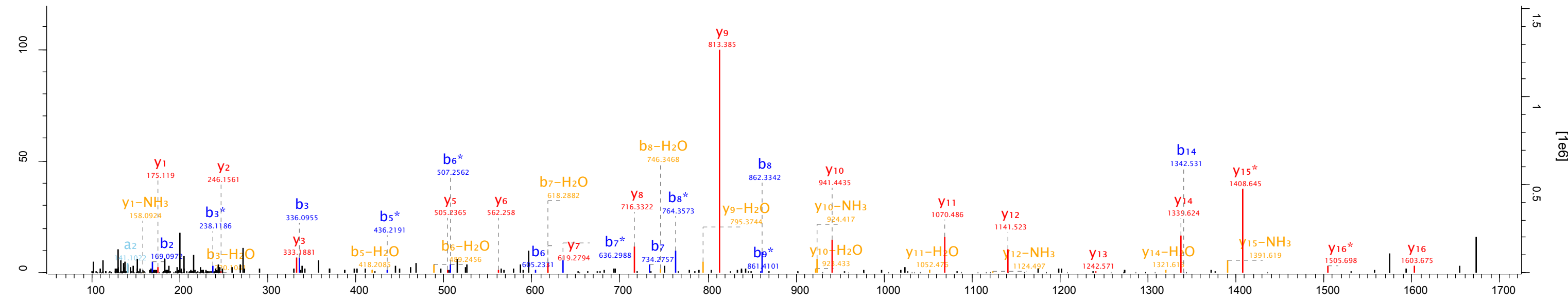
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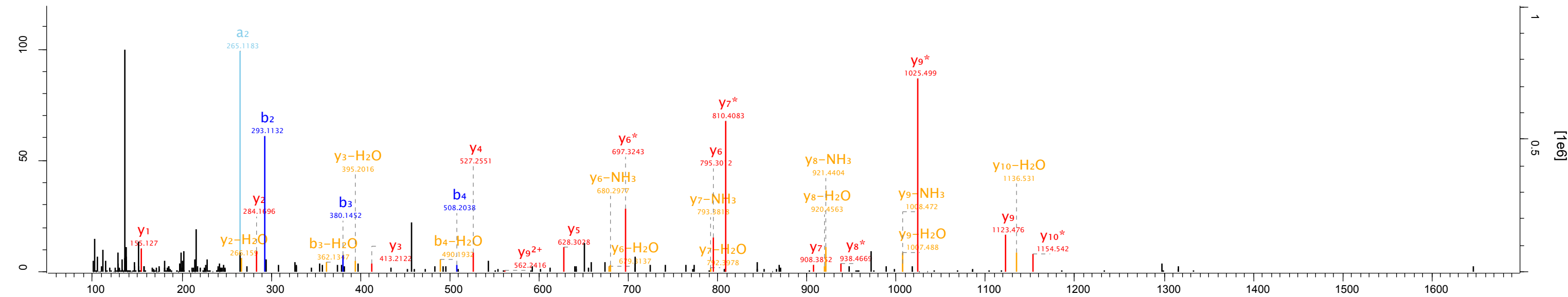
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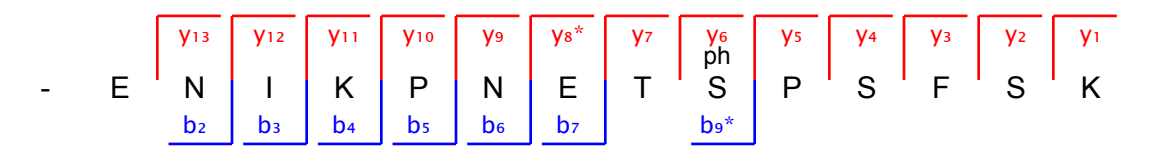
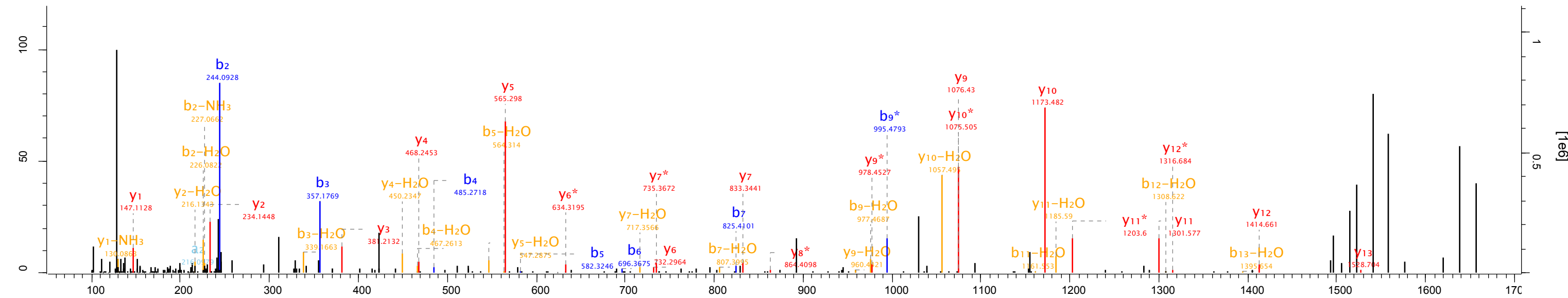


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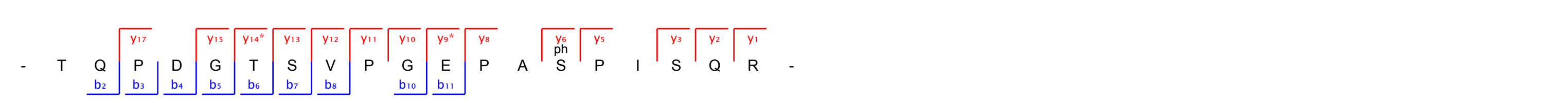
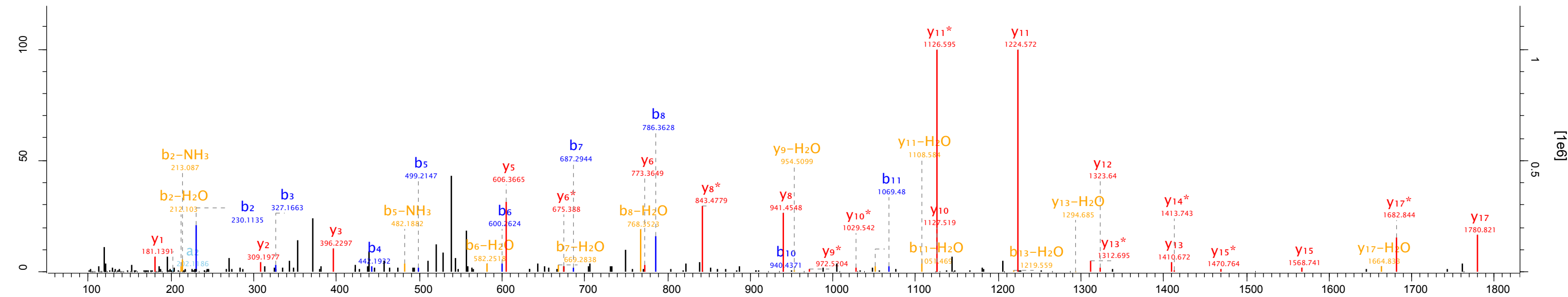


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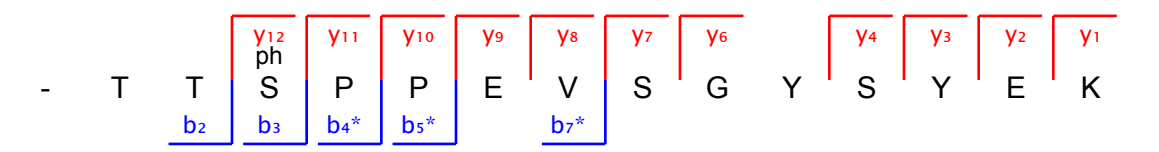
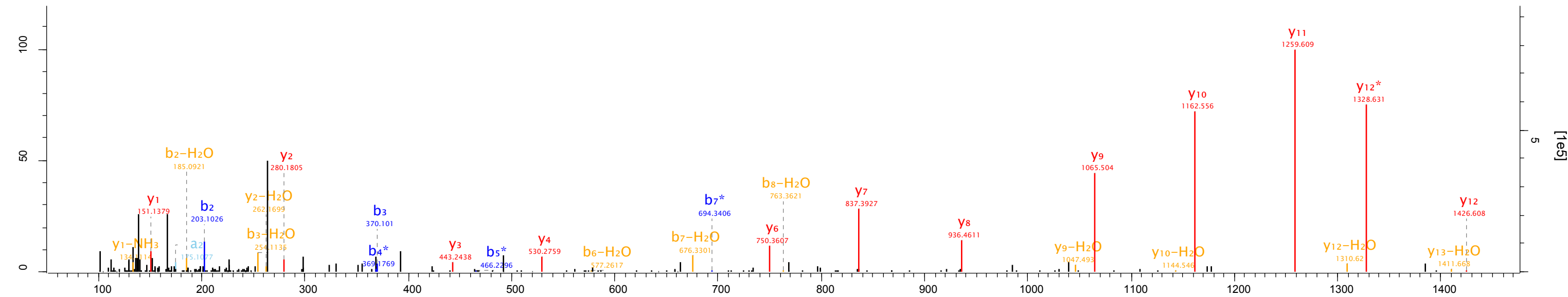
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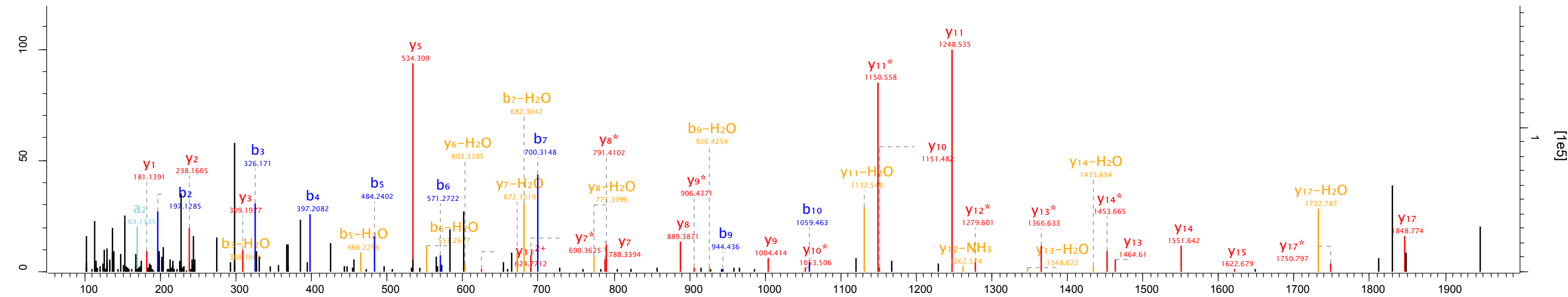
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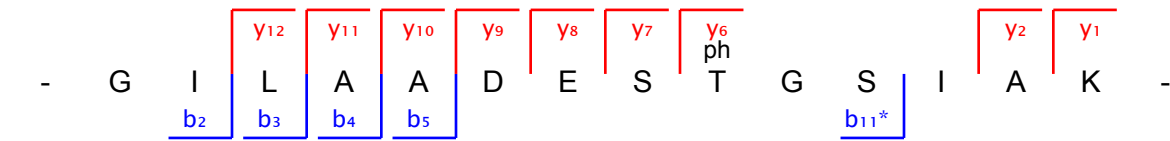
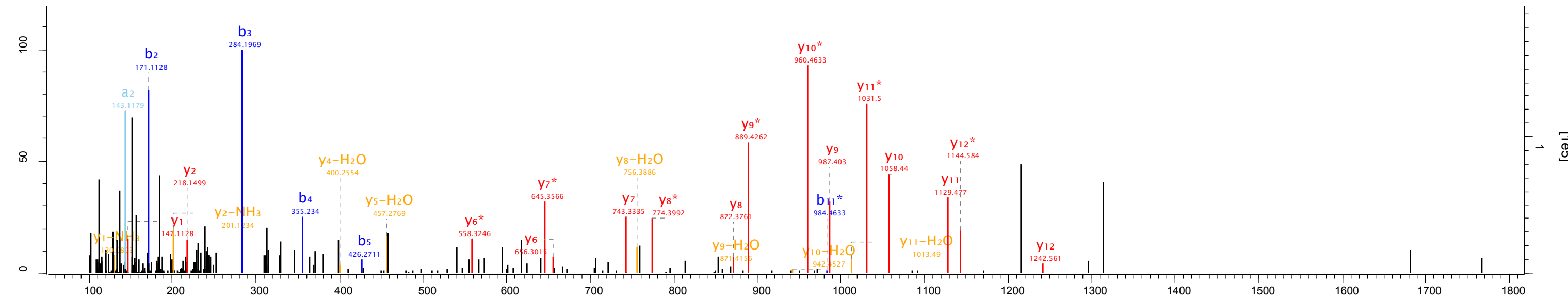


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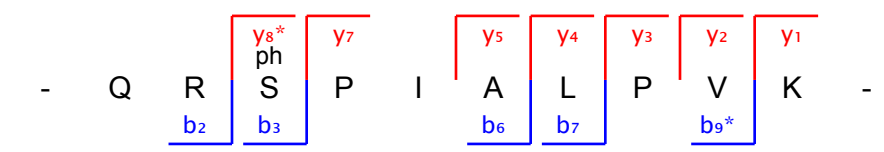
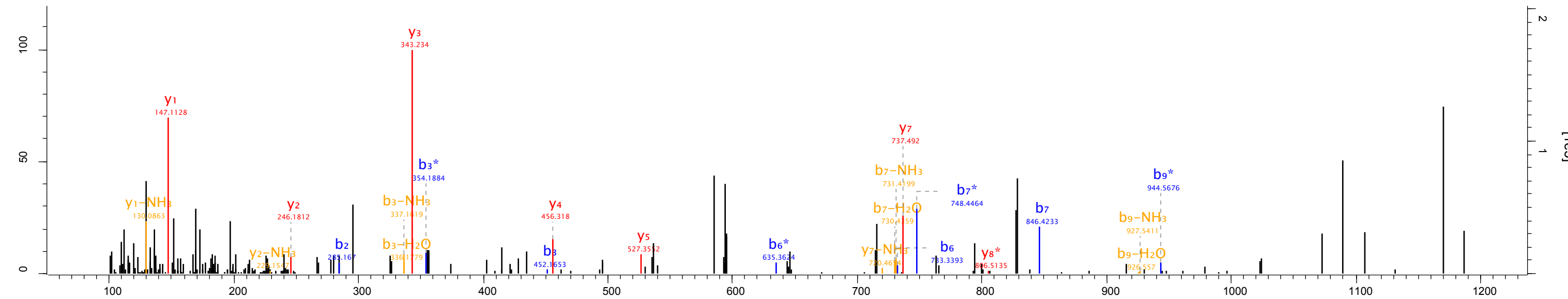


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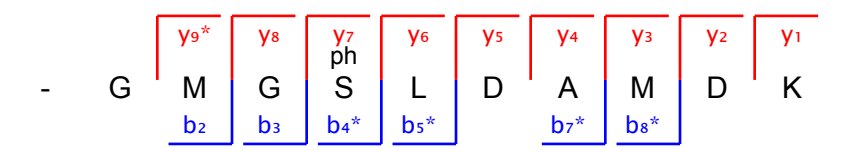
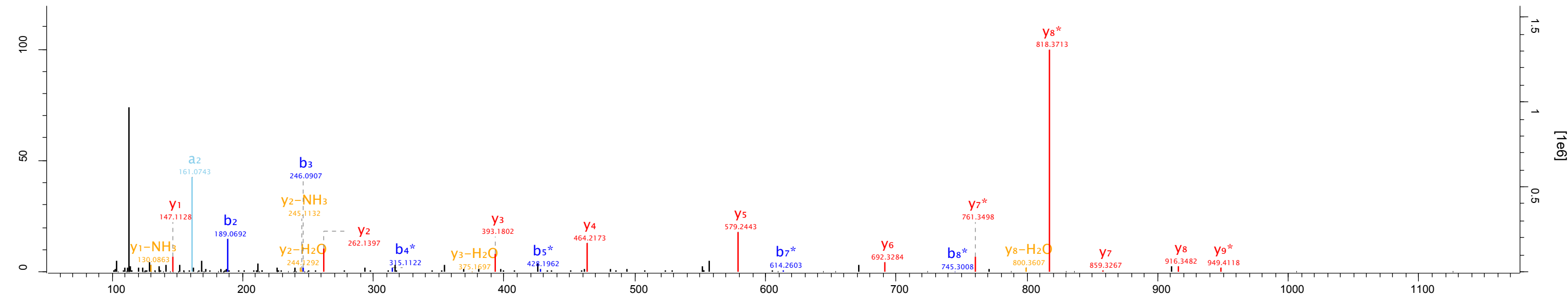




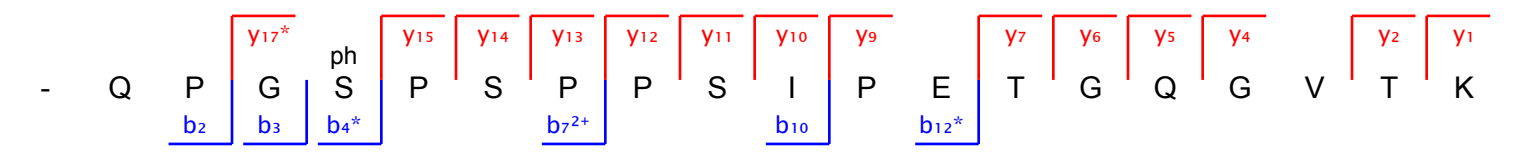
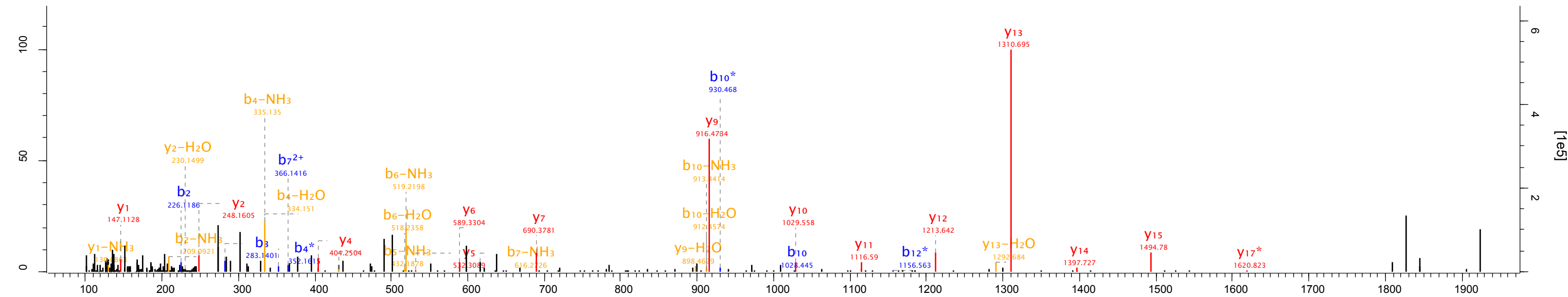
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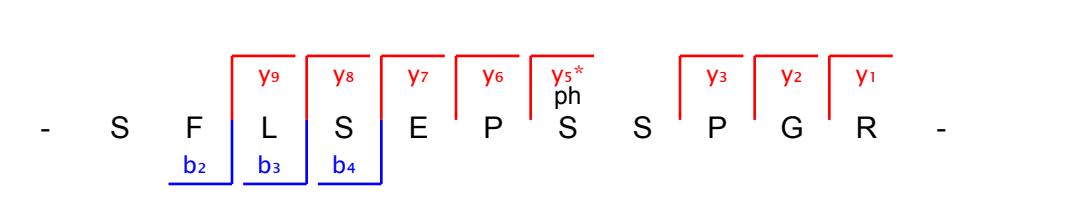
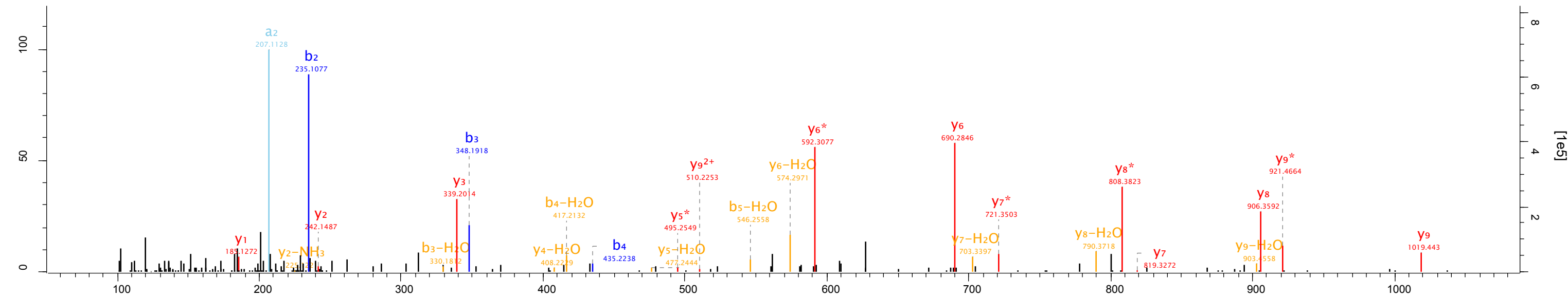
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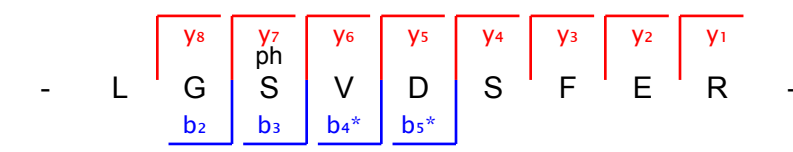
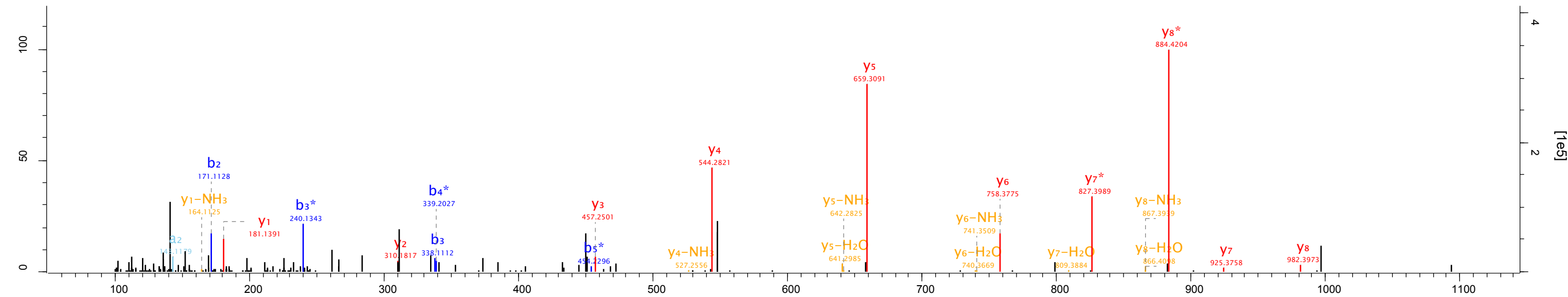
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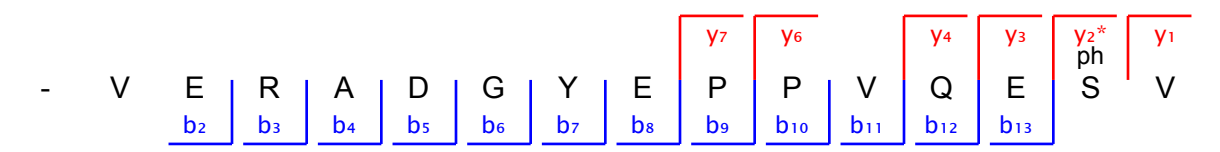
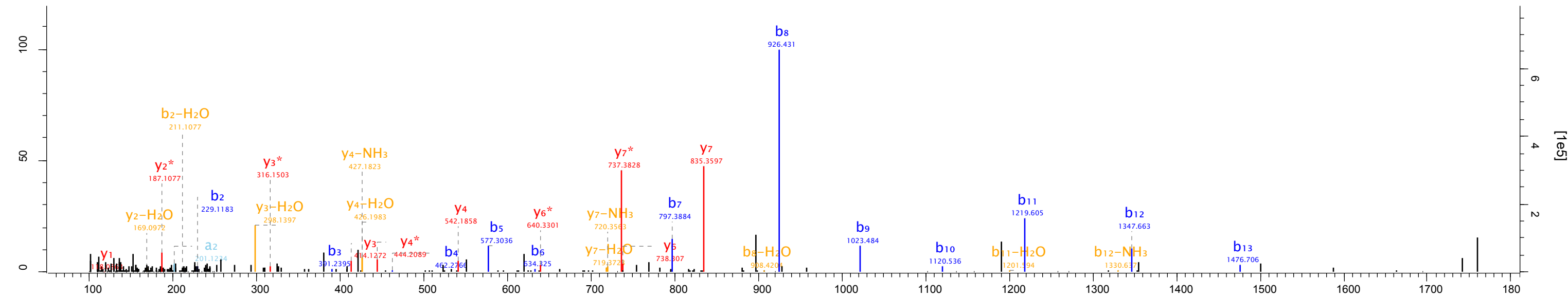
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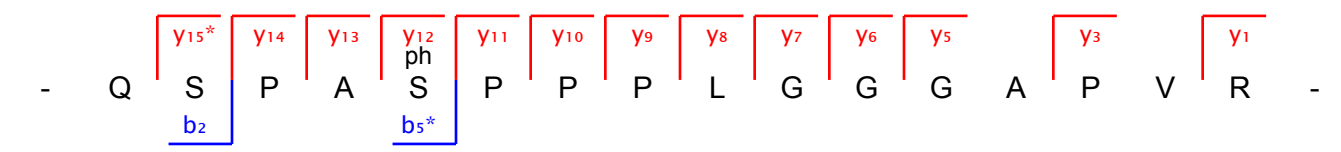
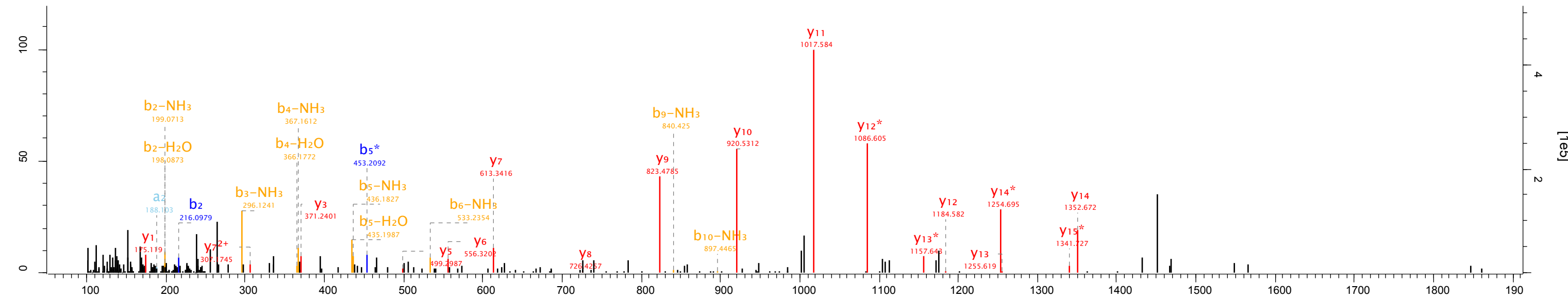
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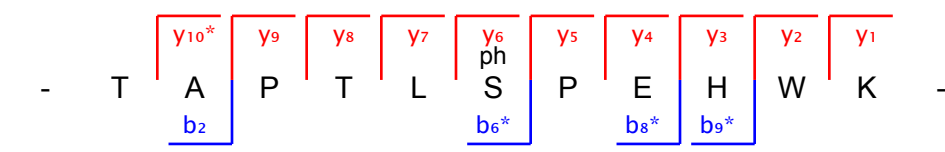
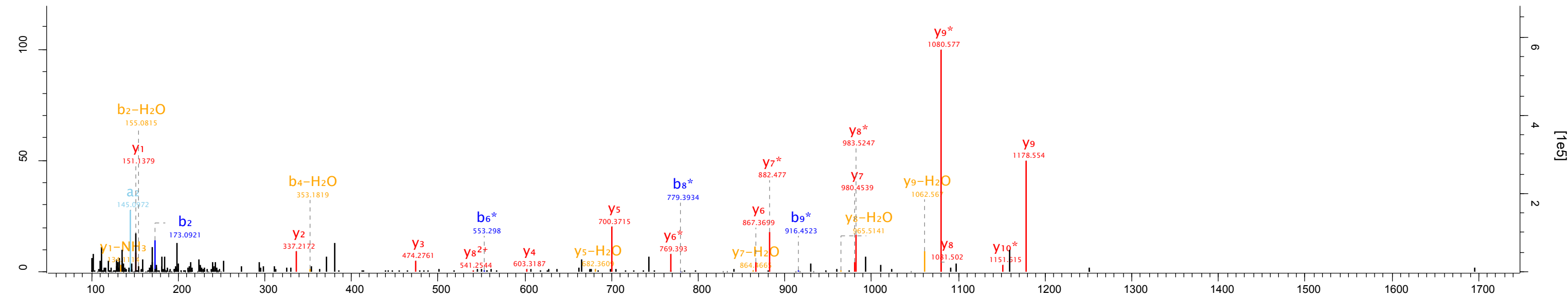
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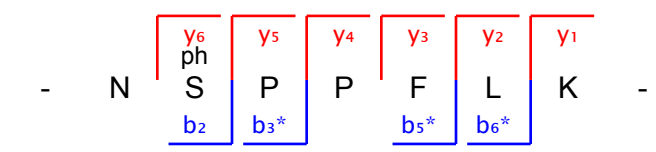
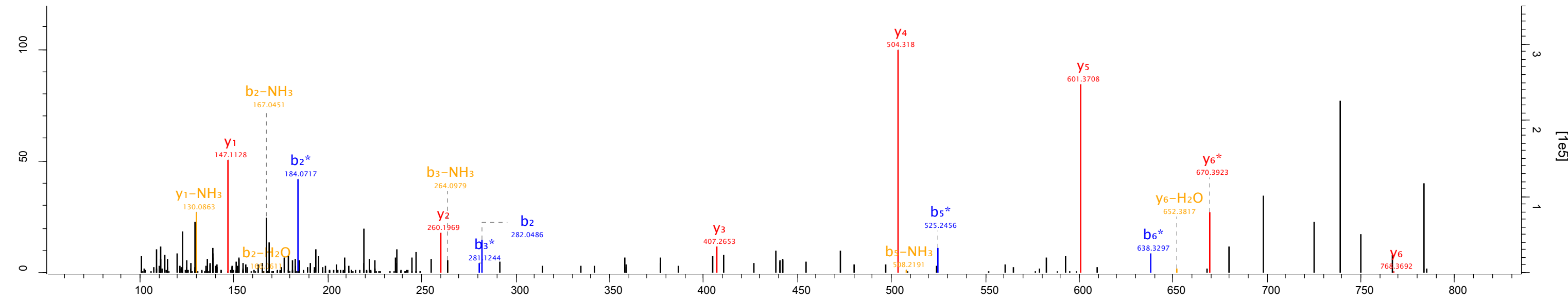
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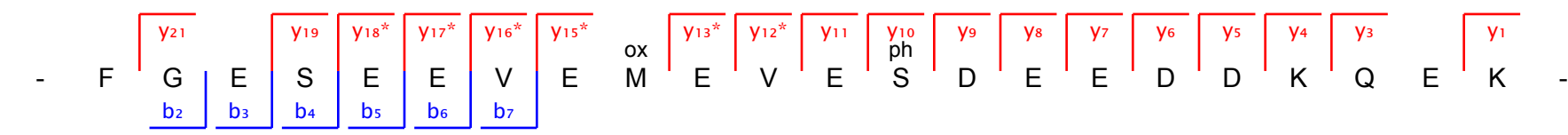
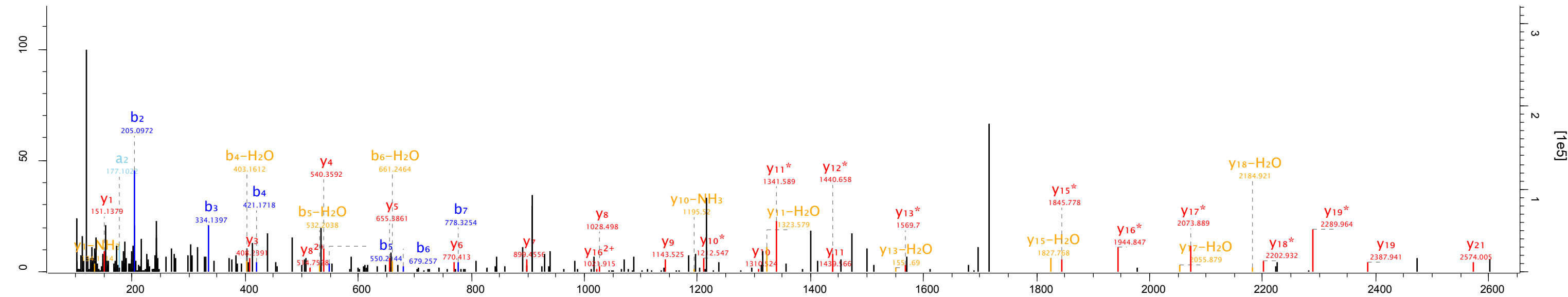
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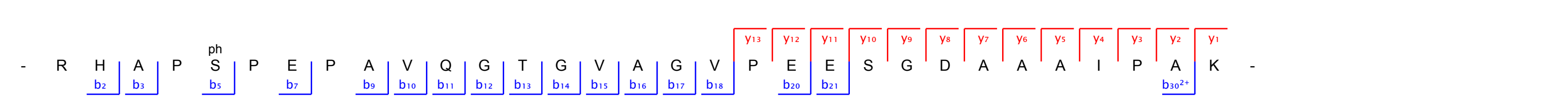
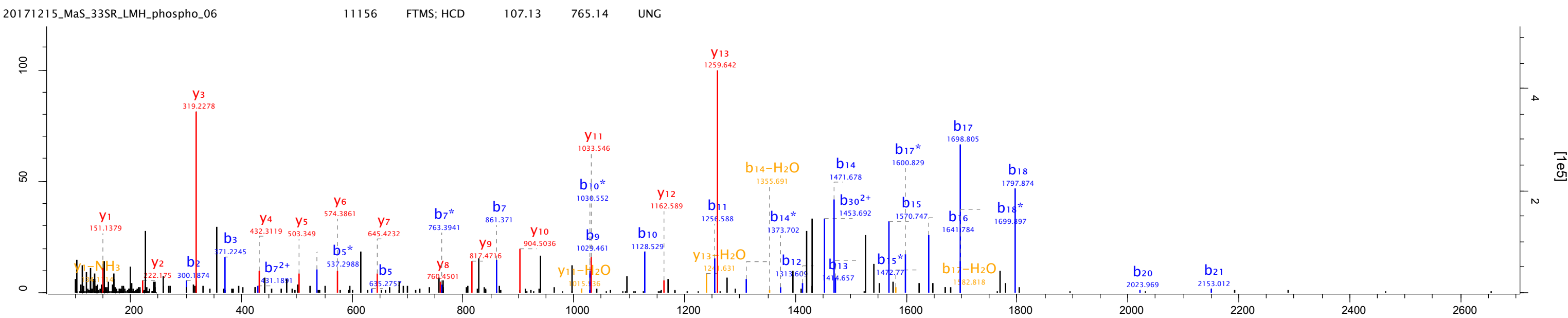
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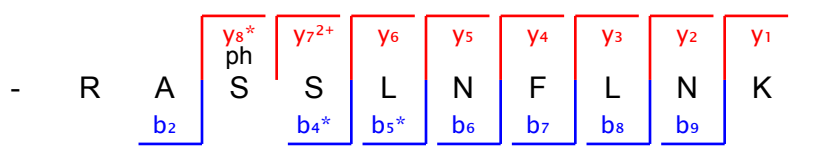
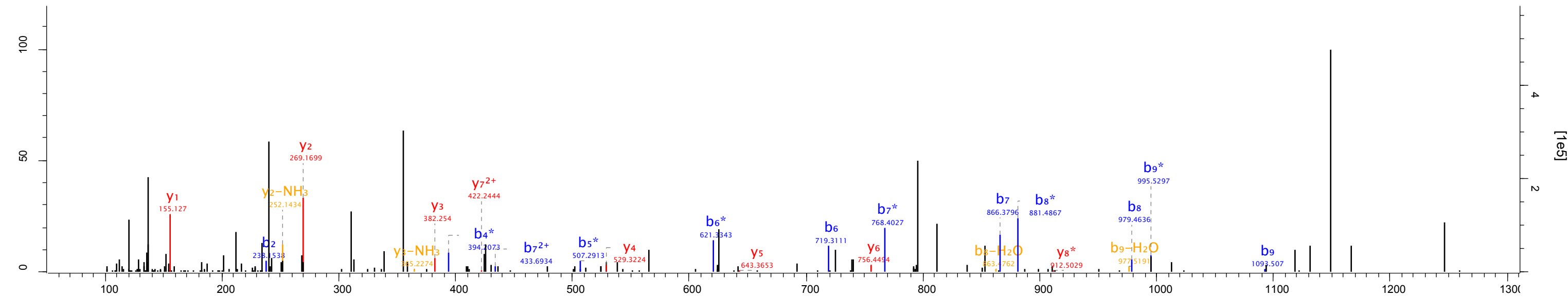
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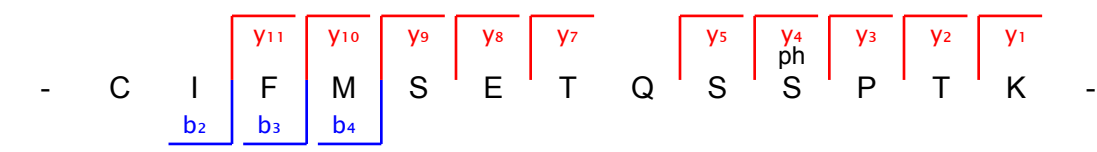
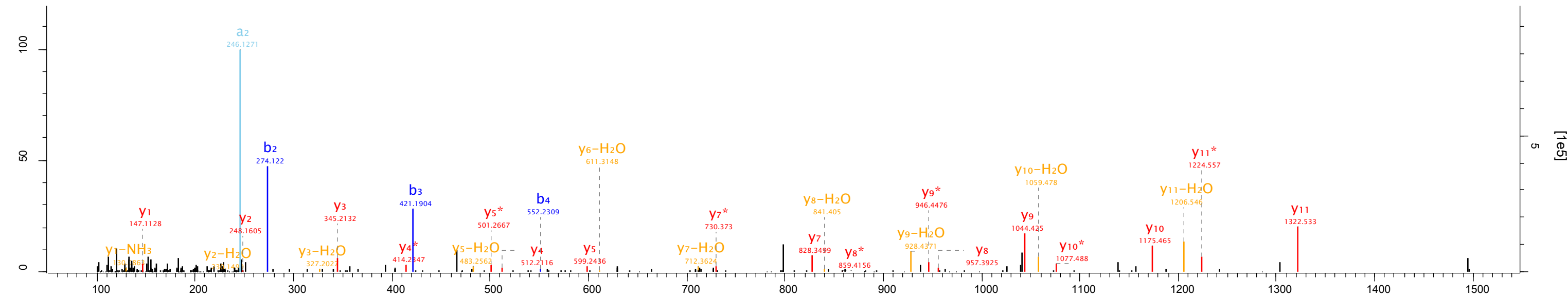
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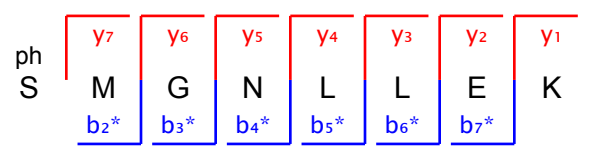
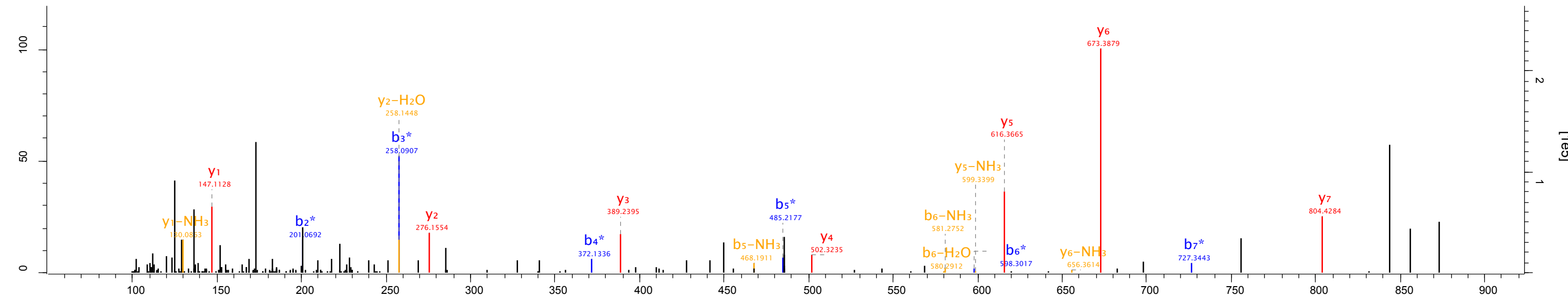
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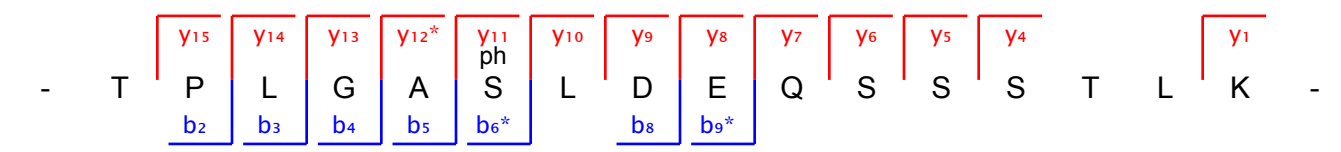
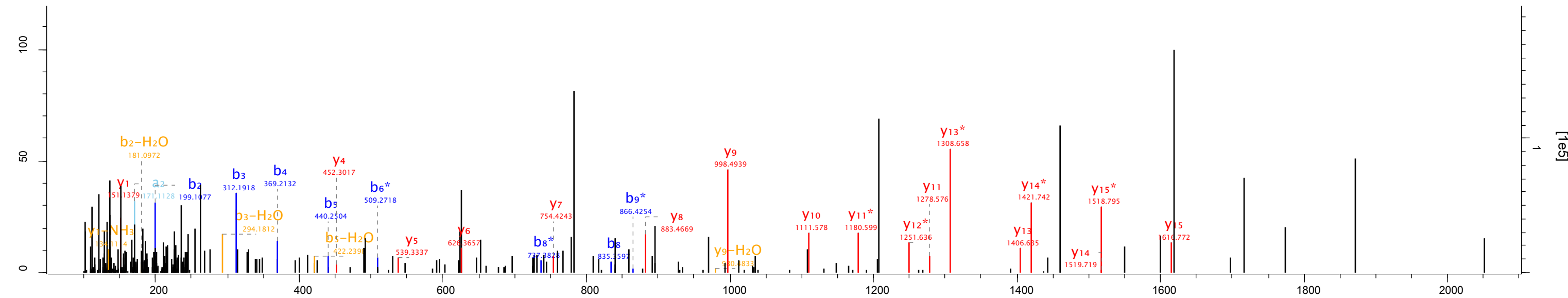
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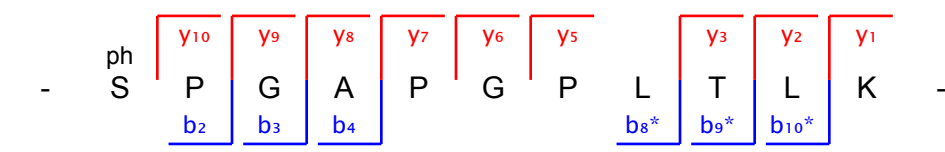
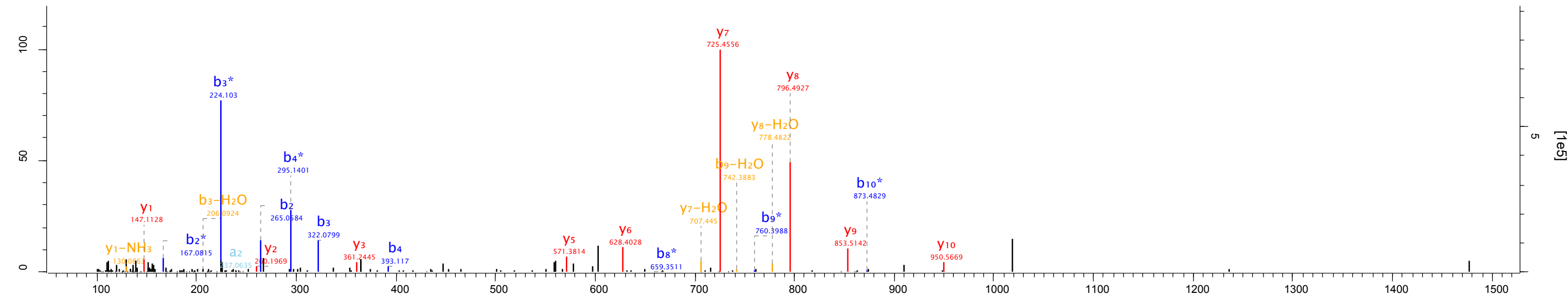
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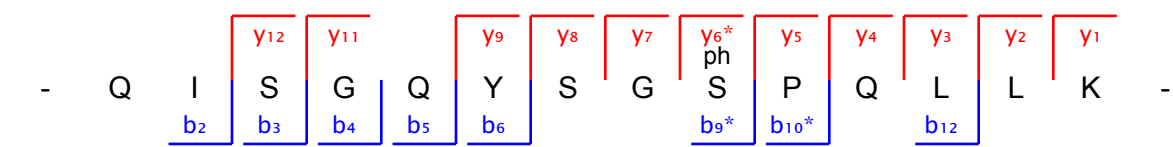
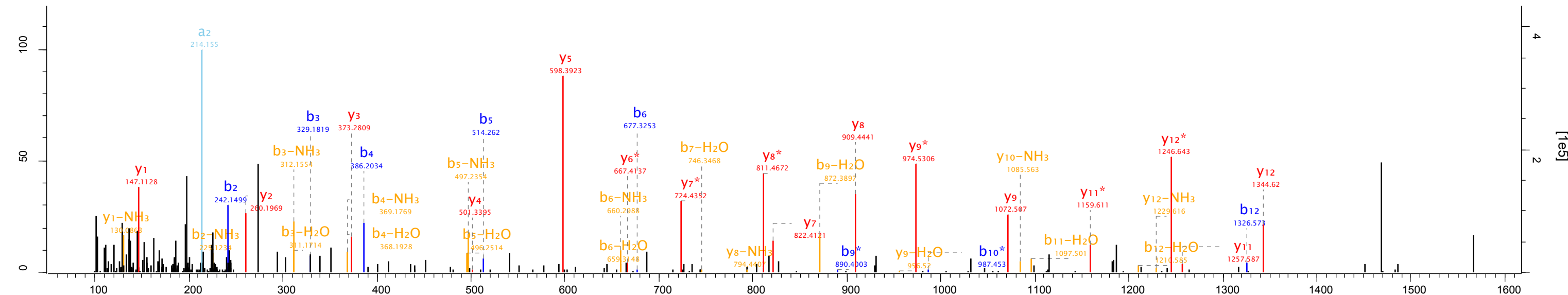


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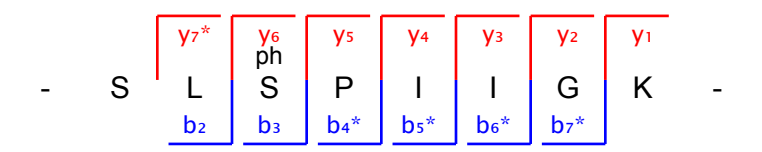
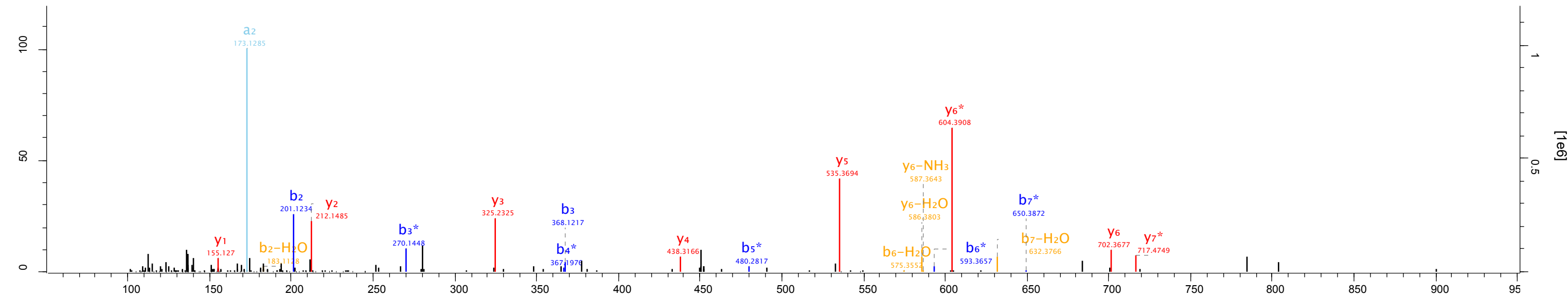


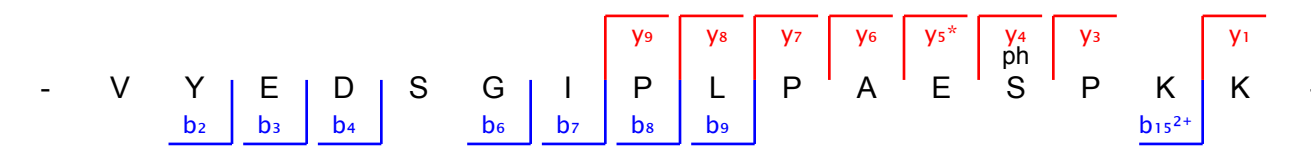
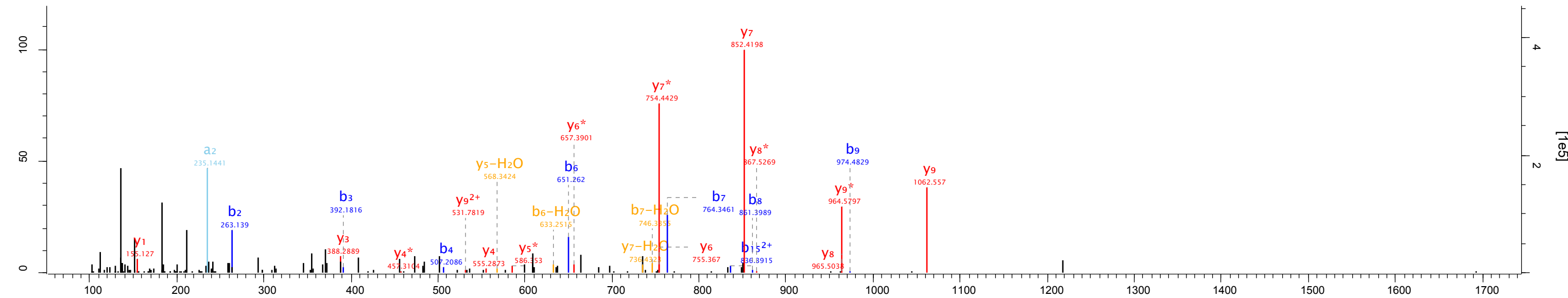
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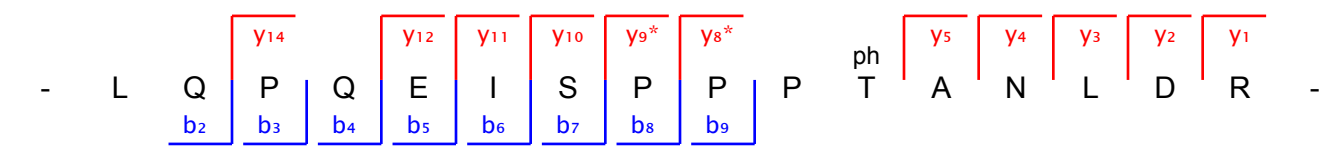
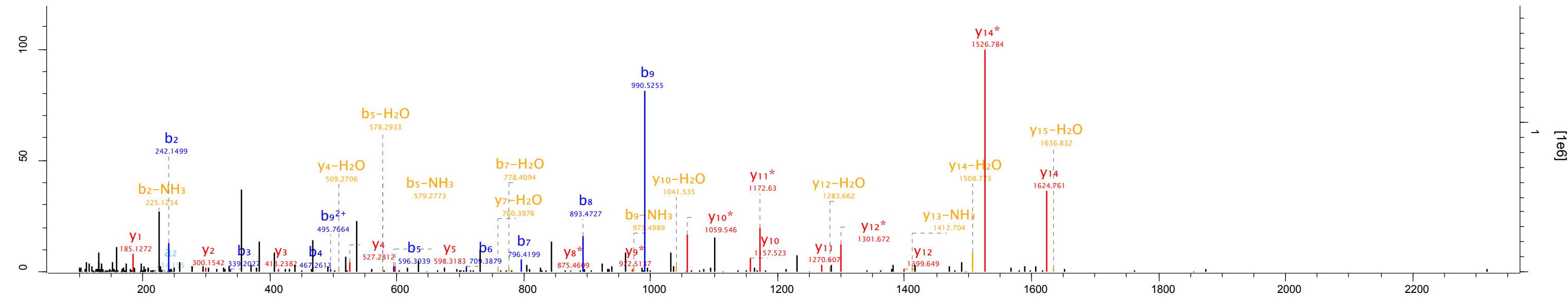


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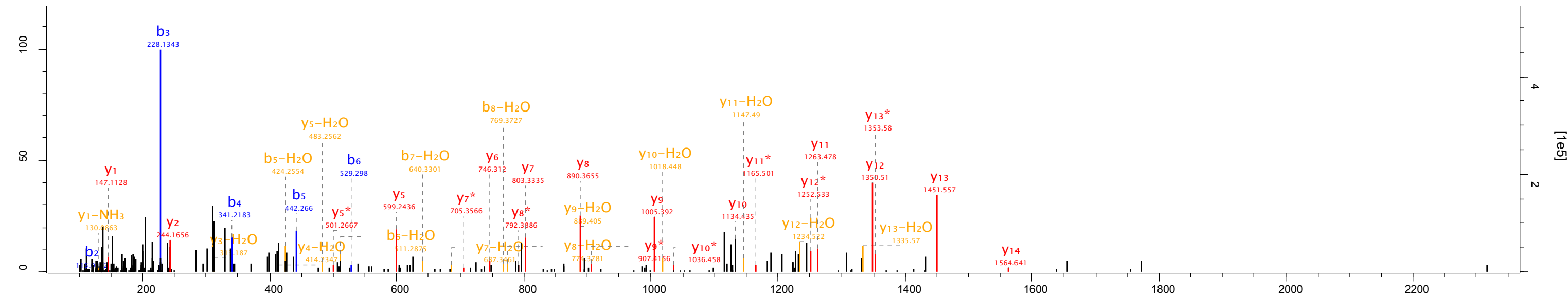




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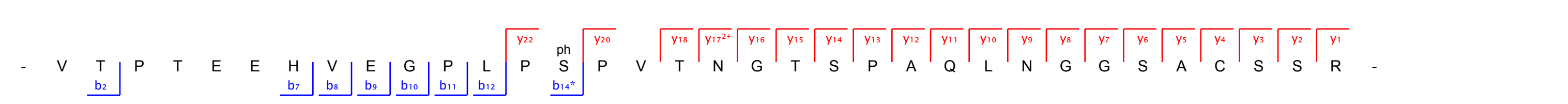
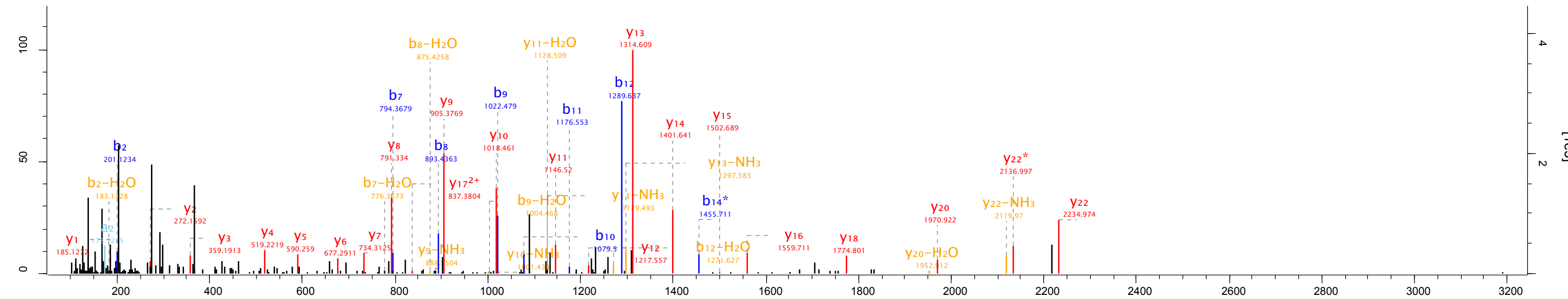


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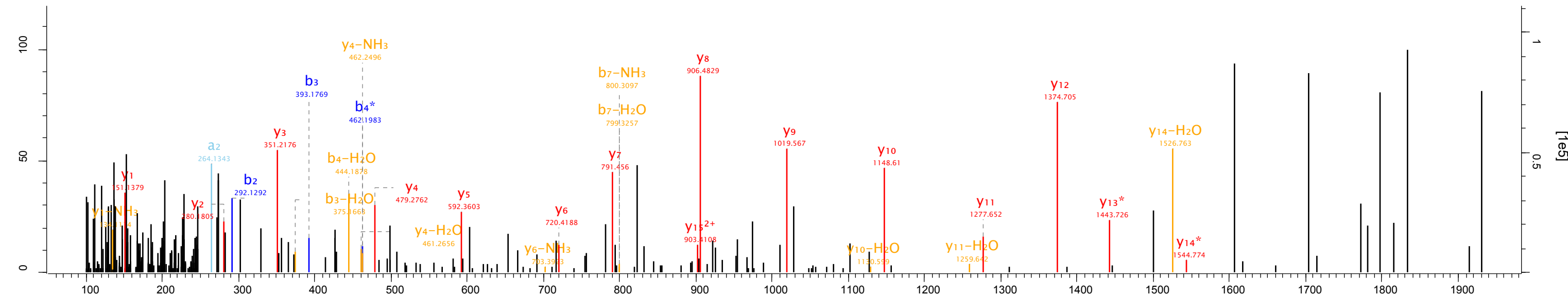


Sequence: - G G L L T S E E D S G F S T S P K -
 Fragmentation sites: b2 (G-G), b3 (G-L), b4 (L-L), b5 (L-T), b6 (L-S), y1 (S-K), y2 (P-K), y5 (S-ph), y6 (F-S), y7 (G-F), y8 (S-G), y9 (D-S), y10 (E-S), y11 (E-E), y12 (S-E), y13 (T-L), y14 (L-L)

Raw file
 20171215_MaS_33SR_LMH_phospho_06
 Scan 13436 Method FTMS; HCD Score 85.04 m/z 1176.21 Gene names SLC9A3R2



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 13516 Method FTMS; HCD Score 86.57 m/z 967.45 Gene names PDAP1

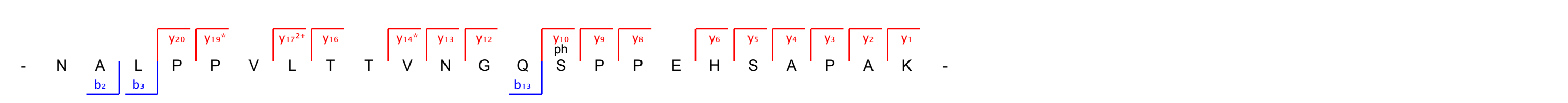
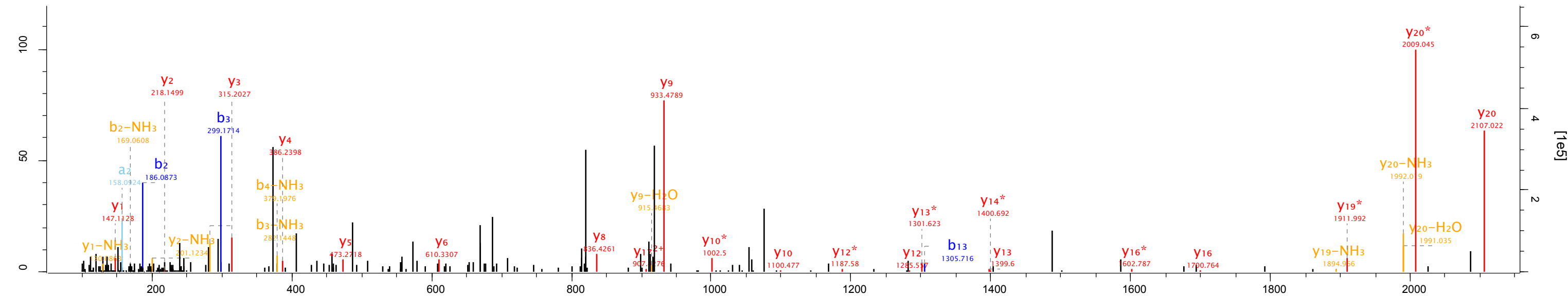


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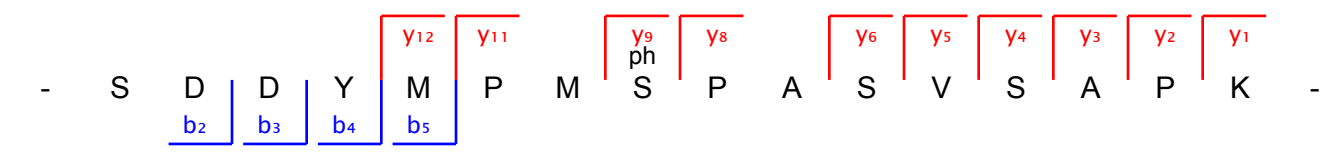
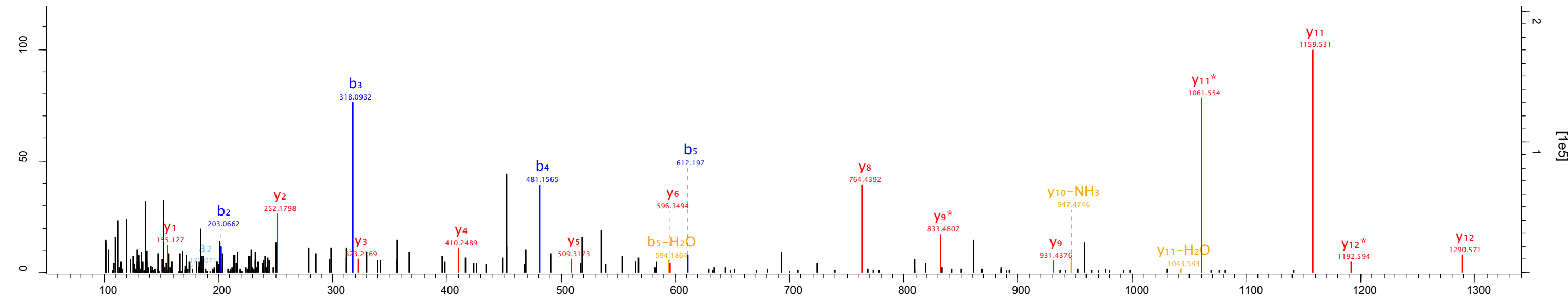
Fragmentation mapping:

- Y15²⁺ (b₂)
- Y14* (b₃)
- Y13* (b₄*)
- Y12
- Y11
- Y10
- Y9
- Y8
- Y7
- Y6
- Y5
- Y4
- Y3
- Y2
- Y1

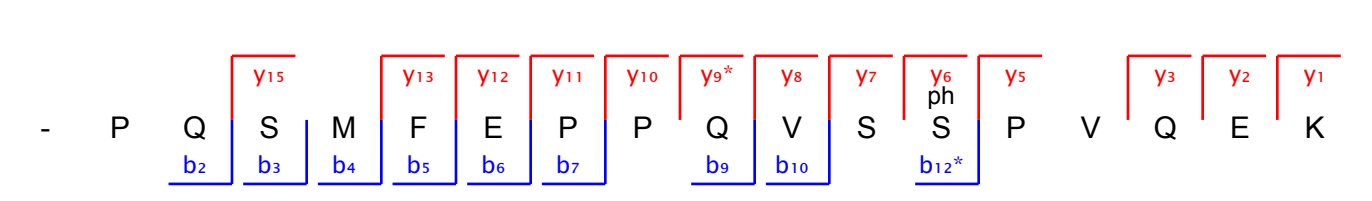
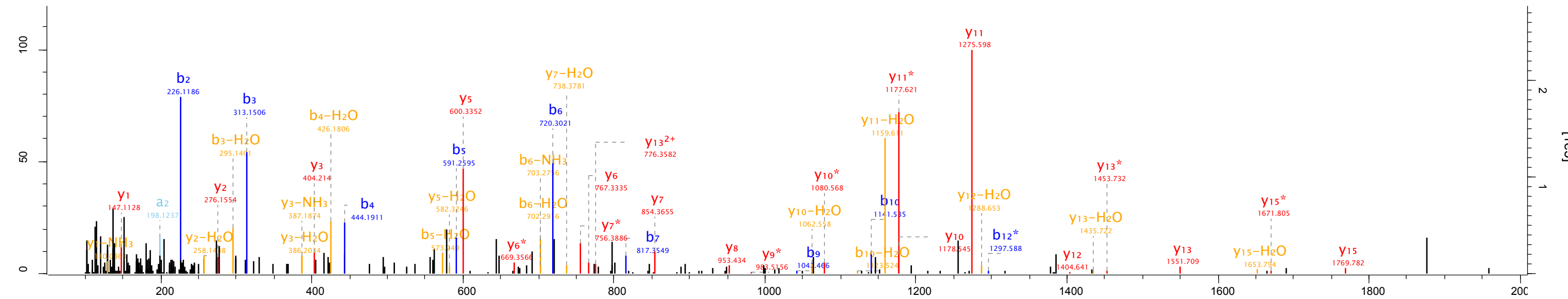
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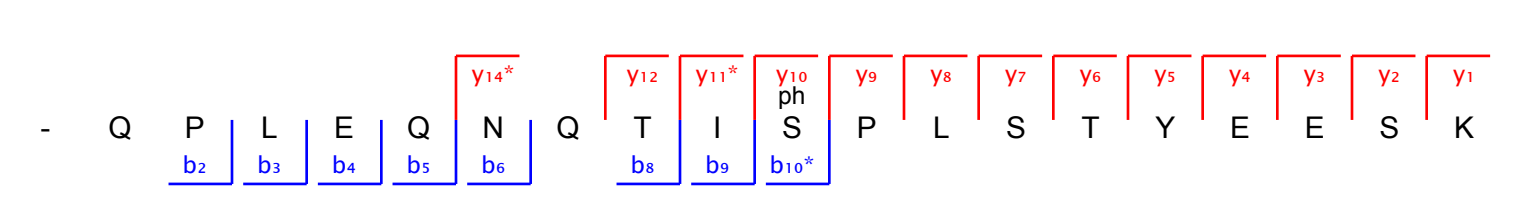
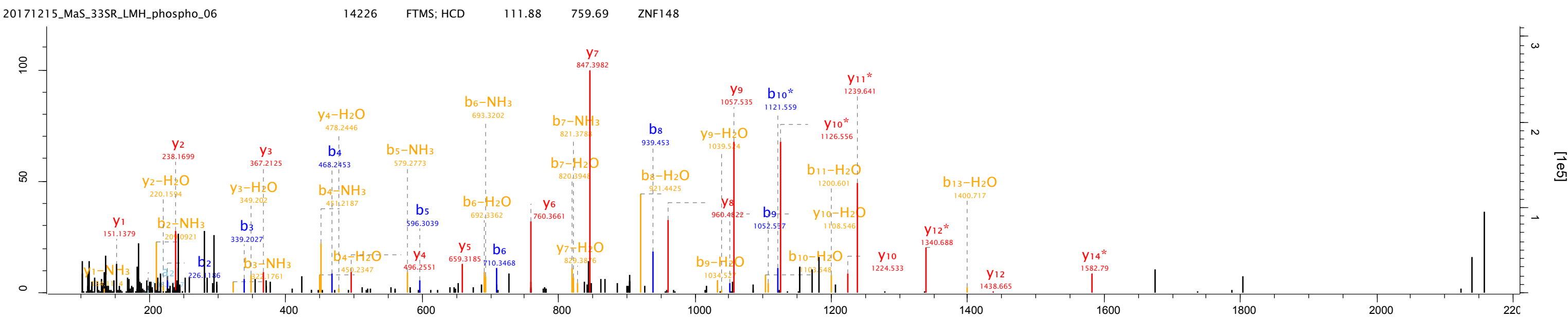
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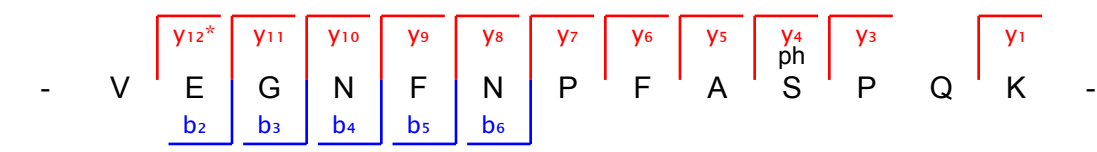
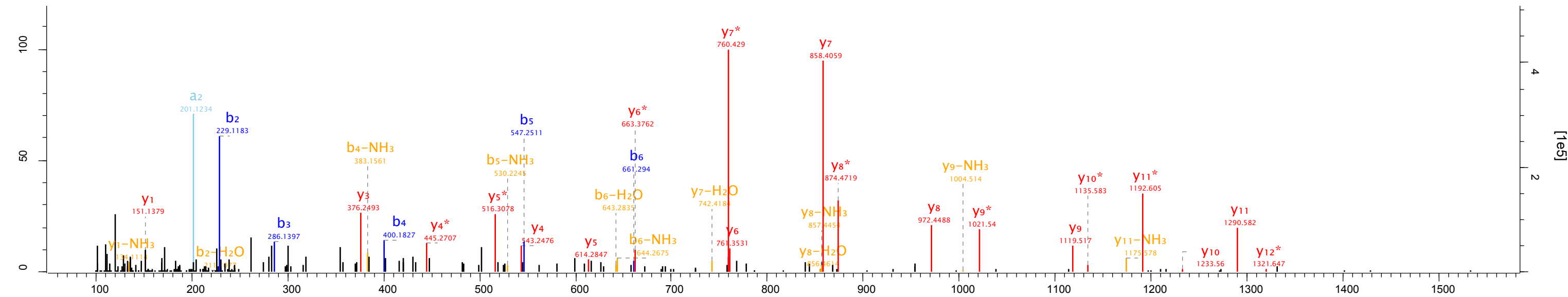
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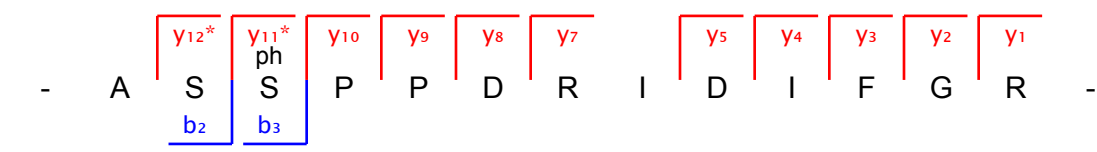
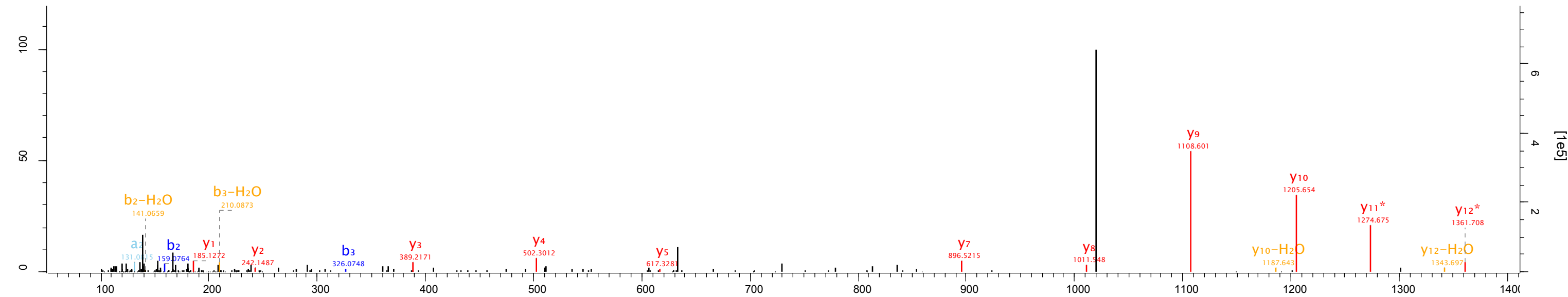
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20171215_MaS_33SR_LMH_phospho_06

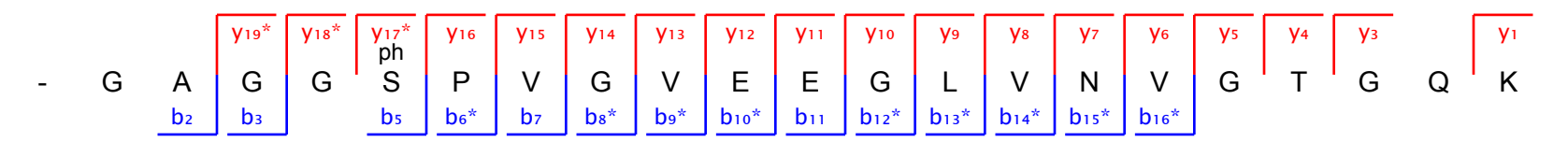
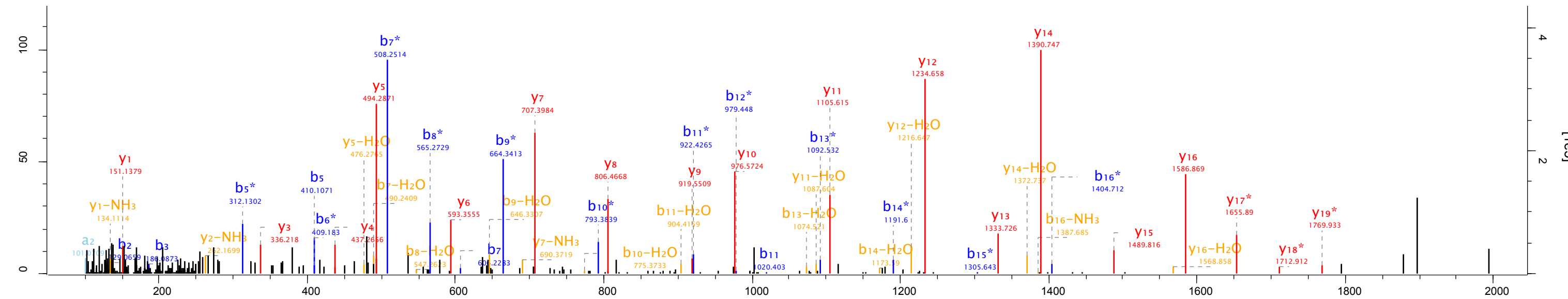
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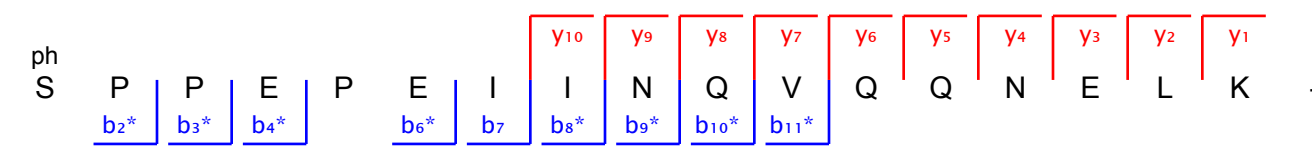
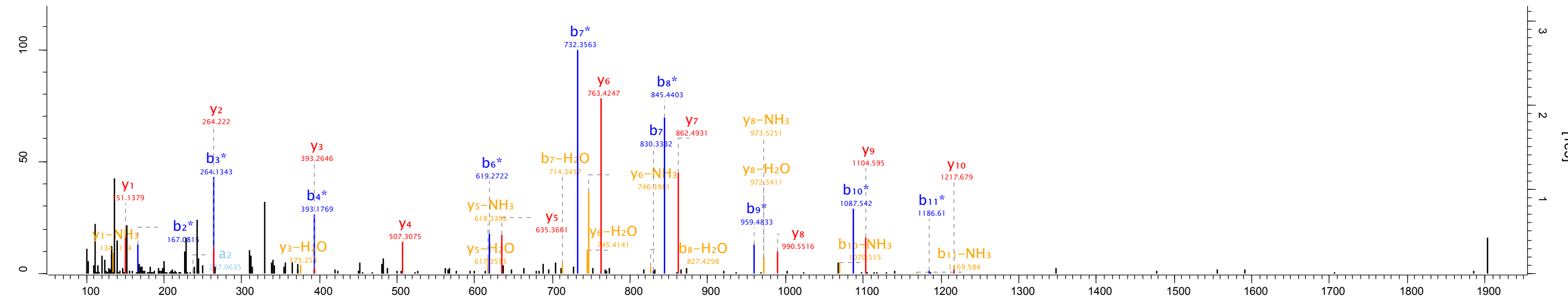
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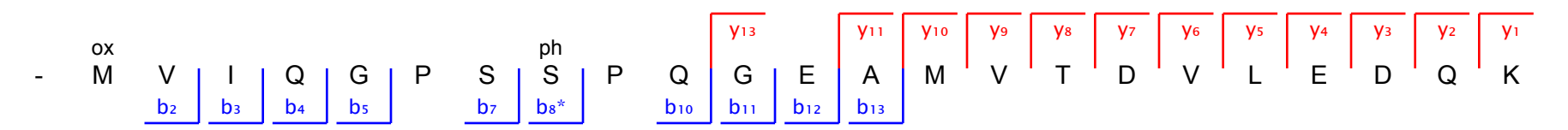
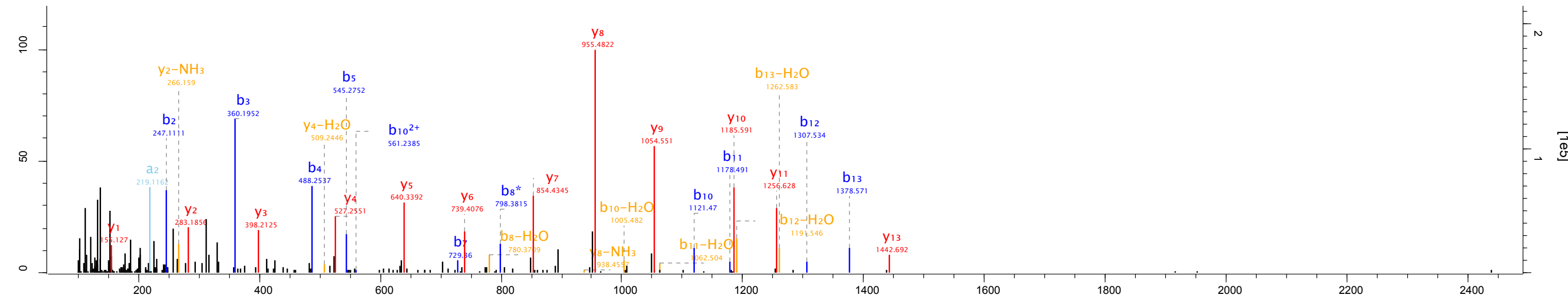
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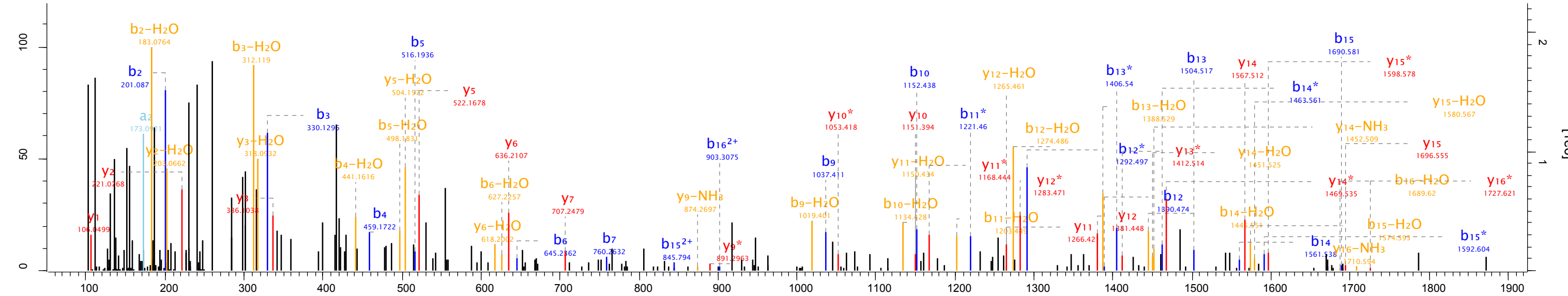


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Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho_06 2236 FTMS; HCD 280.93 1013.34 HNRNPC

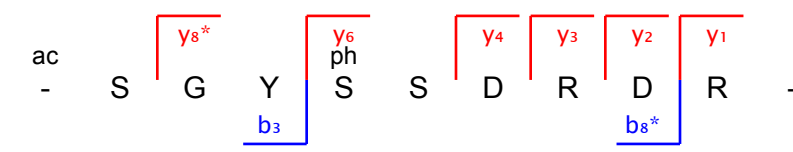
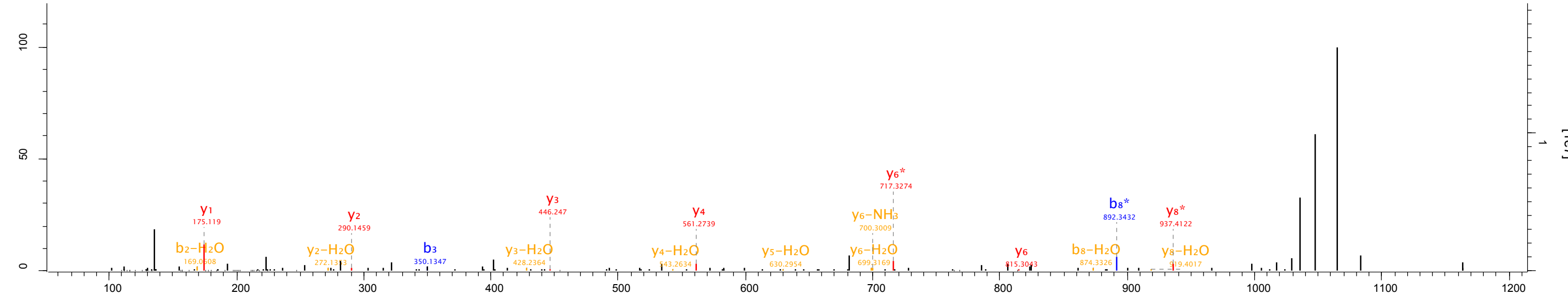


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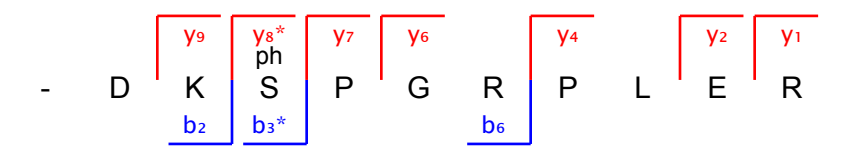
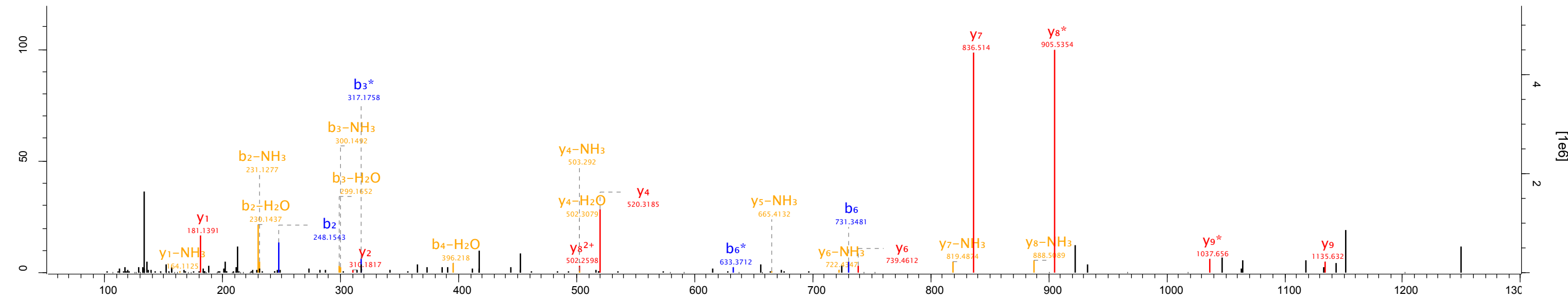
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Raw file Scan Method Score m/z Gene names

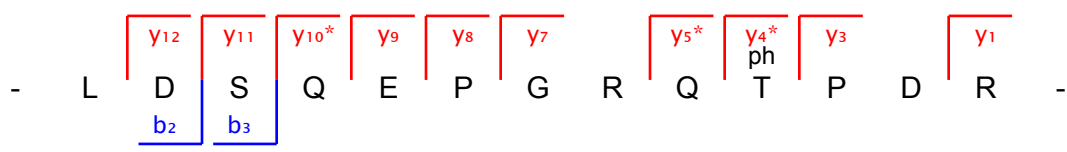
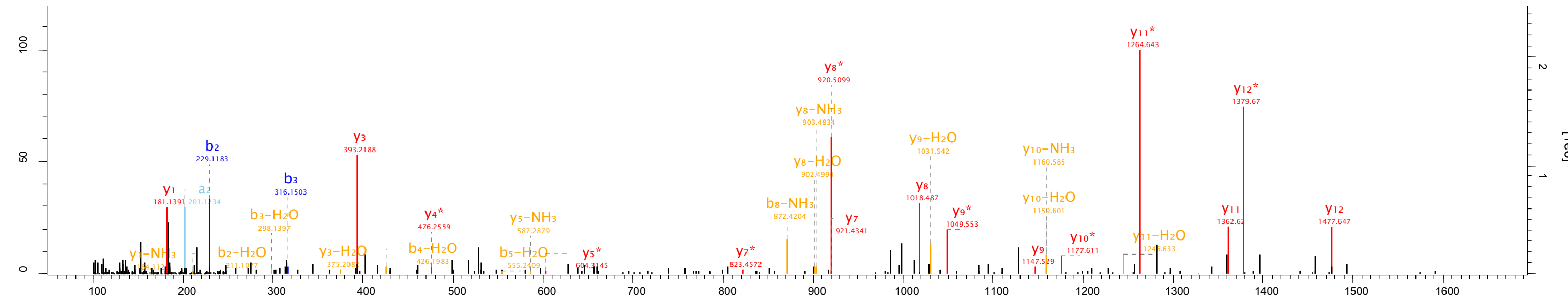
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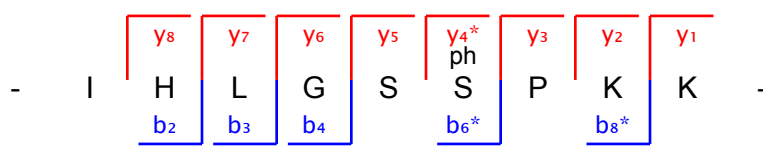
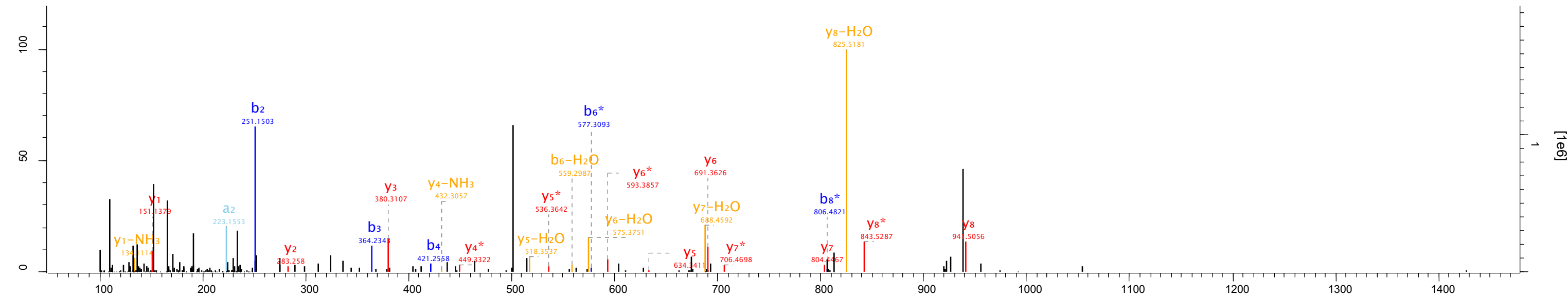
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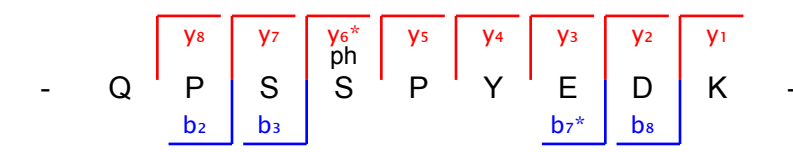
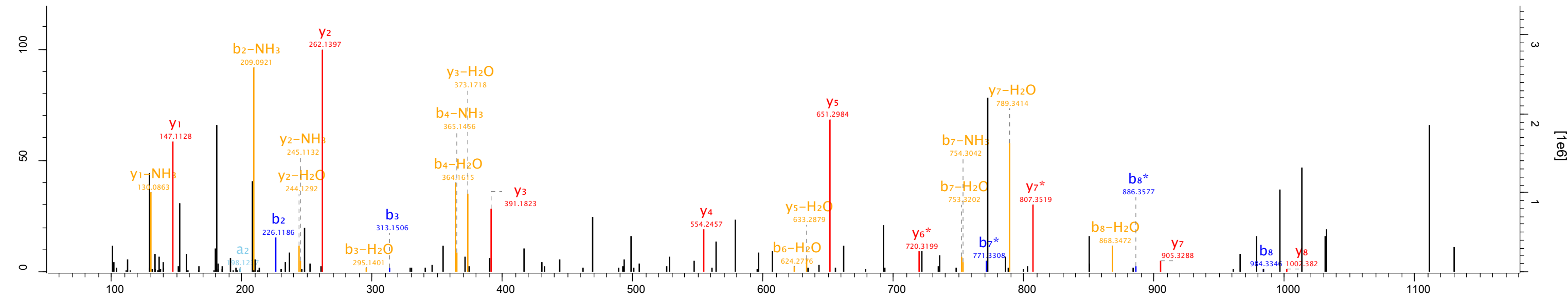
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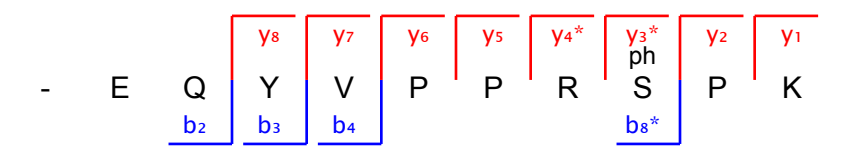
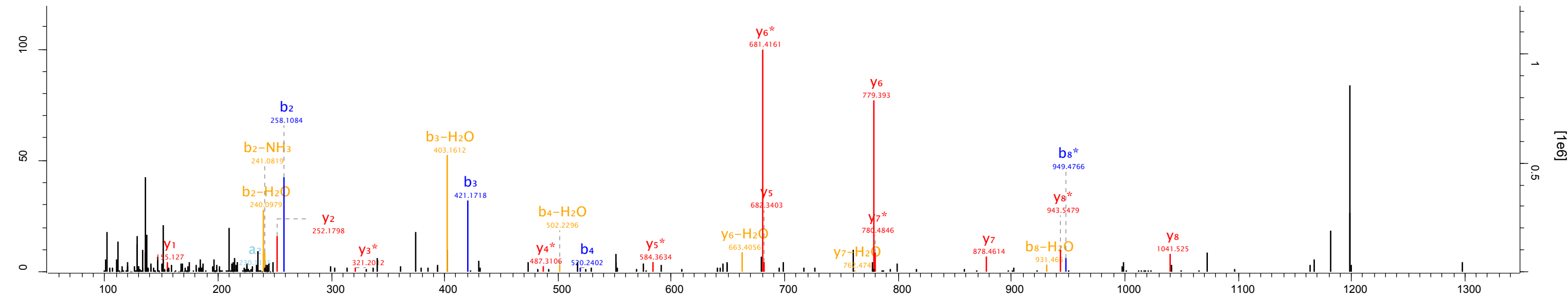
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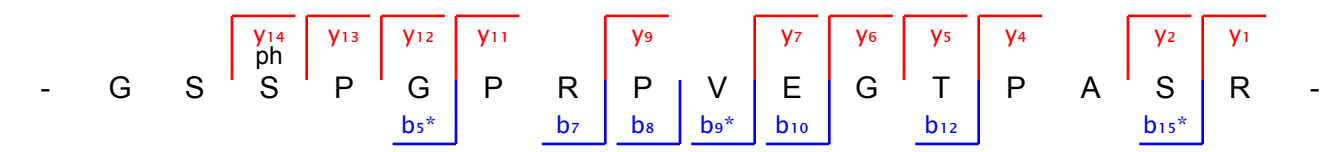
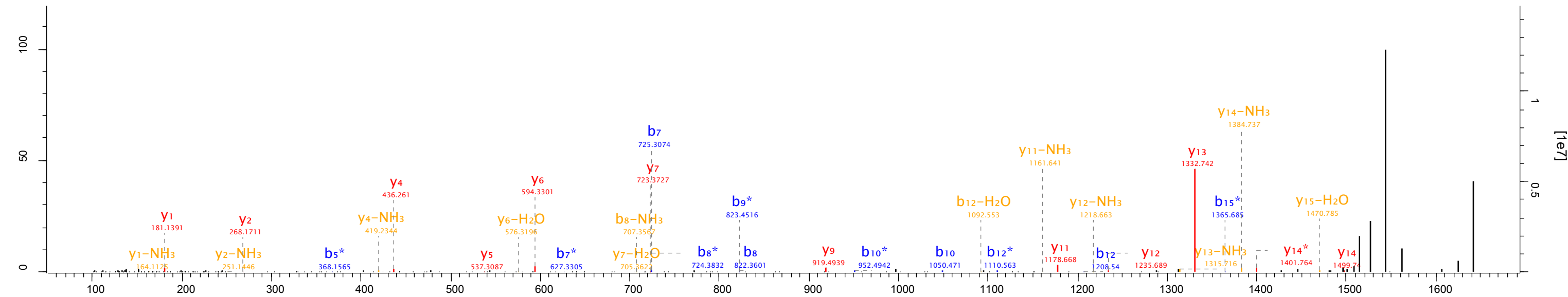
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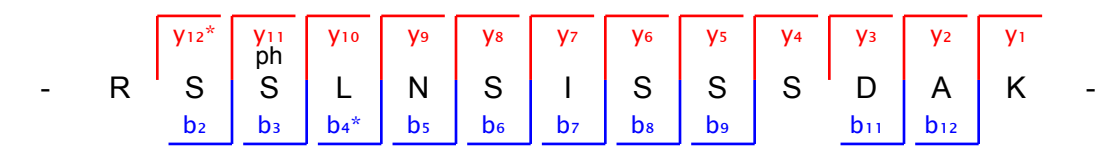
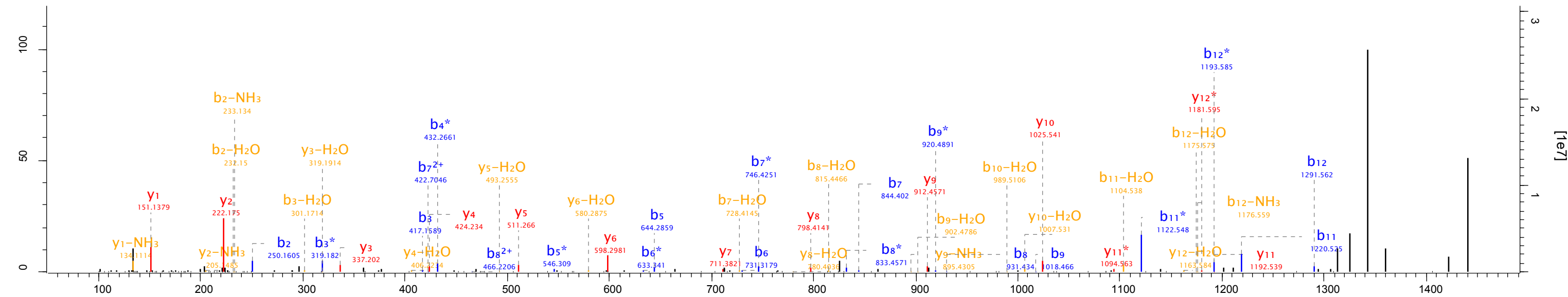
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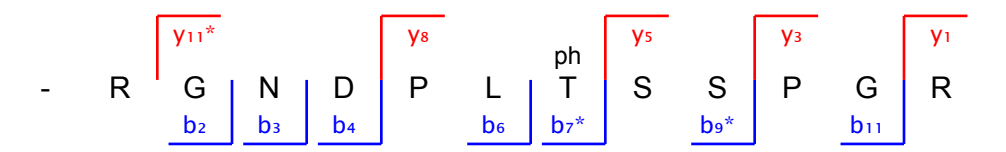
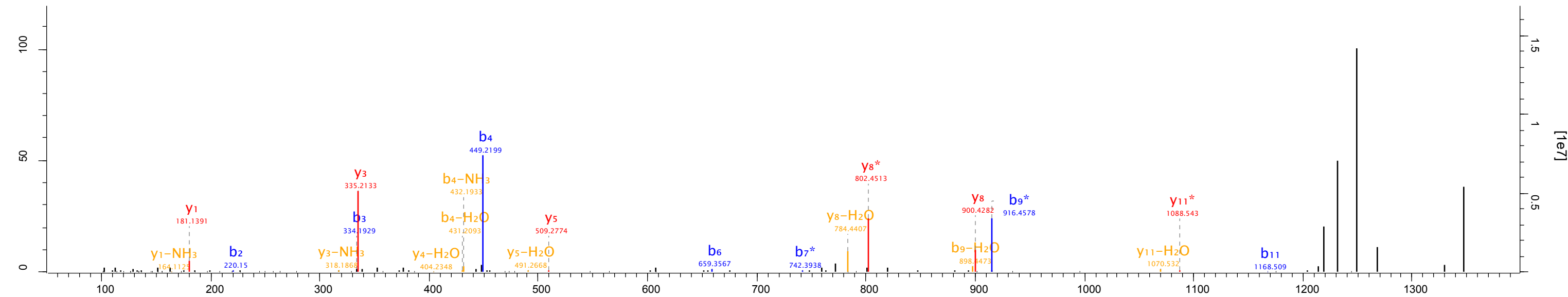
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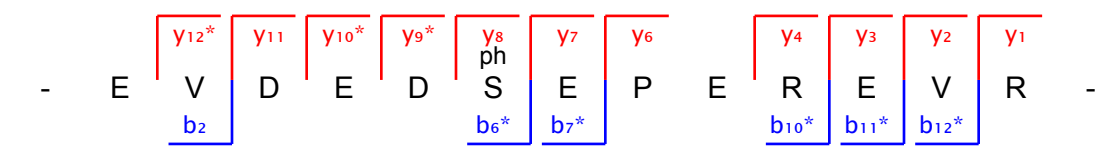
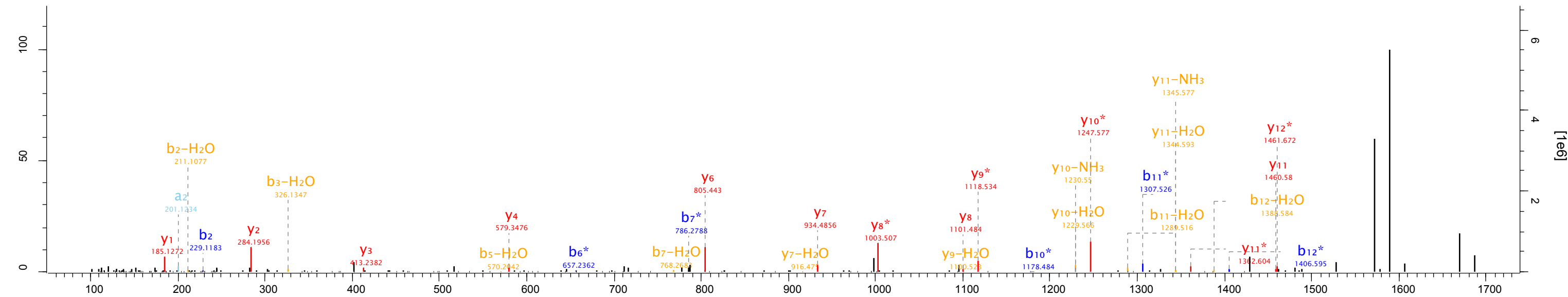
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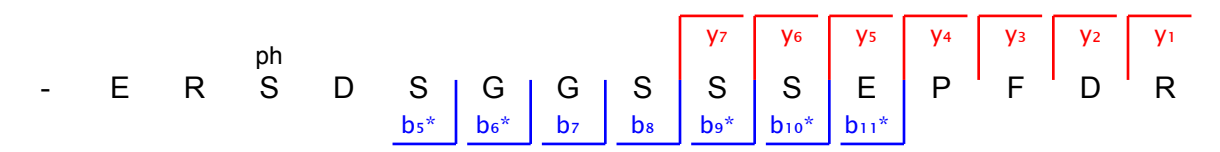
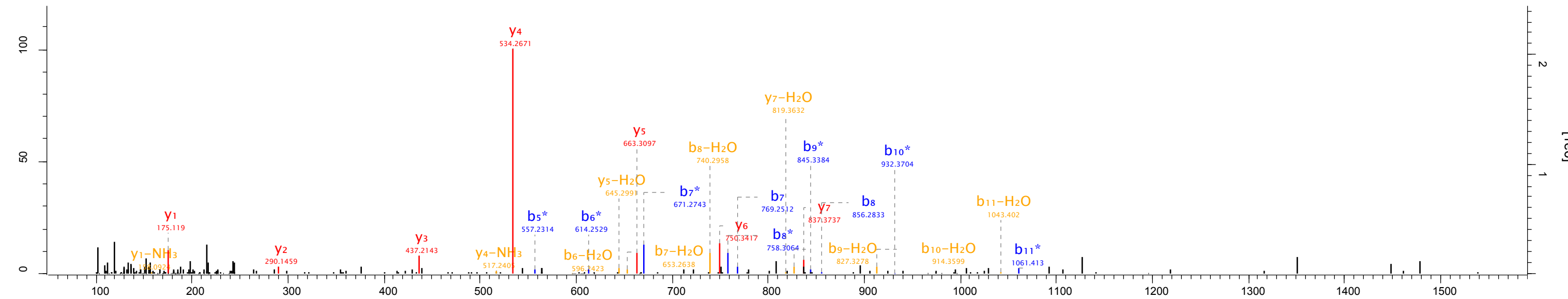
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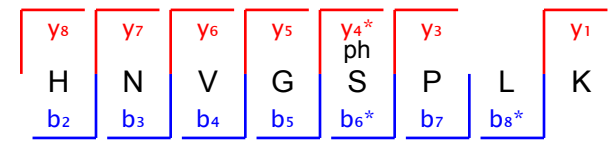
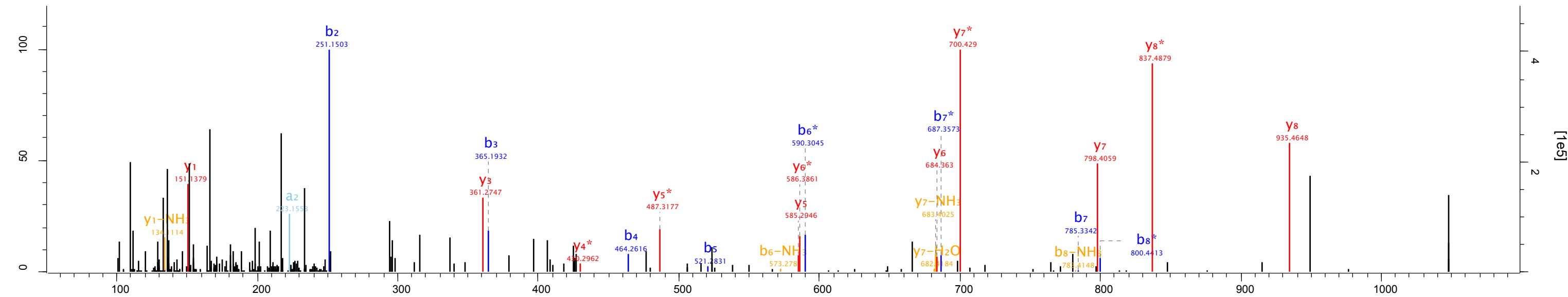
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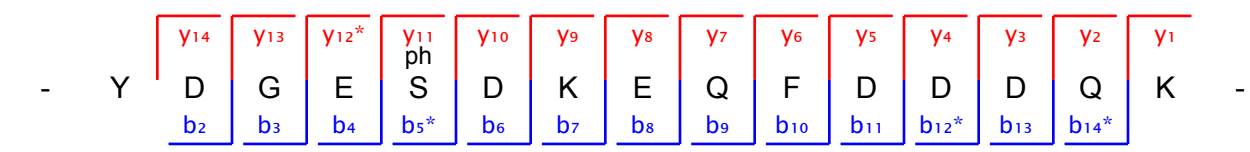
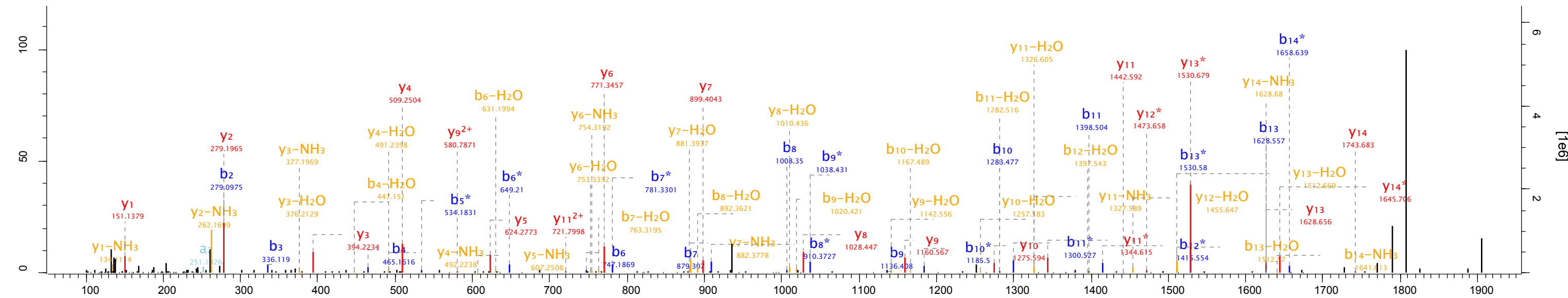
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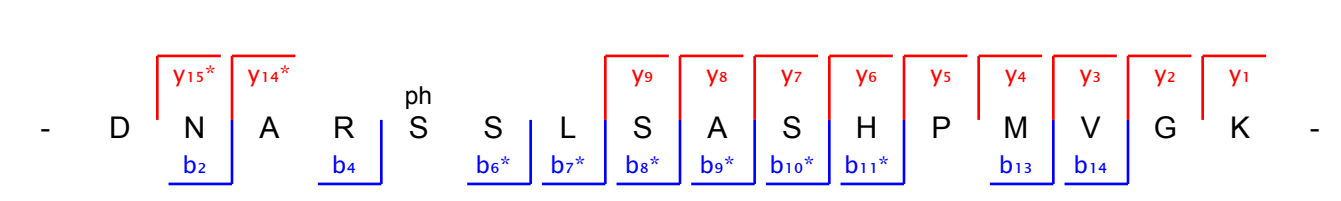
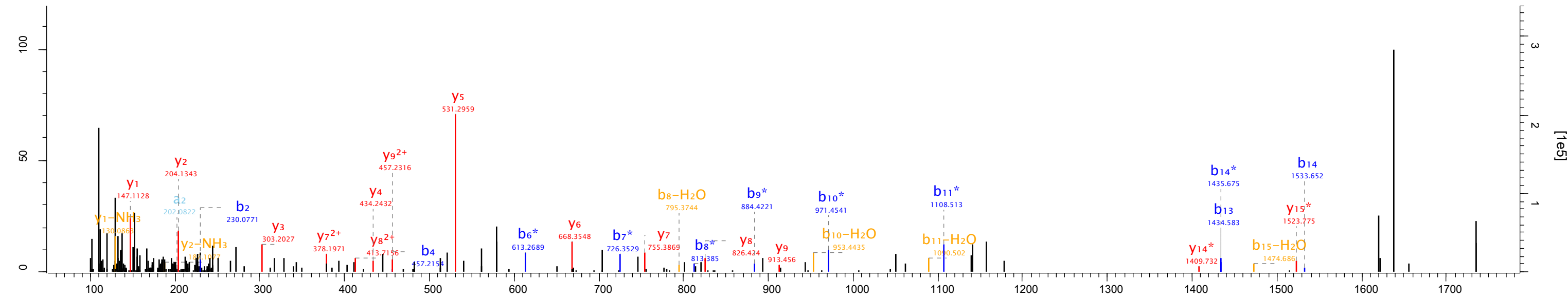
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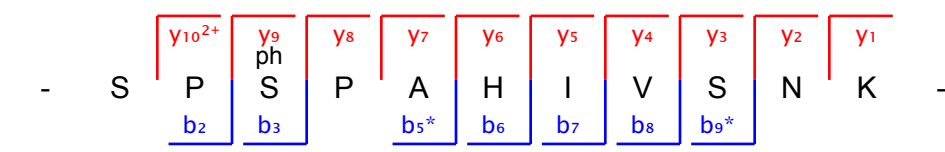
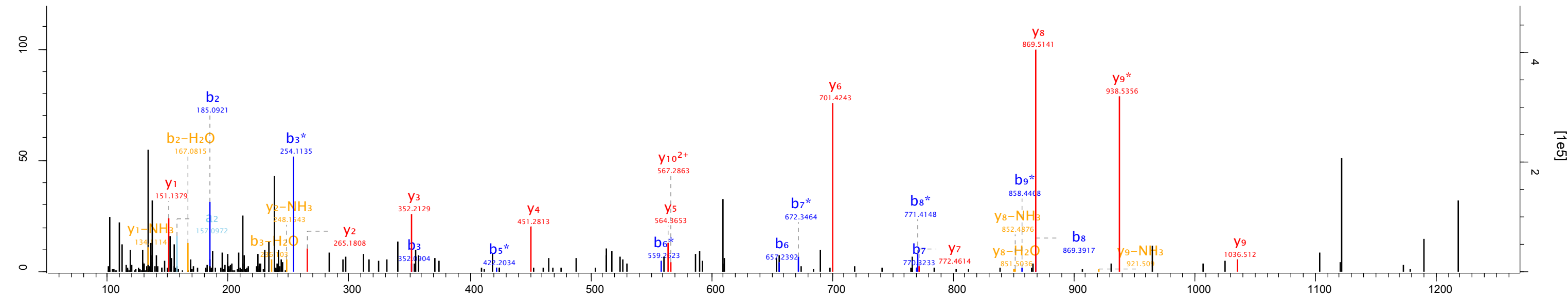
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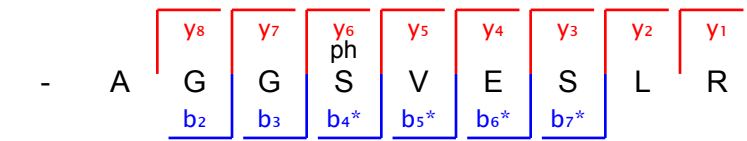
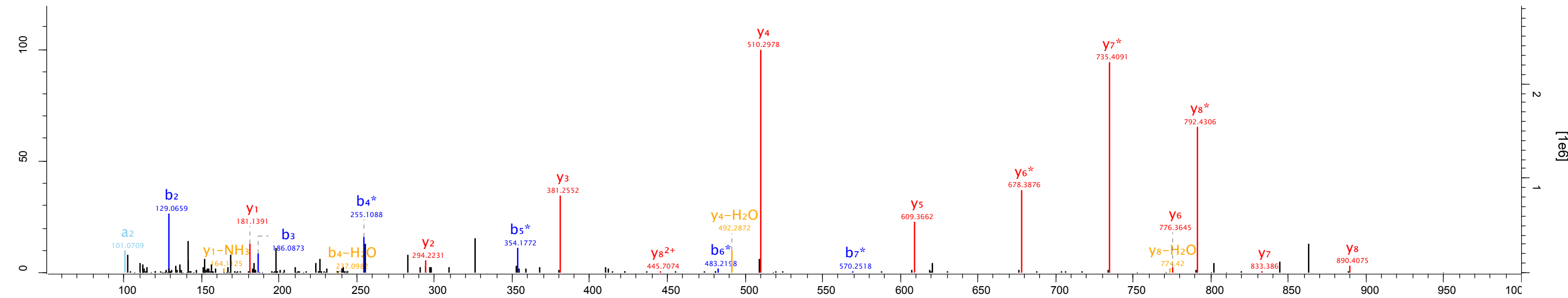
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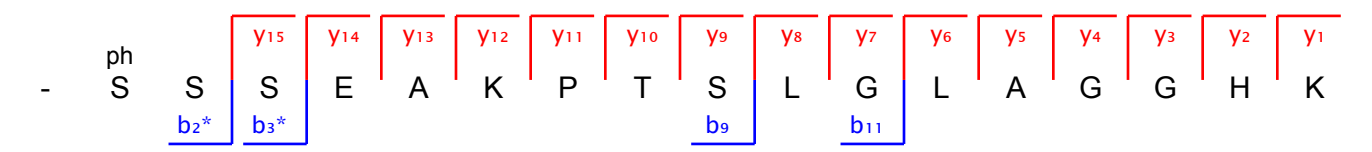
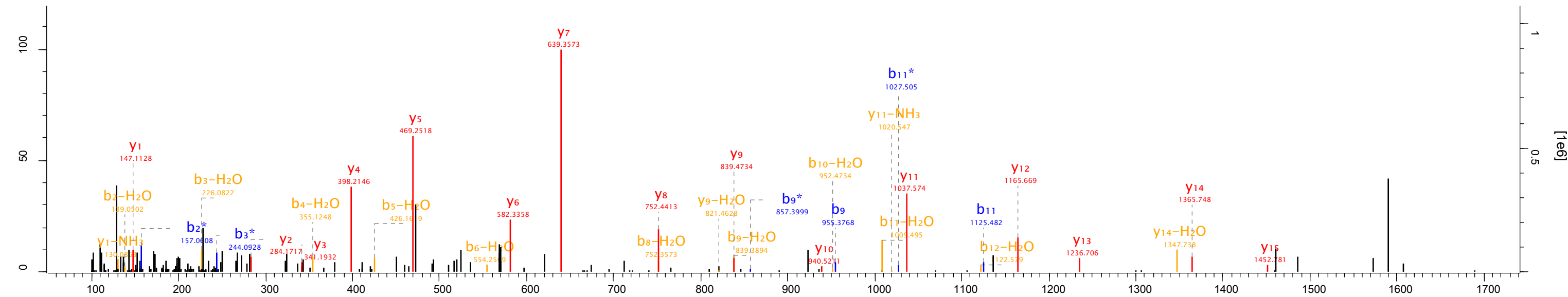
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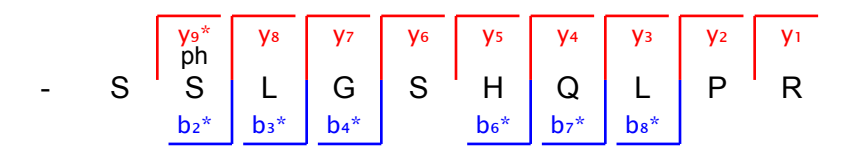
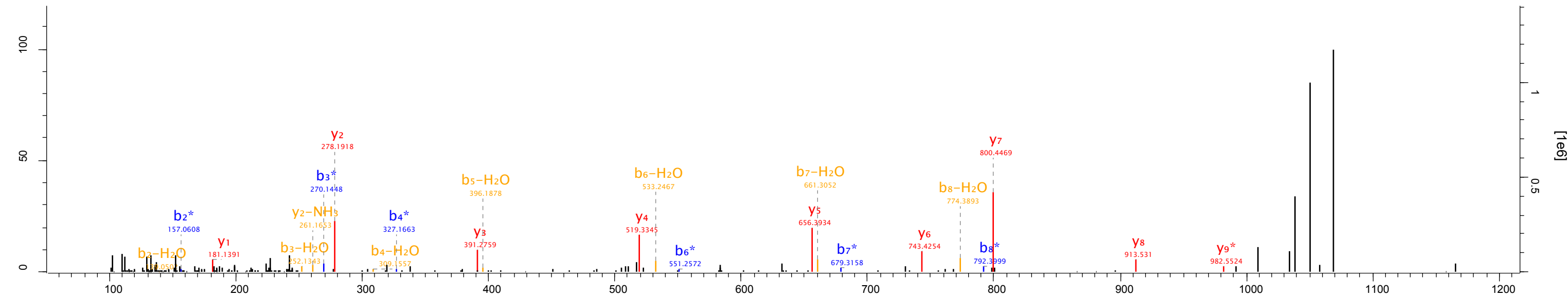
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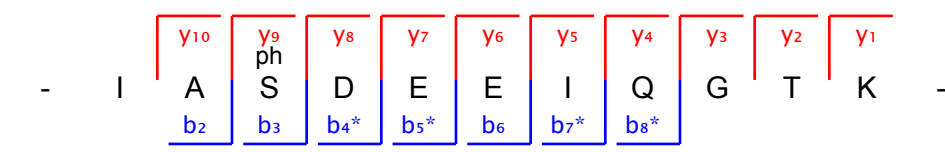
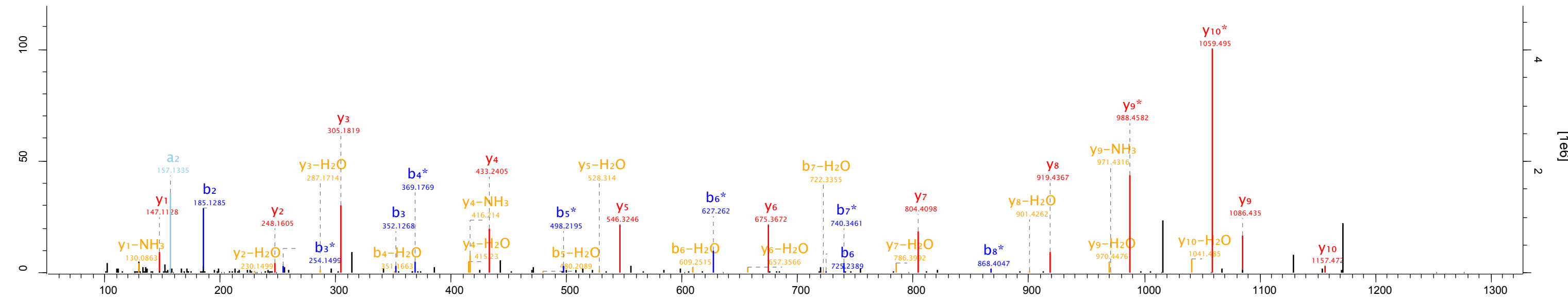
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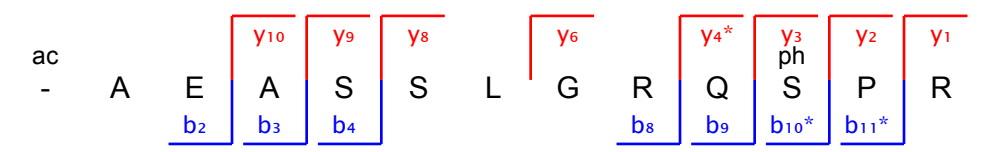
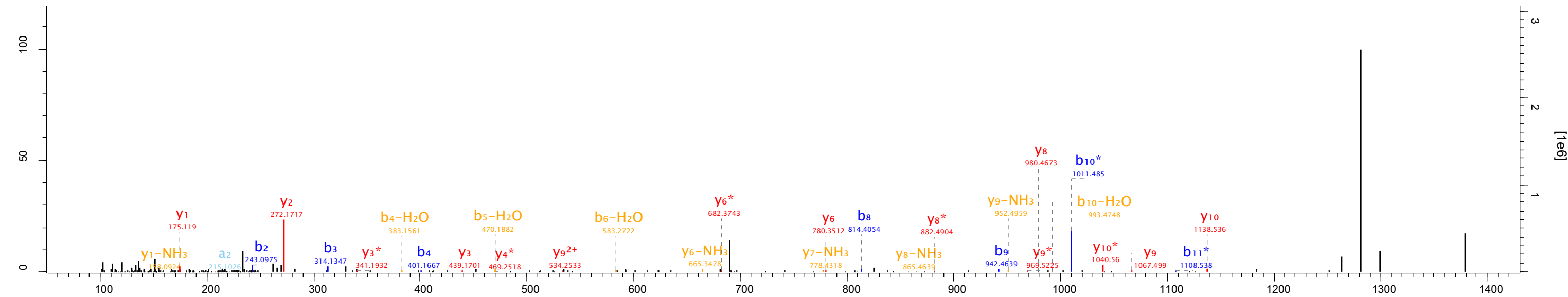
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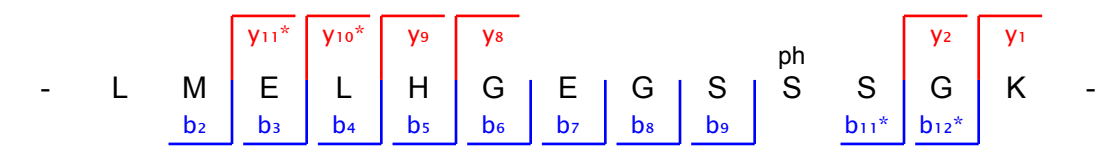
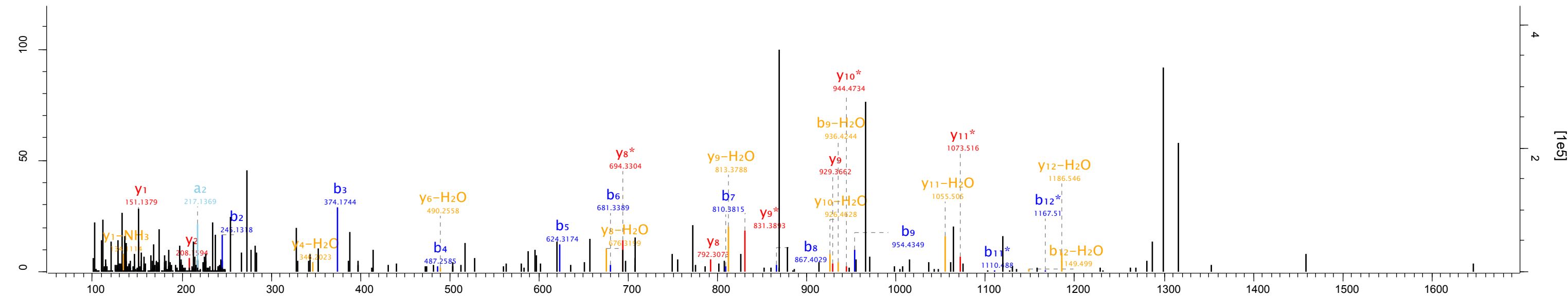
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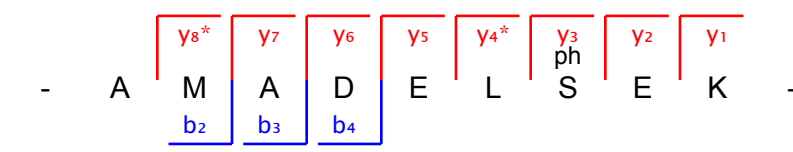
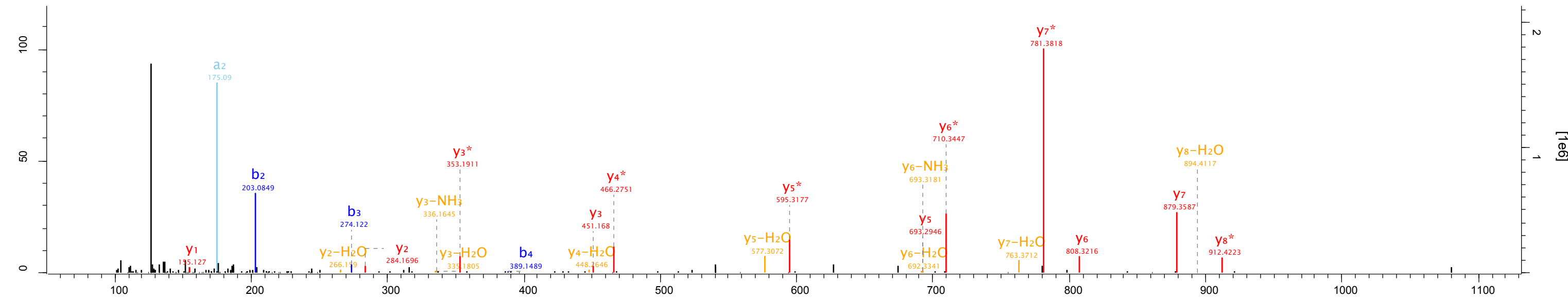
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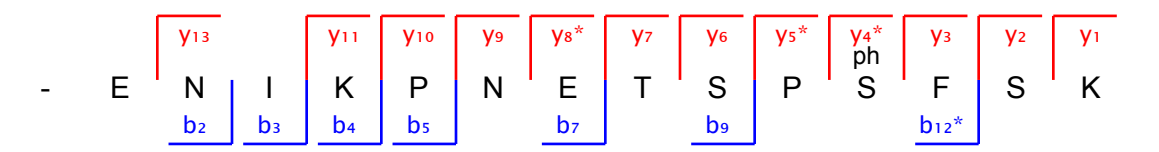
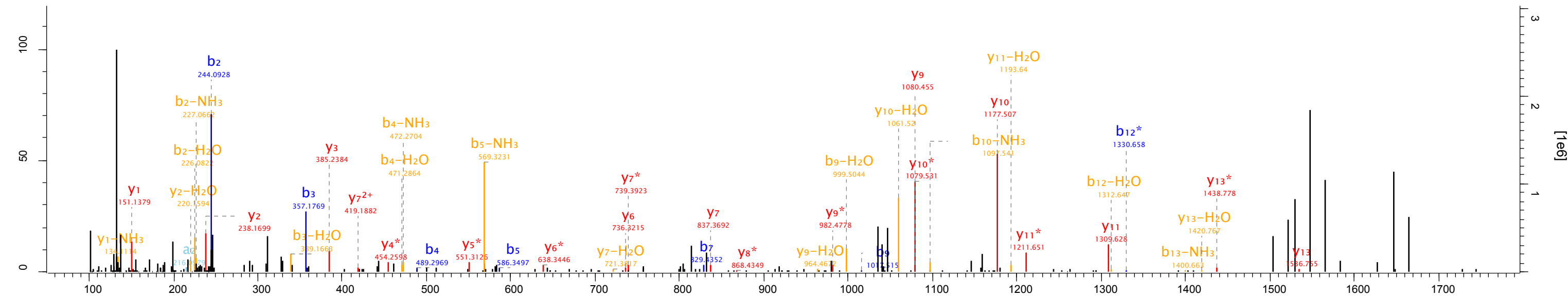
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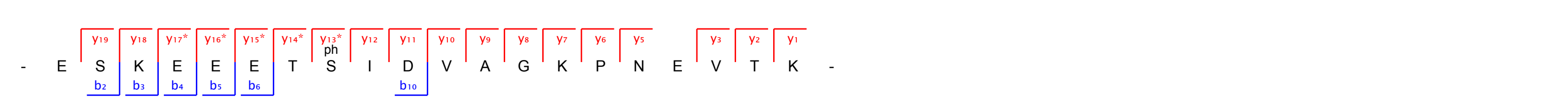
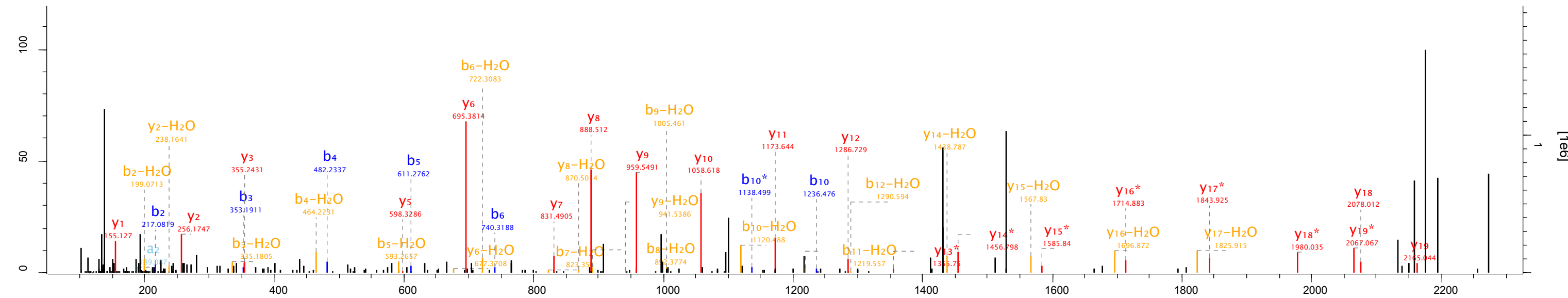
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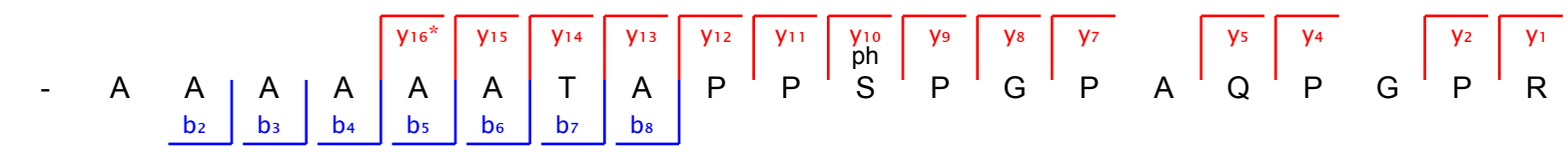
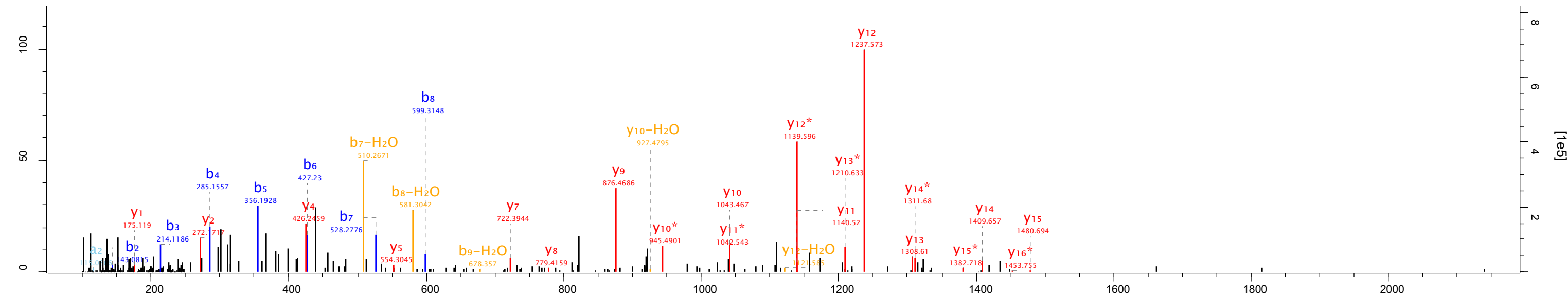
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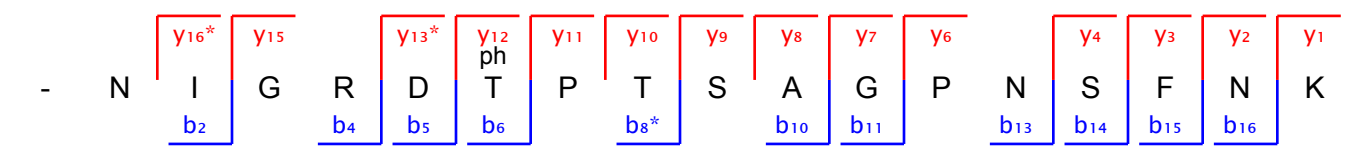
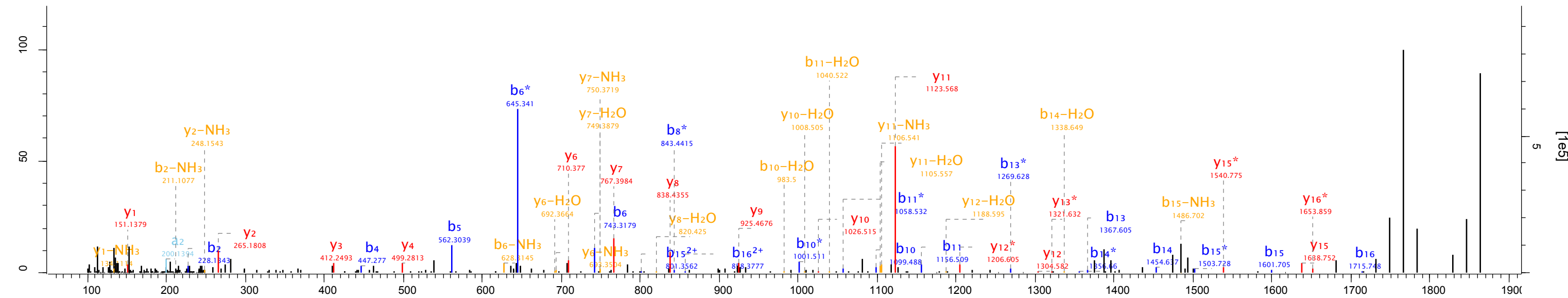
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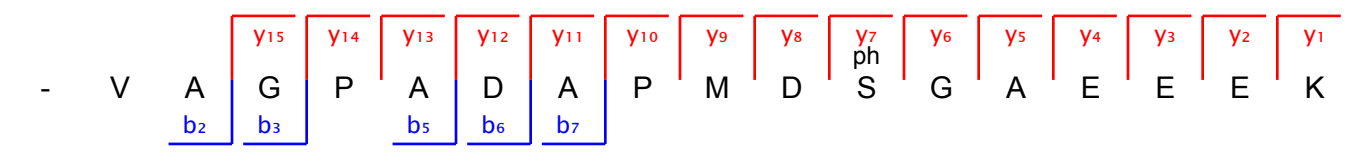
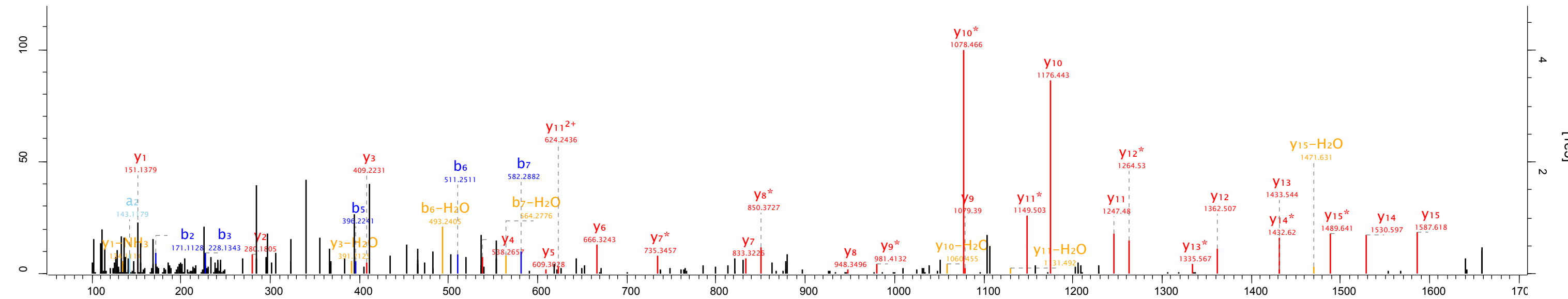
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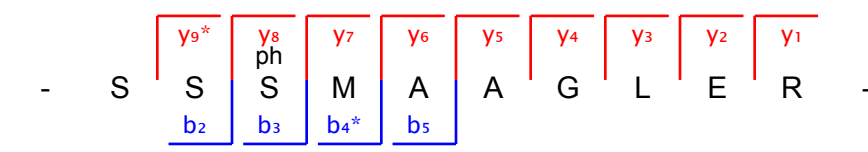
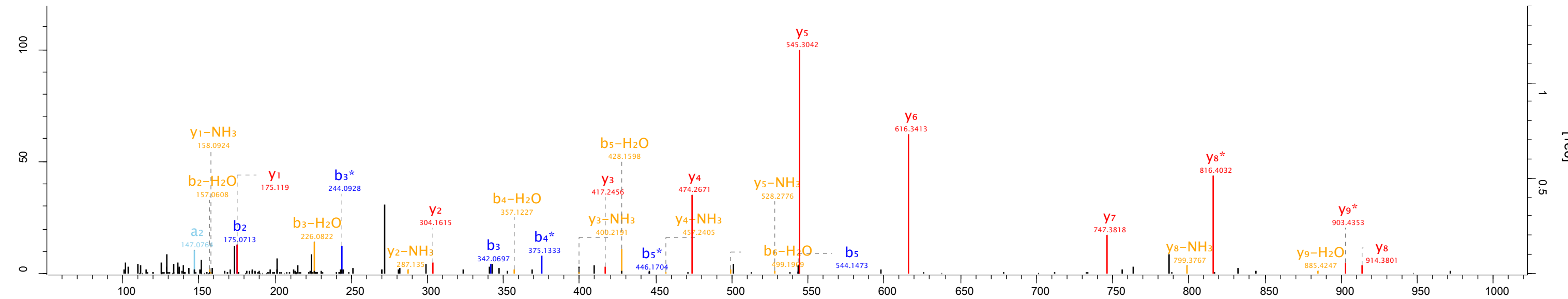
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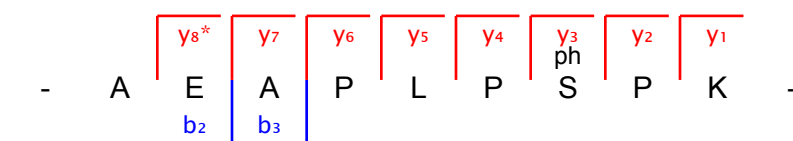
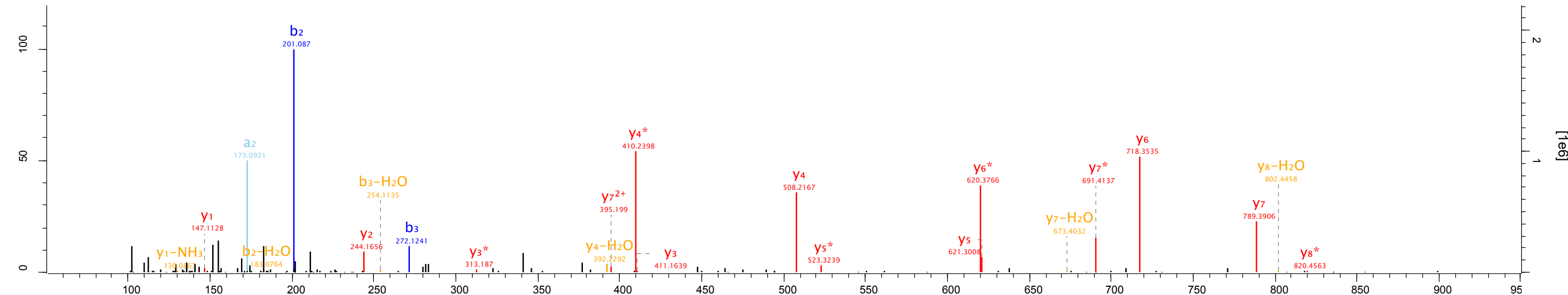
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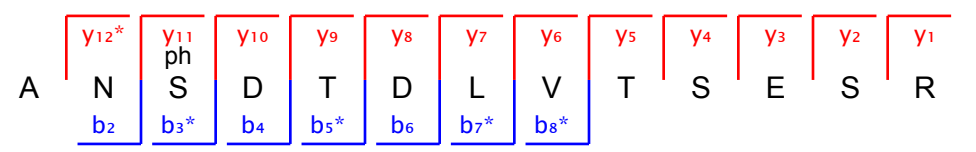
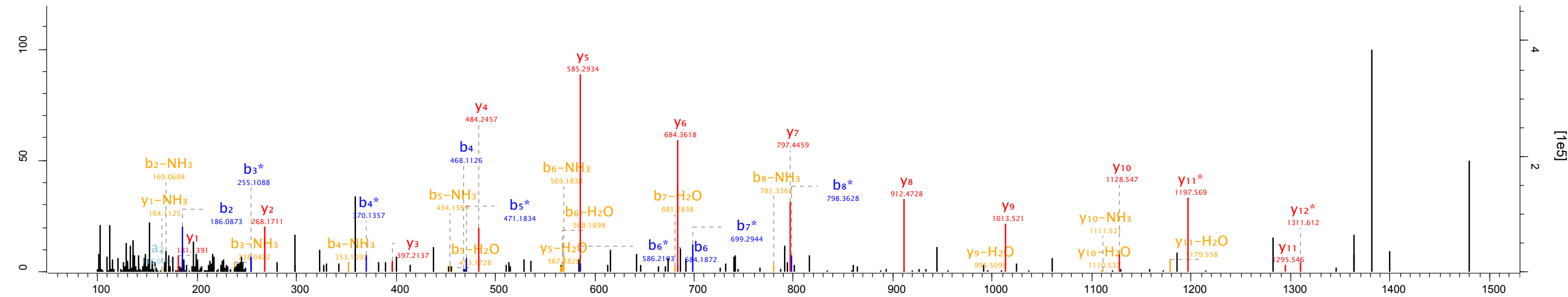
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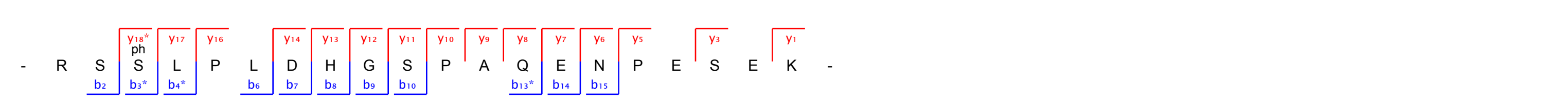
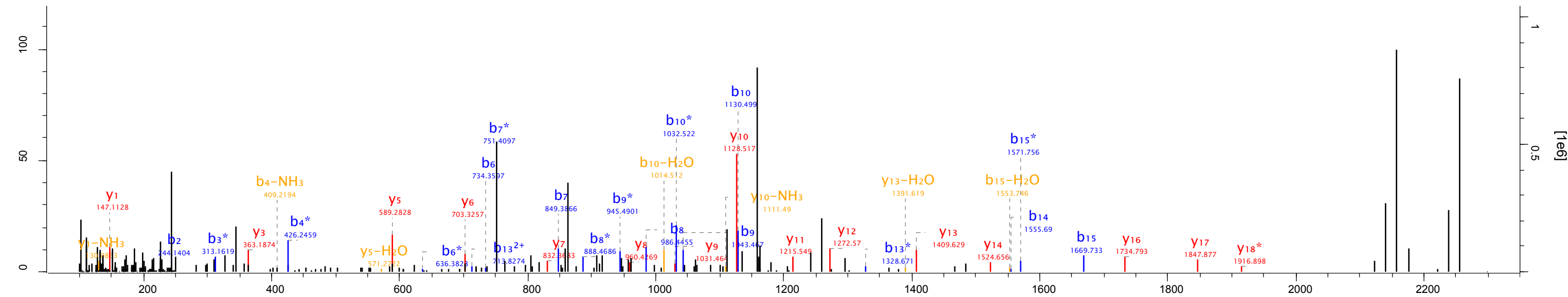
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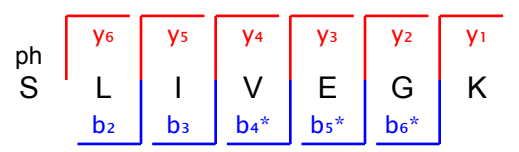
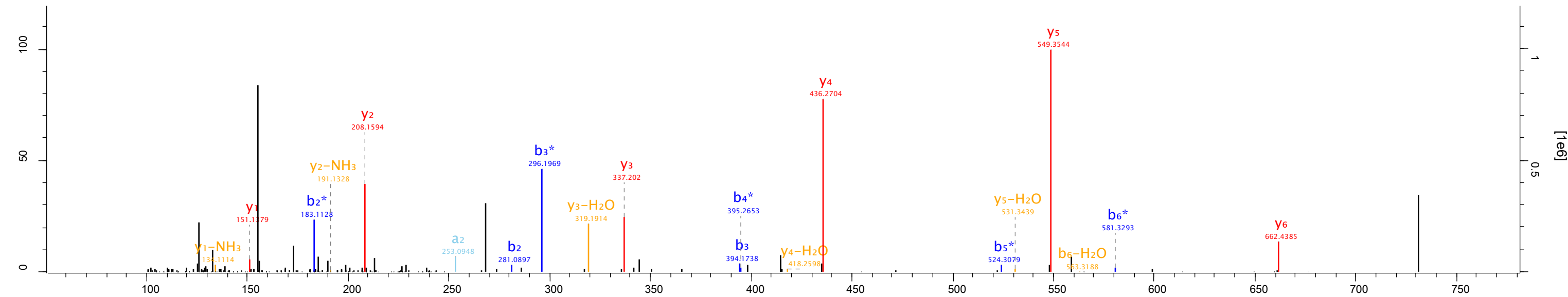
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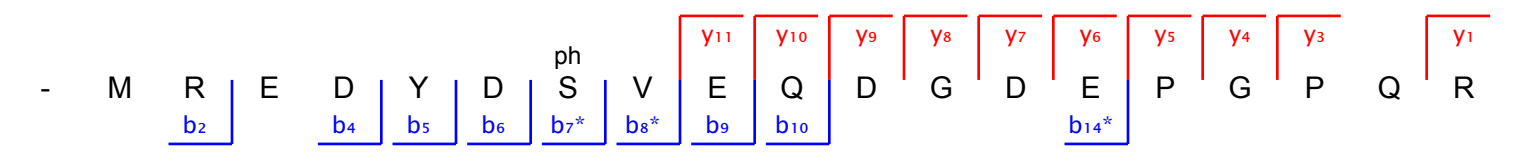
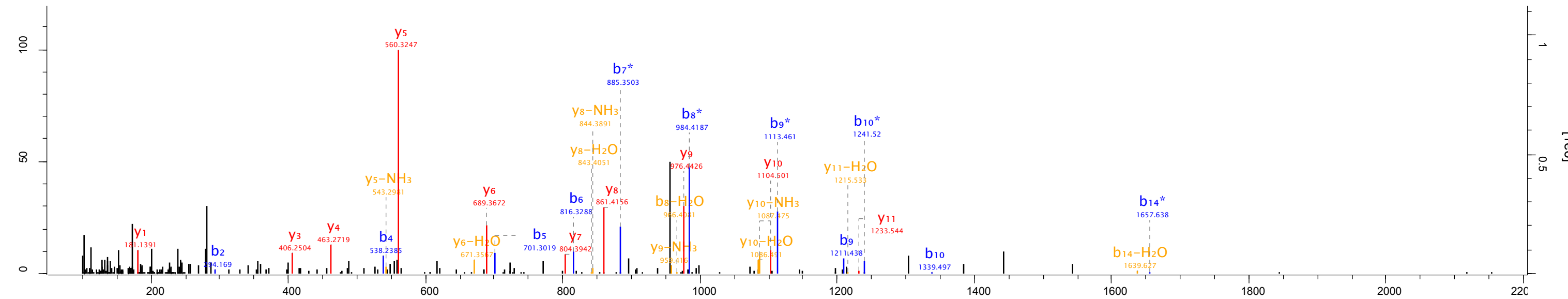
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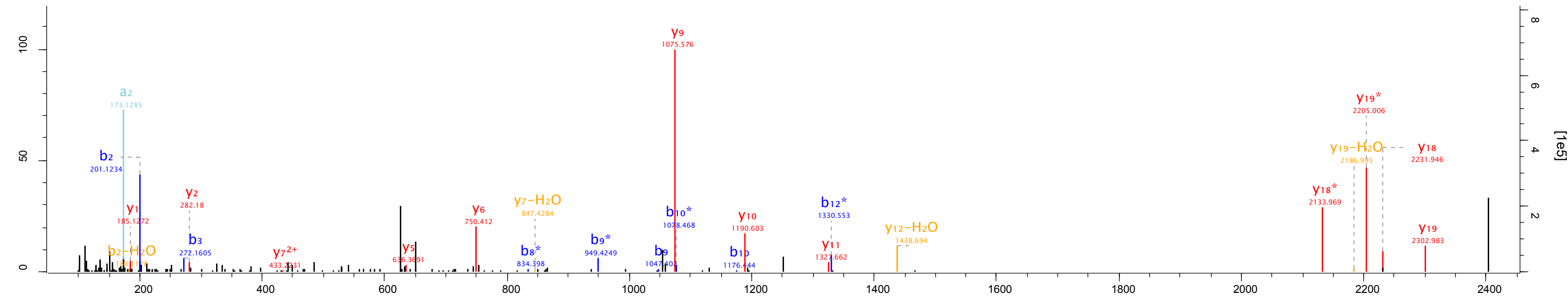


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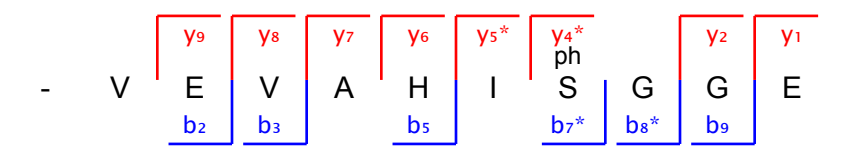
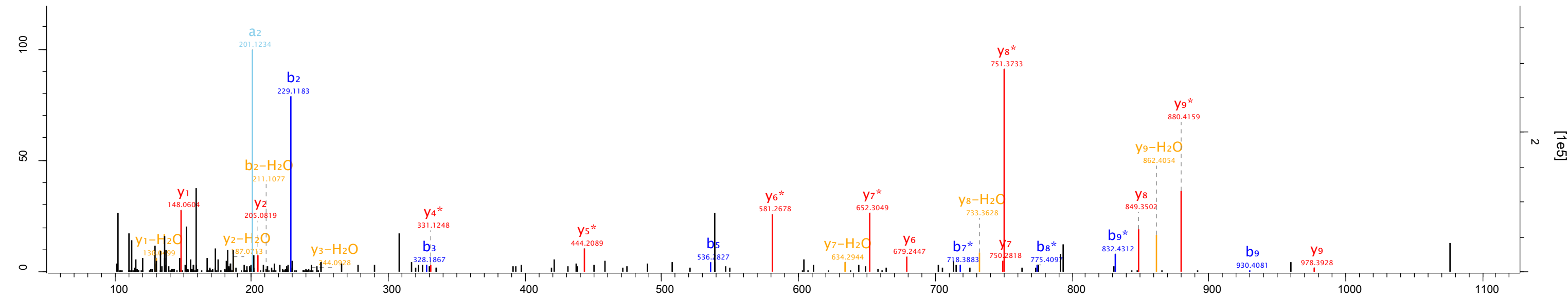


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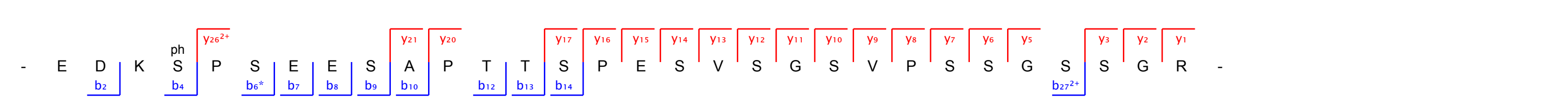
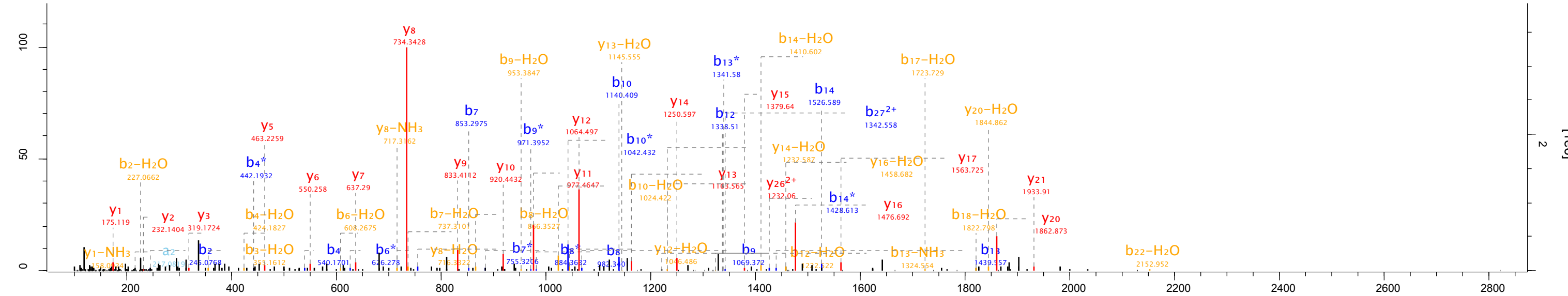
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- b2 (L), b3 (A)
- b8* (D), b9 (D), b10 (E)
- b12* (D)
- y19 (A), y18 (P)
- y11 (H), y10 (D), y9 (P)
- y7^2+ (D), y6 (N), y5 (T)
- y2 (P), y1 (R)

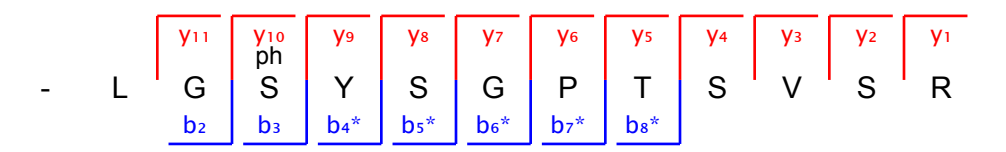
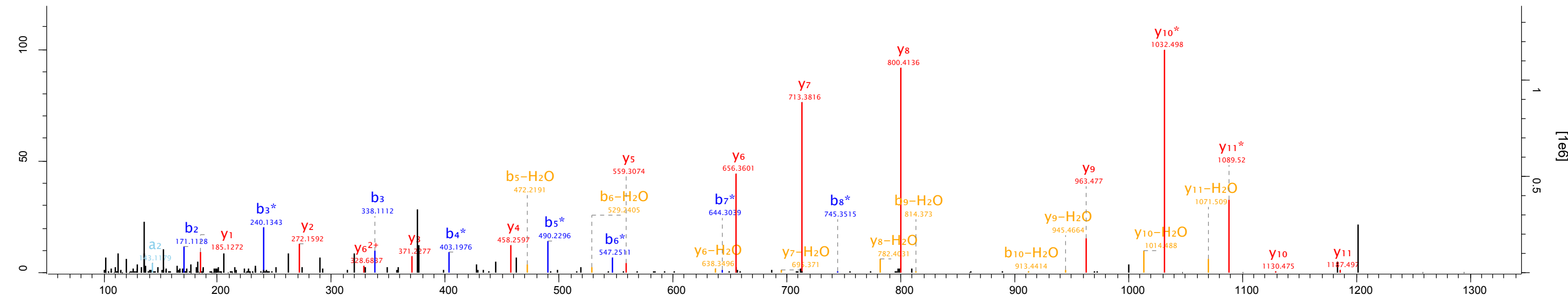
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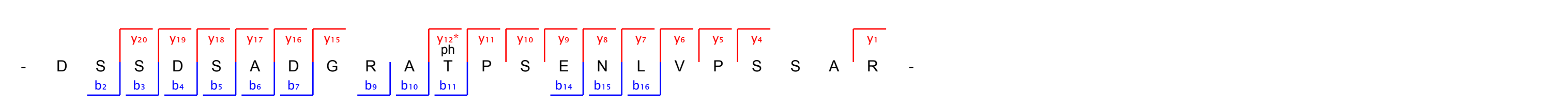
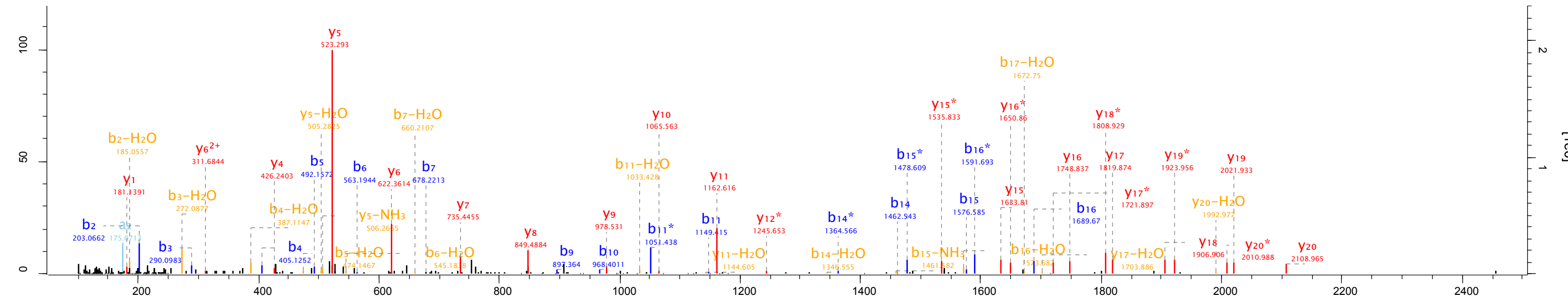
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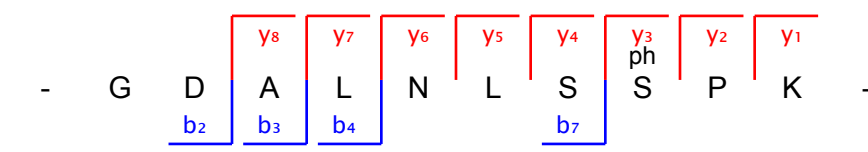
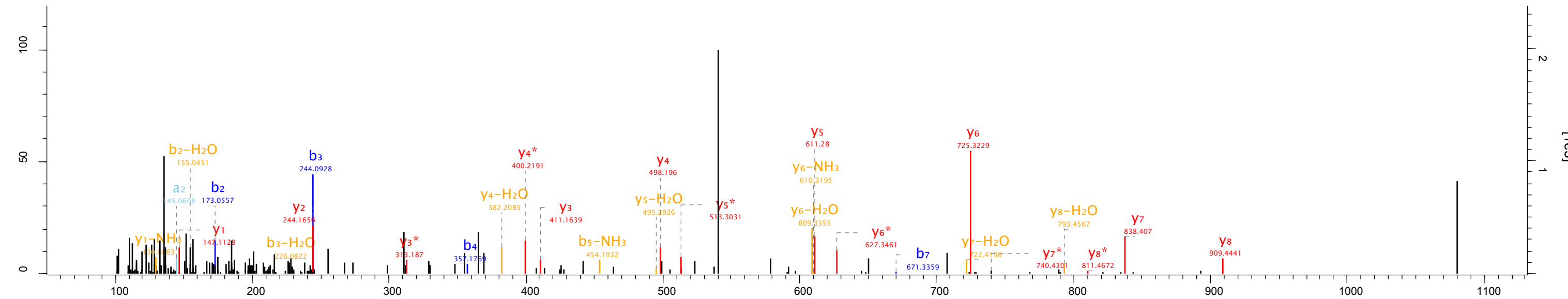
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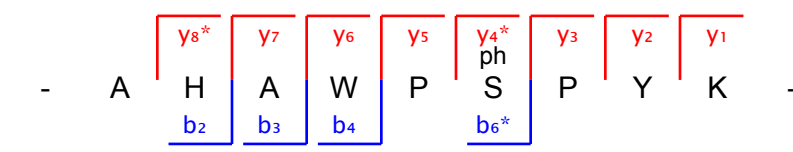
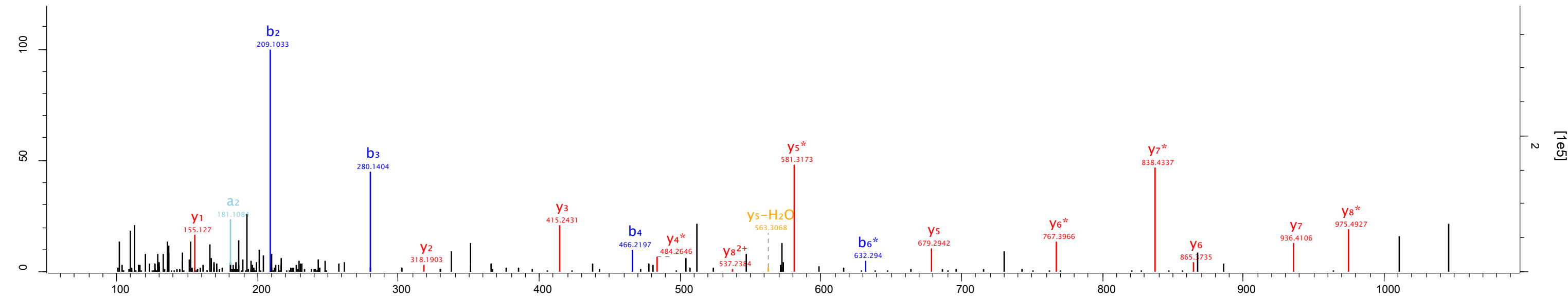
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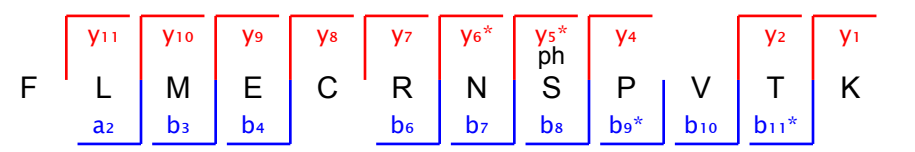
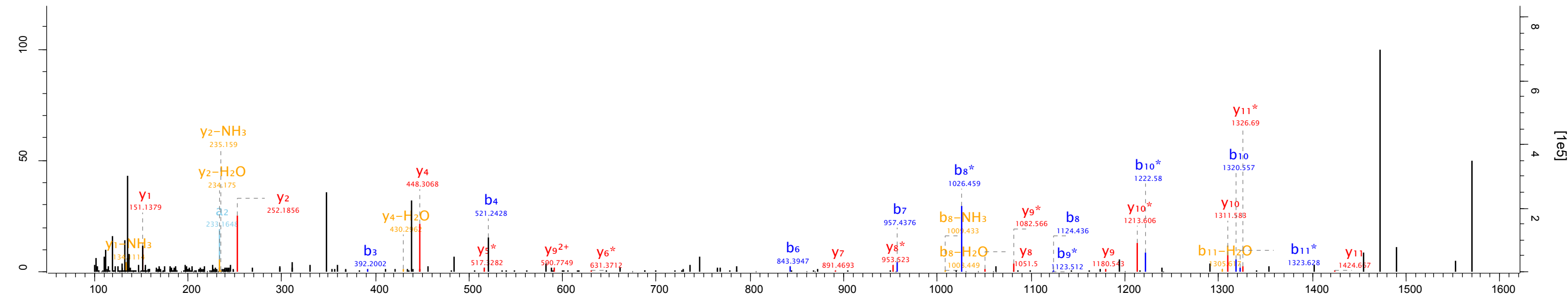
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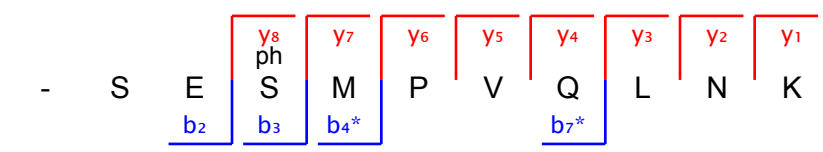
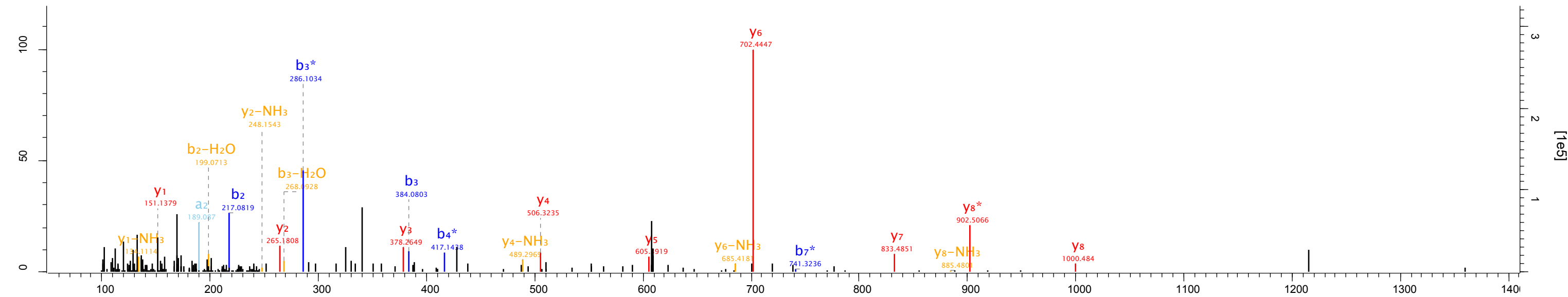
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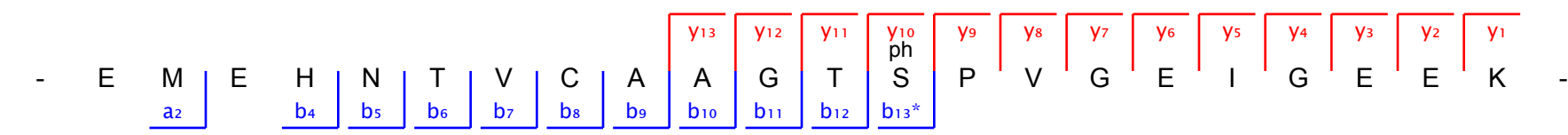
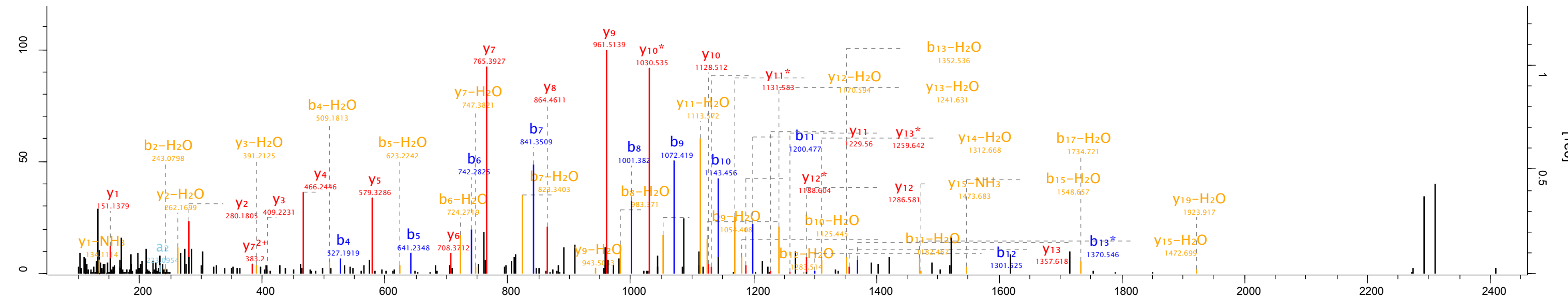
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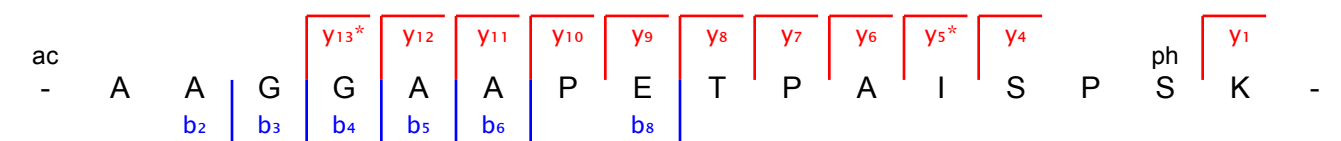
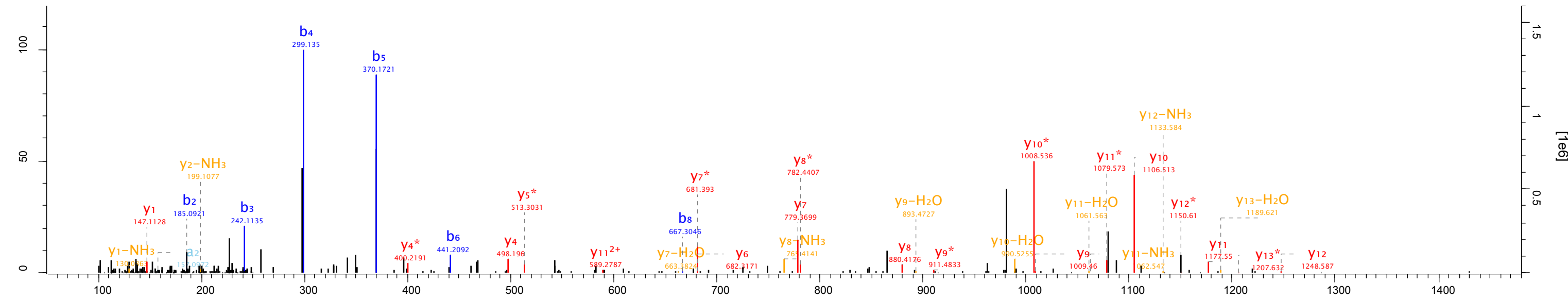
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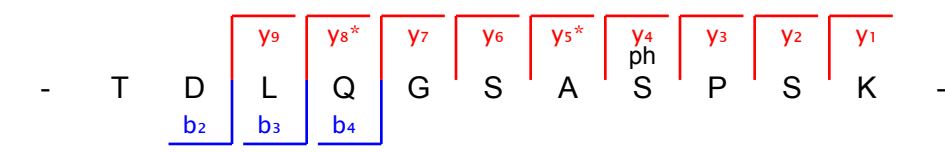
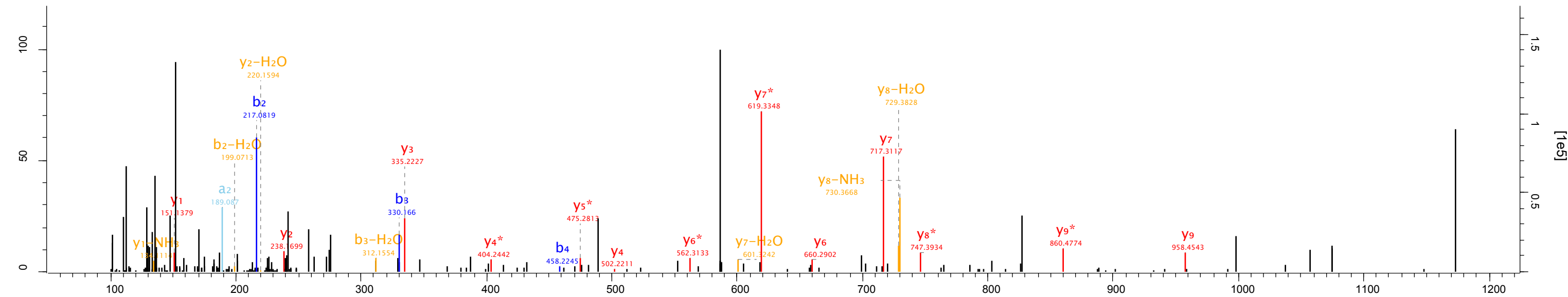
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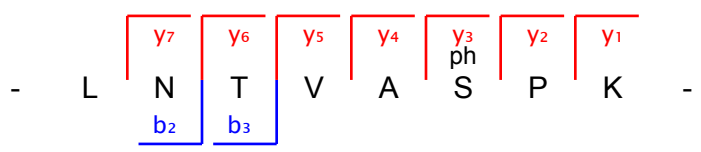
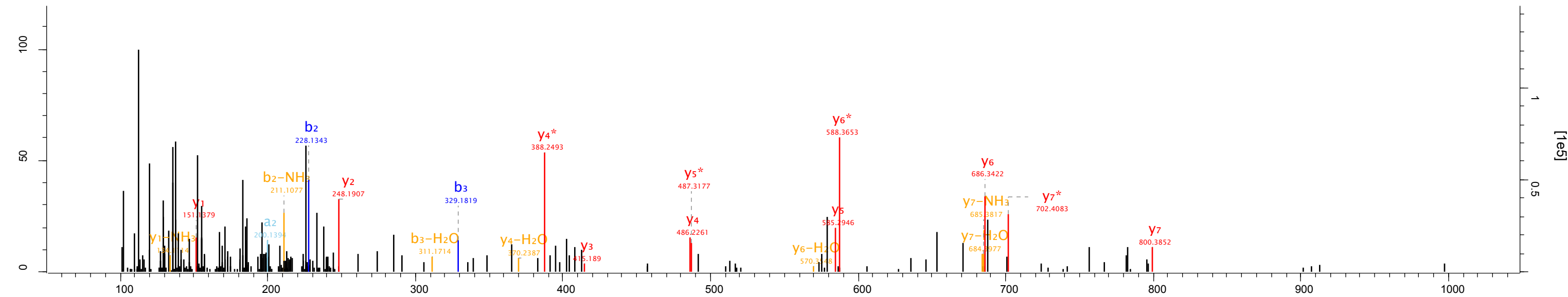
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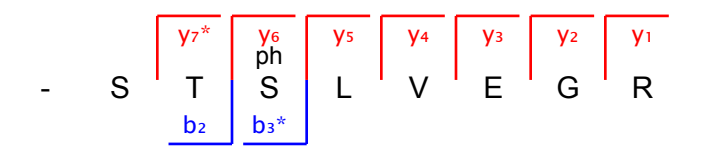
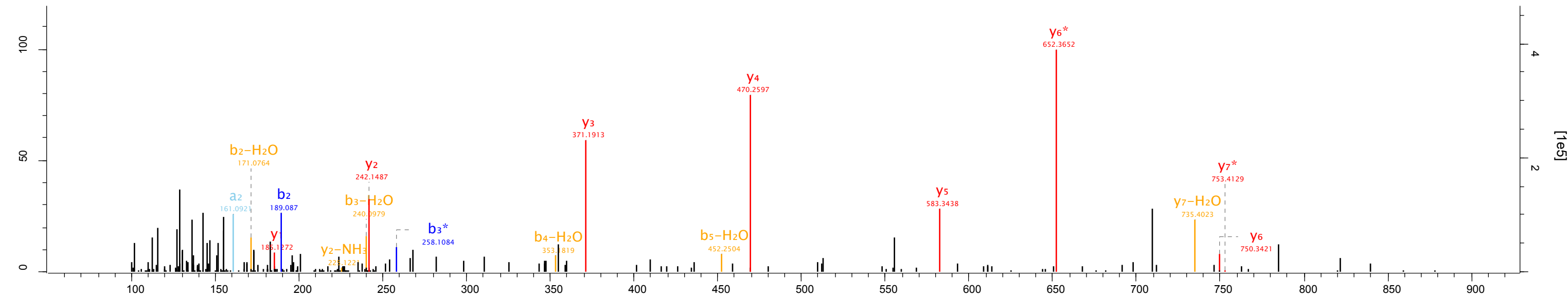
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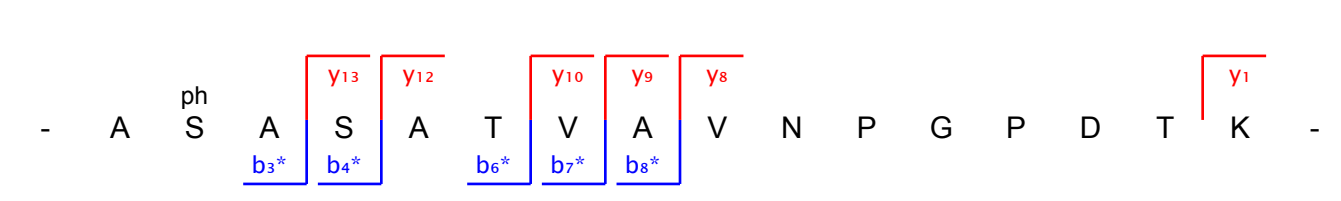
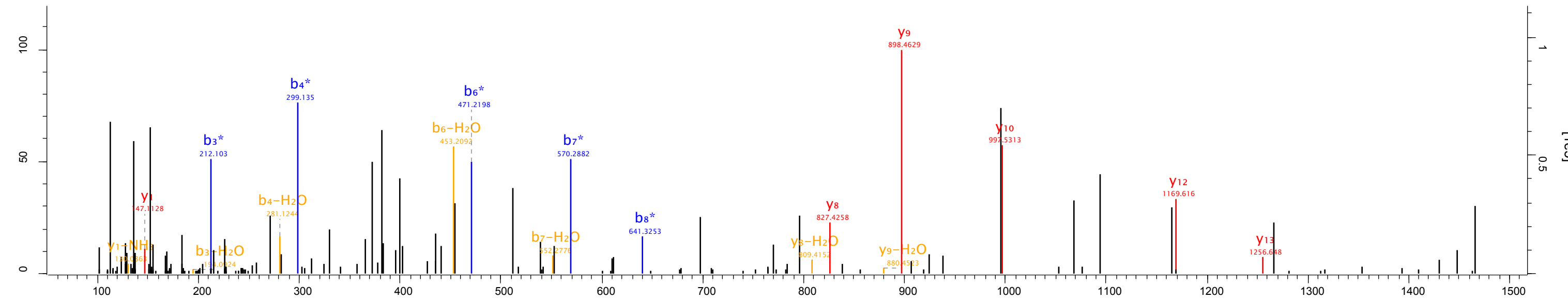
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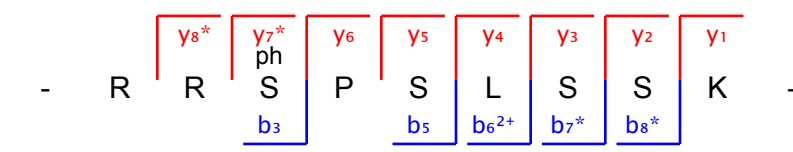
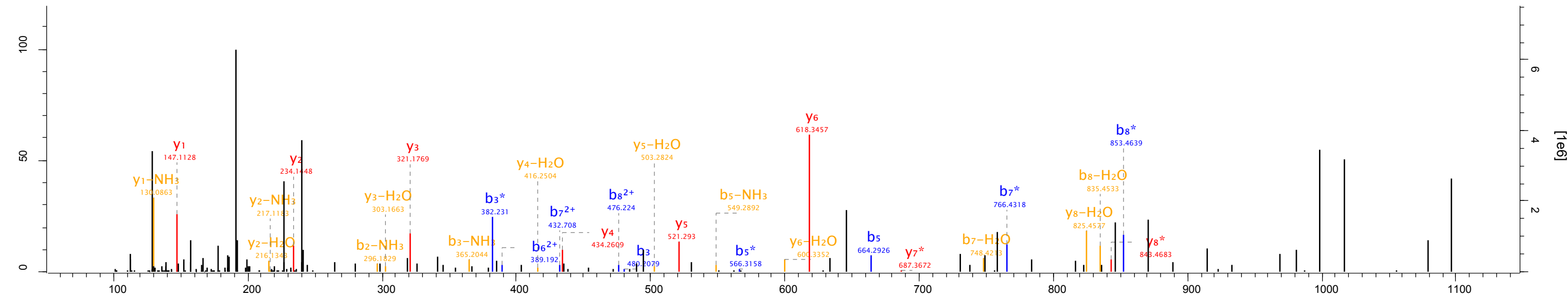
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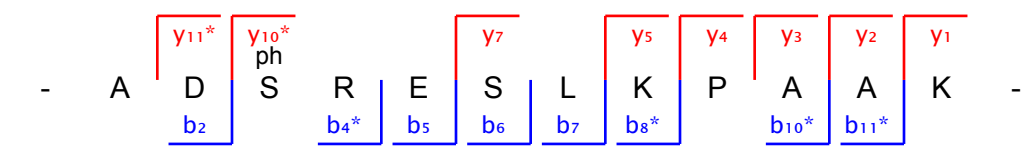
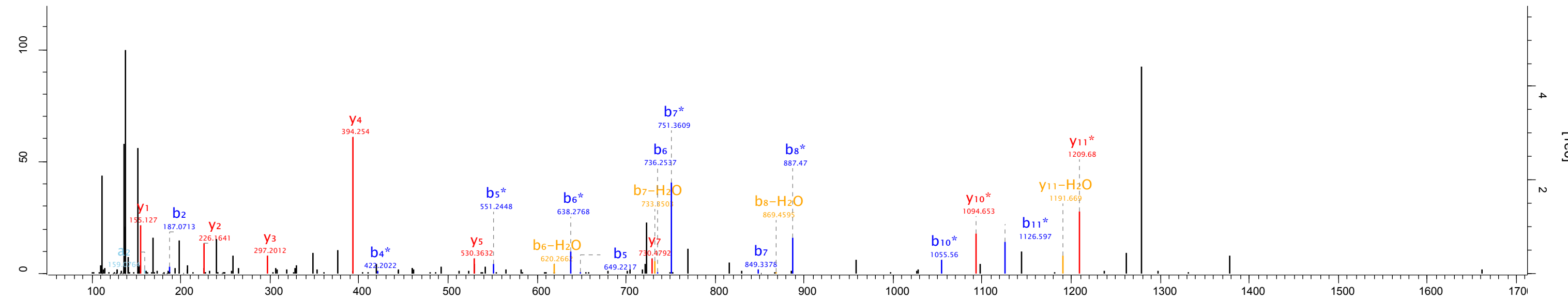
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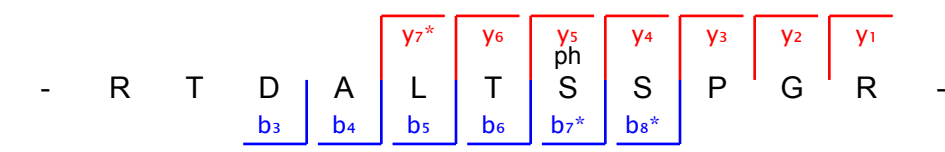
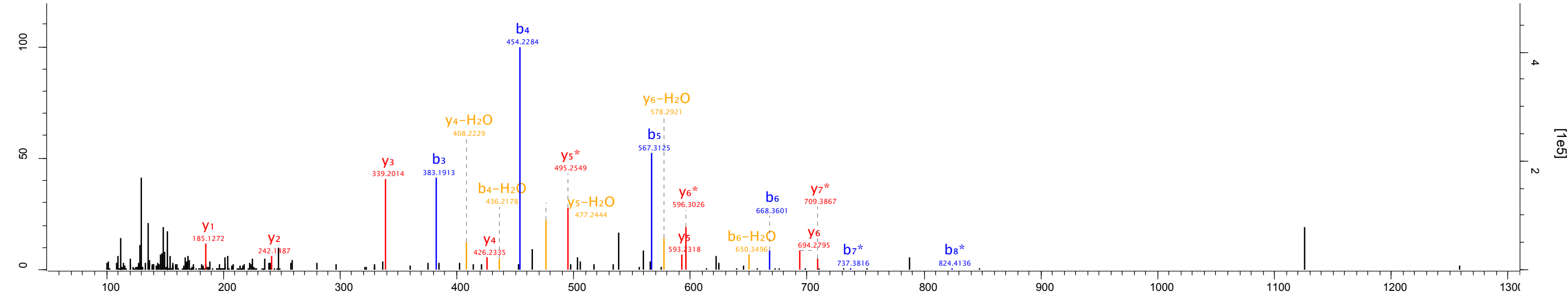
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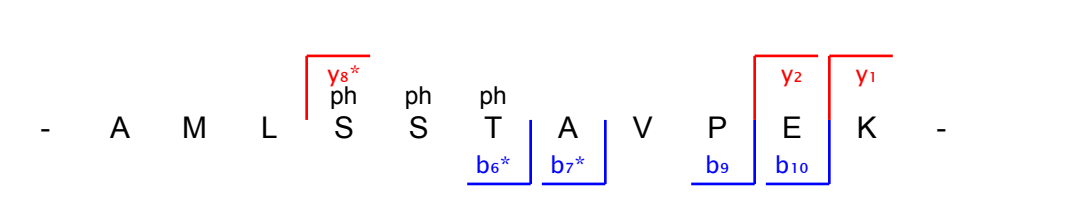
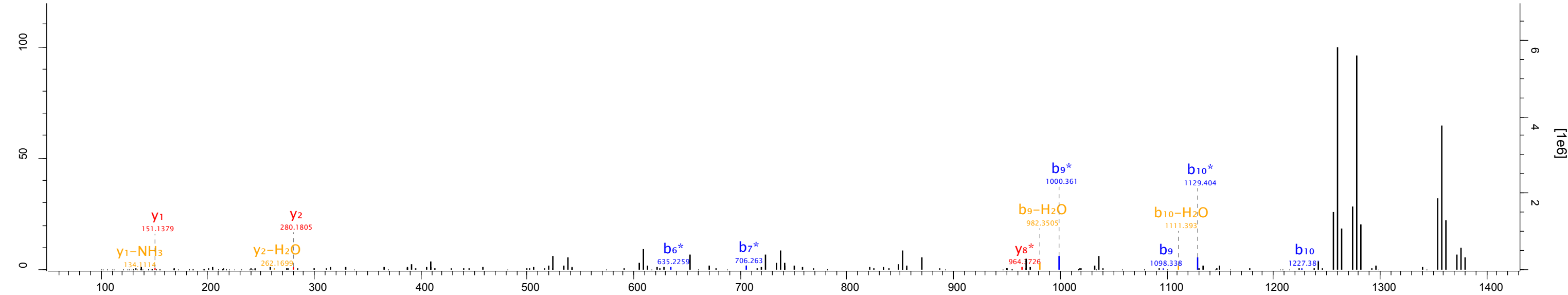
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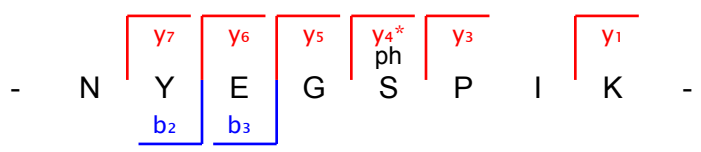
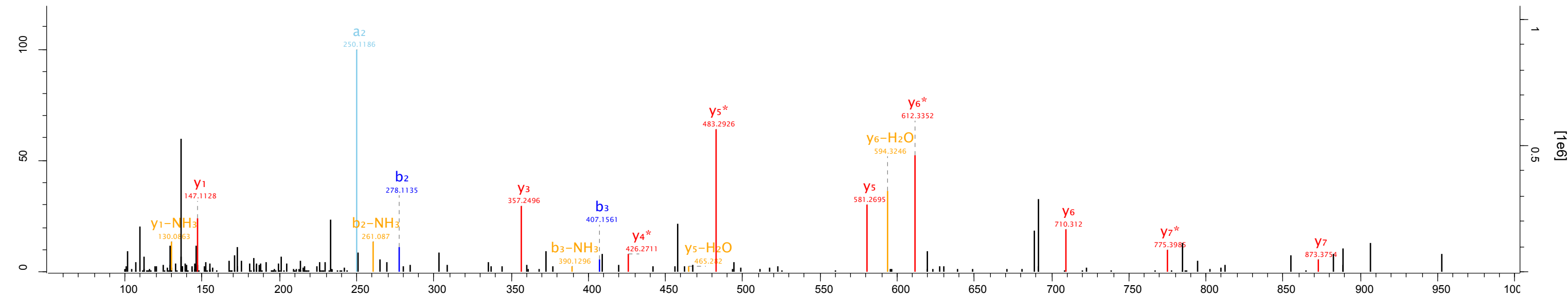
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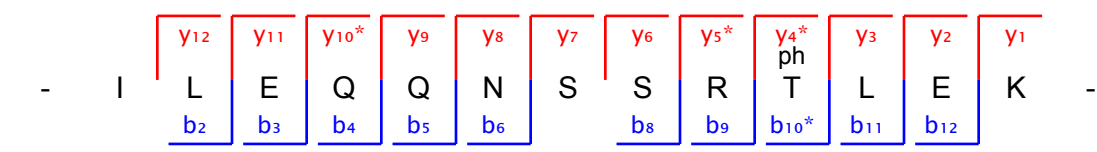
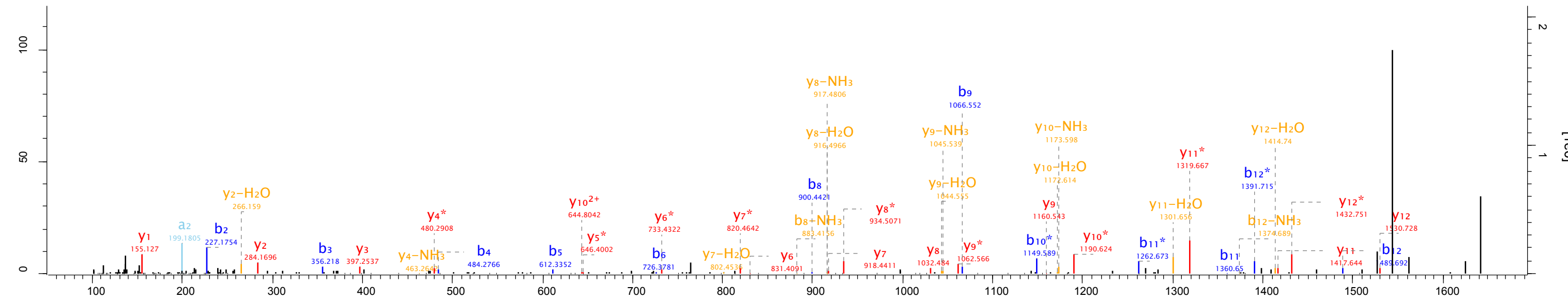
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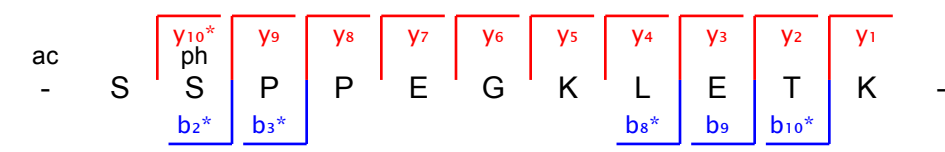
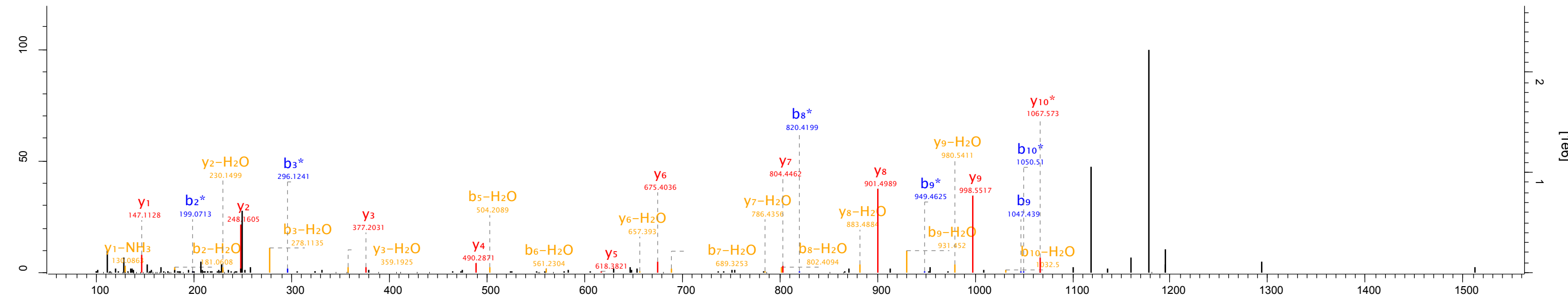
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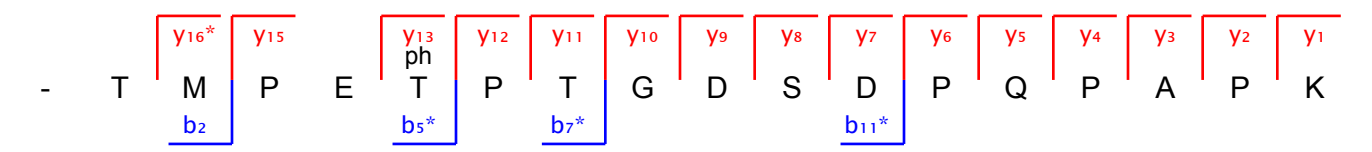
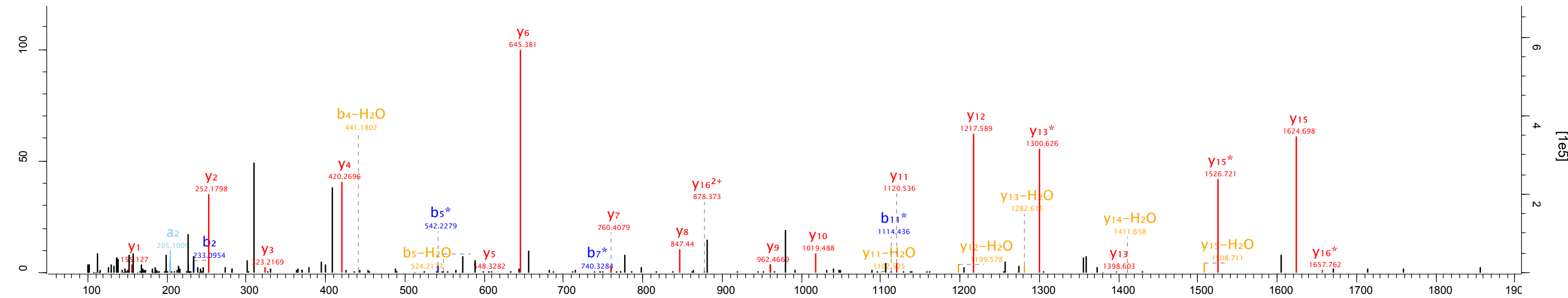
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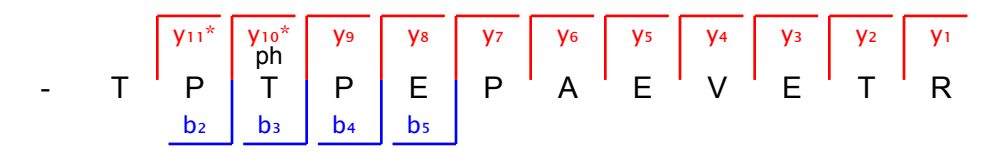
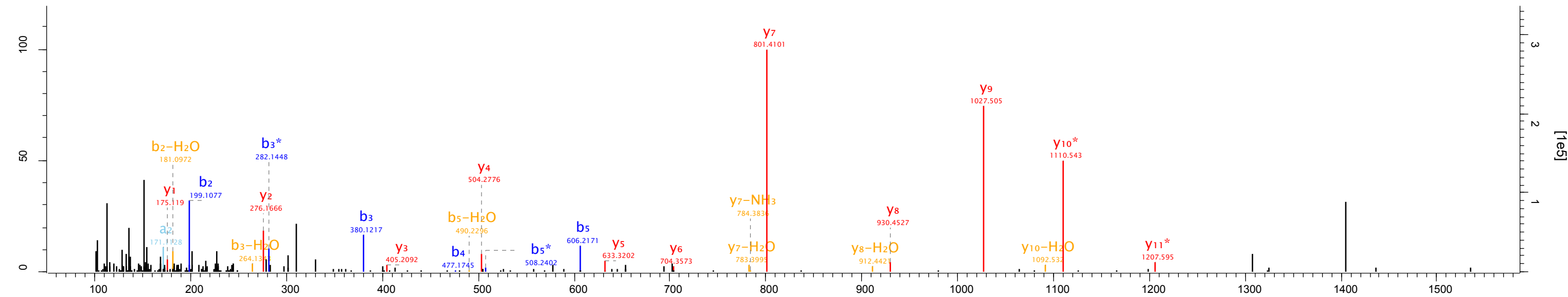
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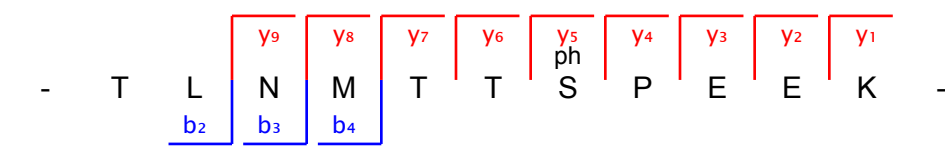
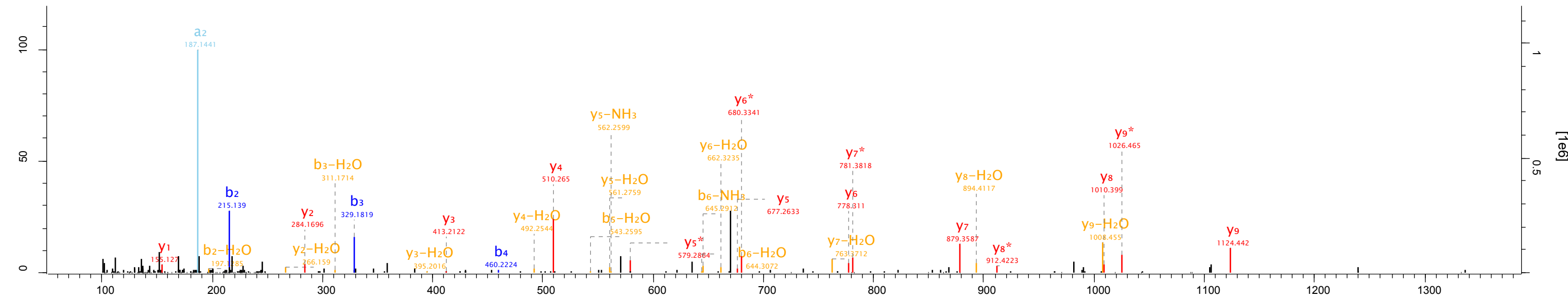
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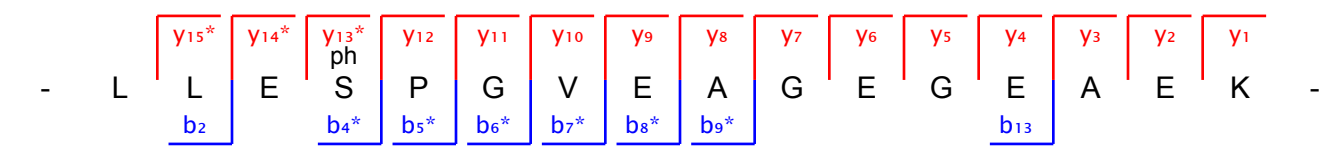
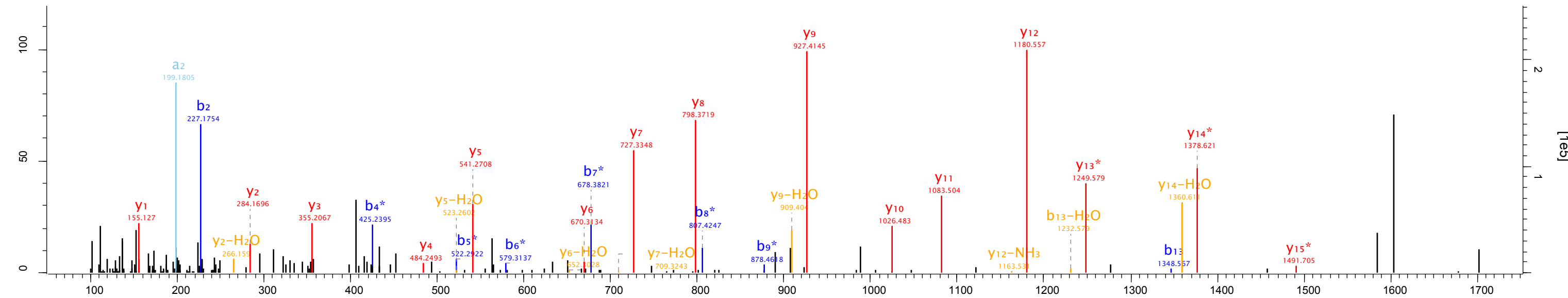
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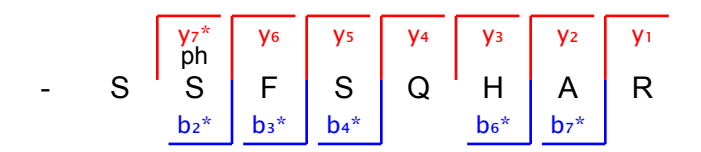
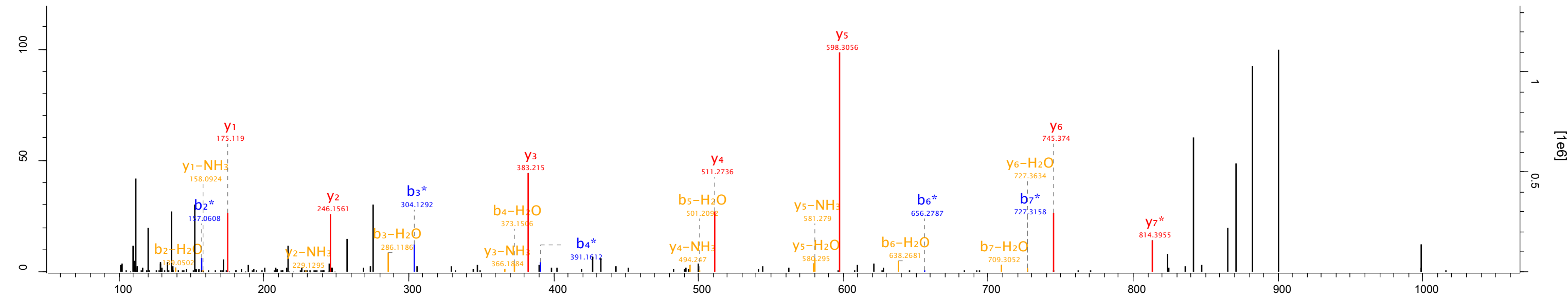
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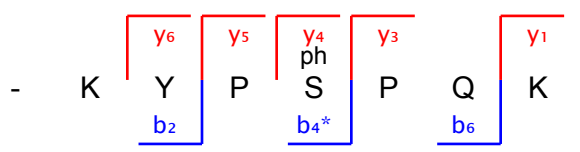
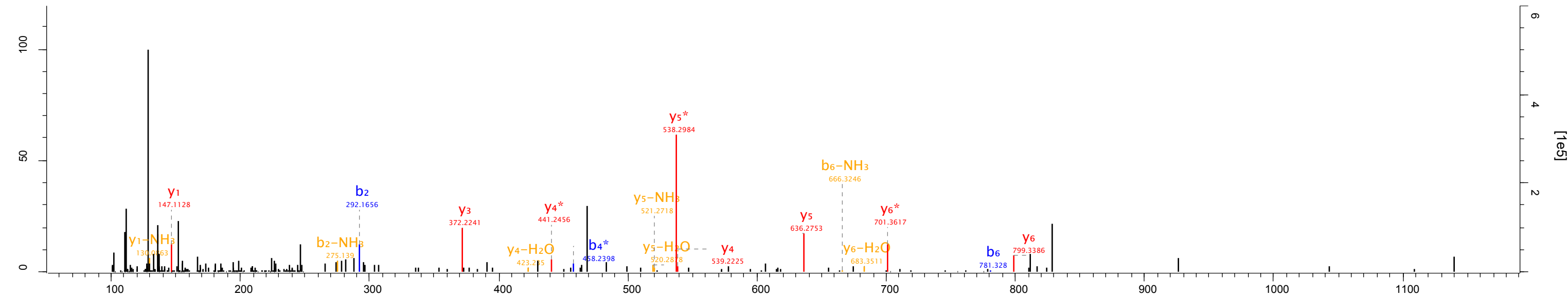
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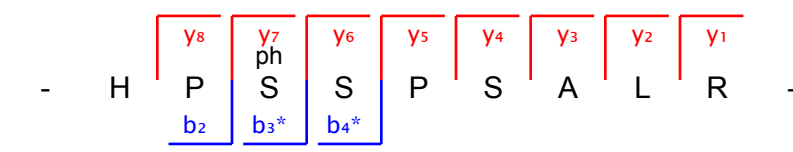
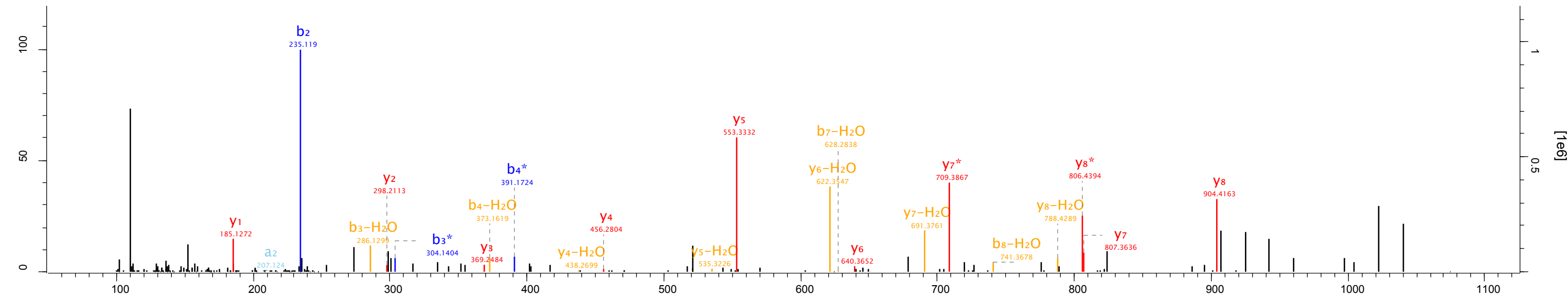
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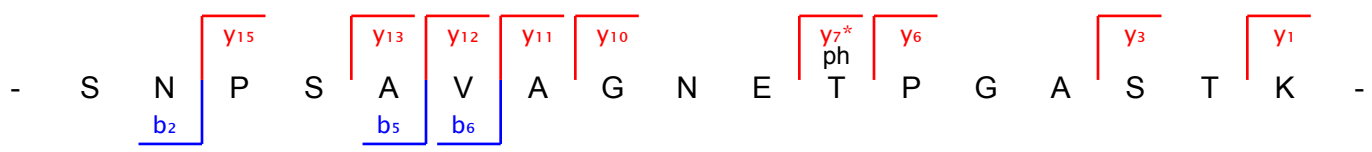
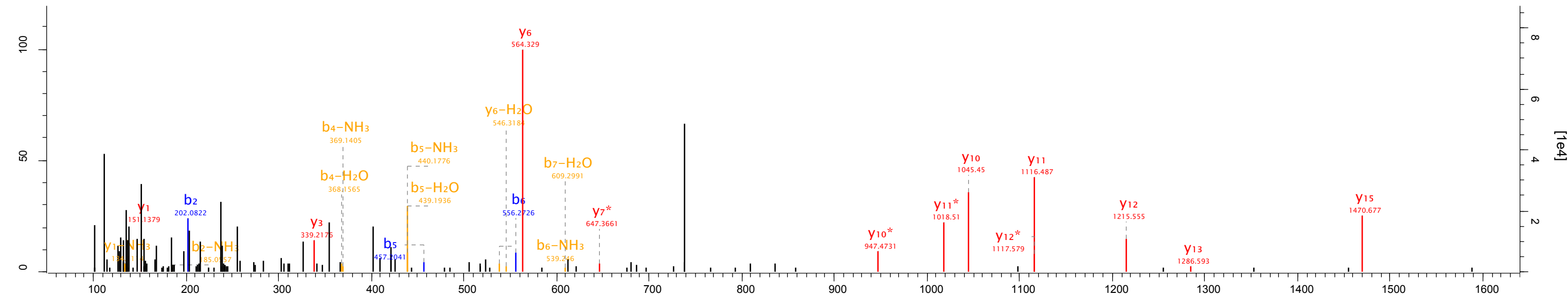
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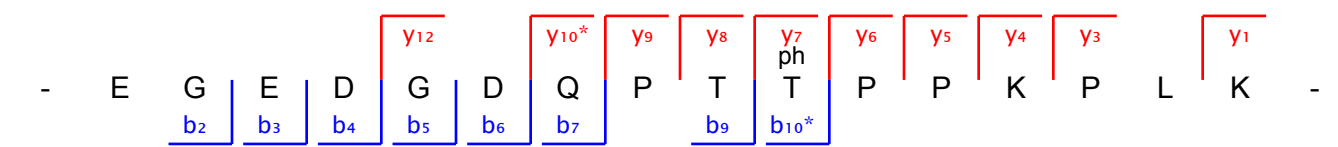
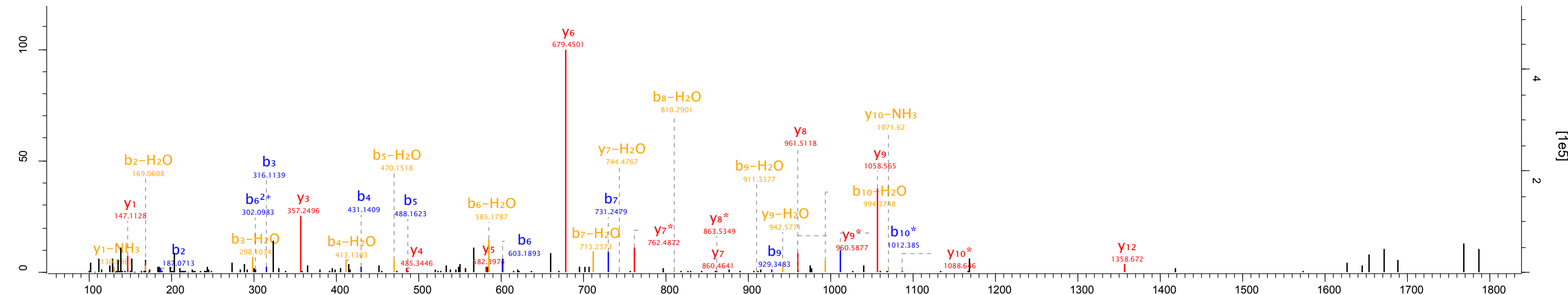
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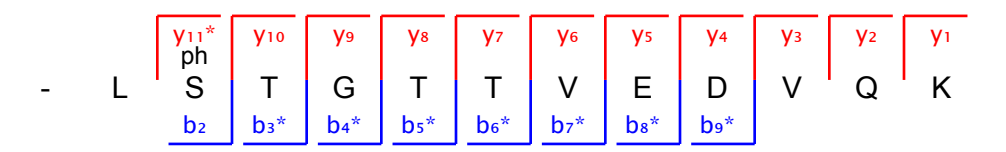
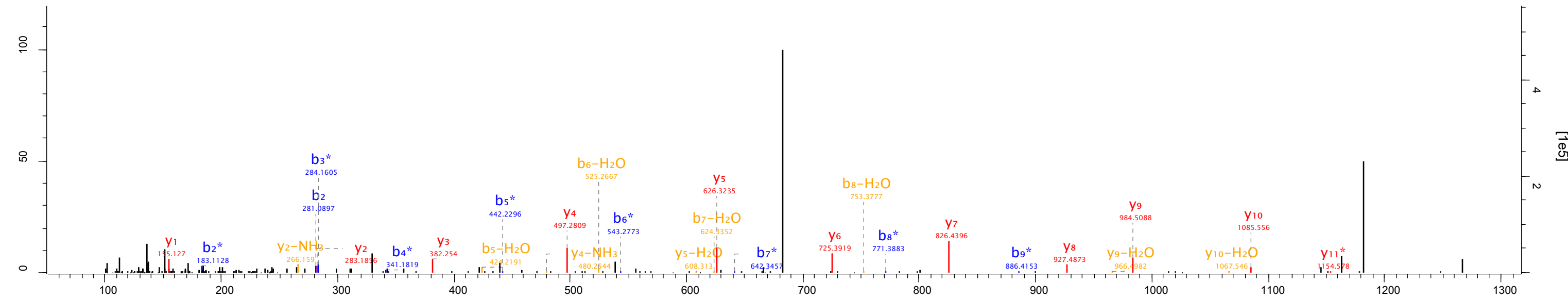
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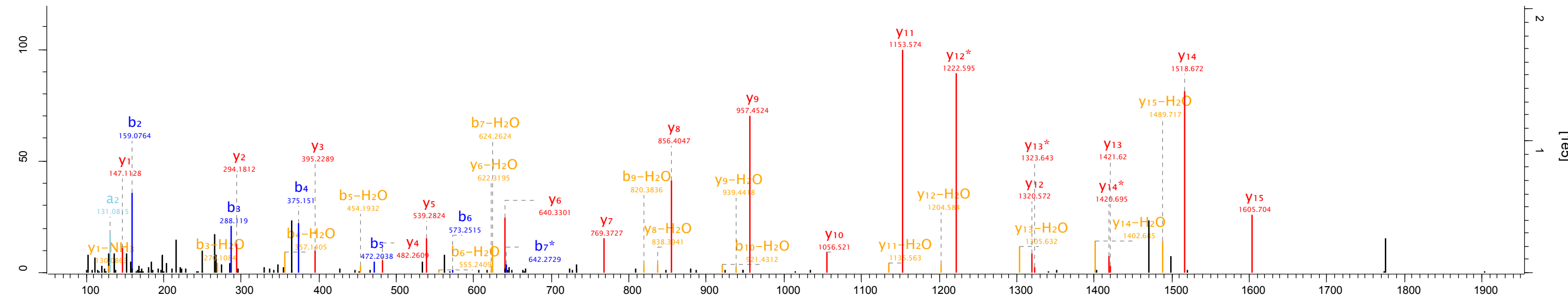
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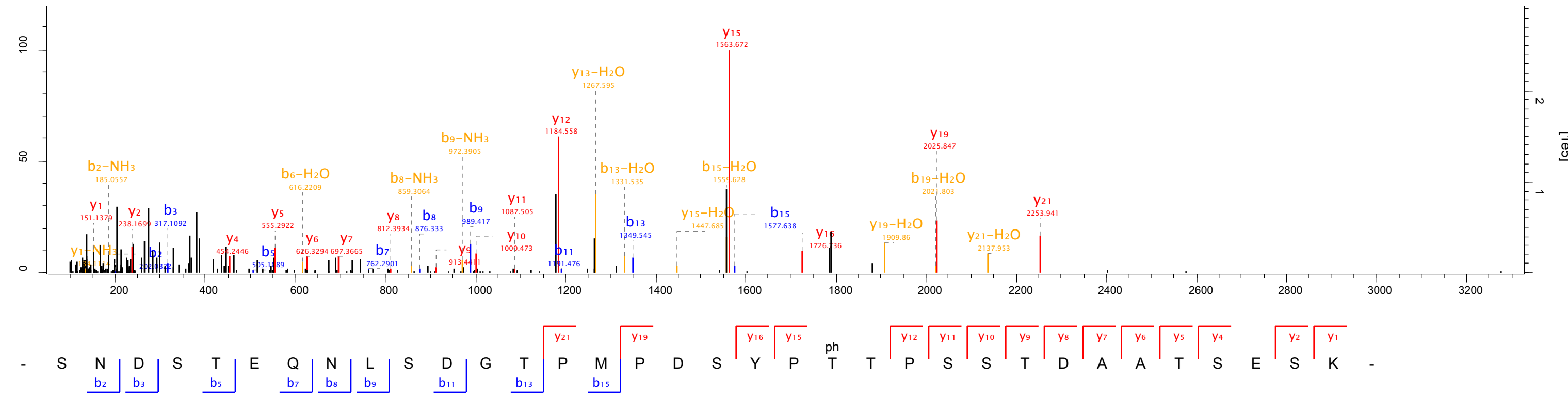


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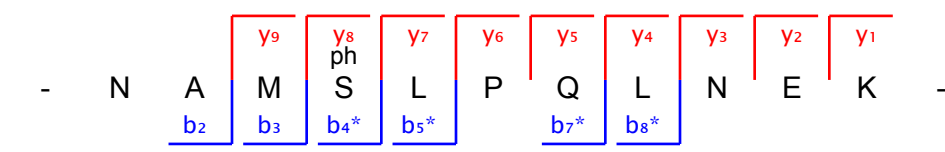
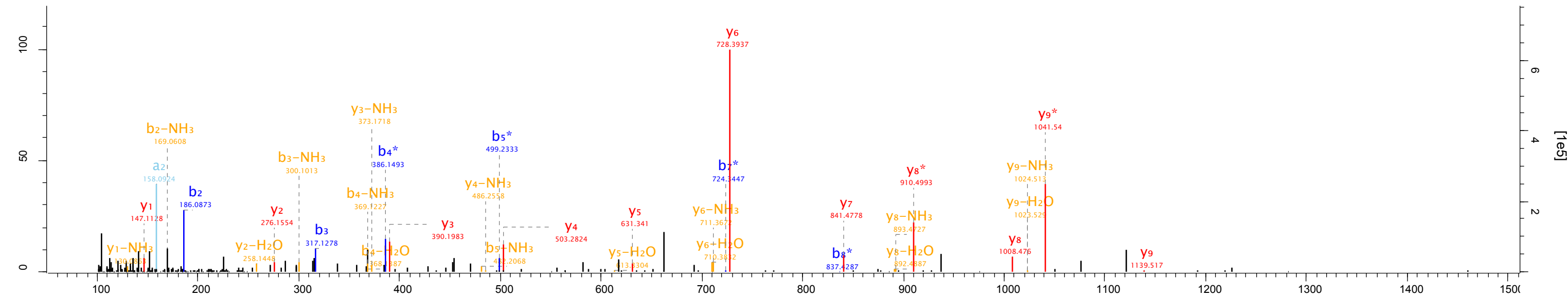


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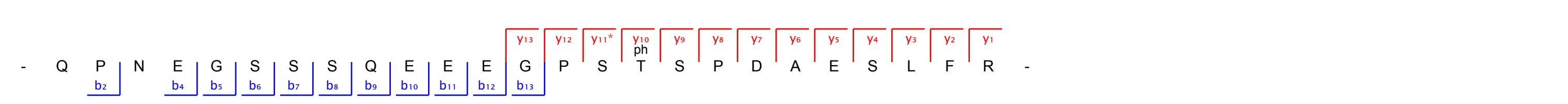
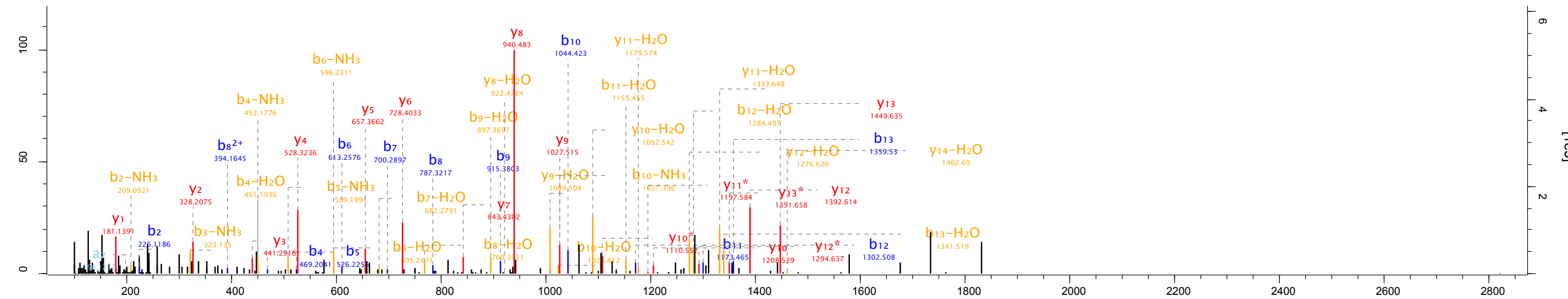
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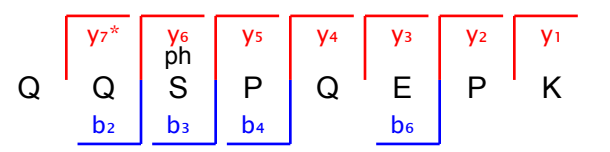
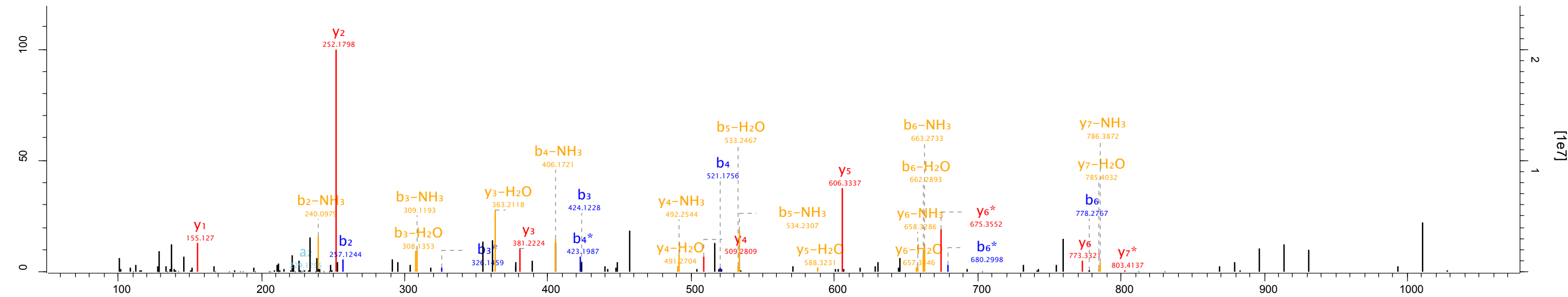
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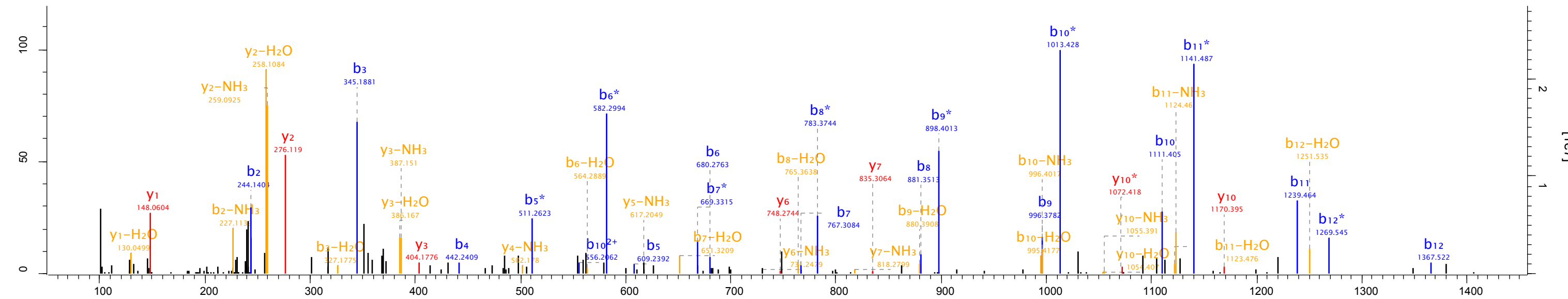
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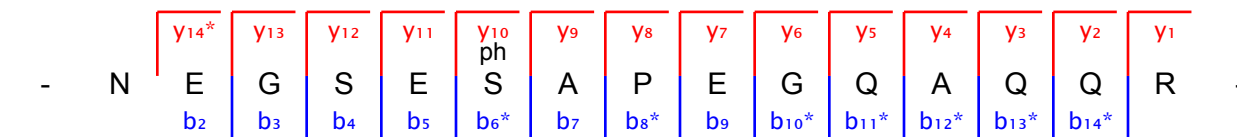
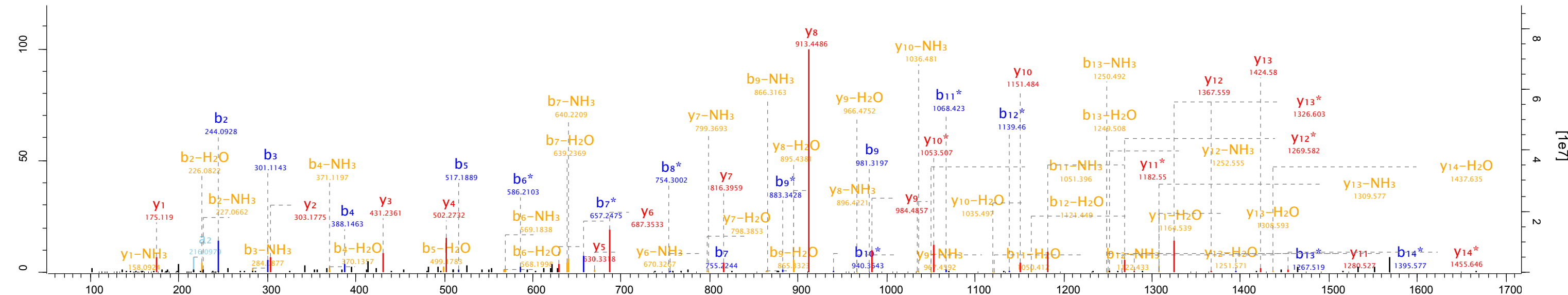


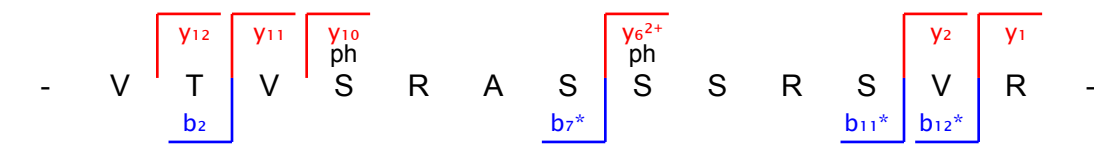
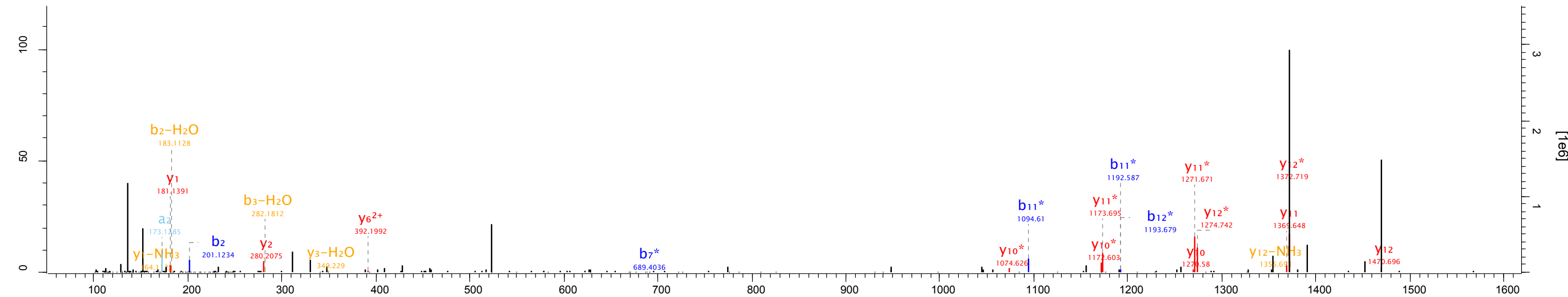
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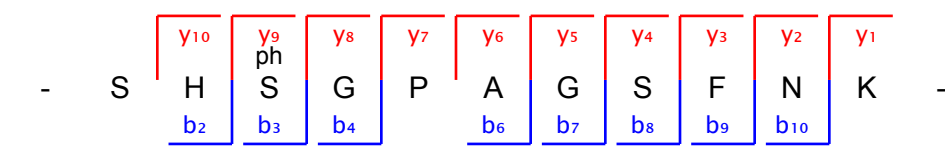
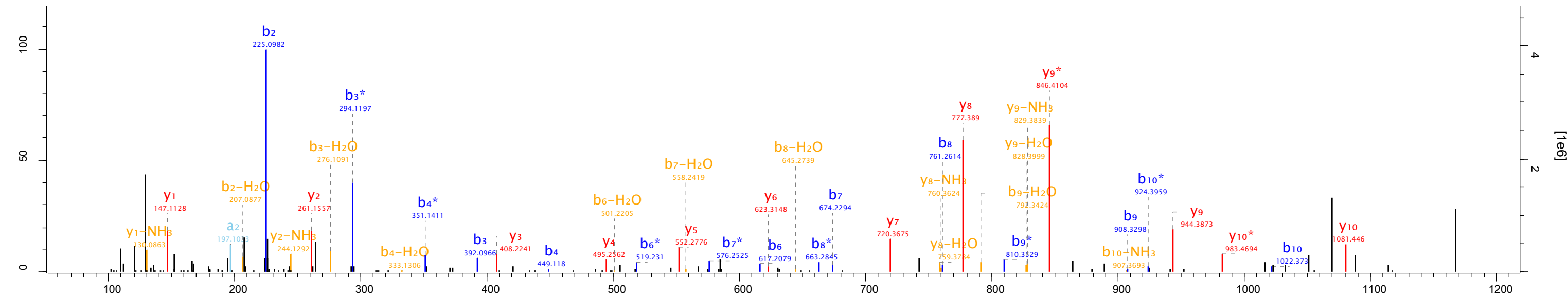
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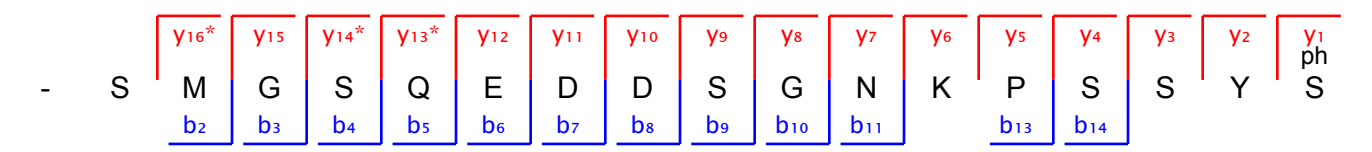
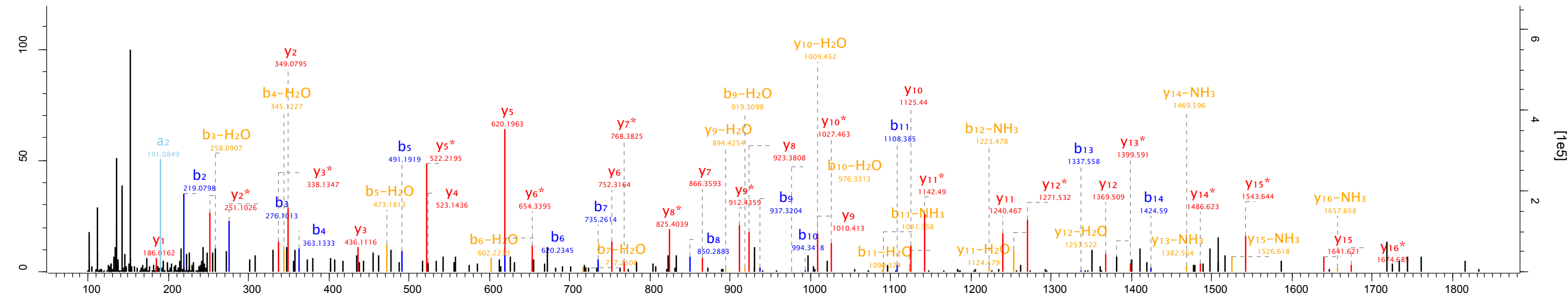


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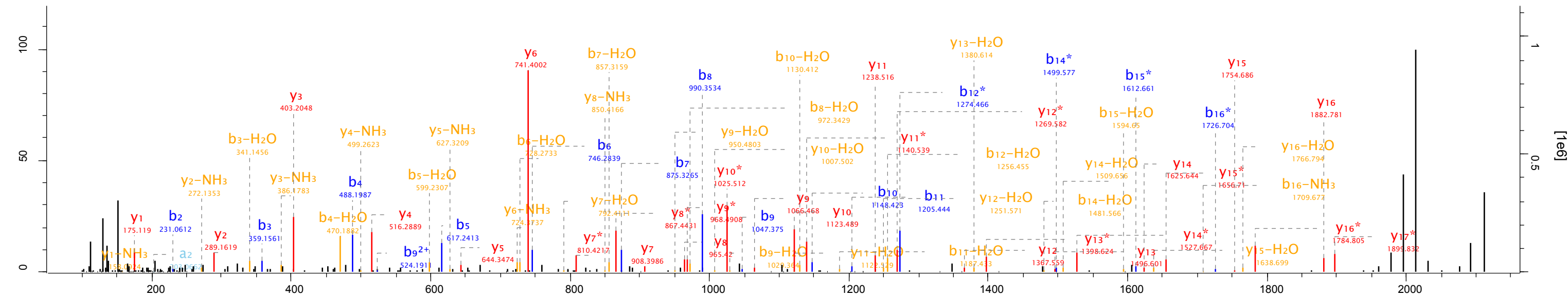


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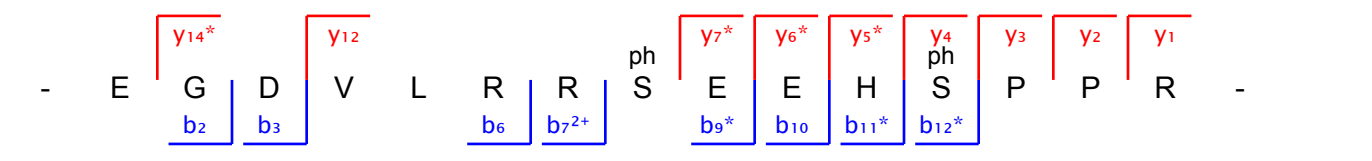
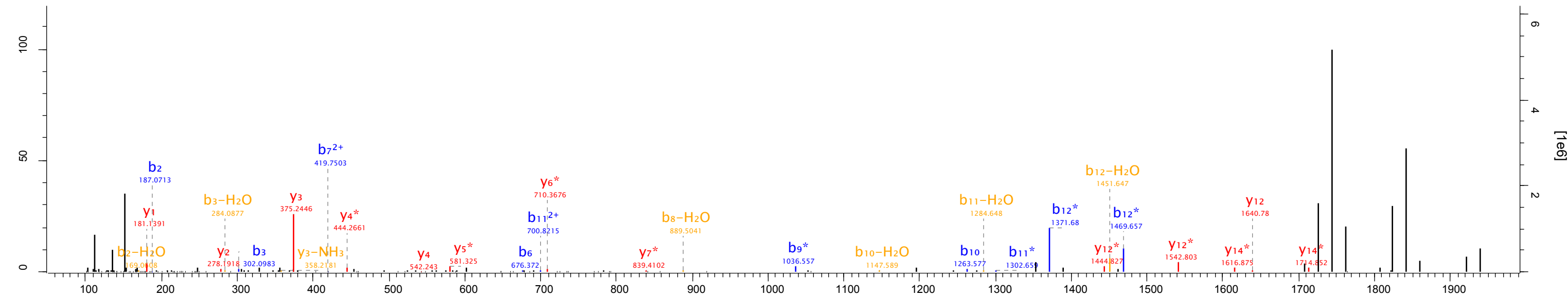
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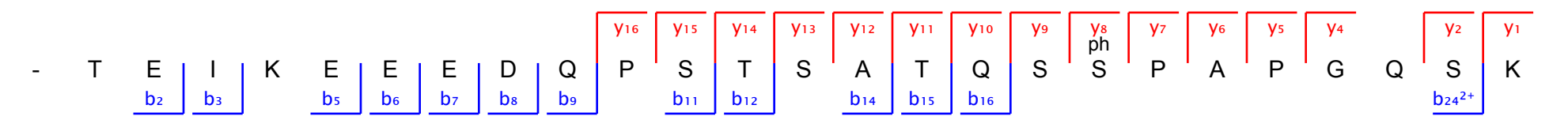
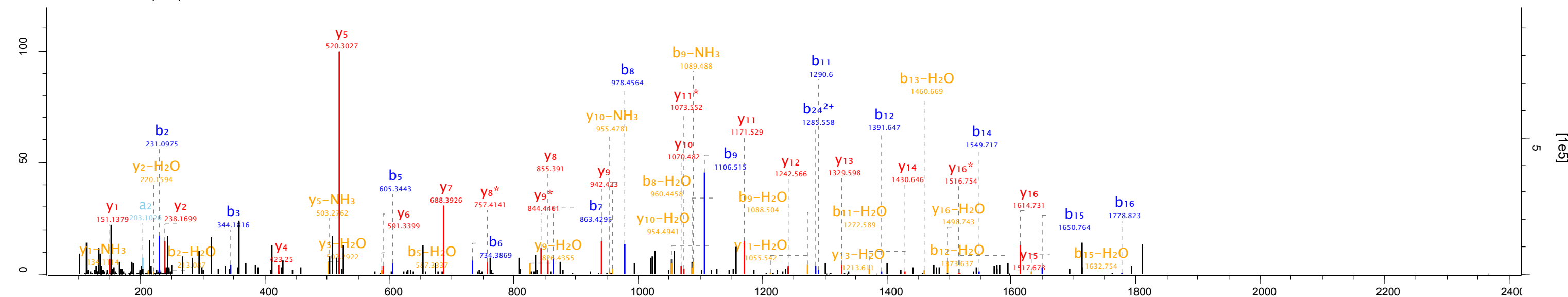


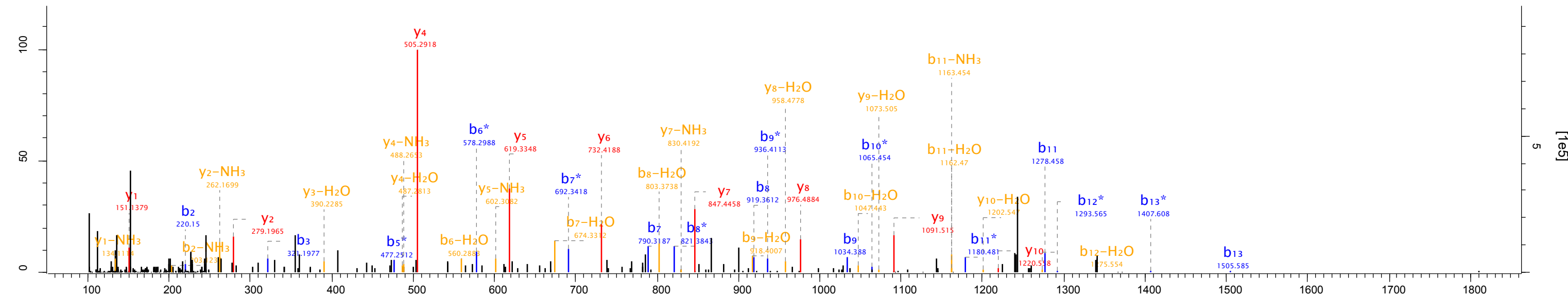
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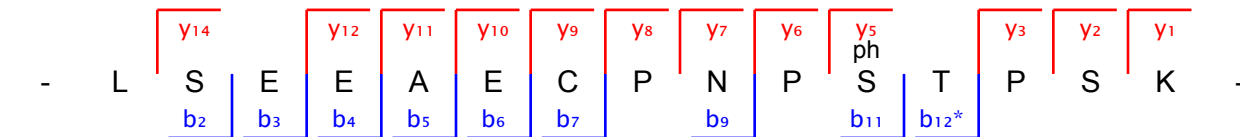
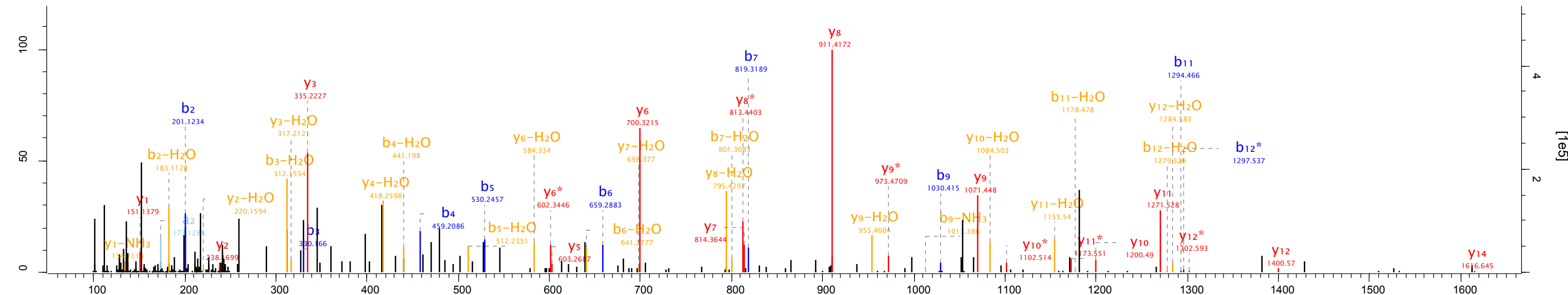
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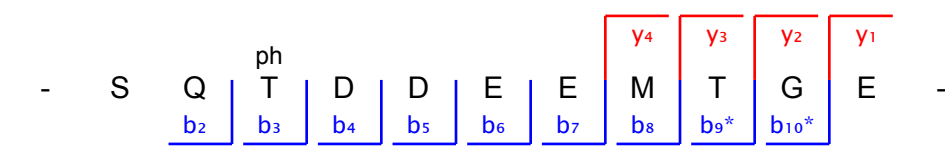
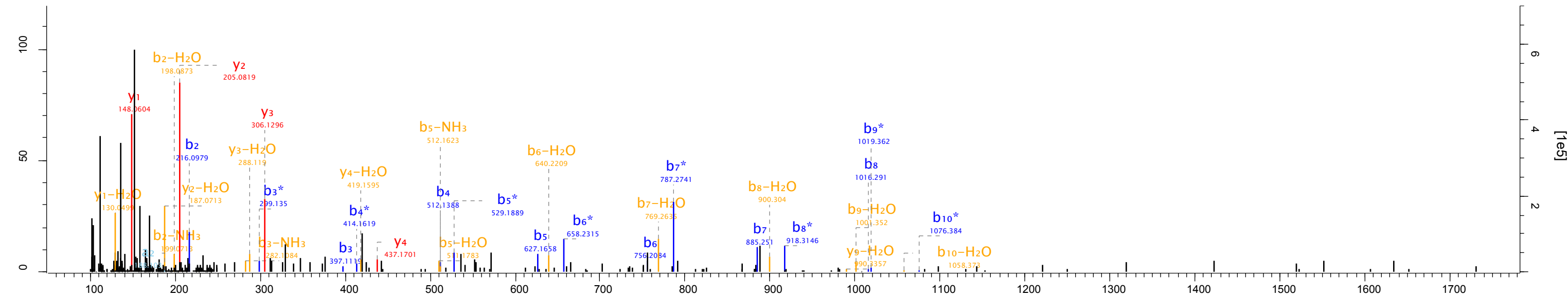


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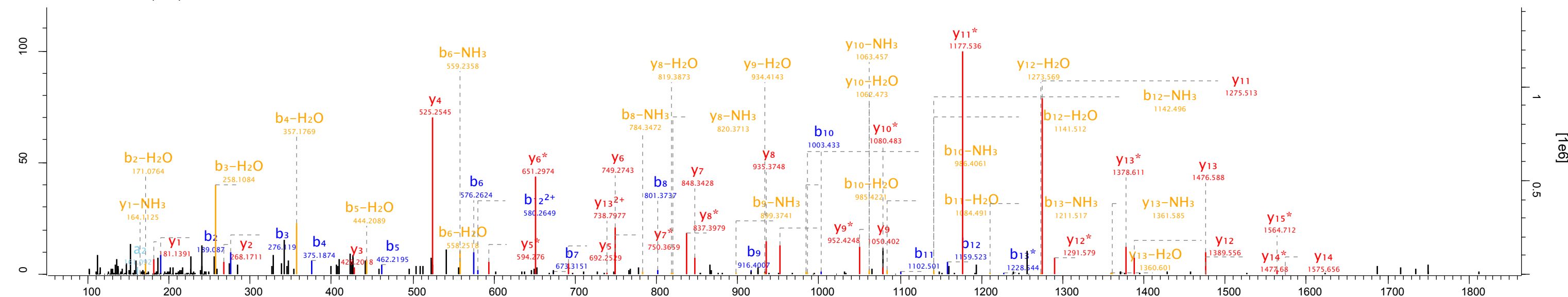


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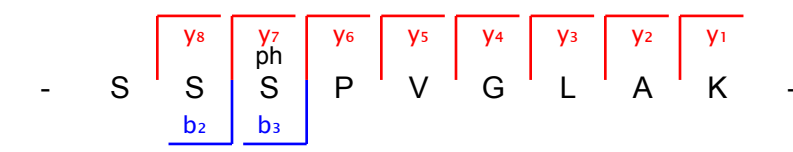
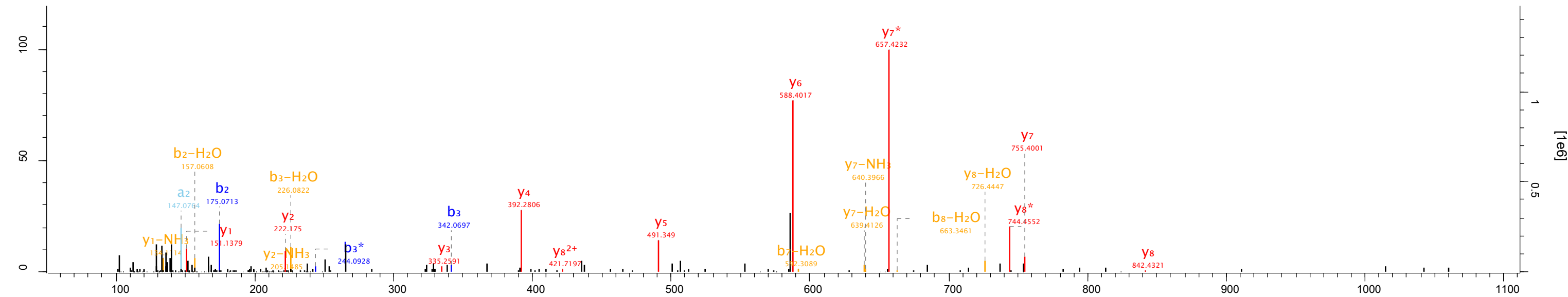
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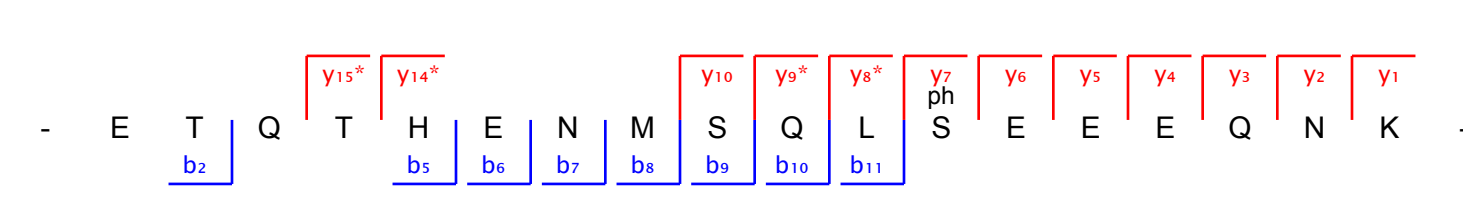
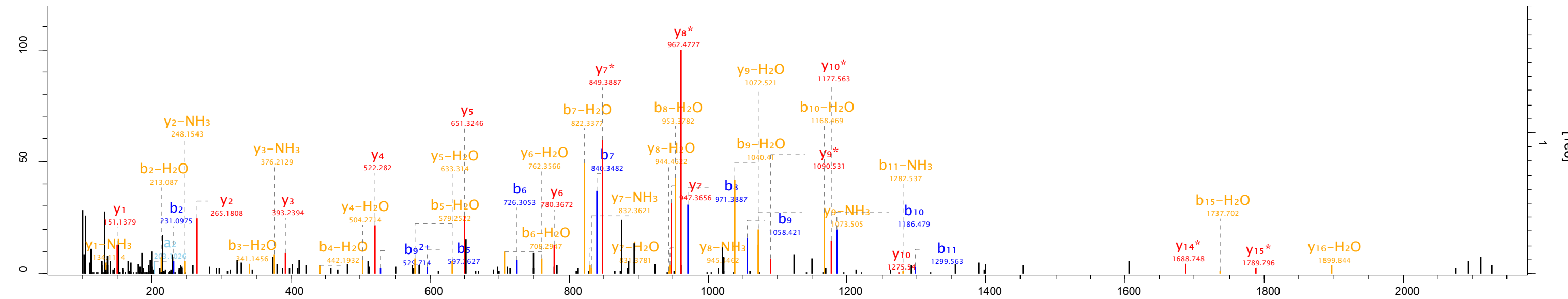


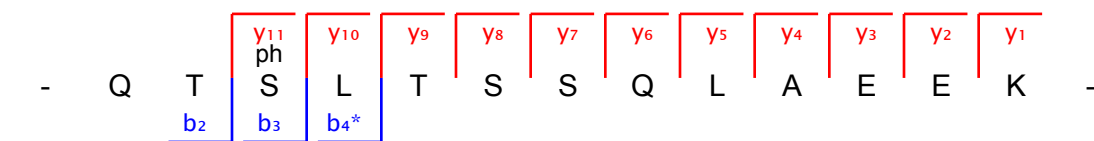
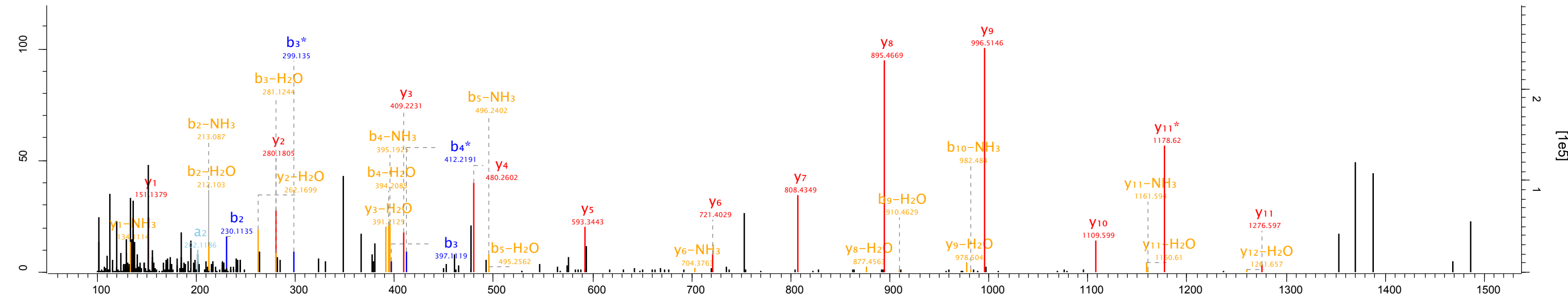
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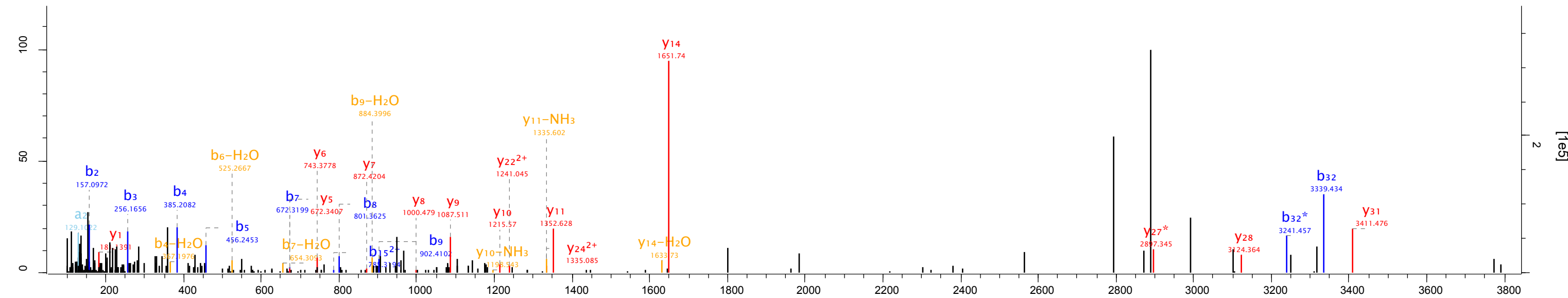


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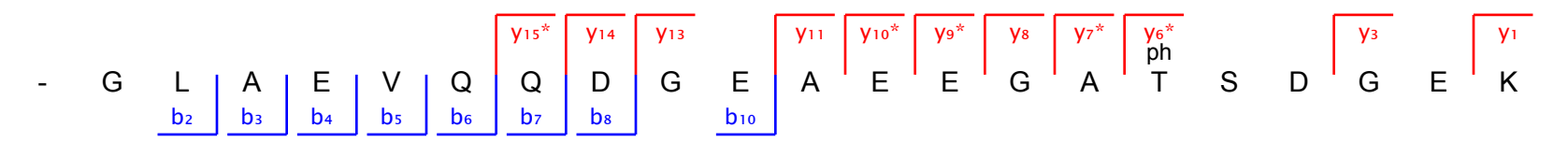
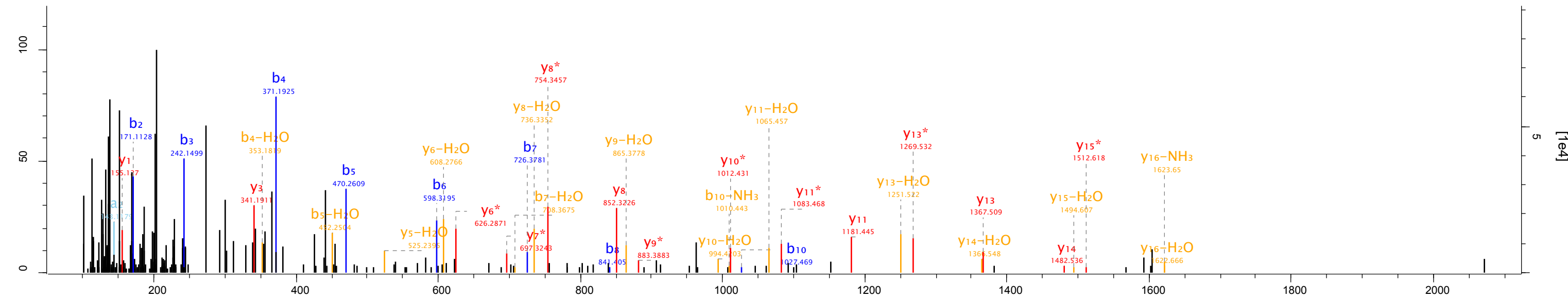




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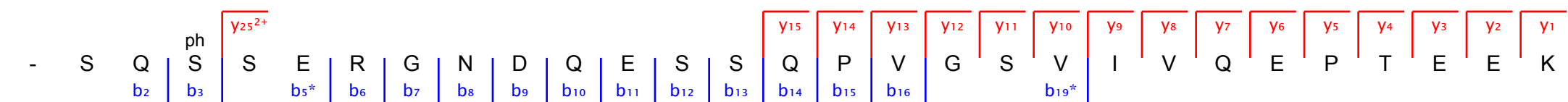
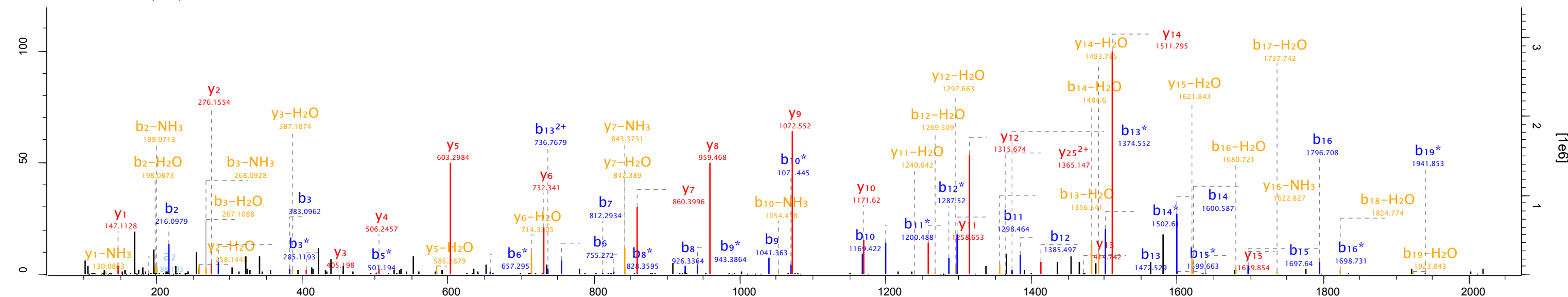


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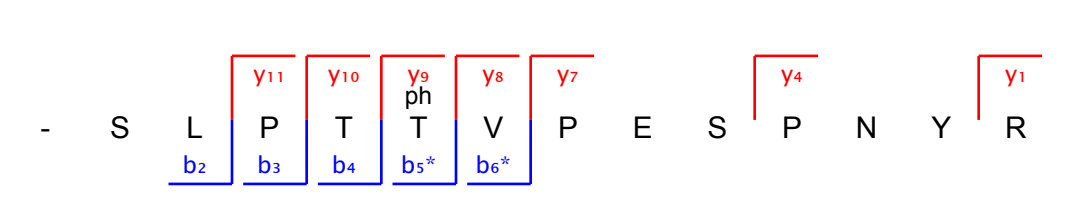
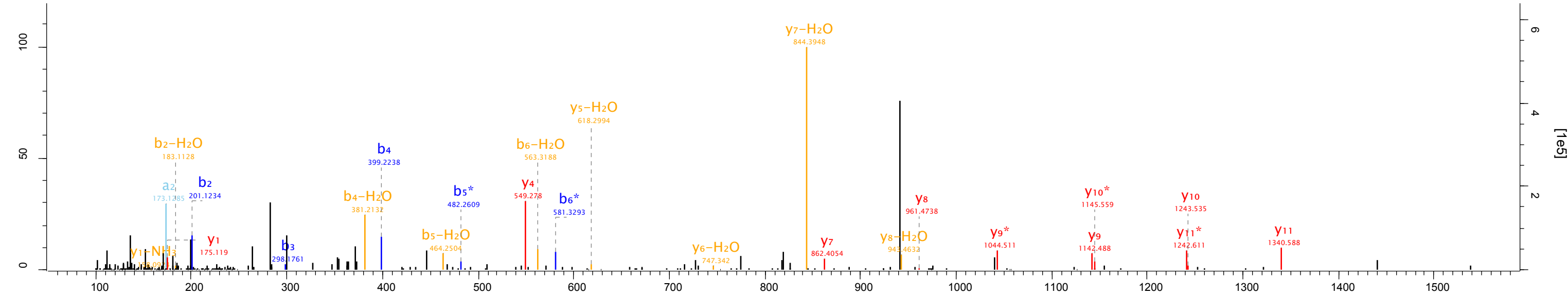
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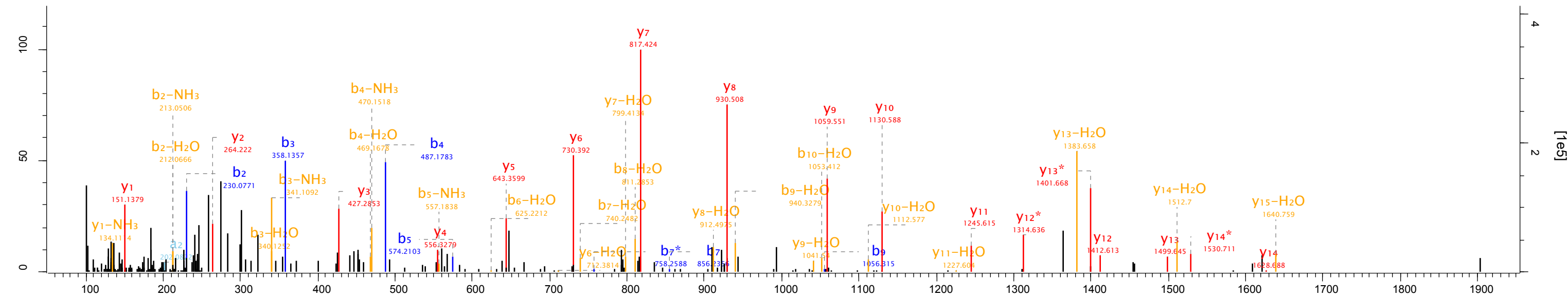
Scan 9516 Method FTMS; HCD Score 203.15 m/z 1038.13 Gene names PAGE2;PAGE2B



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20171215_MaS_33SR_LMH_phospho2_01



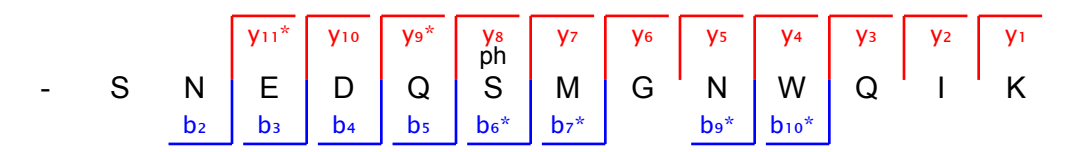
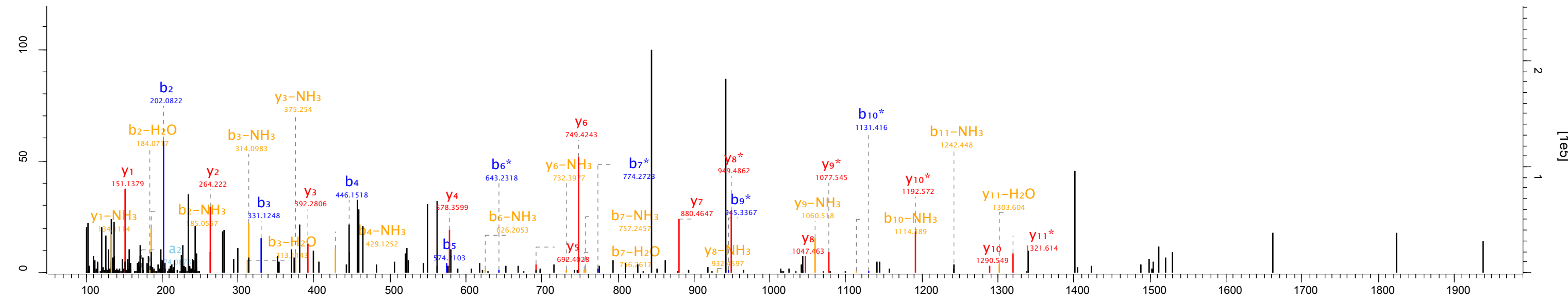


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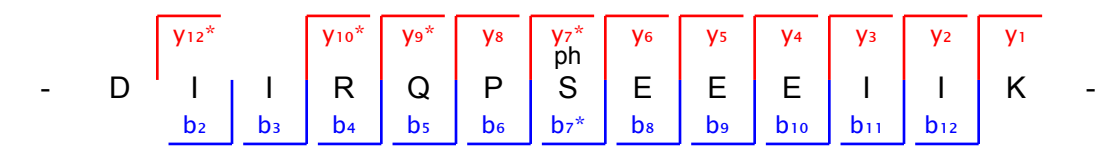
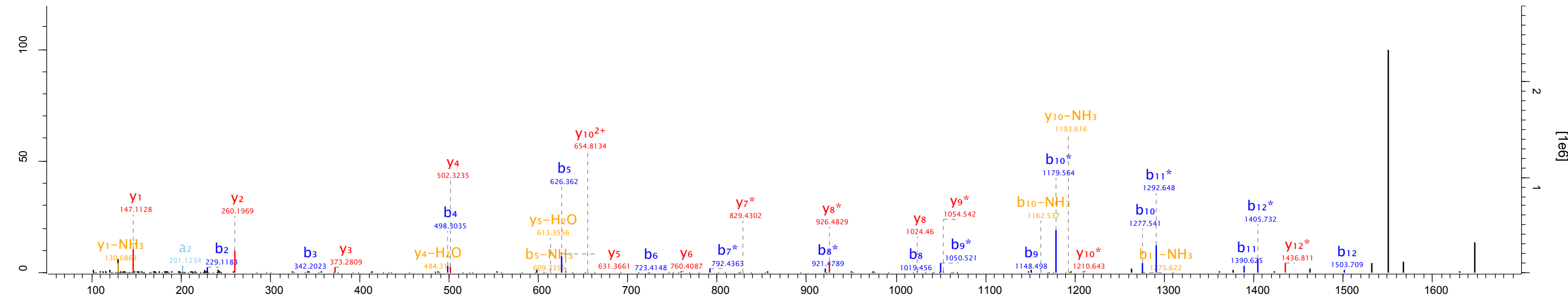
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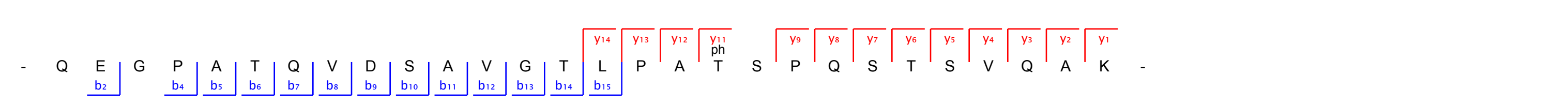
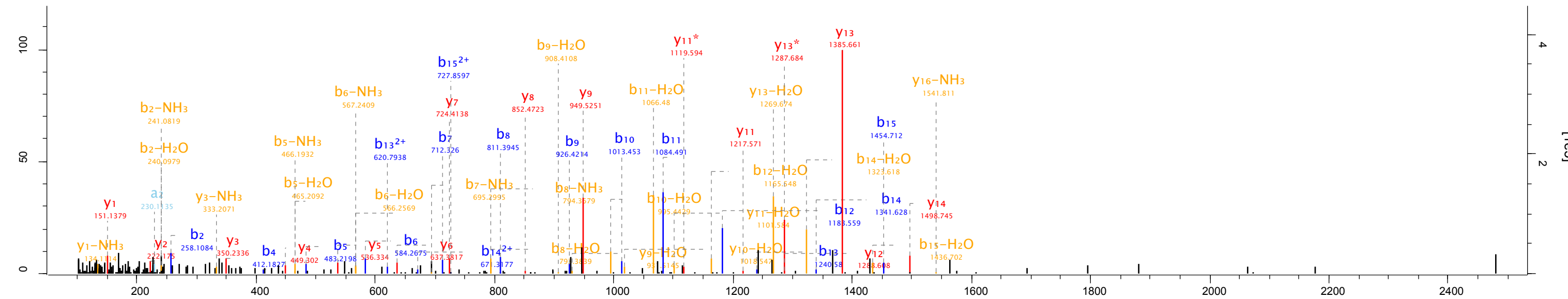
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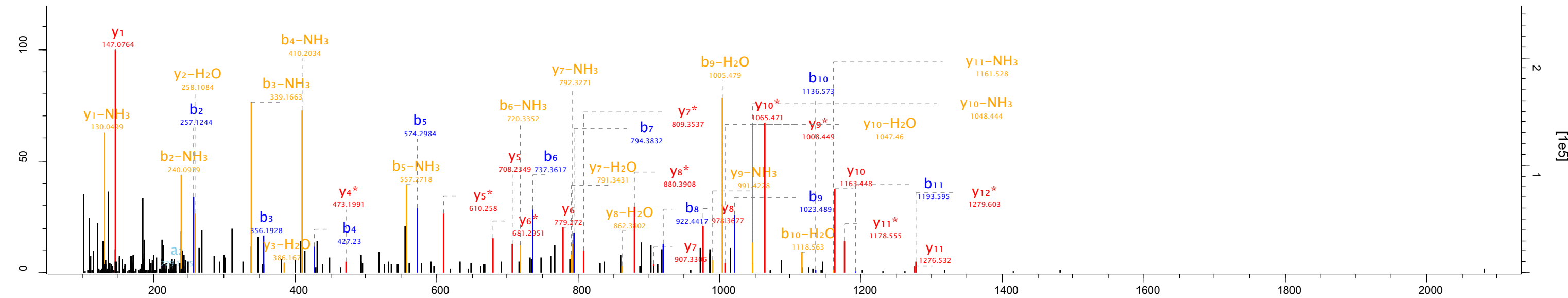


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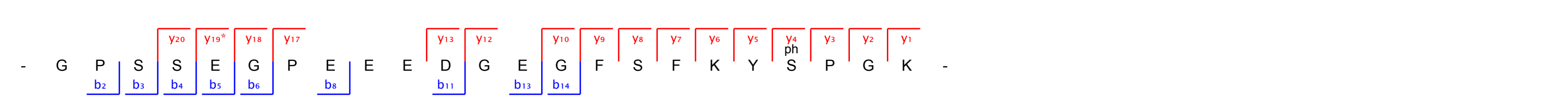
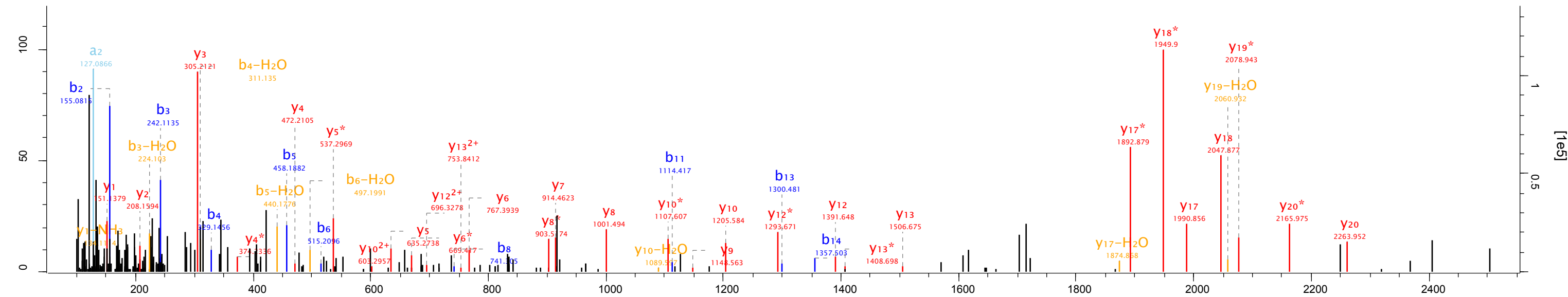
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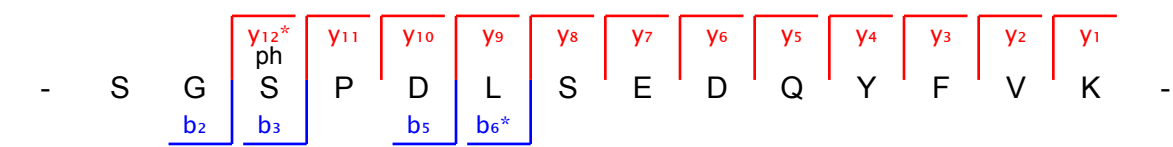
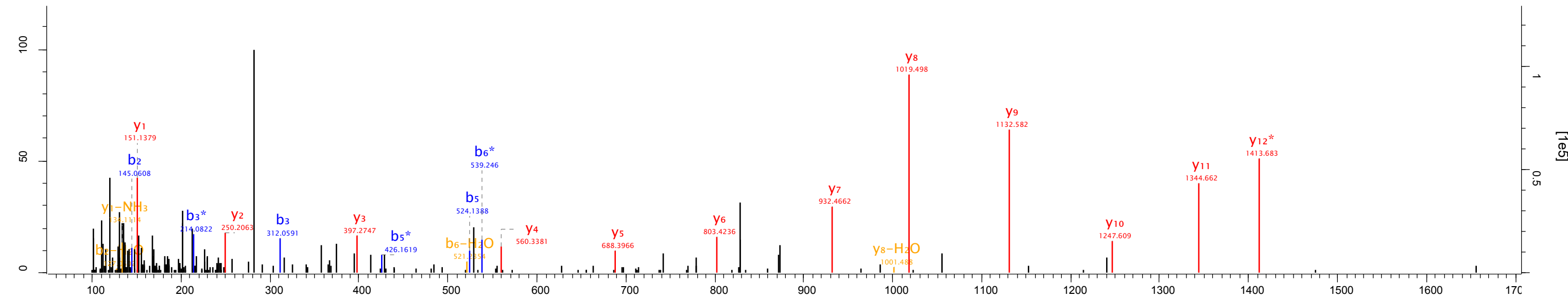


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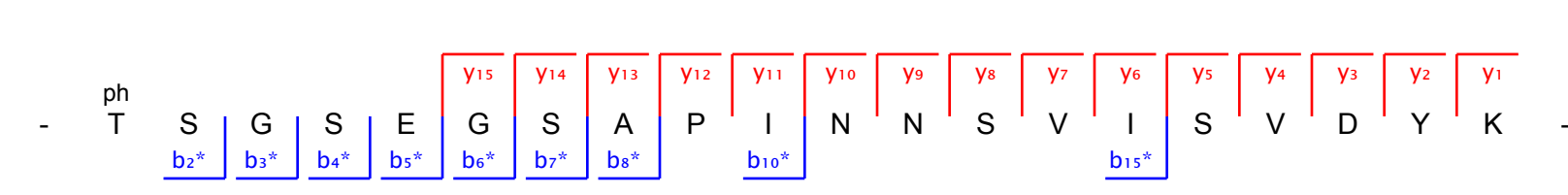
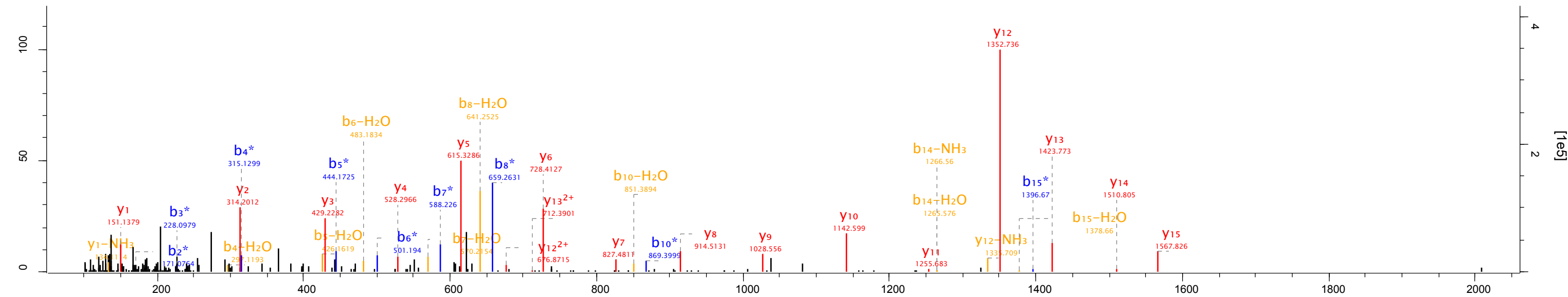
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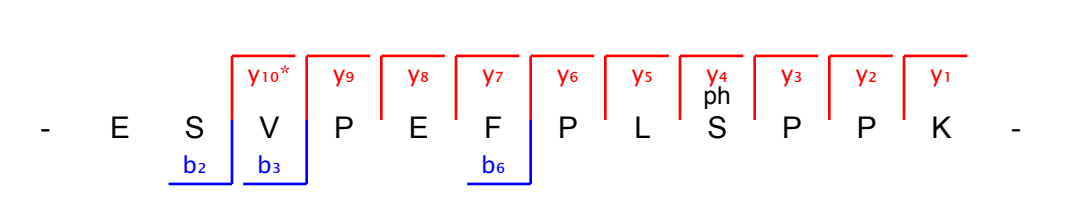
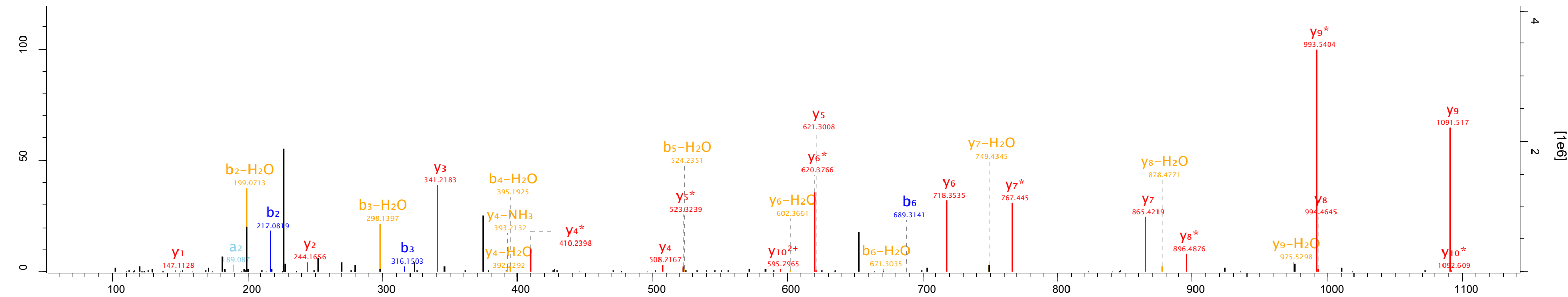
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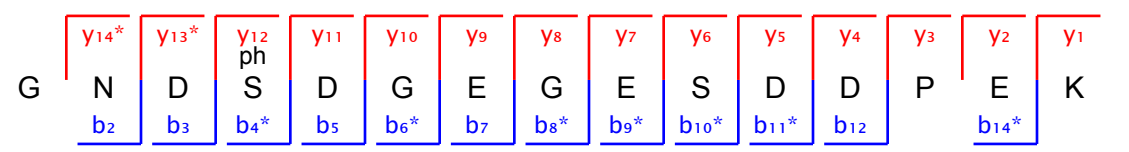
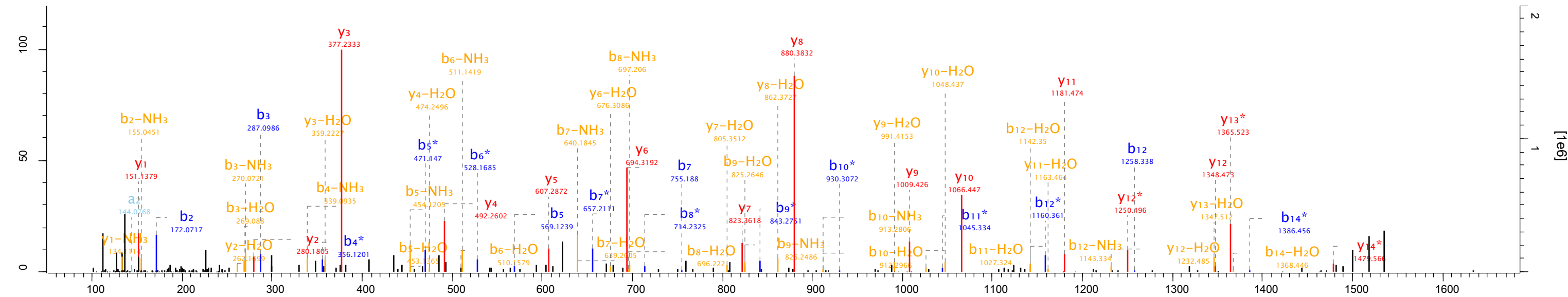
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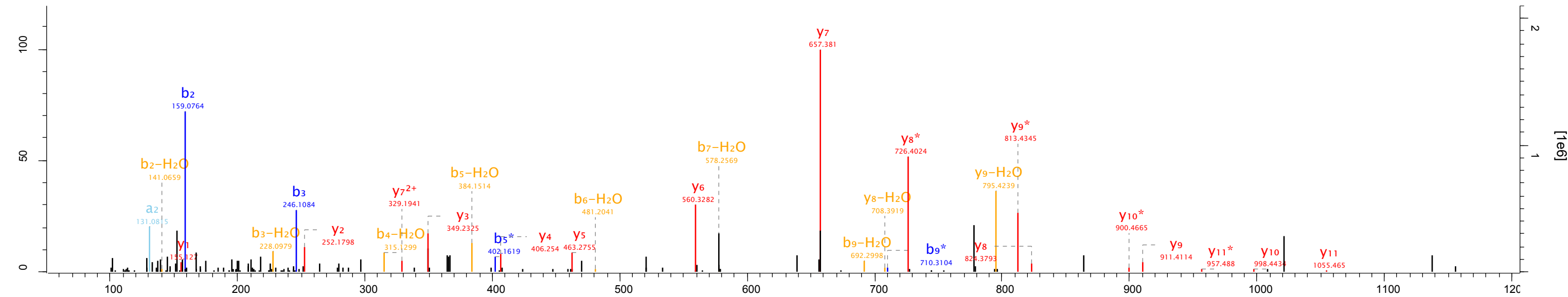


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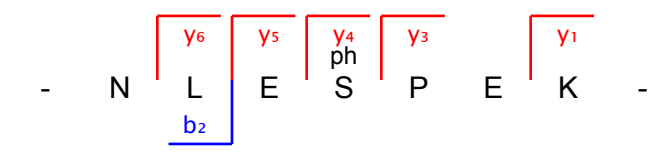
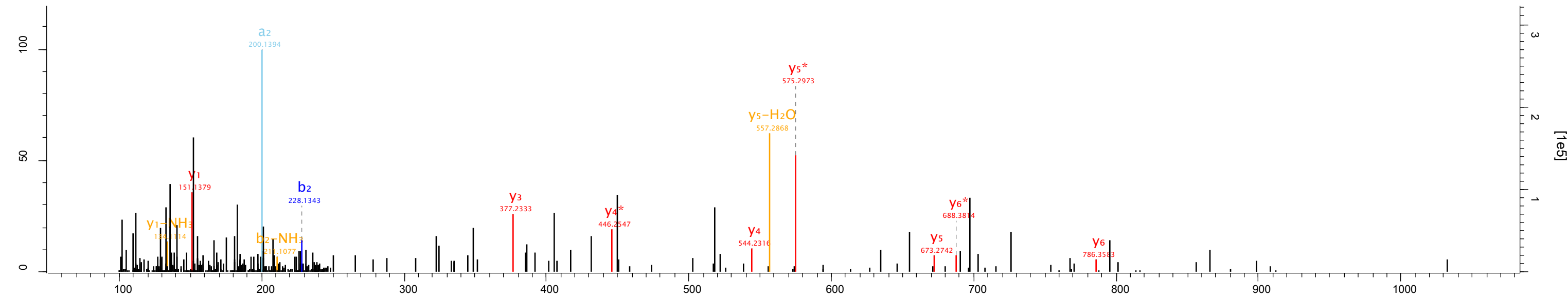


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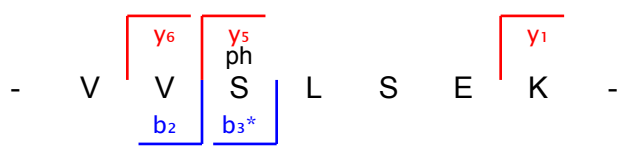
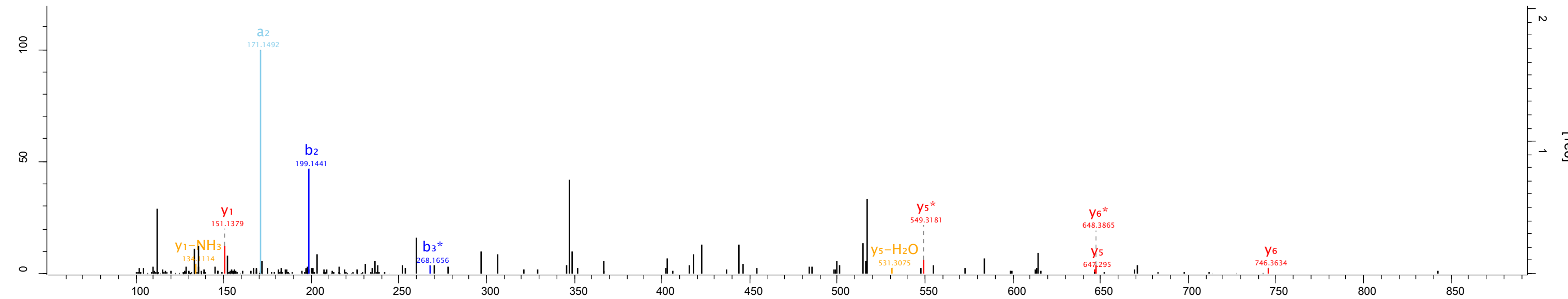
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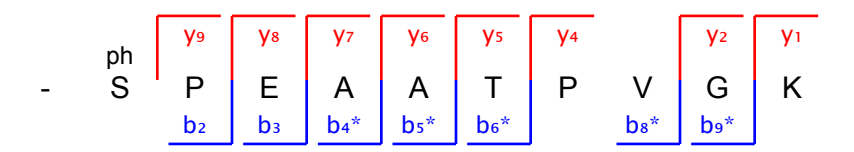
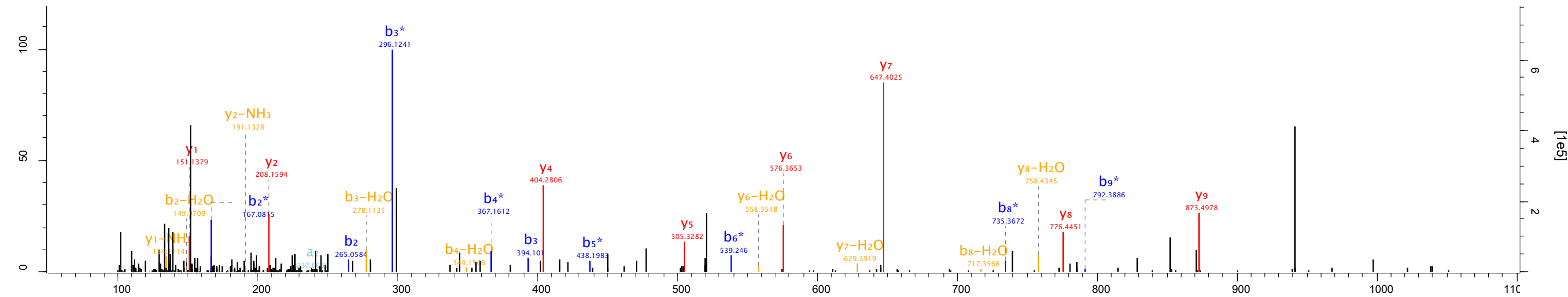
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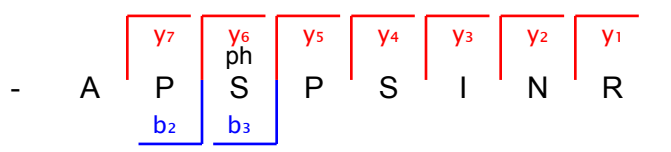
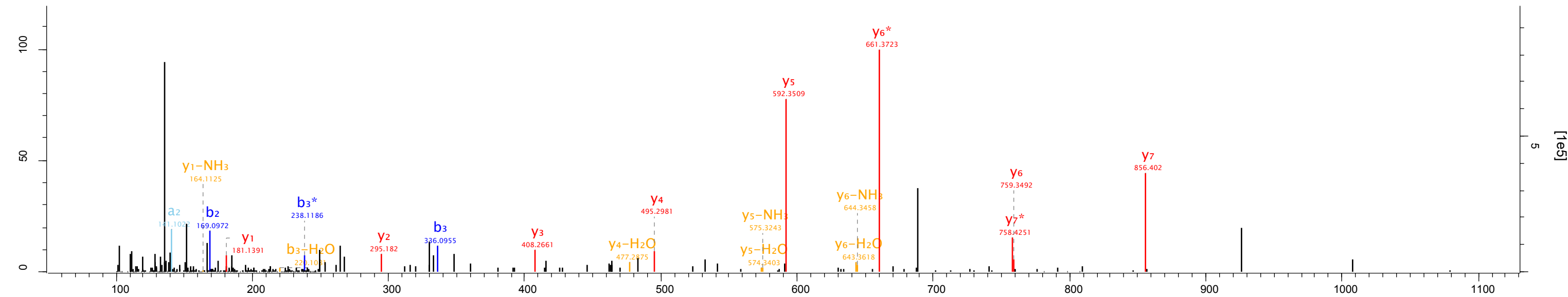
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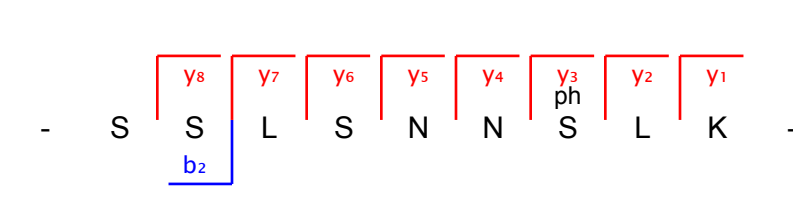
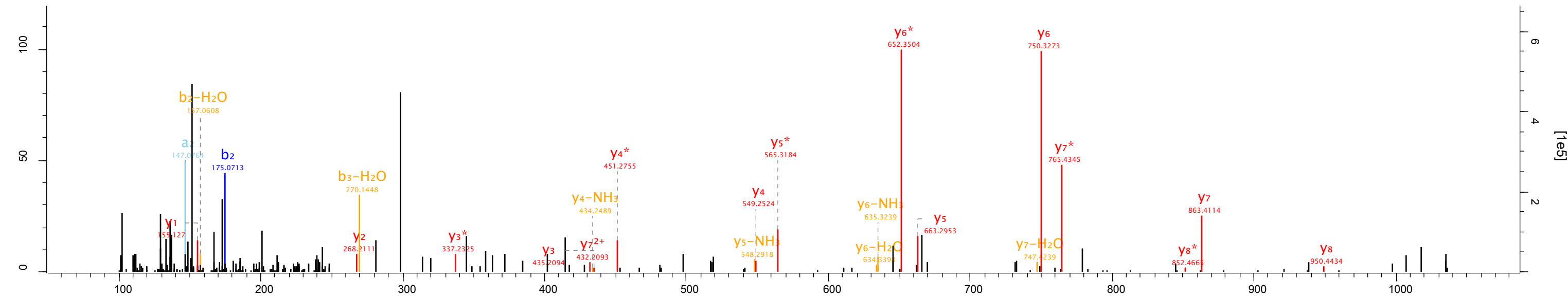
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20171215_MaS_33SR_LMH_phospho2_02

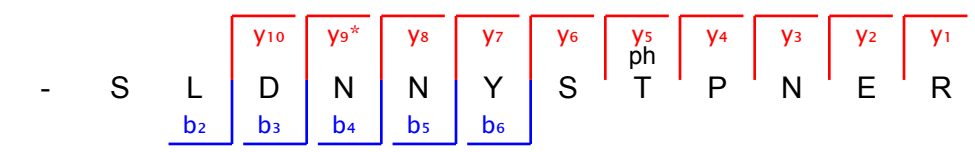
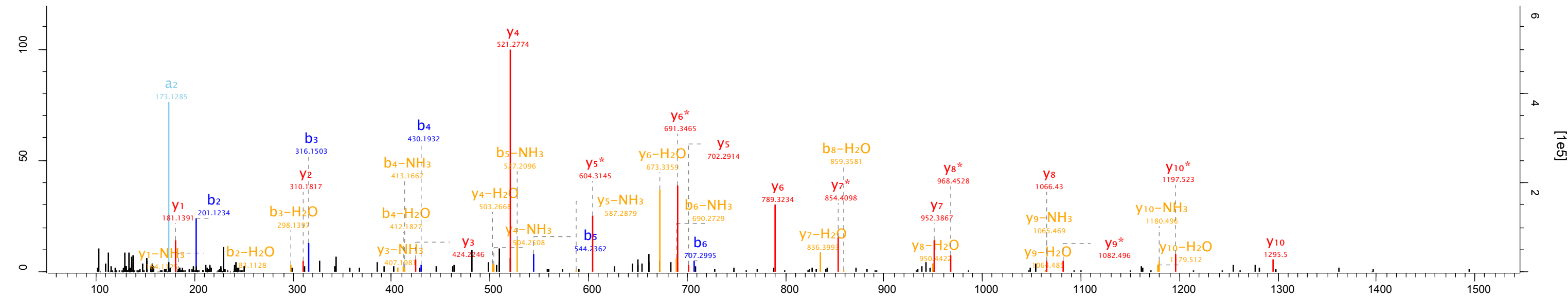
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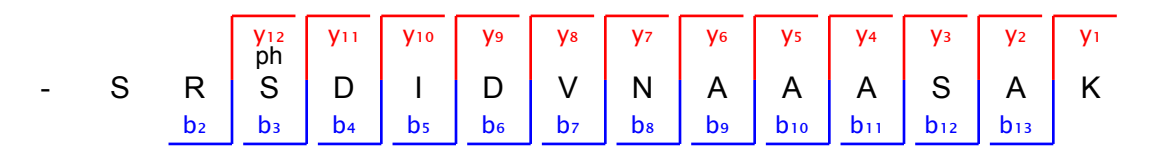
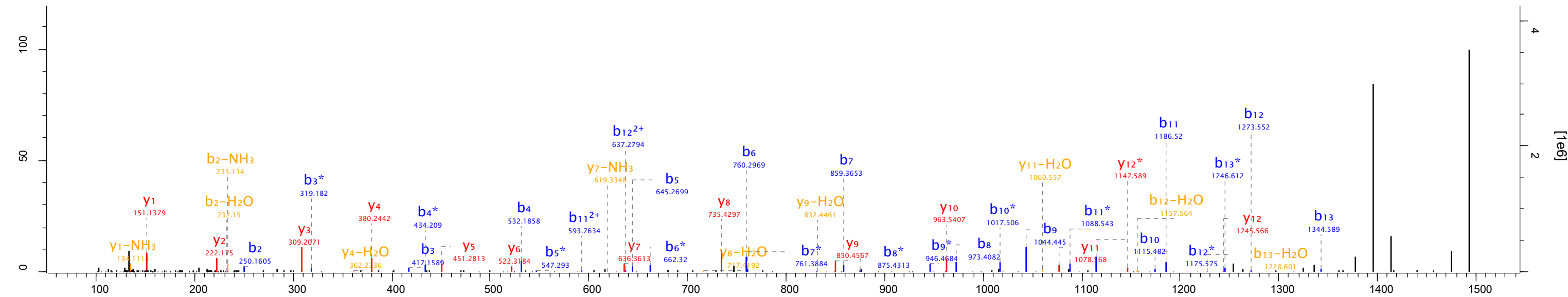
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 Scan: 4796 Method: FTMS; HCD Score: 194 m/z: 748.31 Gene names: CTNND1

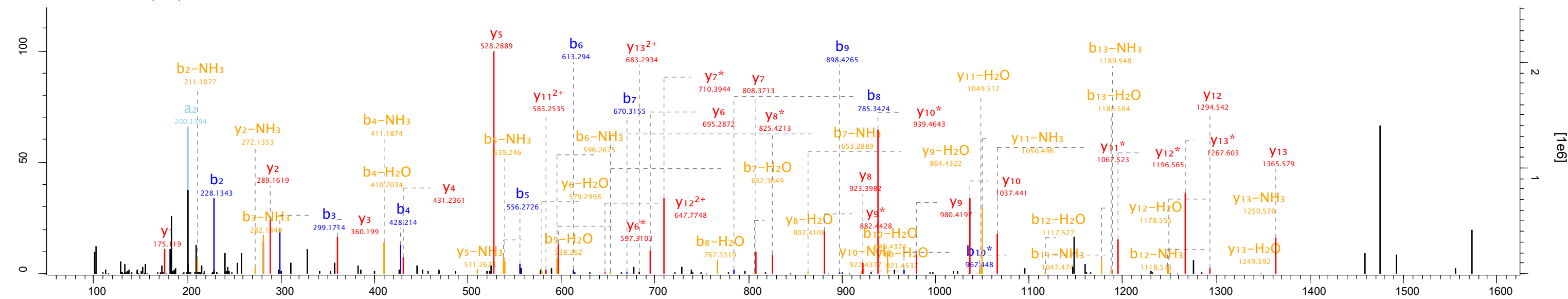


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20171215_MaS_33SR_LMH_phospho2_02

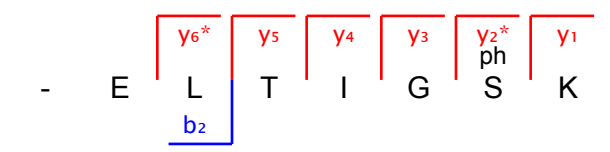
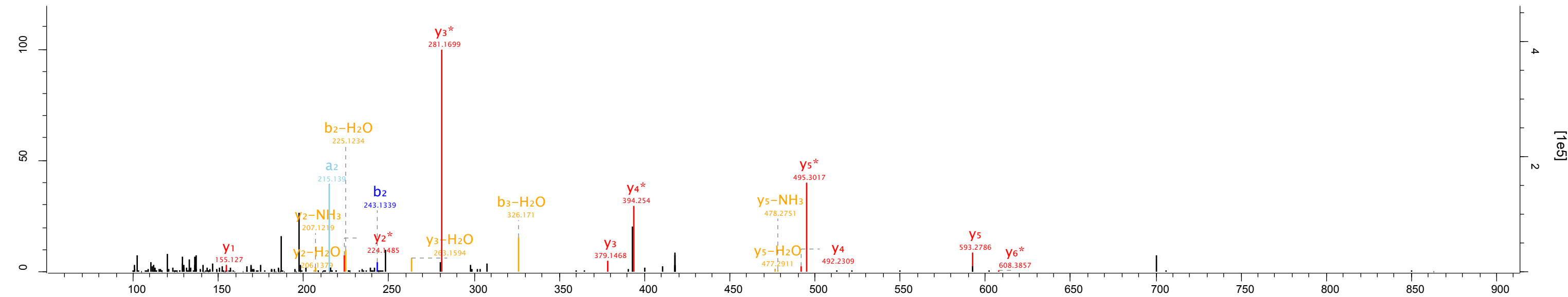
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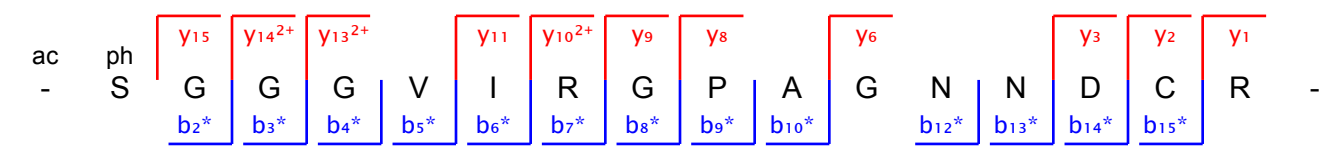
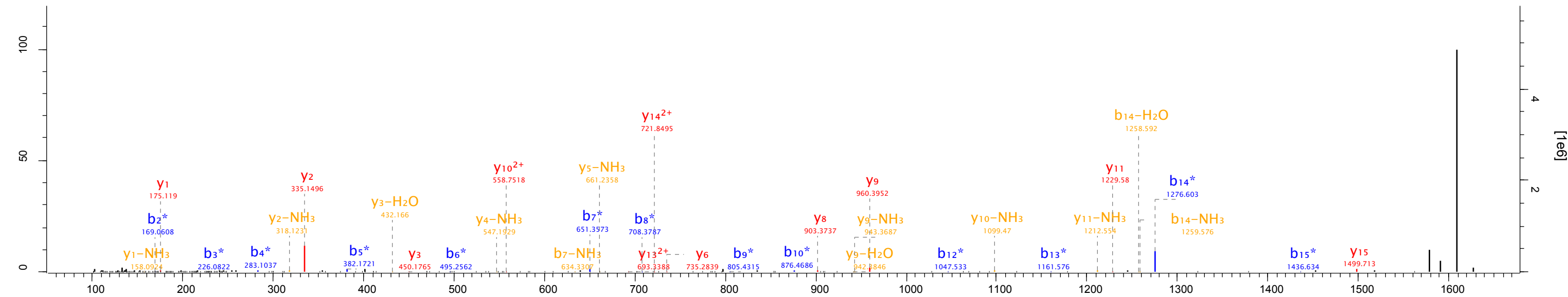
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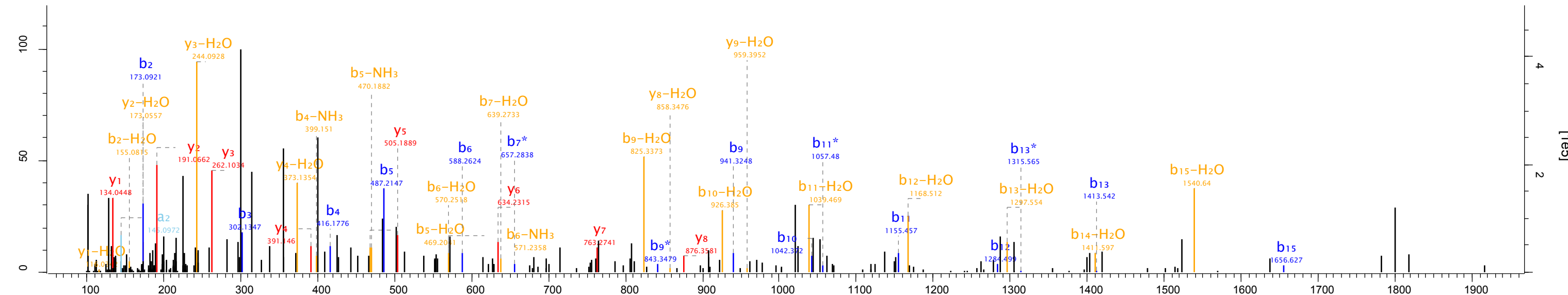
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y₁₁*
y₁₀
y₉
y₈
y₇
y₆ph
y₅
y₄
y₃
y₂
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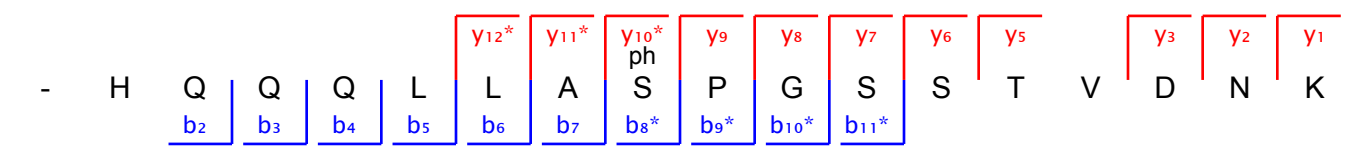
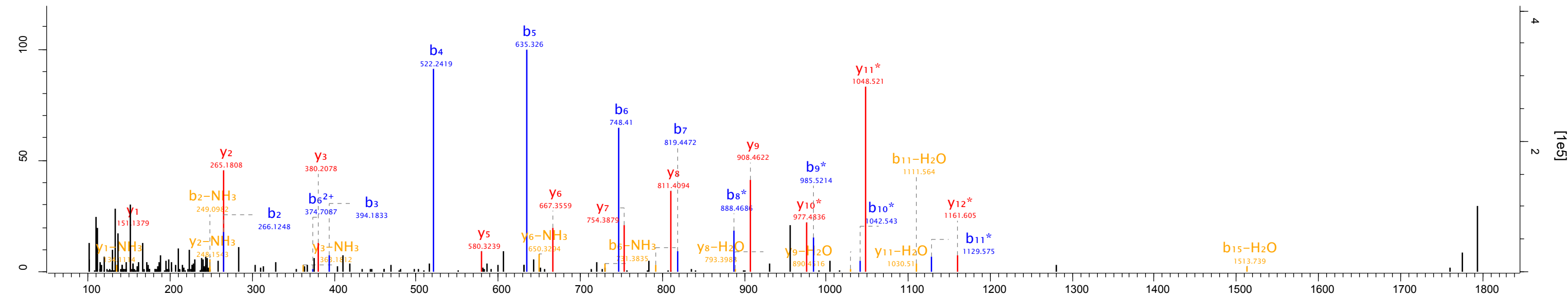


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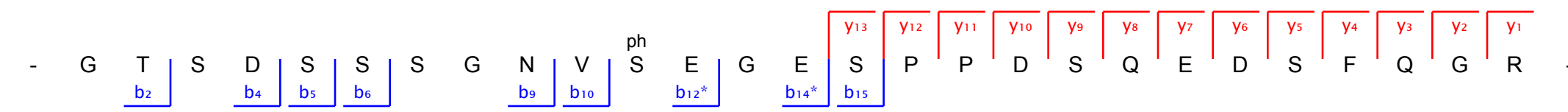
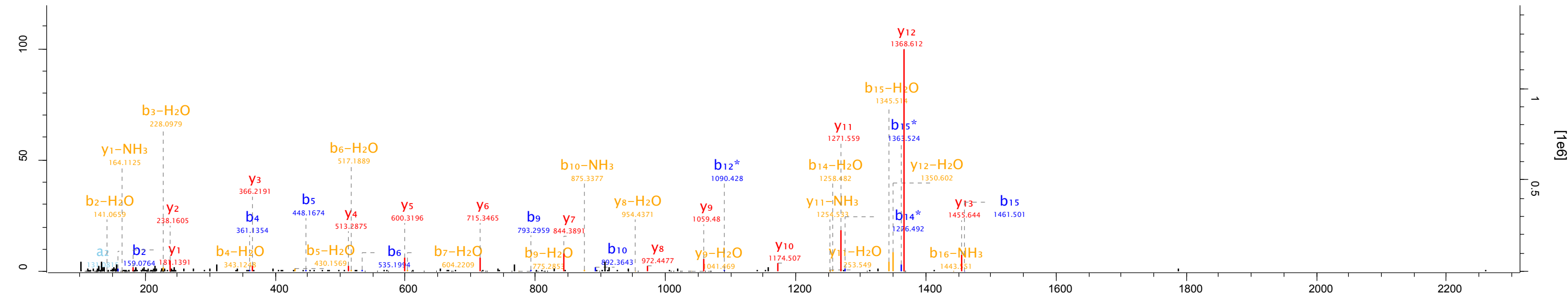


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20171215_MaS_33SR_LMH_phospho2_02

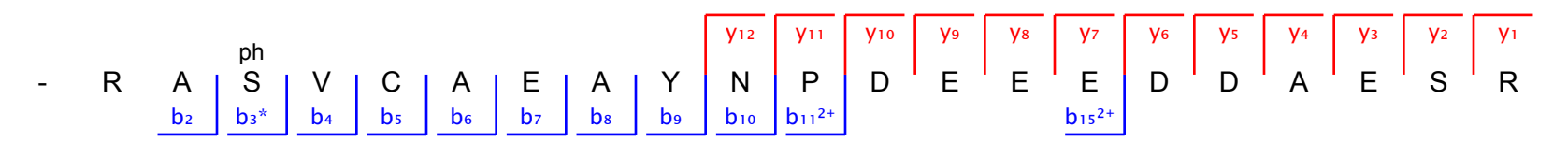
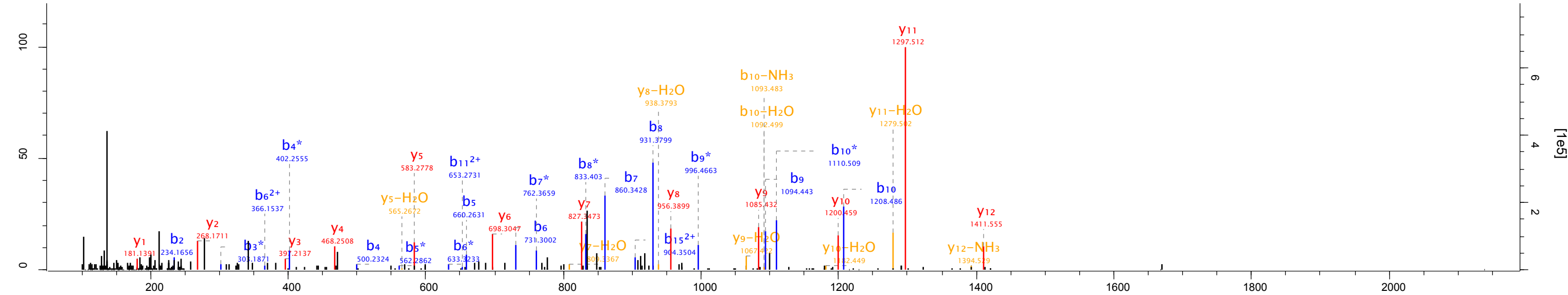
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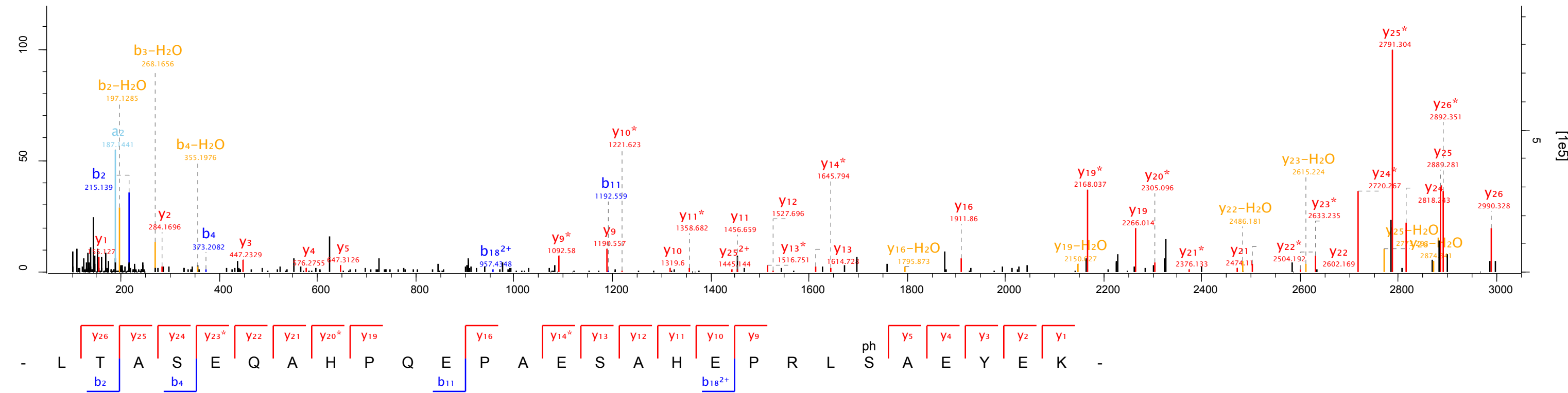


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20171215_MaS_33SR_LMH_phospho2_02

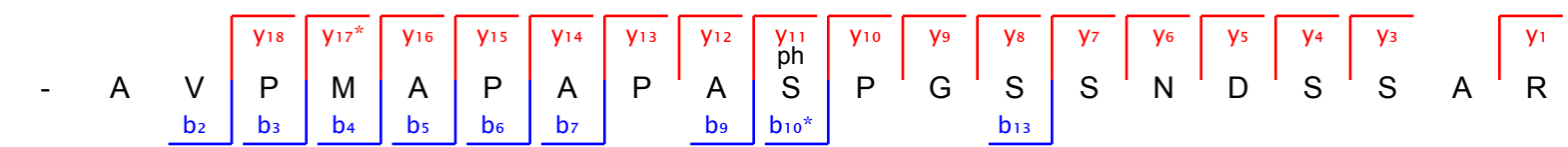
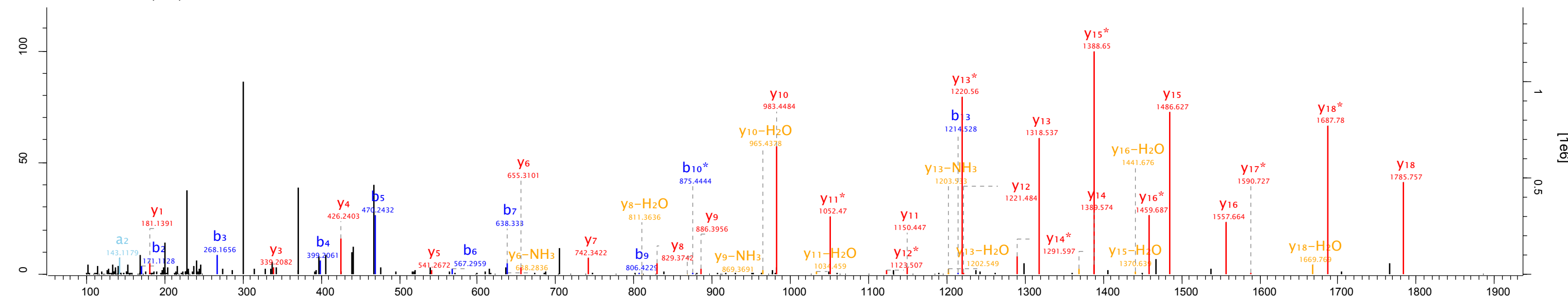
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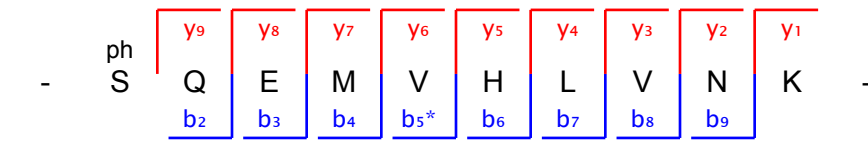
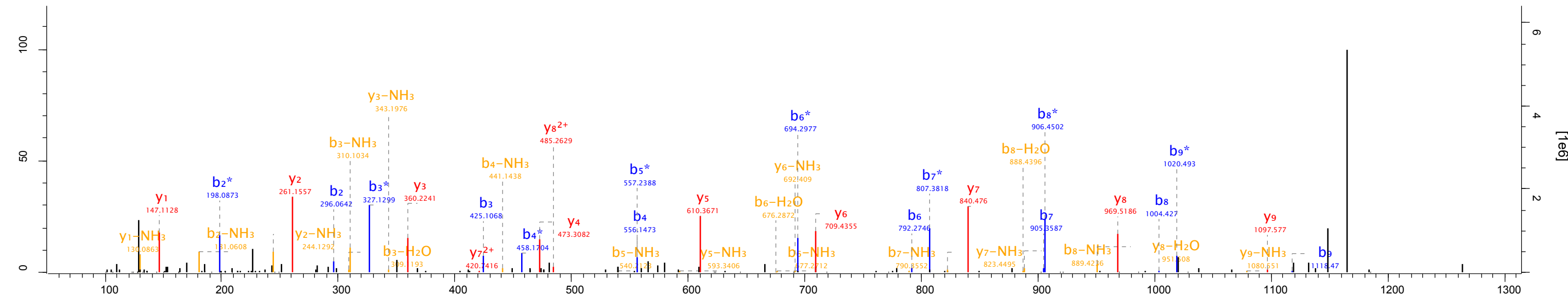




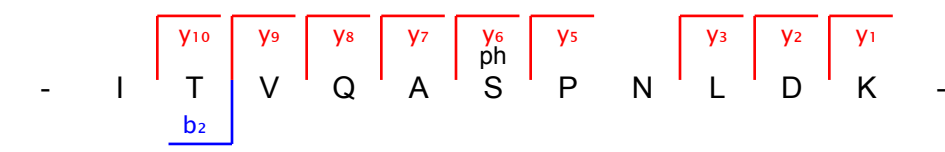
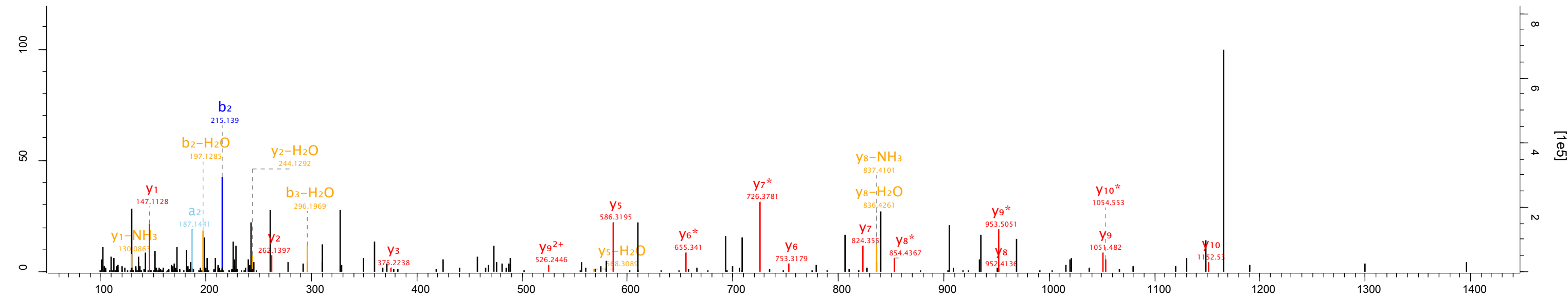
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20171215_MaS_33SR_LMH_phospho2_02

Scan 7706 Method FTMS; HCD Score 186.69 m/z 978.44 Gene names MAP1S



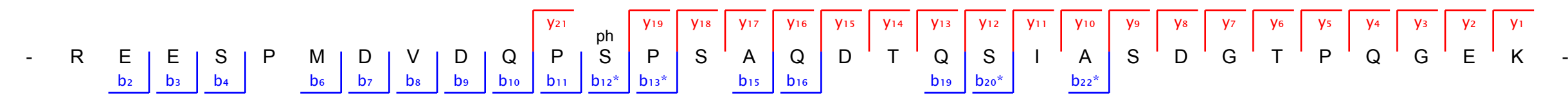
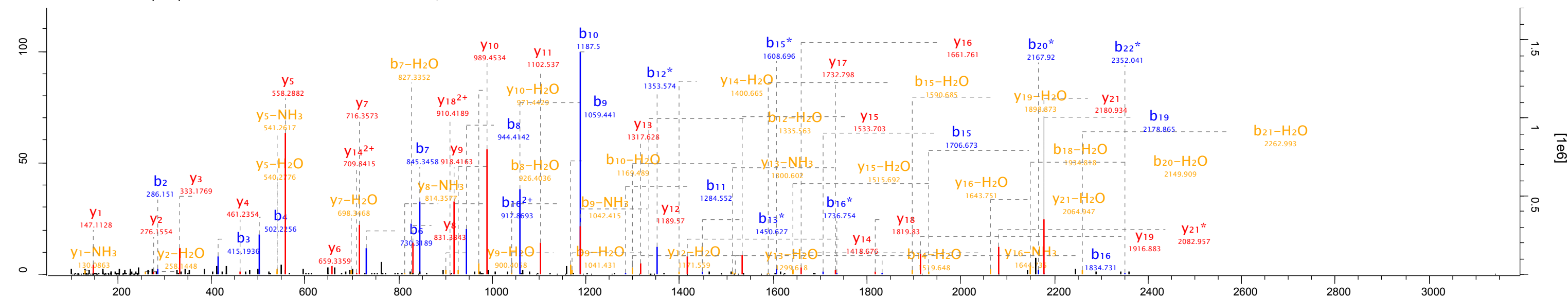


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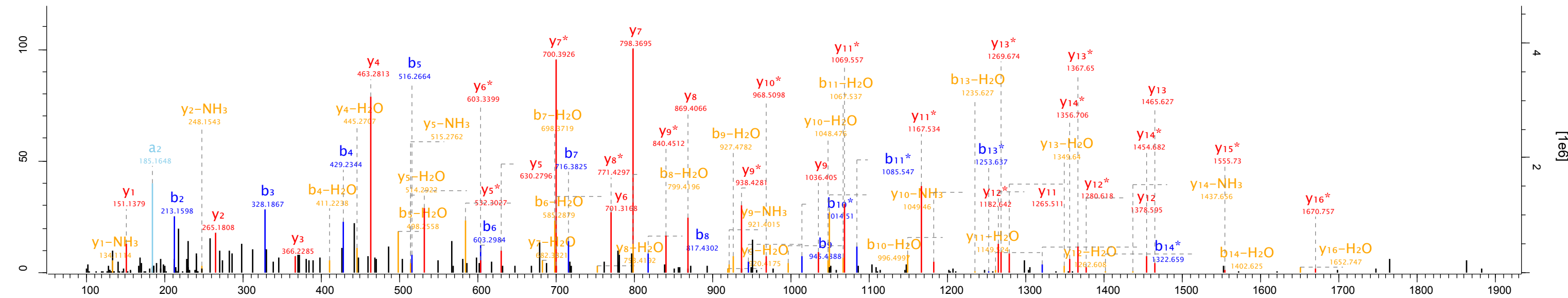


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20171215_MaS_33SR_LMH_phospho2_02

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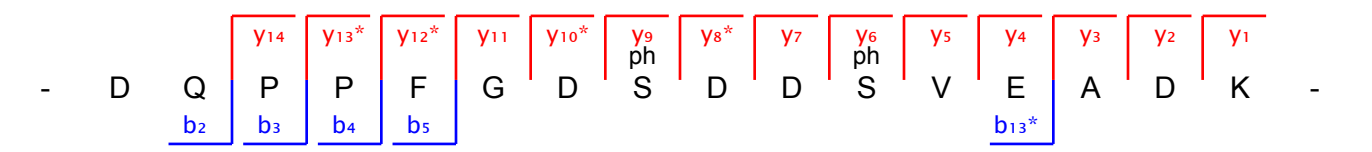
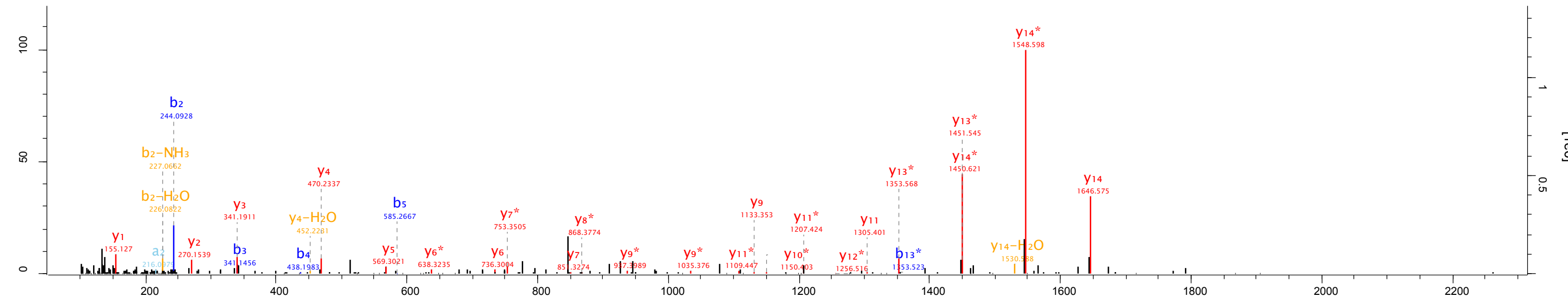
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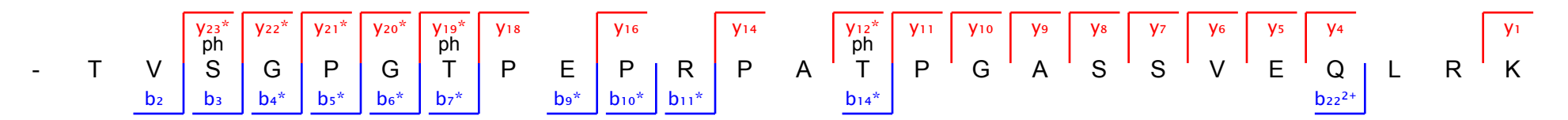
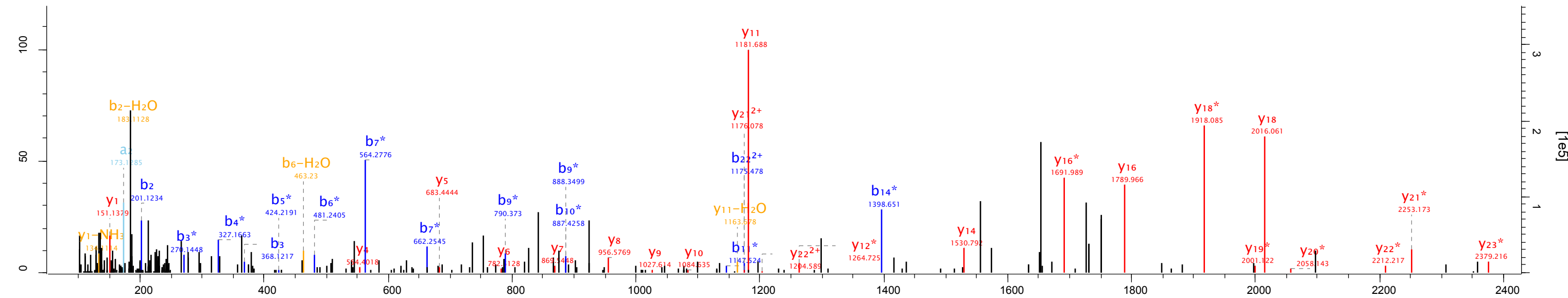
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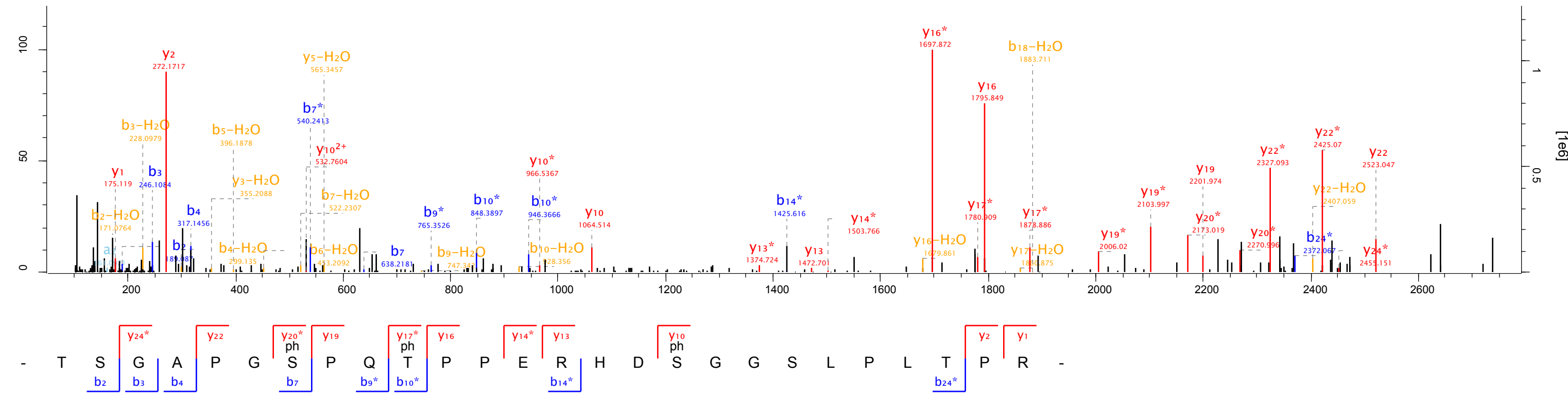
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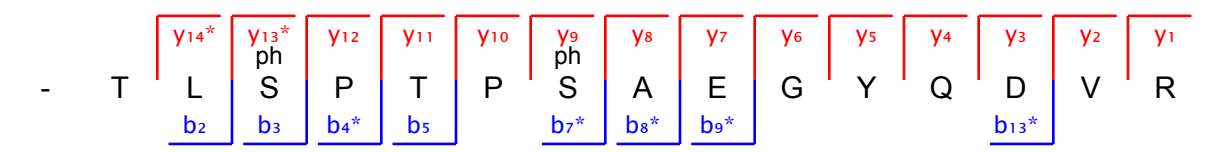
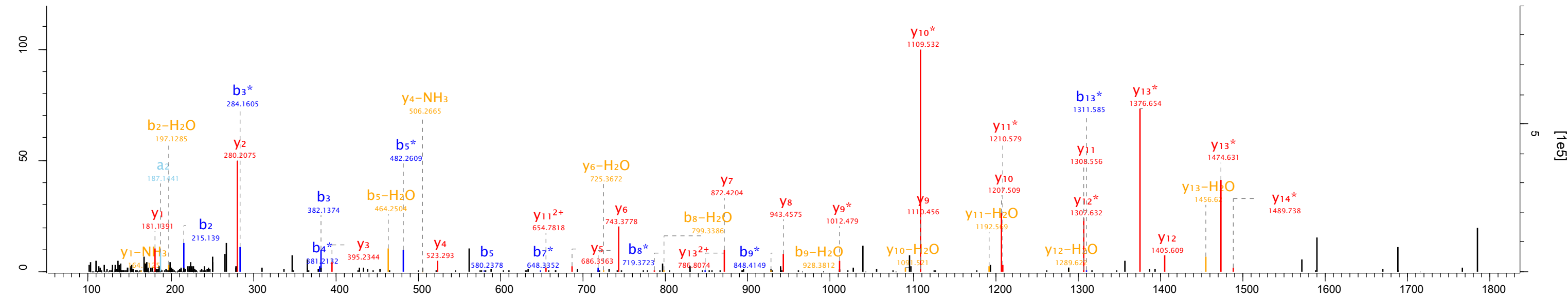
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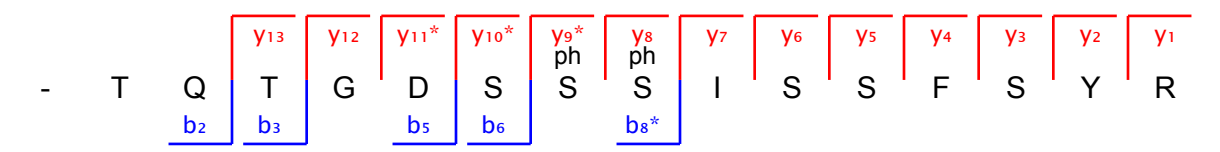
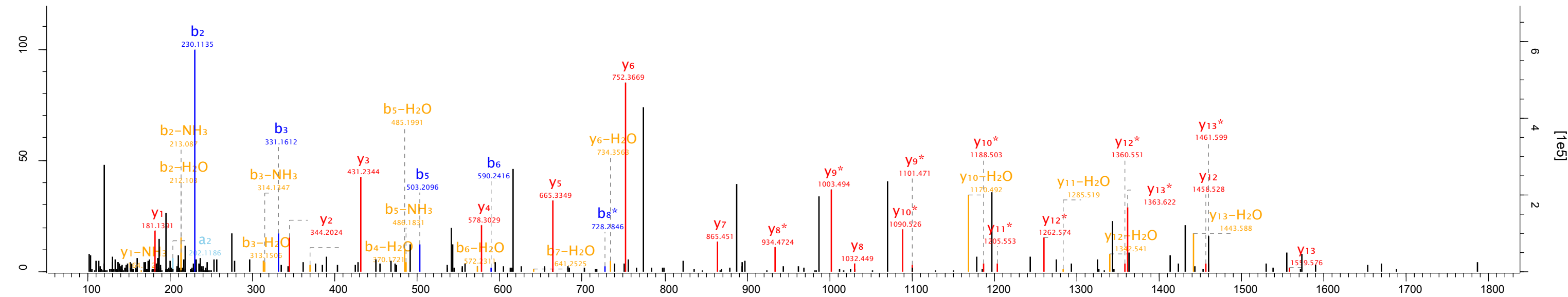
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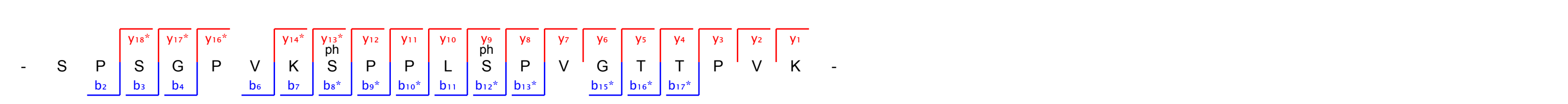
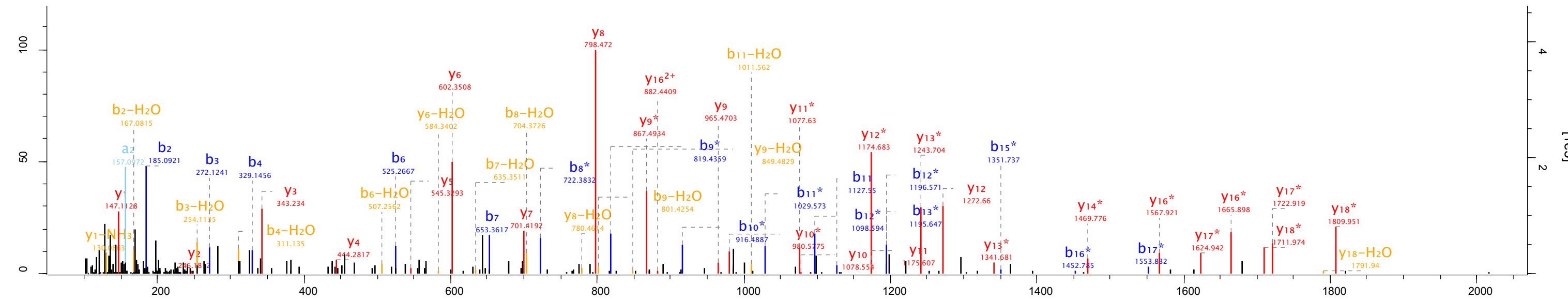
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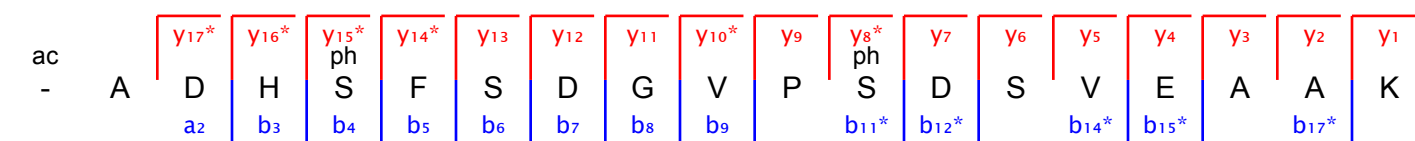
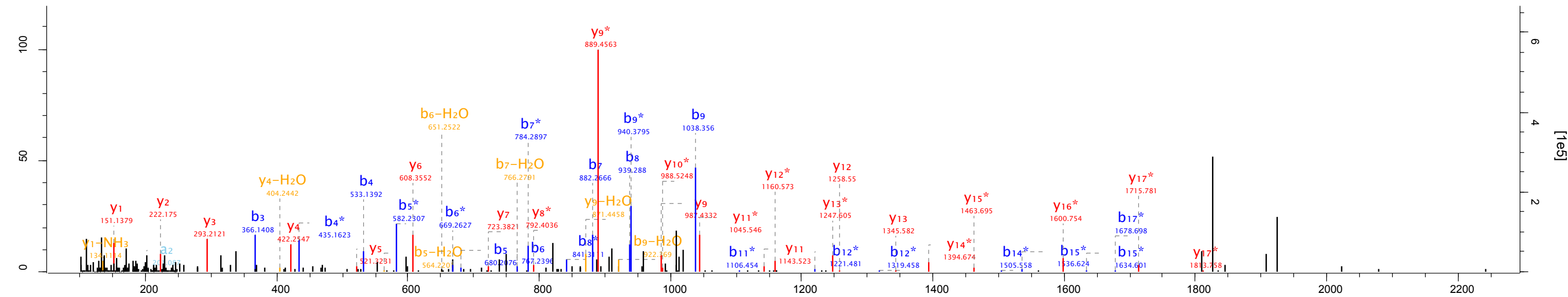
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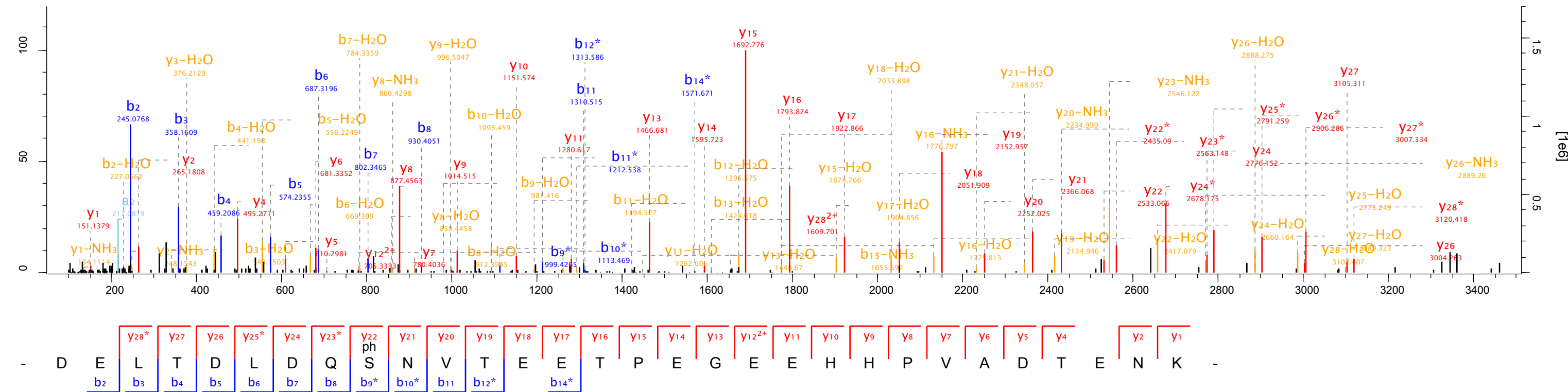
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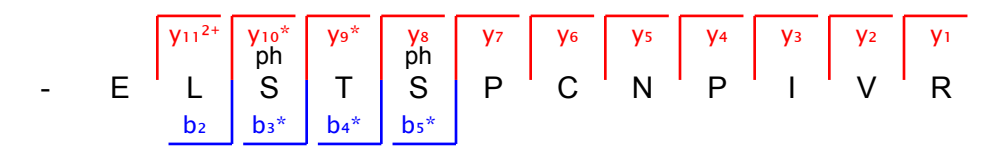
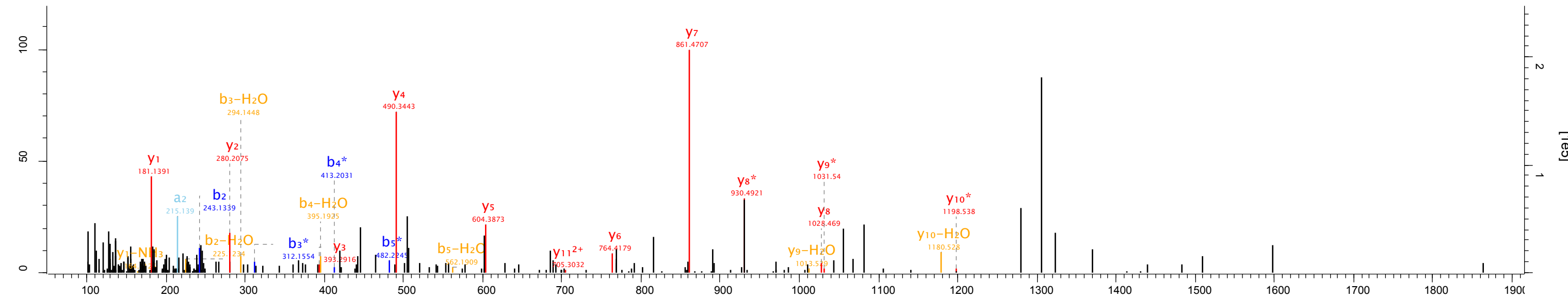
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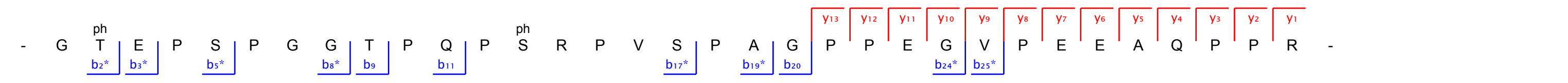
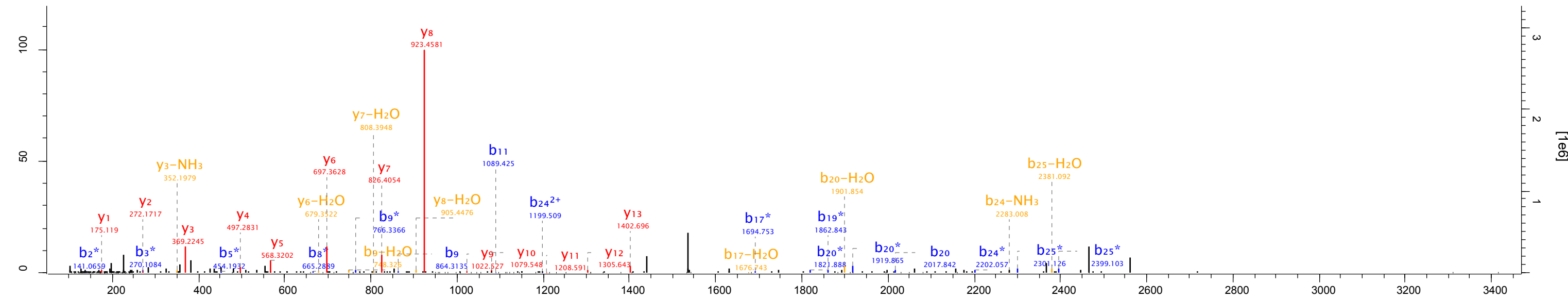
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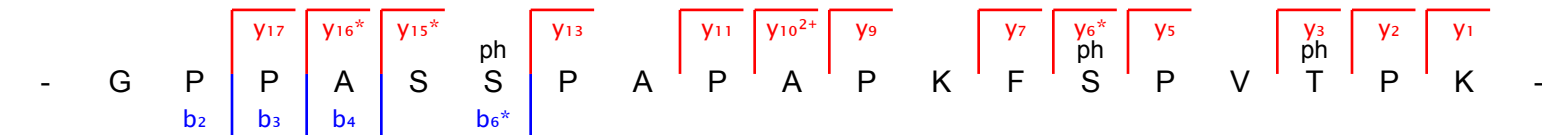
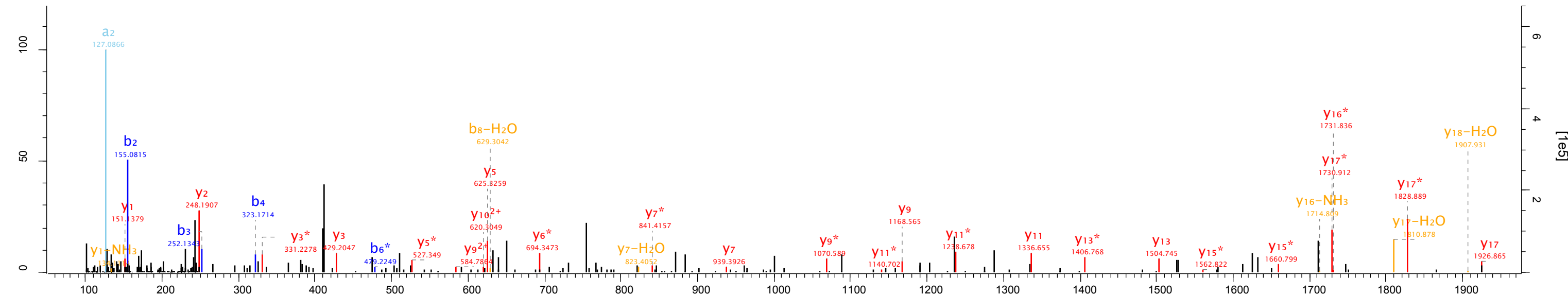


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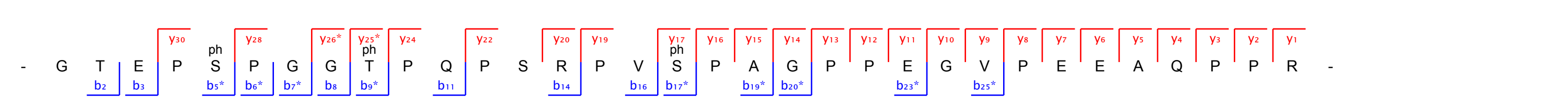
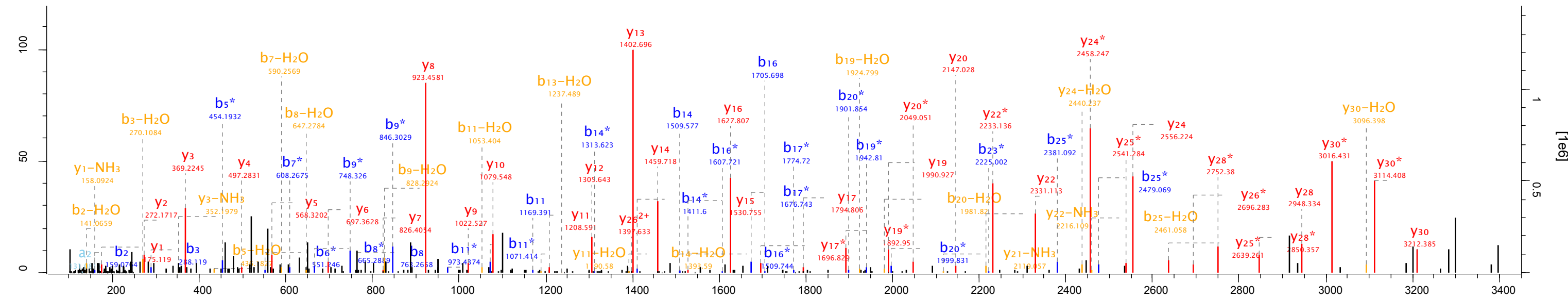


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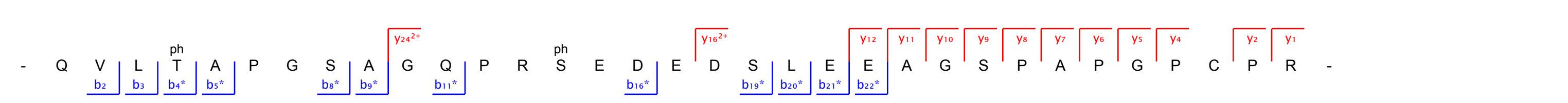
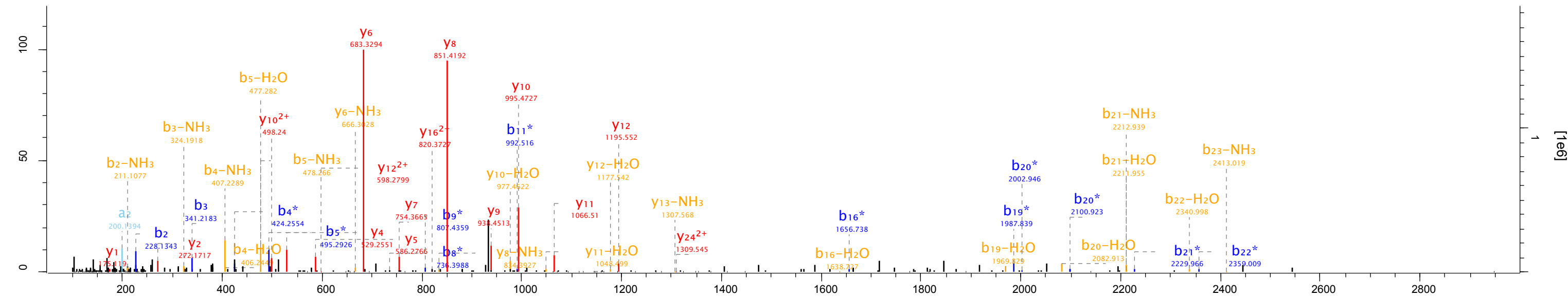


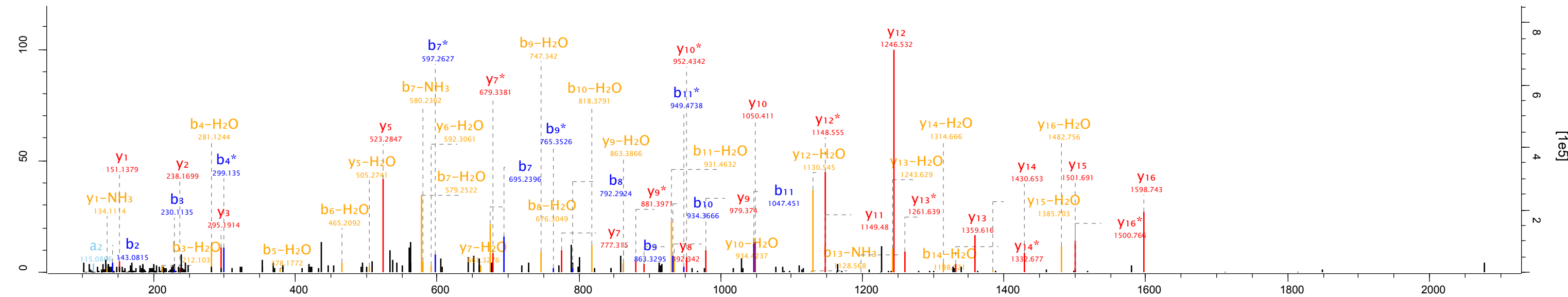


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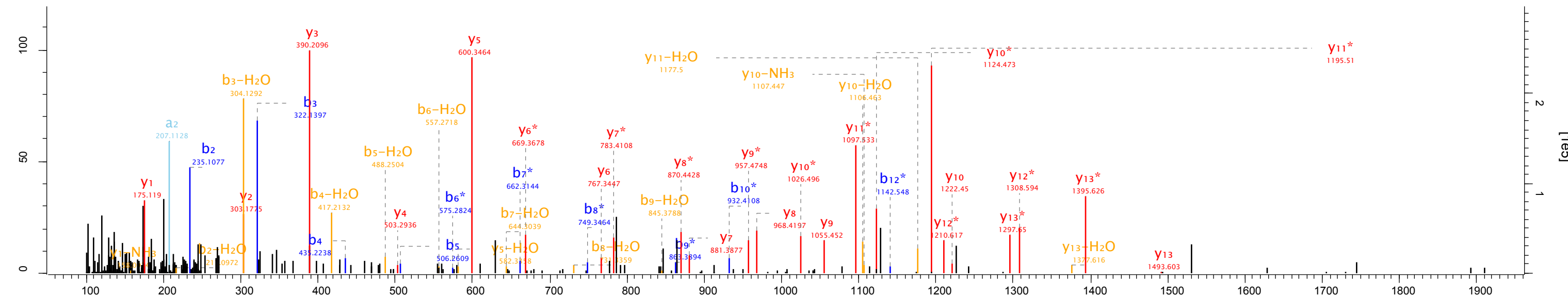


- A A S S P S N P A A L P V A S D S P M G S K -

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

- b₂ (under A)
- b₃ (under S)
- b₄^{*} (under S)
- b₇ (under N)
- b₈ (under P)
- b₉ (under A)
- b₁₀ (under A)
- b₁₁ (under L)
- y₁ (under K)
- y₂ (under S)
- y₃ (under G)
- y₅ (under P)
- y₇ (under S)
- y₈ (under D)
- y₉ (under S)
- y₁₀ (under A)
- y₁₁ (under V)
- y₁₂ (under P)
- y₁₃ (under L)
- y₁₄ (under A)
- y₁₅ (under A)
- y₁₆ (under P)

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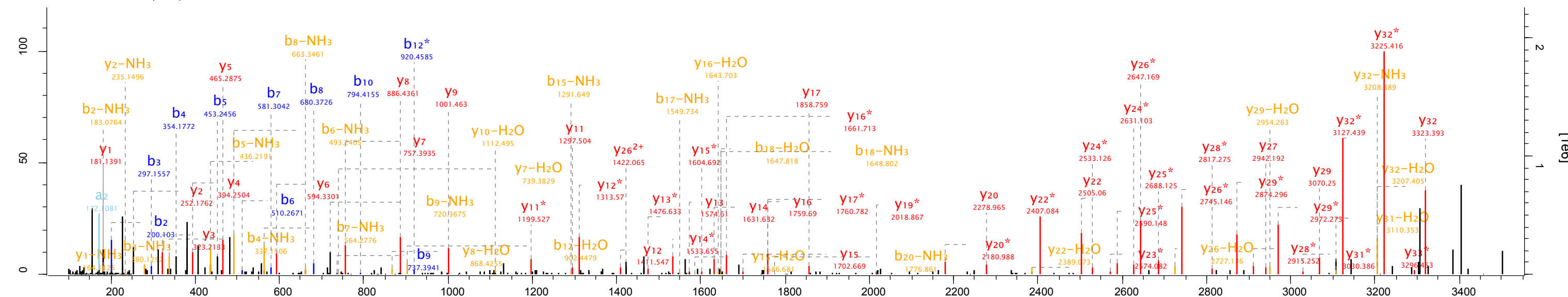
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b2 b3 b4 b5 b6* b7* b8* b9* b10* b12*

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

Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 12676 Method FTMS; HCD Score 223.49 m/z 1175.51 Gene names OTUD5



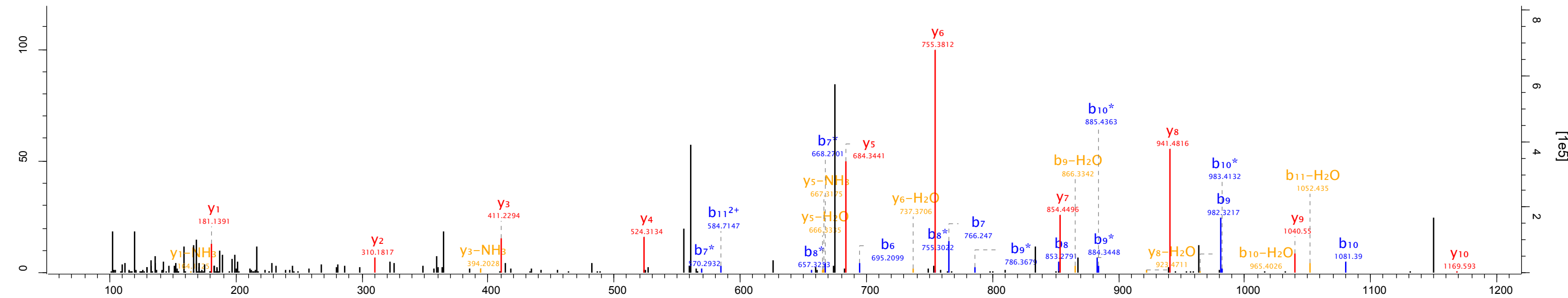
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b₇
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y₂
y₁

Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
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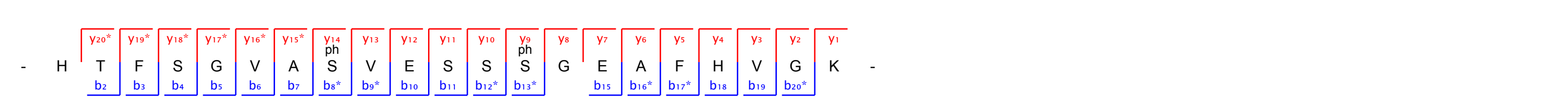
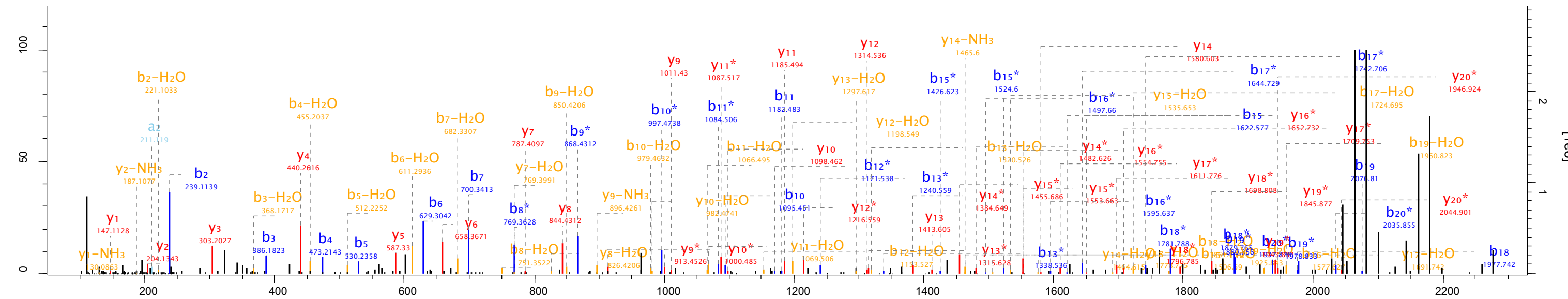


- K G S S G N A S E V S V A C L T E R -

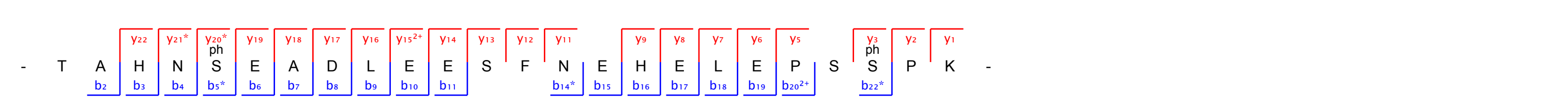
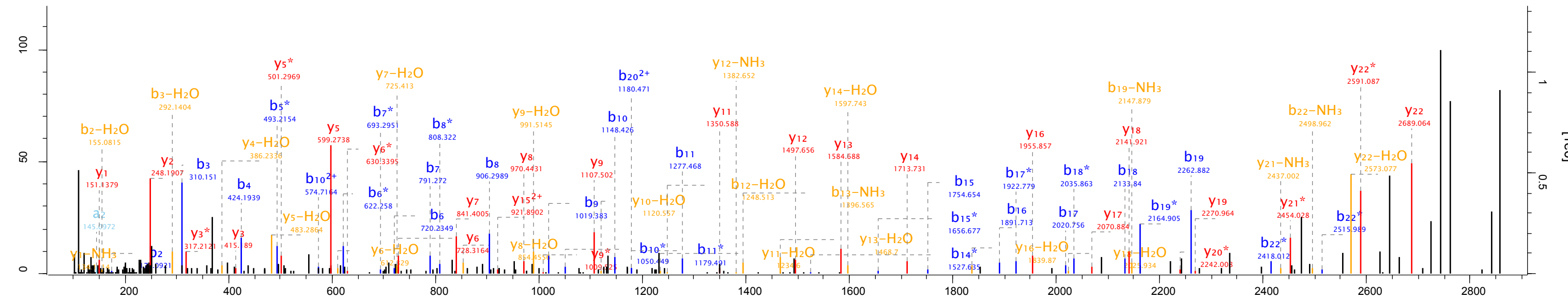
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y₉
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y₅
y₄
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y₂
y₁

b₉
b₁₀
b₁₁²⁺

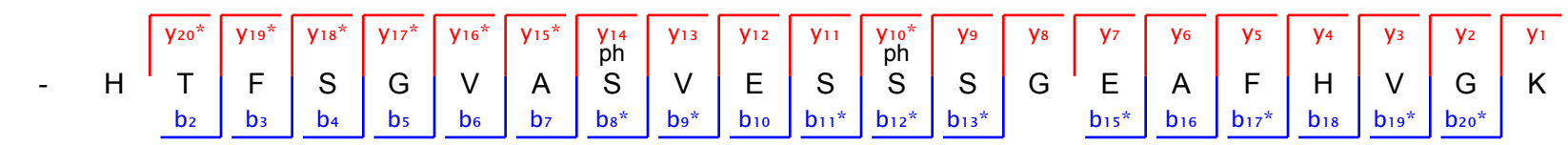
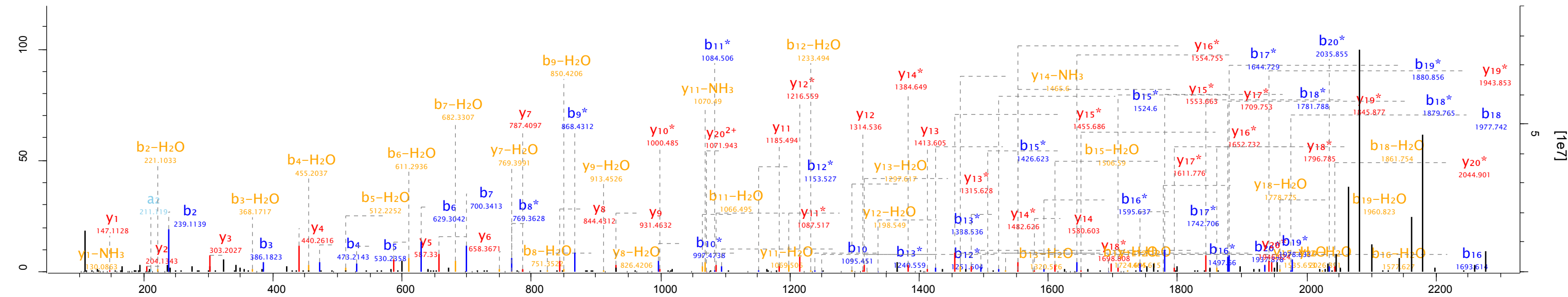
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 Scan: 12876 Method: FTMS; HCD Score: 417.99 m/z: 1140.97



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13566 Method FTMS; HCD Score 185.43 m/z 954.72 Gene names PHF6



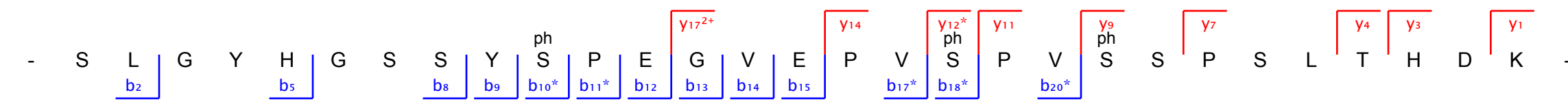
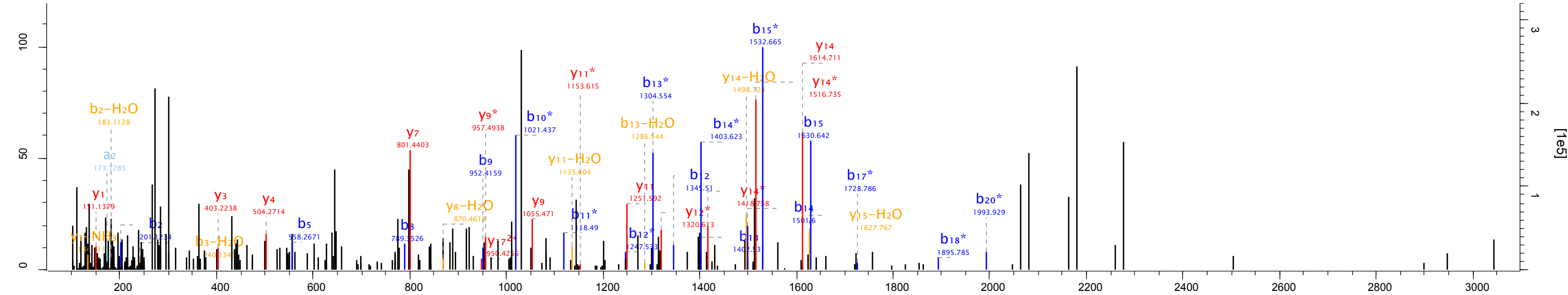
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13836 Method: FTMS; HCD Score: 377.56 m/z: 1140.97



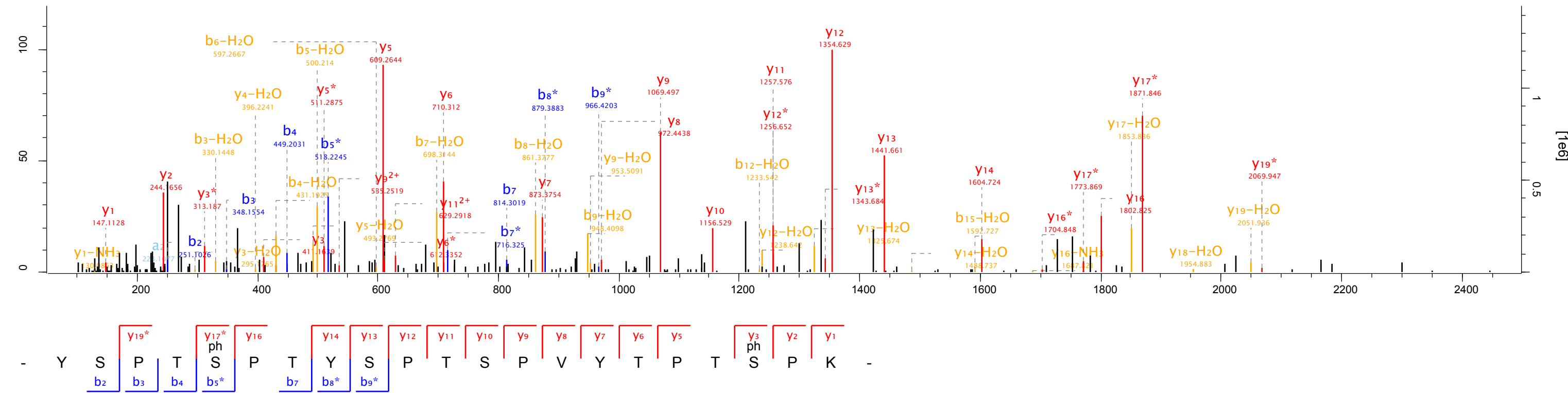
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20171215_MaS_33SR_LMH_phospho2_03

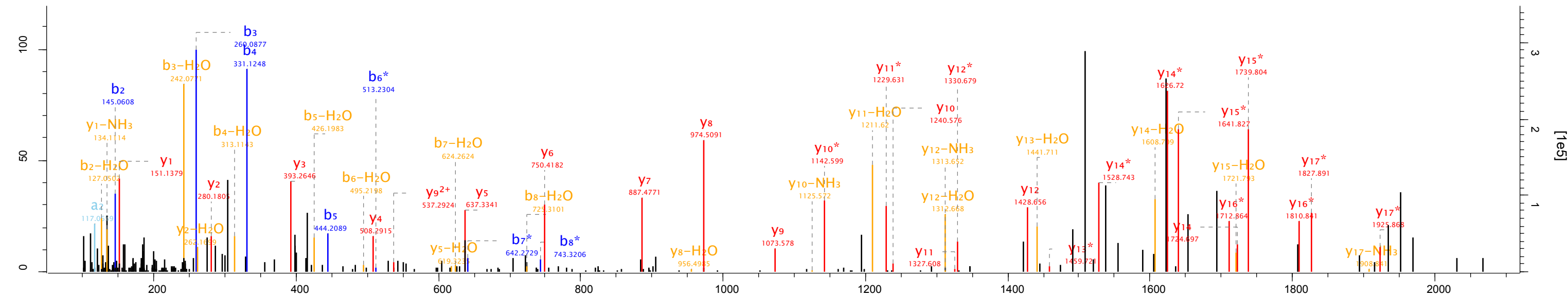
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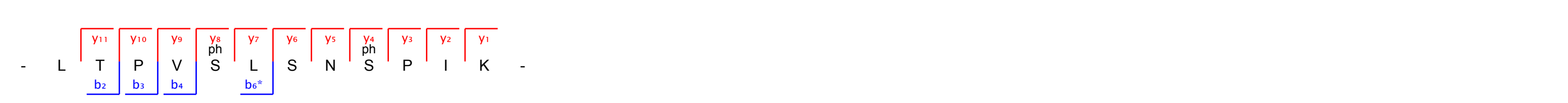
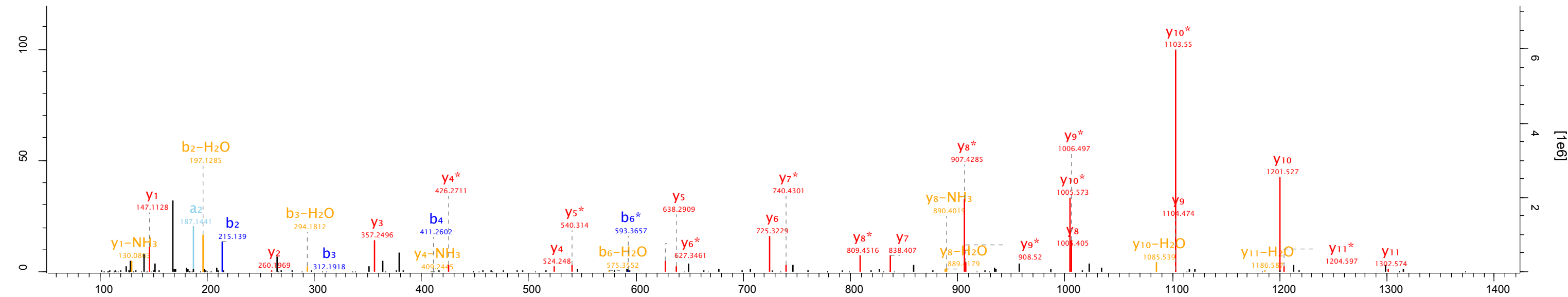
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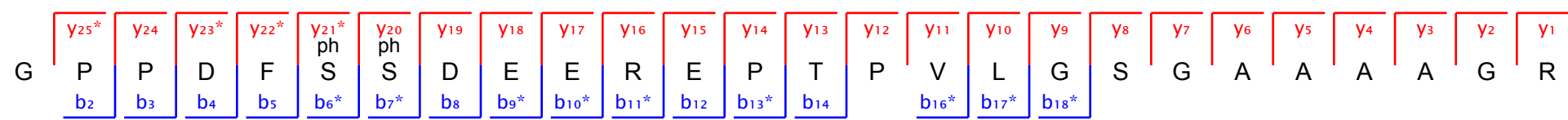
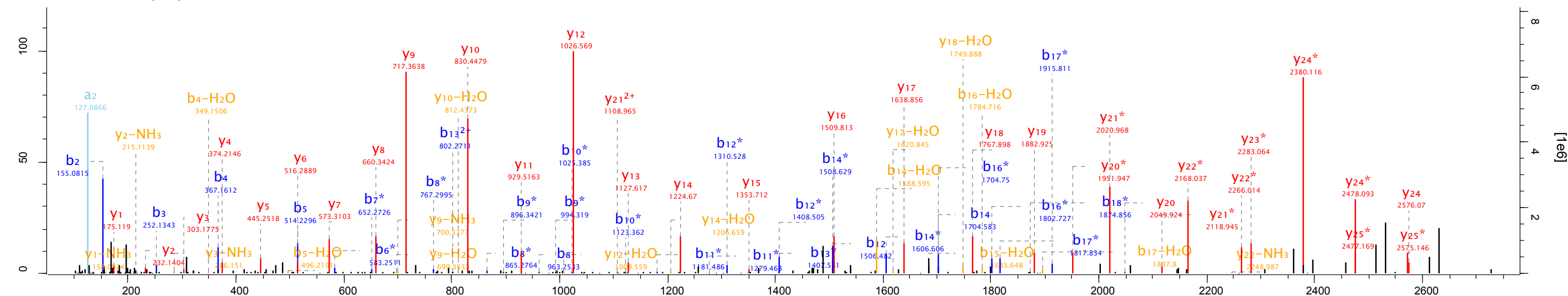
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y₁₀^{ph}
y₉
y₈
y₇
y₆
y₅
y₄
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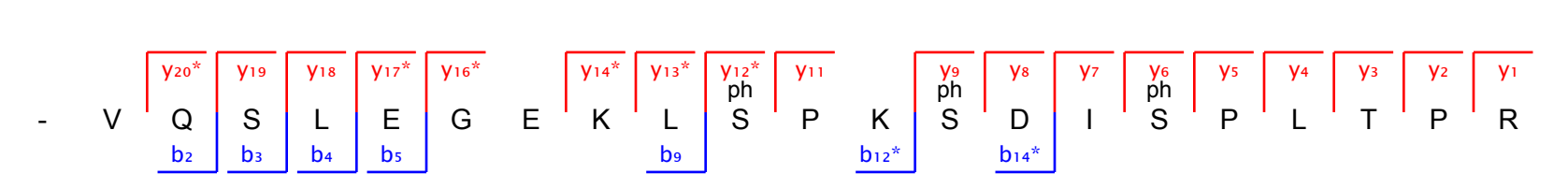
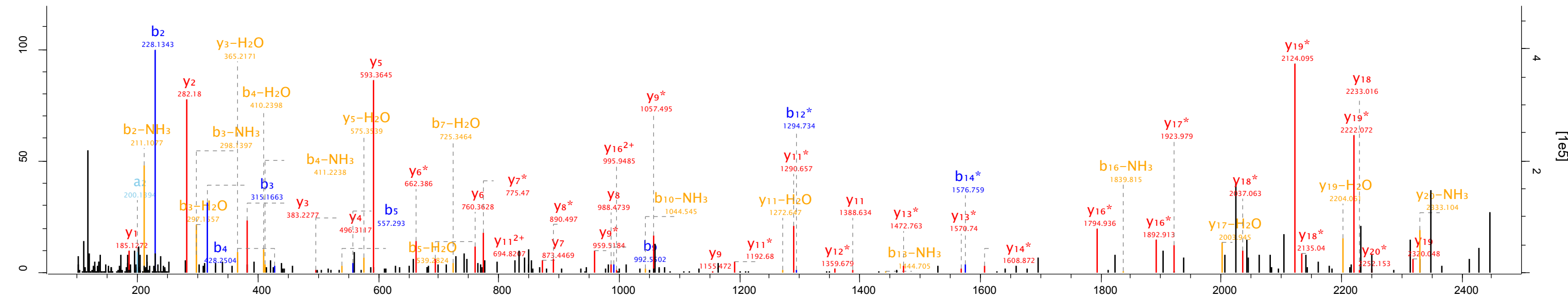


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20171215_MaS_33SR_LMH_phospho2_03

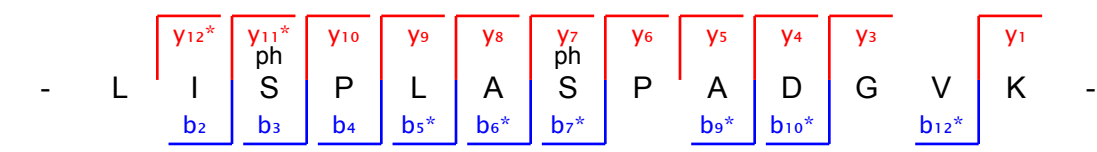
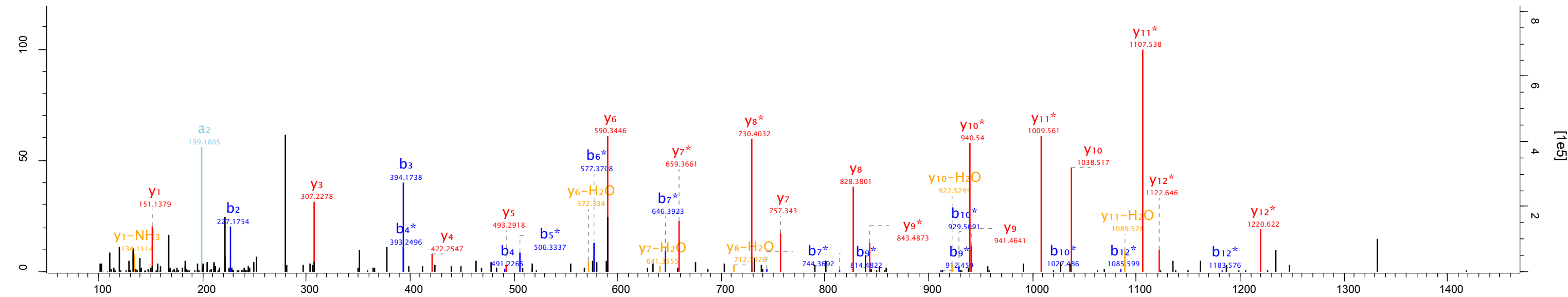
Scan 14476 Method FTMS; HCD Score 289.56 m/z 911.05 Gene names TMPO



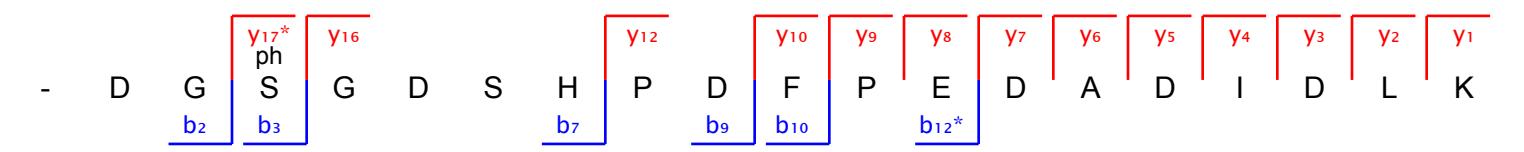
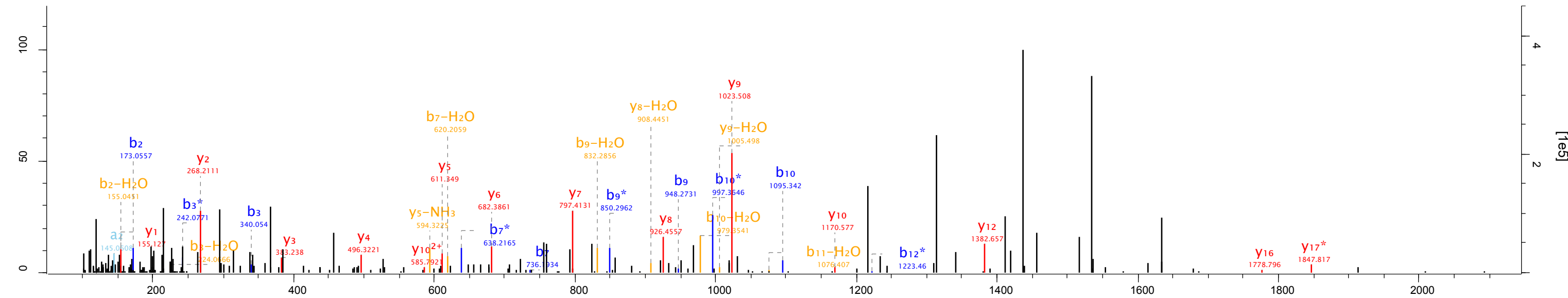
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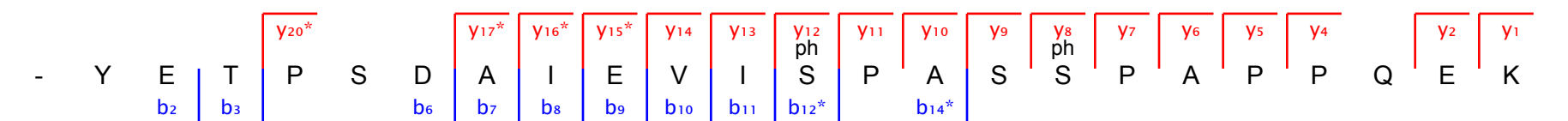
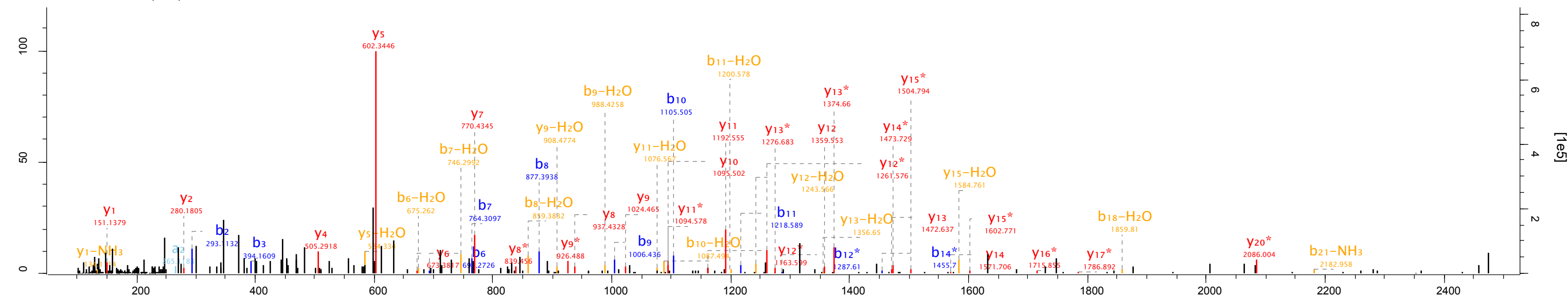


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20171215_MaS_33SR_LMH_phospho2_03

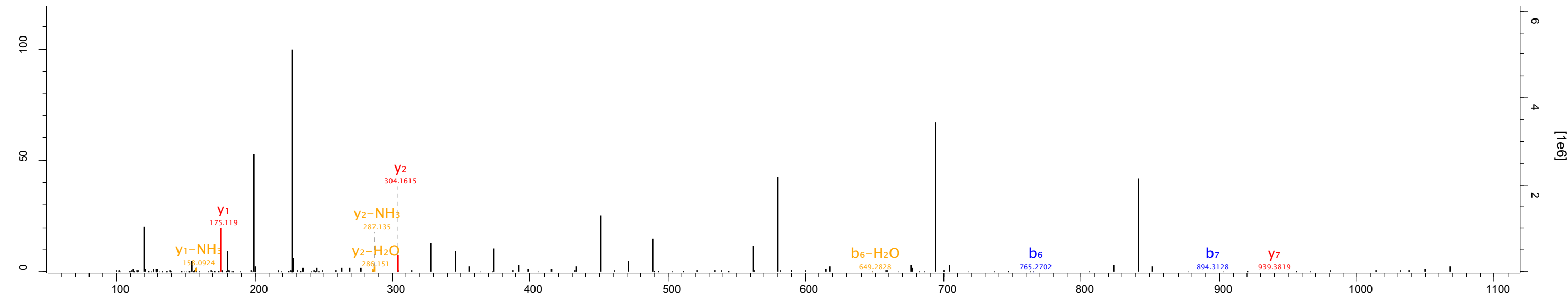
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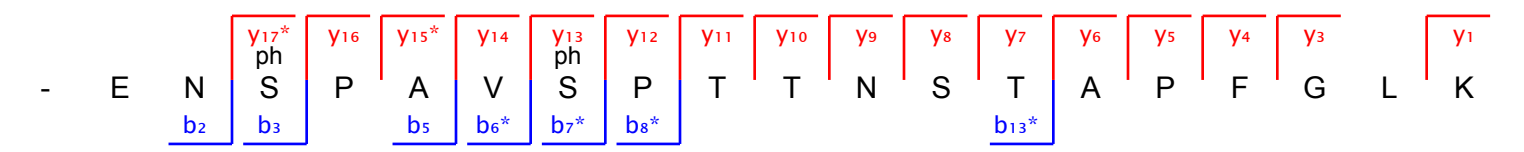
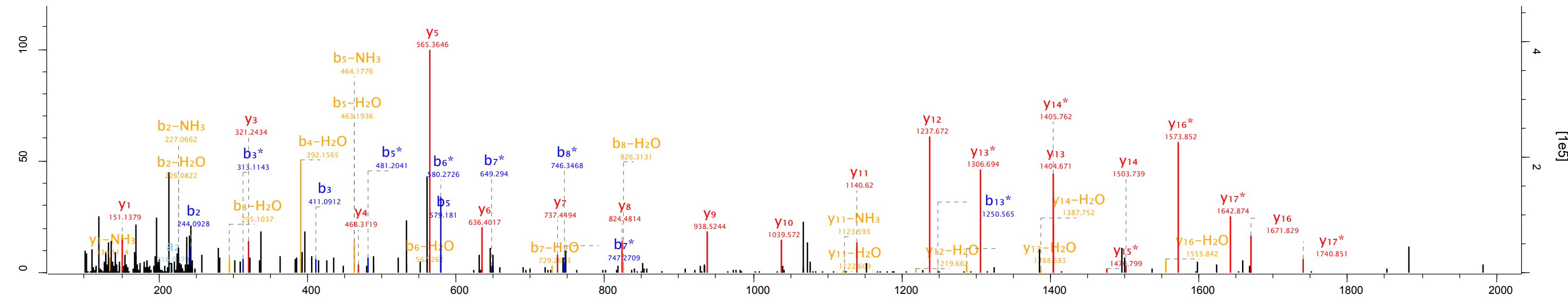
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20171215_MaS_33SR_LMH_phospho2_03

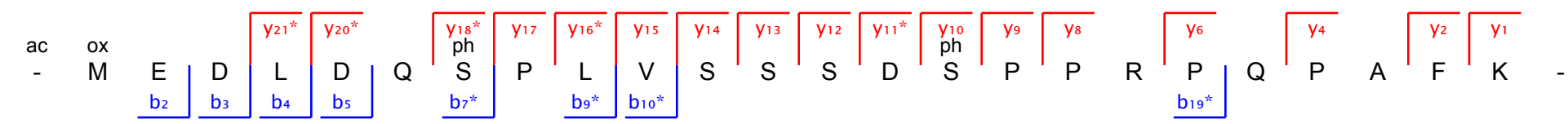
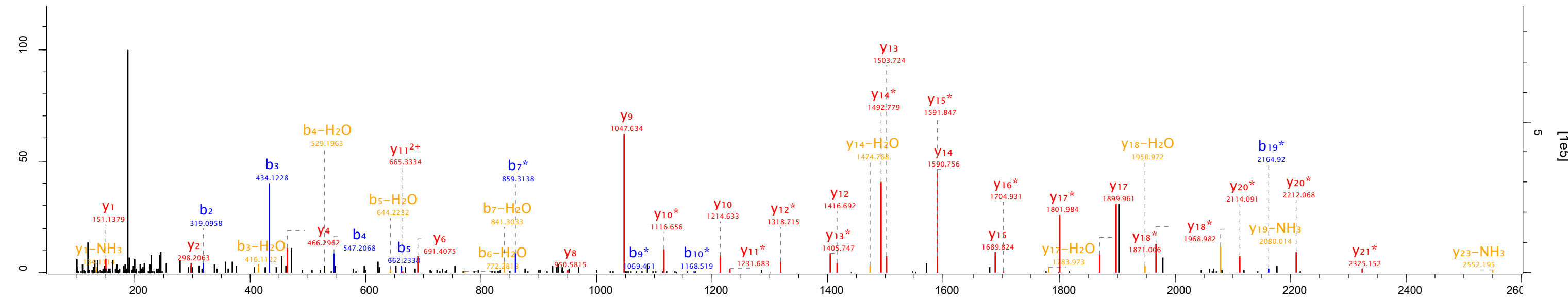
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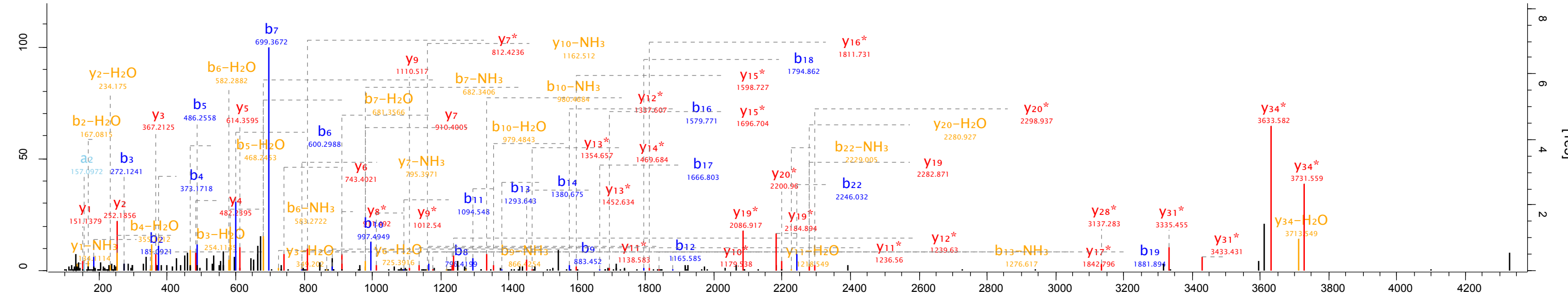
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 Scan: 15506 Method: FTMS; HCD Score: 112.39 m/z: 1041.46 Gene names: LRCH1



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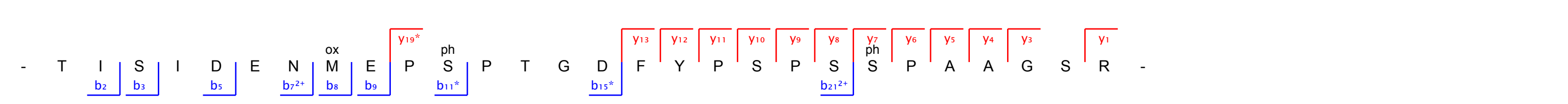
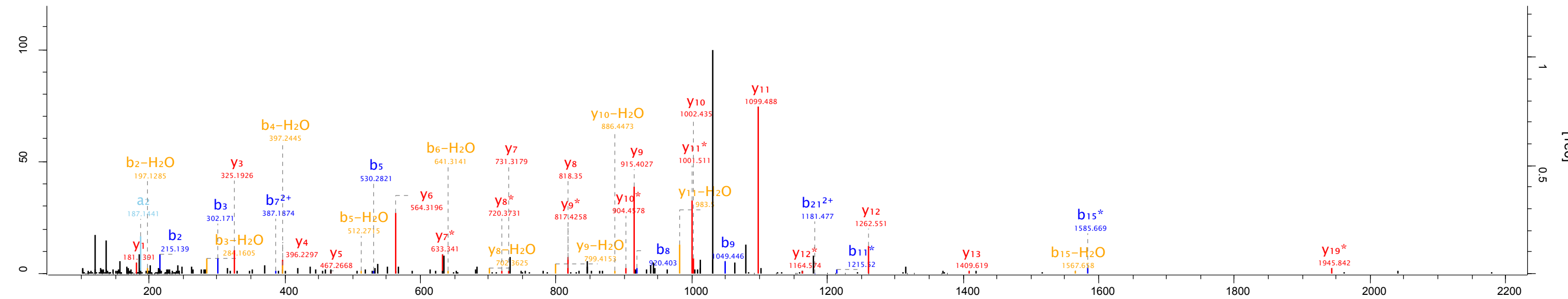


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 Scan: 15816 Method: FTMS; HCD Score: 149.82 m/z: 1510.65 Gene names: PACSIN2

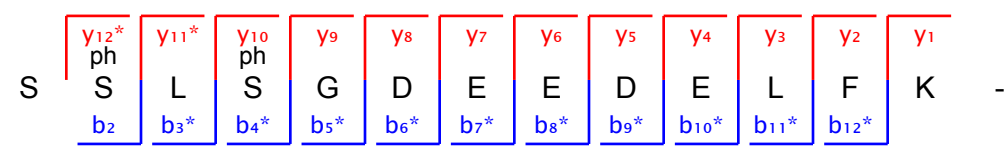
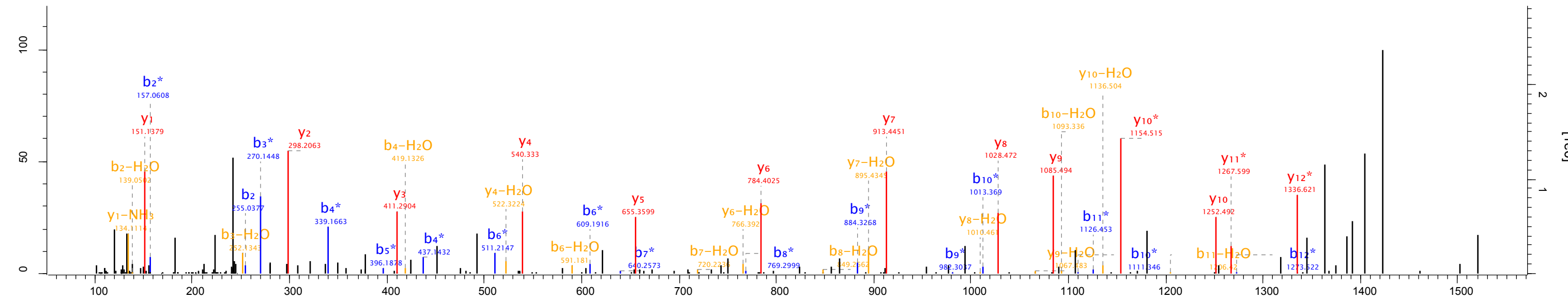


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 y₃ y₂ y₁ y₃₄* y₃₁* y₂₈* y₂₀* y₁₉ y₁₇* y₁₆* y₁₅* y₁₄* y₁₃* y₁₂* y₁₁* y₁₀* y₉ y₈* y₇ y₆ y₅ y₄
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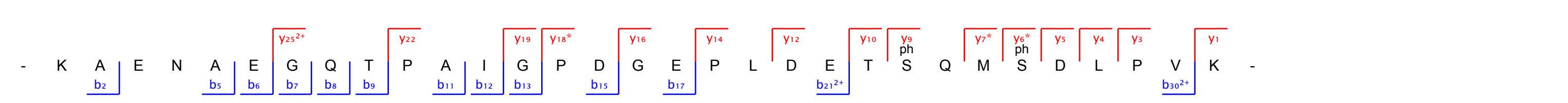
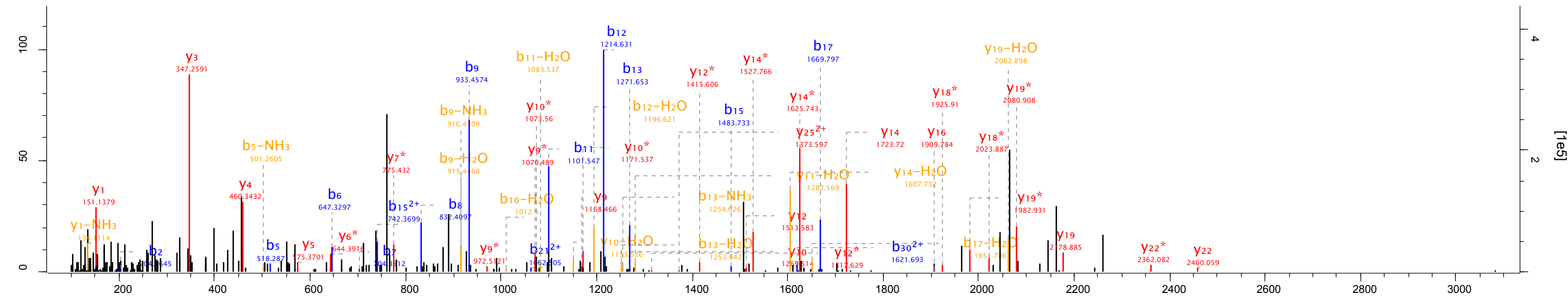
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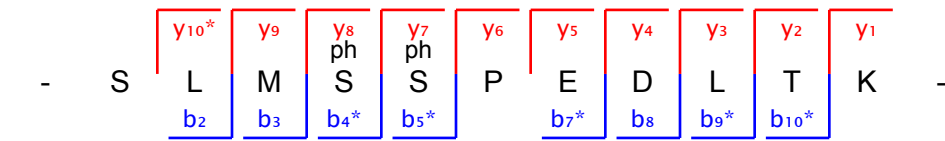
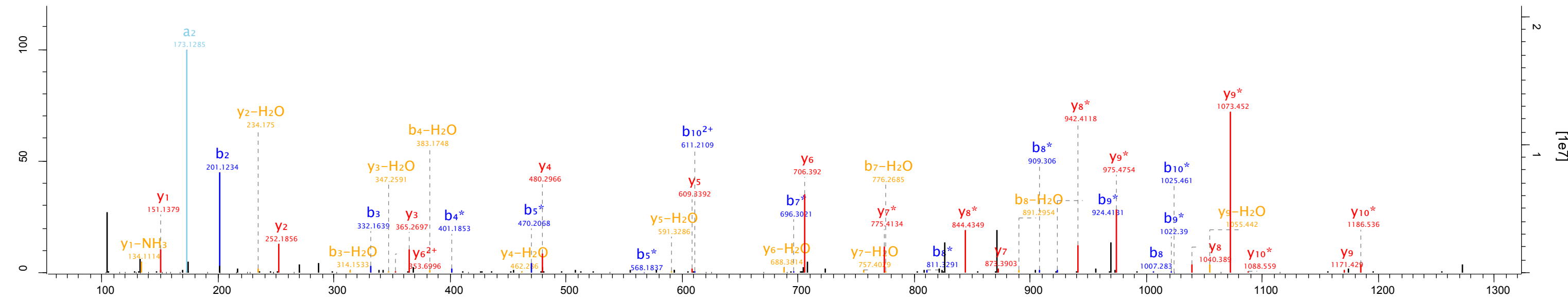
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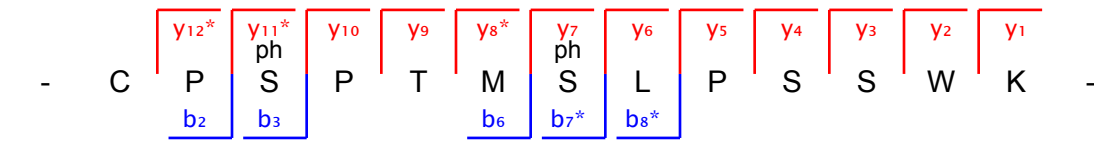
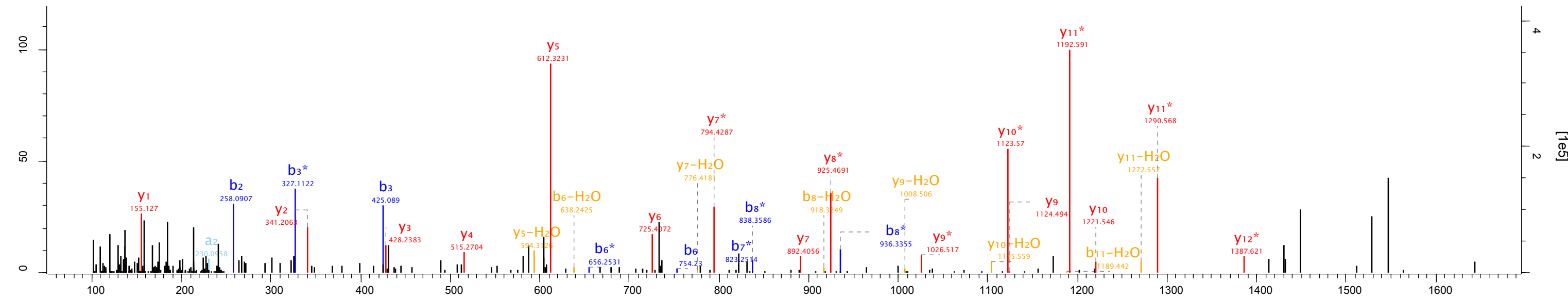


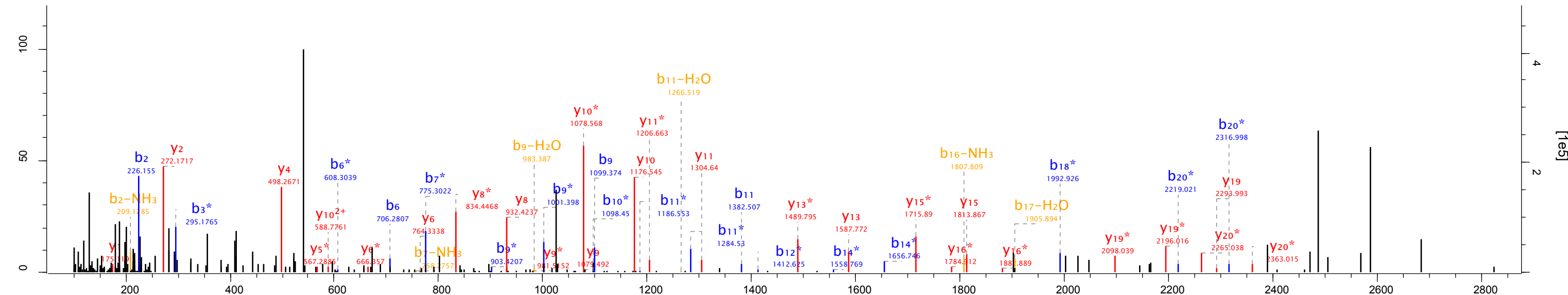
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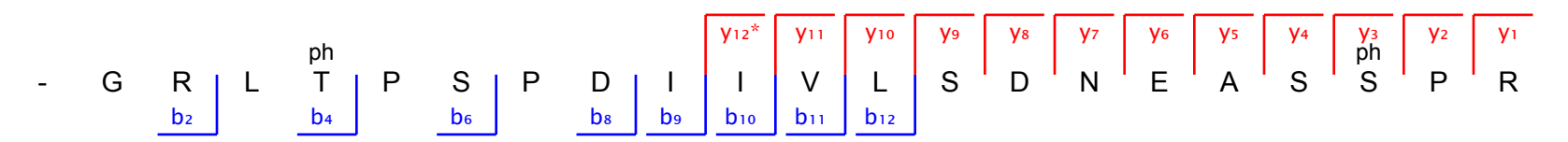
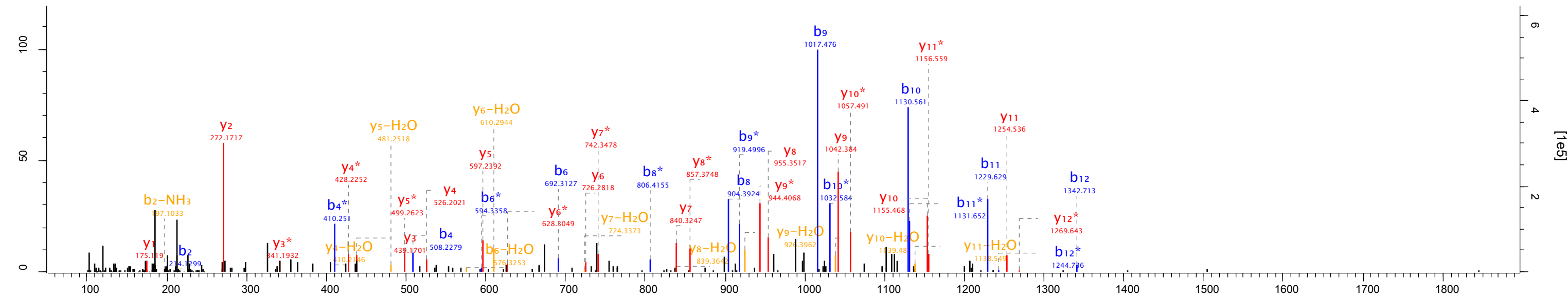


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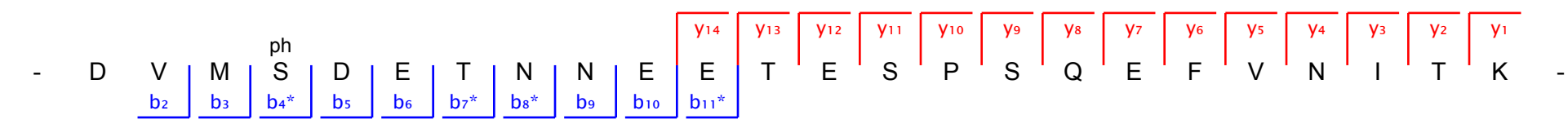
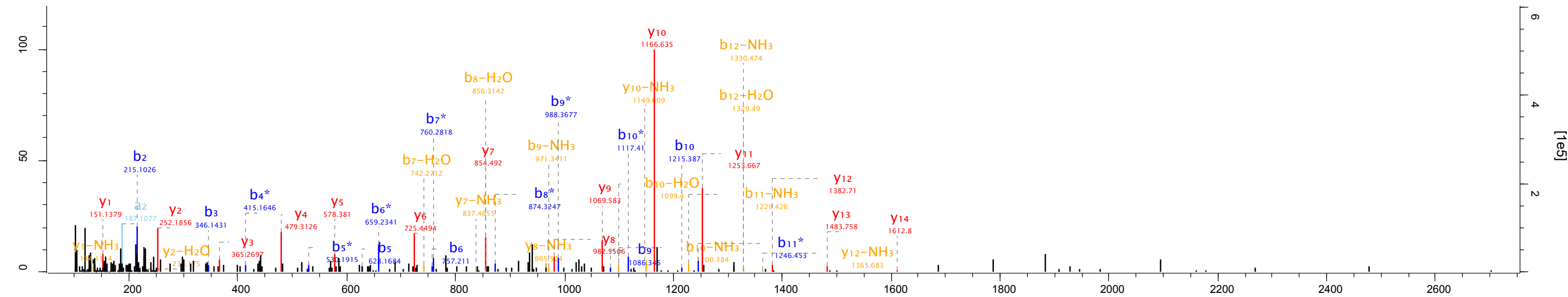
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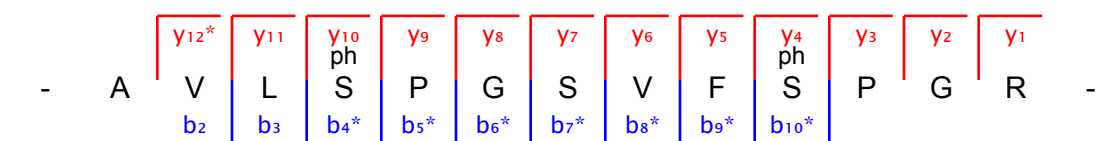
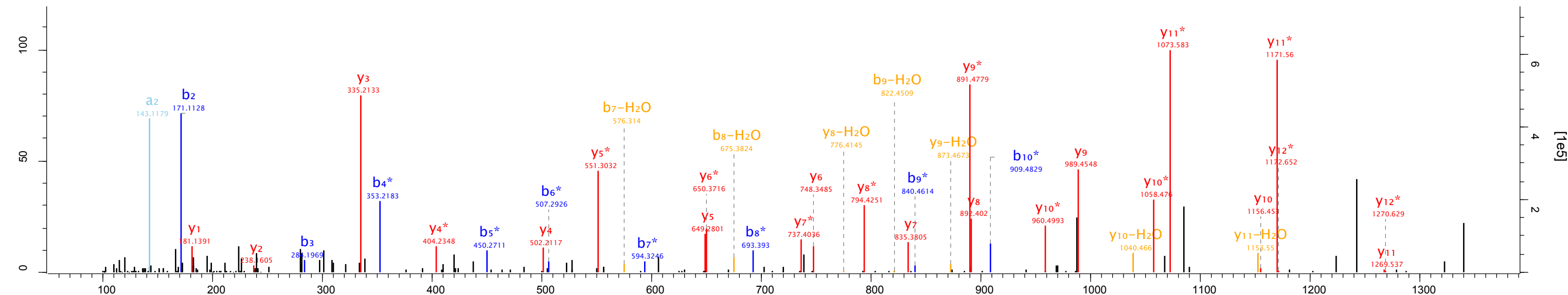
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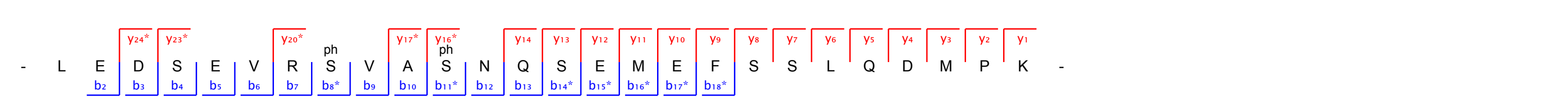
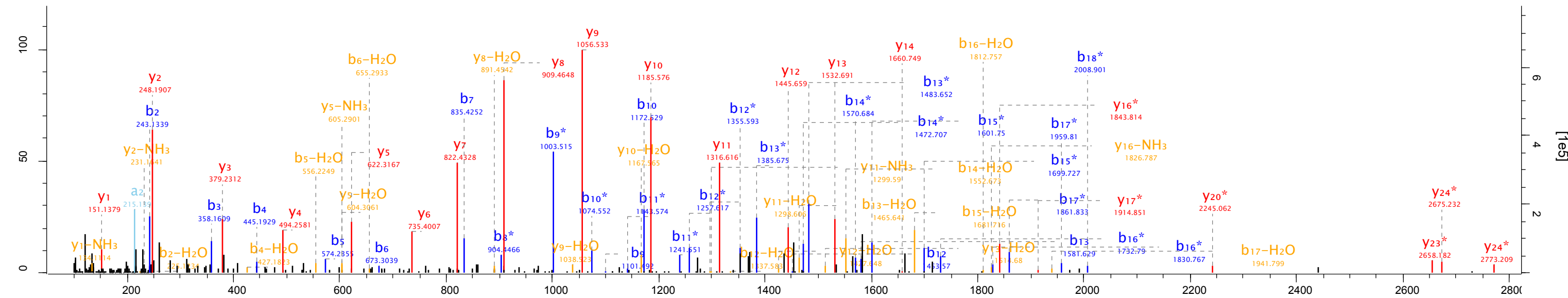
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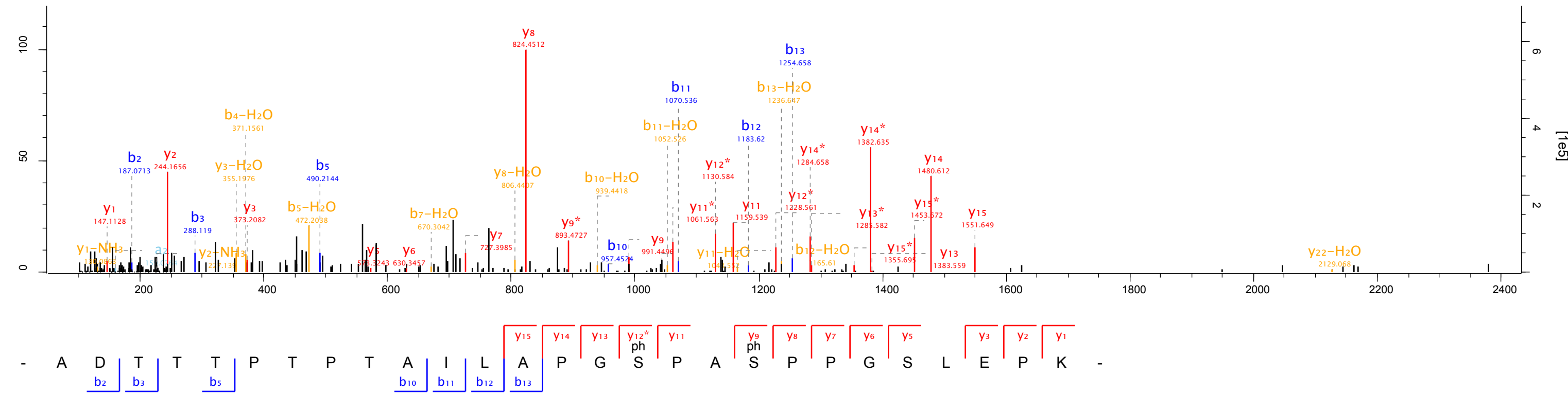


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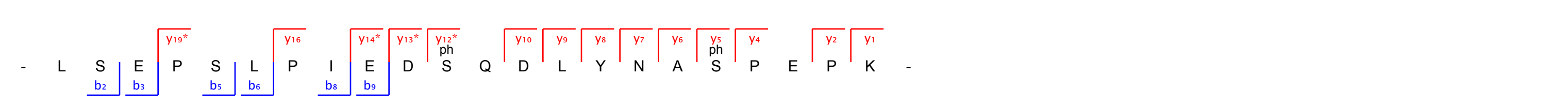
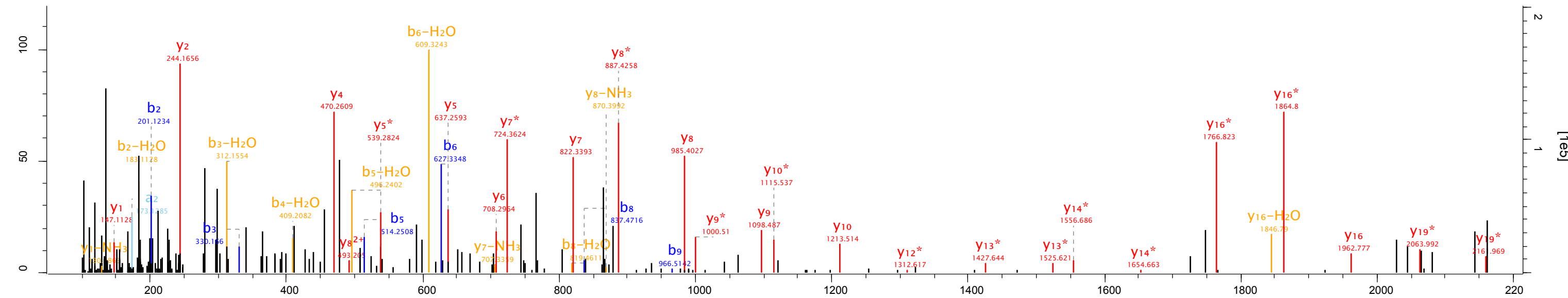


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20171215_MaS_33SR_LMH_phospho2_03

Scan 17956 Method FTMS; HCD Score 46.46 m/z 912.43 Gene names BRD2

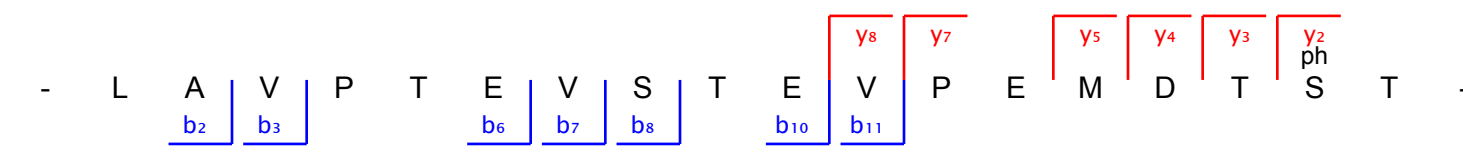
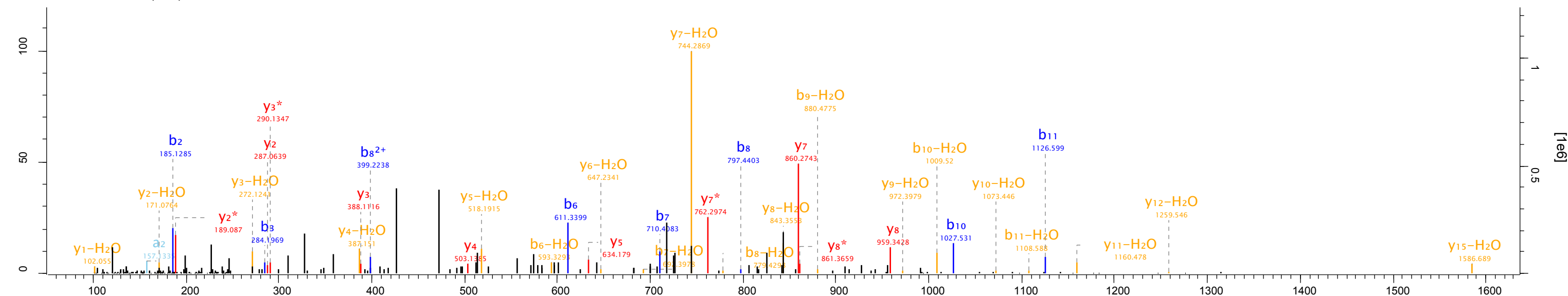


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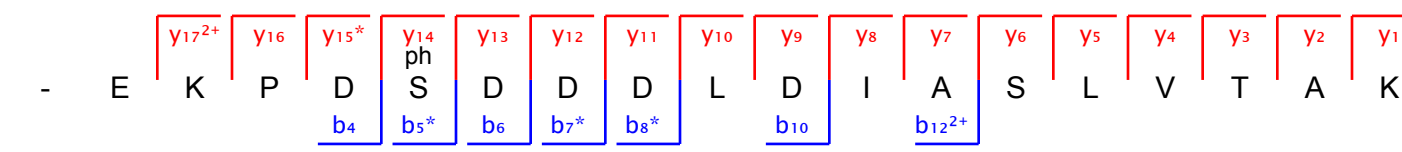
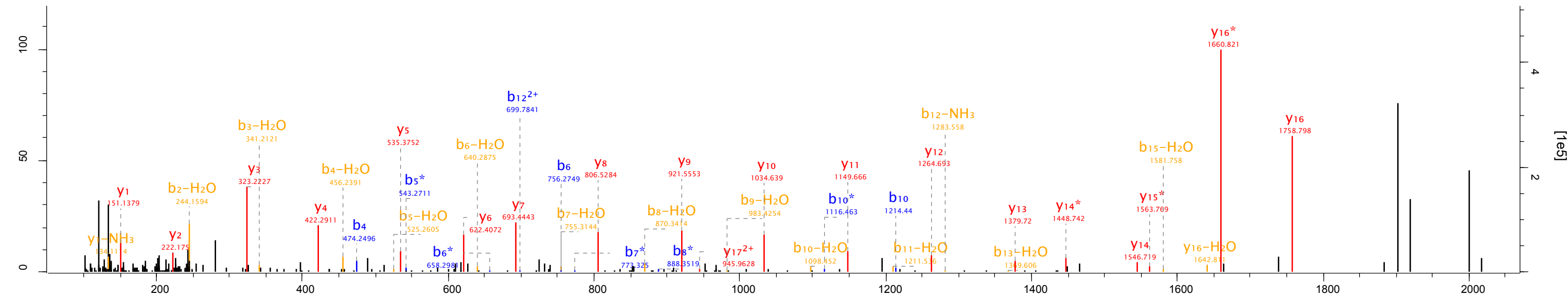


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20171215_MaS_33SR_LMH_phospho2_03

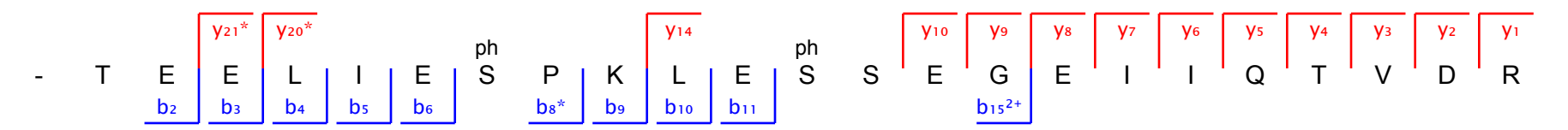
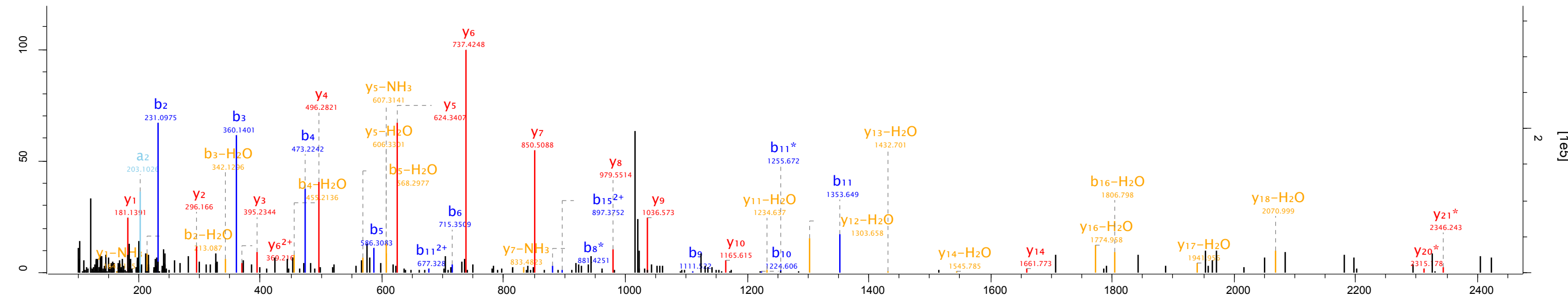
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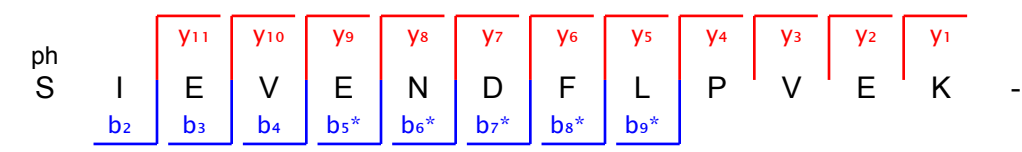
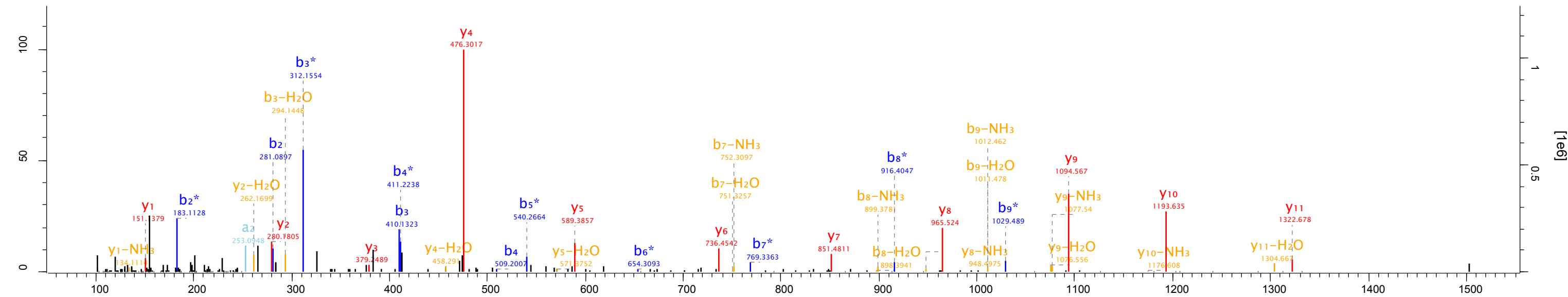
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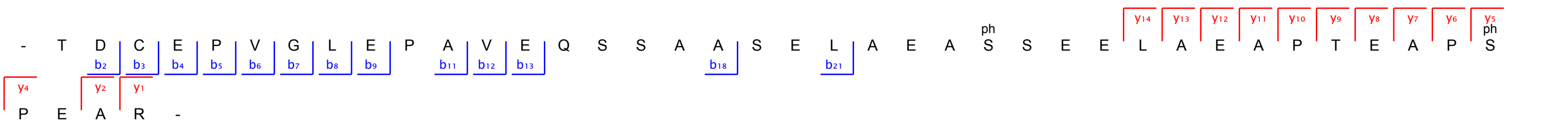
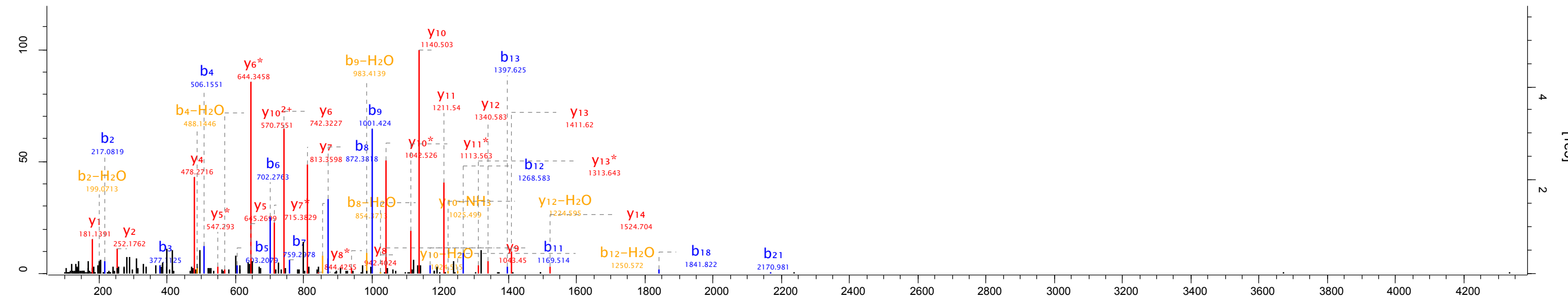
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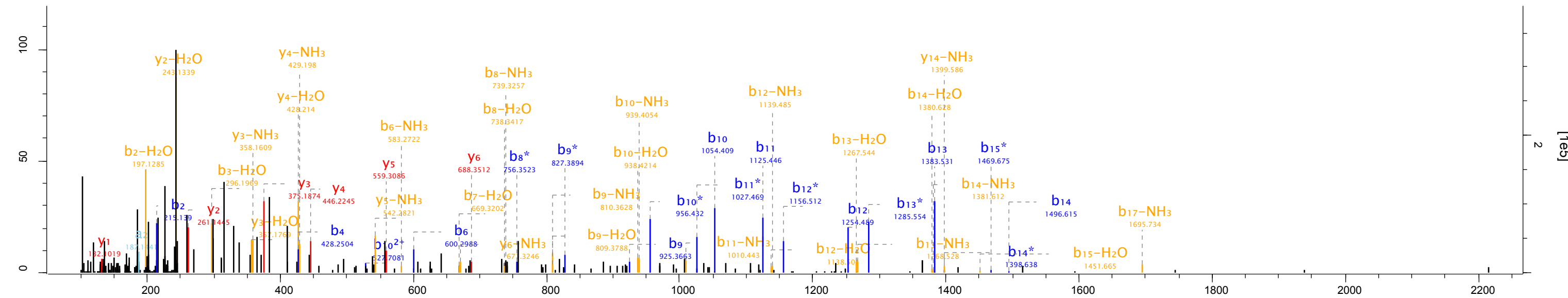
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 Scan: 18266 Method: FTMS; HCD Score: 188.9 m/z: 801.88 Gene names: SH3KBP1



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 18546 Method: FTMS; HCD Score: 72.44 m/z: 1493.98 Gene names: SAFB;SAFB2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18766 Method FTMS; HCD Score 211.35 m/z 971.42 Gene names NAA15

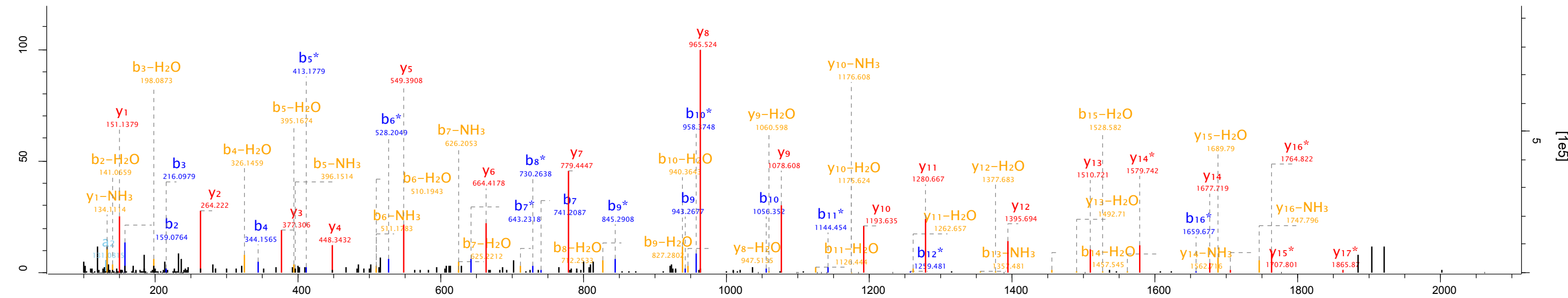


- I T V N G D S ph S A E A E E L A N E I -

Fragmentation sites are indicated by brackets below the sequence:

- b2: T
- b4: N
- b6: D
- b8*: S
- b9: A
- b10: E
- b11: A
- b12: E
- b13: E
- b14: L
- b15*: A

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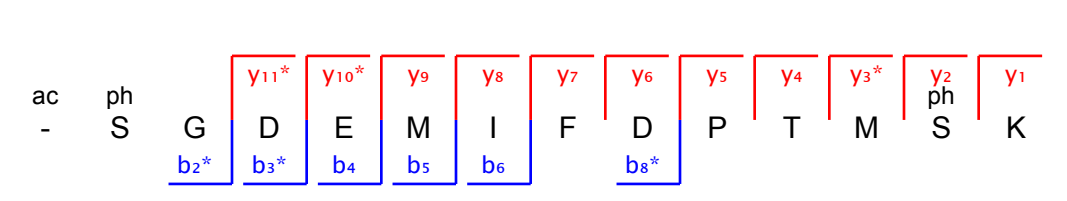
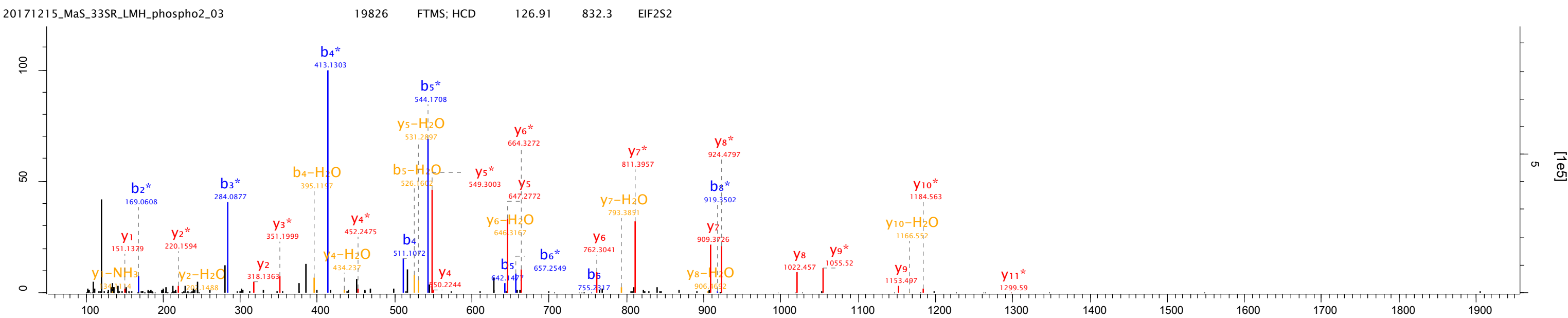


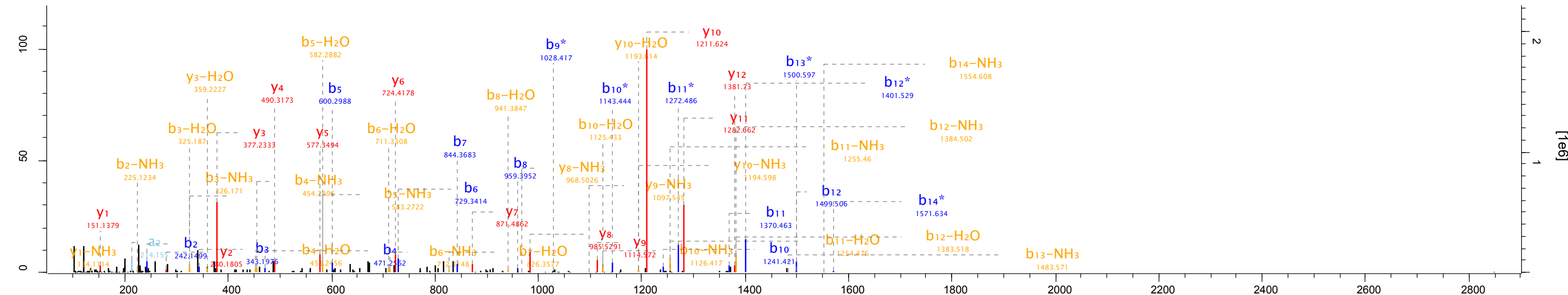
- G T G Q ph S D D S D I W D D T A L I K -

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b₆*
b₇
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b₁₁*
b₁₂*
b₁₆*

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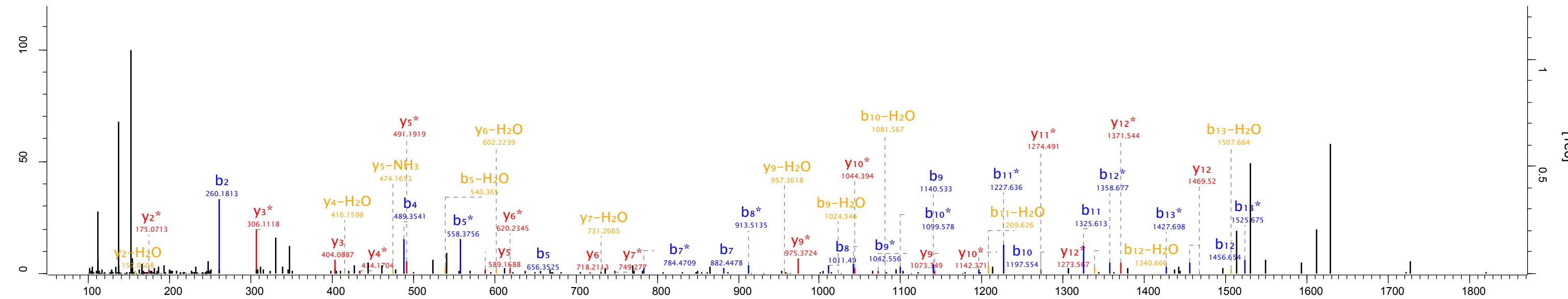
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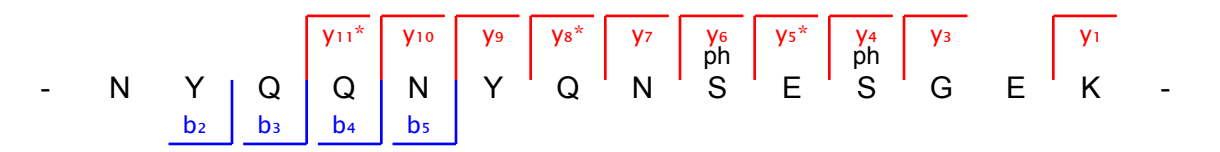
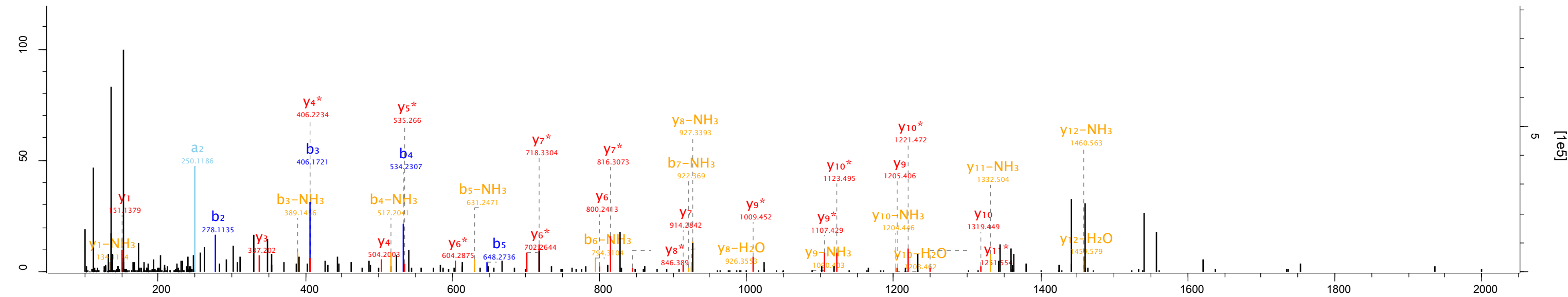
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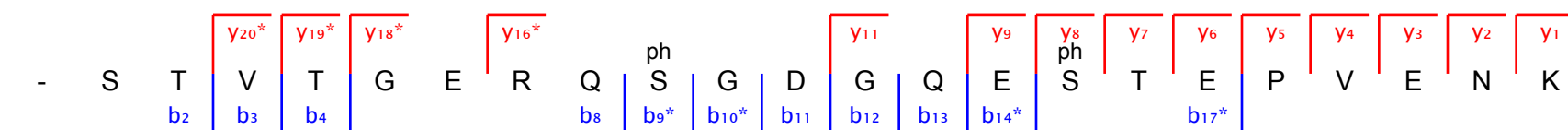
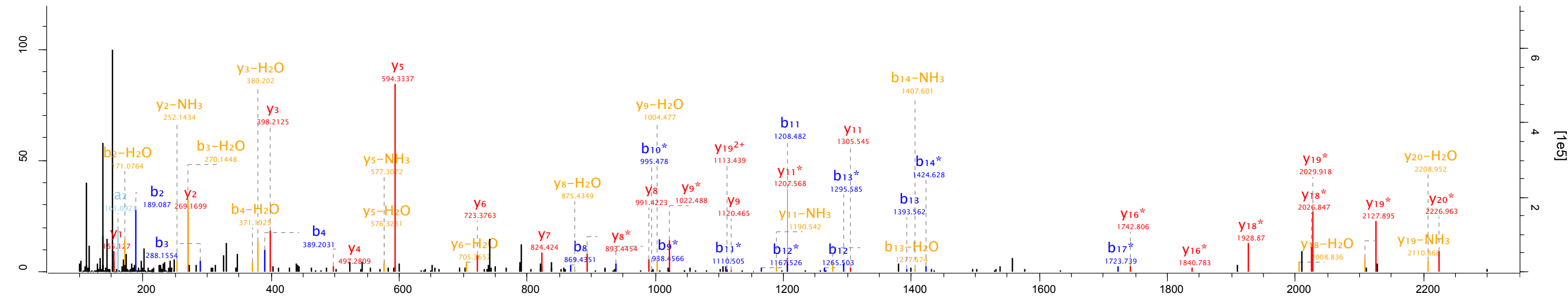
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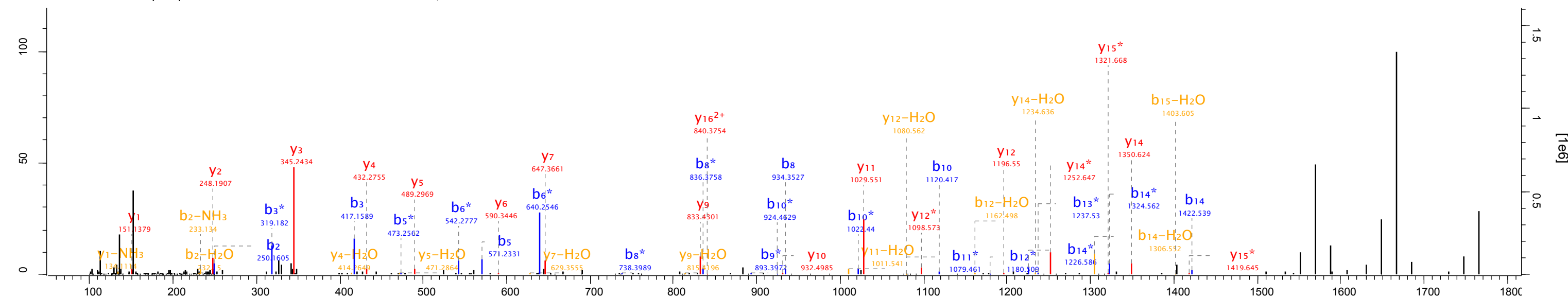
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Scan 4066 Method FTMS; HCD Score 137.03 m/z 884.39 Gene names ADD1



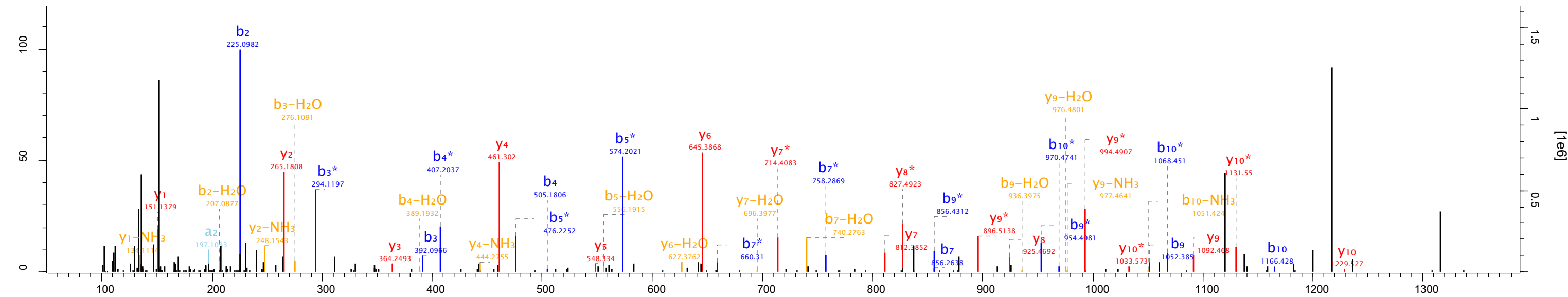
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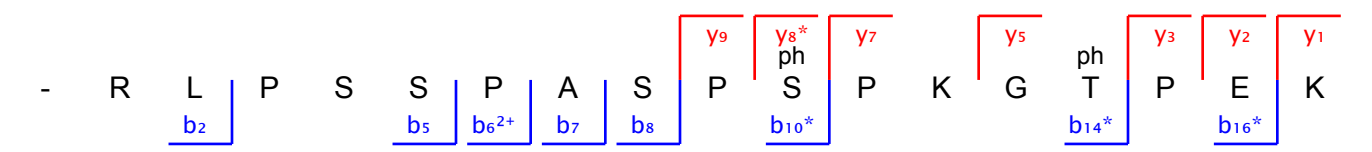
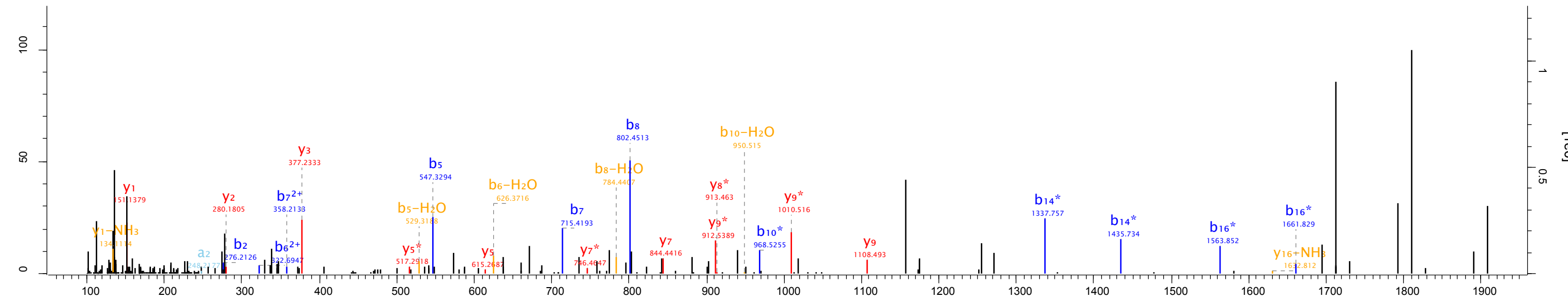
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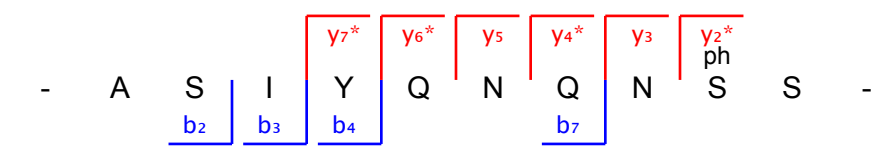
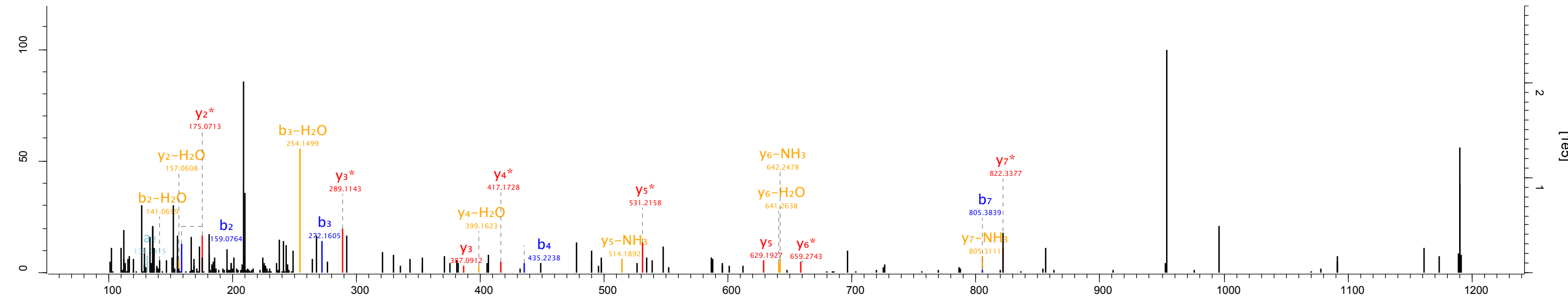
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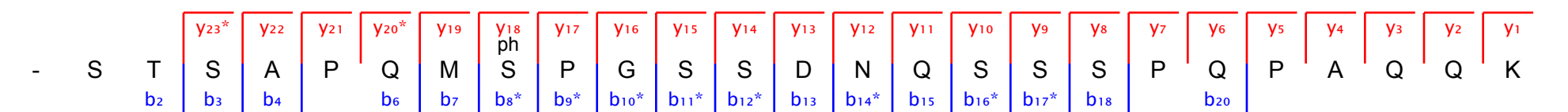
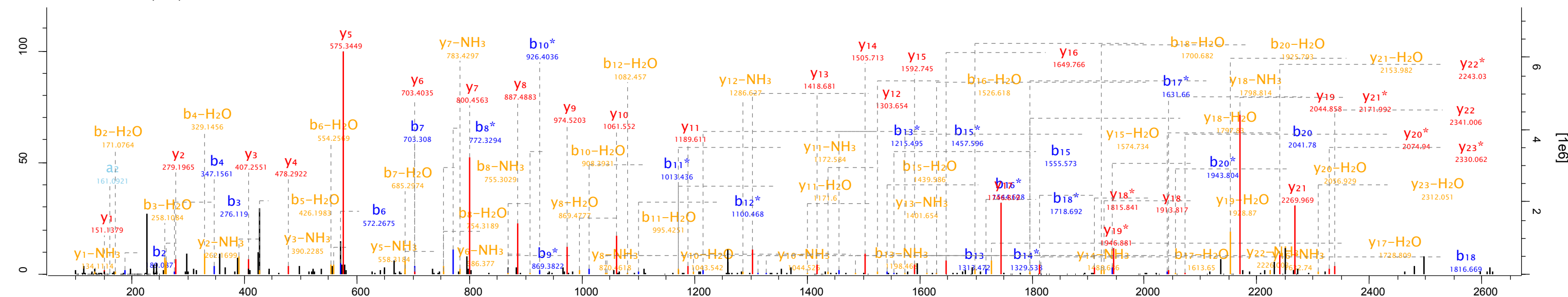
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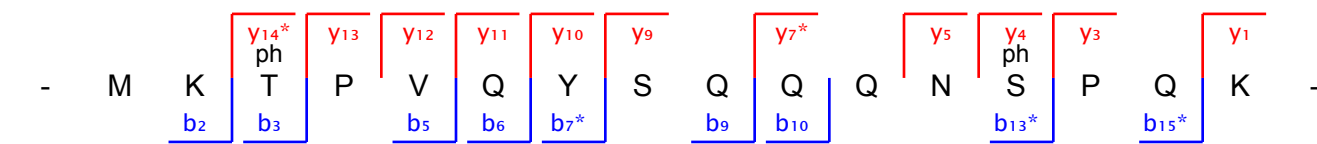
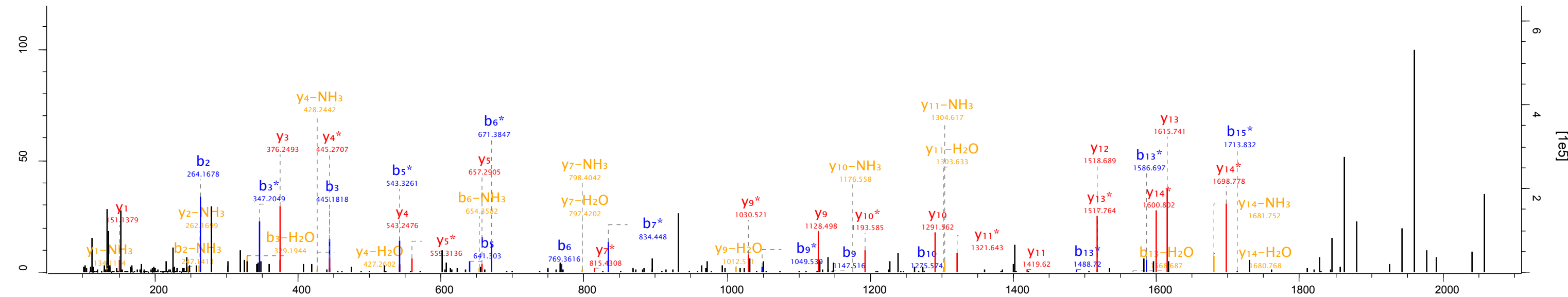


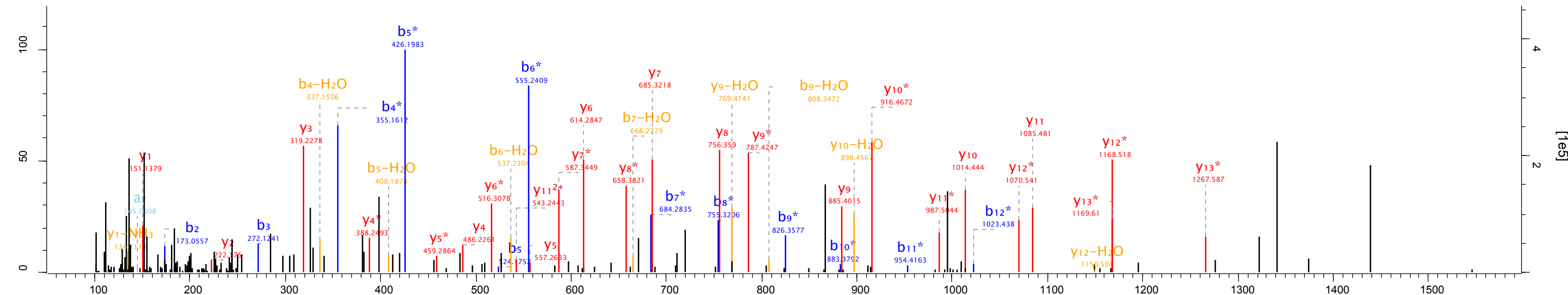
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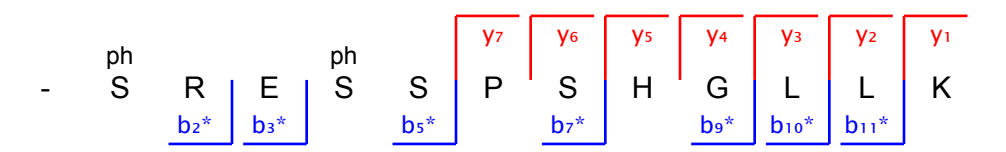
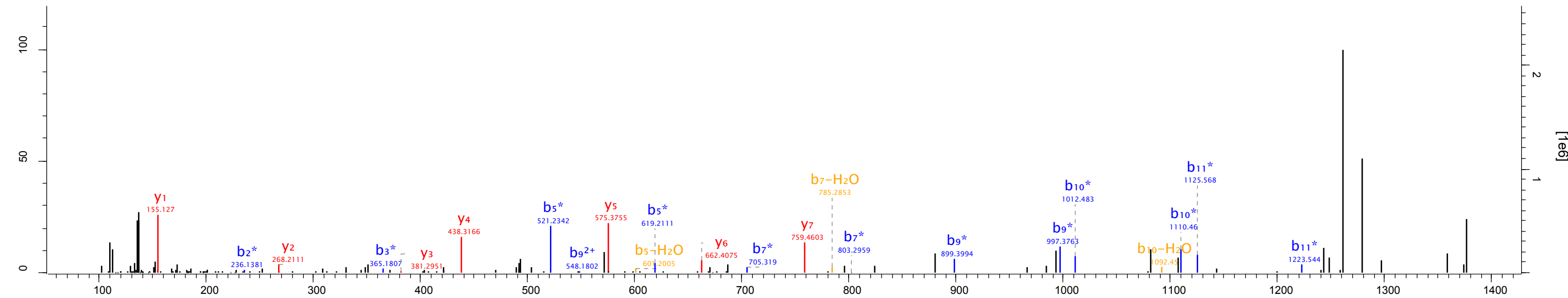




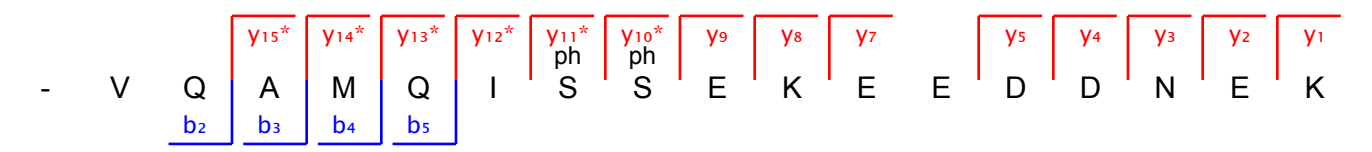
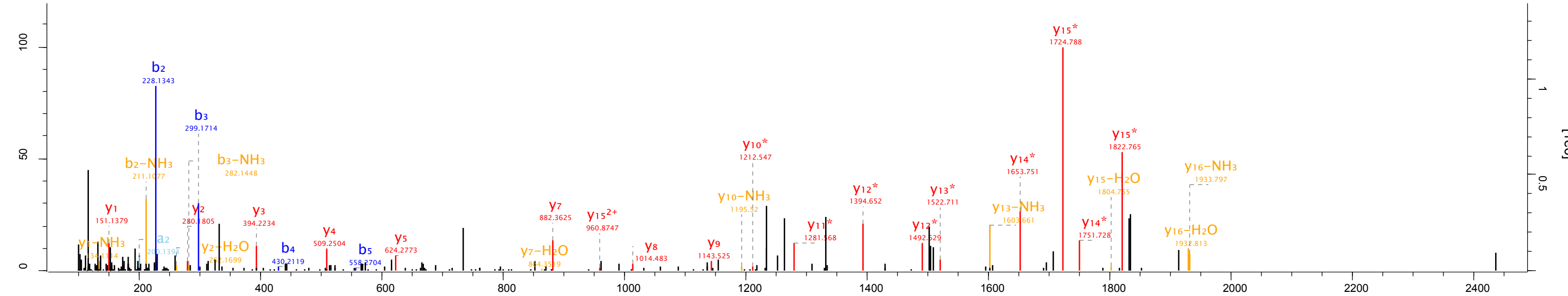
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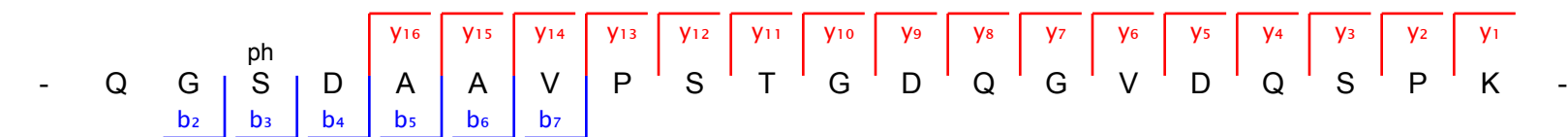
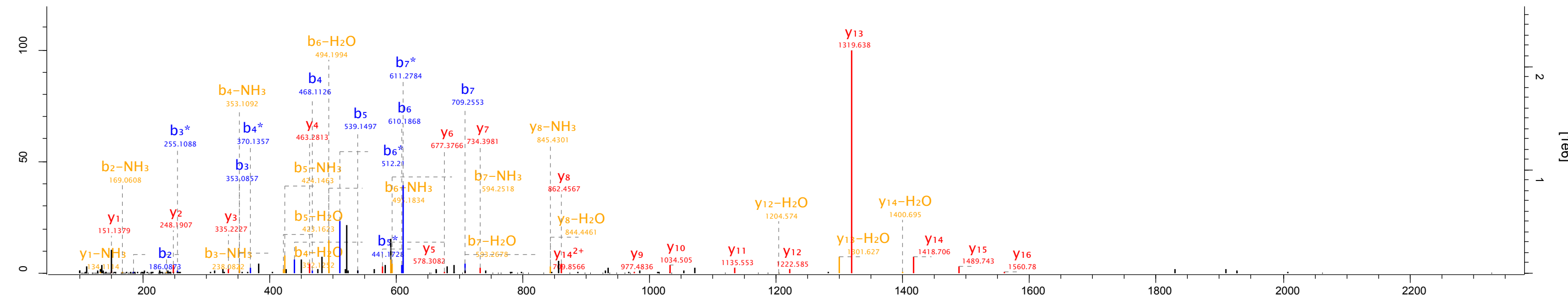


20171215_MaS_33SR_LMH_phospho2_03 5956 FTMS; HCD 73.83 716.96 CDV3



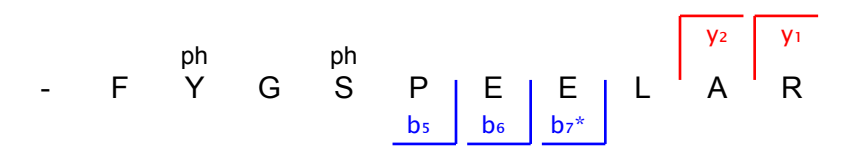
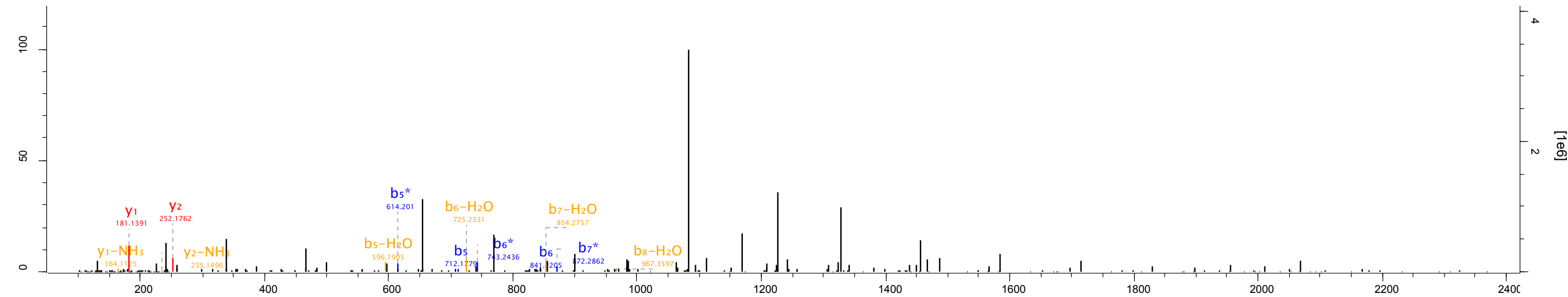
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20171215_MaS_33SR_LMH_phospho2_03

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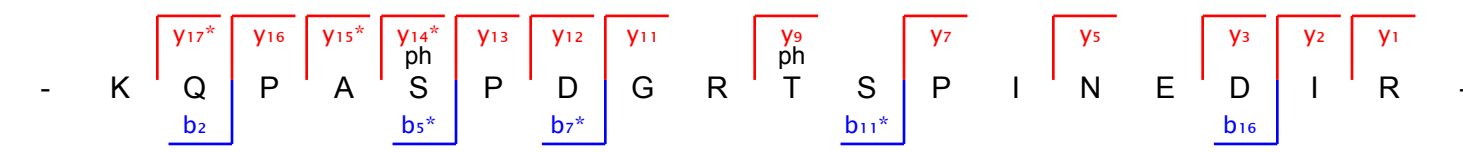
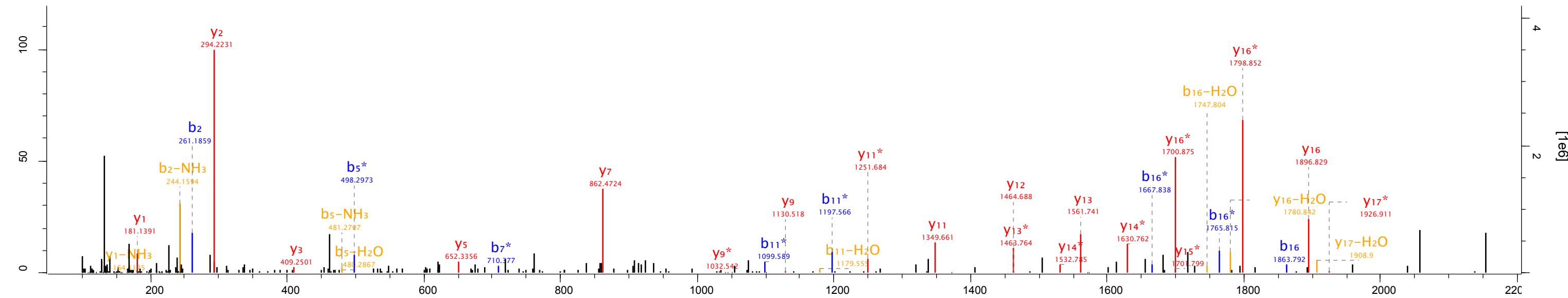


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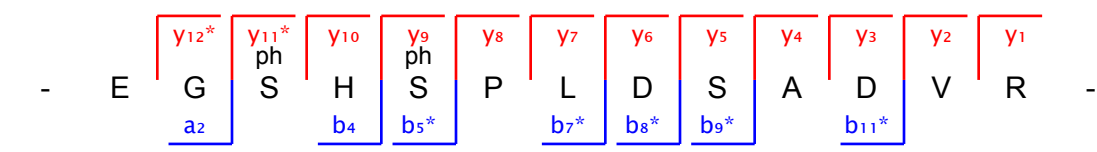
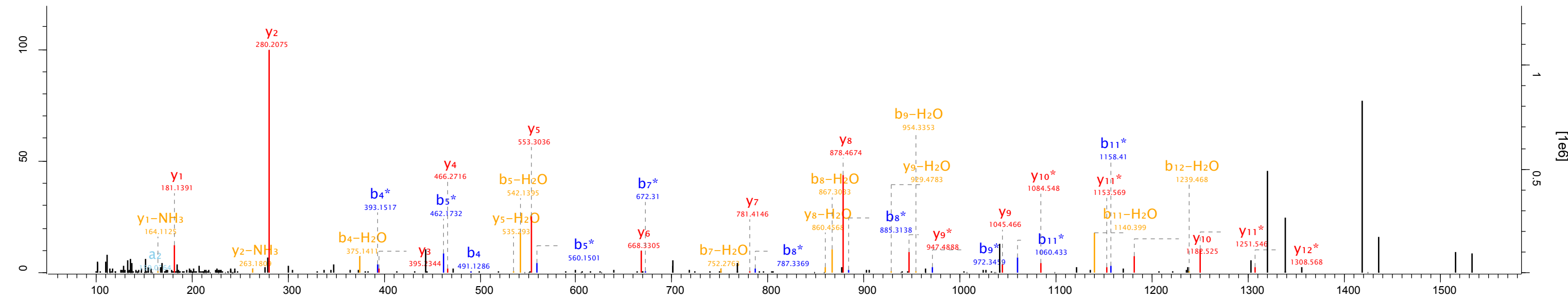
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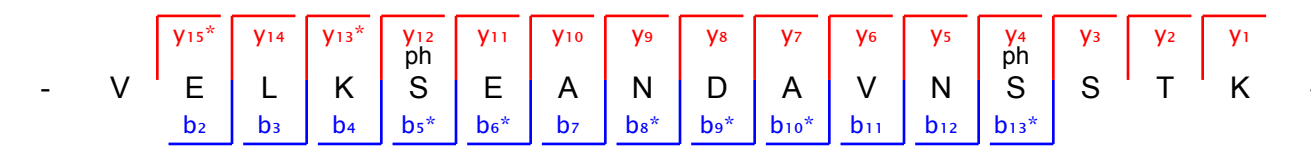
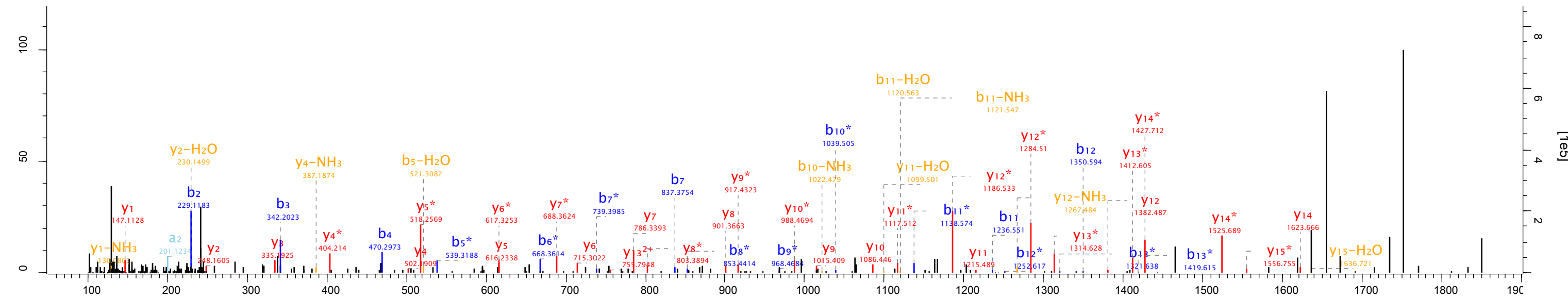


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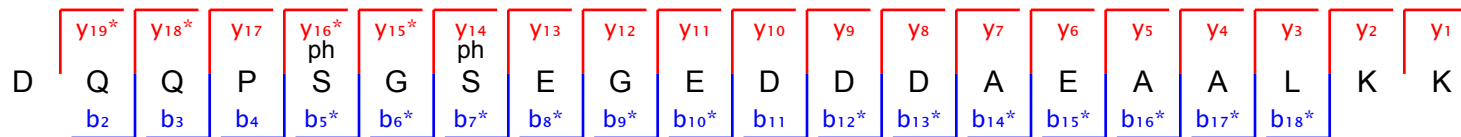
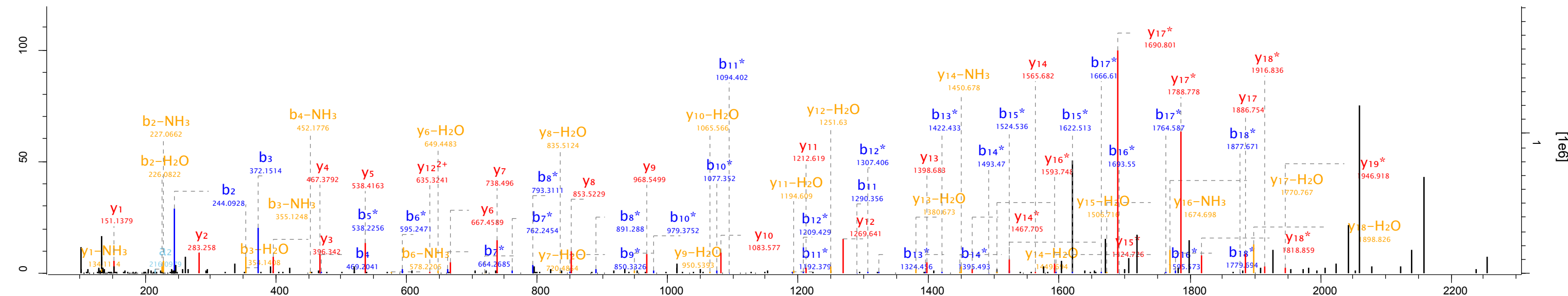


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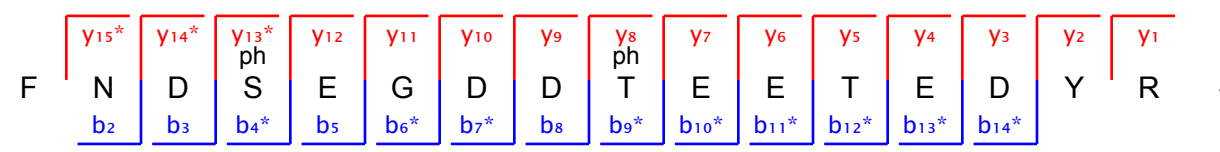
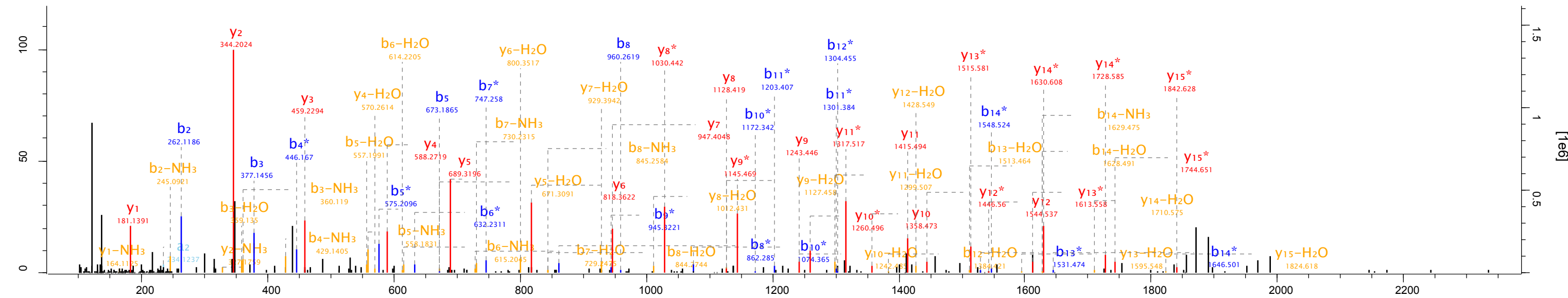
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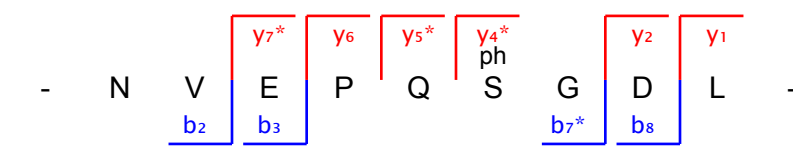
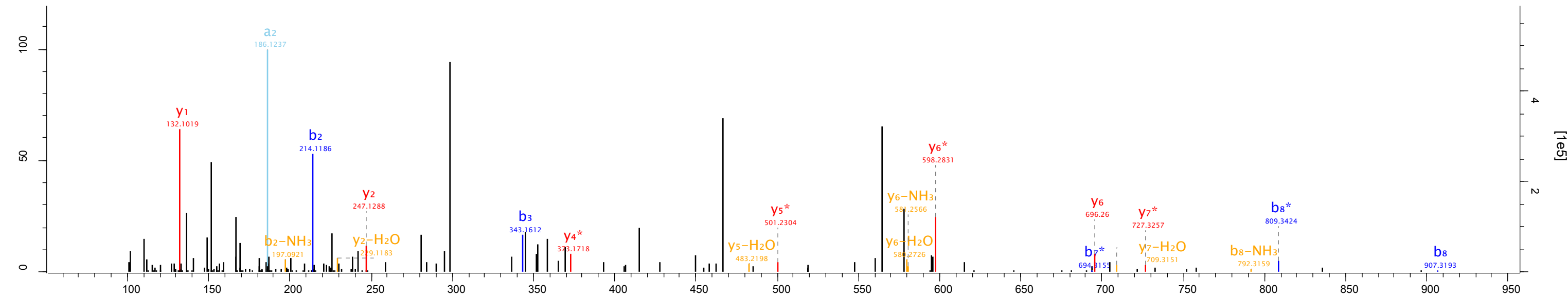
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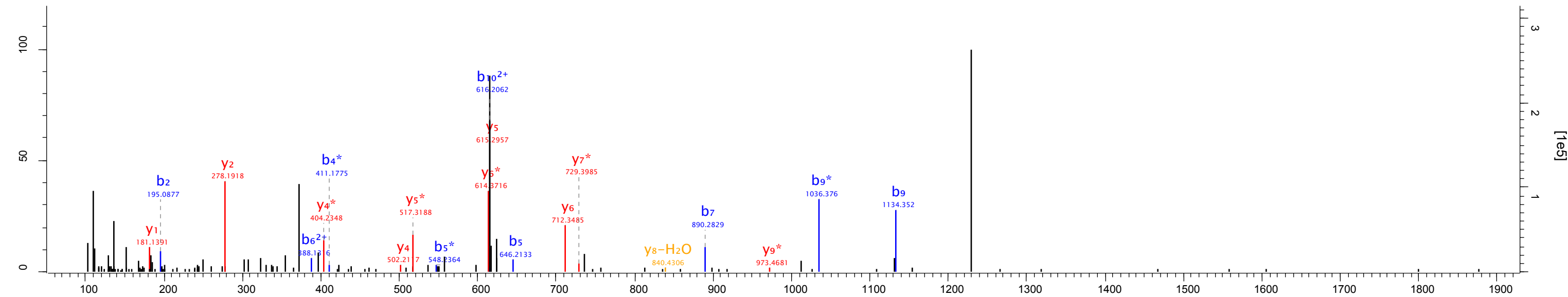
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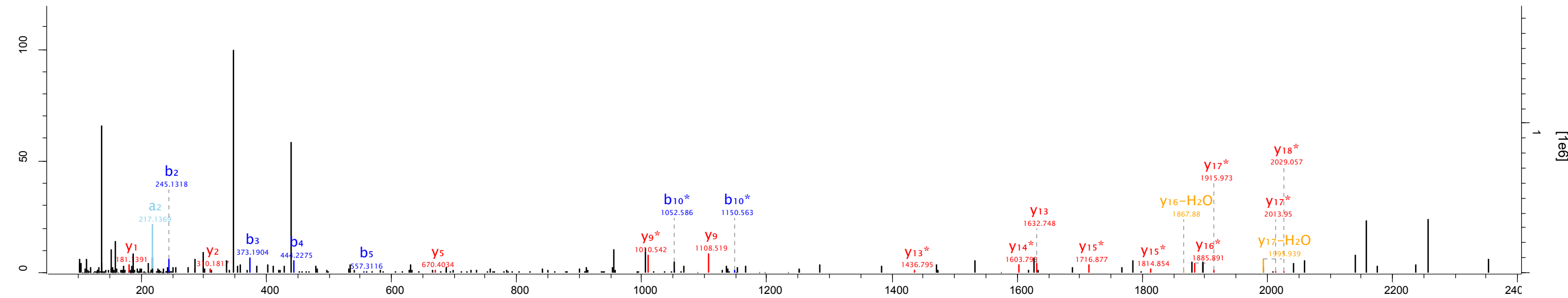
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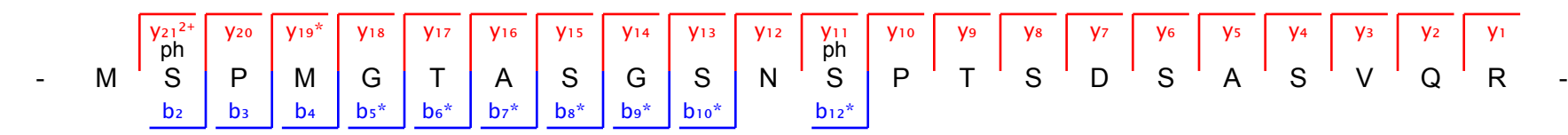
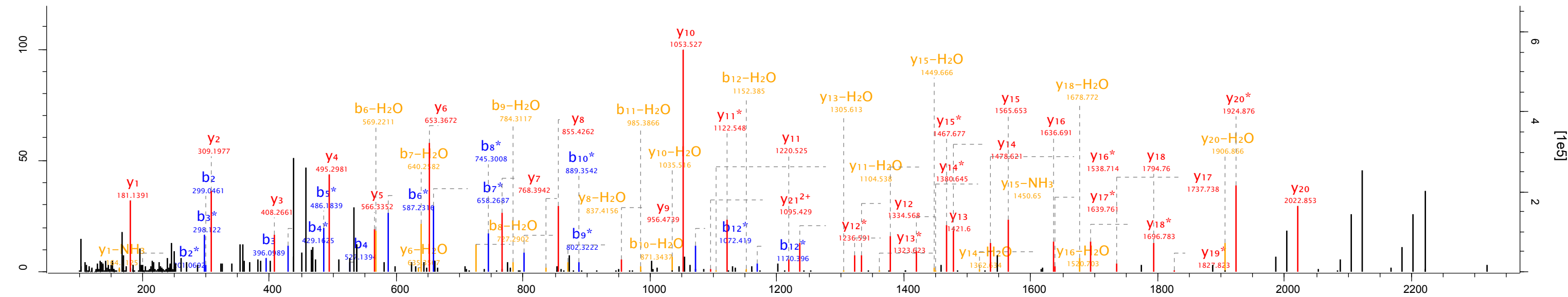


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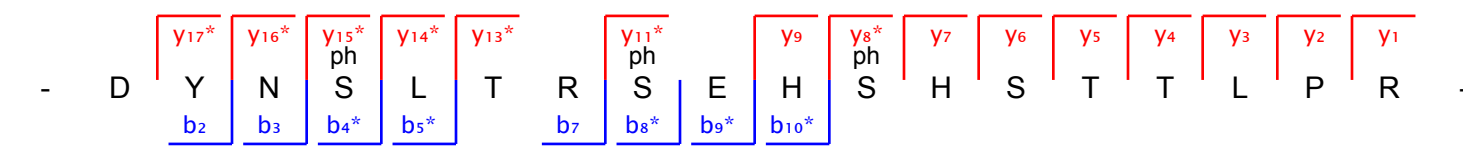
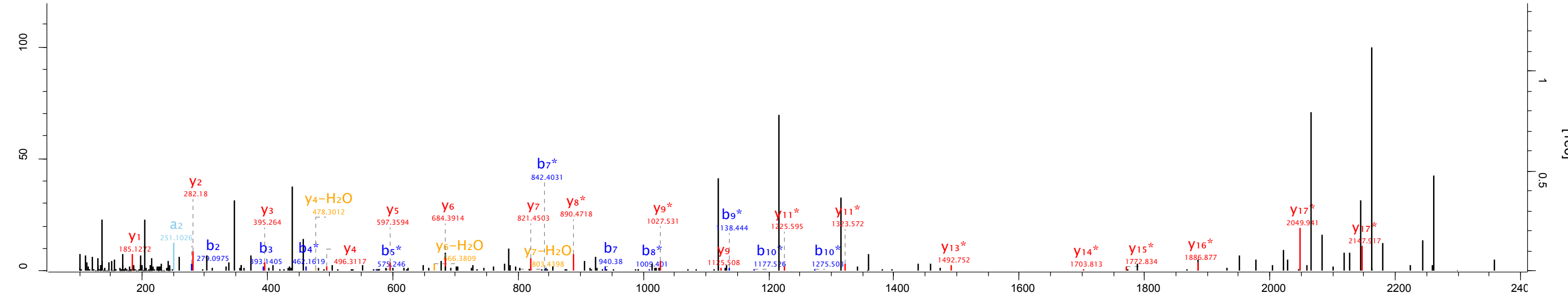
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20171215_MaS_33SR_LMH_phospho2_03

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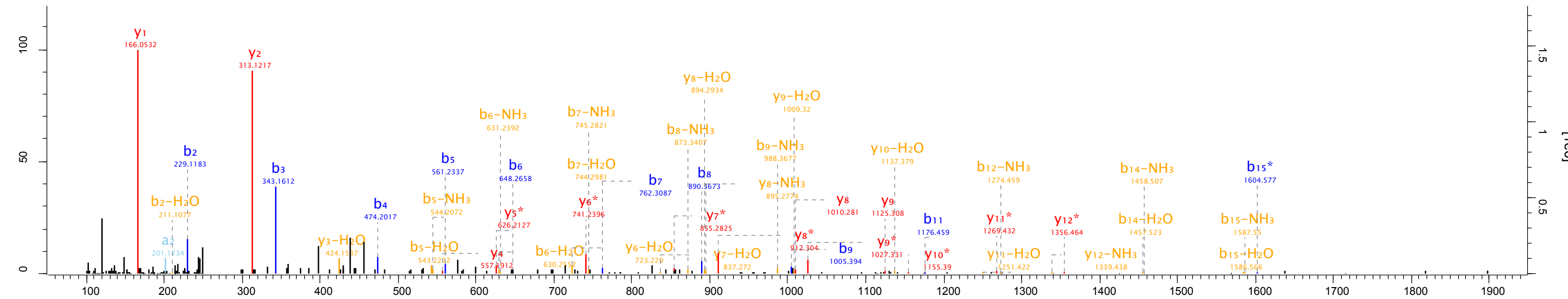


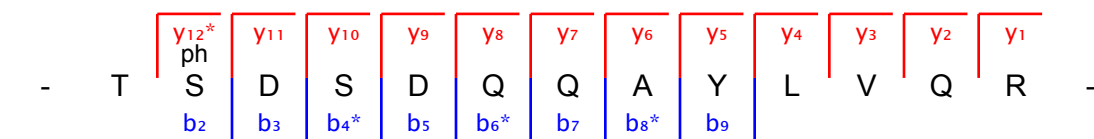
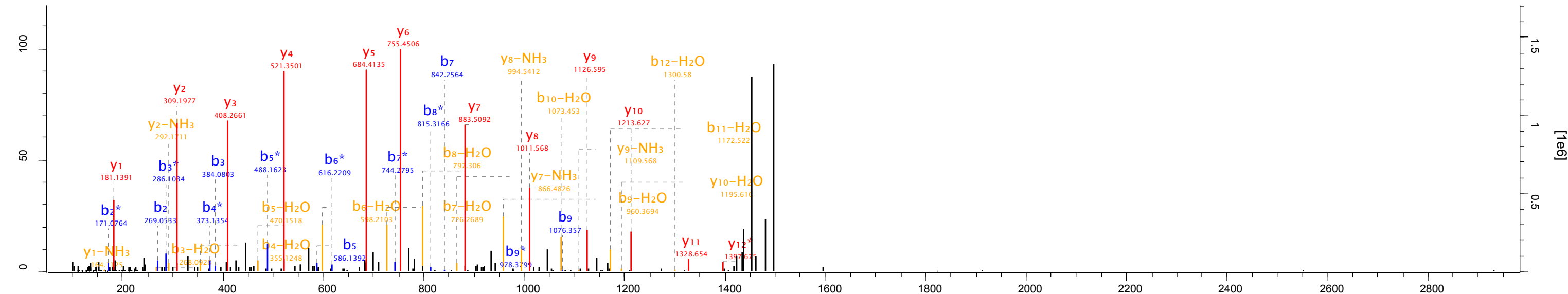
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20171215_MaS_33SR_LMH_phospho2_03 8256 FTMS; HCD 55.43 787.64 ITGB4

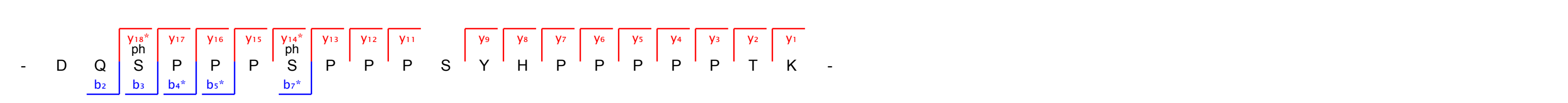
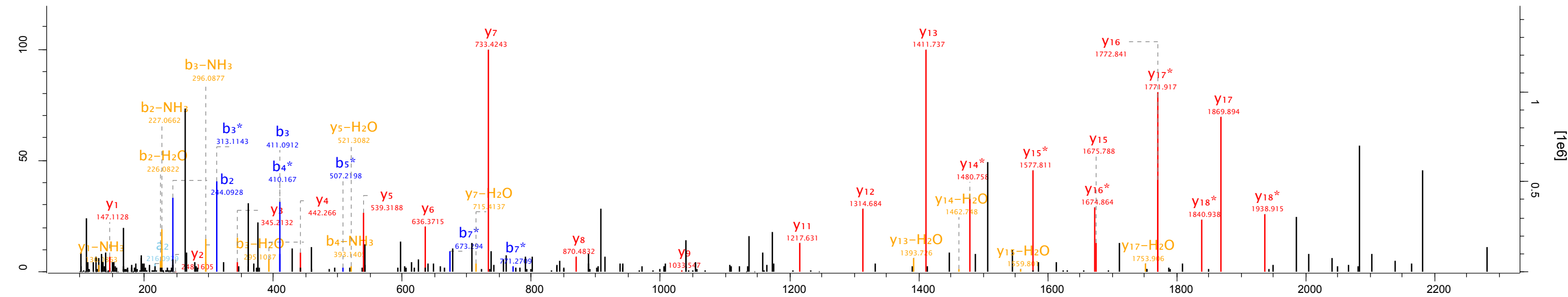


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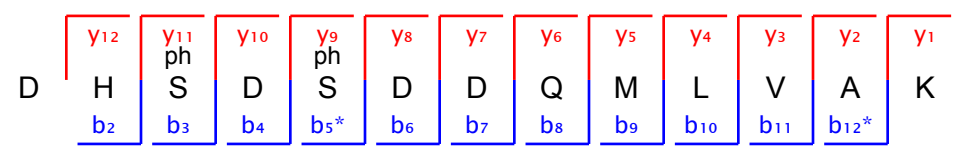
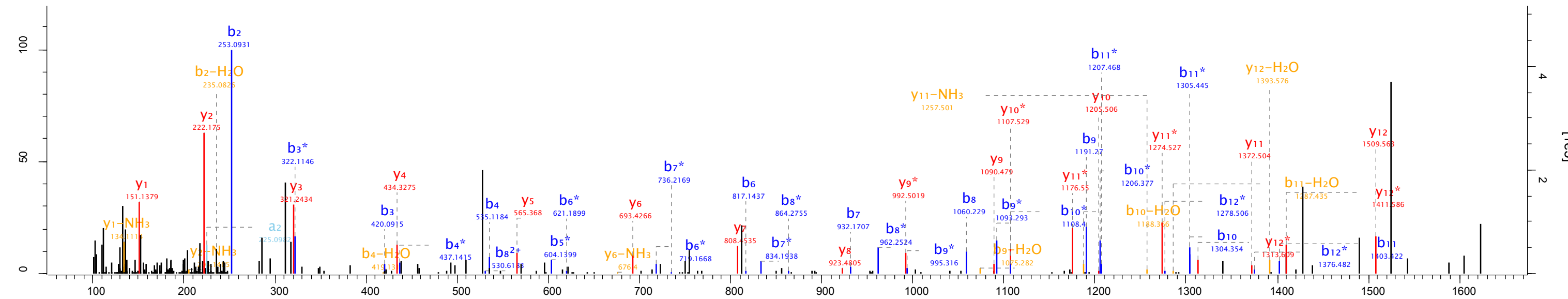




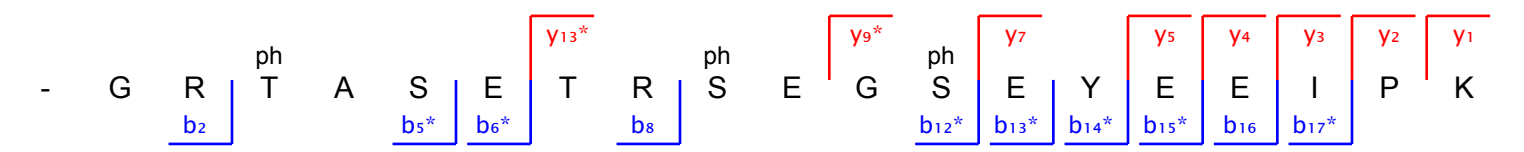
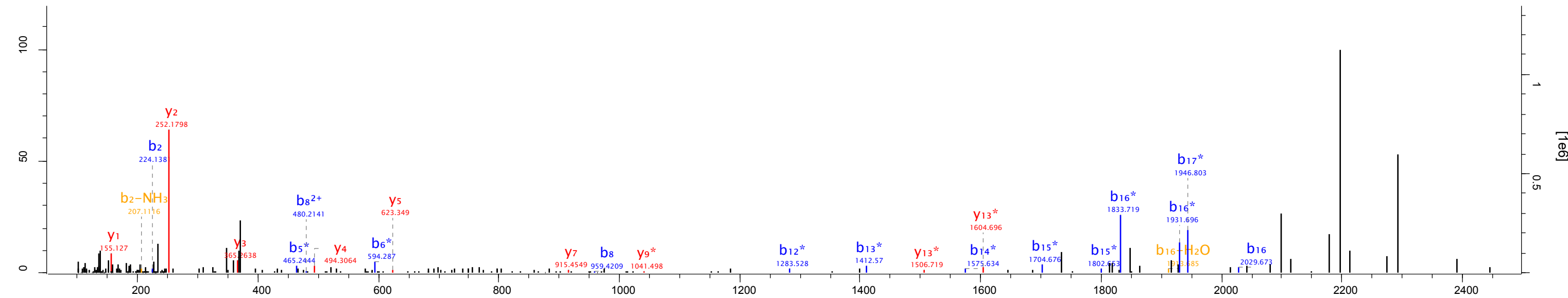
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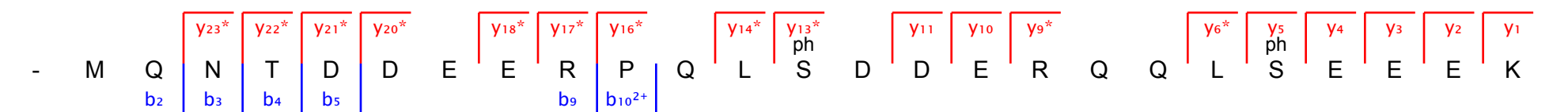
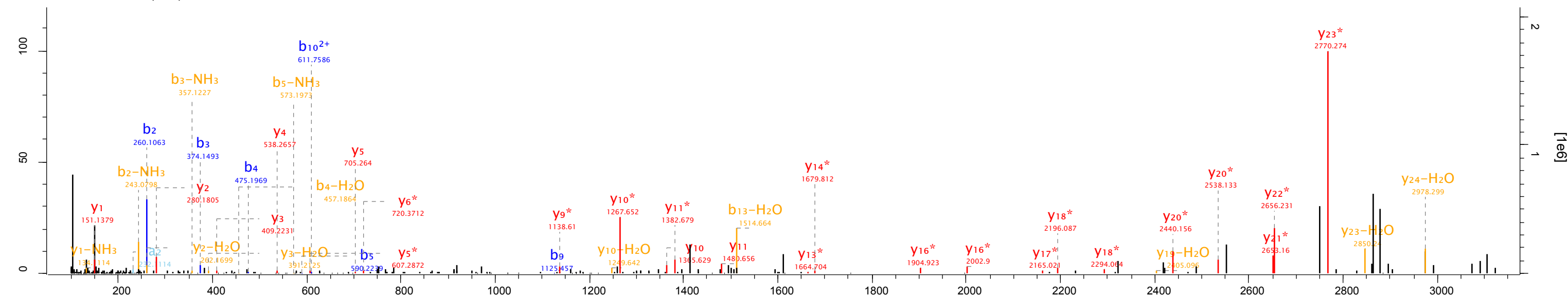


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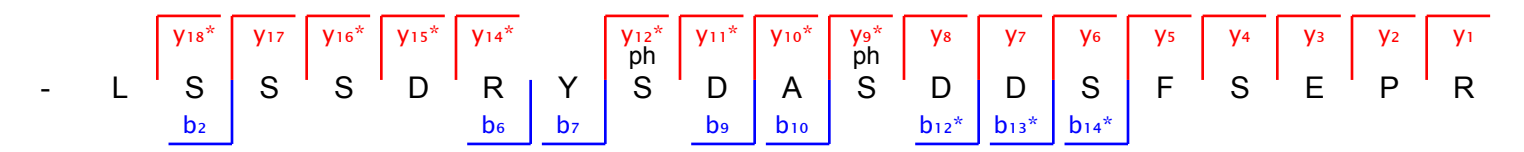
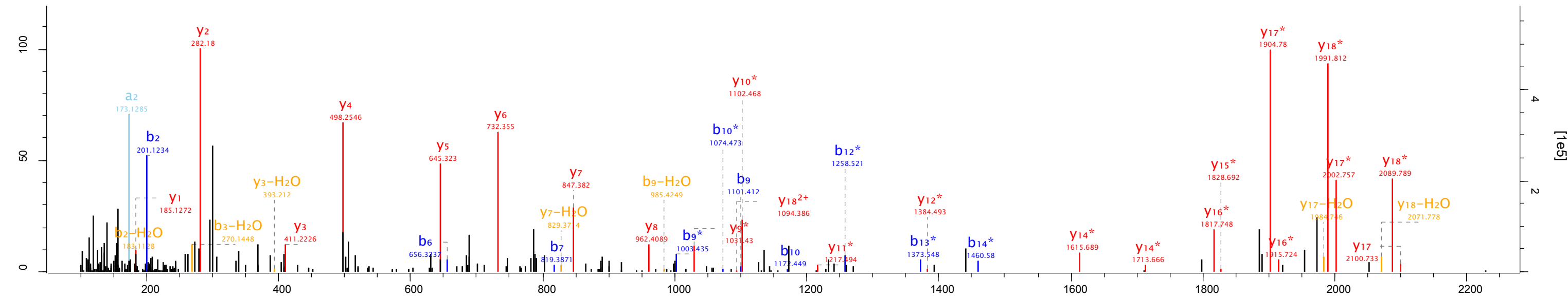


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20171215_MaS_33SR_LMH_phospho2_03

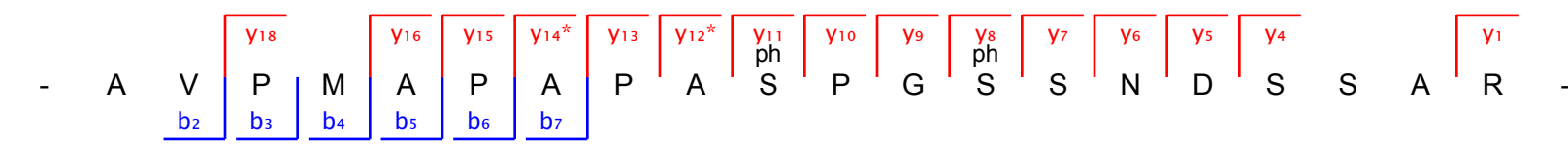
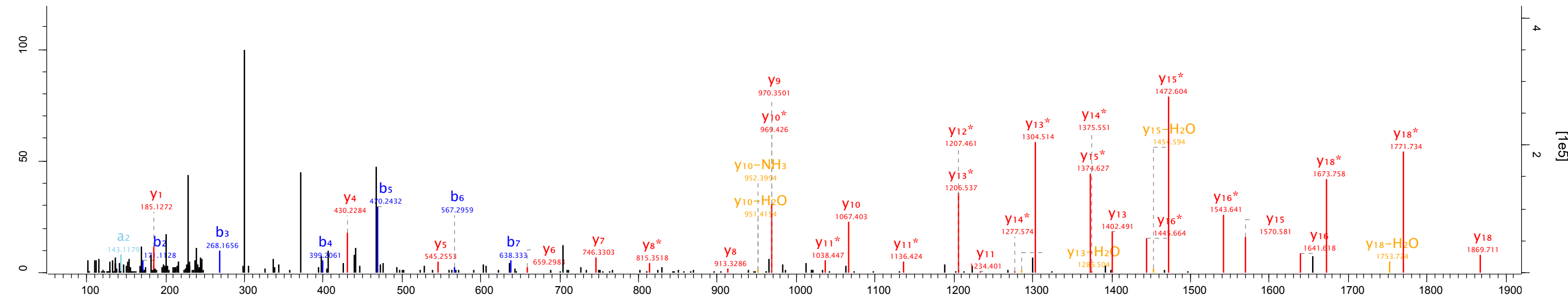
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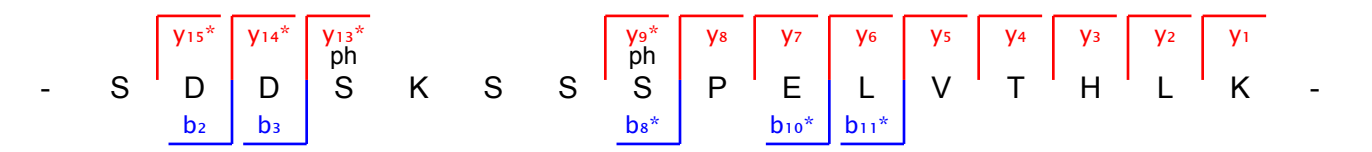
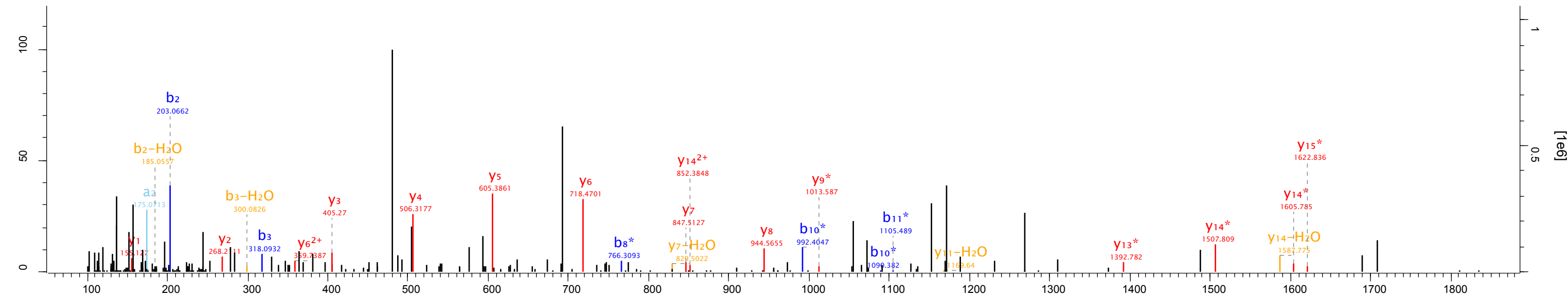
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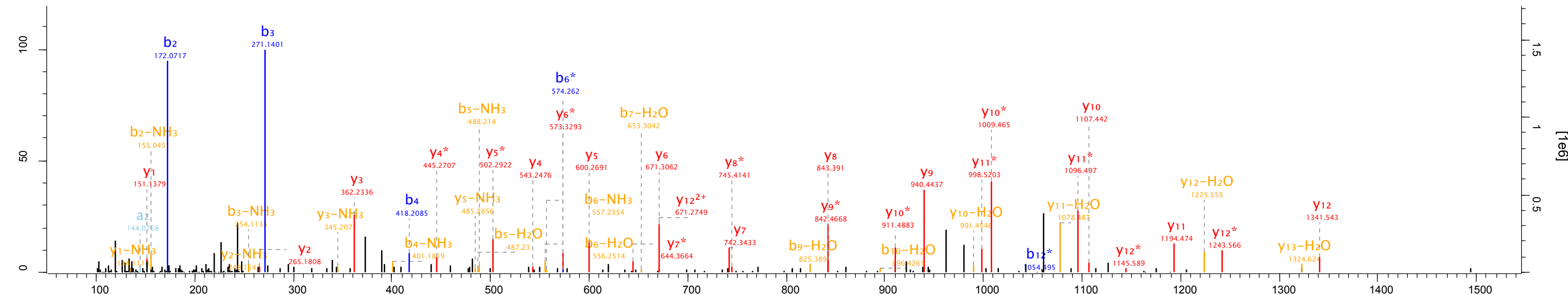


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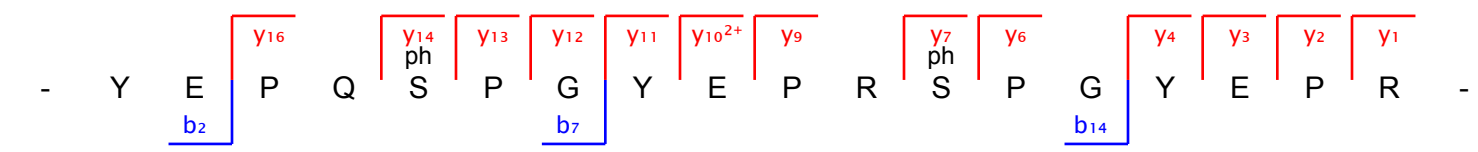
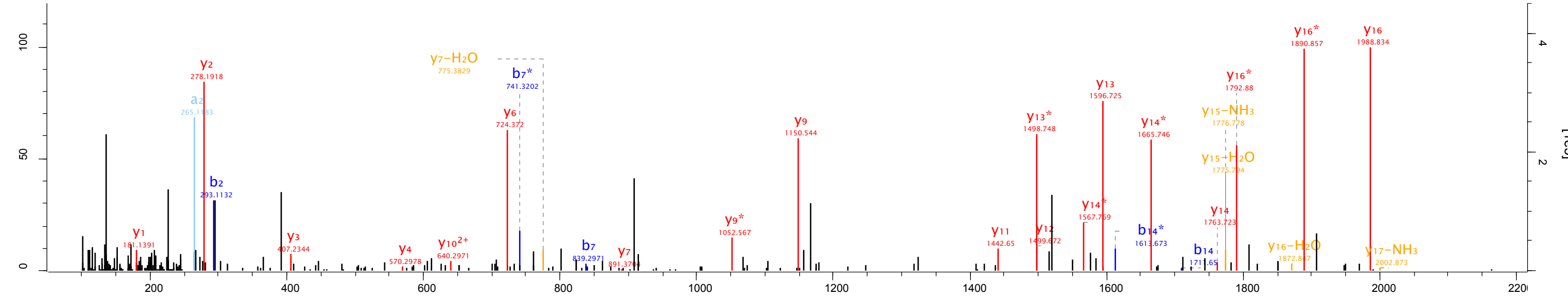


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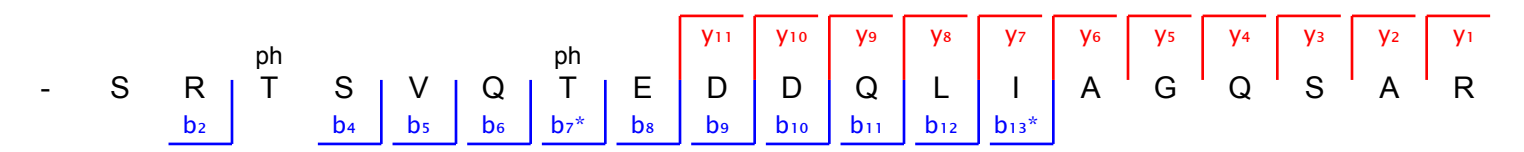
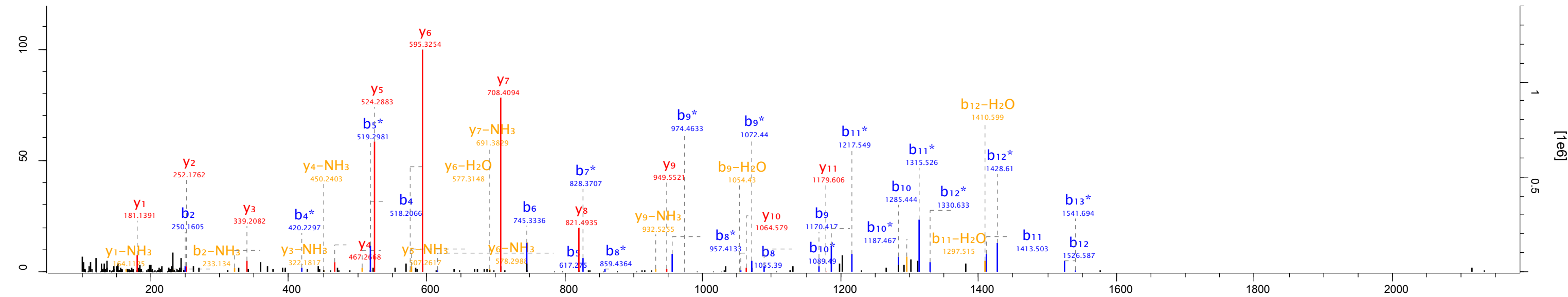
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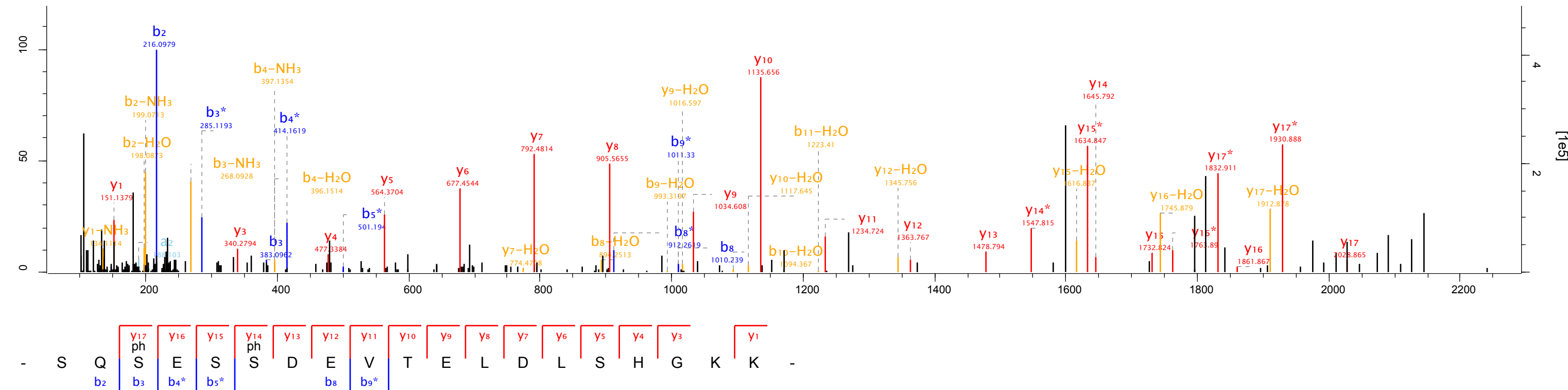
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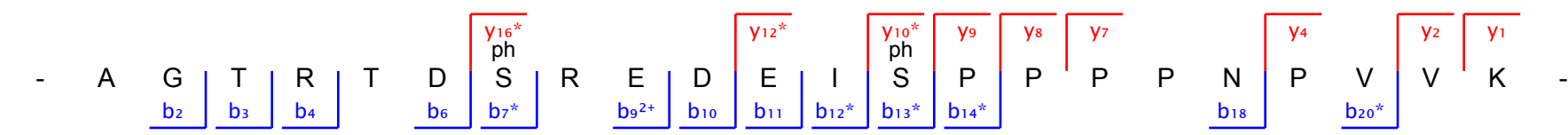
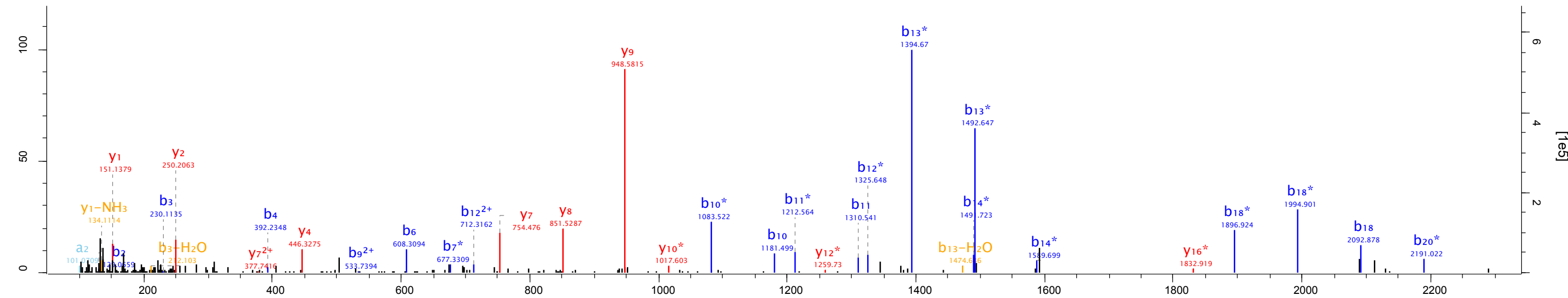


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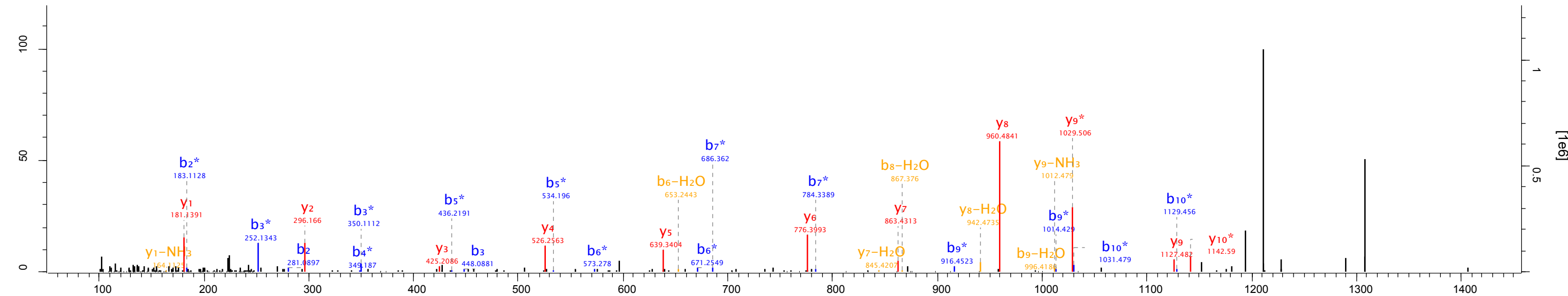
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Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
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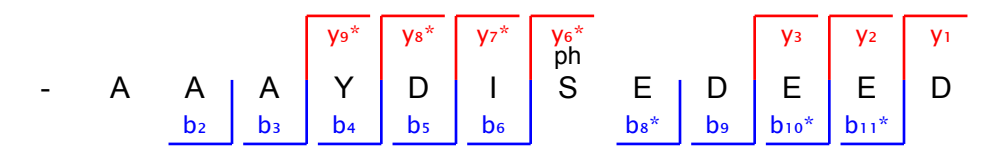
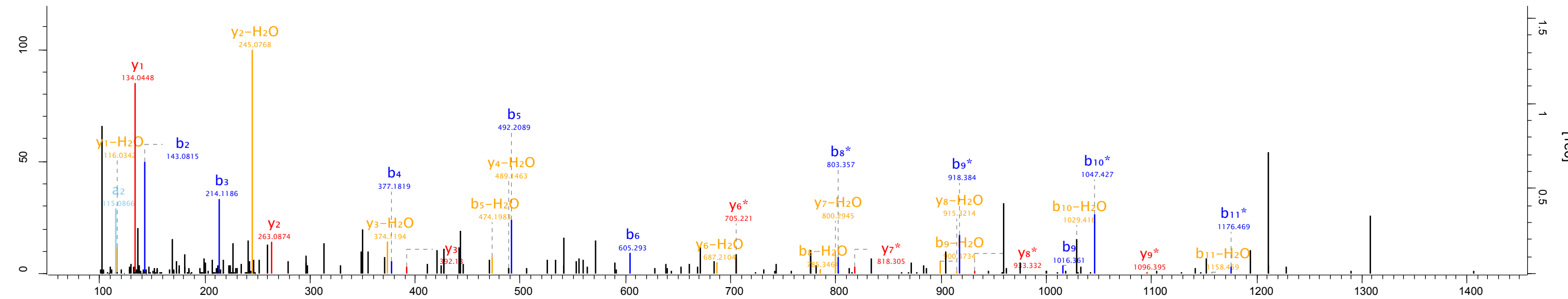


ph S -

y10*	y9 ph	y8	y7	y6	y5	y4	y3	y2	y1
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b2	b3	b4*	b5*	b6*	b7*		b9*	b10*	

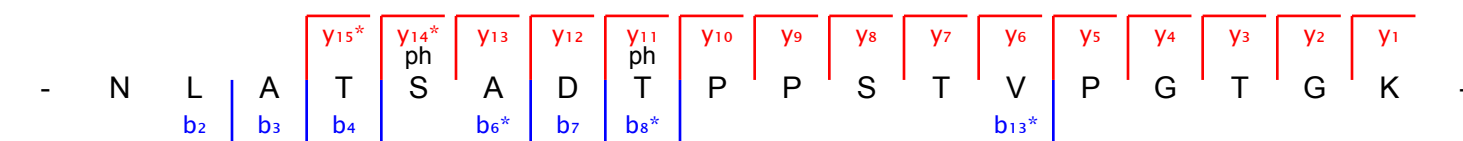
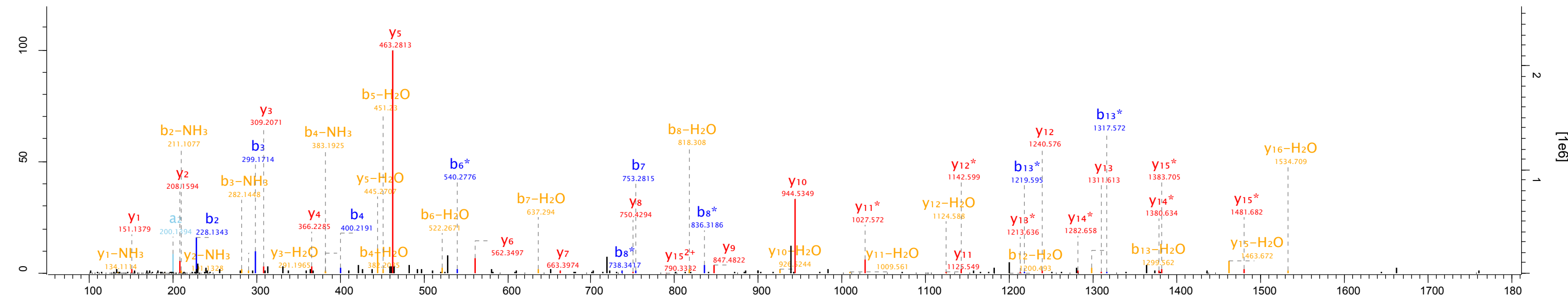
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 9526 Method FTMS; HCD Score 126.21 m/z 704.24 Gene names PCYT1A

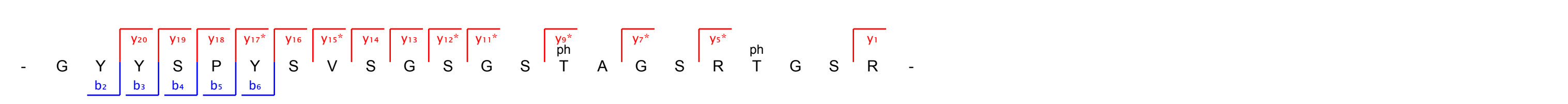
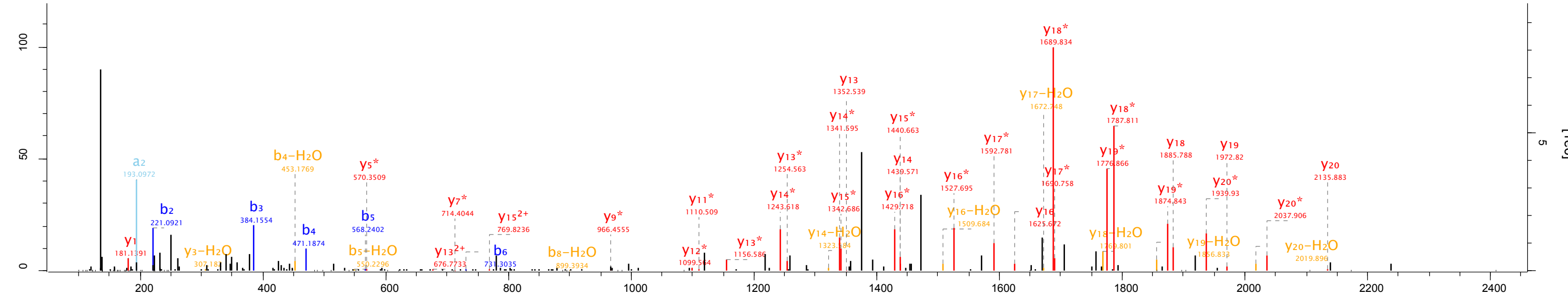


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20171215_MaS_33SR_LMH_phospho2_03

Scan 9696 Method FTMS; HCD Score 123.71 m/z 939.92 Gene names SMG1

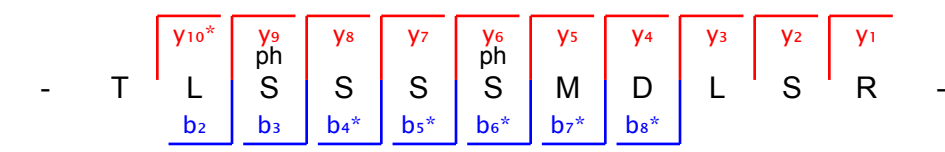
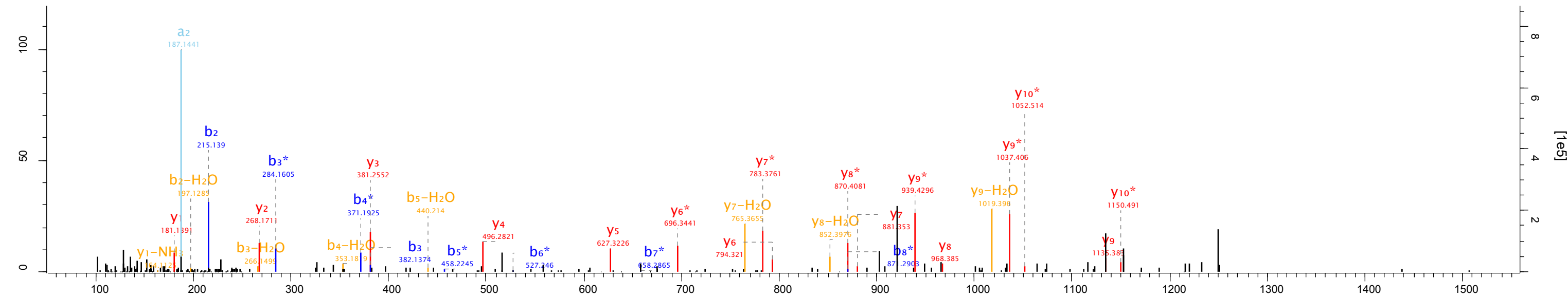


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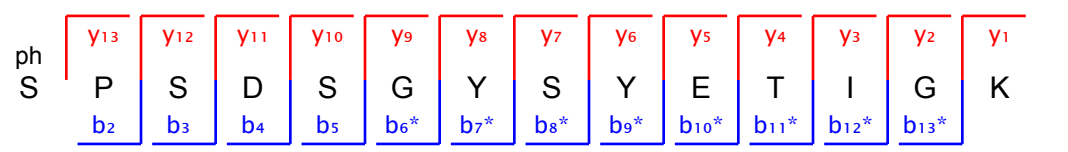
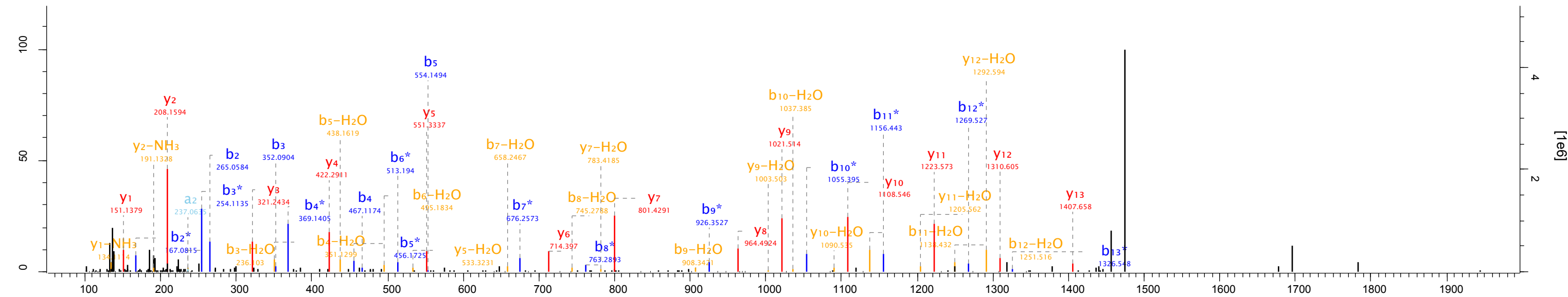


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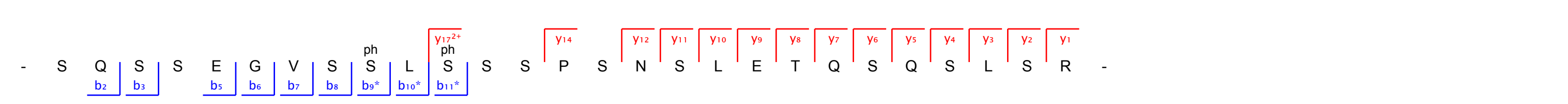
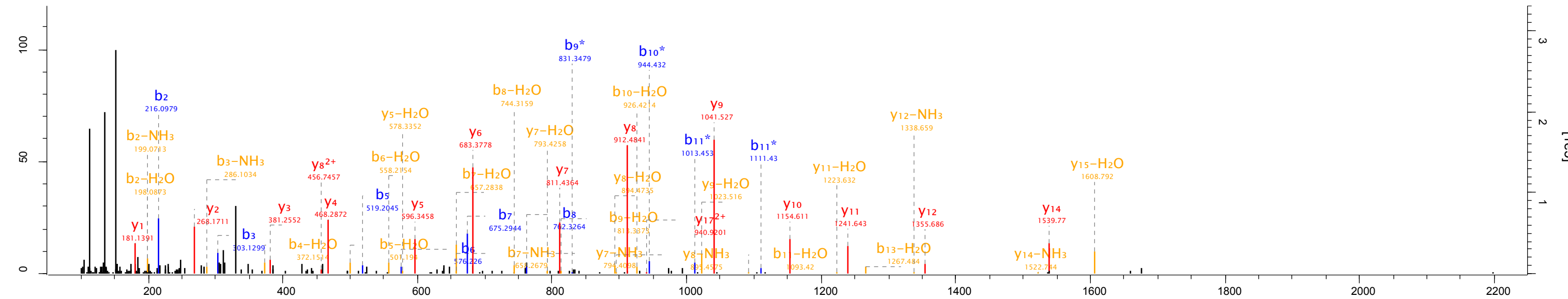
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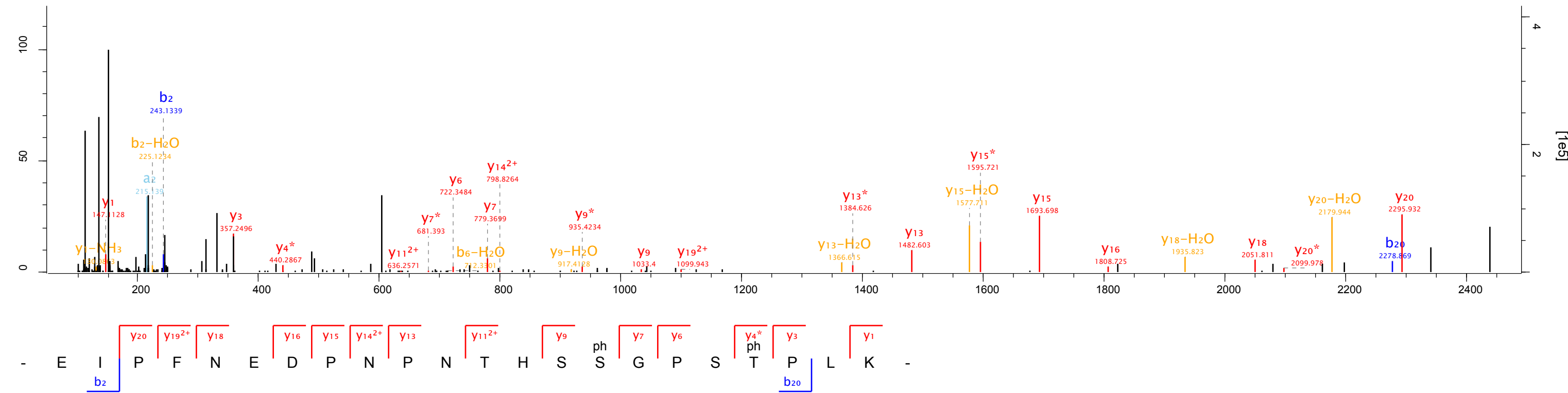
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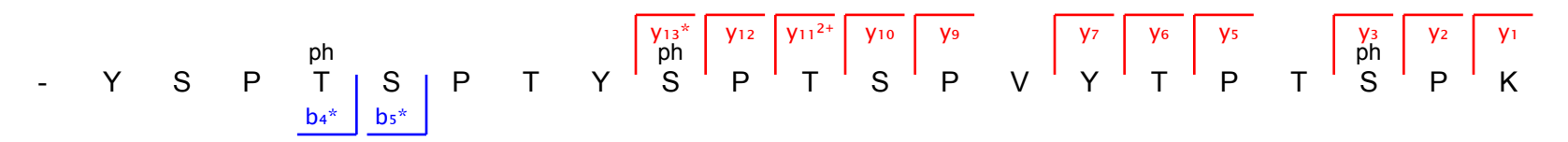
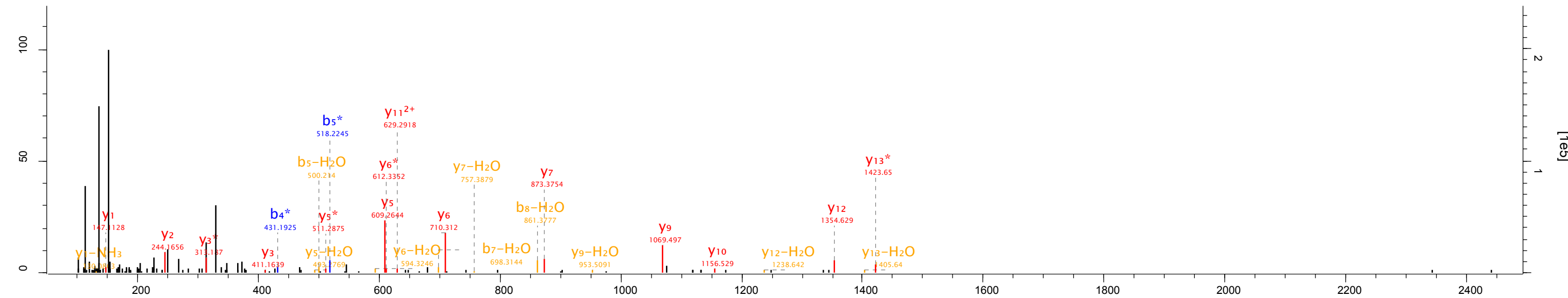
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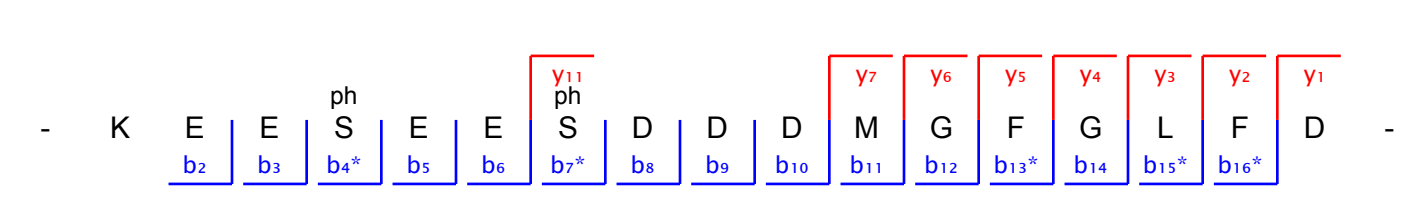
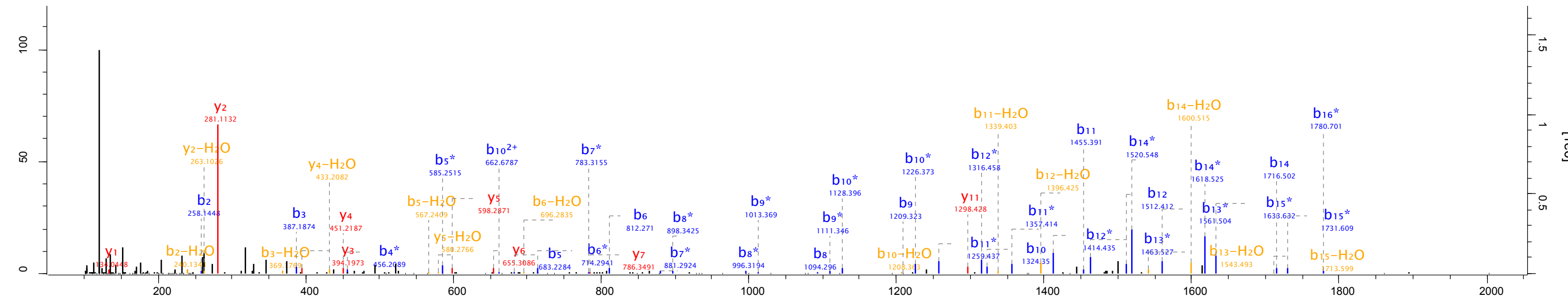
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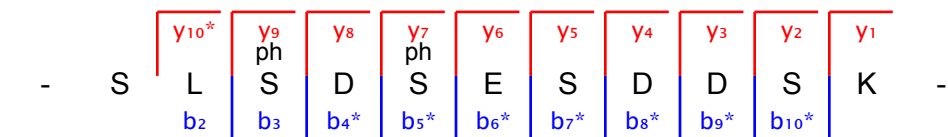
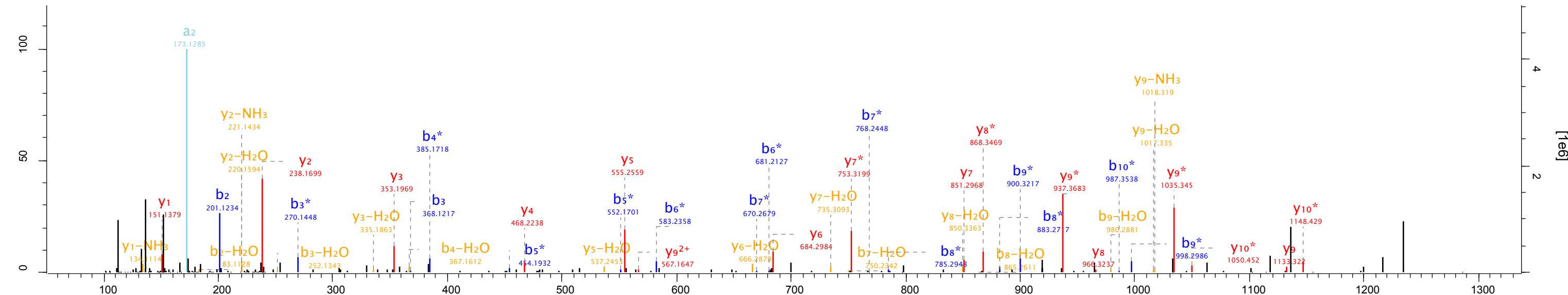


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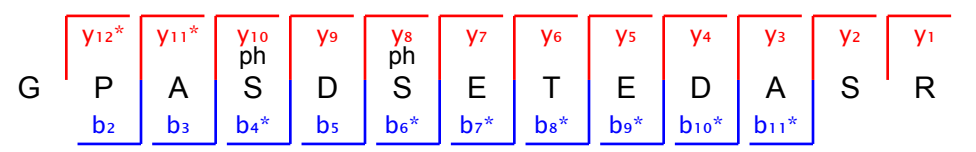
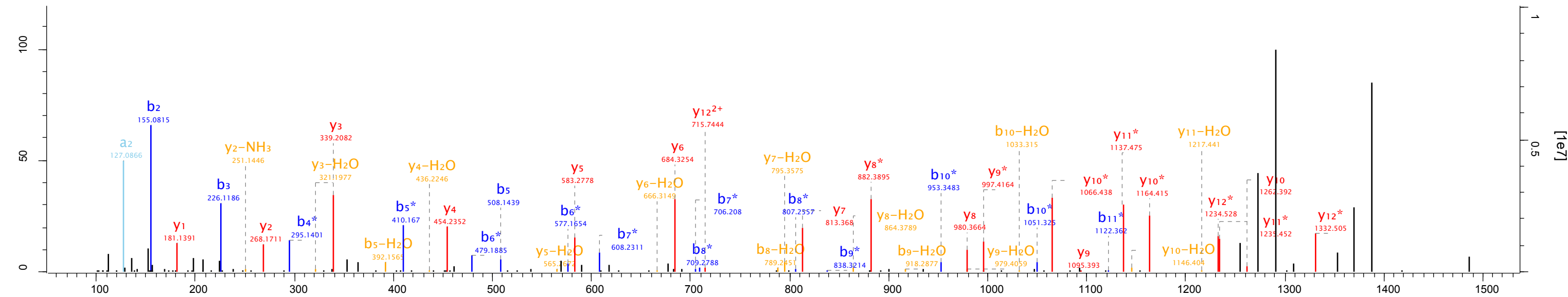


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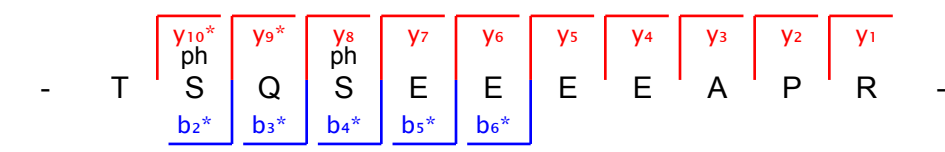
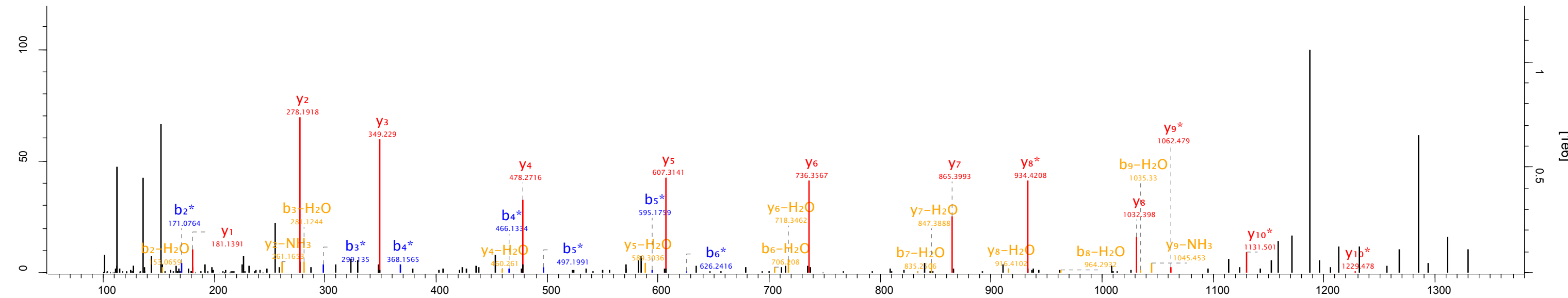




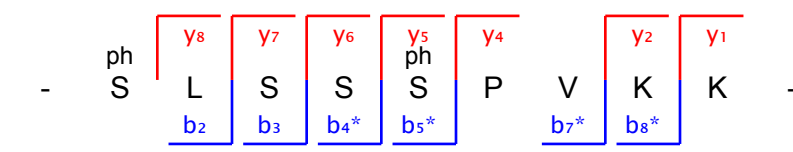
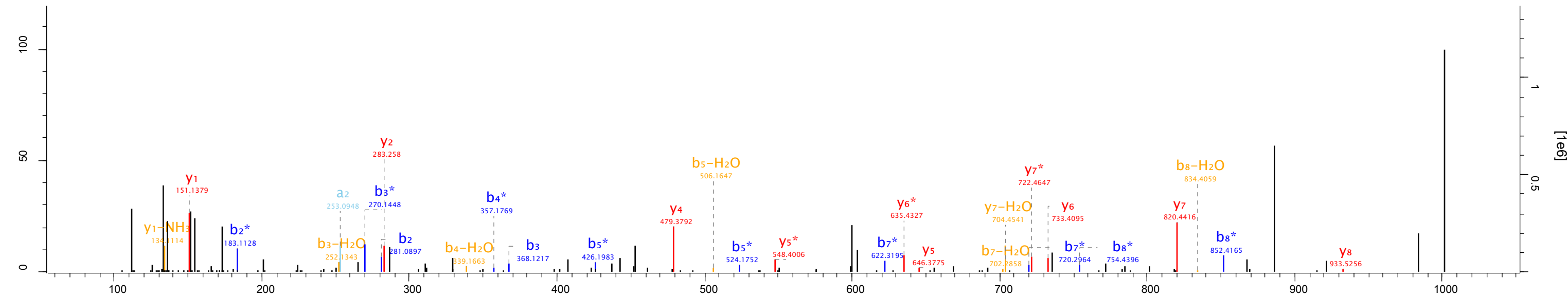
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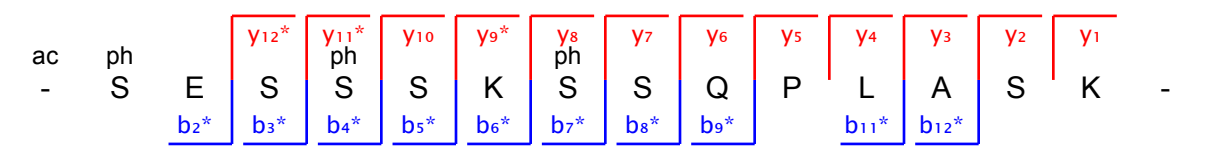
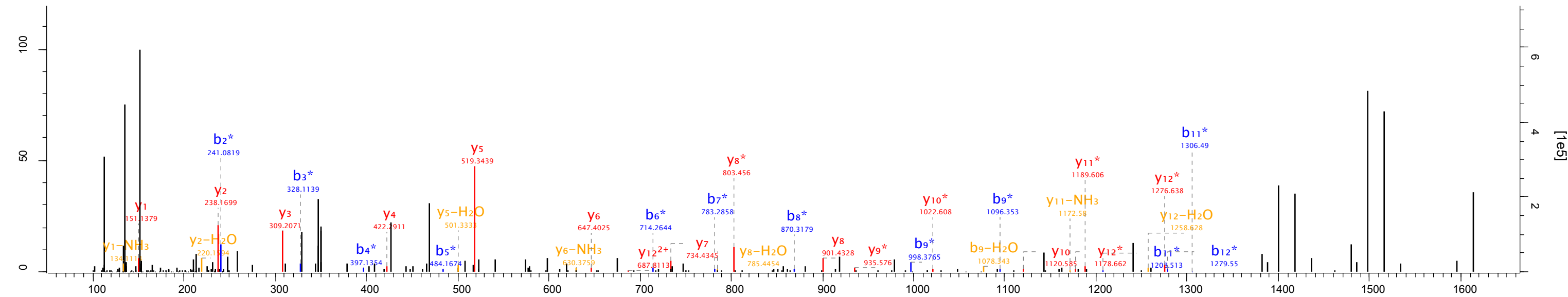
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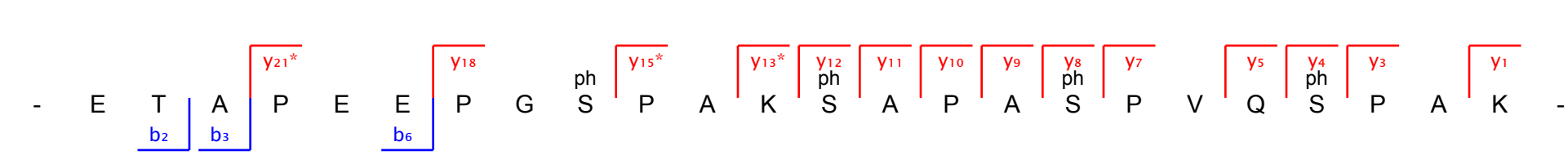
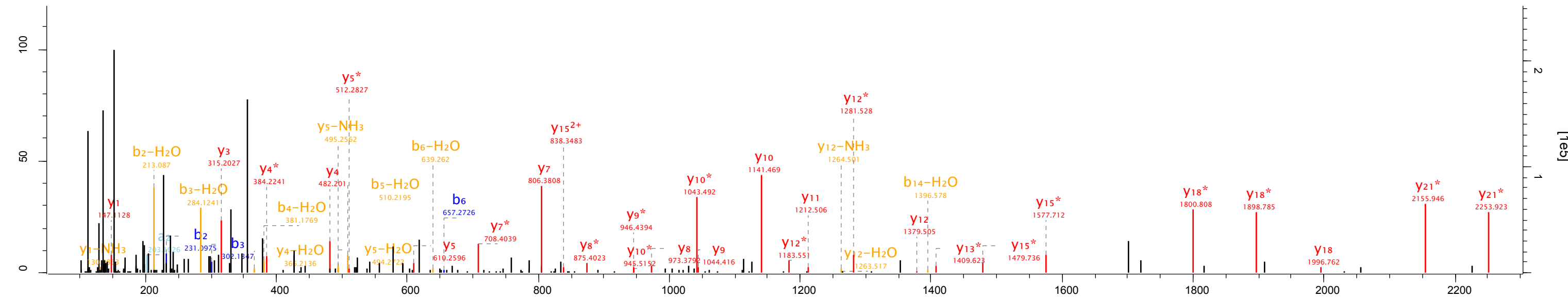
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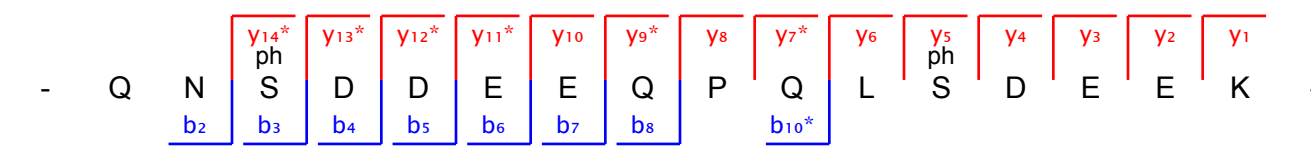
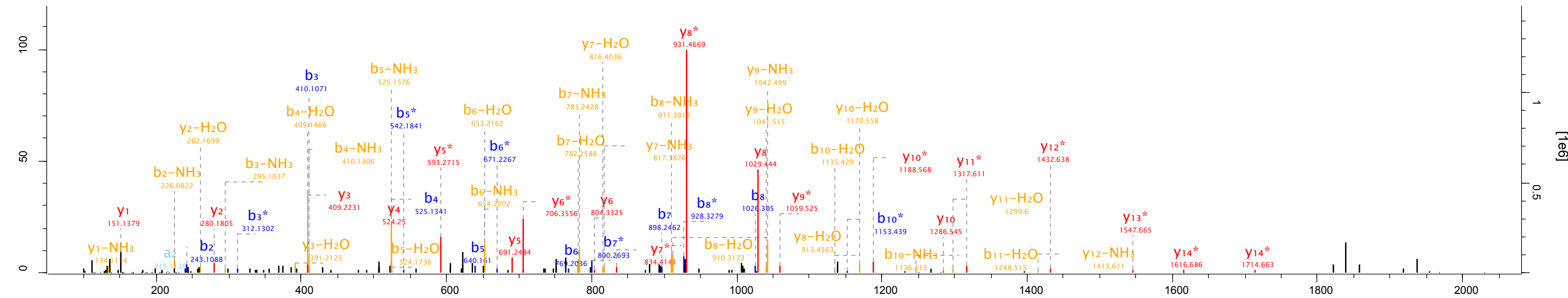
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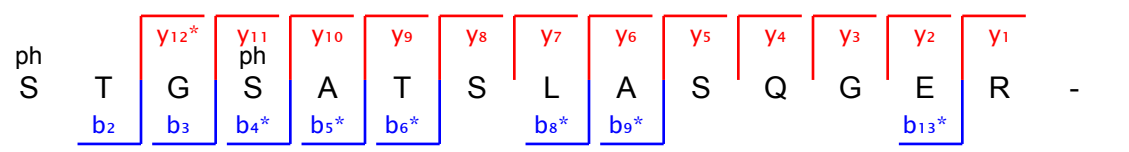
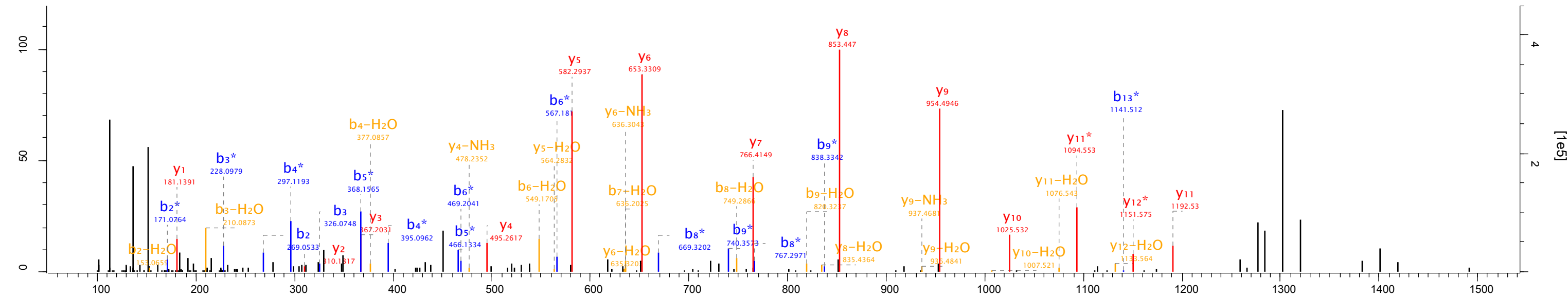
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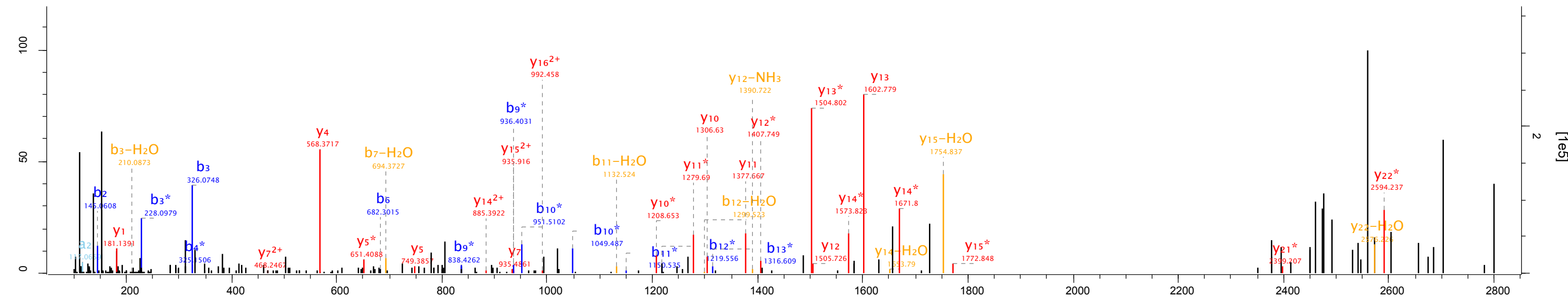


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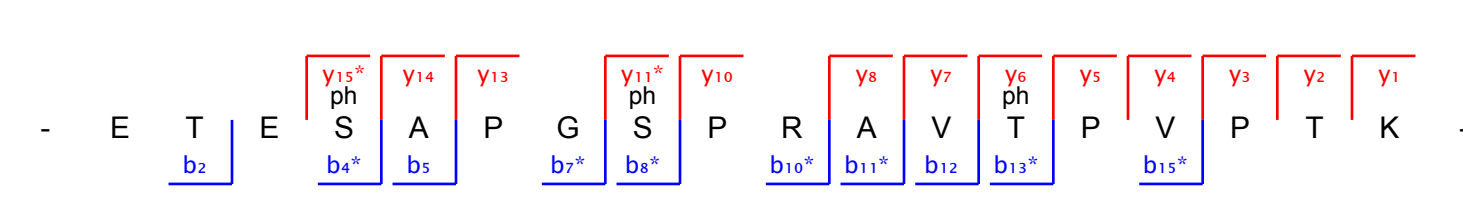
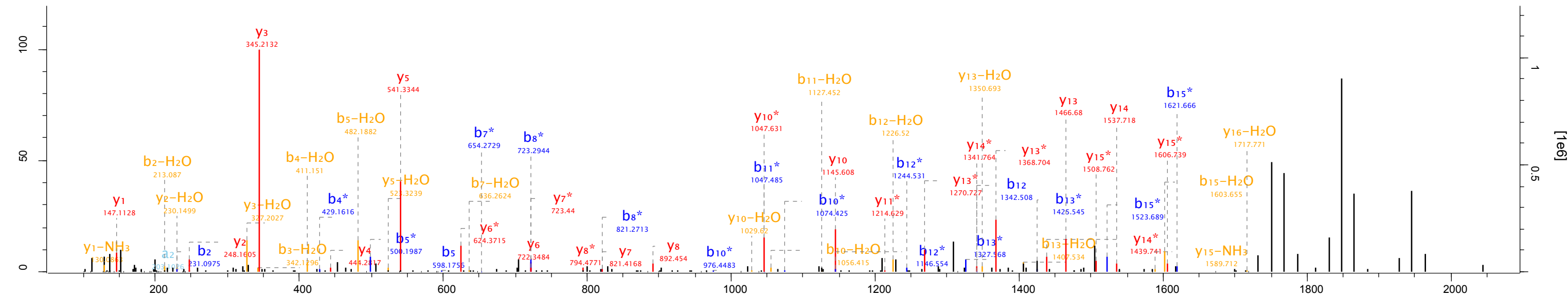
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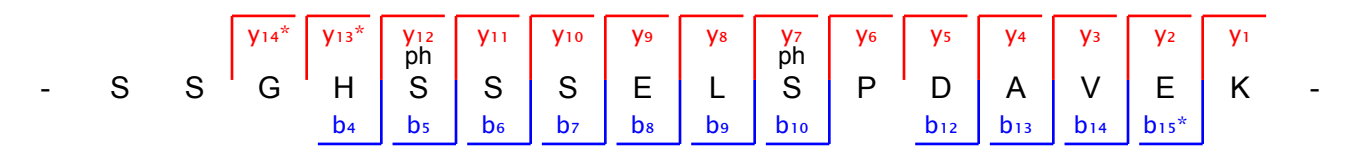
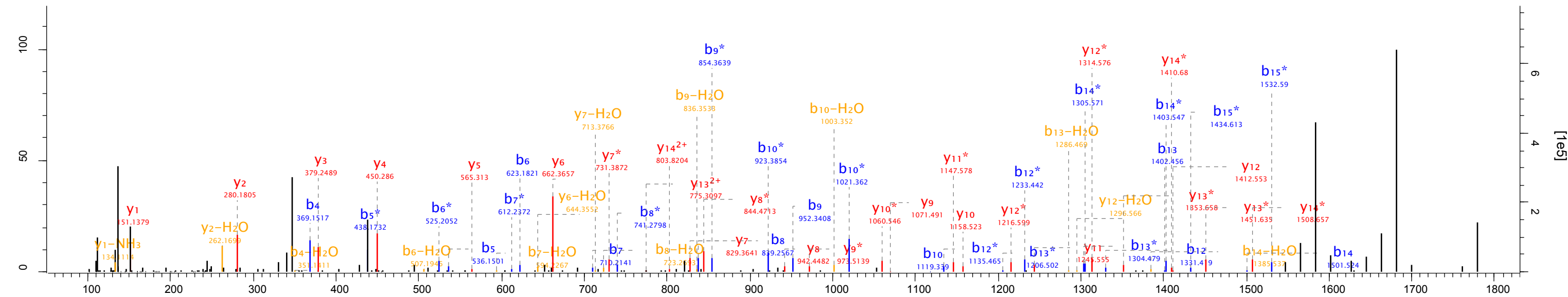
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 b₉* b₁₀* b₁₁* b₁₂* b₁₃*

Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5846 Method FTMS; HCD Score 191.53 m/z 1032.43 Gene names LARP1

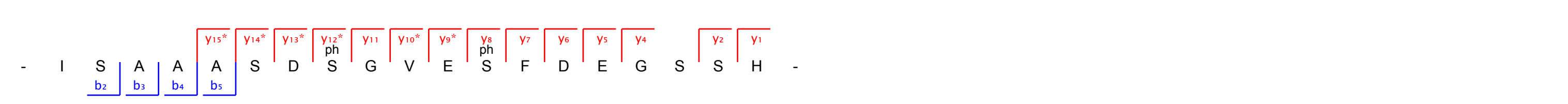
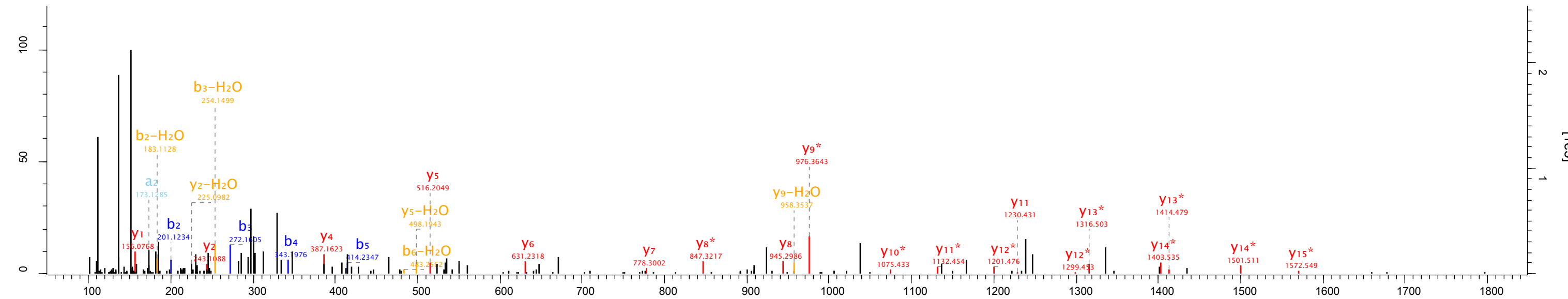


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20171215_MaS_33SR_LMH_phospho2_04

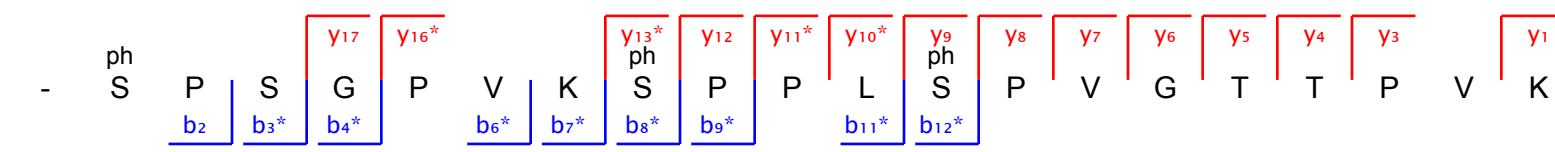
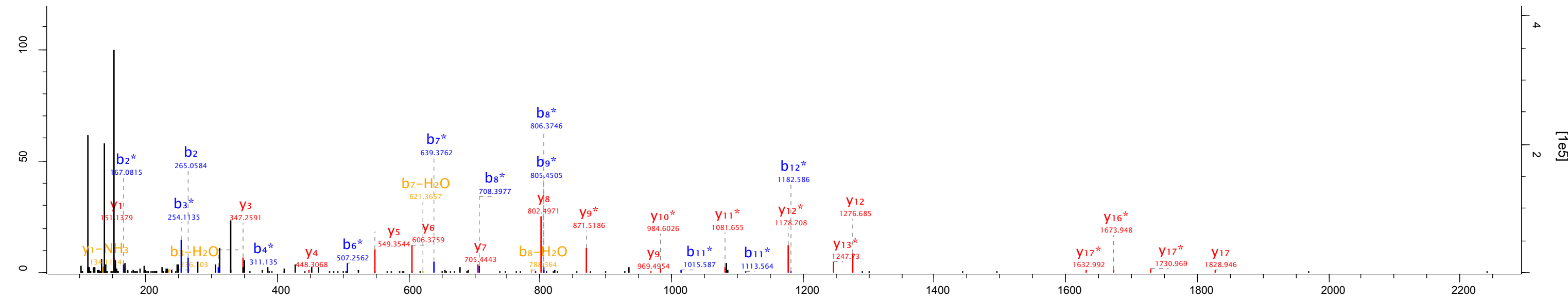
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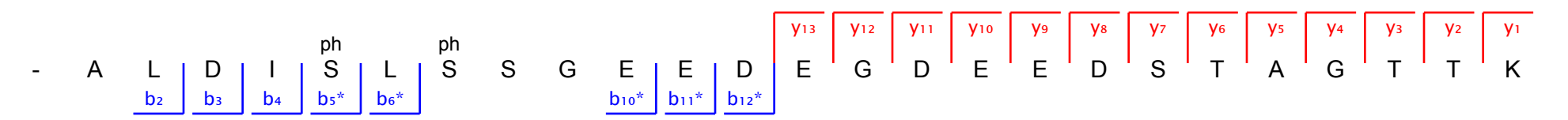
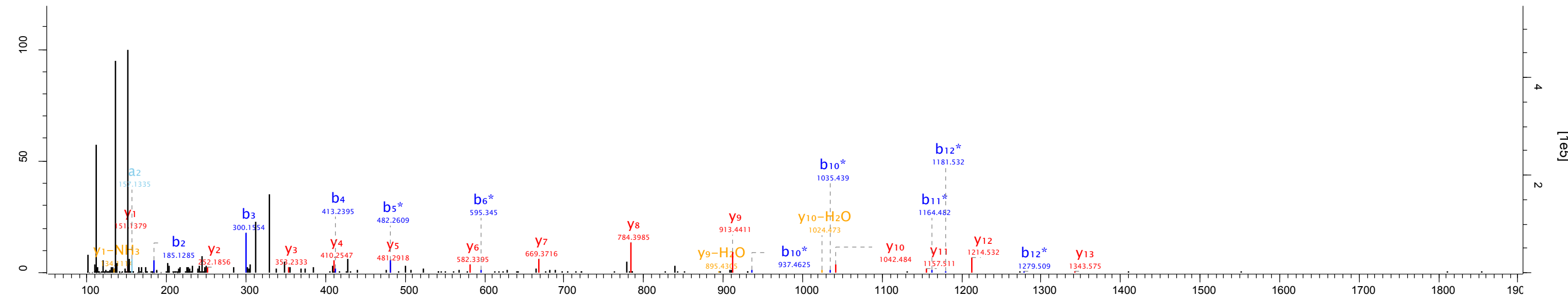
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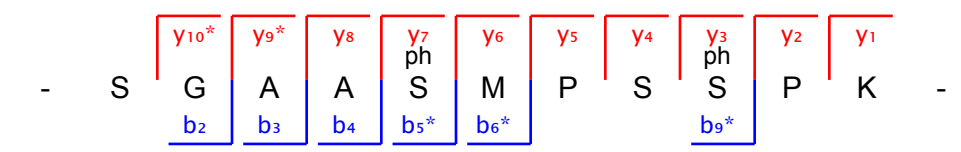
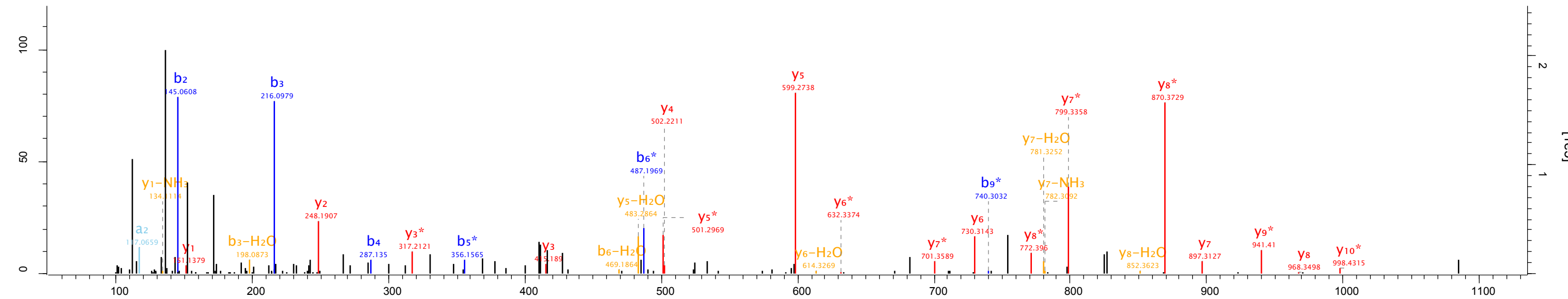
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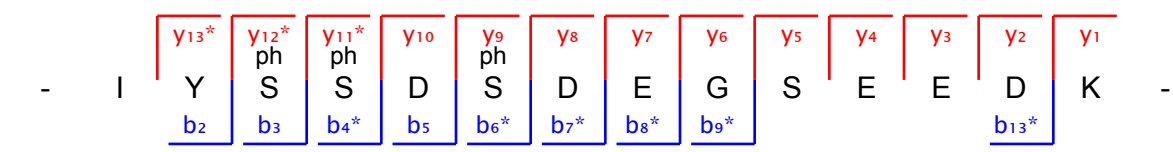
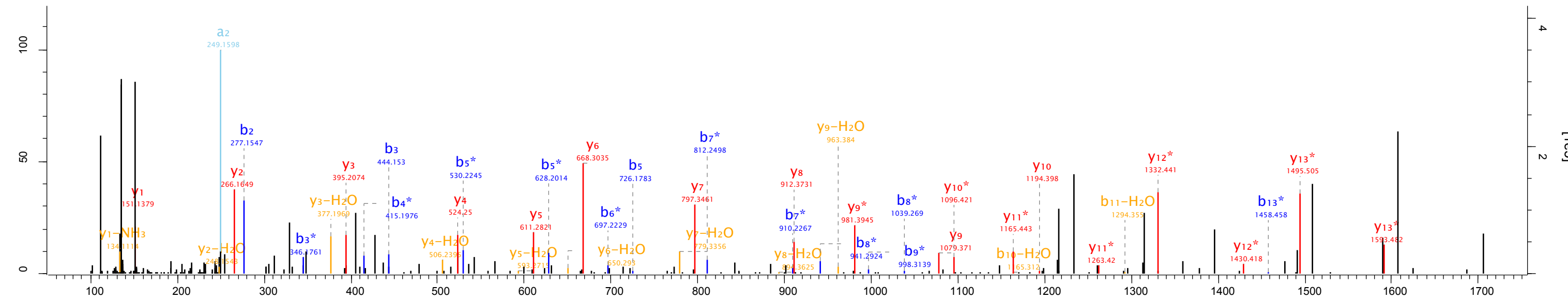
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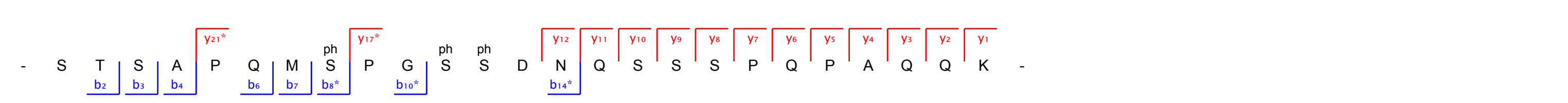
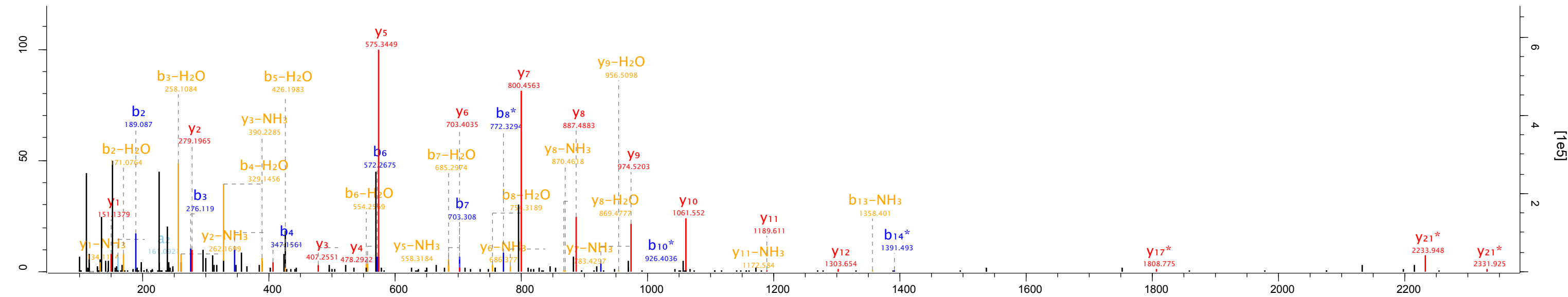
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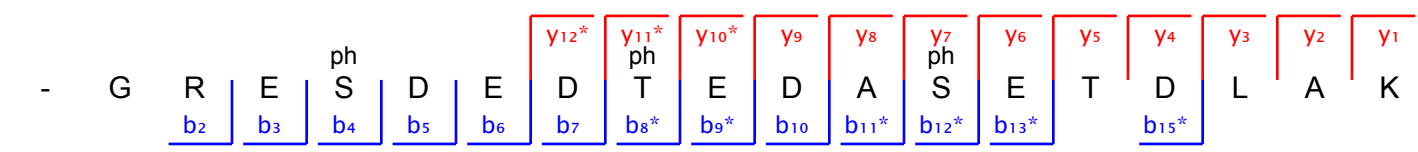
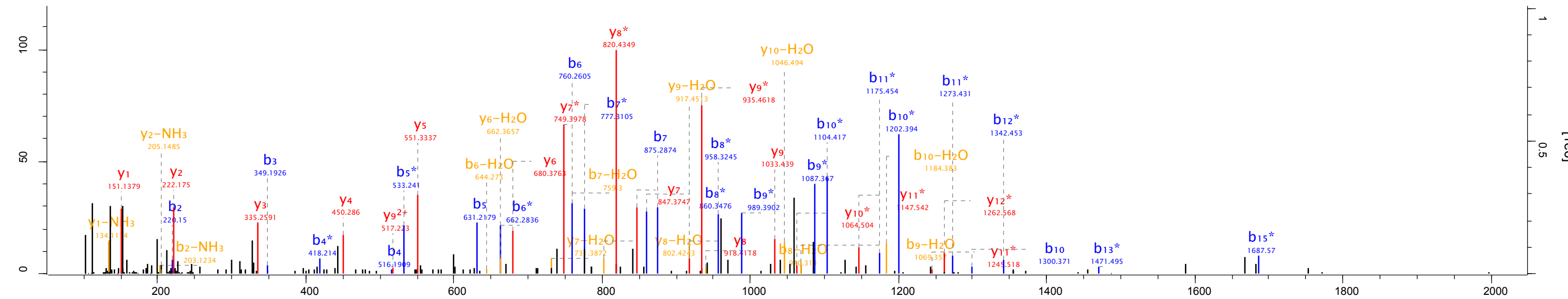


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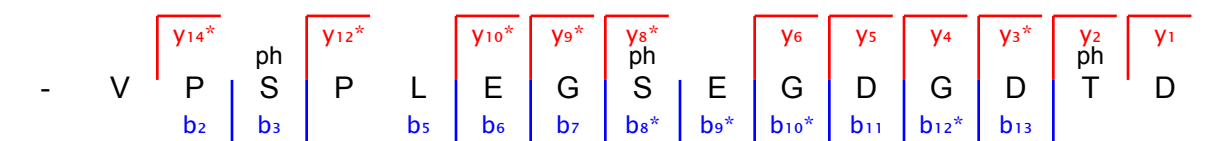
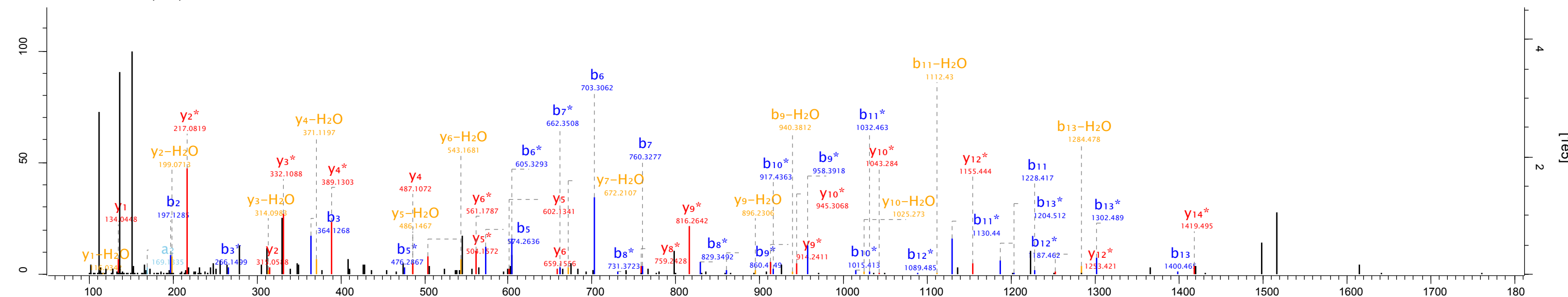
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Scan 4786 Method FTMS; HCD Score 165.17 m/z 739.93 Gene names SUDS3

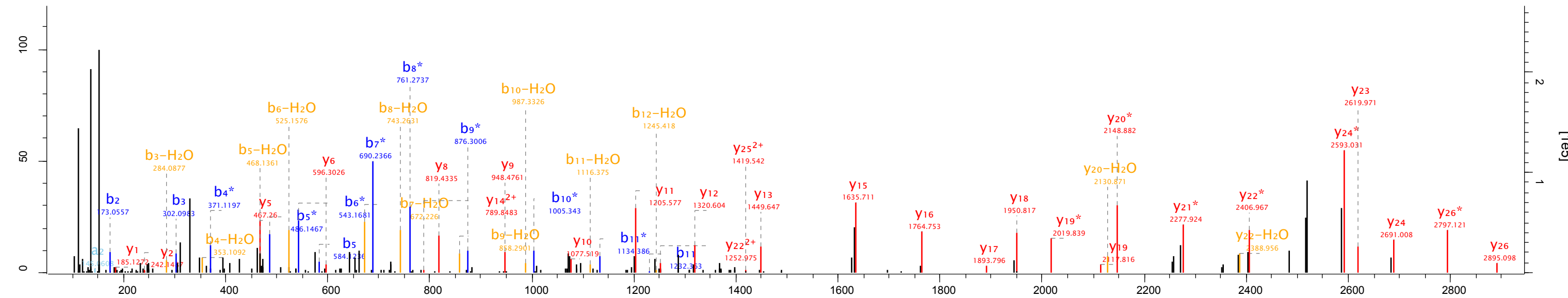


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Scan 6826 Method FTMS; HCD Score 210.66 m/z 857.76 Gene names PUS1



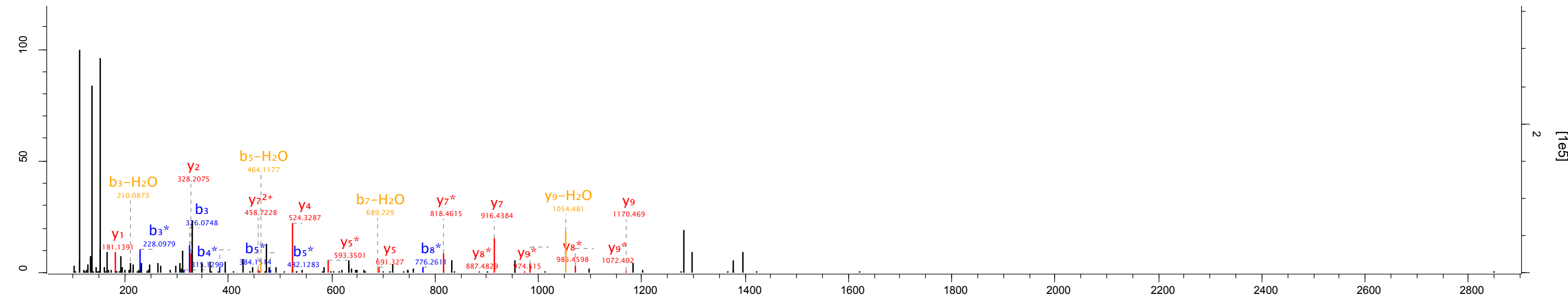
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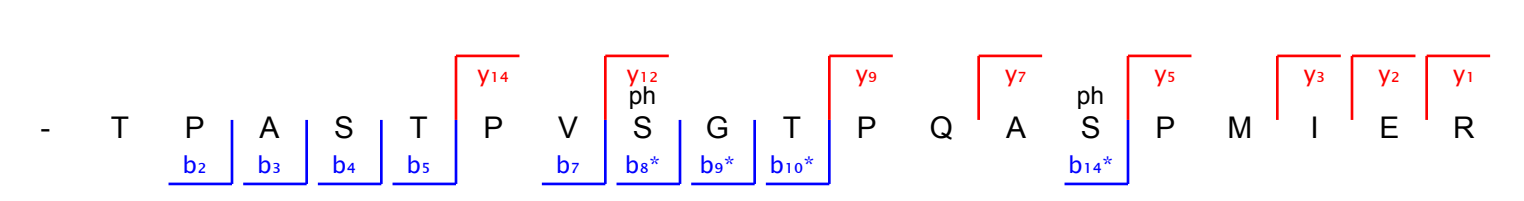
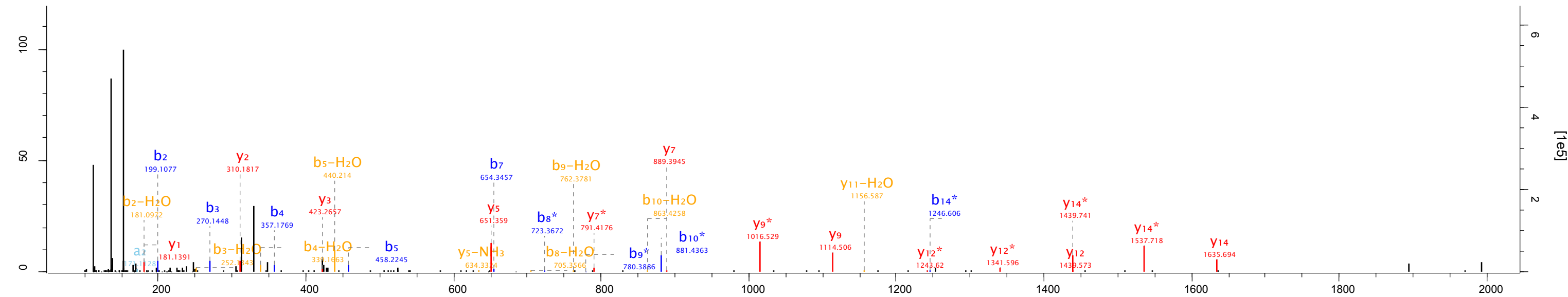
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b₈^{*}
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b₁₀^{*}
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y₂₆
y₂₅²⁺
y₂₄
y₂₃
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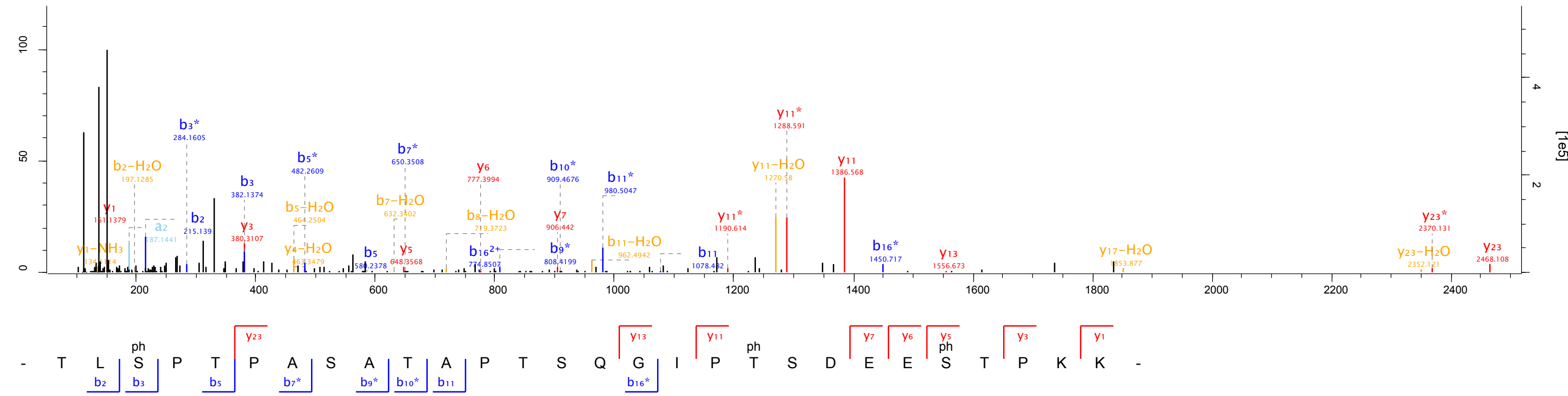


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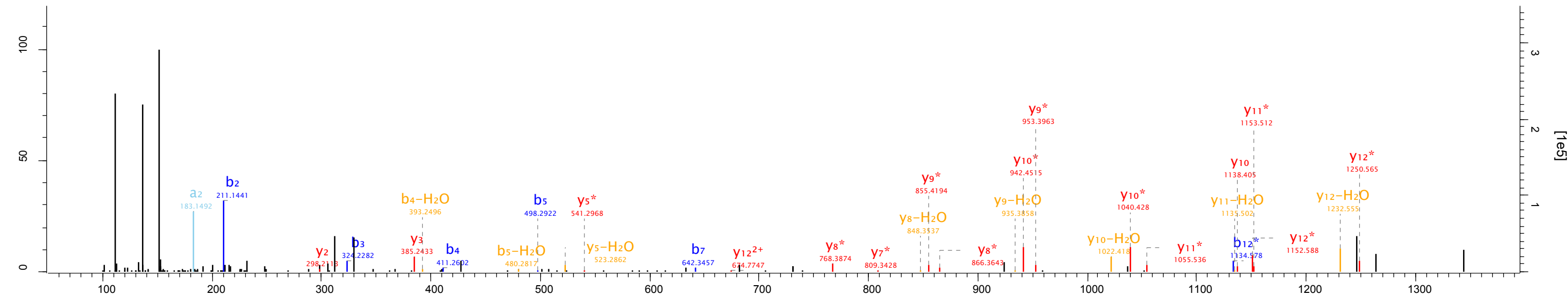


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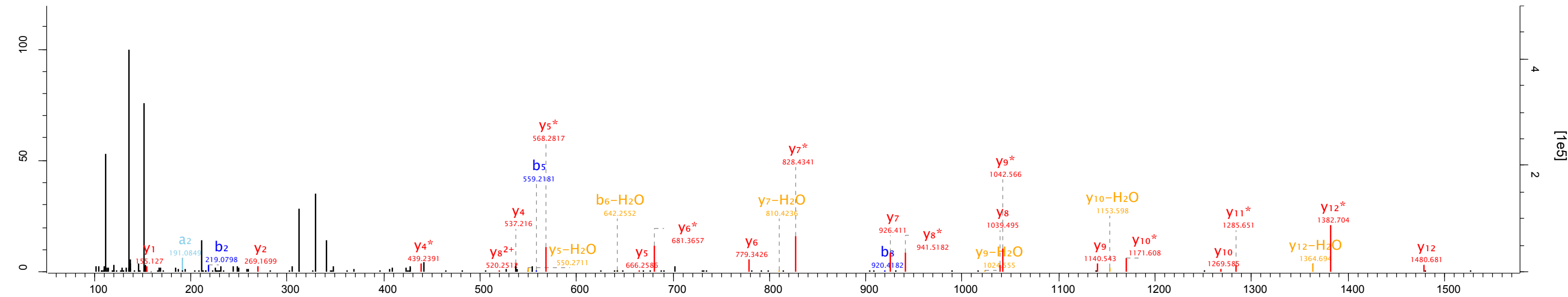
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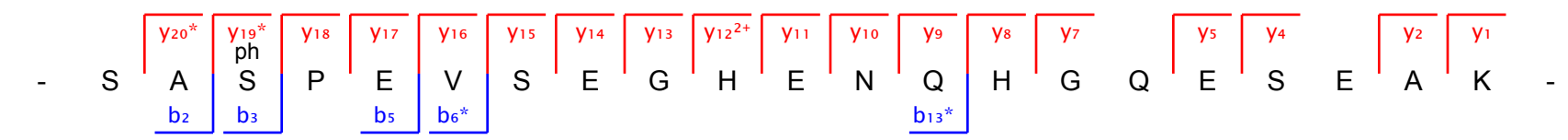
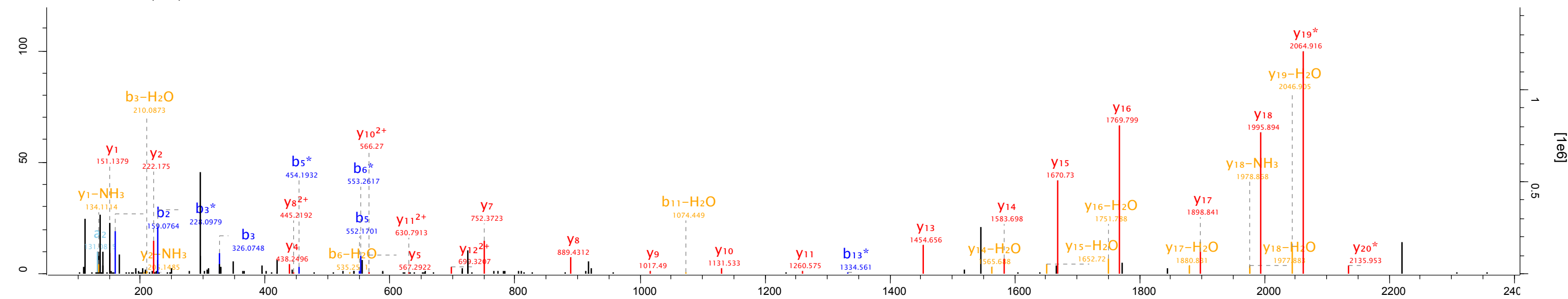


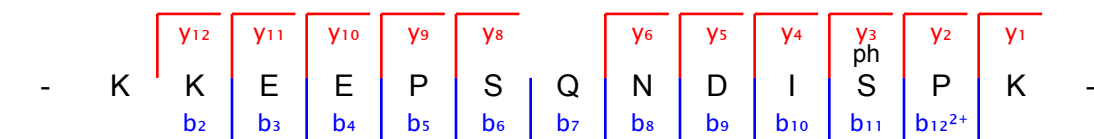
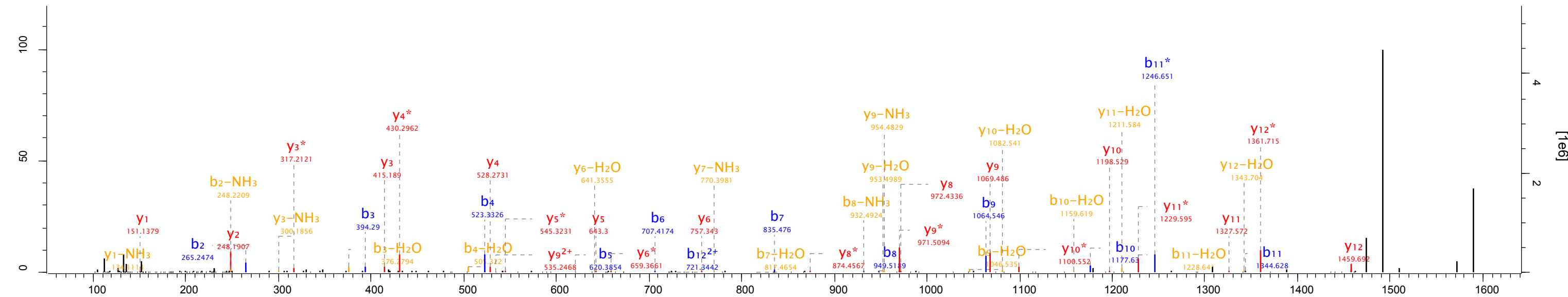
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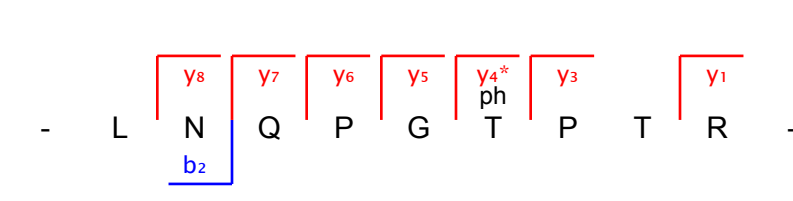
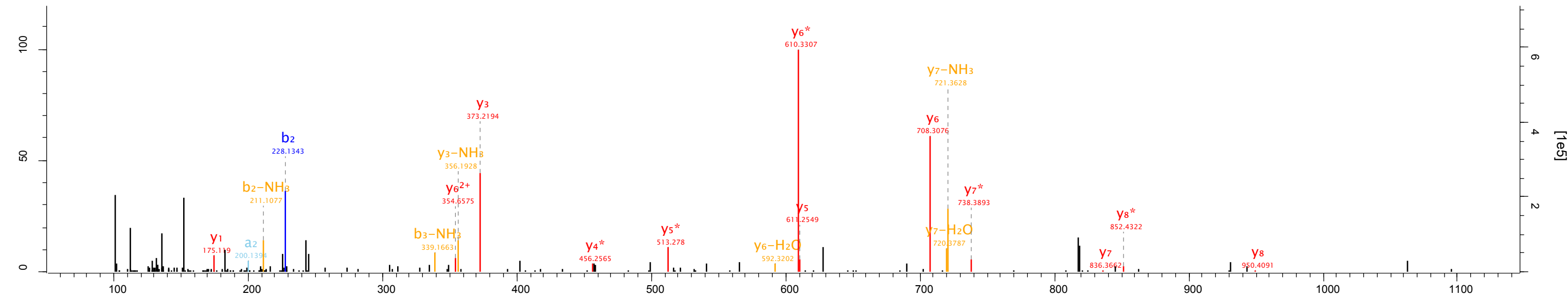
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Scan 2146 Method FTMS; HCD Score 125.39 m/z 774.66 Gene names RNASEH1

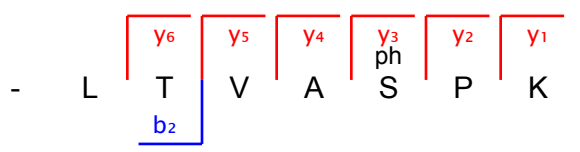
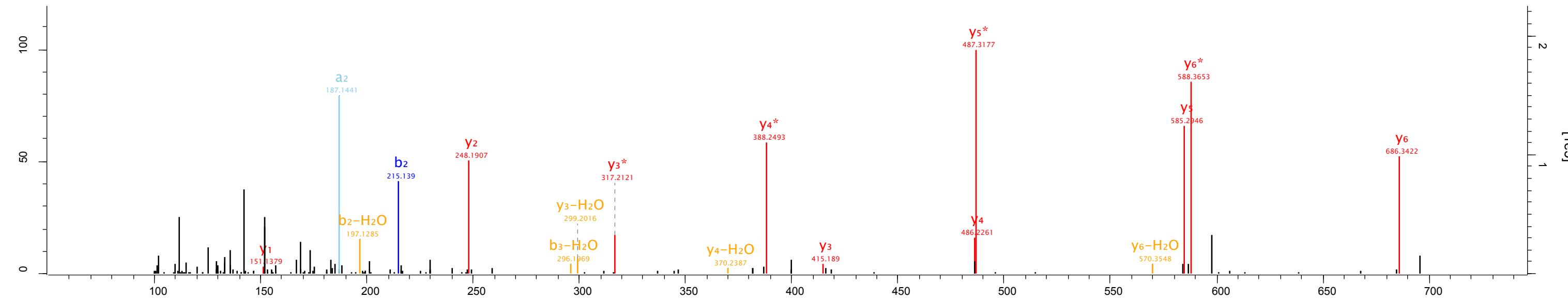




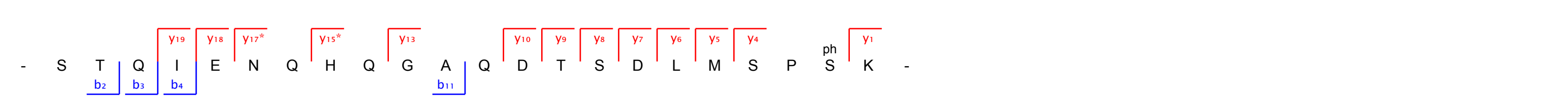
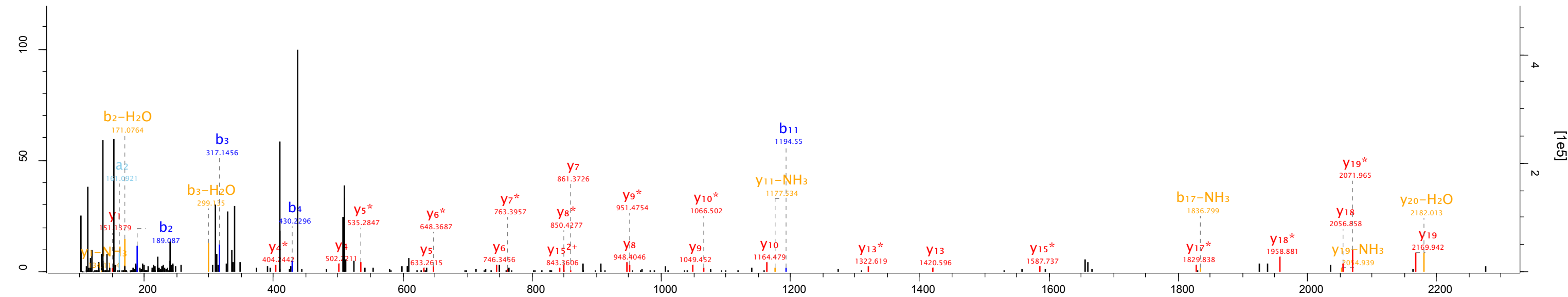
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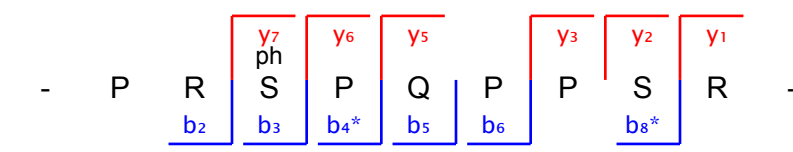
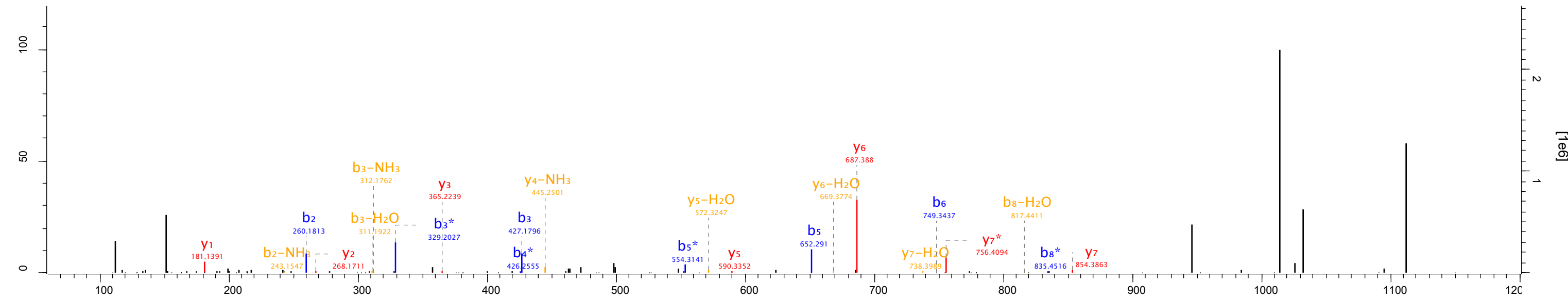
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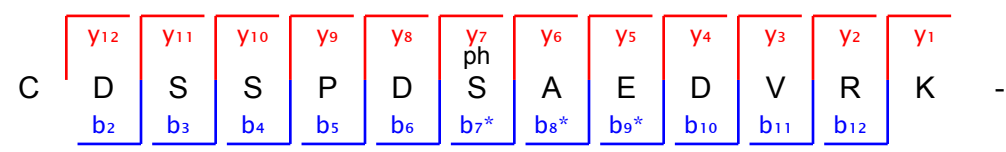
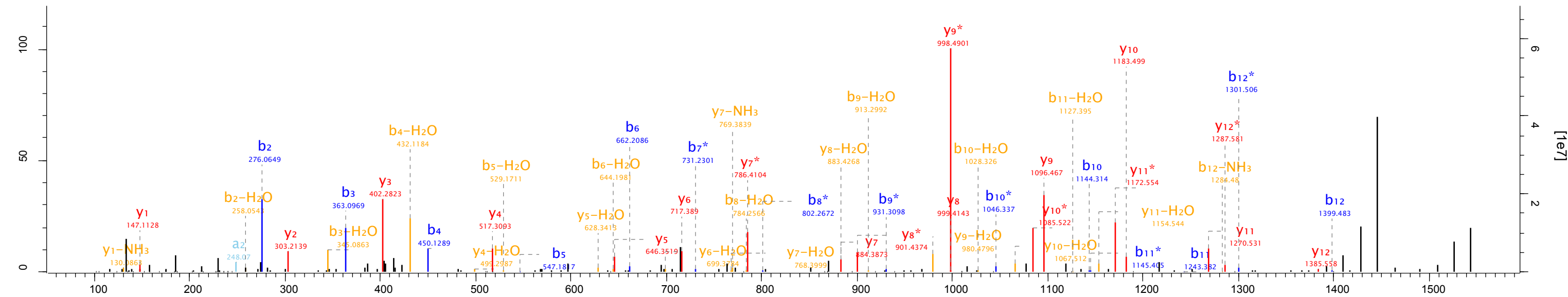
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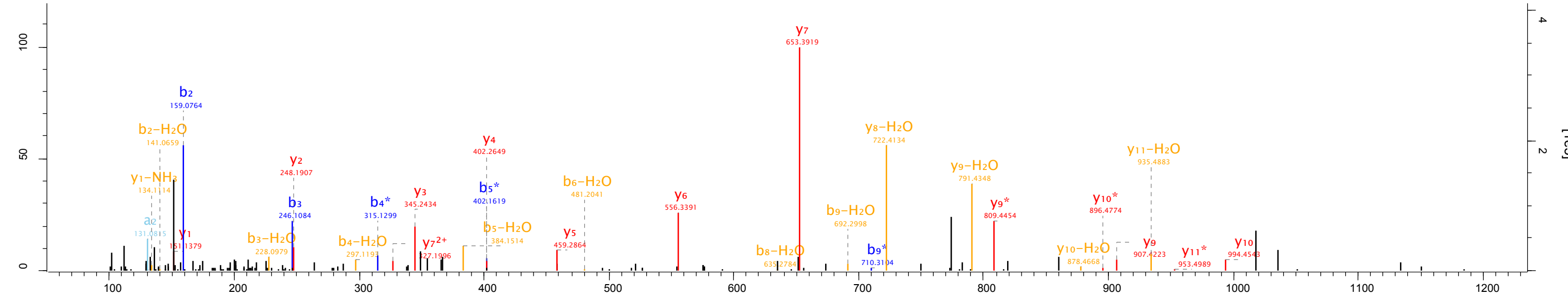
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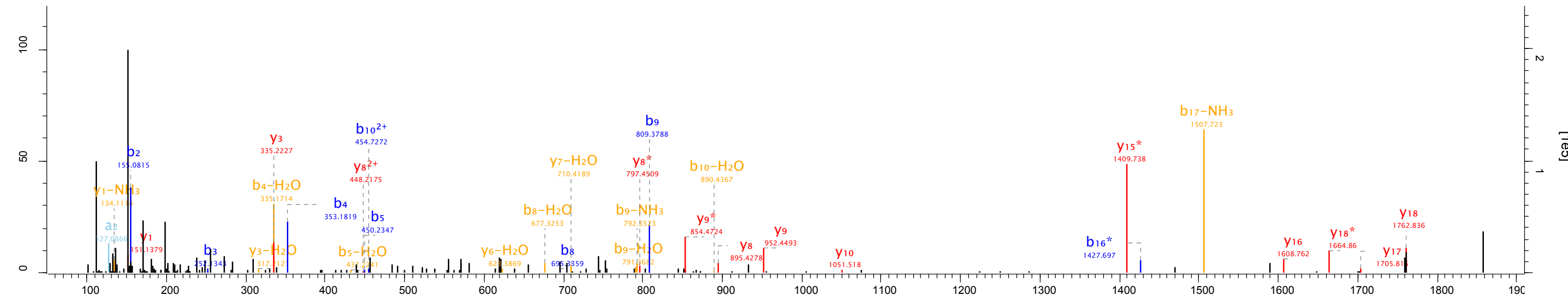


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20171215_MaS_33SR_LMH_phospho2_08

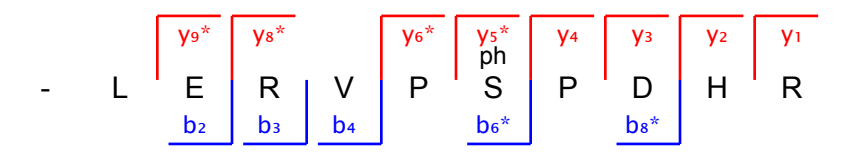
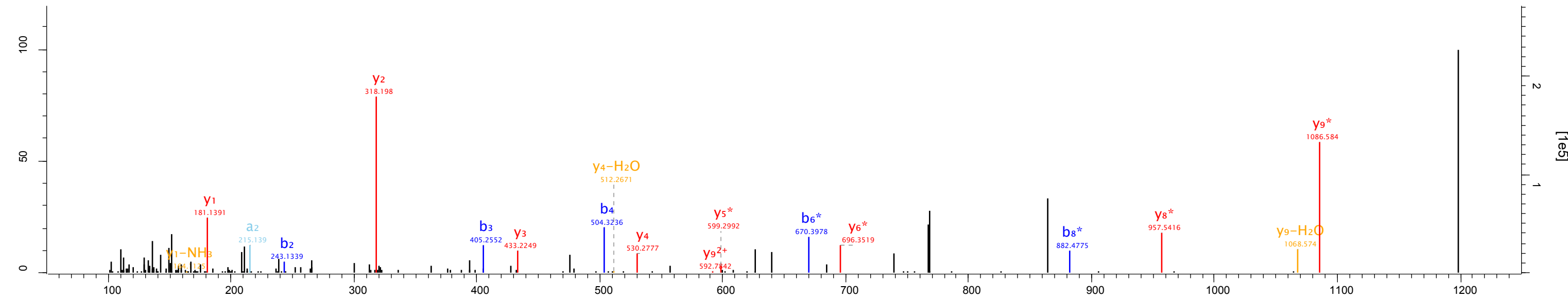




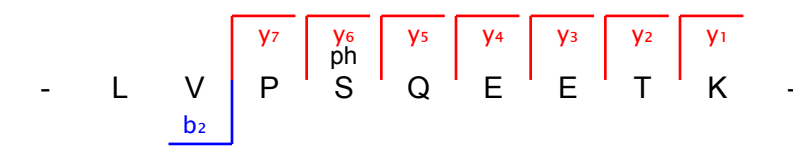
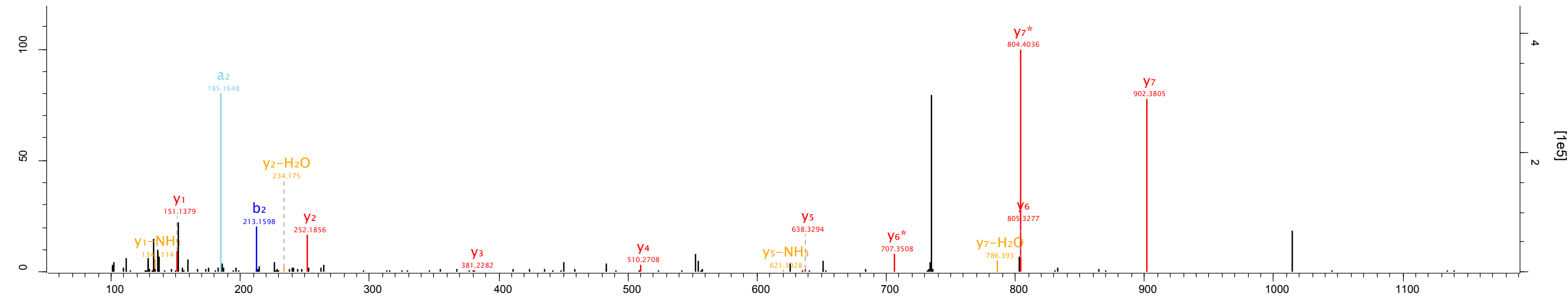
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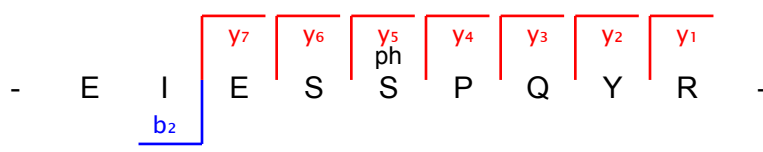
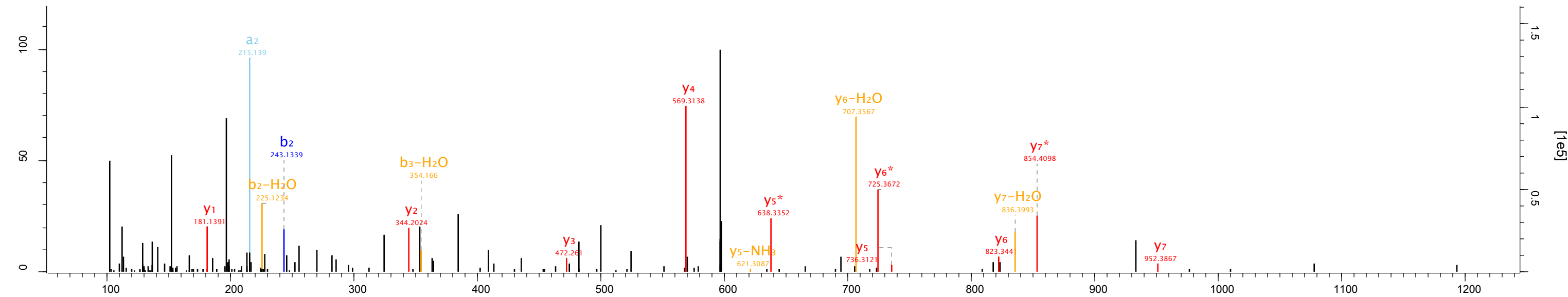
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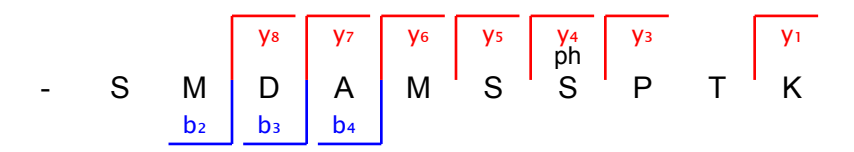
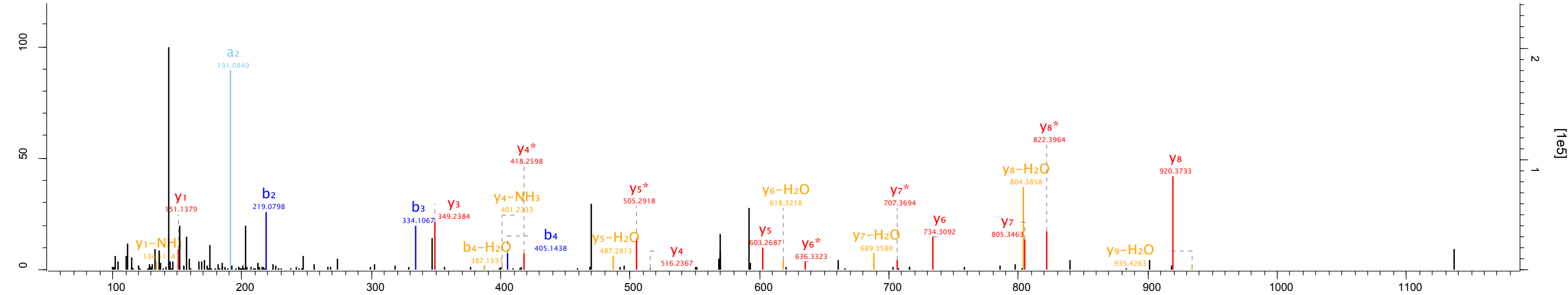
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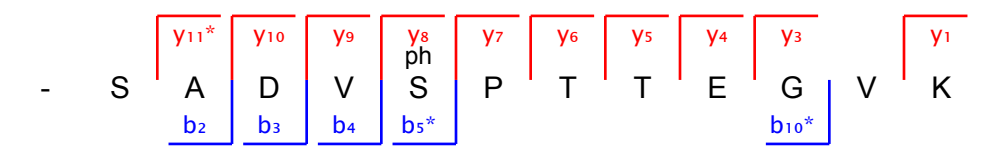
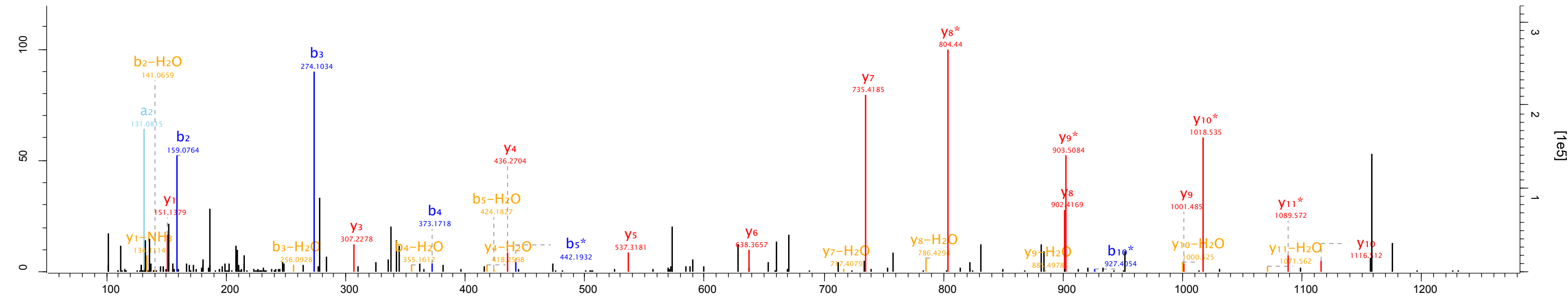
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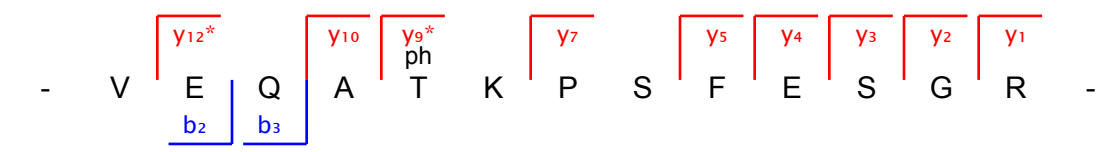
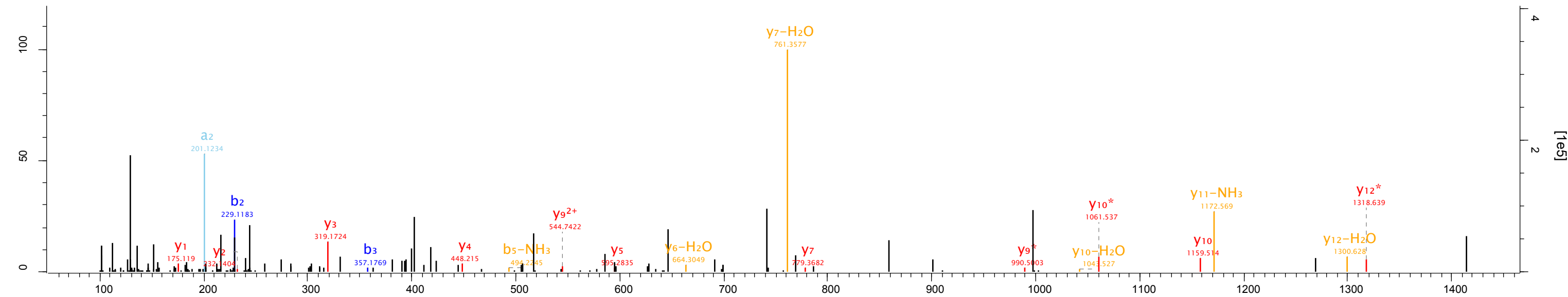
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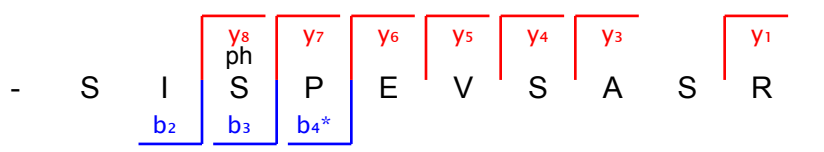
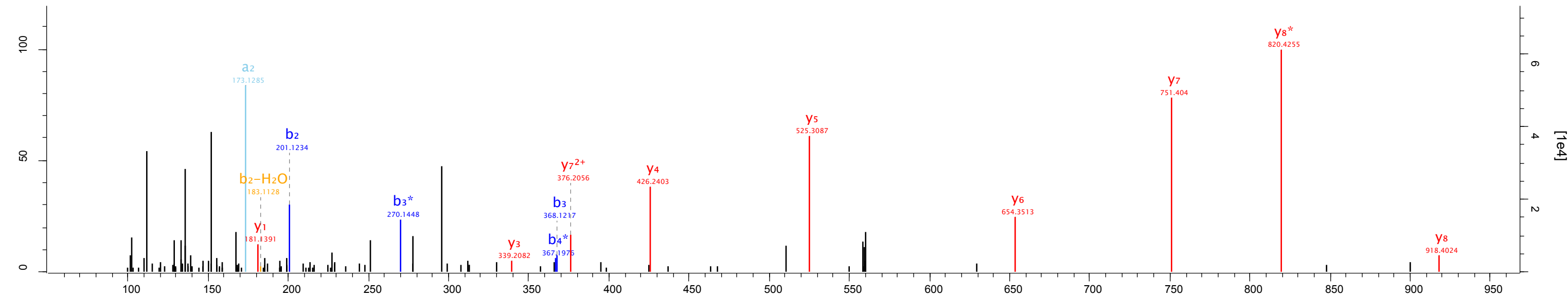
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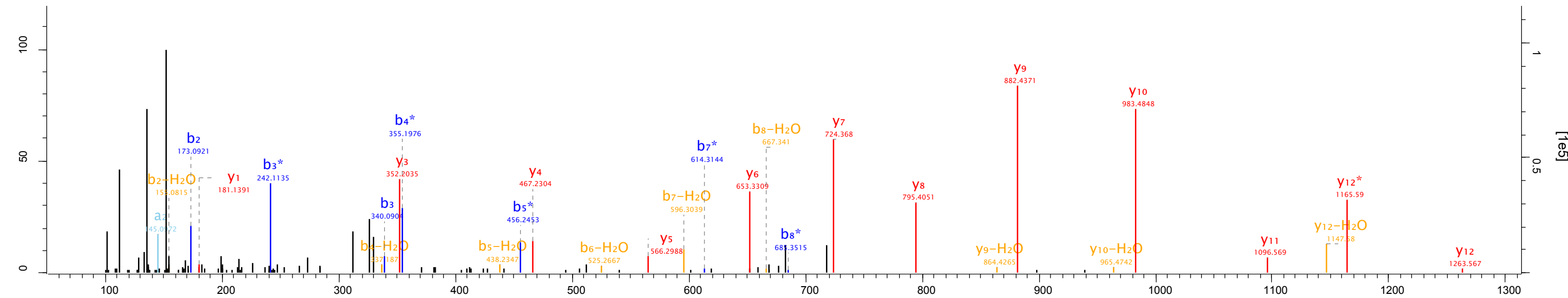


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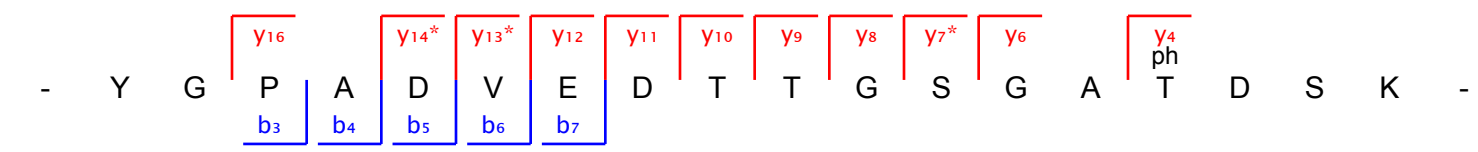
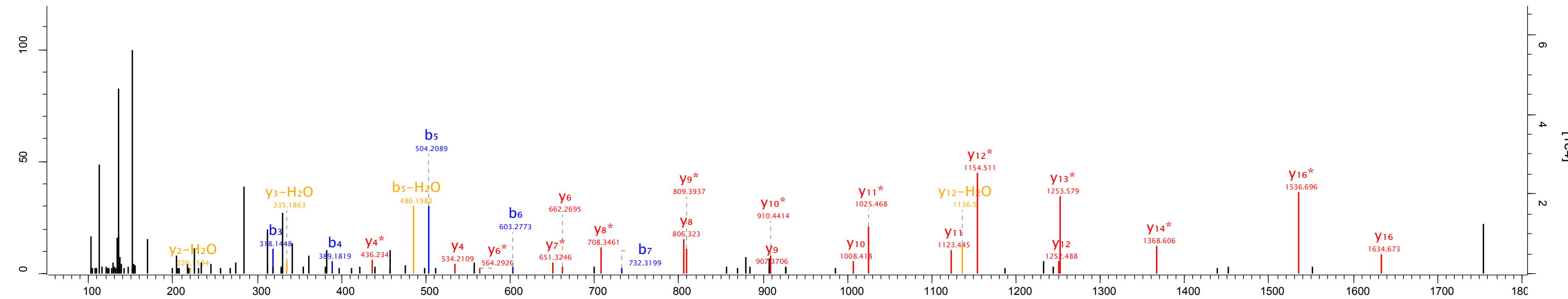


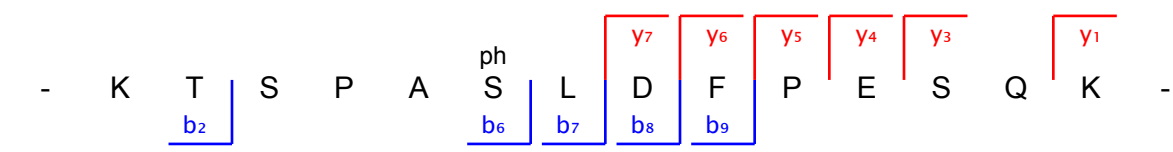
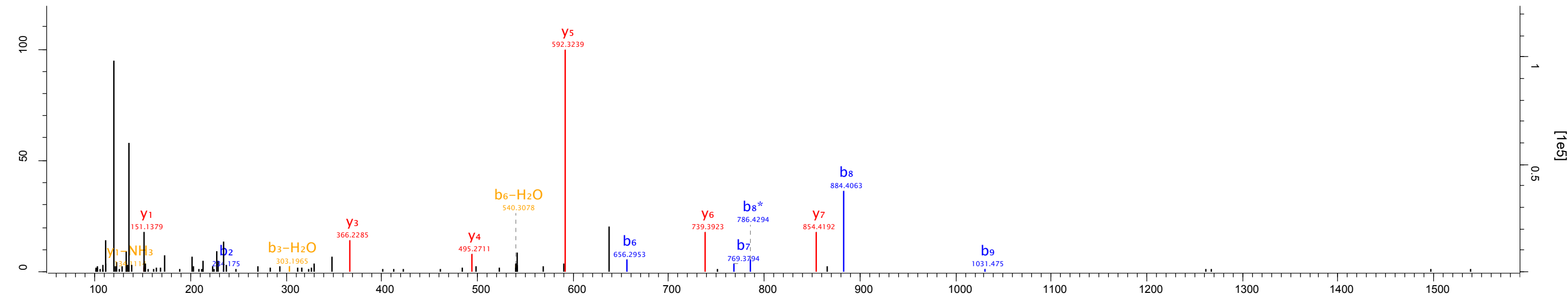


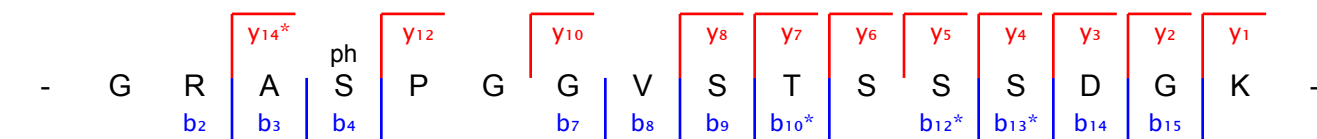
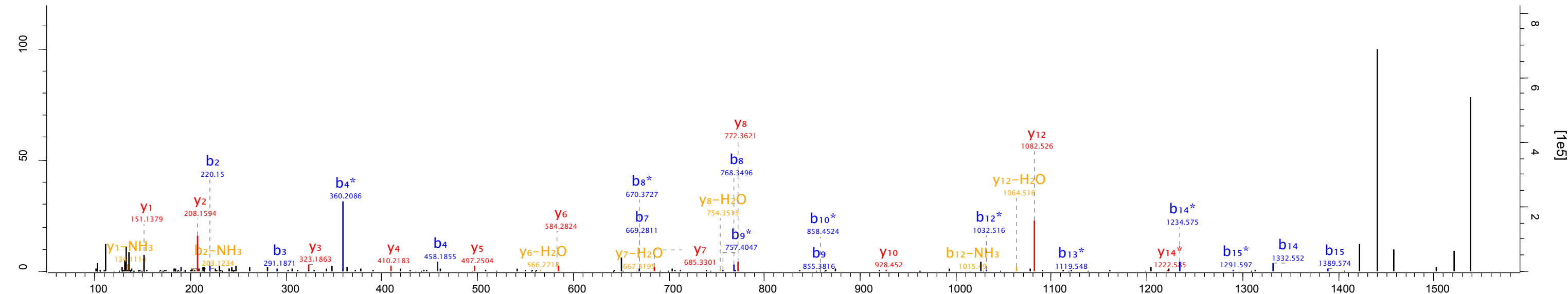
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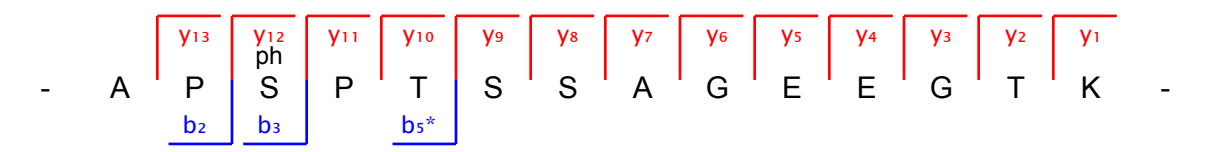
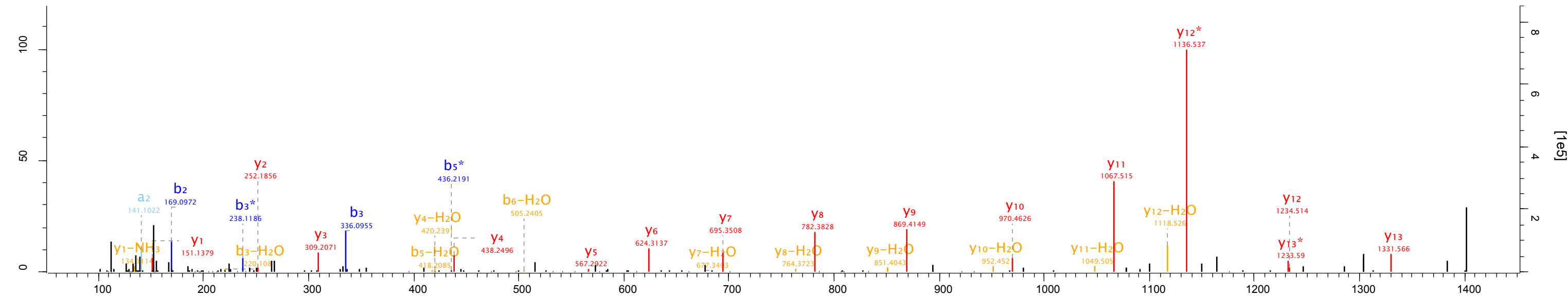
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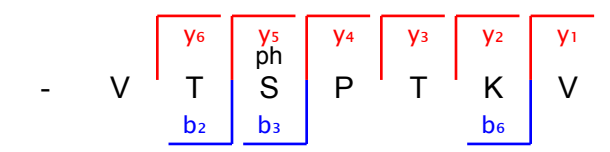
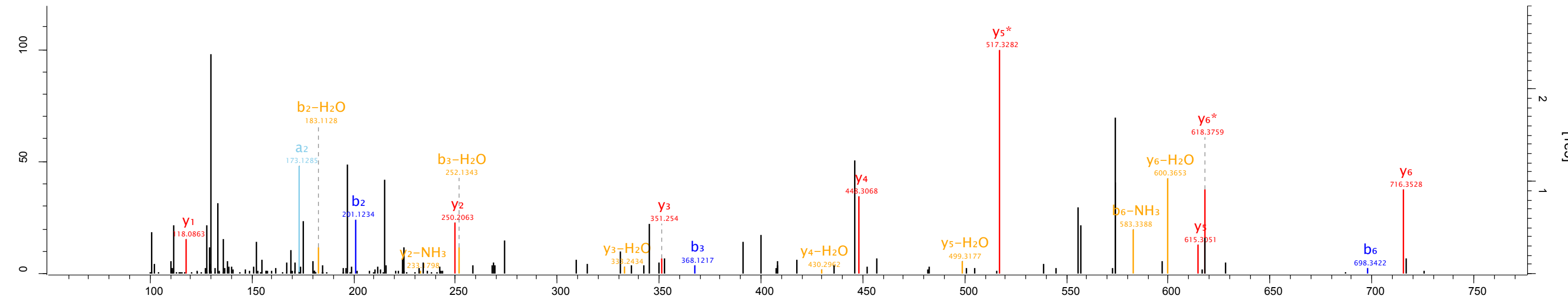


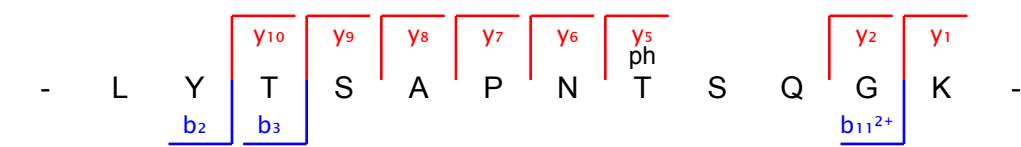
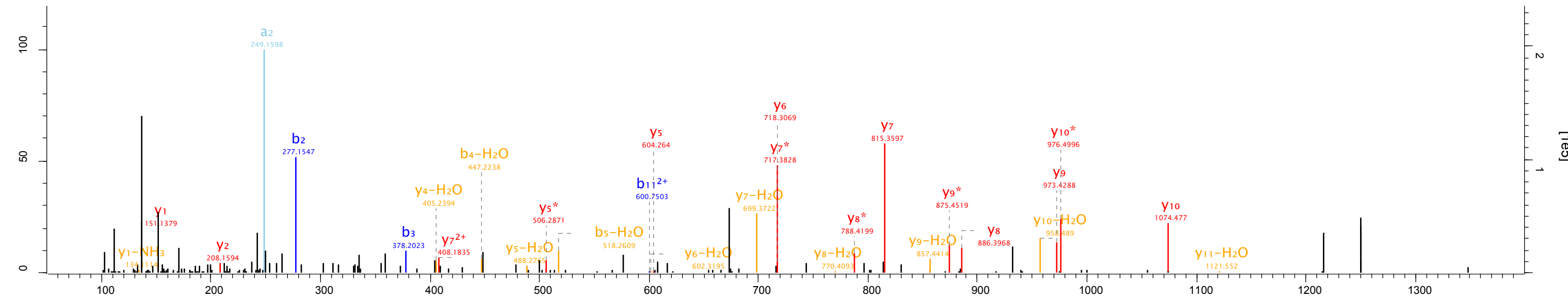


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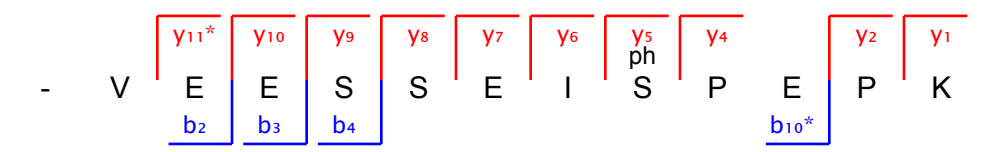
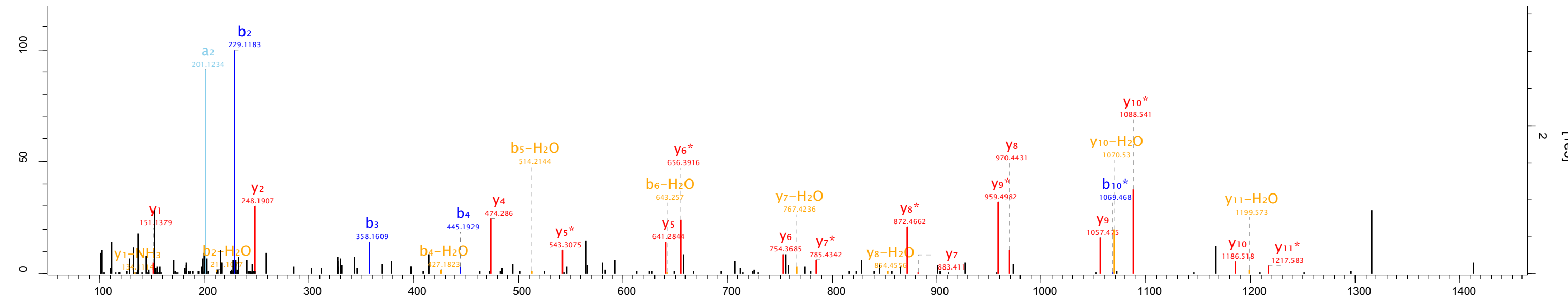


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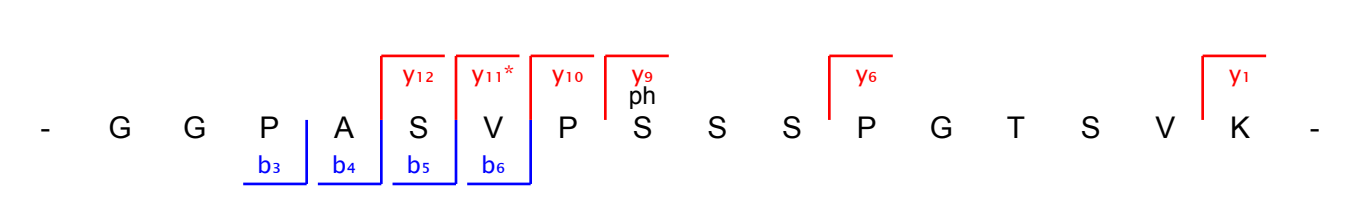
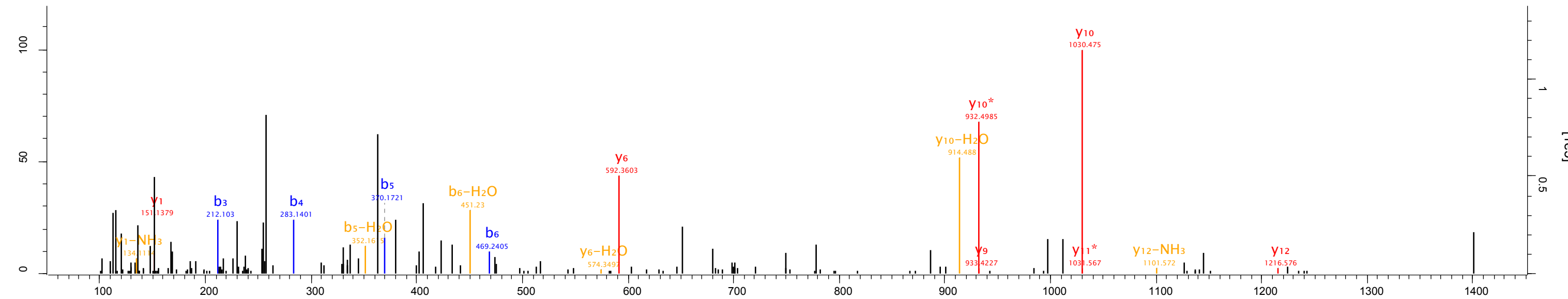




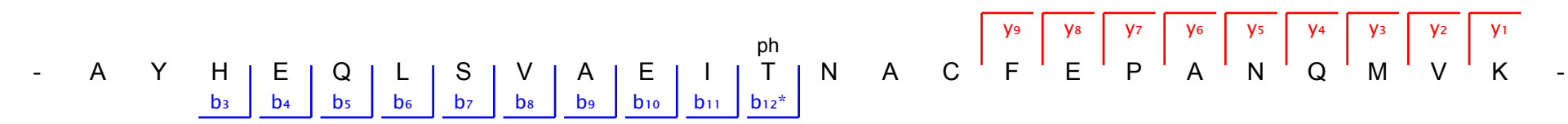
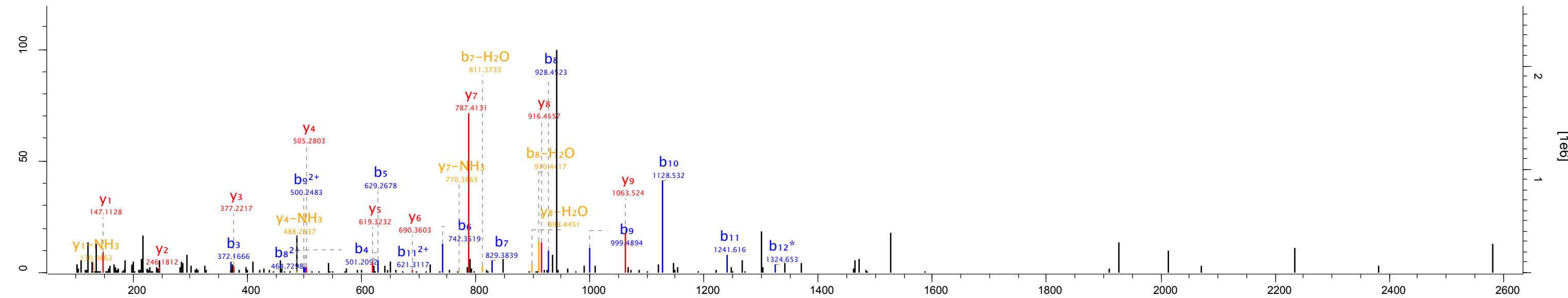
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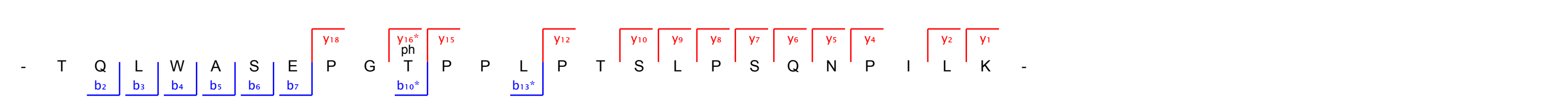
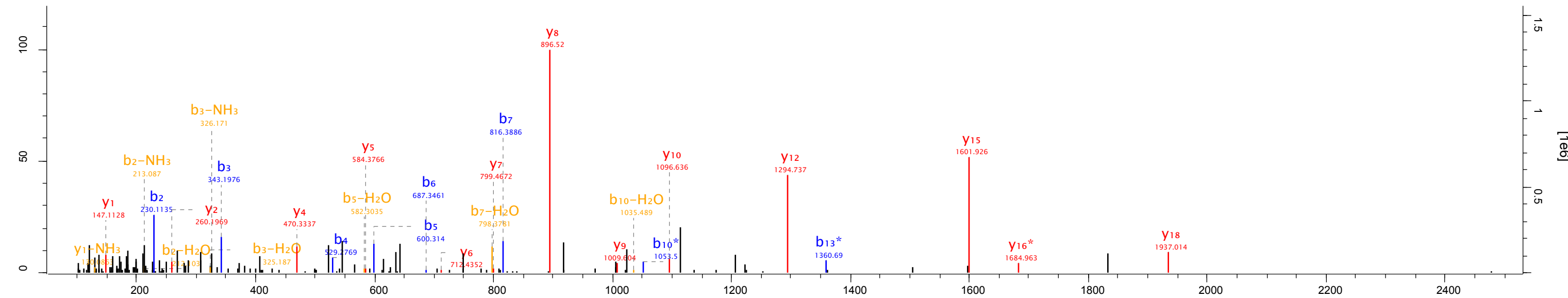
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Raw file: 20171215_MaS_33SR_LMH_proteome_01
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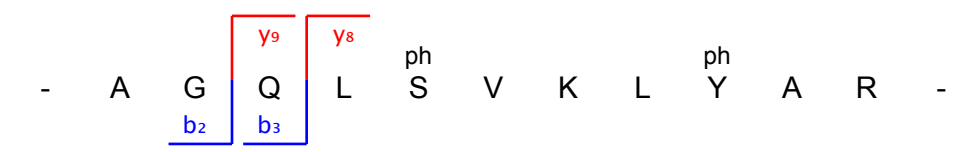
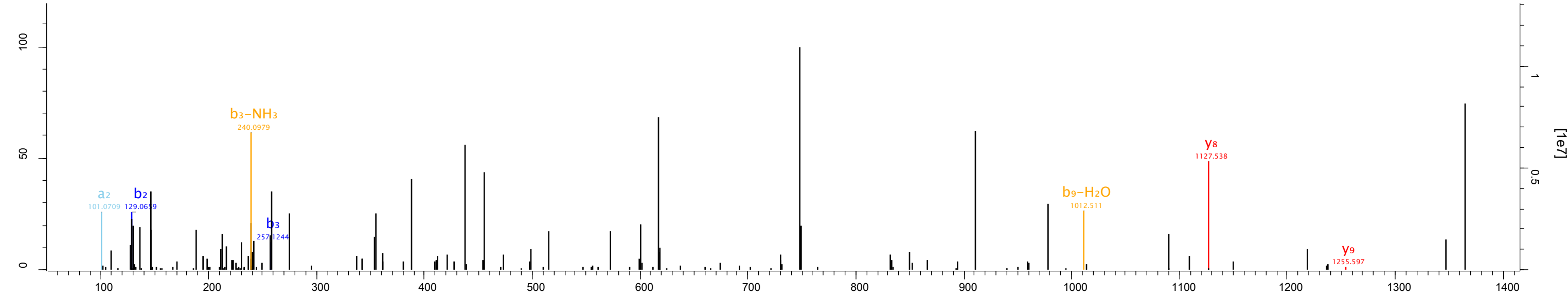
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Raw file

20171215_MaS_33SR_LMH_proteome_01

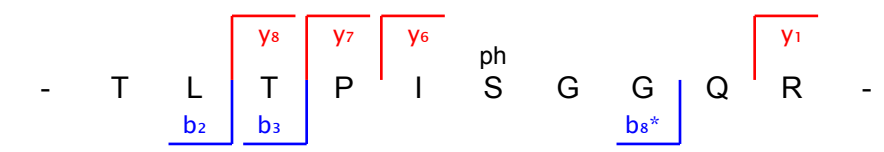
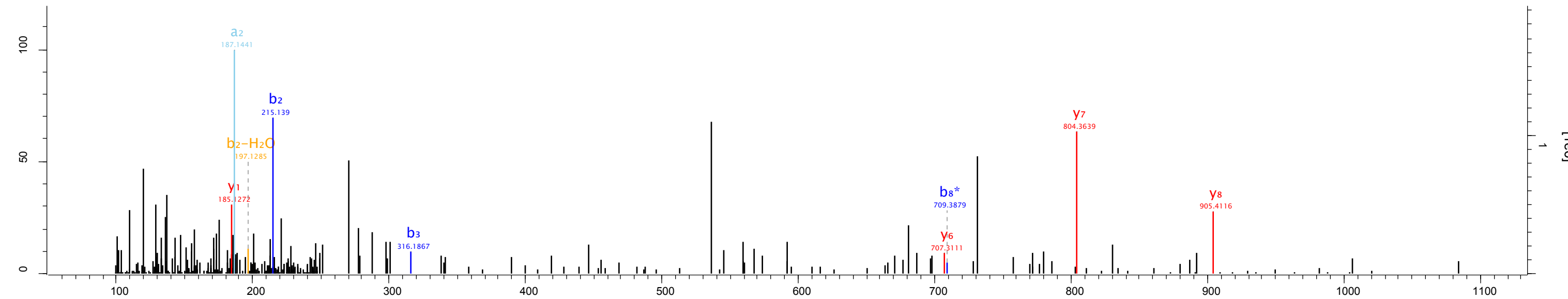
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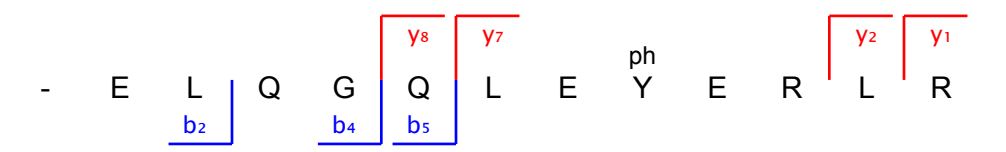
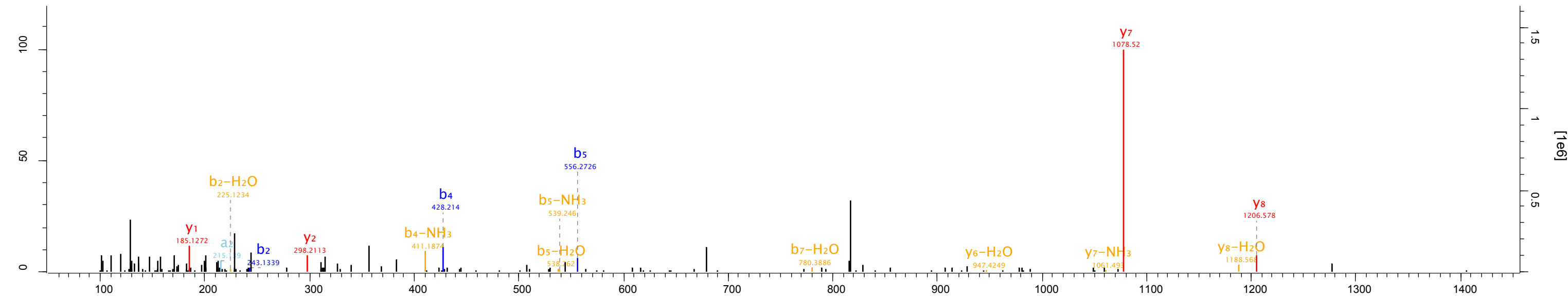
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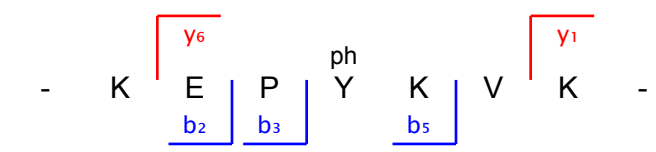
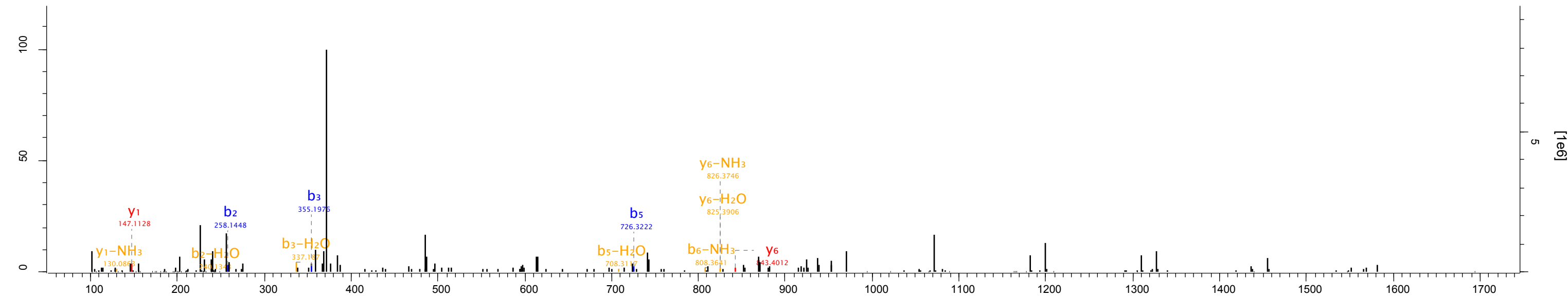
Scan 24176 Method FTMS; HCD Score 43.77 m/z 560.32 Gene names ORC1



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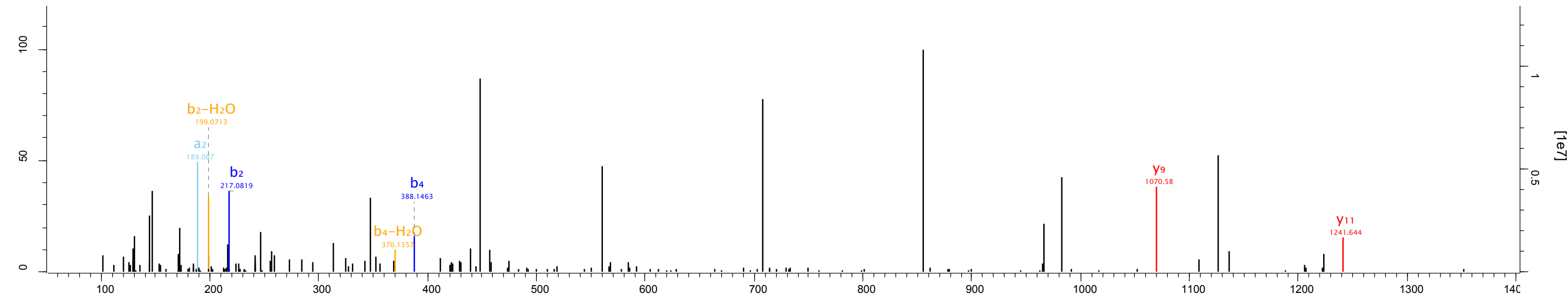


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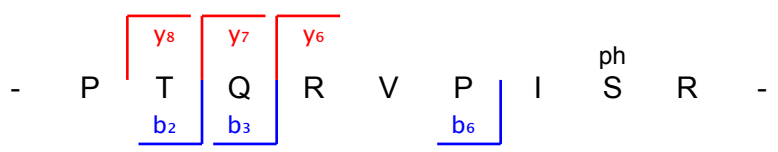
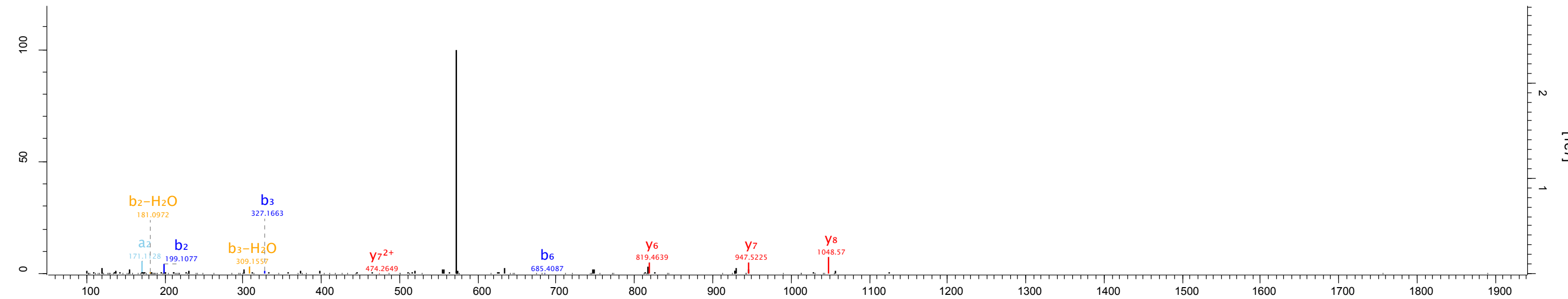


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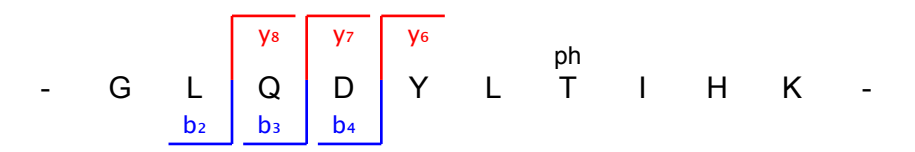
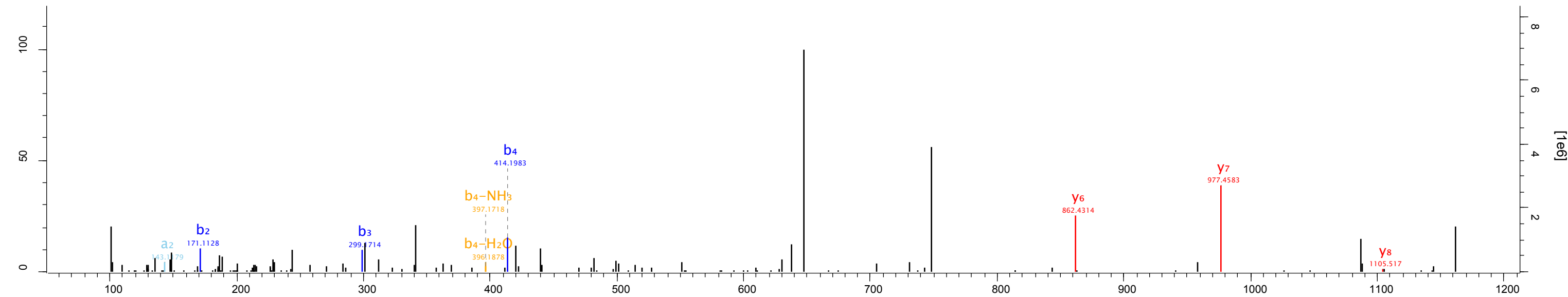
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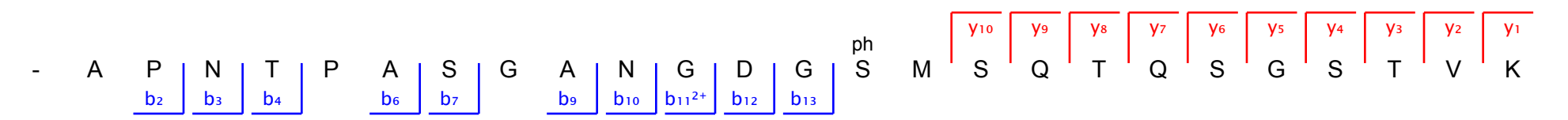
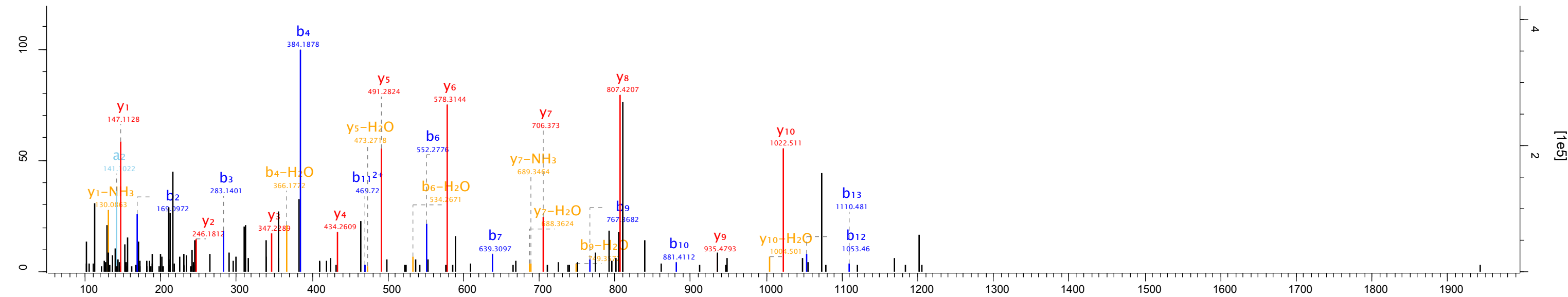
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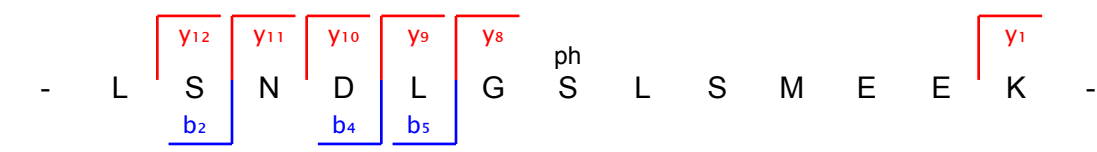
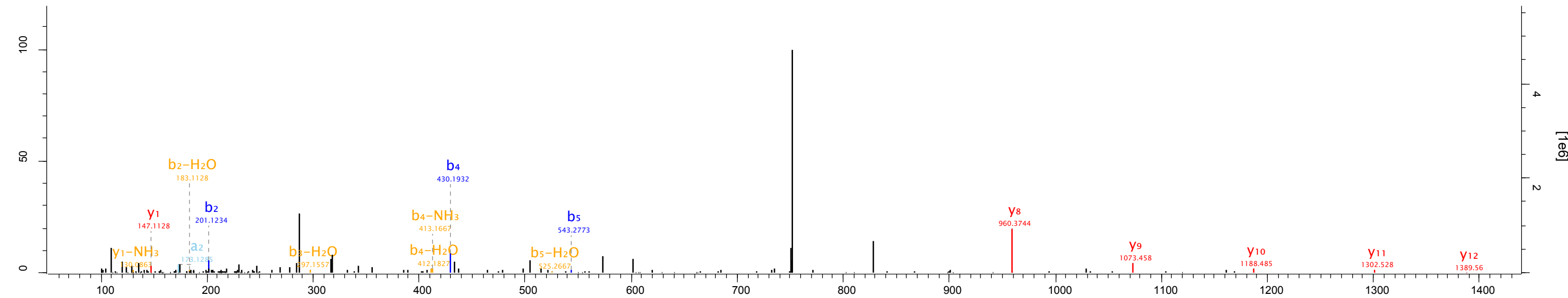
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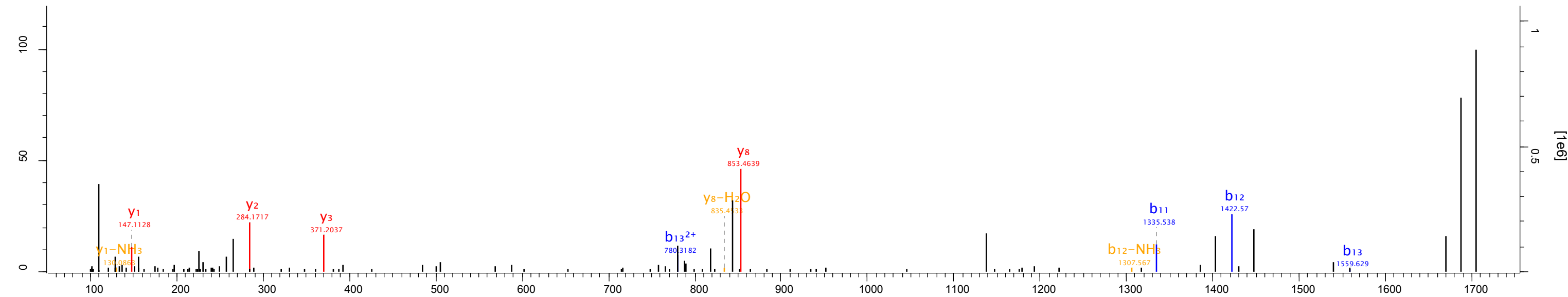
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Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 49416 Method FTMS; HCD Score 41.58 m/z 751.83



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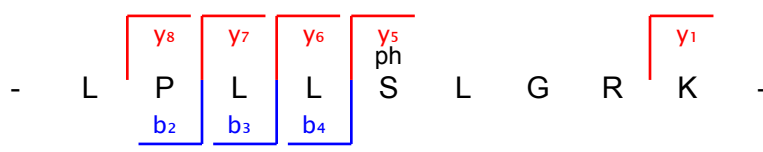
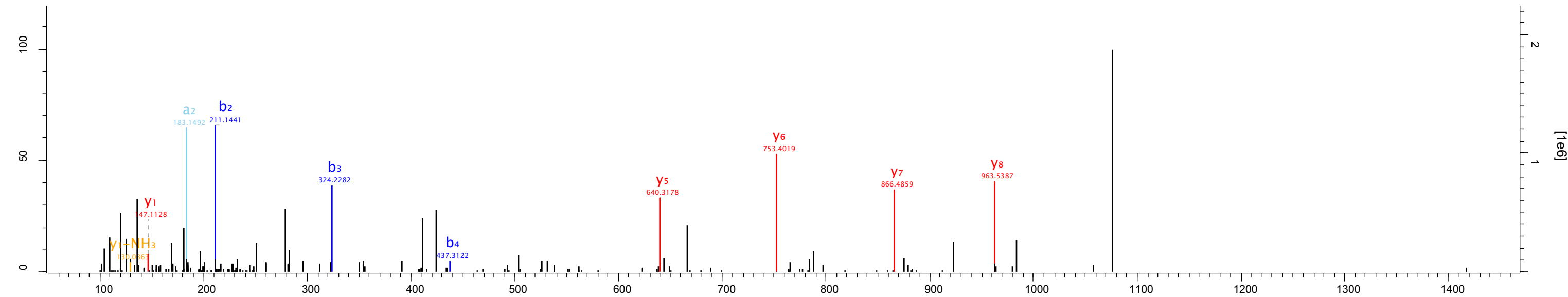
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- y_3 above S
- y_2 above H
- y_1 above K

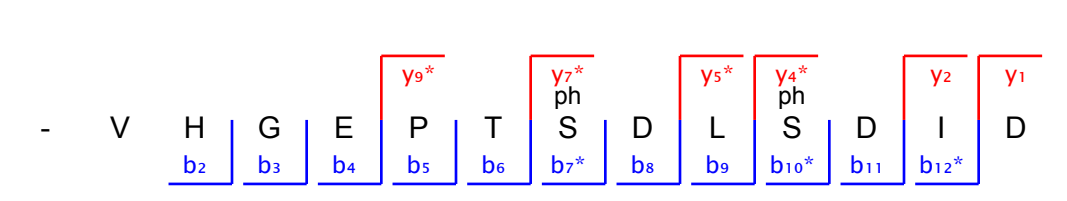
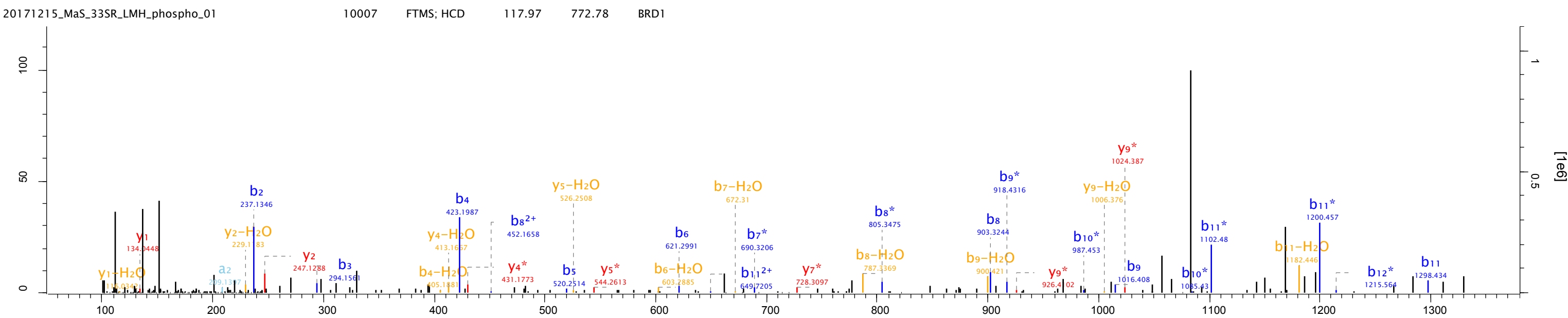
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- b_{11} below P
- b_{12} below S
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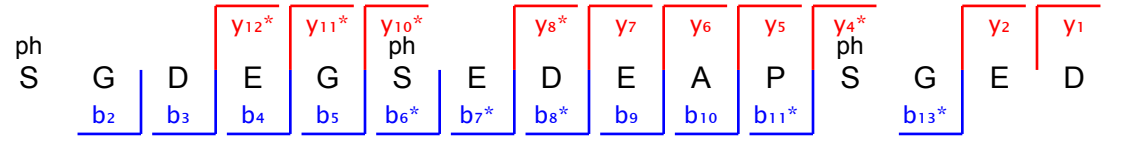
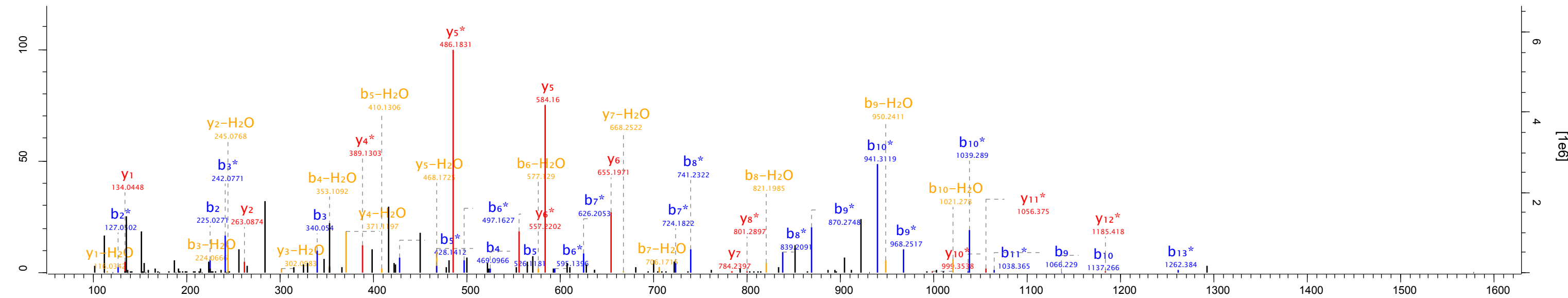
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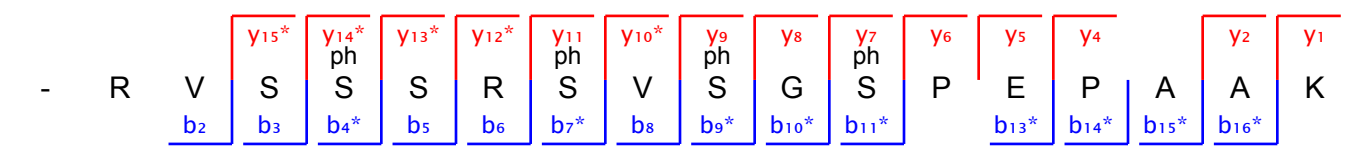
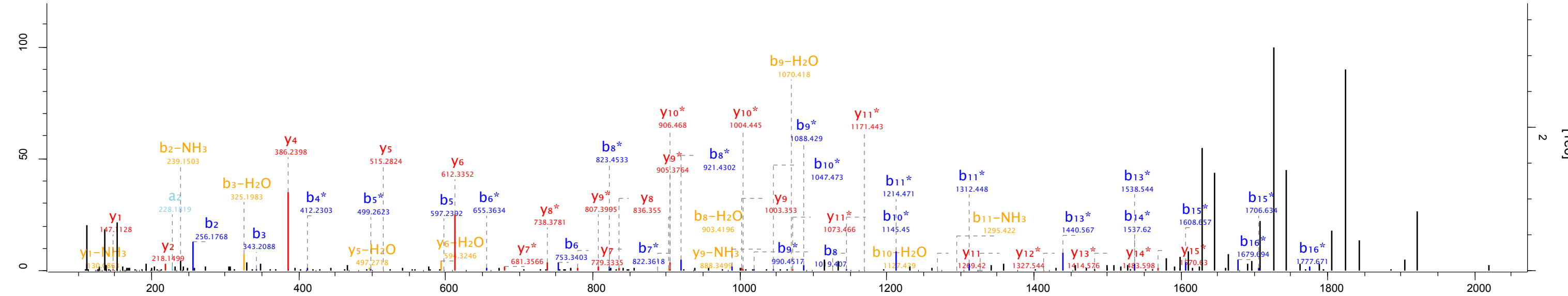


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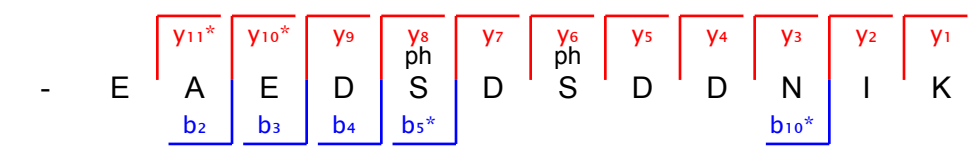
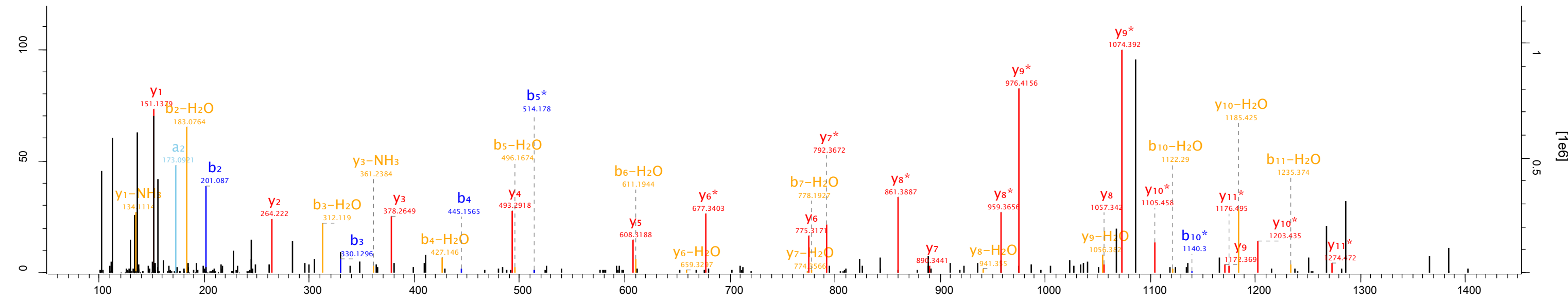


Raw file Scan Method Score m/z Gene names

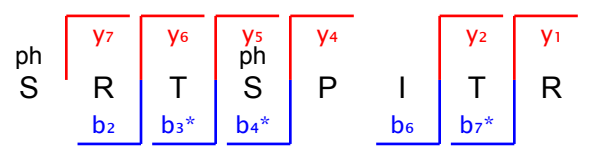
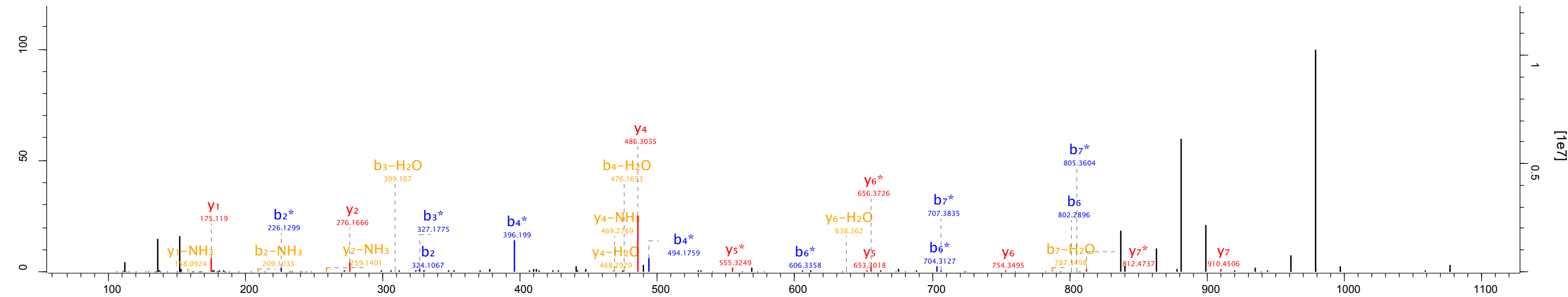
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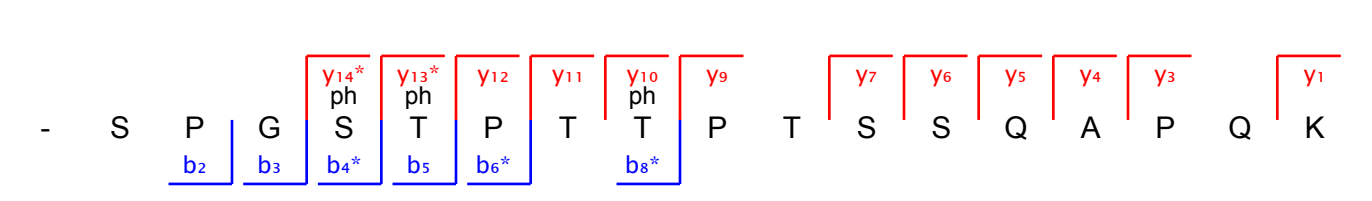
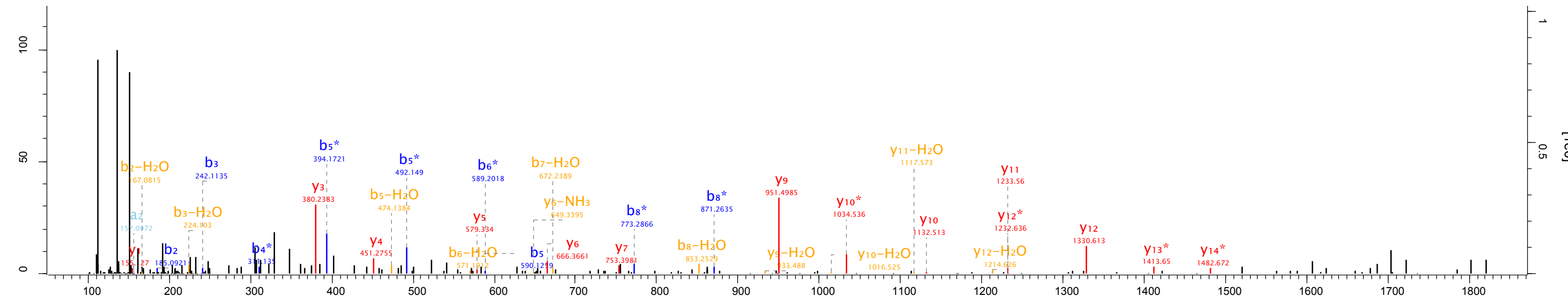
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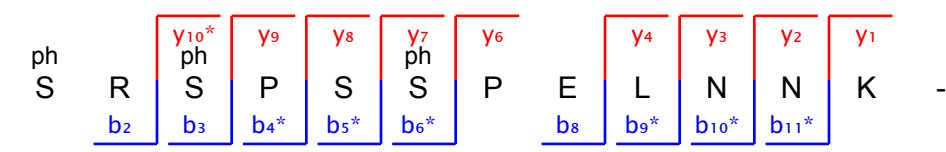
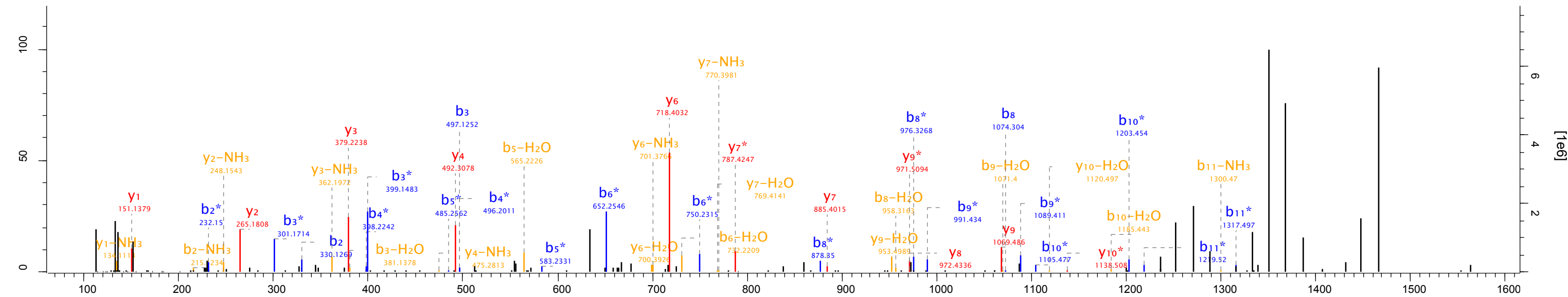
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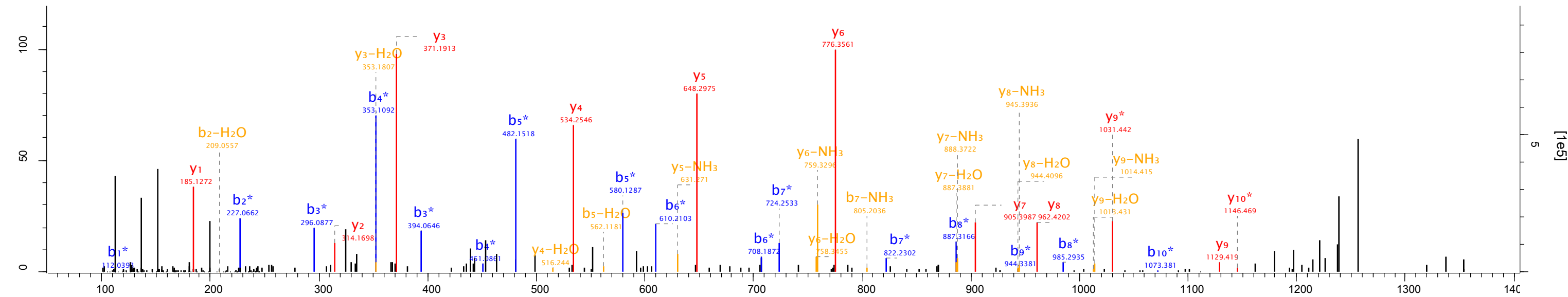
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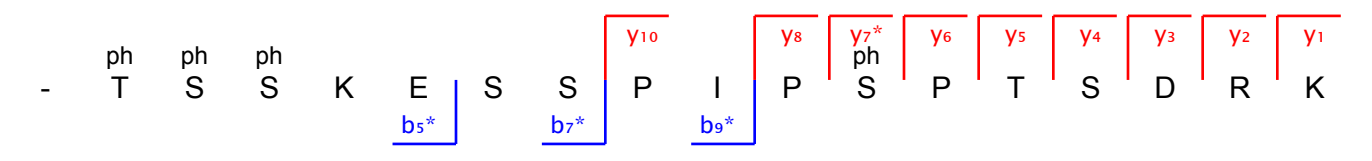
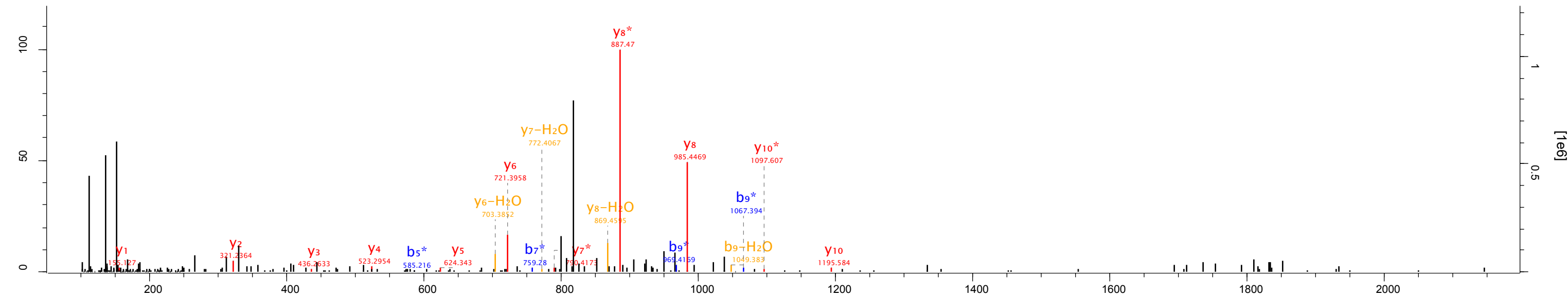


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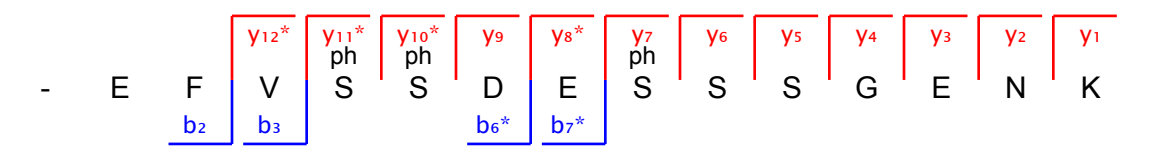
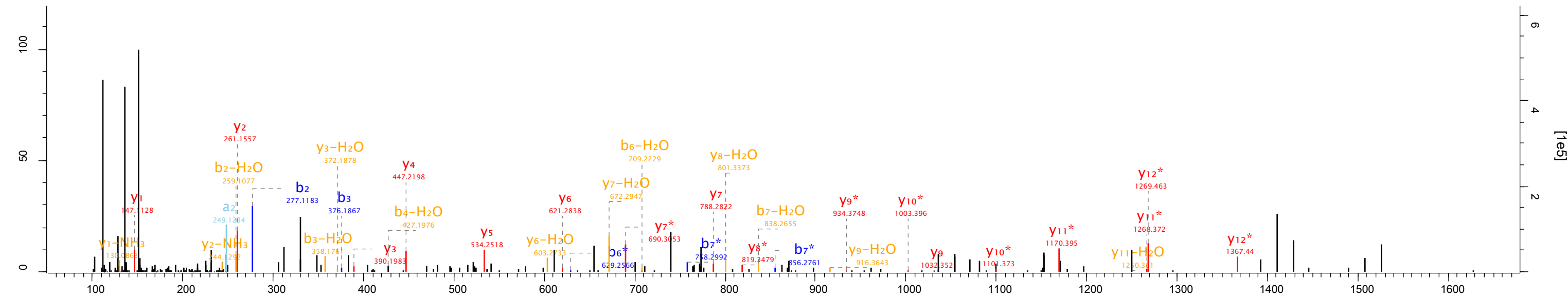


ac - ph S **y₁₀*** **y₉** **y₈** **y₇** **y₆** **y₅** **y₄** **y₃** **y₂** **y₁**
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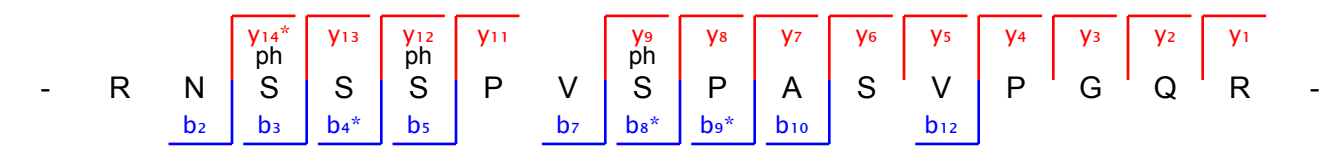
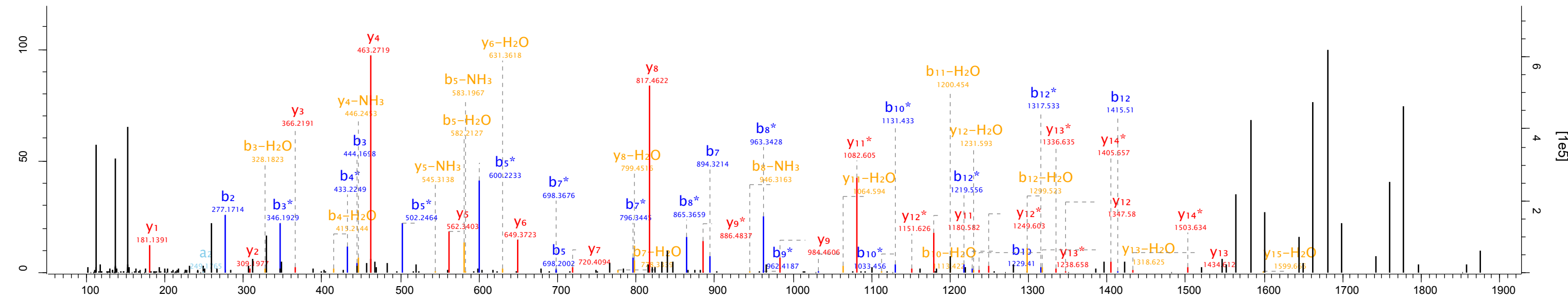
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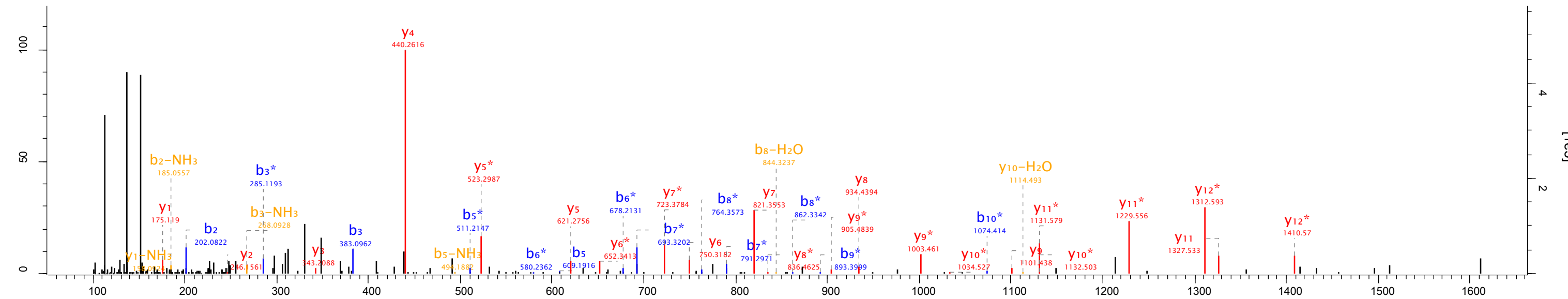
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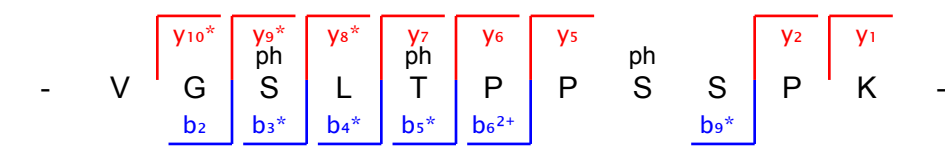
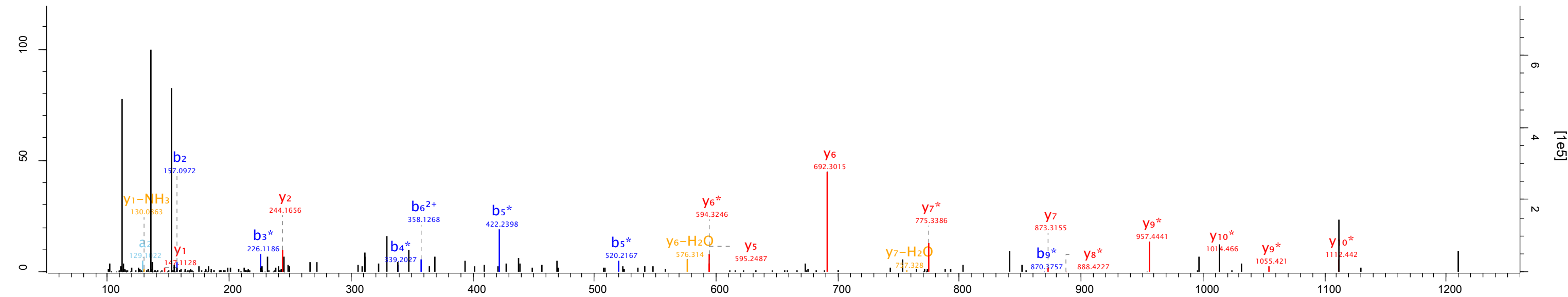
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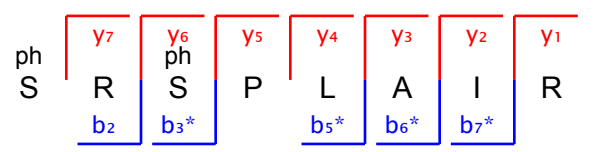
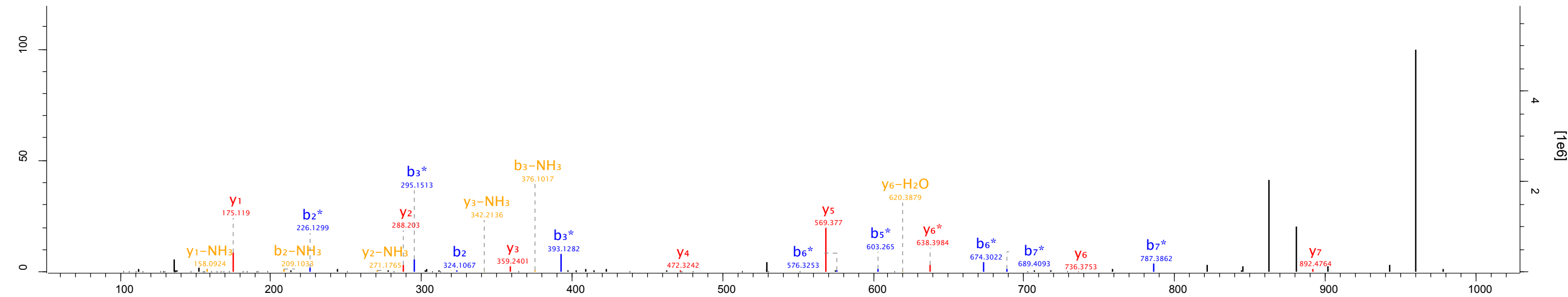
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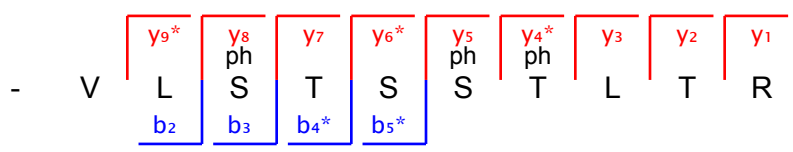
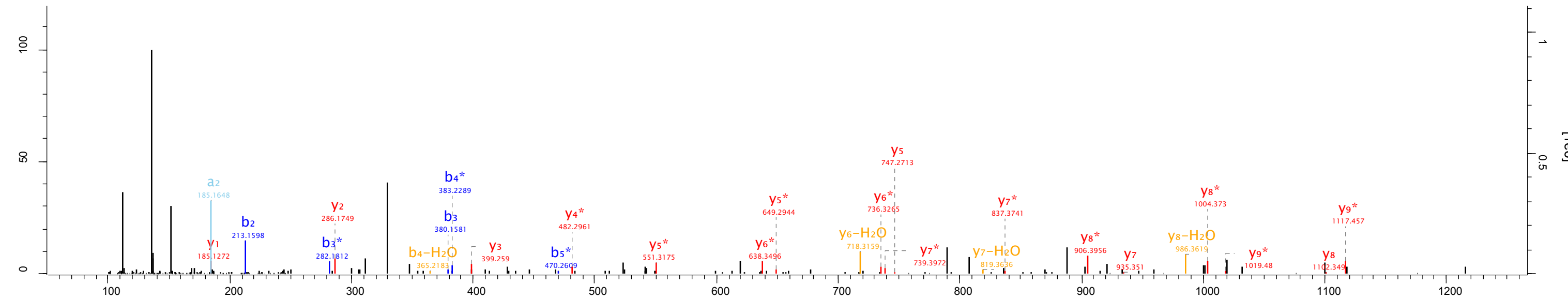
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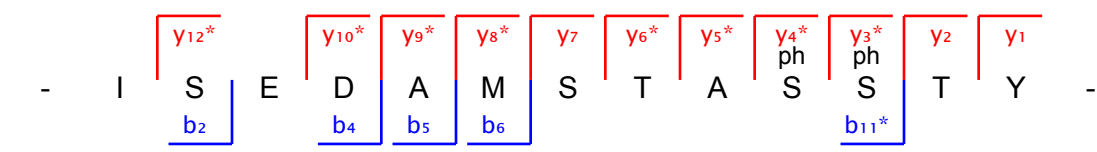
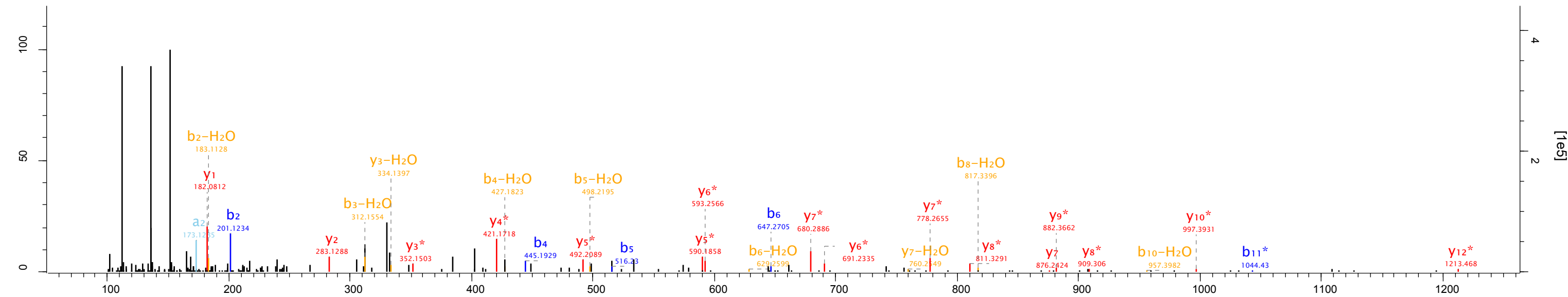
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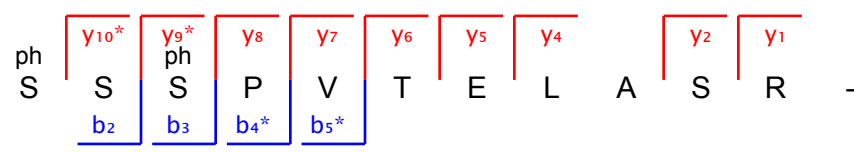
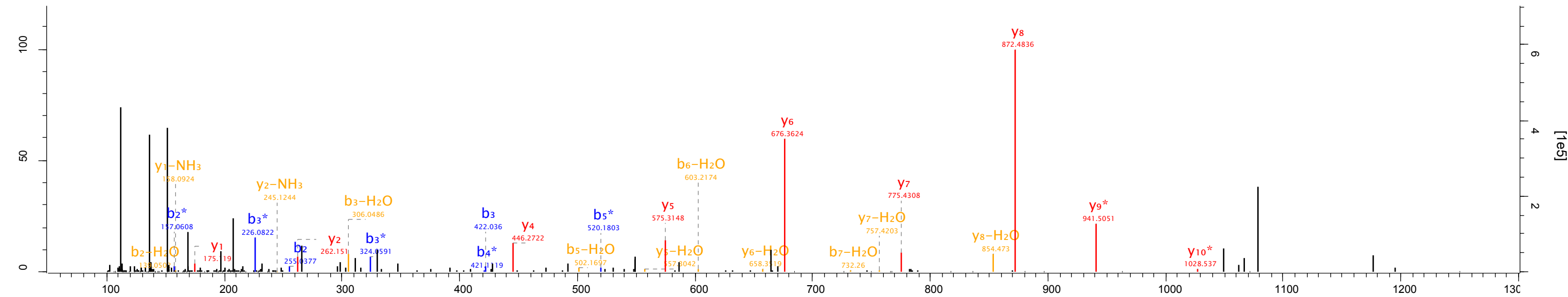
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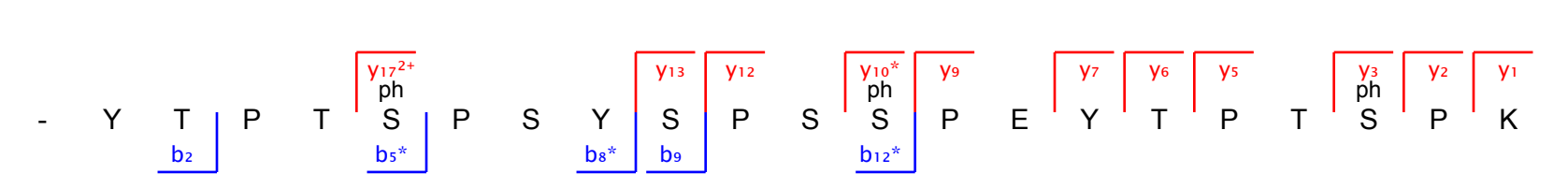
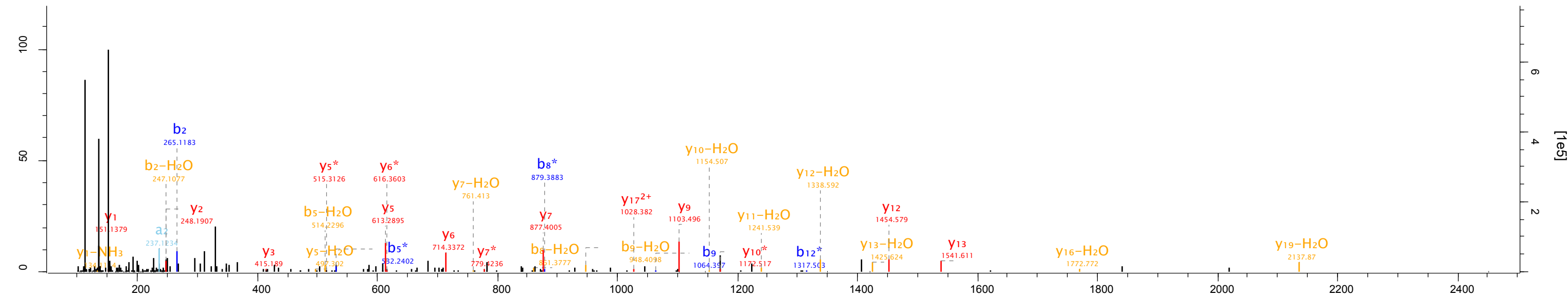
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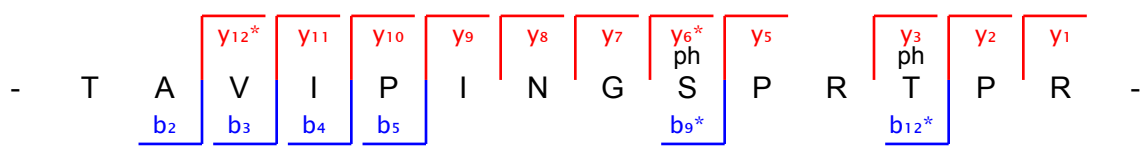
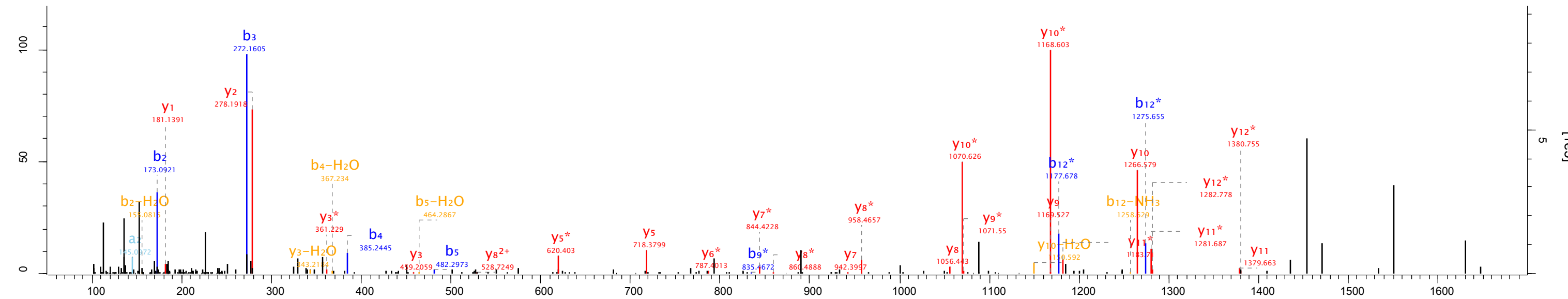


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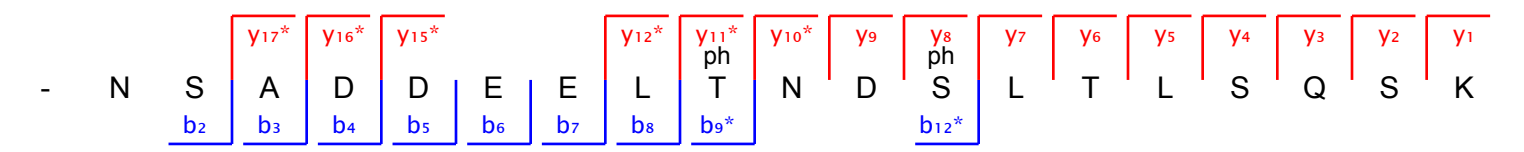
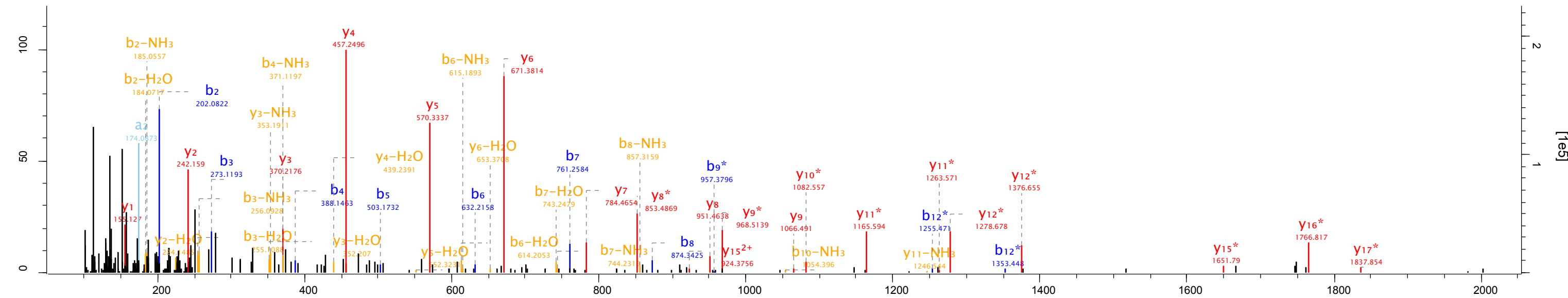


Raw file
20171215_MaS_33SR_LMH_phospho_02

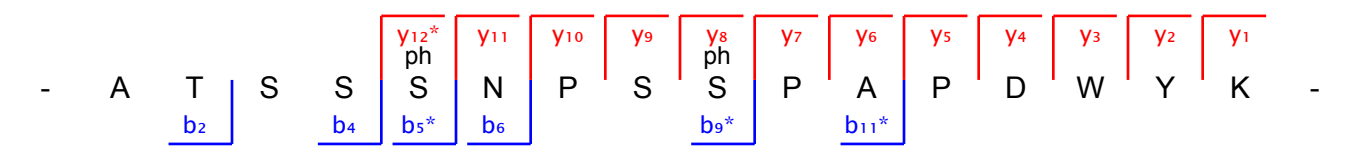
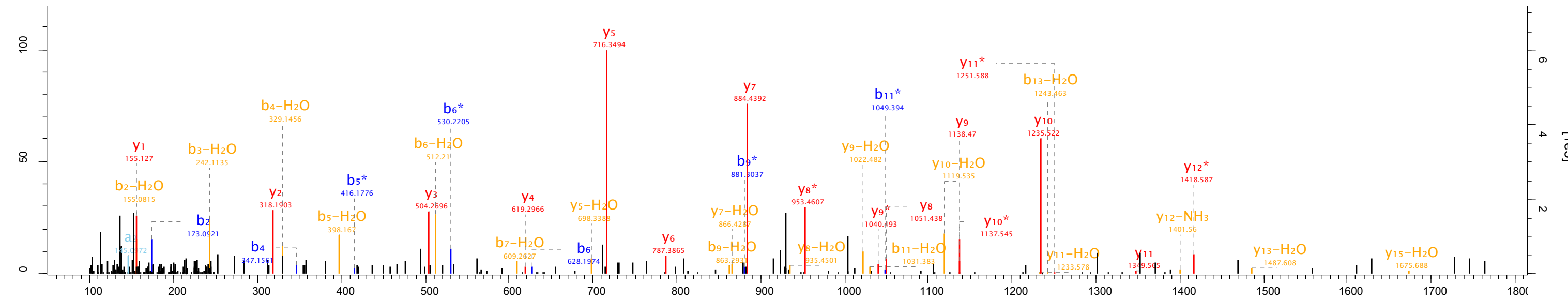
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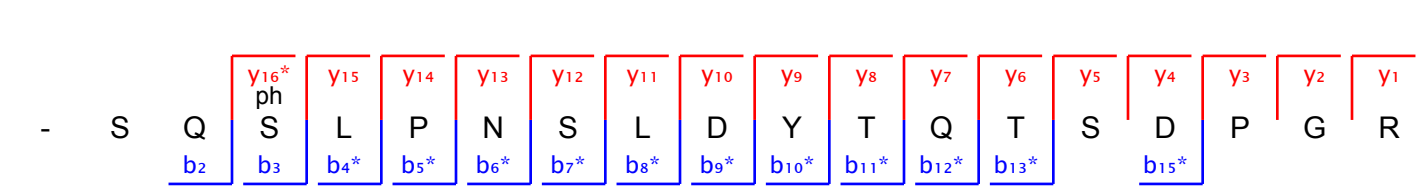
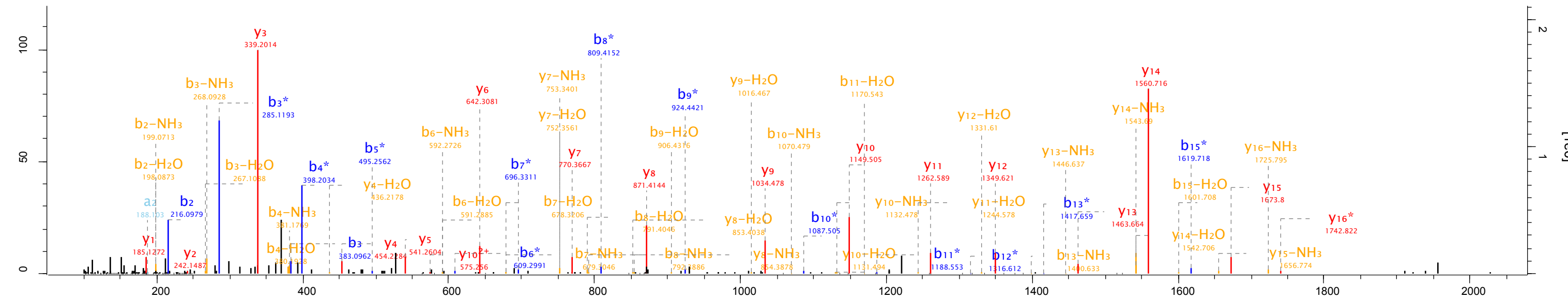
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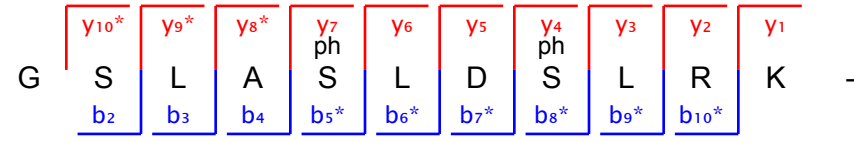
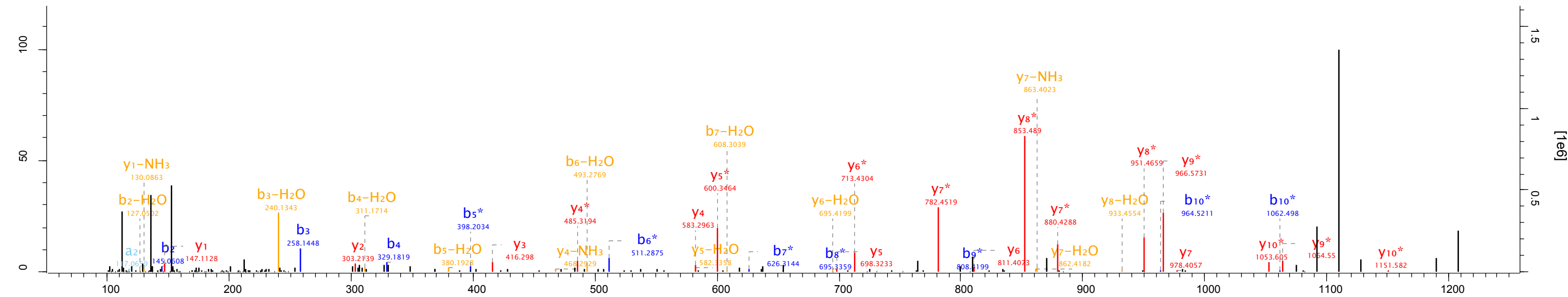
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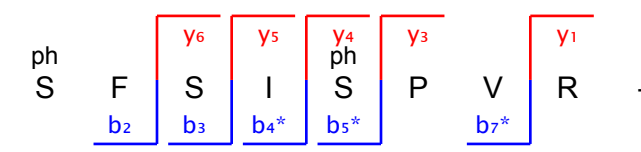
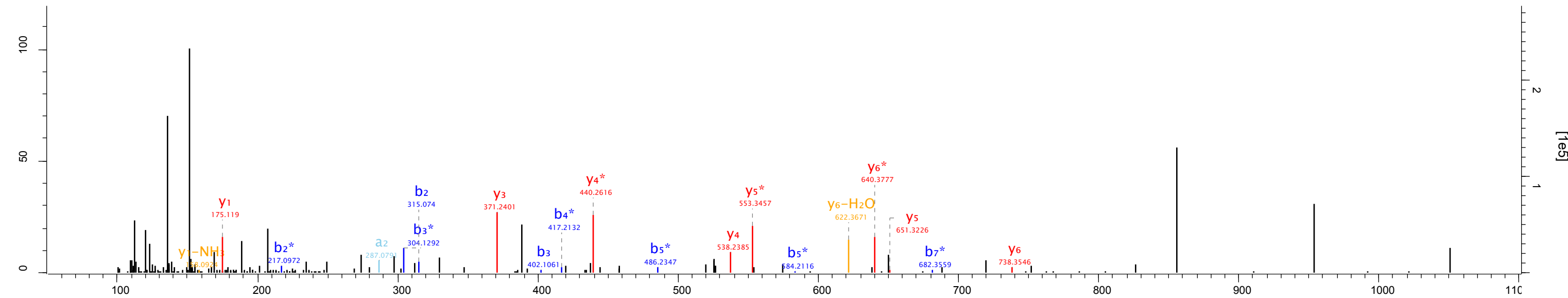
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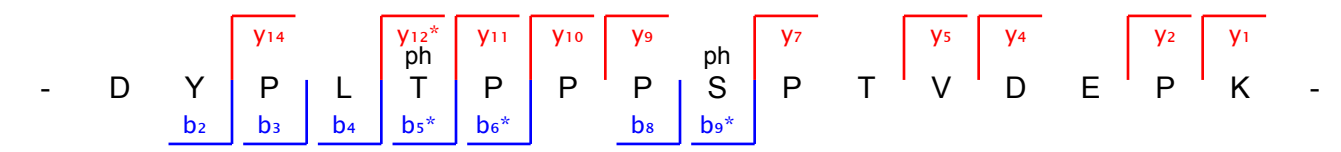
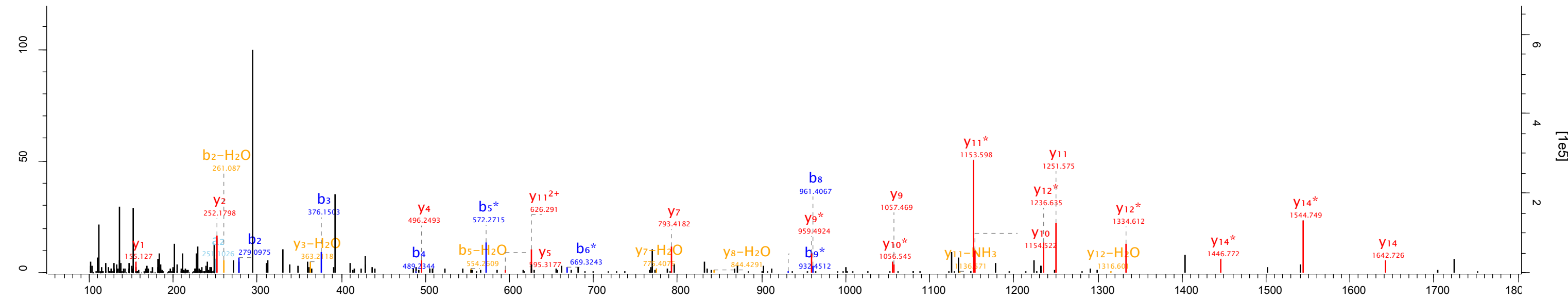
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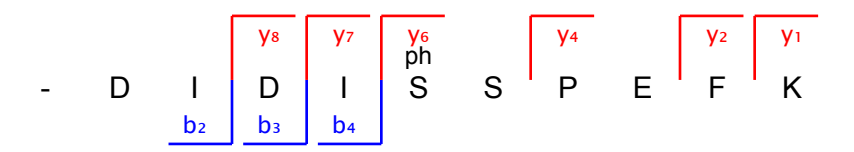
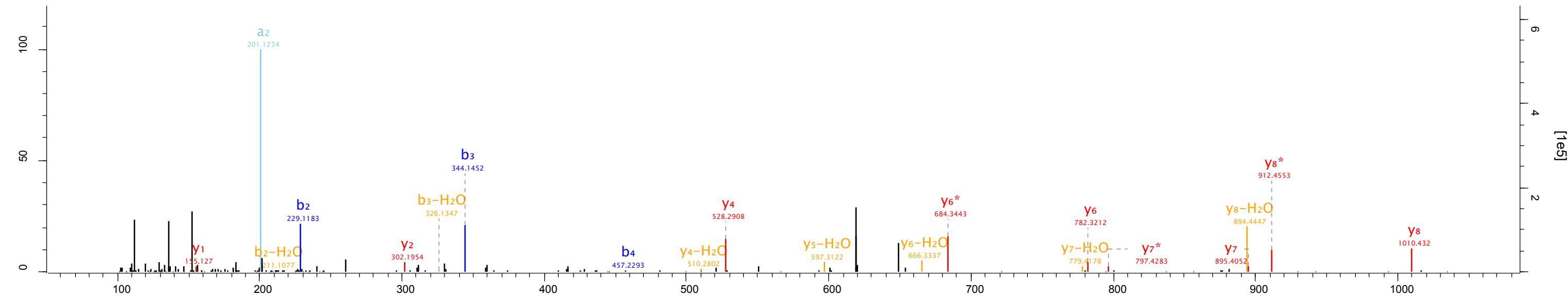
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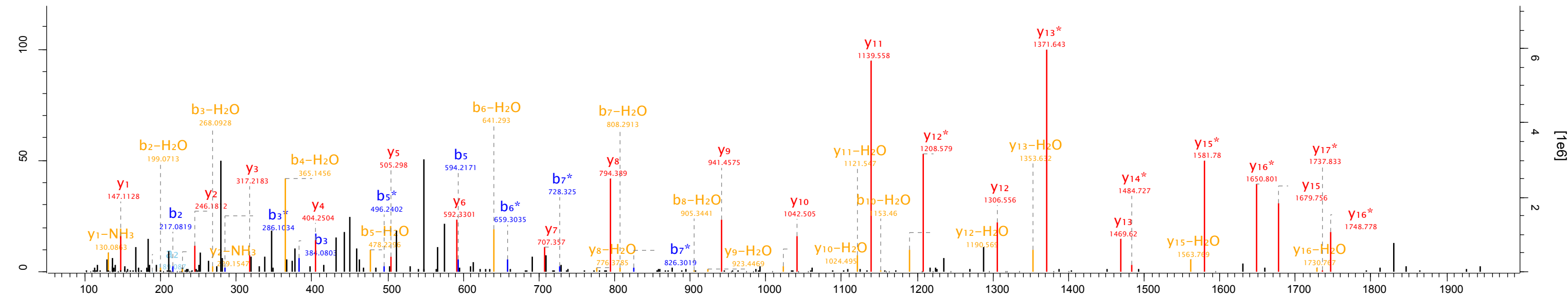
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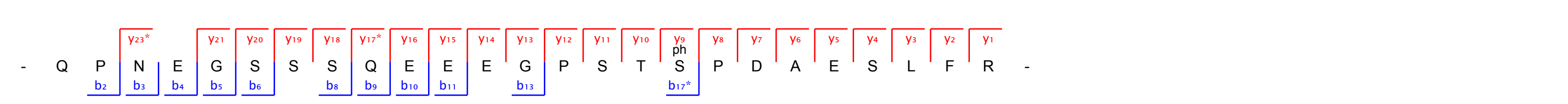
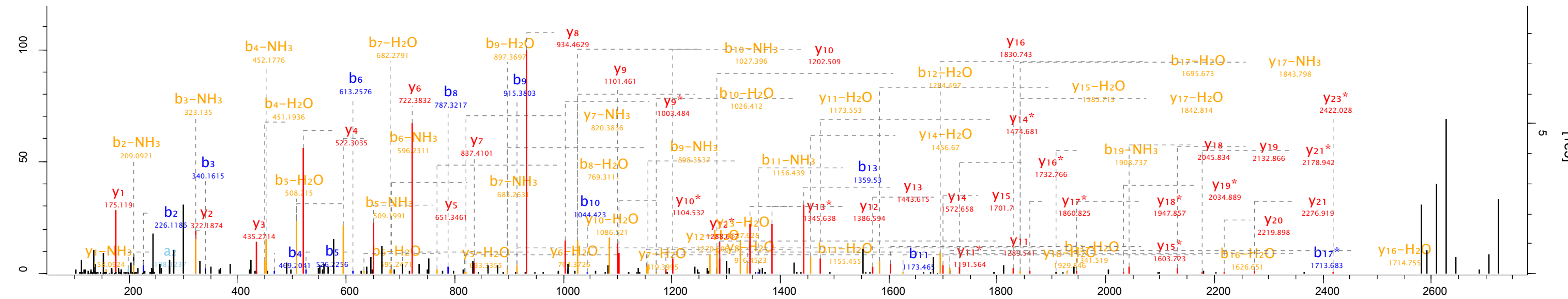
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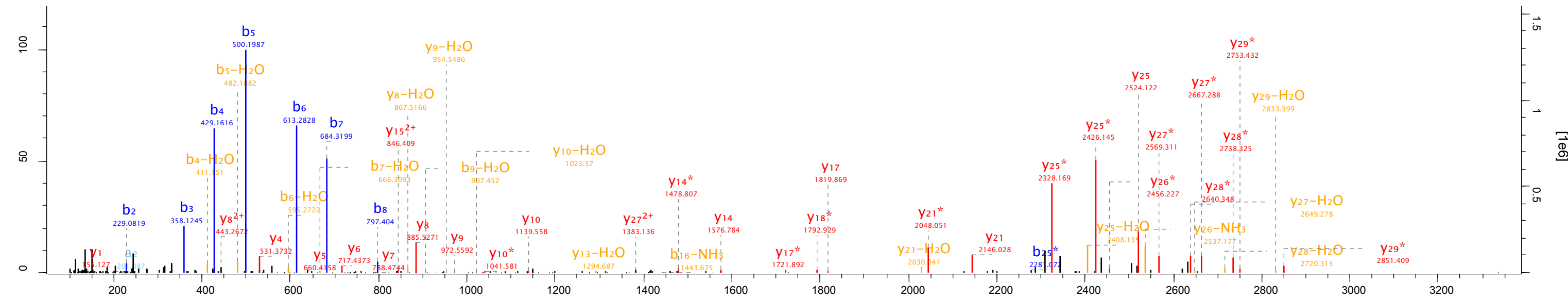
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b₂
b₃
b₅
b₆^{*}
b₇^{*}
y₁₇^{*}
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y₁₅
y₁₄^{*}
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

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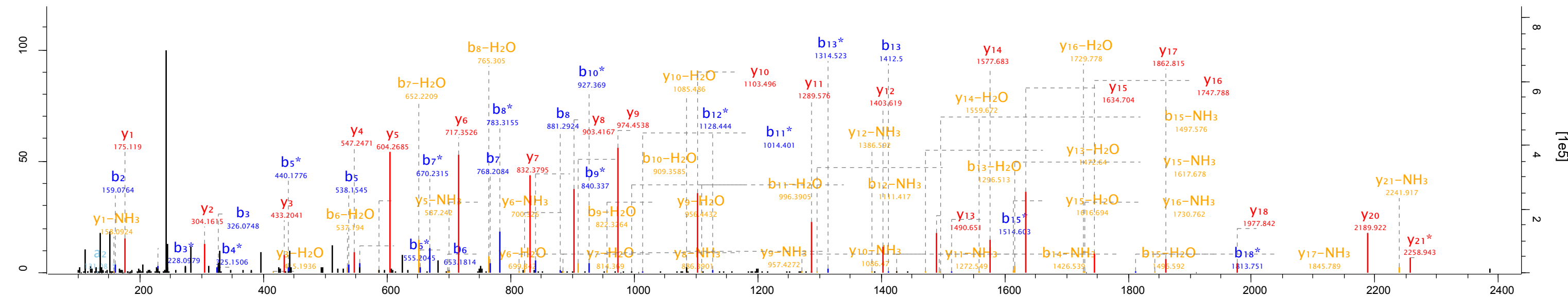
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ac - A D E A A L A L Q P G G S P S A A G A D R E A A S S P A G E P L R K -

Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets: b₂ (D), b₃ (E), b₄ (A), b₅ (A), b₆ (L), b₇ (A), b₈ (L), b₂₅^{*} (S)
- Red brackets: y₂₉^{*} (L), y₂₈^{*} (A), y₂₇^{*} (L), y₂₆^{*} (Q), y₂₅ (P), y₂₁ (P), y₁₈^{*} (A), y₁₇ (G), y₁₅²⁺ (D), y₁₄ (R), y₁₀ (S), y₉ (S), y₈ (P), y₇ (A), y₆ (G), y₅ (E), y₄ (P), y₁ (K)

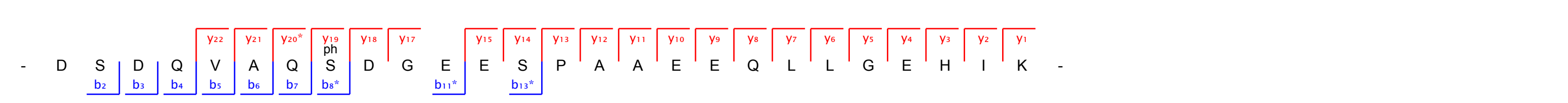
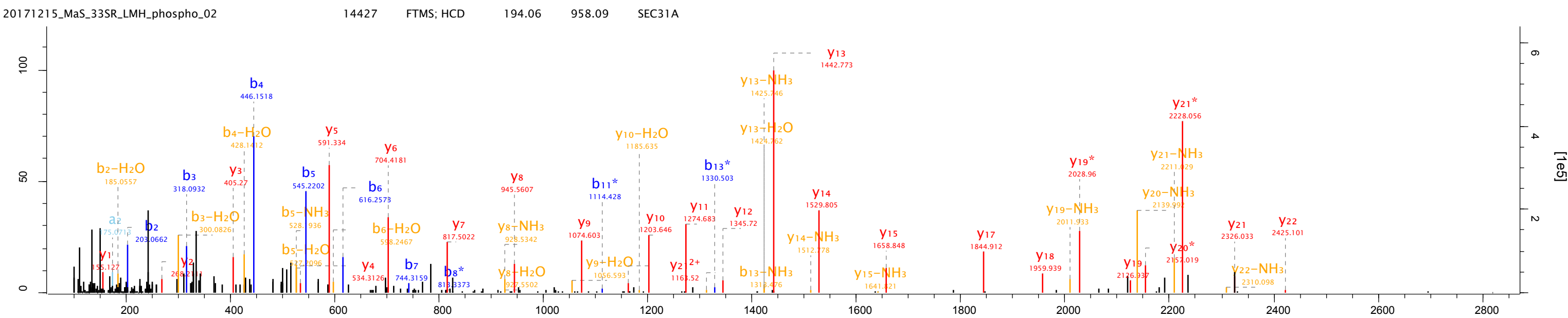


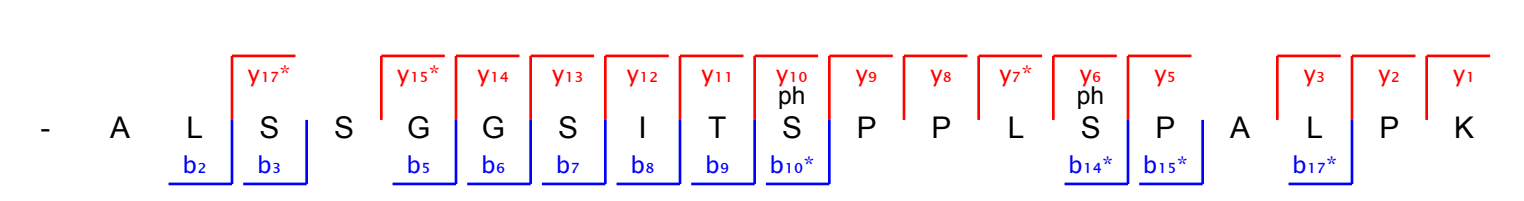
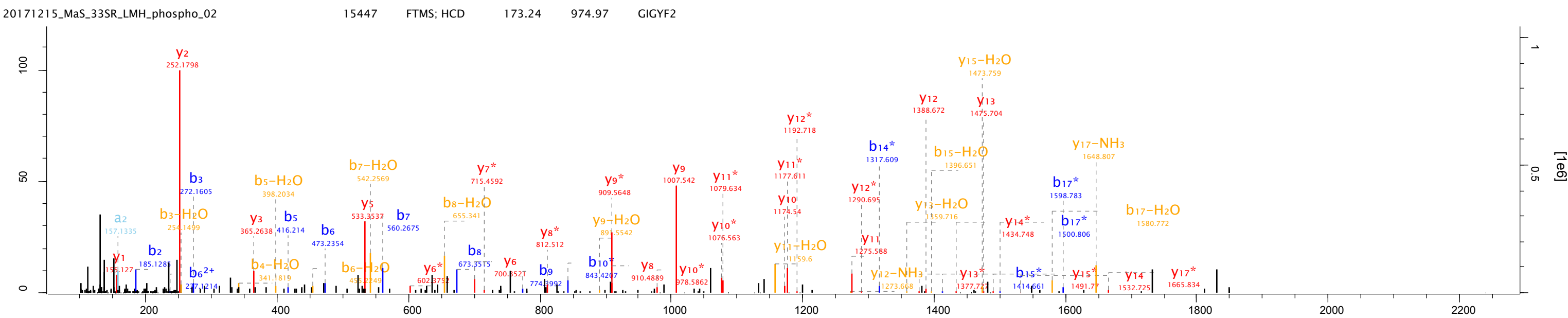
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b₆
b₇
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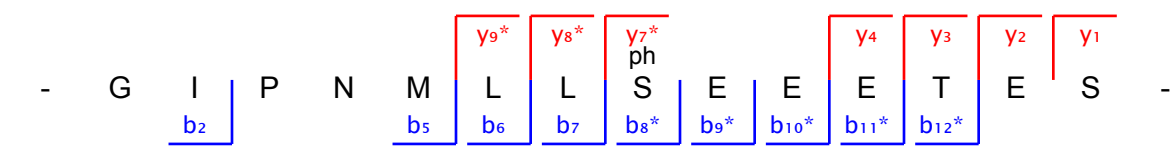
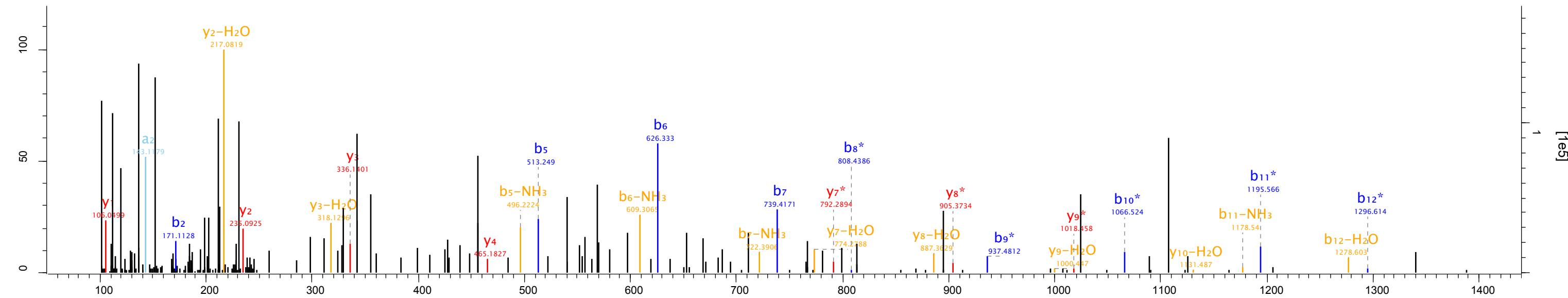
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y₉
y₈
y₇
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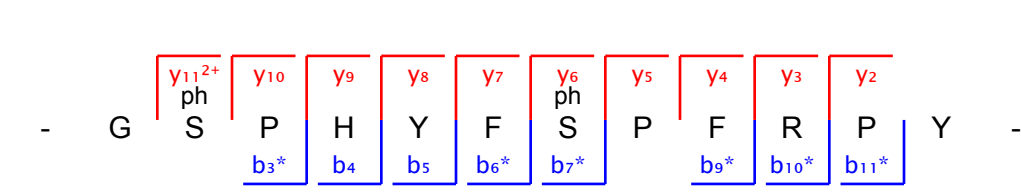
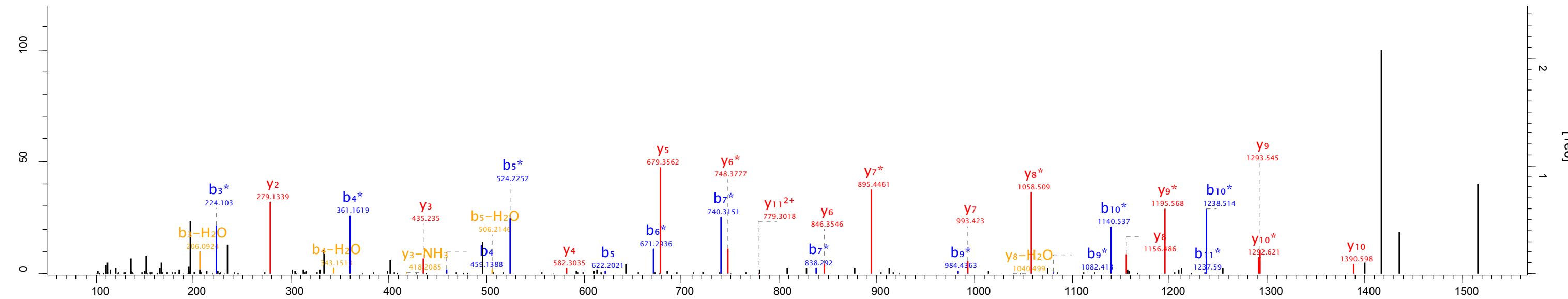


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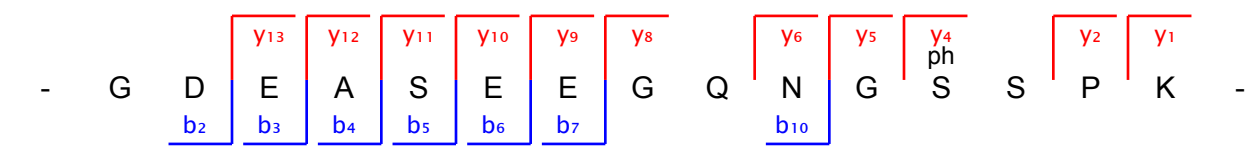
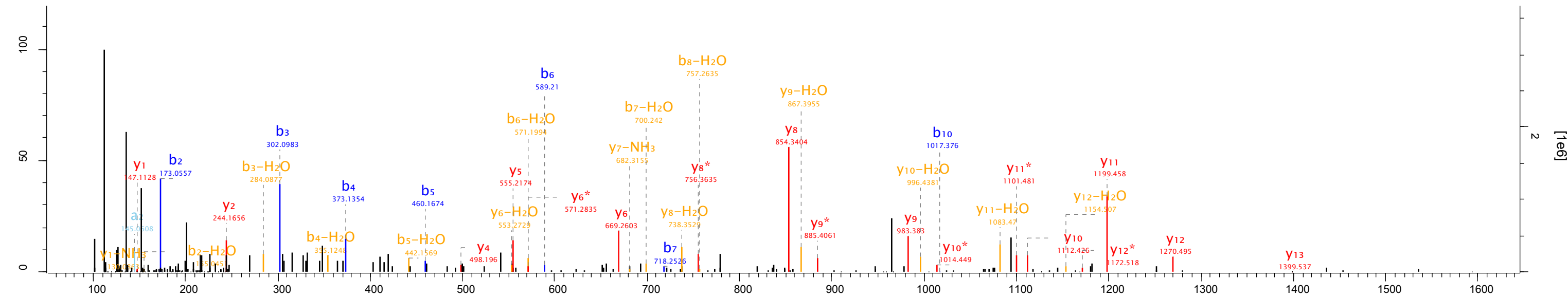
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20171215_MaS_33SR_LMH_phospho_02

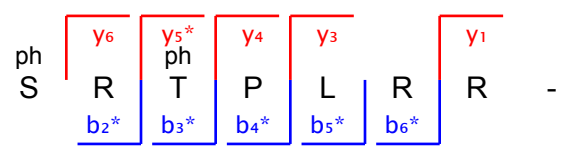
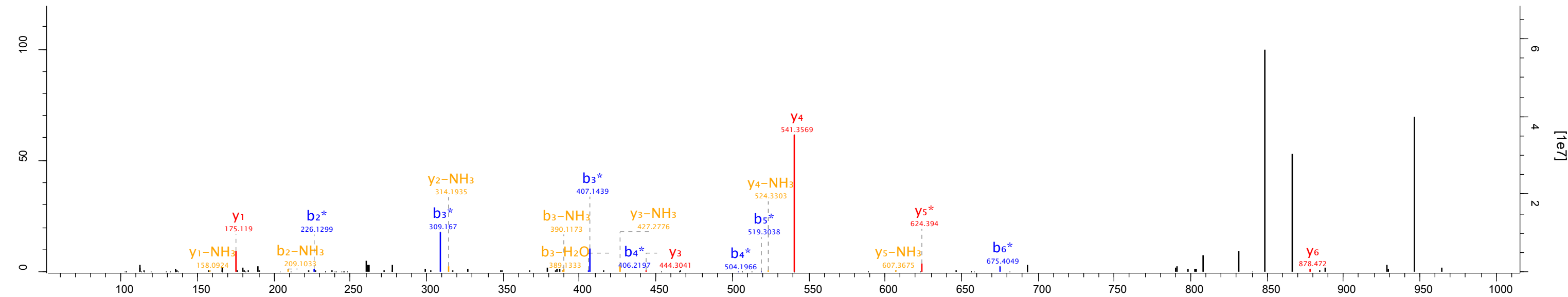


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20171215_MaS_33SR_LMH_phospho_02

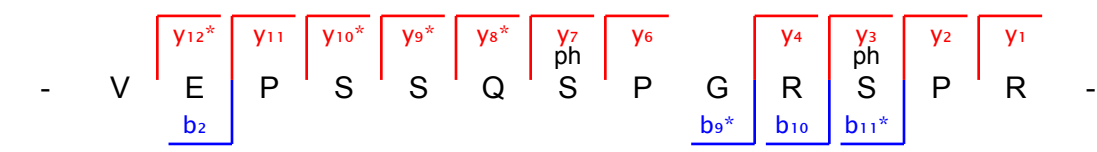
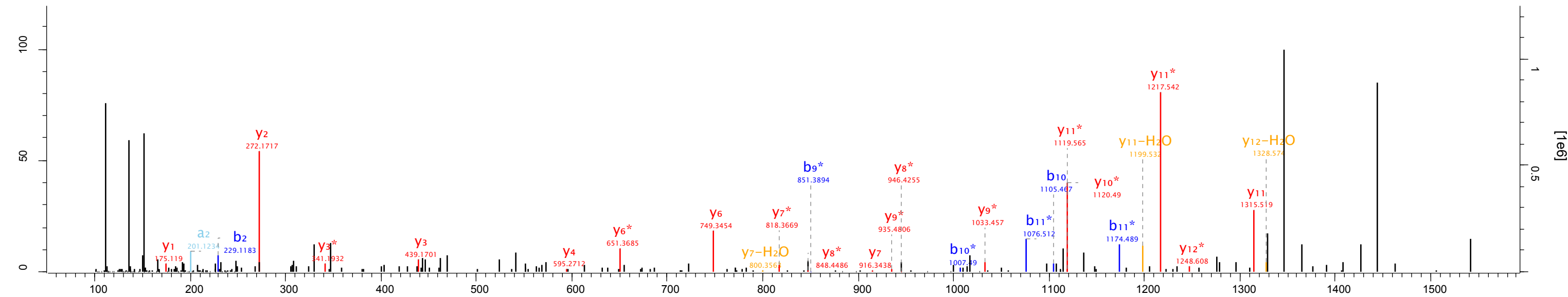
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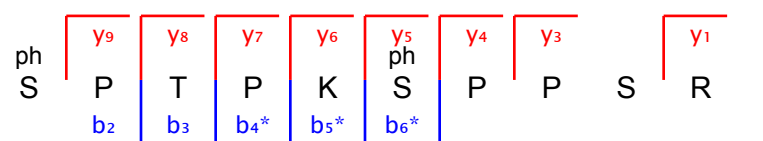
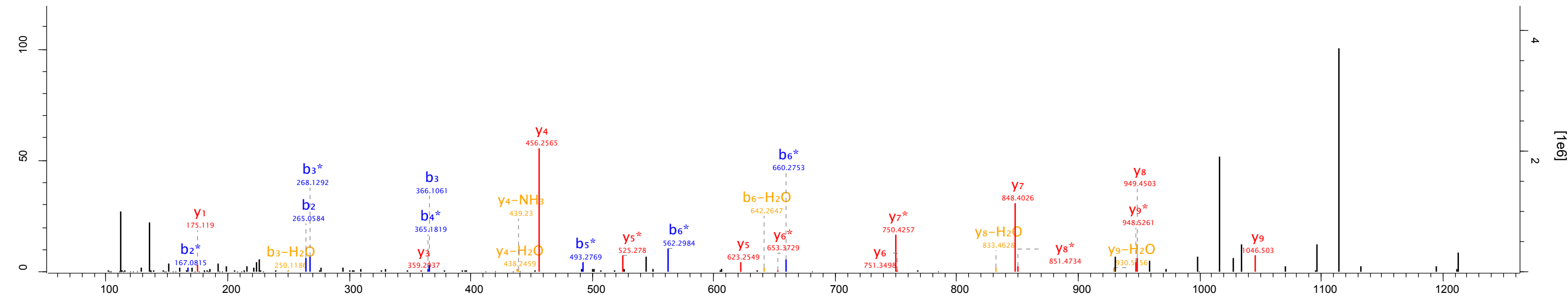
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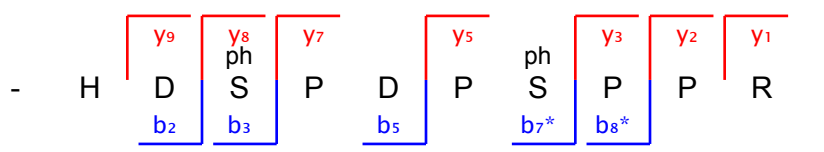
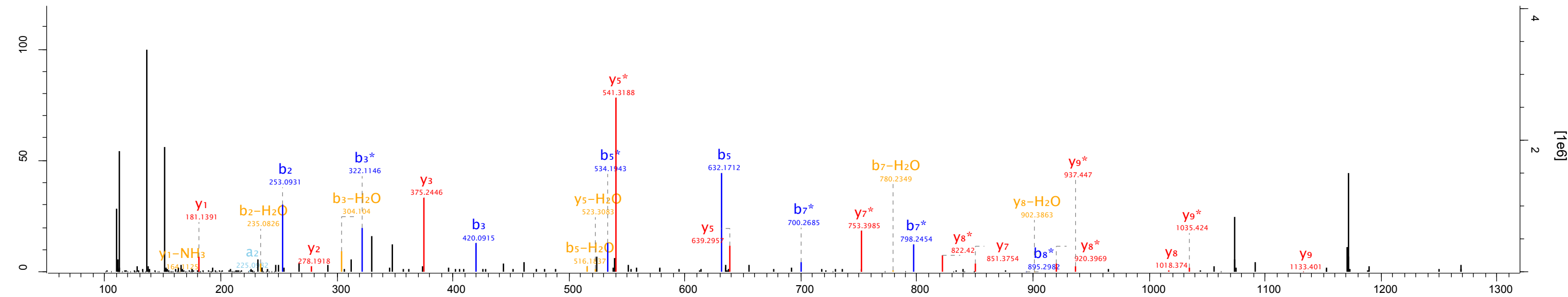
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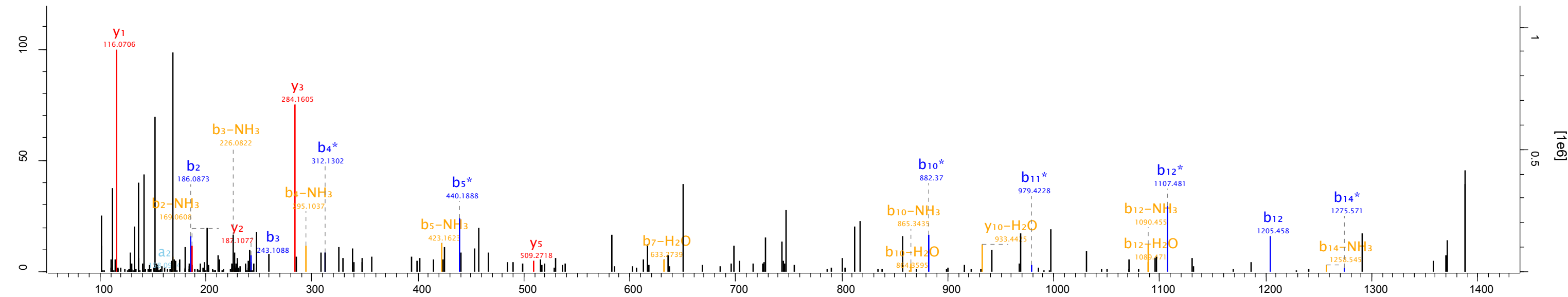
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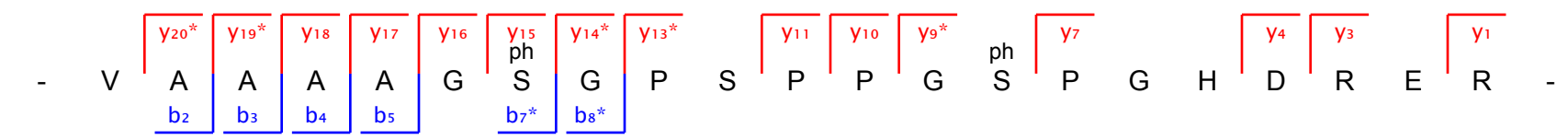
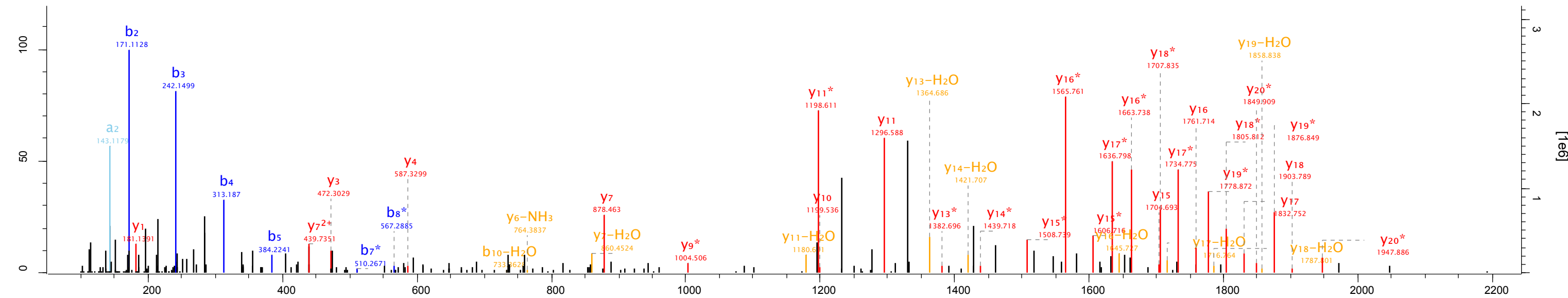
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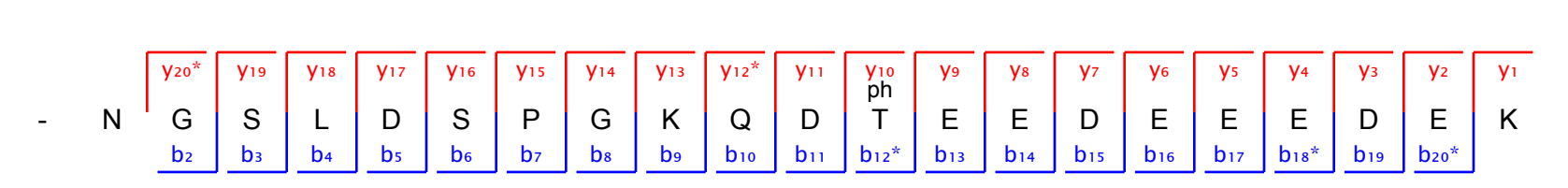
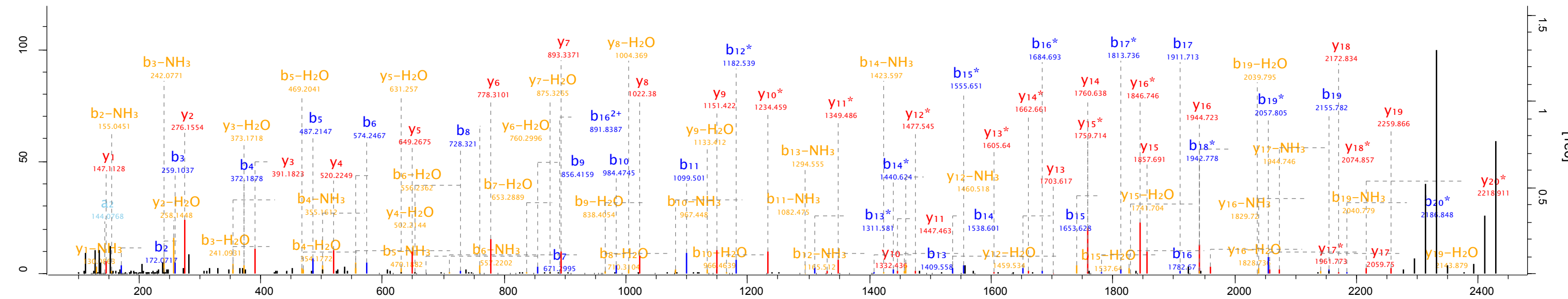
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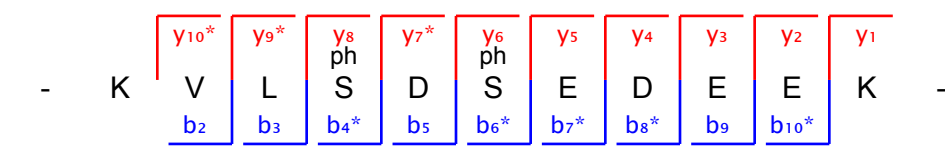
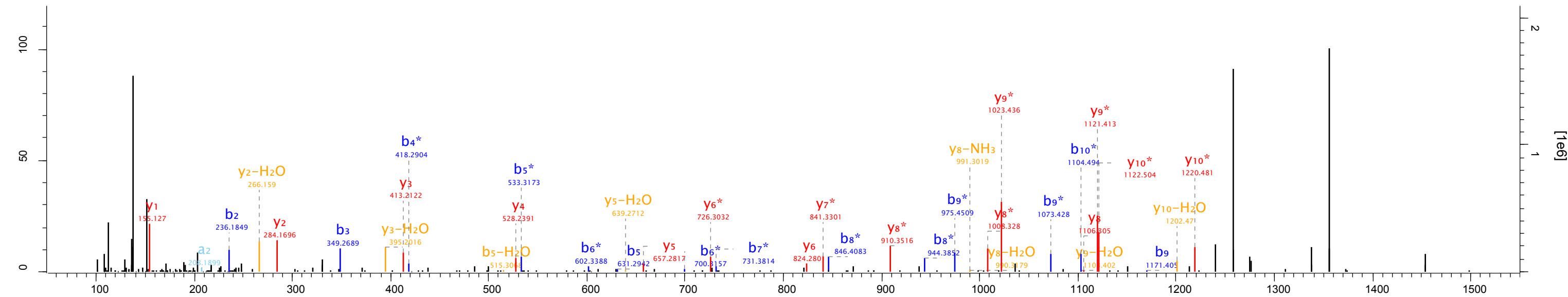
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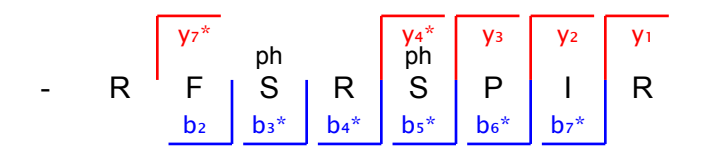
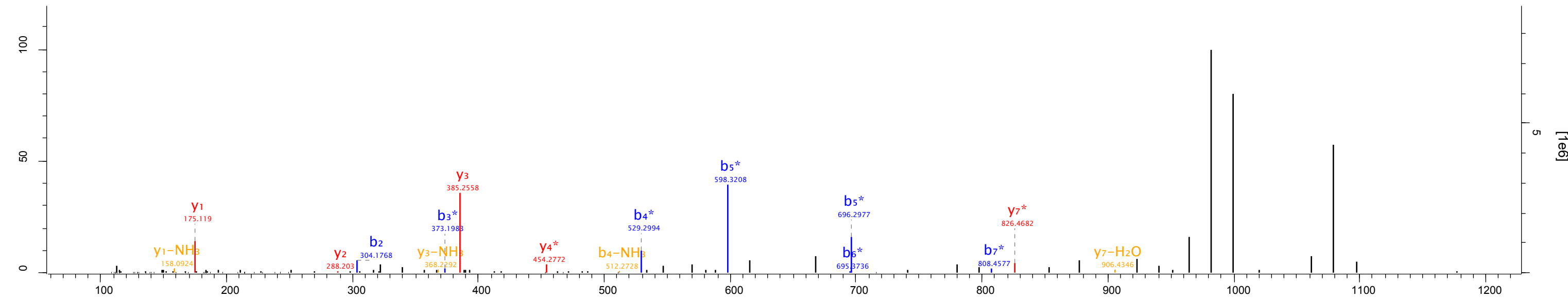
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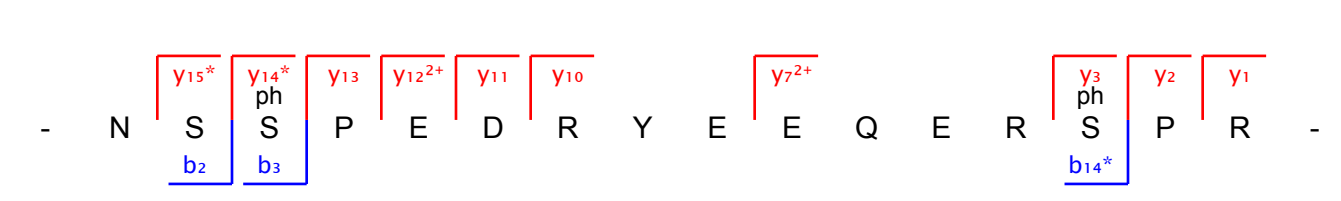
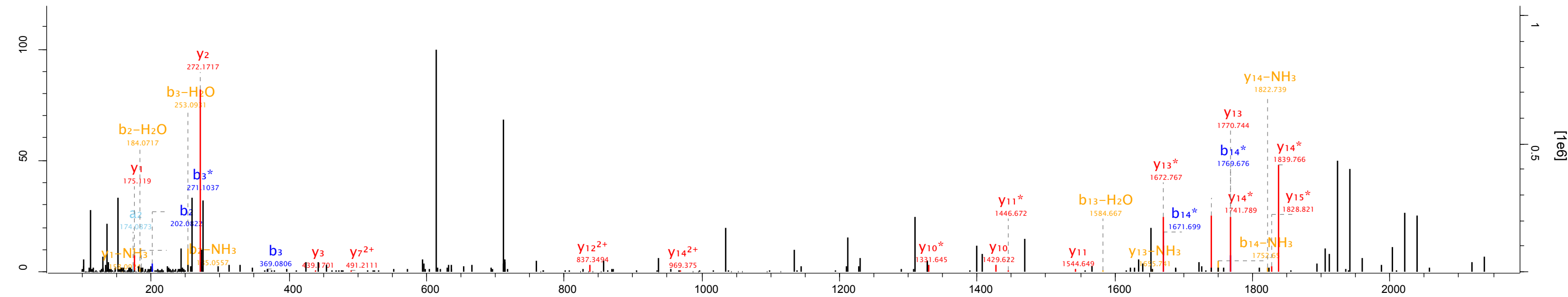
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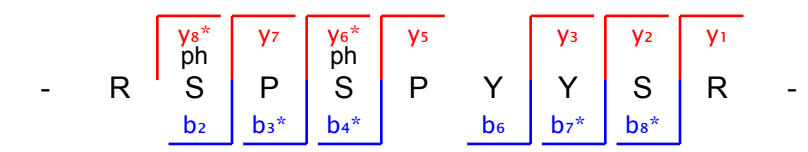
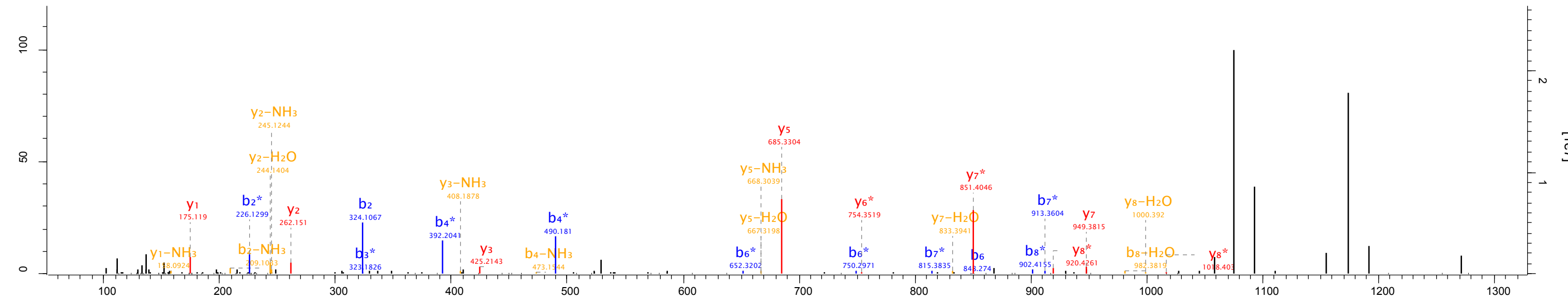
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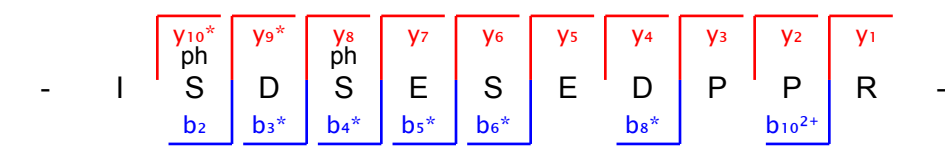
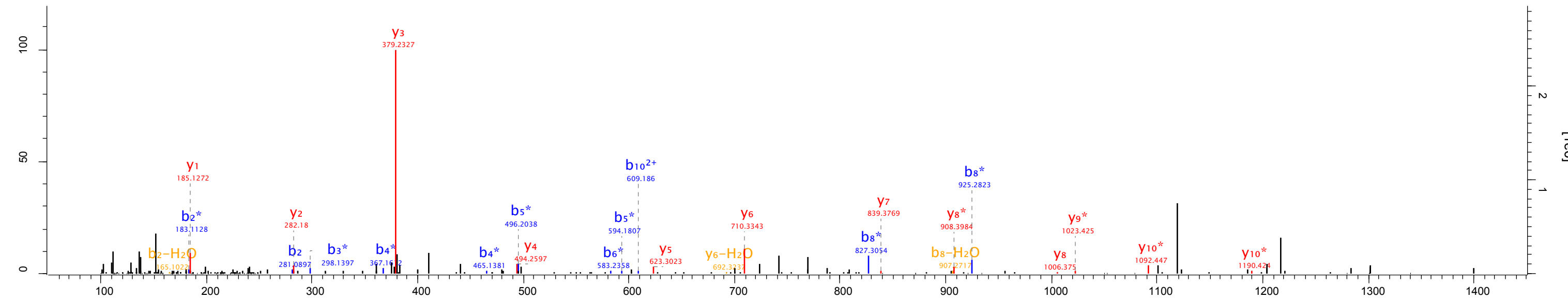
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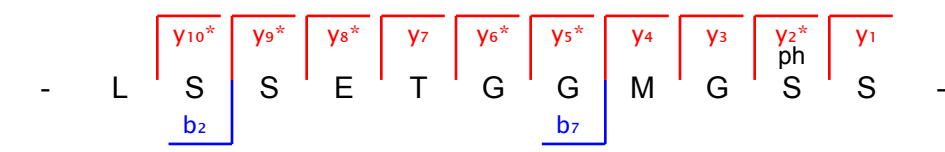
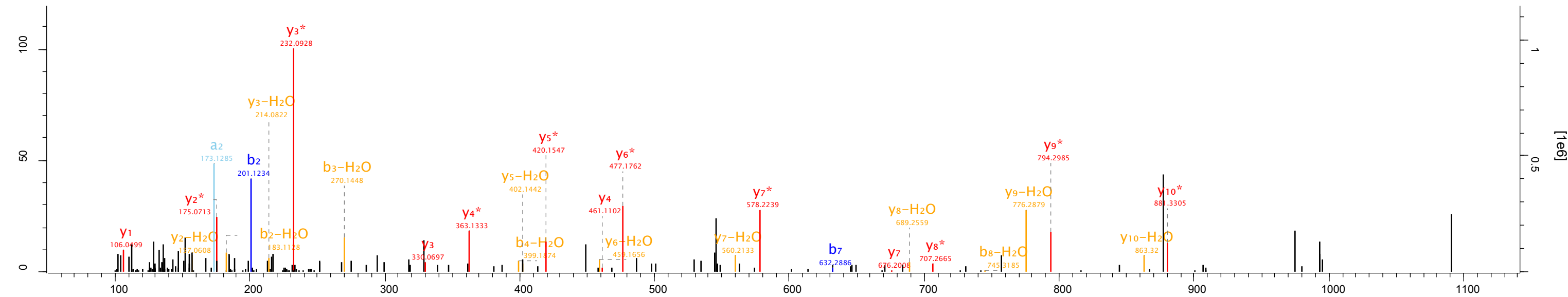
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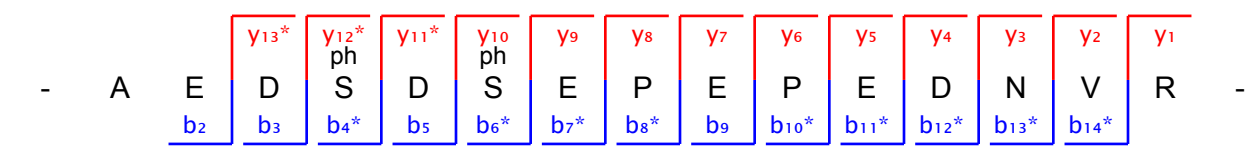
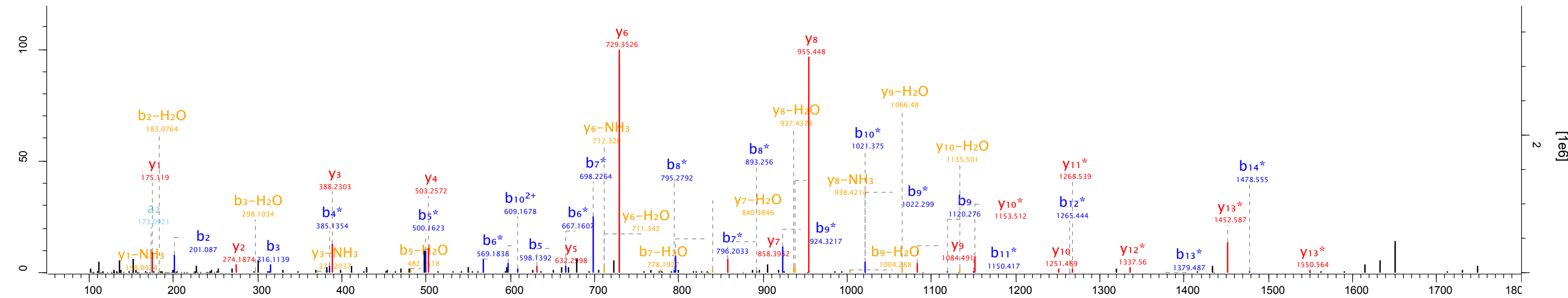
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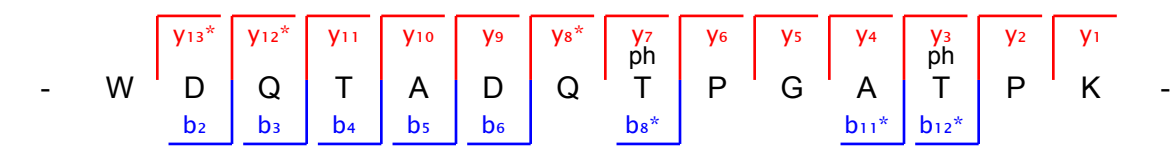
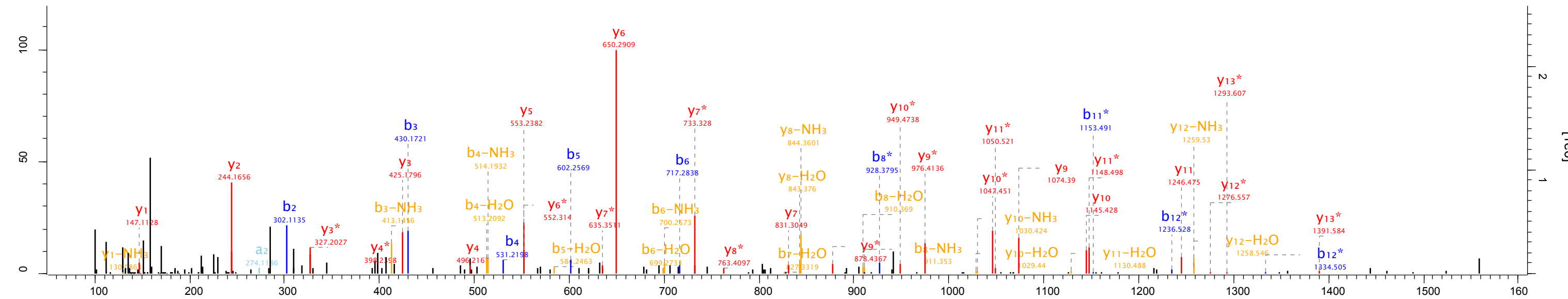


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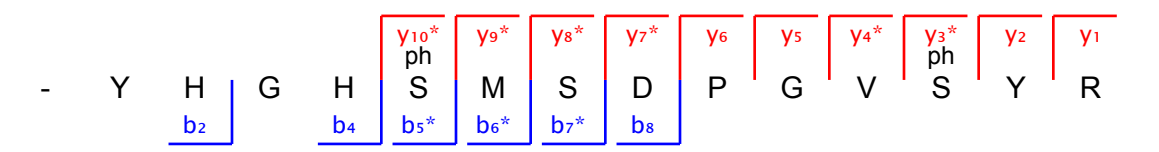
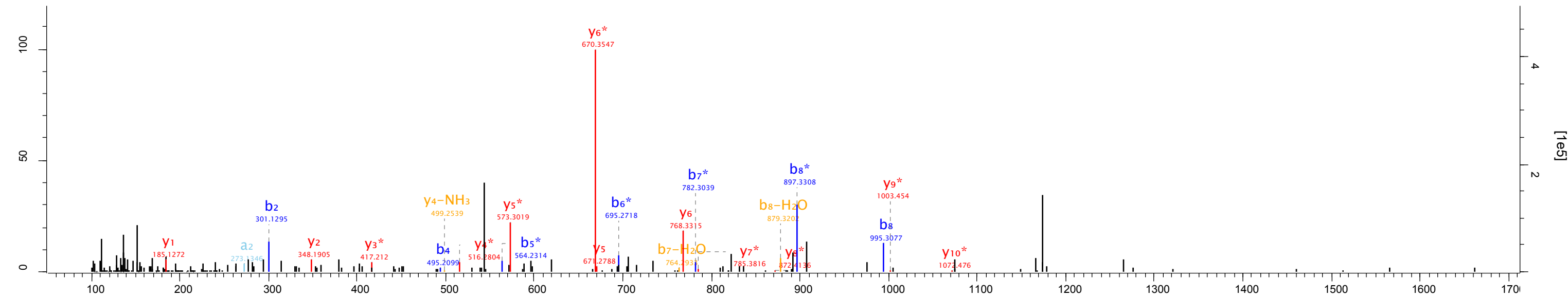


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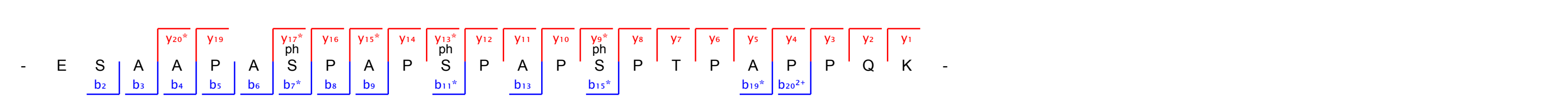
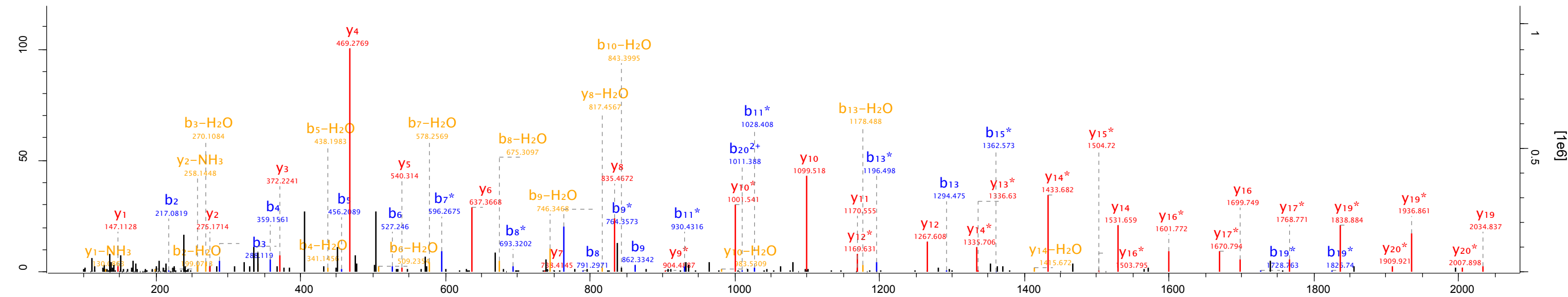
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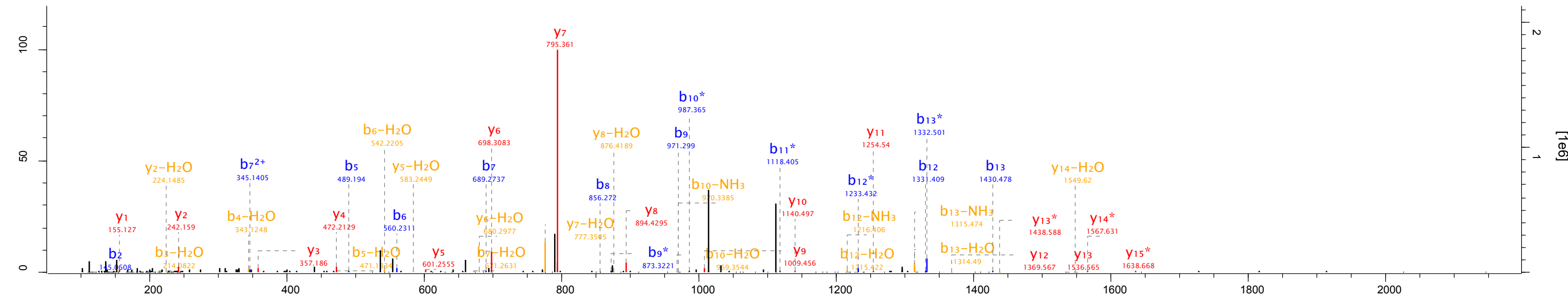


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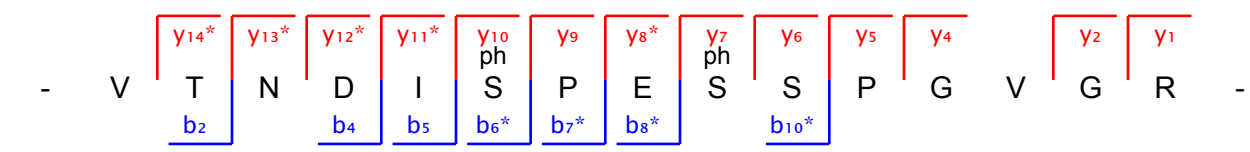
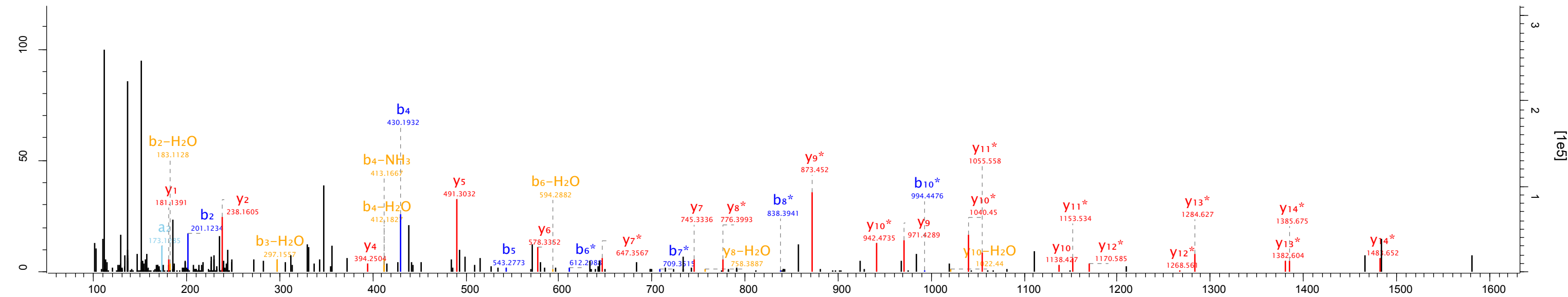


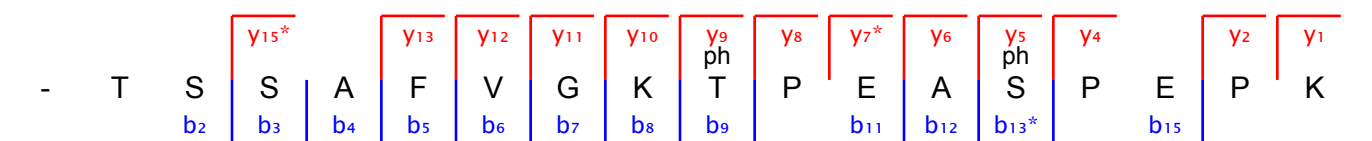
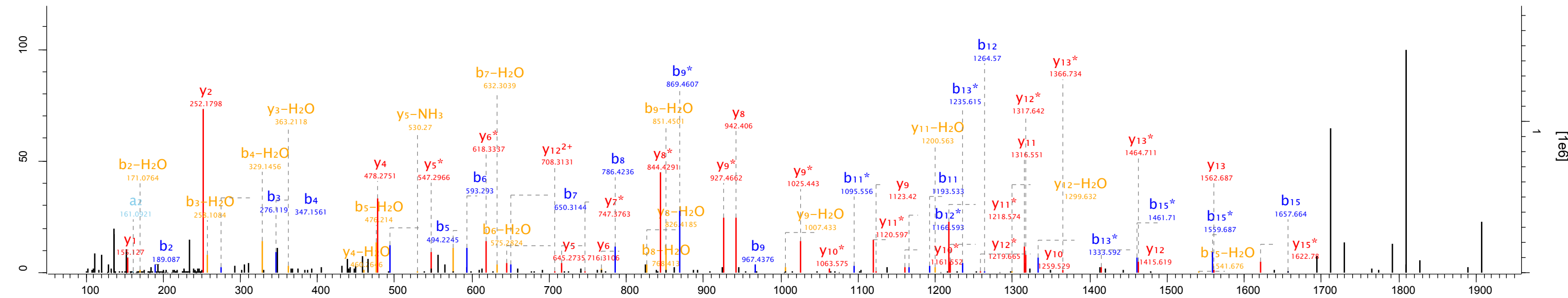


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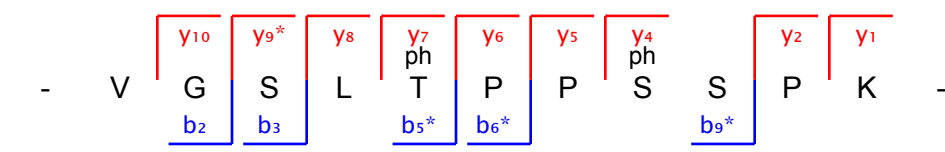
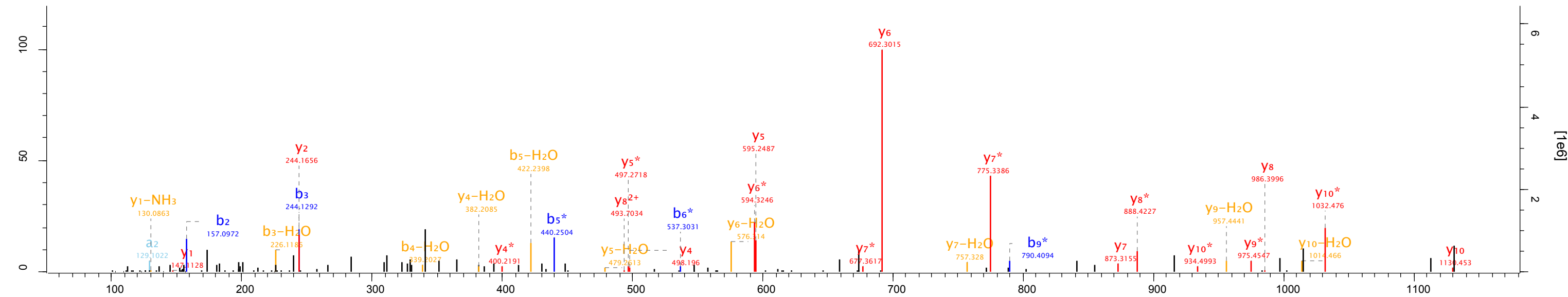
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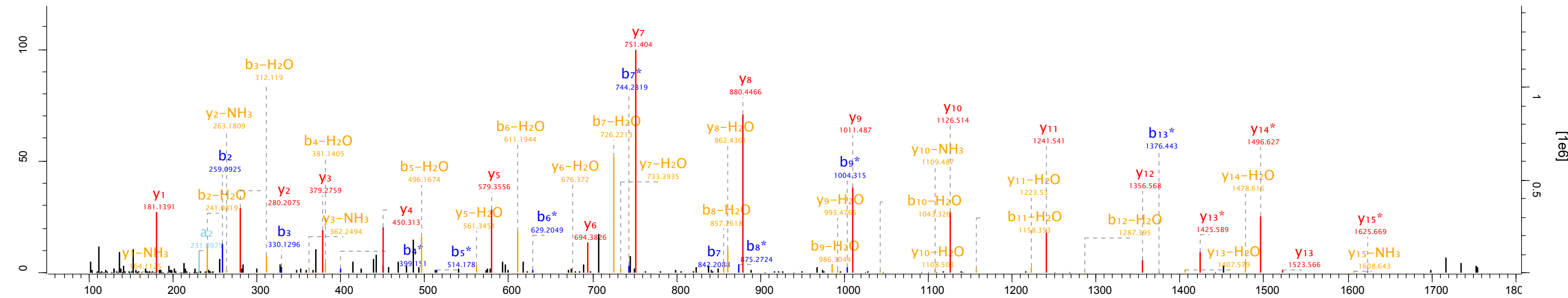




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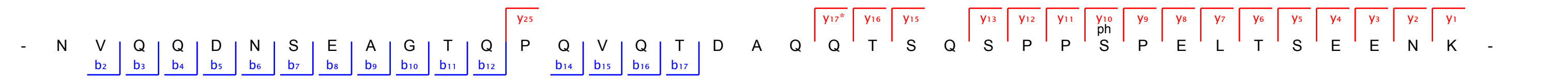
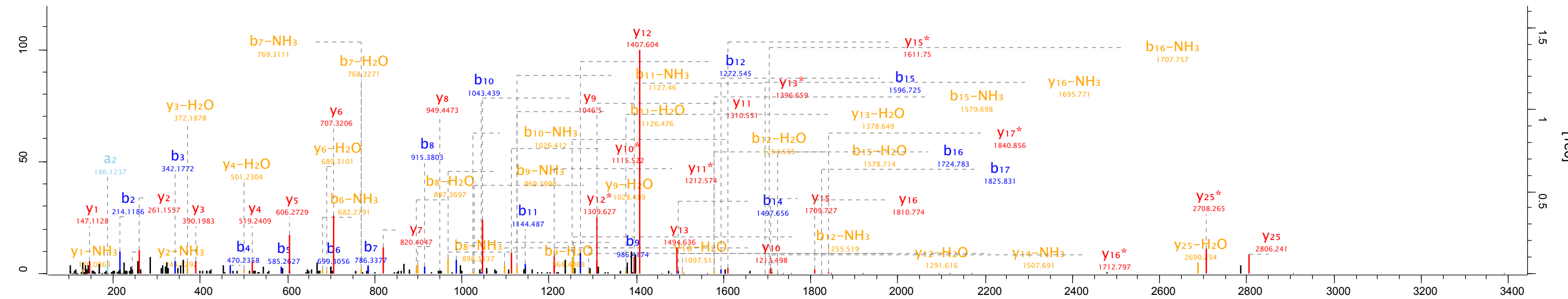


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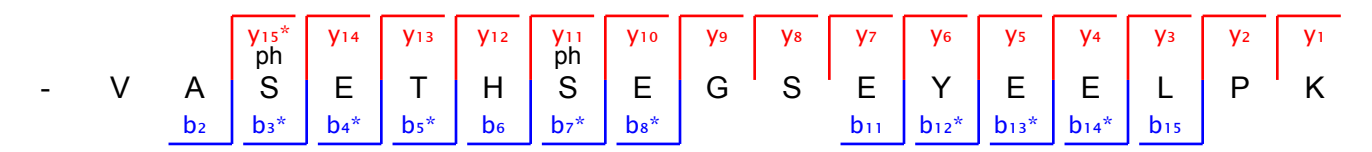
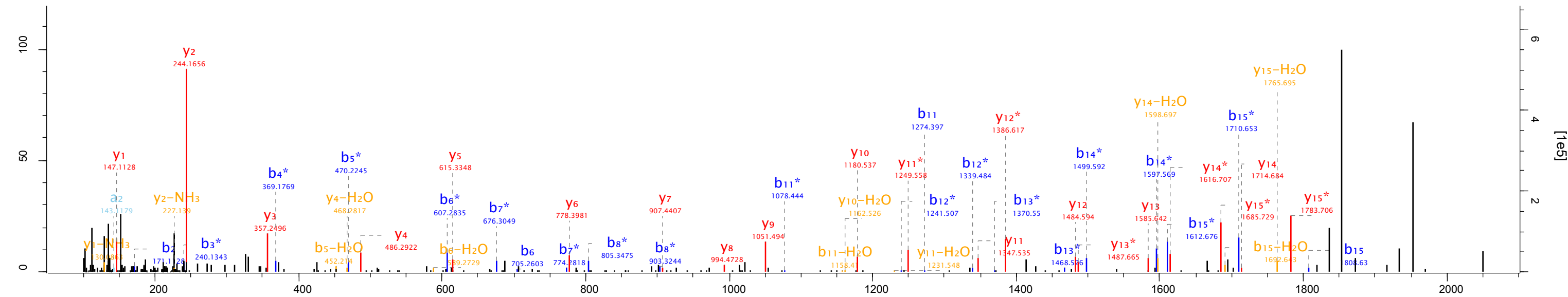


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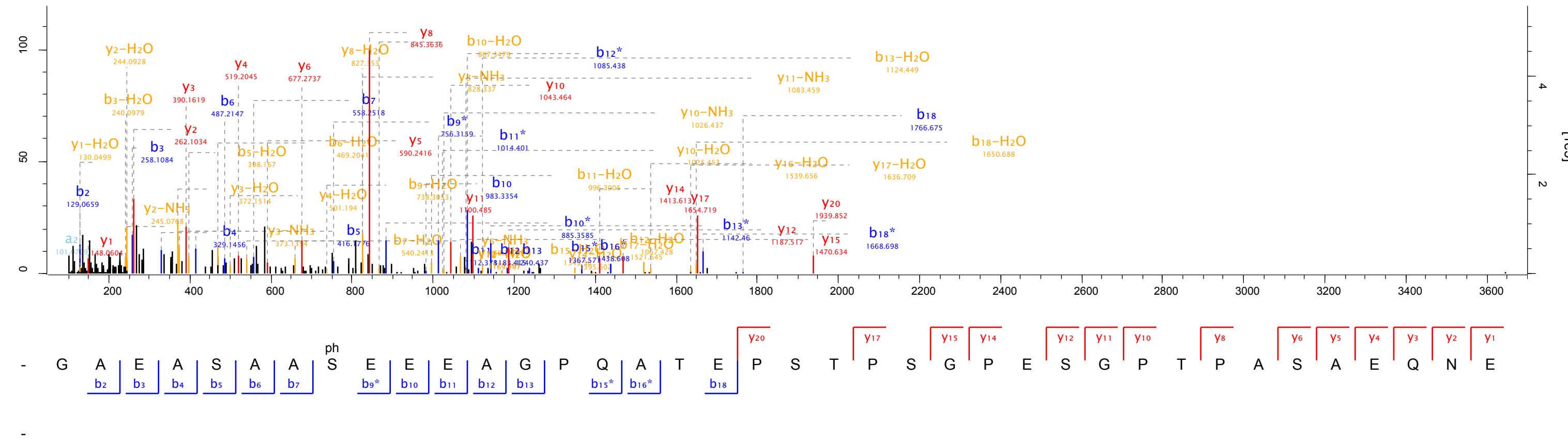
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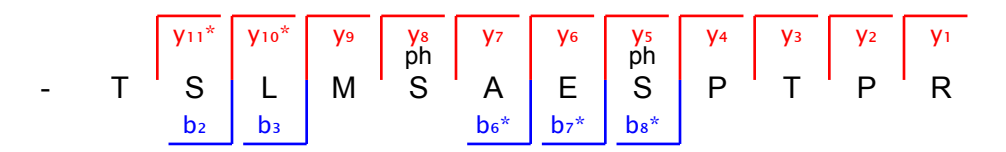
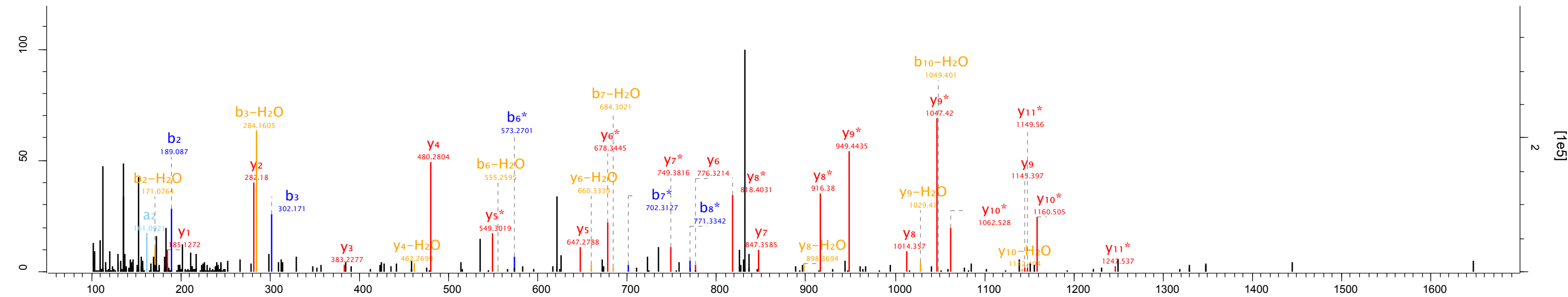
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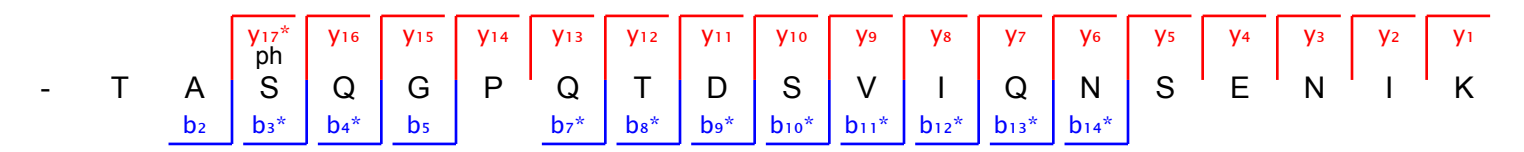
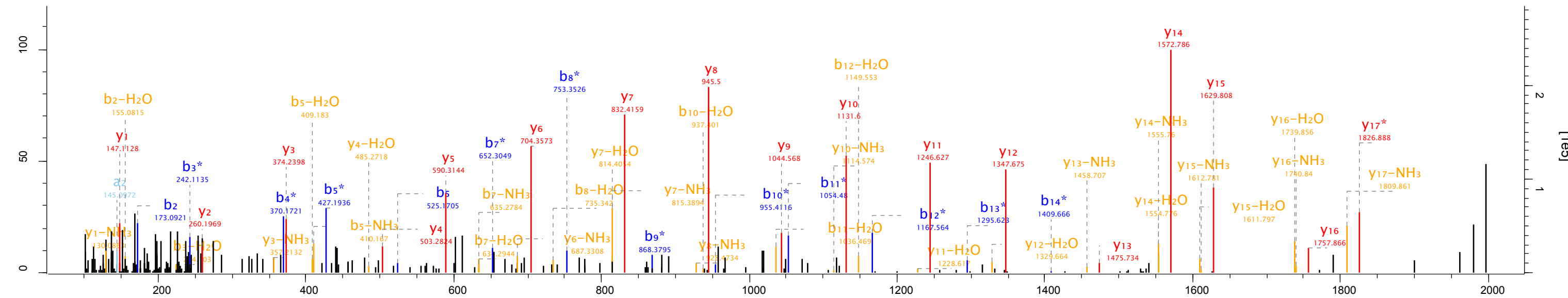
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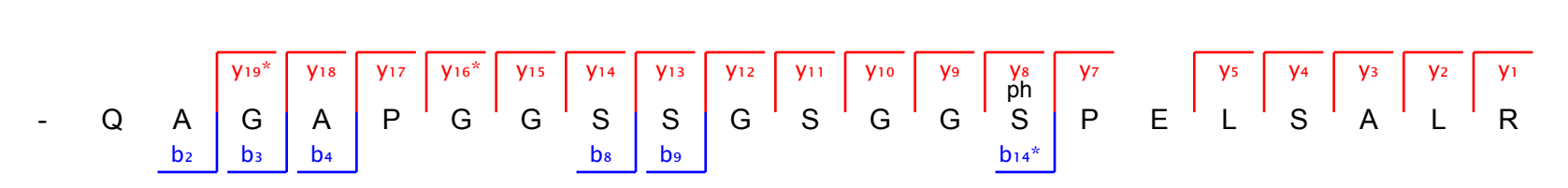
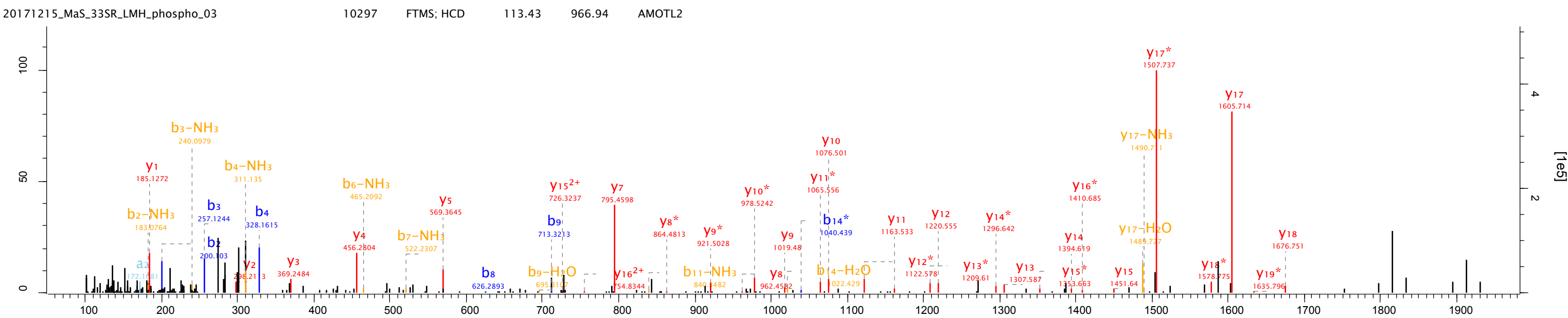
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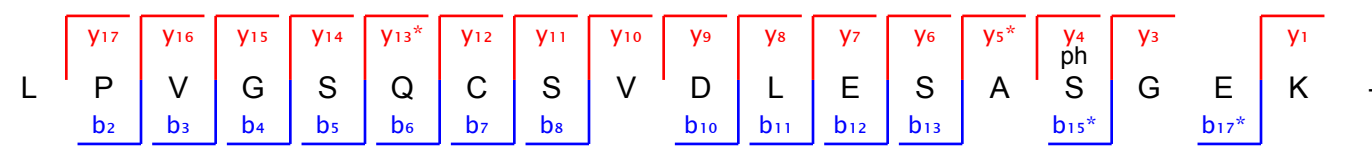
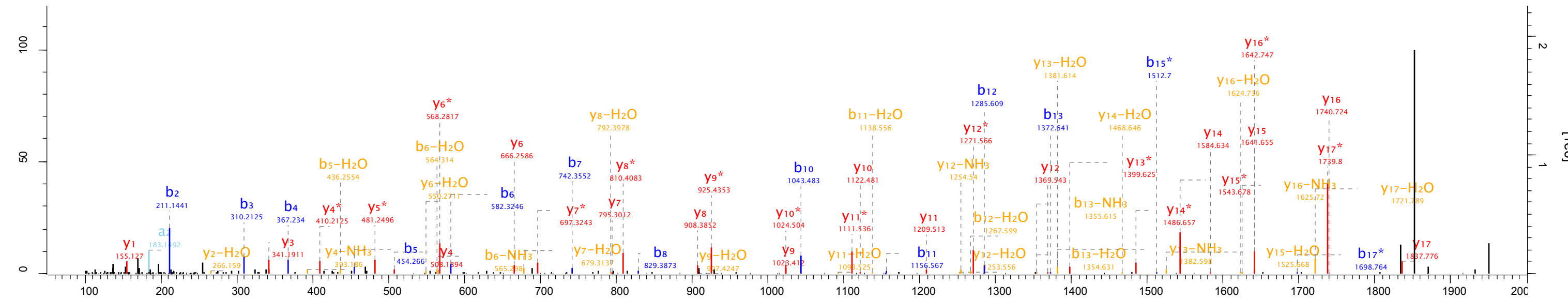
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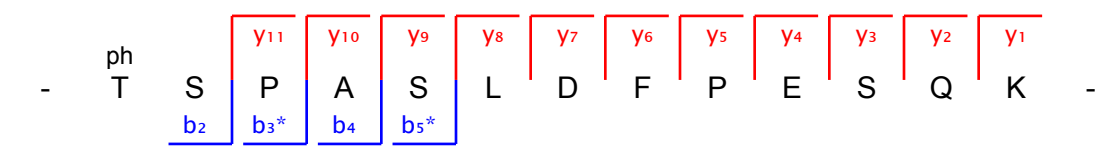
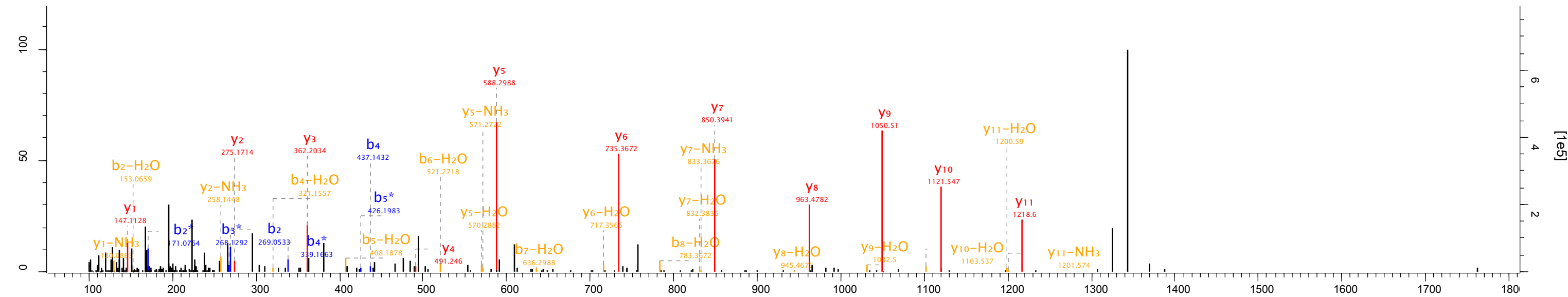
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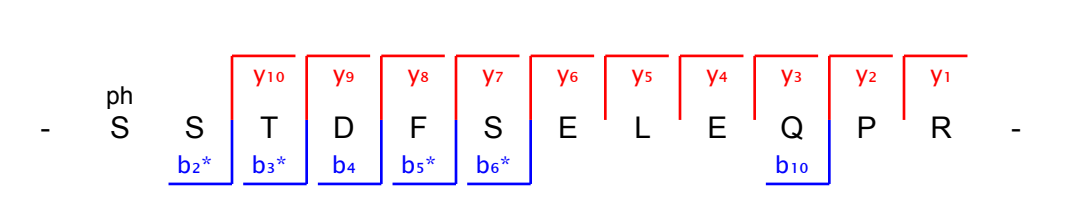
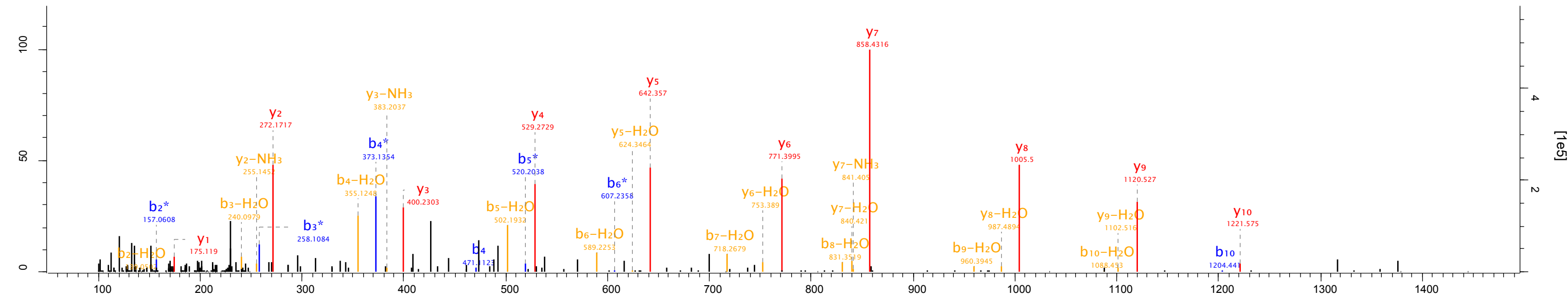
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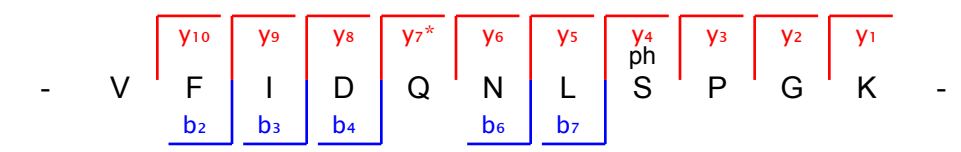
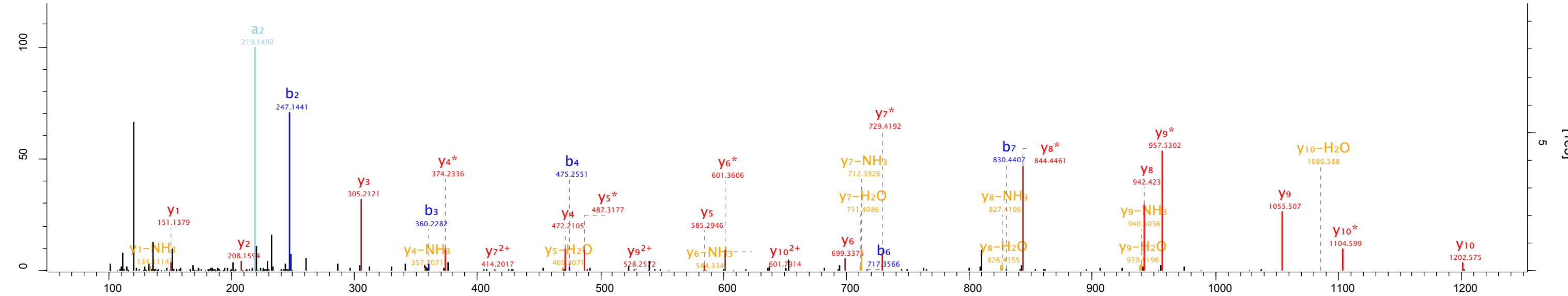
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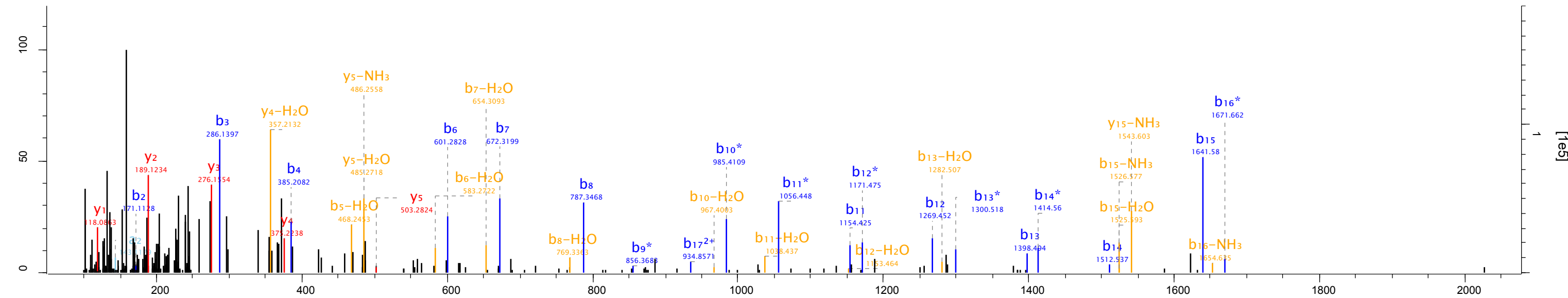
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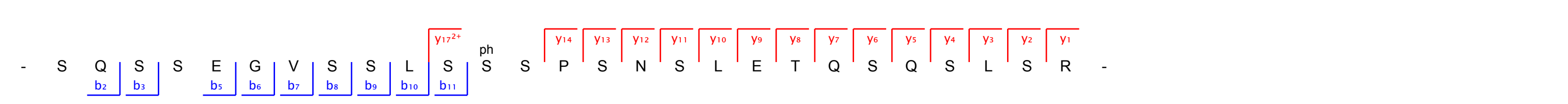
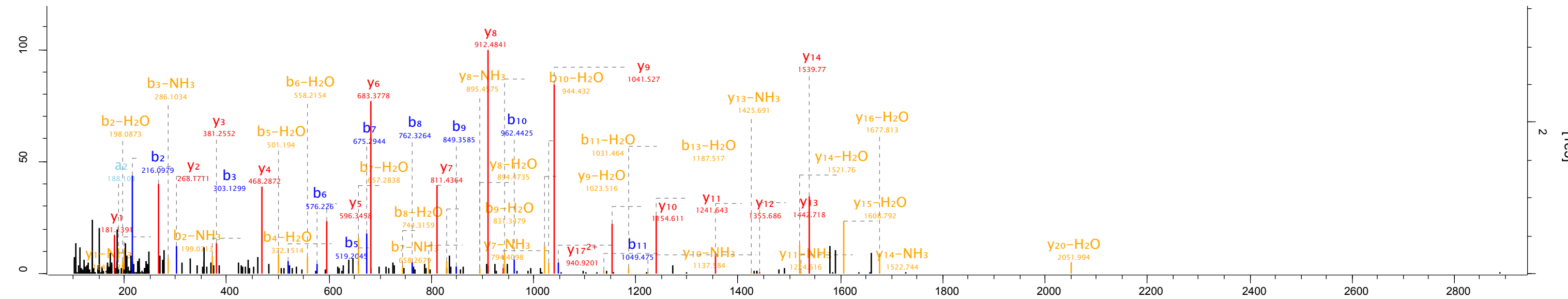
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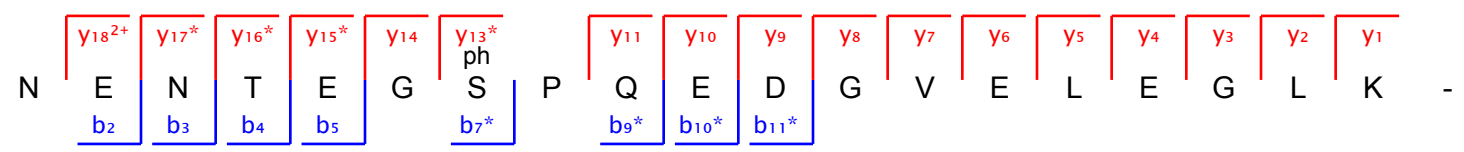
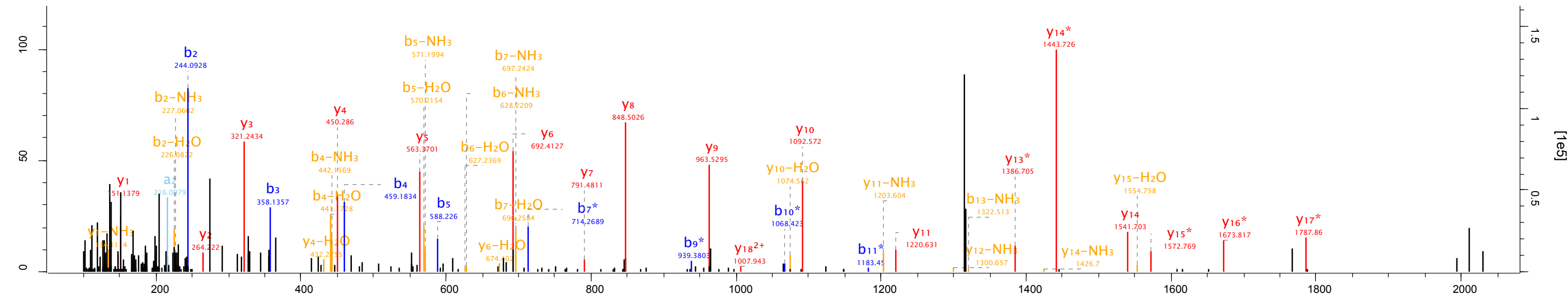
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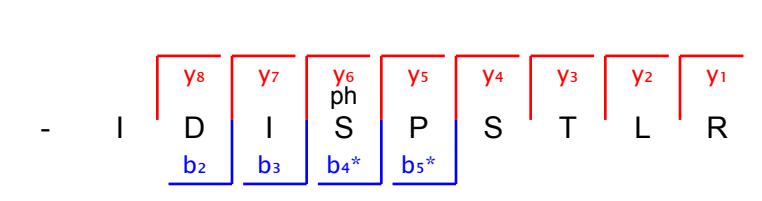
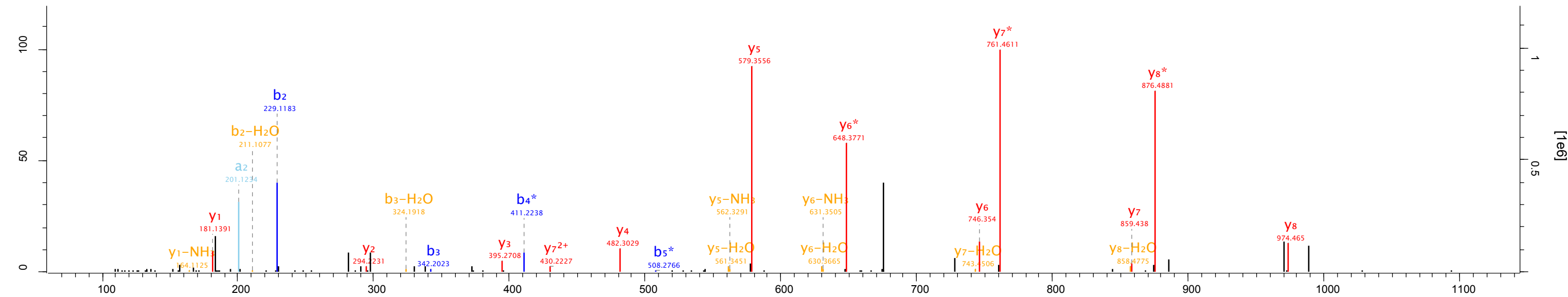
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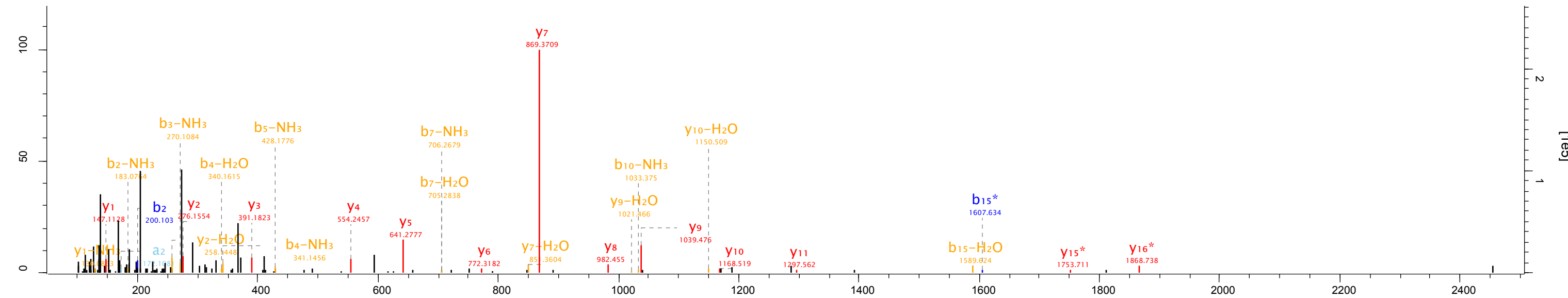
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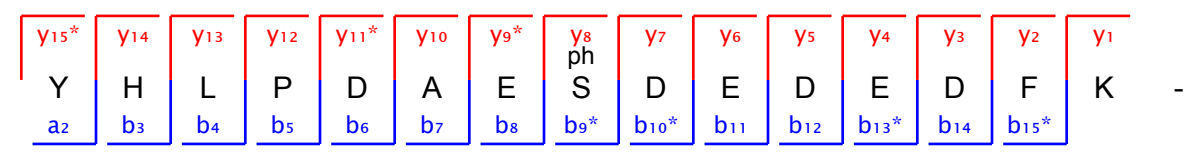
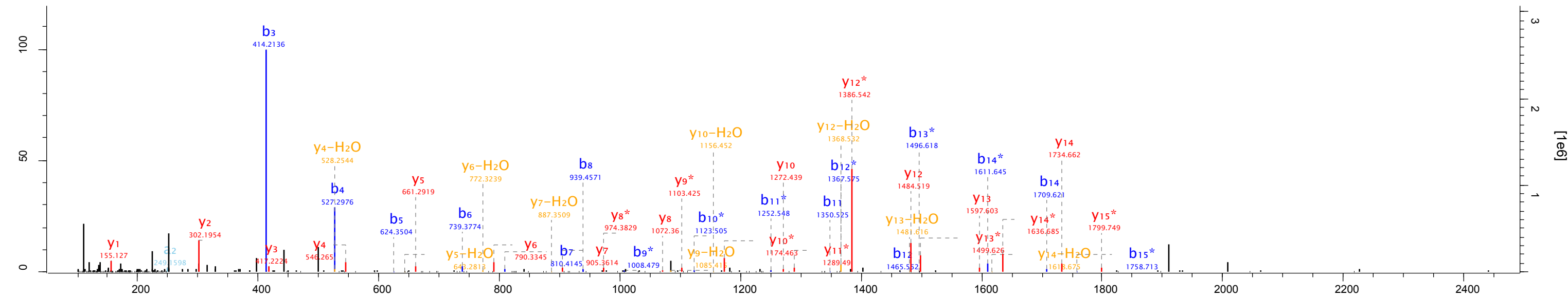
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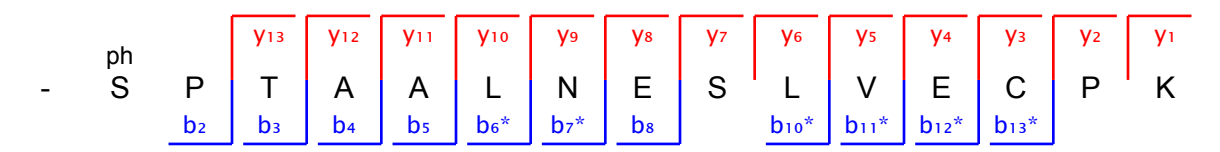
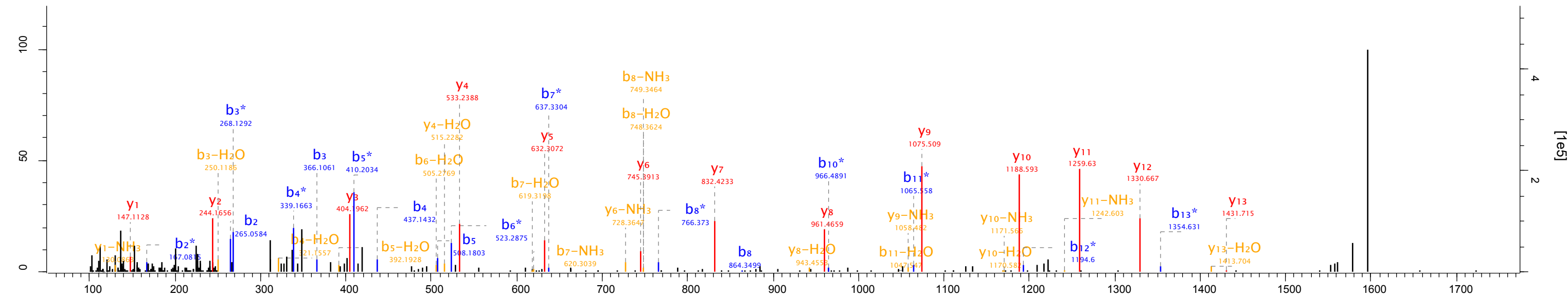
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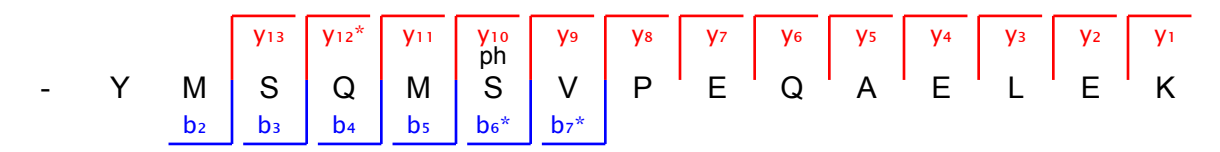
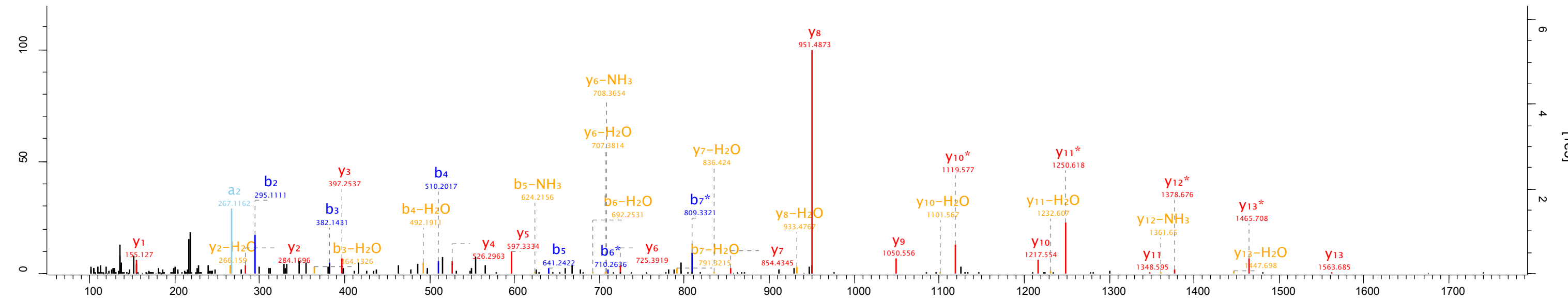
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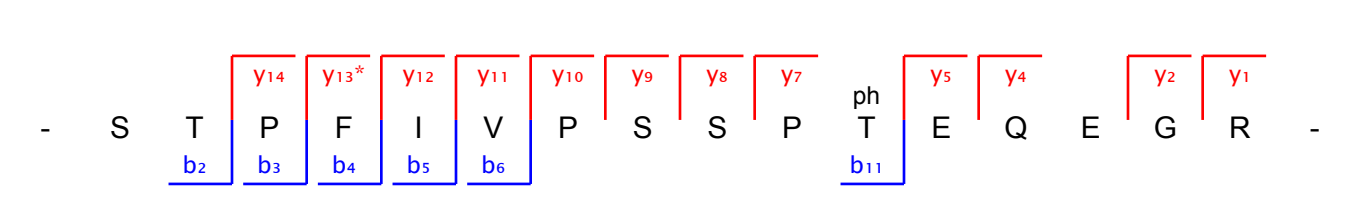
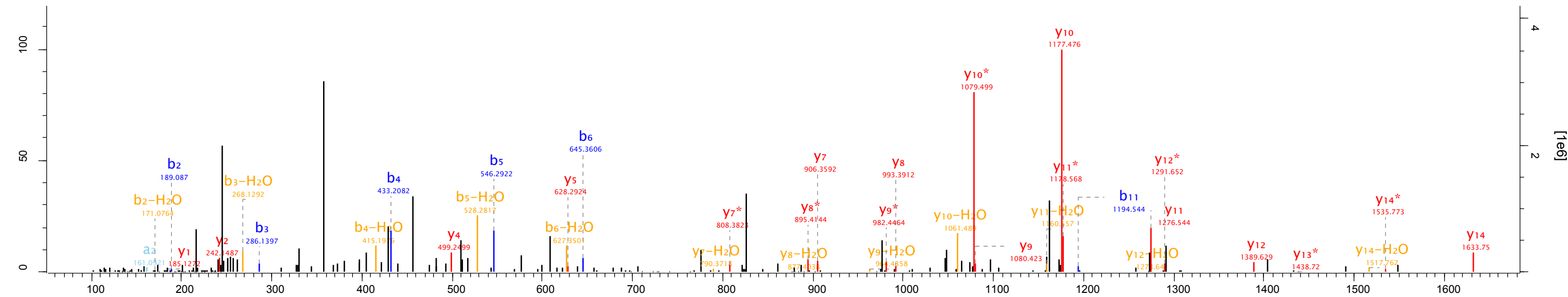
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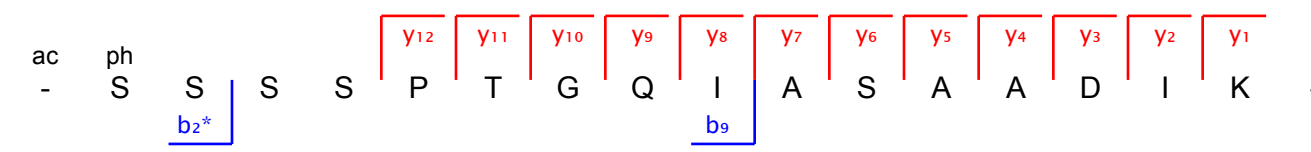
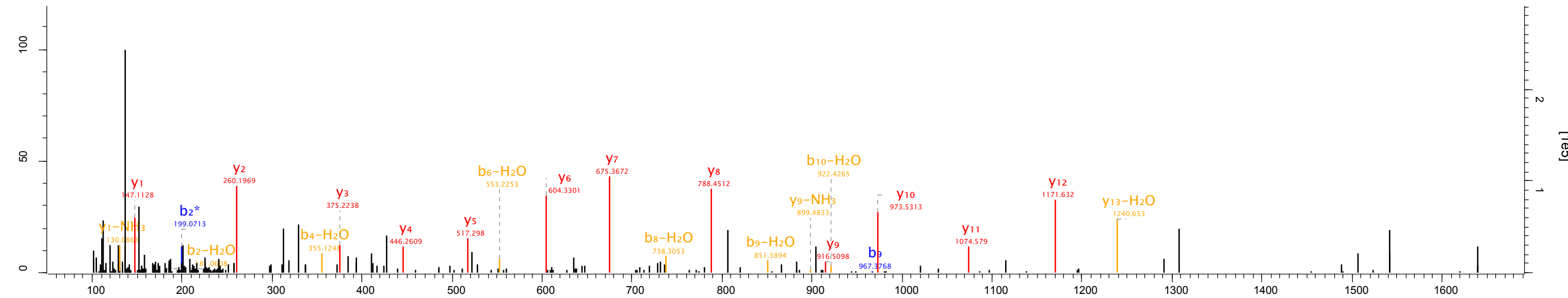
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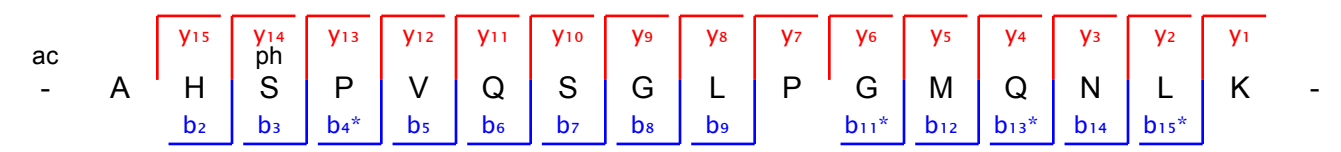
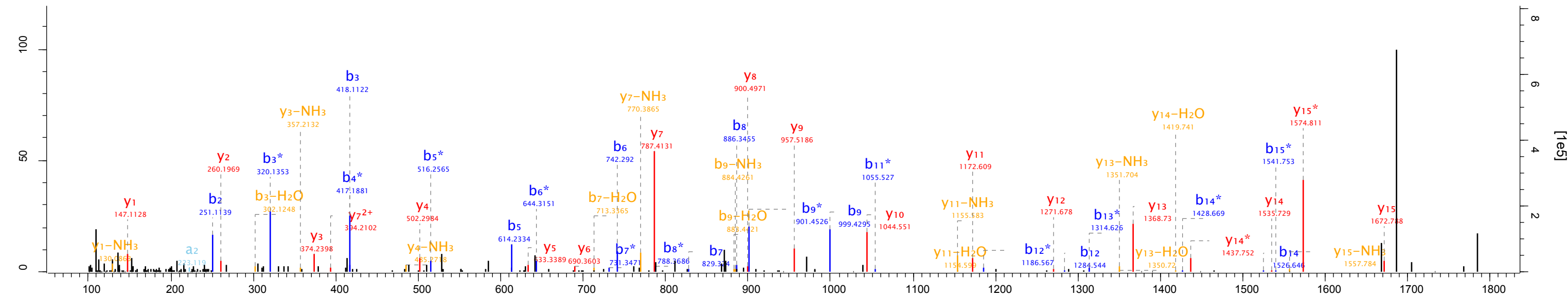
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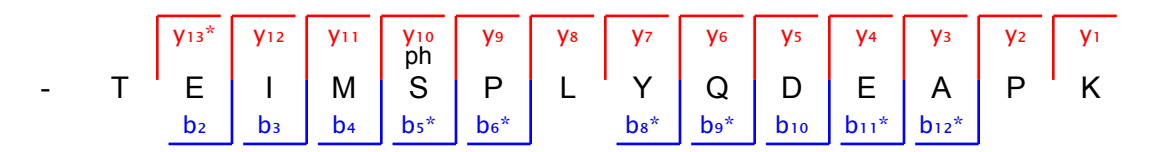
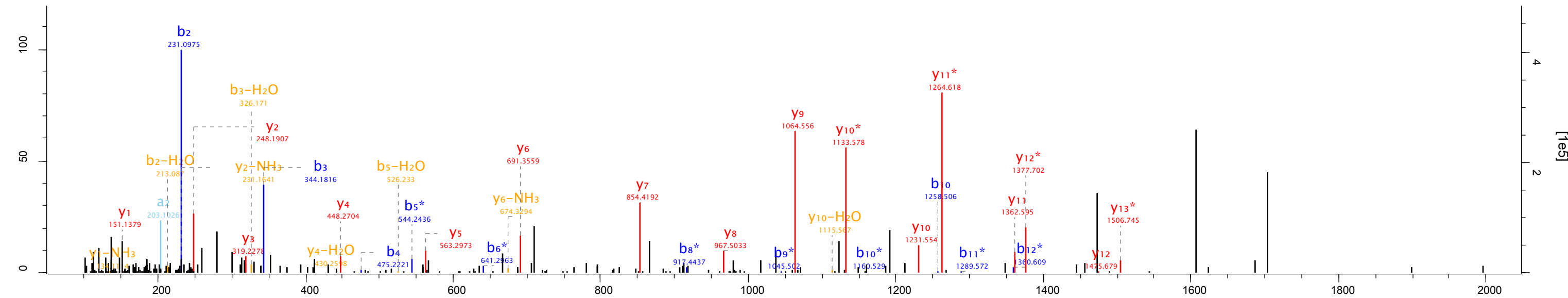
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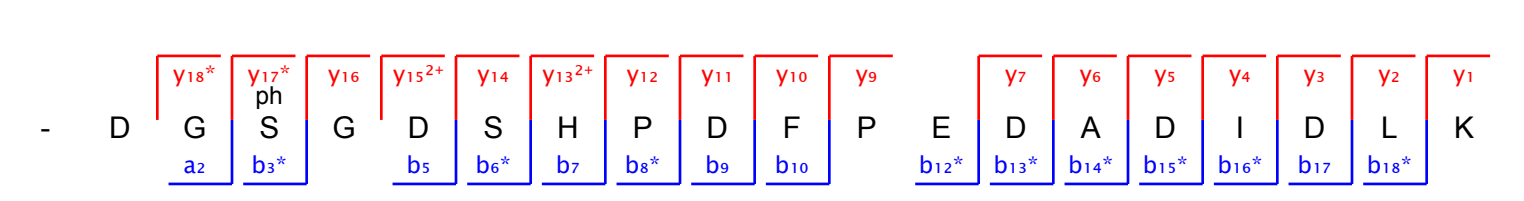
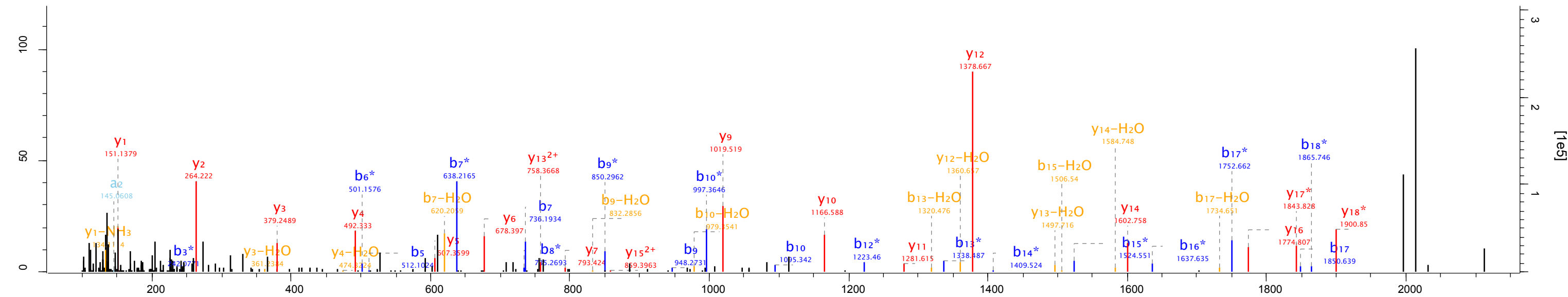
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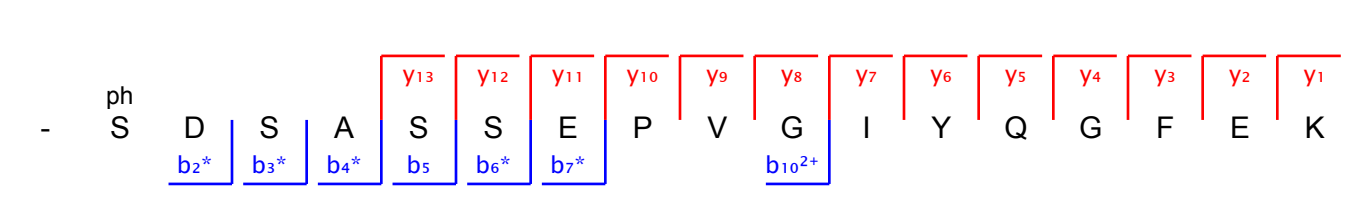
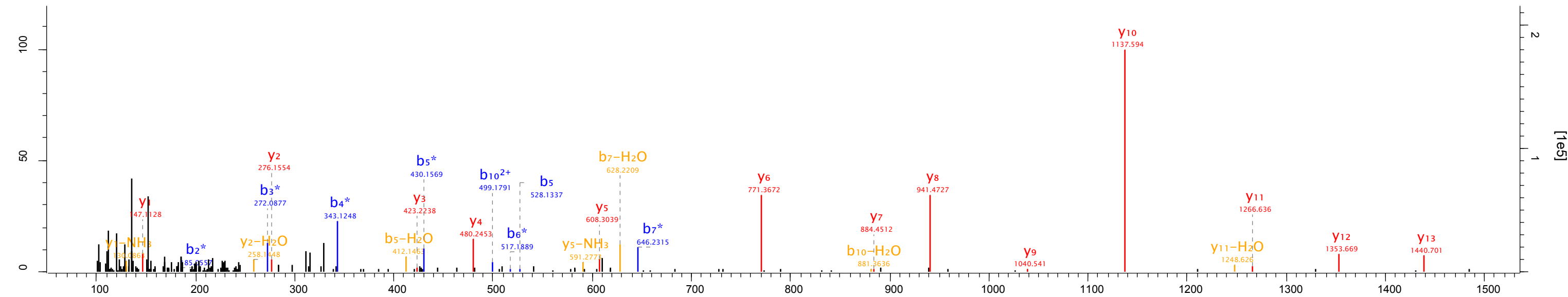
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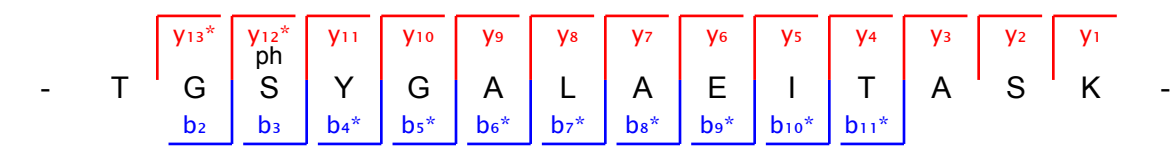
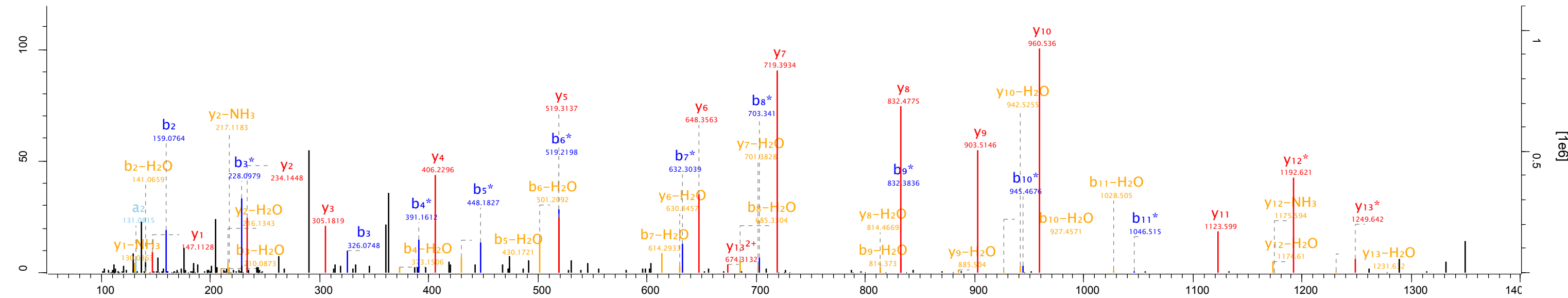
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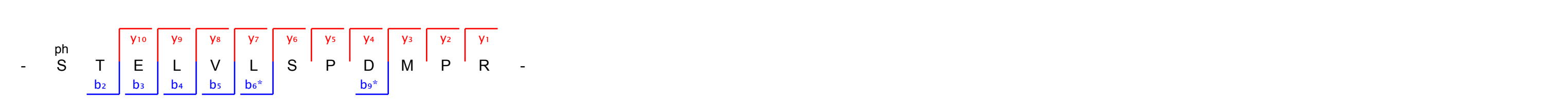
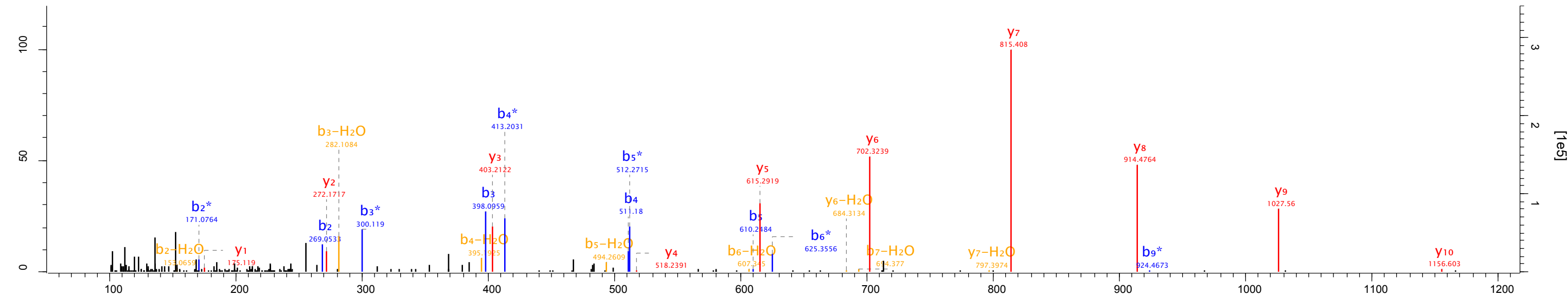
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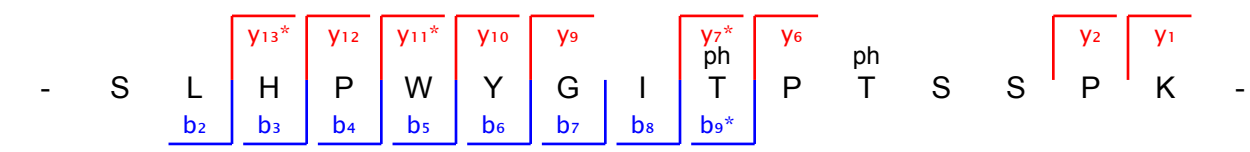
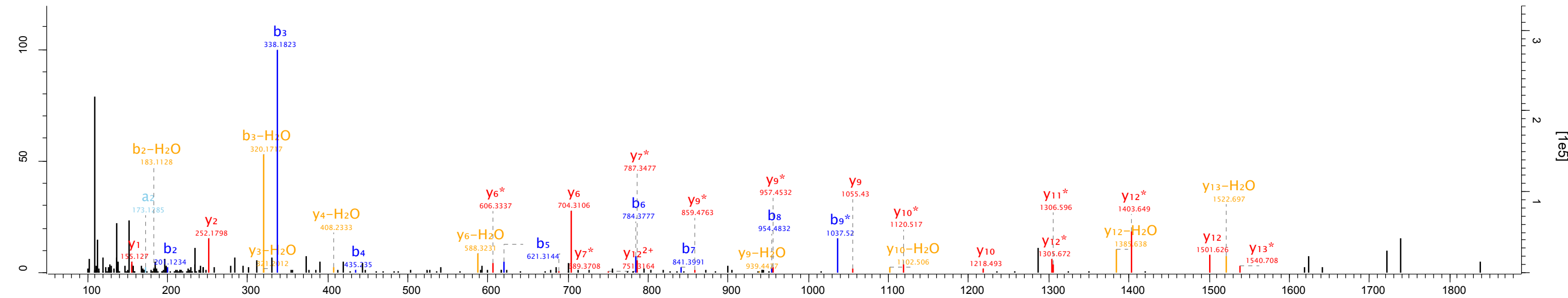
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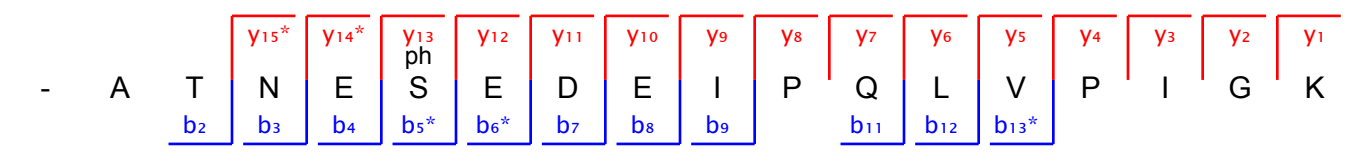
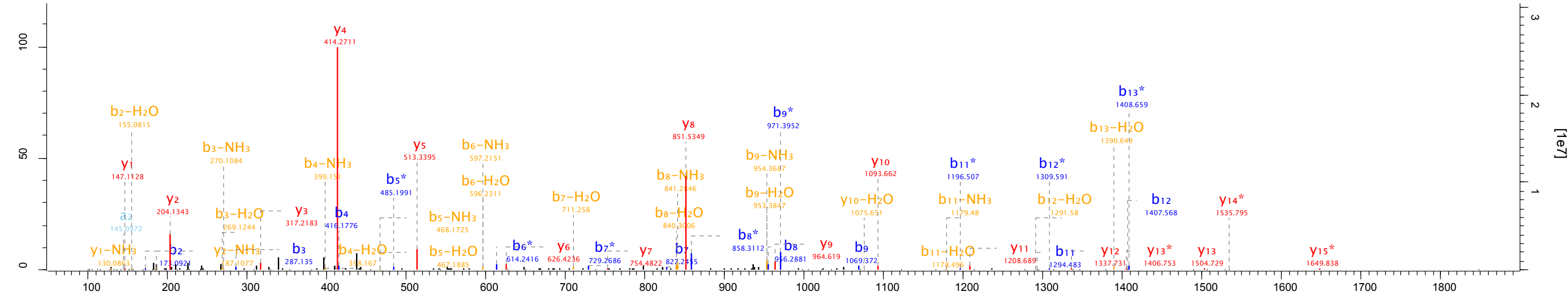
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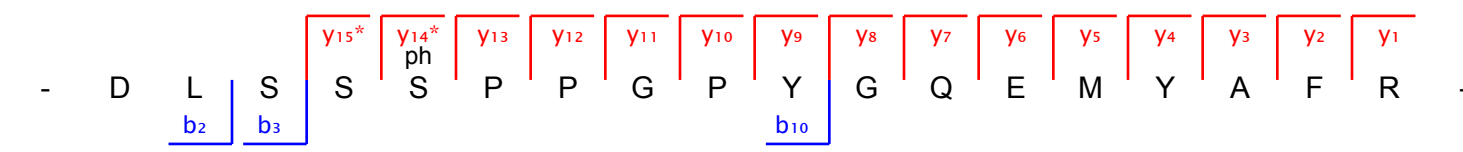
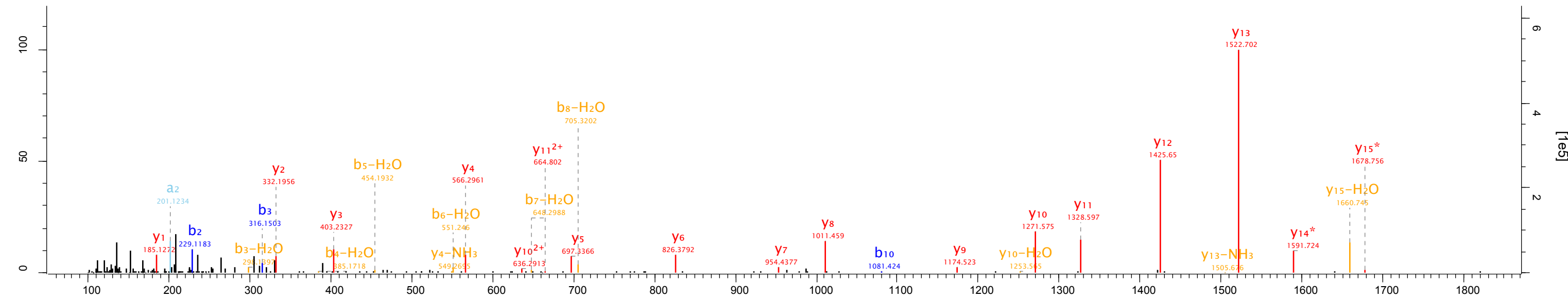
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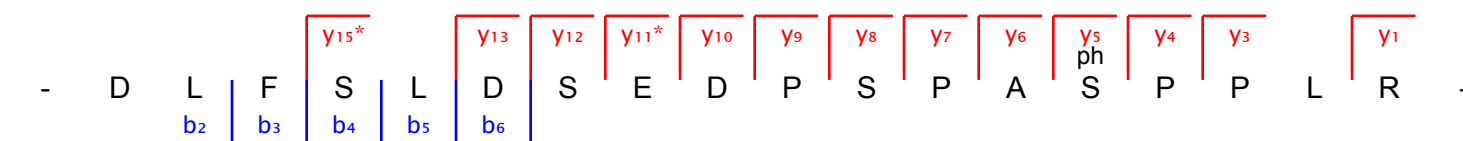
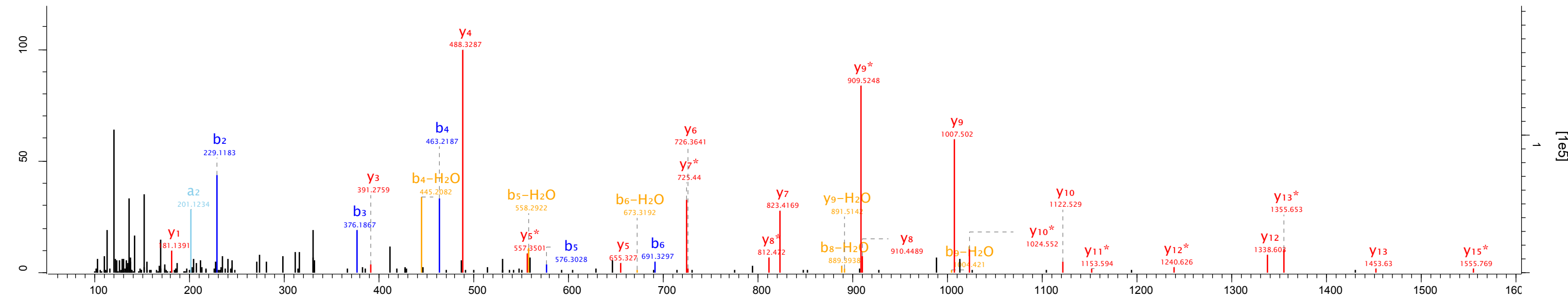
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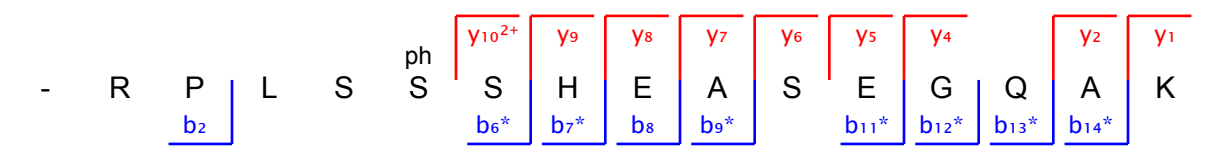
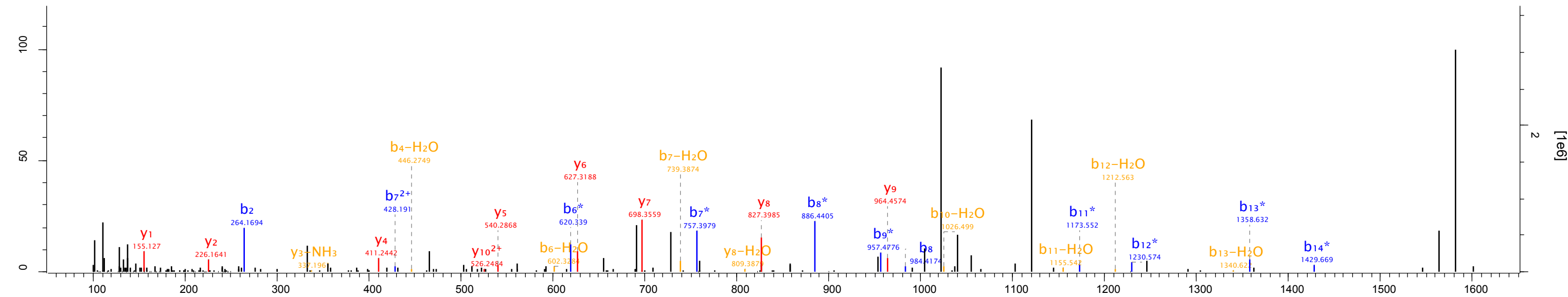
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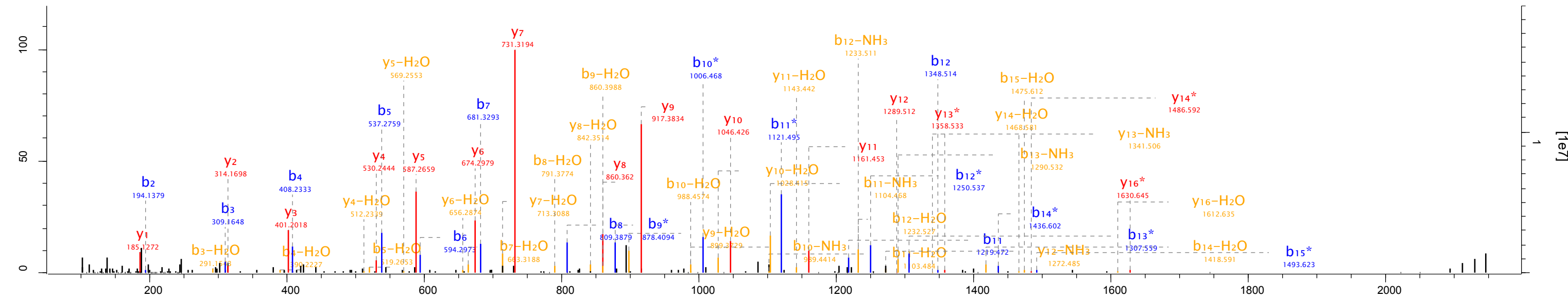
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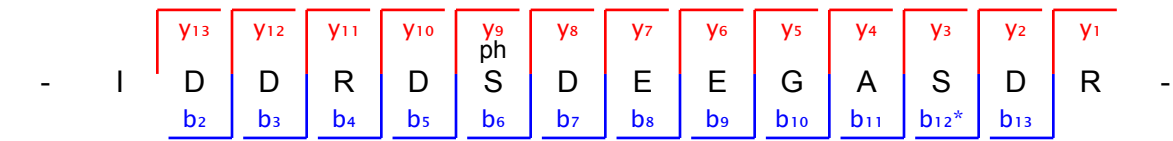
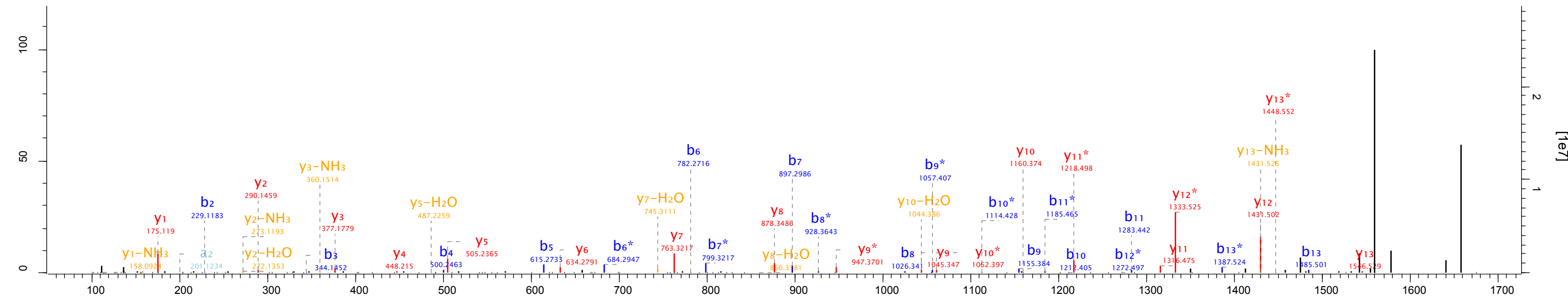


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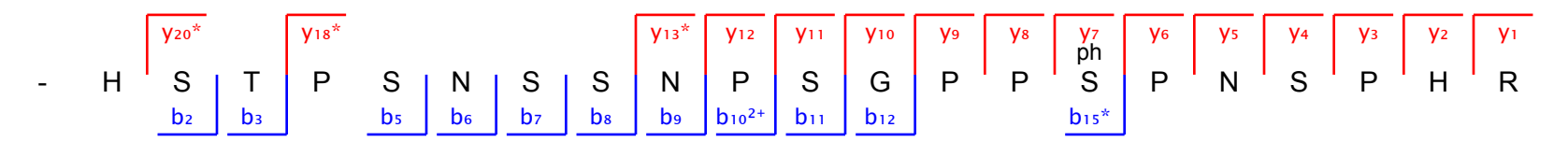
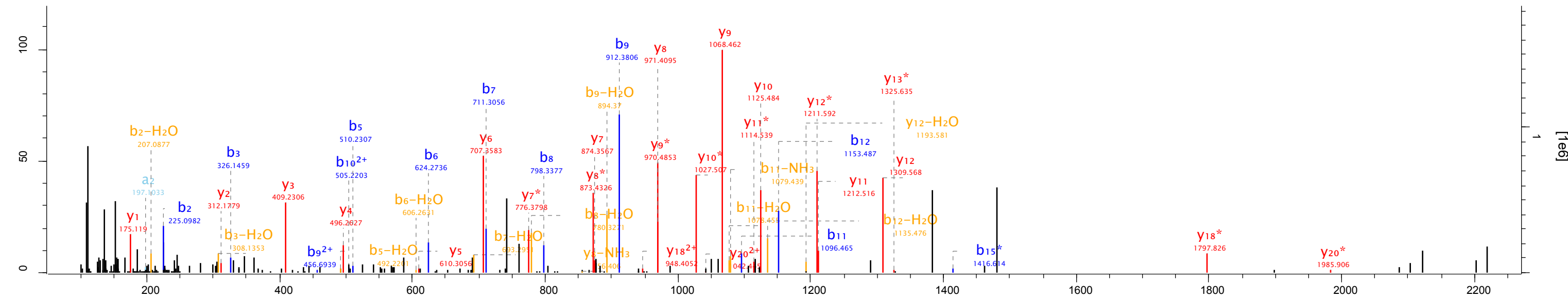
b₂
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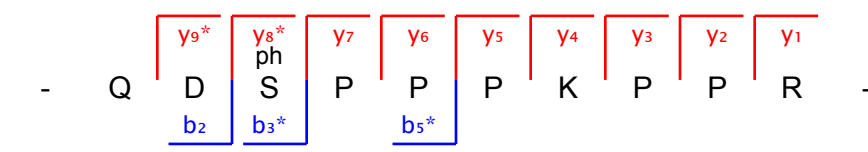
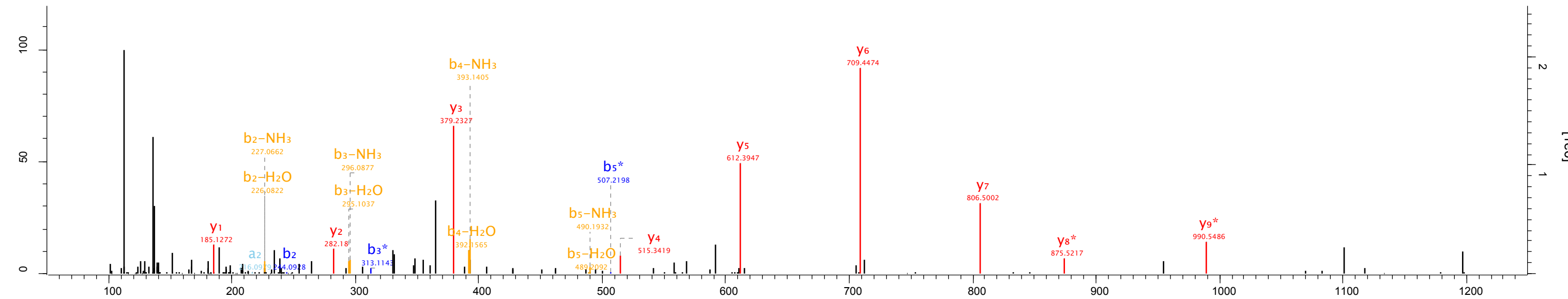
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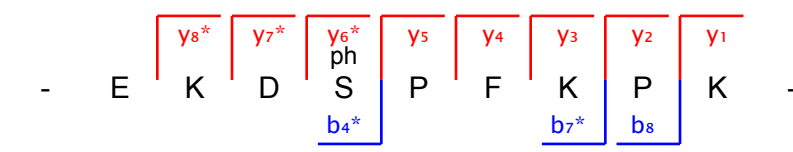
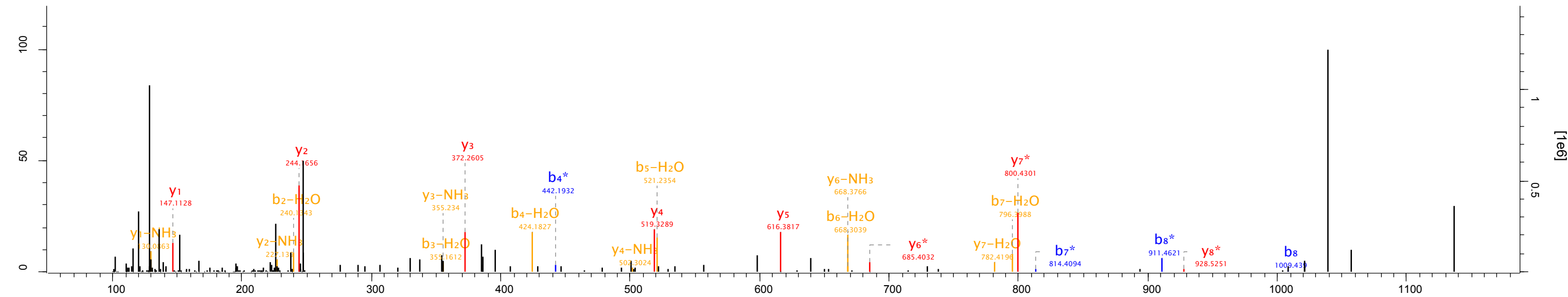
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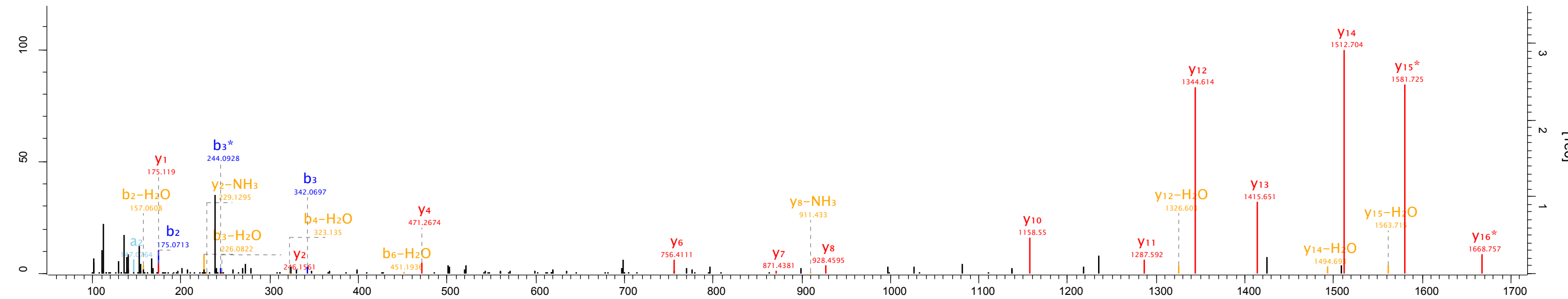
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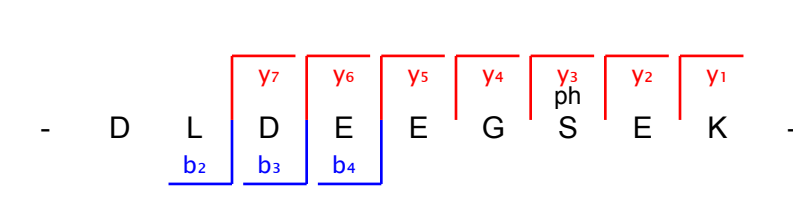
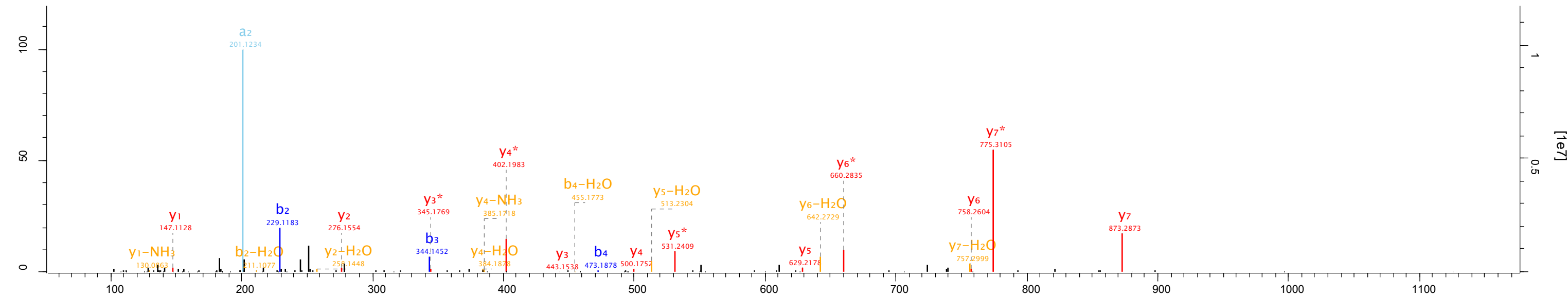
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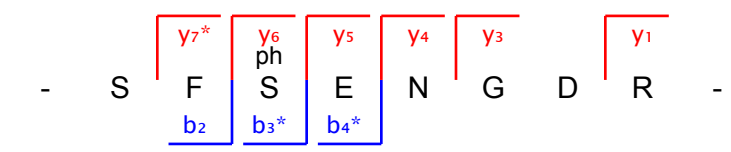
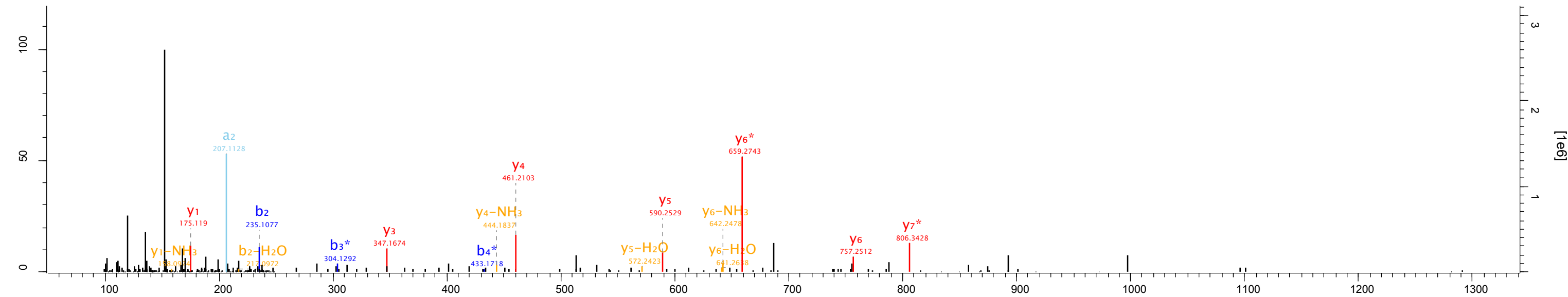
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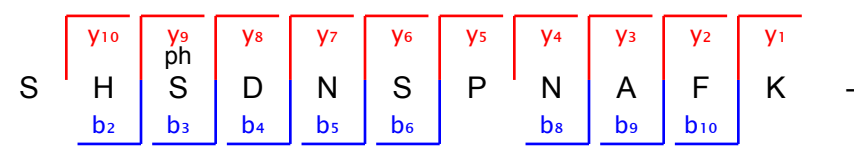
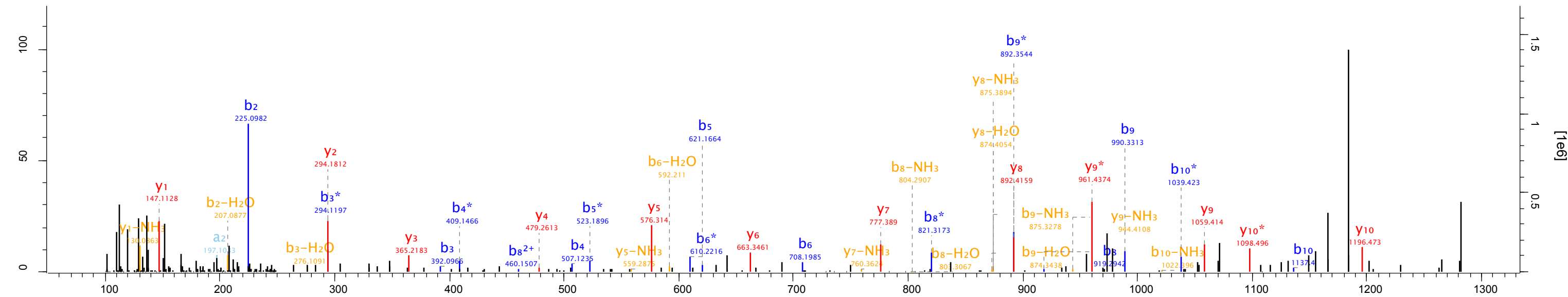
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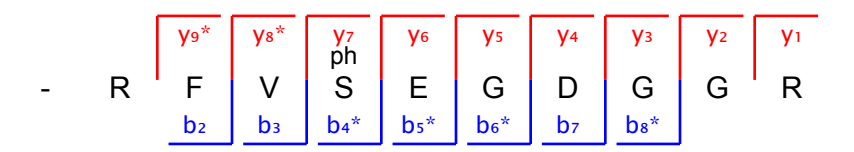
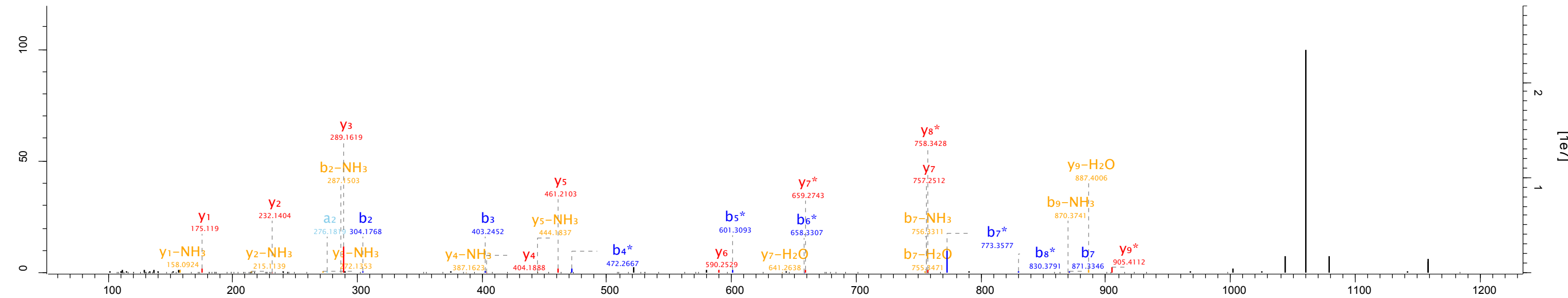
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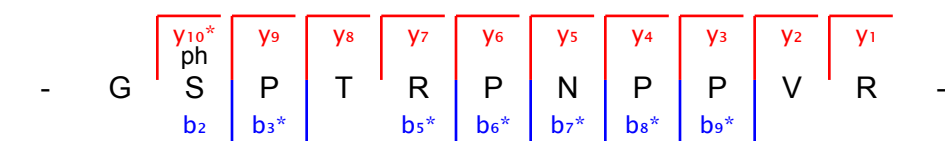
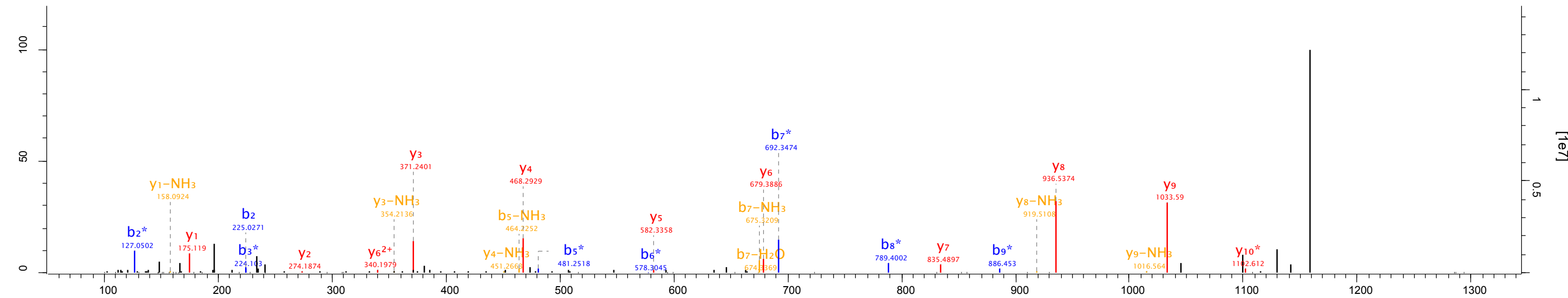
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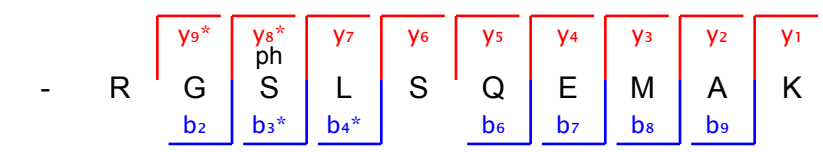
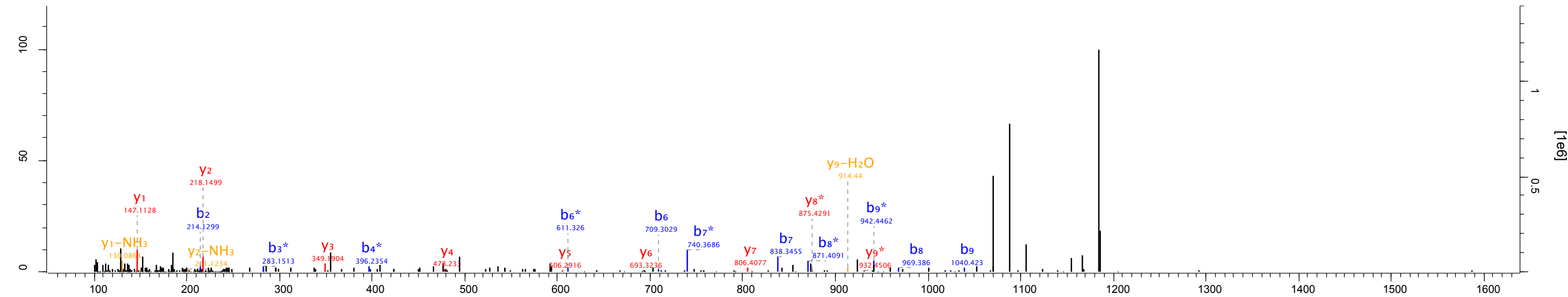
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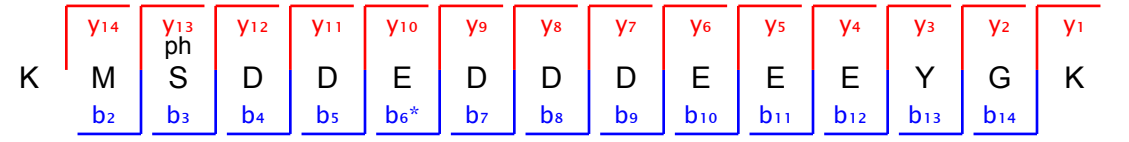
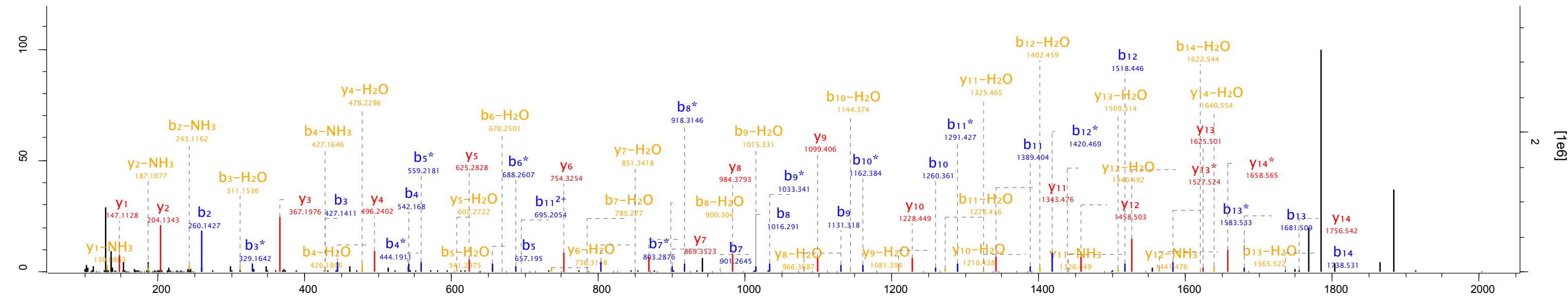
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20171215_MaS_33SR_LMH_phospho_03

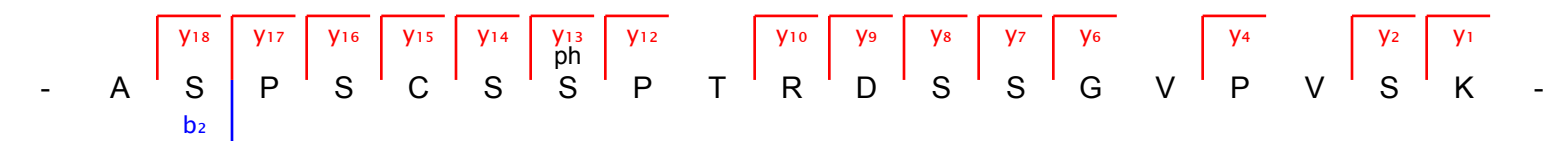
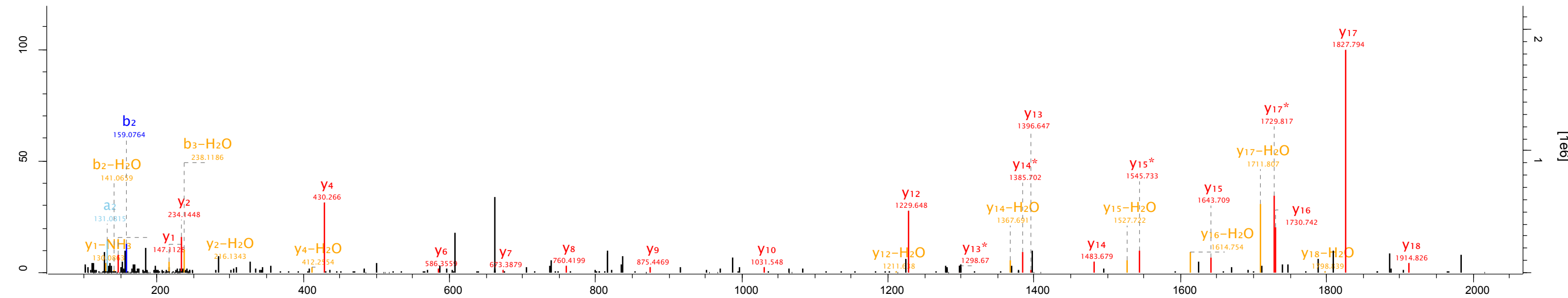
Scan	Method	Score	m/z	Gene names
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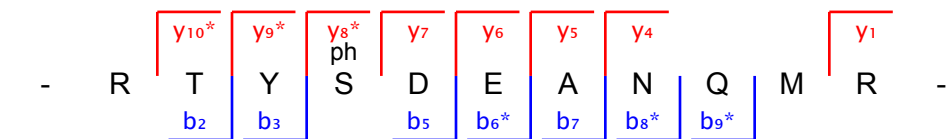
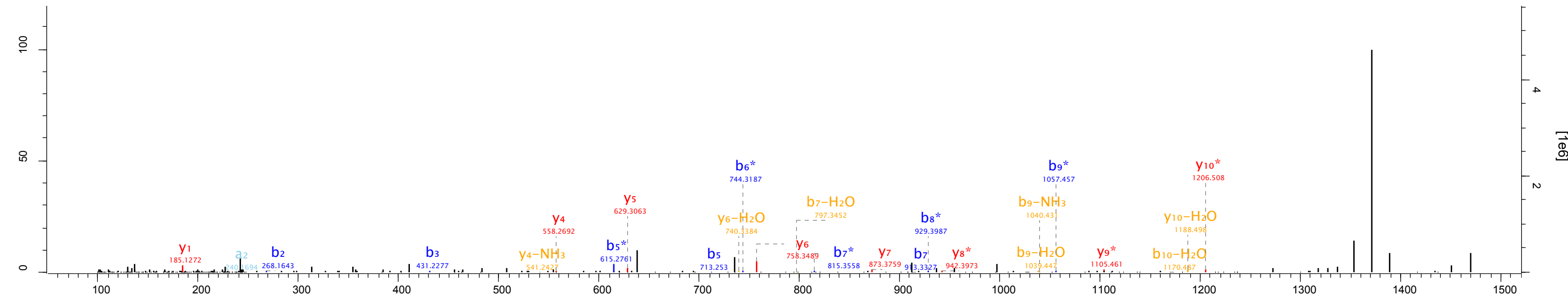


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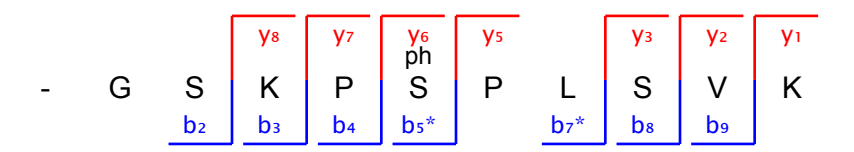
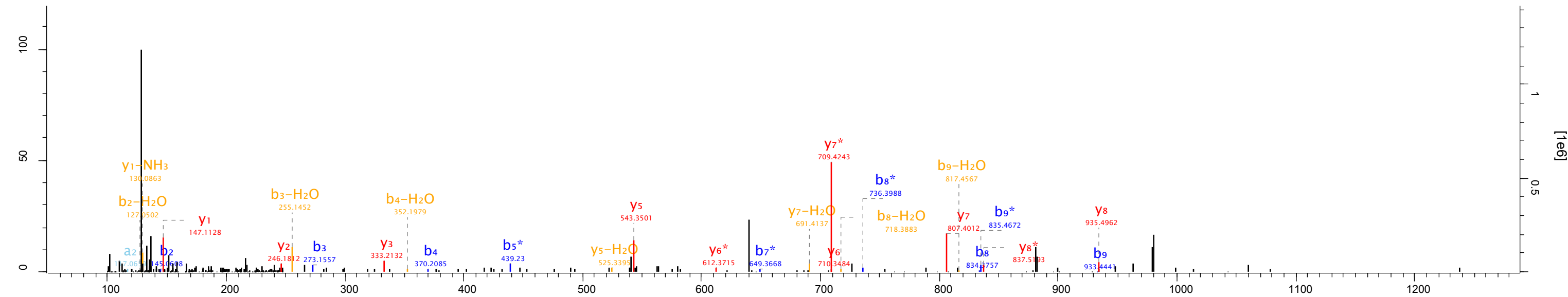


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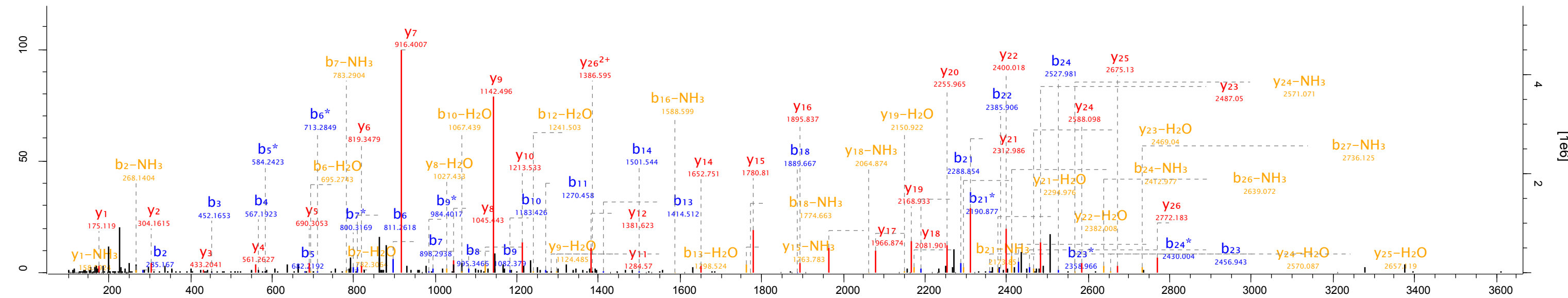




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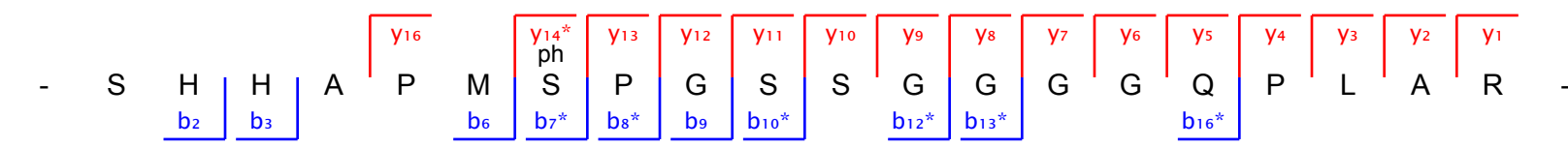
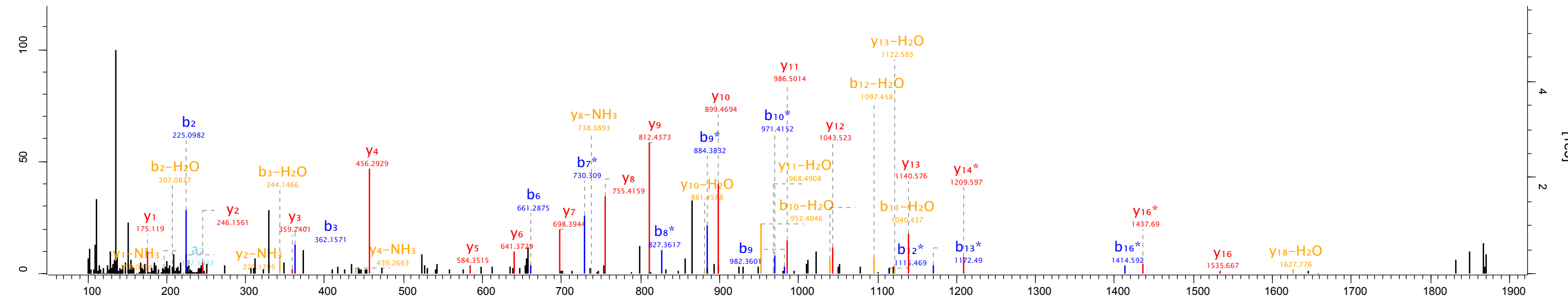
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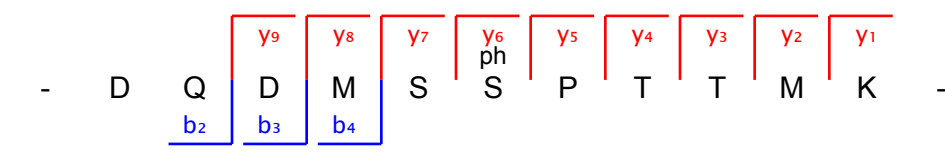
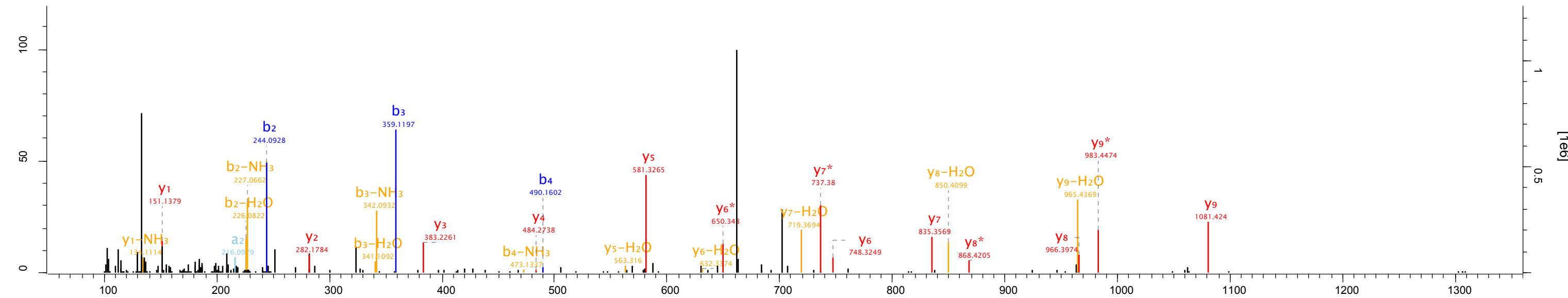
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y1 y2 y3 y4 y5 y6 y7 y8 y9 y10 y11 y12 y13 y14 y15 y16 y17 y18 y19 y20 y21 y22 y23 y24 y25 y26 y27 y28 y29 y30 y31 y32 y33 y34 y35 y36 y37 y38 y39 y40 y41 y42 y43 y44 y45 y46 y47 y48 y49 y50 y51 y52 y53 y54 y55 y56 y57 y58 y59 y60 y61 y62 y63 y64 y65 y66 y67 y68 y69 y70 y71 y72 y73 y74 y75 y76 y77 y78 y79 y80 y81 y82 y83 y84 y85 y86 y87 y88 y89 y90 y91 y92 y93 y94 y95 y96 y97 y98 y99 y100

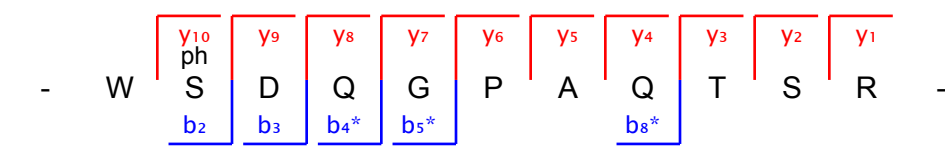
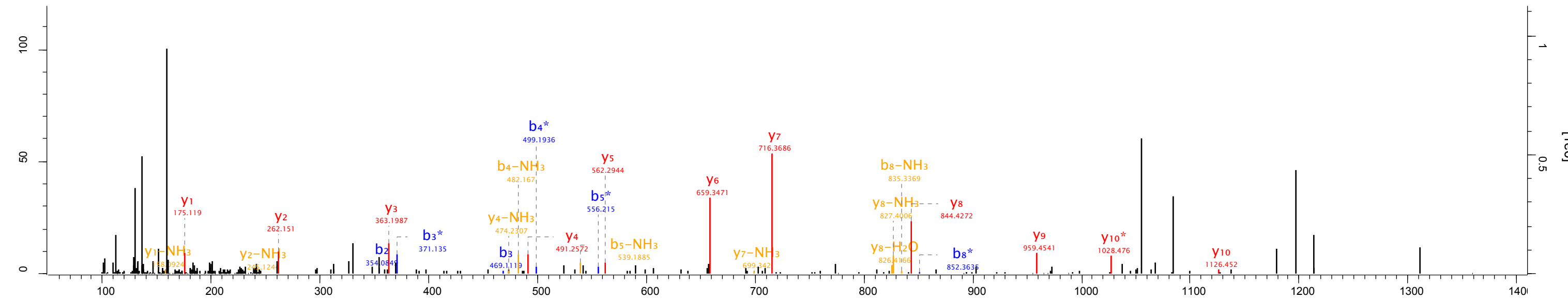
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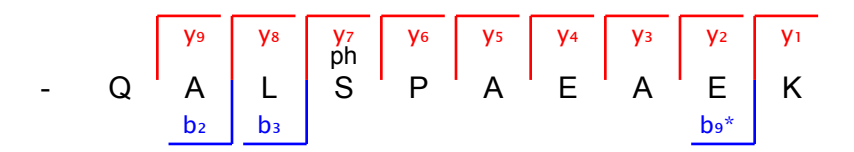
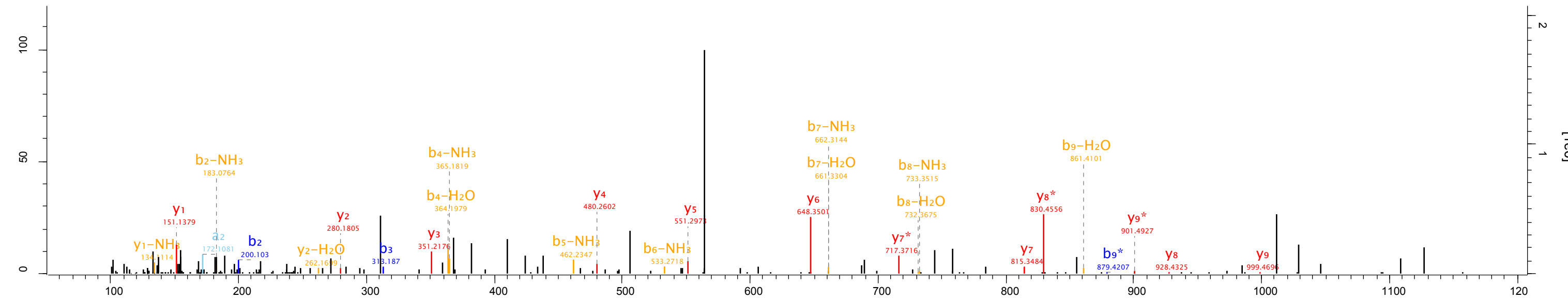
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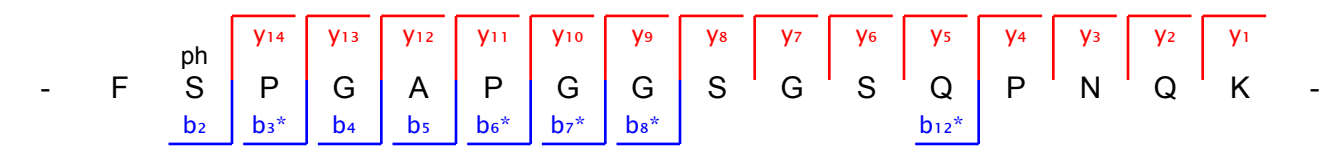
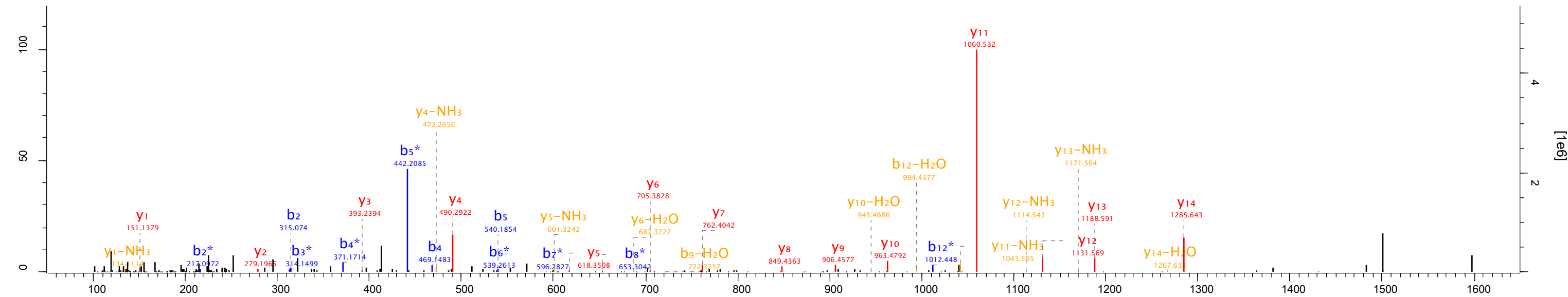
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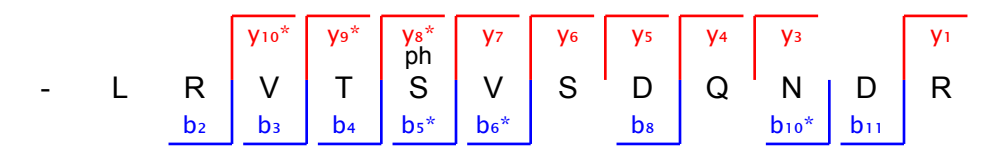
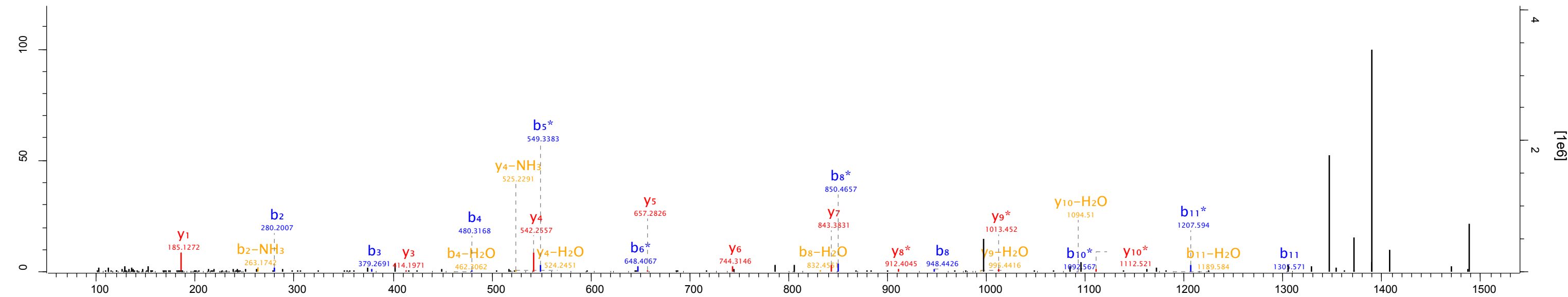
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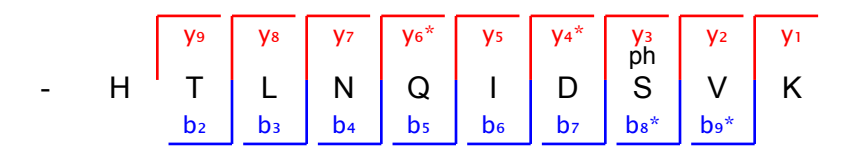
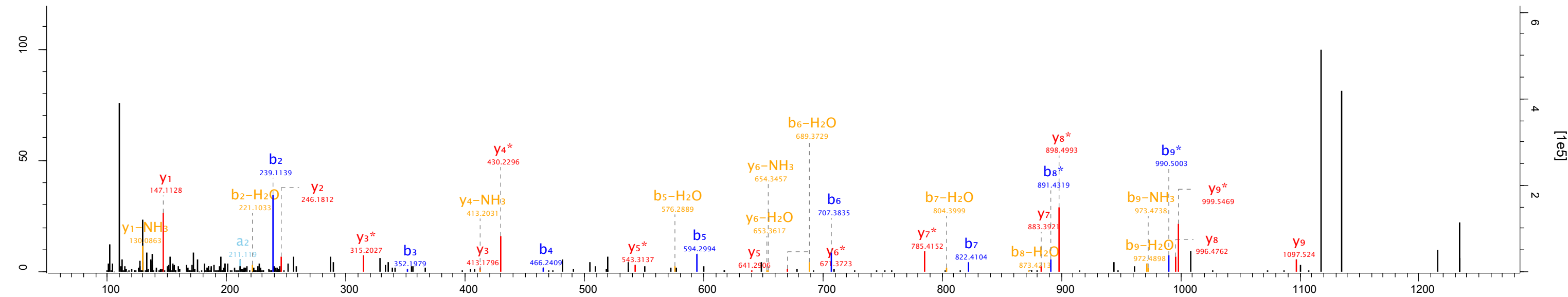
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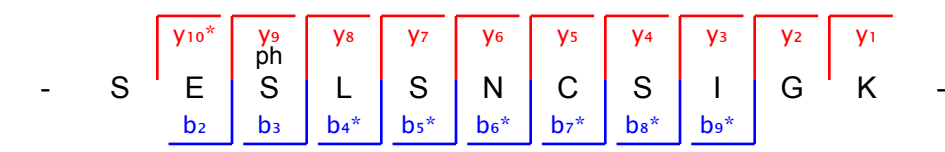
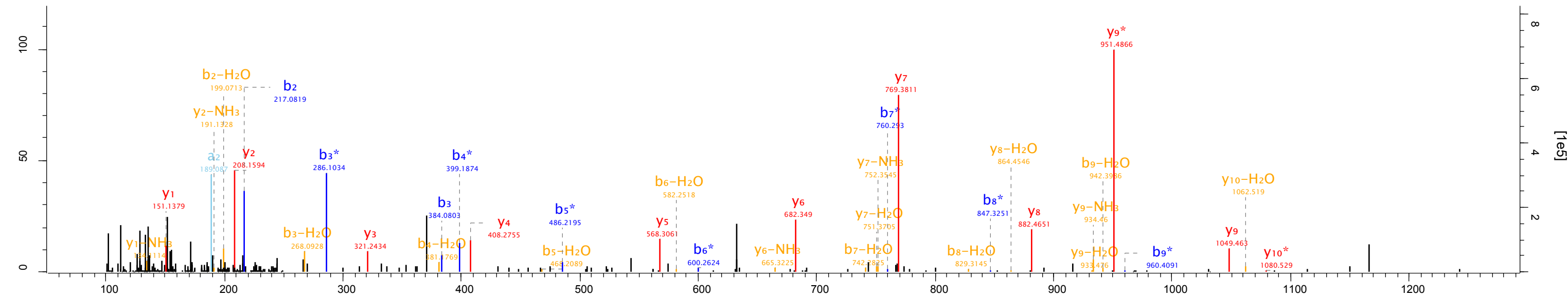
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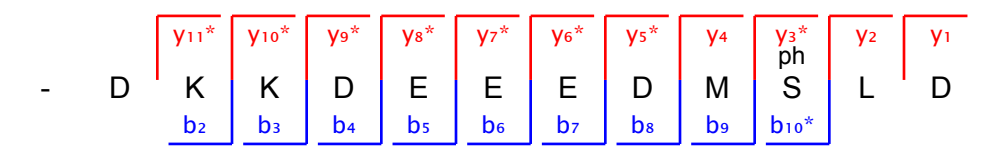
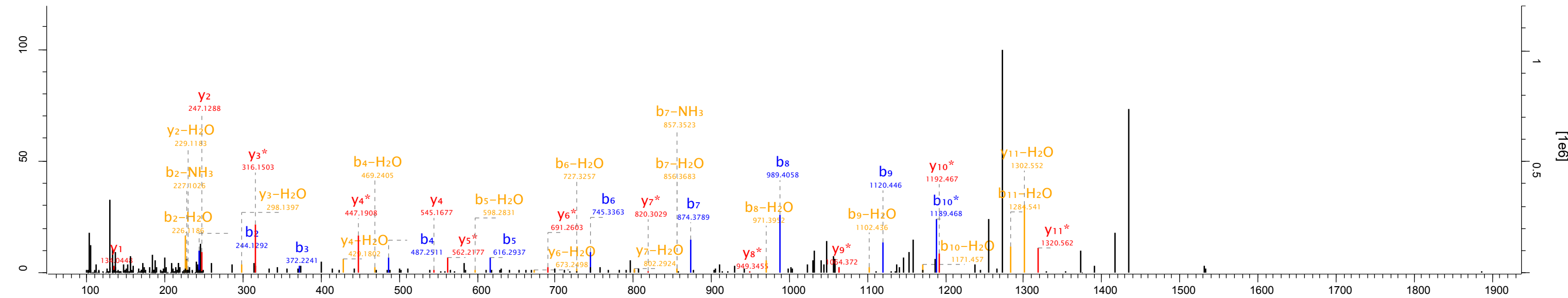
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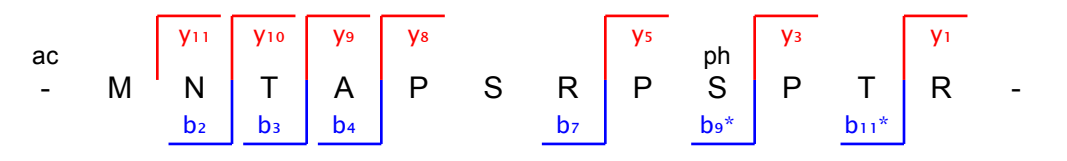
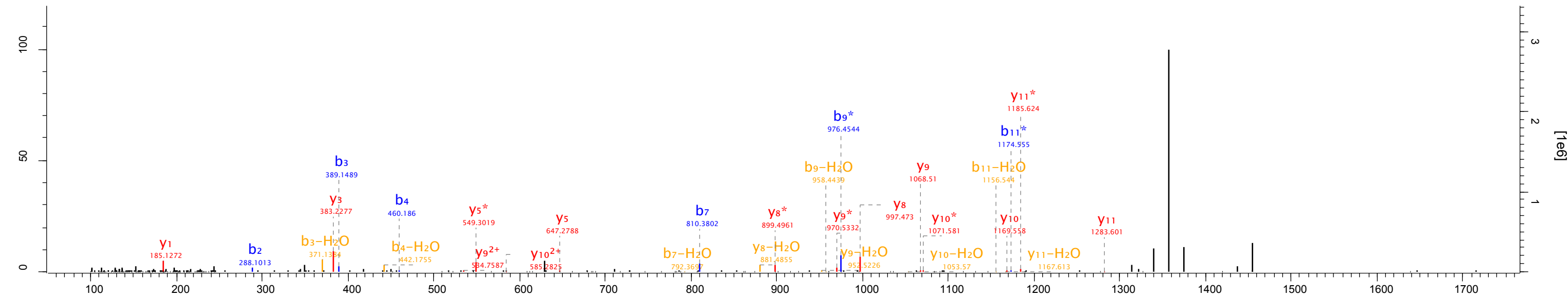
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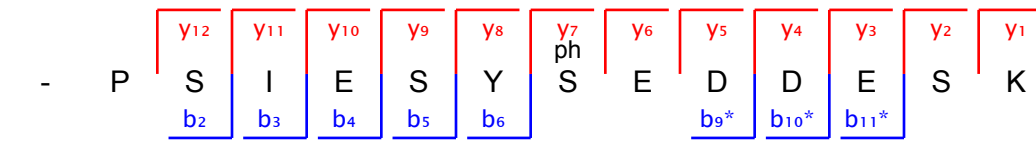
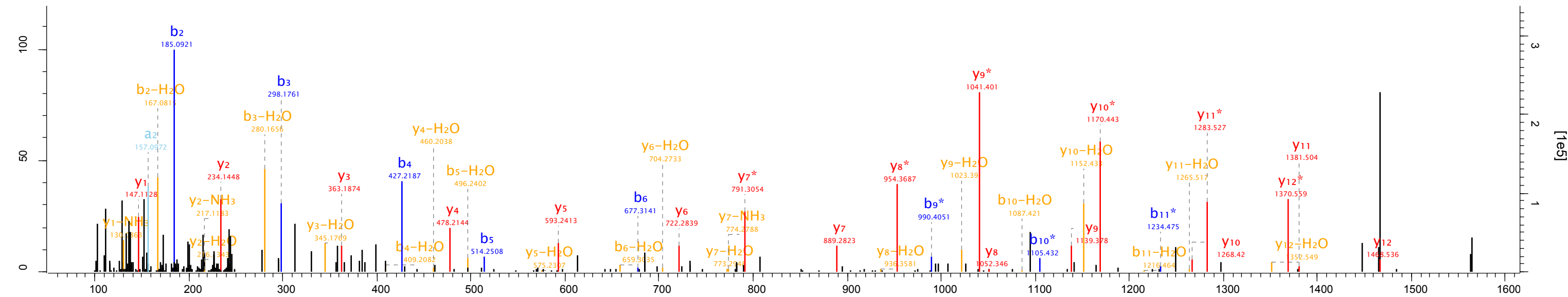


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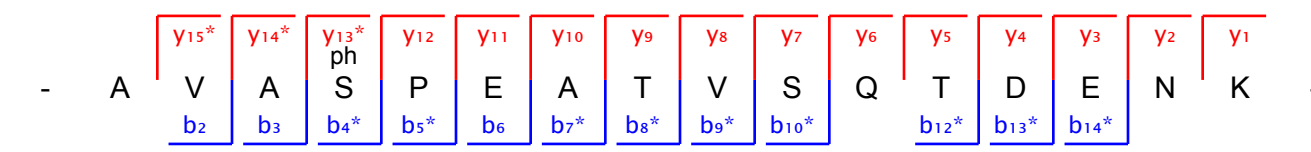
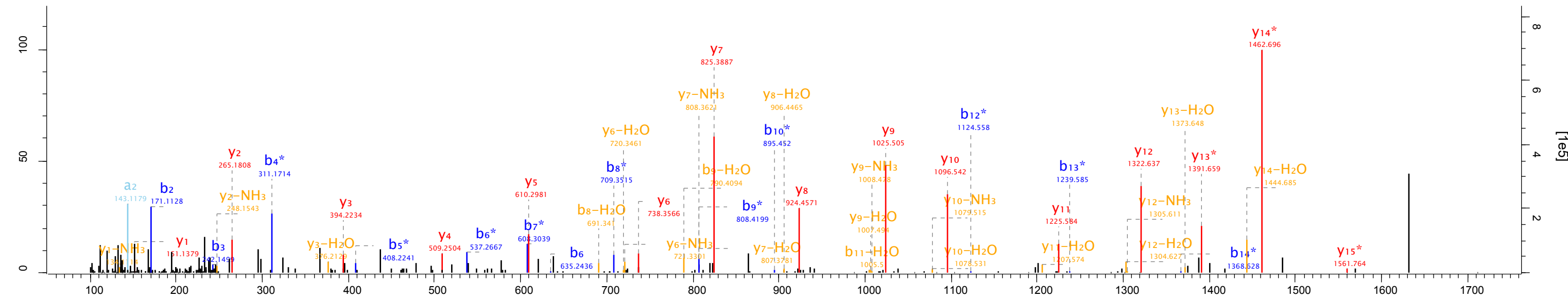


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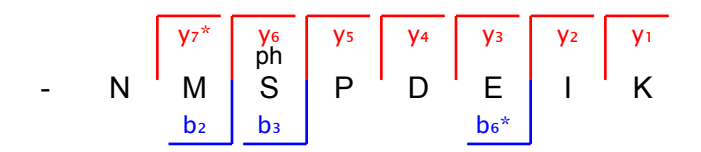
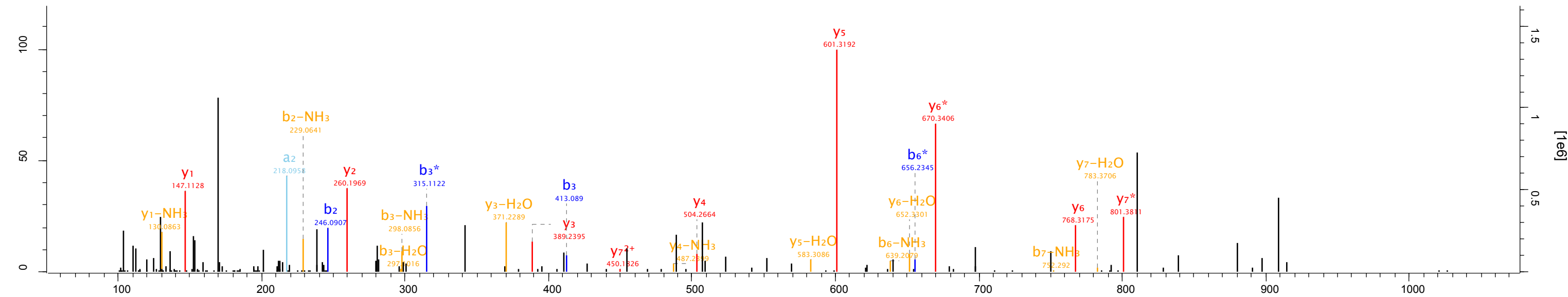


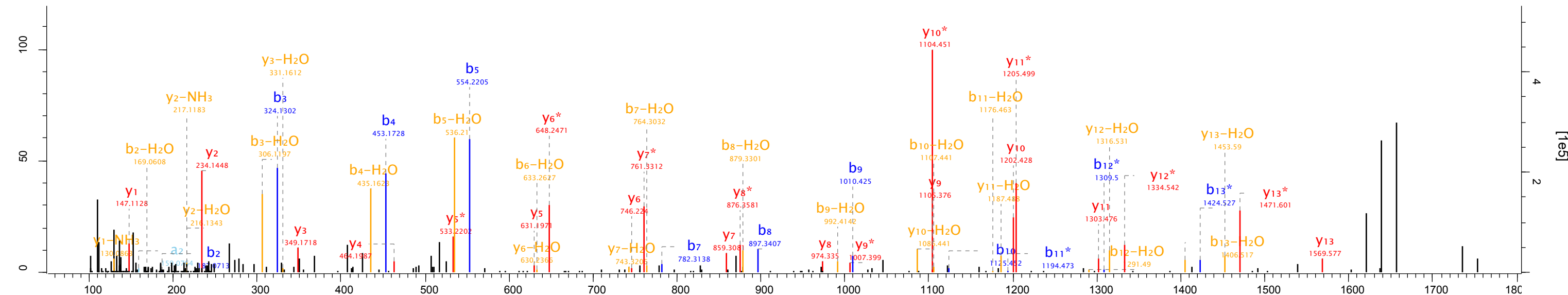


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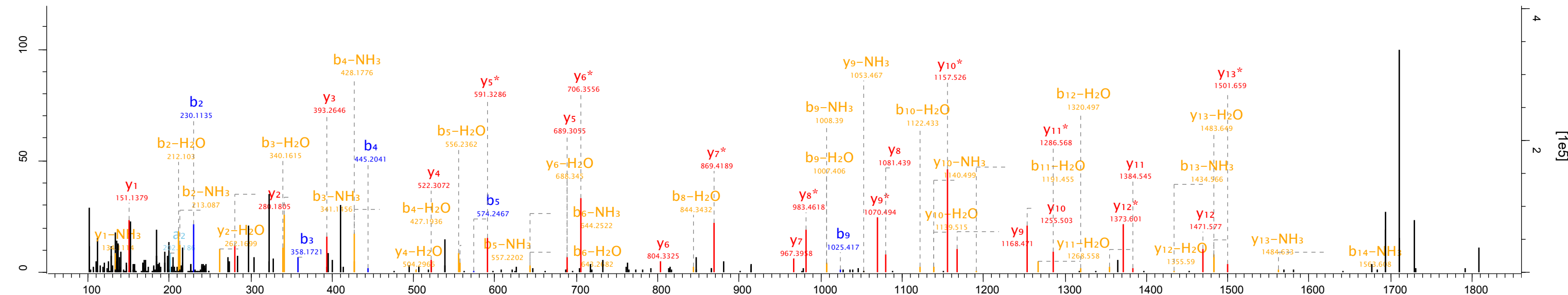




- E G H E T P M D I D S D D S K -

Fragmentation scheme showing b and y ions for the peptide sequence: E G H E T P M D I D S D D S K. The b ions (blue) are b₂ through b₁₃*, and the y ions (red) are y₁ through y₁₃. The y₅ ion is labeled 'ph'.

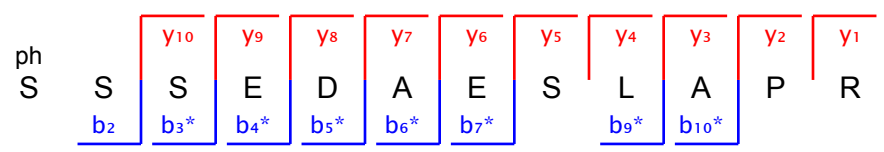
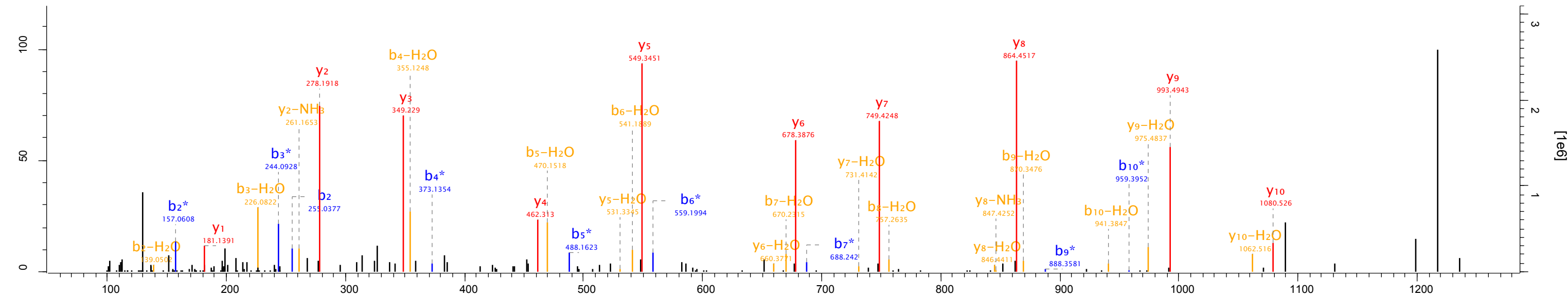
Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 6497 Method FTMS; HCD Score 221.51 m/z 915.37 Gene names ATRX



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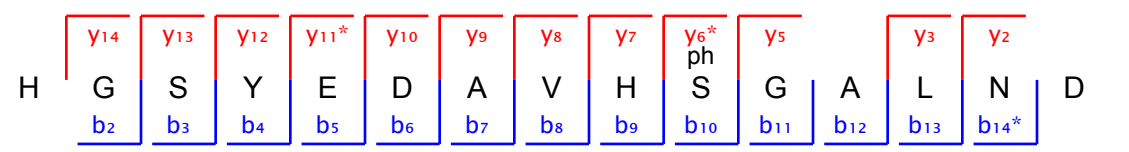
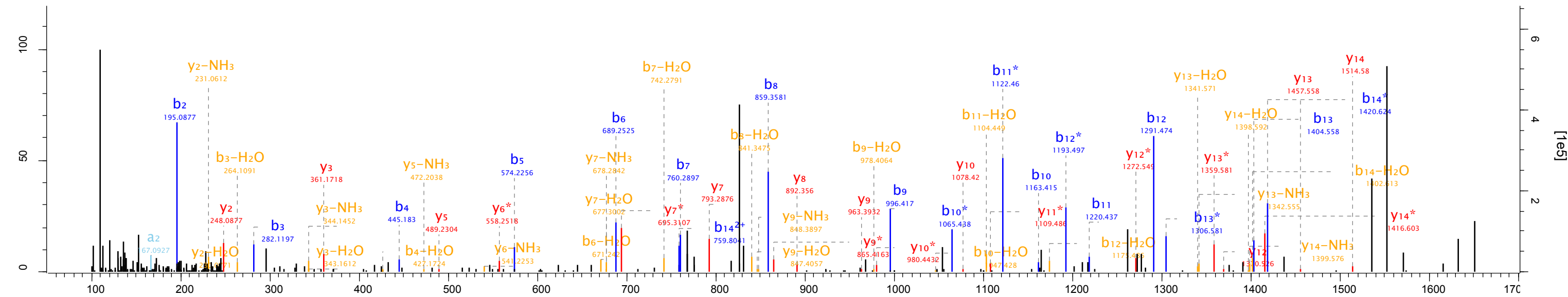
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y₆
y₅
ph
y₄
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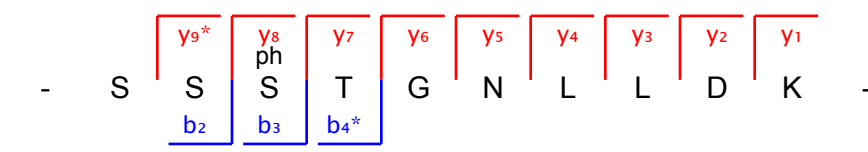
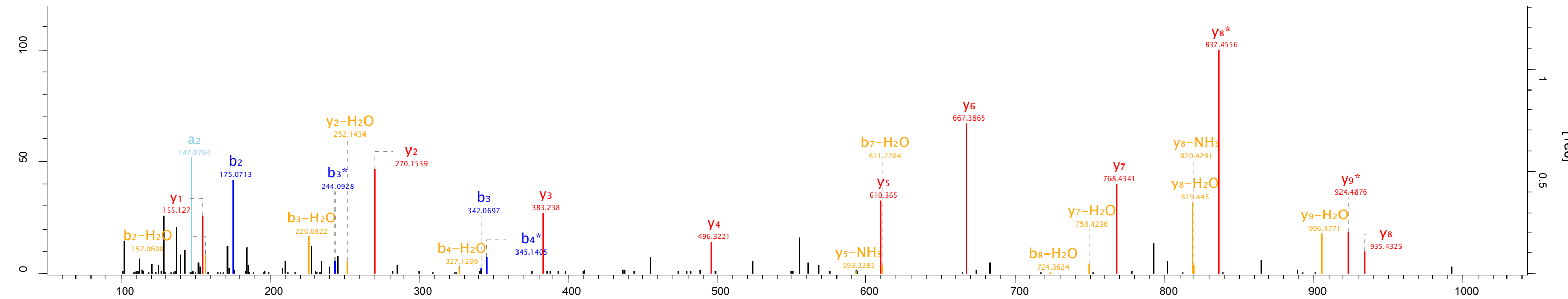


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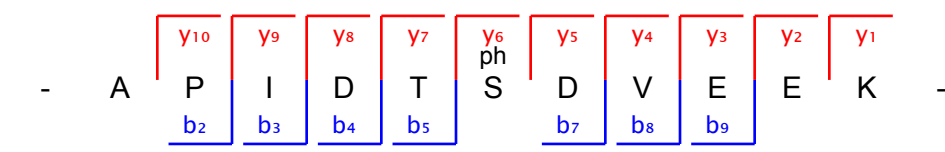
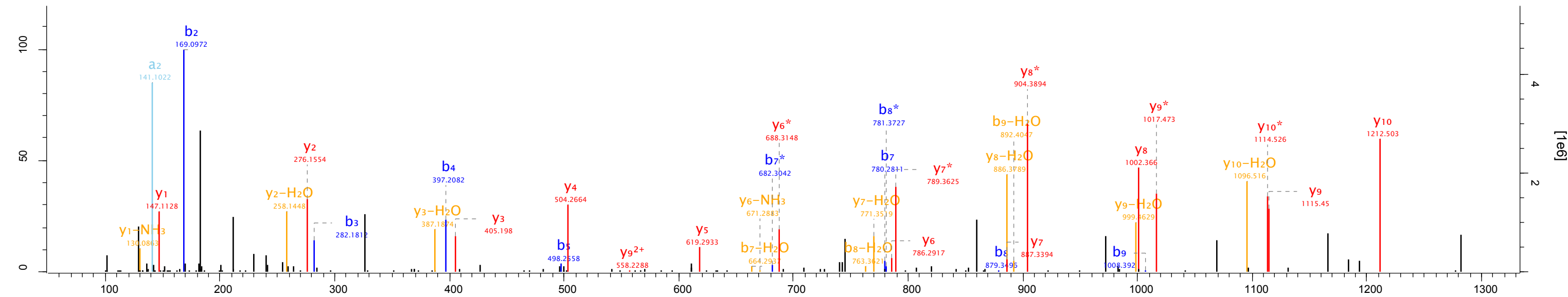
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6827 FTMS; HCD 273.52 826.32 TCP1



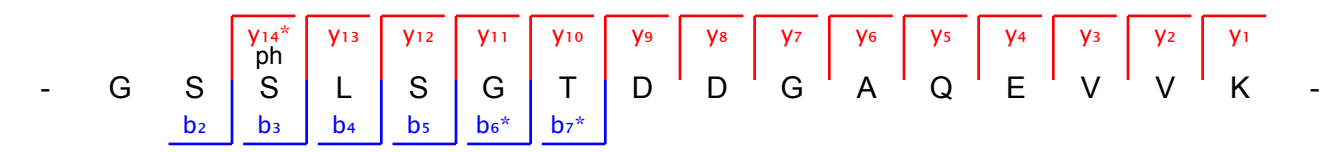
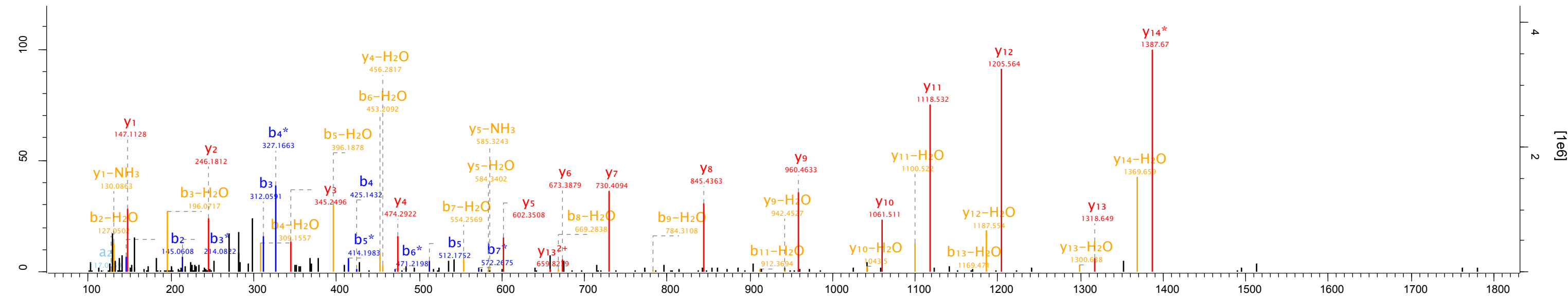
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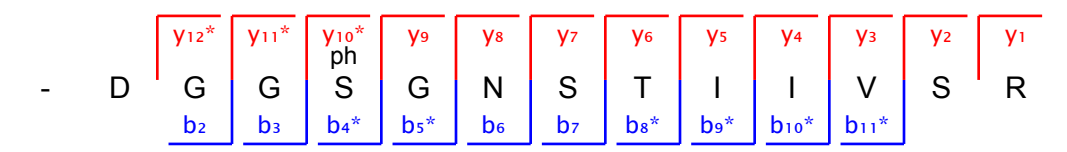
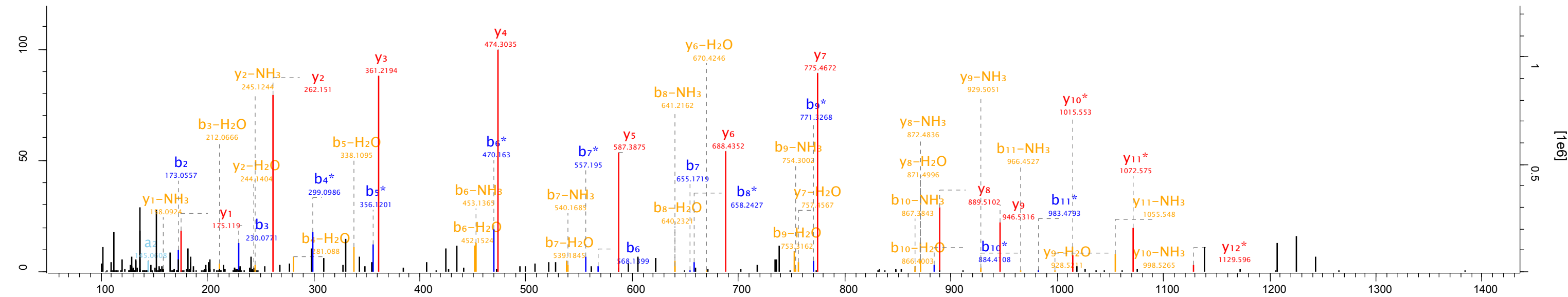
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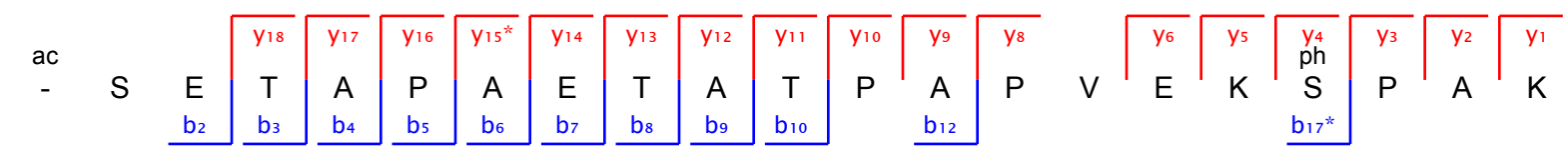
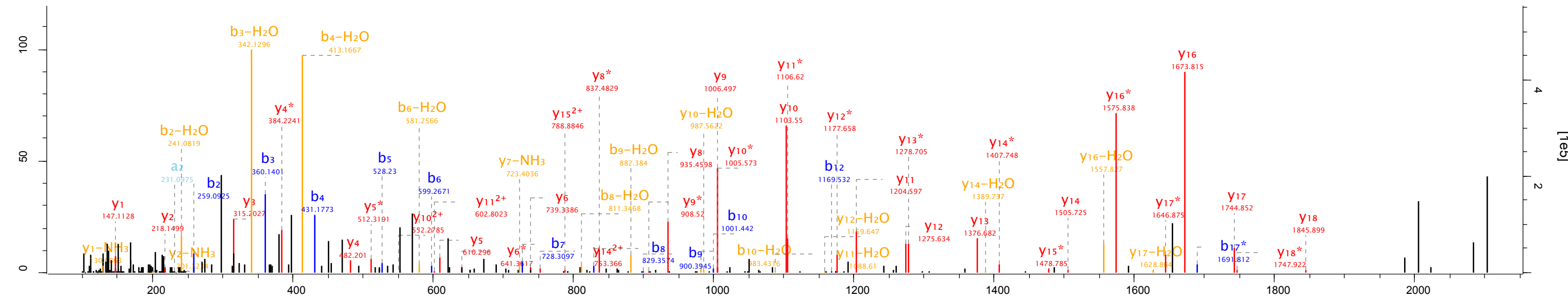
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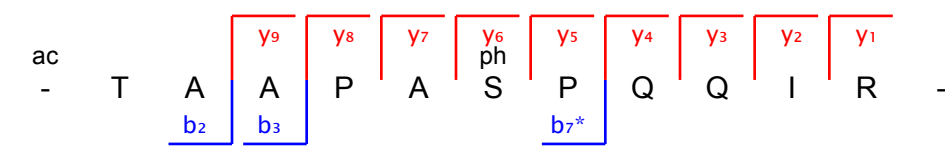
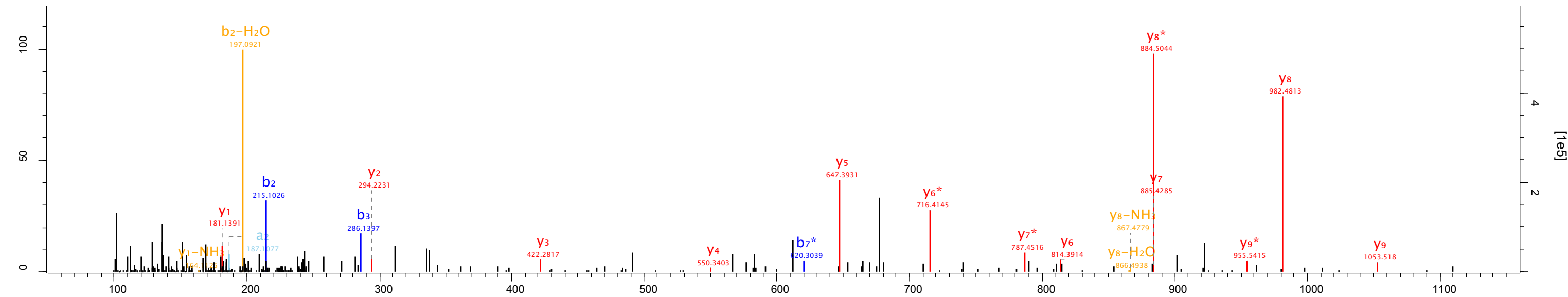
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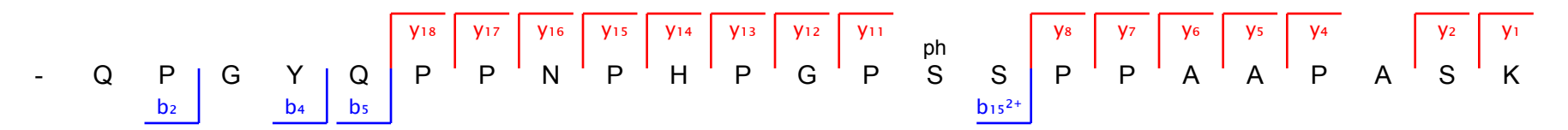
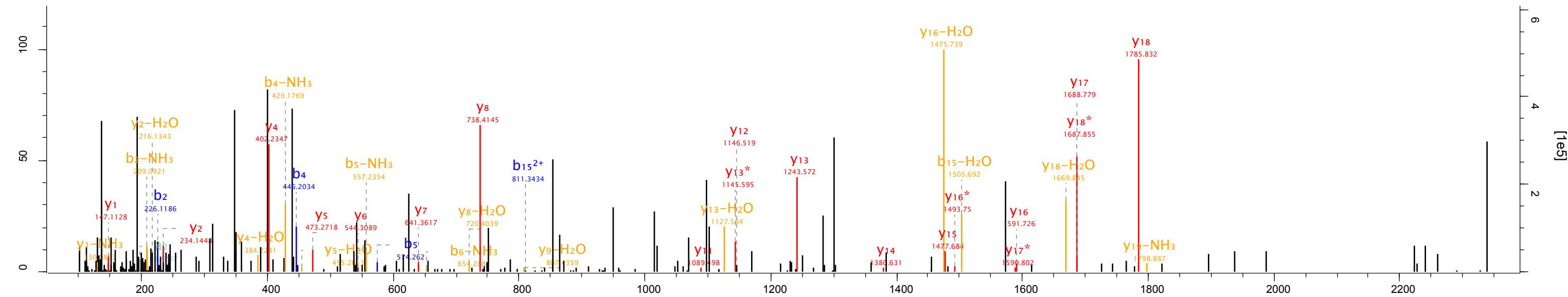
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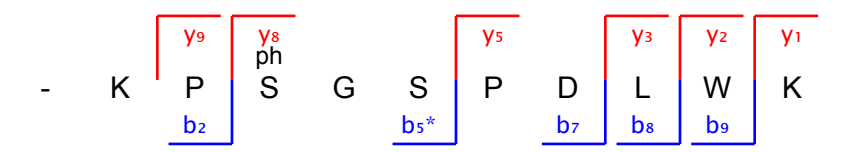
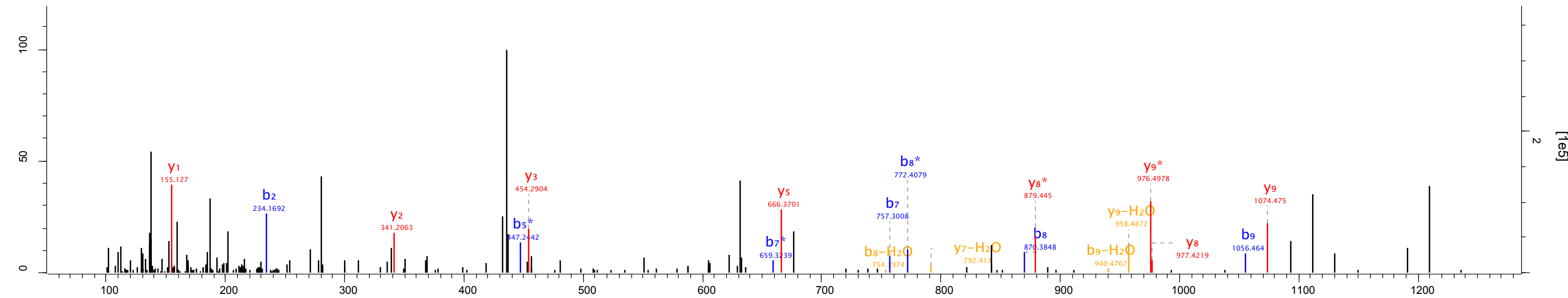
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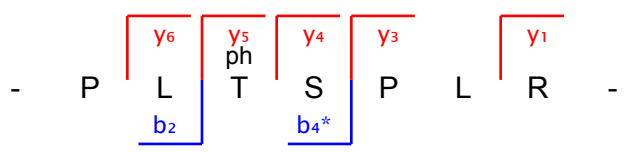
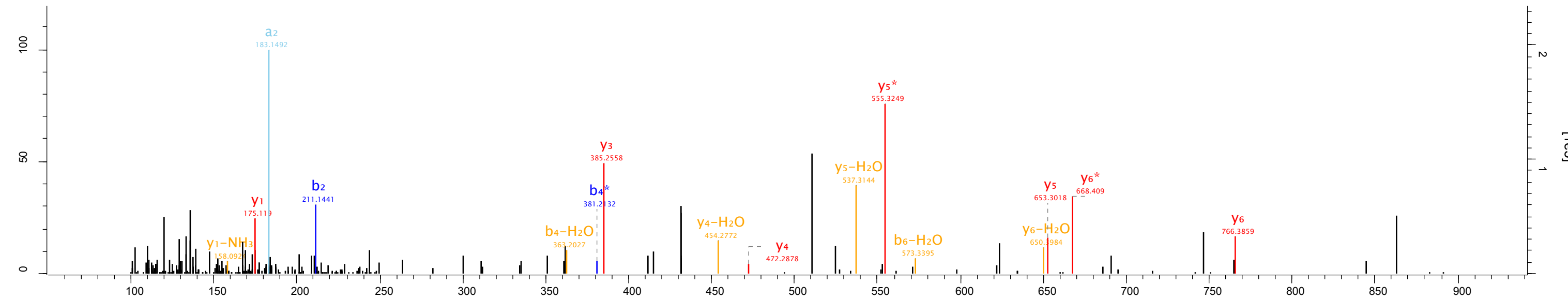
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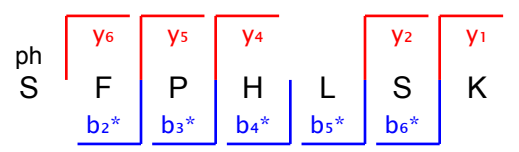
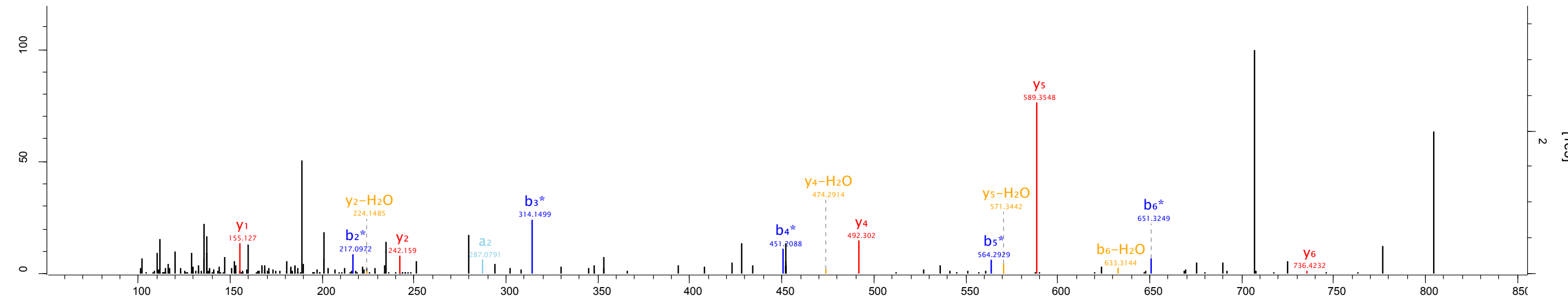
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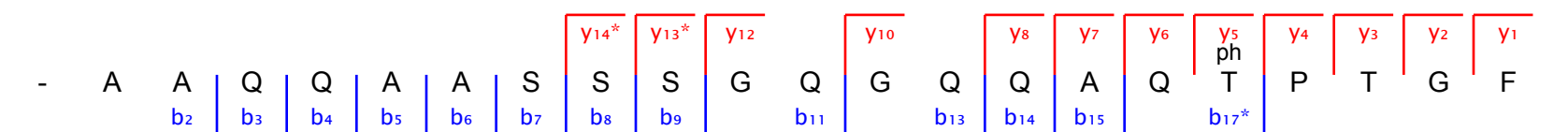
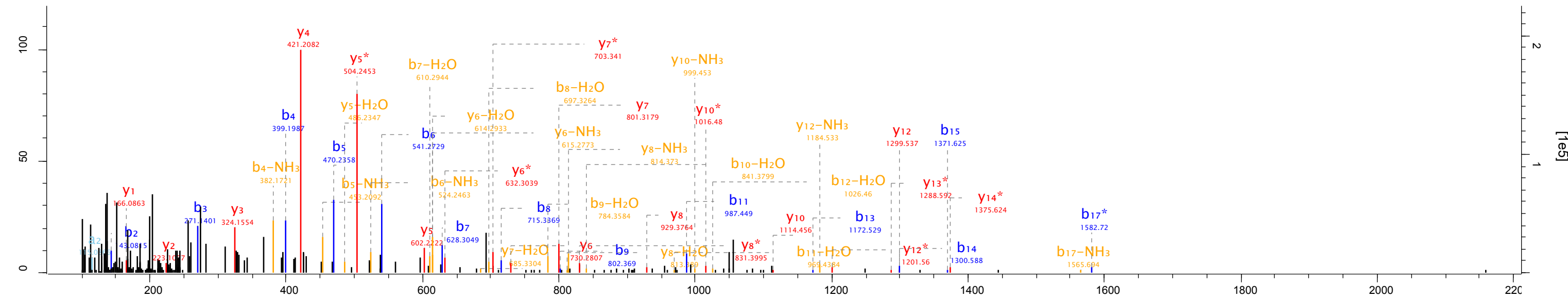


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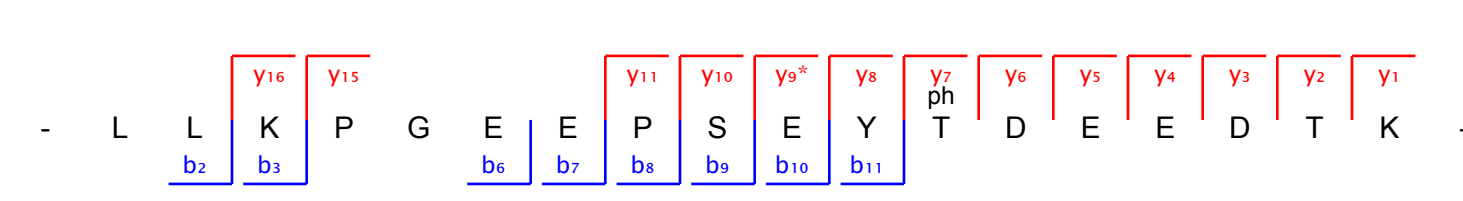
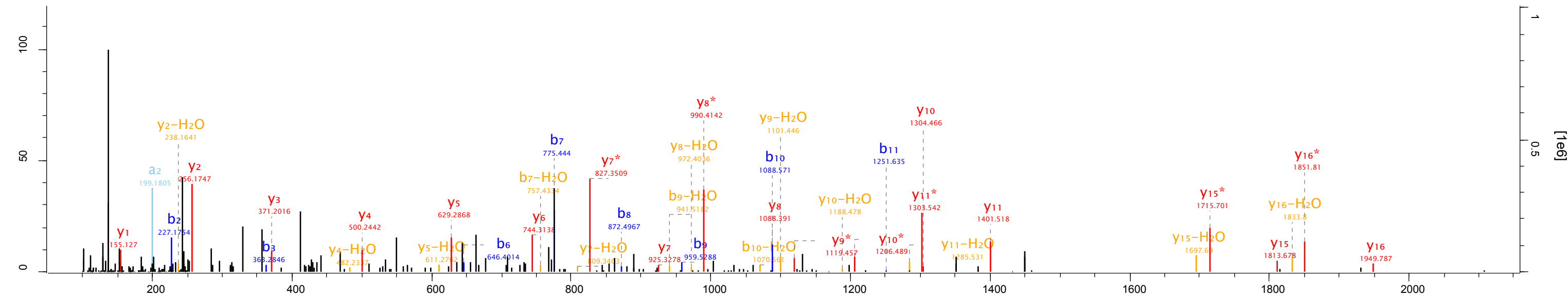


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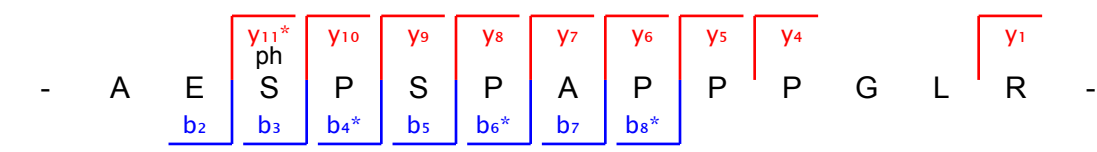
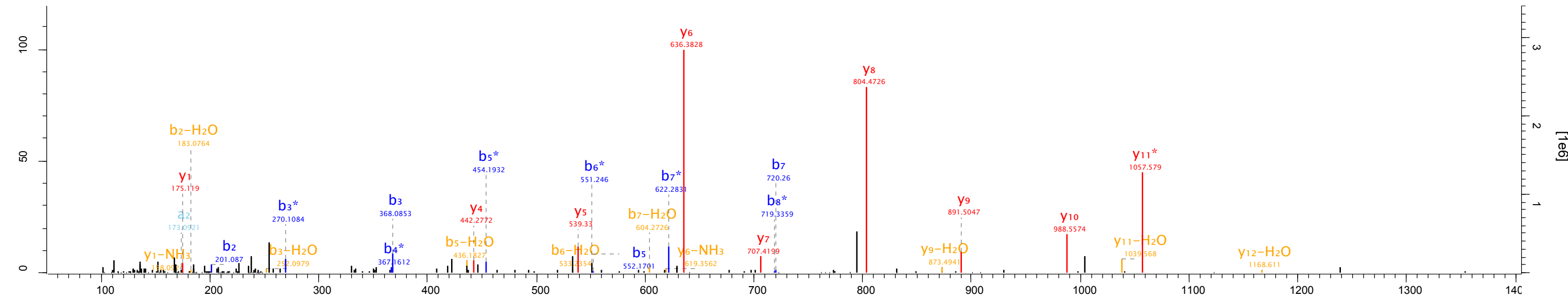




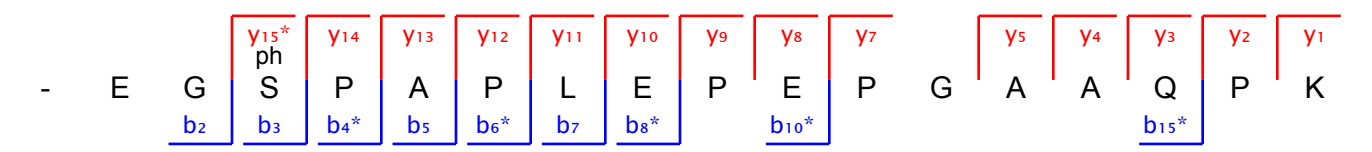
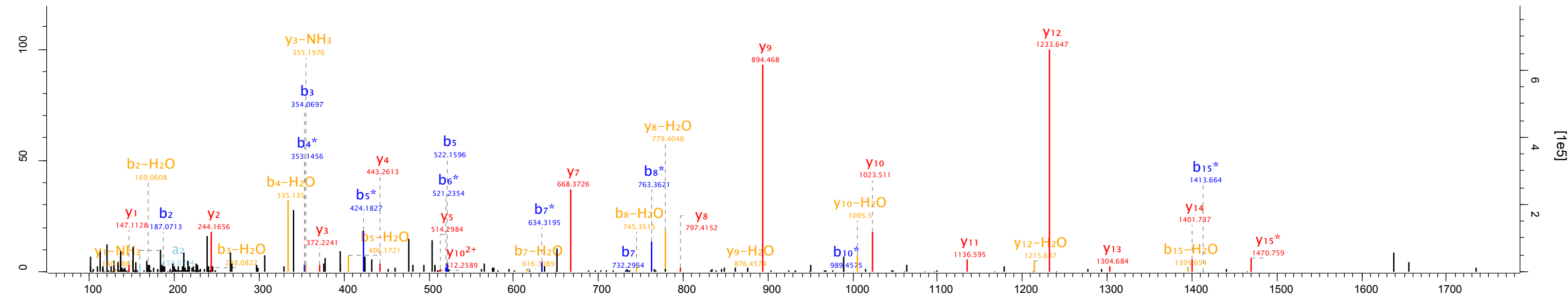
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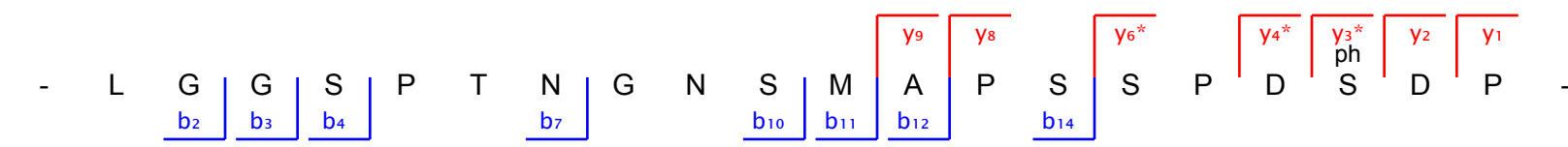
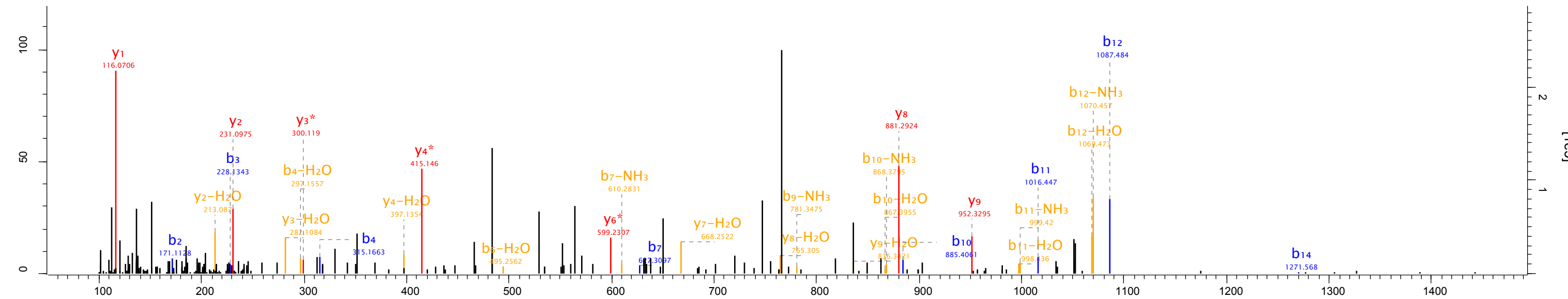
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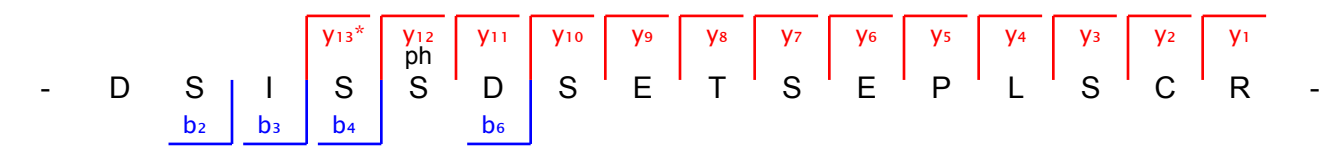
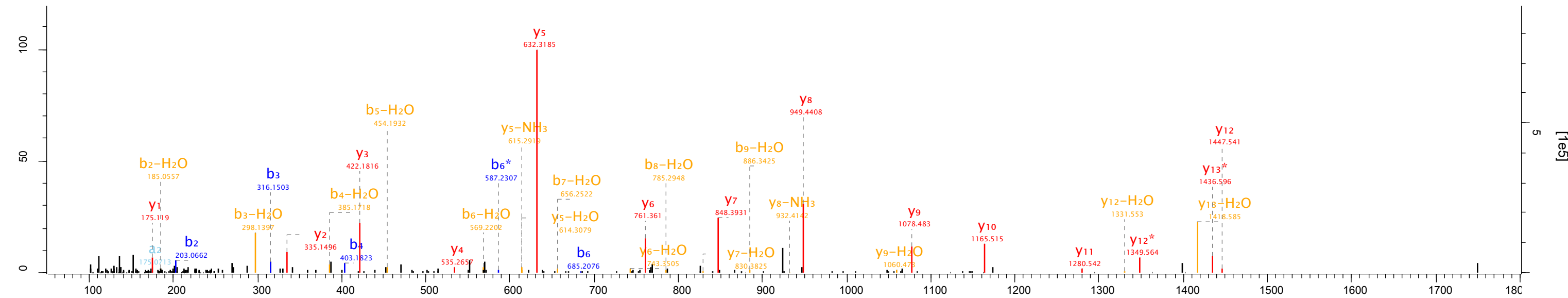
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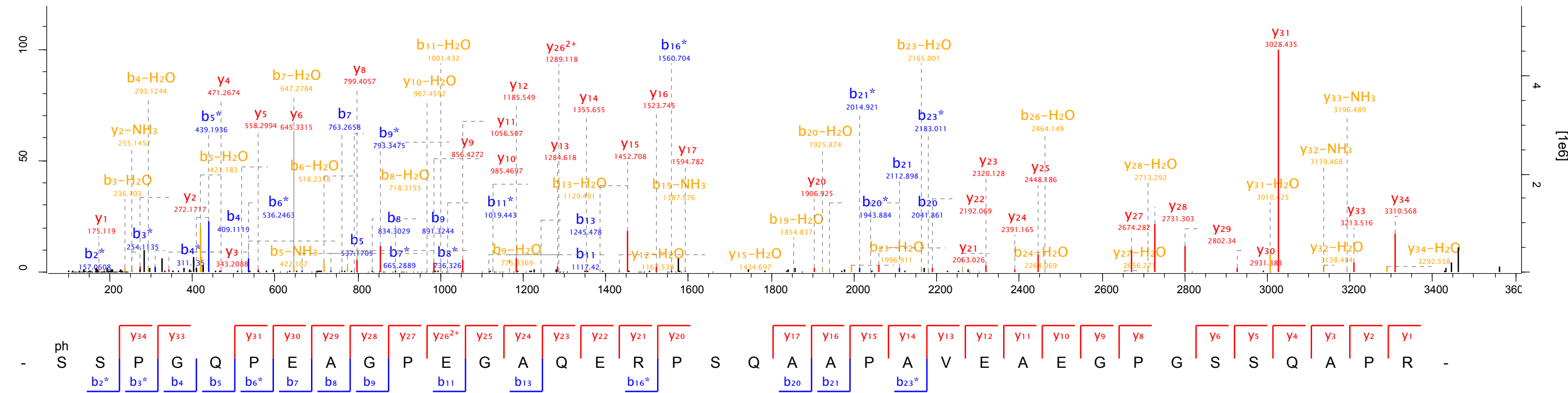
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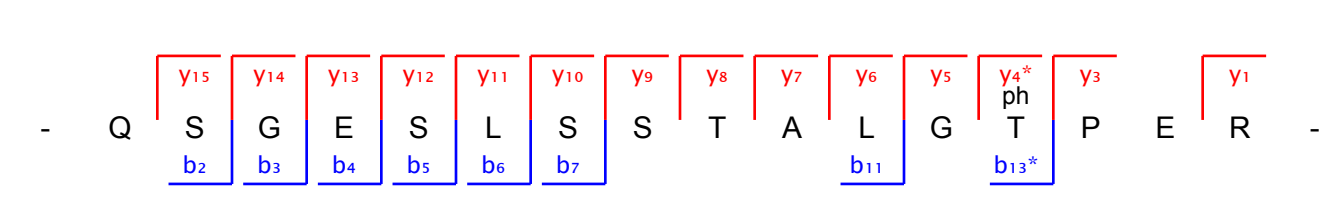
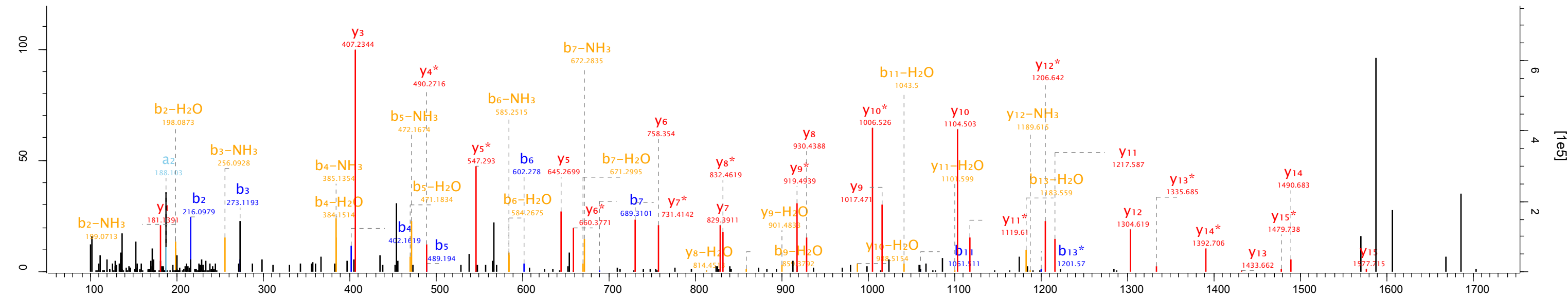
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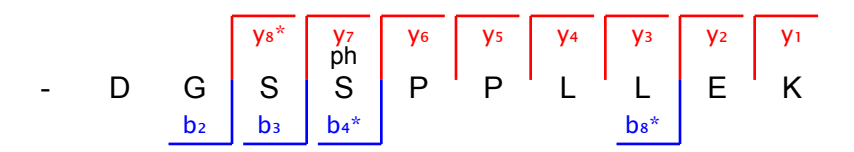
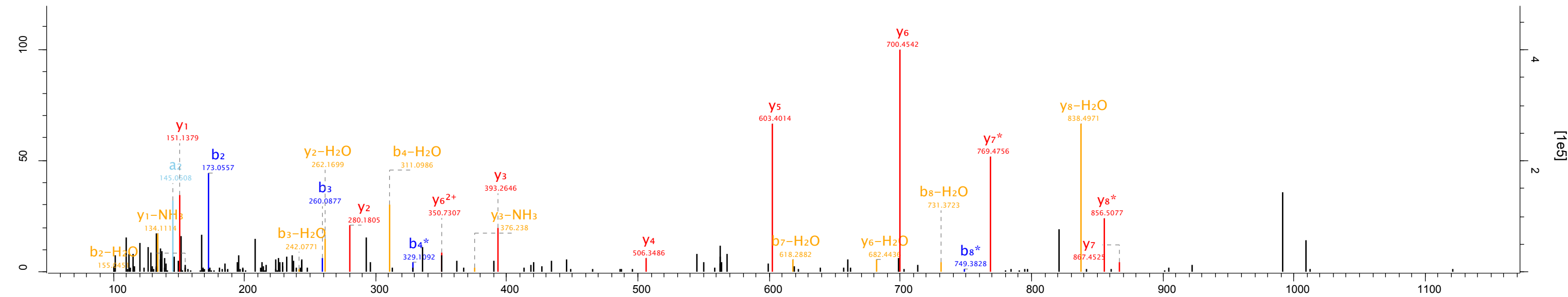
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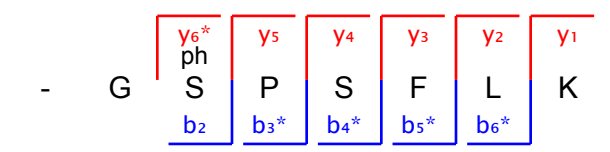
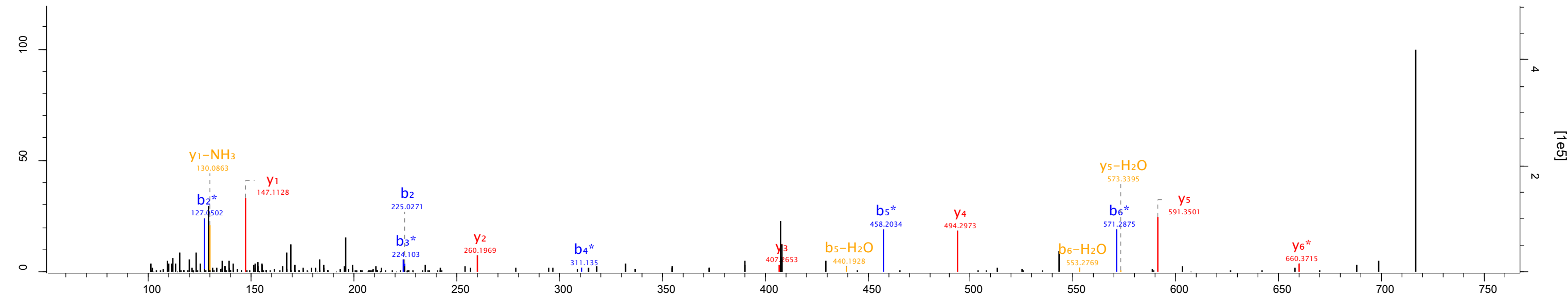
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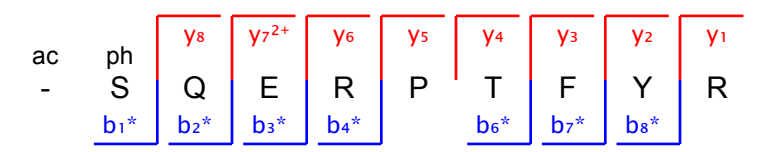
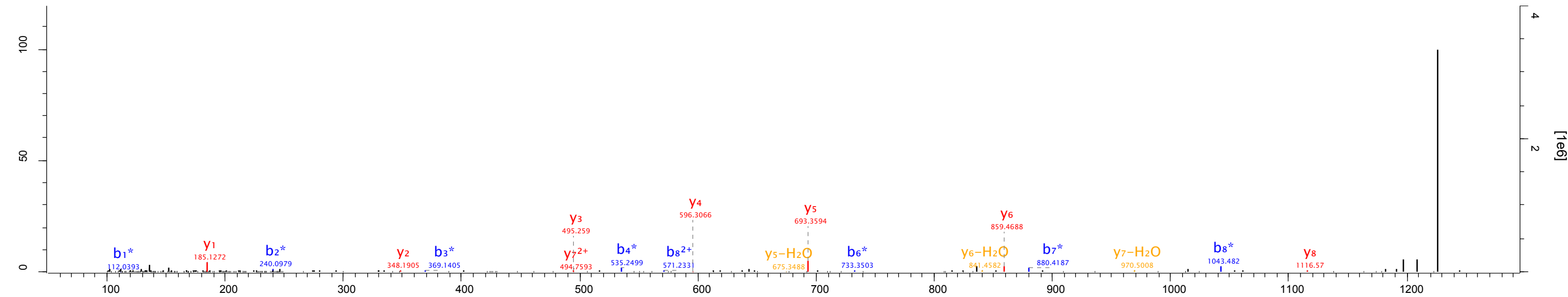
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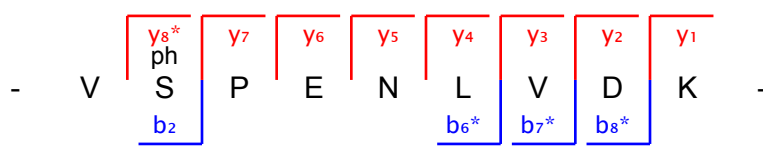
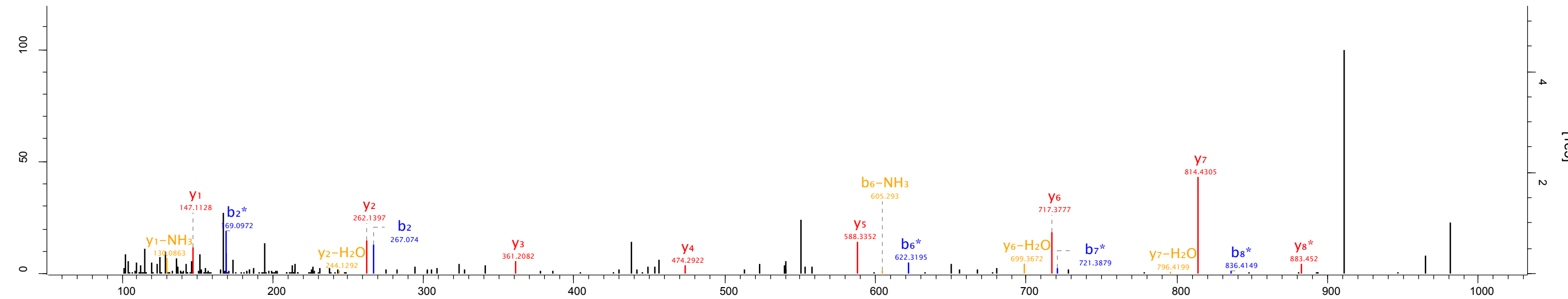
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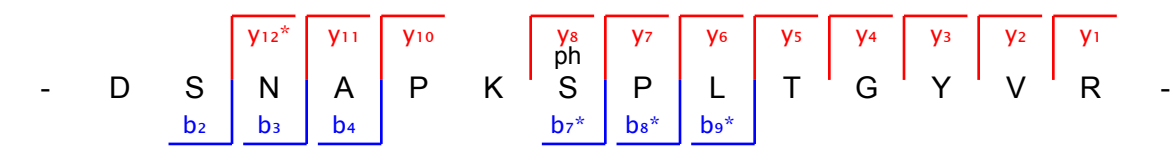
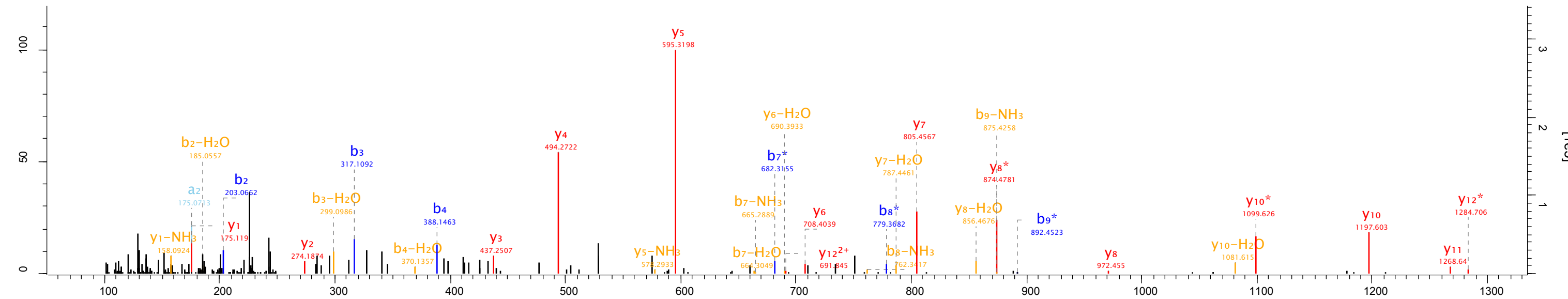
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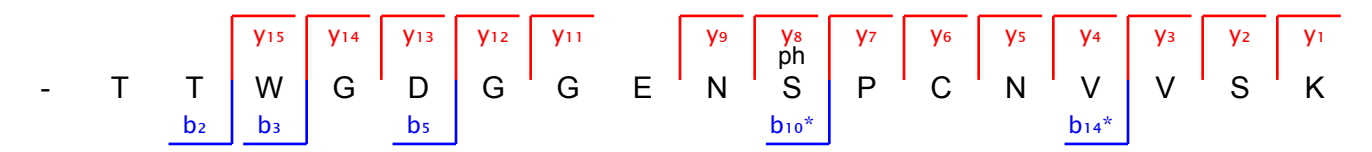
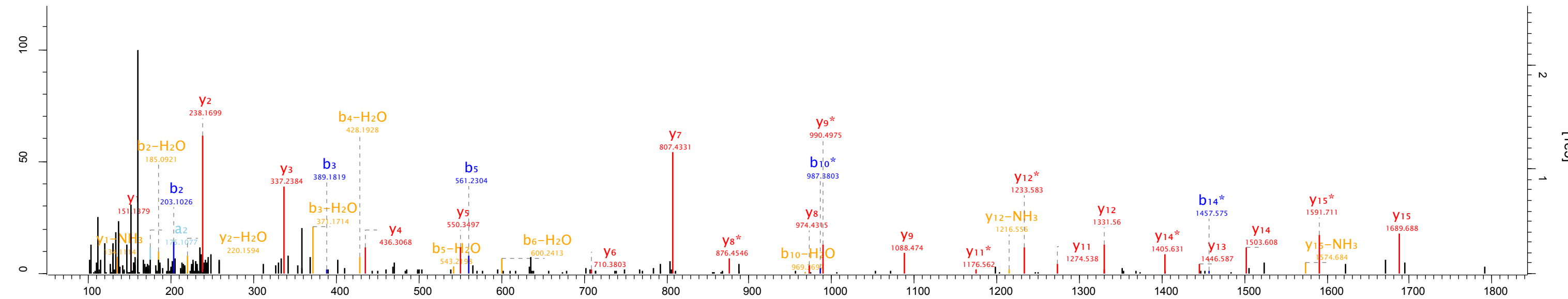
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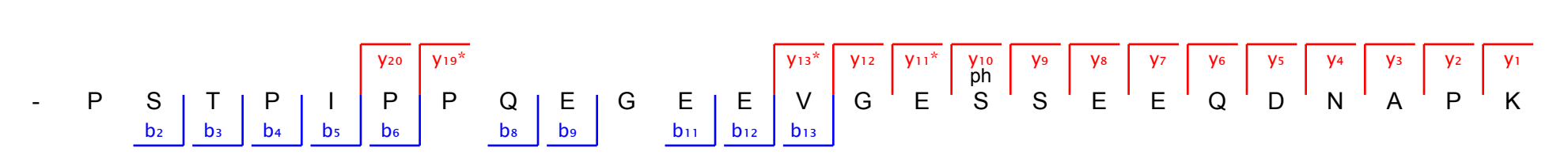
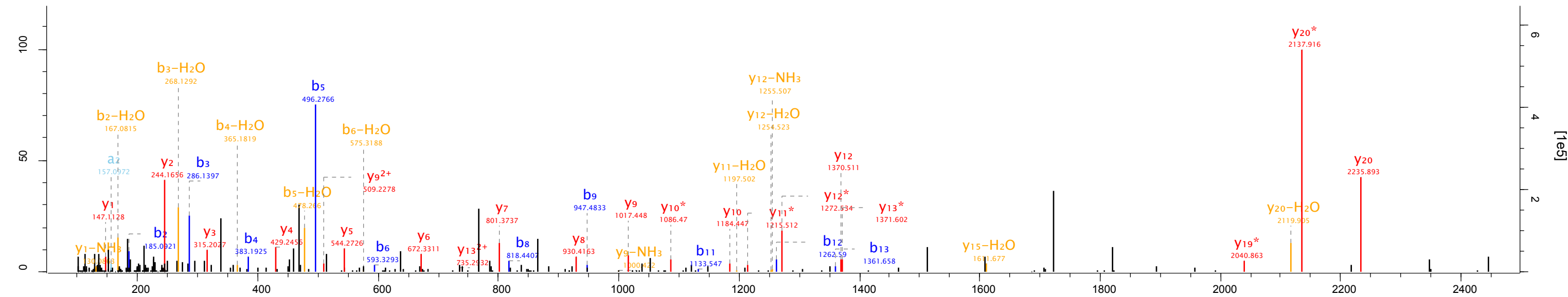
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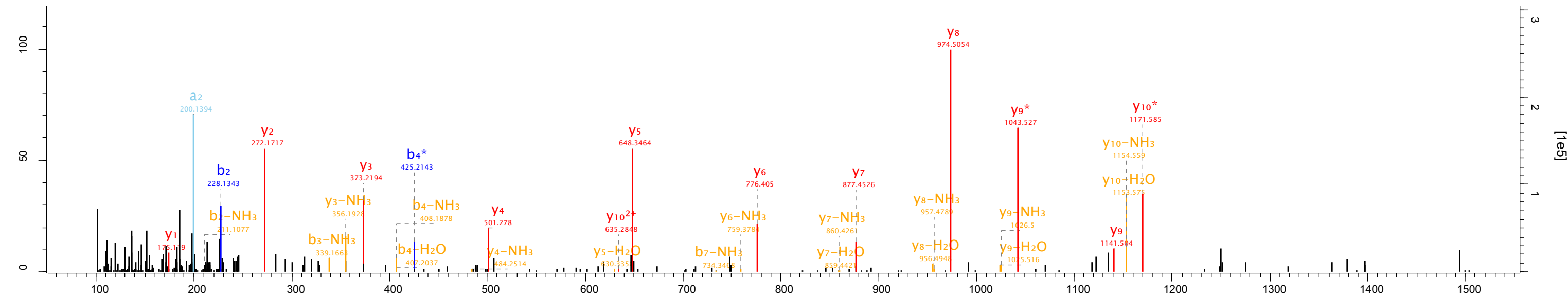
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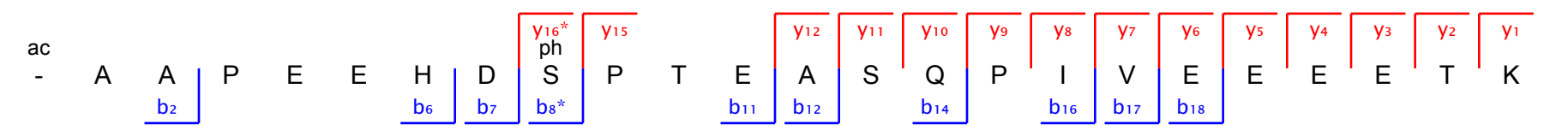
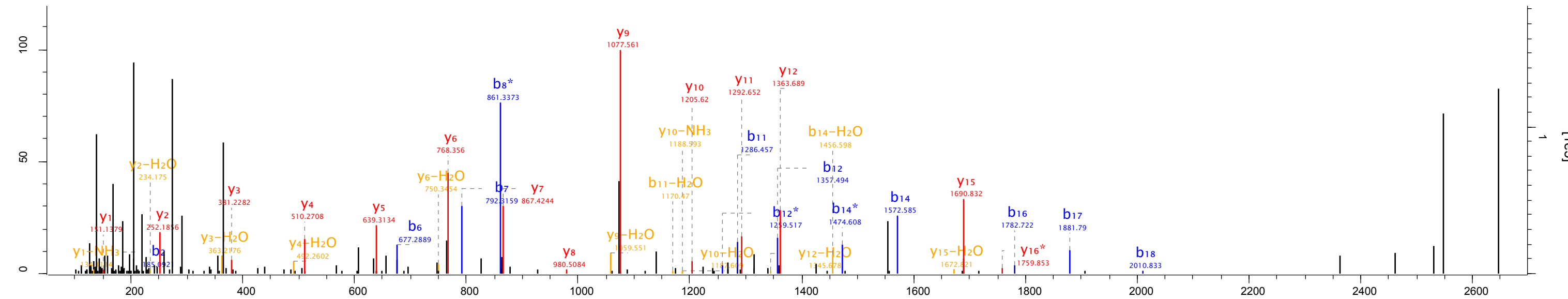
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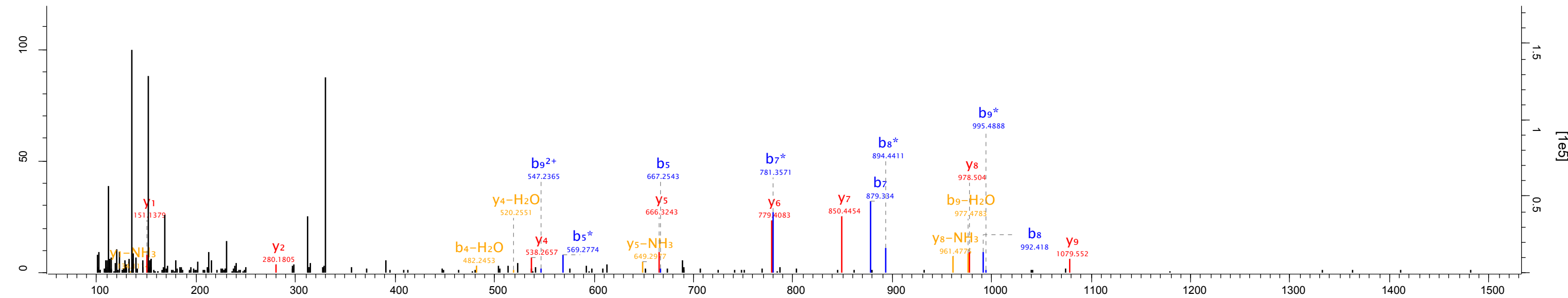
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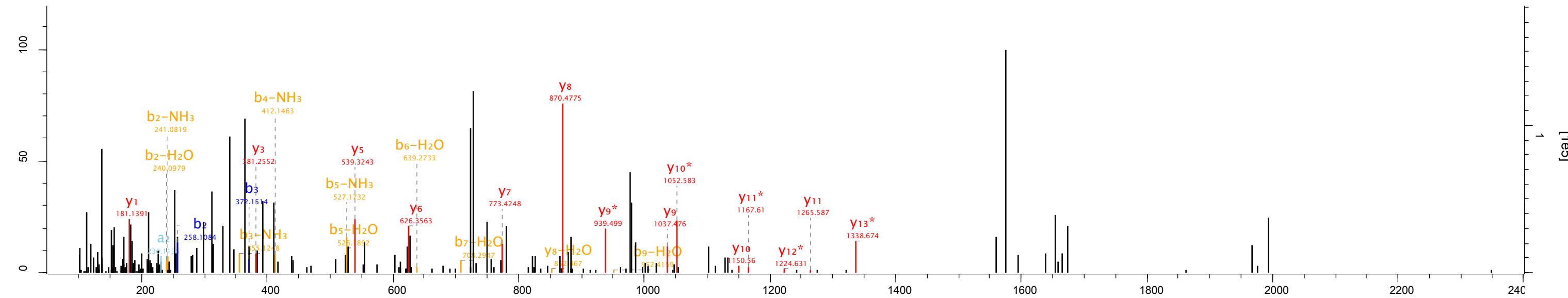
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Labels below the sequence: b5 (under S), b7 (under D), b8 (under I), b9* (under T), y9 (above T), y8 (above Q), y7 (above A), y6 (above I), y5 (above Q), y4 (above E), y2 (above E), y1 (above K).

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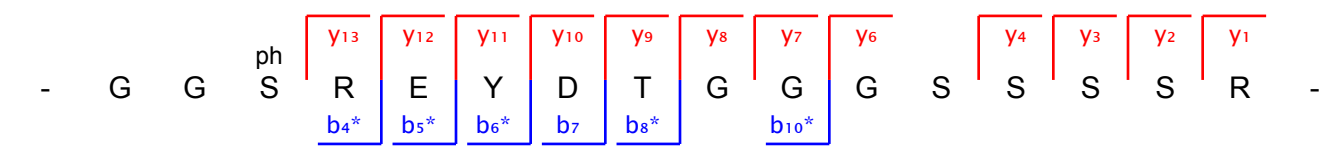
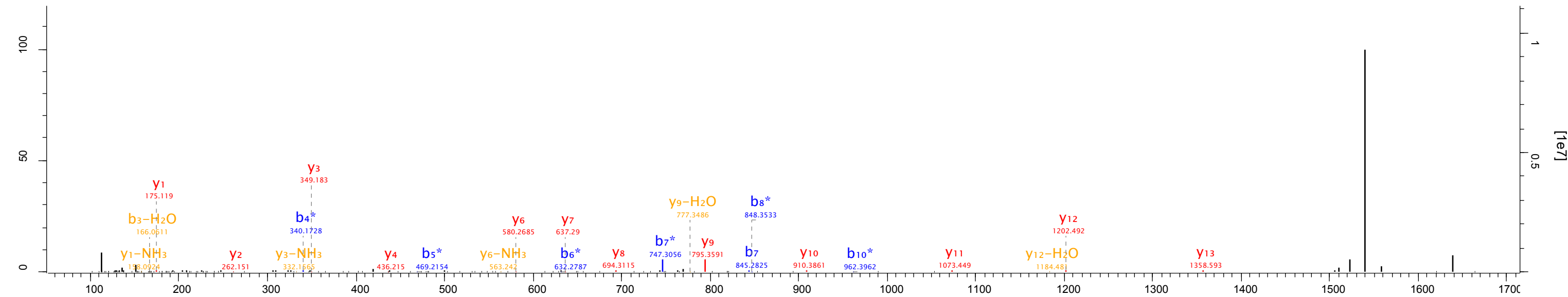


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Fragmentation mapping:

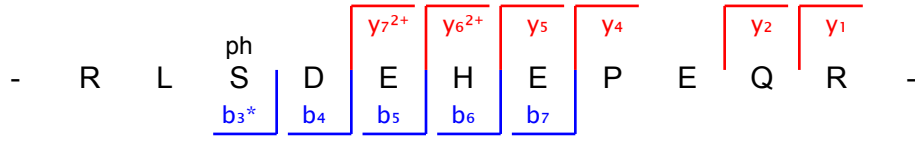
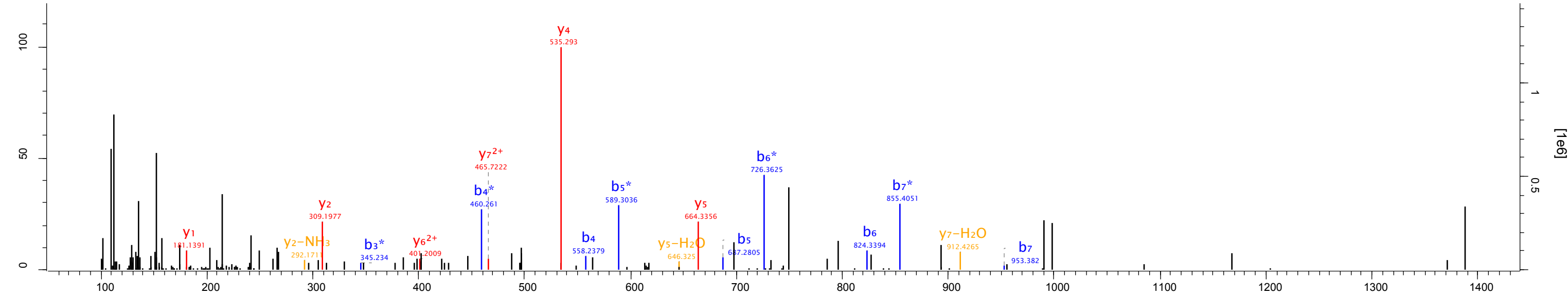
- Red brackets above the sequence indicate y-ion fragments: y13* (N-G), y12* (G-D), y11 (D-L), y10 (L-S), y9-ph (S-P), y8 (P-F), y7 (F-S), y6 (S-G), y5 (G-T), y3 (T-S), y1 (S-L).
- Blue brackets below the sequence indicate b-ion fragments: b2 (E-N), b3 (N-G).

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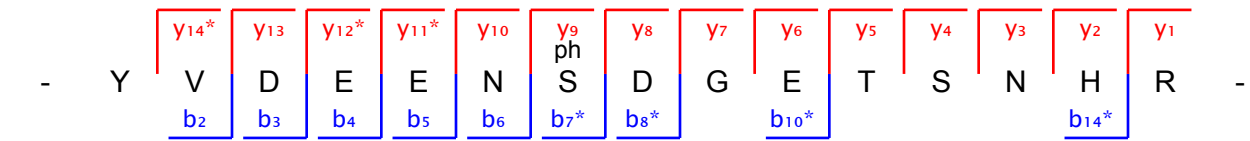
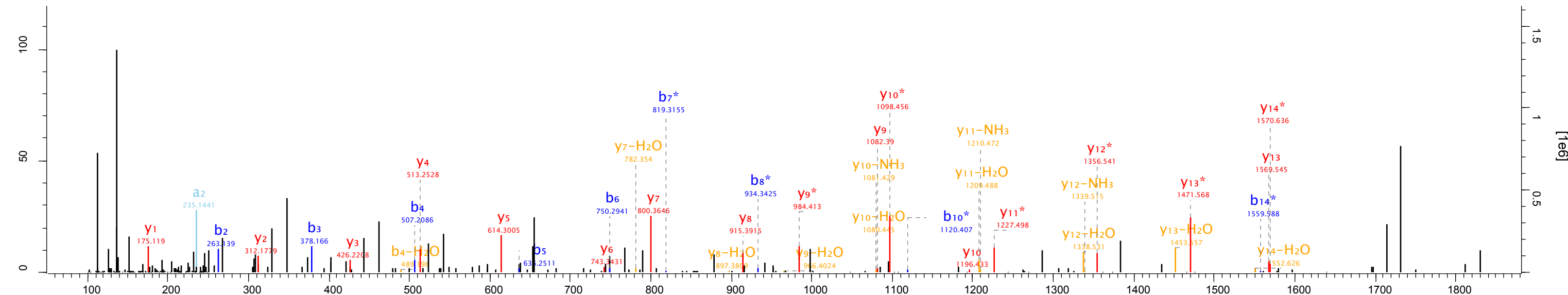


Raw file Scan Method Score m/z Gene names

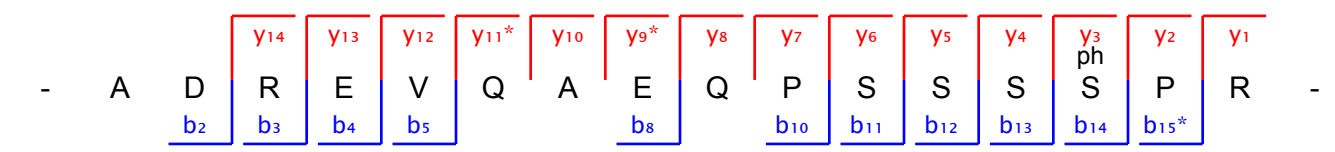
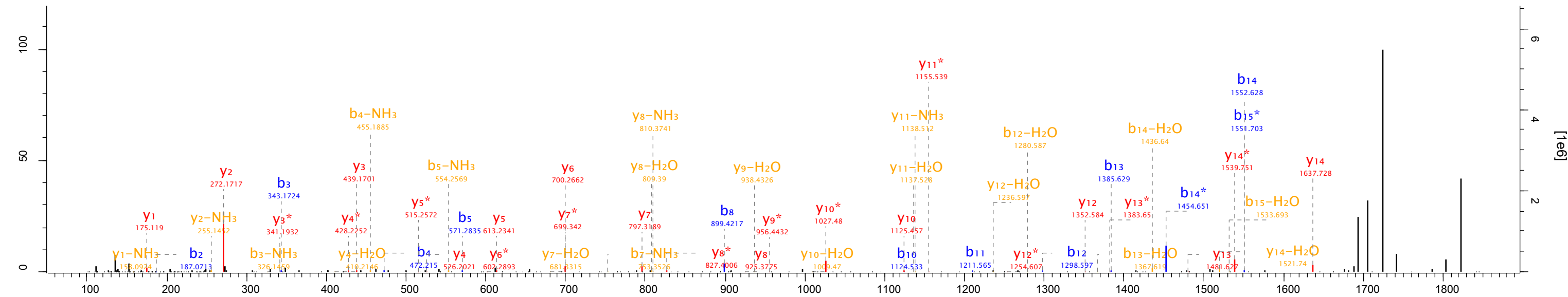
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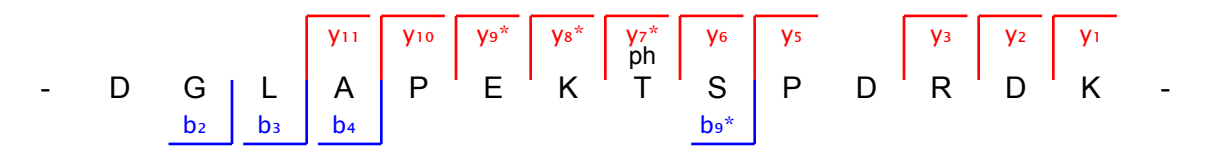
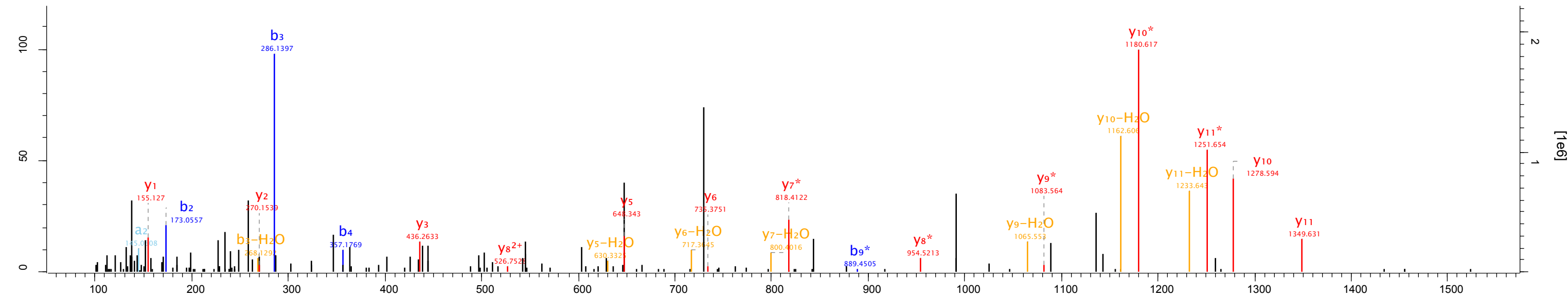
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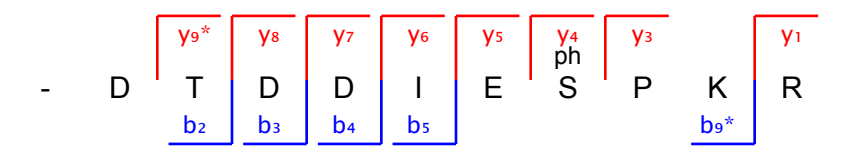
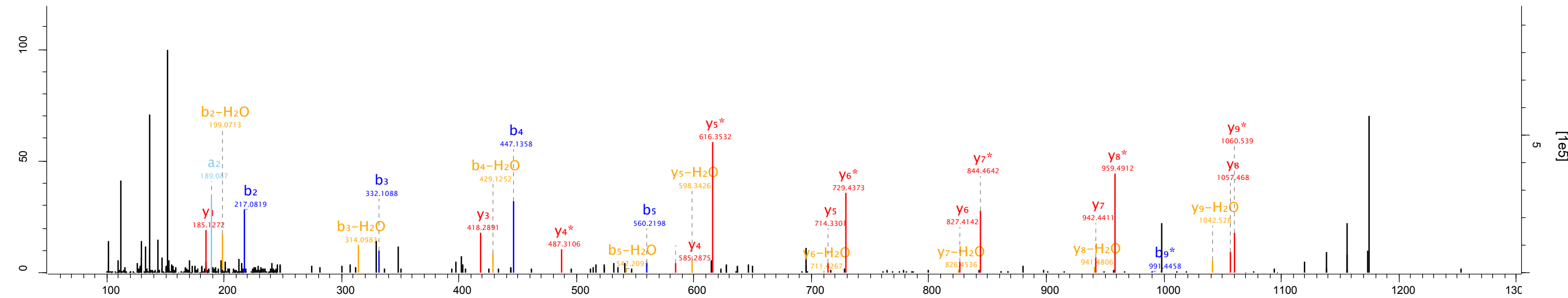
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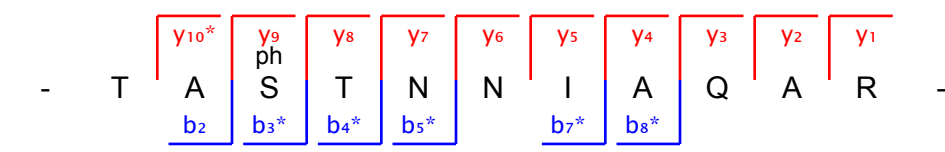
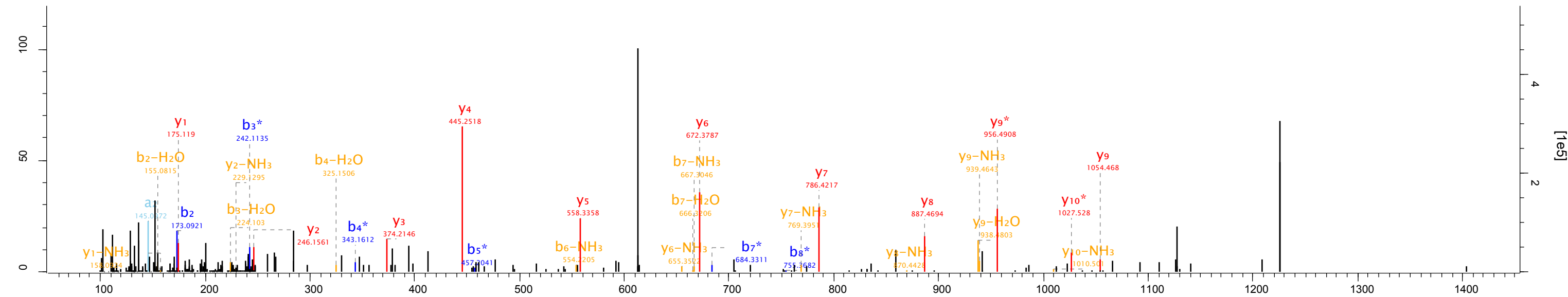
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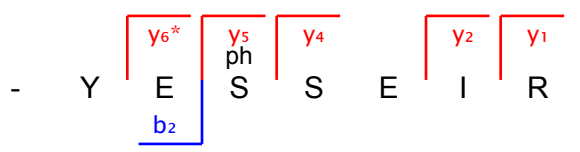
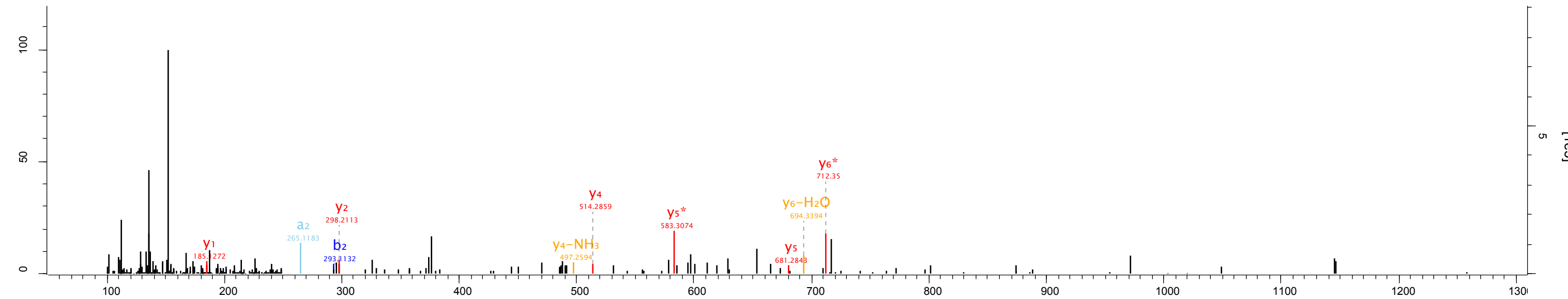
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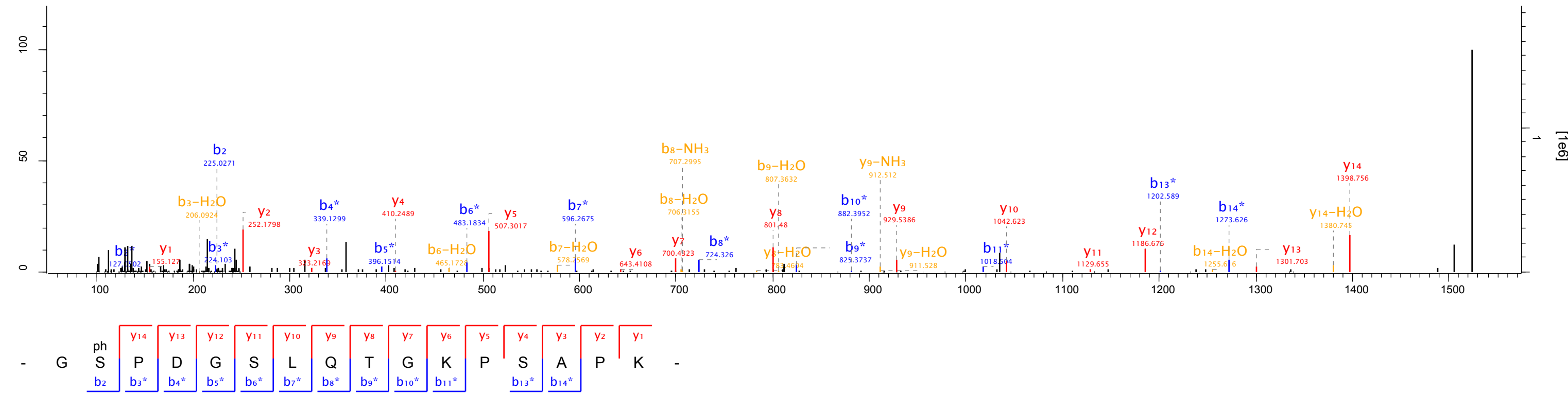


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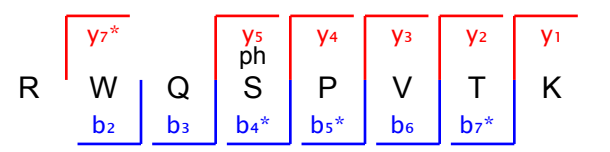
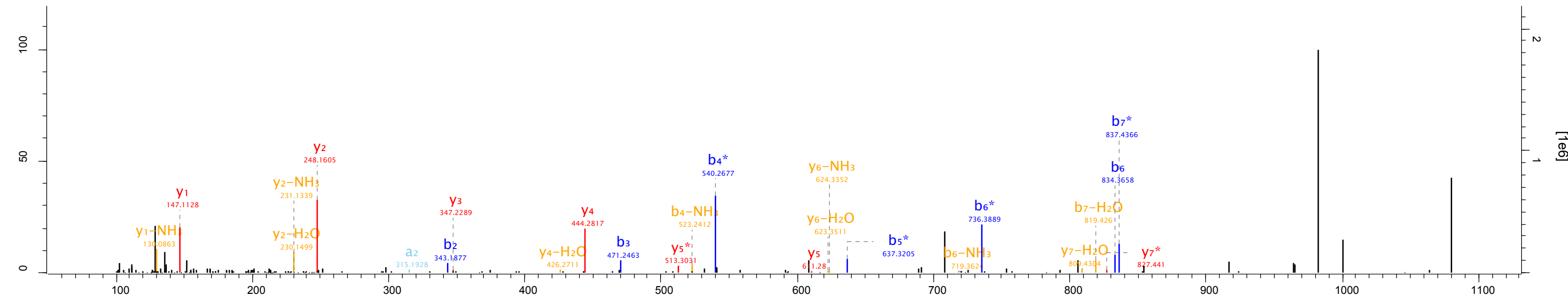


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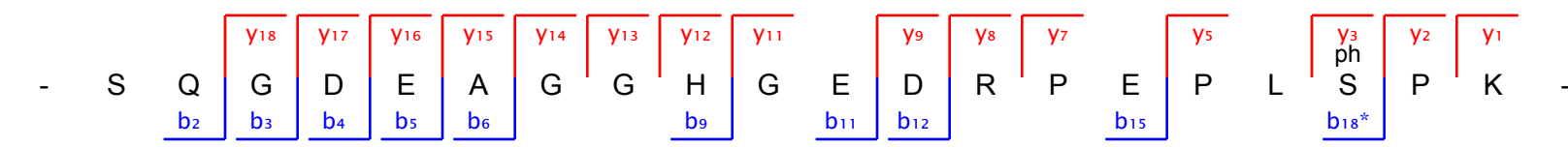
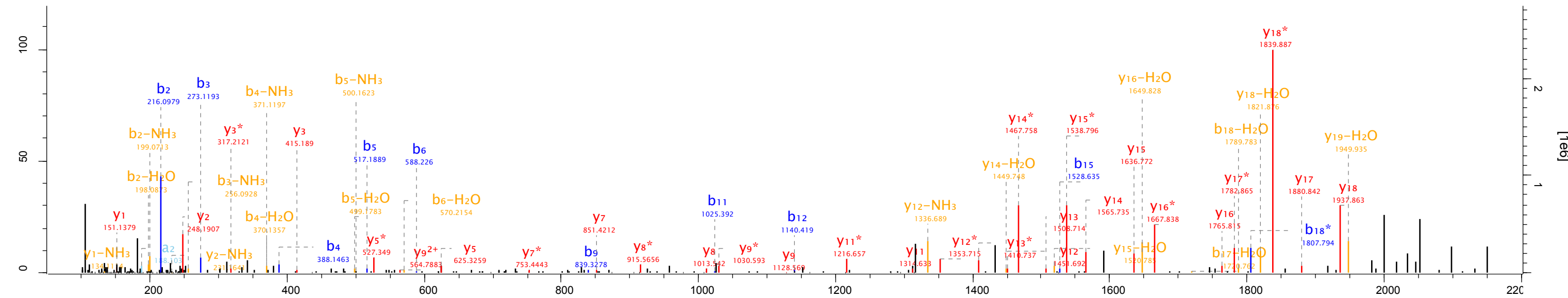




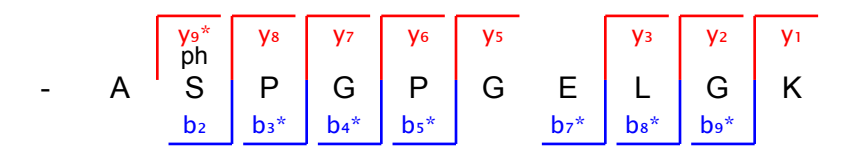
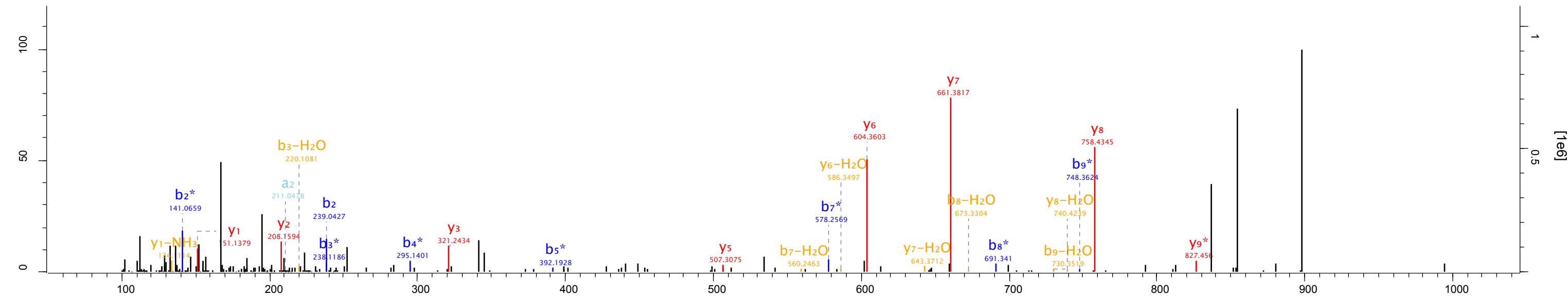
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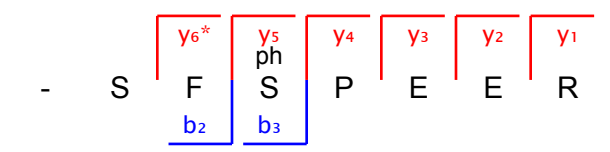
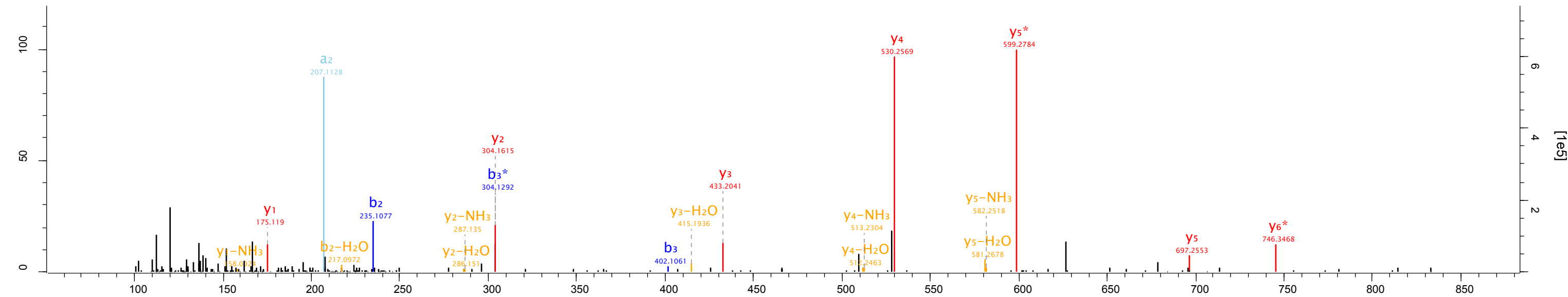
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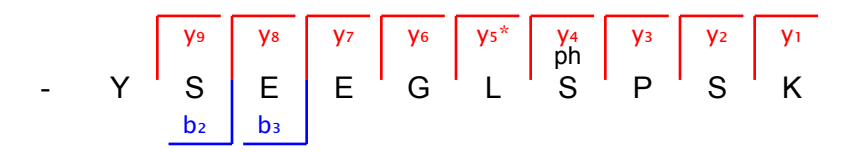
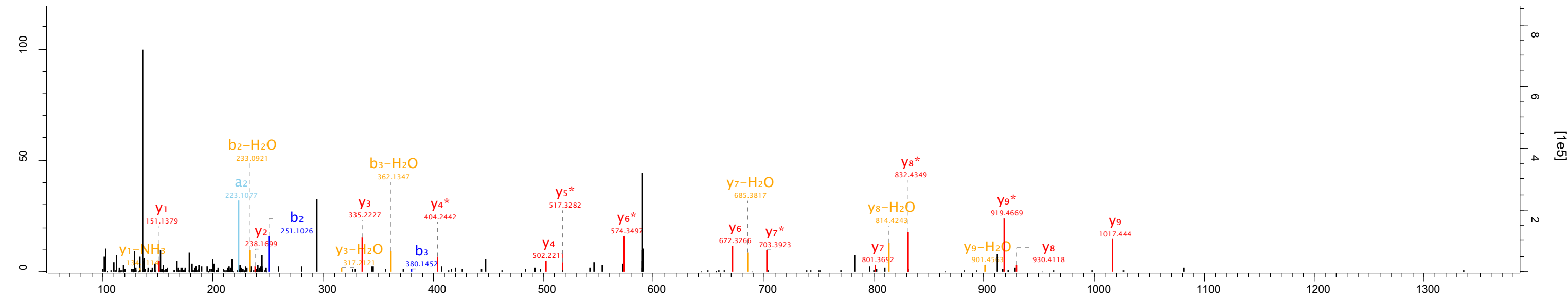
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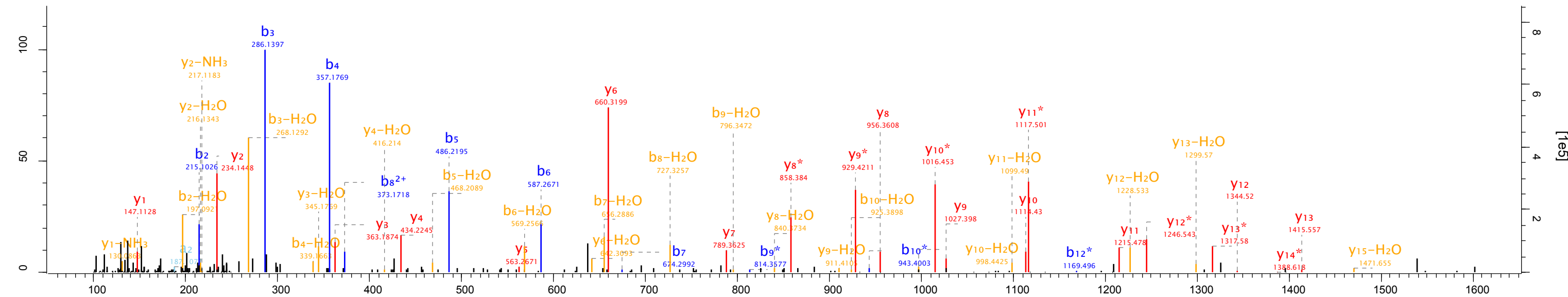


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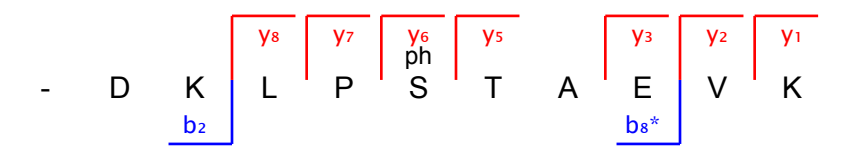
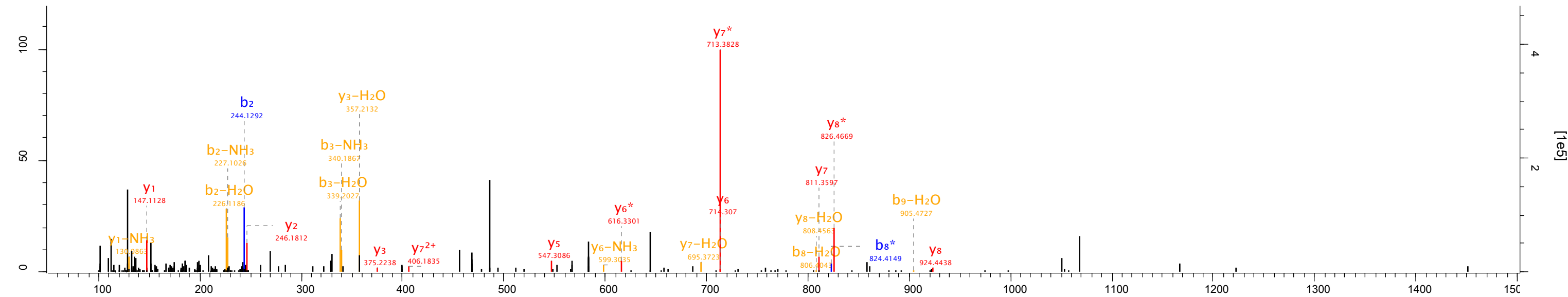
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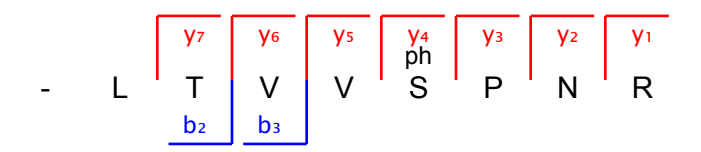
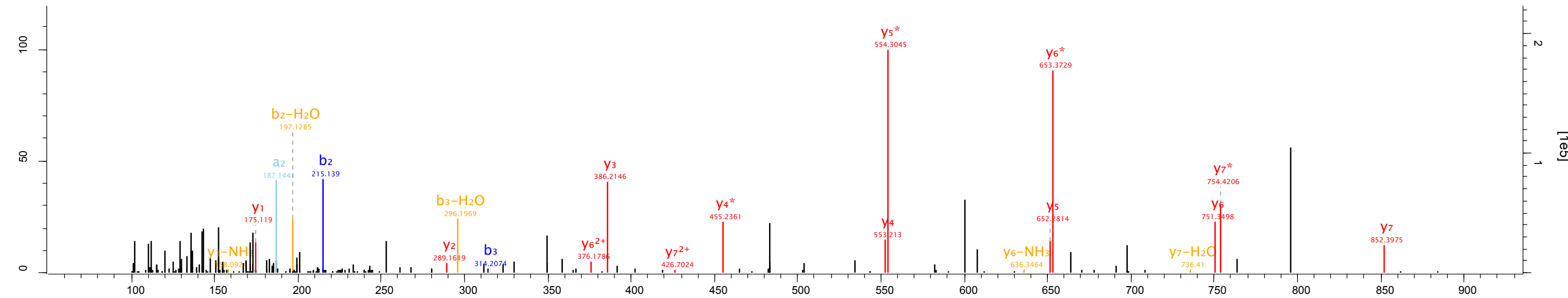
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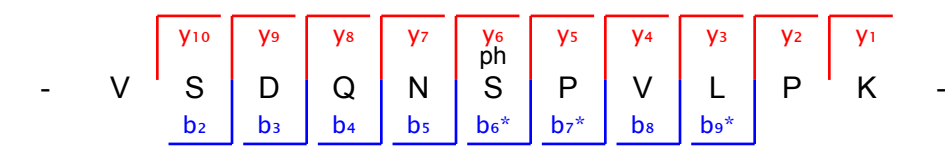
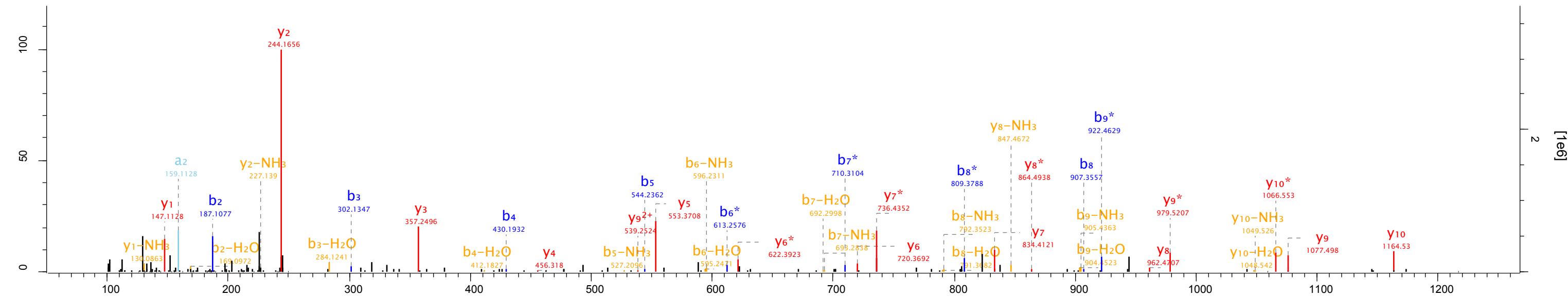
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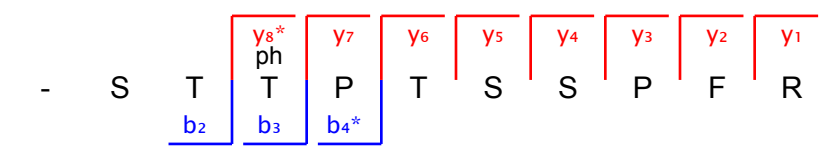
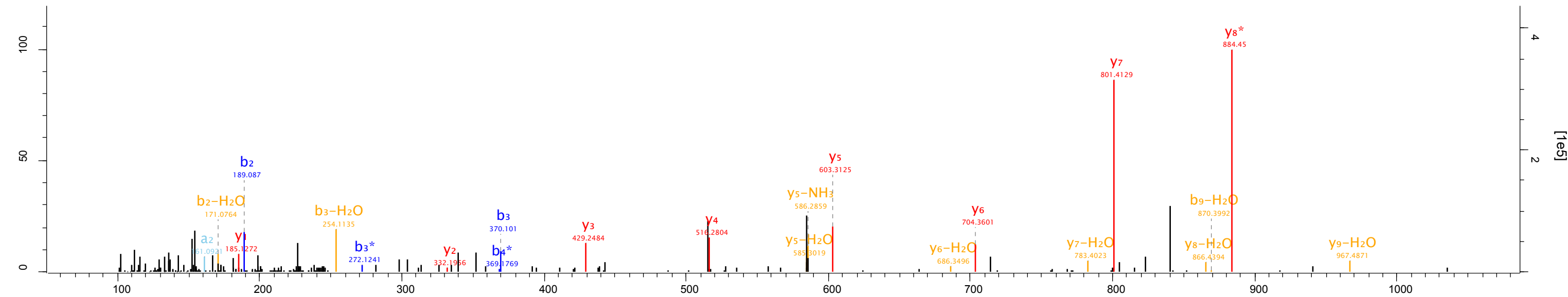
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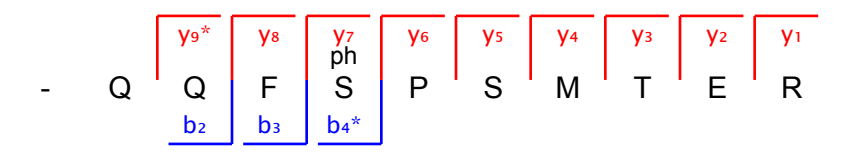
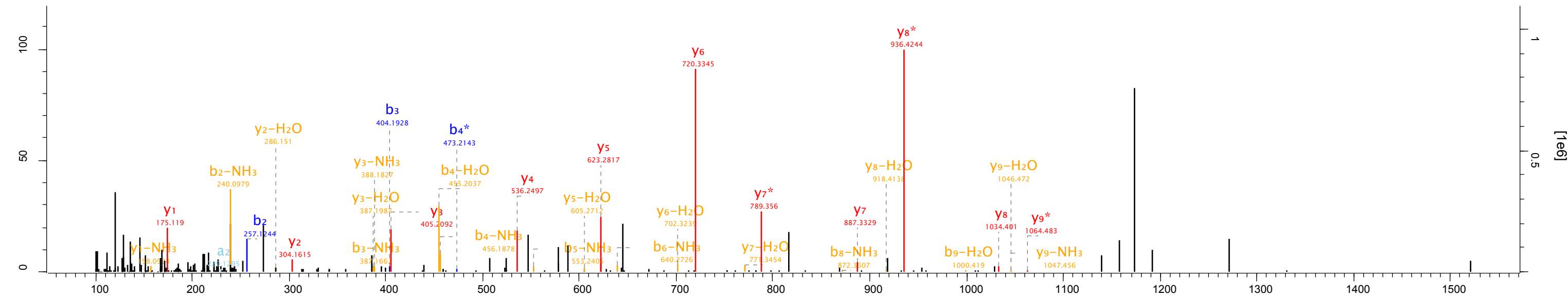
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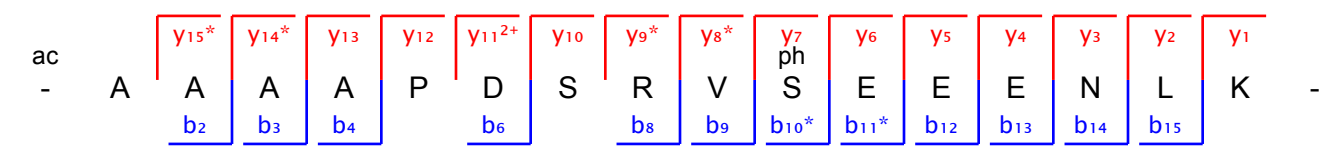
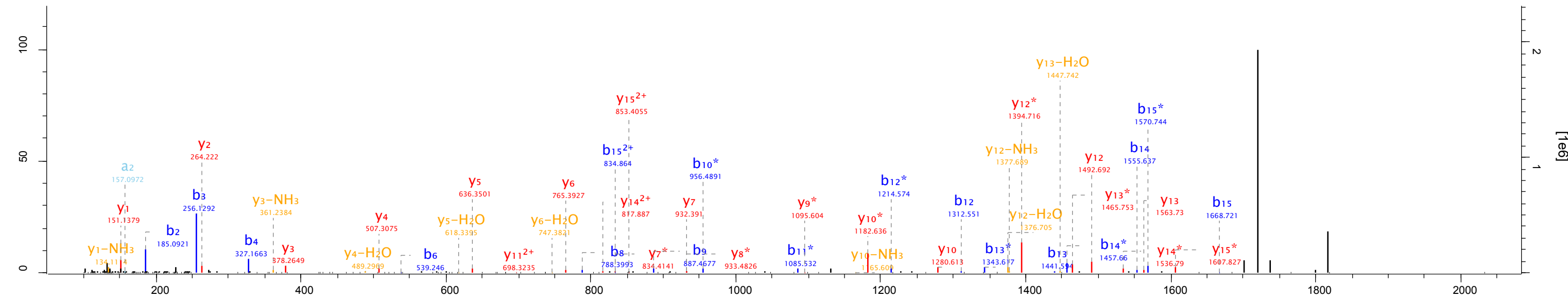
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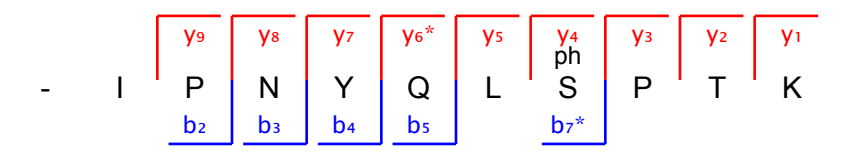
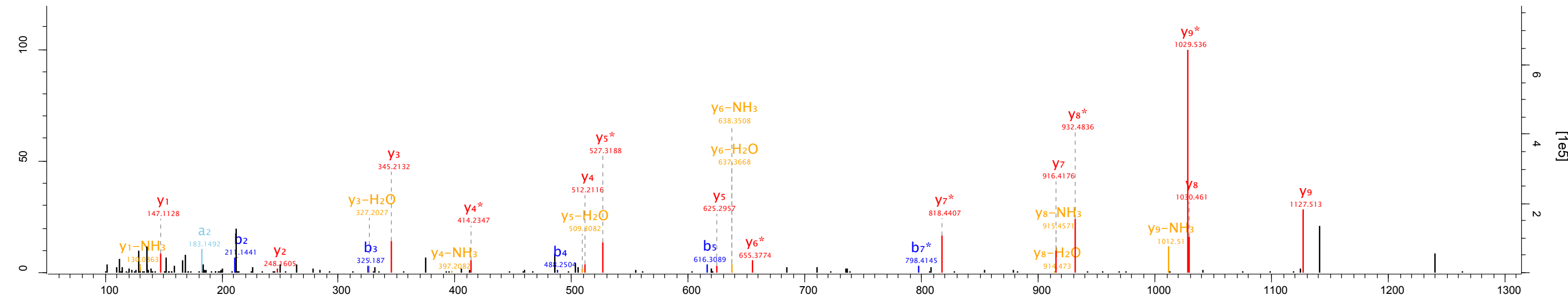
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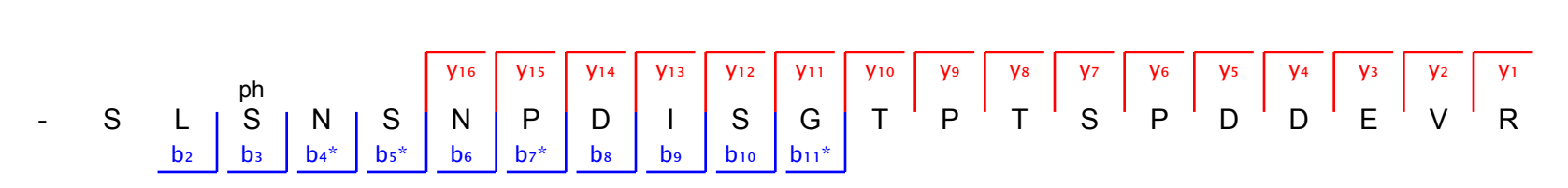
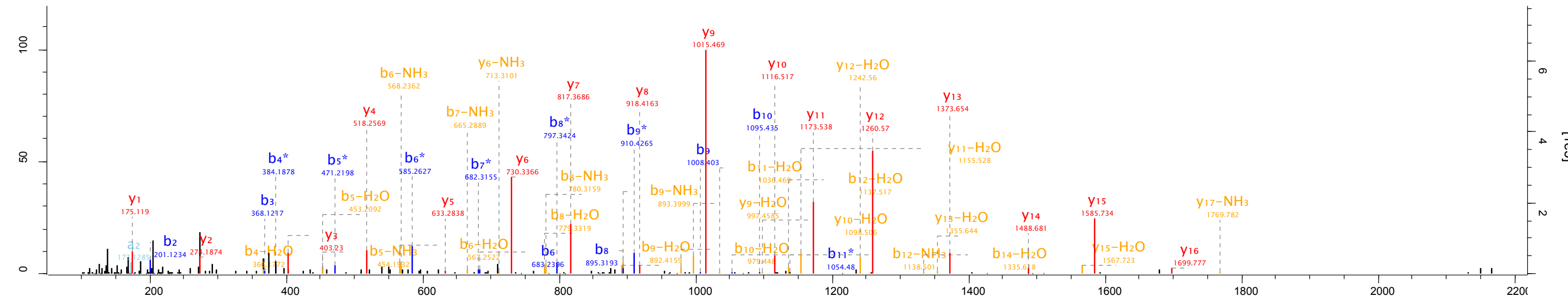


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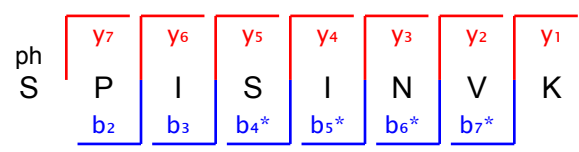
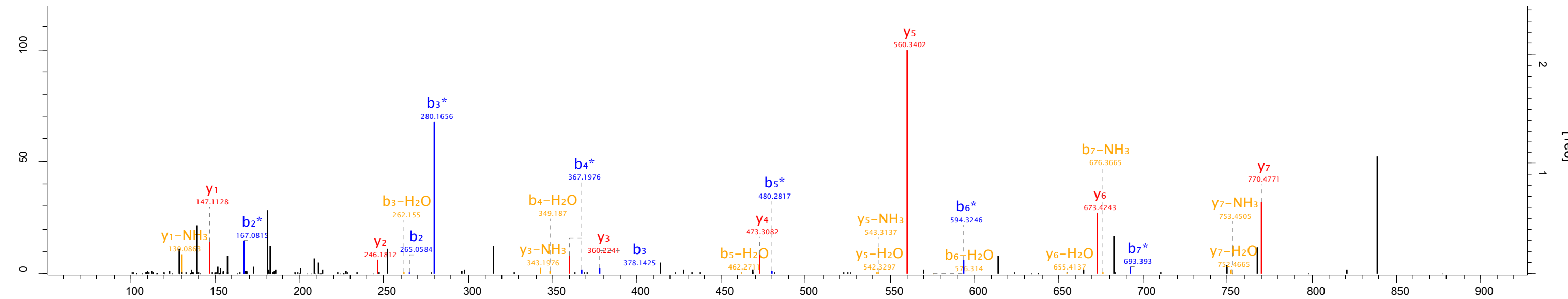


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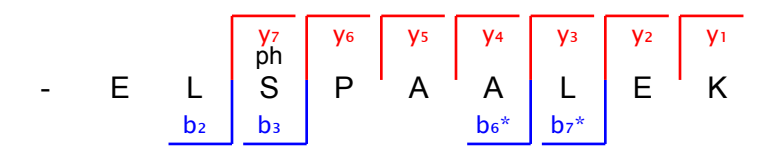
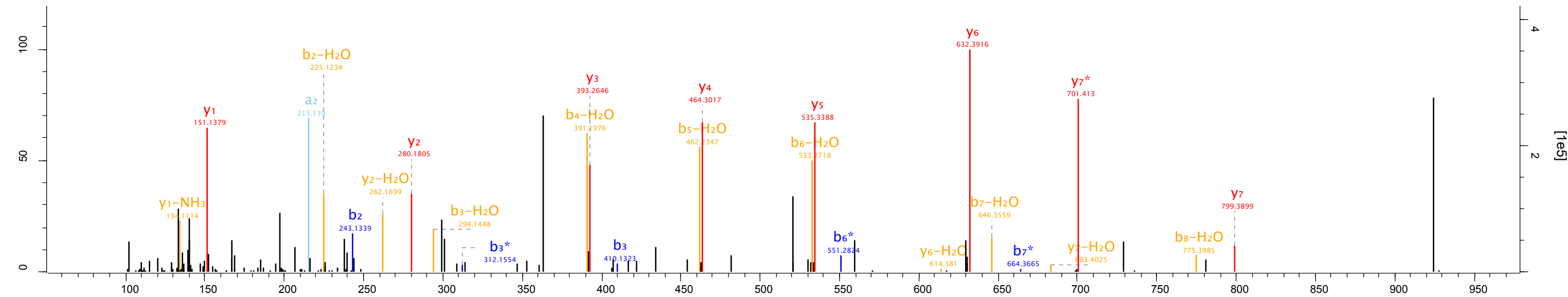
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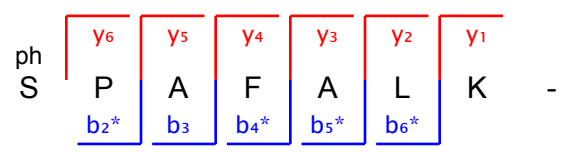
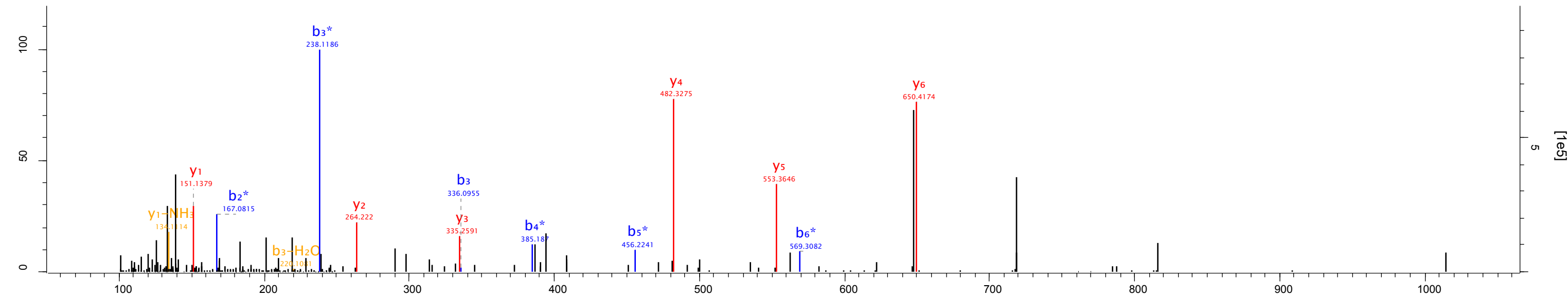
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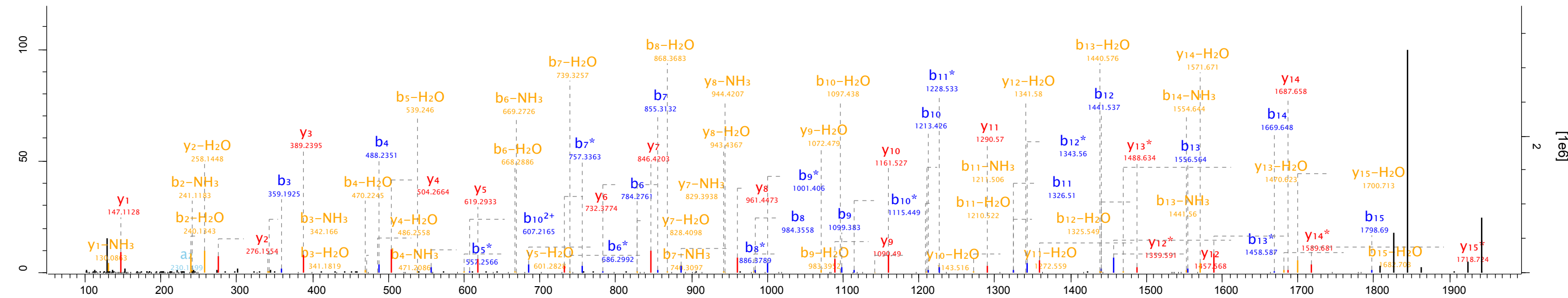
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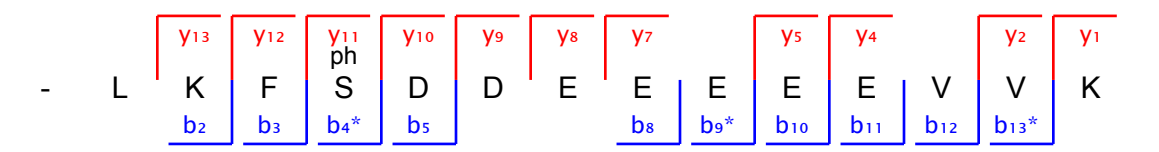
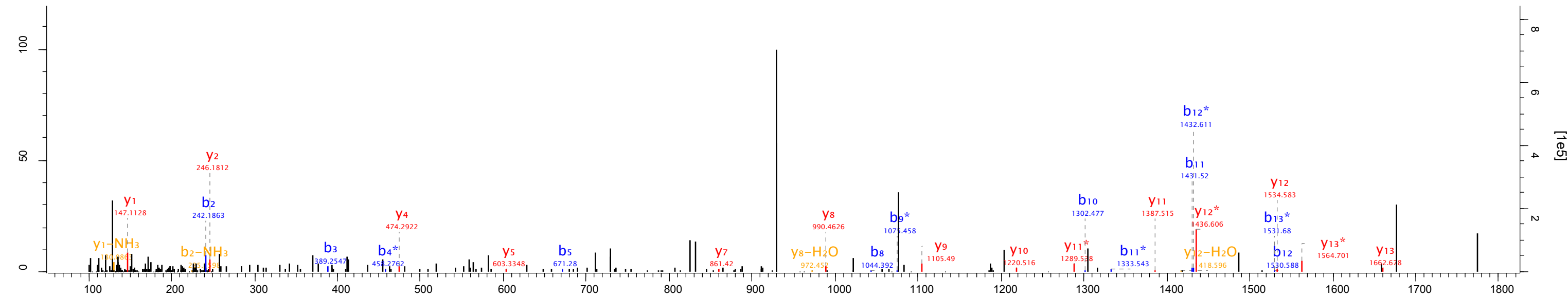


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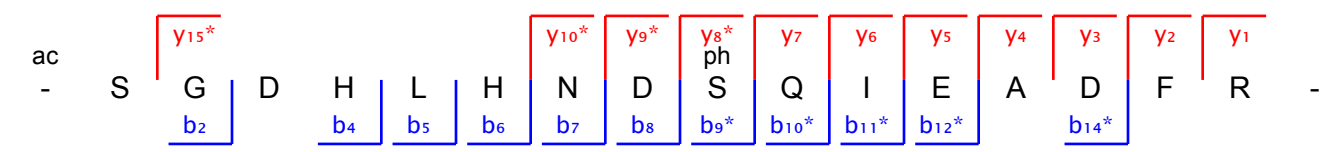
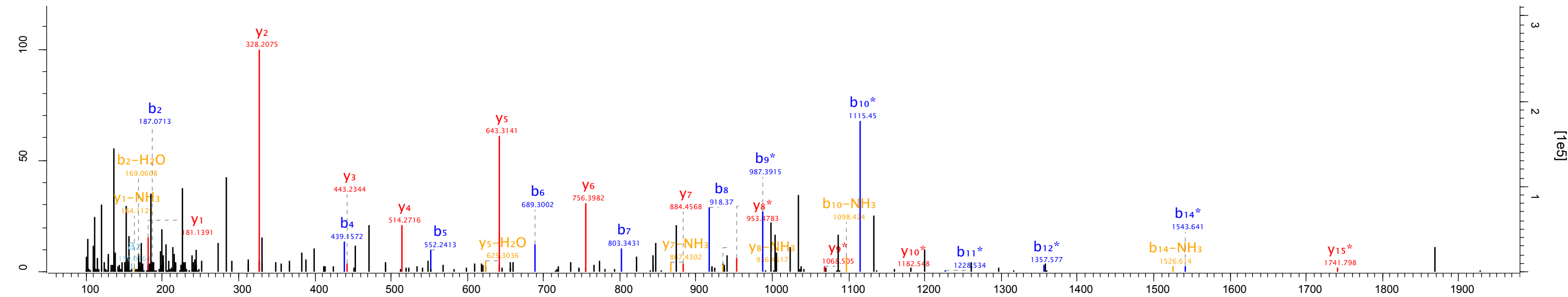
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a₂
b₃
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b₅*
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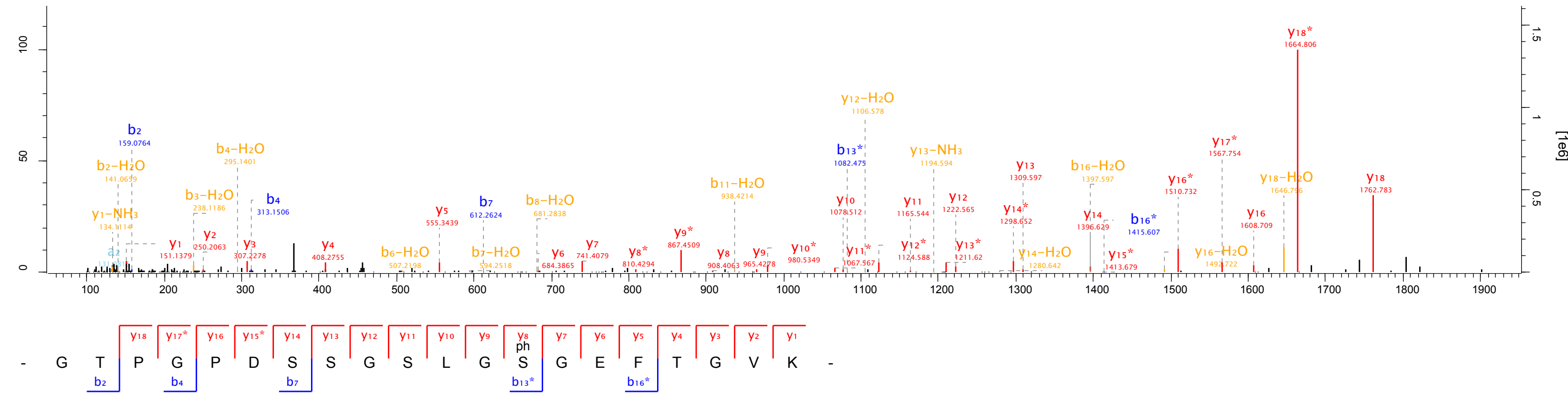
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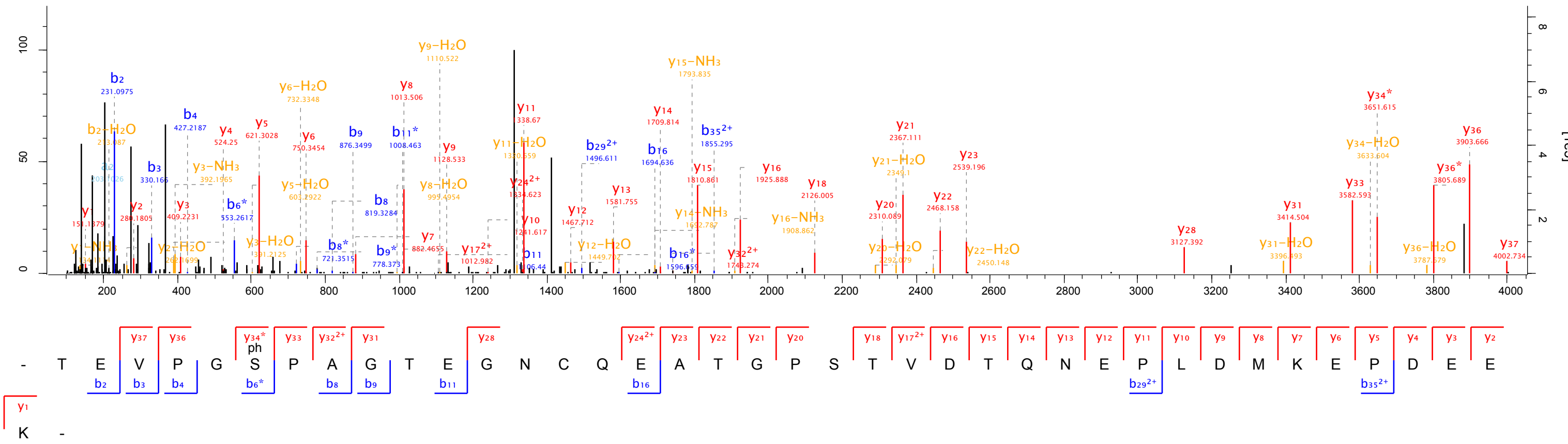
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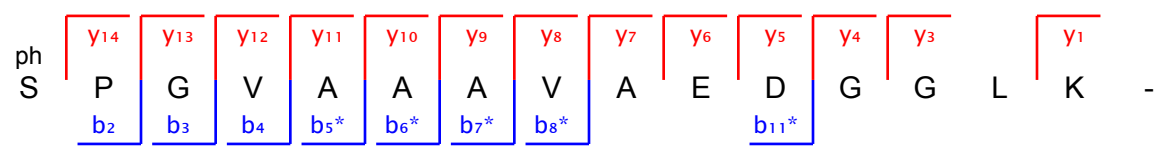
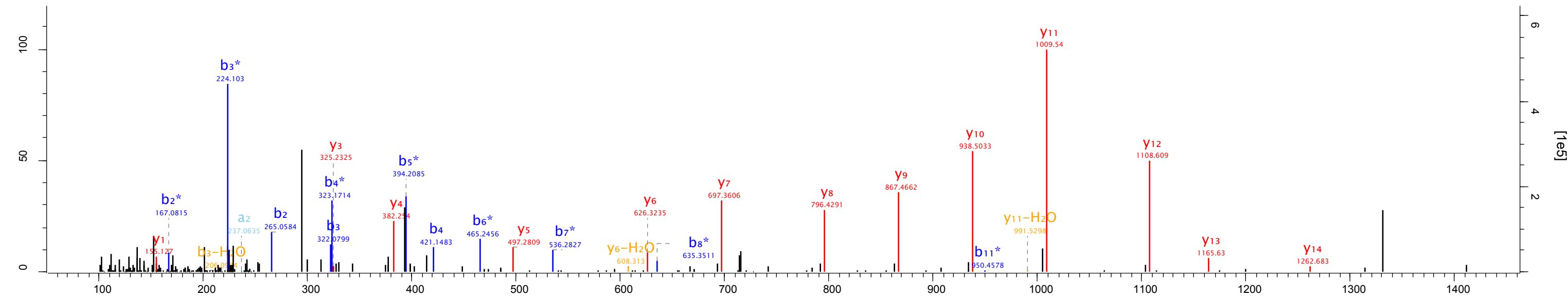
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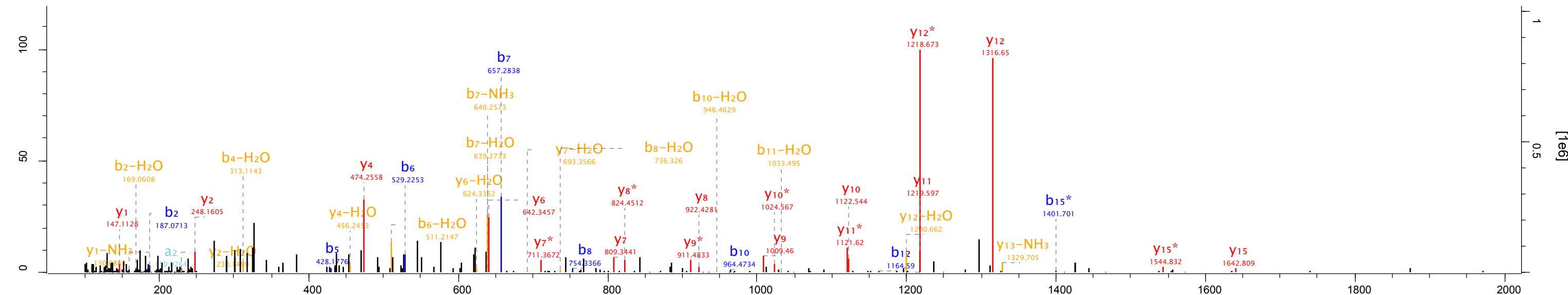


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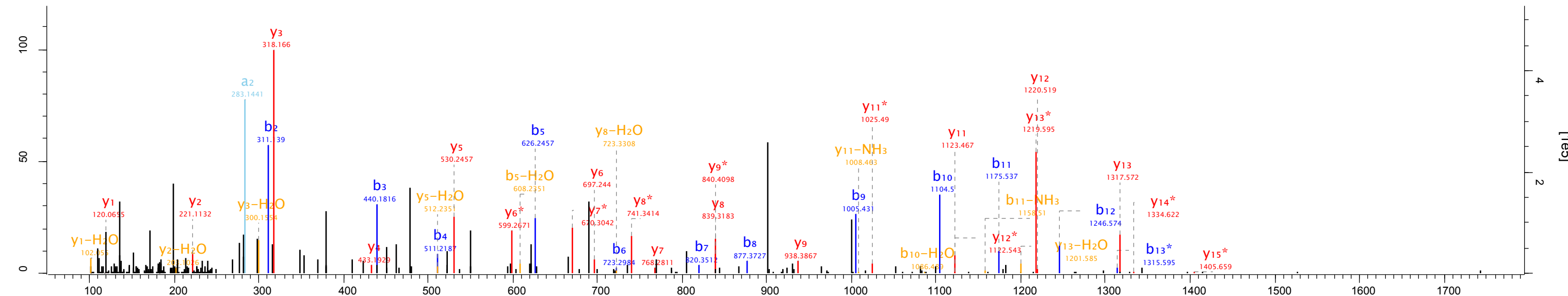
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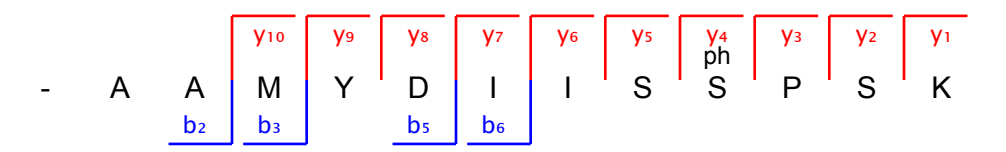
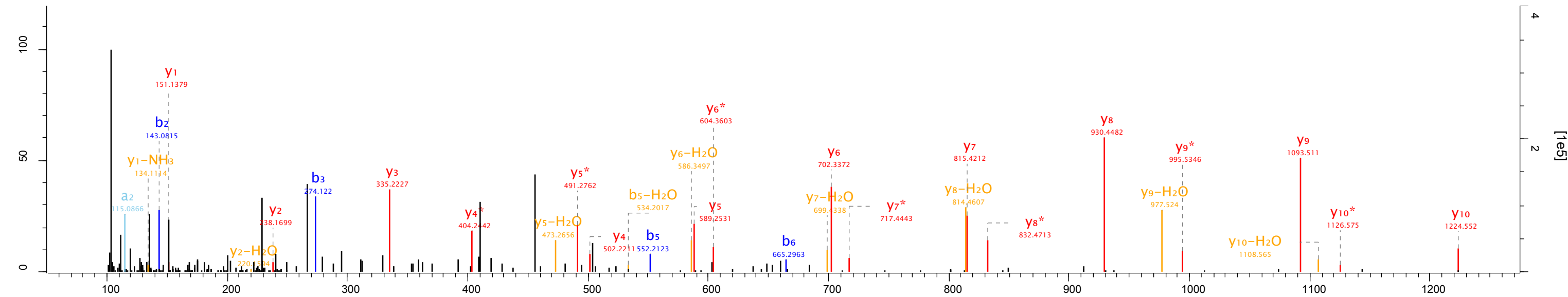
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b₂
b₅
b₆
b₇
b₈
b₁₀
b₁₂
b₁₅*
y₁₅
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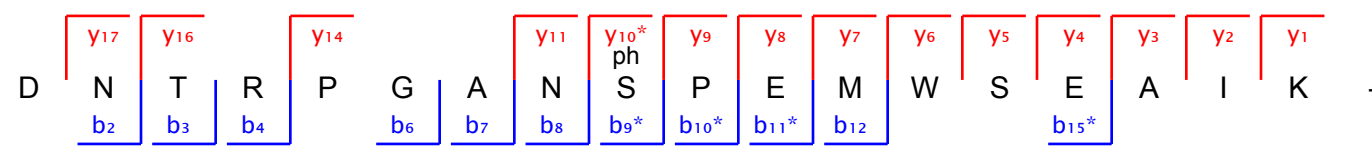
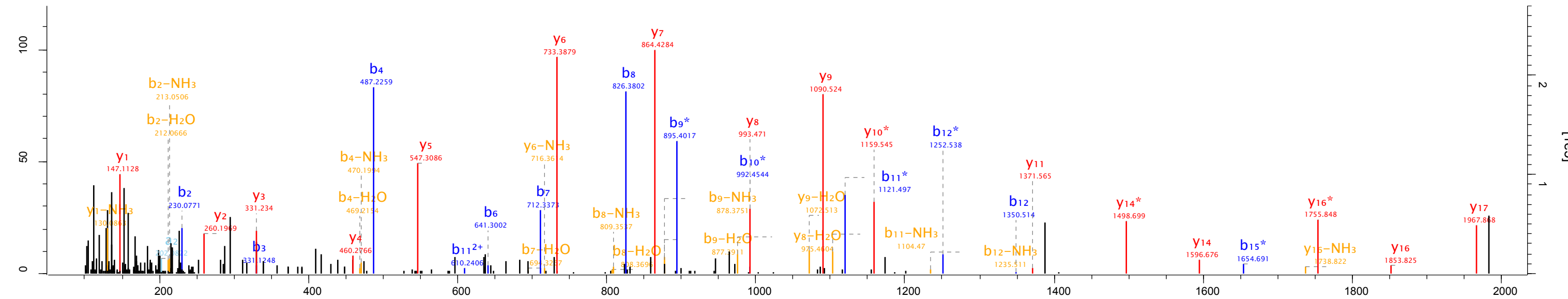


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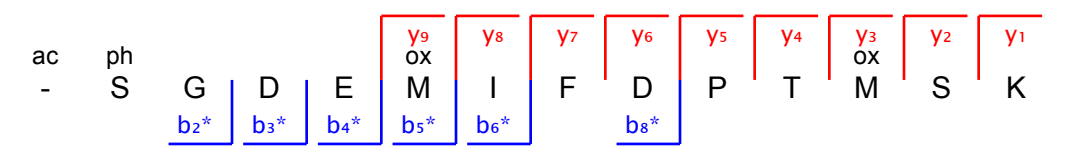
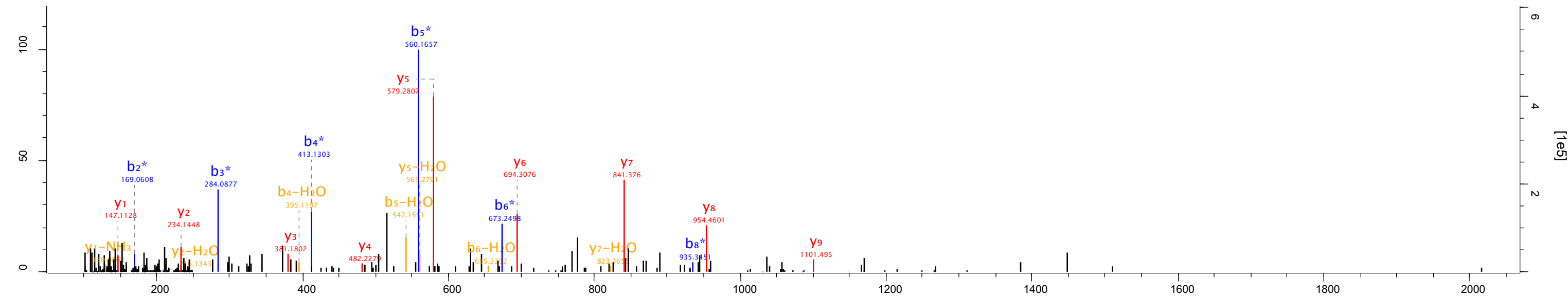
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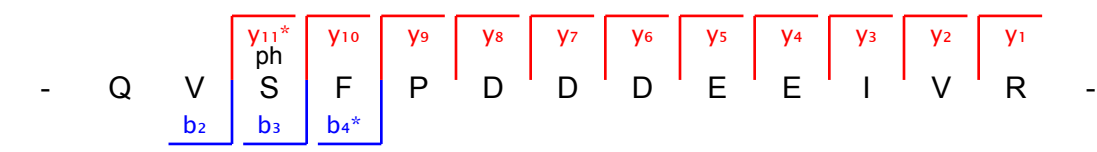
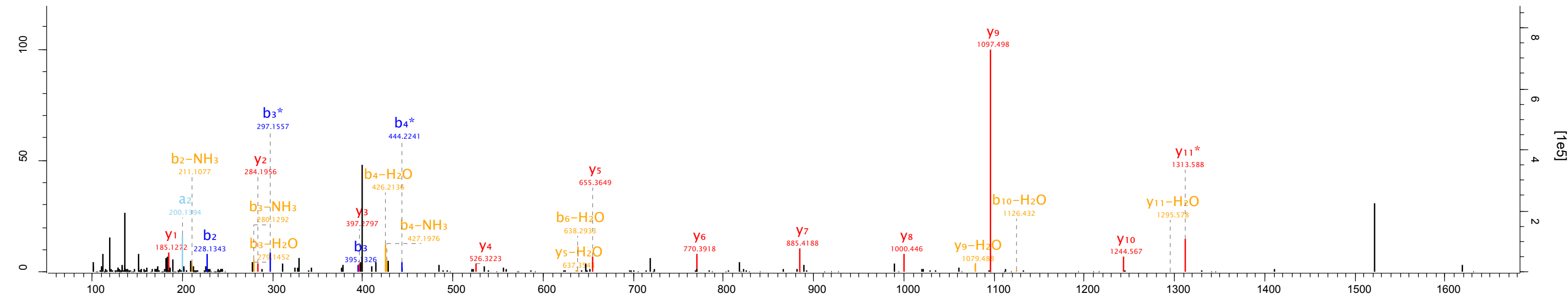
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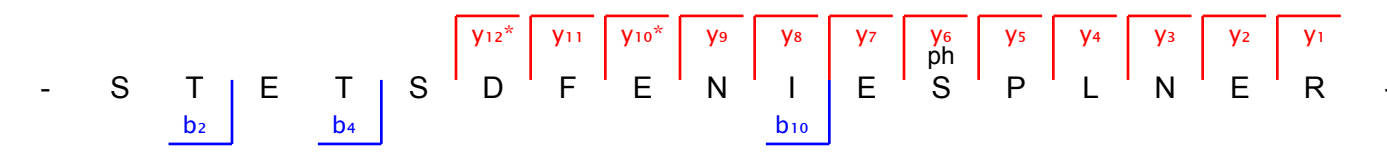
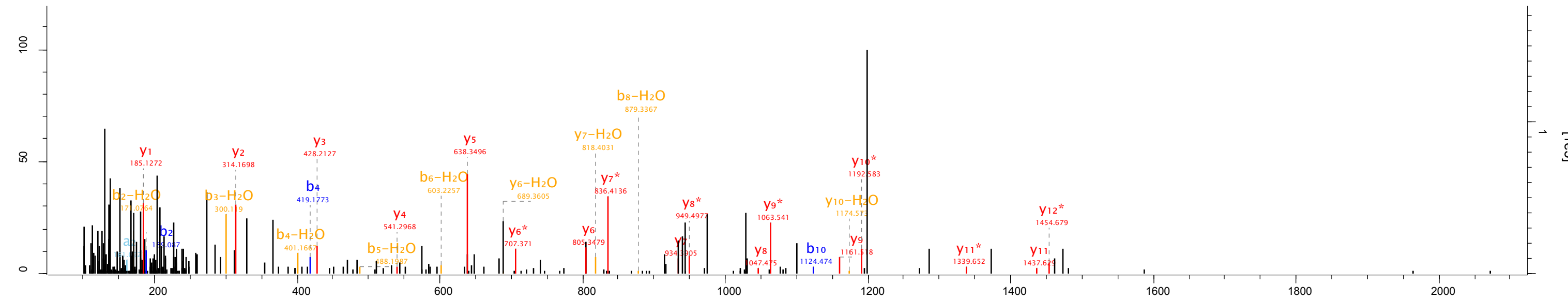
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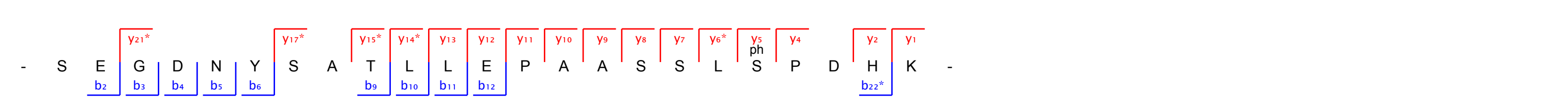
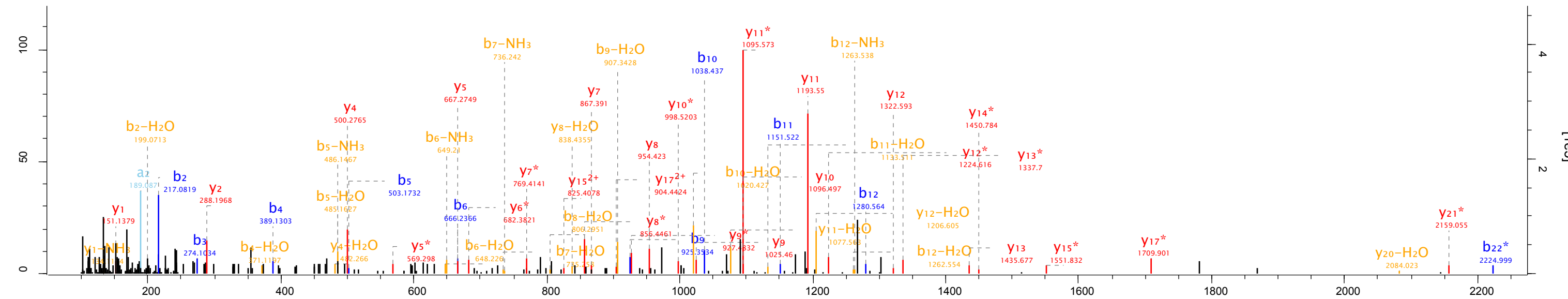
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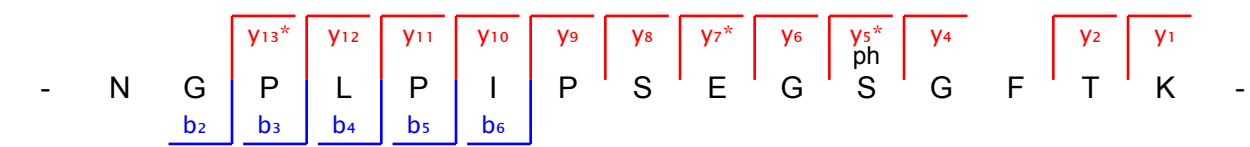
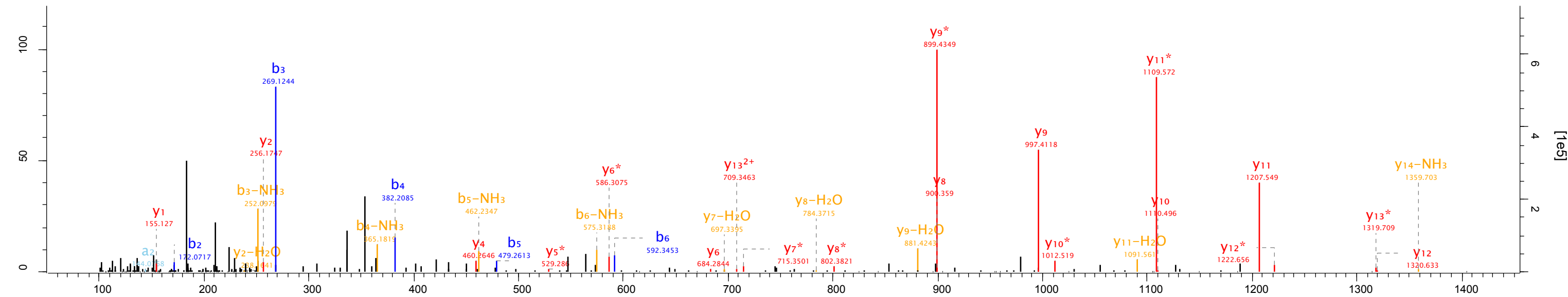
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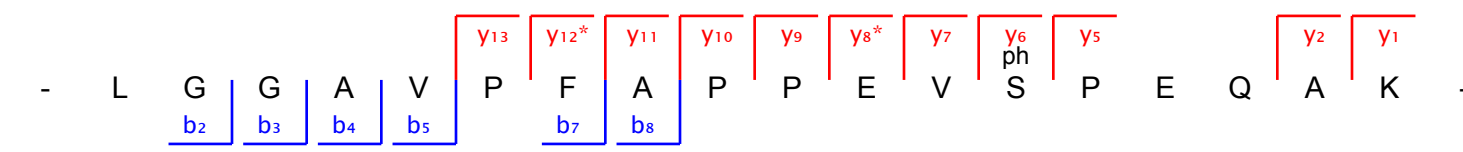
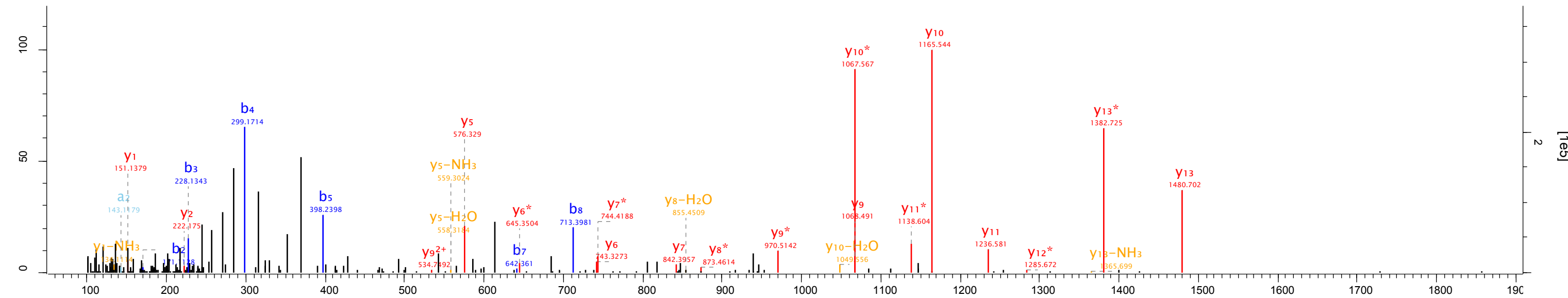
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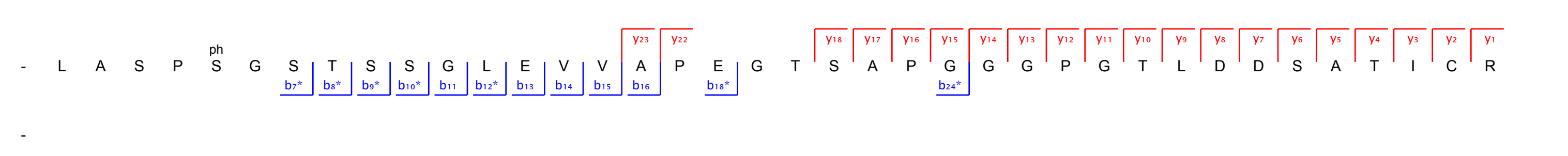
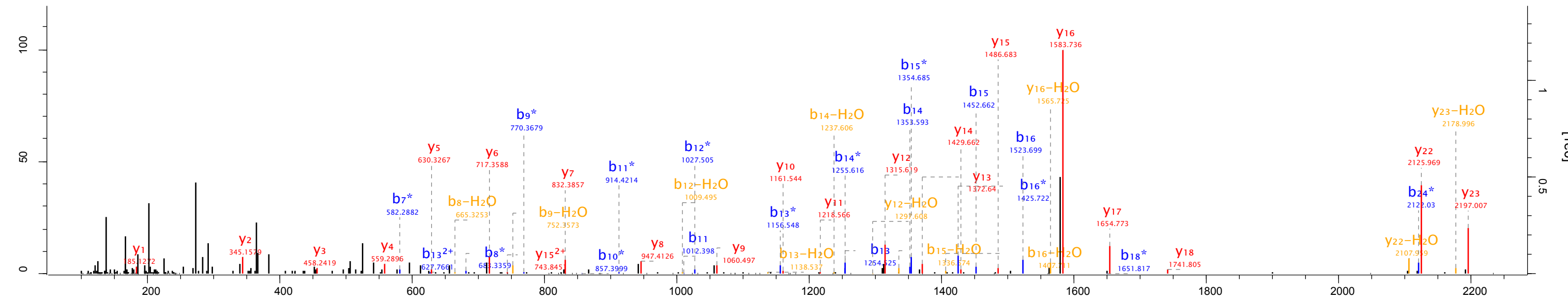
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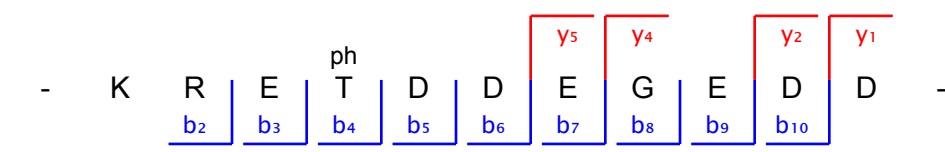
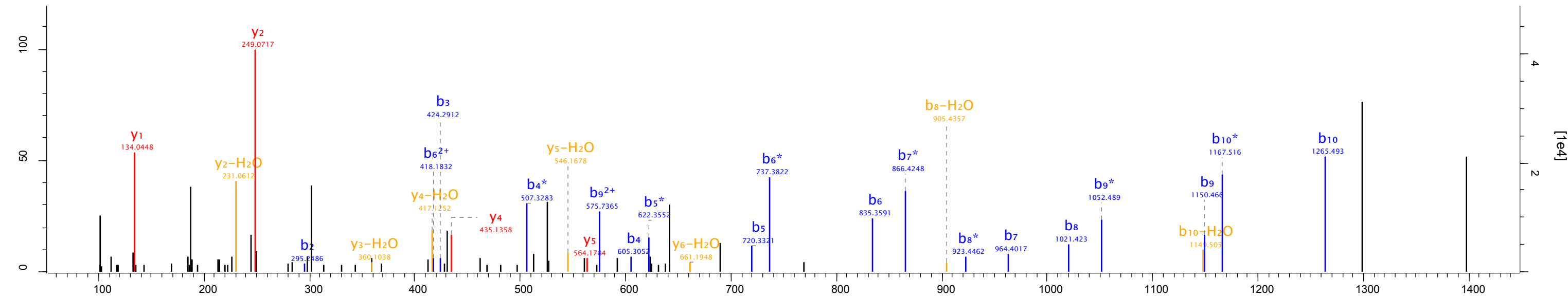
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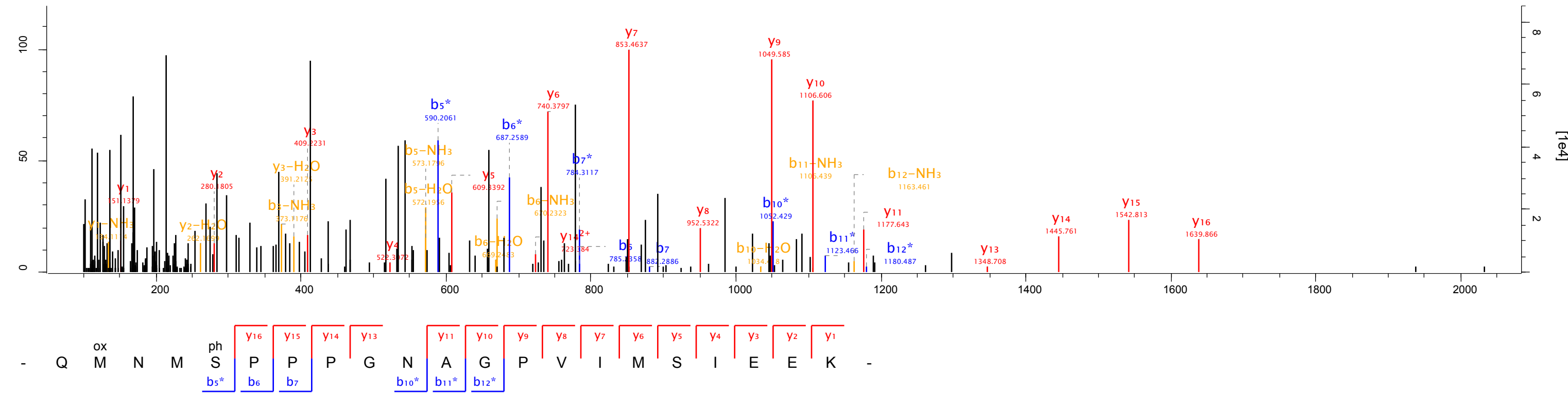
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Raw file

20171215_MaS_33SR_LMH_phospho_06

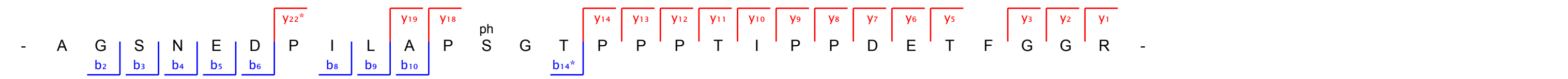
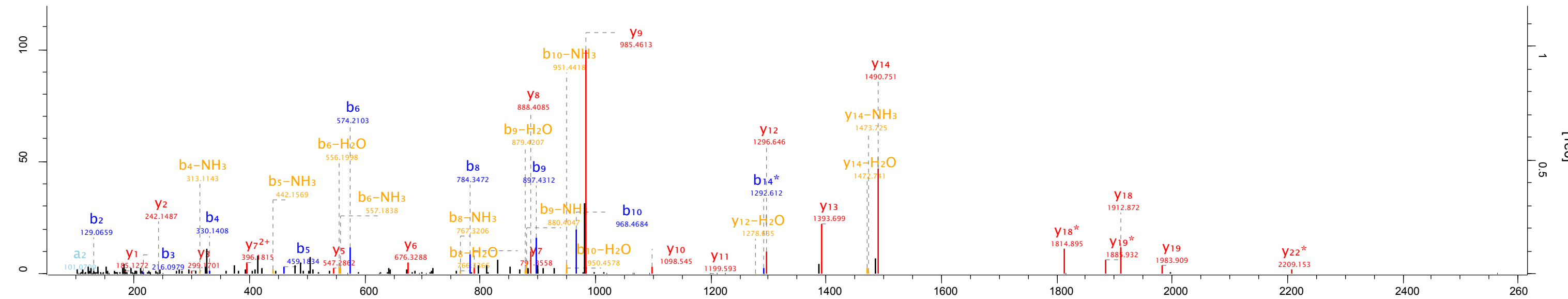
Scan	Method	Score	m/z	Gene names
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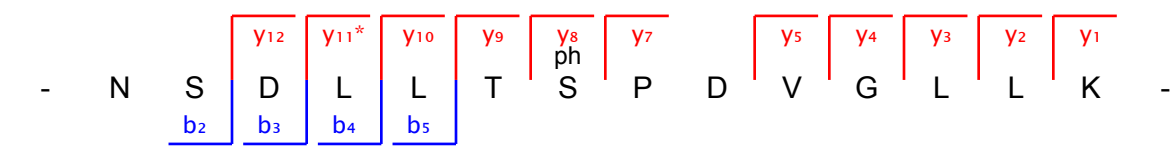
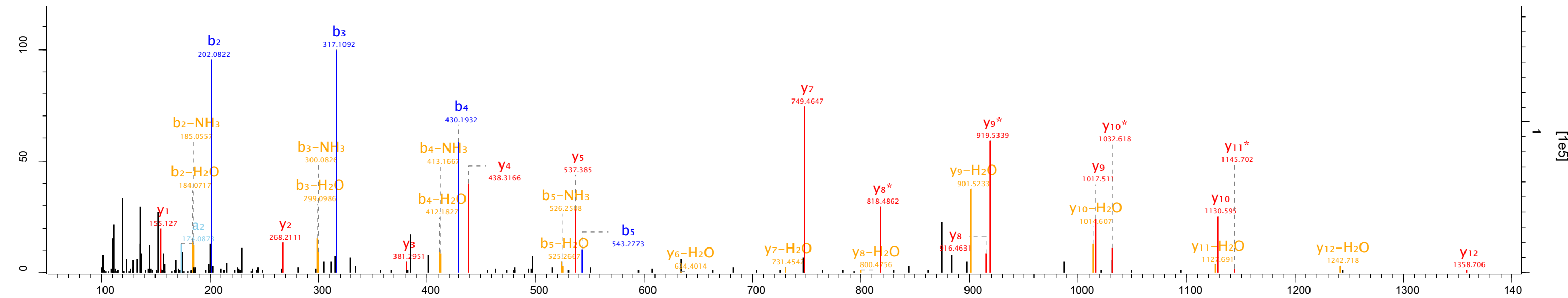
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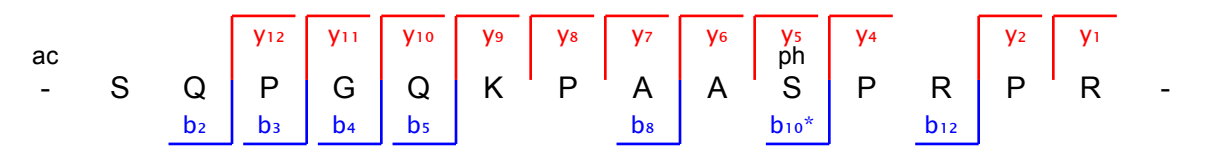
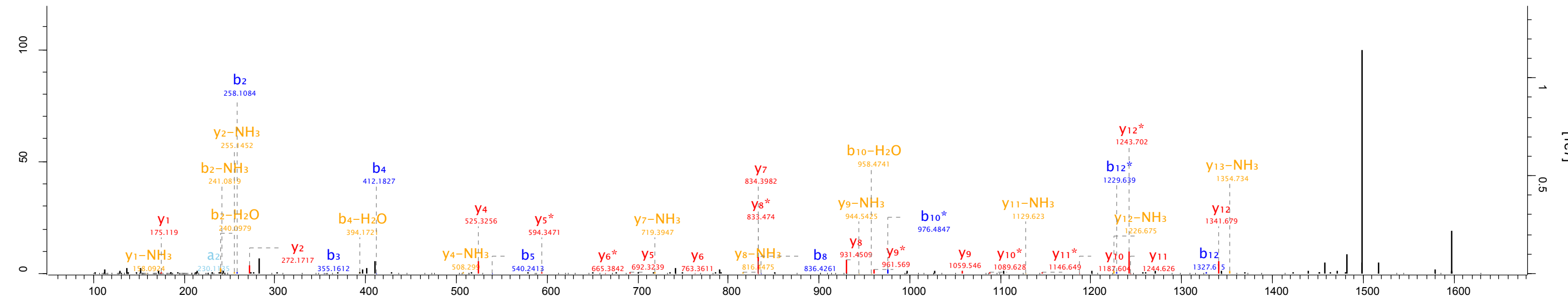
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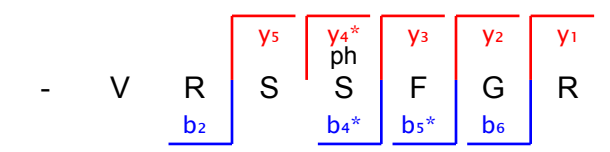
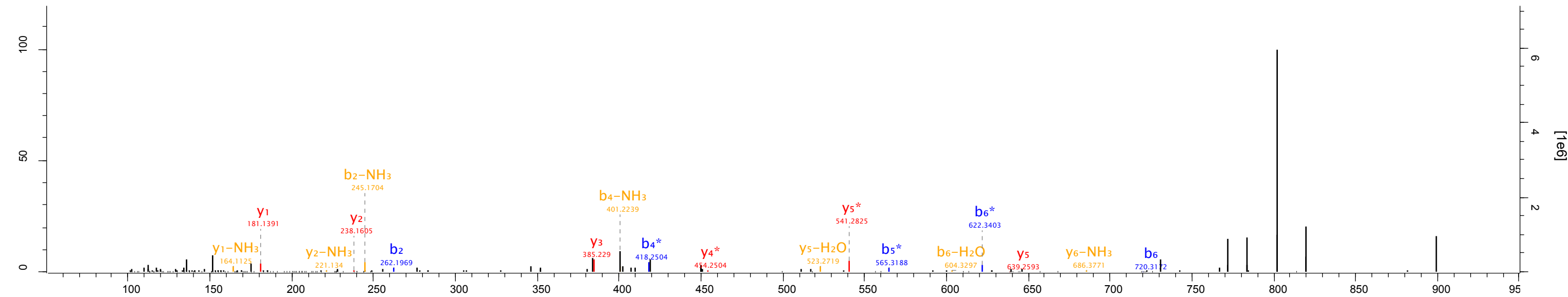
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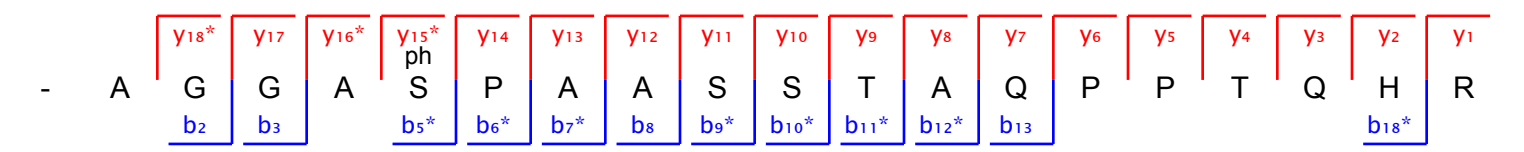
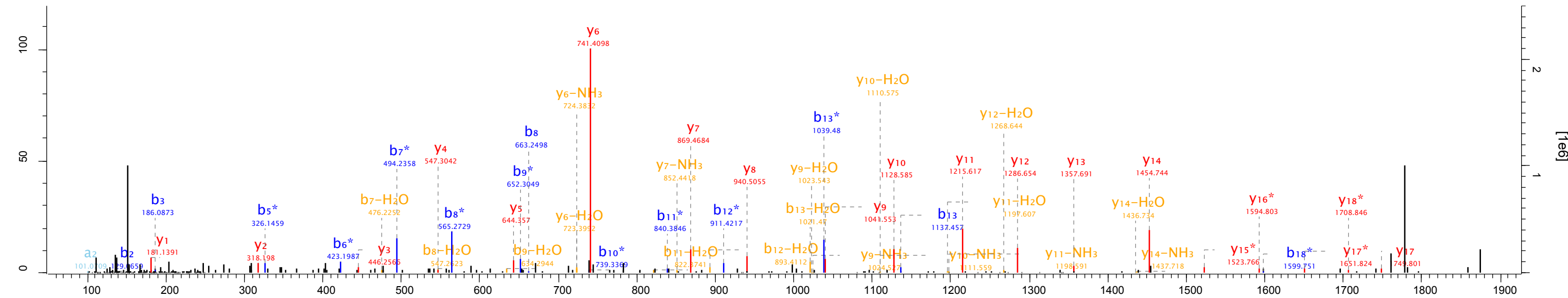
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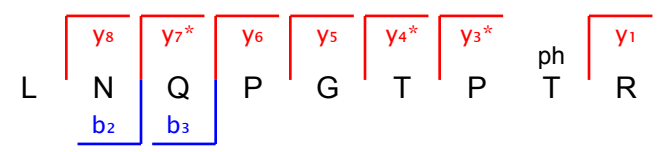
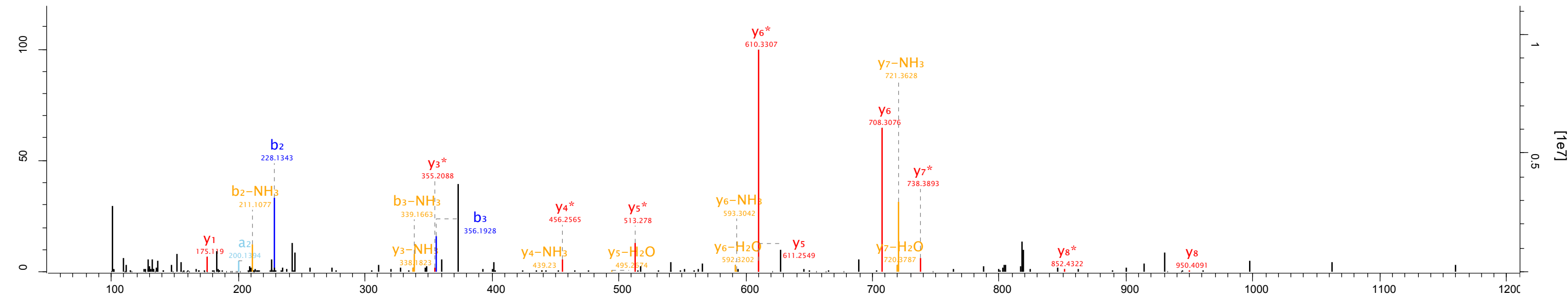
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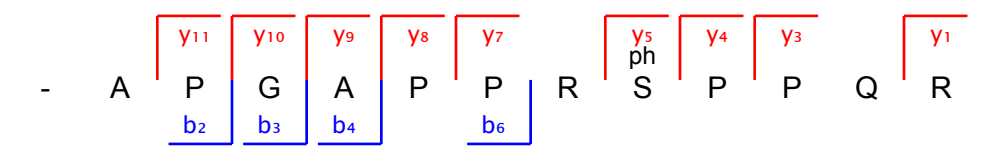
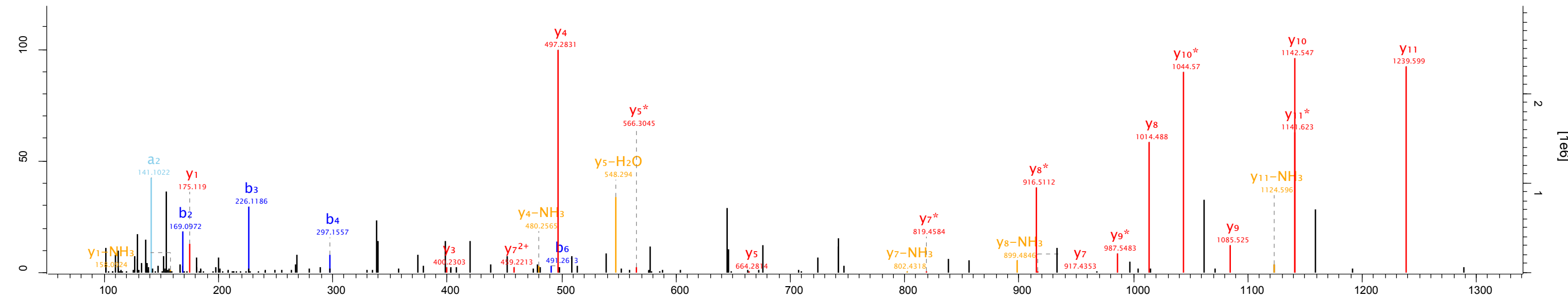
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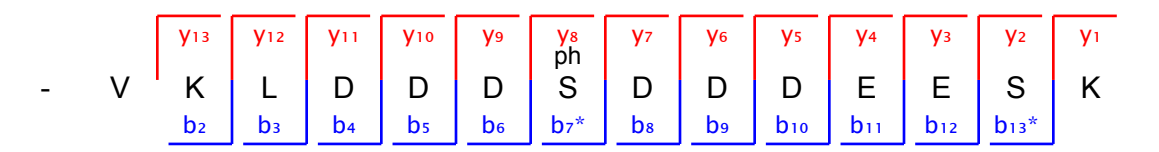
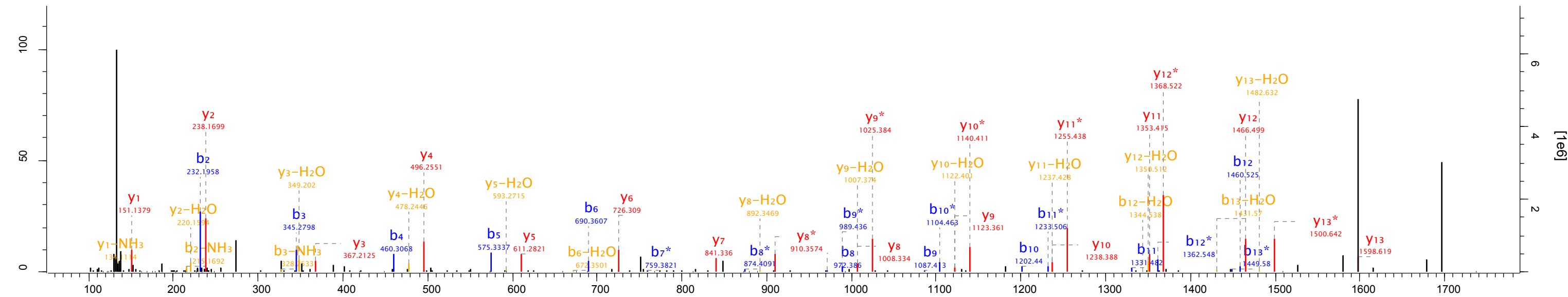
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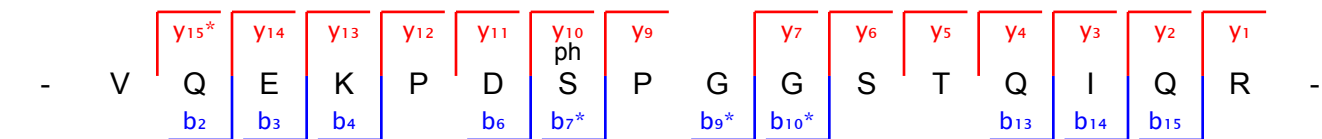
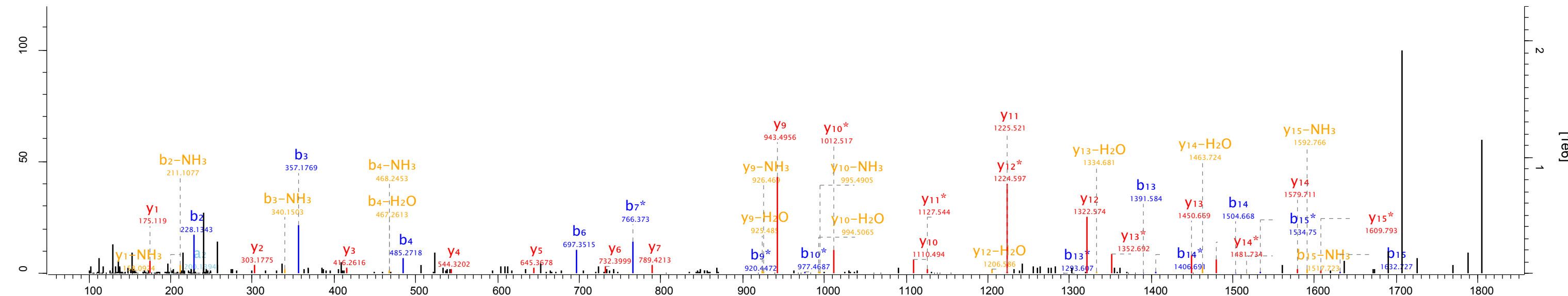
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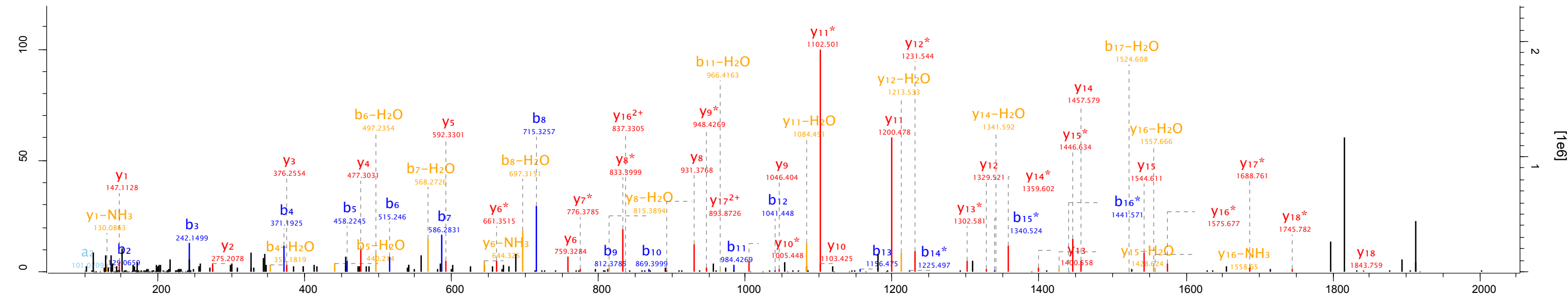
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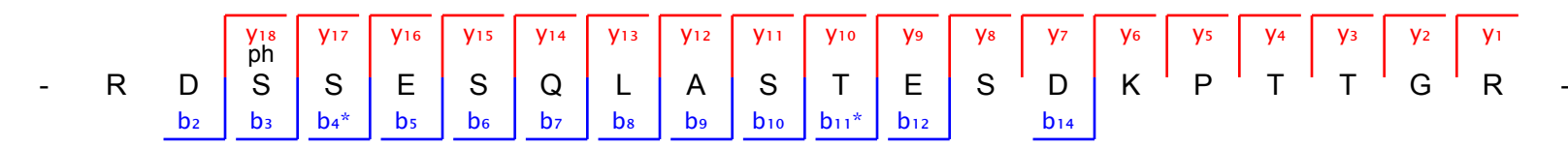
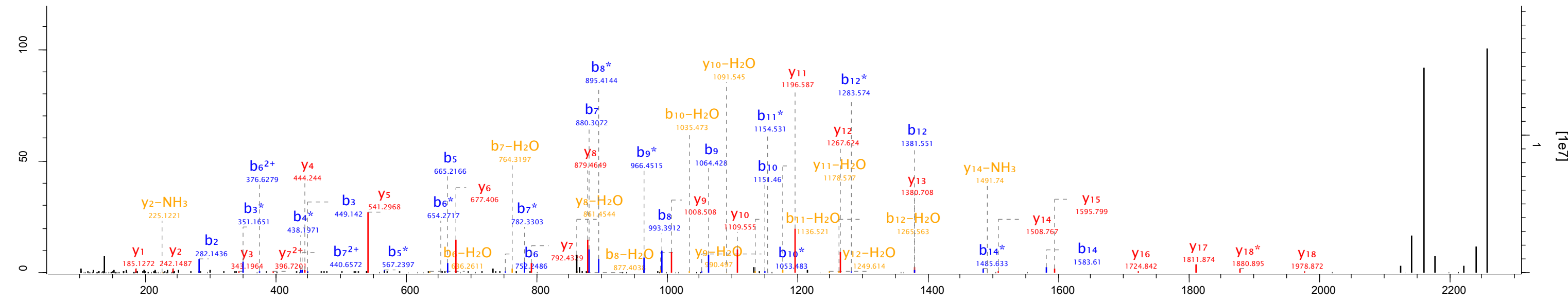


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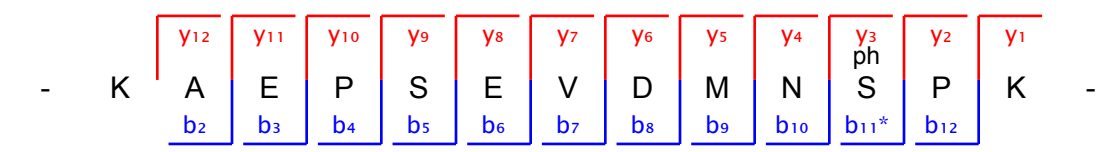
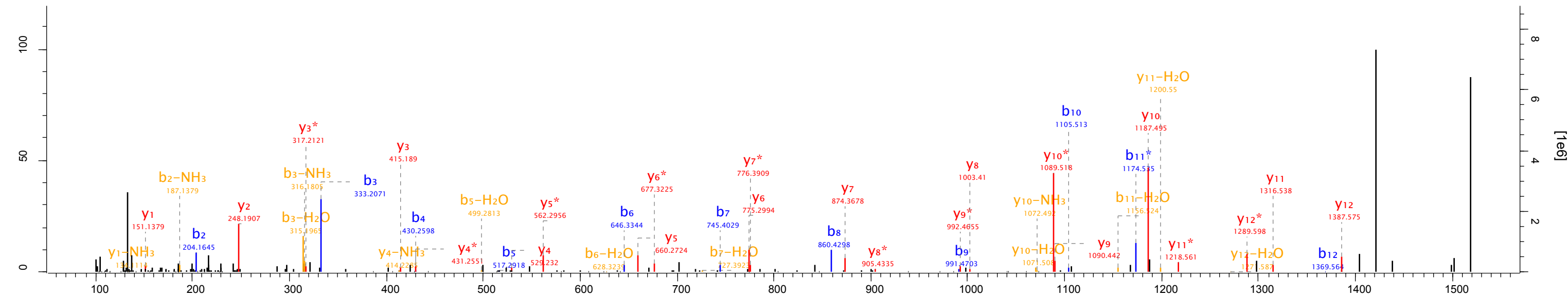
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y₁₈ y₁₇* y₁₆* y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇* y₆ ph y₅ y₄ y₃ y₂ y₁

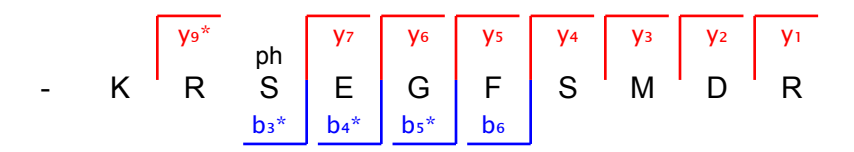
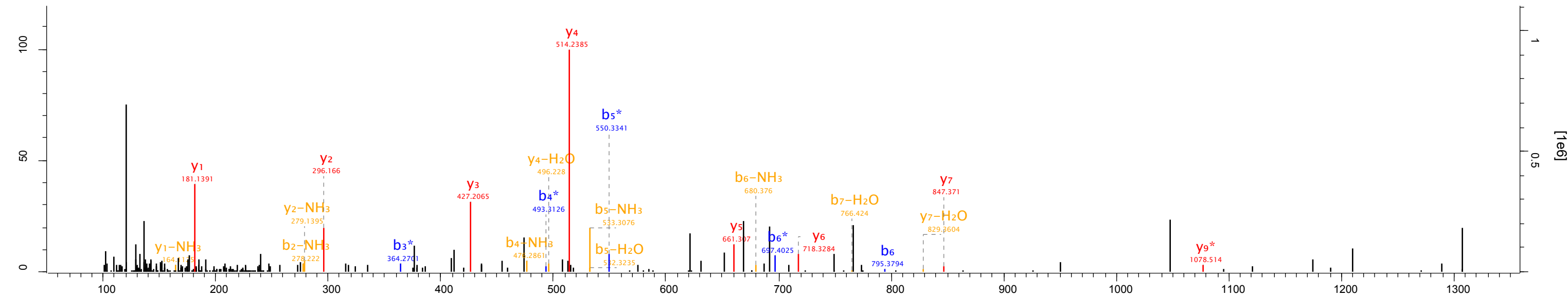
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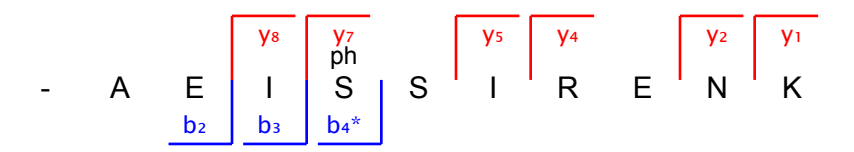
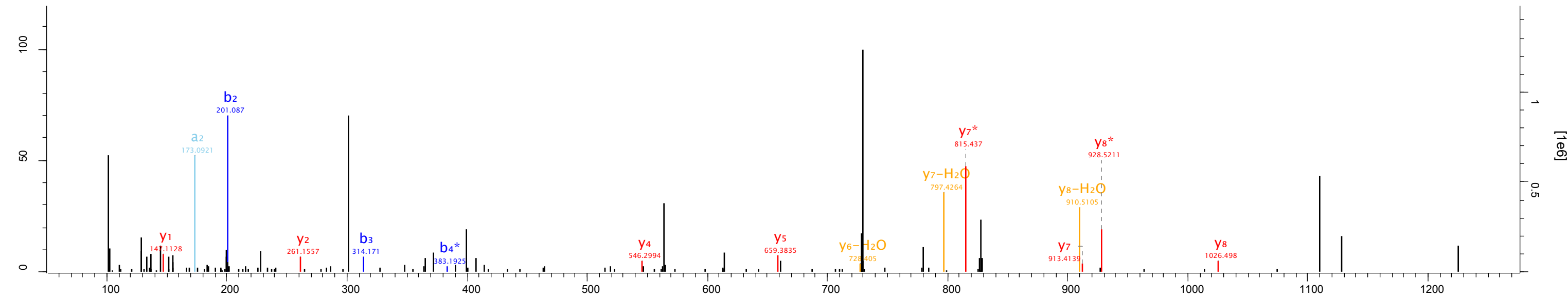
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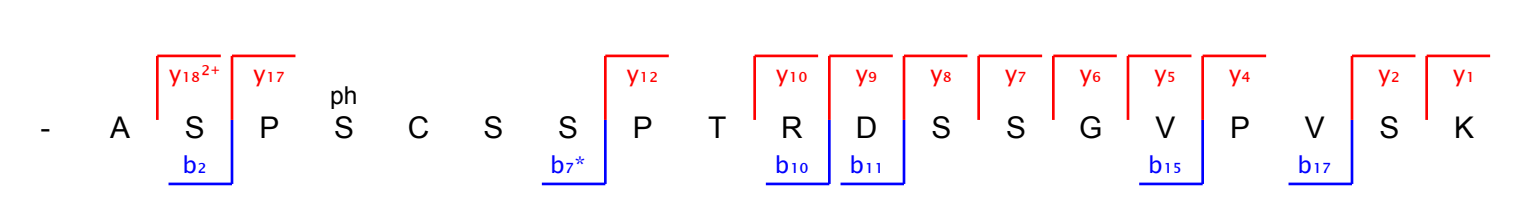
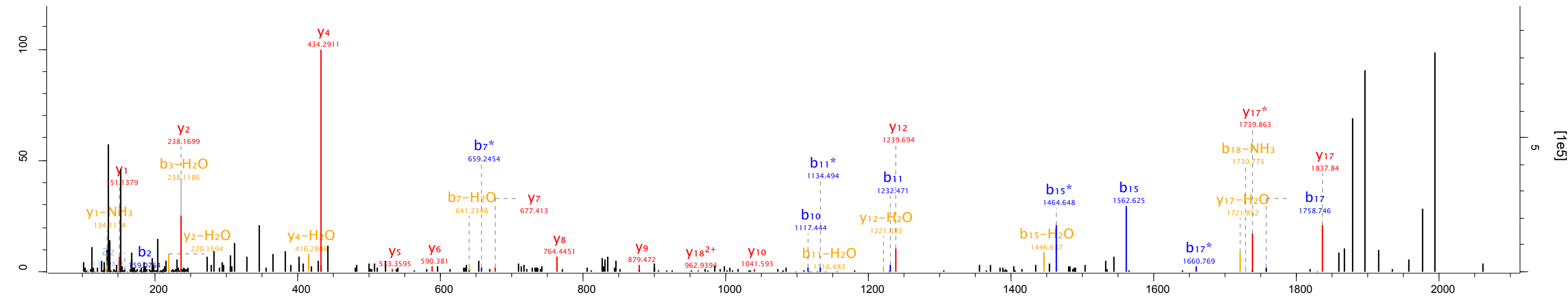
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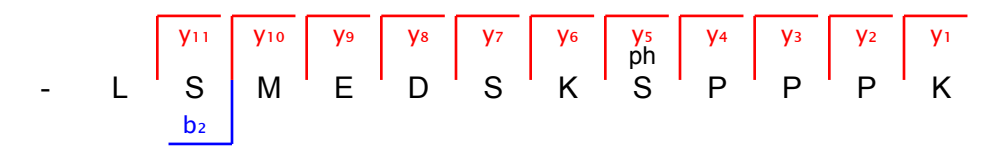
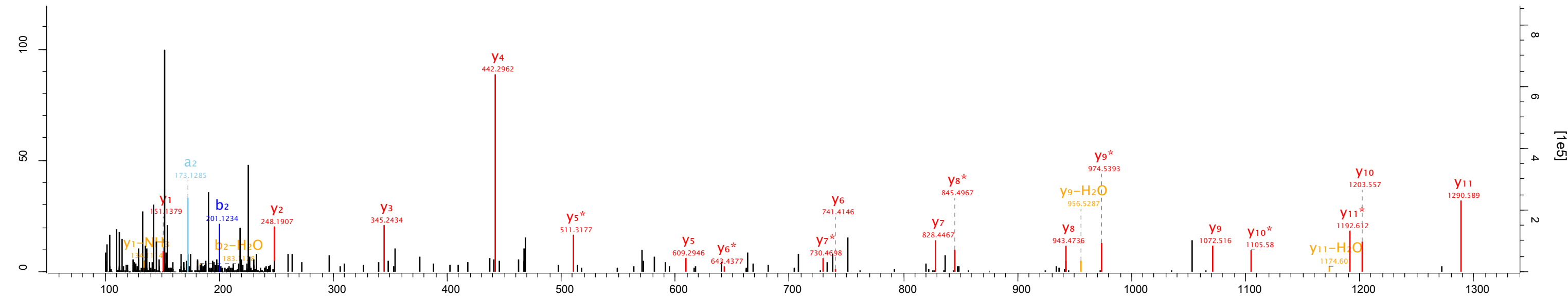
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 4217 FTMS; HCD 79.43 998.96 C12orf45



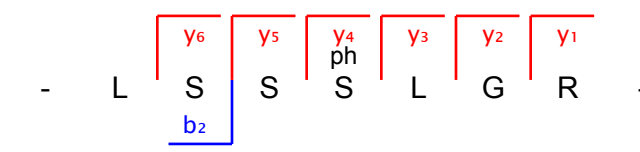
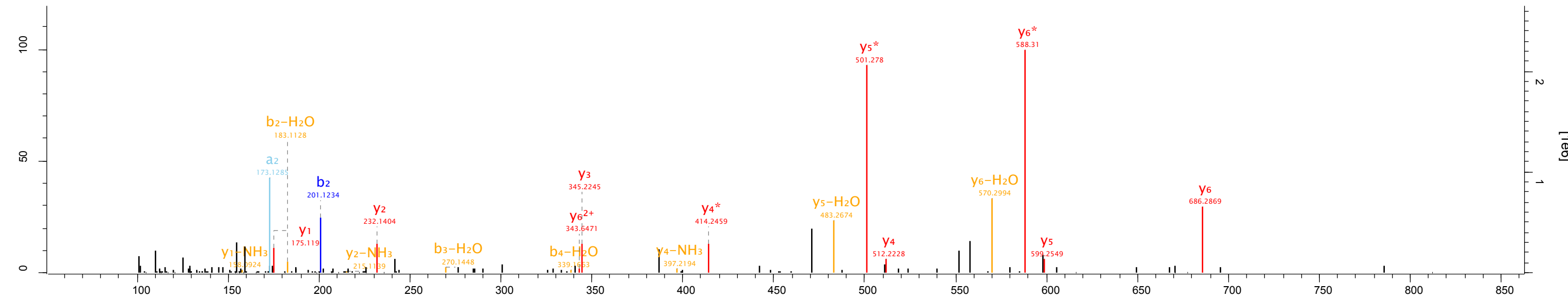
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20171215_MaS_33SR_LMH_phospho_06

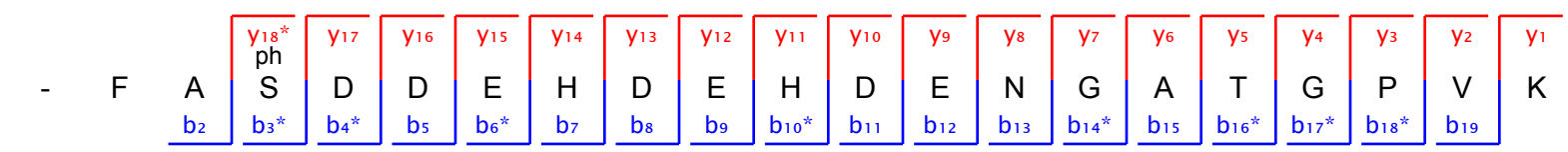
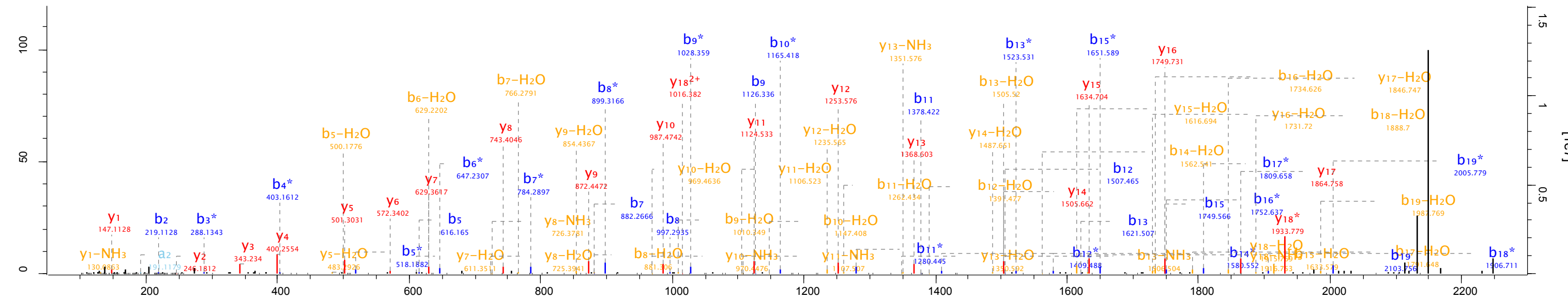
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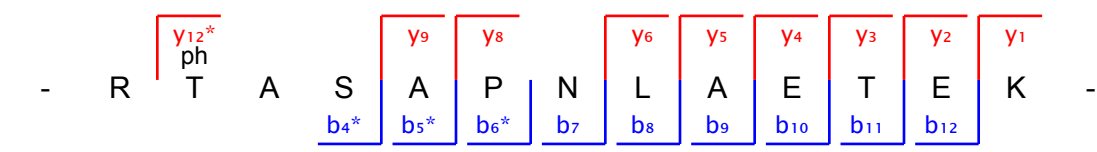
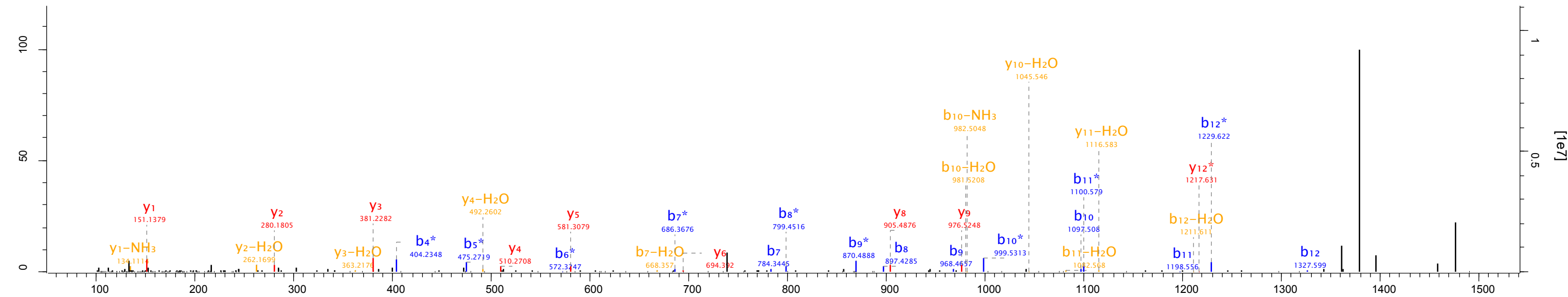
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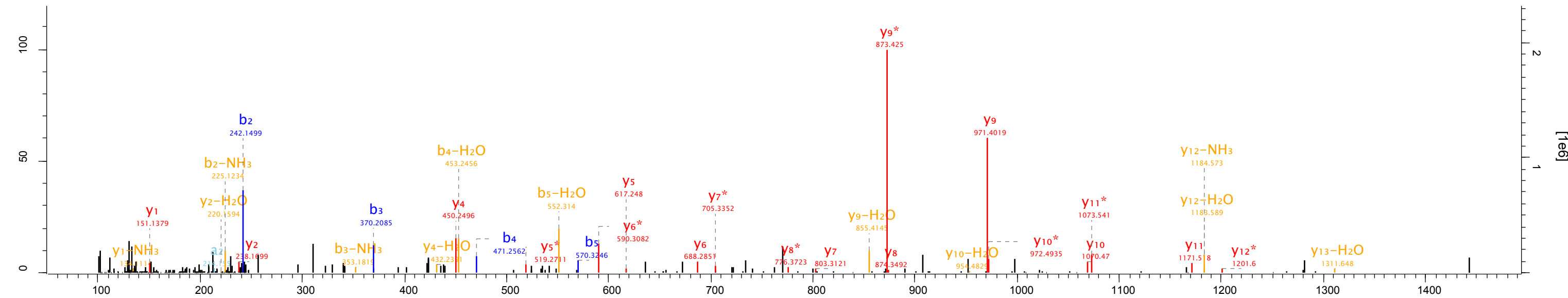
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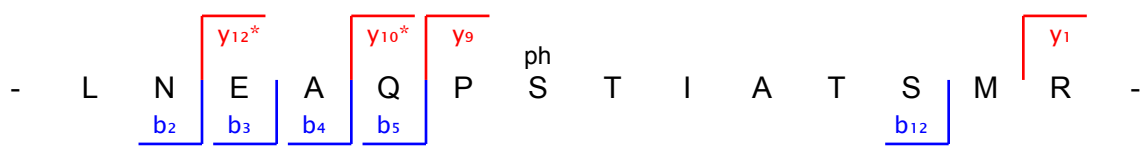
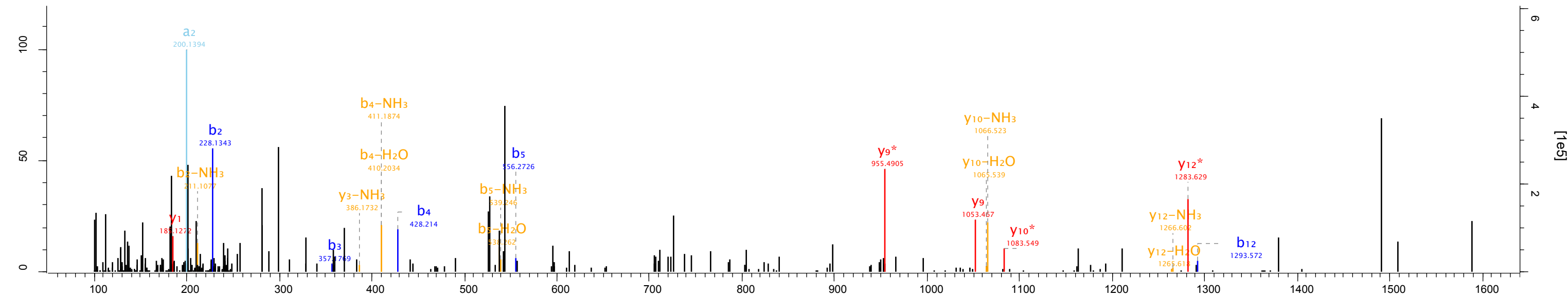


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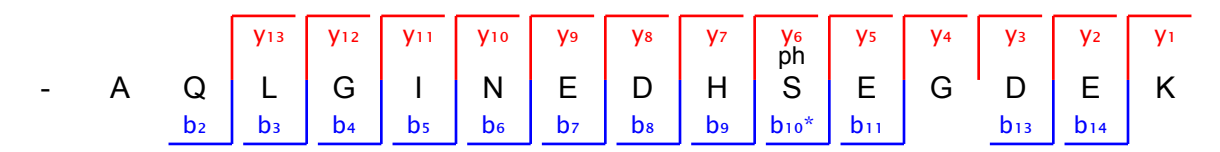
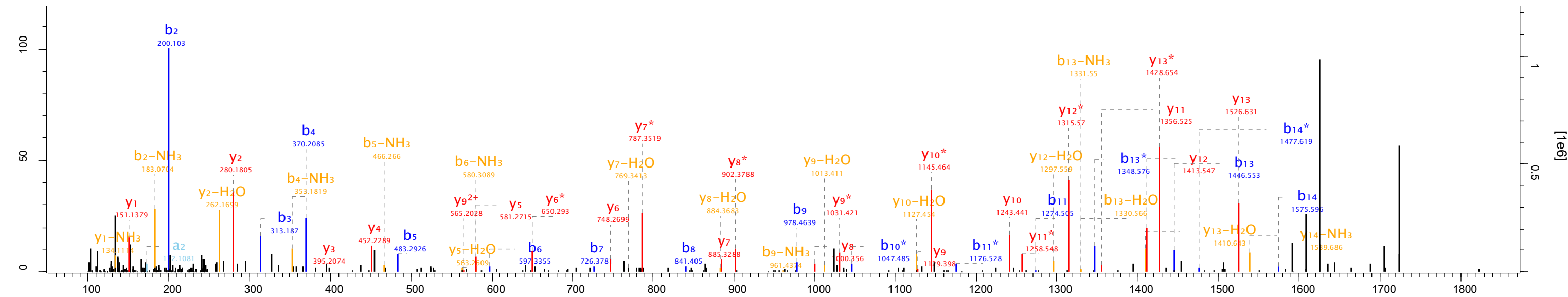
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- b3: L-Q-Q
- b4: L-Q-Q-T
- b5: L-Q-Q-T-V
- y1: V-P
- y2: P-A
- y3: A-D
- y4: D-A
- y5: A-S_{ph}
- y6: S_{ph}-P
- y7: P-D
- y8: D-S
- y9: S-K
- y10: K-

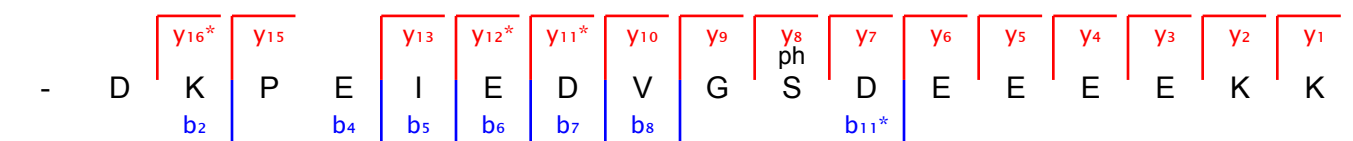
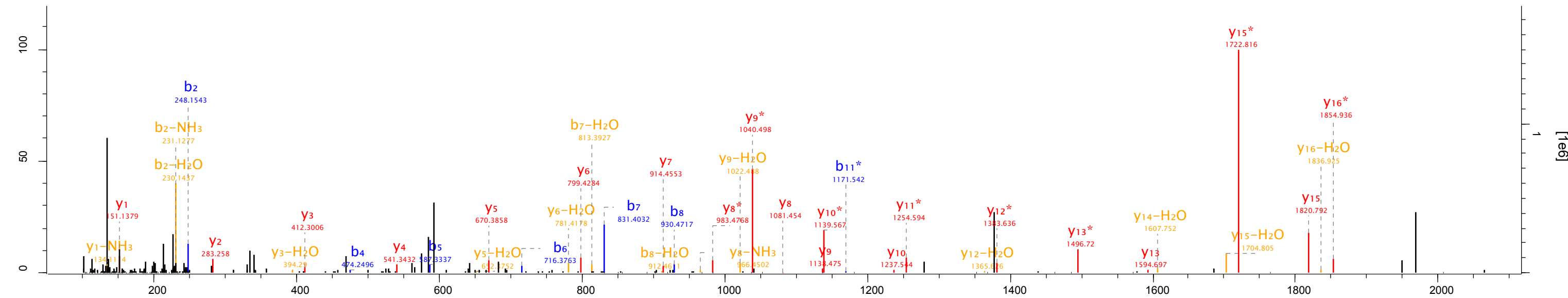
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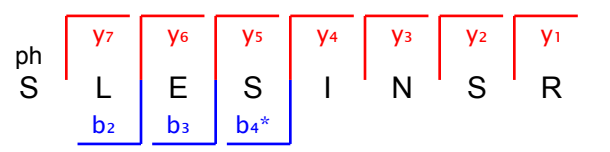
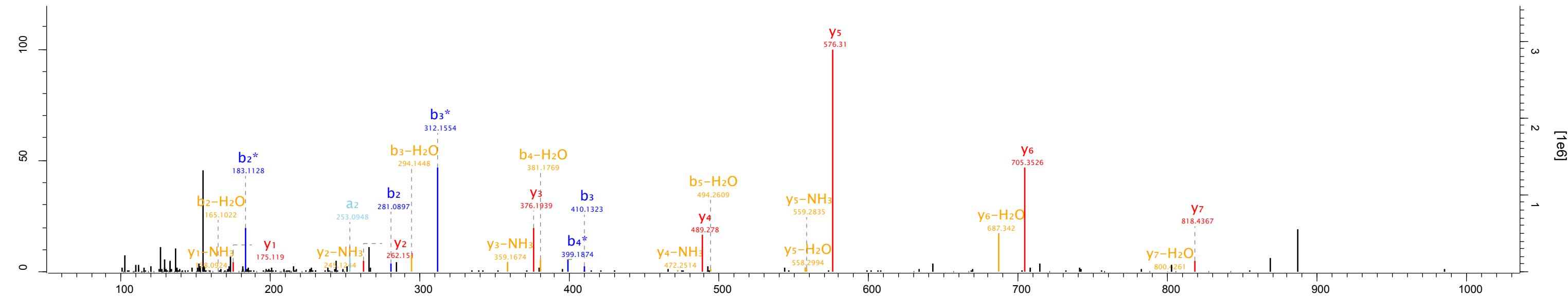
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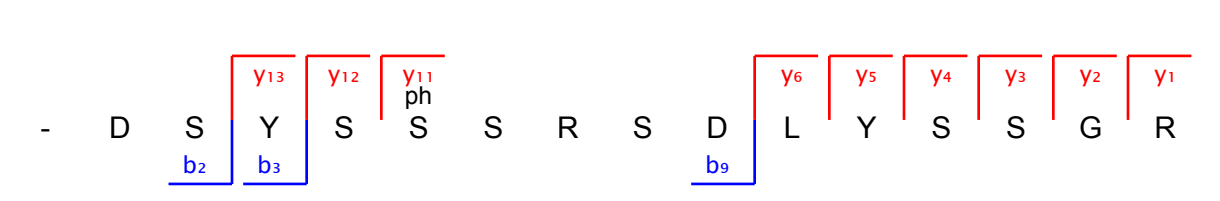
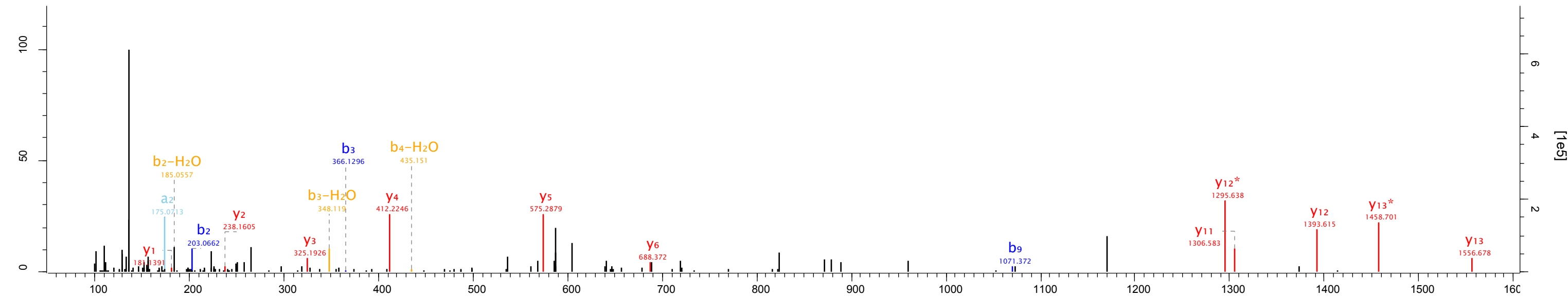
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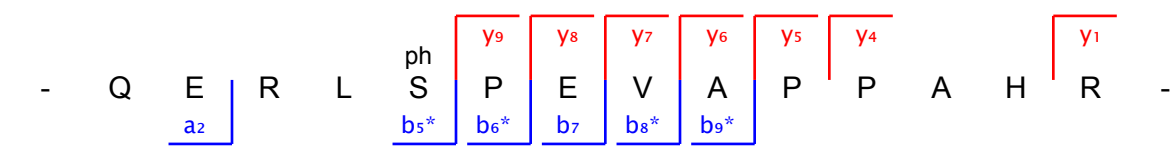
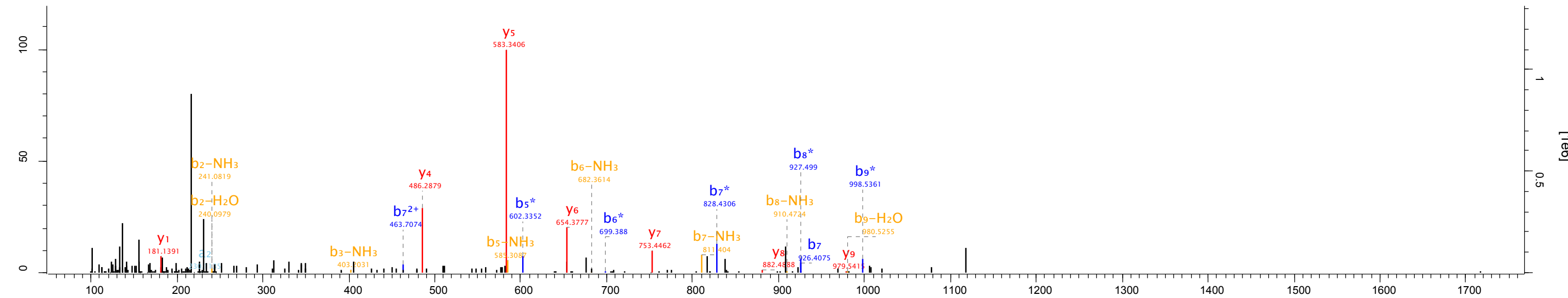


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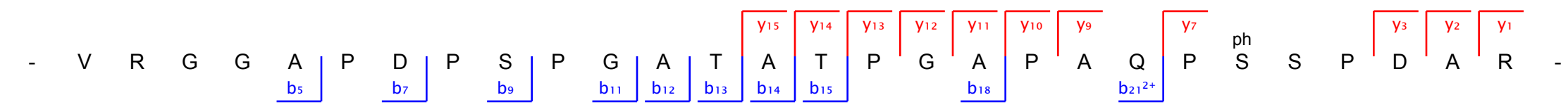
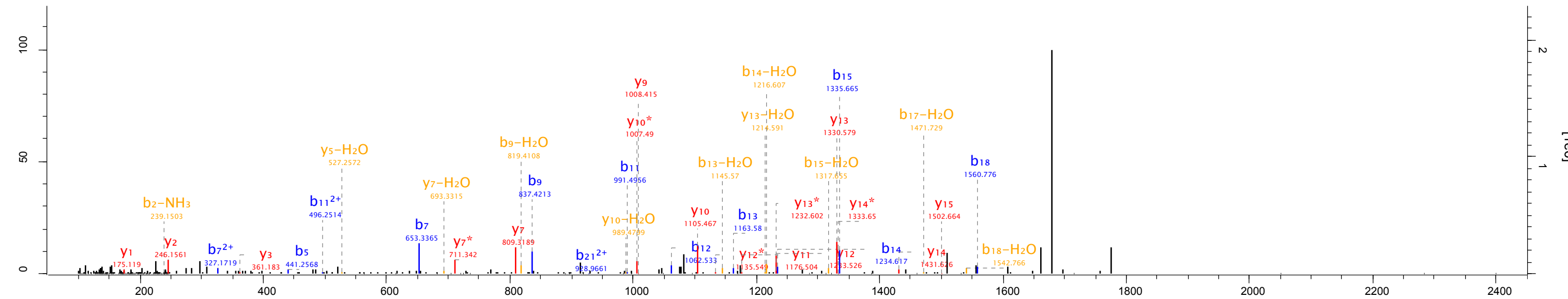


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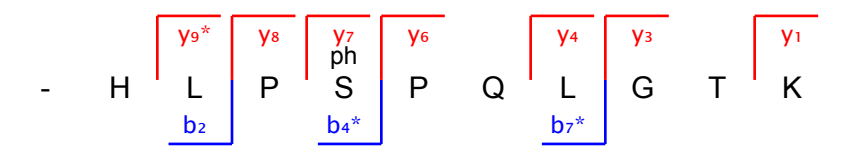
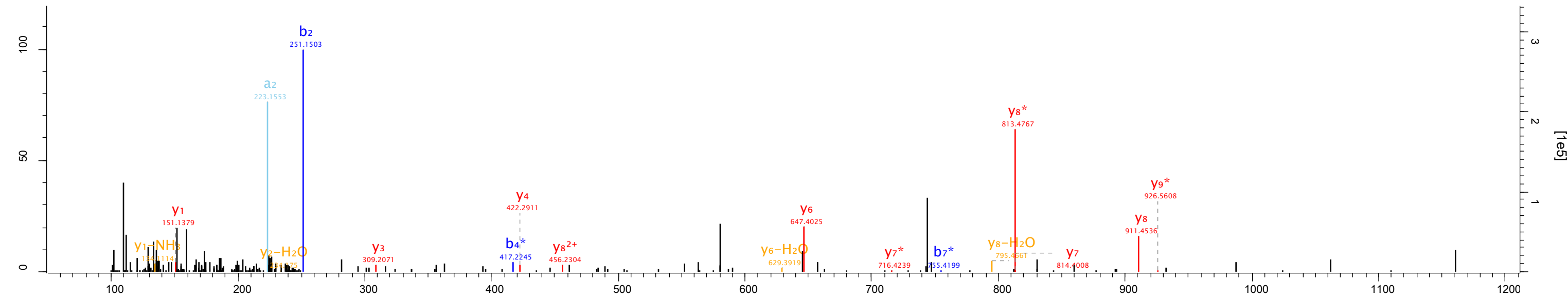




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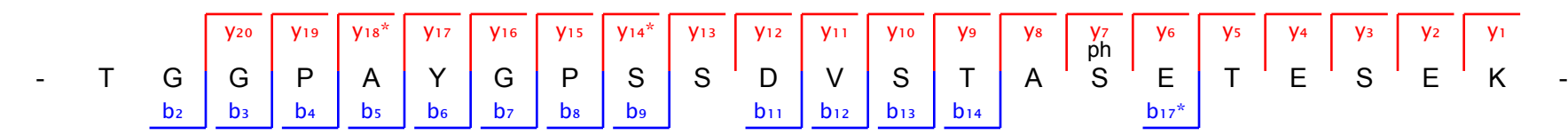


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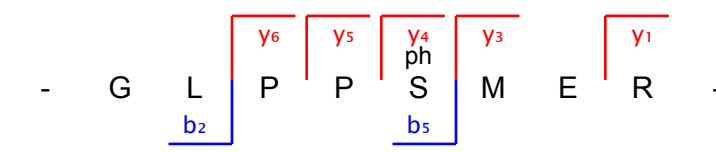
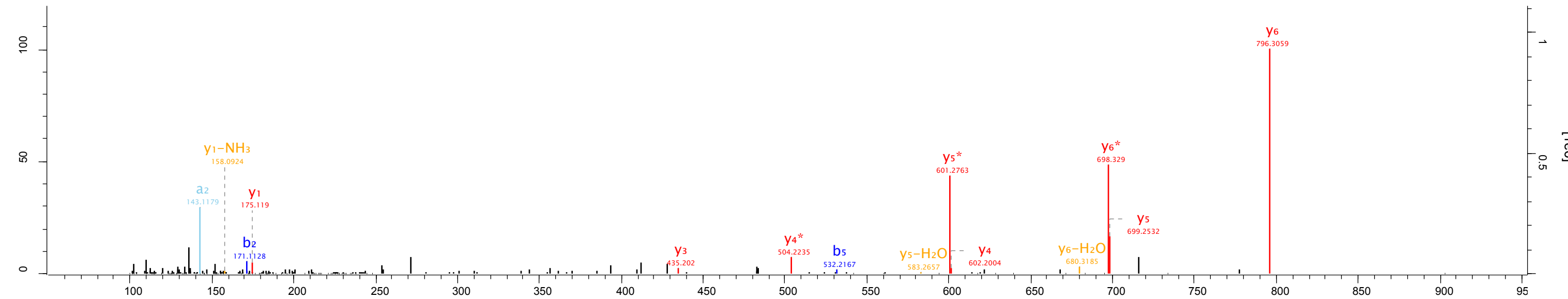


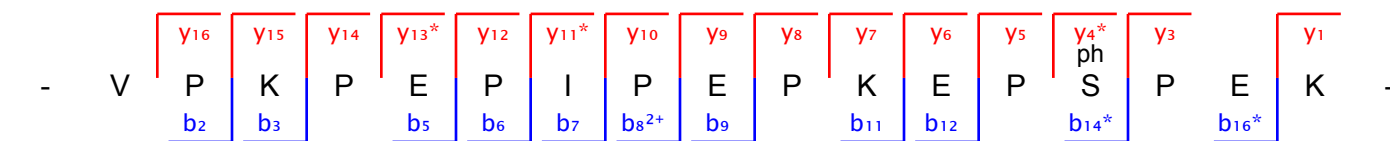
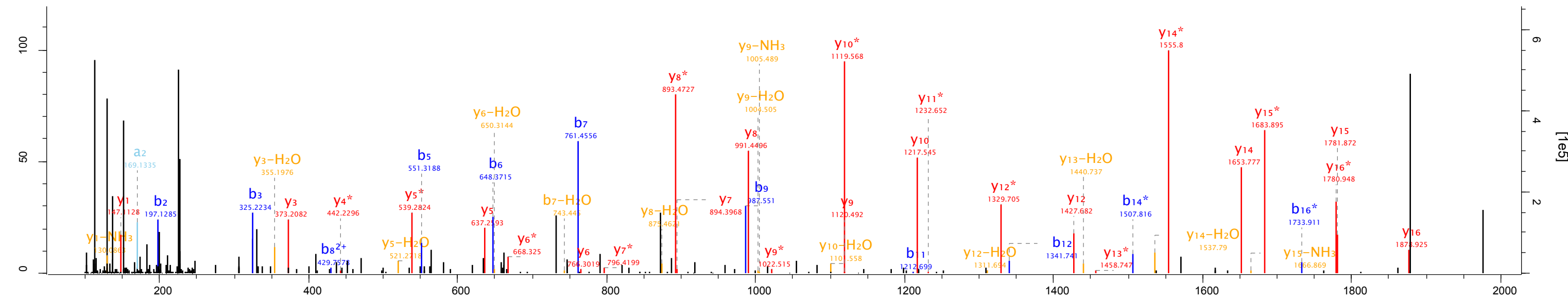
20171215_MaS_33SR_LMH_phospho_06

7397 FTMS; HCD 222.01 1118.96 FXR2

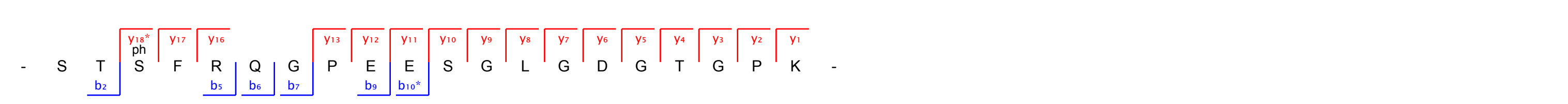
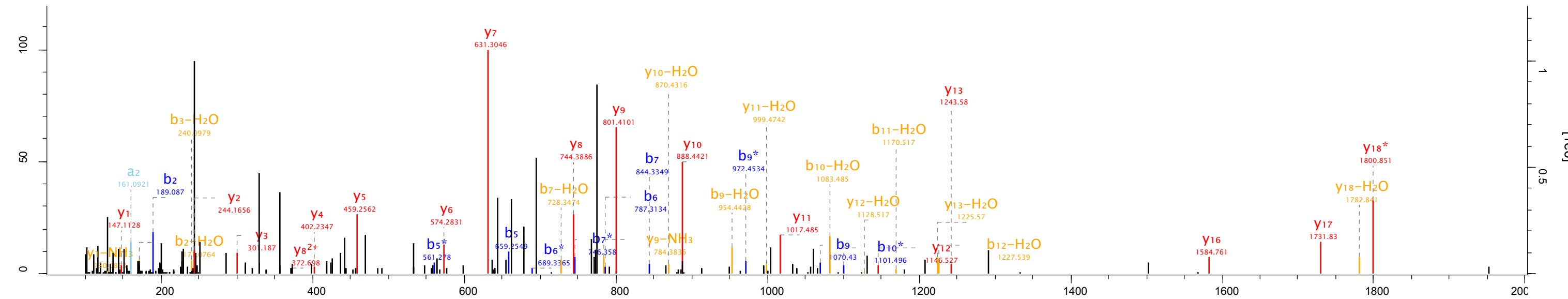


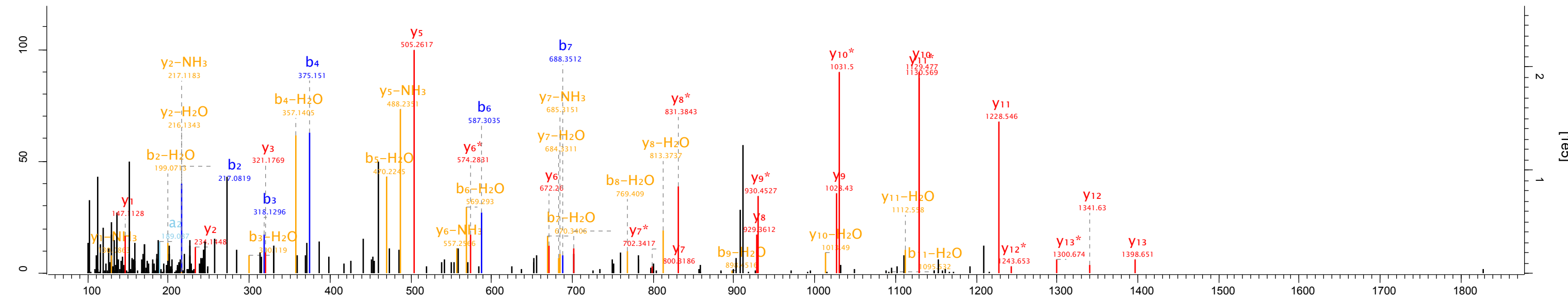
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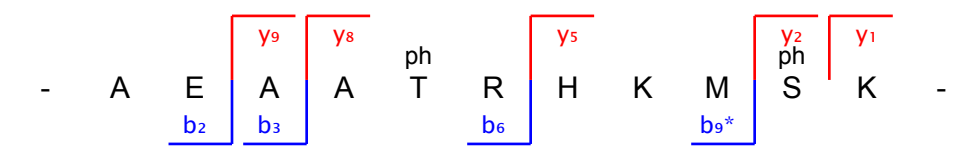
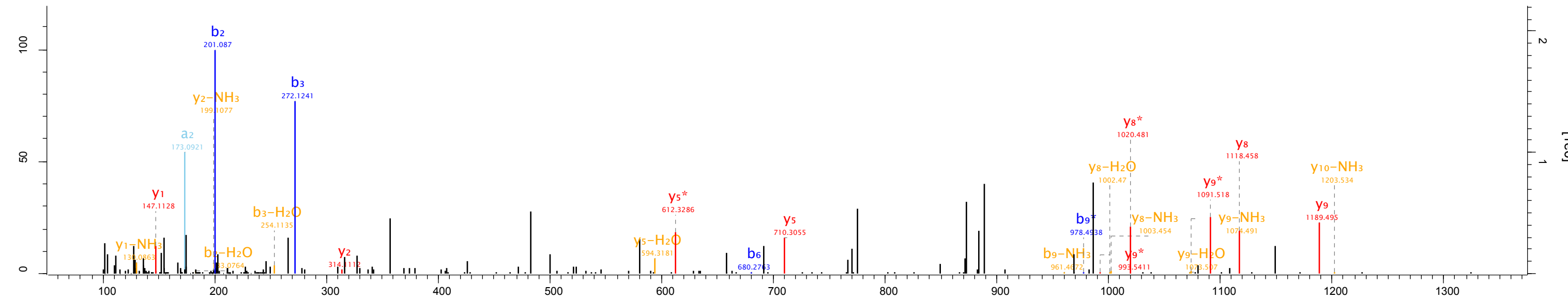




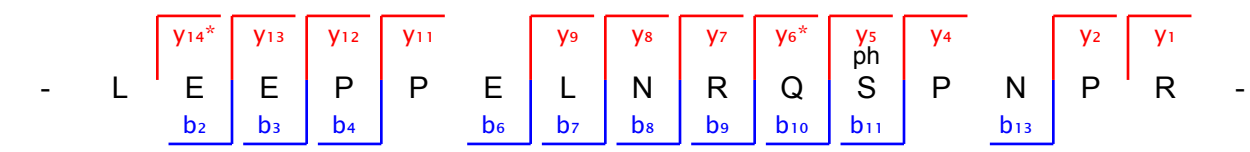
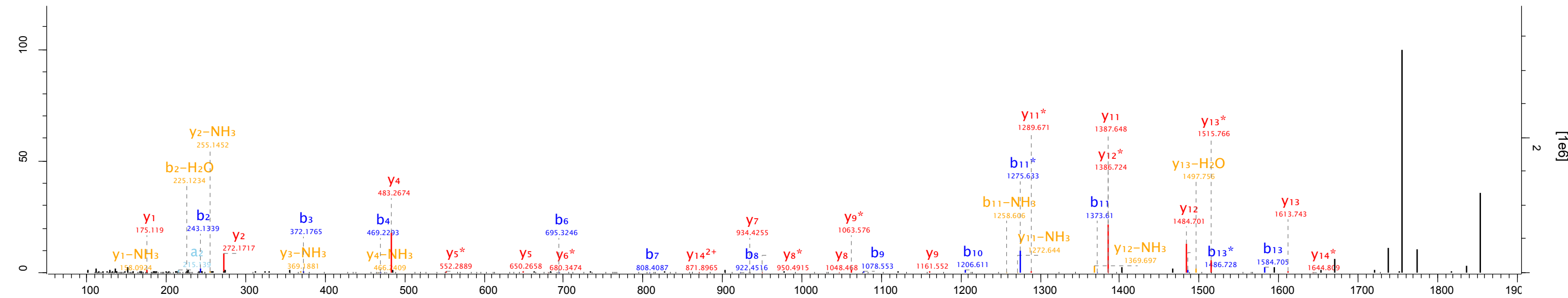
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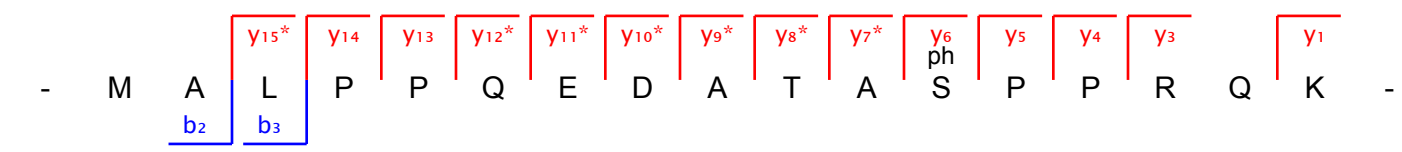
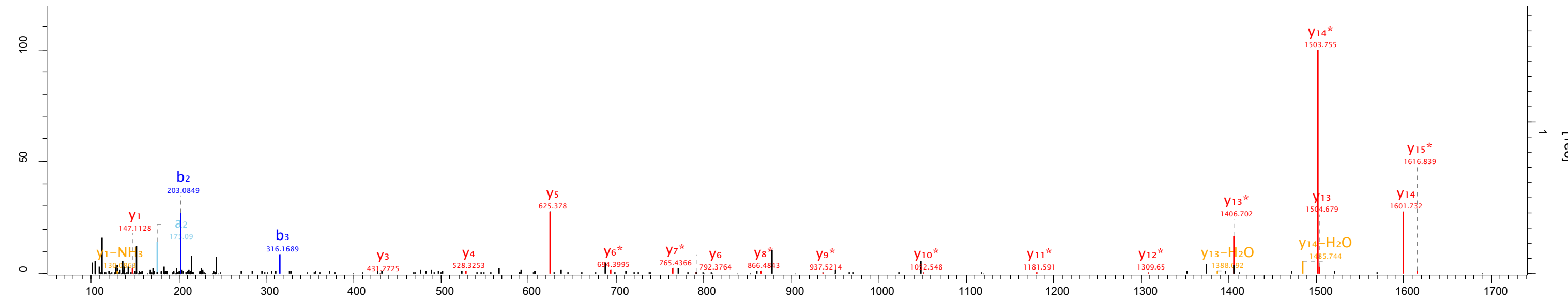
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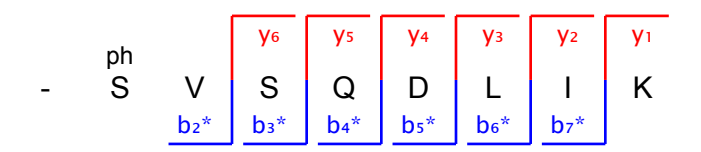
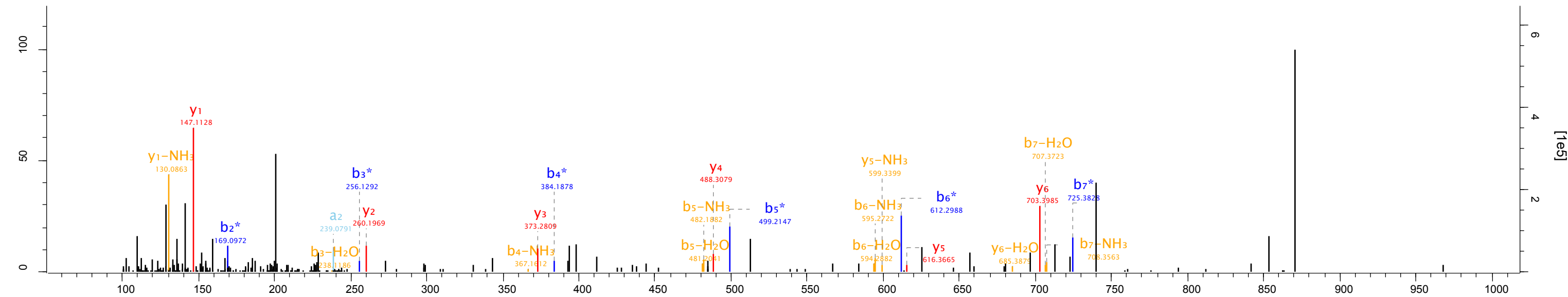
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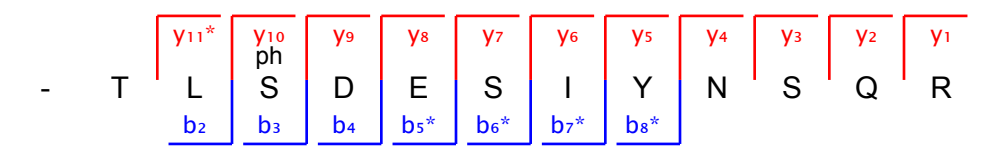
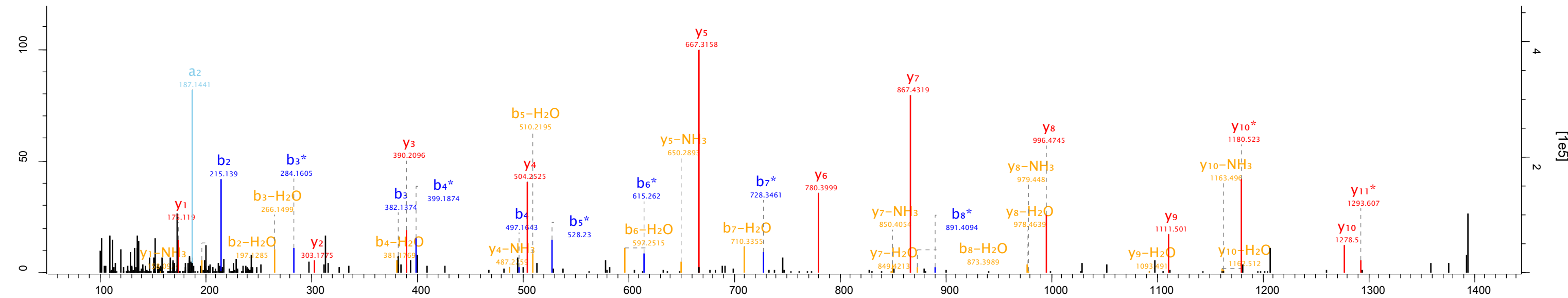
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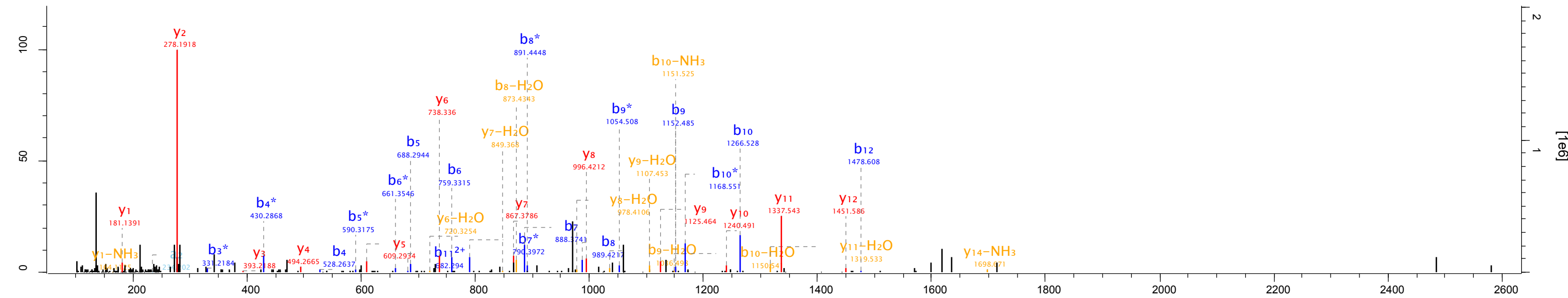


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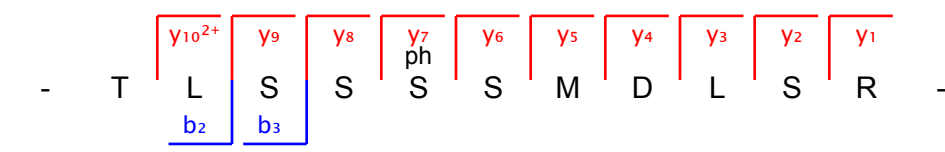
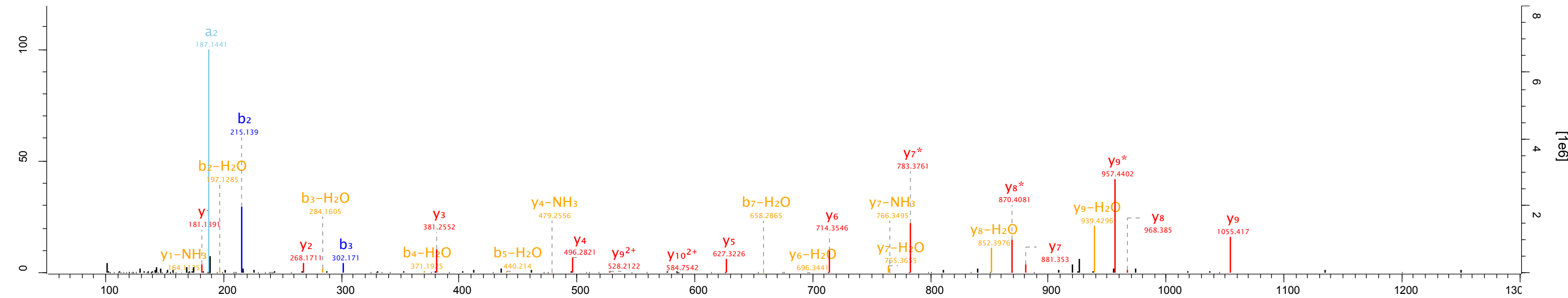


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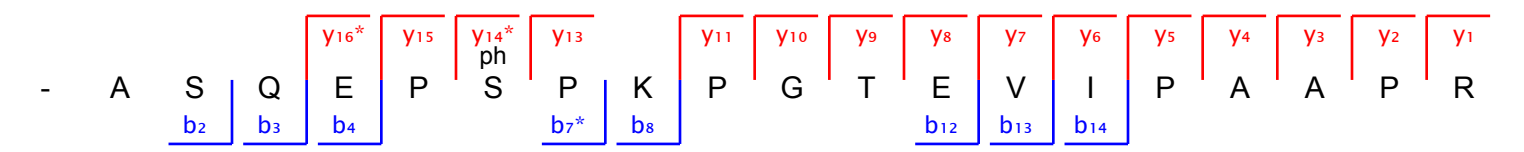
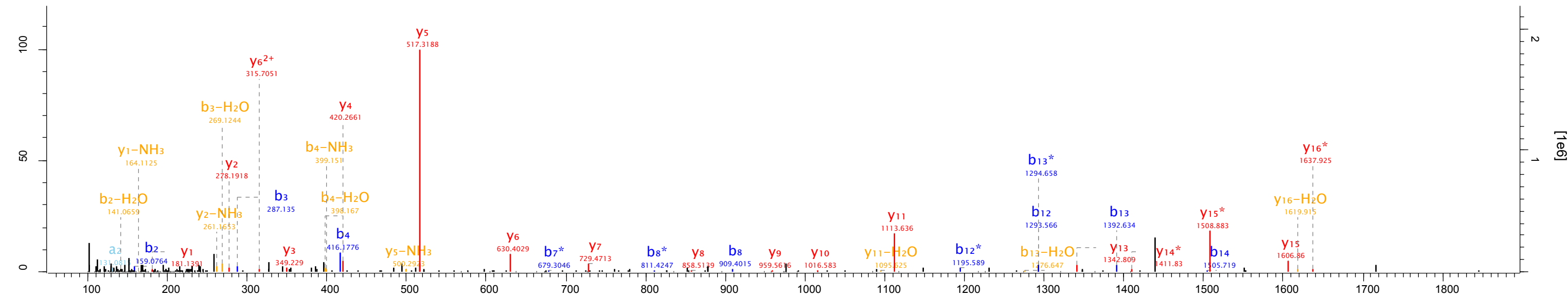
a₂
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b₄
b₅
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b₇
b₈
b₉
b₁₀
b₁₁²⁺
b₁₂

y₁₂
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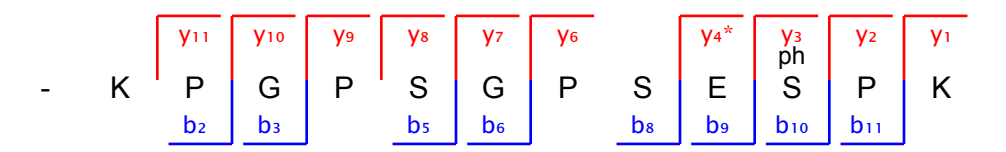
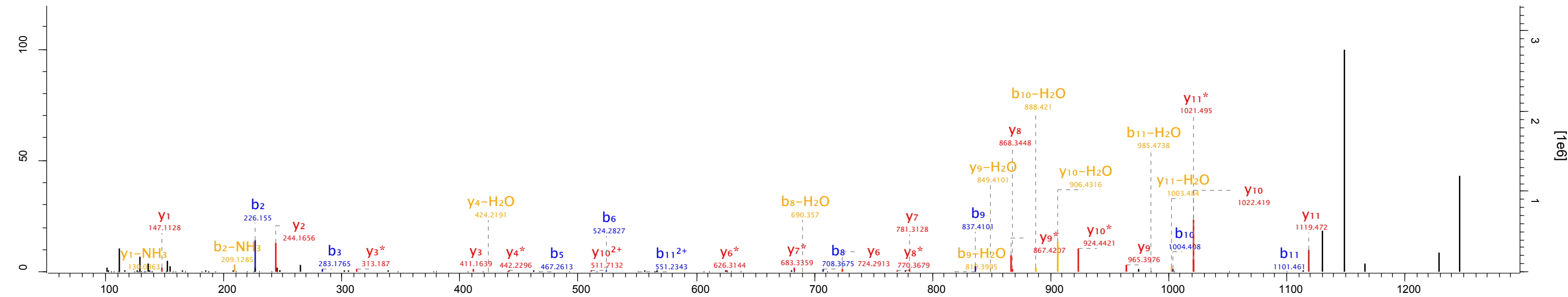
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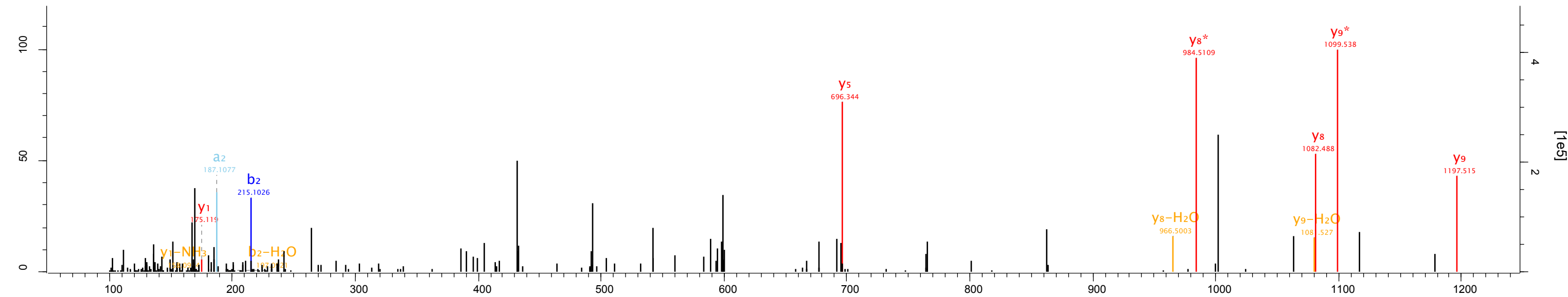
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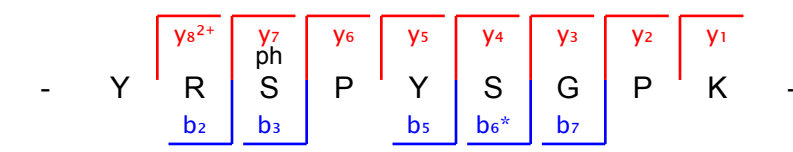
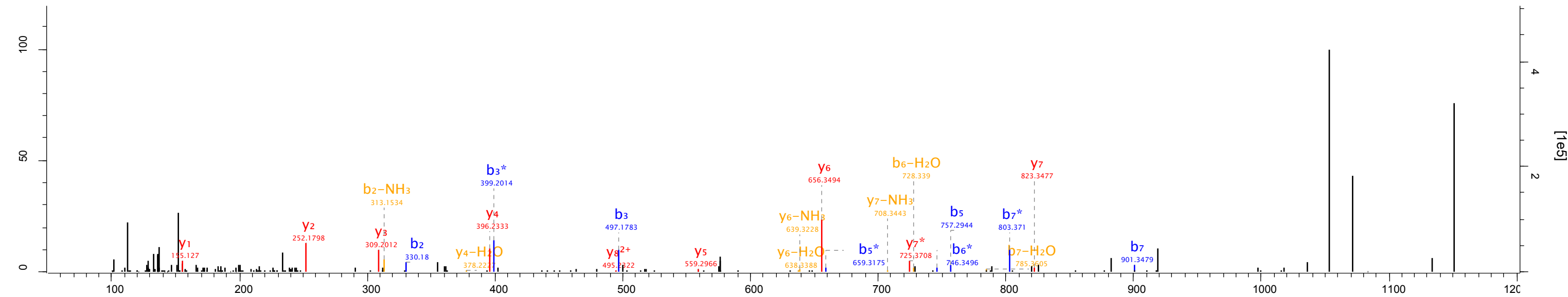
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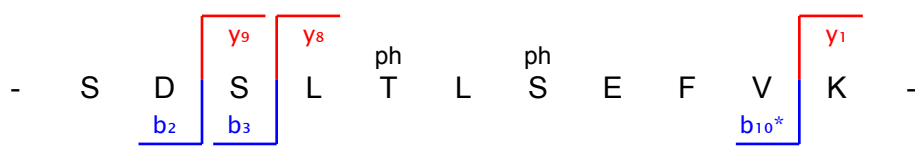
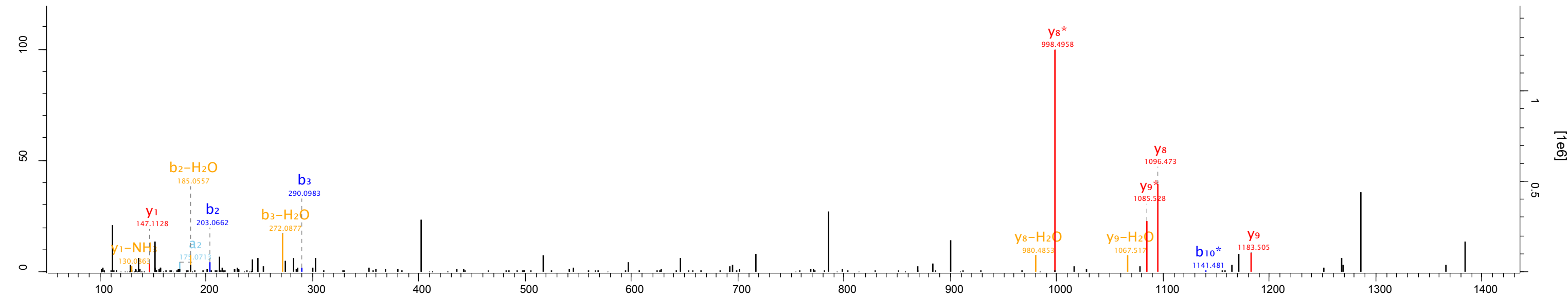
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20171215_MaS_33SR_LMH_phospho_07

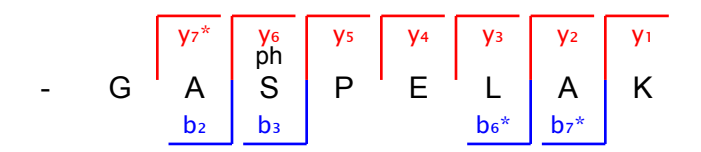
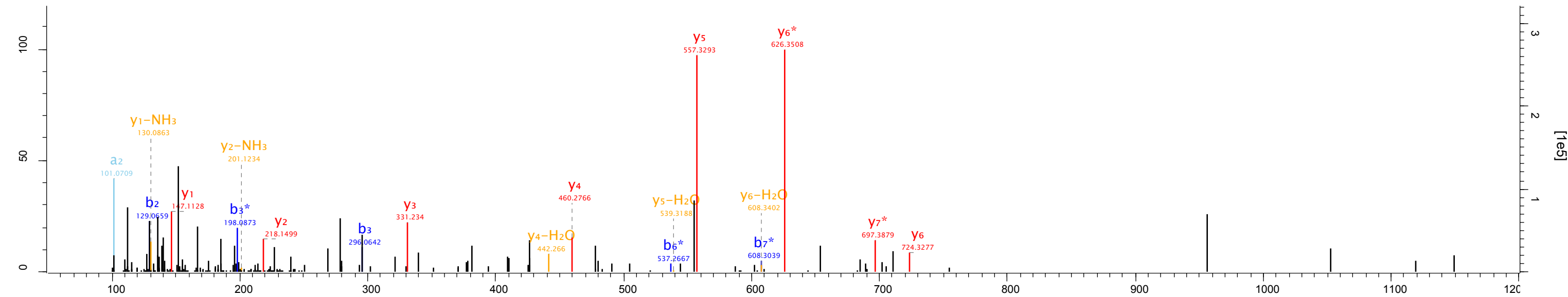
Scan	Method	Score	m/z	Gene names
3097	FTMS; HCD	109.69	576.76	RBM39



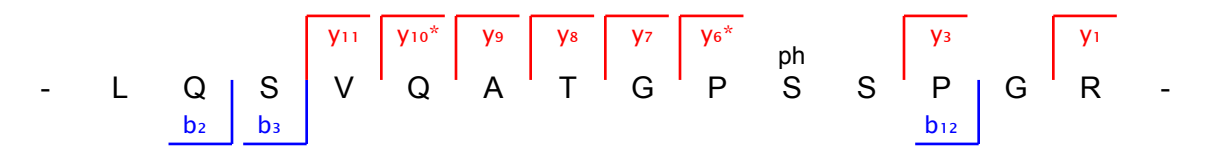
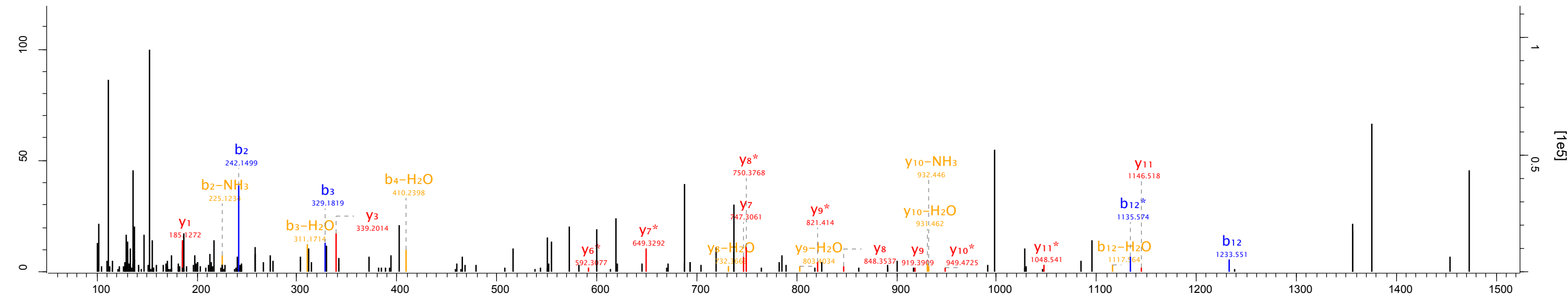
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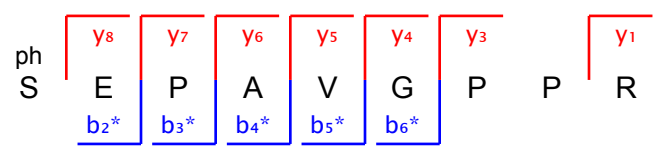
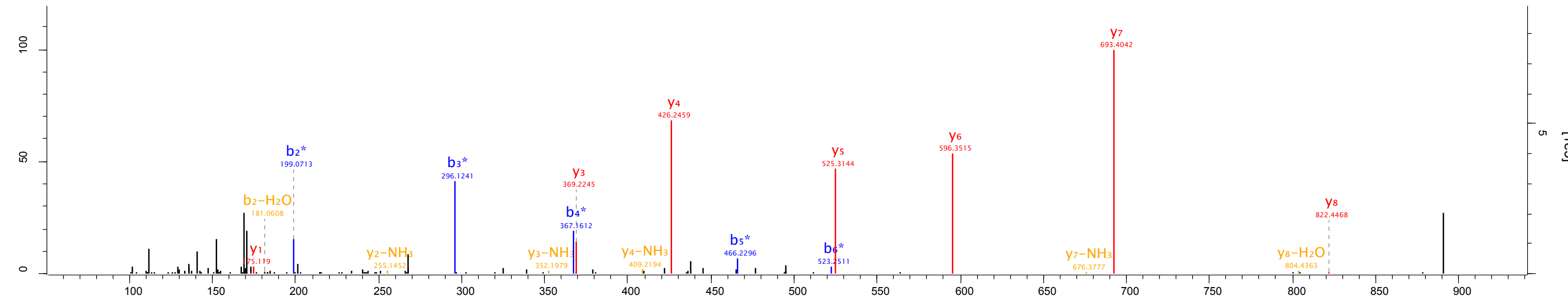
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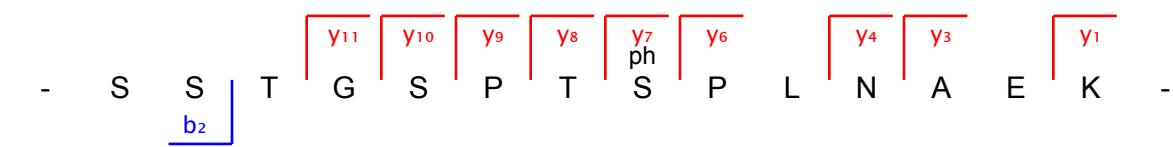
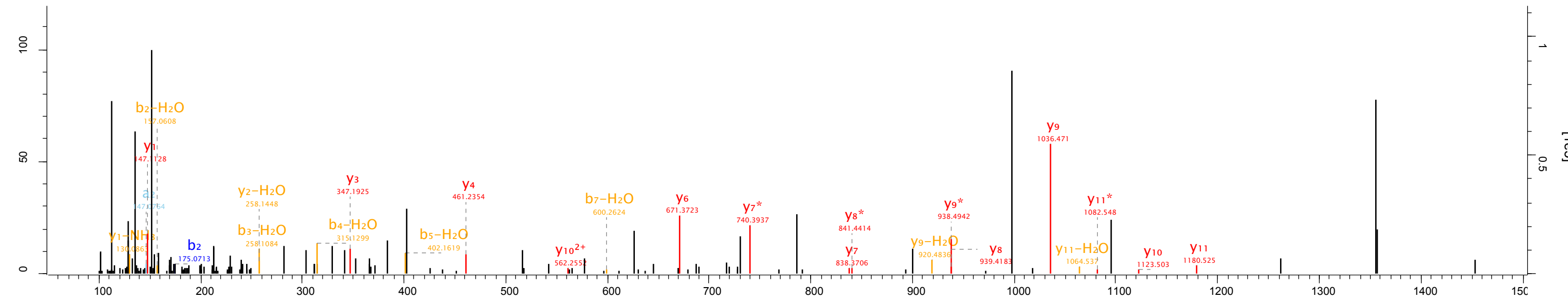
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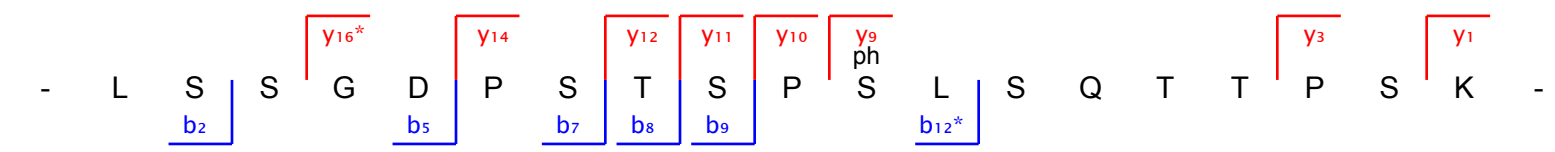
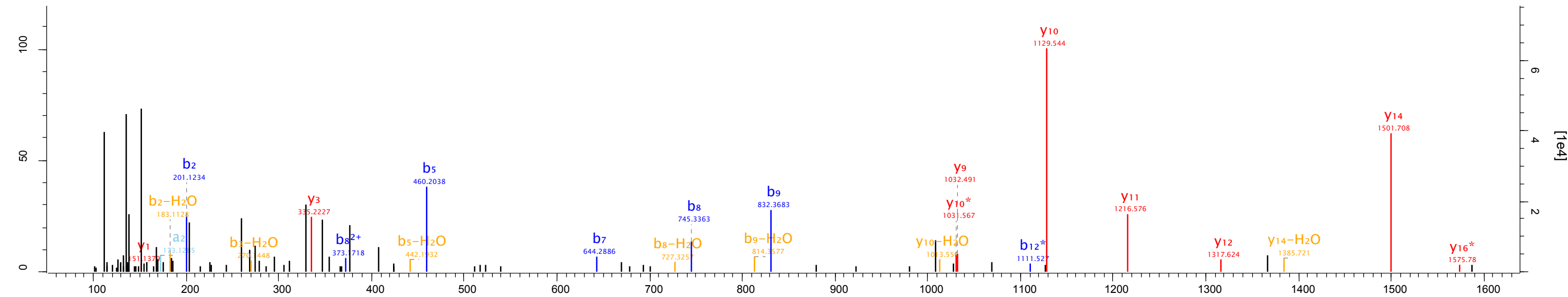


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Raw file Scan Method Score m/z Gene names

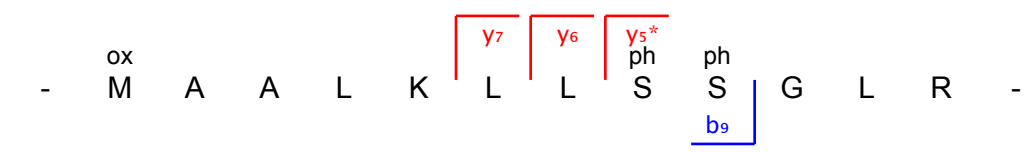
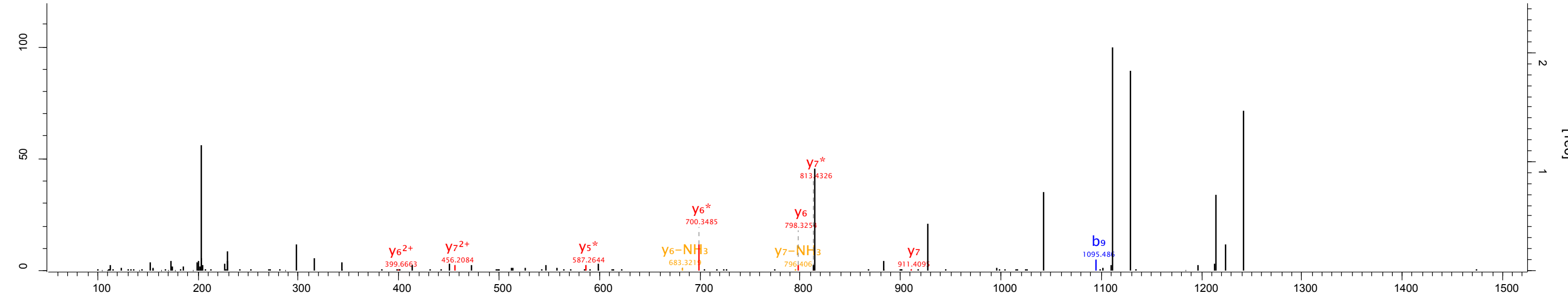
20171215_MaS_33SR_LMH_phospho_07 5767 FTMS; HCD 54.56 980.95 EYA3



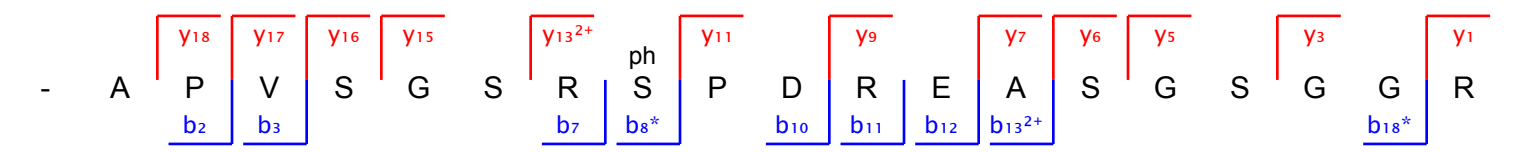
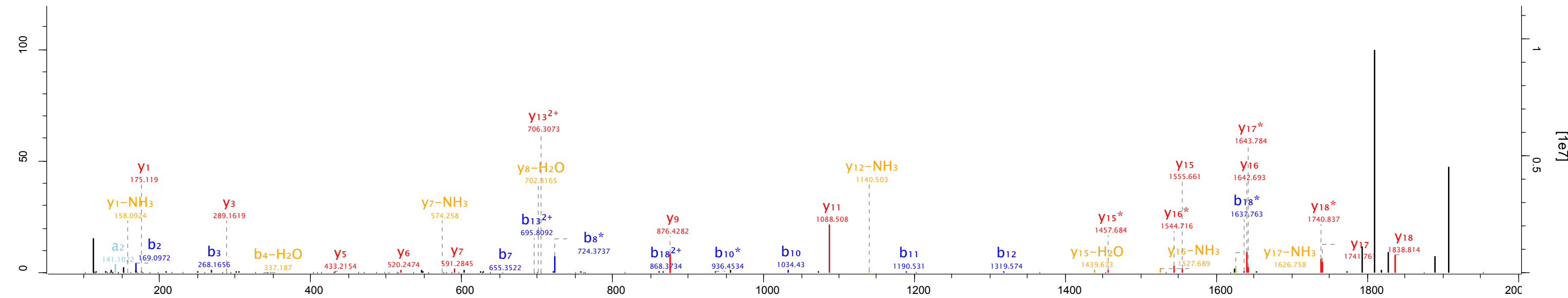
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20171215_MaS_33SR_LMH_phospho_08

Scan	Method	Score	m/z	Gene names
15097	FTMS; HCD	40.28	723.36	OXCT1



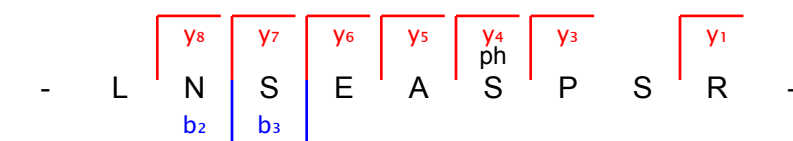
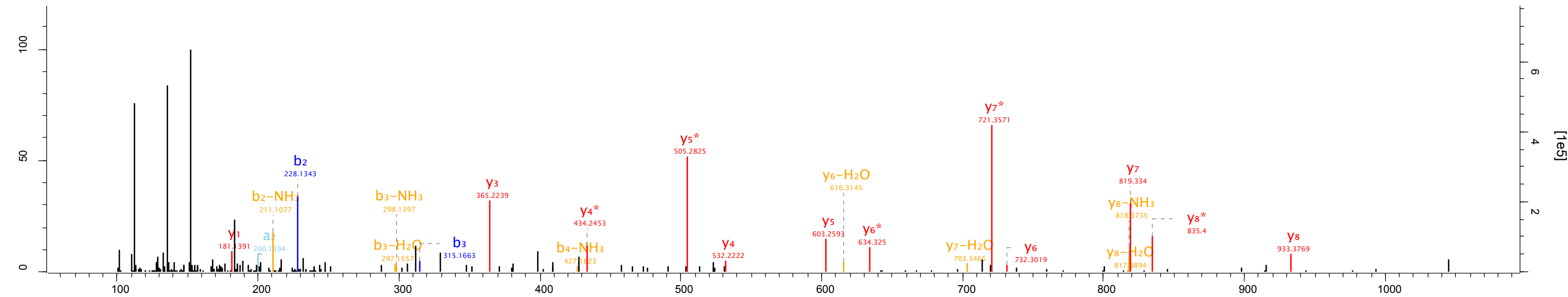
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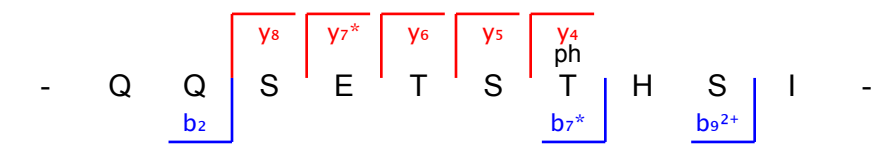
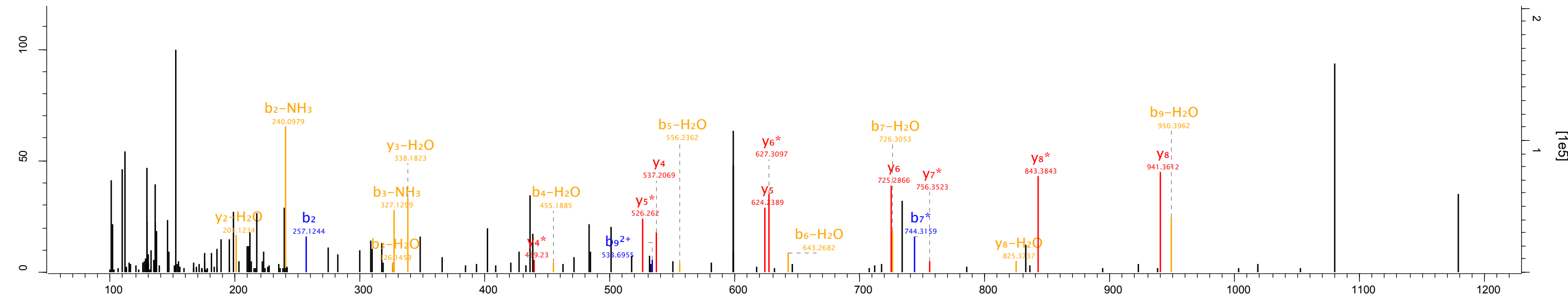


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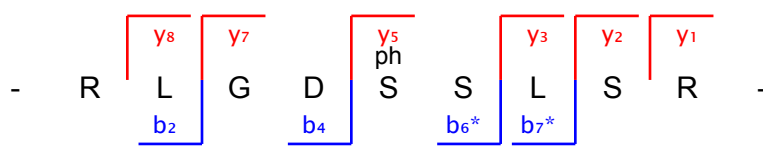
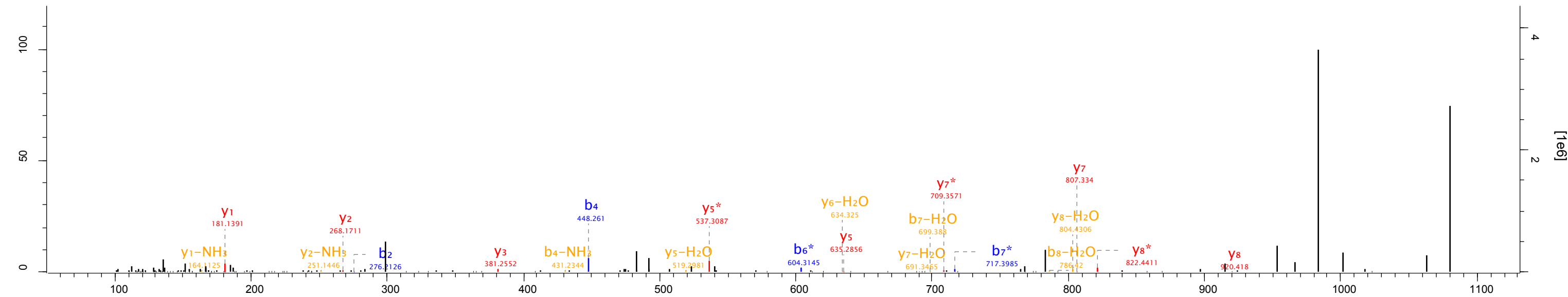
20171215_MaS_33SR_LMH_phospho_08

Scan	Method	Score	m/z	Gene names
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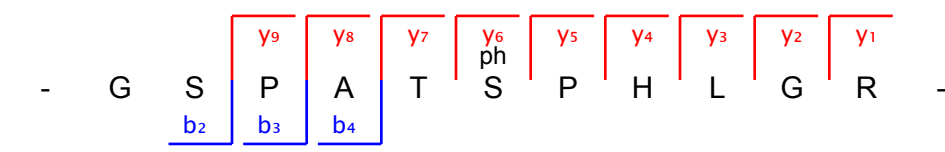
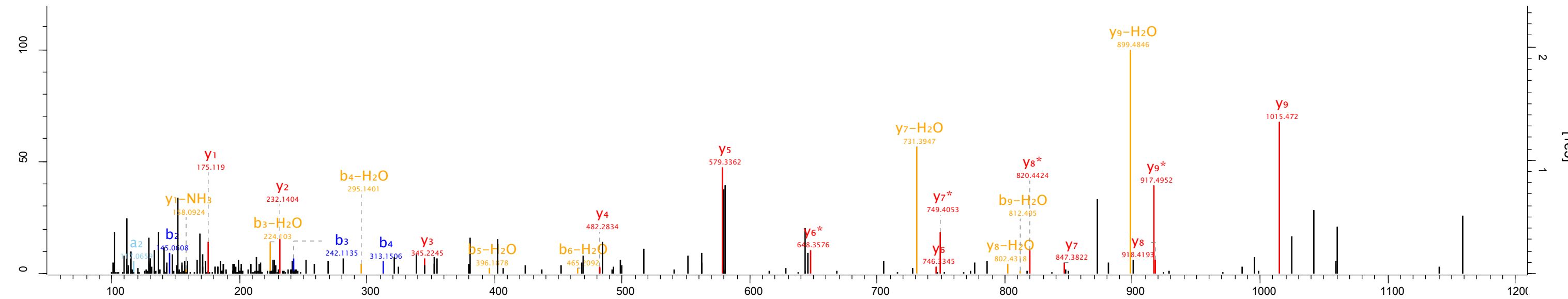




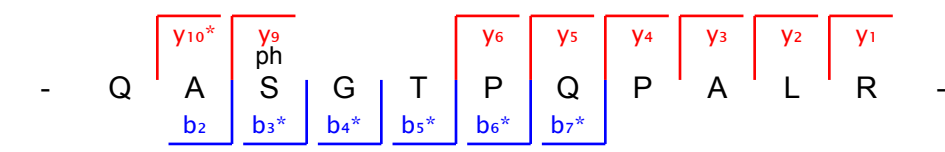
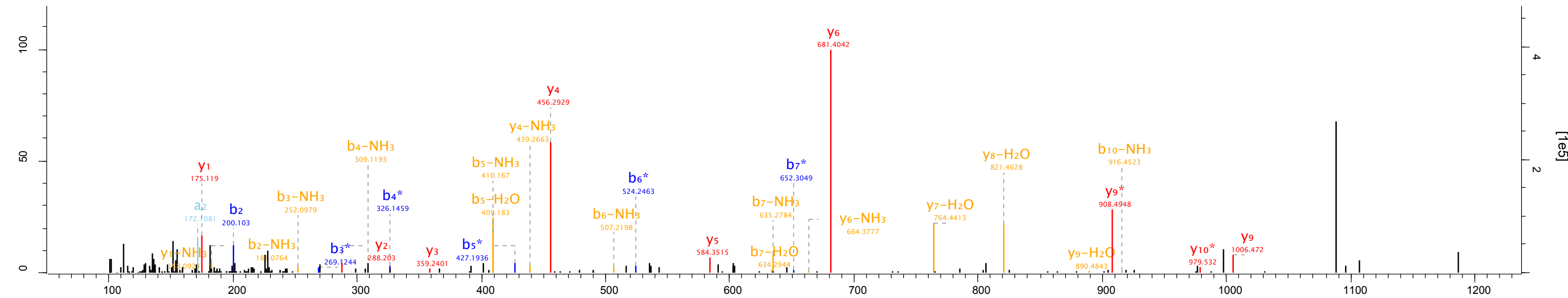
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 Scan: 3437 Method: FTMS; HCD Score: 60.36 m/z: 541.77 Gene names: EIF3A



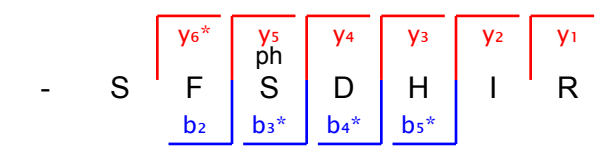
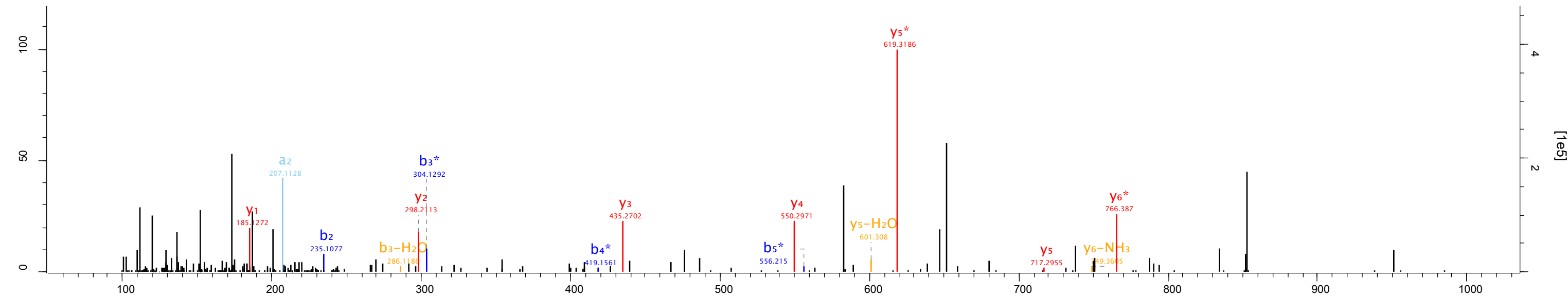
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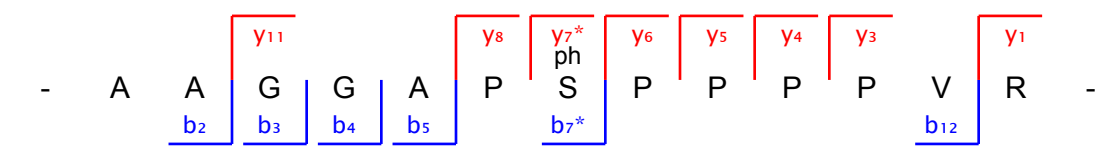
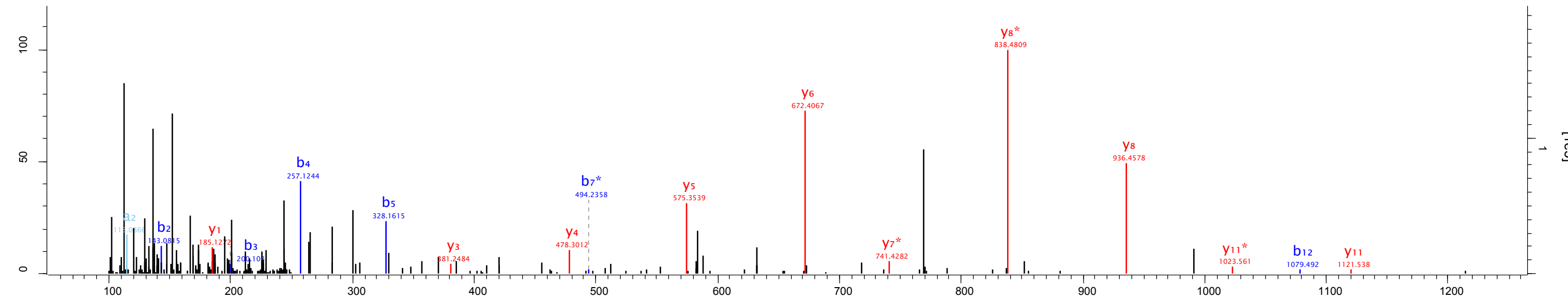
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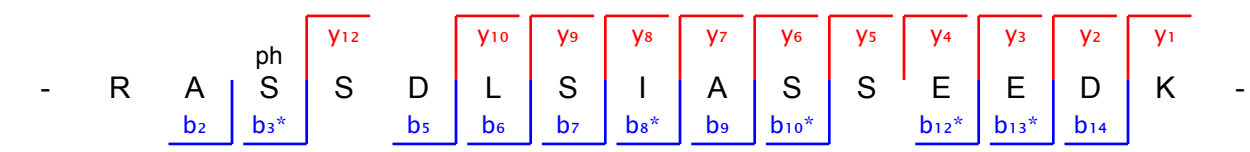
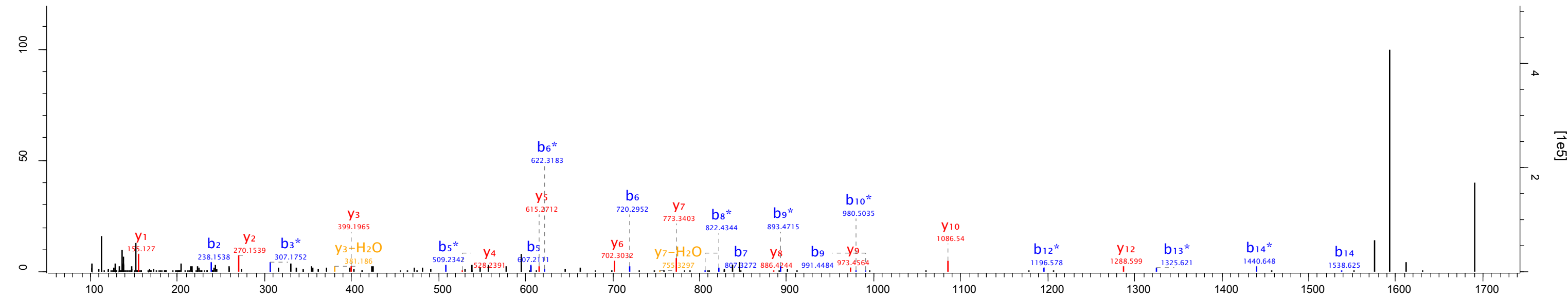
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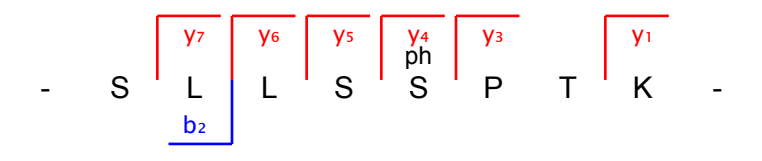
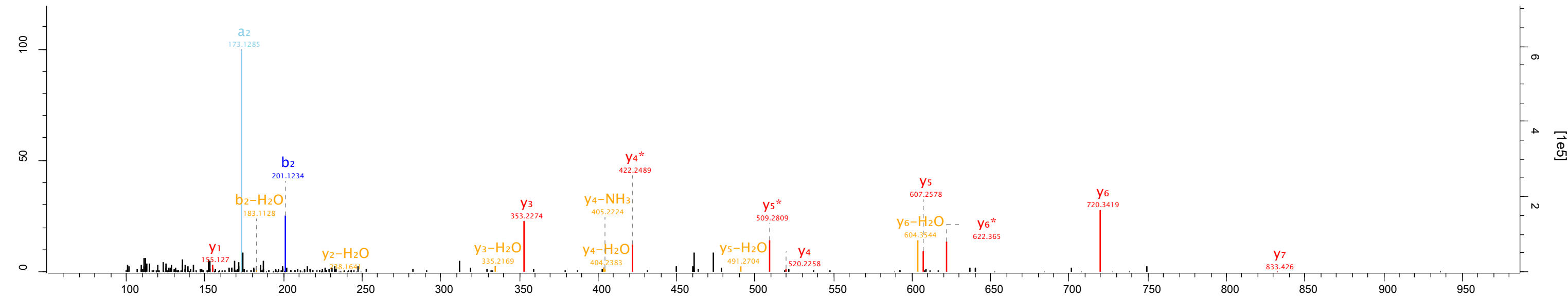
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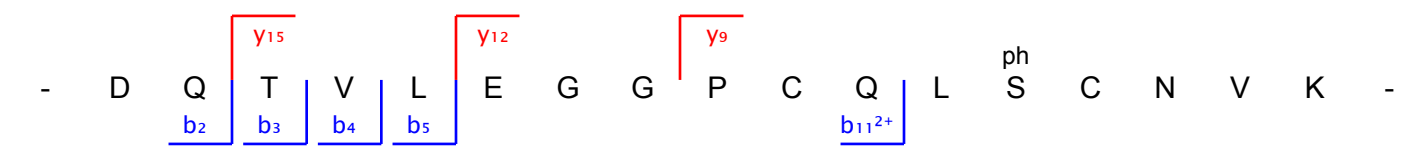
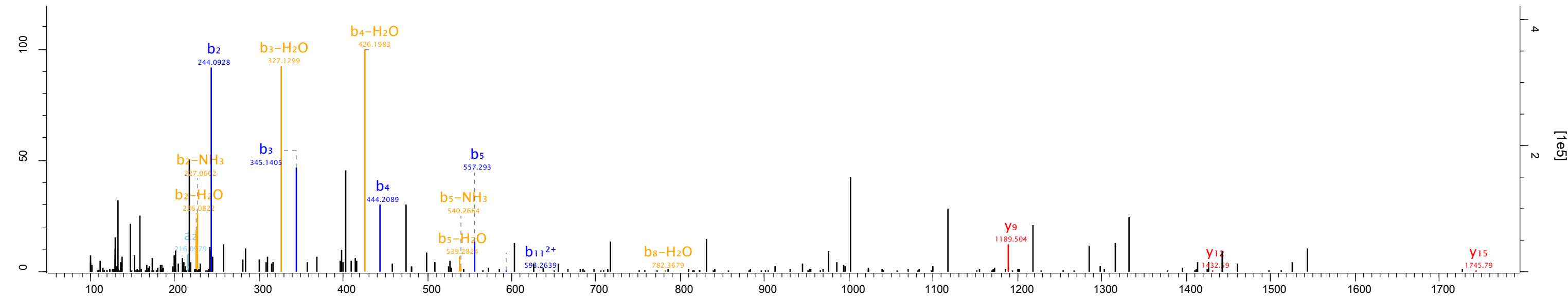
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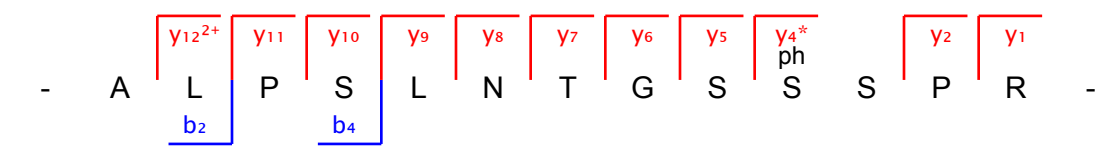
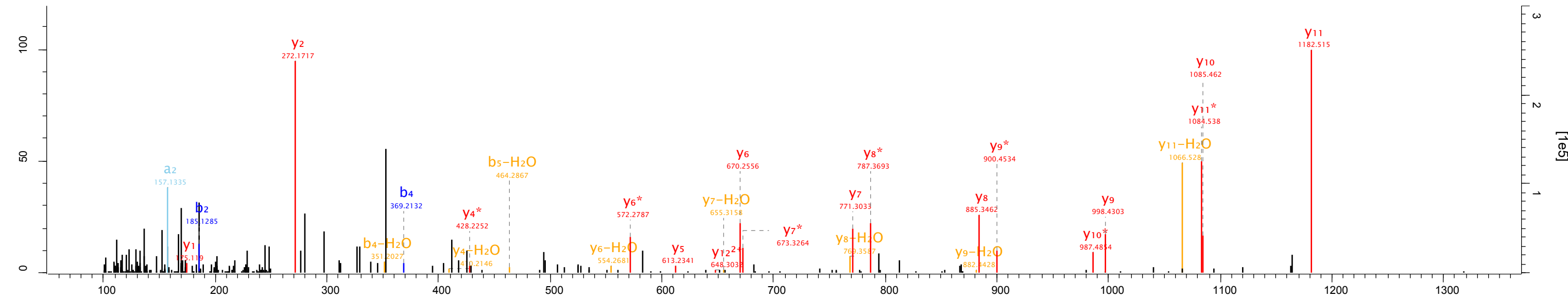
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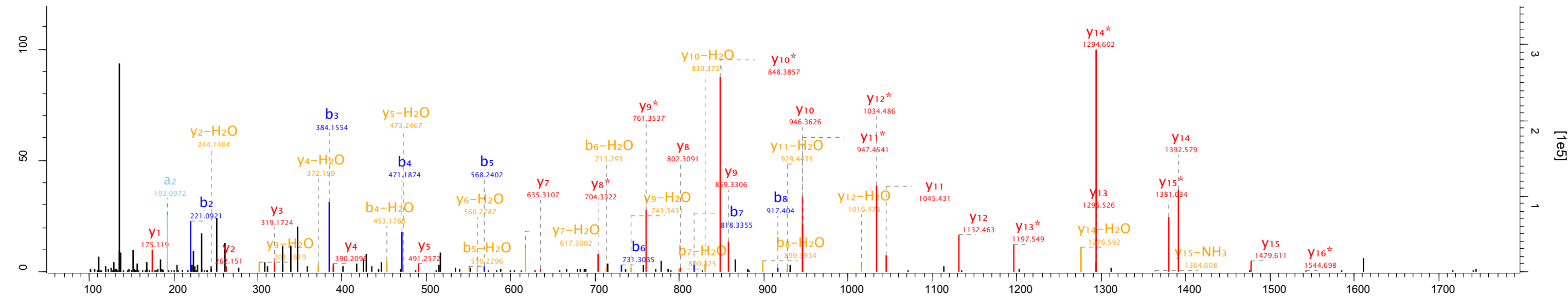
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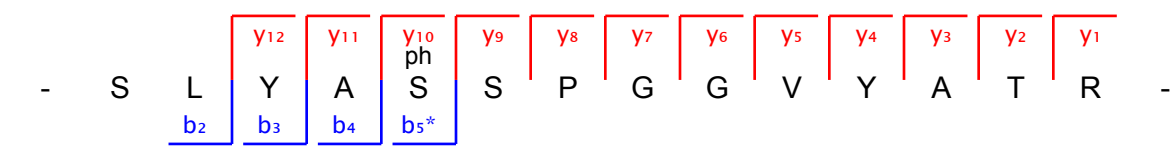
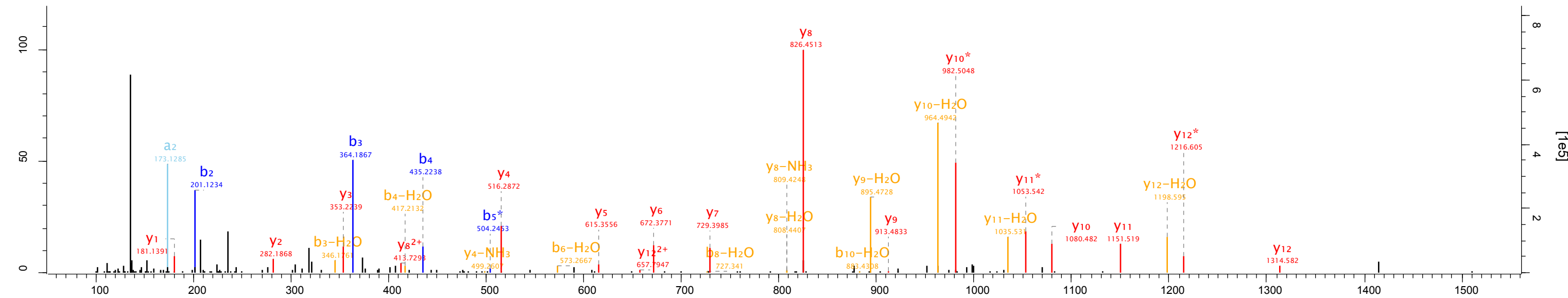
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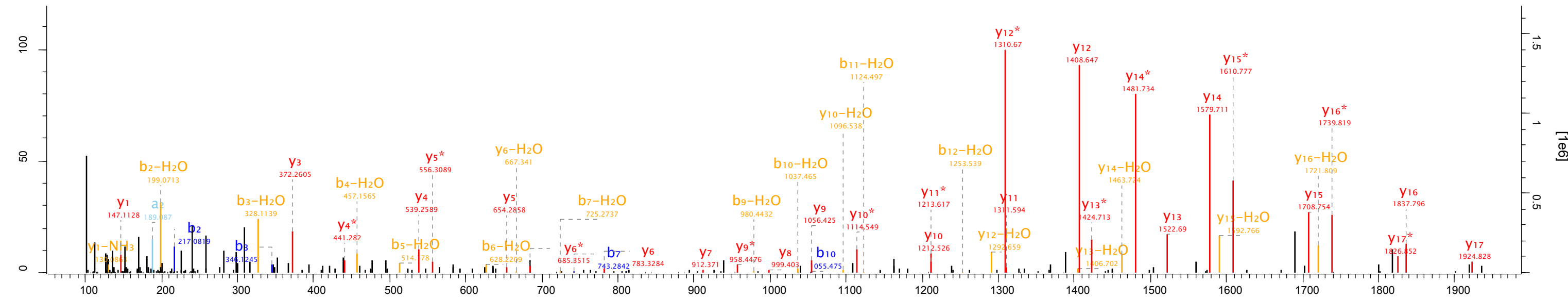
- G Y Y Y S P Y S V S G S G S T A G S R -

Fragmentation scheme showing b and y ions for the peptide sequence: Y Y Y S P Y S V S G S G S T A G S R. The b ions are labeled b2 through b8, and the y ions are labeled y1 through y16*.

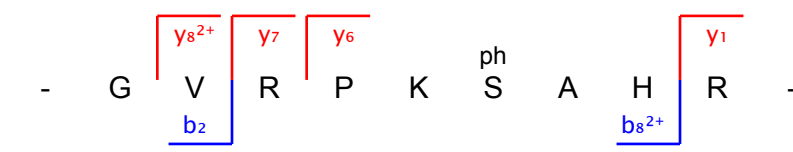
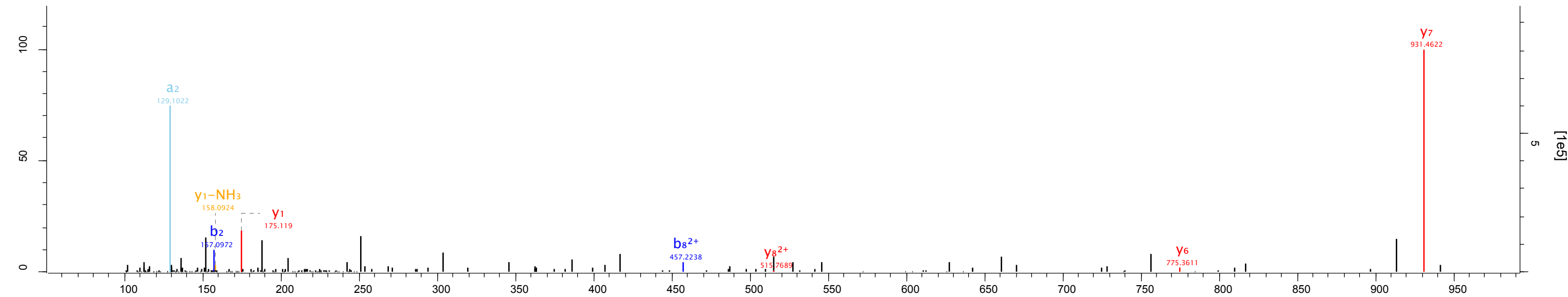
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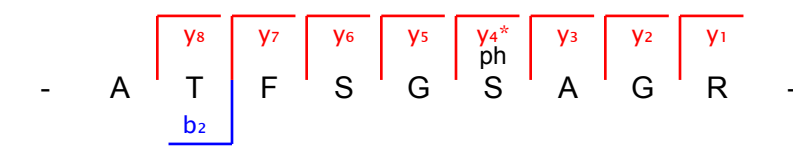
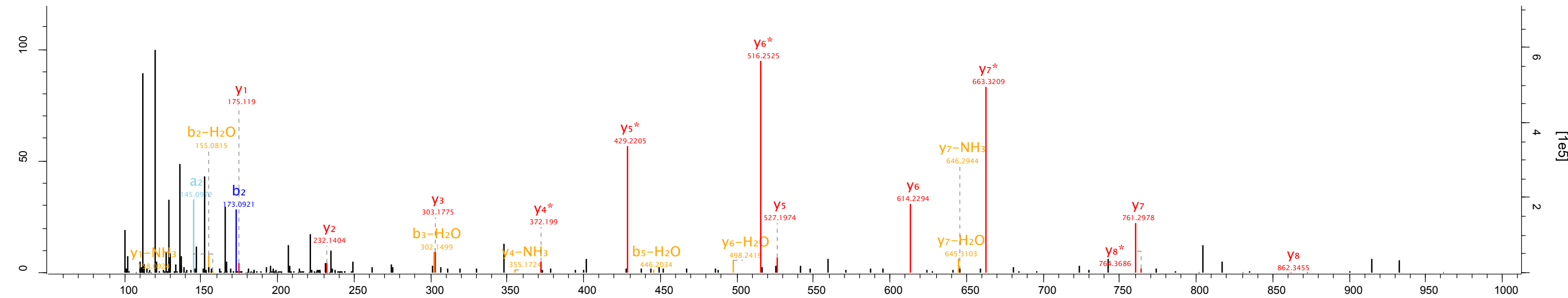
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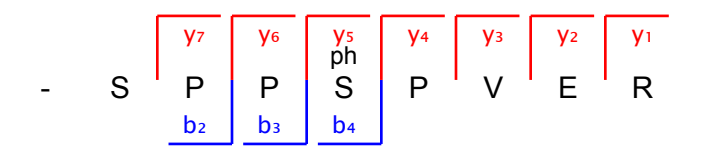
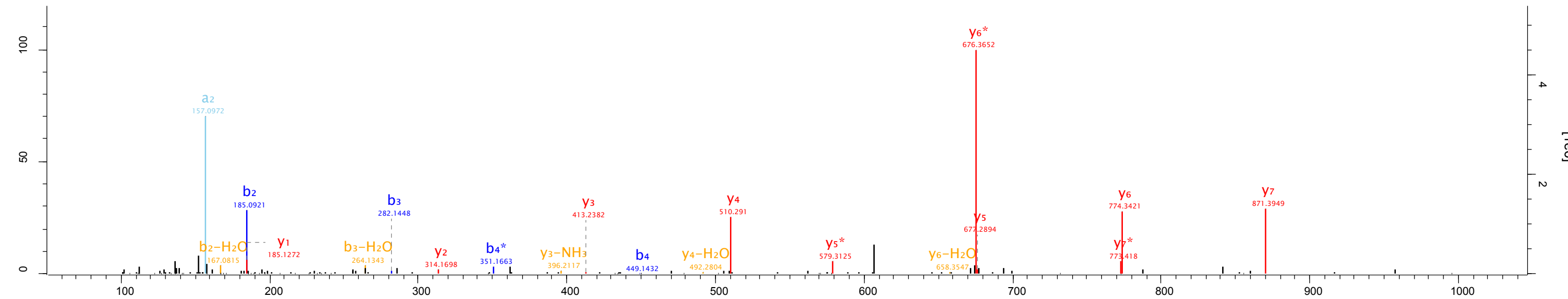
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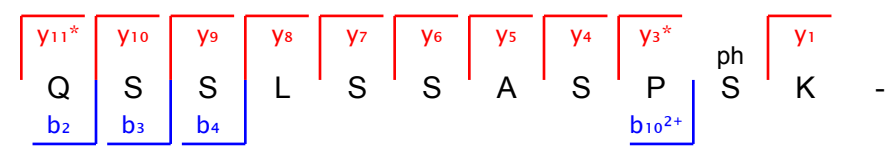
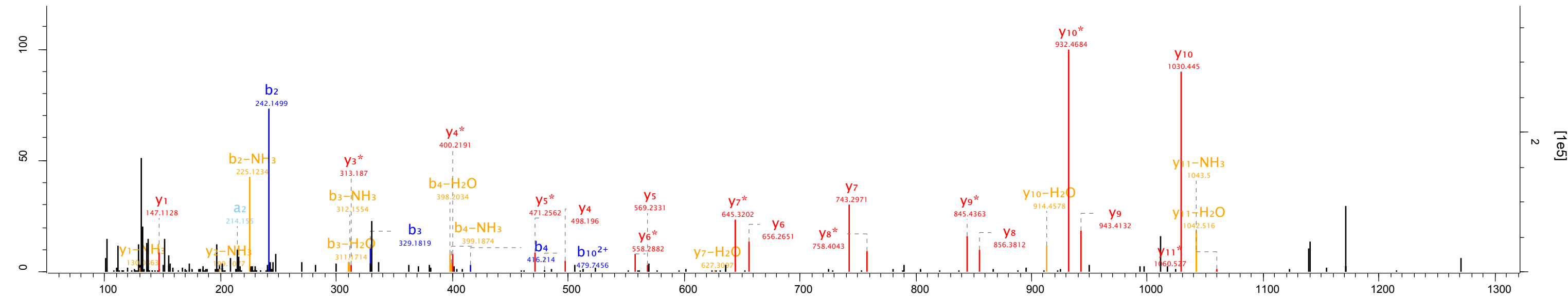
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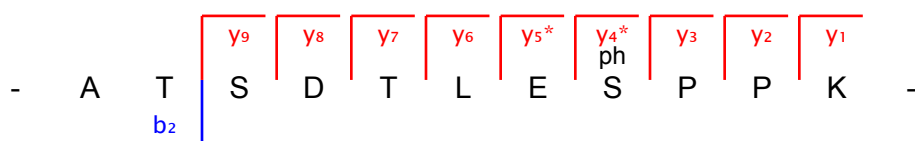
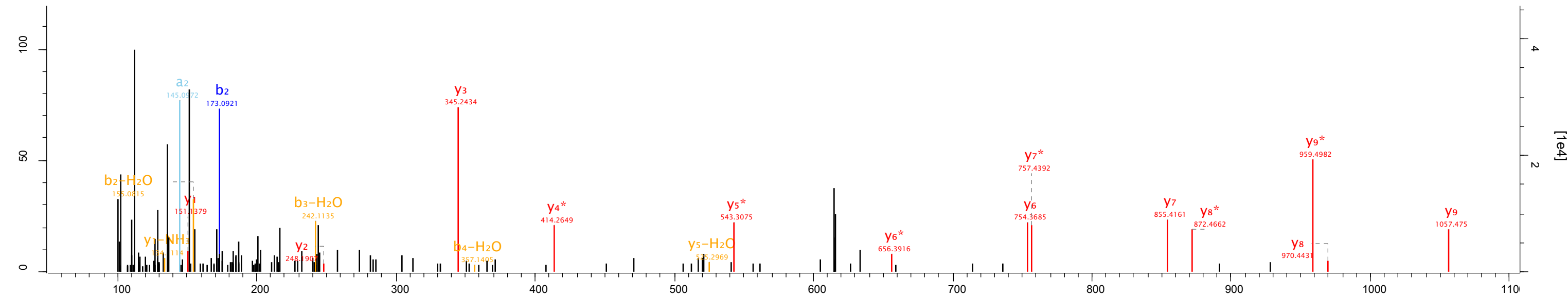
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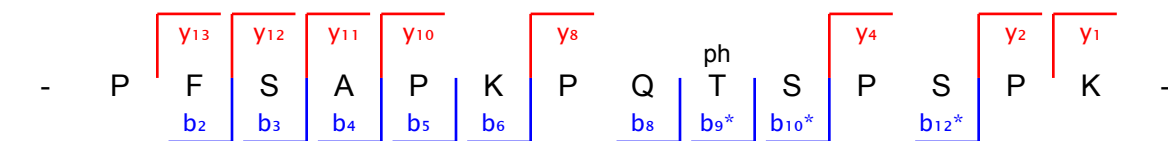
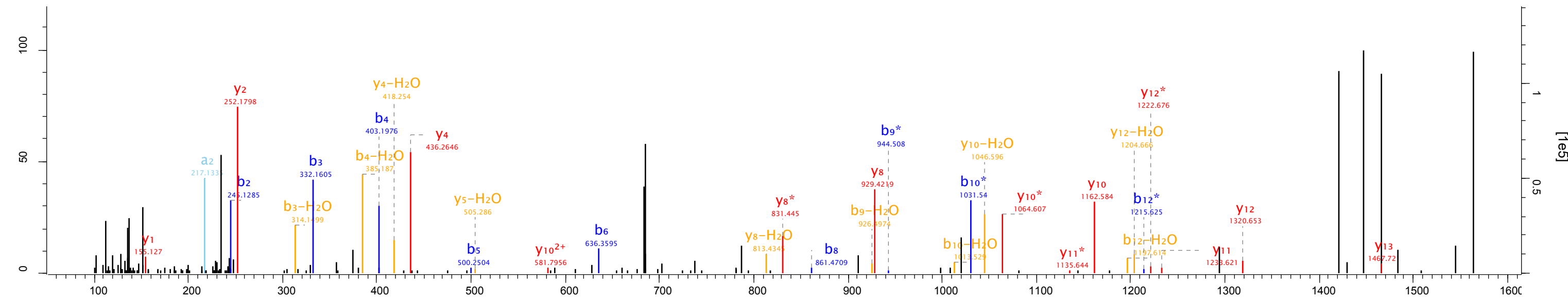


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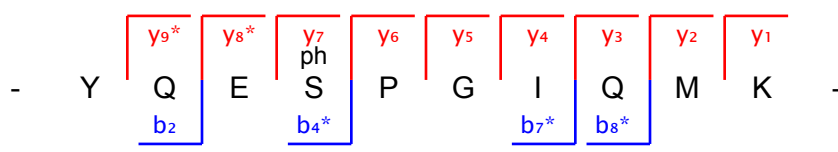
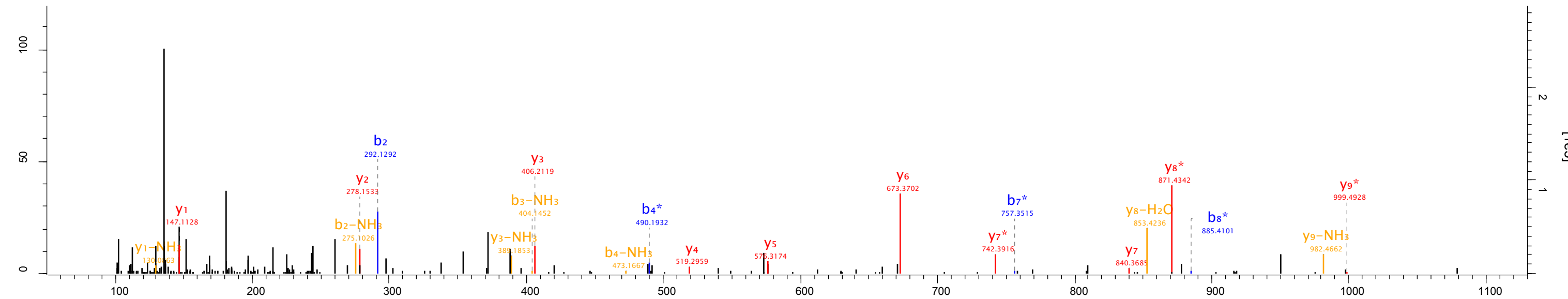


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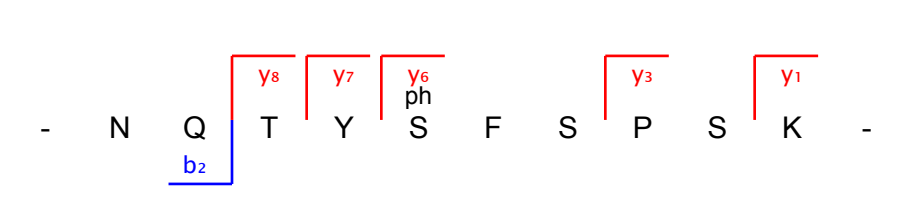
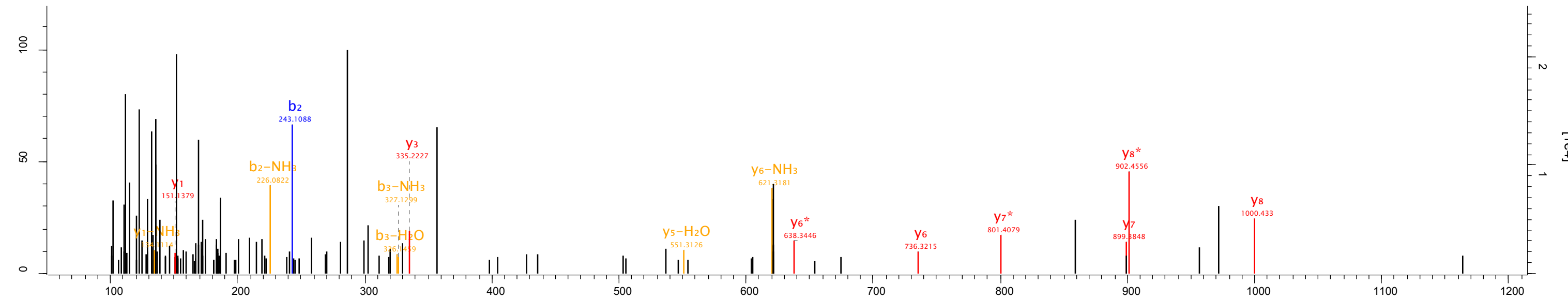


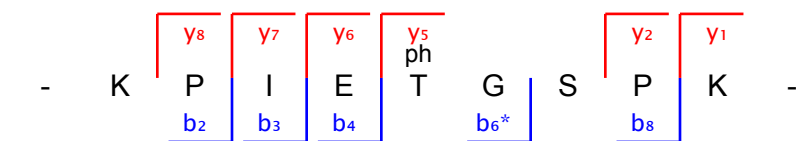
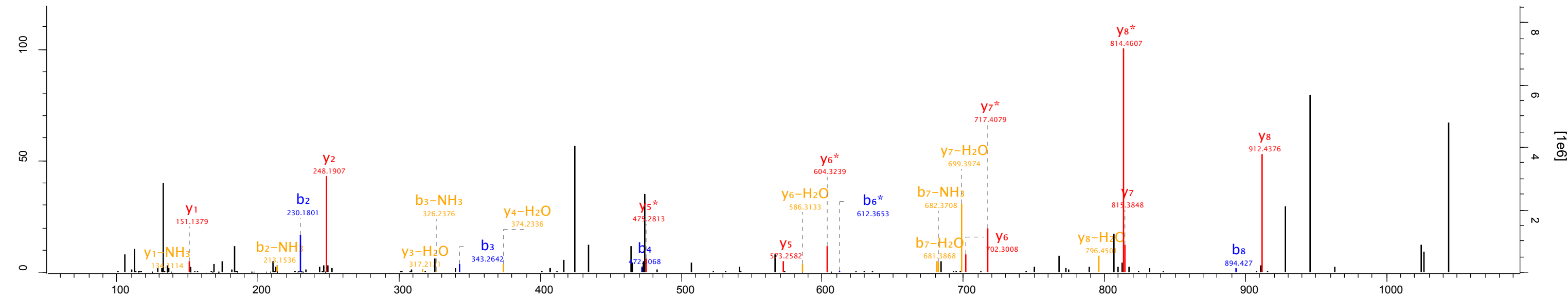


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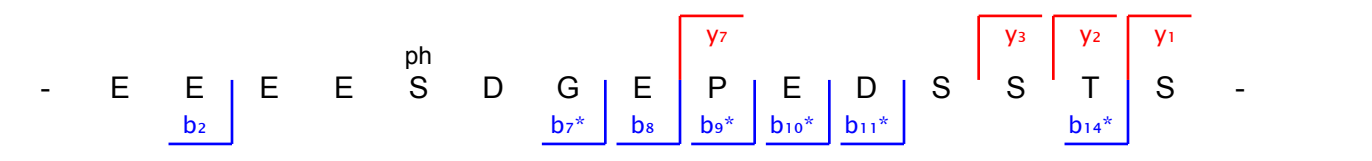
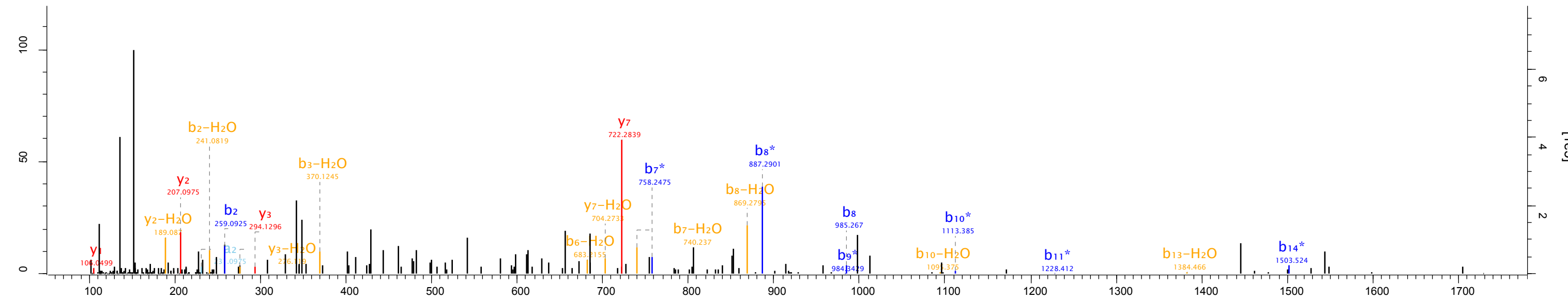


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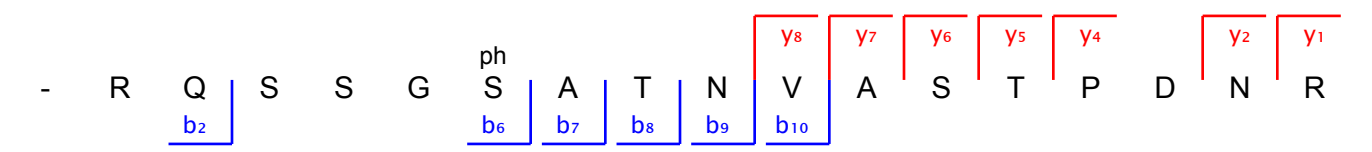
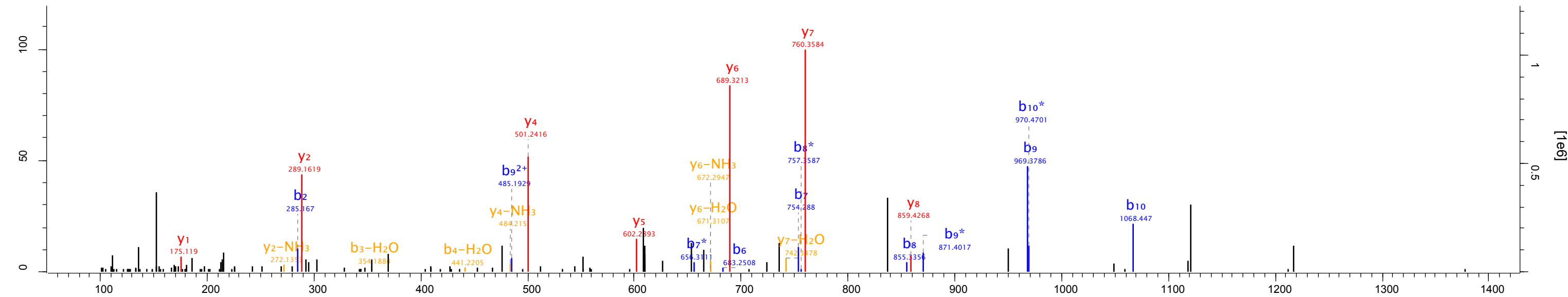
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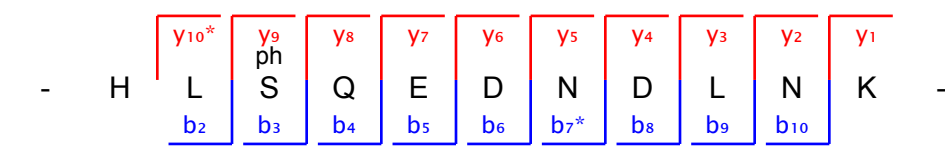
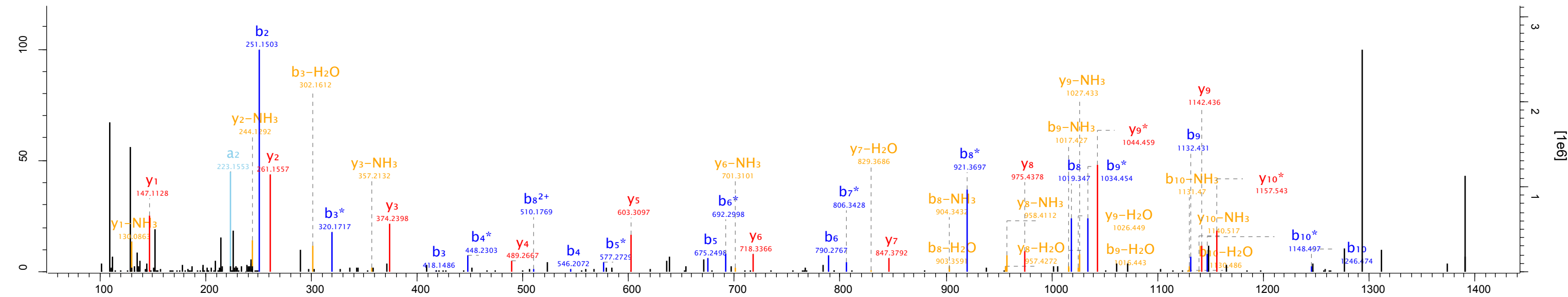


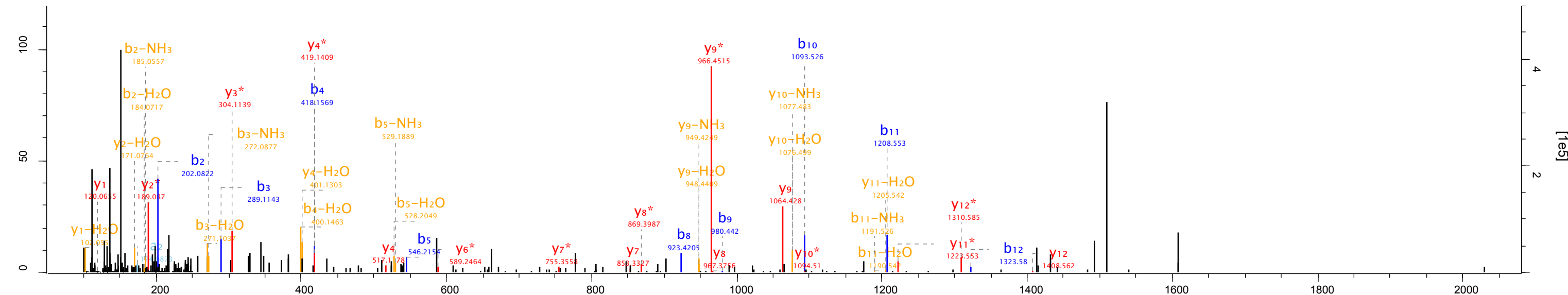
Raw file

20171215_MaS_33SR_LMH_phospho2_01

Scan	Method	Score	m/z	Gene names
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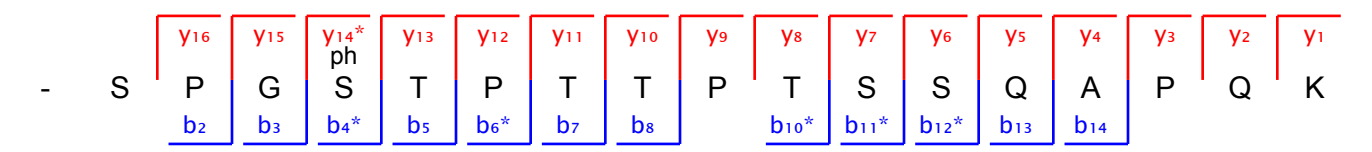
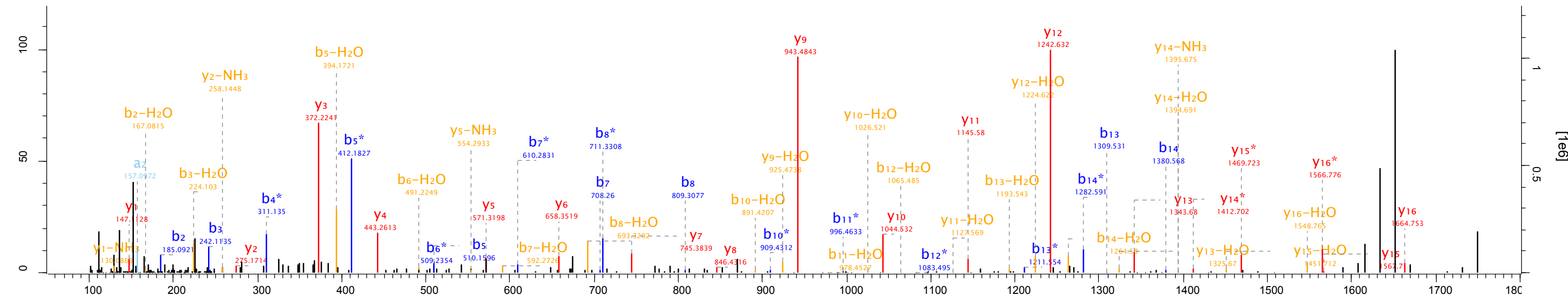
- S N S E Q P N R G L D D S T -

b₂
b₃
b₄
b₅
b₈
b₉
b₁₀
b₁₁
b₁₂

y₁₂
y₁₁*
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y₉
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y₄
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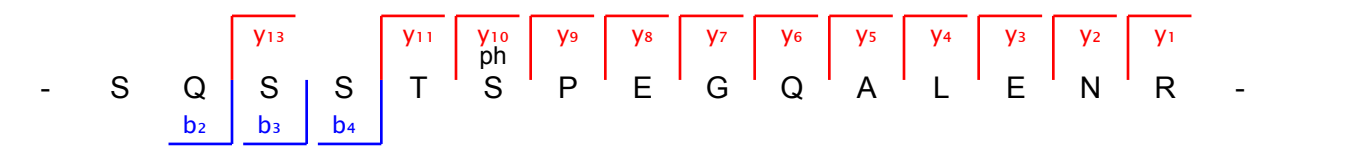
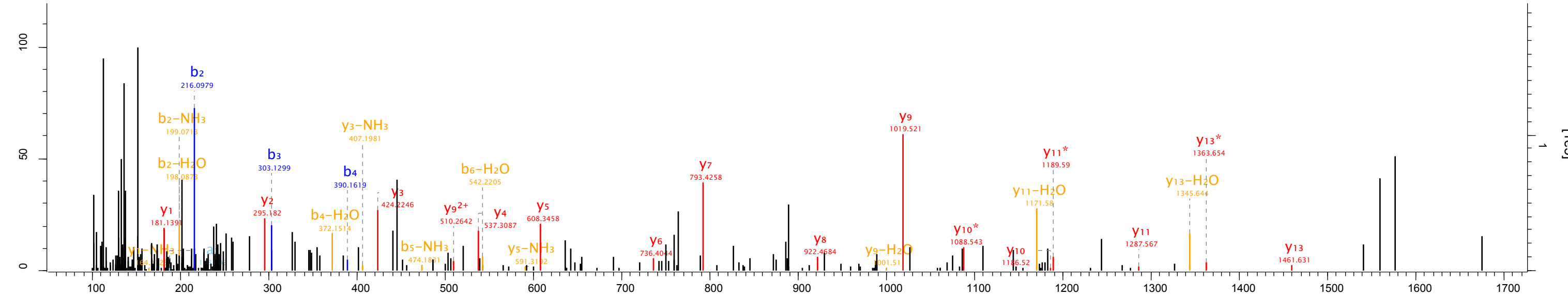
ph
S

Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 3797 Method FTMS; HCD Score 272.06 m/z 876.4 Gene names NUP214



Raw file Scan Method Score m/z Gene names

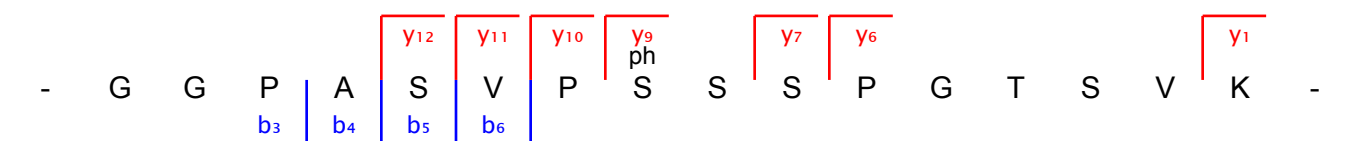
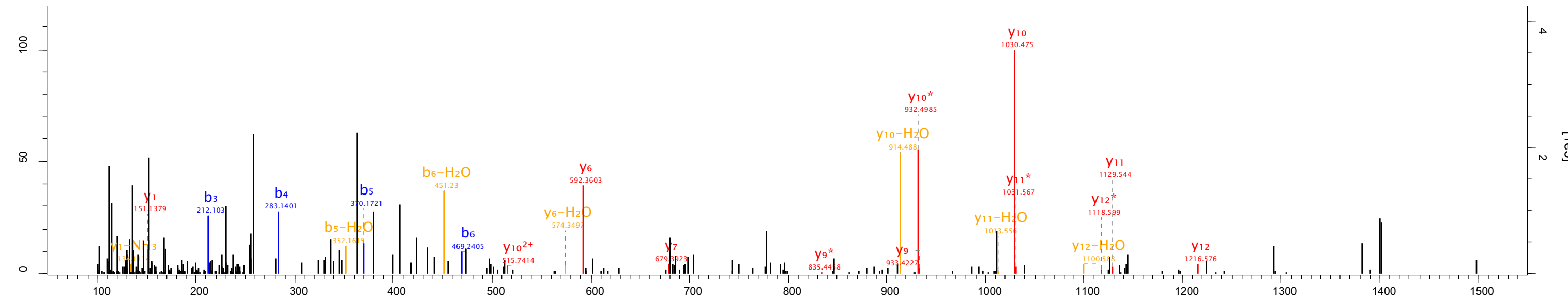
20171215_MaS_33SR_LMH_phospho2_01 5197 FTMS; HCD 59.98 838.86 SH3BP5



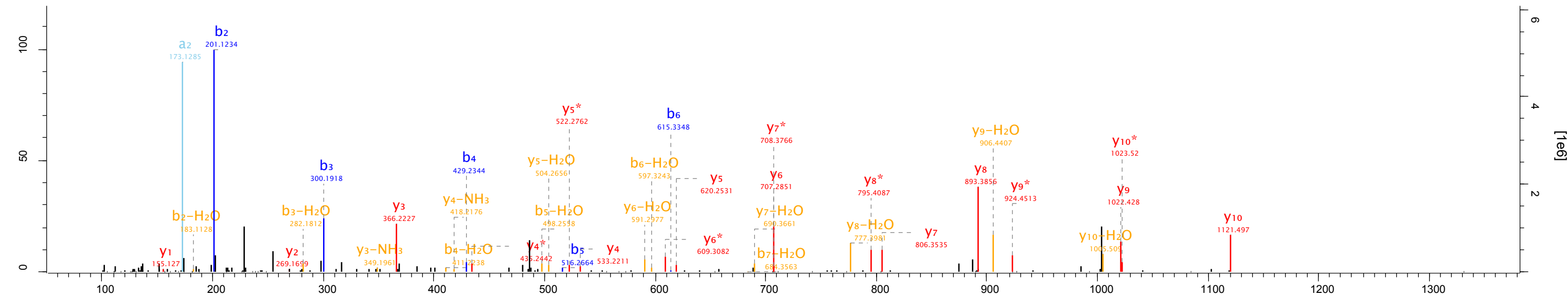
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20171215_MaS_33SR_LMH_phospho2_01

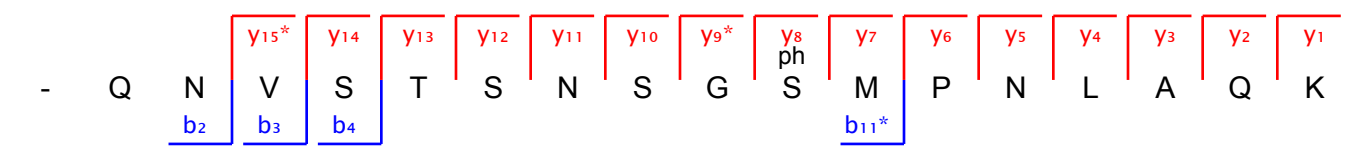
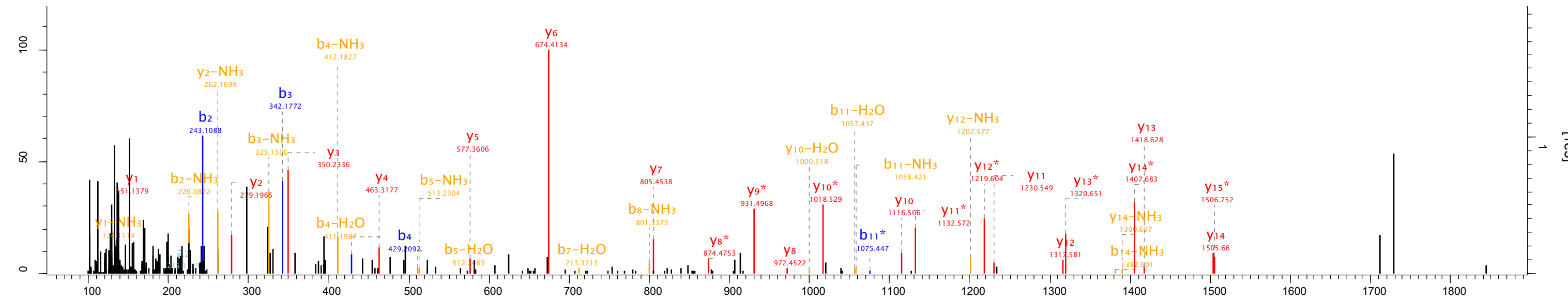
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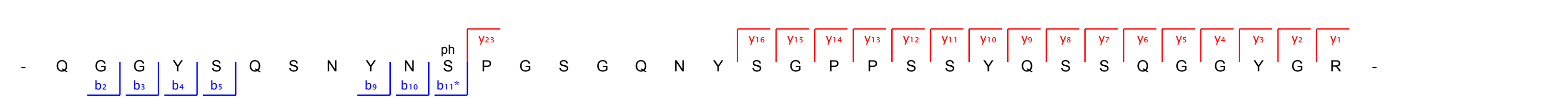
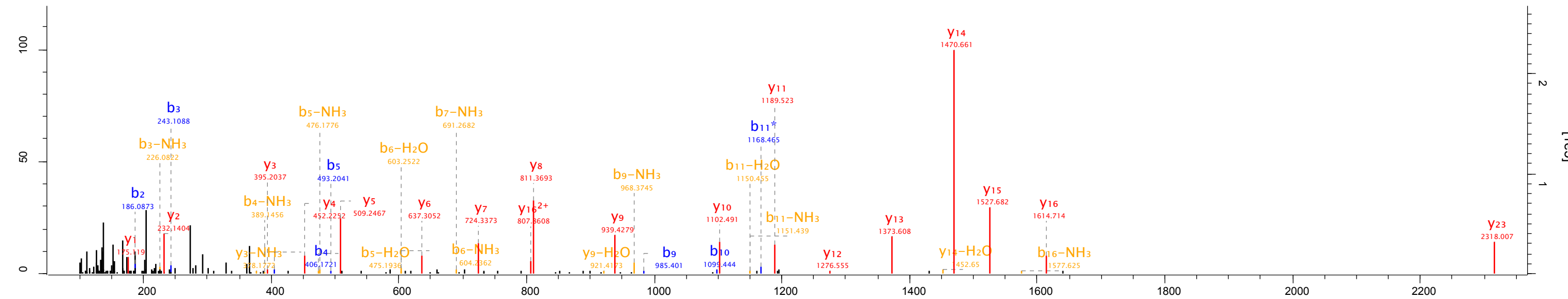
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 Scan: 6507 Method: FTMS; HCD Score: 188.39 m/z: 661.31 Gene names: PPA2



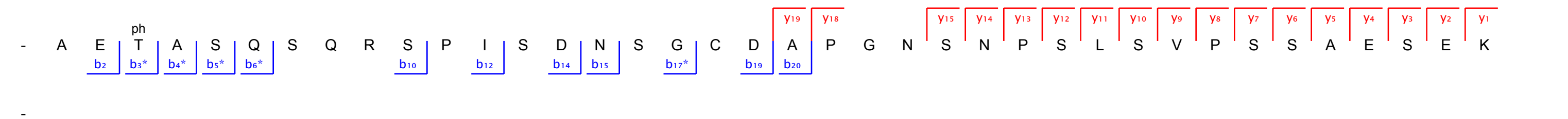
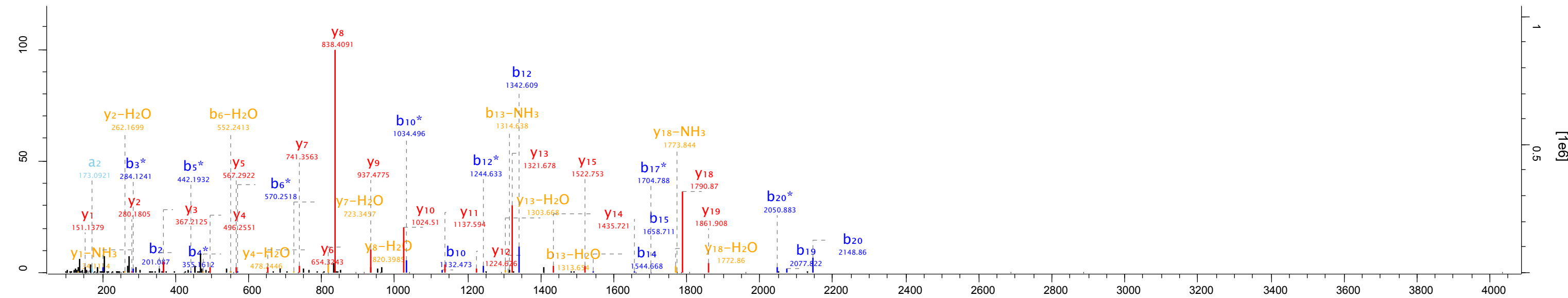
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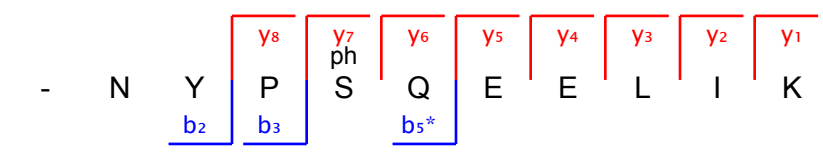
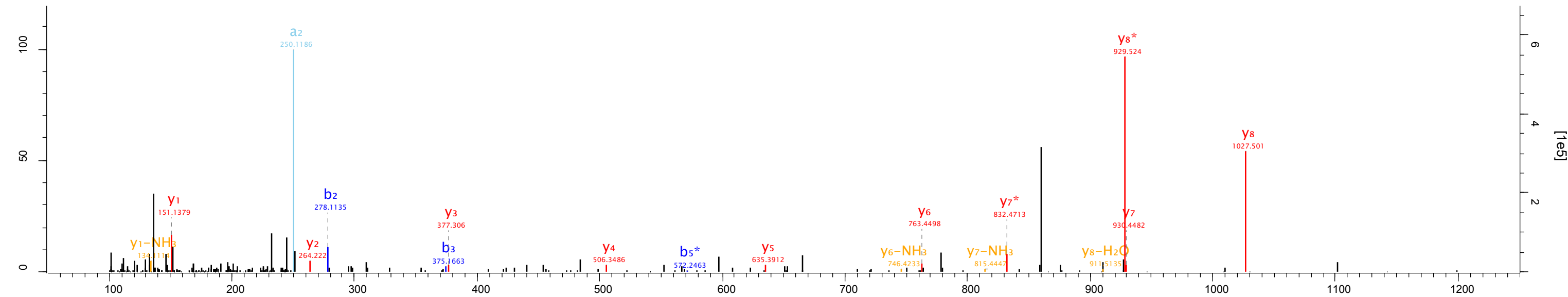
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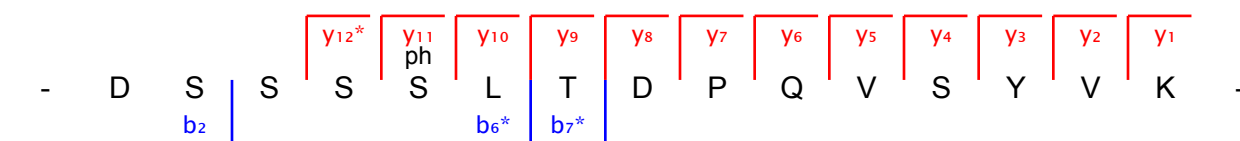
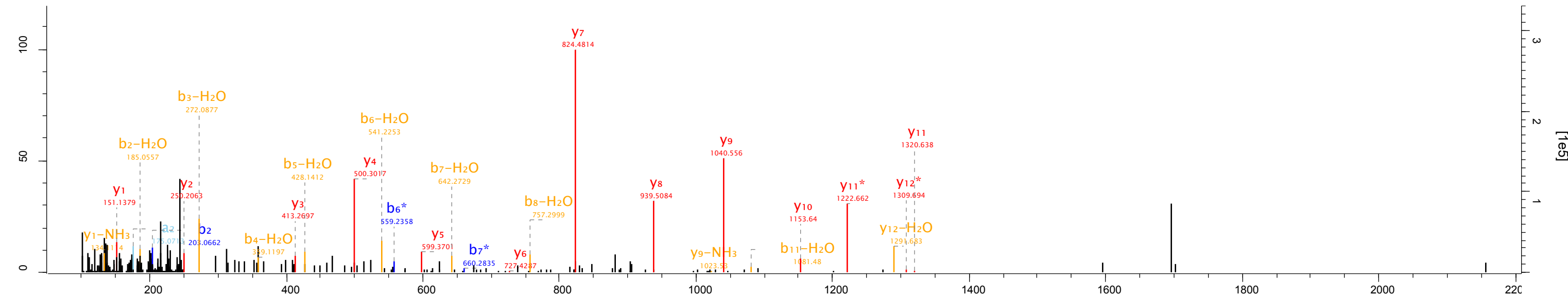


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 Scan: 8937 Method: FTMS; HCD Score: 93.57 m/z: 1314.25 Gene names: SCAF11

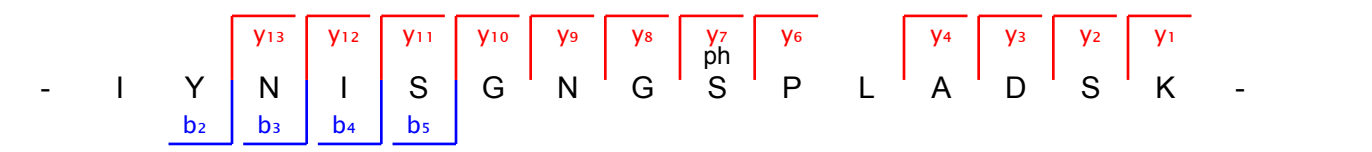
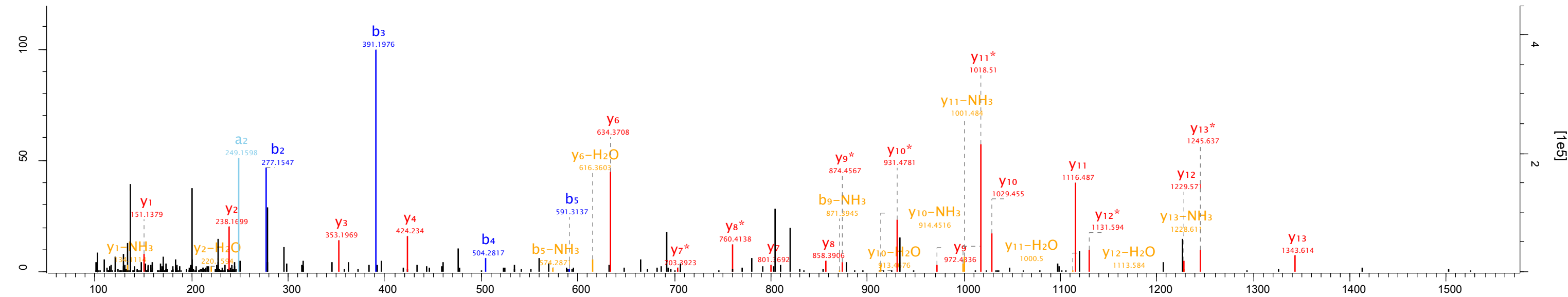


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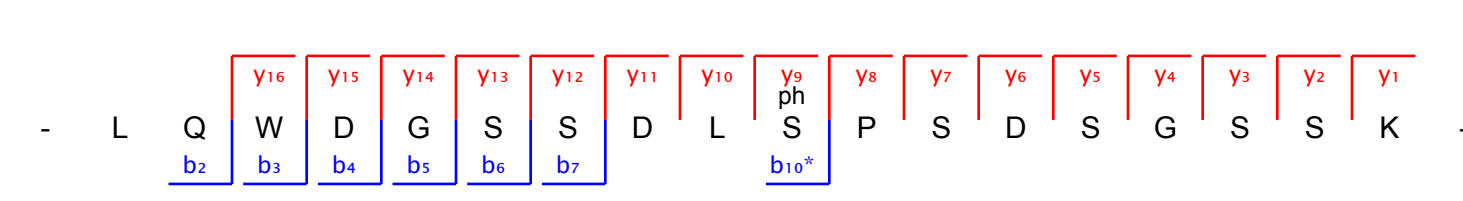
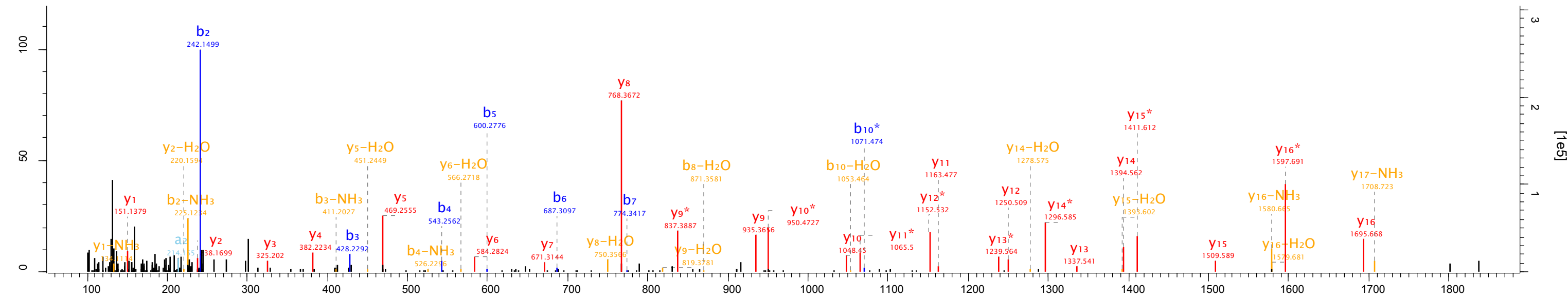


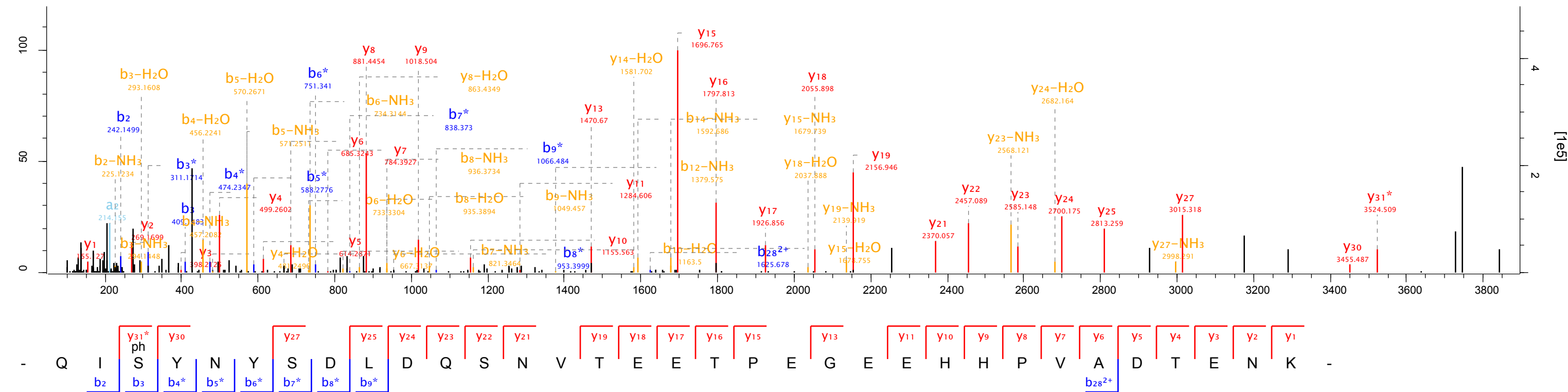


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 10497 Method FTMS; HCD Score 135.43 m/z 810.39 Gene names CDCA8

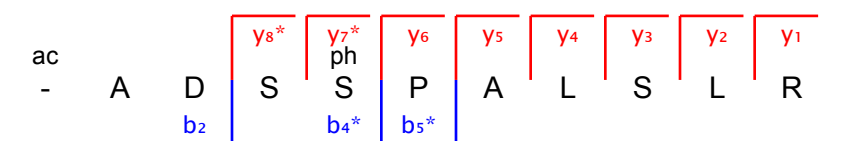
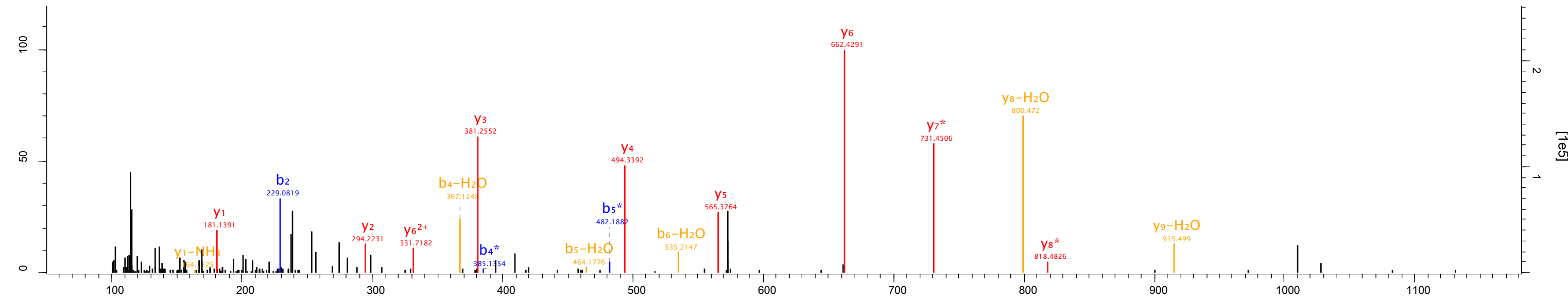


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 10947 Method FTMS; HCD Score 192.58 m/z 969.41 Gene names ATXN7L3

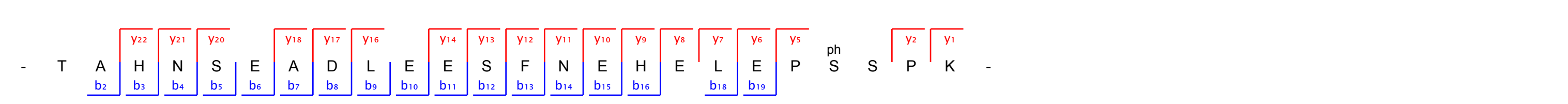
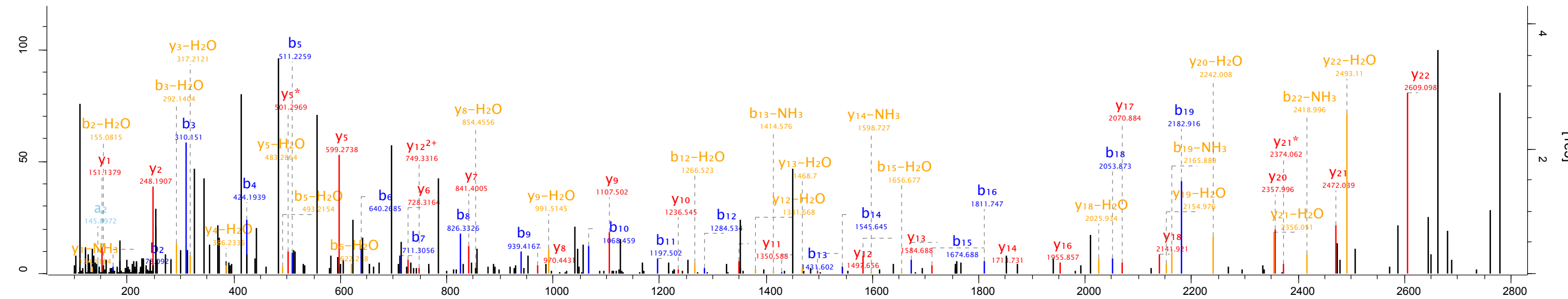




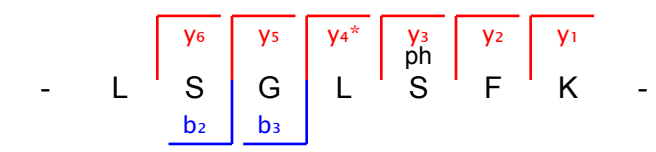
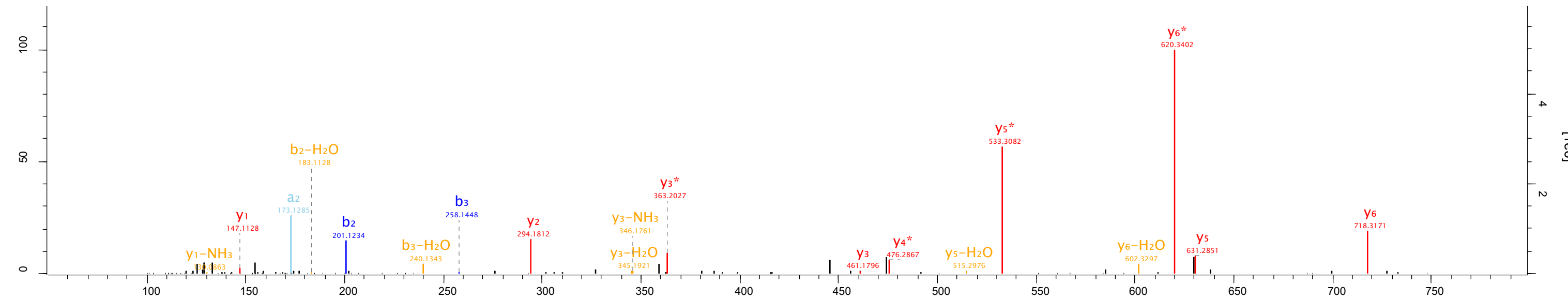
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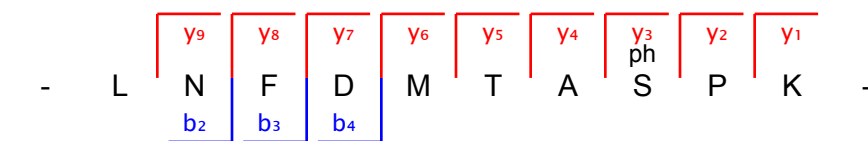
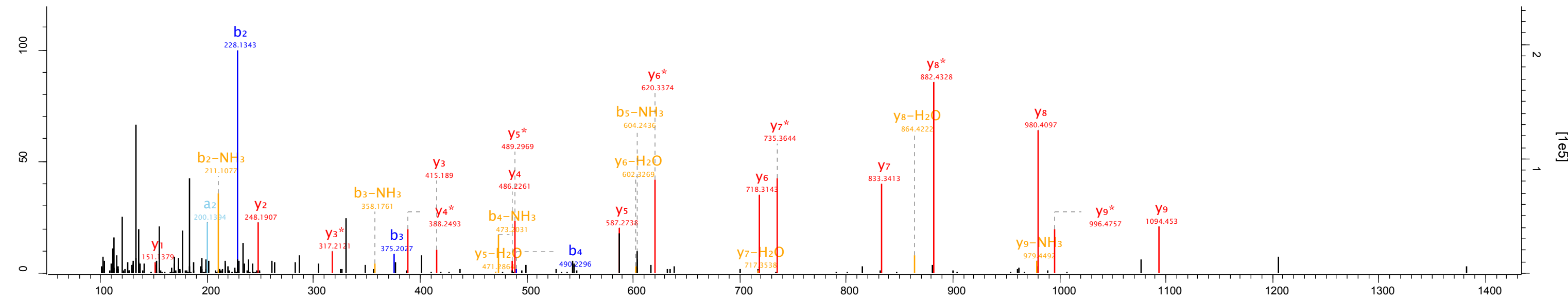
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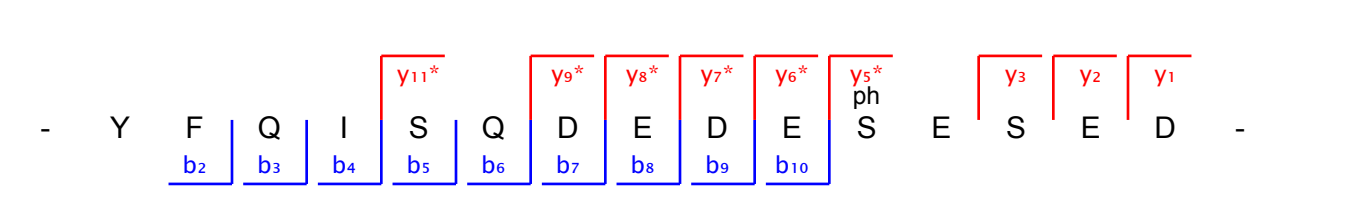
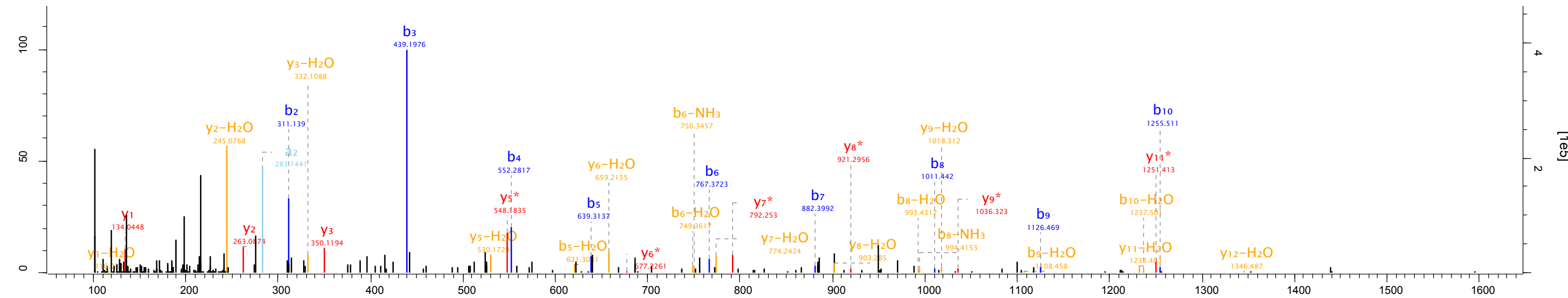
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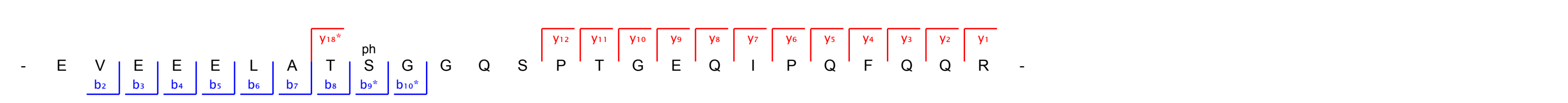
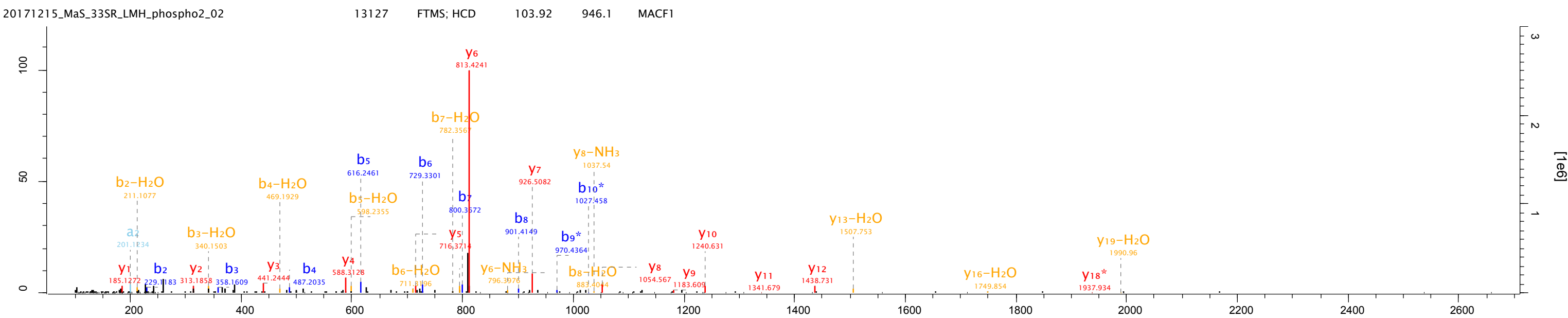
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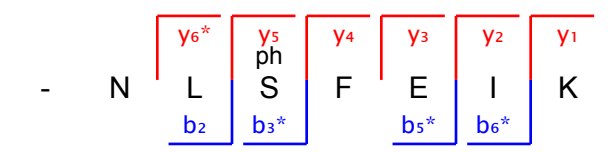
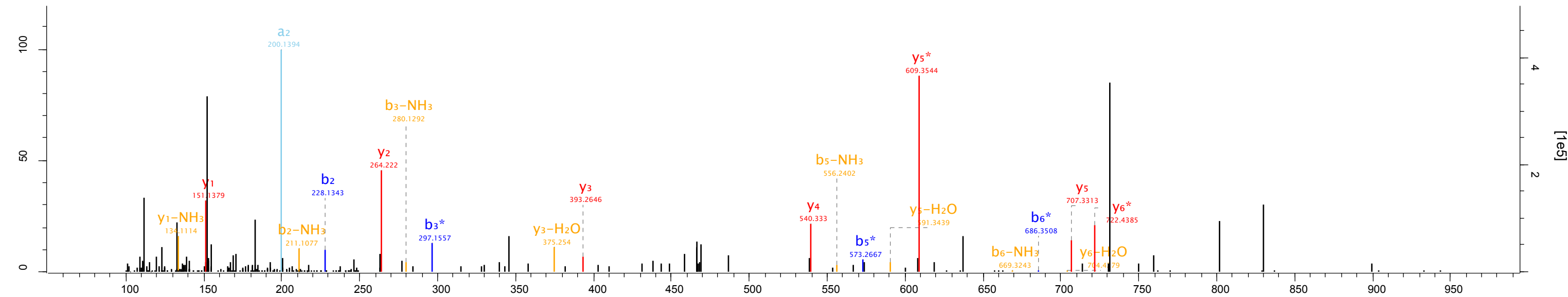
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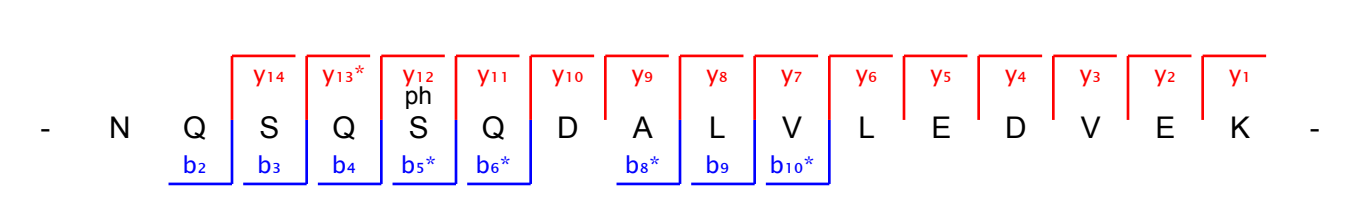
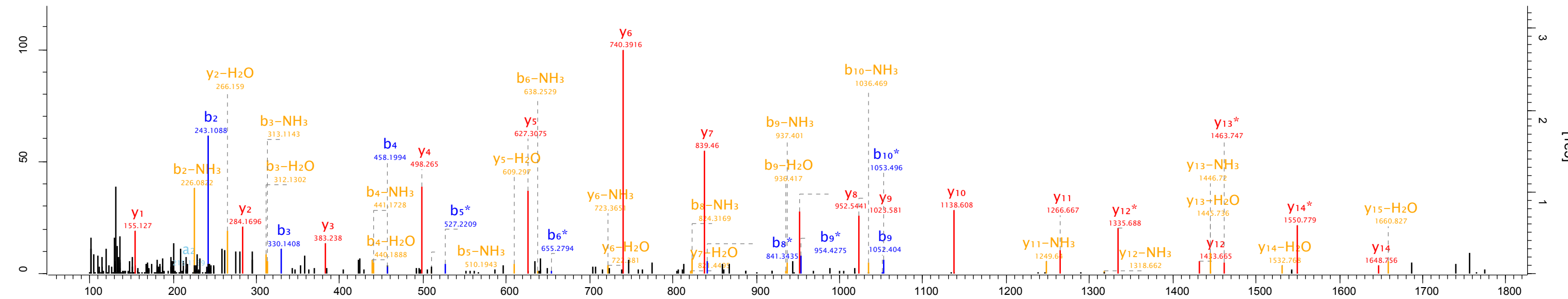
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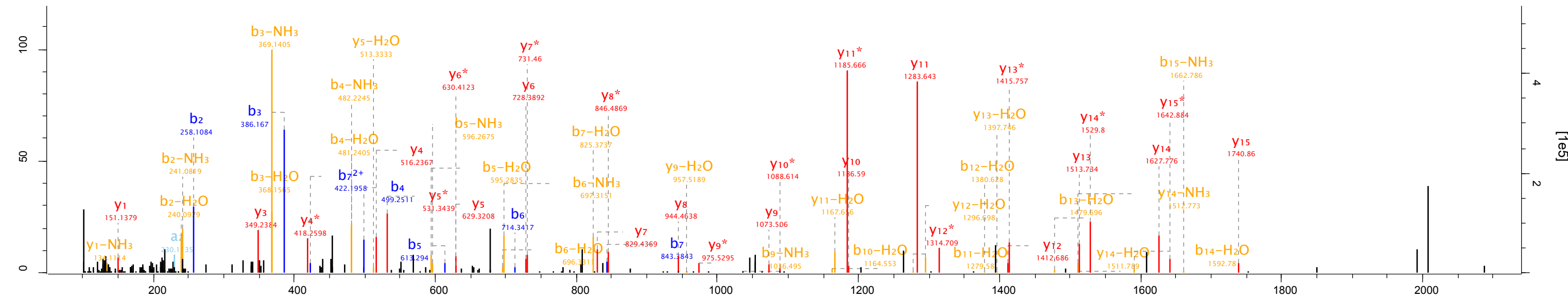
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Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 13607 Method: FTMS; HCD Score: 218.25 m/z: 945.93 Gene names: ABCC2



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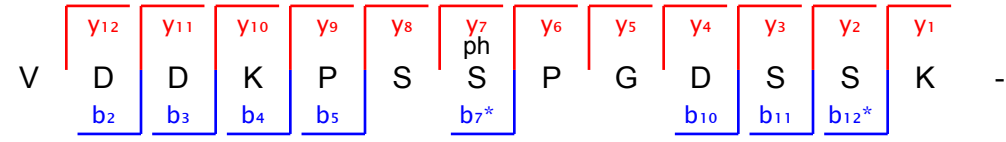
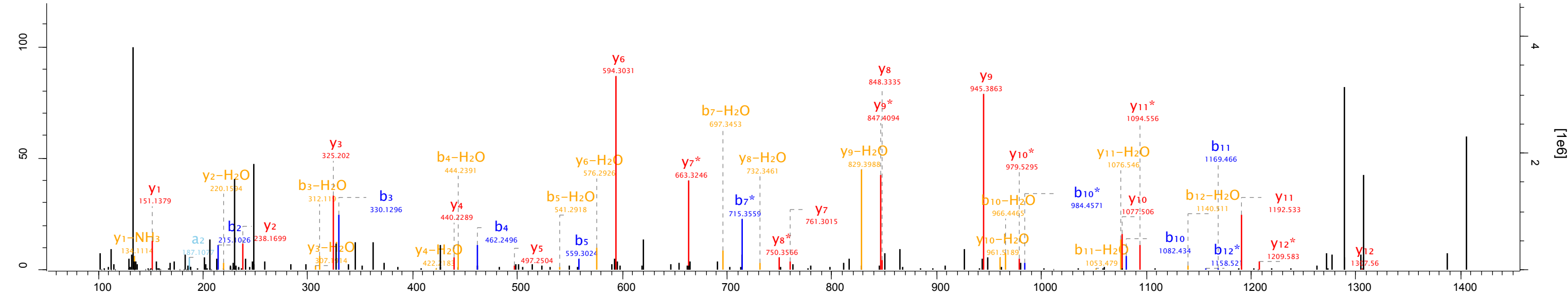
- Q E Q I N T E P L E D T V L S P T K -

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

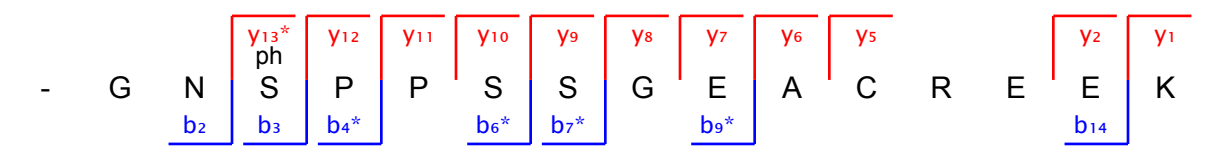
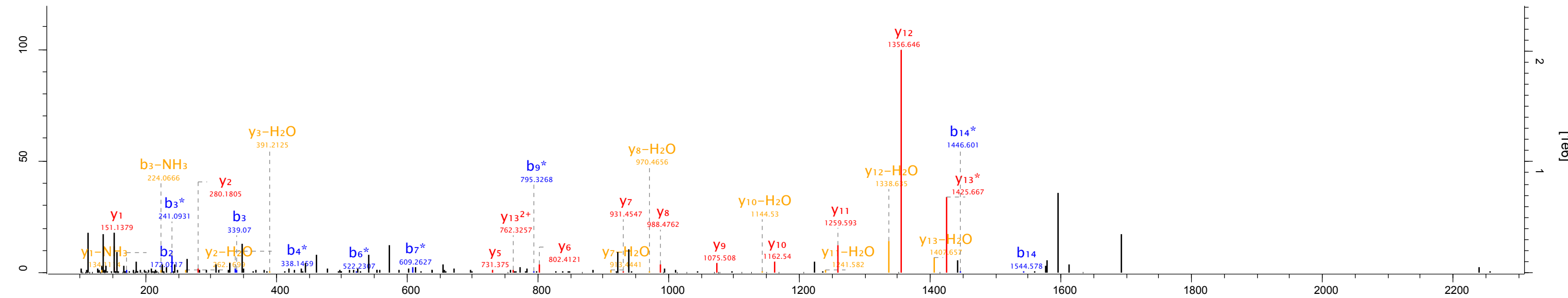
Fragmentation sites (b and y ions) are indicated by brackets below the sequence:

- b₂ (E)
- b₃ (EQ)
- b₄ (EQI)
- b₅ (EQIN)
- b₆ (EQINT)
- b₇ (EQINTE)
- y₁ (K)
- y₃ (SP)
- y₄ (SPL)
- y₅ (SPLD)
- y₆ (SPLDT)
- y₇ (SPLDTE)
- y₈ (SPLDTEV)
- y₉ (SPLDTEVL)
- y₁₀ (SPLDTEVLS)
- y₁₁ (SPLDTEVLSPT)
- y₁₂ (SPLDTEVLSPTK)
- y₁₃ (SPLDTEVLSPTK)
- y₁₄ (SPLDTEVLSPTK)
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20171215_MaS_33SR_LMH_phospho2_02 1947 FTMS; HCD 160.76 703.82 CBX8

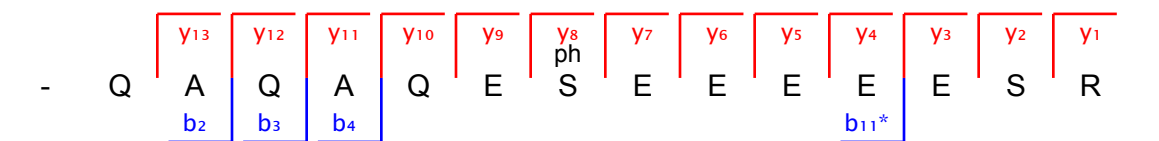
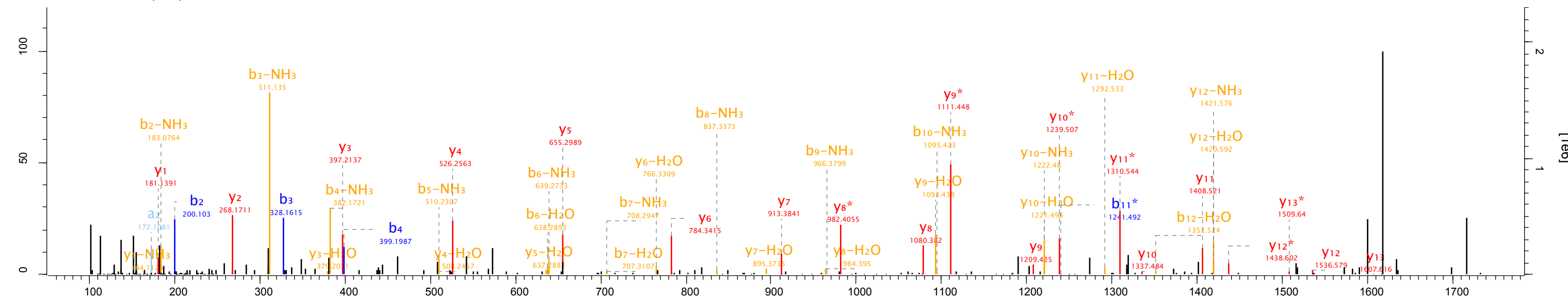


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 2347 Method FTMS; HCD Score 65.16 m/z 847.86 Gene names NAA10

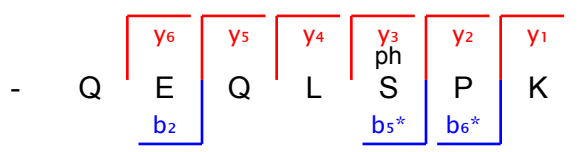
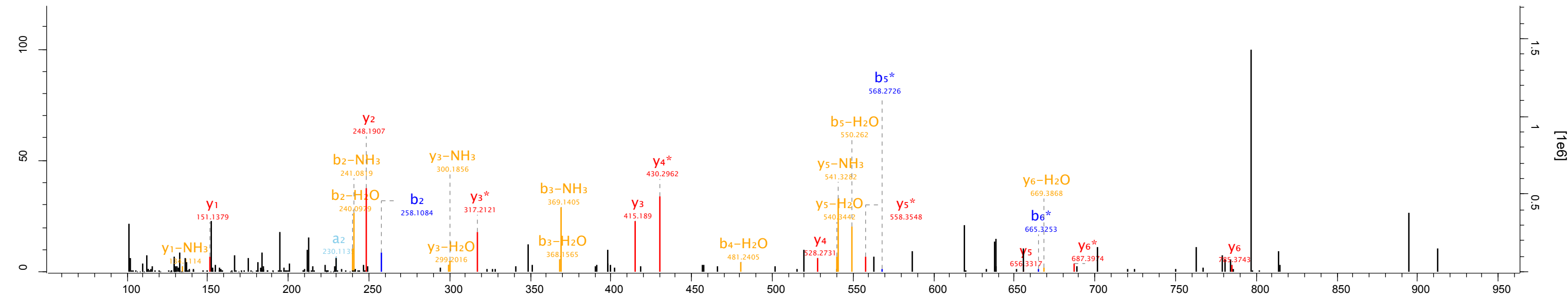


Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 2357 Method FTMS; HCD Score 184.21 m/z 868.34 Gene names DNAJC17

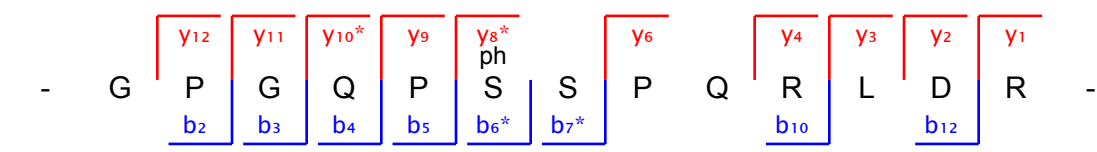
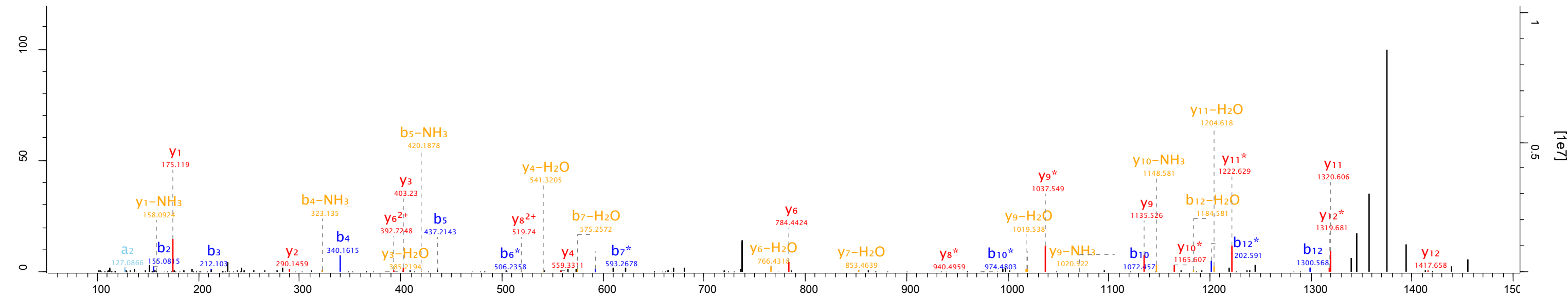


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 2947 Method FTMS; HCD Score 117.28 m/z 457.22 Gene names NCOA3

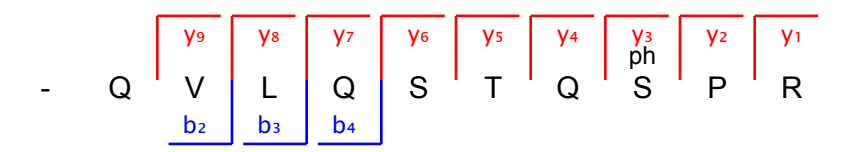
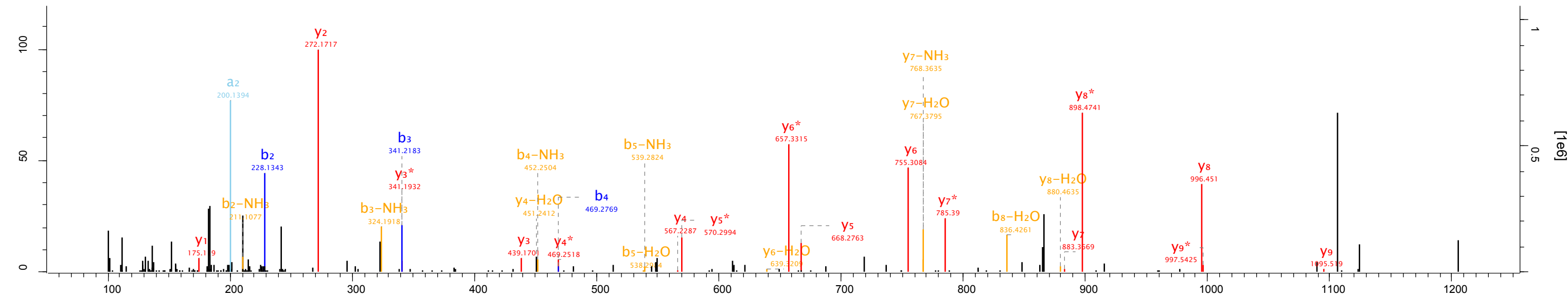


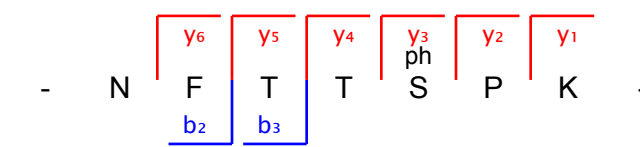
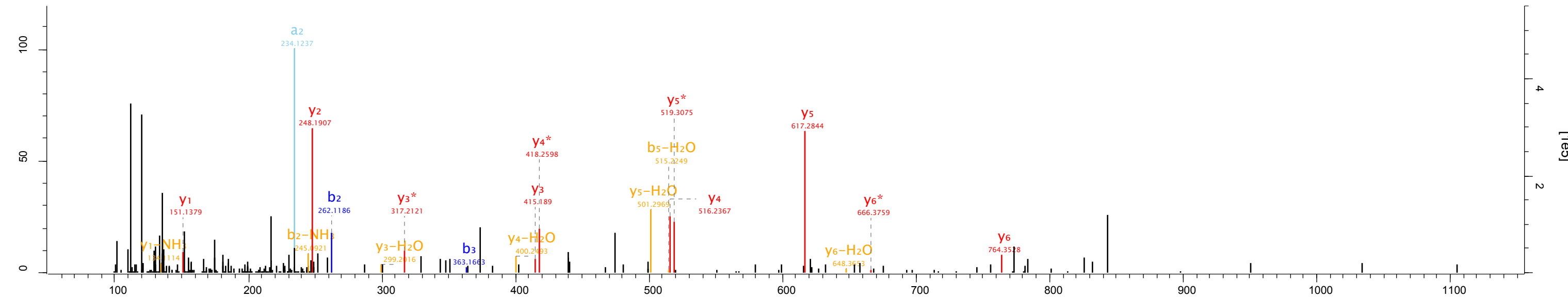
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20171215_MaS_33SR_LMH_phospho2_02

Scan 3537 Method FTMS; HCD Score 172.32 m/z 737.84 Gene names CD2BP2



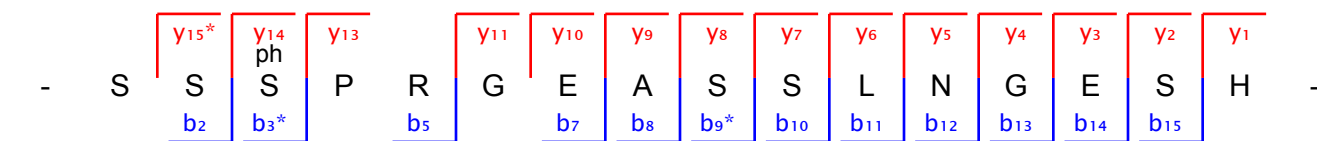
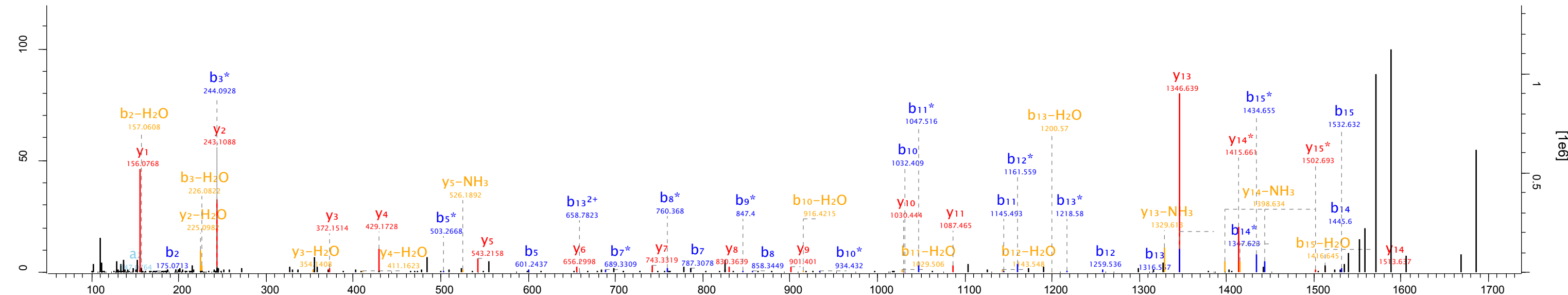
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 Scan: 3917 Method: FTMS; HCD Score: 175.88 m/z: 612.29 Gene names: AKAP2

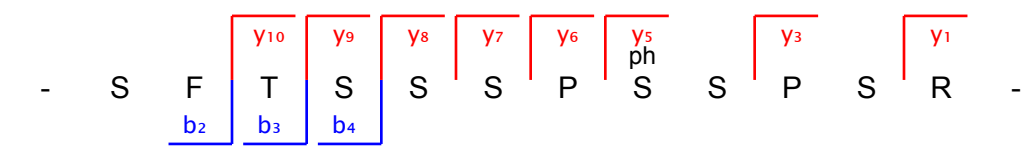
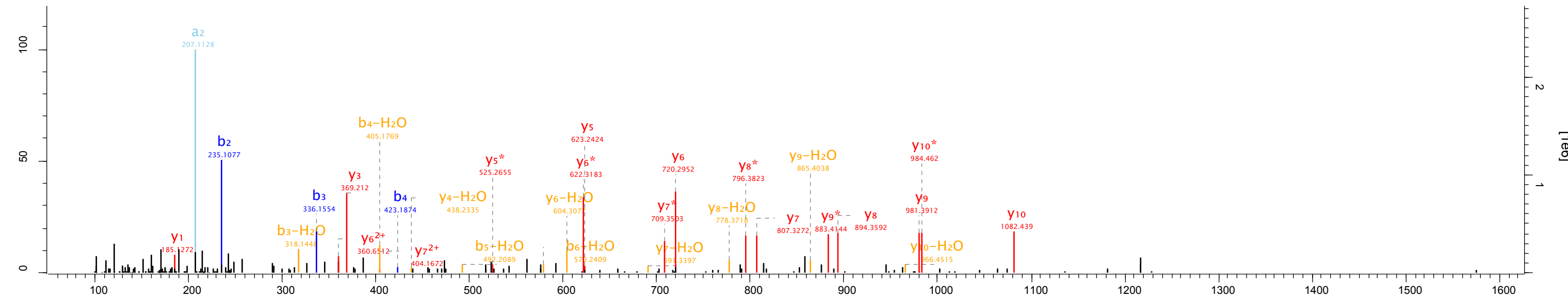




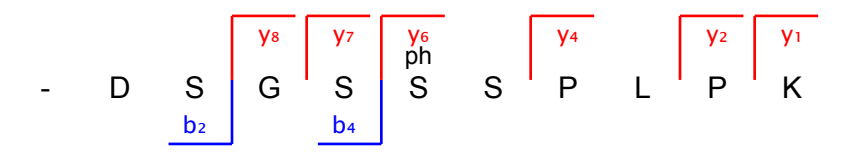
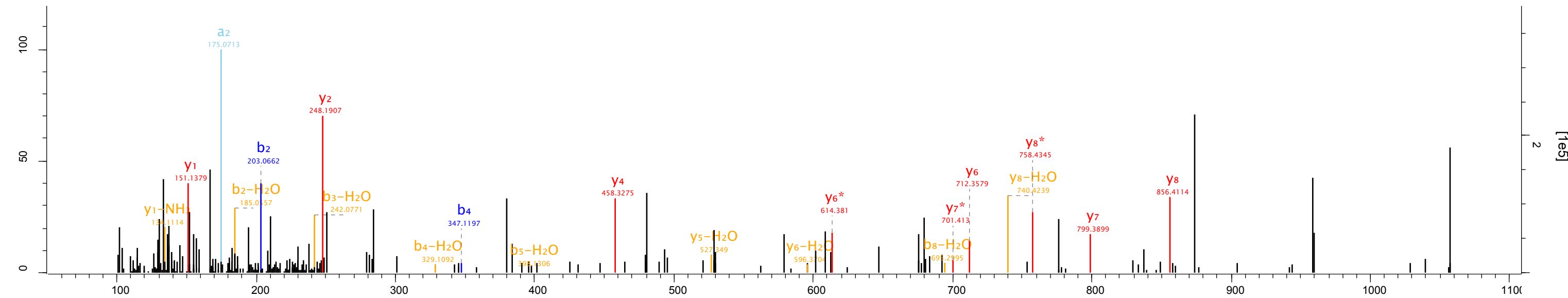
Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 4017 Method FTMS; HCD Score 160.12 m/z 844.36 Gene names YAF2

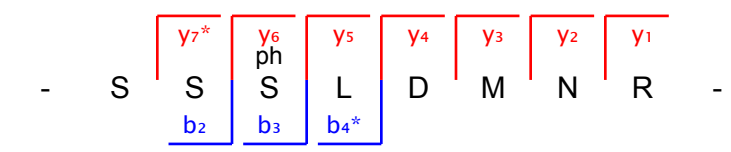
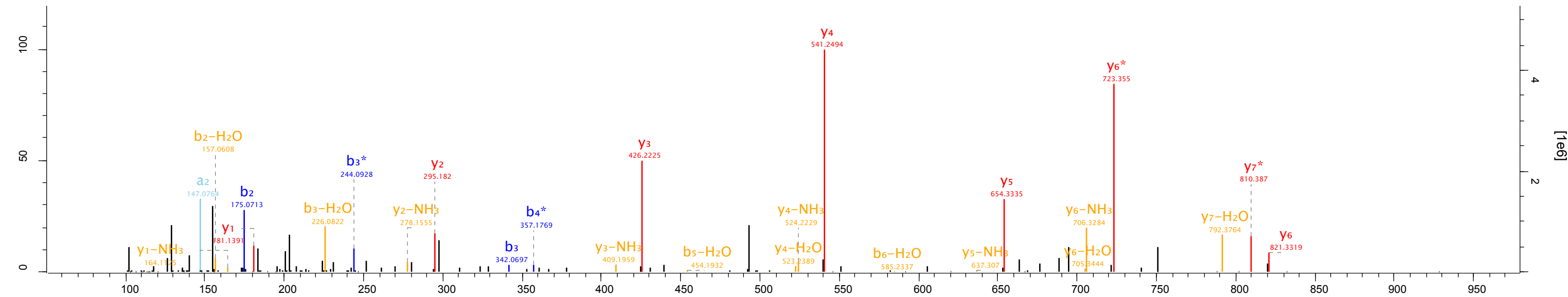




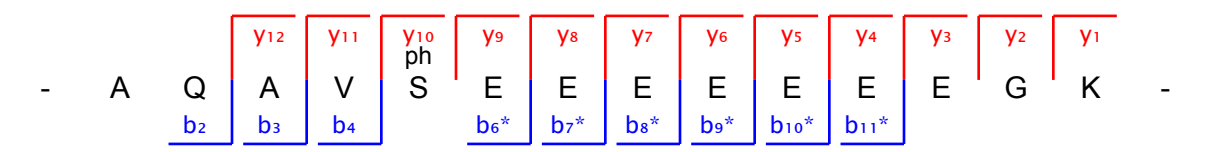
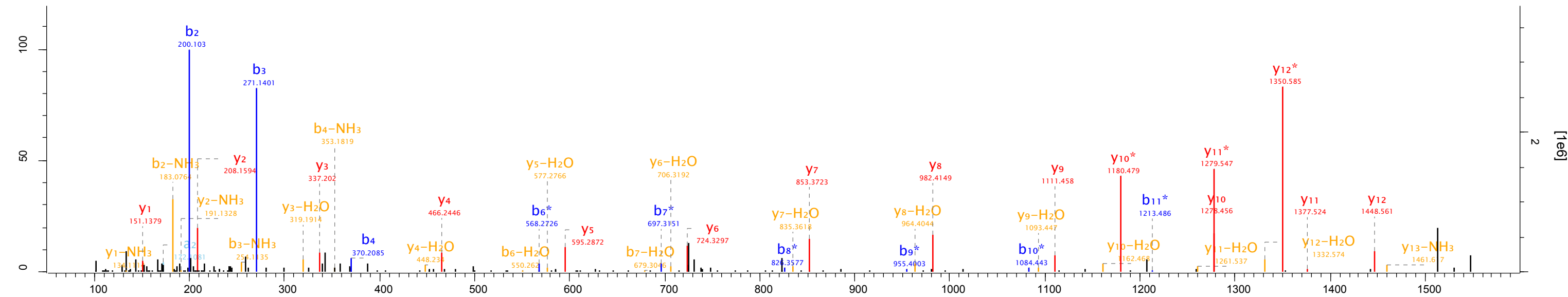
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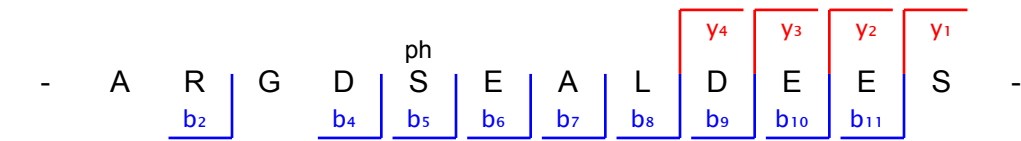
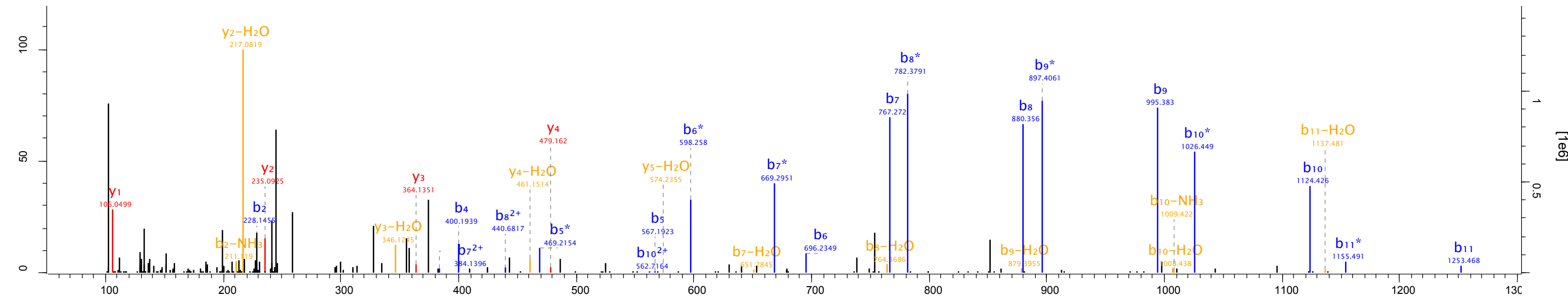


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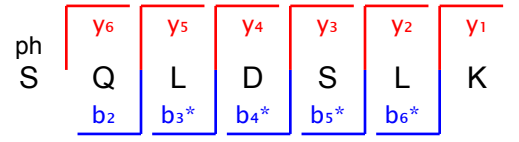
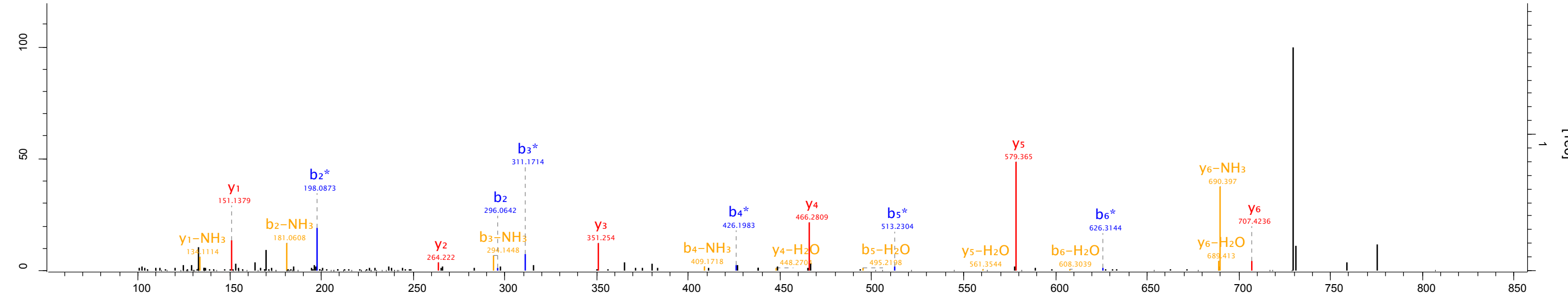


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 Scan: 4297 Method: FTMS; HCD Score: 196.71 m/z: 824.33 Gene names: DDX24

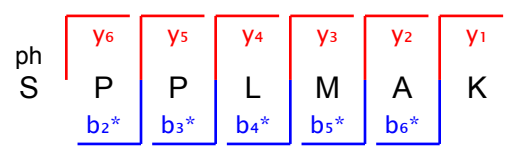
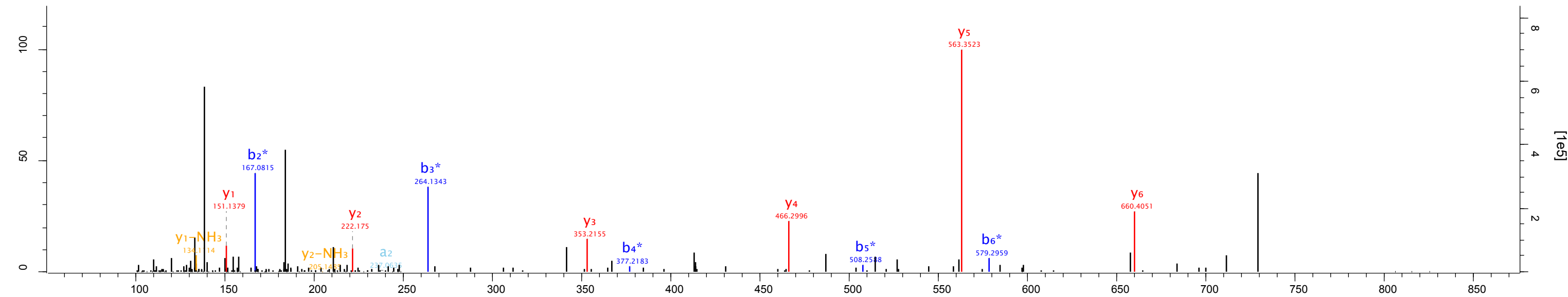


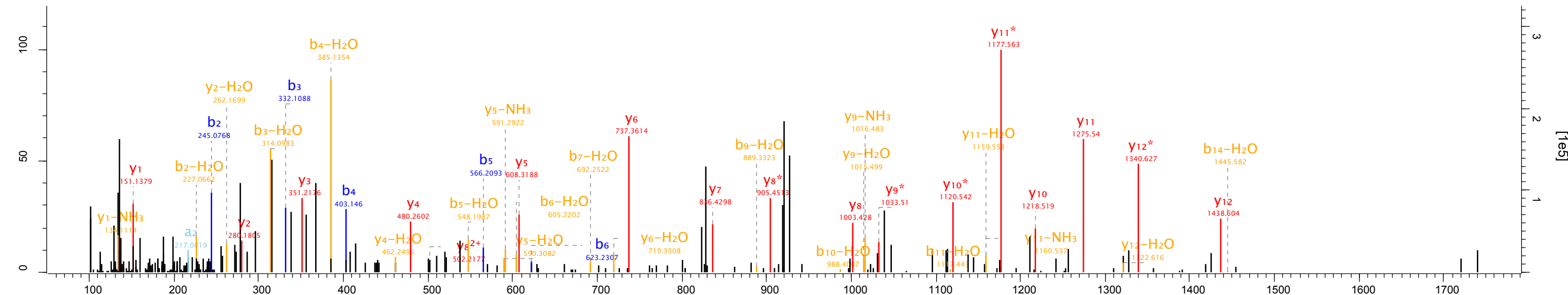


20171215_MaS_33SR_LMH_phospho2_02



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 5977 Method FTMS; HCD Score 69.81 m/z 414.21 Gene names DENND4C



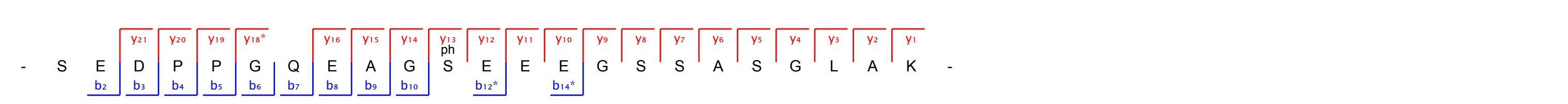
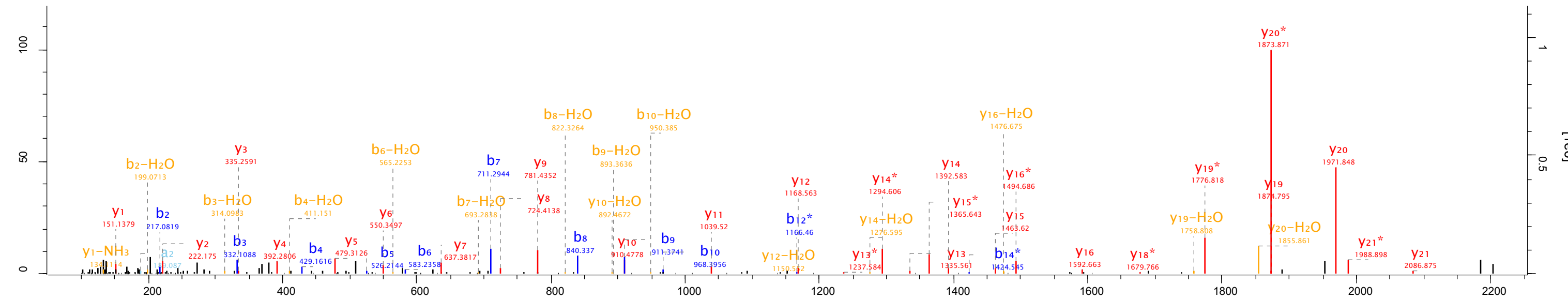


- E D S A Y G S Q S_{ph} V E Q E A E K -

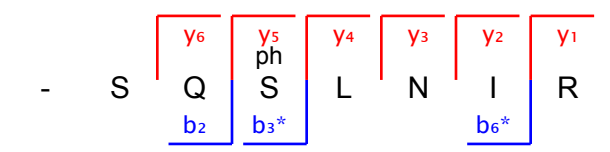
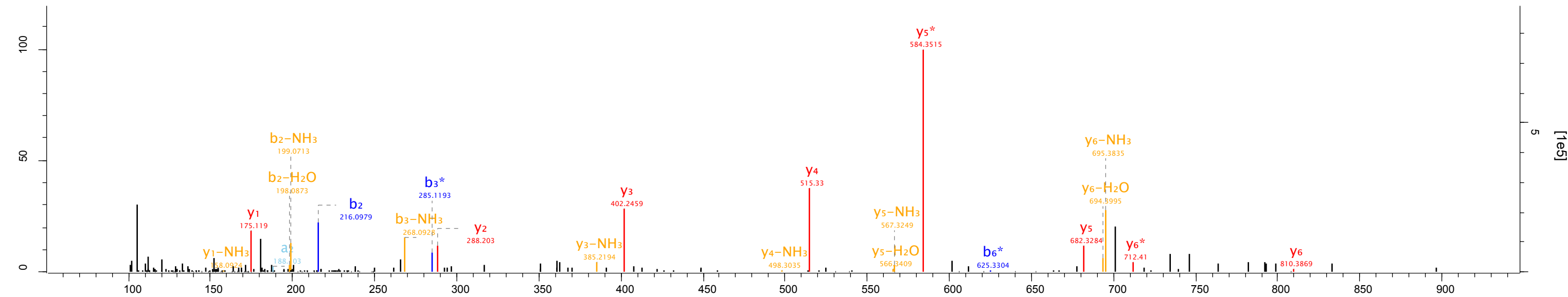
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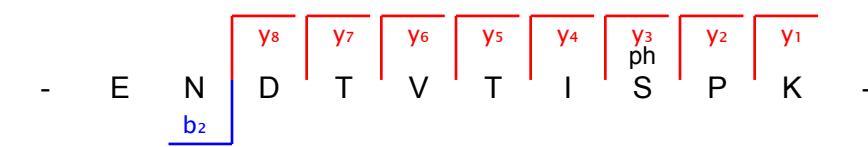
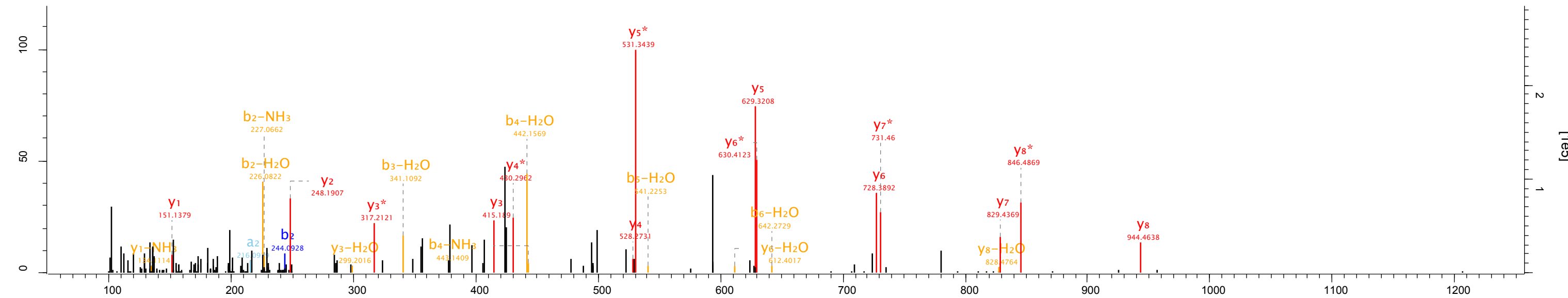
- b₂ (under D)
- b₃ (under S)
- b₄ (under A)
- b₅ (under Y)
- b₆ (under G)
- y₁₂ (under Y)
- y₁₁ (under G)
- y₁₀ (under S)
- y₉* (under Q)
- y₈ (under S_{ph})
- y₇ (under V)
- y₆ (under E)
- y₅ (under Q)
- y₄ (under E)
- y₃ (under A)
- y₂ (under E)
- y₁ (under K)

Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6127 Method FTMS; HCD Score 192.5 m/z 1152.48 Gene names CLUH

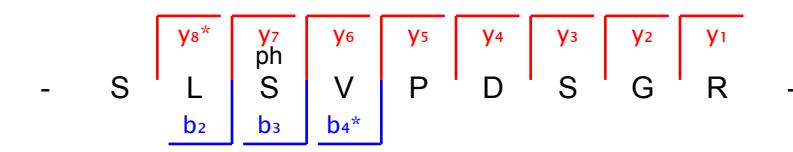
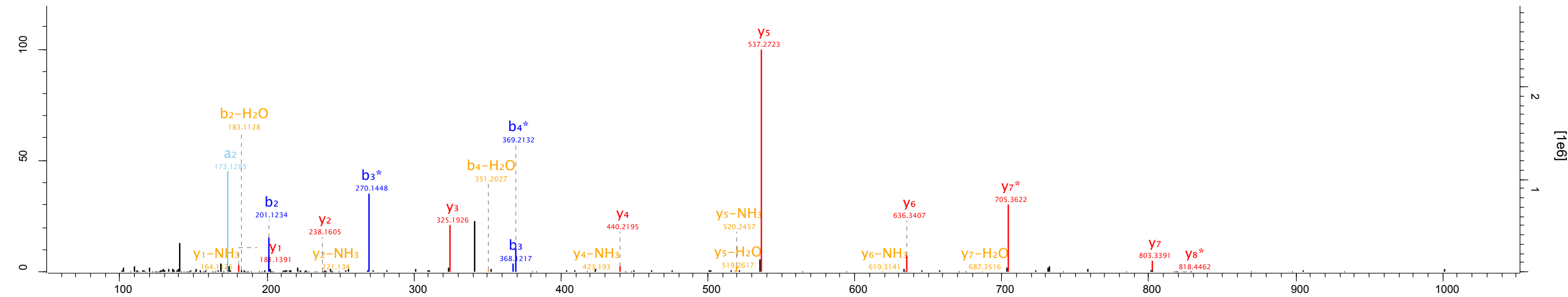


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 6137 Method: FTMS; HCD Score: 125.83 m/z: 449.21 Gene names: PIK3C2A

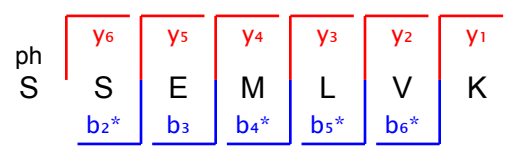
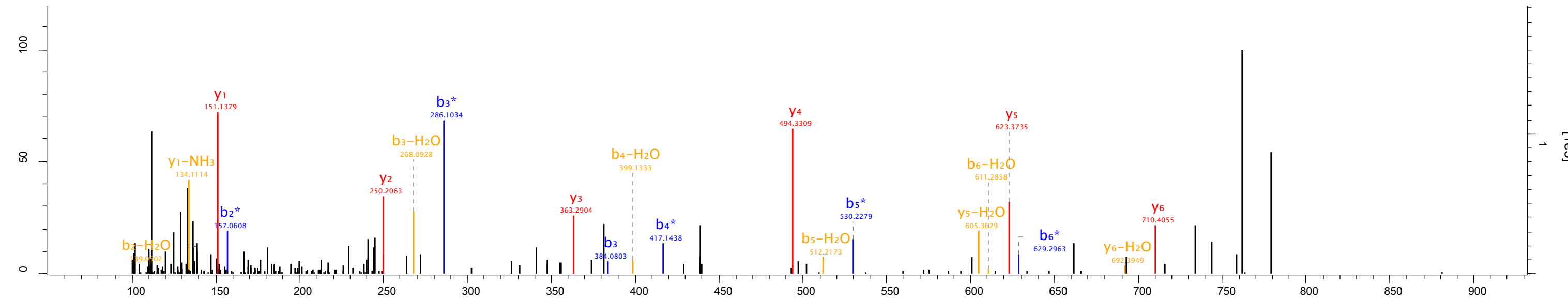




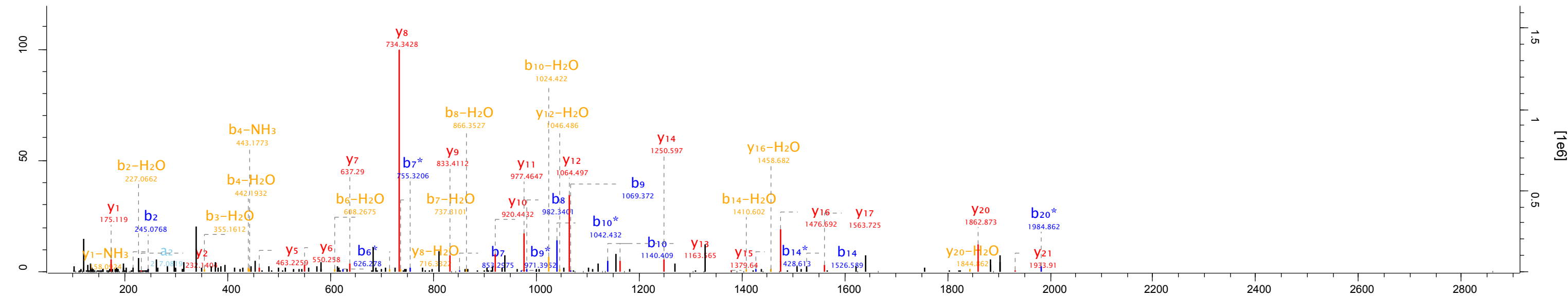
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 Scan: 6467 Method: FTMS; HCD Score: 84.82 m/z: 502.23 Gene names: GIGYF1



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6587 Method FTMS; HCD Score 120.87 m/z 439.21 Gene names KLC2



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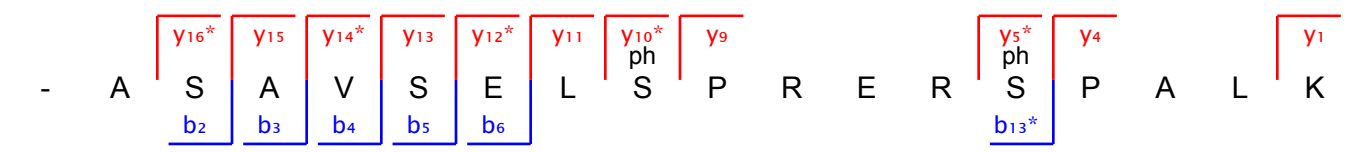
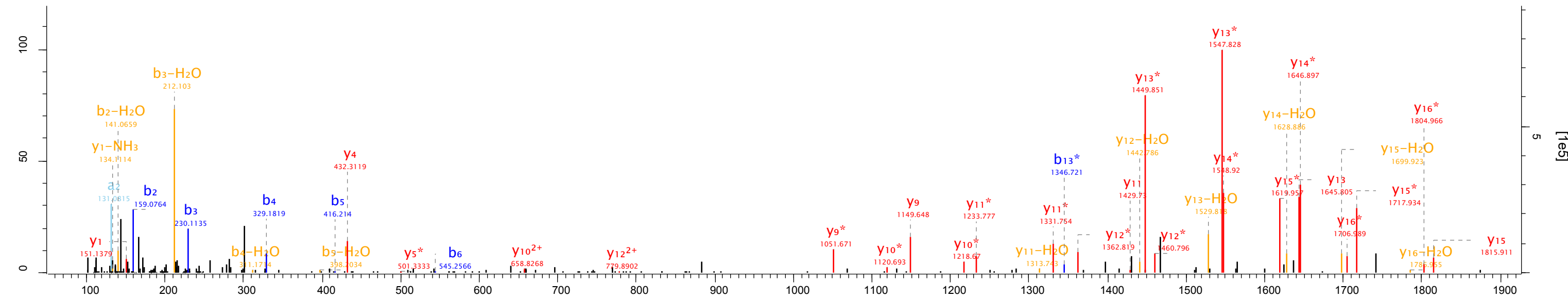
- E D K S P S E E S A P T T S P E S V S G S V P S S G S S G R -

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

- b₂ (D)
- b₆^{*} (S)
- b₇ (E)
- b₈ (E)
- b₉ (S)
- b₁₀ (A)
- b₁₄ (S)
- b₂₀^{*} (G)
- y₁ (R)
- y₂ (G)
- y₅ (G)
- y₆ (S)
- y₇ (S)
- y₈ (P)
- y₉ (V)
- y₁₀ (S)
- y₁₁ (G)
- y₁₂ (S)
- y₁₃ (V)
- y₁₄ (S)
- y₁₅ (E)
- y₁₆ (P)
- y₁₇ (S)
- y₂₀ (P)
- y₂₁ (A)

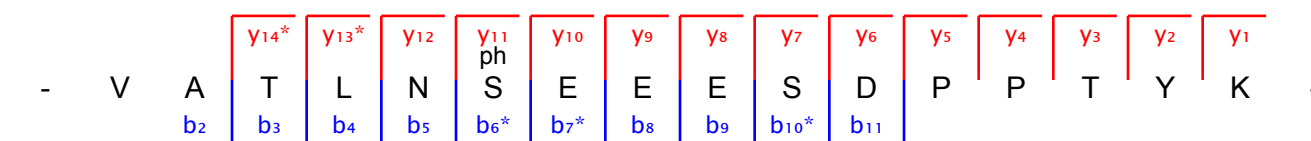
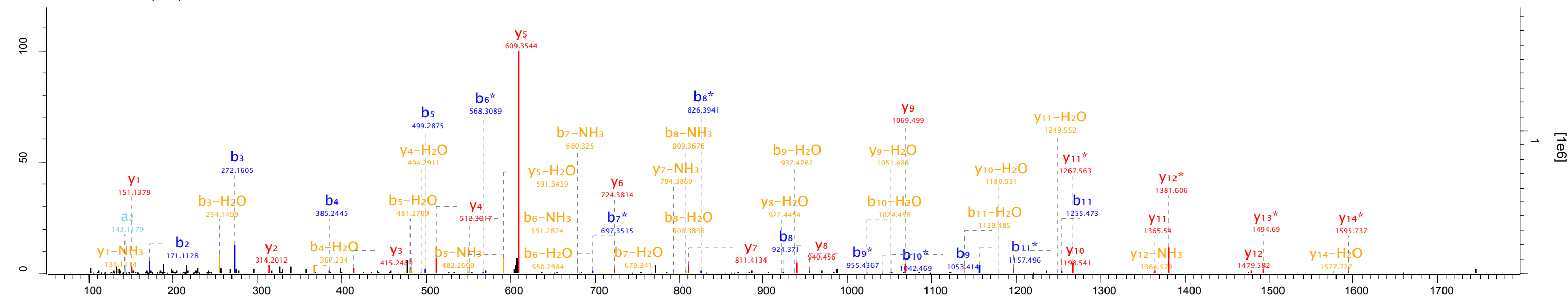
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20171215_MaS_33SR_LMH_phospho2_02

Scan 8037 Method FTMS; HCD Score 171.39 m/z 658.67 Gene names THRAP3

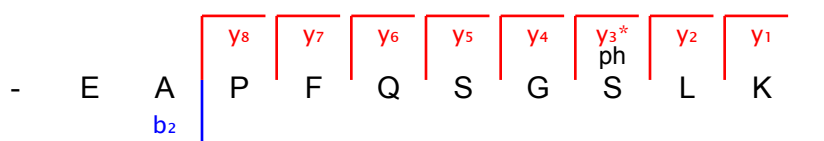
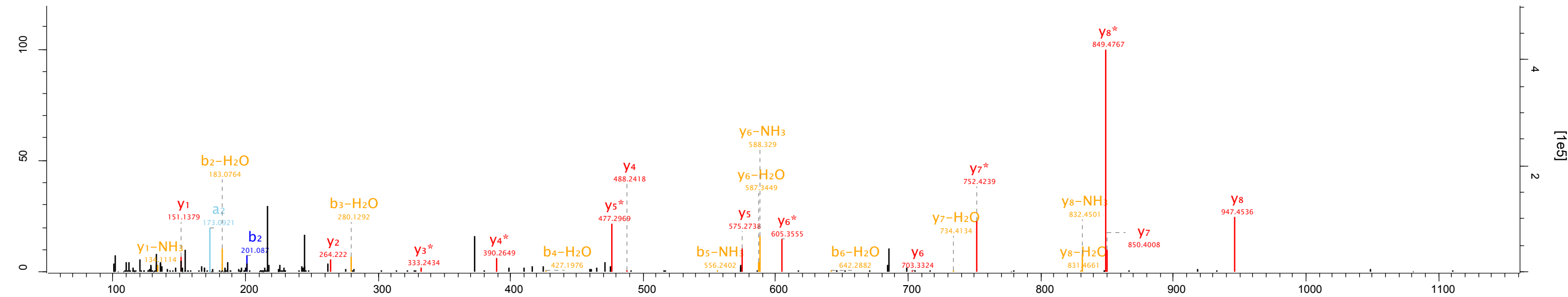


Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan 8397 Method FTMS; HCD Score 228.86 m/z 932.41 Gene names HDLBP

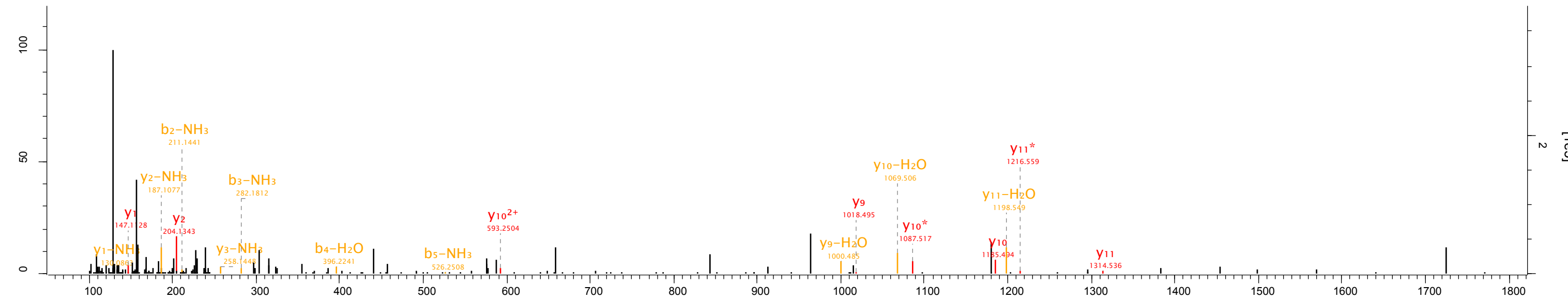


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Raw file
20171215_MaS_33SR_LMH_phospho2_02

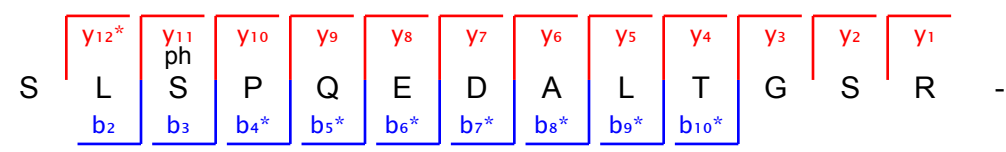
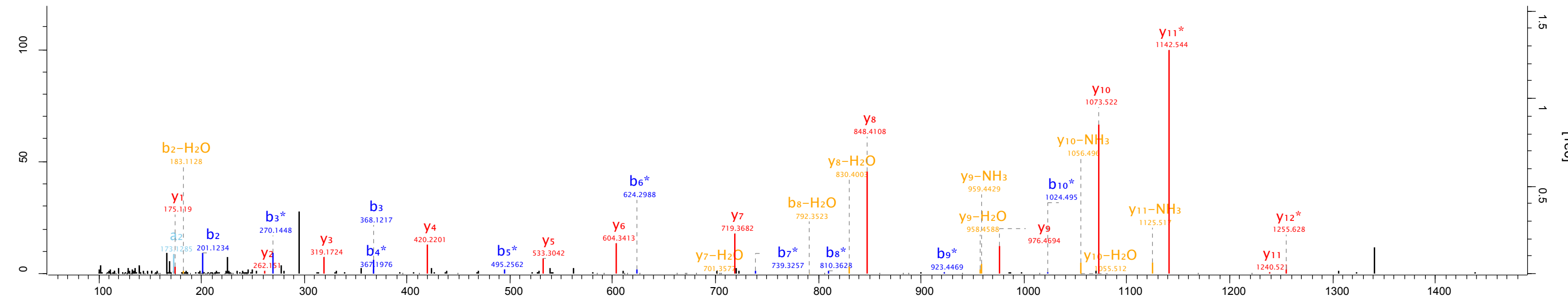
Scan 9097 Method FTMS; HCD Score 42.71 m/z 576.59



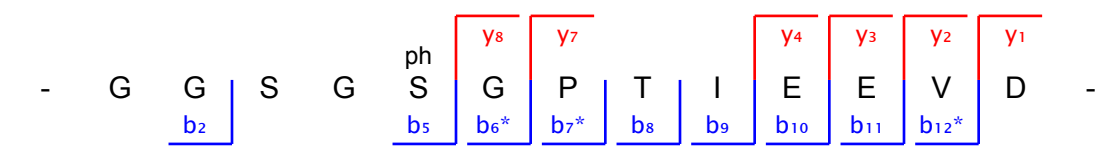
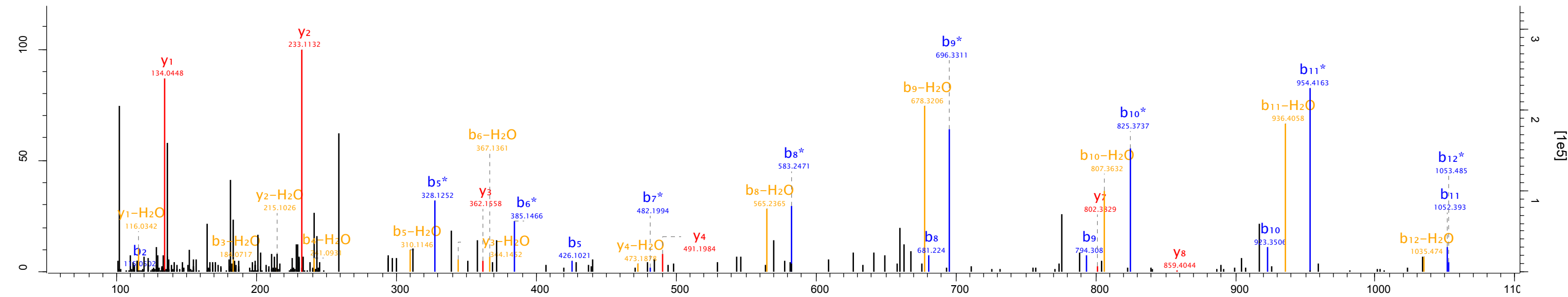
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Red brackets above the sequence indicate fragmentation sites: y11 (E), y10 ph (S), y9 (Y), y2 (G), and y1 (K).

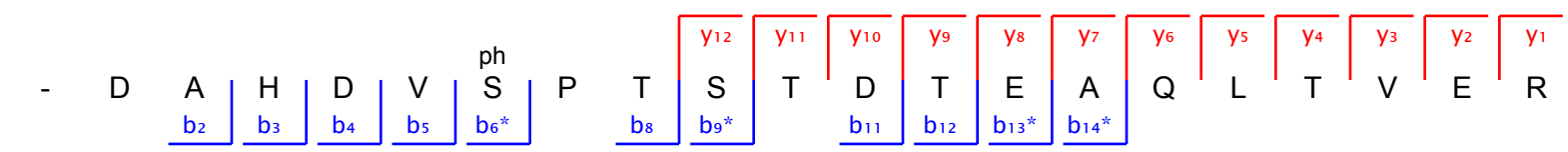
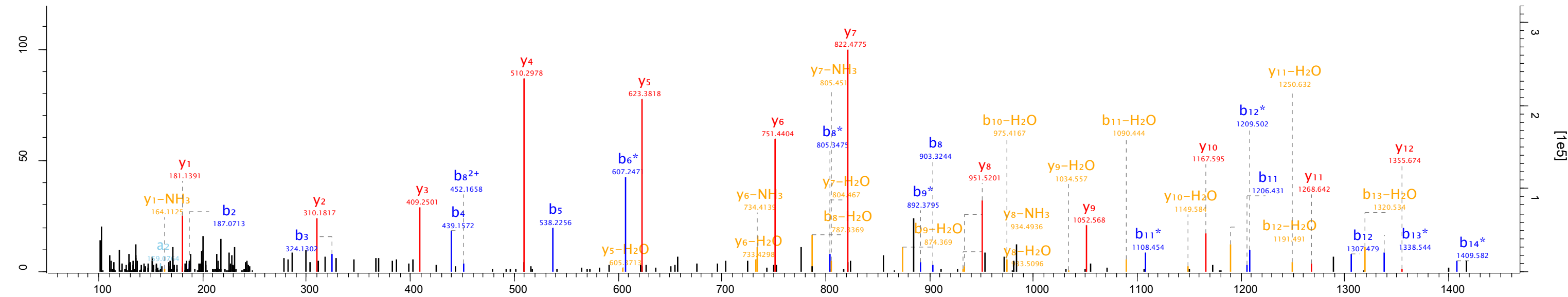
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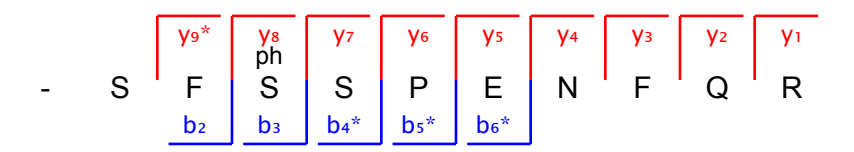
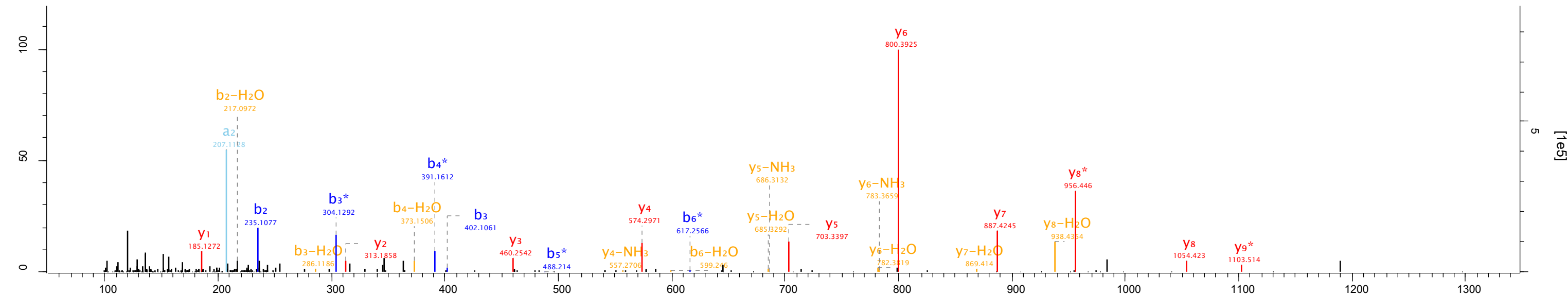
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 Scan: 9277 Method: FTMS; HCD Score: 147.7 m/z: 642.75 Gene names: HSPA1A



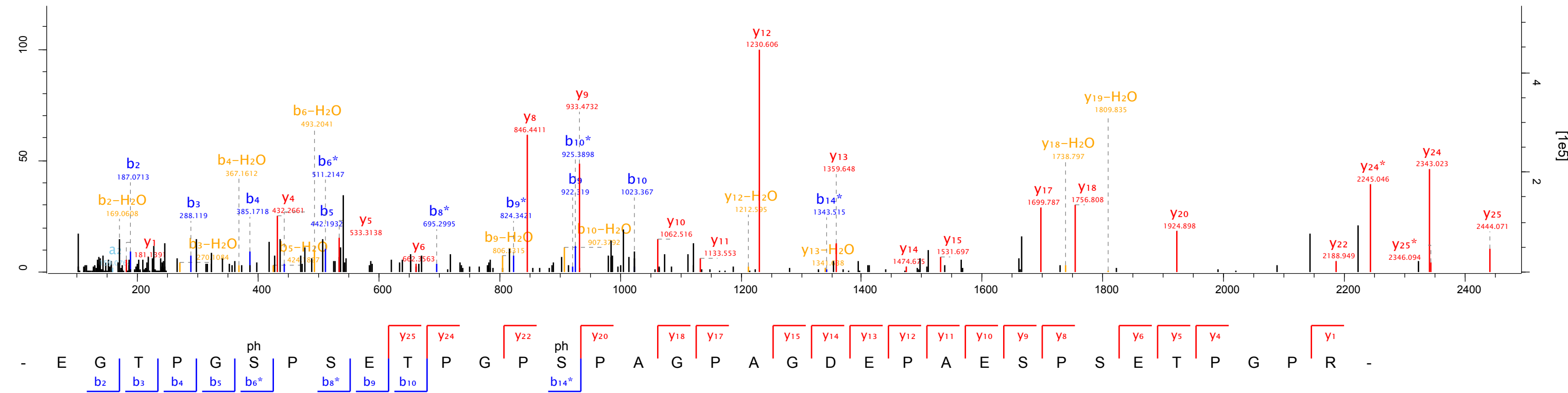
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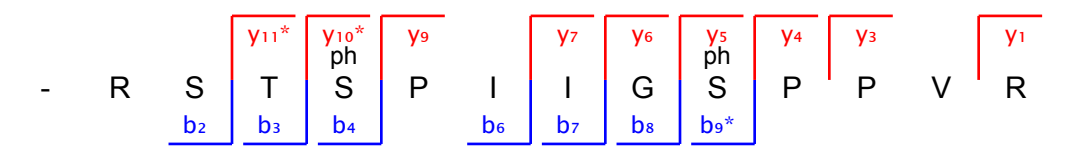
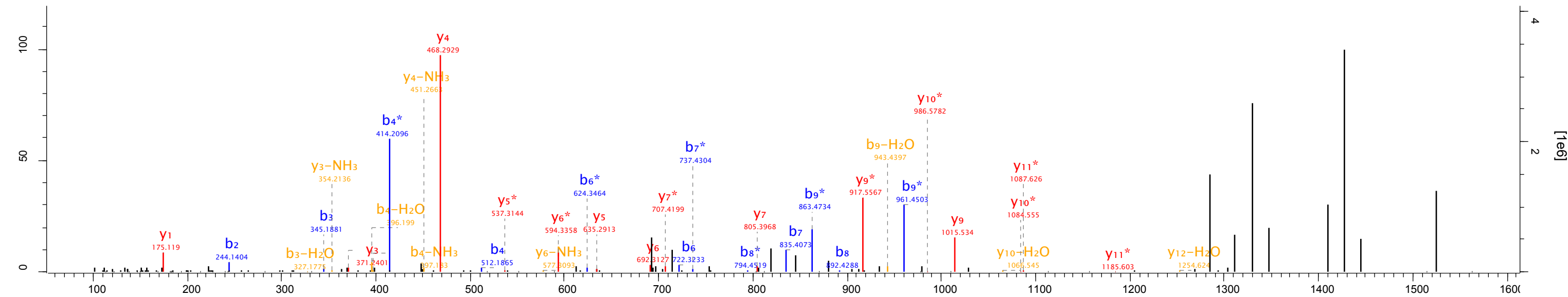
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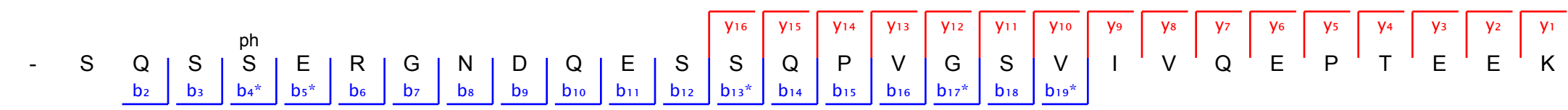
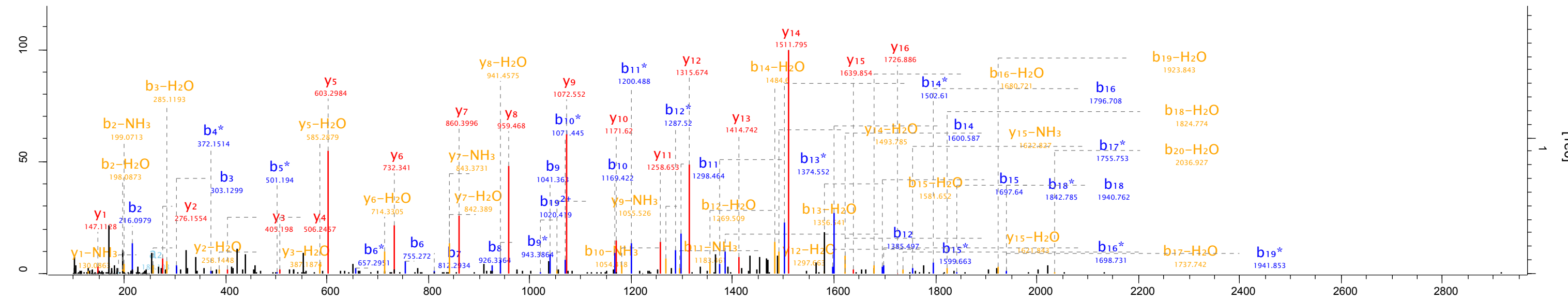
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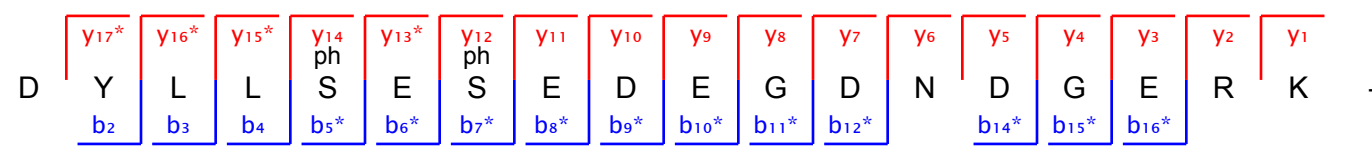
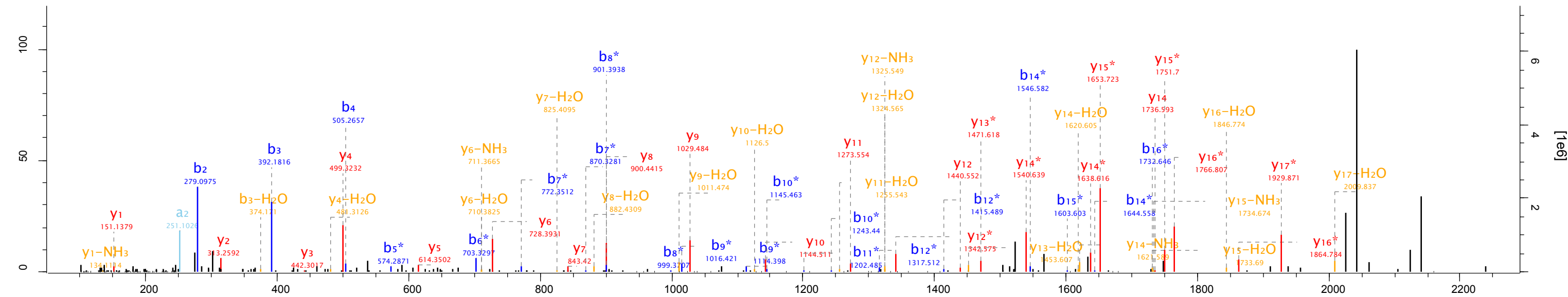
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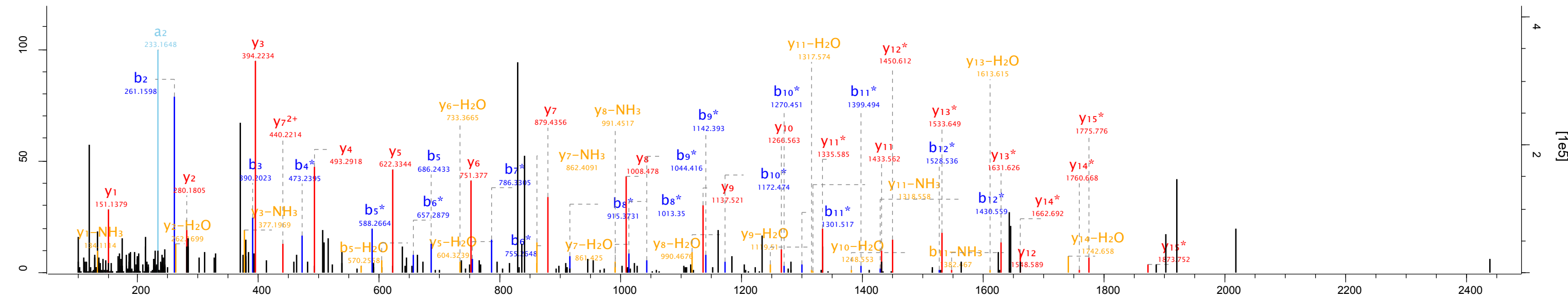
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 Scan: 10457 Method: FTMS; HCD Score: 228.2 m/z: 1038.47 Gene names: PAGE2;PAGE2B



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10487 Method FTMS; HCD Score 268.36 m/z 1121.43 Gene names UTP14A



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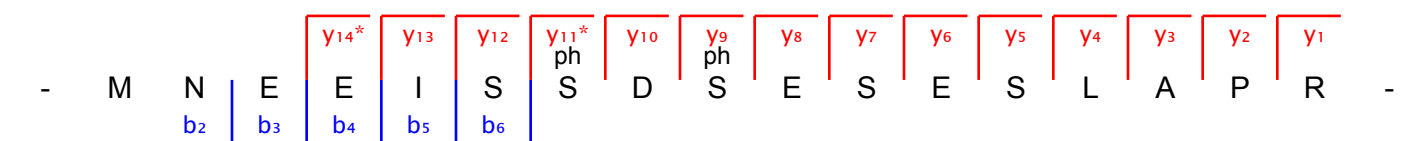
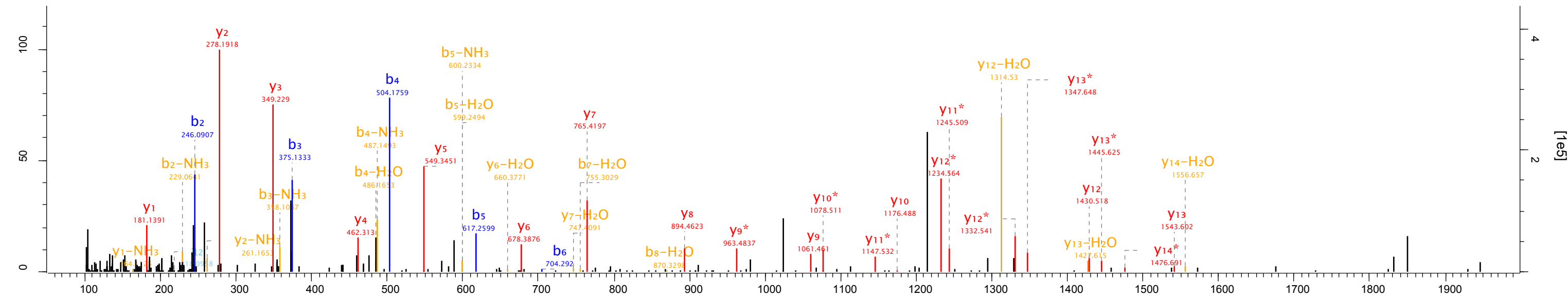


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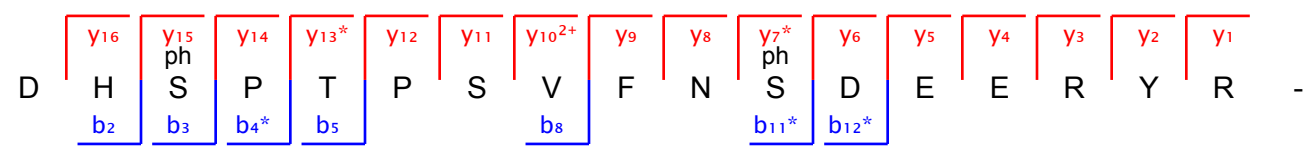
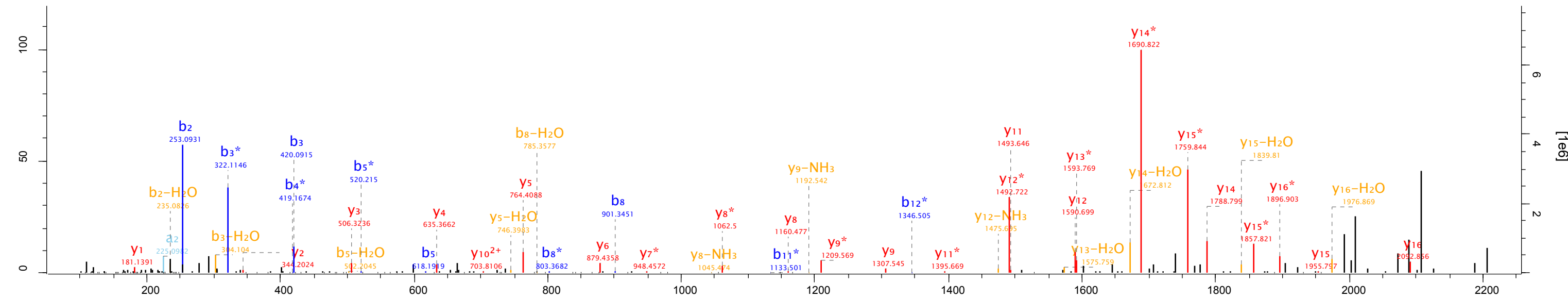
y15*
y14*
y13*
y12
y11
y10
y9
y8
y7
y6
y5
y4
y3
y2
y1

b2
b3
b4*
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b6*
b7*
b8*
b9*
b10*
b11*
b12*

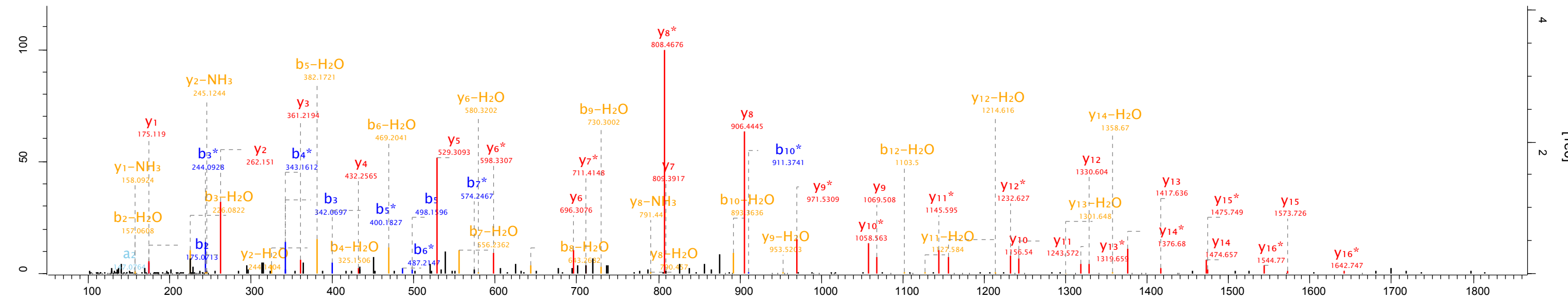
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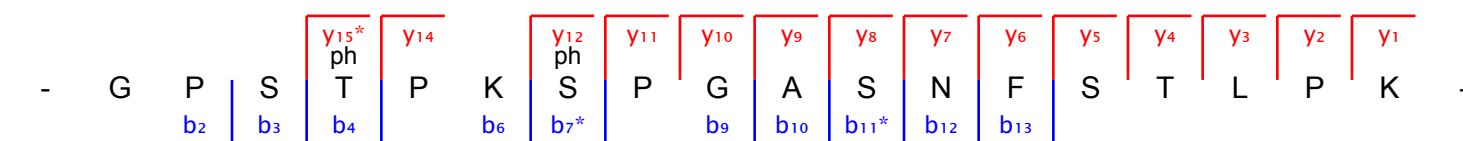
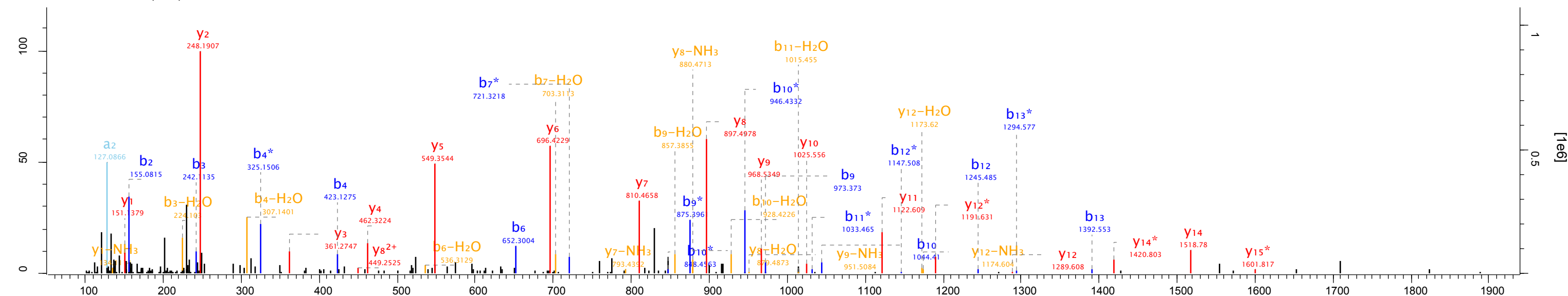


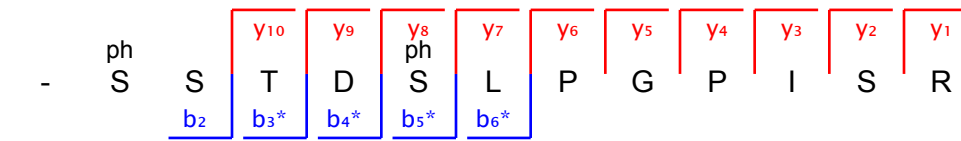
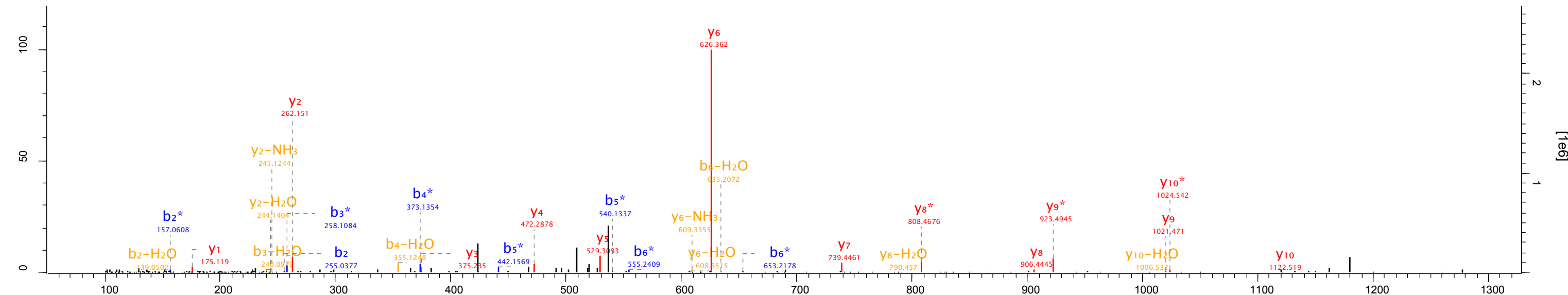
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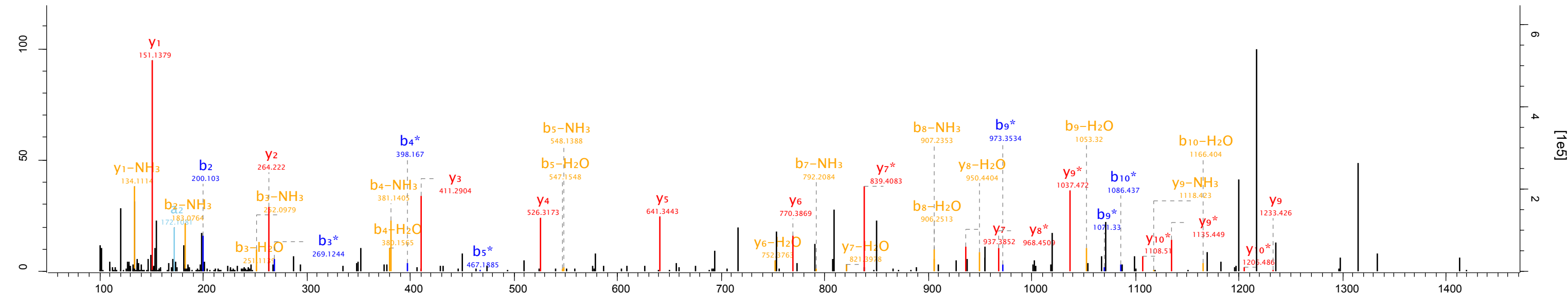


Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 10867 Method FTMS; HCD Score 198.22 m/z 647.97 Gene names USP15

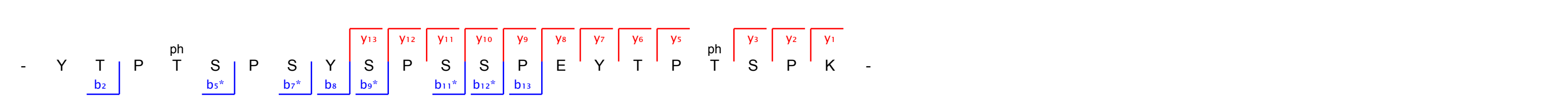
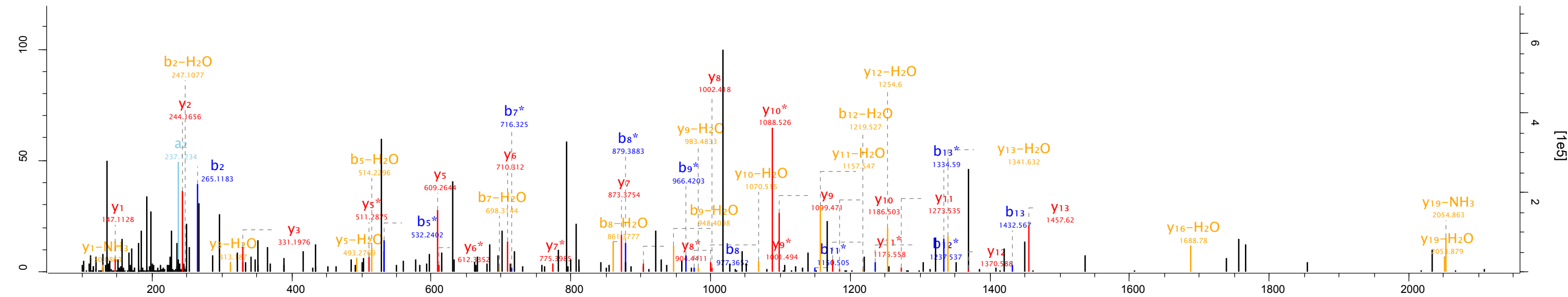




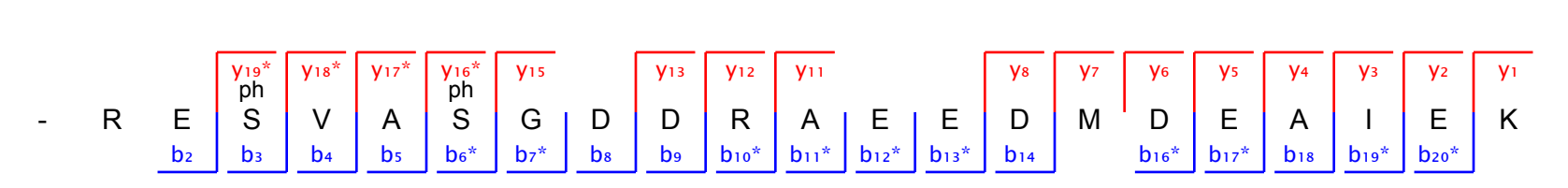
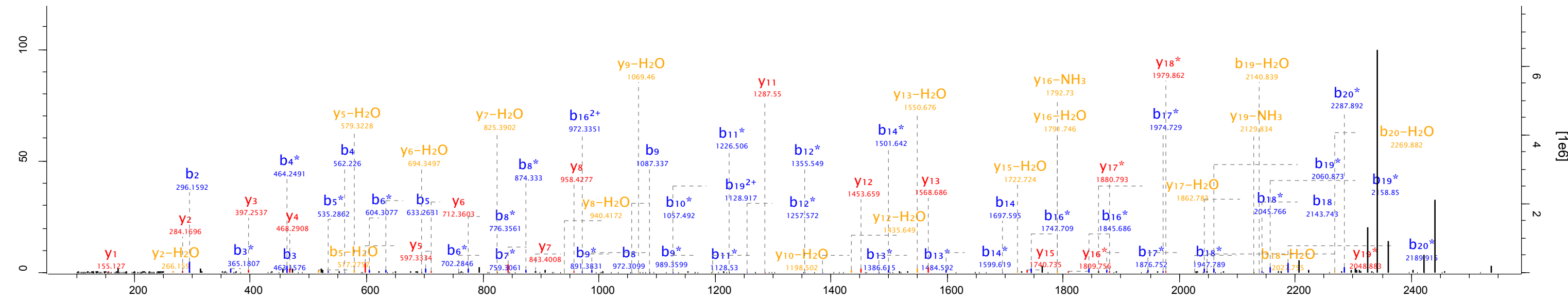


- Q -
 A S E S E D D F I K -
 b₂ b₃* b₄* b₅* b₉* b₁₀*

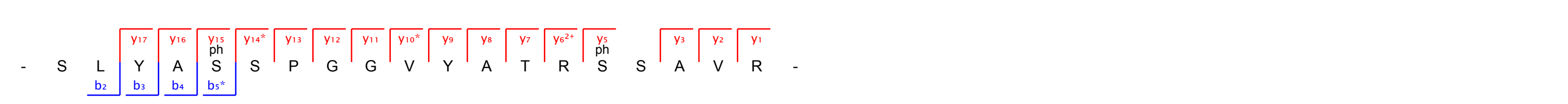
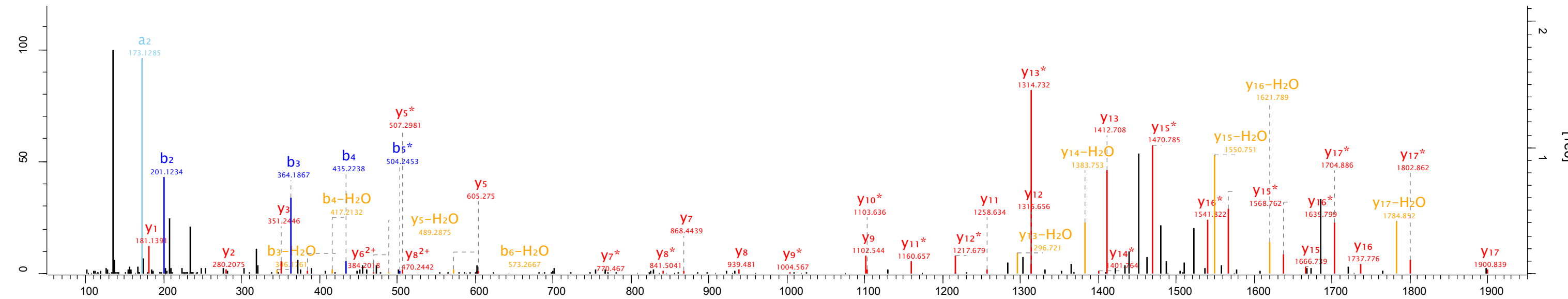
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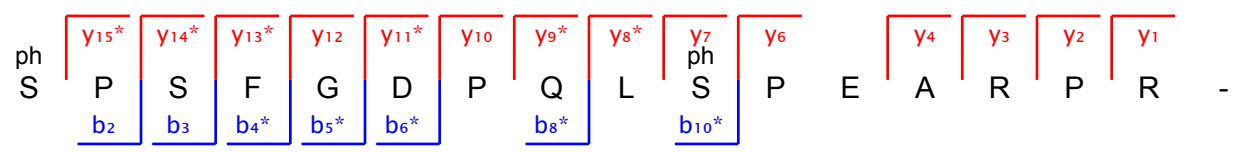
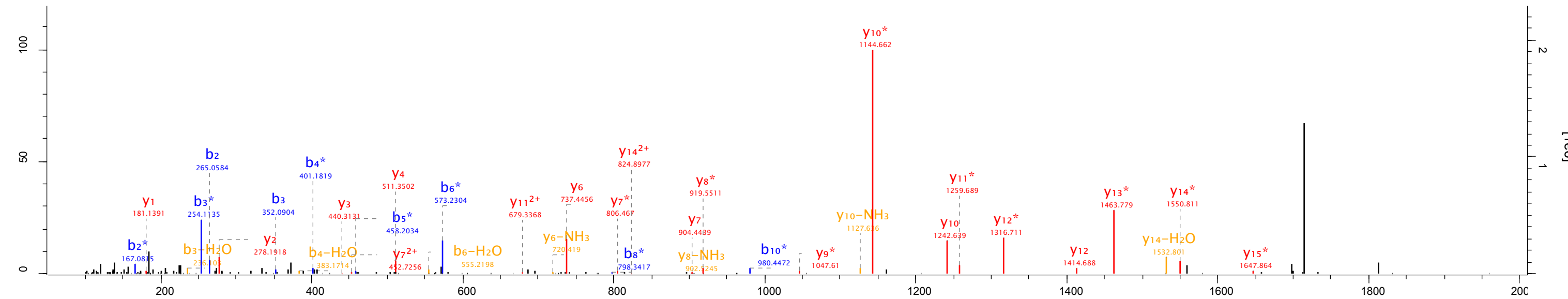
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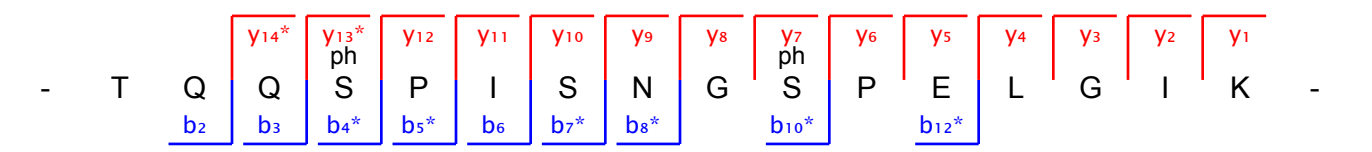
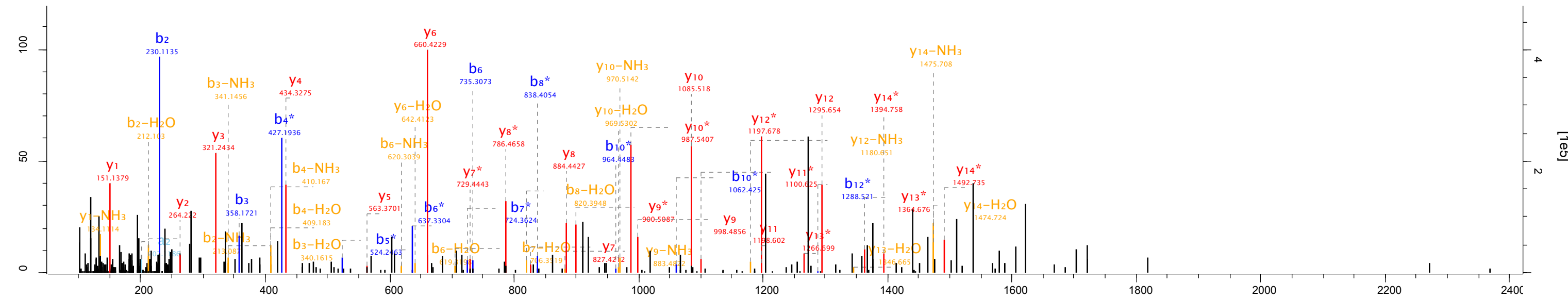
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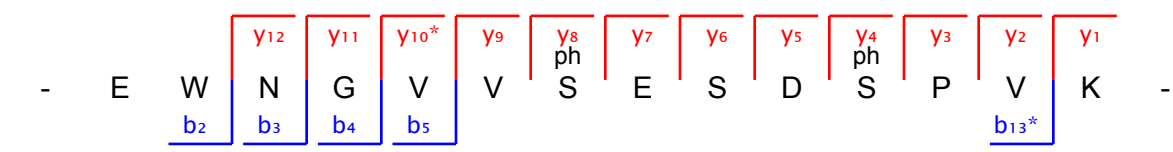
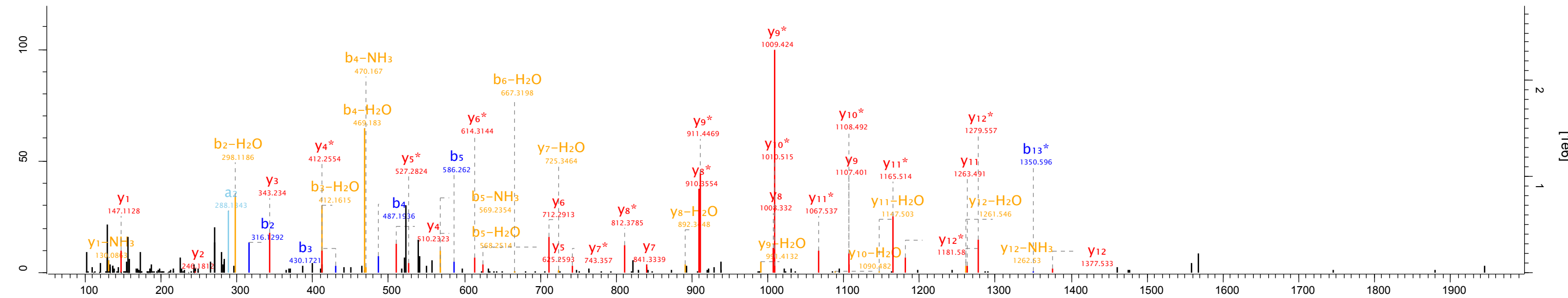
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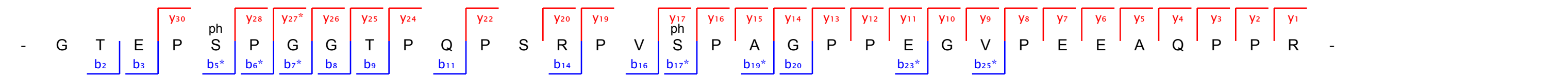
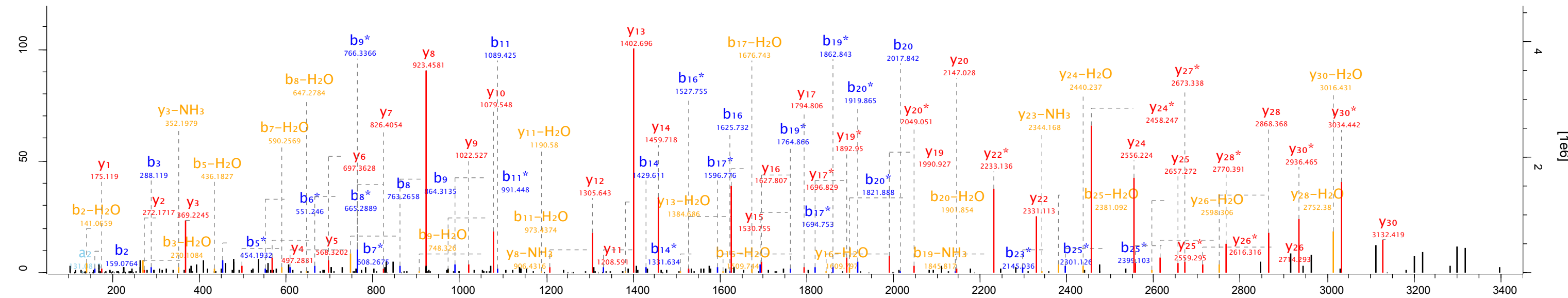
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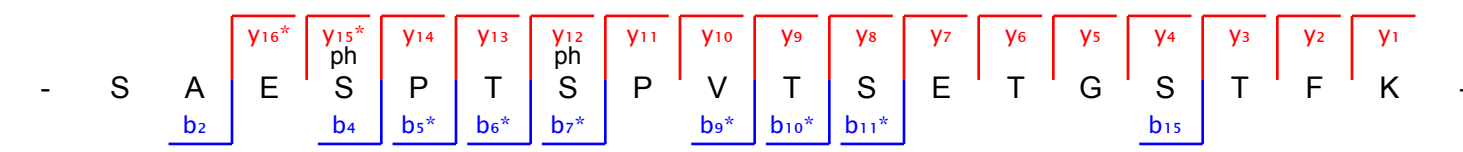
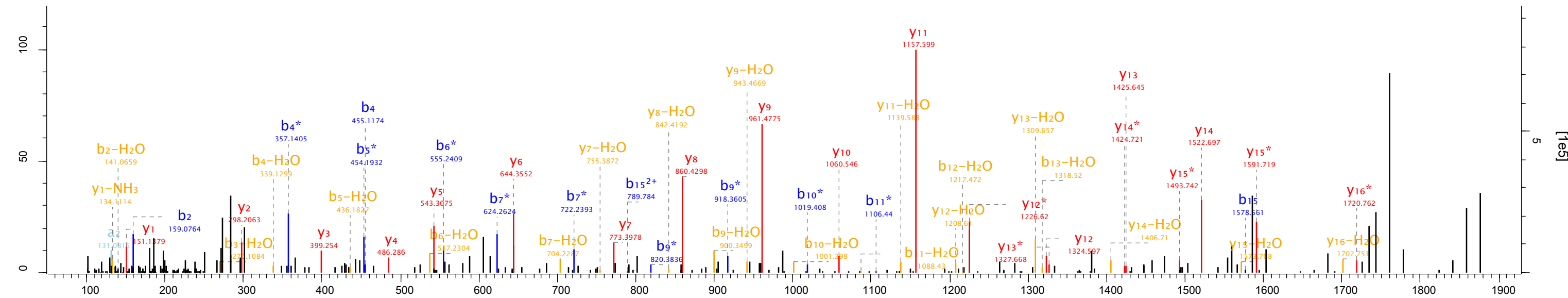
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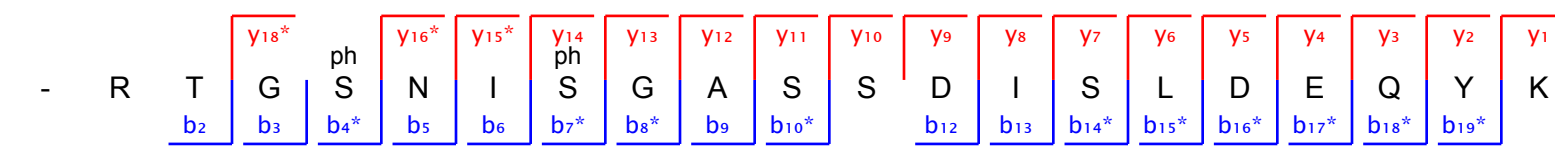
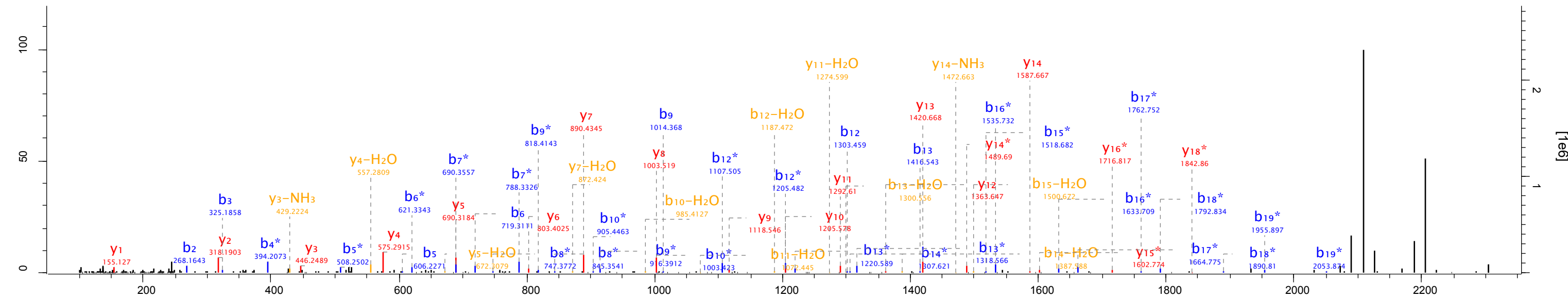
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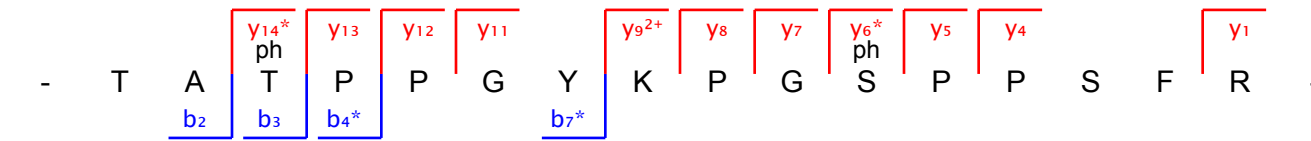
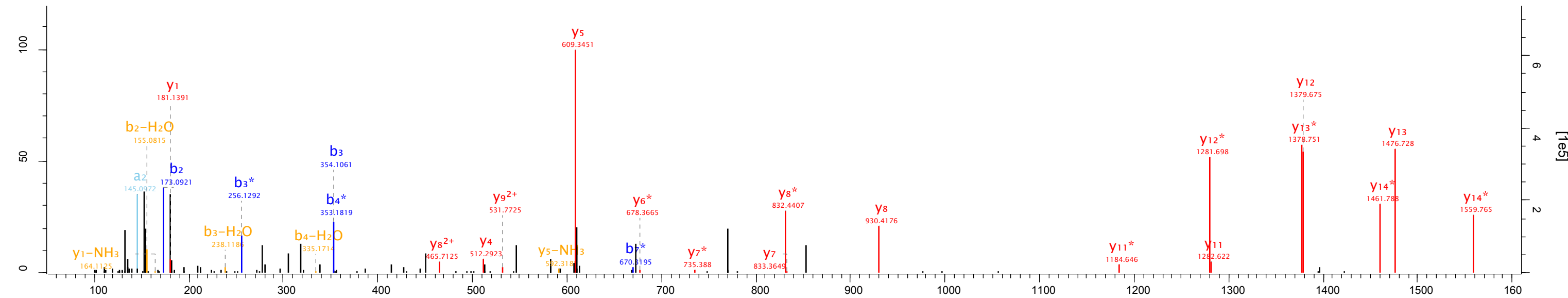


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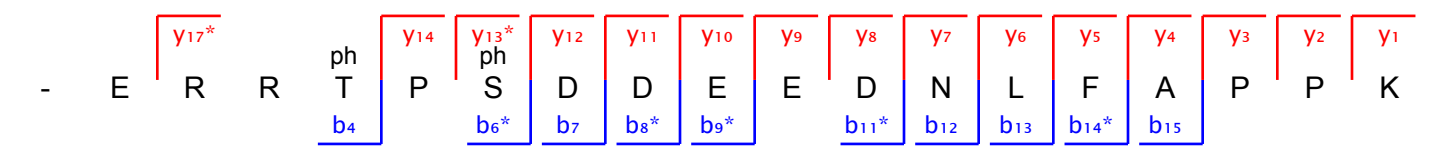
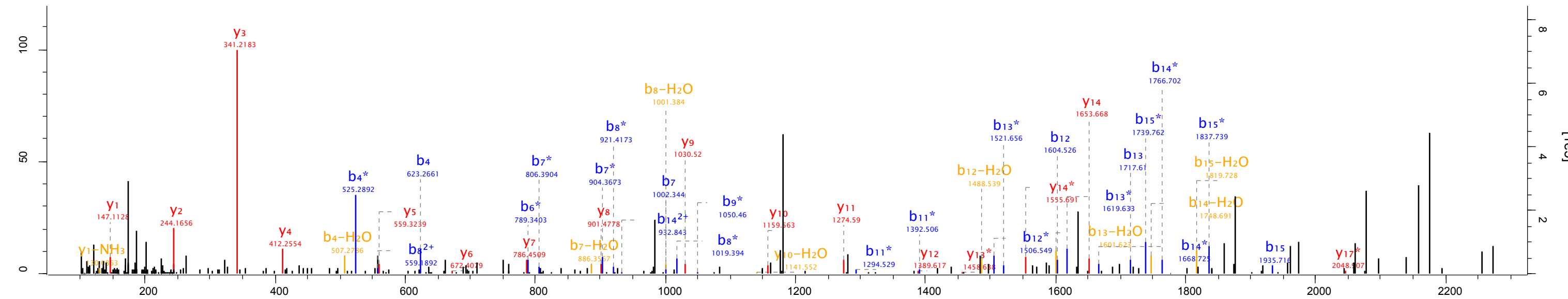


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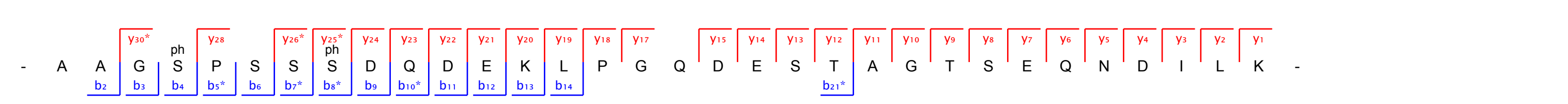
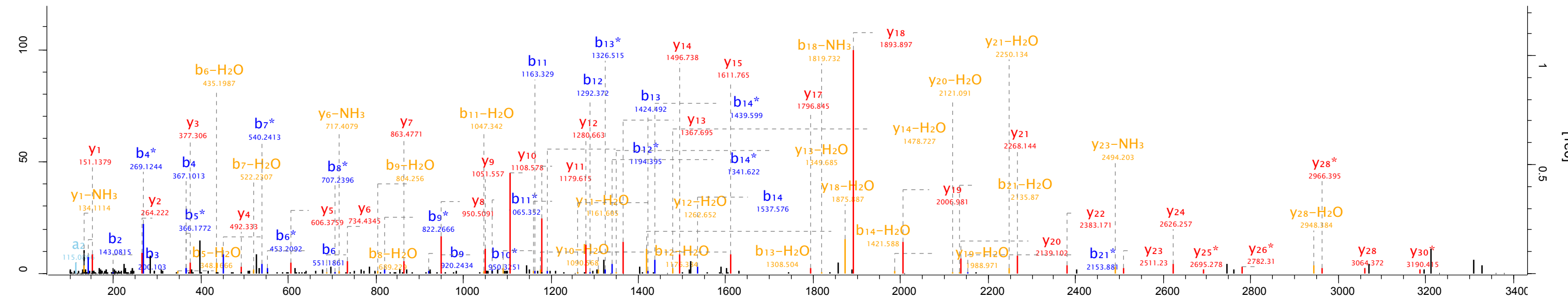




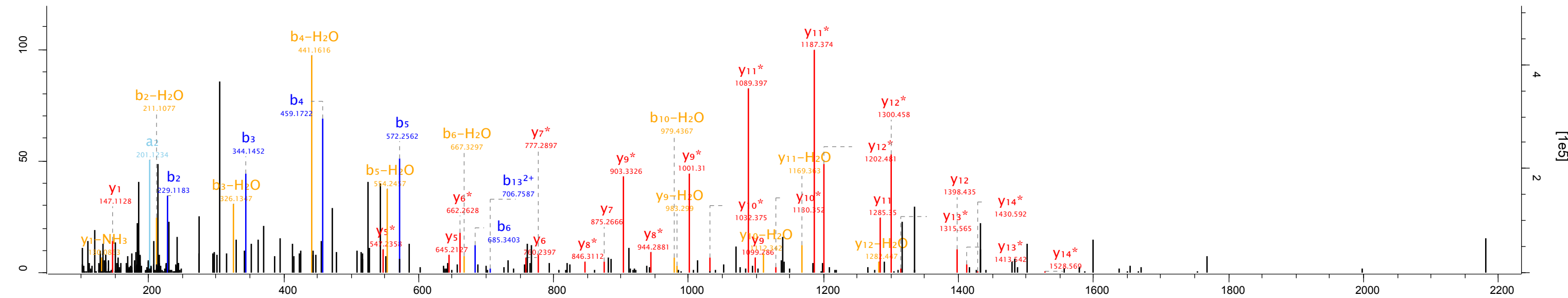
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 Scan: 12007 Method: FTMS; HCD Score: 156.51 m/z: 759.32 Gene names: FAM21A;FAM21C



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 Scan: 12197 Method: FTMS; HCD Score: 250.24 m/z: 1144.49 Gene names: PRRC2C

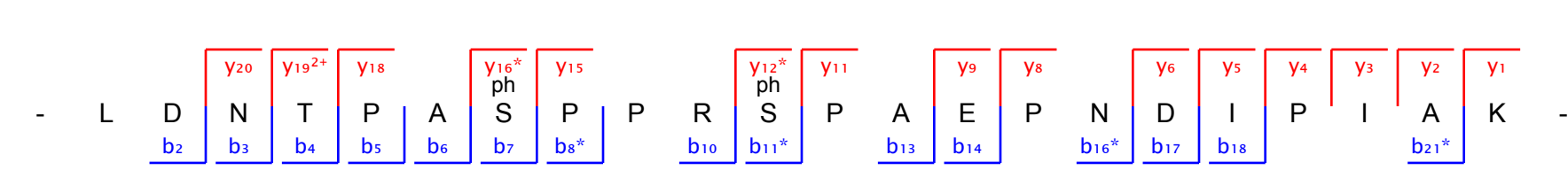
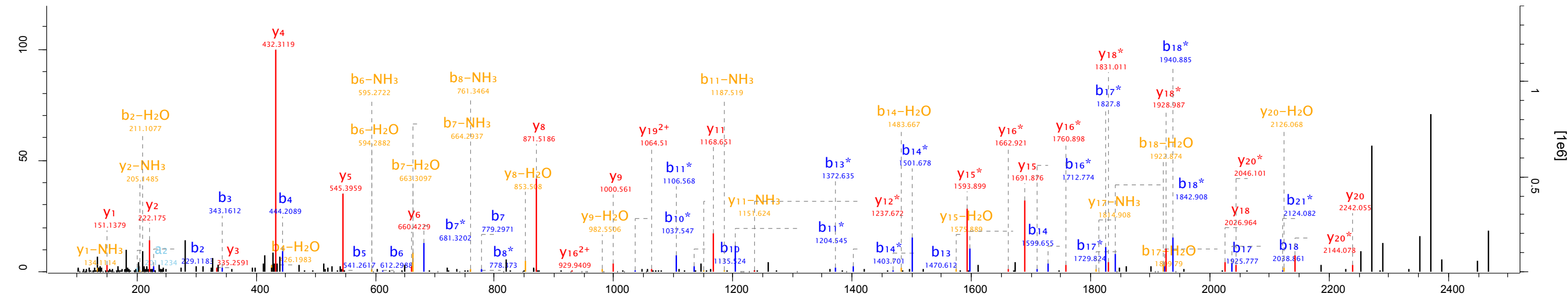


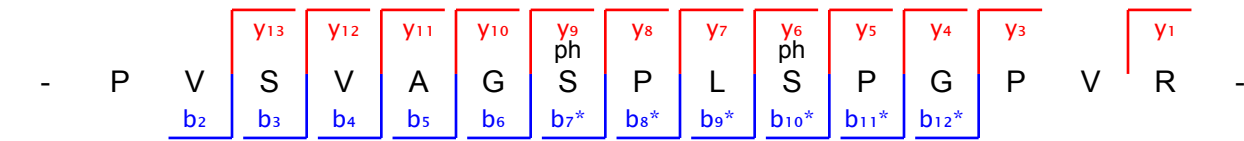
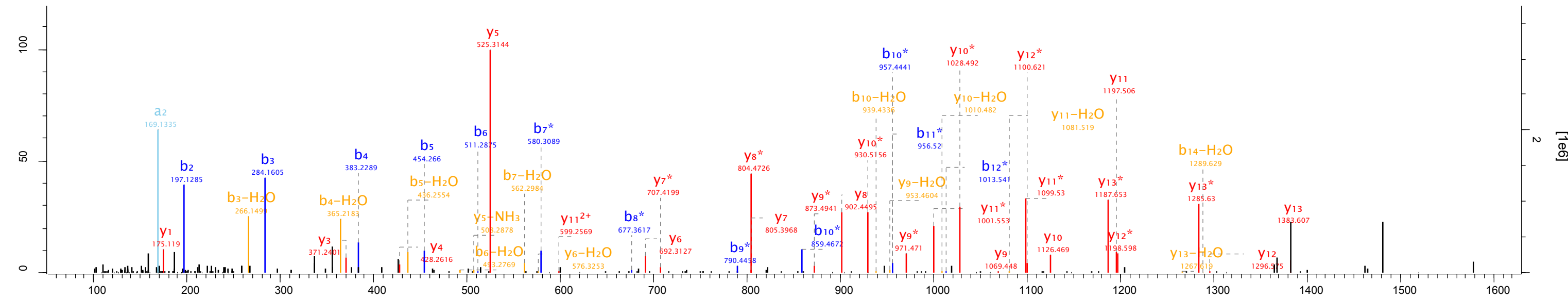
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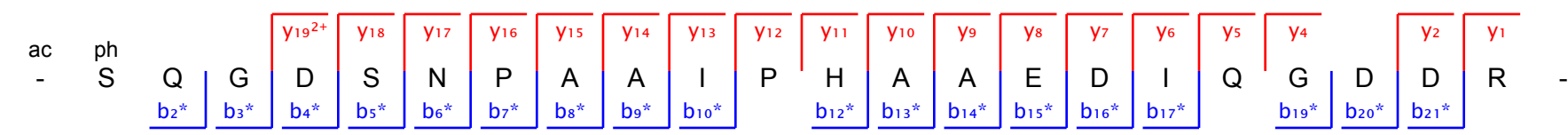
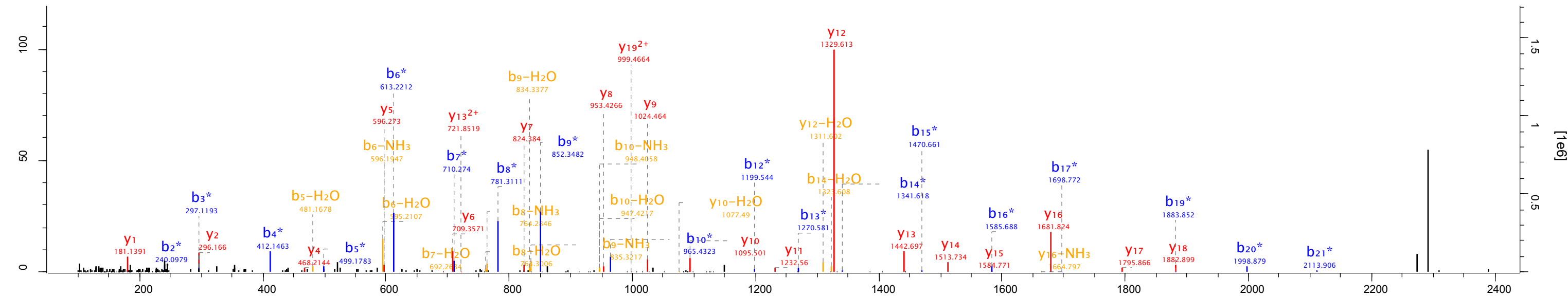
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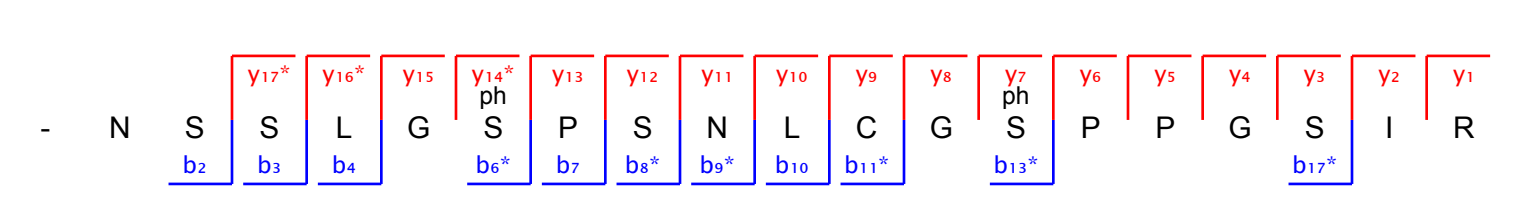
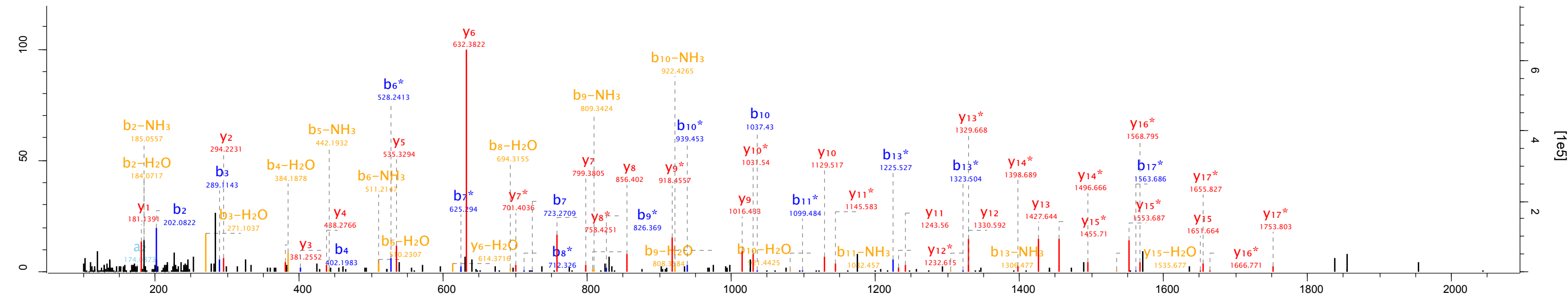




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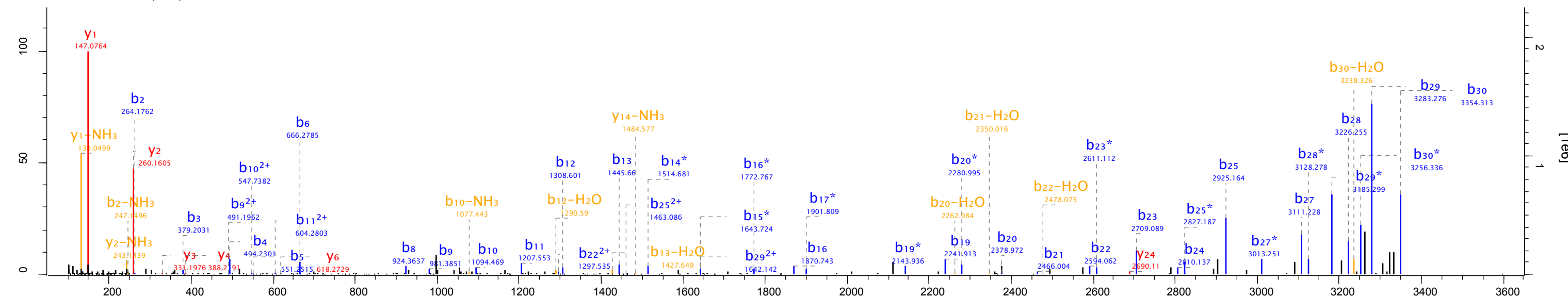


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 Scan: 12517 Method: FTMS; HCD Score: 155.4 m/z: 1026.93 Gene names: UNK



Raw file
20171215_MaS_33SR_LMH_phospho2_03

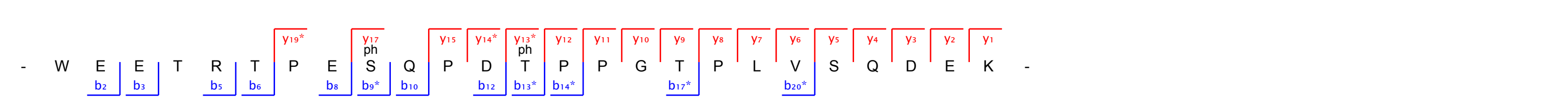
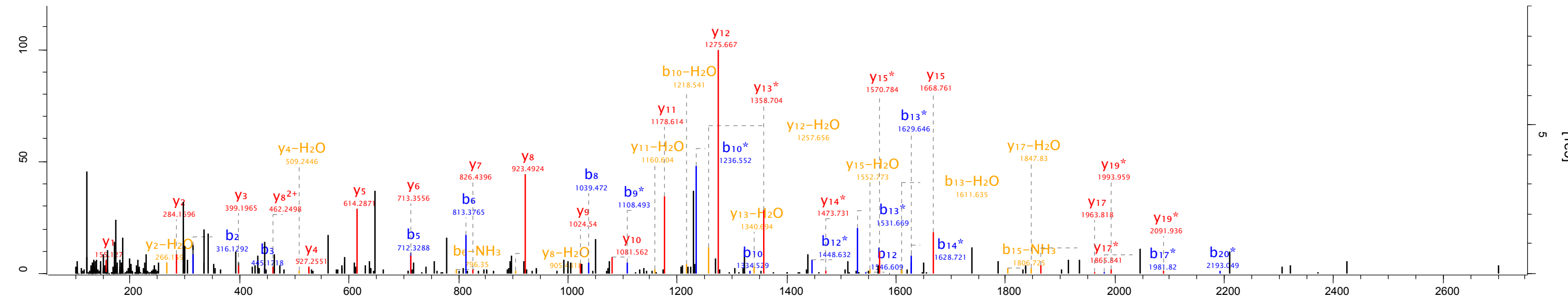
Scan 12557 Method FTMS; HCD Score 234.02 m/z 904.37 Gene names RALY

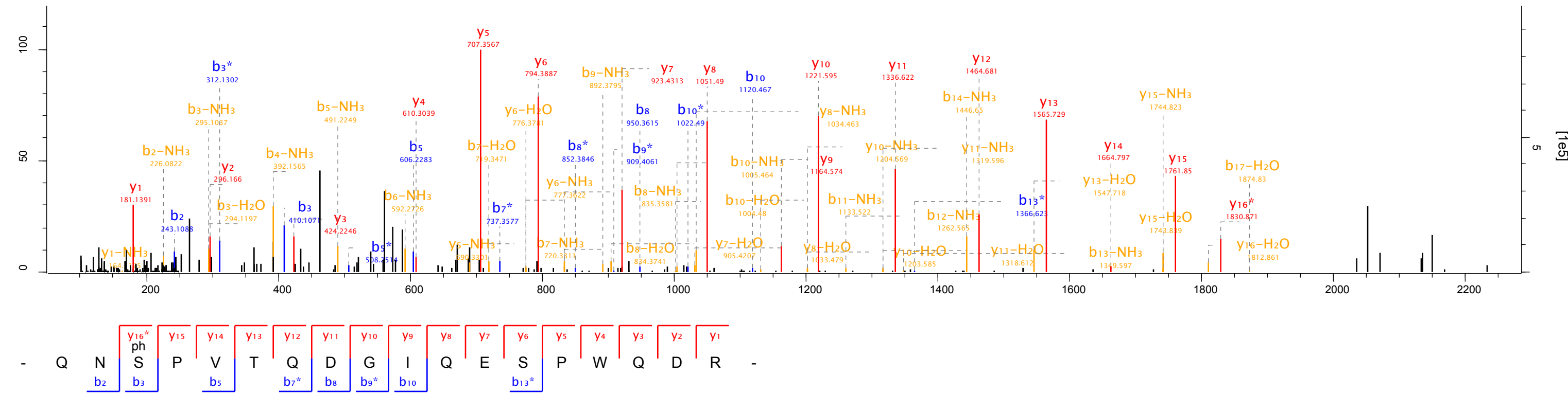


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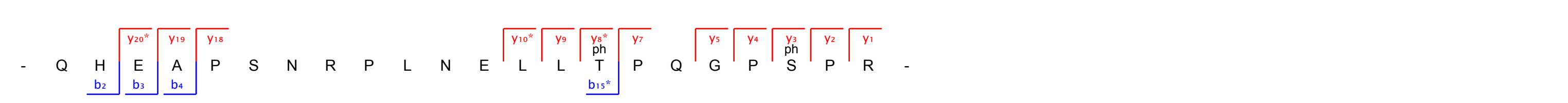
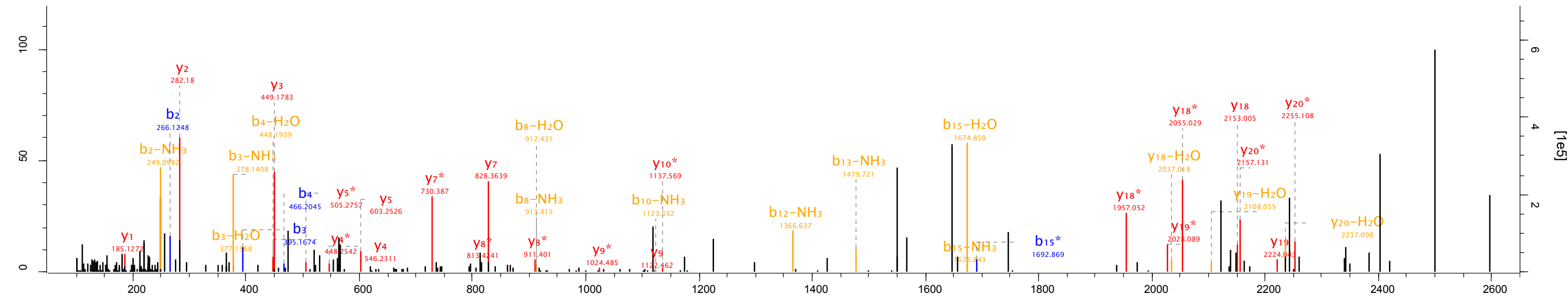
Fragmentation mapping: b2 (R), b3 (D), b4 (D), b5 (G), b6 (D), b8 (E), b9 (G), b10 (L), b11 (L), b12 (T), b13 (H), b14* (S), b15* (E), b16 (E), b17* (E), b19 (E), b20 (H), b21 (S), b22 (Q), b23 (D), b24 (T), b25 (D), b27 (A), b28 (D), b29 (G), b30 (A), y24 (E), y4 (G), y3 (A), y2 (L), y1 (Q).

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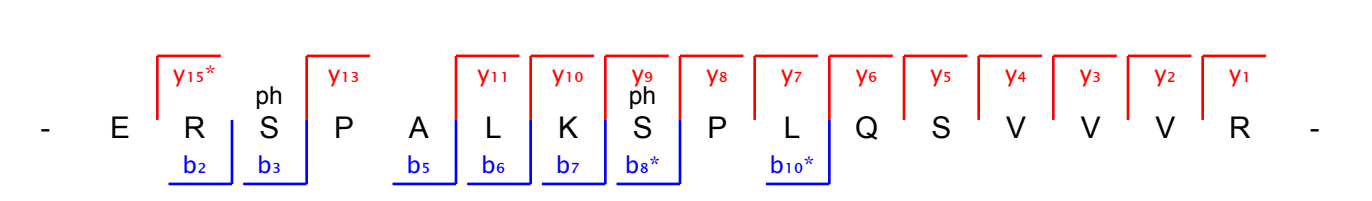
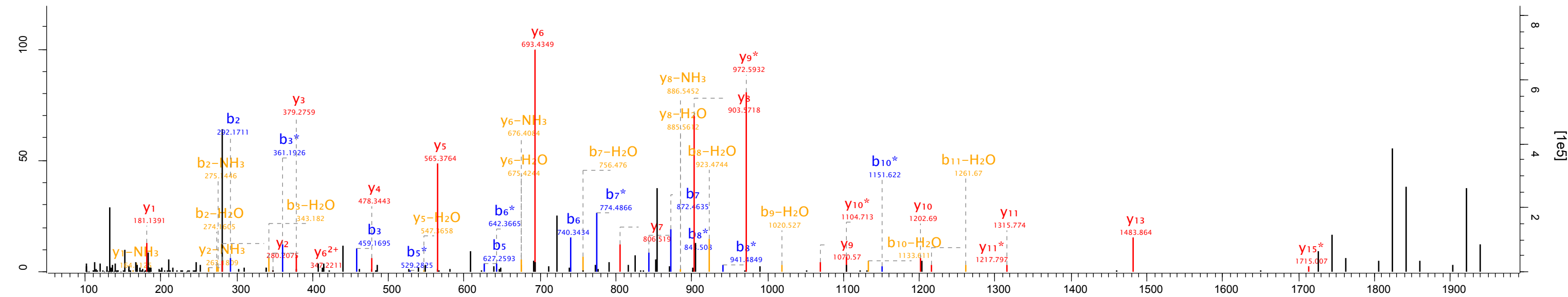




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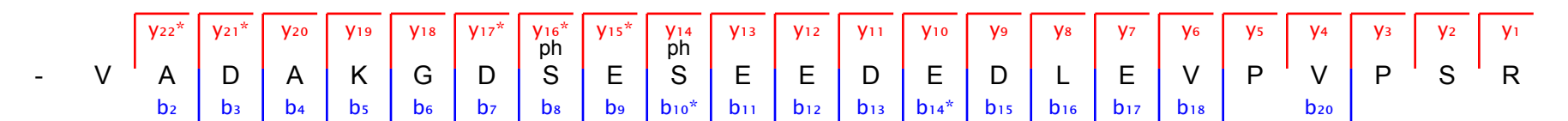
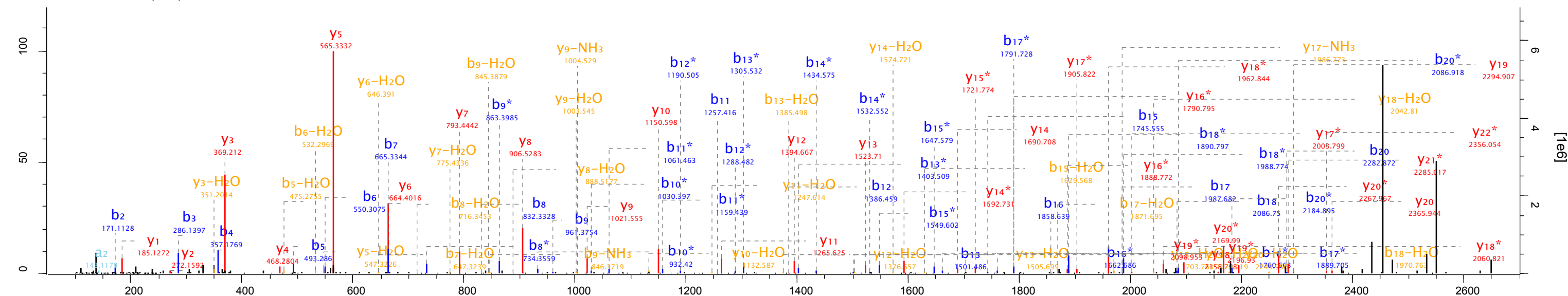


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 Scan: 12847 Method: FTMS; HCD Score: 146.17 m/z: 648.01 Gene names: THRAP3

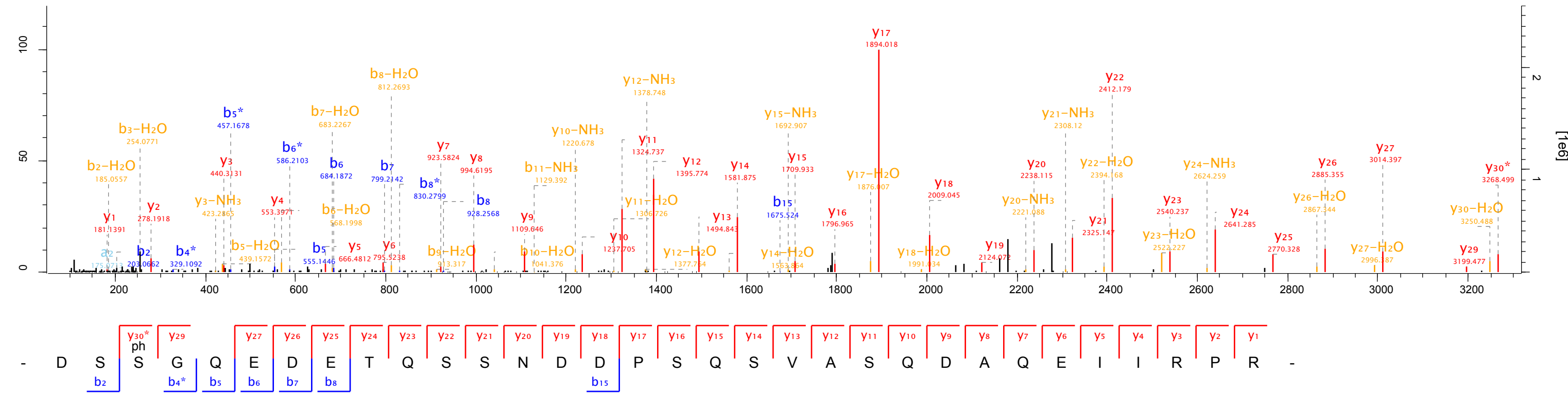


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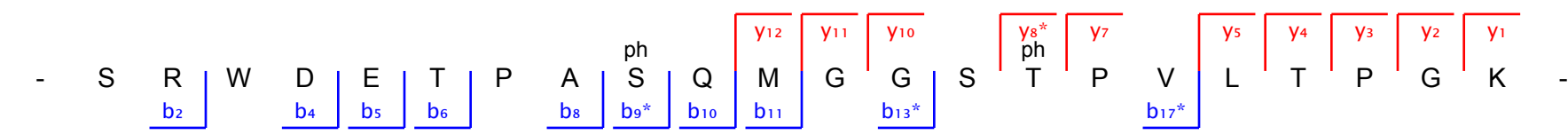
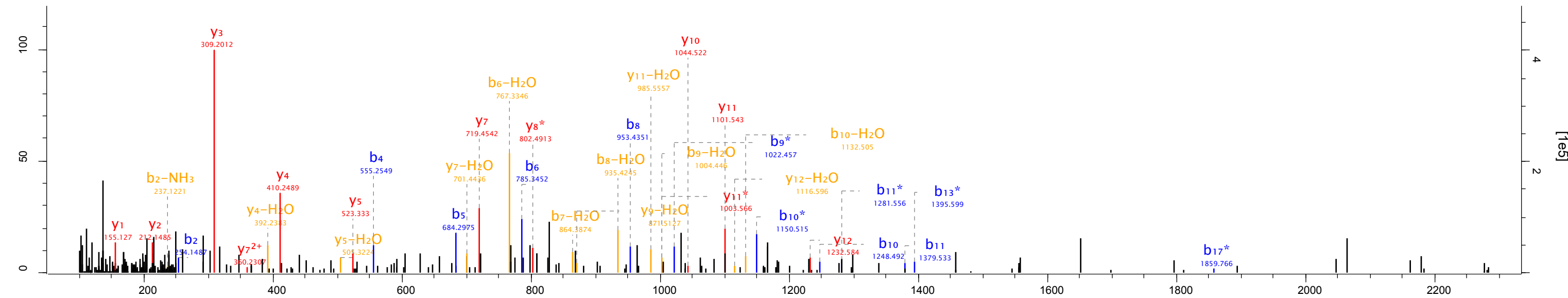
Scan 12897 Method FTMS; HCD Score 359.18 m/z 1326.54 Gene names PRKAR2A



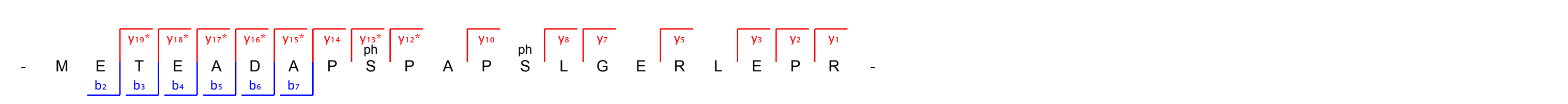
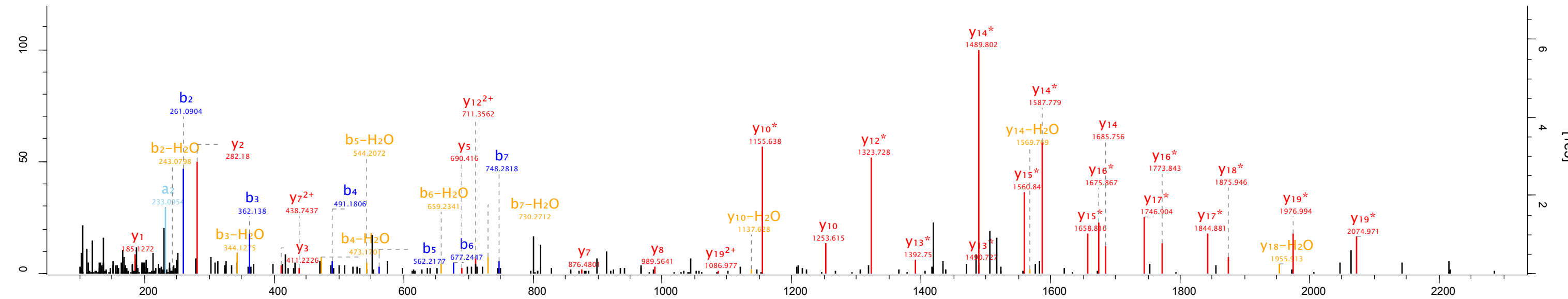
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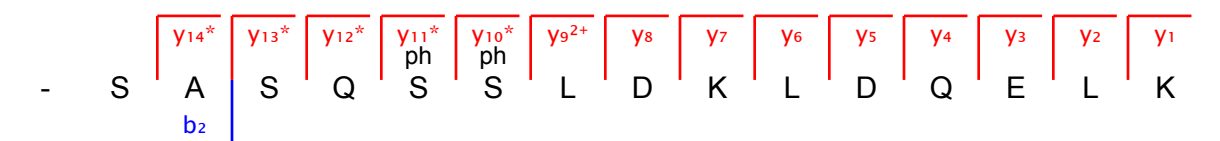
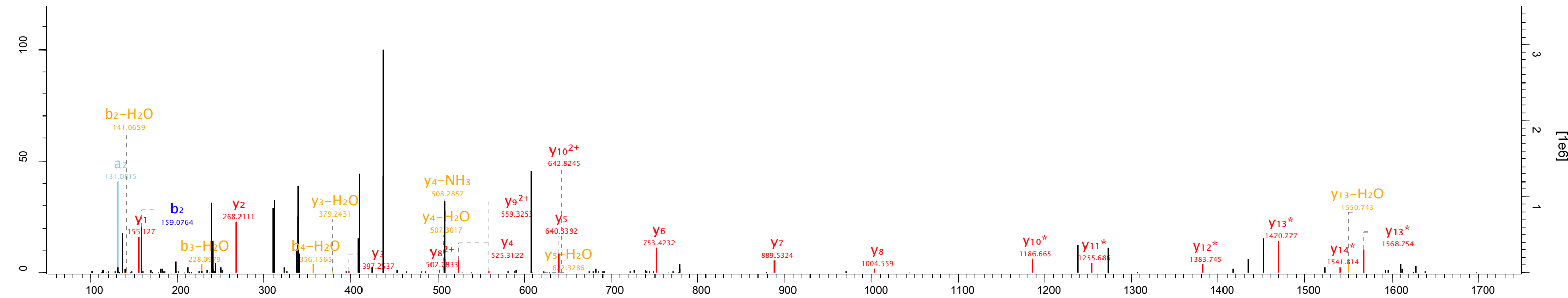
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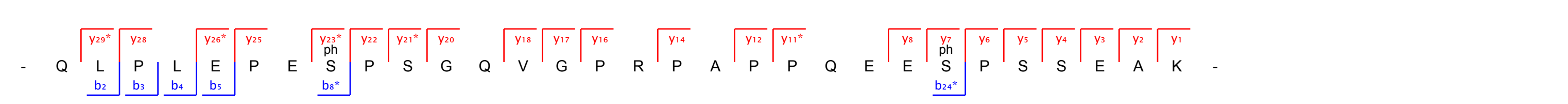
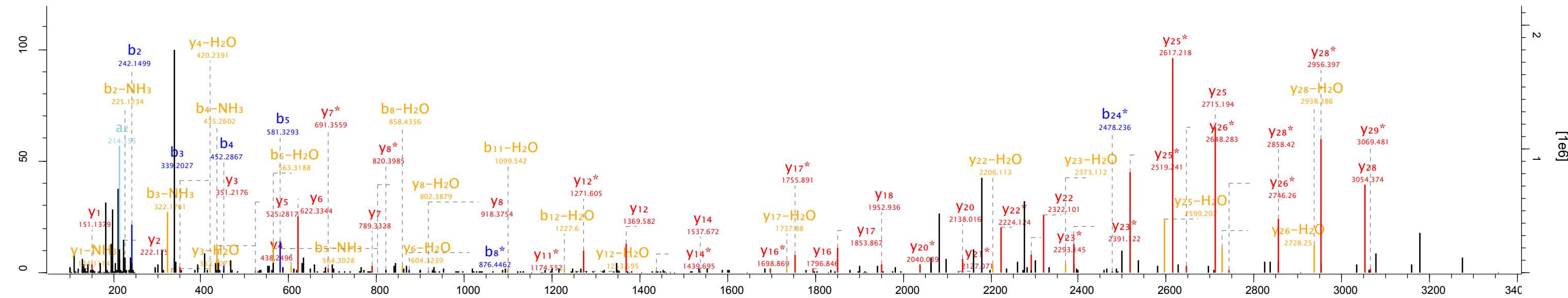
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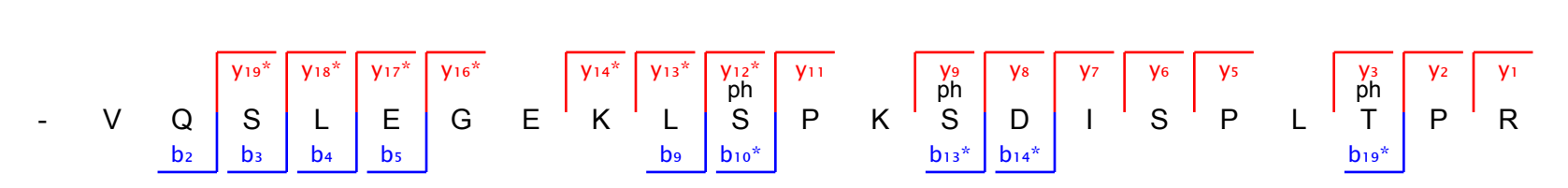
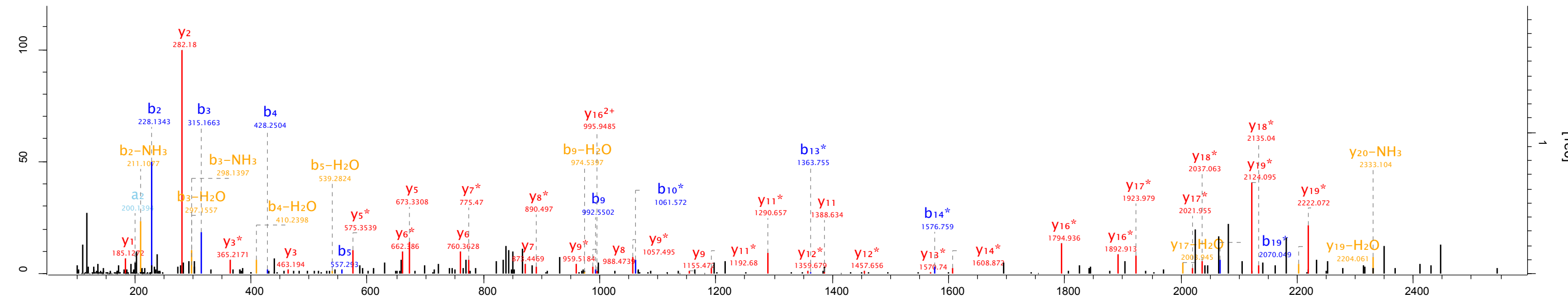
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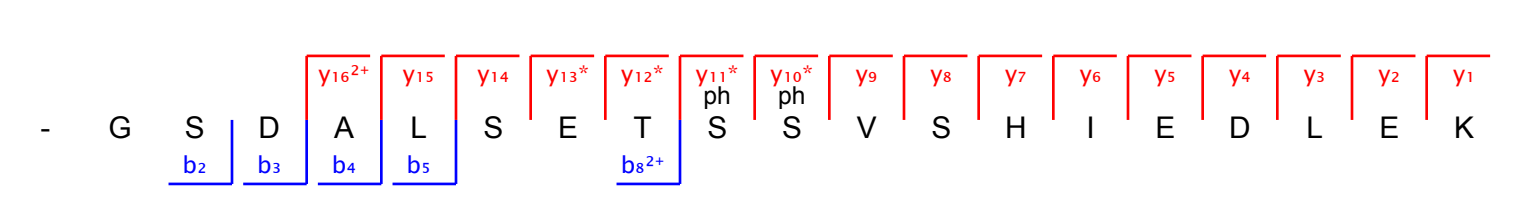
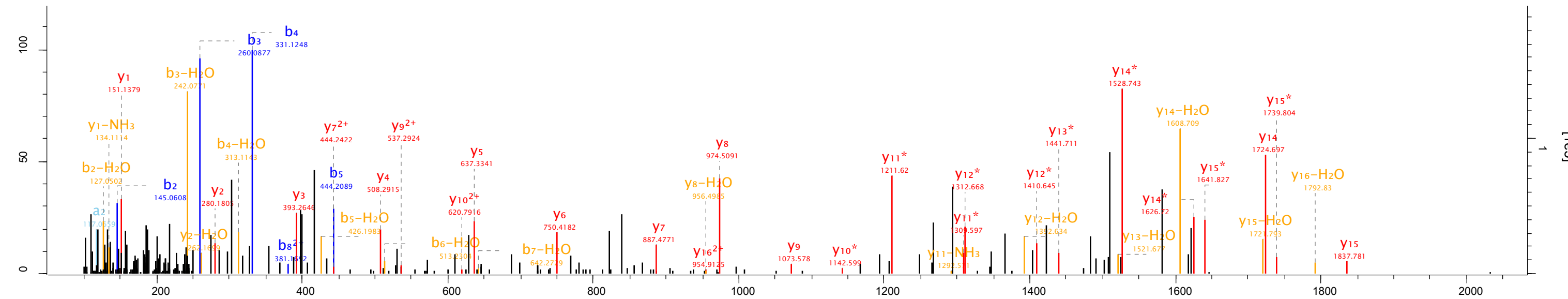
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 Scan: 13727 Method: FTMS; HCD Score: 142.65 m/z: 1099.84 Gene names: MAP7D1



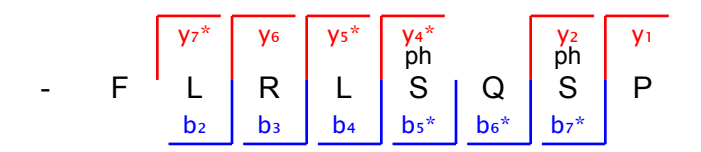
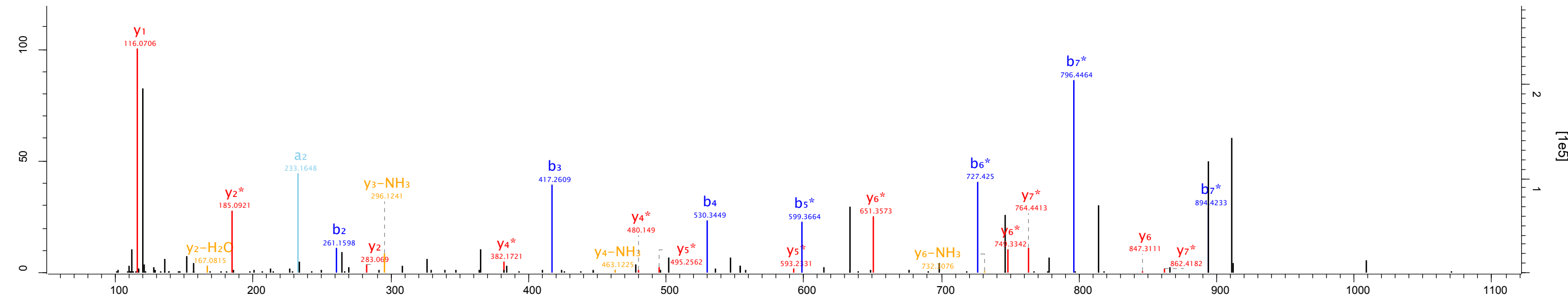
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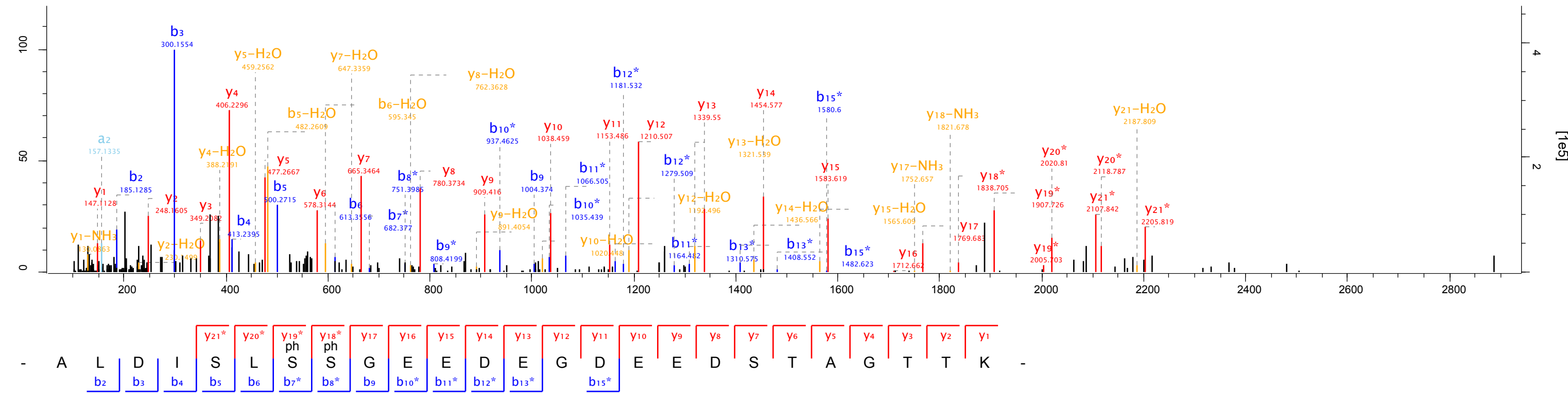
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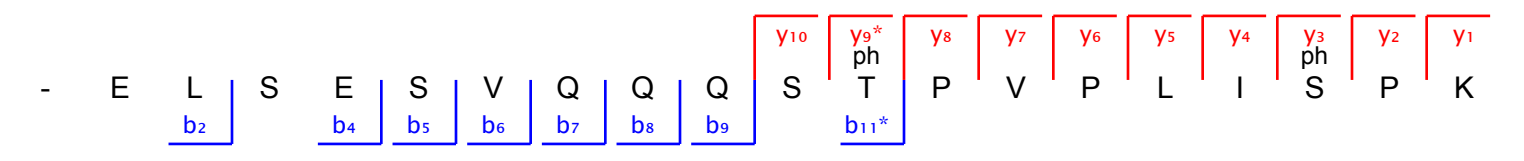
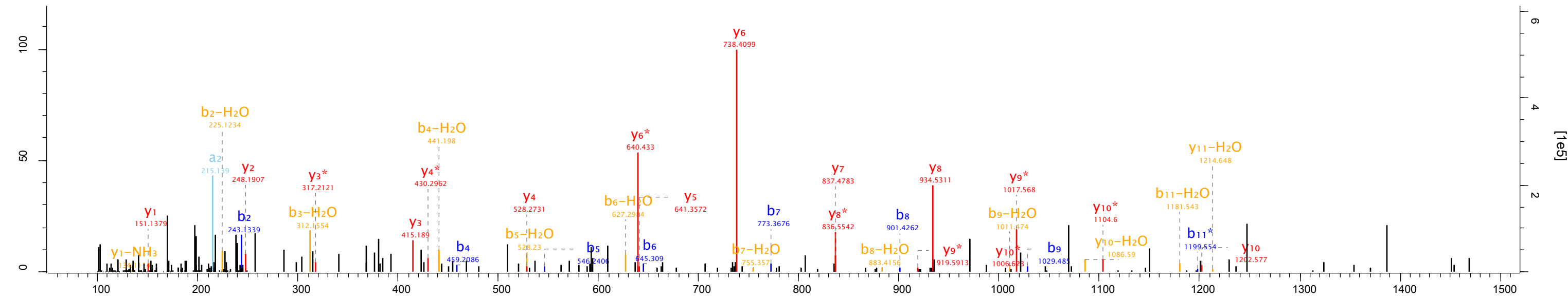
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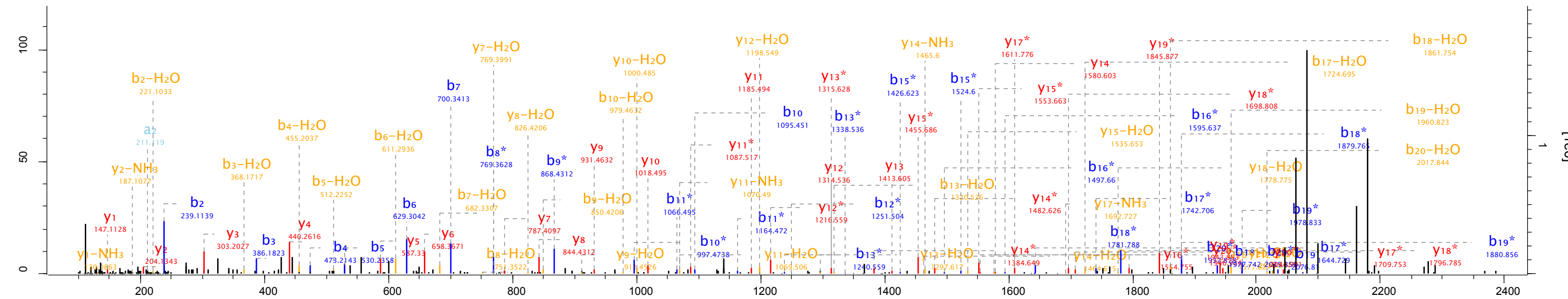
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14417 Method FTMS; HCD Score 44.66 m/z 744.35 Gene names ZMYND8



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
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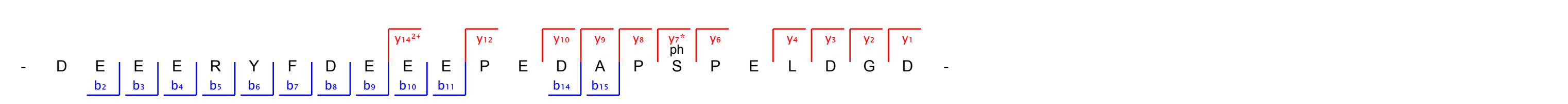
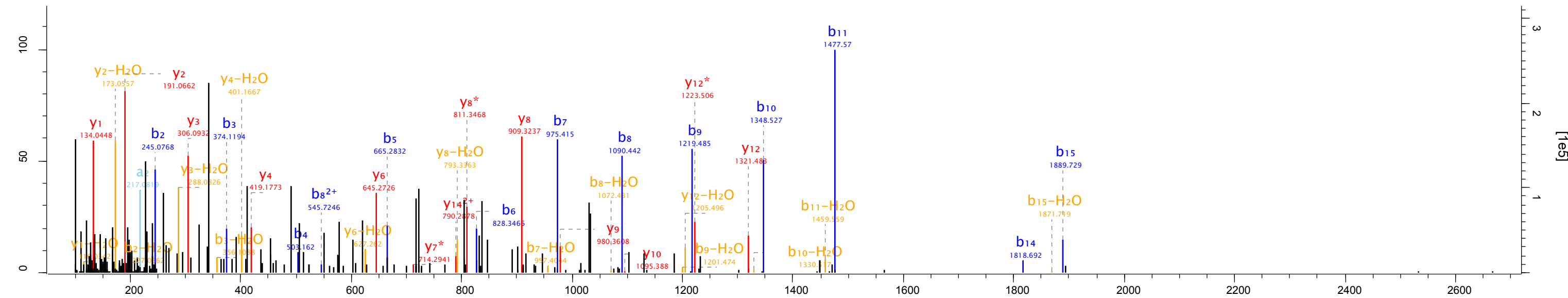


Protein sequence: H T F S G V A S V E S S G E A F H V G K

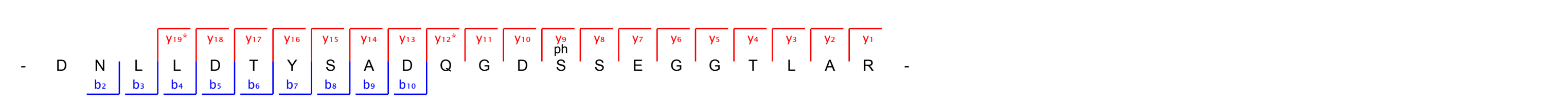
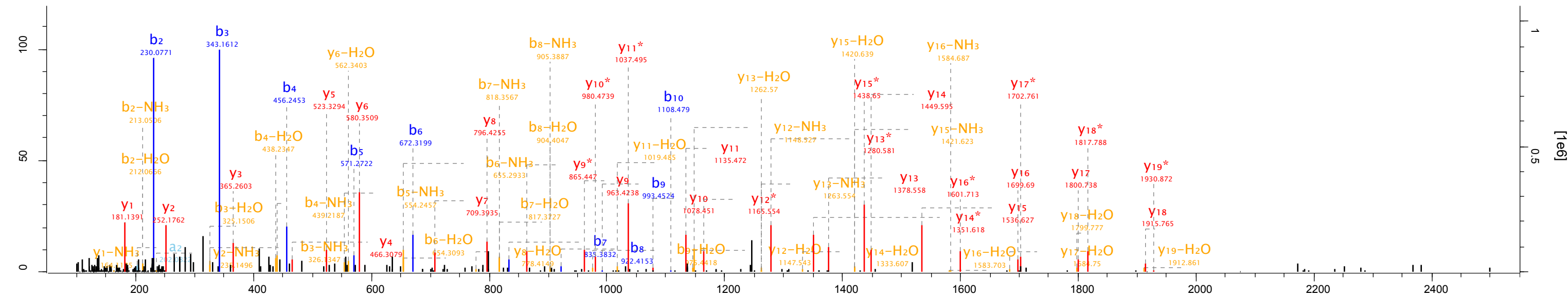
Fragmentation mapping (b and y ions):

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b ₂	b ₃	b ₄	b ₅	b ₆	b ₇	b ₈ *	b ₉ *	b ₁₀	b ₁₁ *	b ₁₂ *	b ₁₃ *		b ₁₅ *	b ₁₆ *	b ₁₇ *	b ₁₈	b ₁₉	b ₂₀ *	K

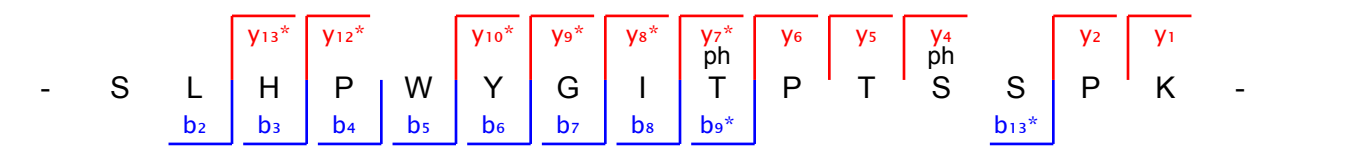
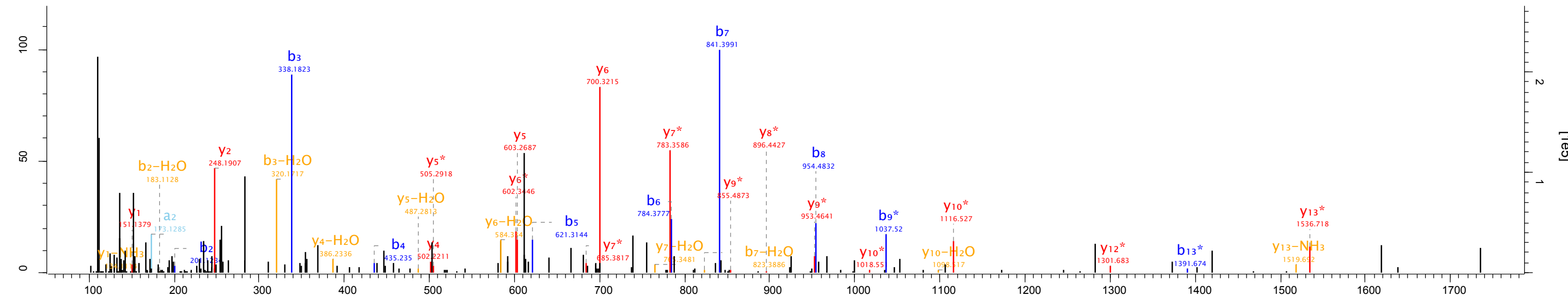
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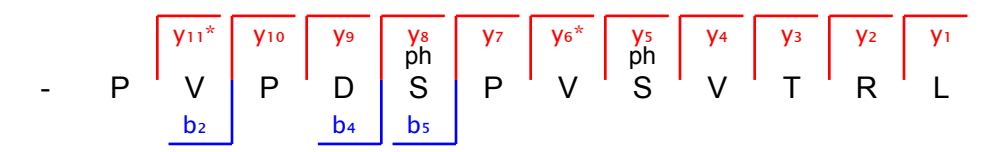
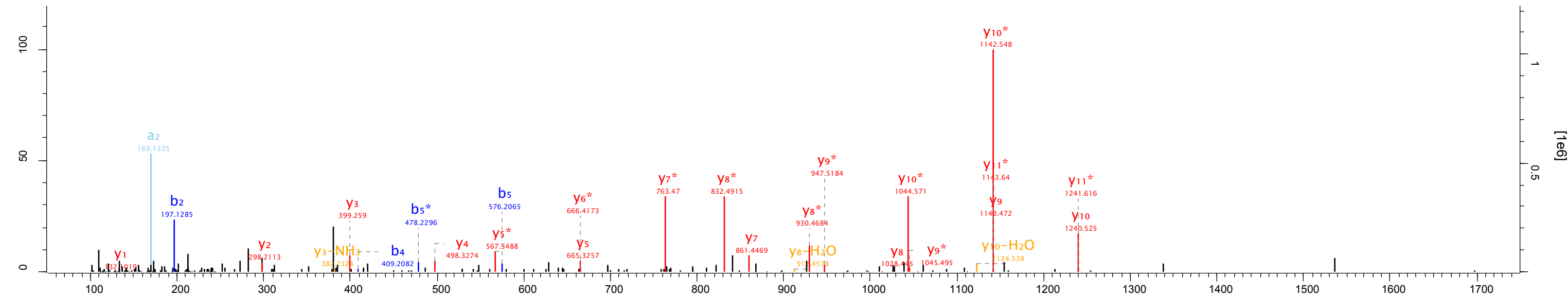
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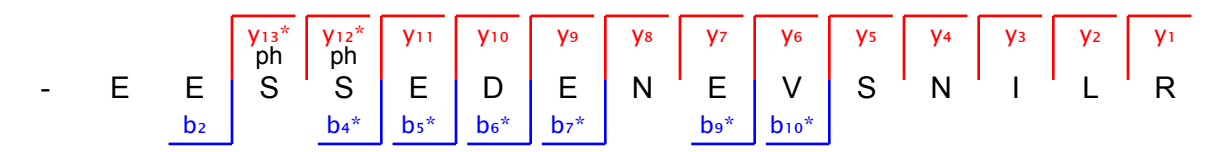
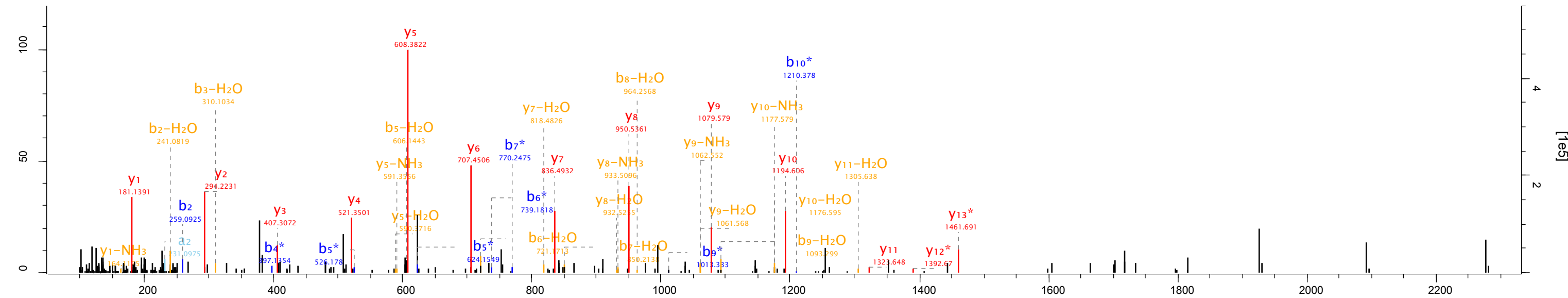
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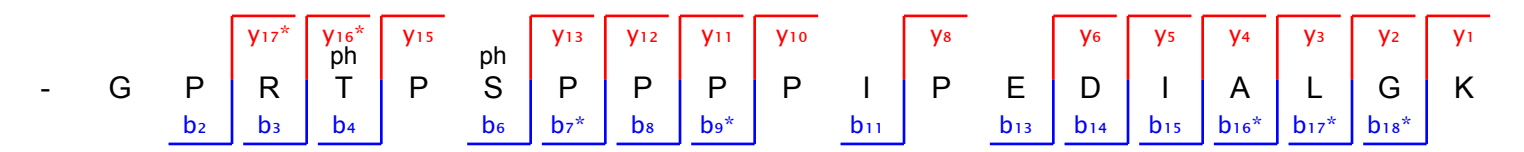
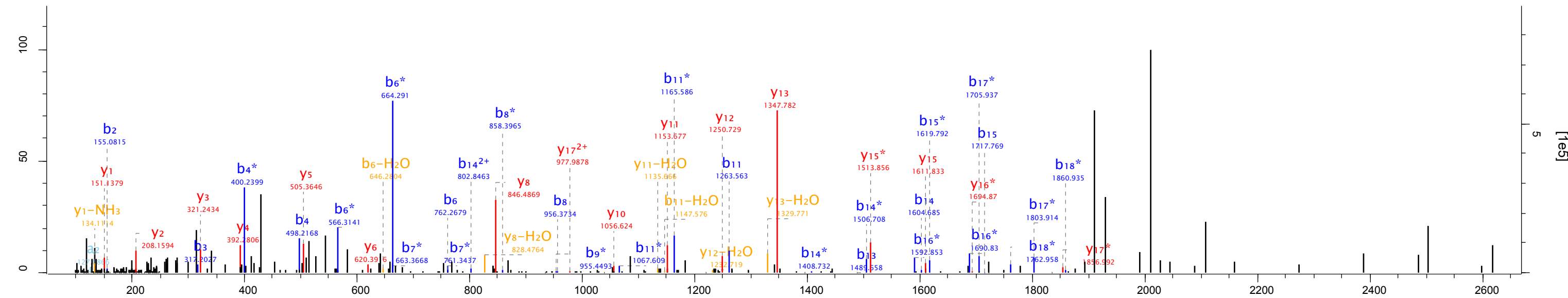
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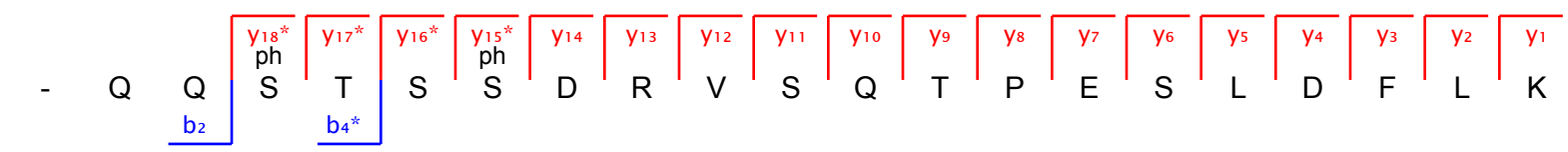
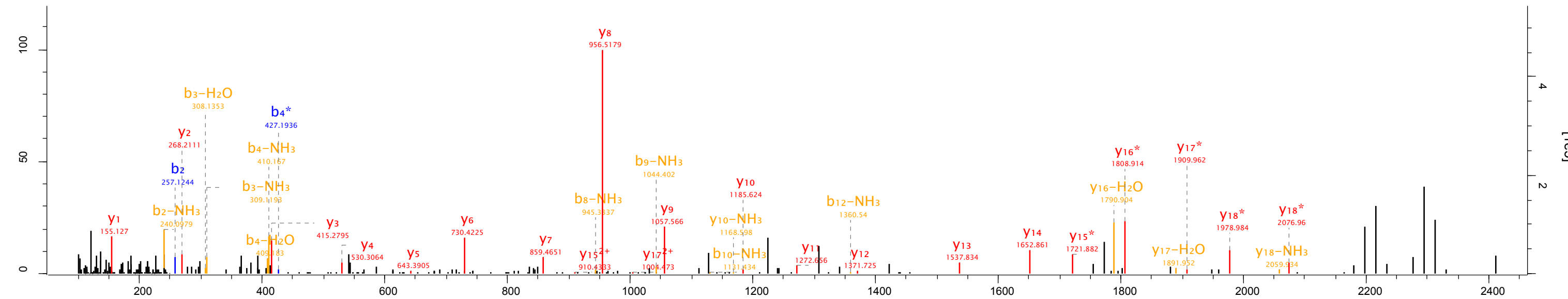
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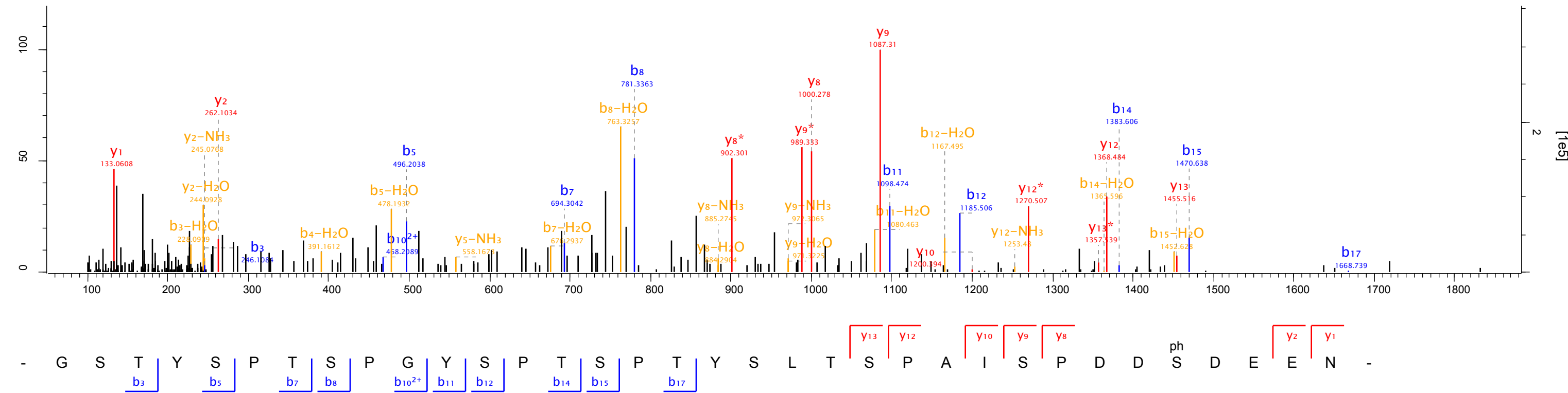


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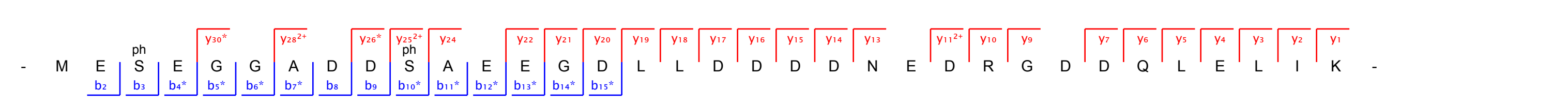
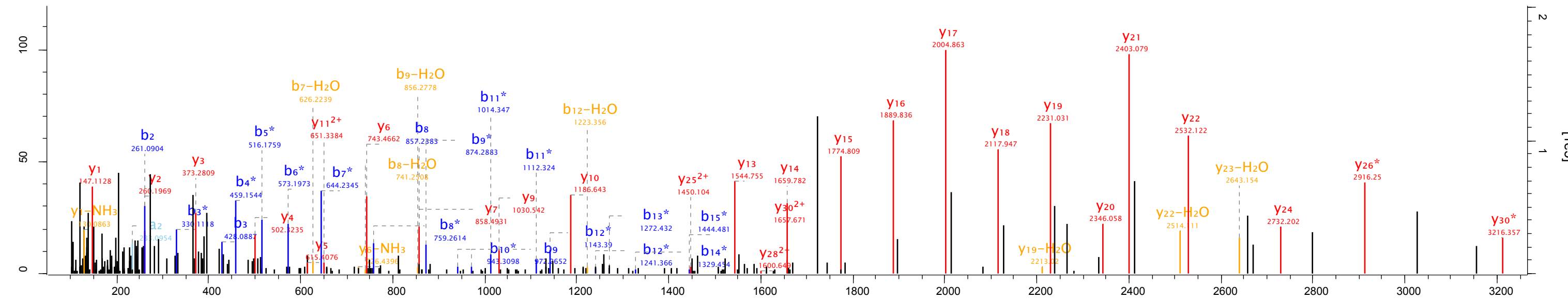


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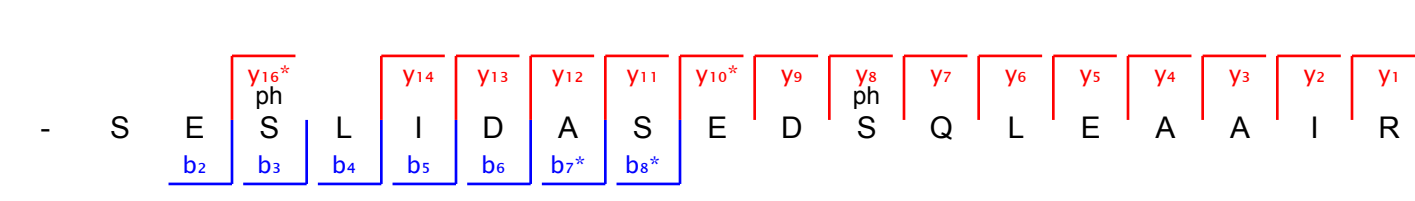
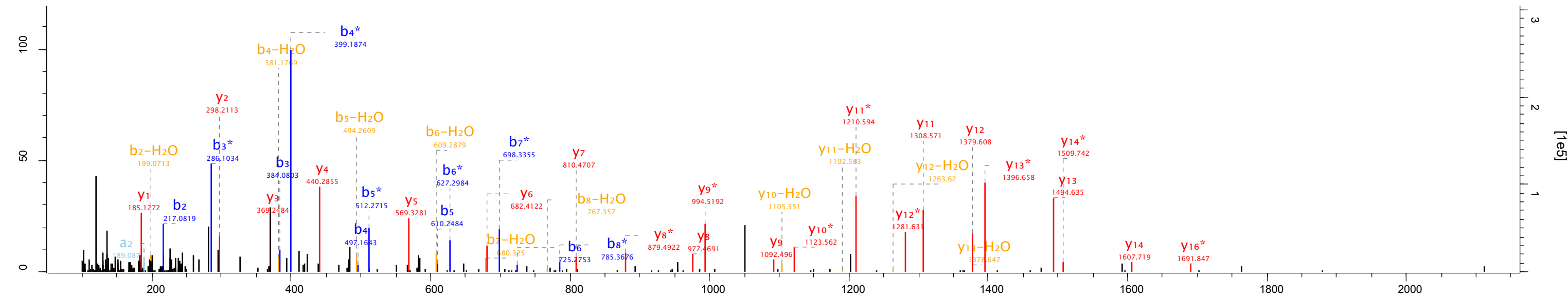




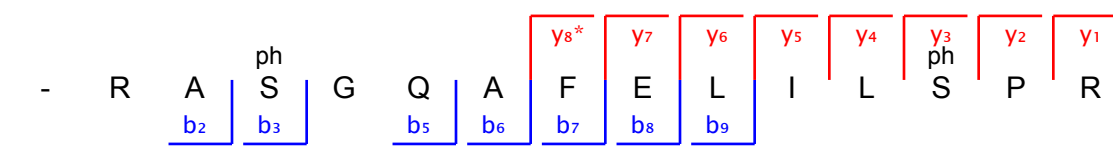
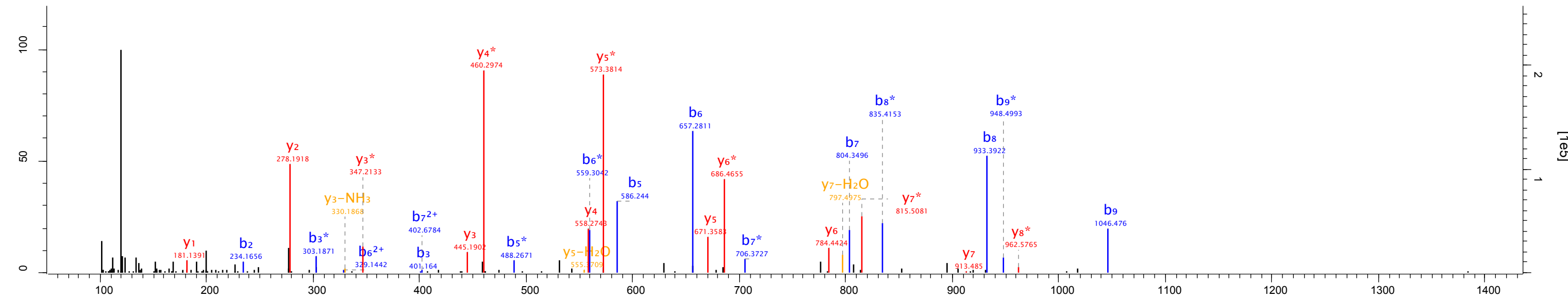
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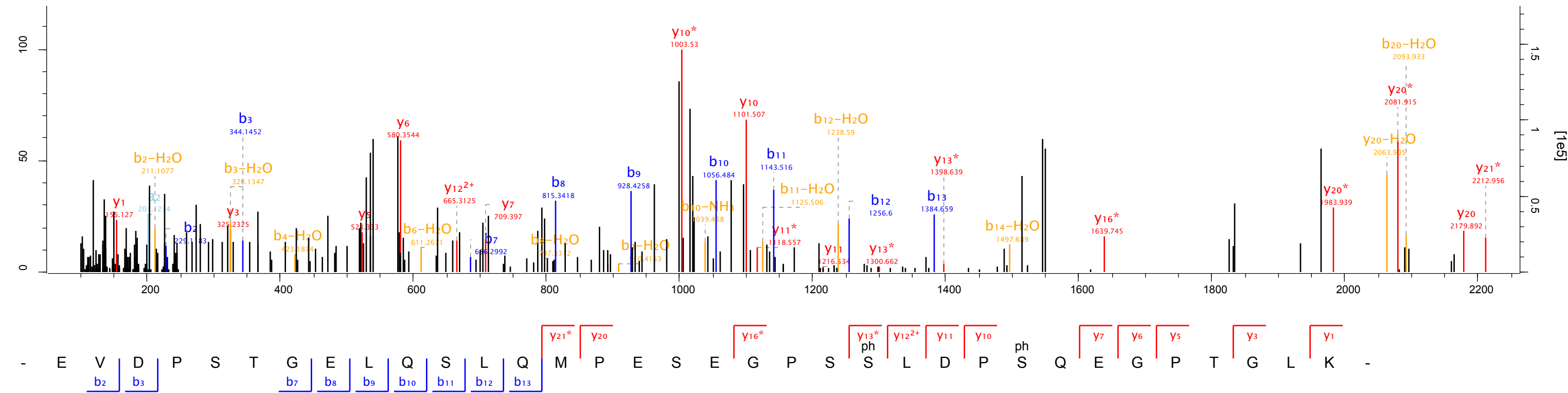
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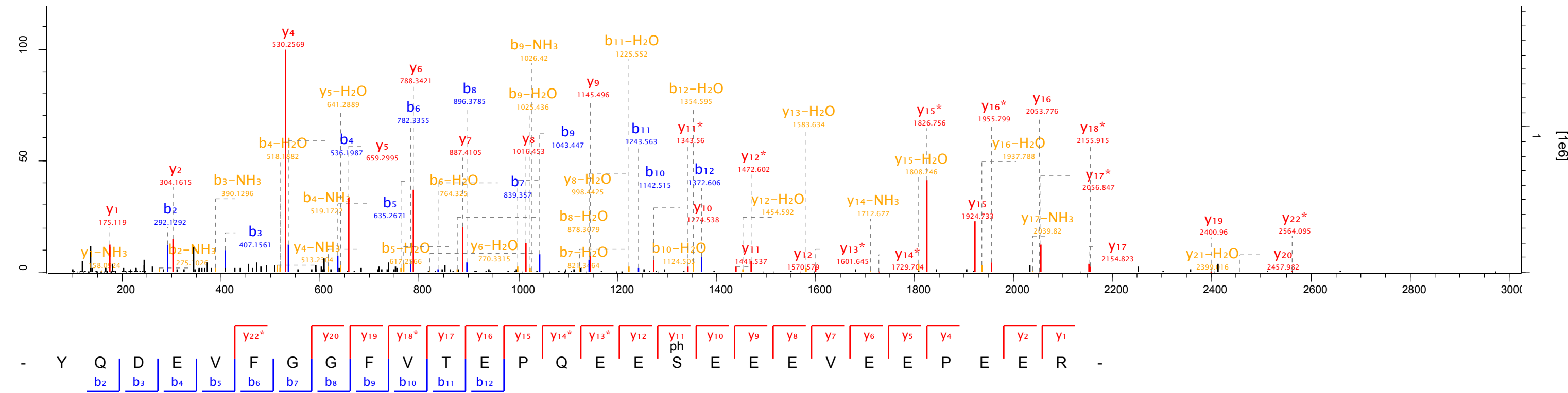
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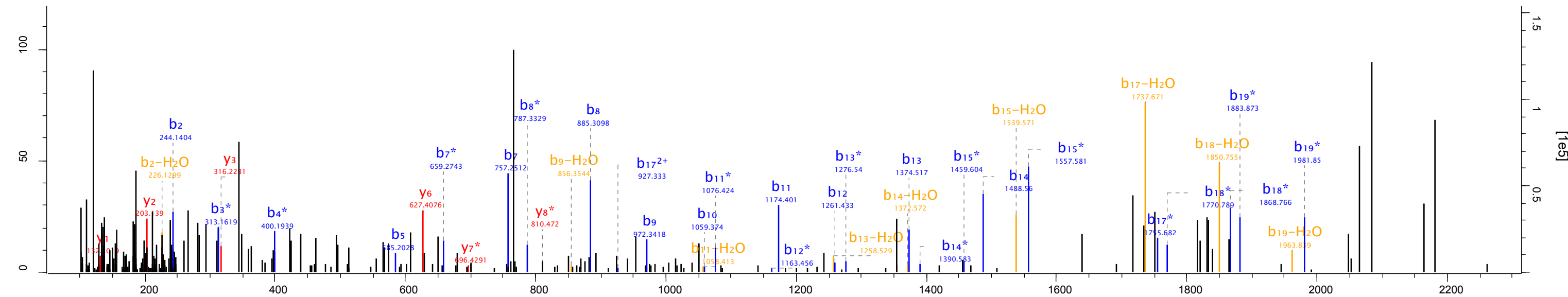


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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18627 Method FTMS; HCD Score 260.53 m/z 1648.67 Gene names G3BP1

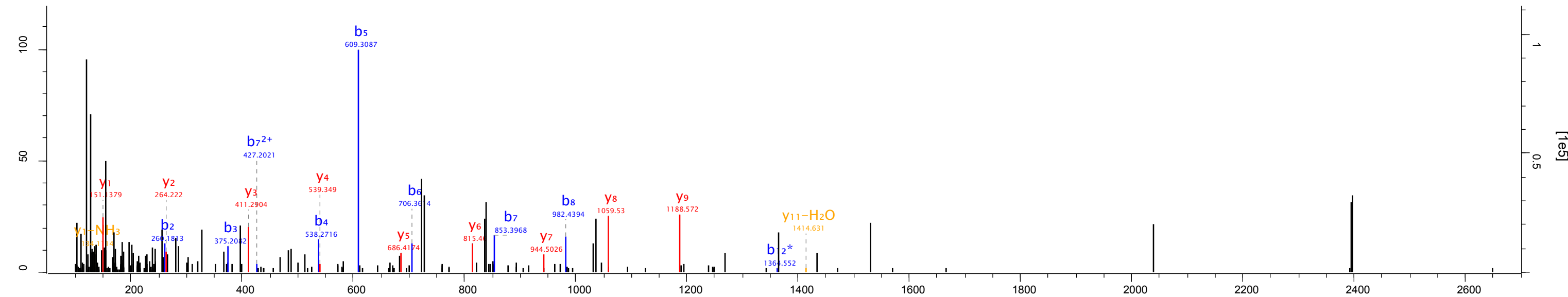




- R S S S S G D Q S S D S L N S P T L L A L -

b₂
b₃^{*}
b₄^{*}
b₅
b₇
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃
b₁₄
b₁₅^{*}
b₁₇^{*}
b₁₈^{*}
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y₈^{*}
y₇^{*}
y₆
y₃
y₂
y₁

ph
 ph
 ph

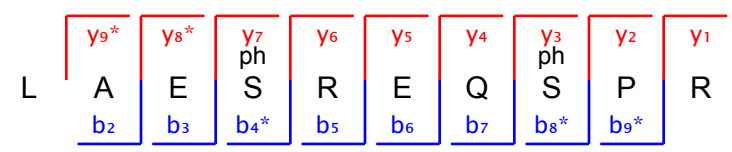
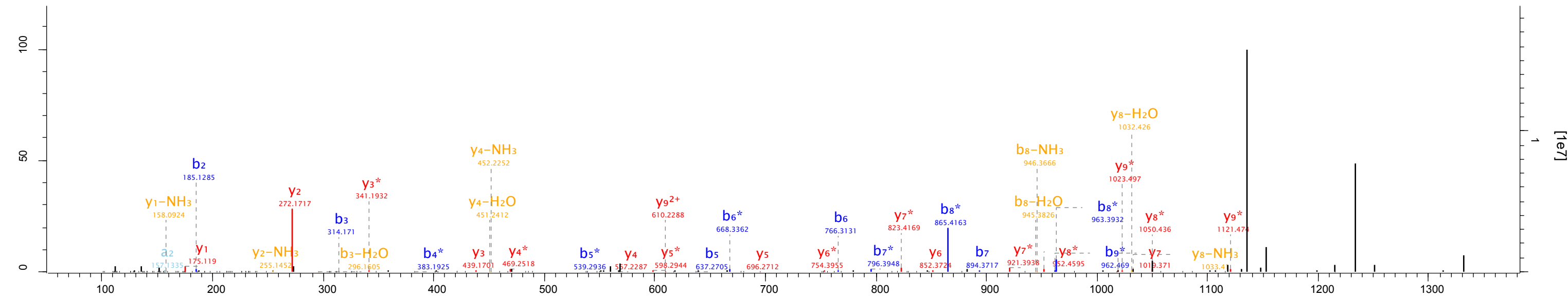


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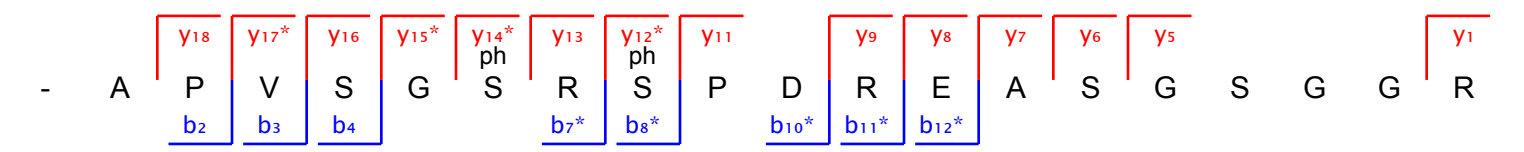
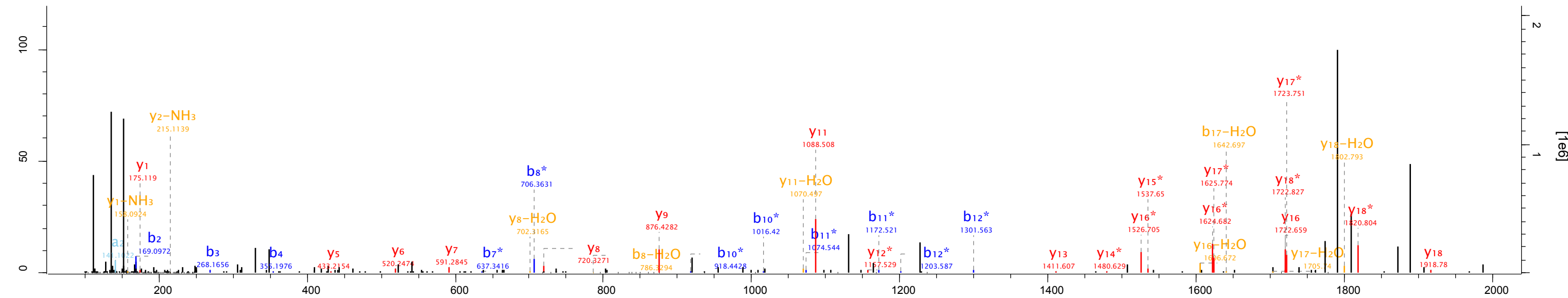
Fragmentation mapping (b and y ions) is shown below the sequence:

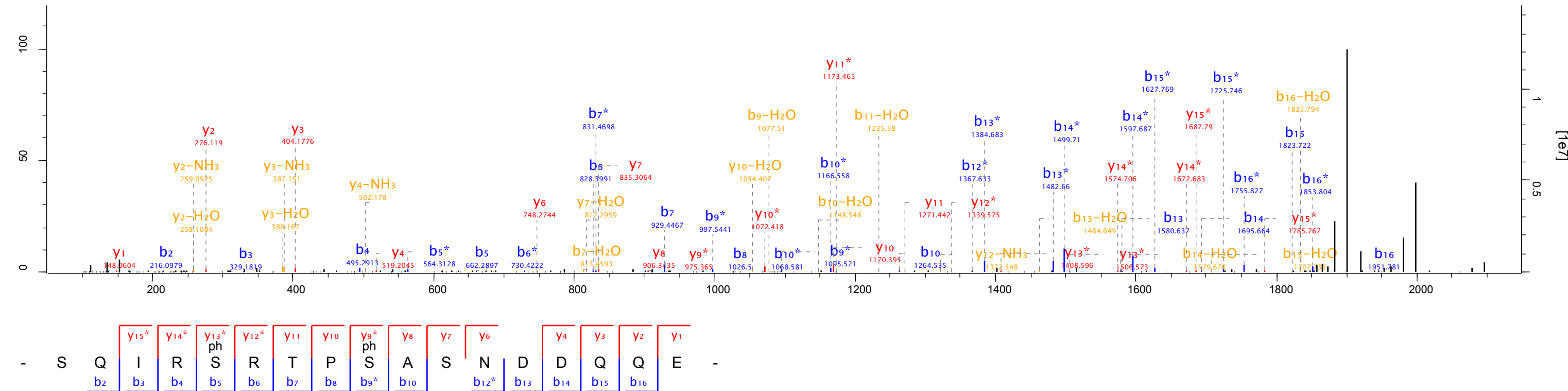
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- b3: DP
- b4: DYP
- b5: DYAP
- b6: DYAPox
- b7: DYAPoxM
- b8: DYAPoxME
- b12*: D
- y1: K
- y2: IK
- y3: IKF
- y4: IKFQ
- y5: IKFE
- y6: IKFEE
- y7: IKFEEDE
- y8: IKFEEDE
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 2477 Method FTMS; HCD Score 126.31 m/z 666.77 Gene names PPP1R18

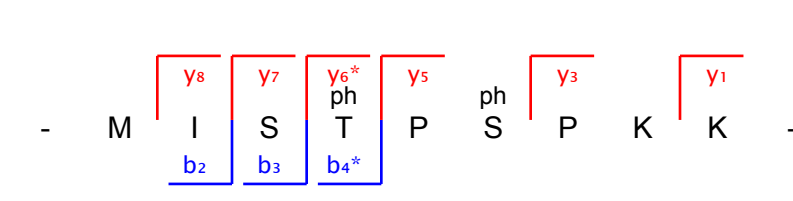
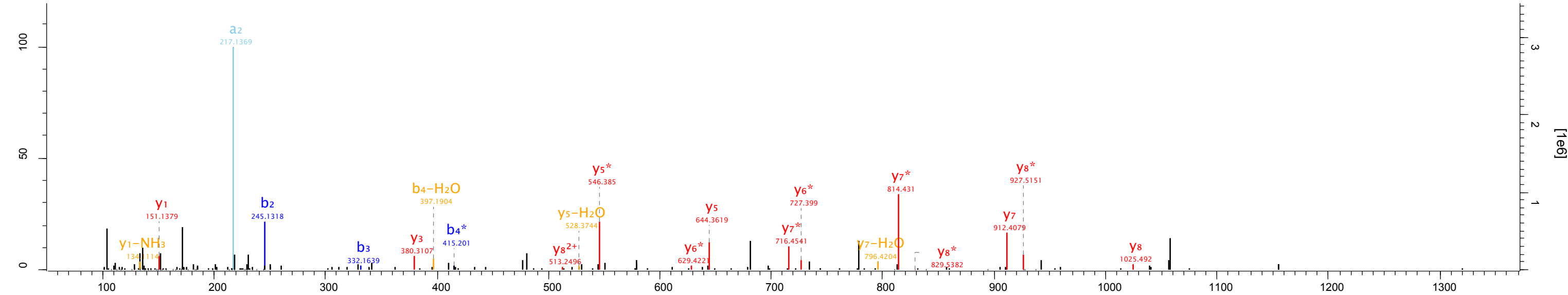


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 2727 Method FTMS; HCD Score 70.57 m/z 664.62 Gene names NKAP

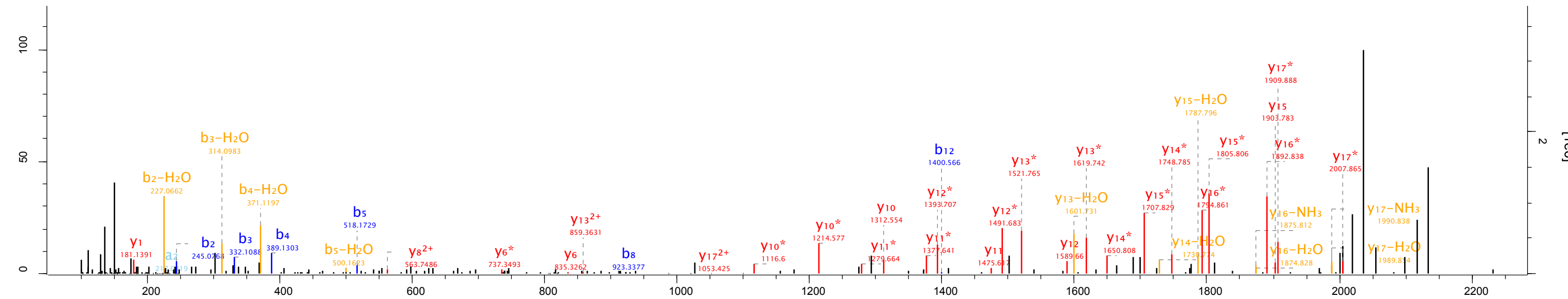




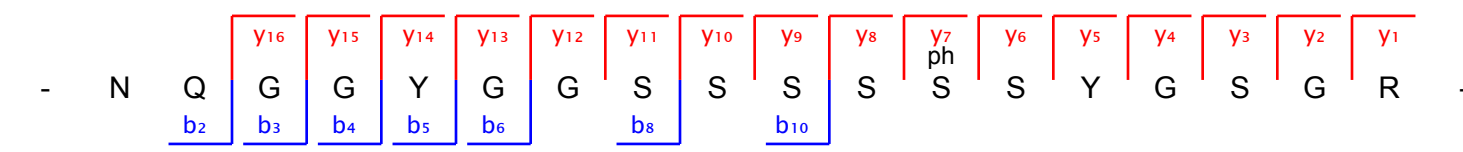
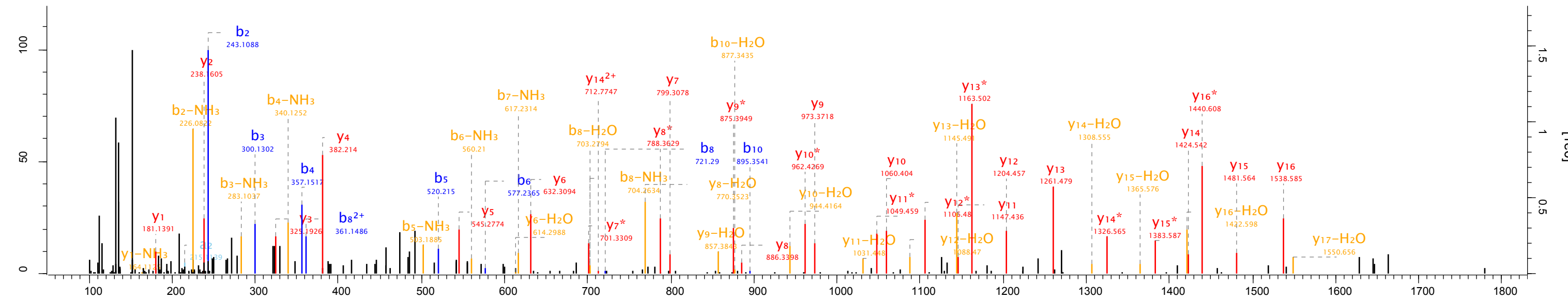
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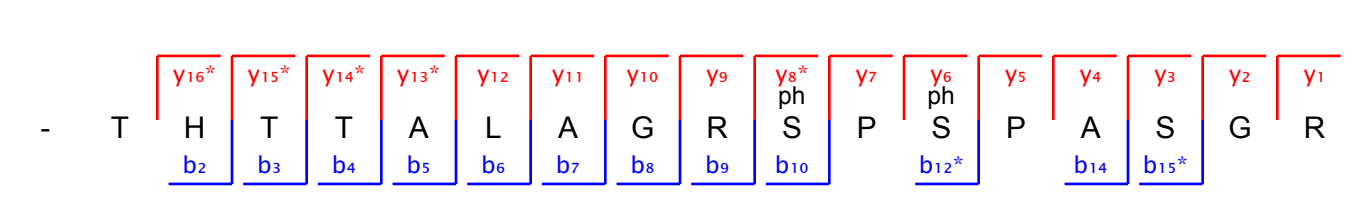
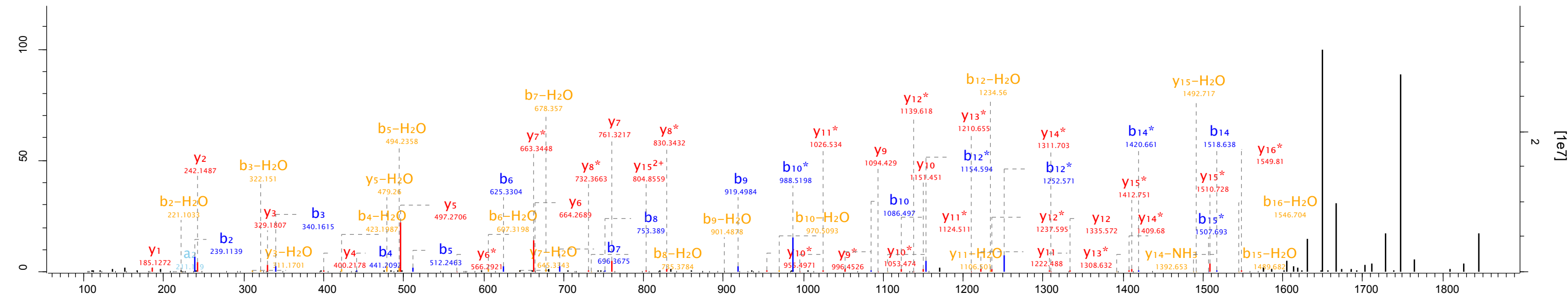
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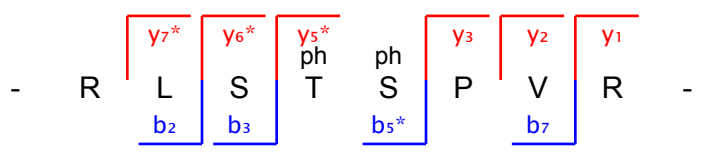
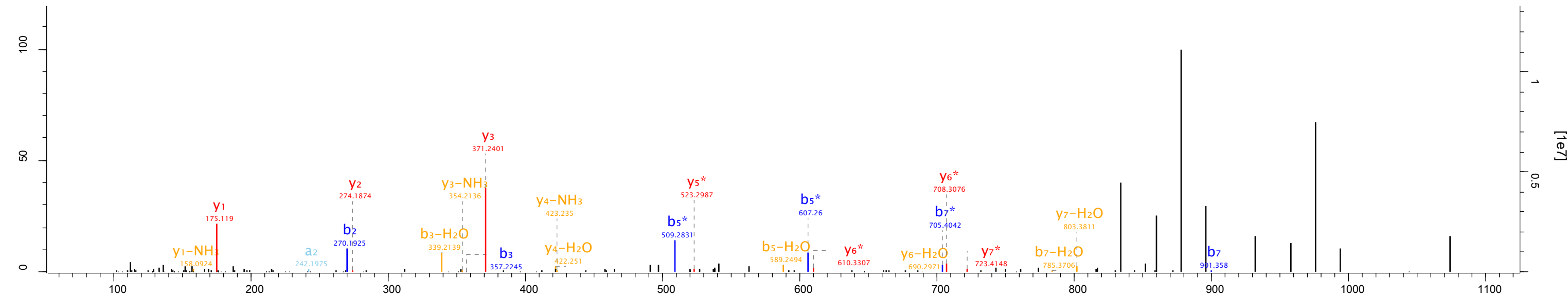
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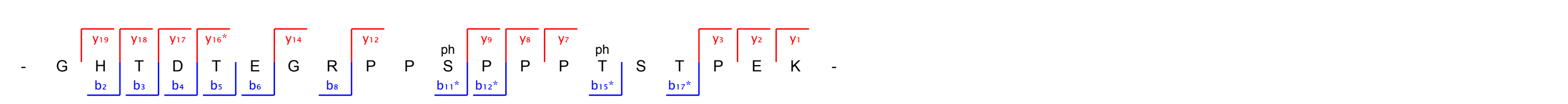
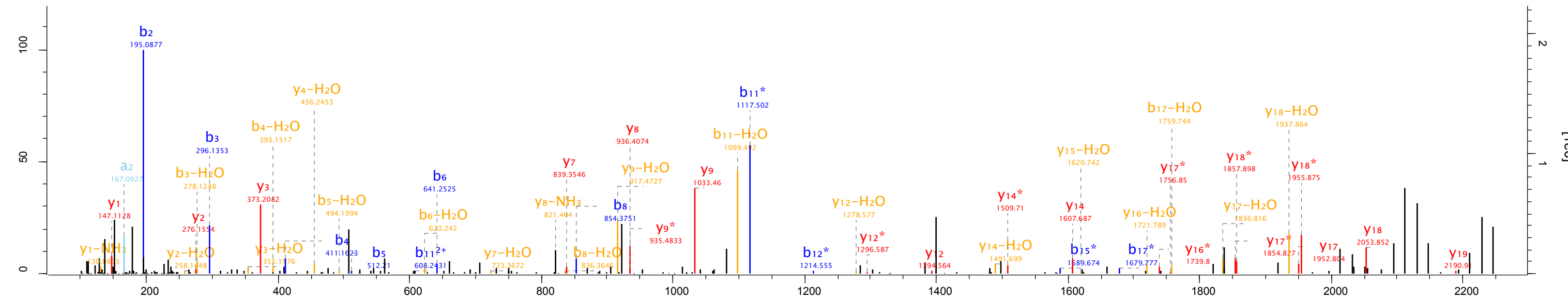
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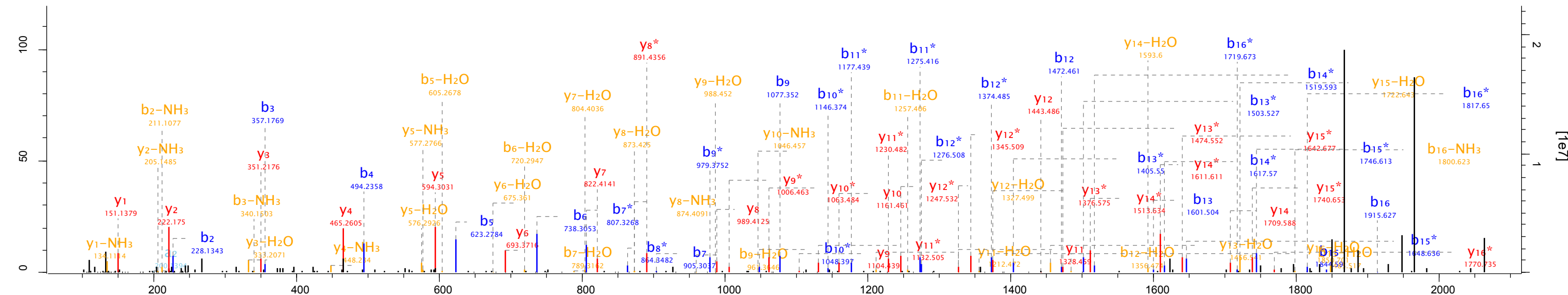
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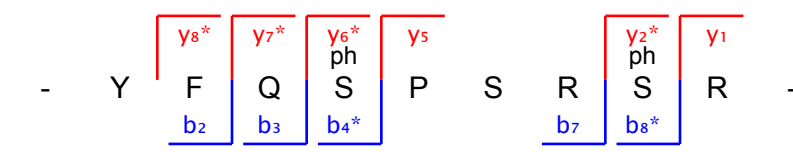
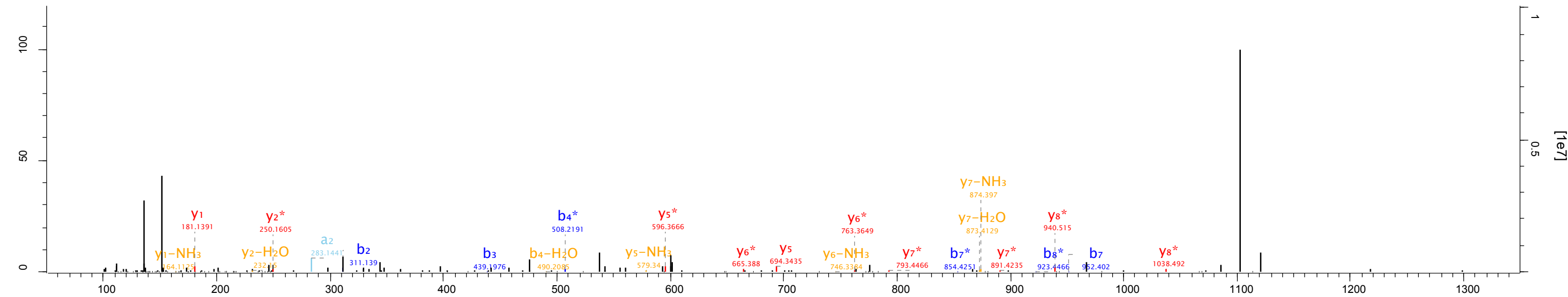


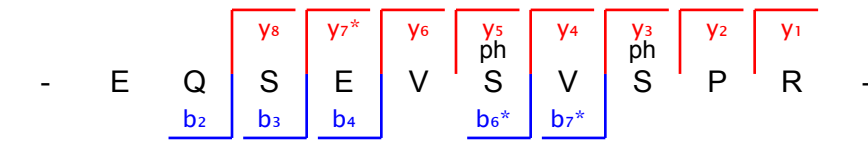
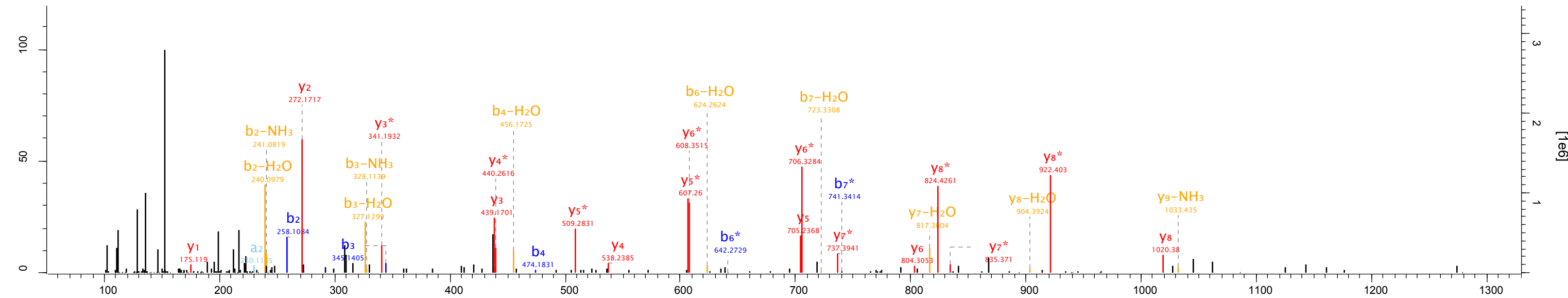
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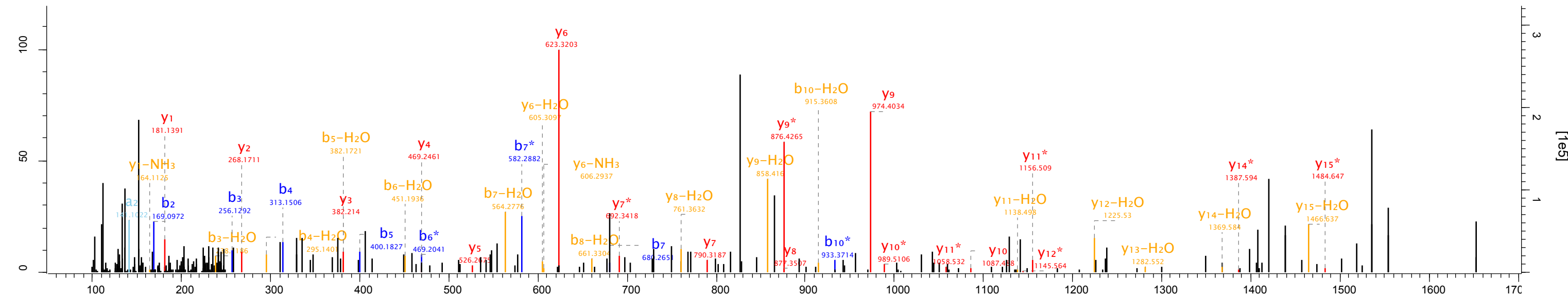
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y15*
y14
y13*
y12
y11
y10
y9
y8
y7
y6
y5
y4
y3
y2
y1

b2
b3
b4
b5
b6
b7
b8*
b9
b10*
b11*
b12
b13
b14*
b15
b16

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4317 Method FTMS; HCD Score 63.8 m/z 650.27 Gene names SRSF7





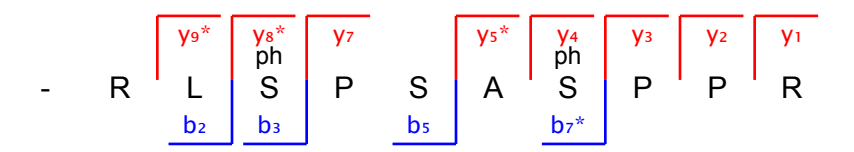
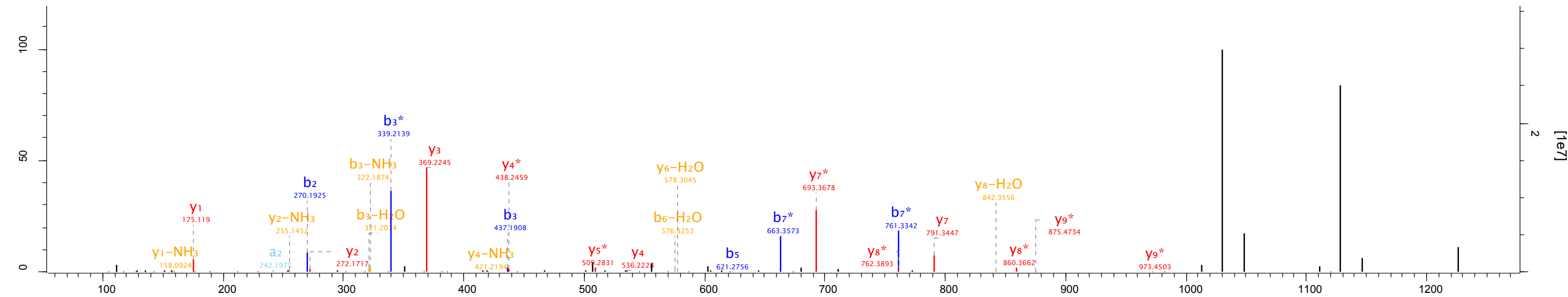


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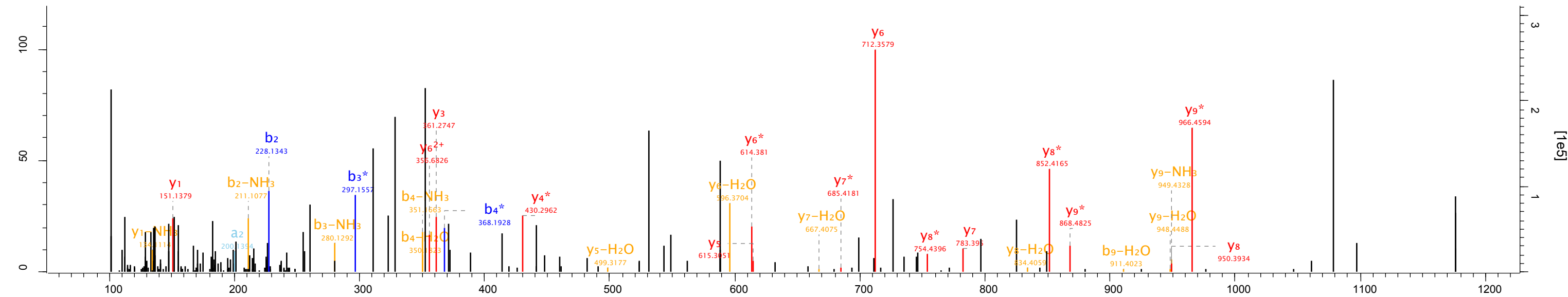
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y₁₅* y₁₄* y₁₂* y₁₁* ph y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

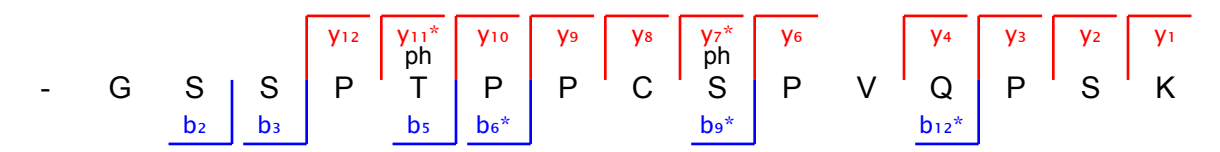
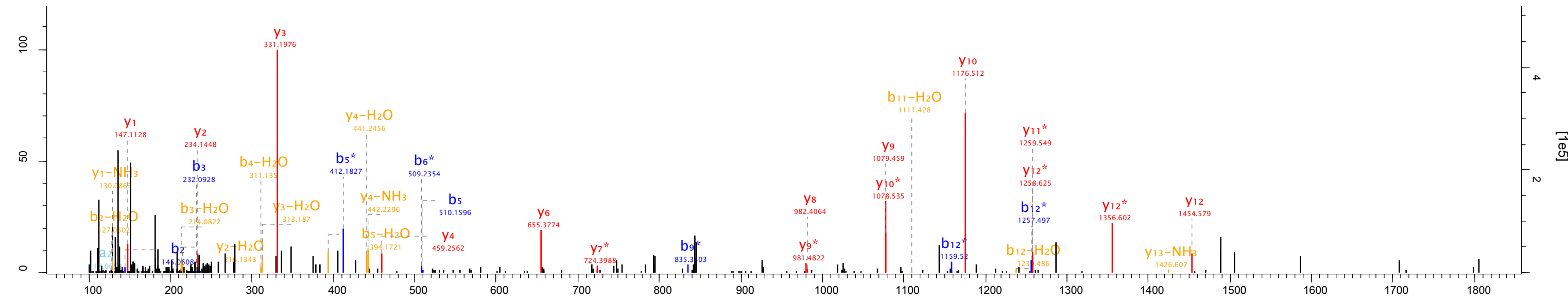
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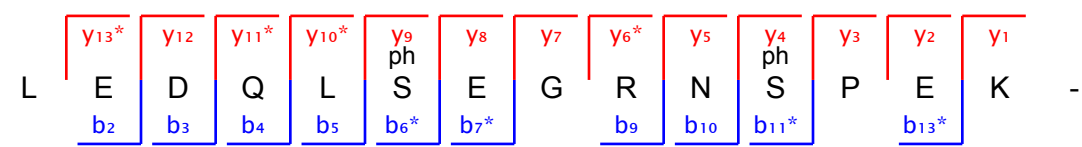
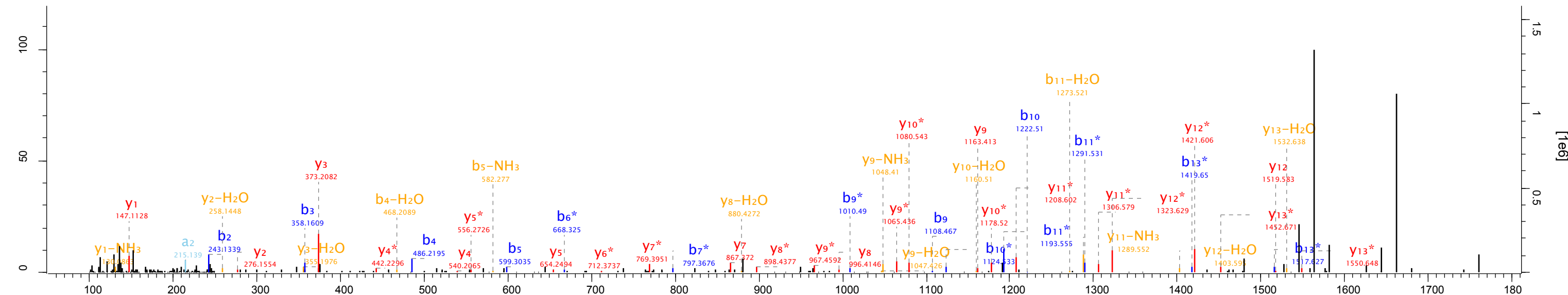
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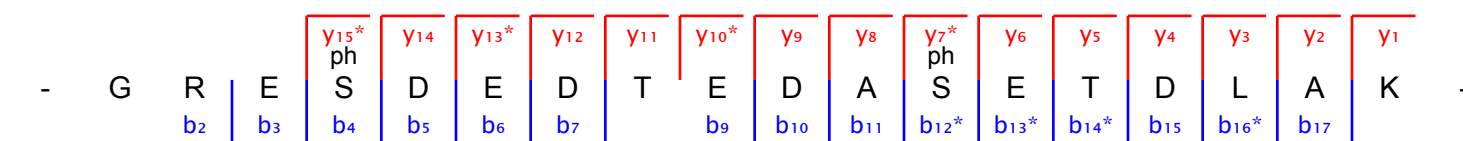
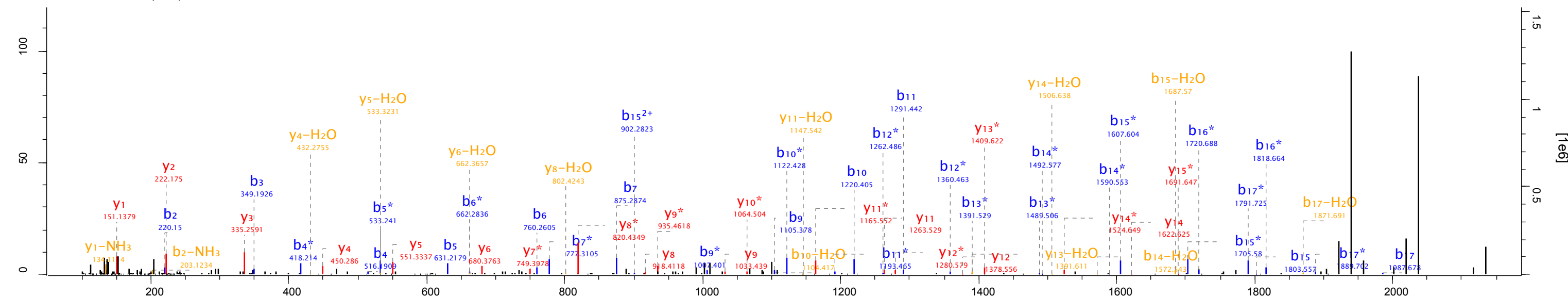


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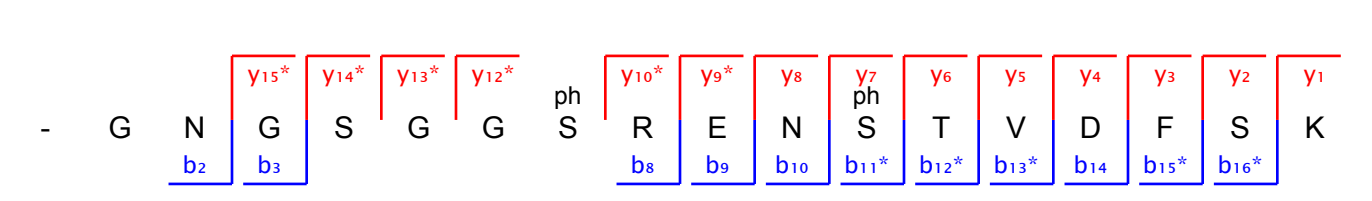
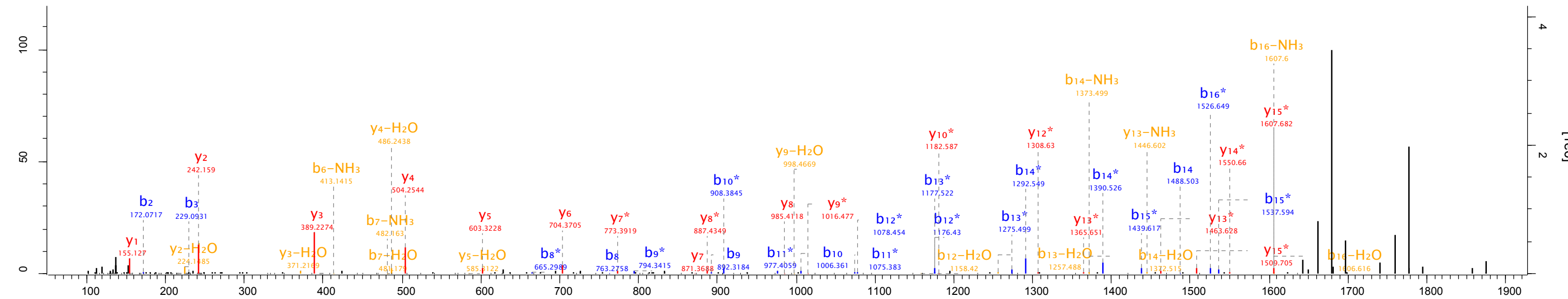


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20171215_MaS_33SR_LMH_phospho2_03

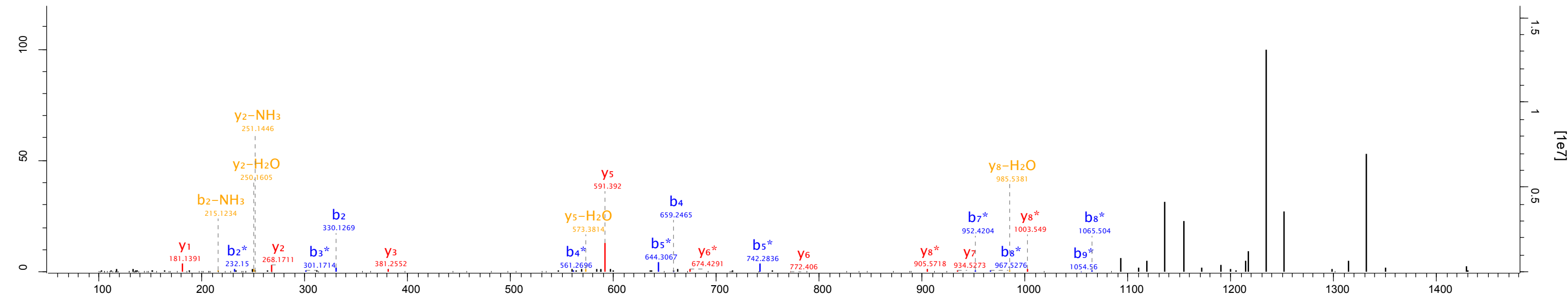
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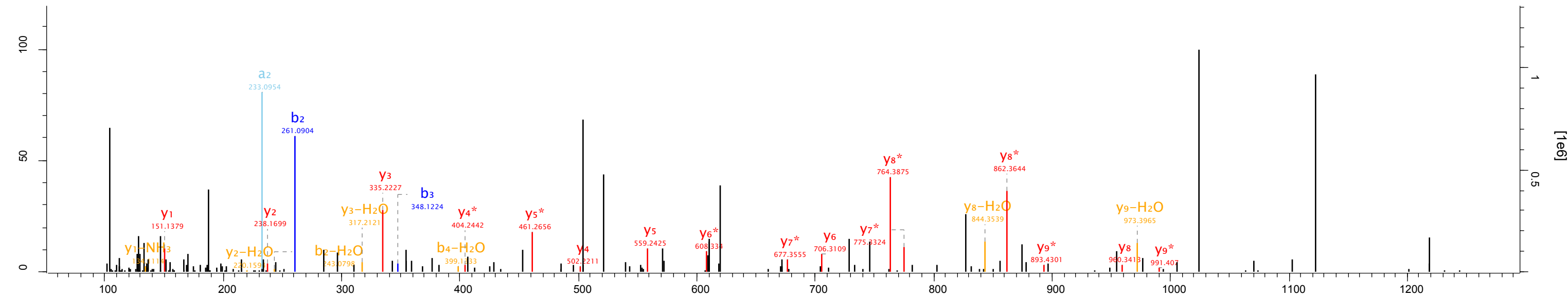


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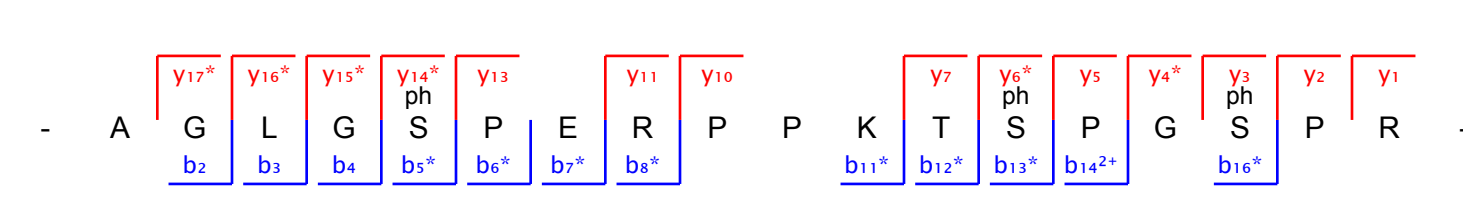
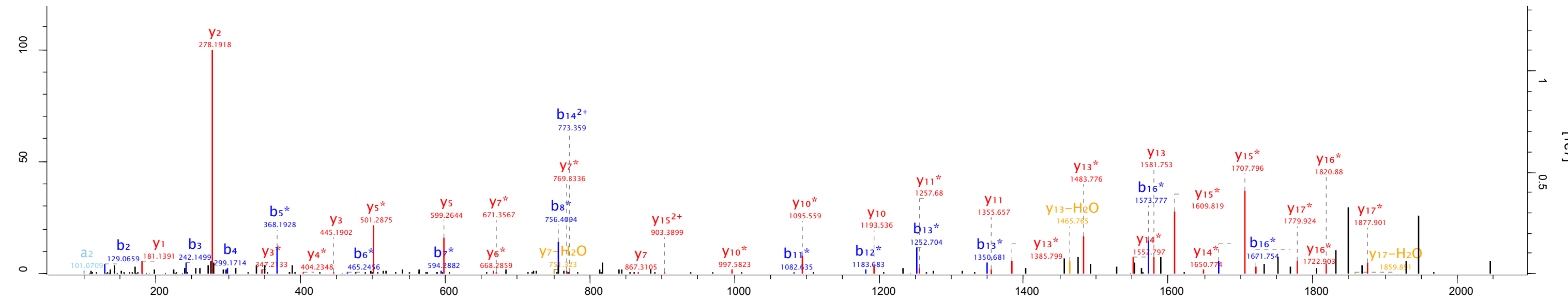


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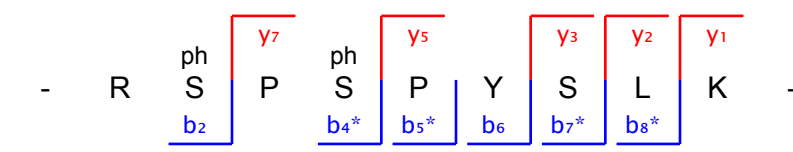
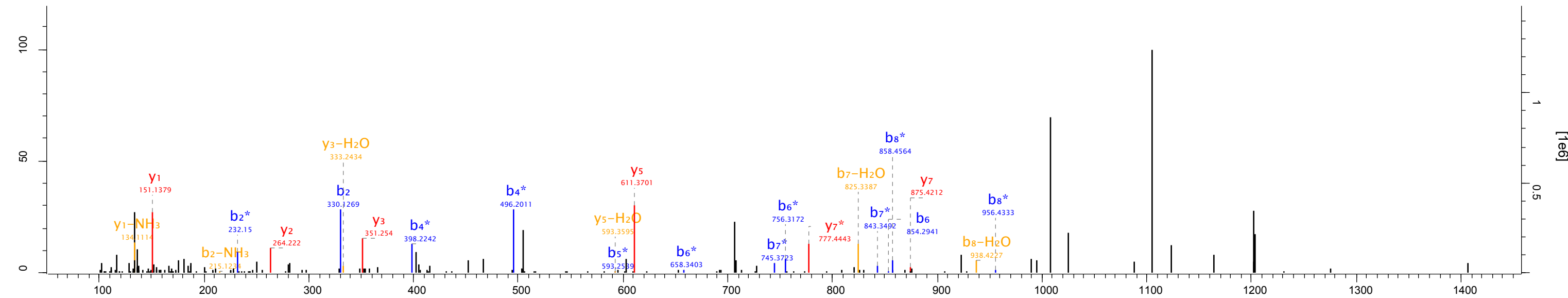
20171215_MaS_33SR_LMH_phospho2_03



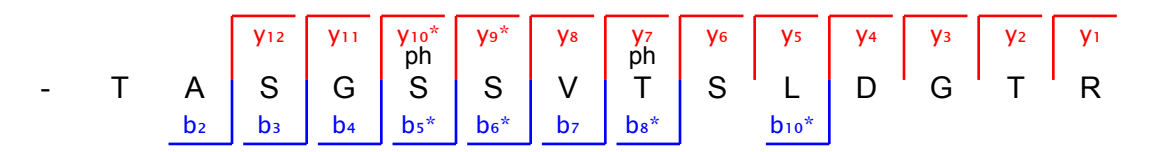
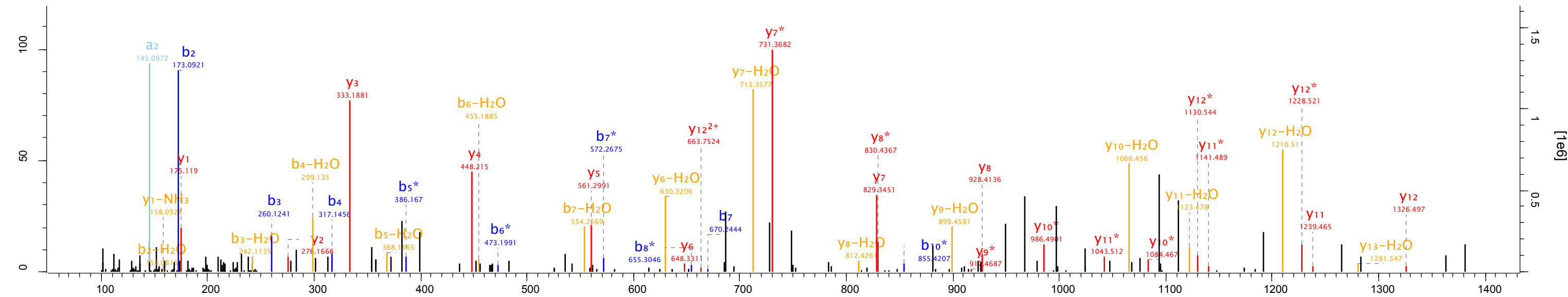
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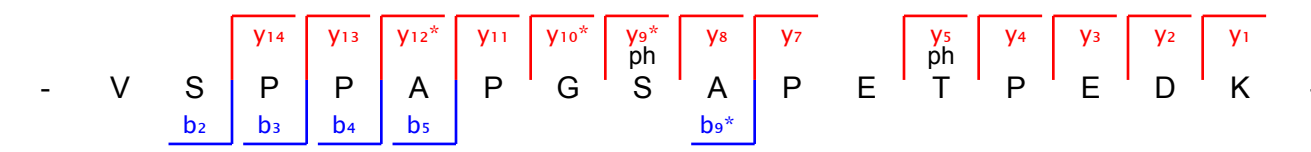
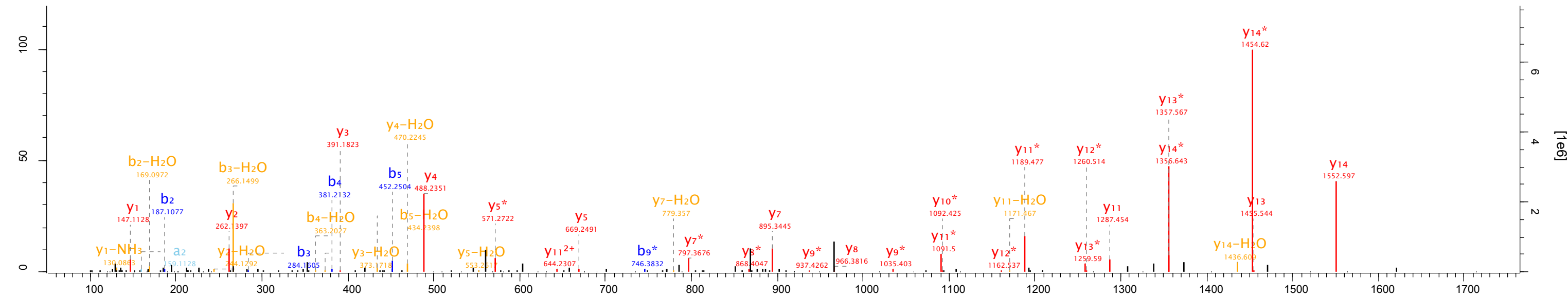


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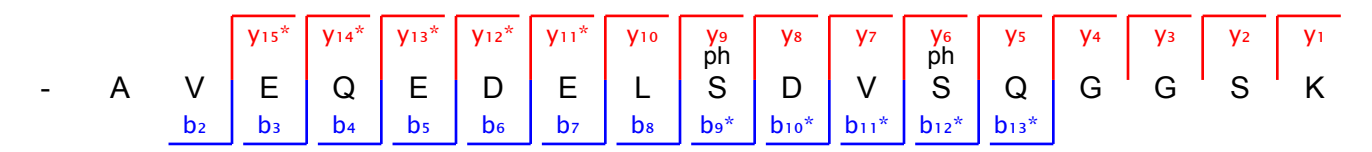
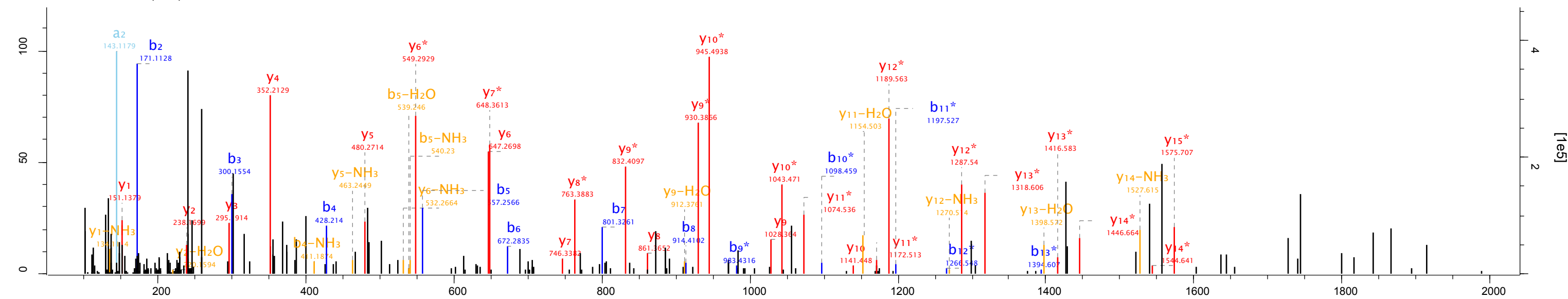
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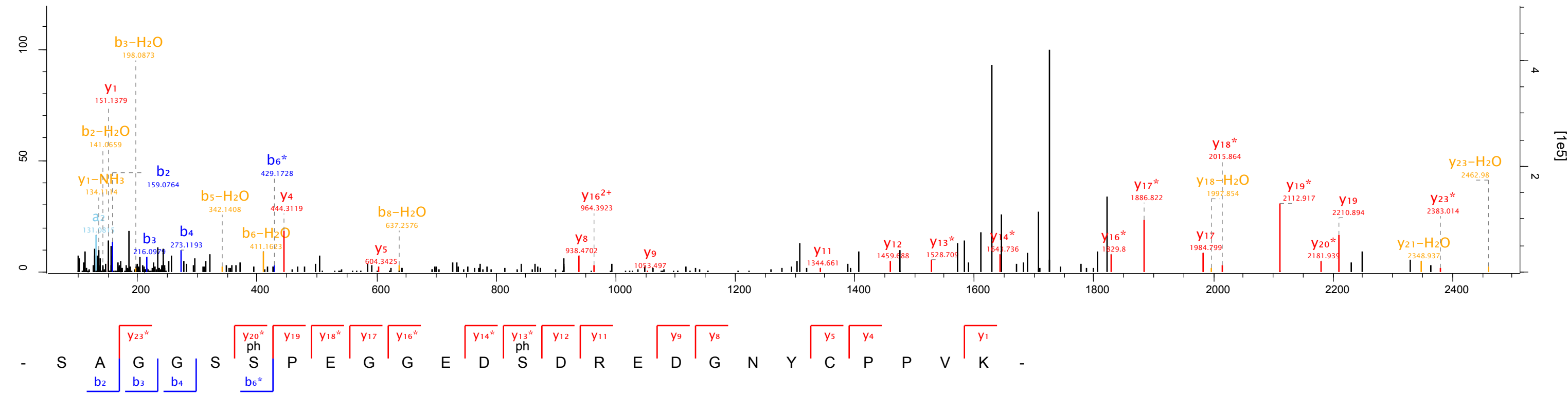


Raw file
20171215_MaS_33SR_LMH_phospho2_03

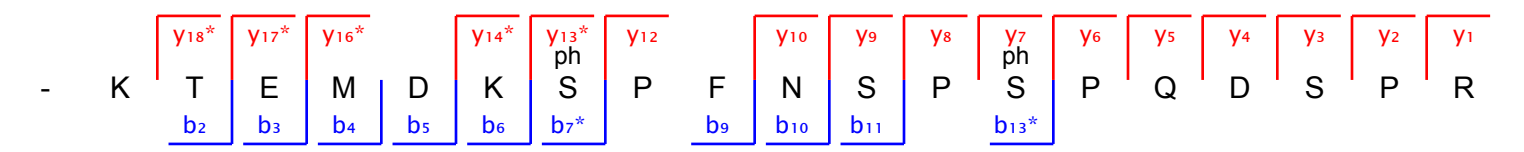
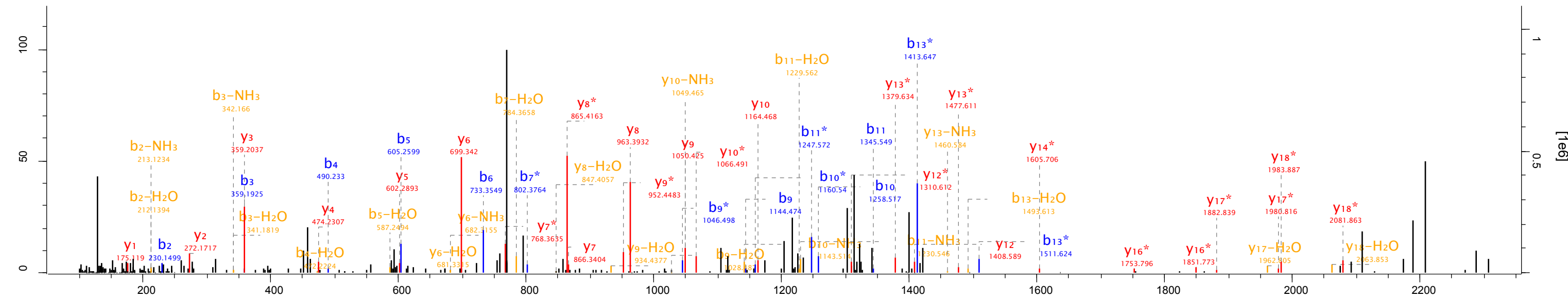
Scan 6817 Method FTMS; HCD Score 162.41 m/z 971.89 Gene names SPAG9

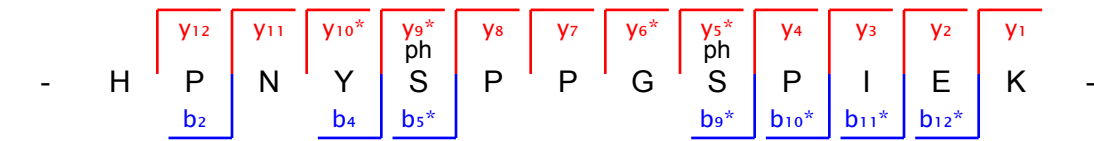
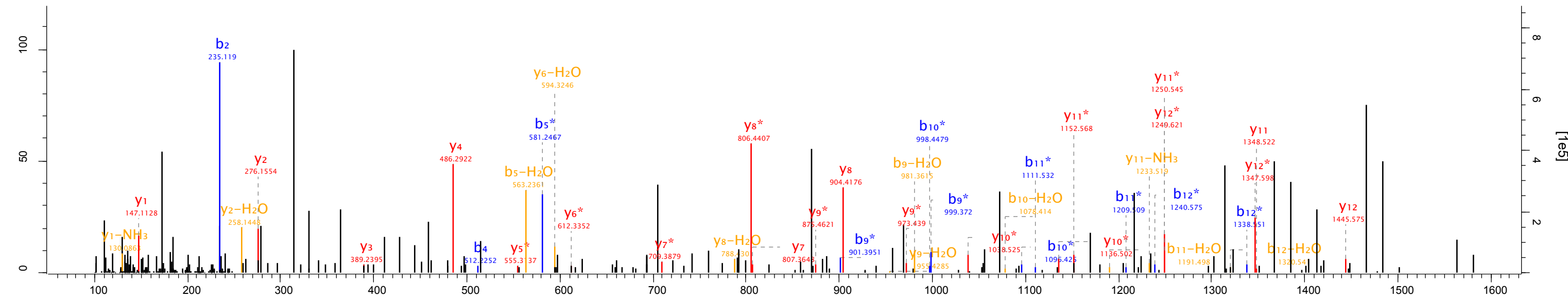


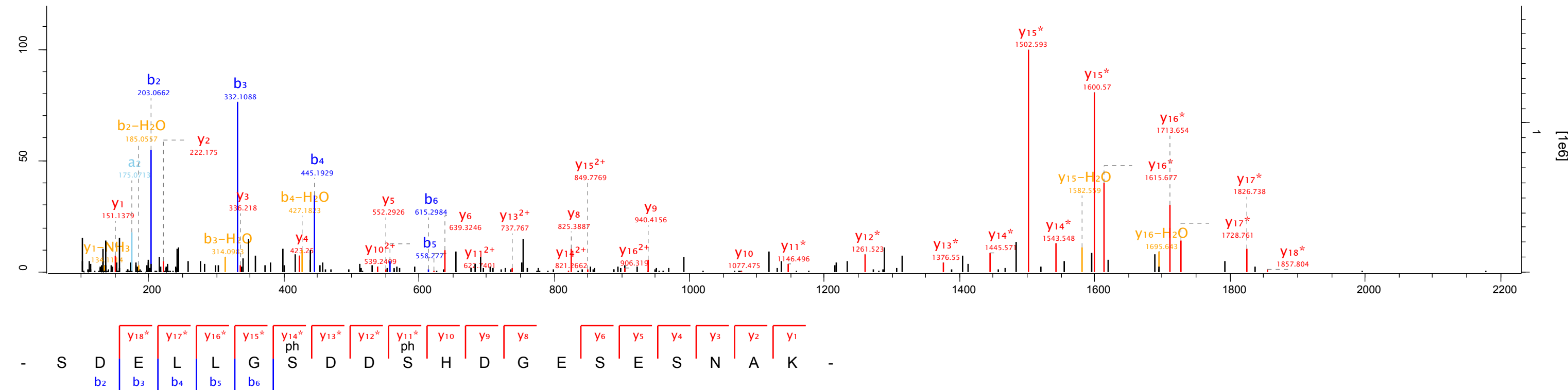
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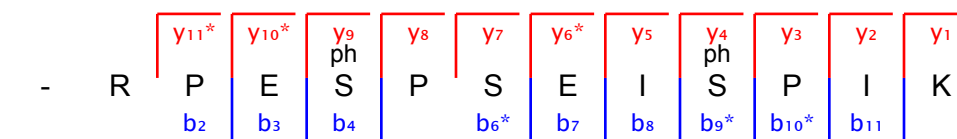
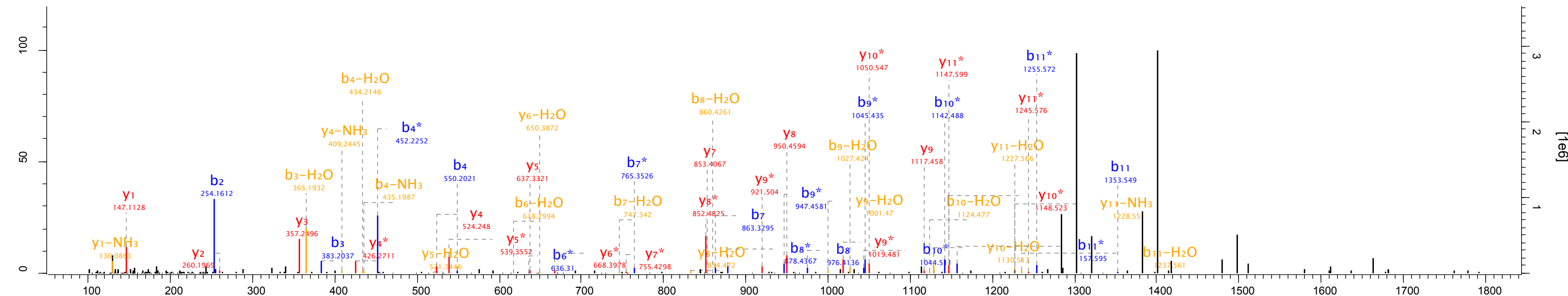


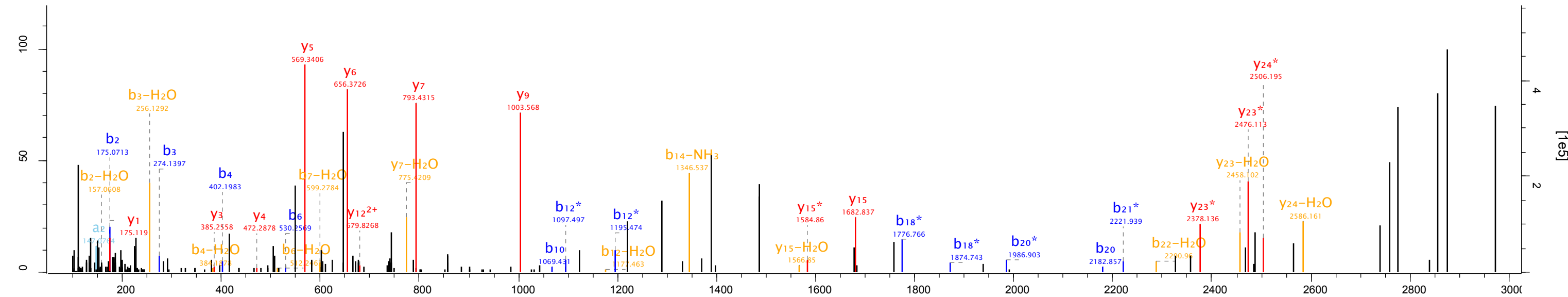
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- S S V Q G A S S R E G S P A R S T P L H S P S P I R -

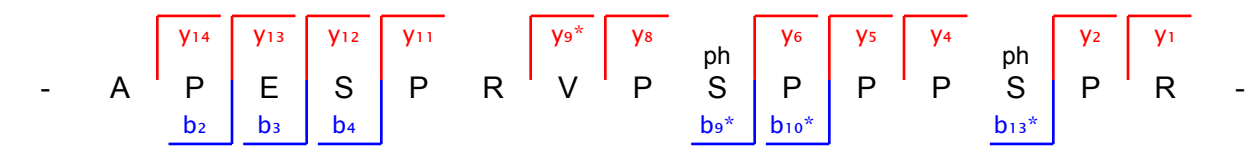
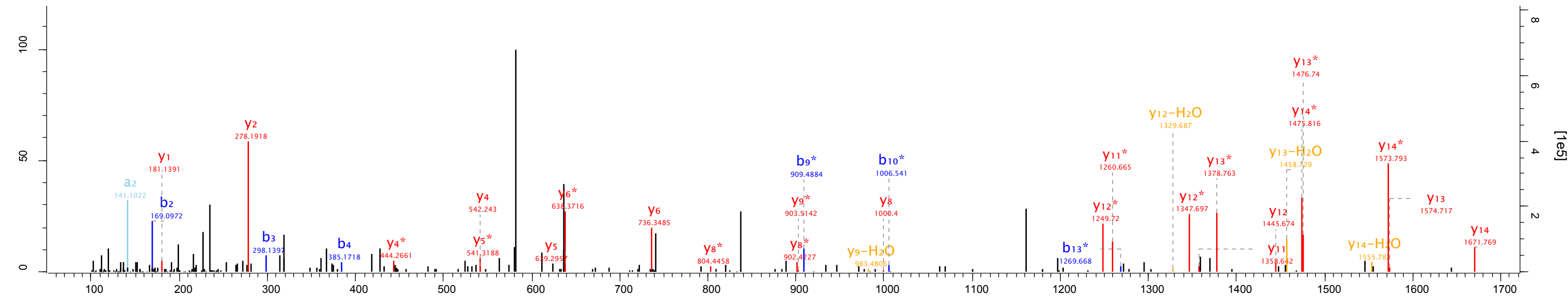
Fragmentation sites are indicated by brackets below the sequence:

- b2 (S-S)
- b3 (S-V)
- b4 (V-Q)
- b6 (A-S)
- b10 (E-G)
- b12* (S-P)
- b18* (T-P)
- b20 (L-P)
- b21* (L-H)

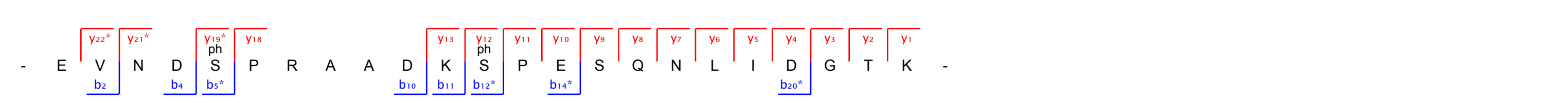
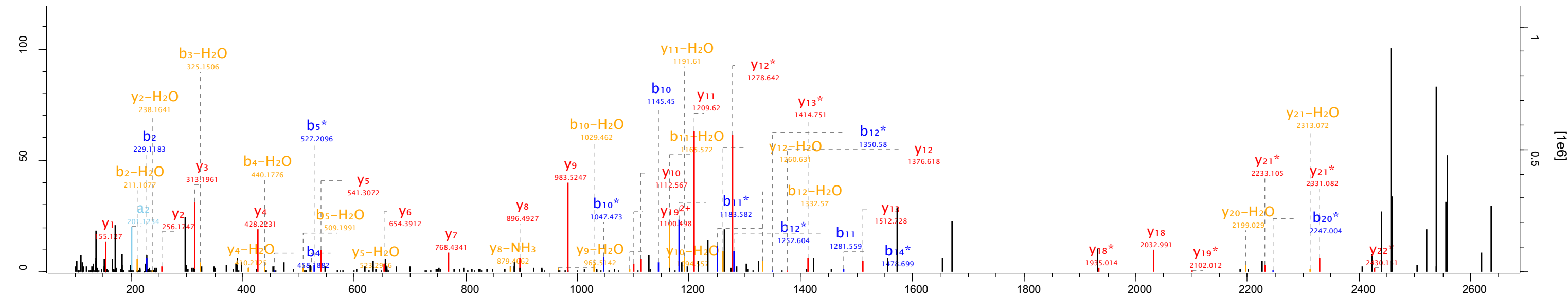
Y-ion fragmentation sites are indicated by brackets above the sequence:

- y1 (I-R)
- y3 (P-S)
- y4 (S-P)
- y5 (P-S)
- y6 (S-P)
- y7 (H-S)
- y9 (P-S)
- y12²⁺ (S-P)
- y15 (P-S)
- y23* (S-P)
- y24* (Q-G)

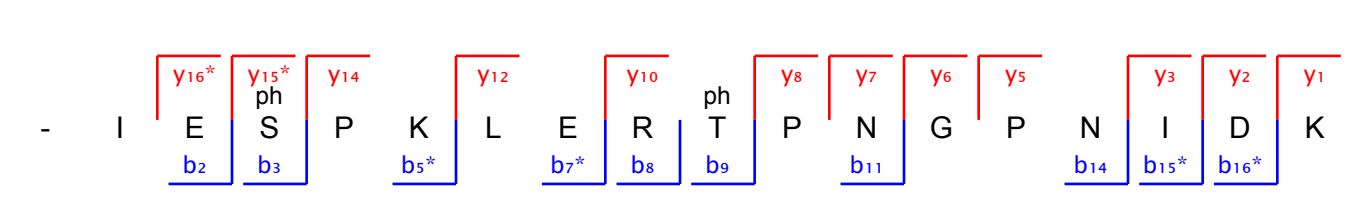
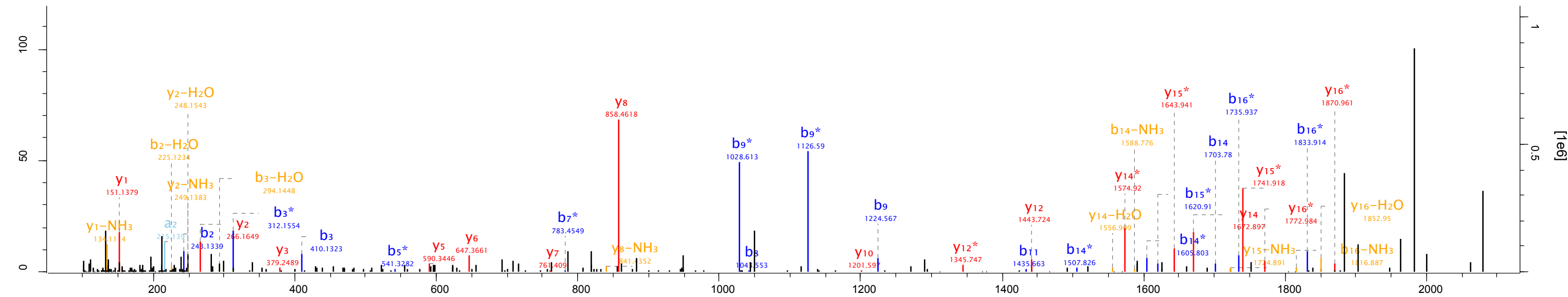
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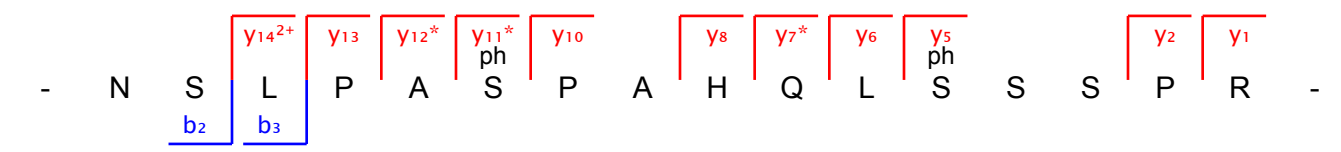
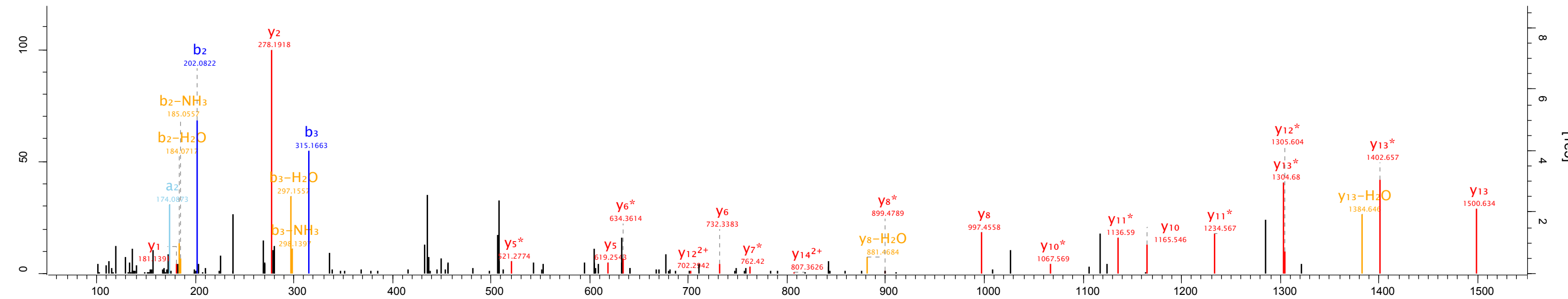
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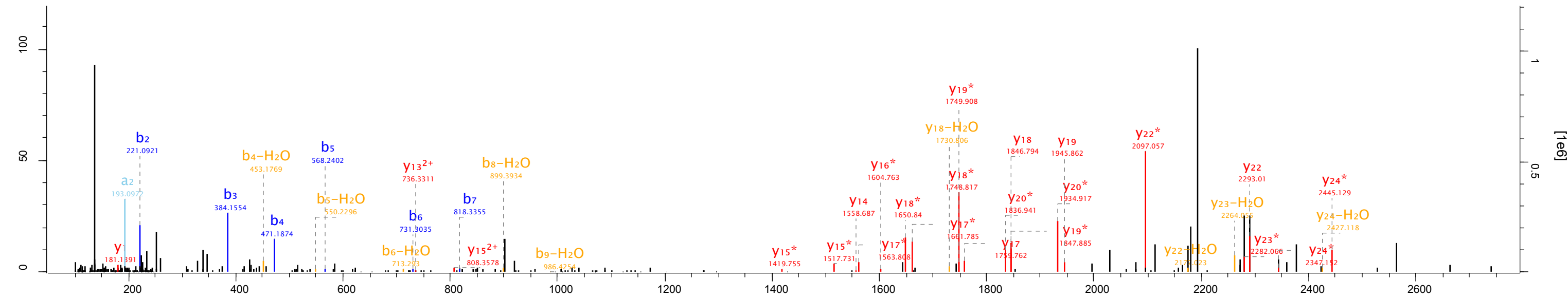
Raw file

20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
8297	FTMS; HCD	84.33	605.6	DOT1L



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 8497 Method FTMS; HCD Score 82.26 m/z 921.73 Gene names PLEC

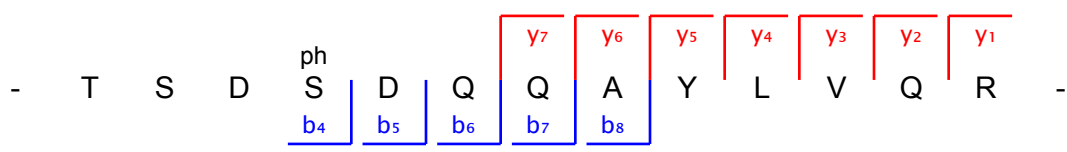
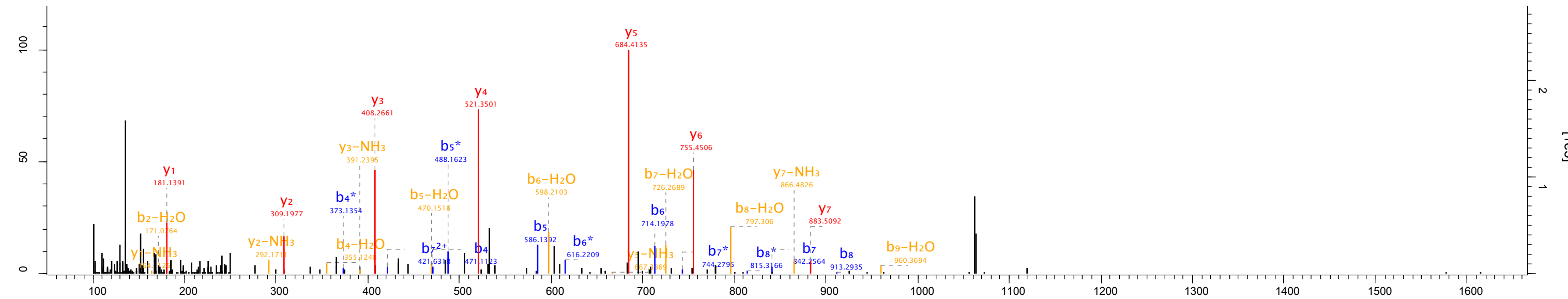


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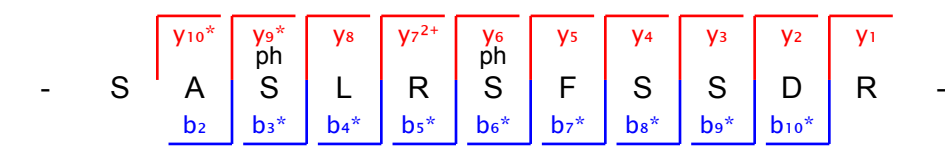
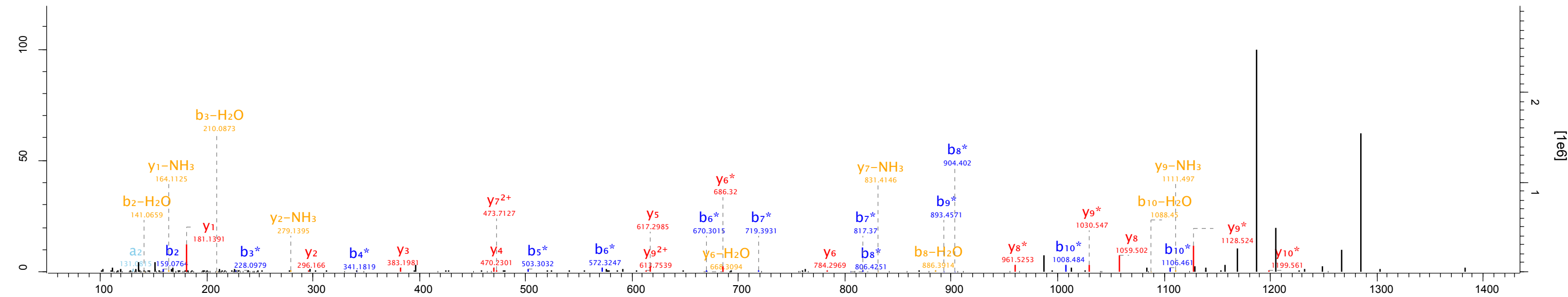
Fragmentation mapping (b and y ions):

- b ions (blue boxes):** b₂ (Y), b₃ (Y), b₄ (S), b₅ (P), b₆ (Y), b₇ (S)
- y ions (red boxes):** y₂₄^{*} (Y), y₂₃^{*} (S), y₂₂ (P), y₂₀^{*} (S), y₁₉ (V), y₁₈ (S), y₁₇ (G), y₁₆^{*} (S), y₁₅^{*} (G), y₁₄ (S), y₁₃²⁺ (T)

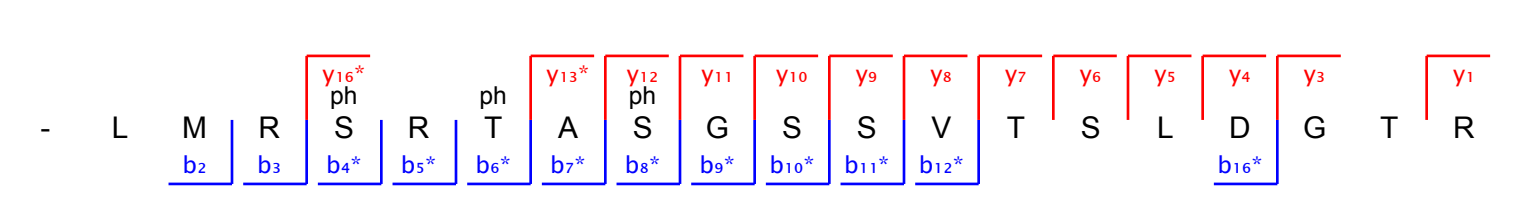
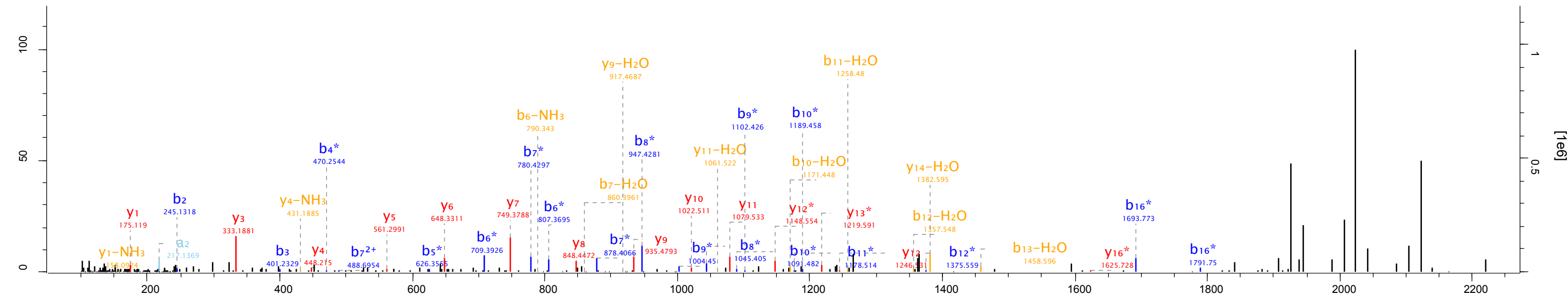
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 Scan: 8597 Method: FTMS; HCD Score: 100.21 m/z: 692.79 Gene names: ANK3

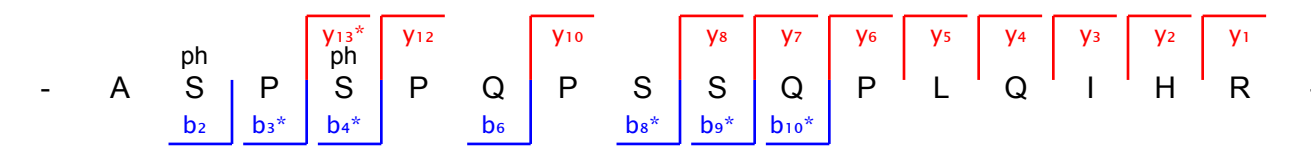
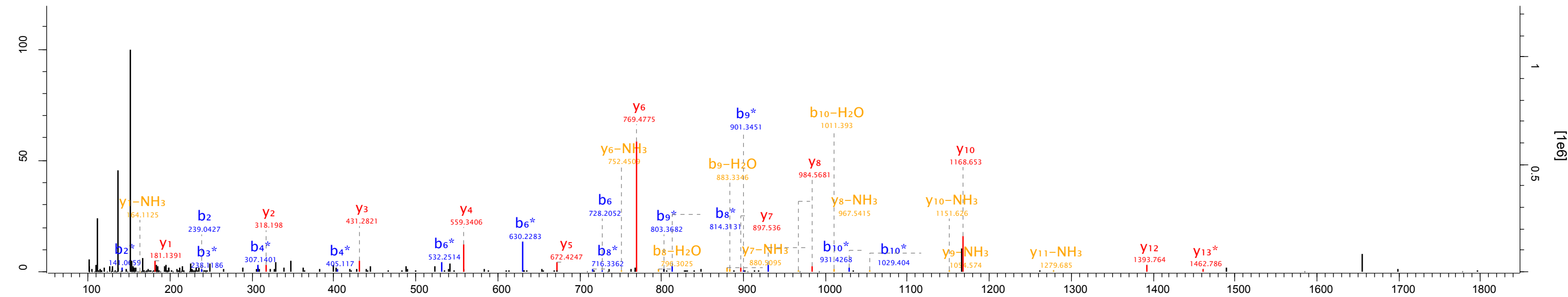


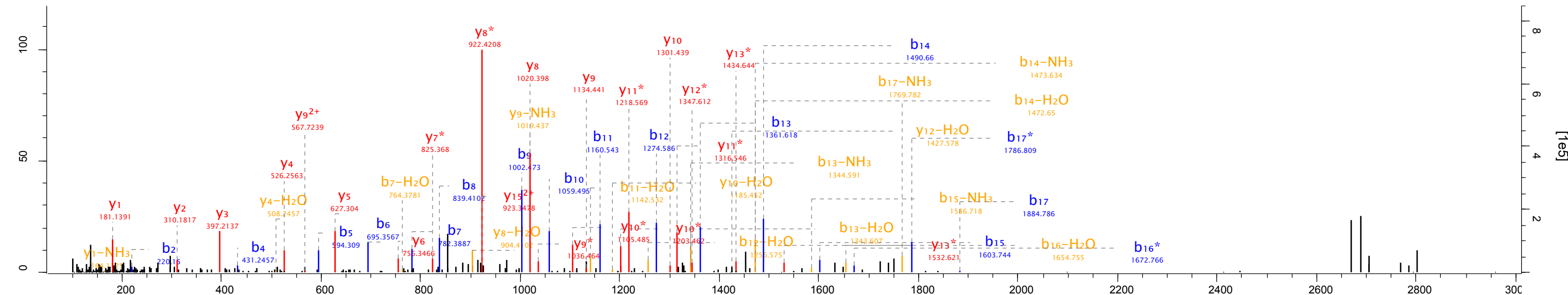
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Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 8797 Method FTMS; HCD Score 83.87 m/z 632.62 Gene names EML4





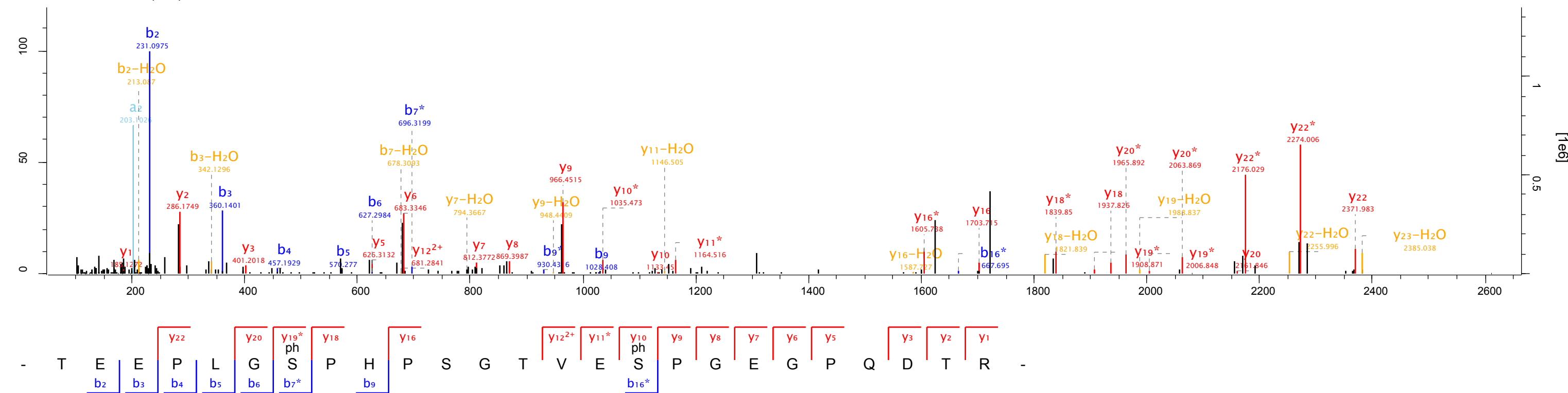
- R G P N Y T S G Y G T N S E L S N P S E T E S E R -

b₂
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃
b₁₄
b₁₅
b₁₆^{*}
b₁₇

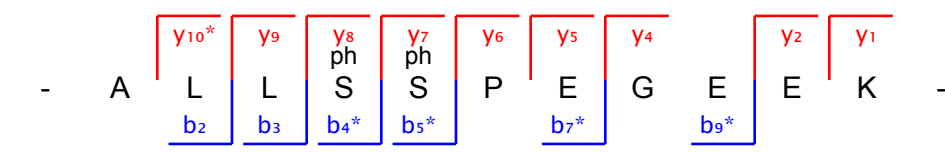
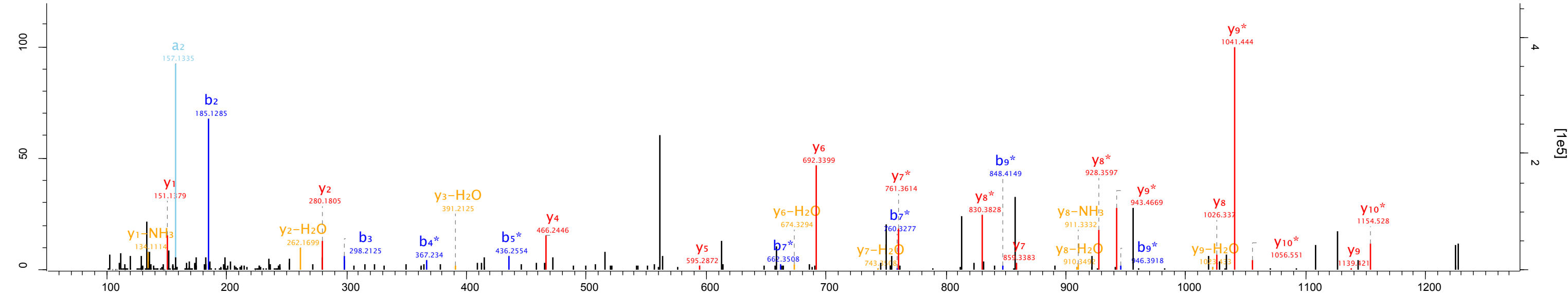
y₁₅²⁺
y₁₃^{*}
y₁₂^{*}
y₁₁^{*}
y₁₀
ph
y₉
y₈
y₇^{*}
ph
y₆
y₅
y₄
y₃
y₂
y₁

Raw file
20171215_MaS_33SR_LMH_phospho2_03

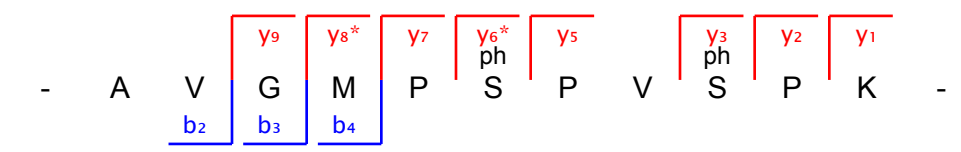
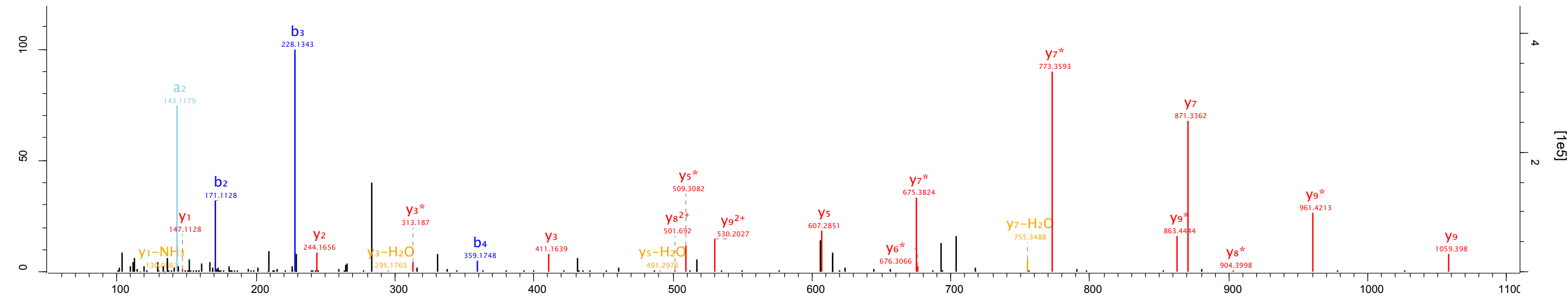
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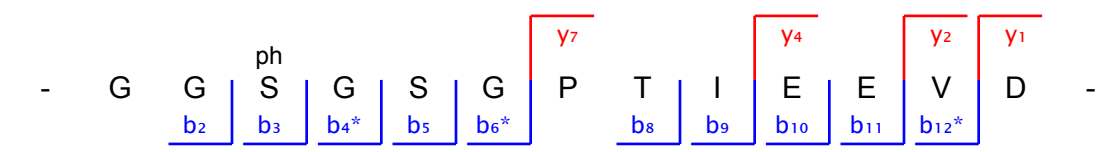
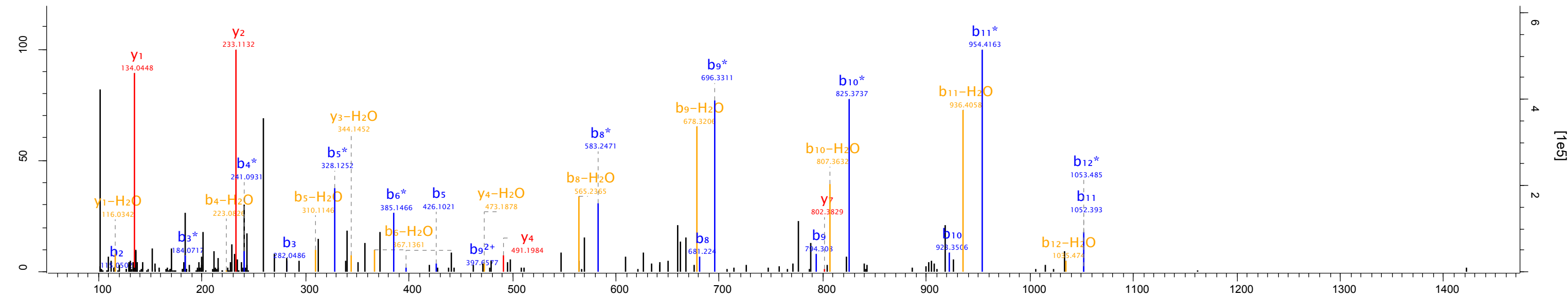
20171215_MaS_33SR_LMH_phospho2_03 9577 FTMS; HCD 108.66 662.27 MYCBP2



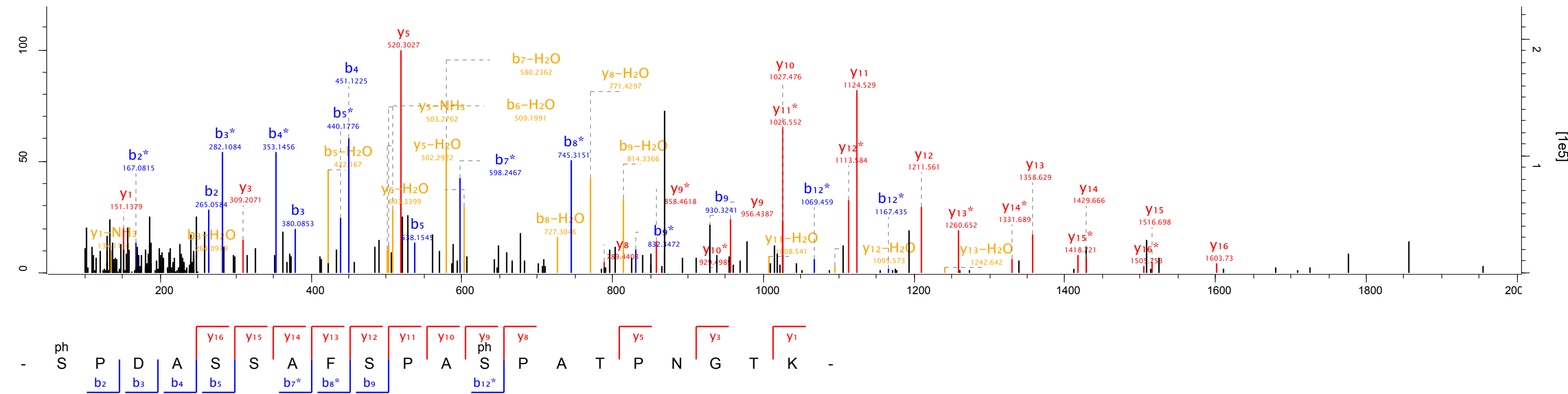
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 Scan: 9817 Method: FTMS; HCD Score: 90.73 m/z: 615.26 Gene names: AFF4



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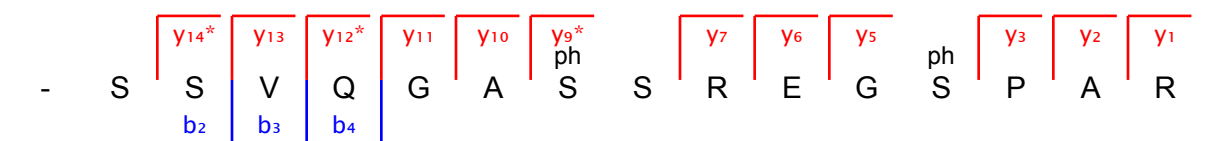
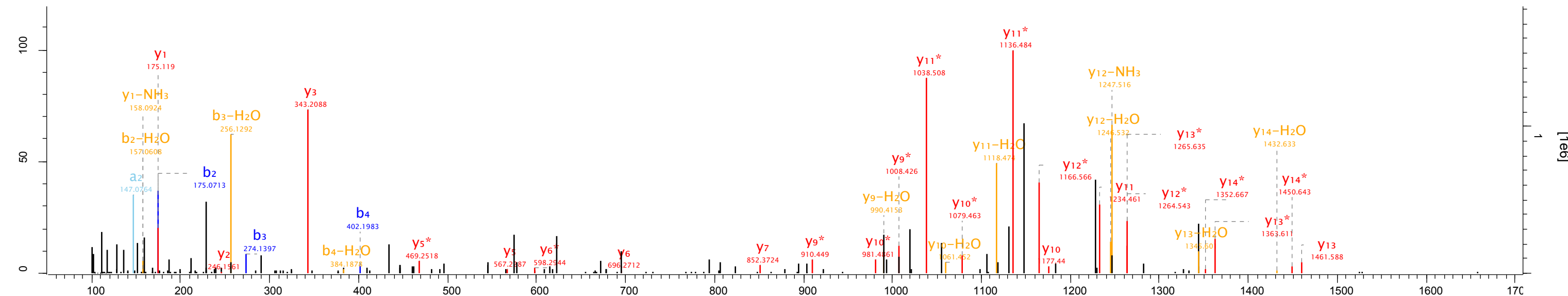


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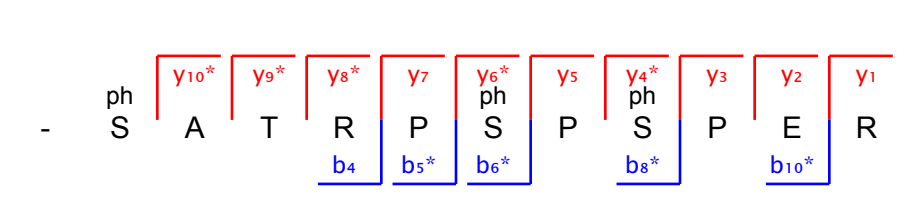
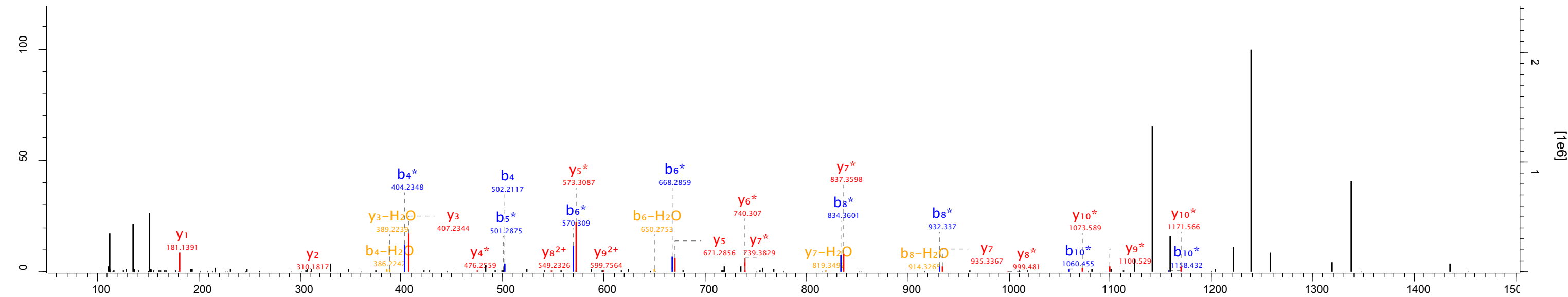


Raw file
20171215_MaS_33SR_LMH_phospho2_04

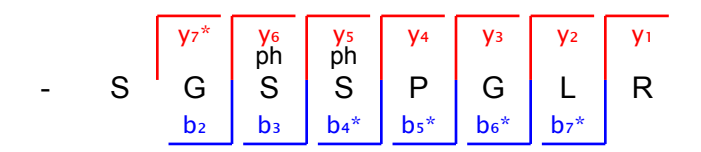
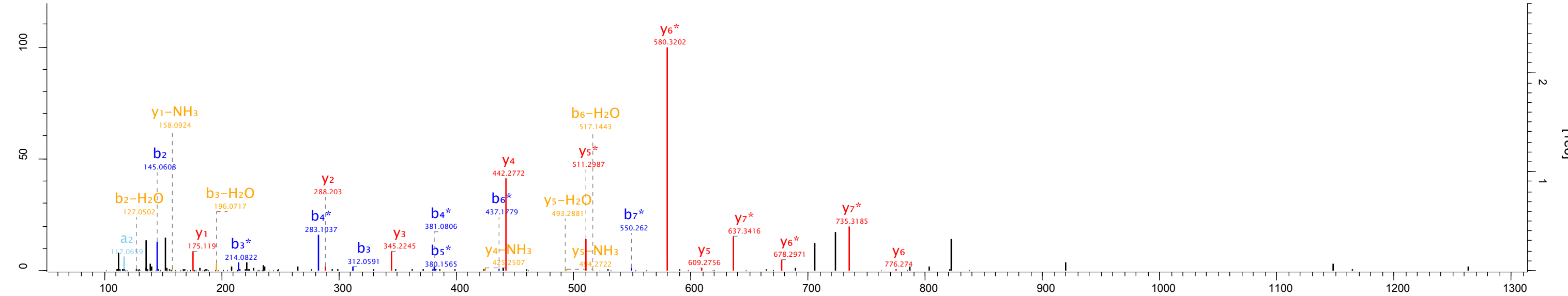
Scan 2397 Method FTMS; HCD Score 135.21 m/z 545.89 Gene names BAG3



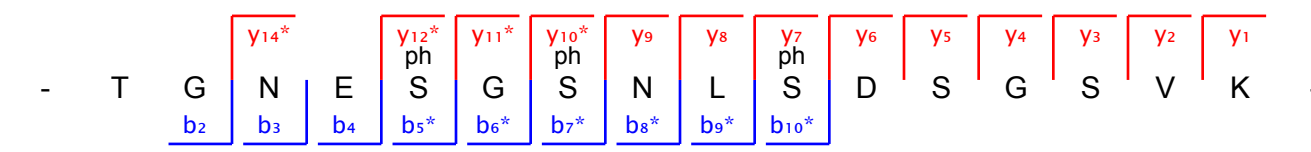
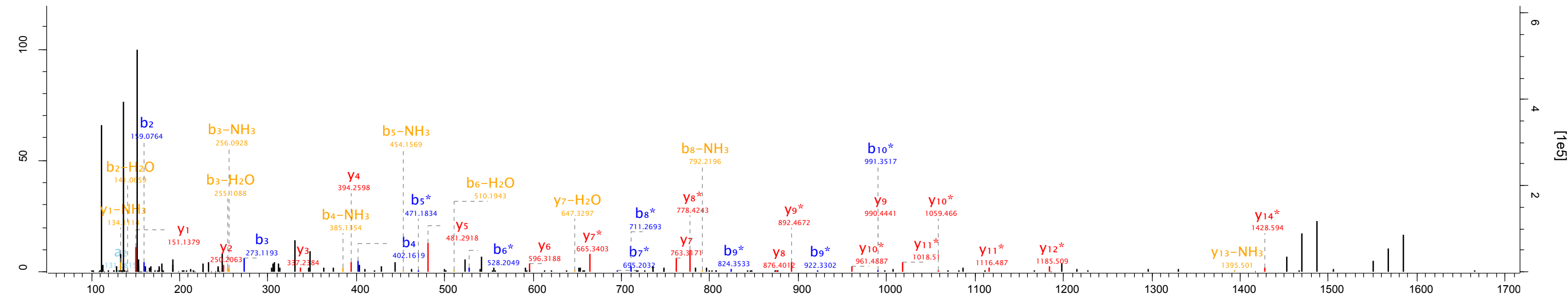
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 20171215_MaS_33SR_LMH_phospho2_04
 Scan 2597 Method FTMS; HCD Score 100.07 m/z 718.77 Gene names SRRM2



20171215_MaS_33SR_LMH_phospho2_04 3307 FTMS; HCD 136.5 460.67 SRRM2

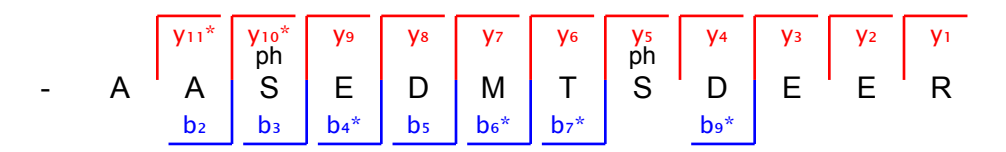
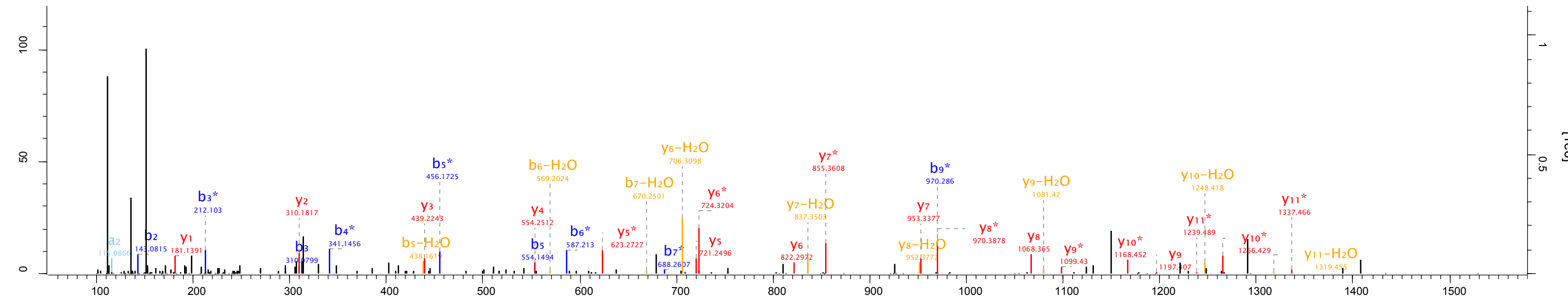


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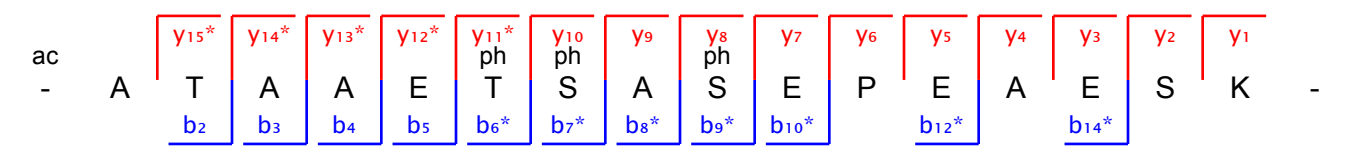
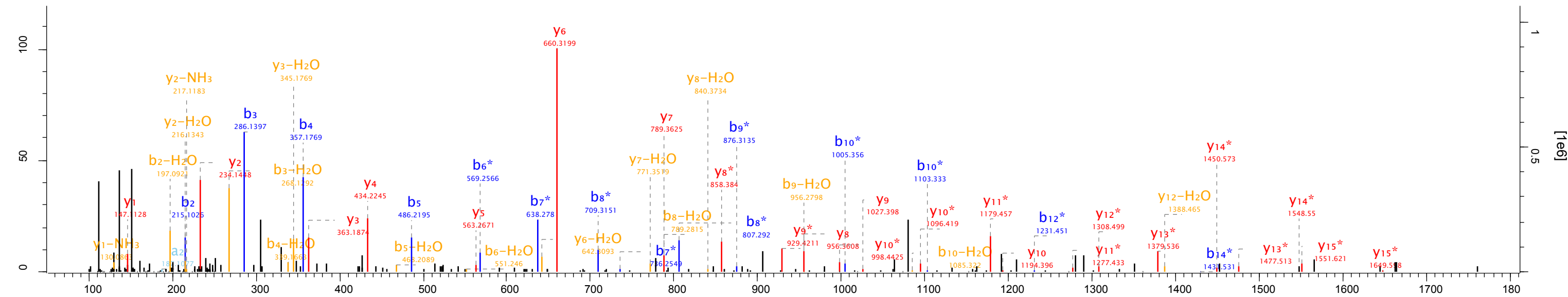


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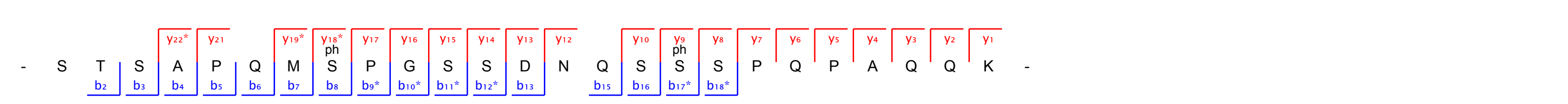
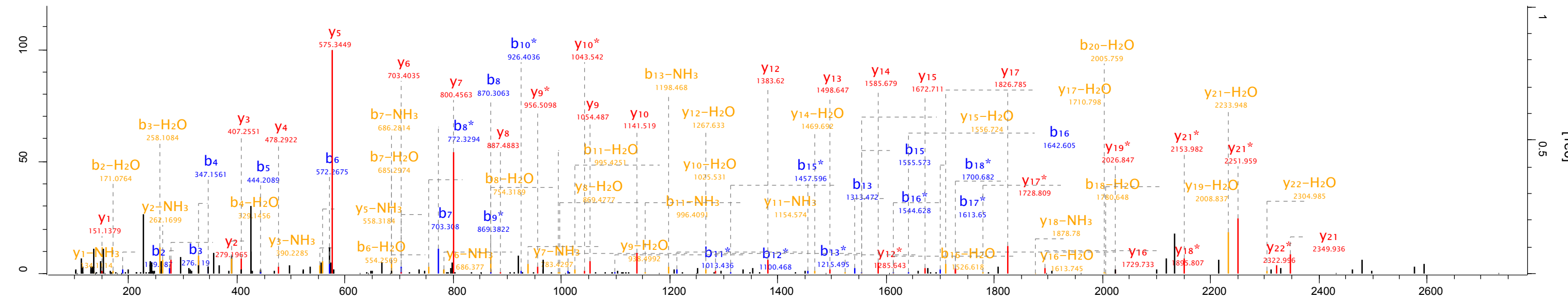
Scan Method Score m/z Gene names
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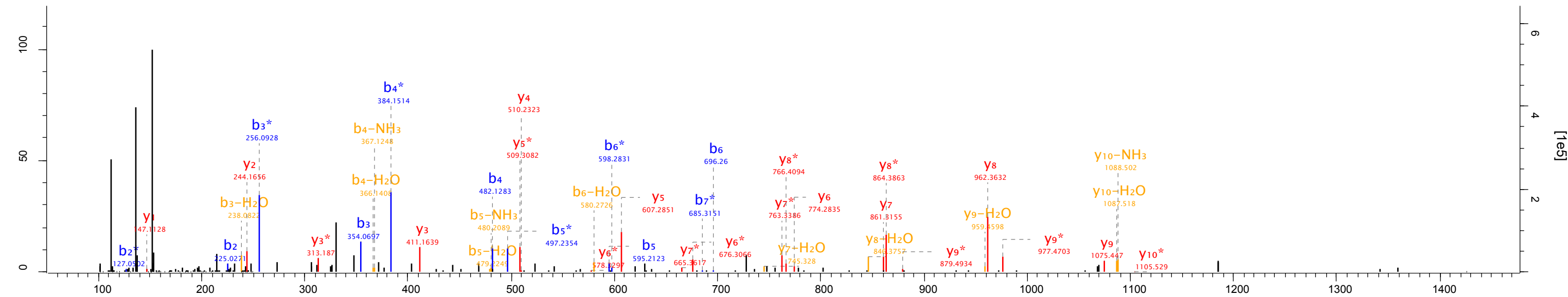
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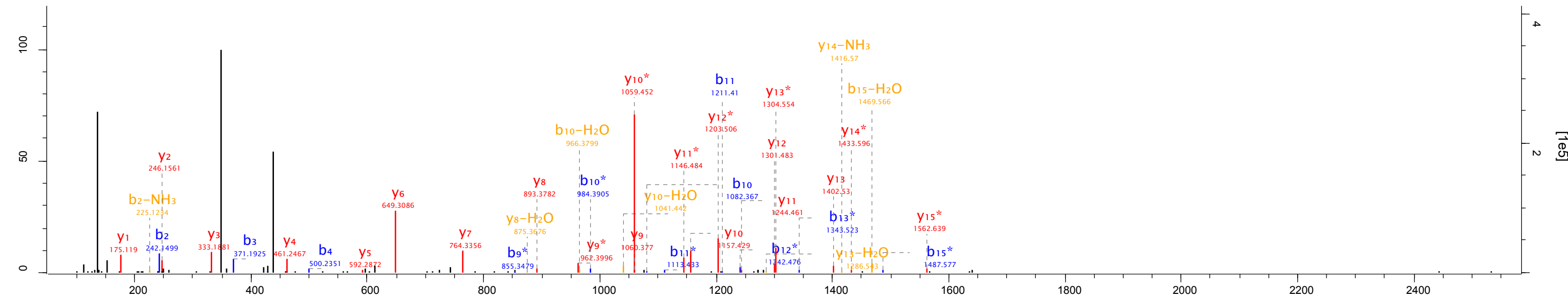


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 Scan: 4437 Method: FTMS; HCD Score: 221.86 m/z: 1349.04 Gene names: UBAP2L



Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5587 Method FTMS; HCD Score 124.1 m/z 778.79 Gene names PPIP5K2



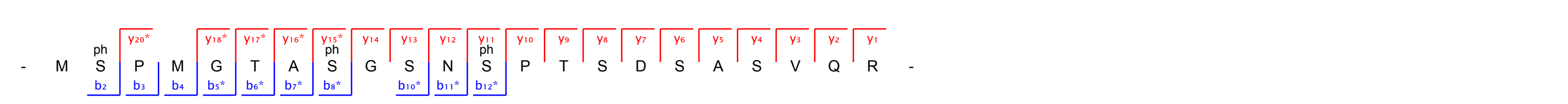
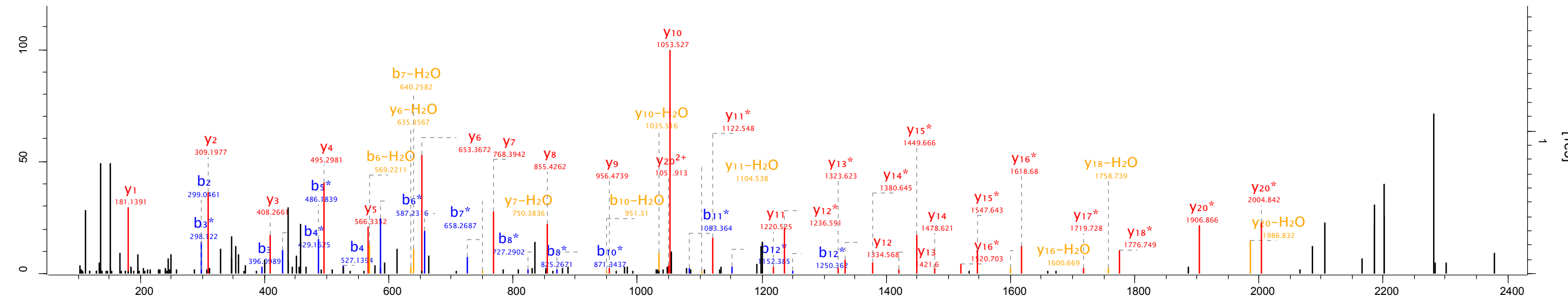


- L Q E E G G G ph S D E E E T G S P S E D G M Q S A R -

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

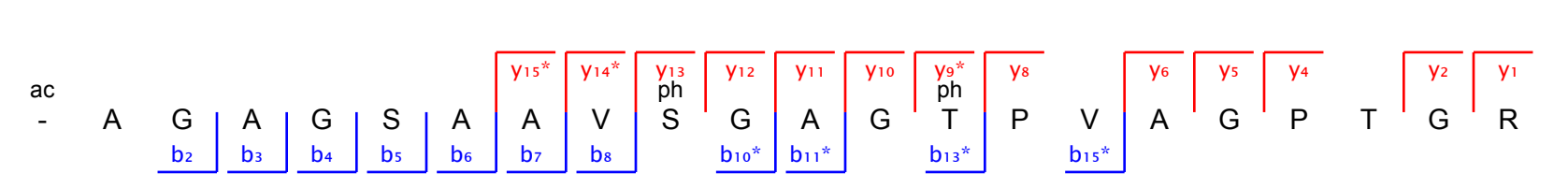
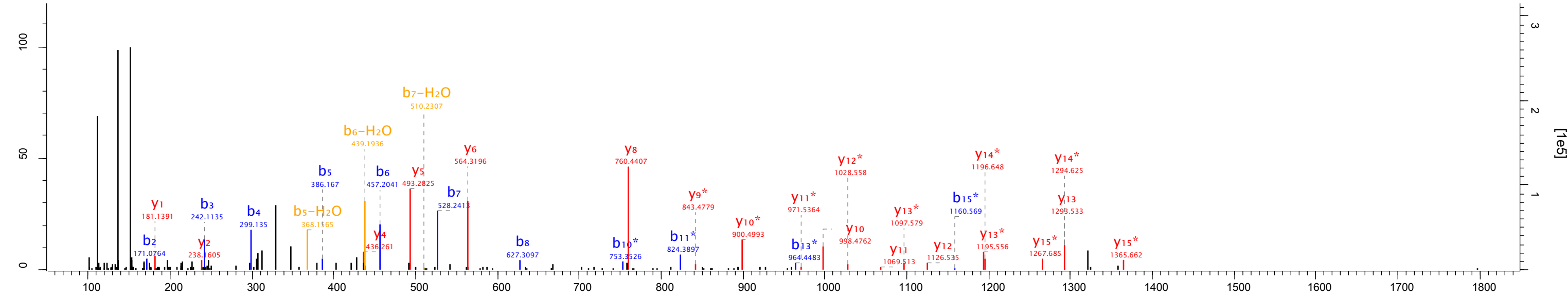
- Q: b₂, b₃, b₄
- E: b₉^{*}, b₁₀
- E: b₁₁, b₁₂^{*}, b₁₃^{*}
- T: b₁₅^{*}
- S: b₉^{*}, b₁₀, b₁₁, b₁₂^{*}, b₁₃^{*}, b₁₅^{*}
- P: y₁₀
- S: y₉, y_{ph}
- E: y₈
- D: y₇
- G: y₆
- M: y₅
- Q: y₄
- S: y₃
- A: y₂
- R: y₁

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 Scan: 7027 Method: FTMS; HCD Score: 144.55 m/z: 1200.93 Gene names: ZFAND5

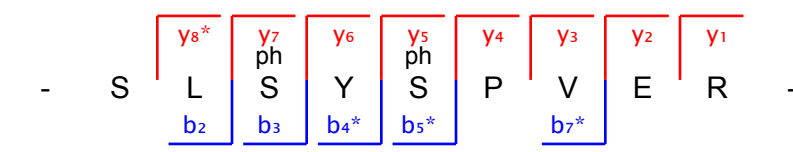
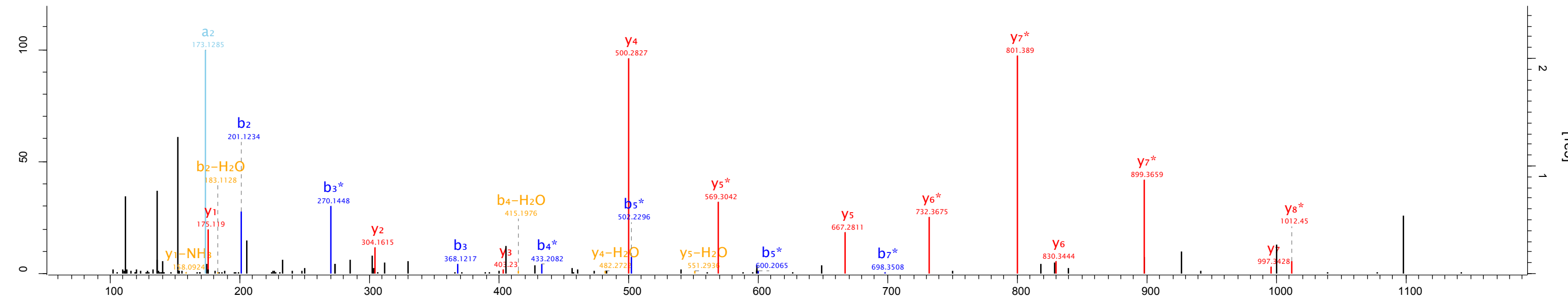


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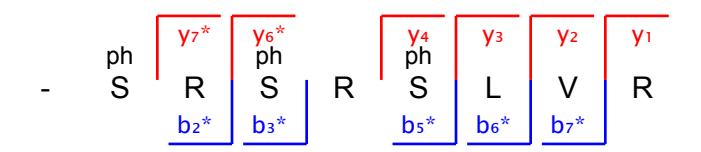
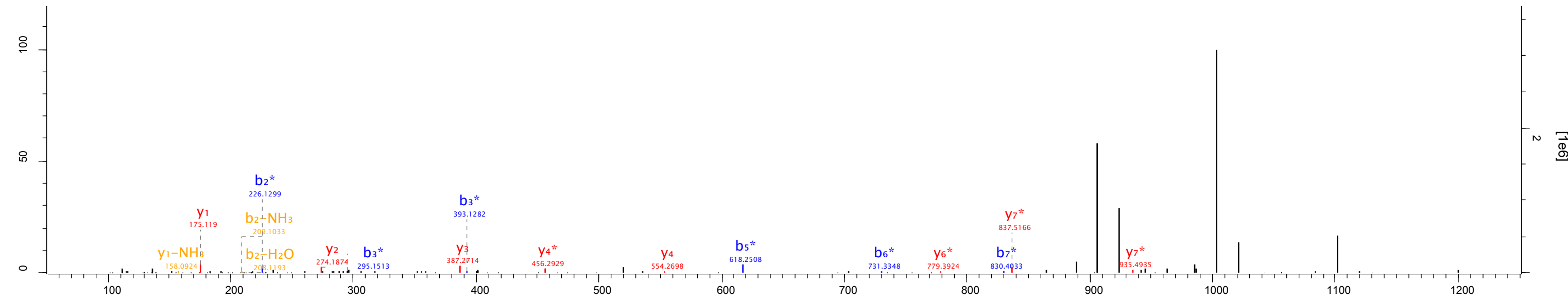
20171215_MaS_33SR_LMH_phospho2_04



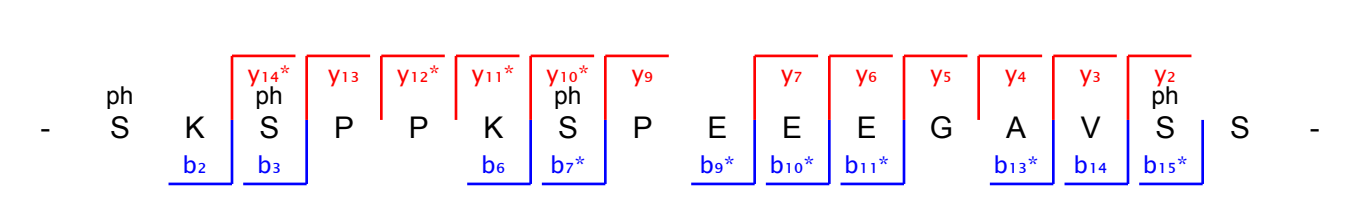
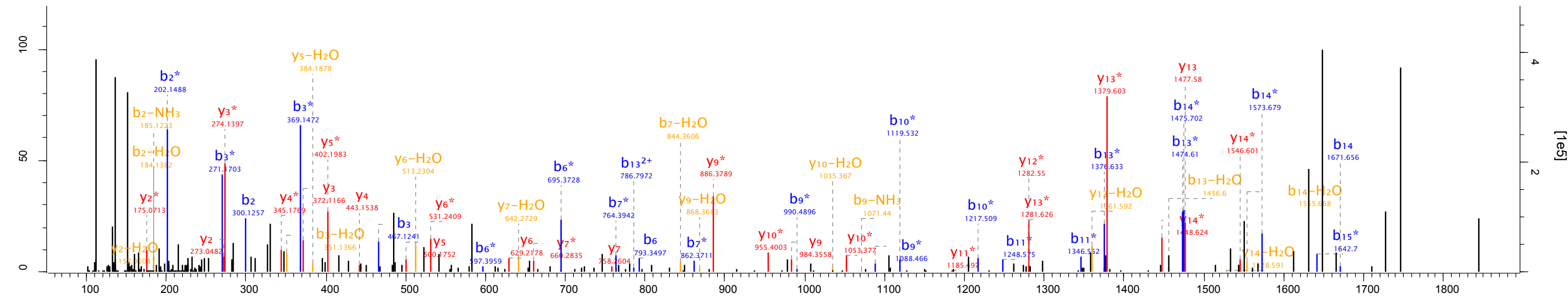
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 Scan: 7887 Method: FTMS; HCD Score: 101.43 m/z: 599.23 Gene names: SRRM2



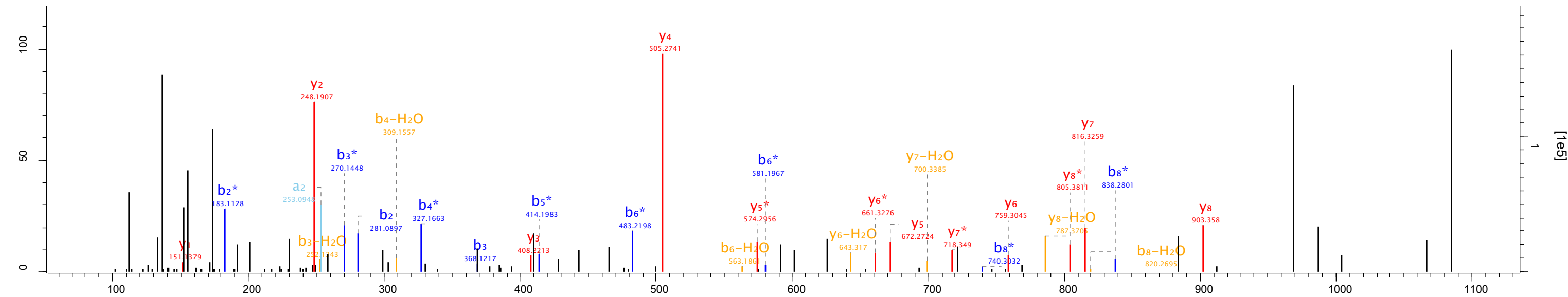
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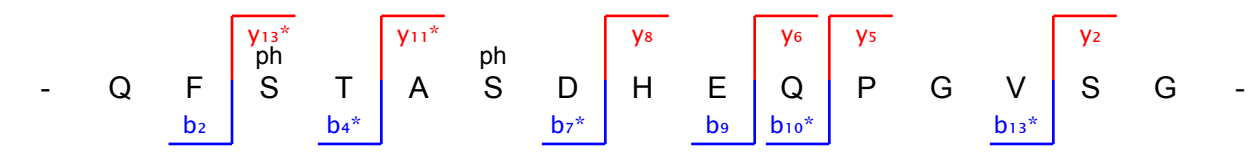
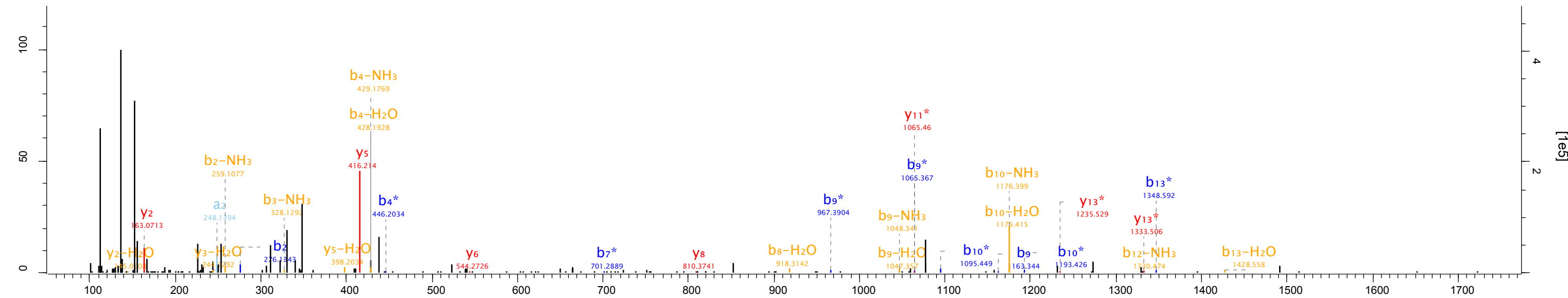
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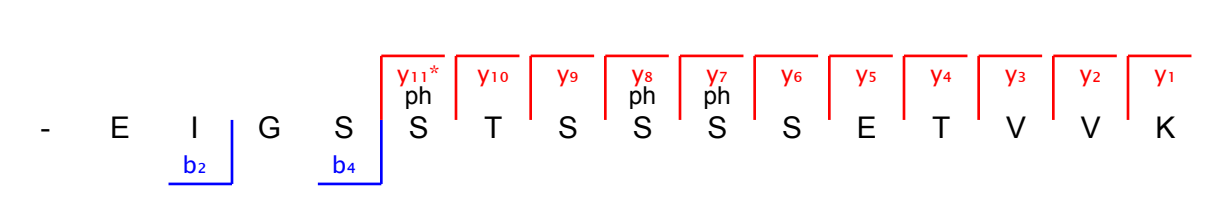
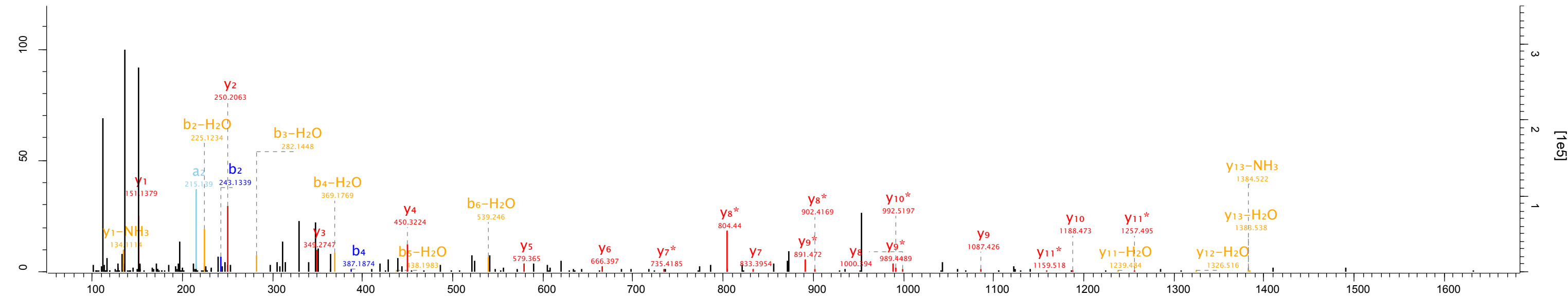
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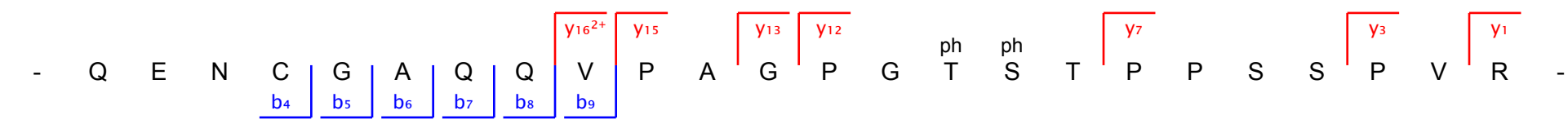
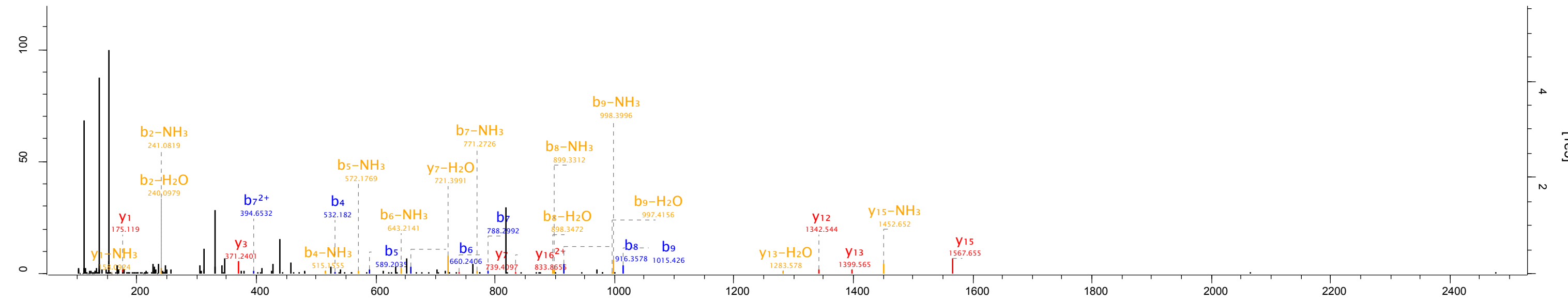
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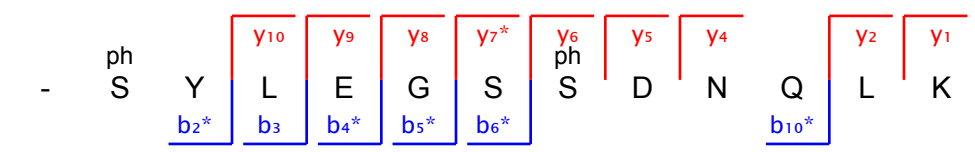
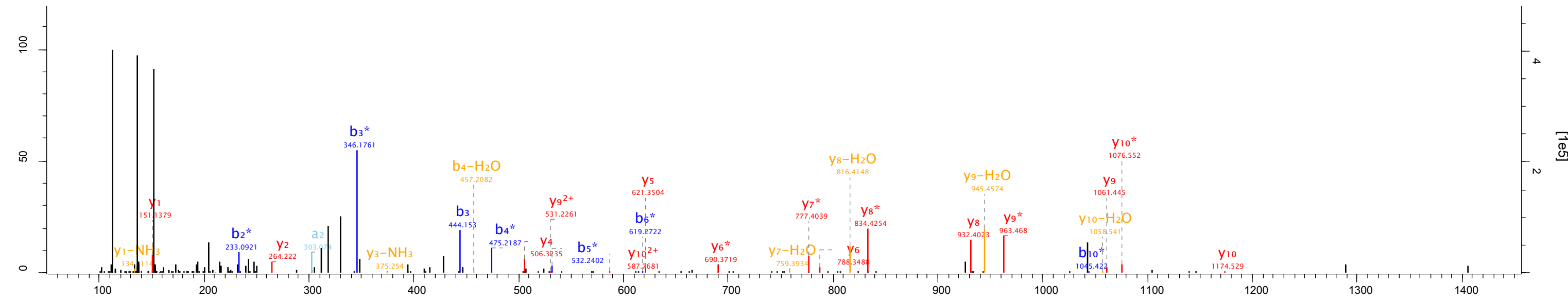
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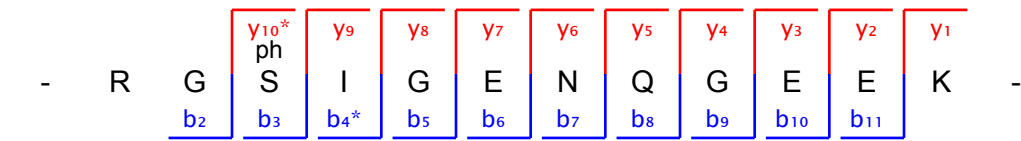
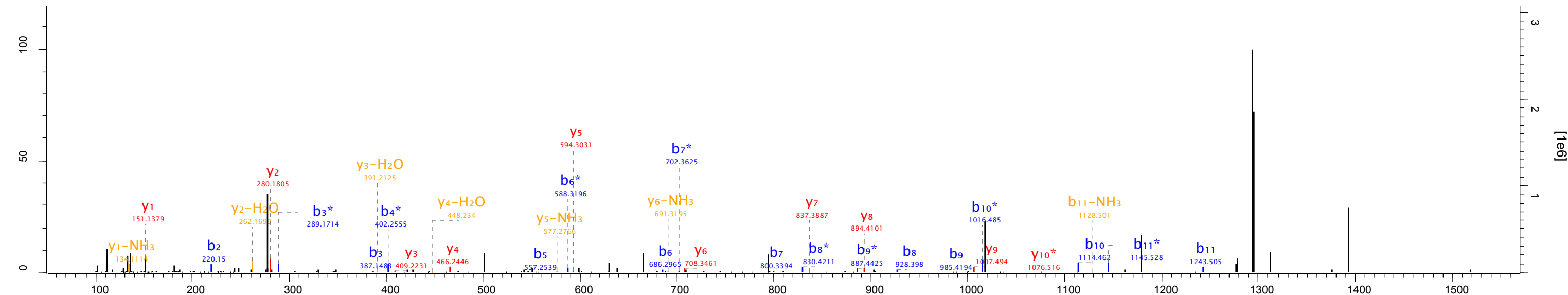


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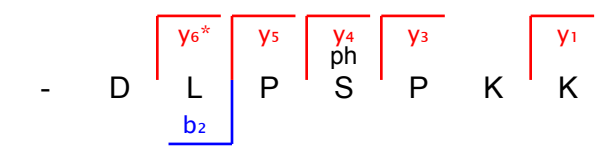
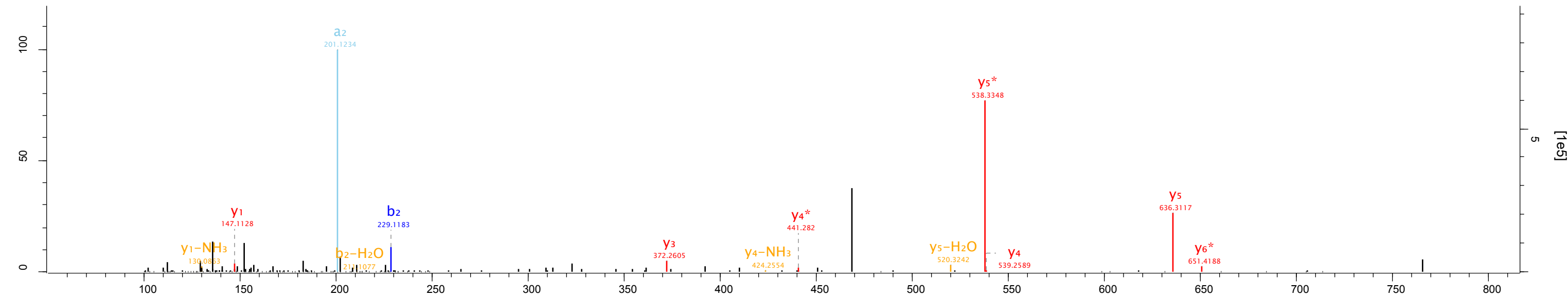


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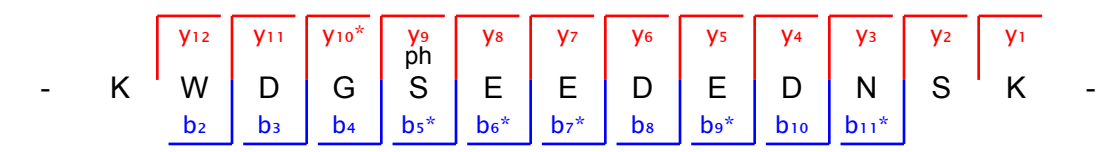
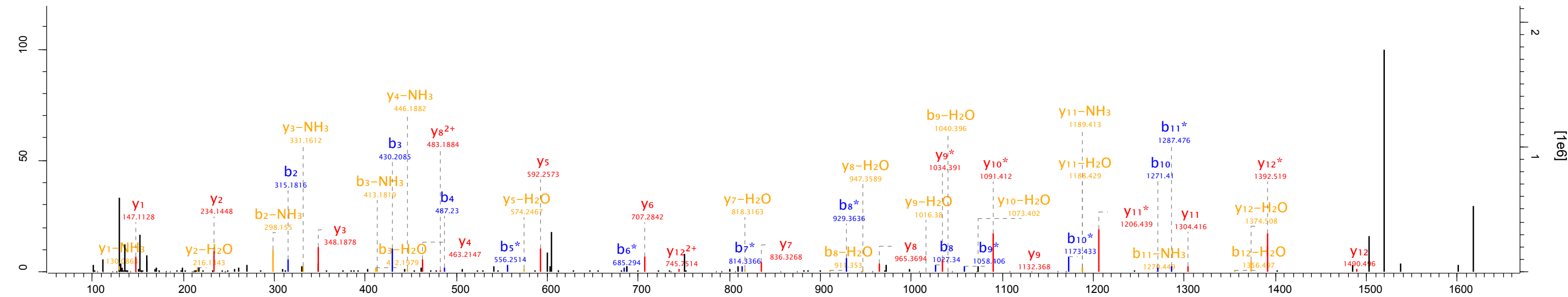


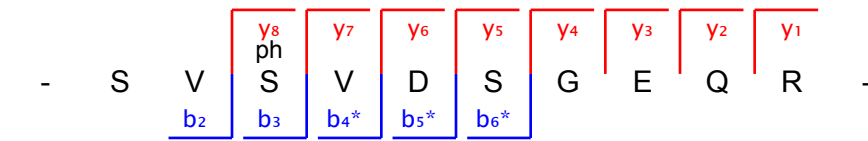
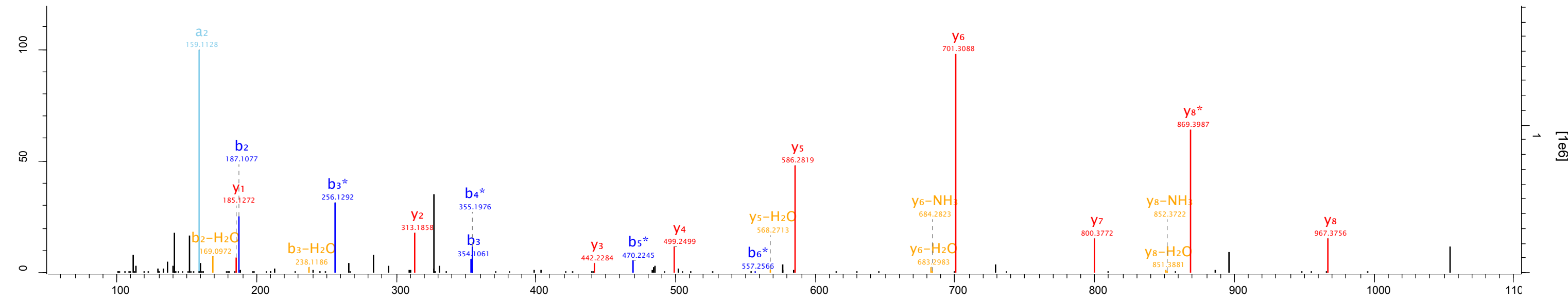


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 Scan 2817 Method FTMS; HCD Score 66.3 m/z 432.71 Gene names BBX

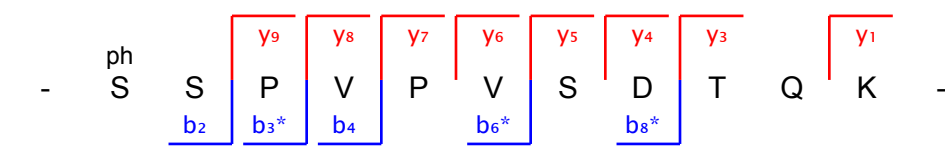
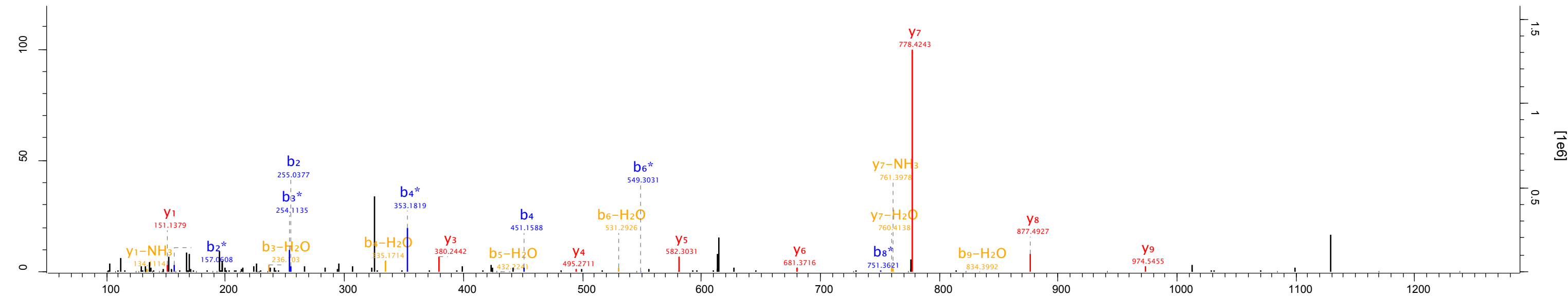


Raw file 20171215_MaS_33SR_LMH_phospho2_06 Scan 2867 Method FTMS; HCD Score 235.72 m/z 809.8 Gene names EIF5B





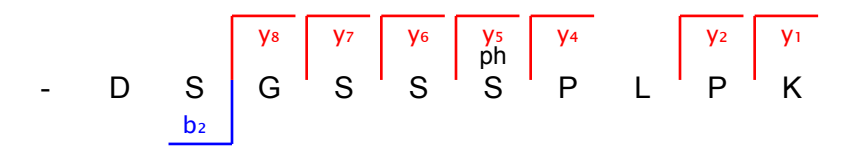
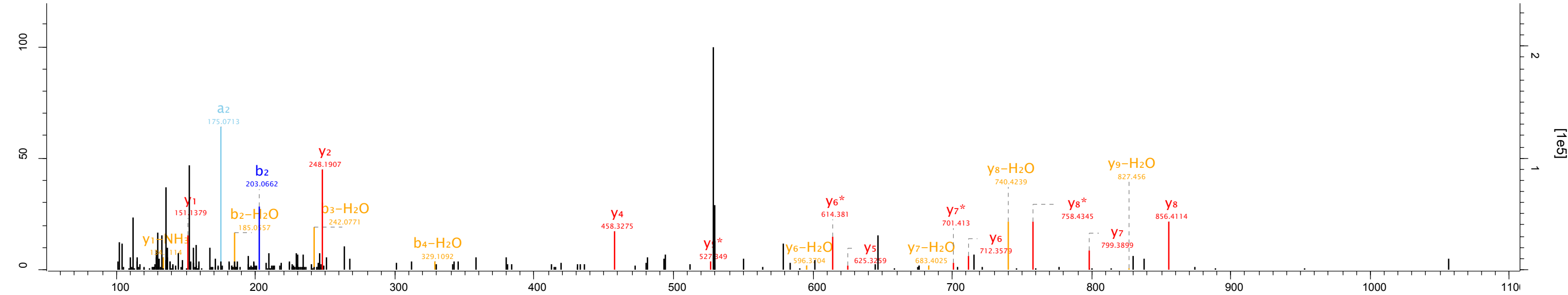
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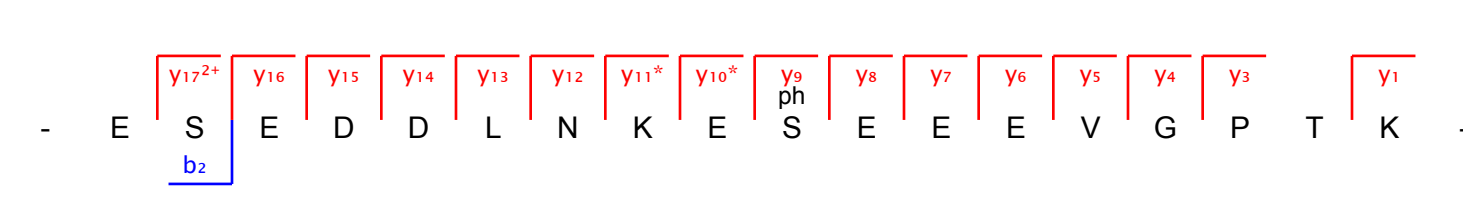
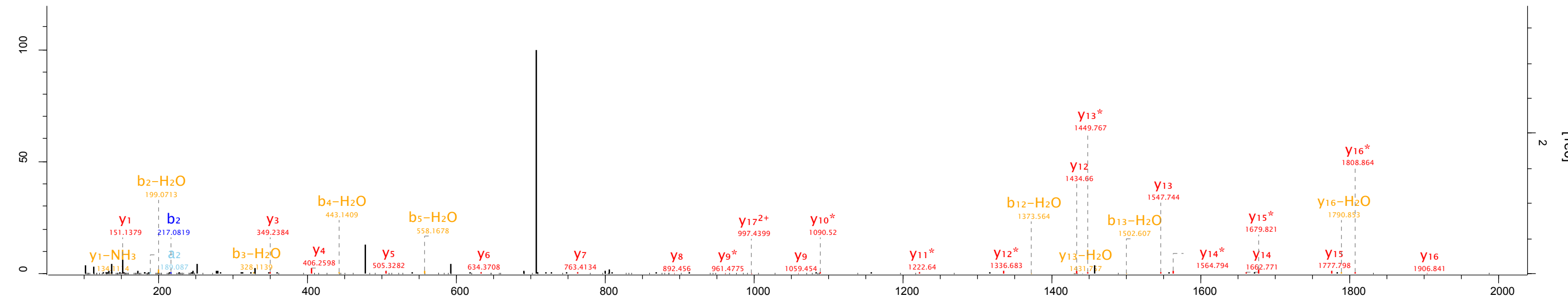
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20171215_MaS_33SR_LMH_phospho2_06

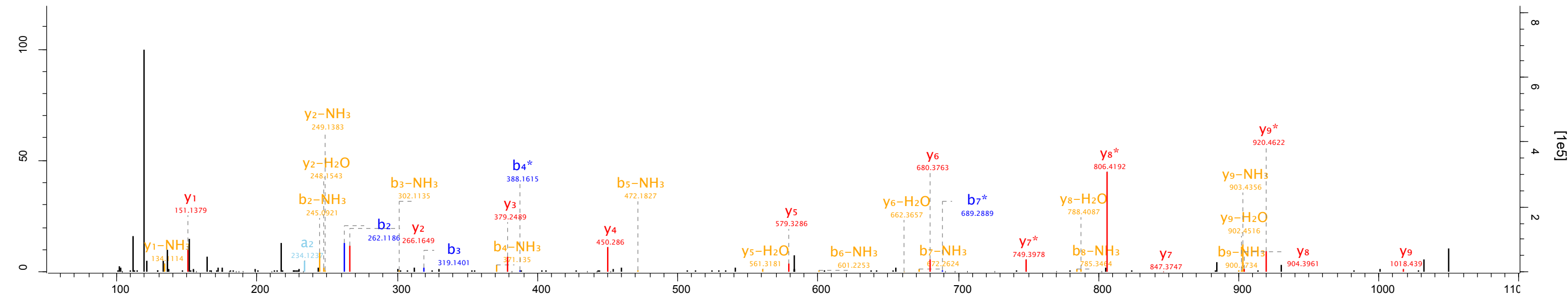
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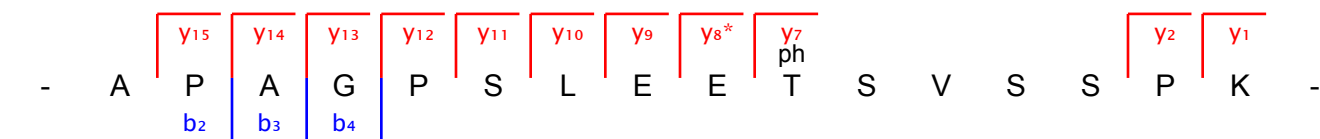
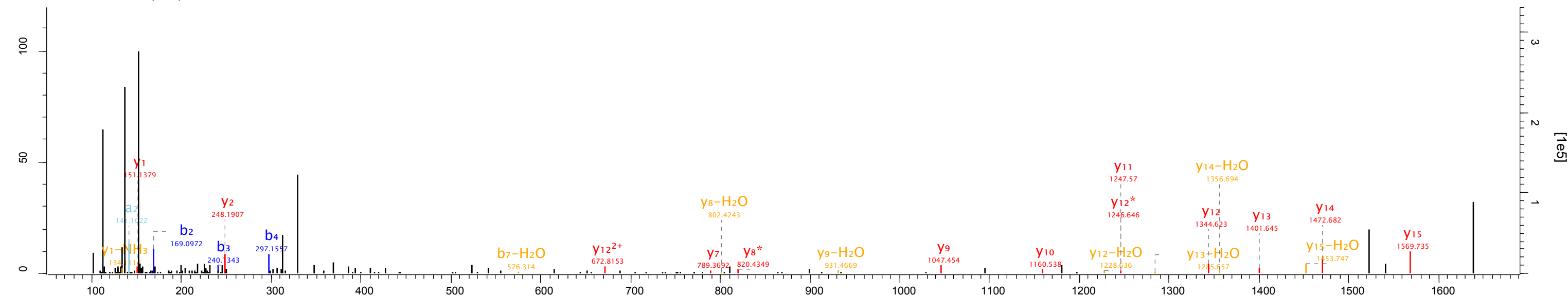


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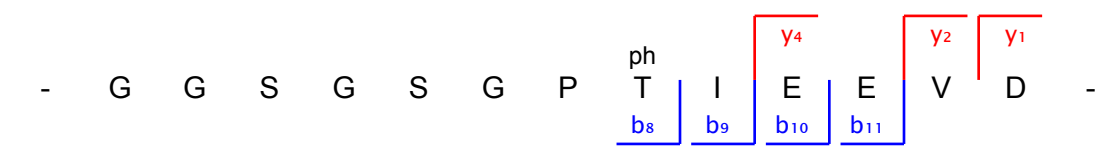
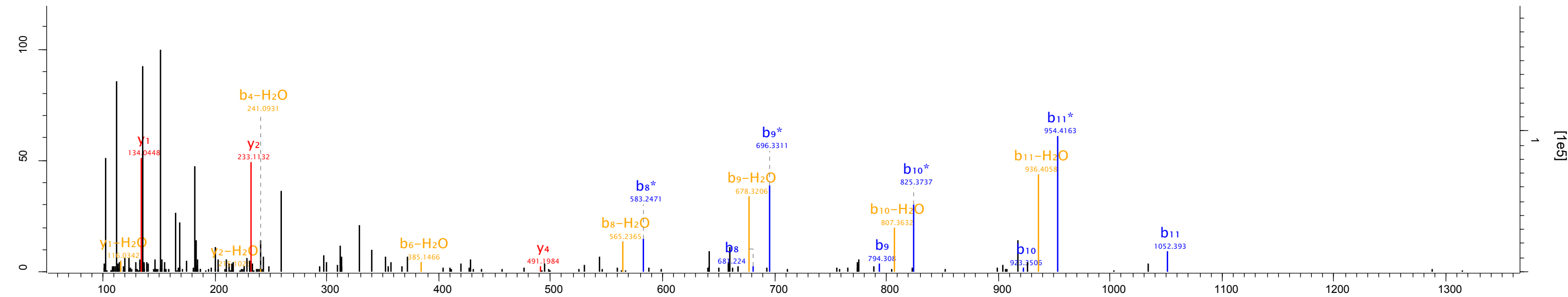


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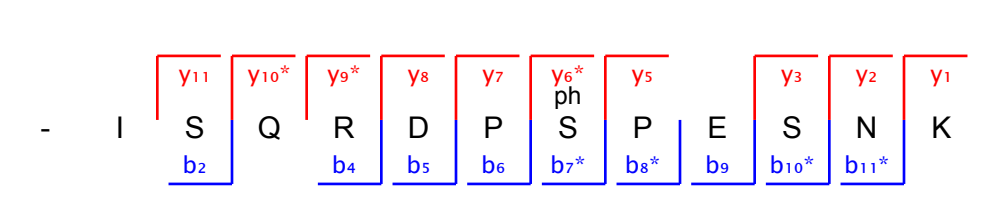
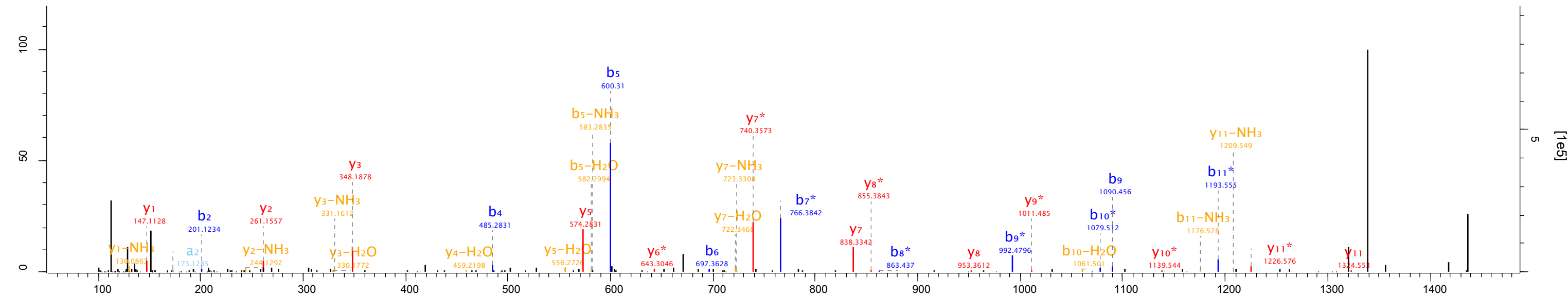




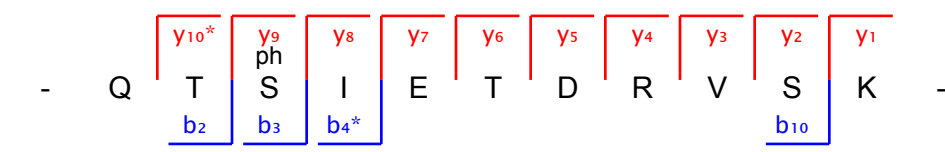
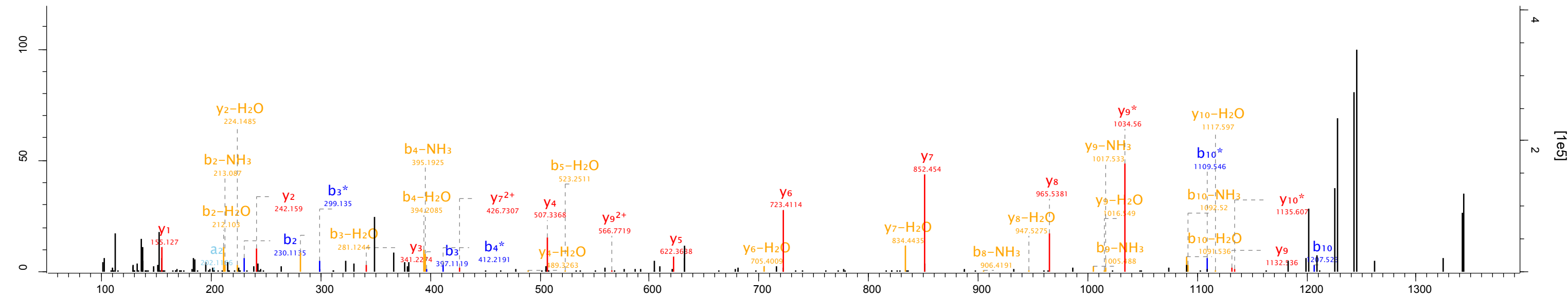
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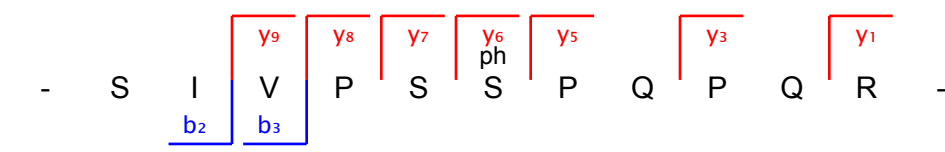
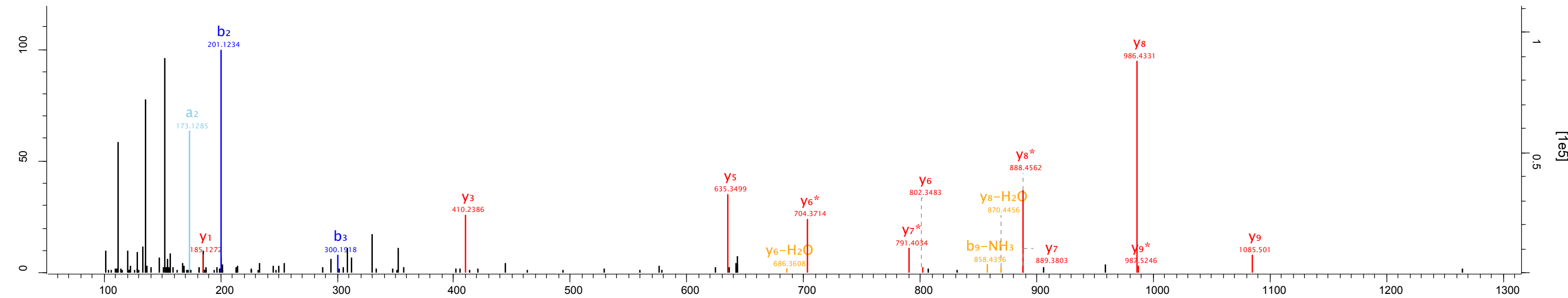
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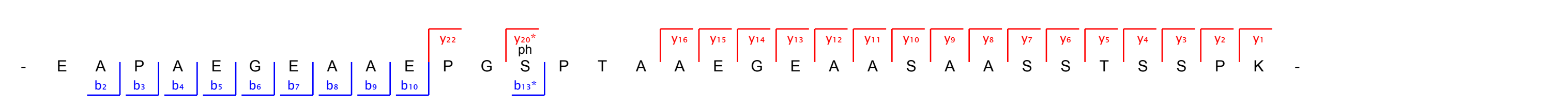
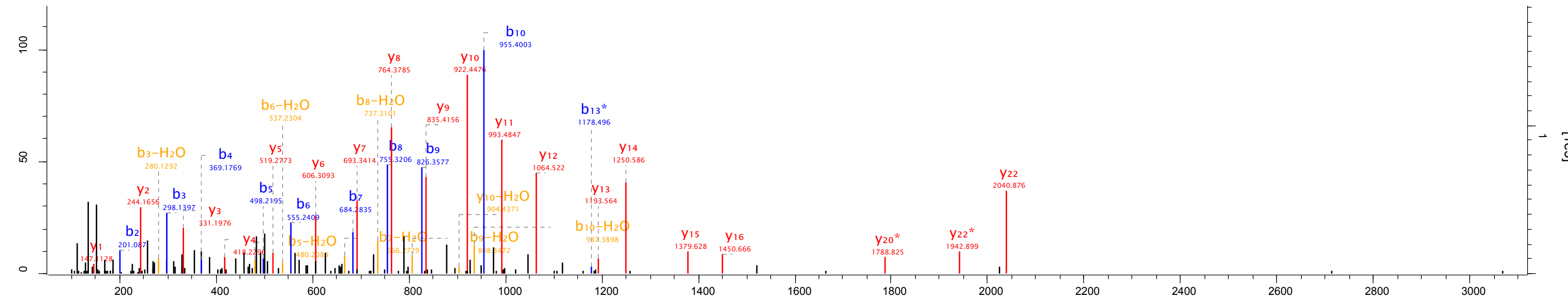
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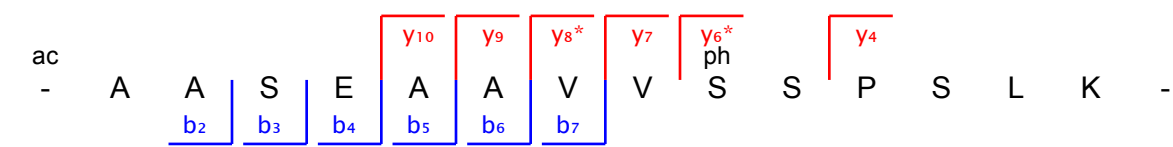
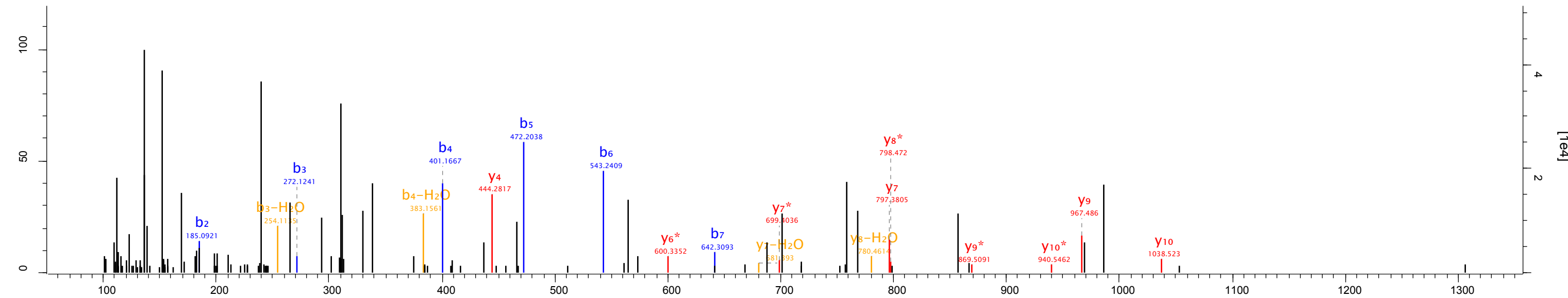
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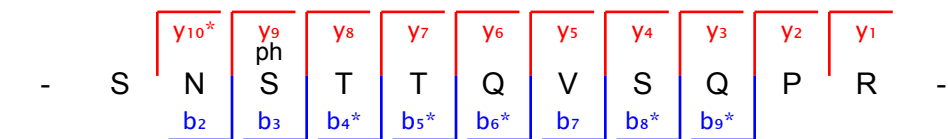
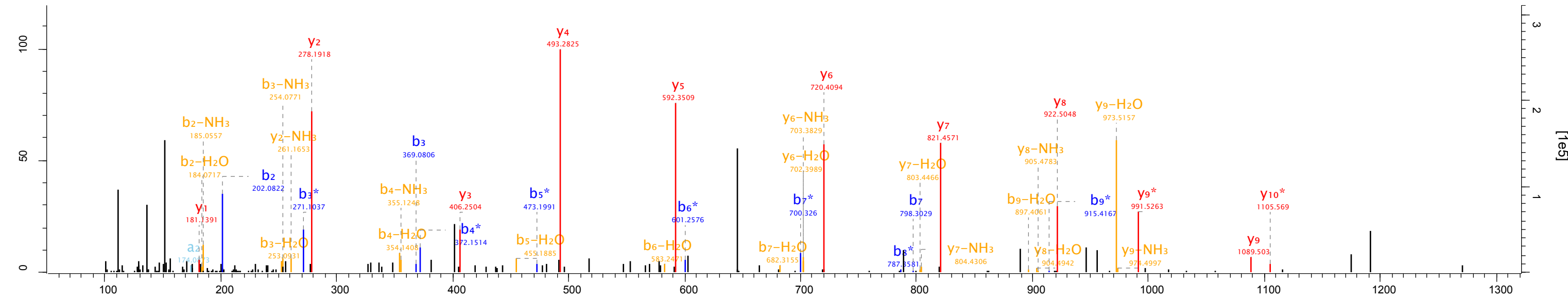


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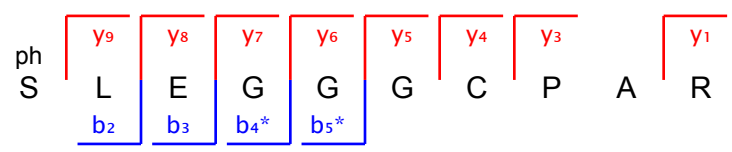
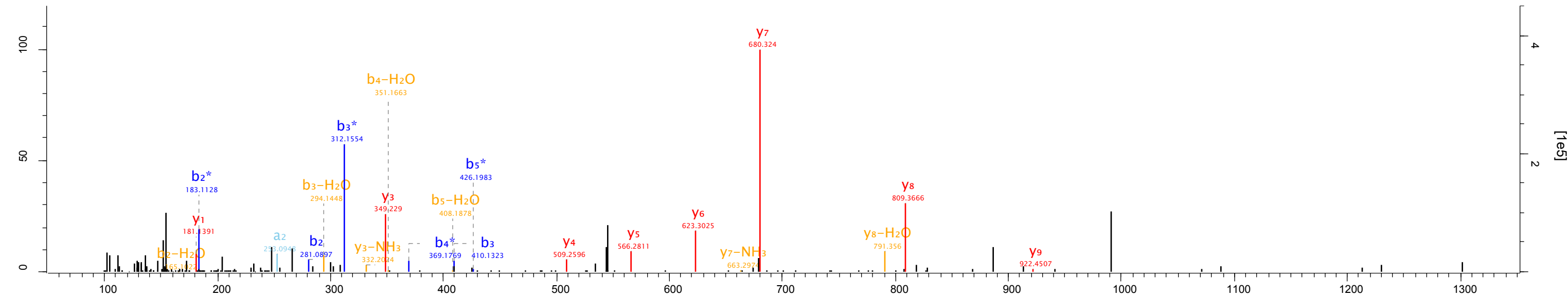


Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 10017 Method FTMS; HCD Score 46.34 m/z 719.85 Gene names TRUB1





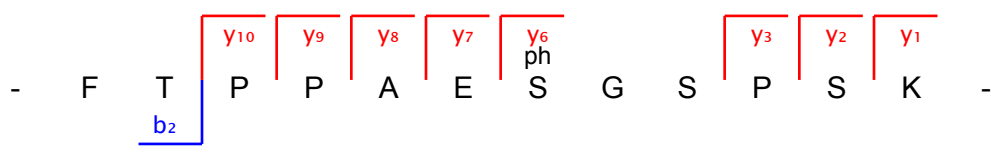
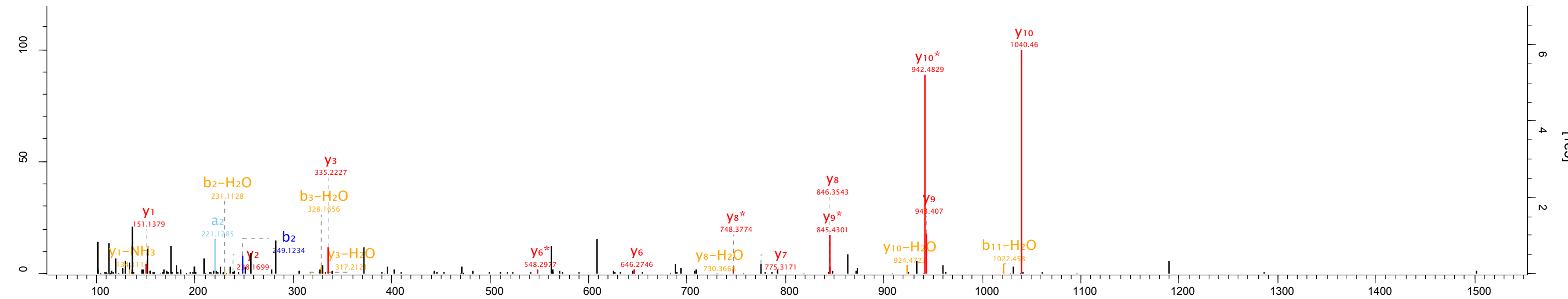
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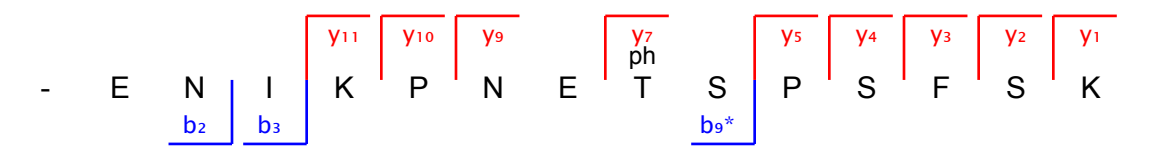
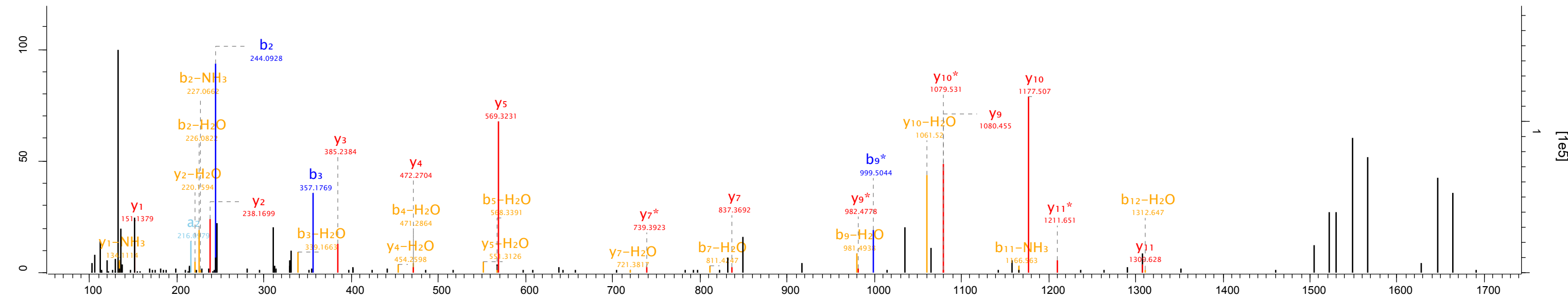
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20171215_MaS_33SR_LMH_phospho2_09

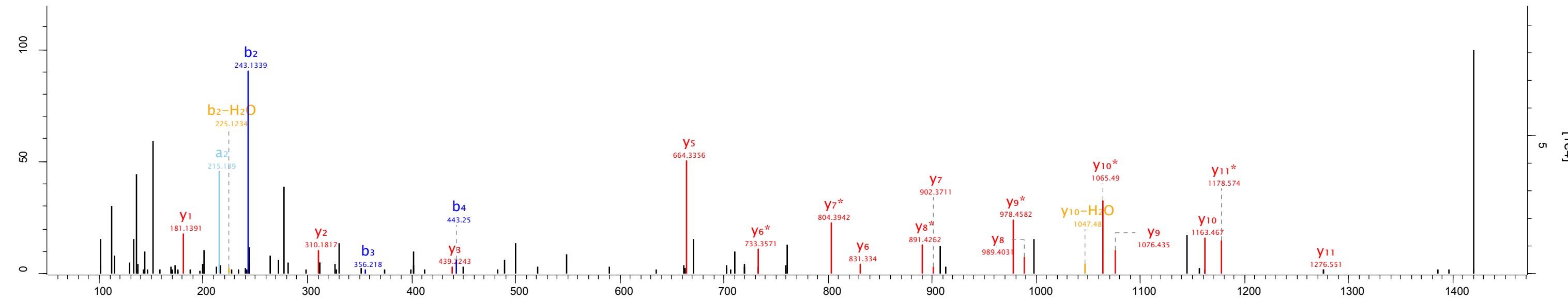
Scan	Method	Score	m/z	Gene names
4747	FTMS; HCD	46.89	644.79	RAPH1



Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 5067 Method FTMS; HCD Score 106.28 m/z 833.4 Gene names ATXN2



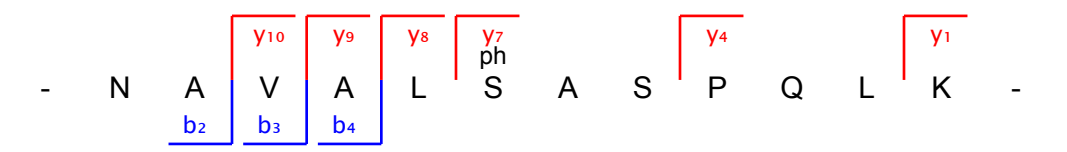
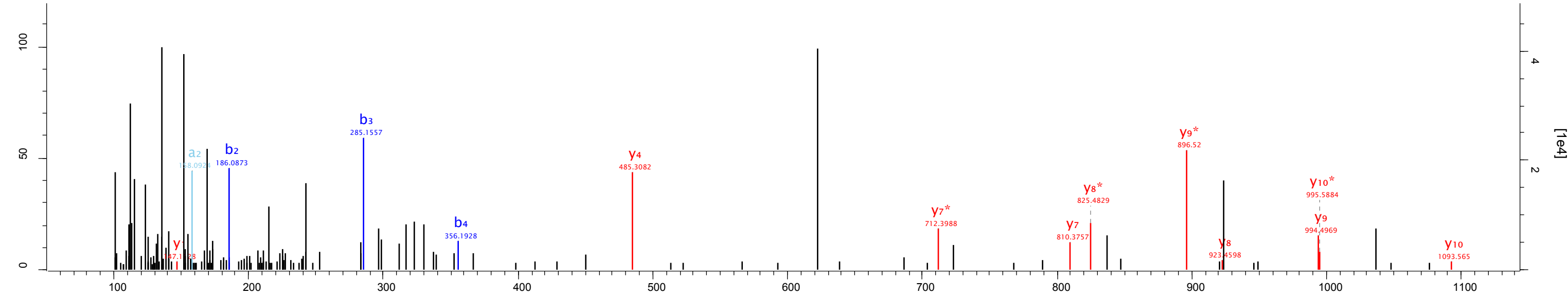
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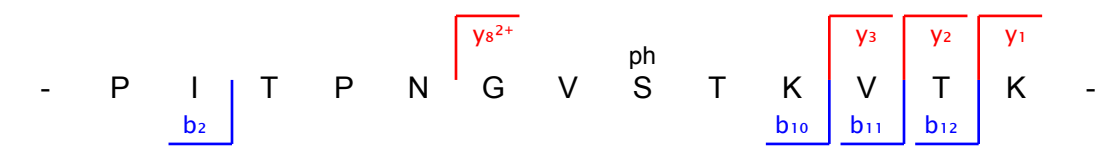
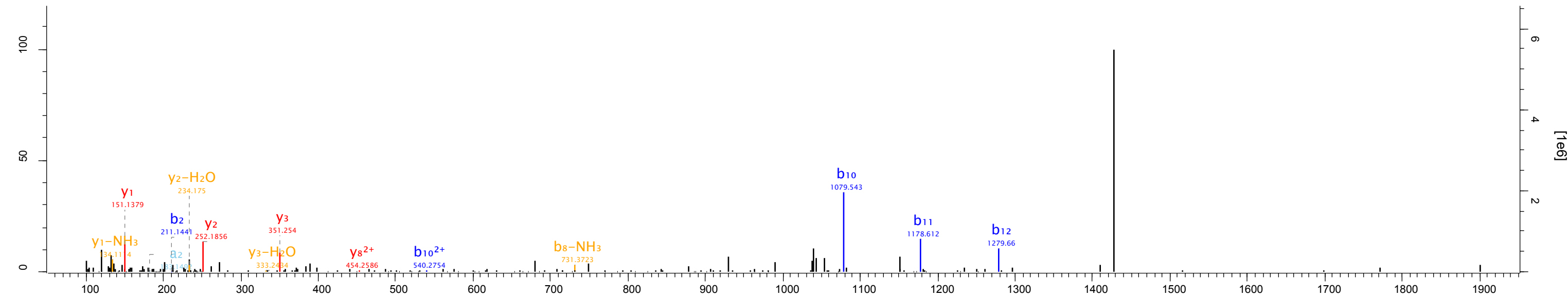
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20171215_MaS_33SR_LMH_phospho2_09

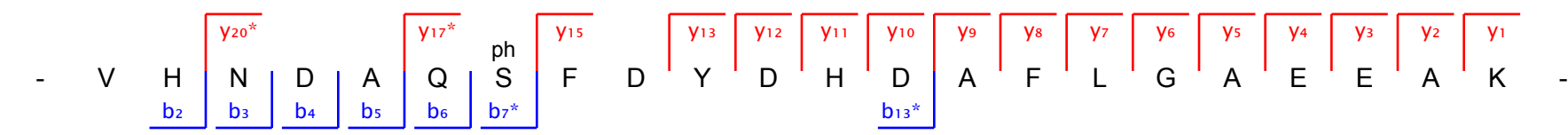
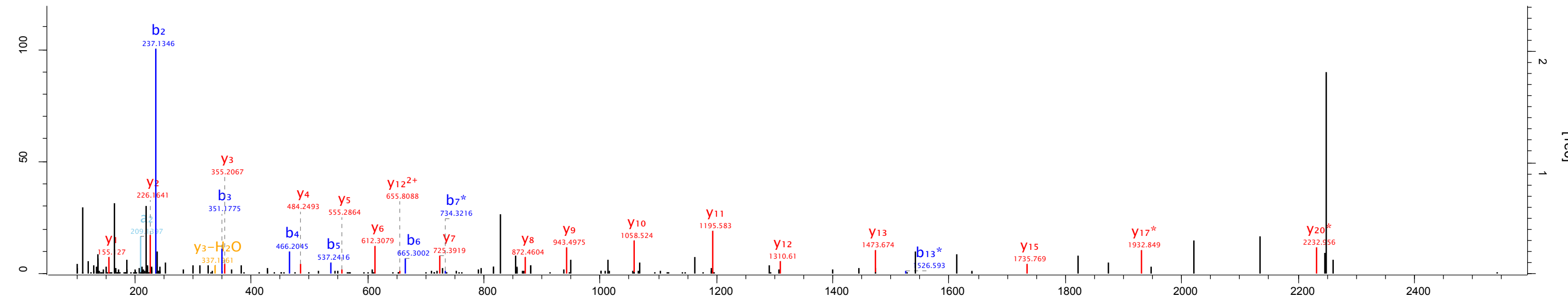
Scan	Method	Score	m/z	Gene names
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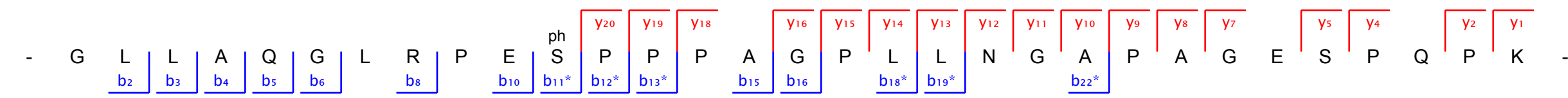
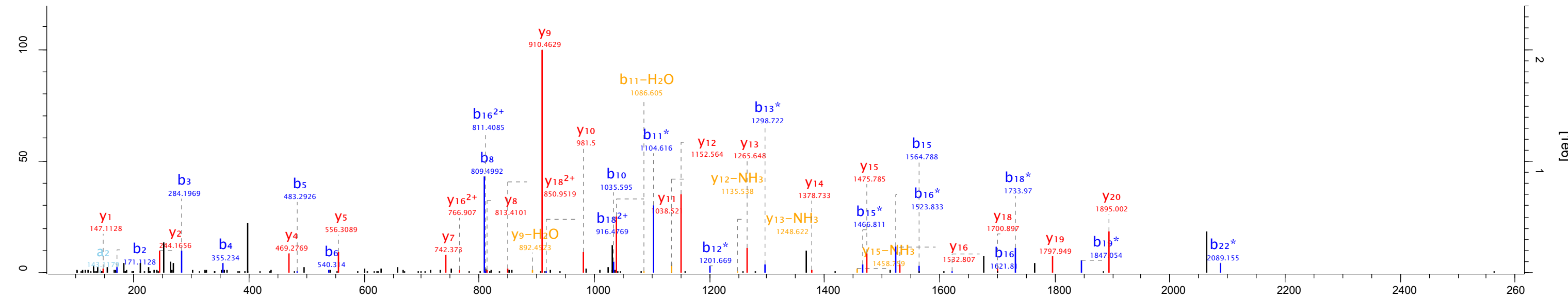
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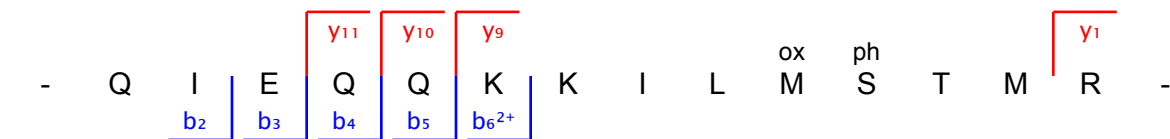
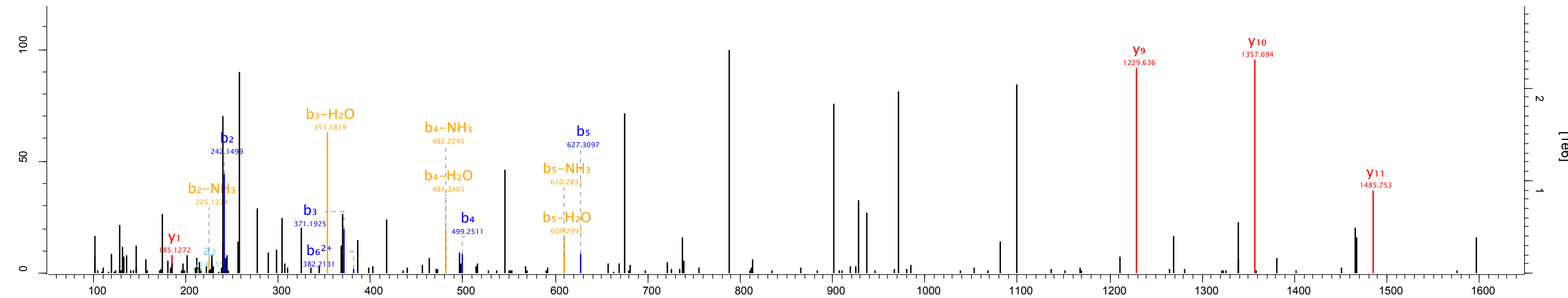


20171215_MaS_33SR_LMH_proteome_01 50757 FTMS; HCD 89.72 856.36 CALU

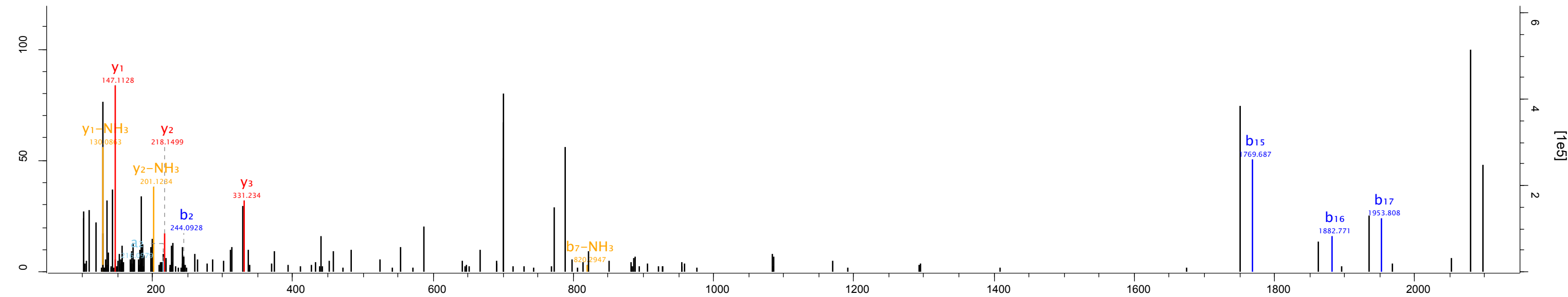


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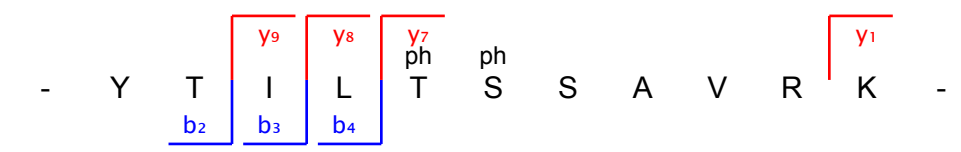
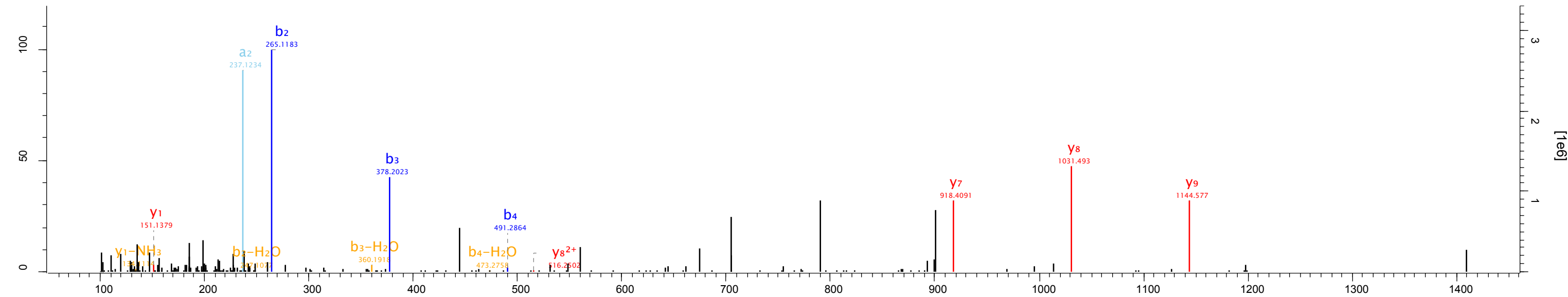




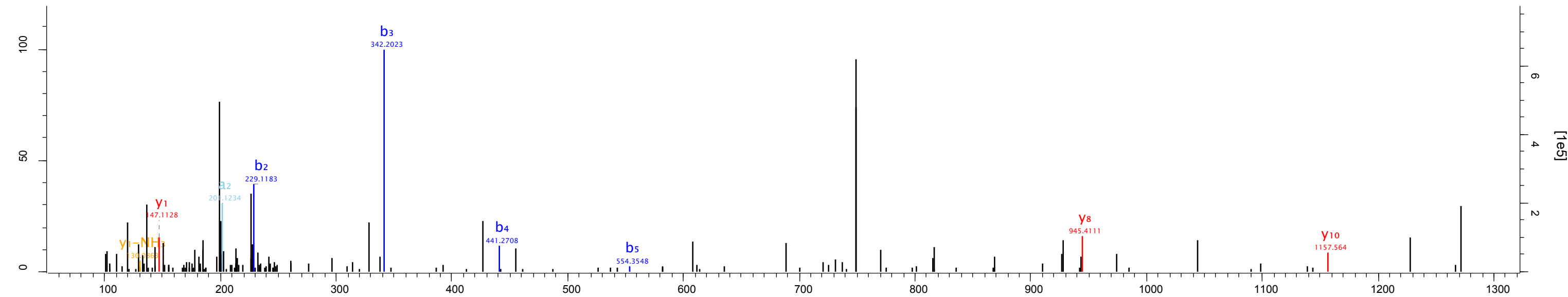
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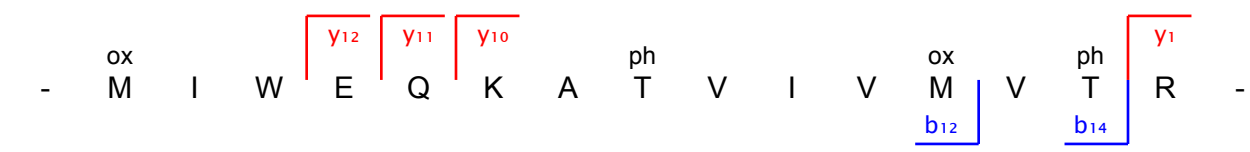
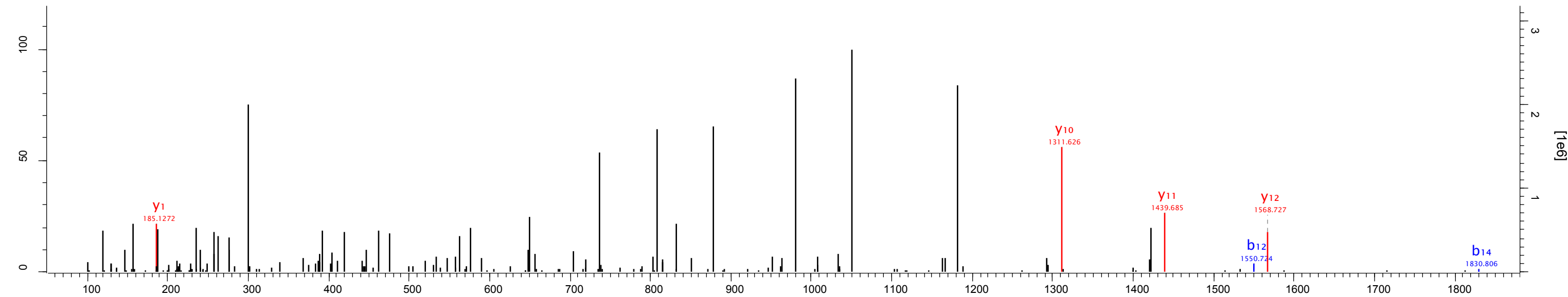
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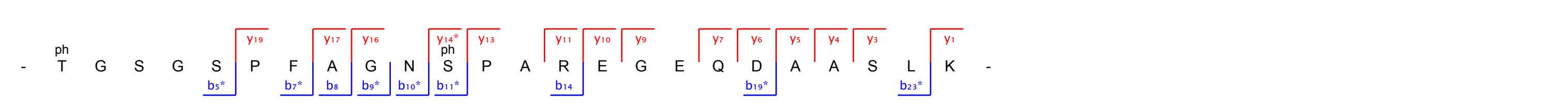
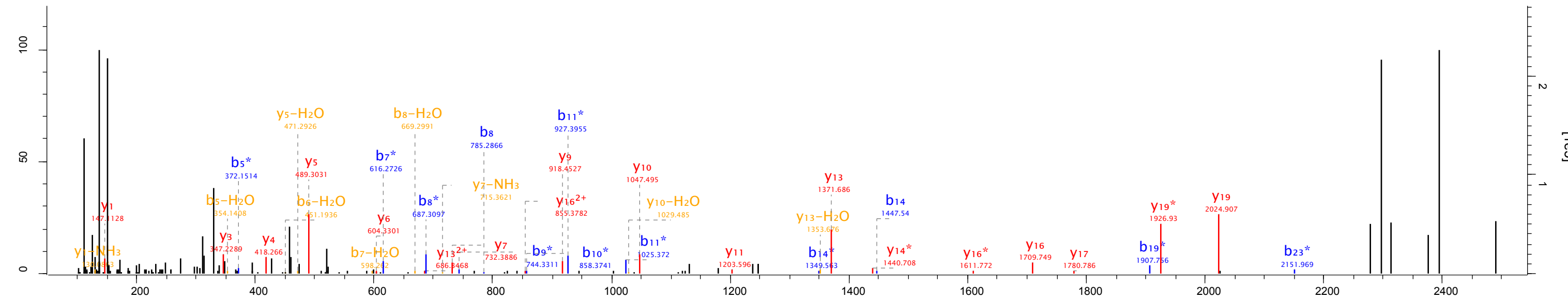
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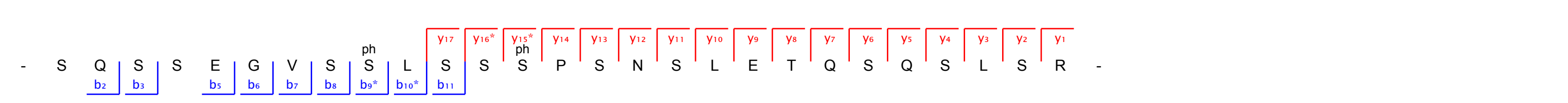
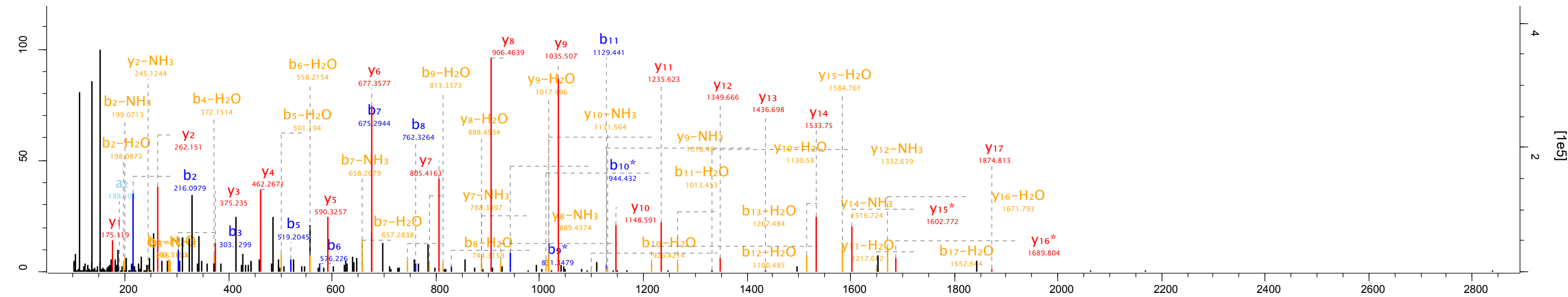
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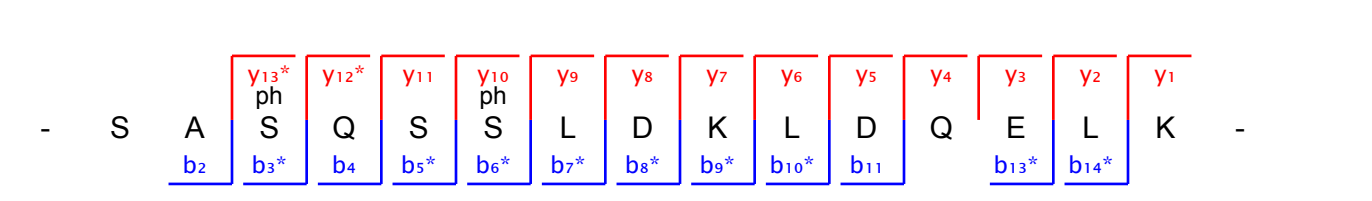
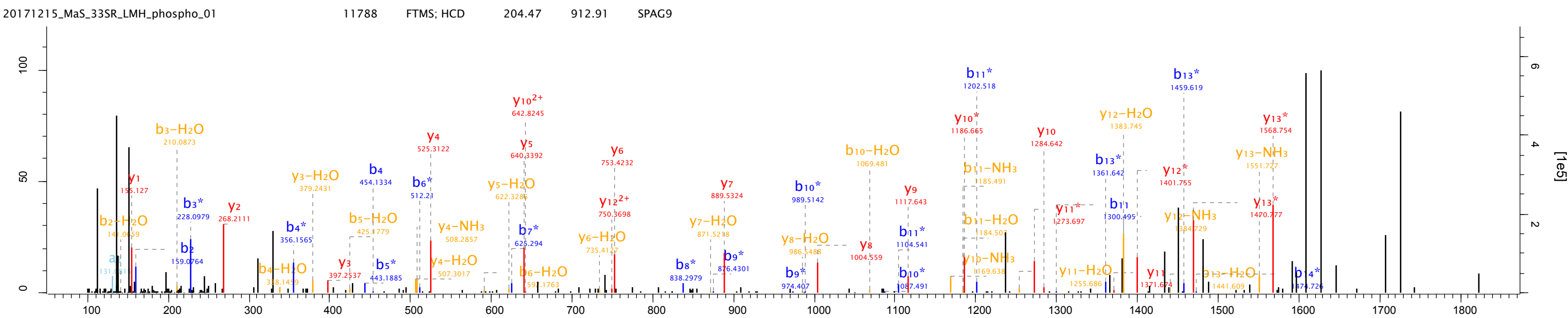
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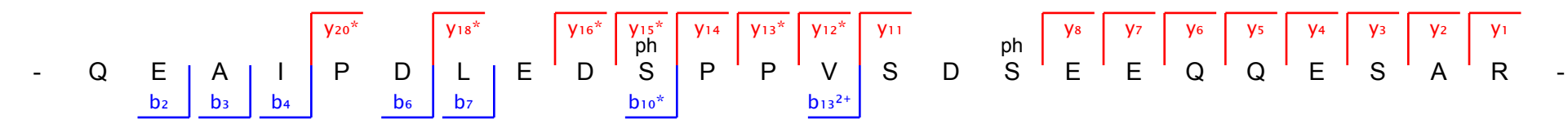
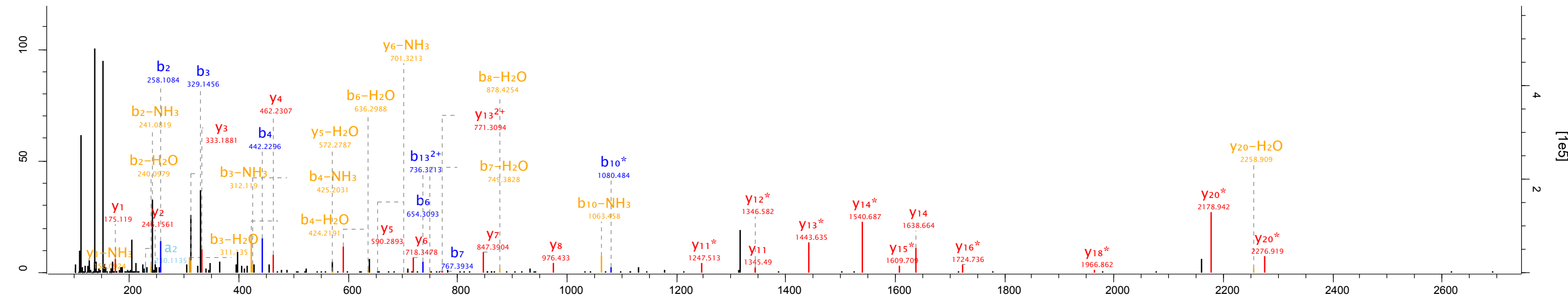
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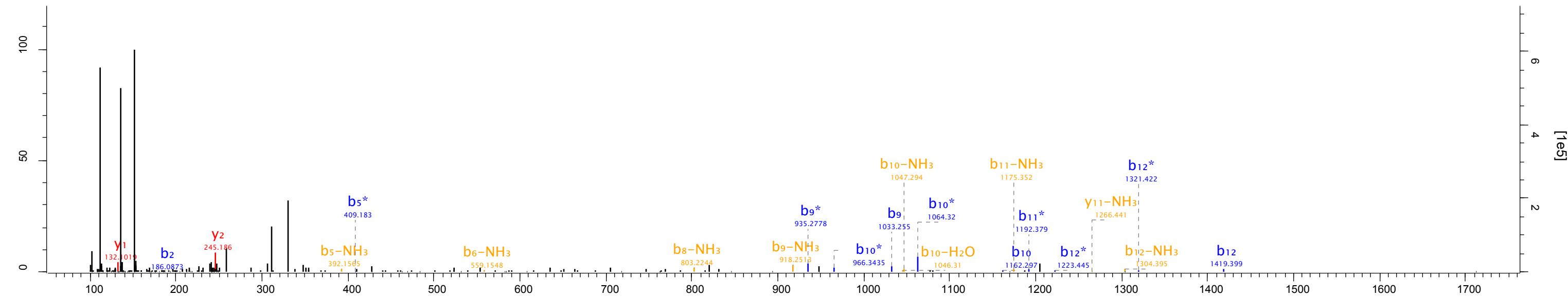
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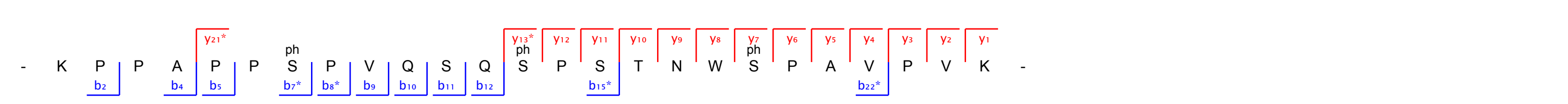
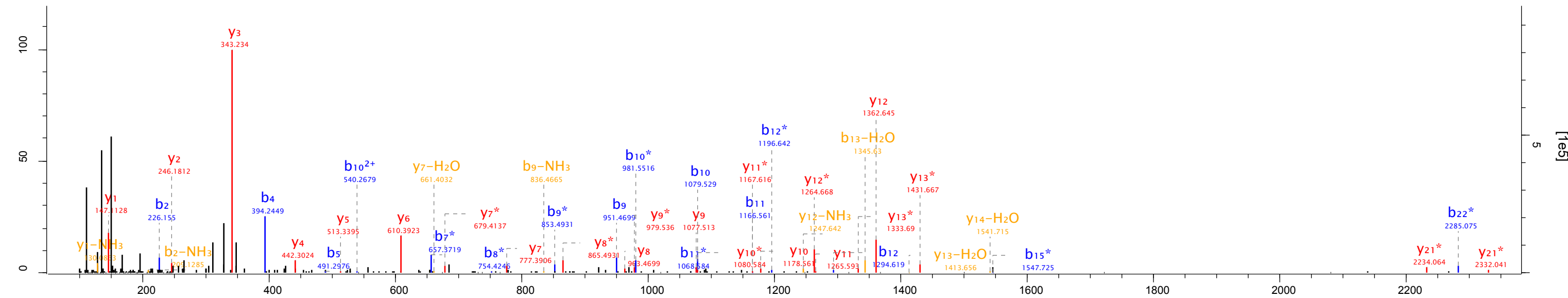
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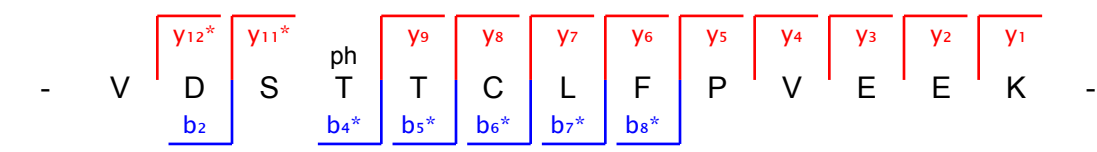
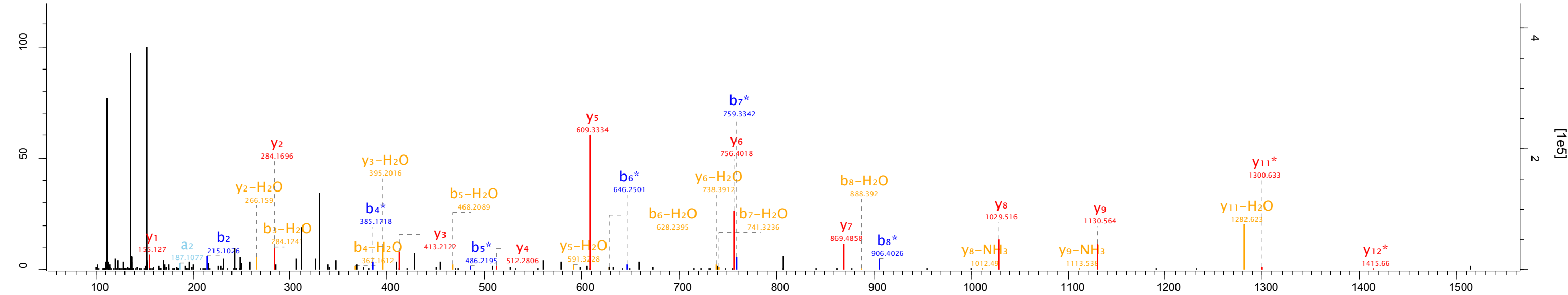
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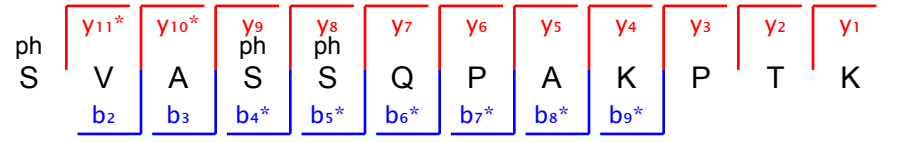
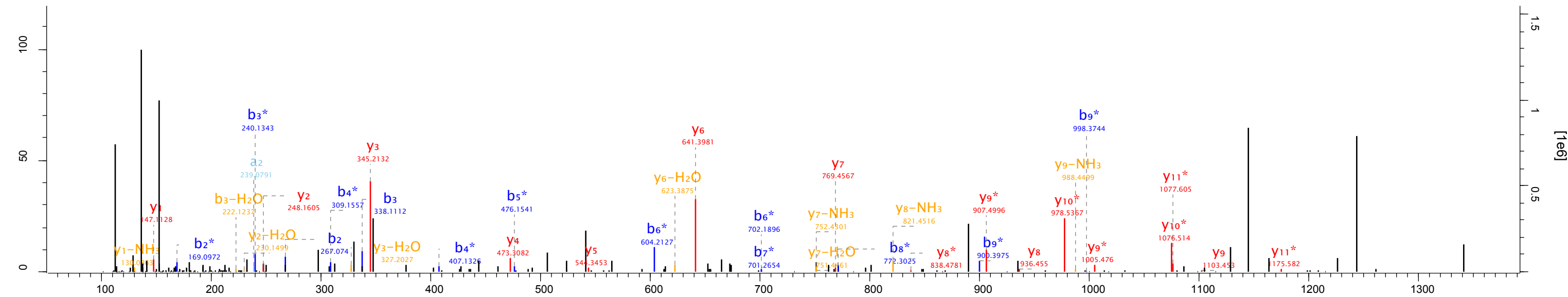
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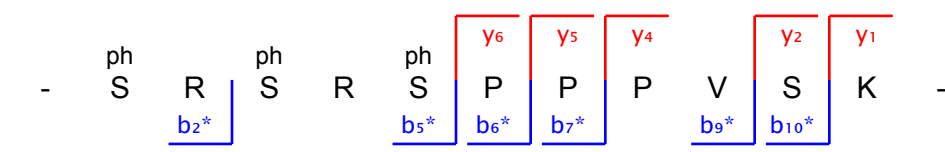
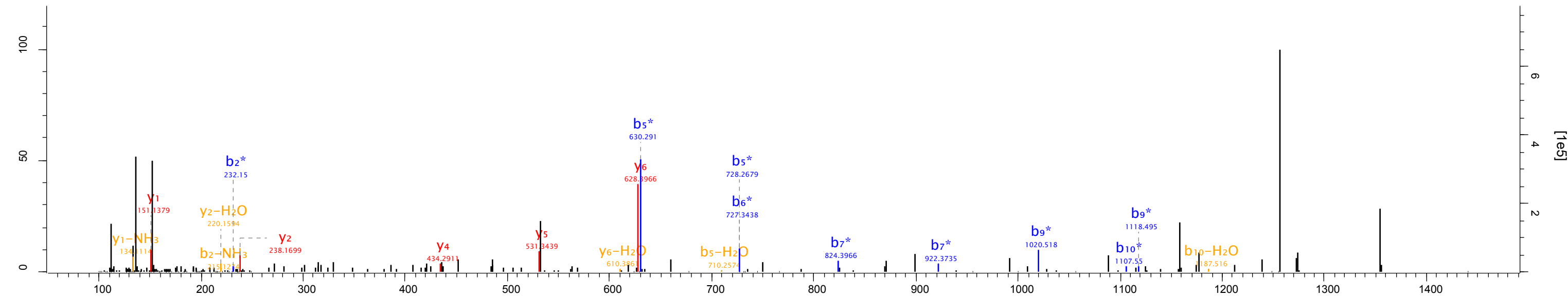
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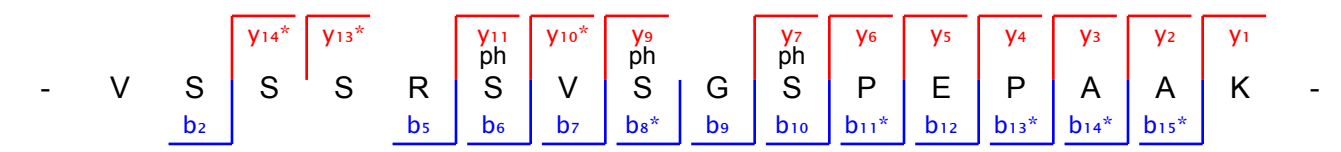
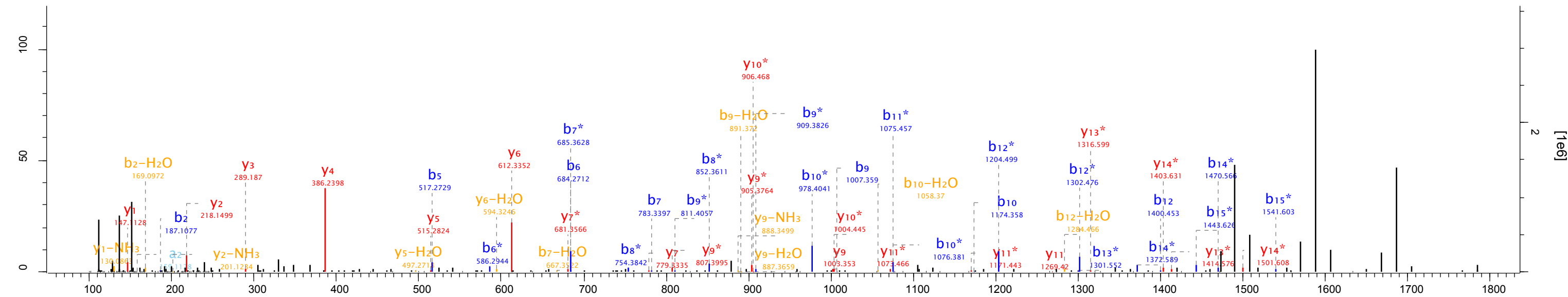
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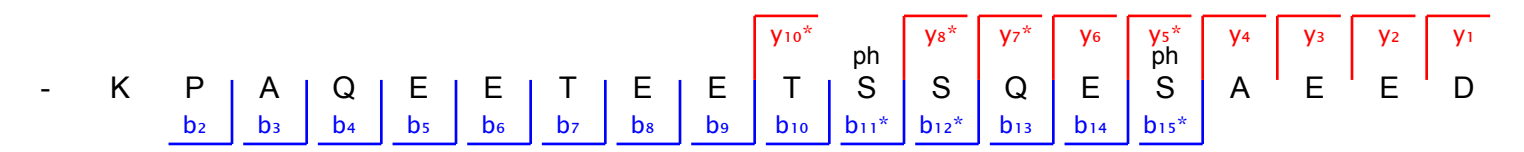
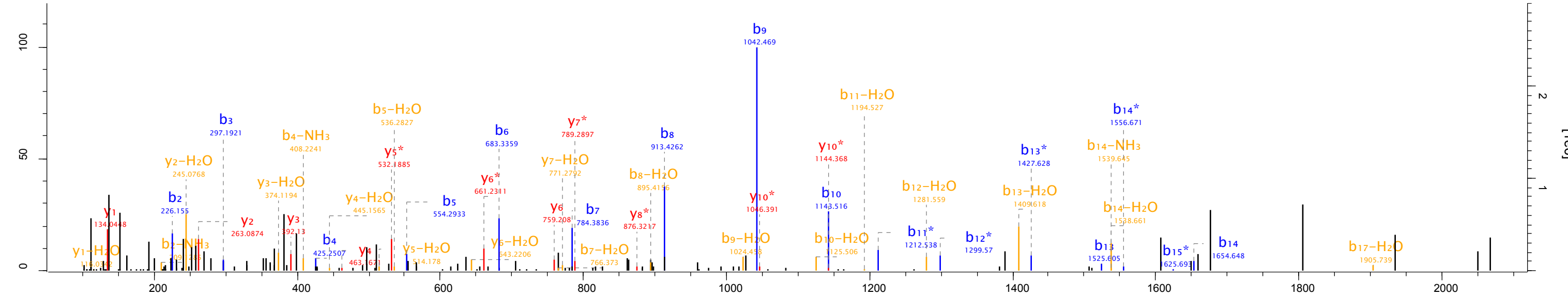
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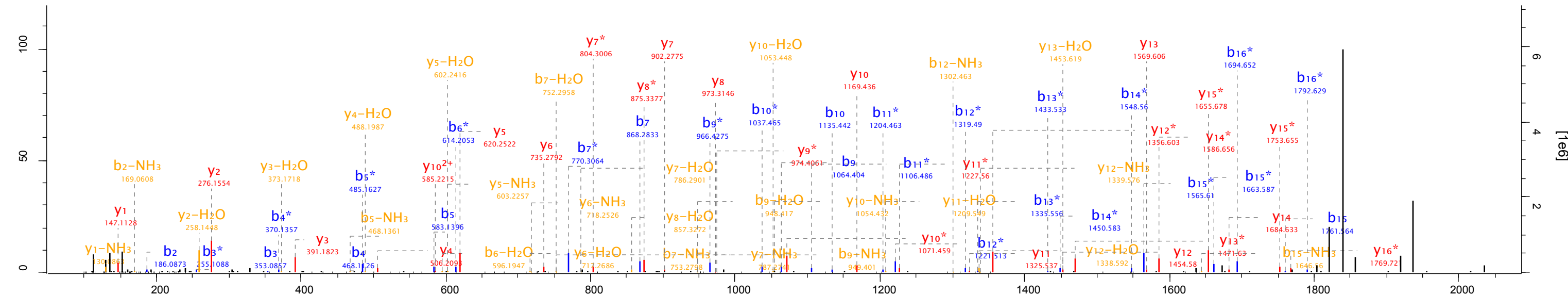


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20171215_MaS_33SR_LMH_phospho_01 2938 FTMS; HCD 149.41 1142.41 HMGA2



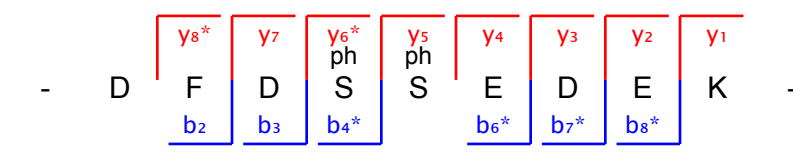
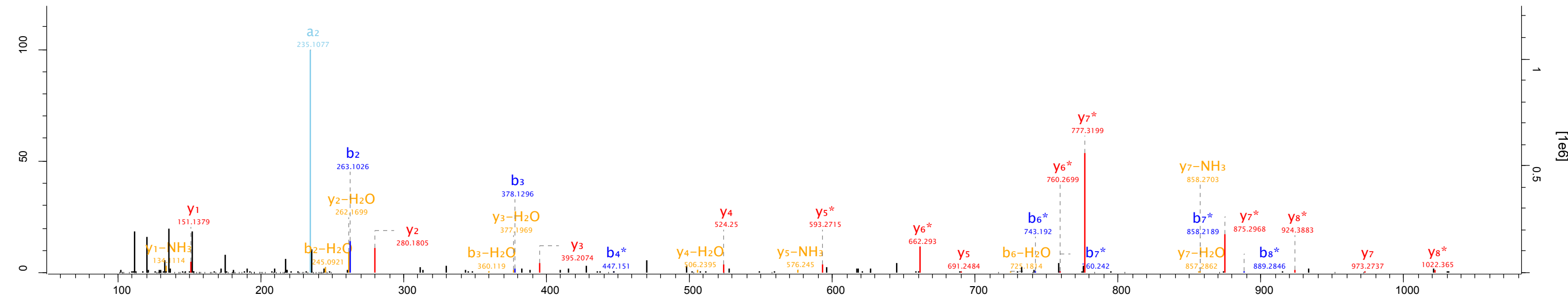


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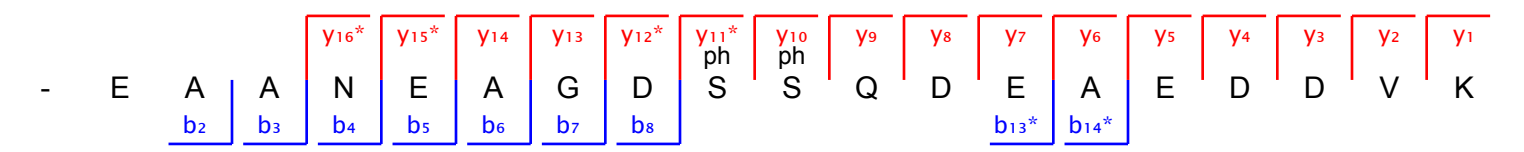
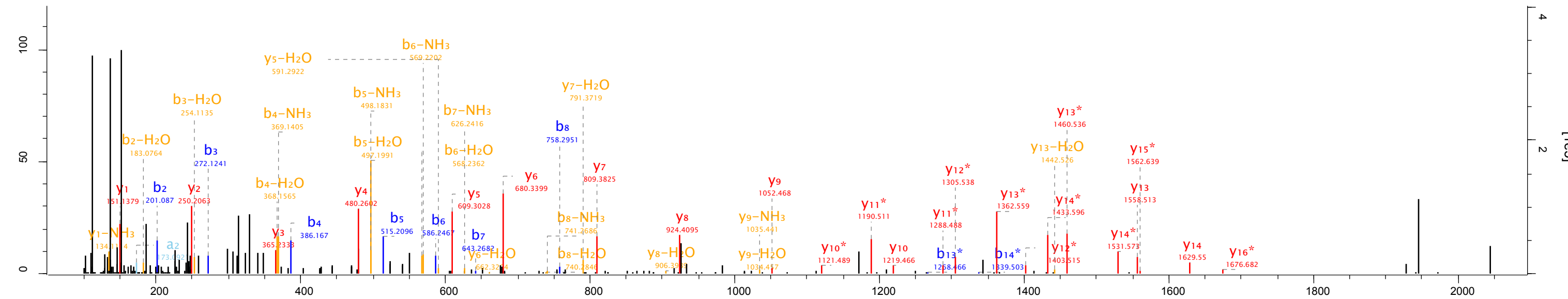
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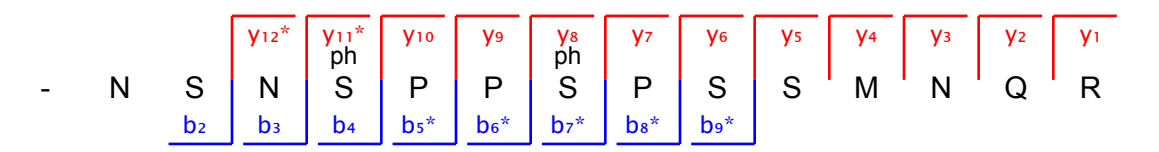
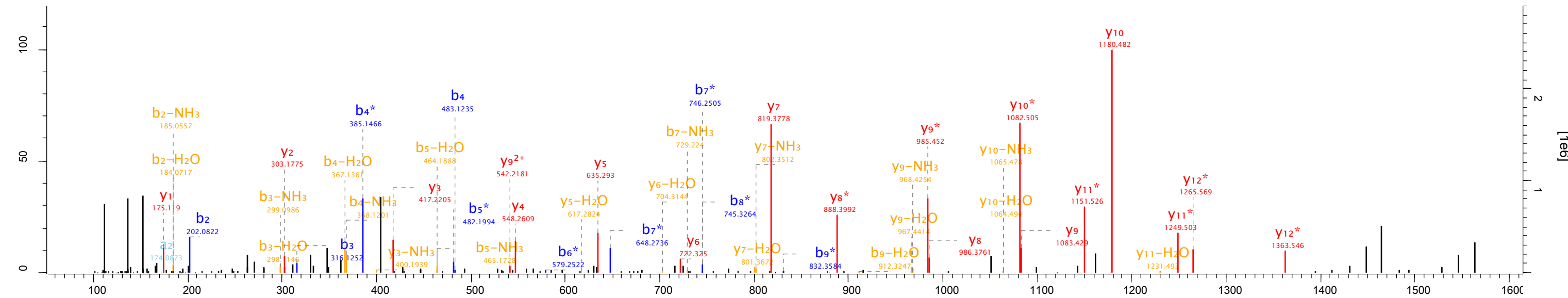
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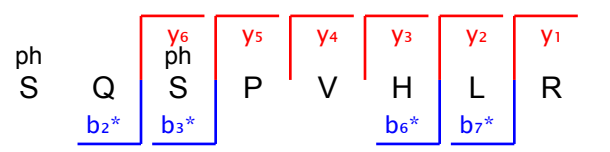
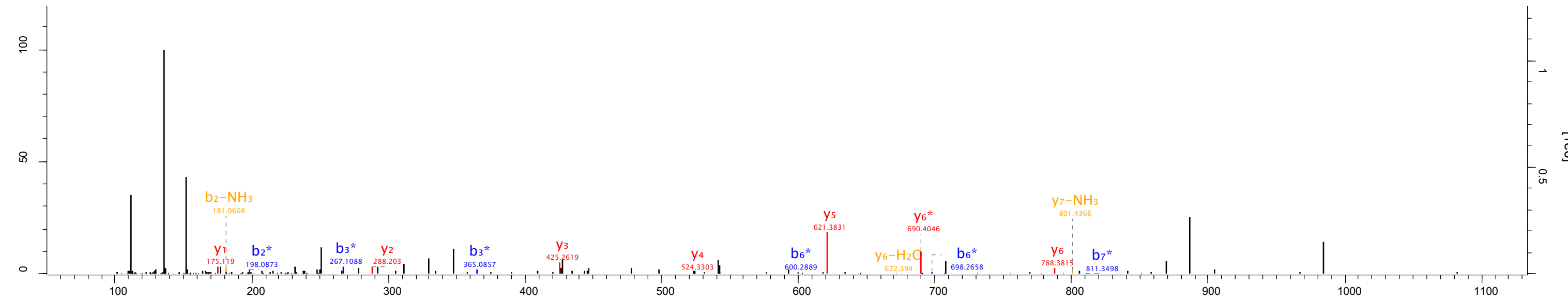
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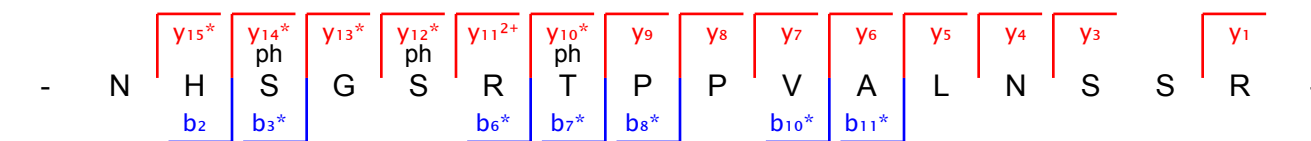
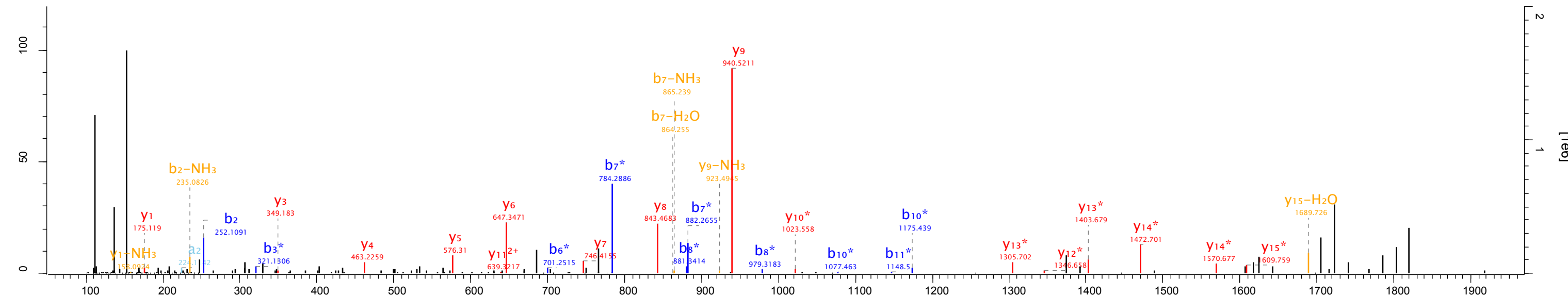
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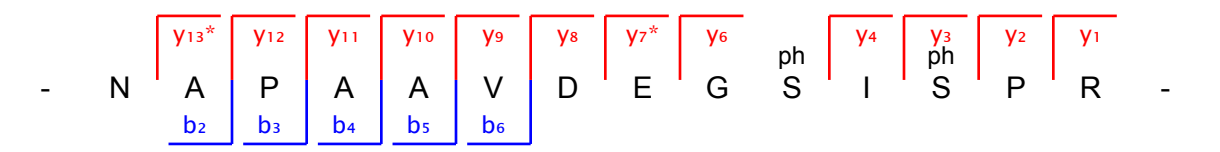
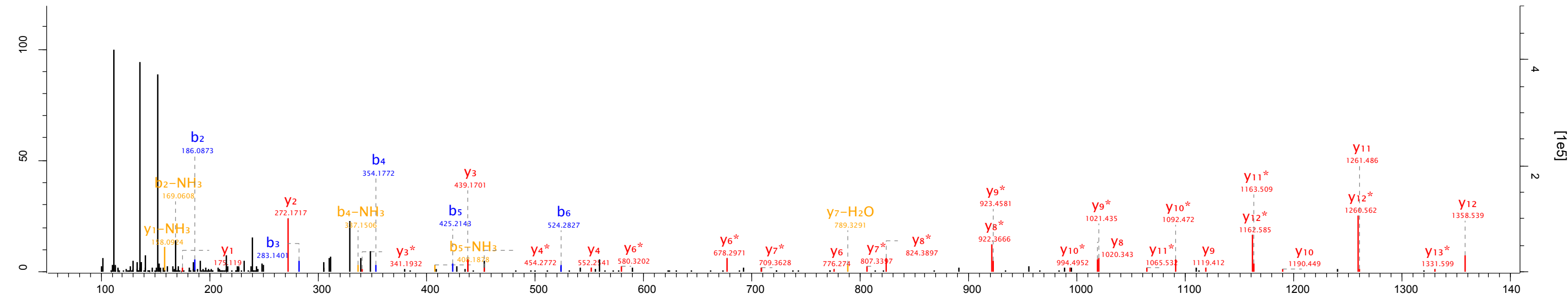
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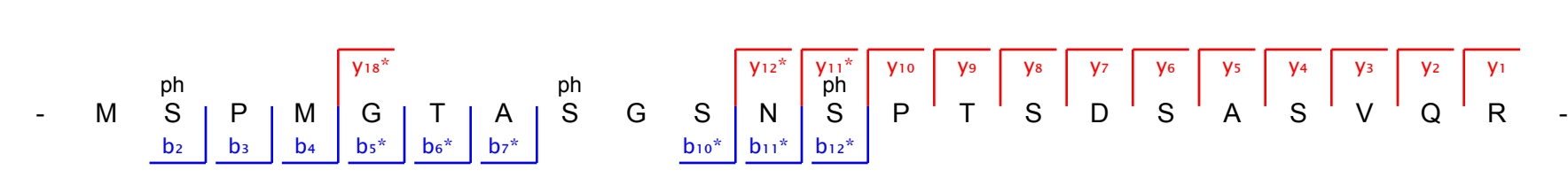
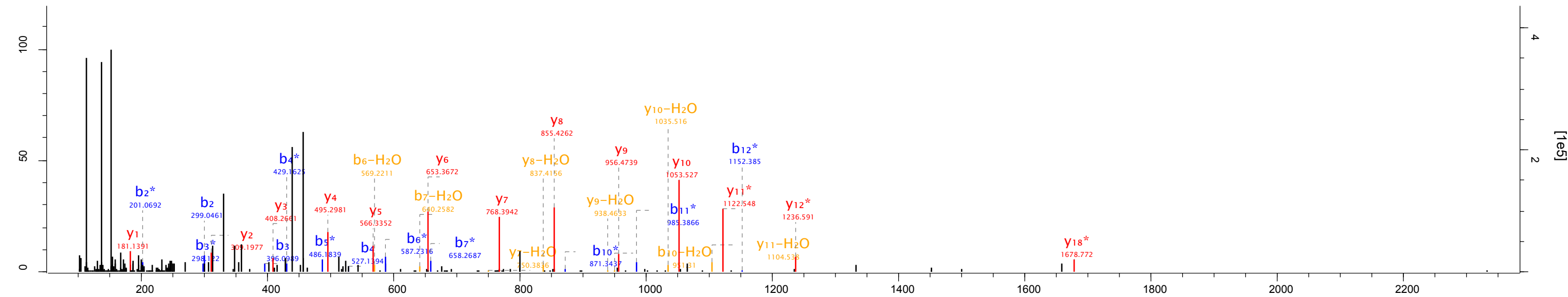
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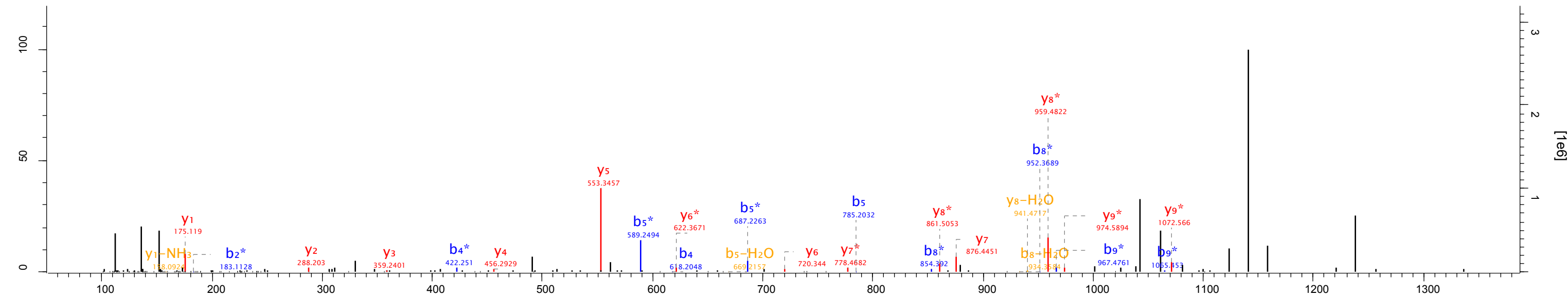
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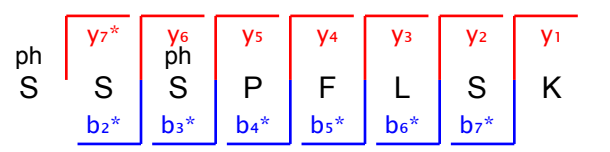
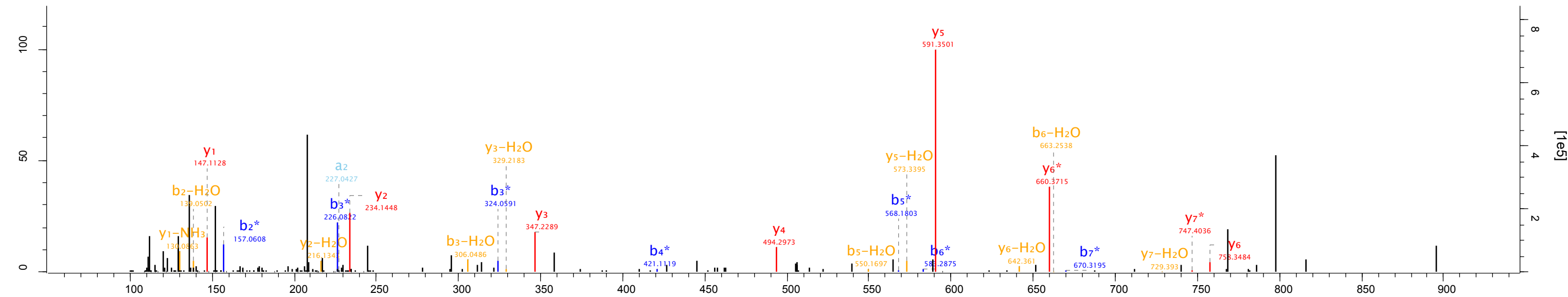
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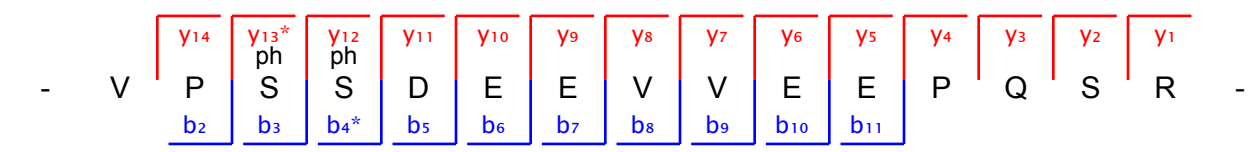
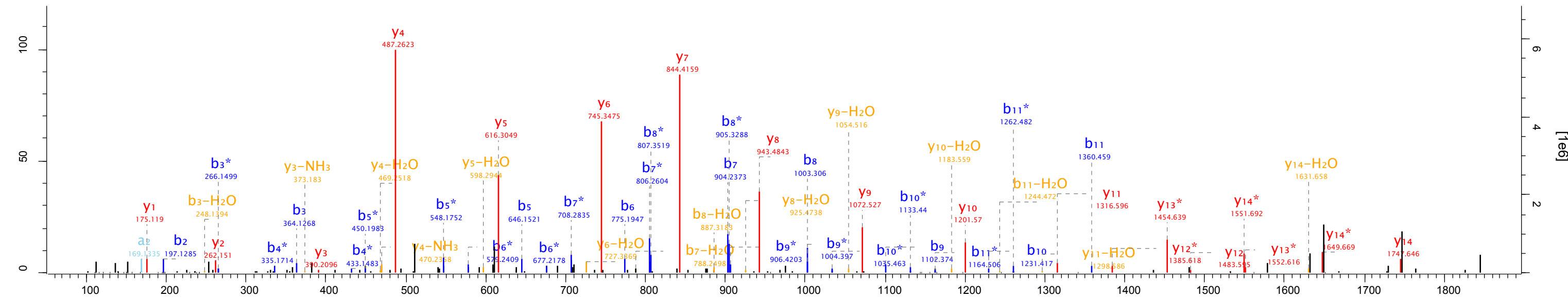
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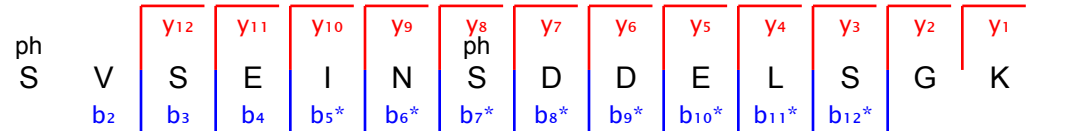
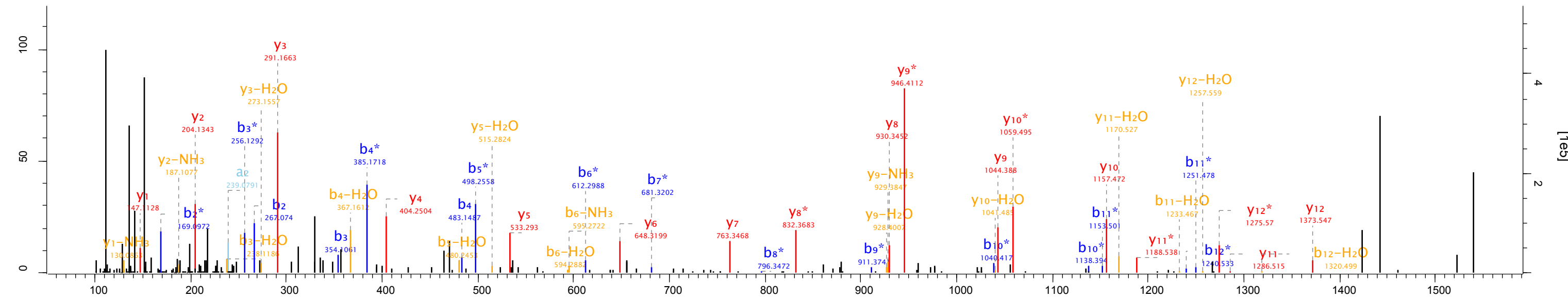
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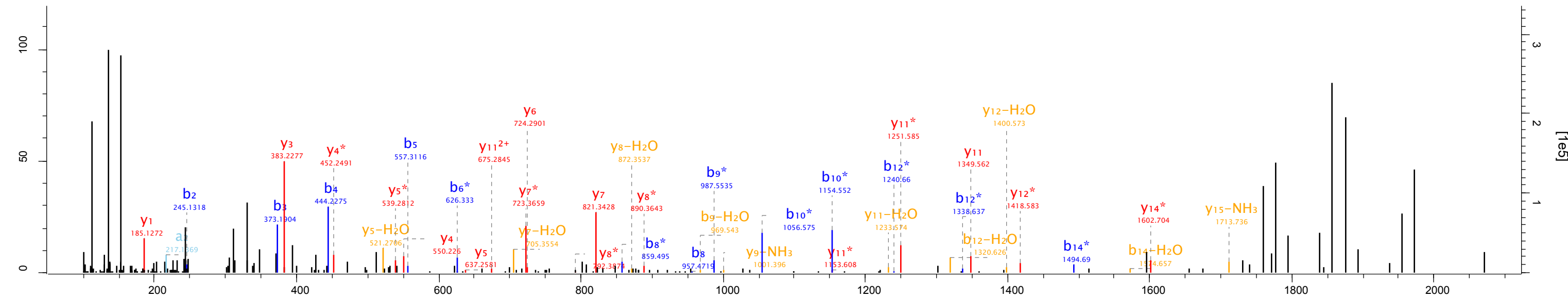
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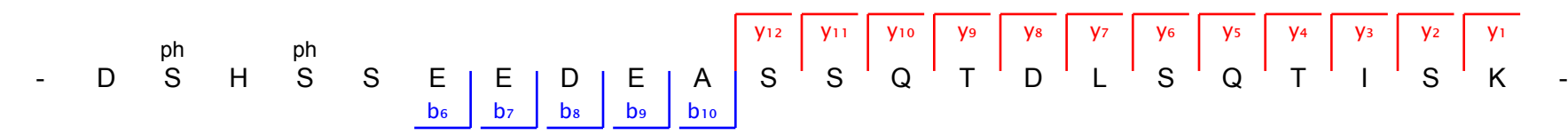
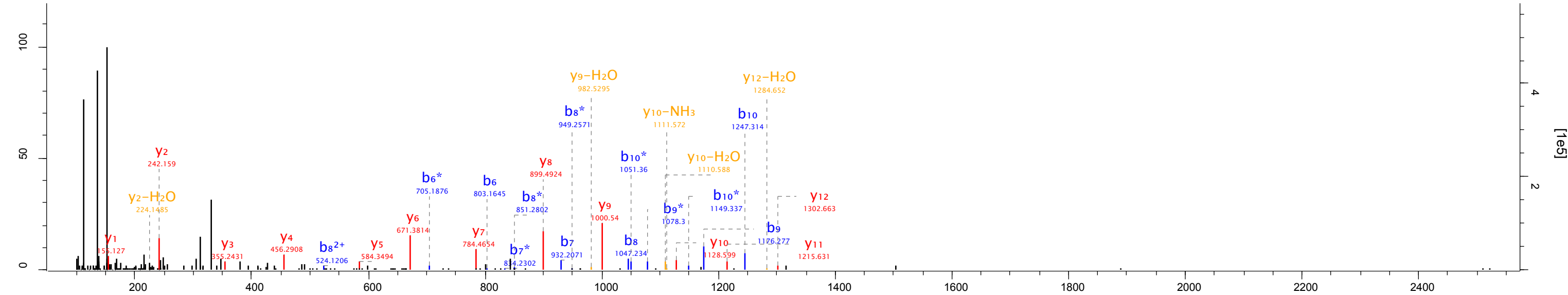
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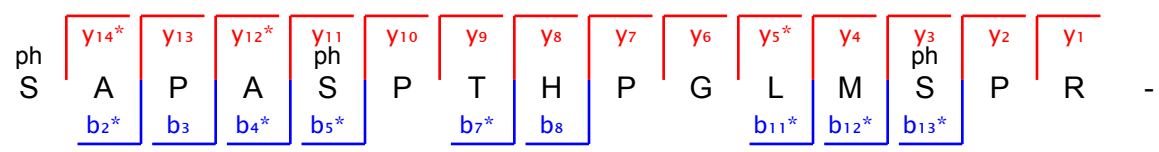
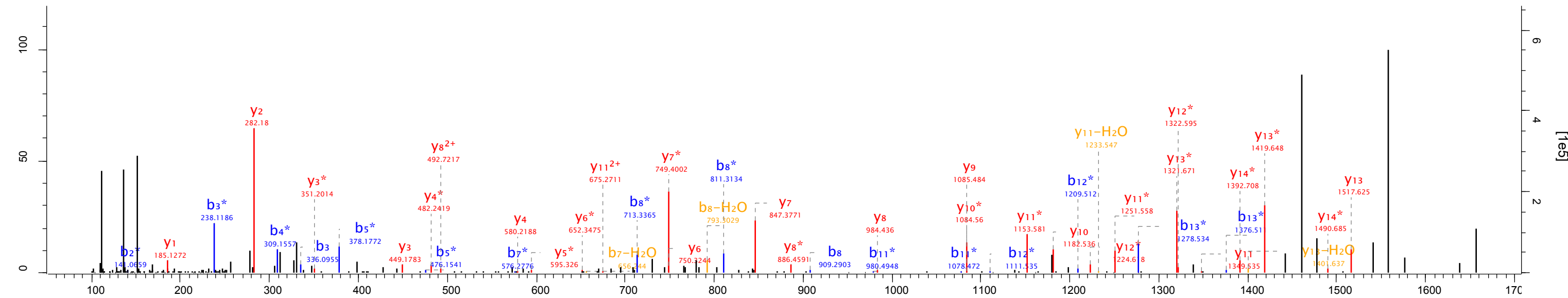
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20171215_MaS_33SR_LMH_phospho_01

Scan 8398 Method FTMS; HCD Score 76.49 m/z 851 Gene names TOR1AIP1

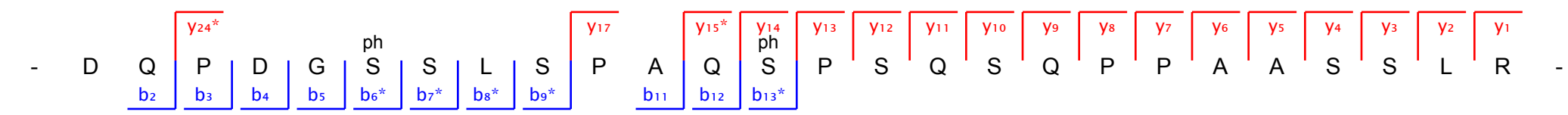
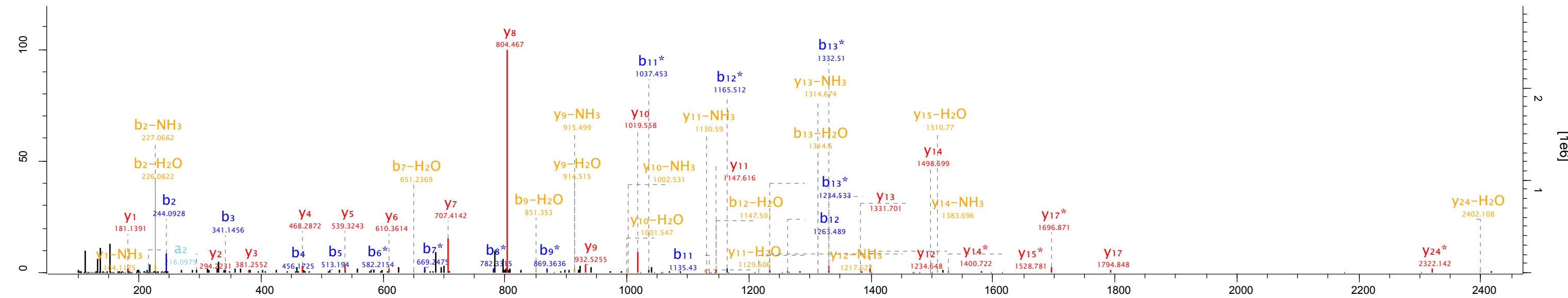


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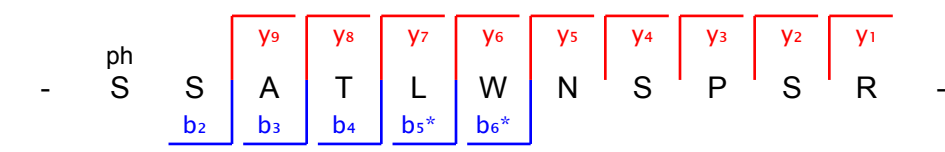
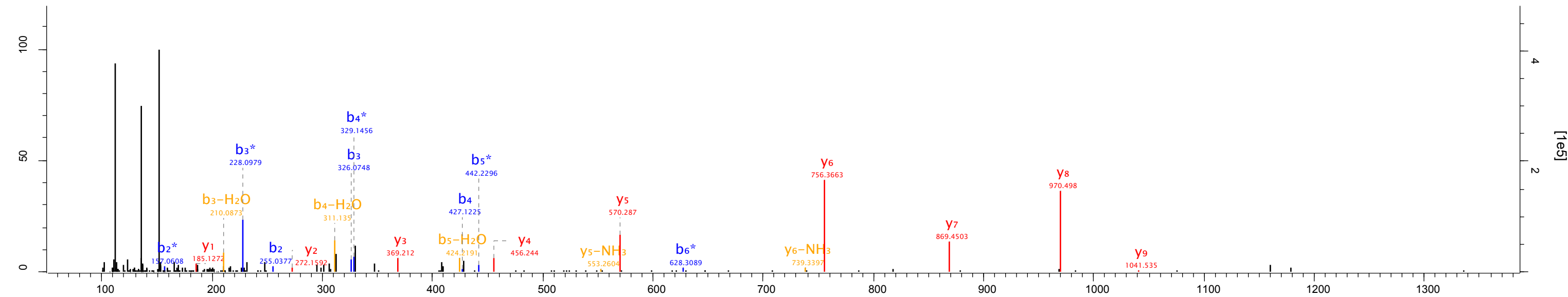


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20171215_MaS_33SR_LMH_phospho_01

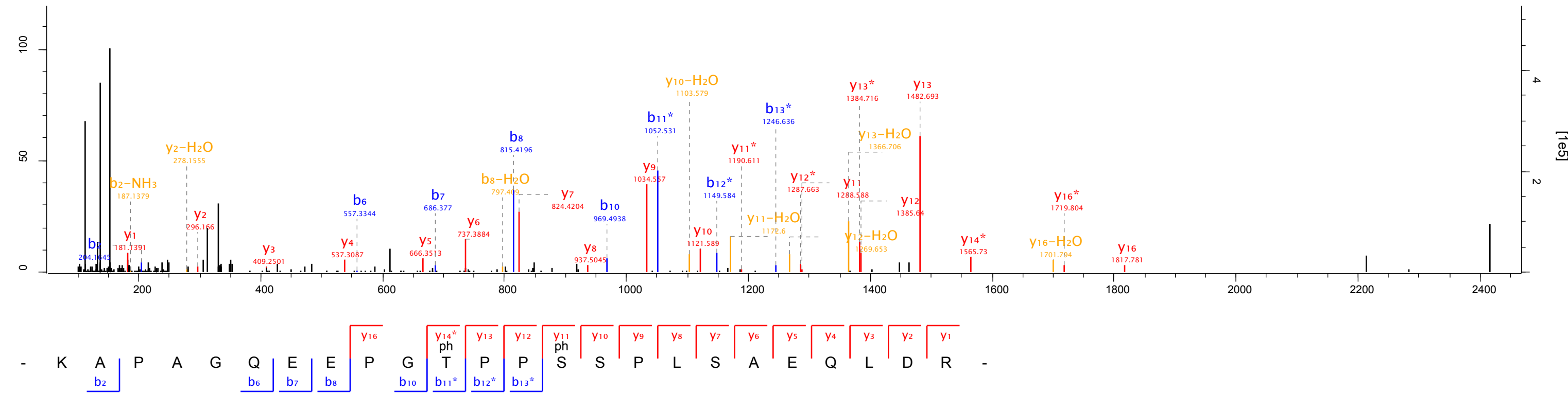
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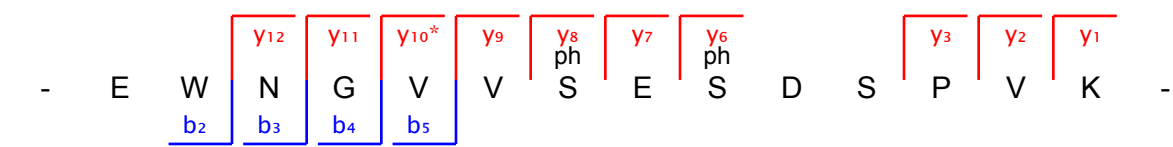
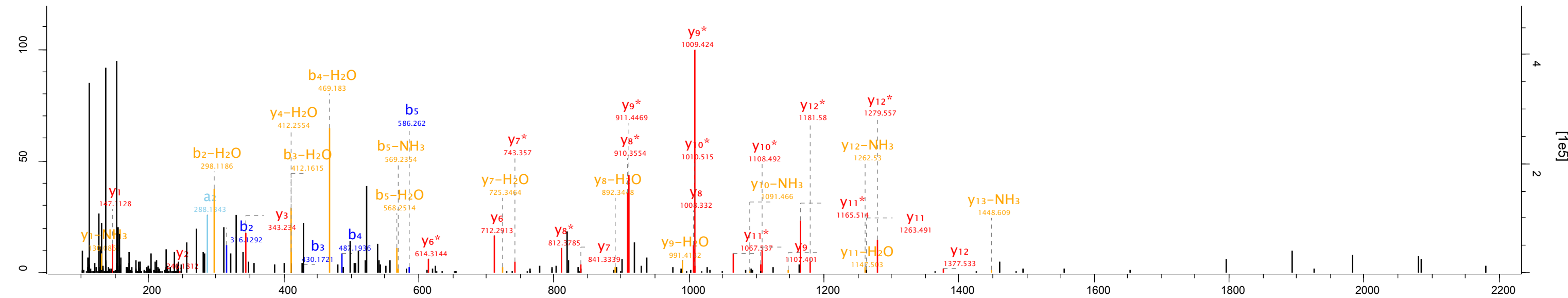
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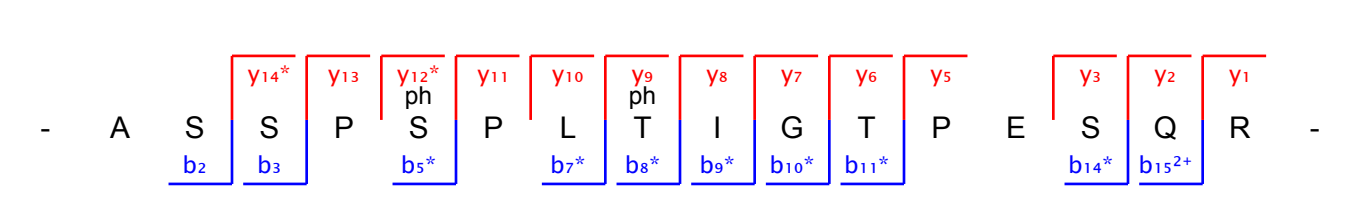
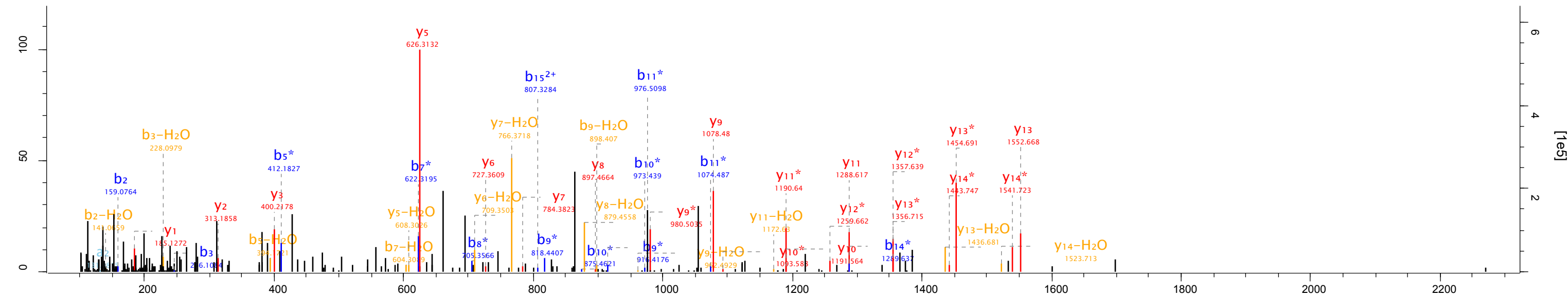
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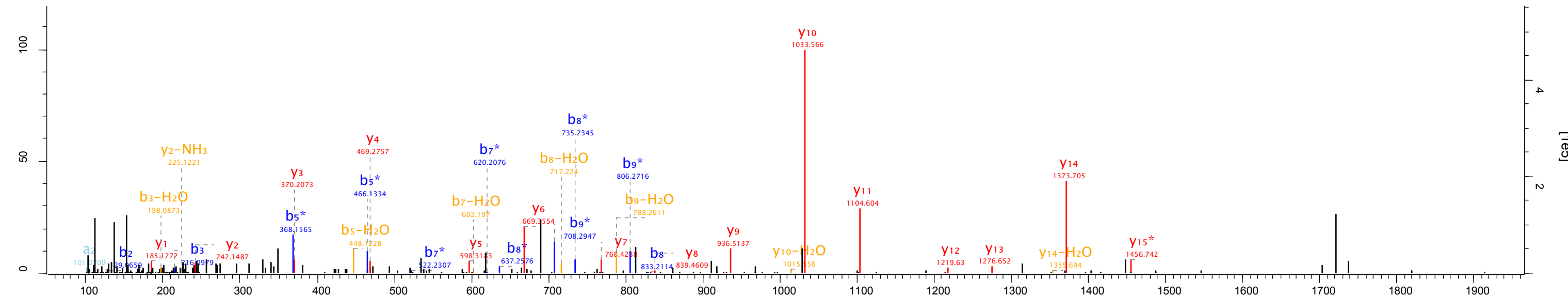
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Raw file: 20171215_MaS_33SR_LMH_phospho_02
 Scan: 10018 Method: FTMS; HCD Score: 129.91 m/z: 899.39 Gene names: DCP1A



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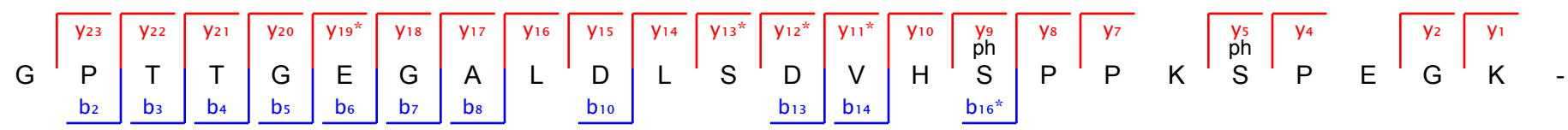
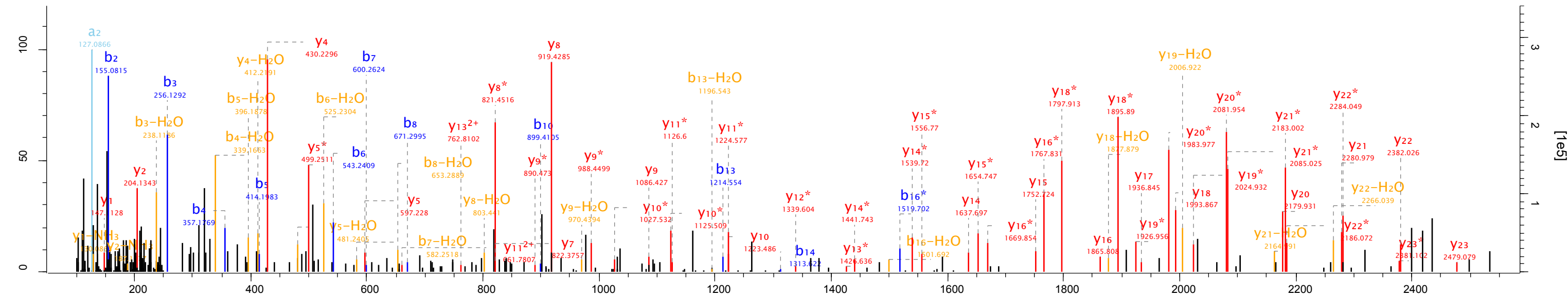


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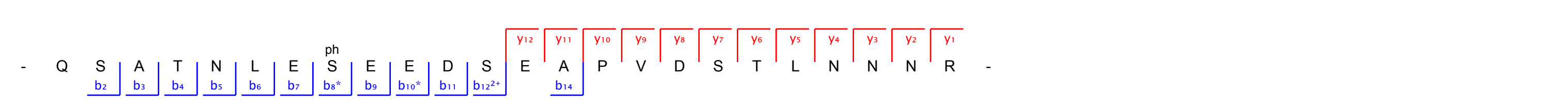
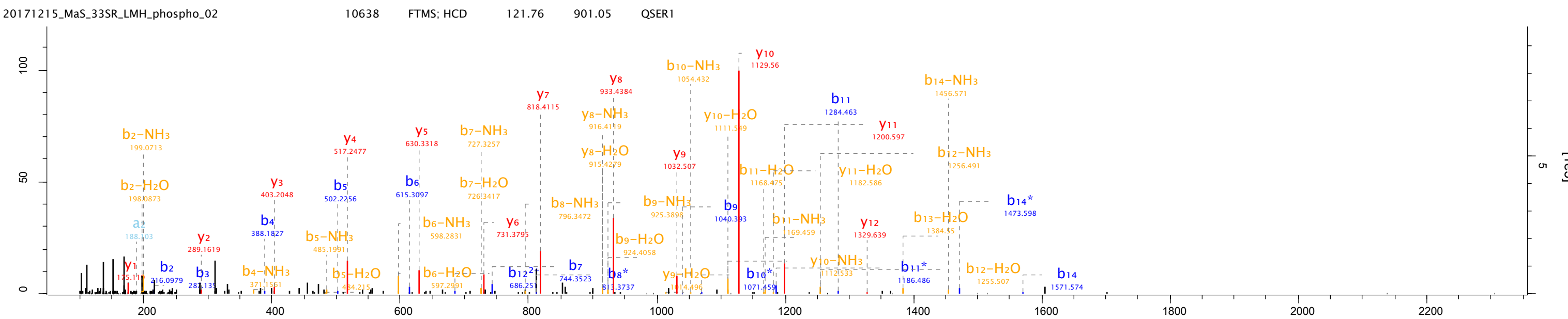
Fragmentation sites are indicated by brackets below the amino acid sequence:

- b2 (under G)
- b3 (under S)
- b5* (under T)
- b7* (under G)
- b8 (under D)
- b9* (under A)

Raw file: 20171215_MaS_33SR_LMH_phospho_02
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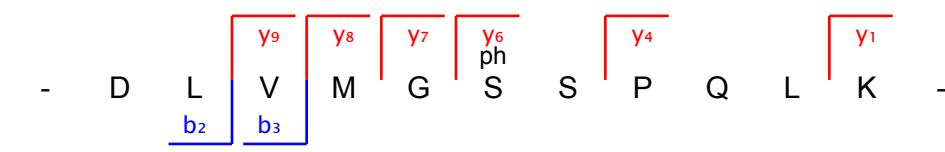
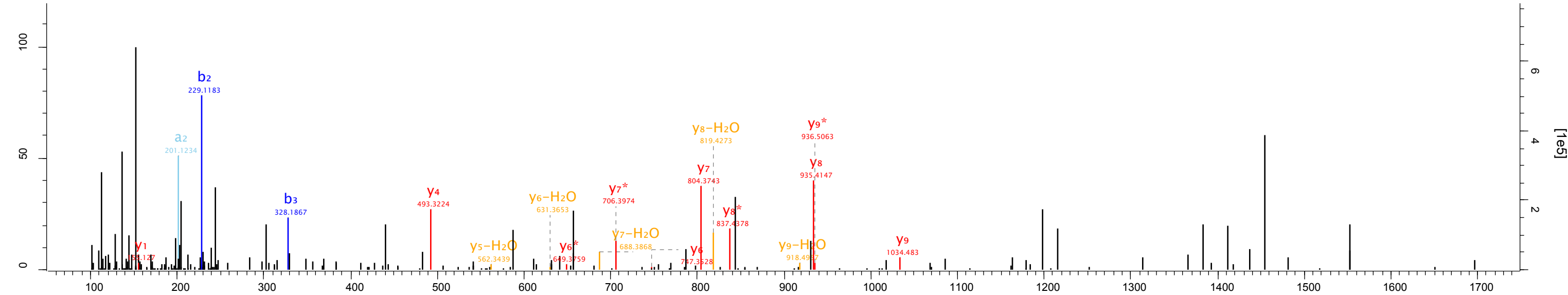
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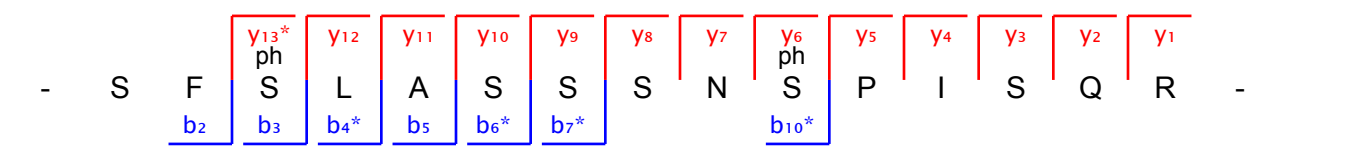
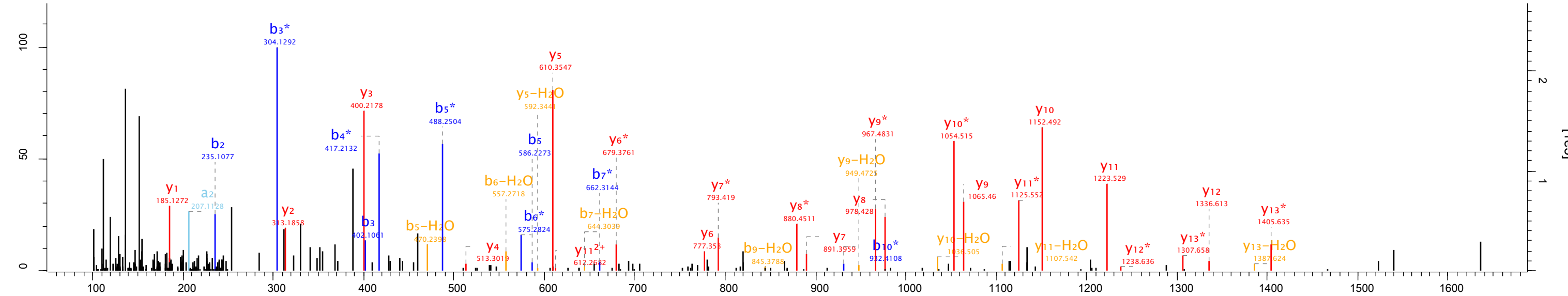
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20171215_MaS_33SR_LMH_phospho_02

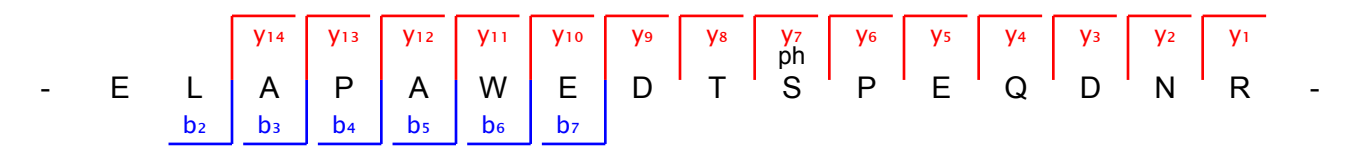
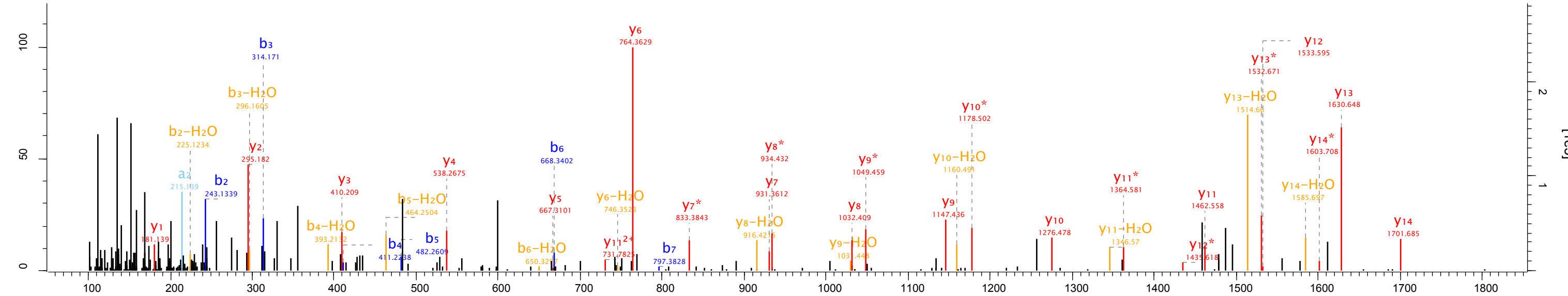
Scan	Method	Score	m/z	Gene names
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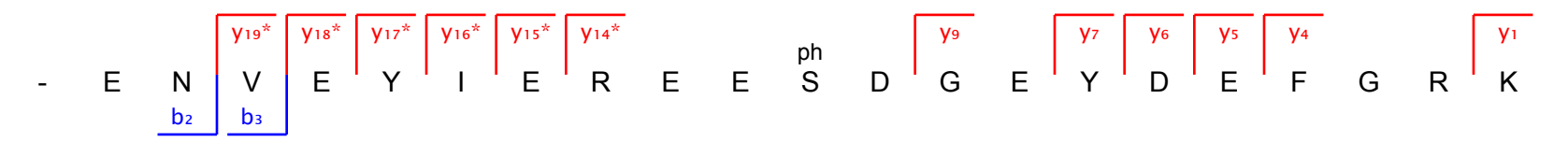
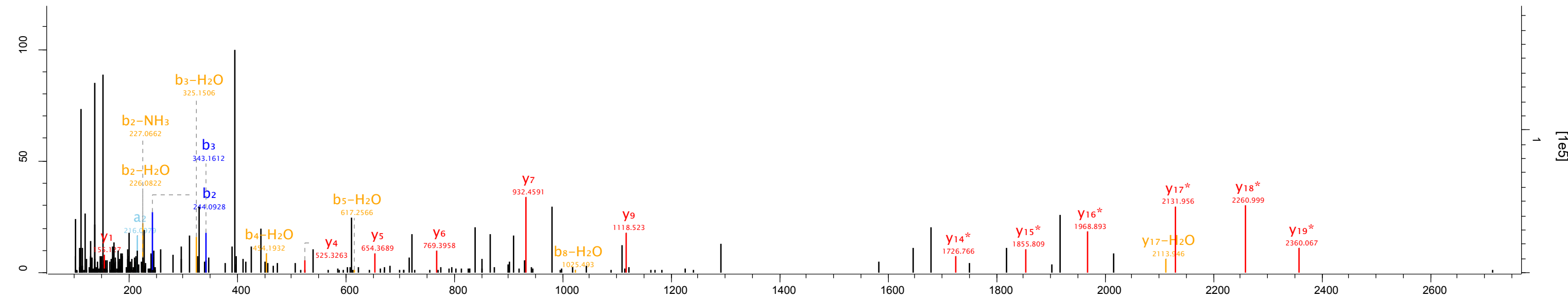
20171215_MaS_33SR_LMH_phospho_02 11488 FTMS; HCD 180.63 869.36 OSBPL11

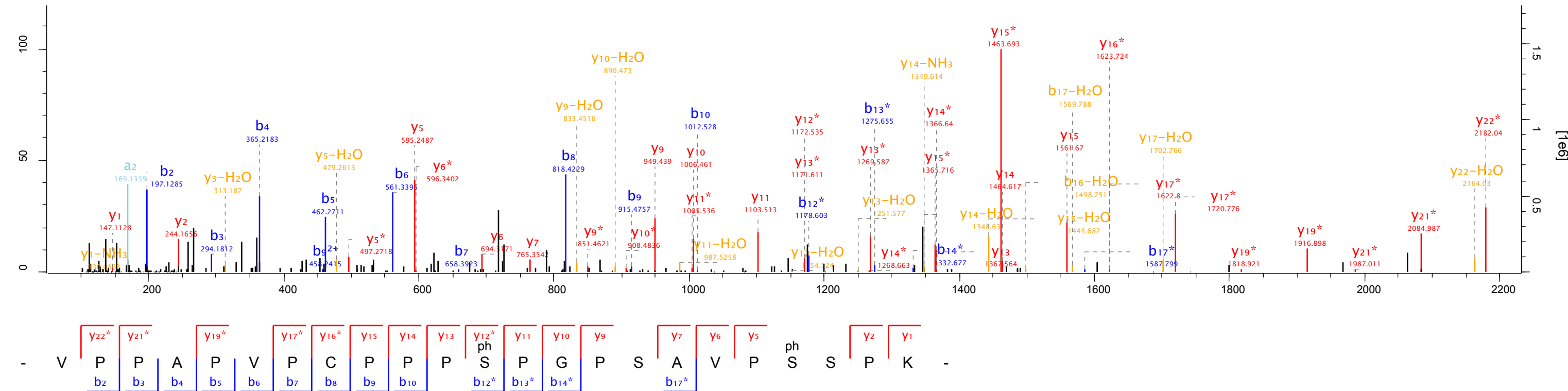


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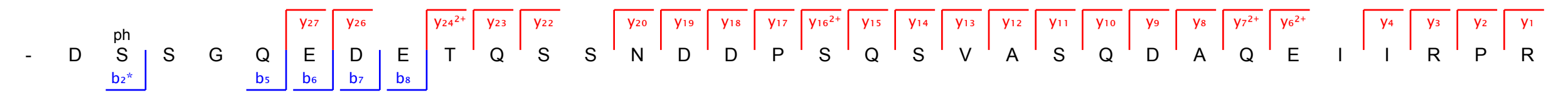
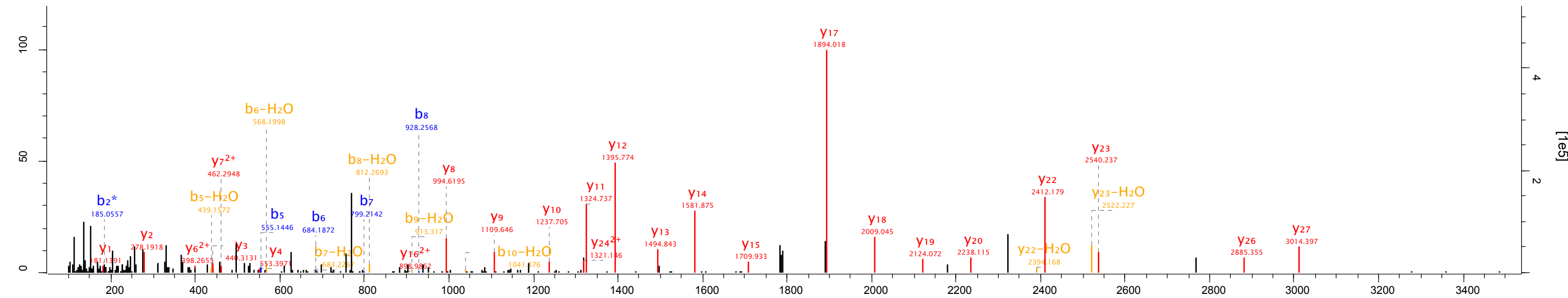


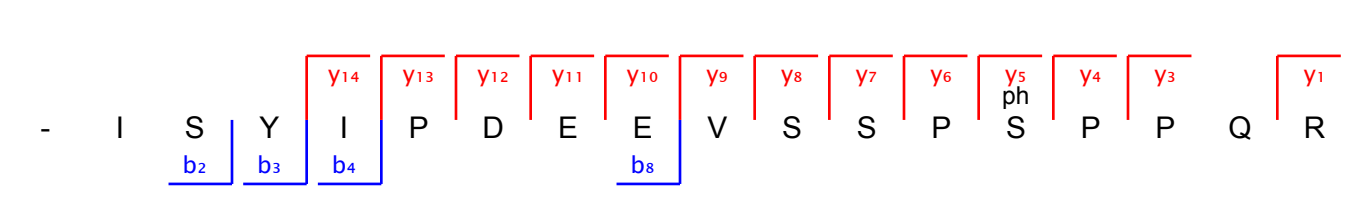
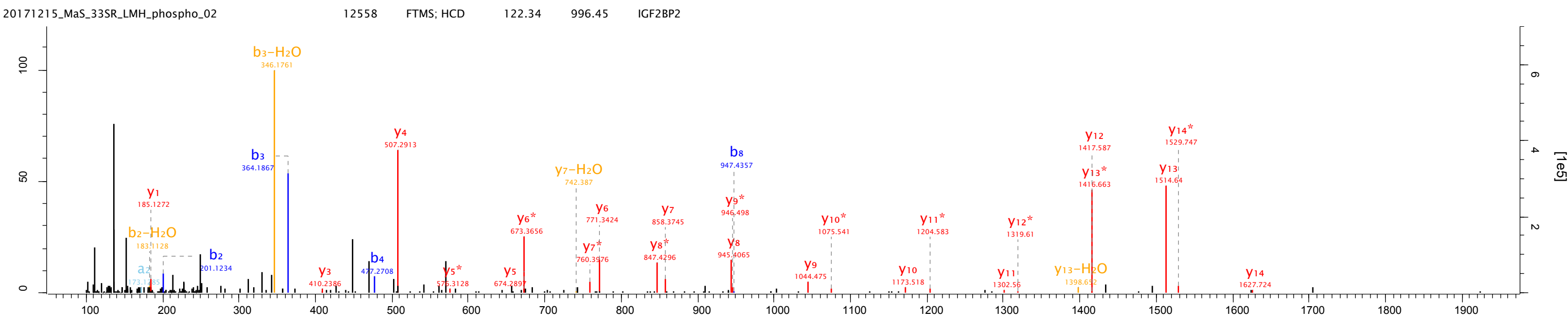
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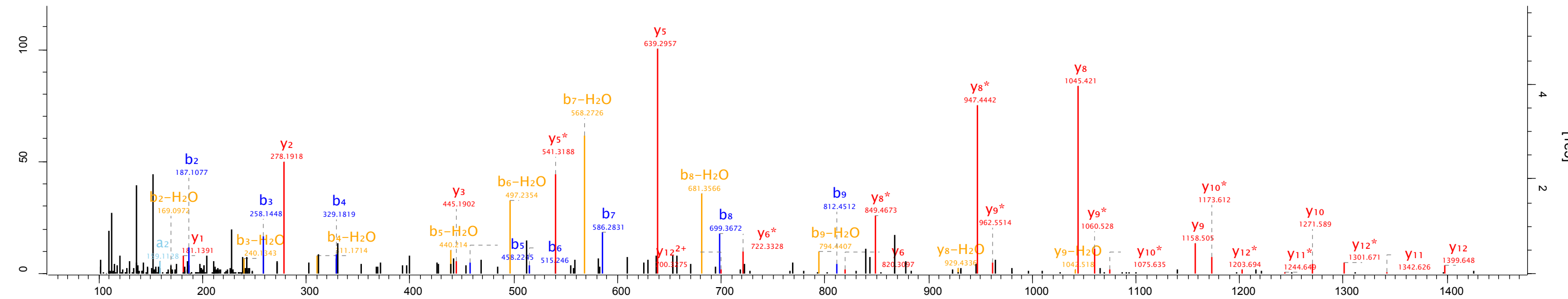


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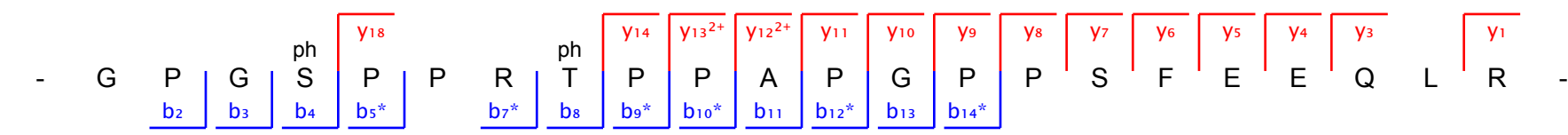
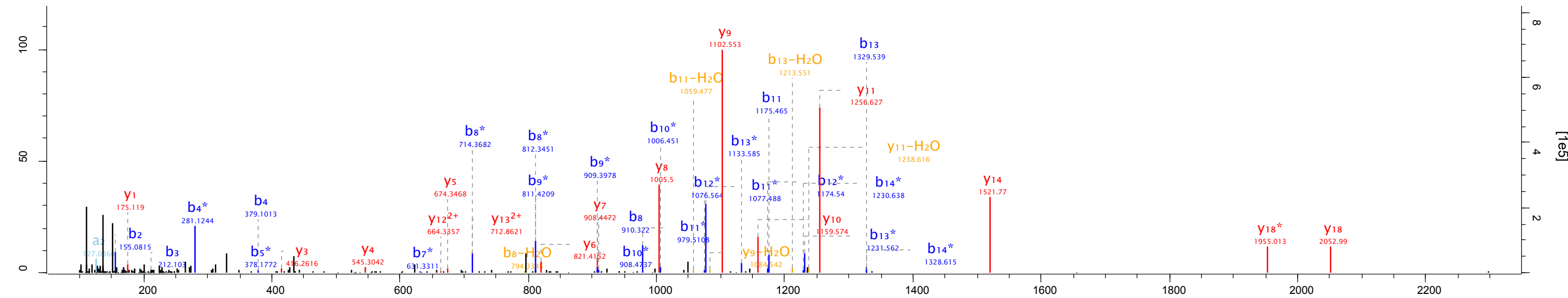
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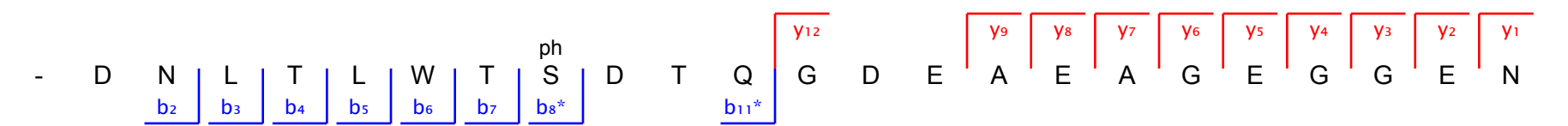
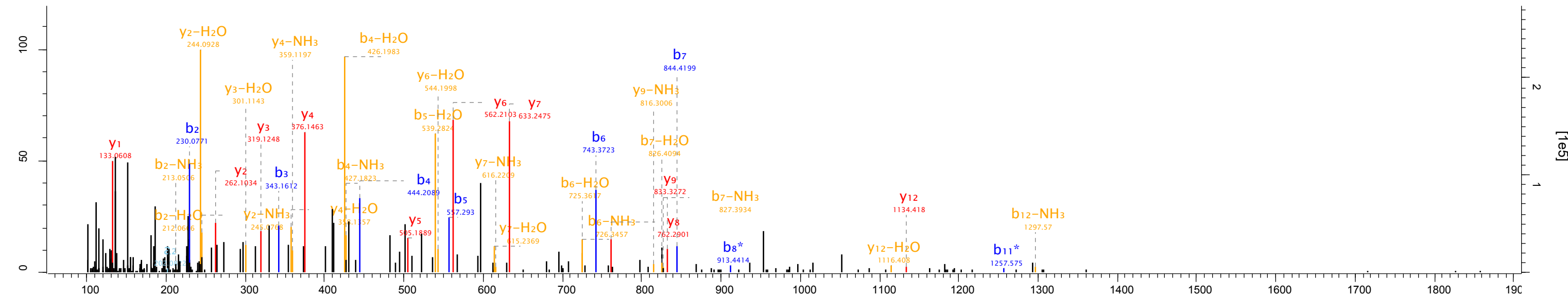
- S V A A E G A L L P Q T P P S P R -

b2
b3
b4
b5
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y11
y10
y9
y8
y6 ph
y5
y3 ph
y2
y1

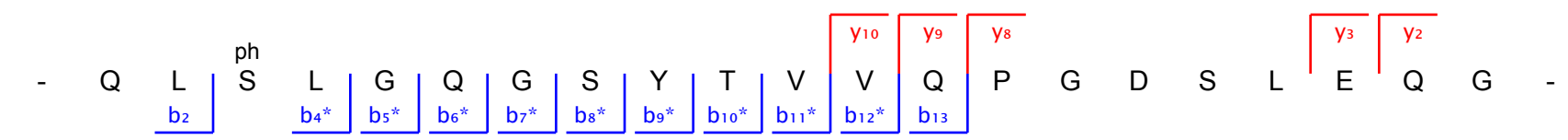
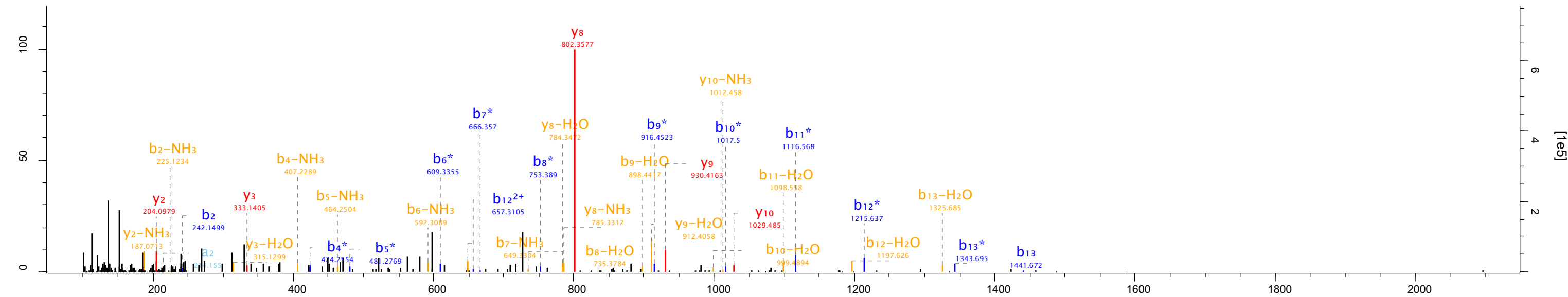
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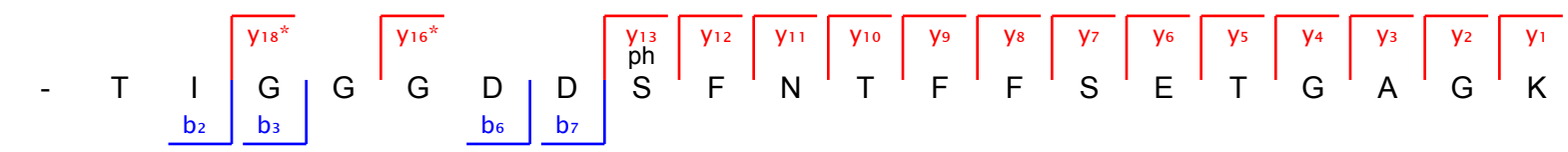
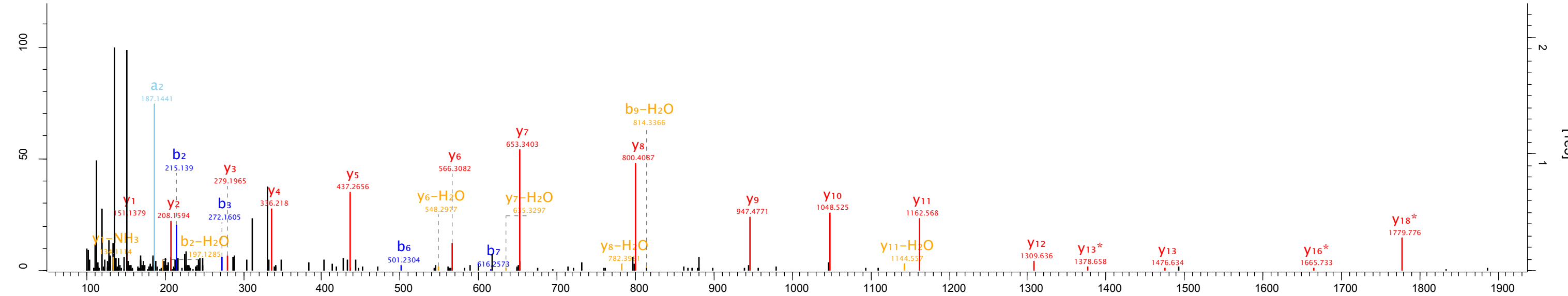
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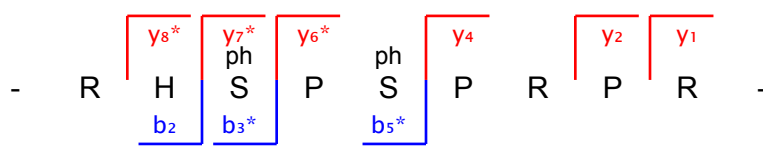
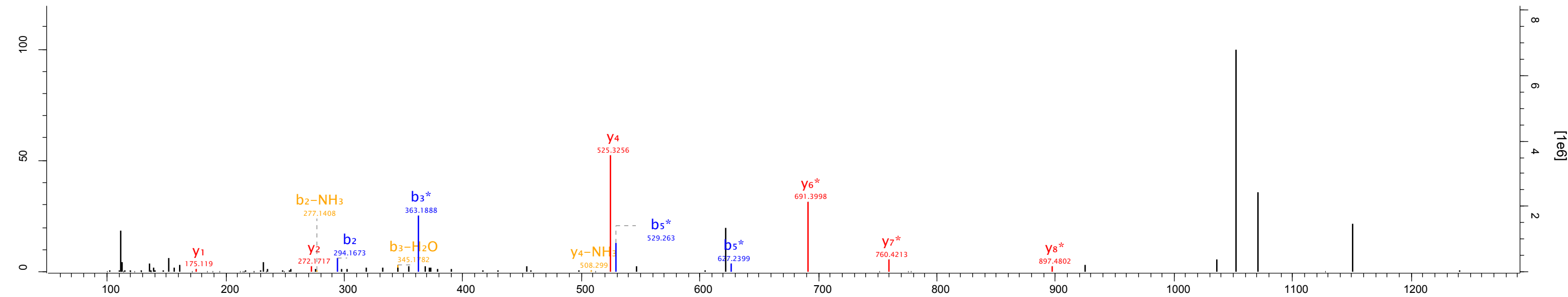
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20171215_MaS_33SR_LMH_phospho_02

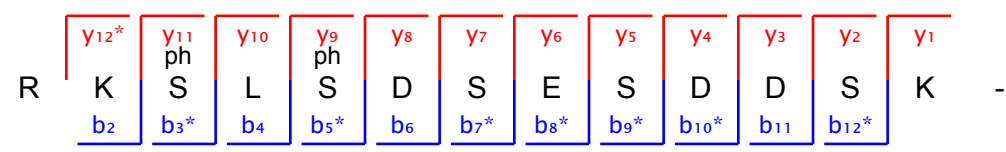
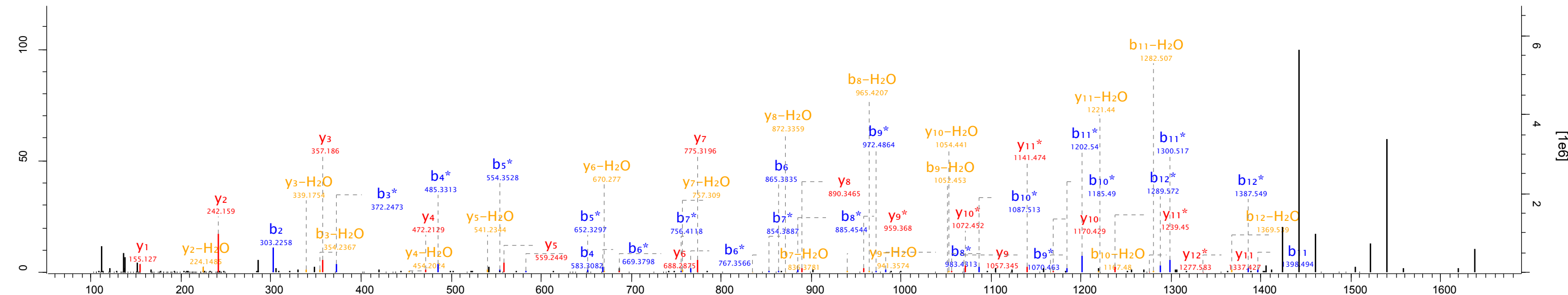
Scan	Method	Score	m/z	Gene names
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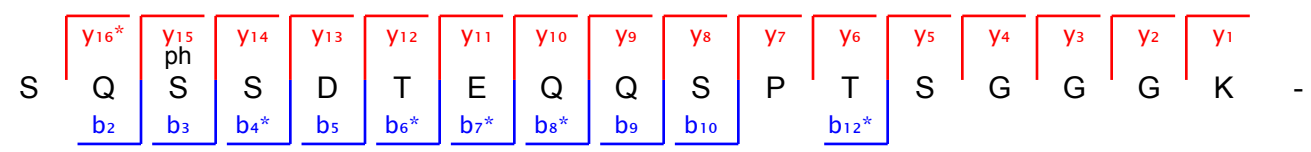
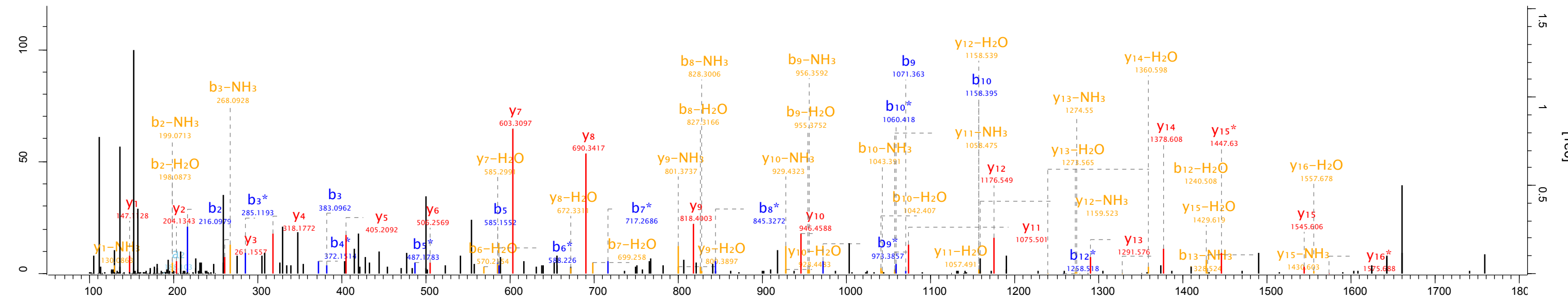
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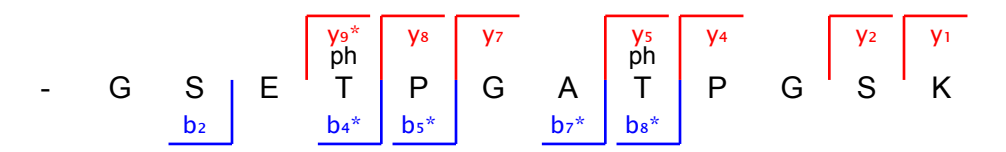
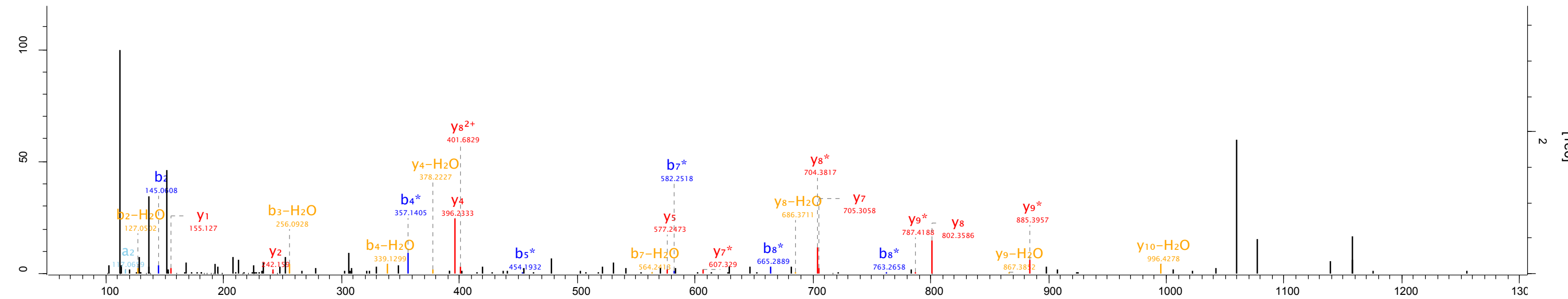
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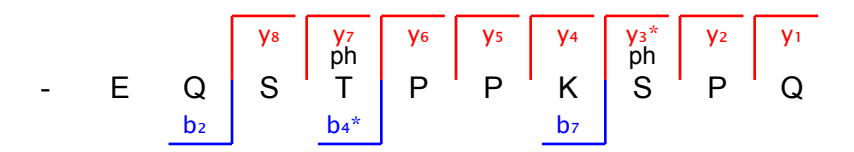
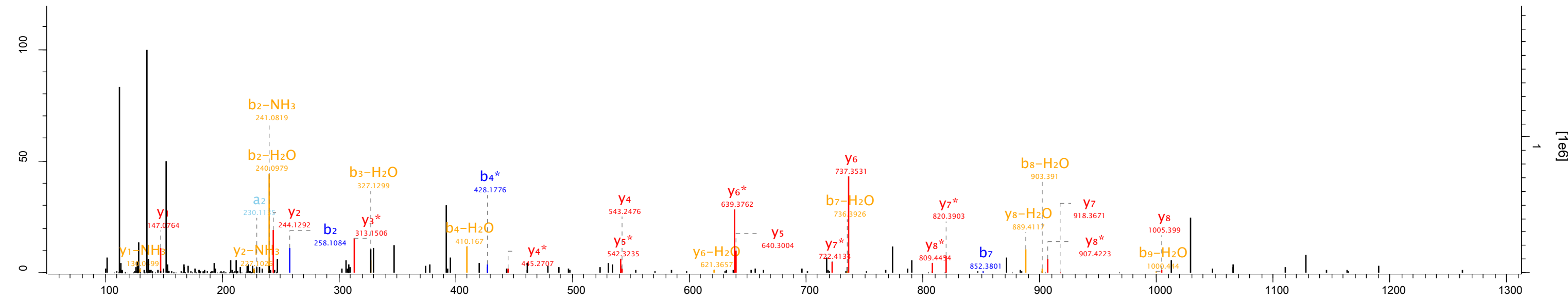
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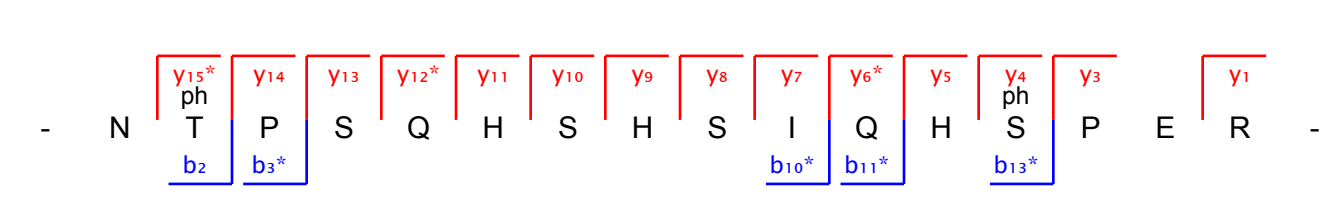
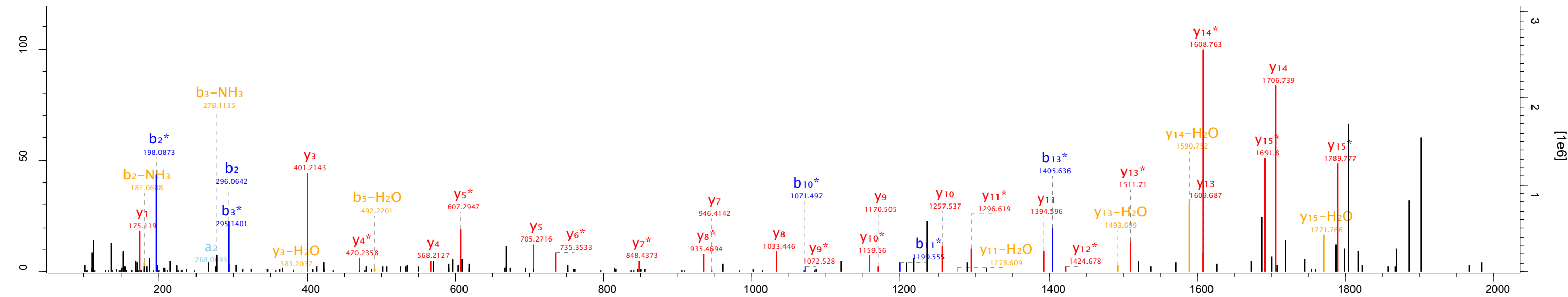
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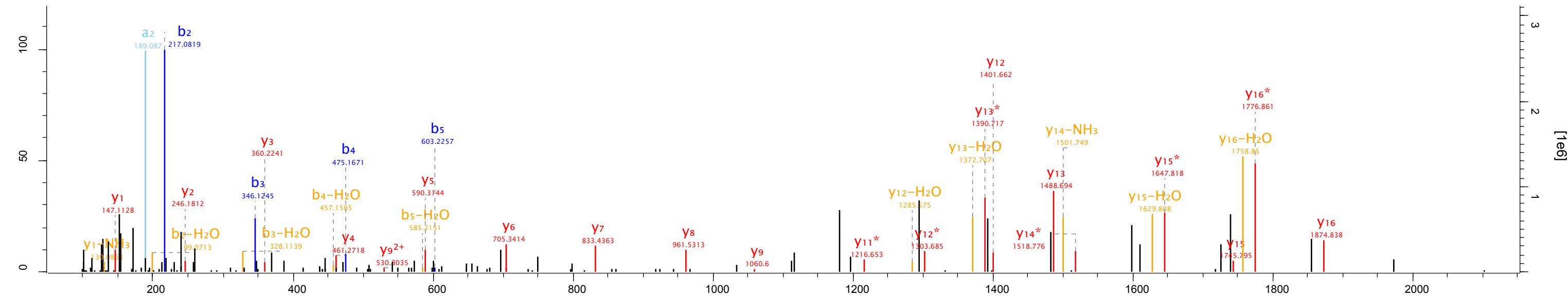
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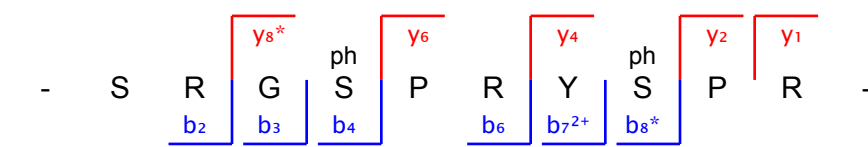
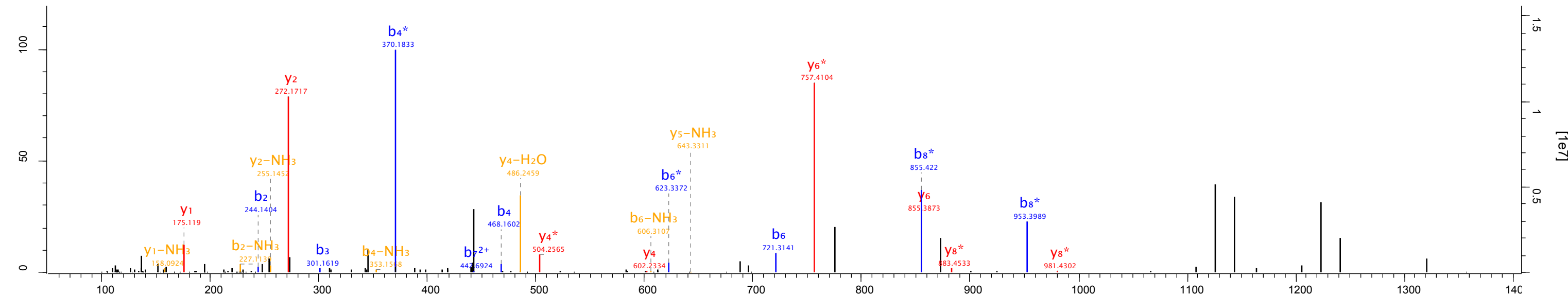
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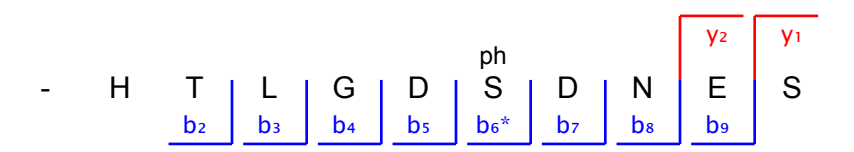
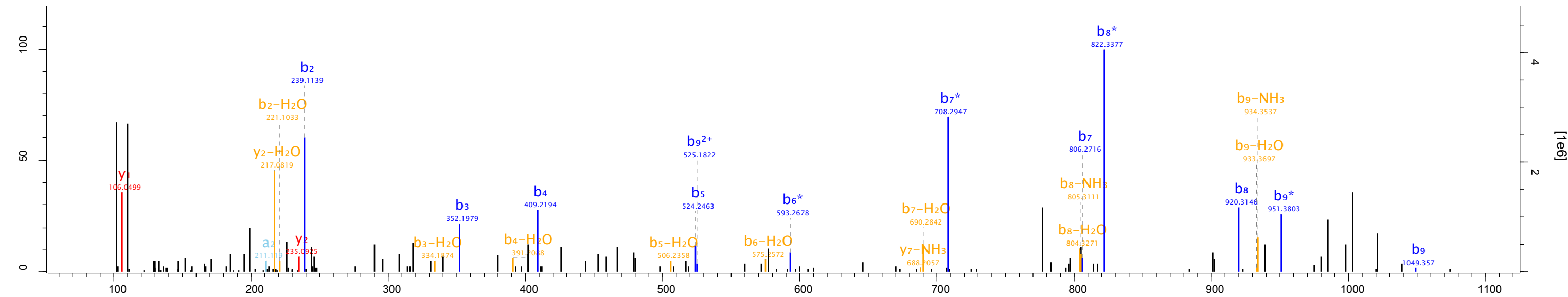
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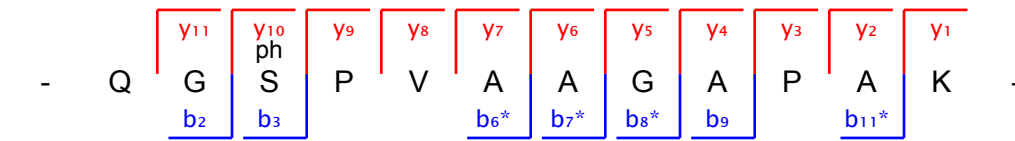
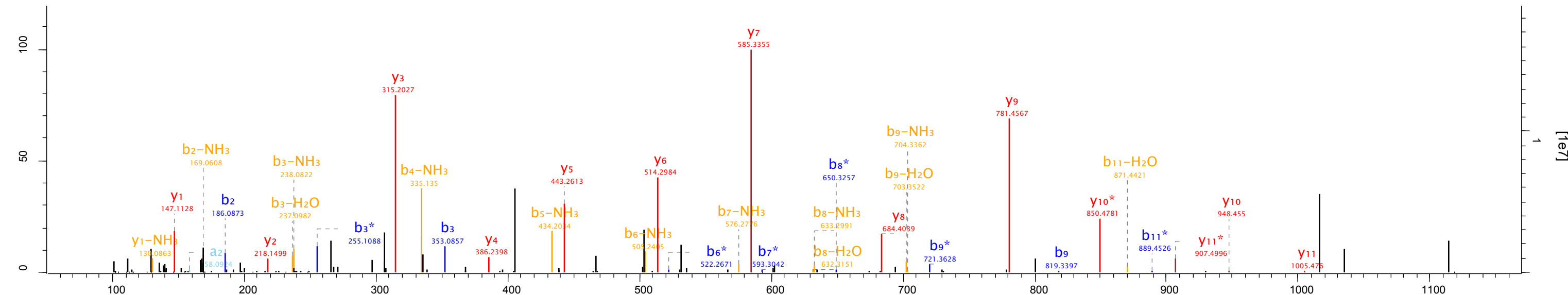


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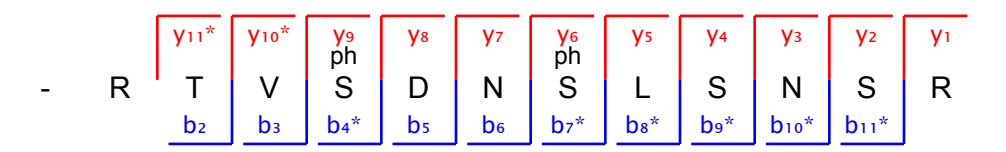
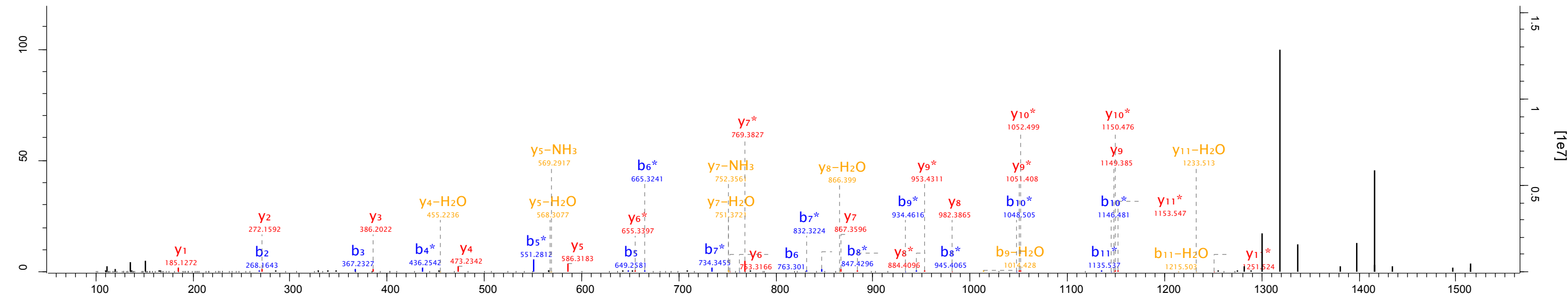


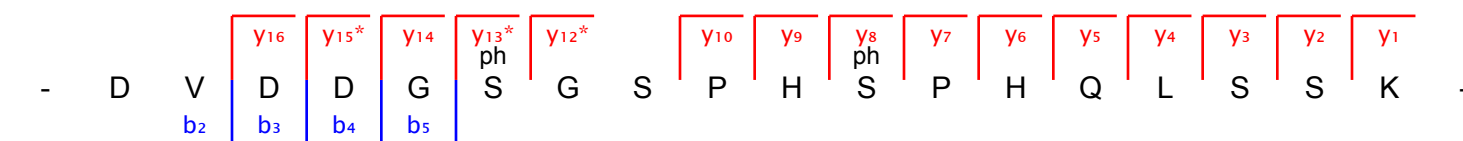
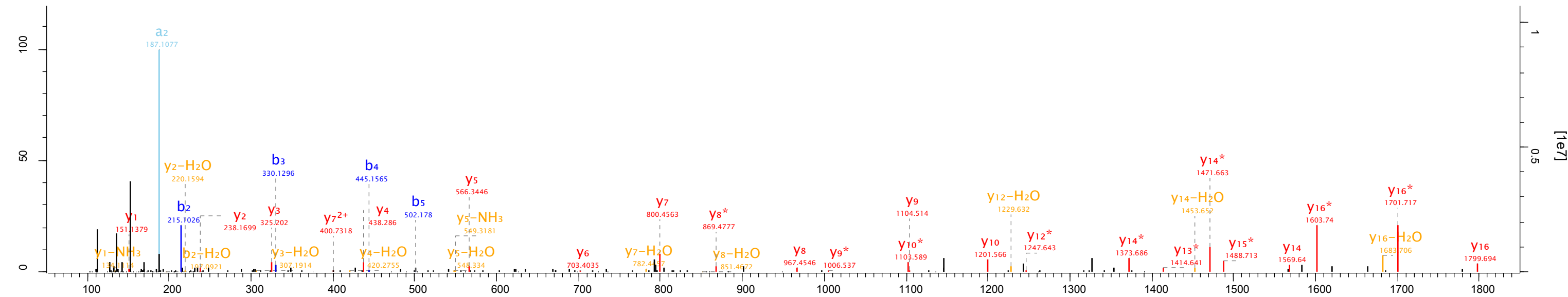
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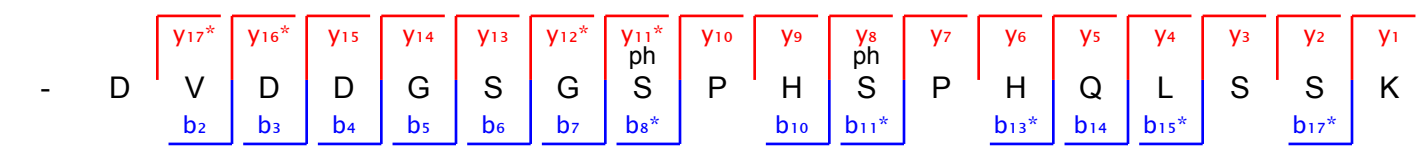
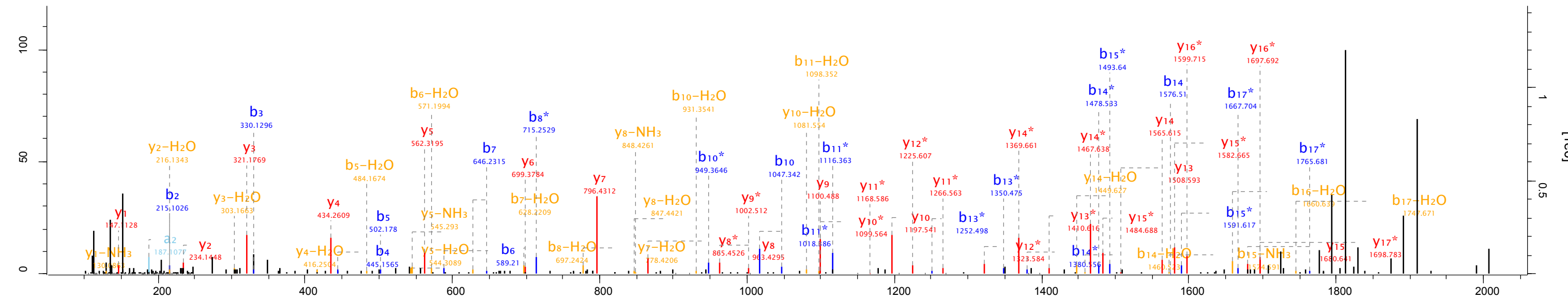


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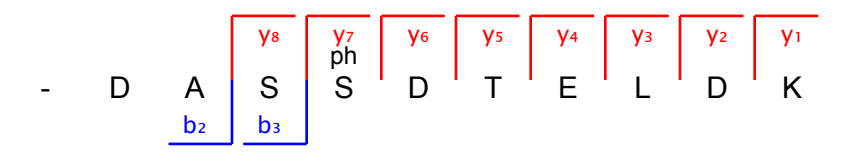
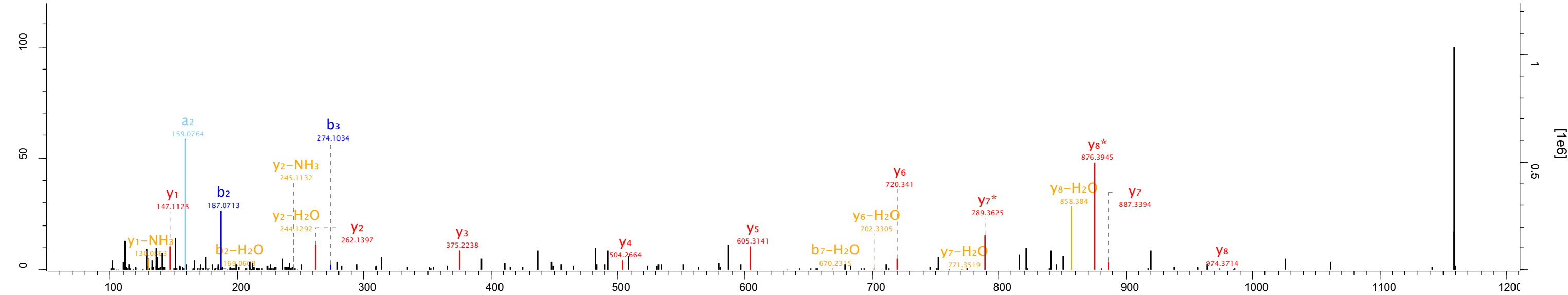


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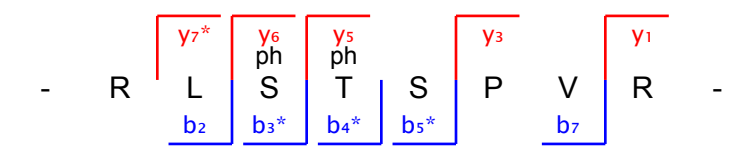
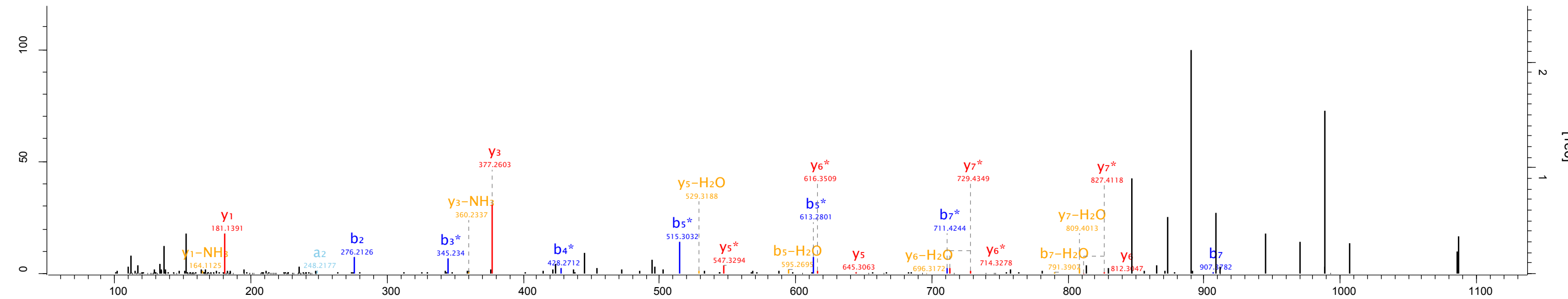


20171215_MaS_33SR_LMH_phospho_02

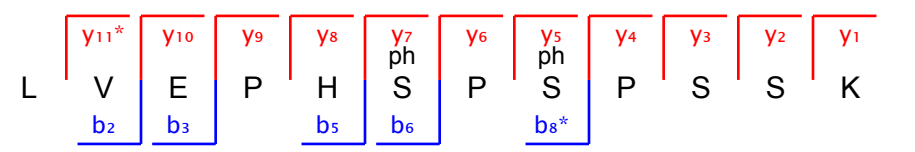
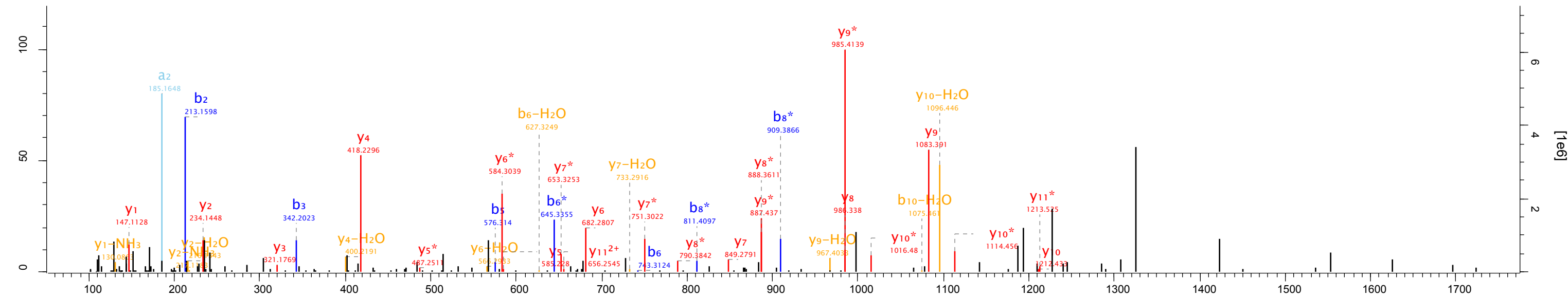
3638 FTMS; HCD 47.62 580.72 ZFPM2



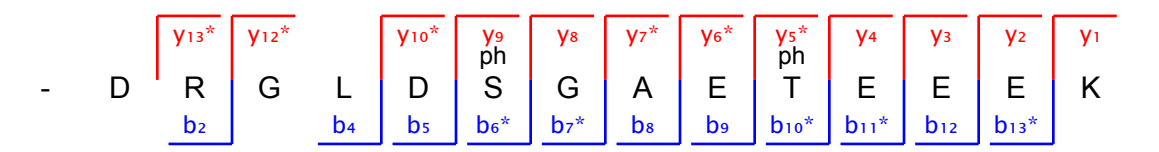
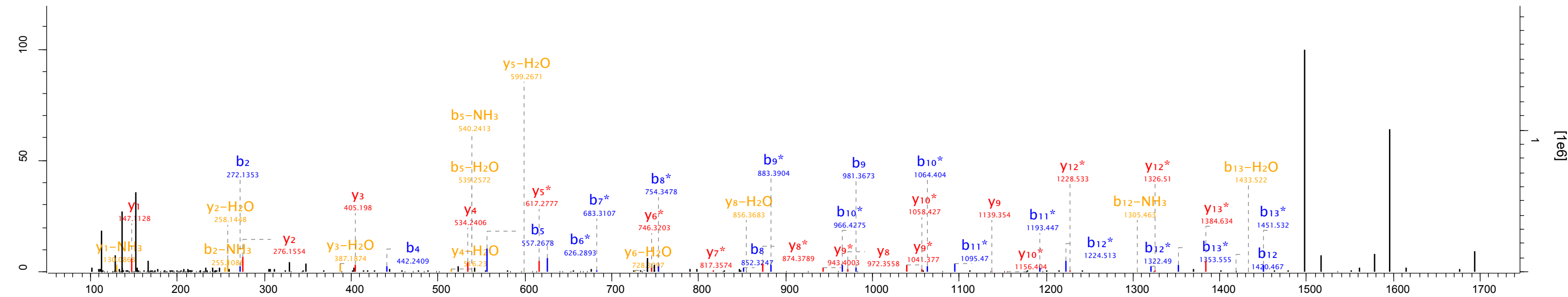
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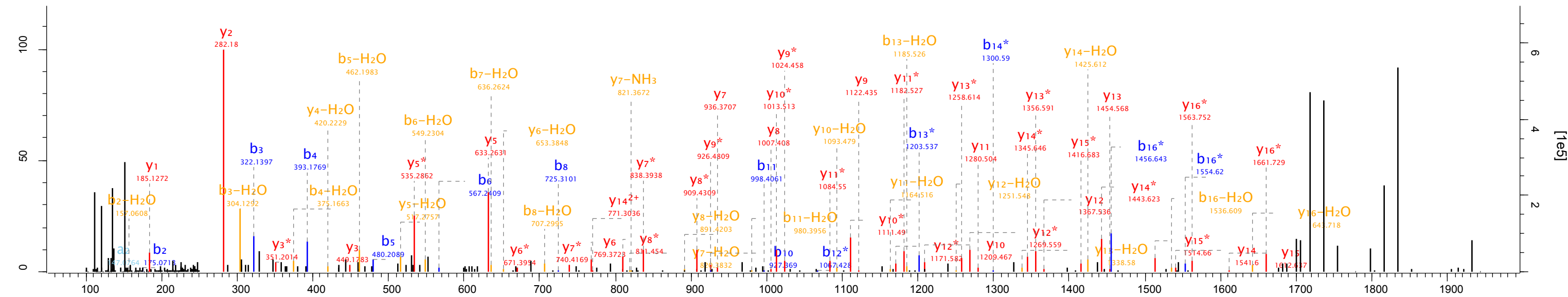
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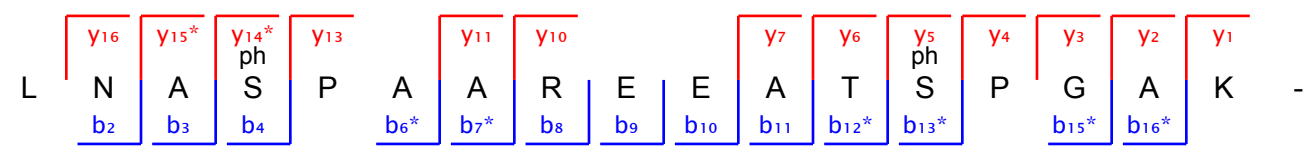
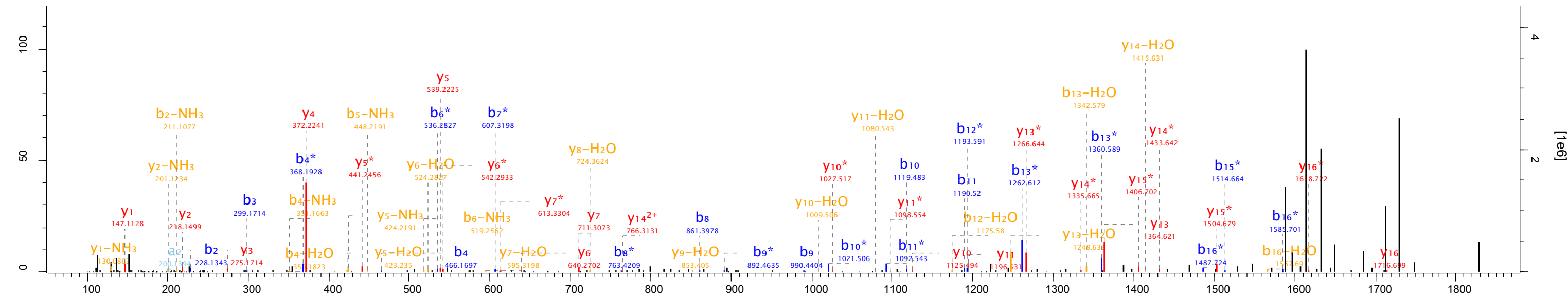


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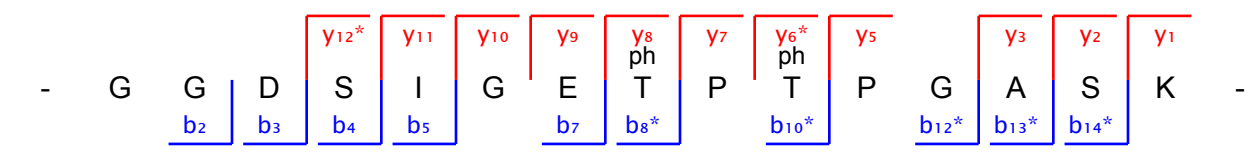
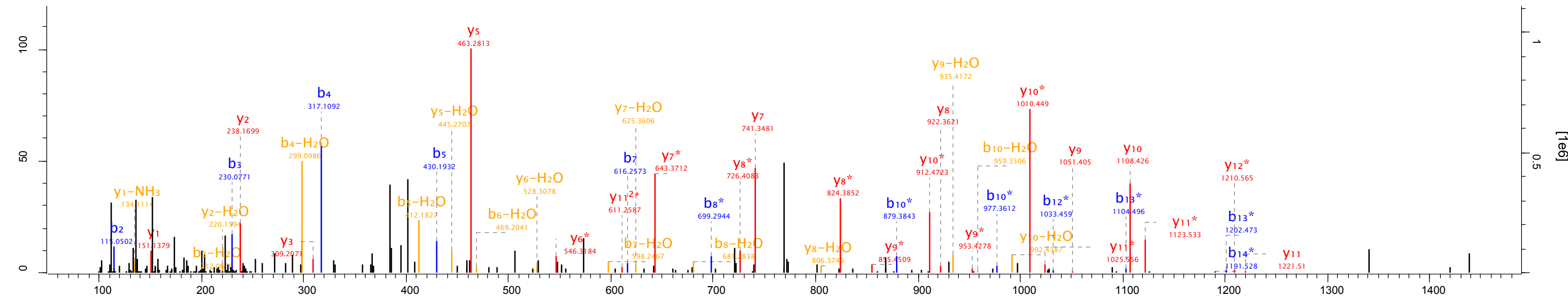


Raw file
20171215_MaS_33SR_LMH_phospho_02

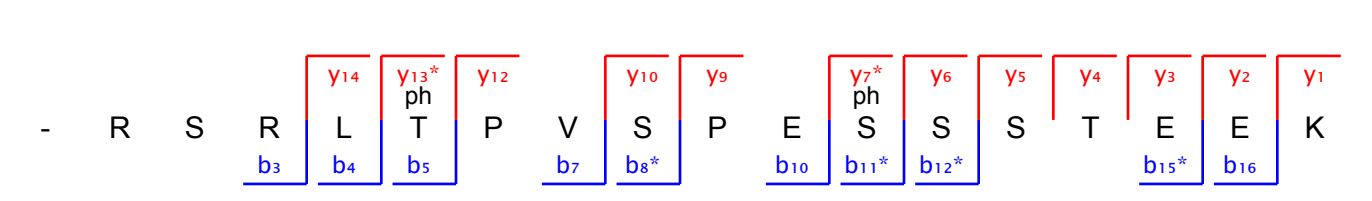
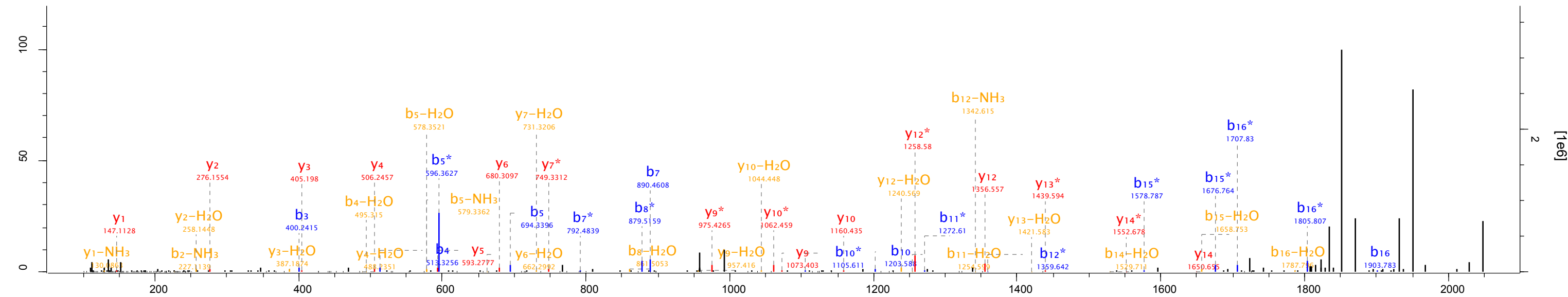
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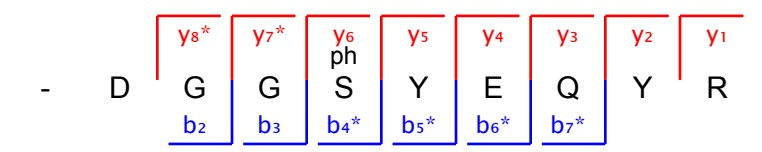
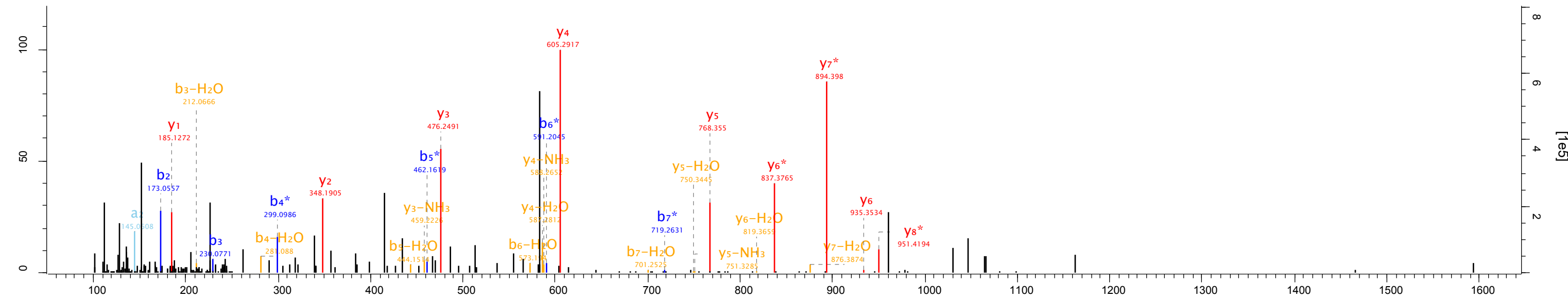
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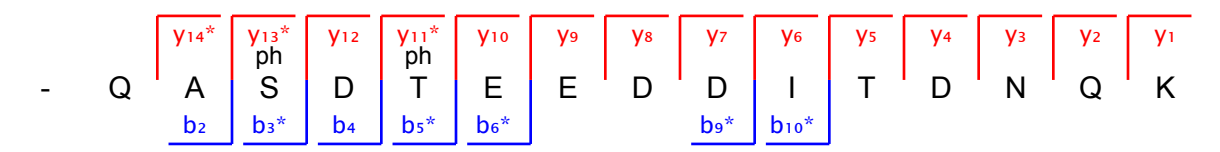
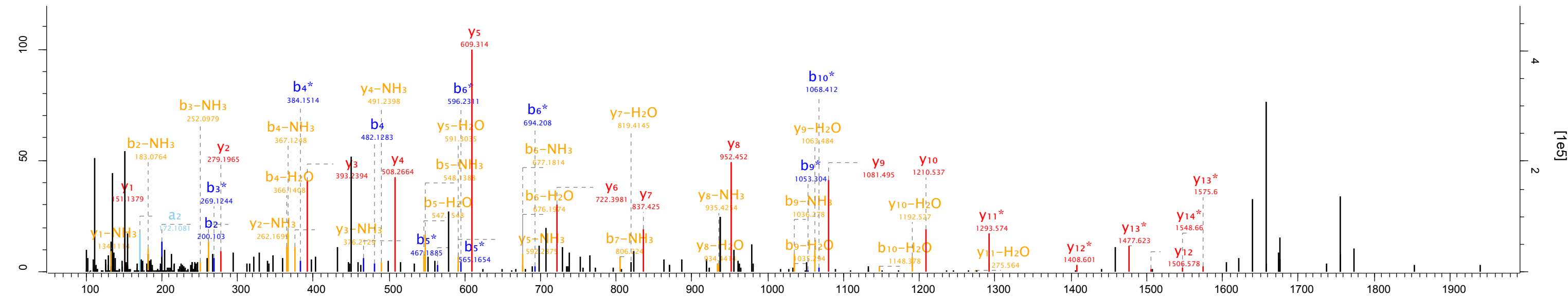
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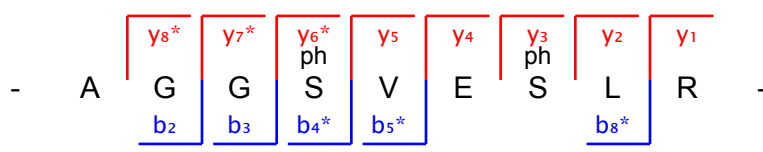
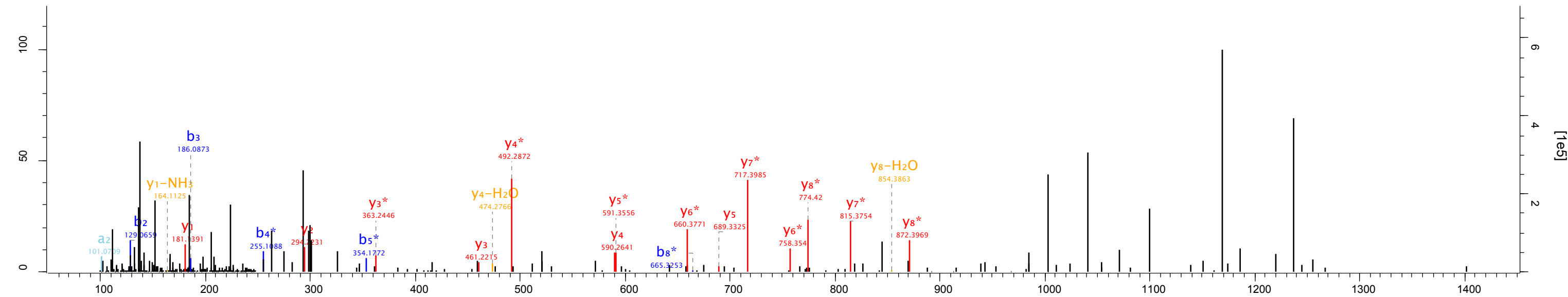
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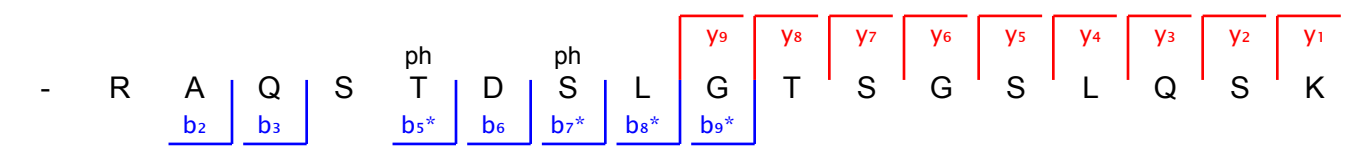
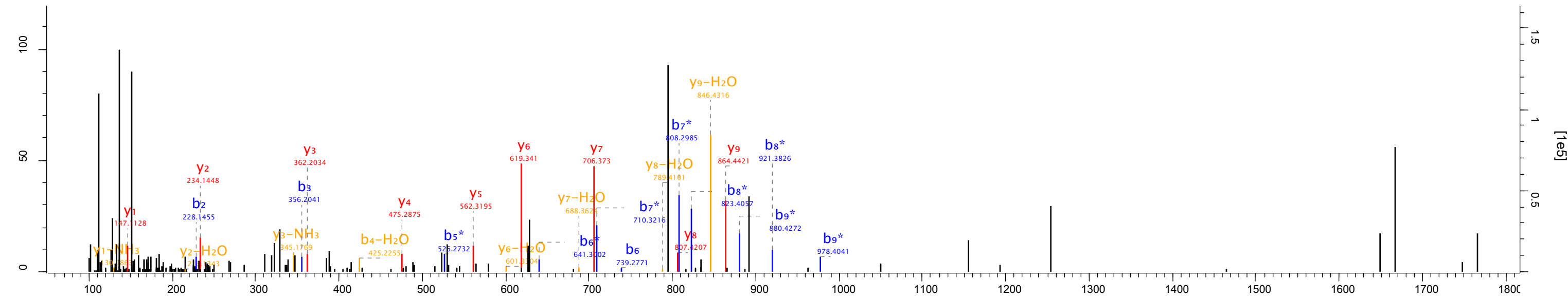
Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 5158 Method FTMS; HCD Score 155.7 m/z 937.34 Gene names UBN2



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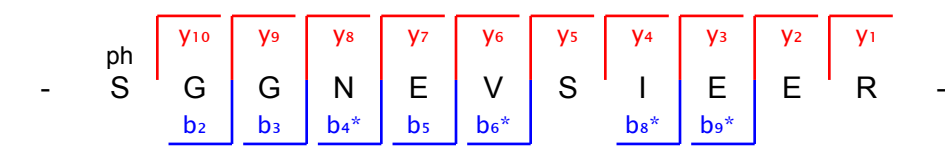
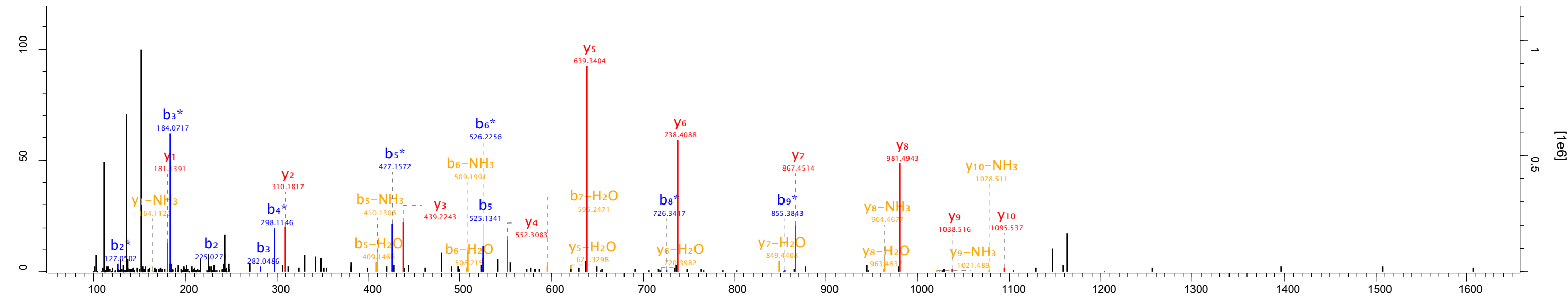


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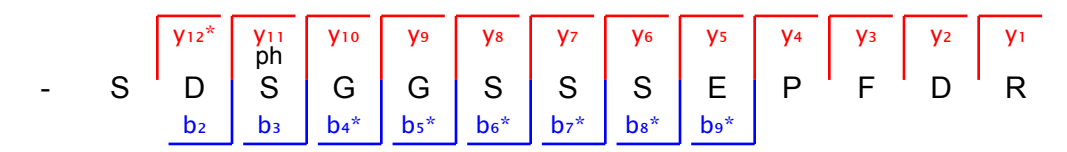
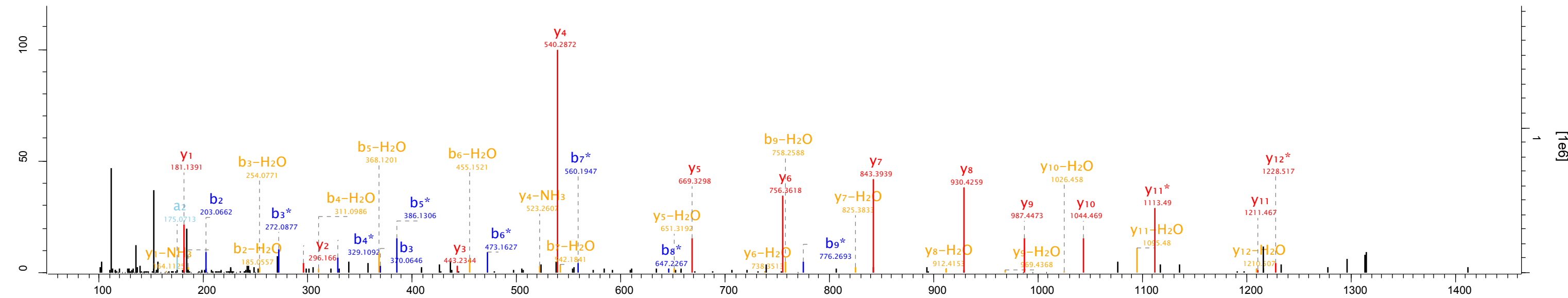


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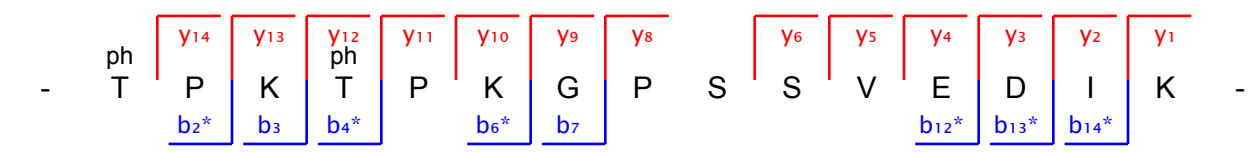
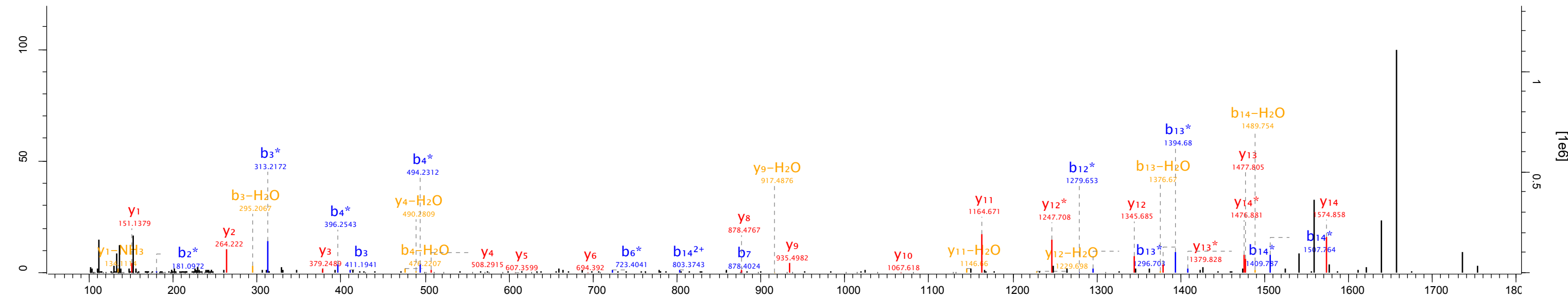
Scan 5778 Method FTMS; HCD Score 129.01 m/z 631.77 Gene names WDR43

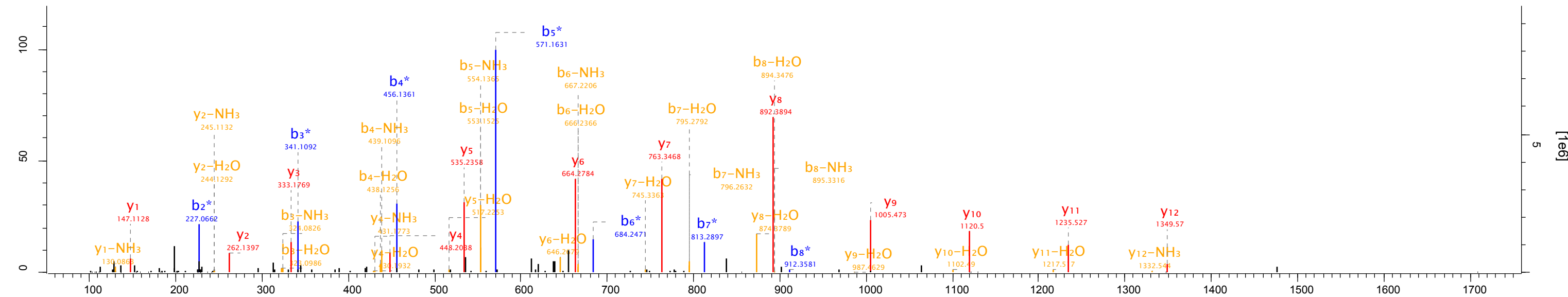


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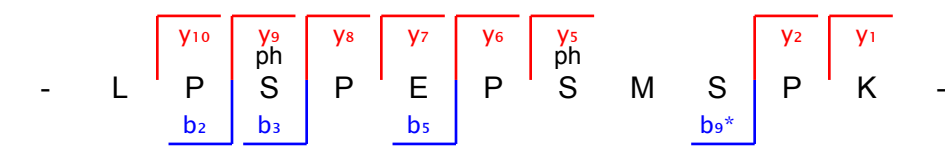
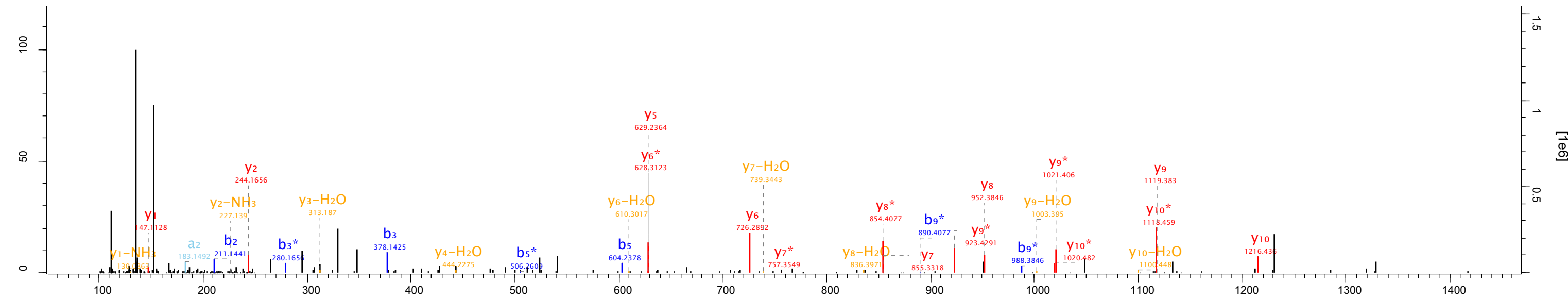




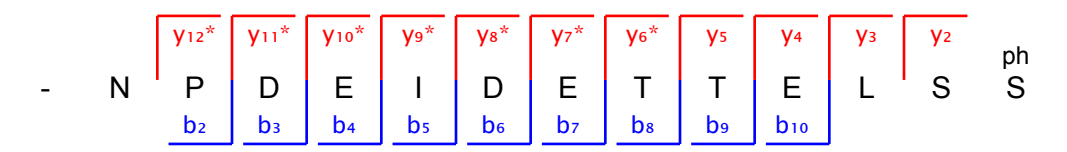
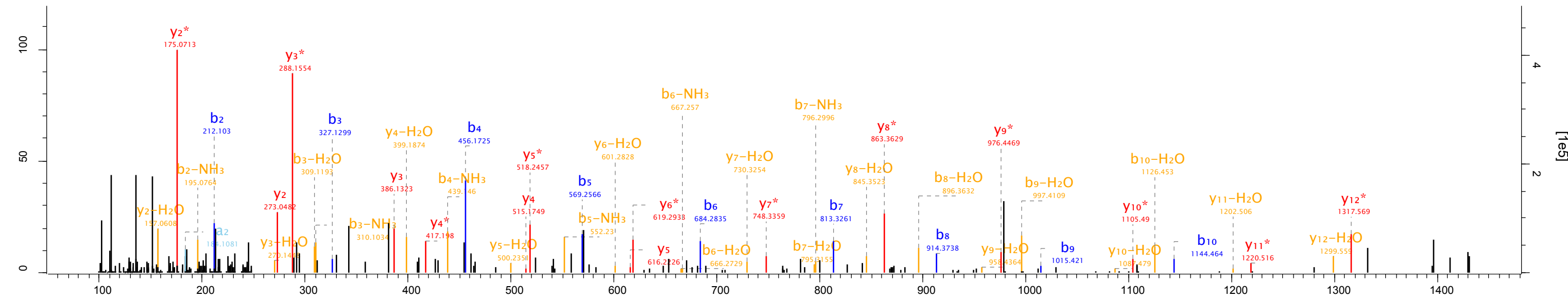
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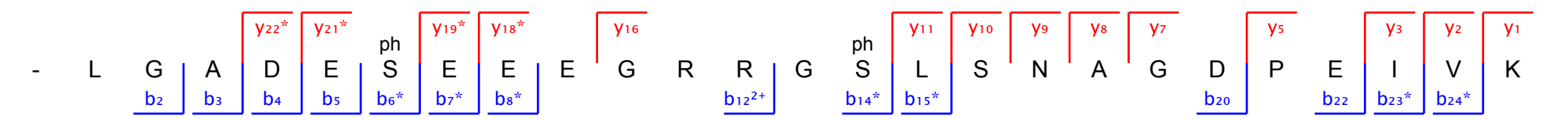
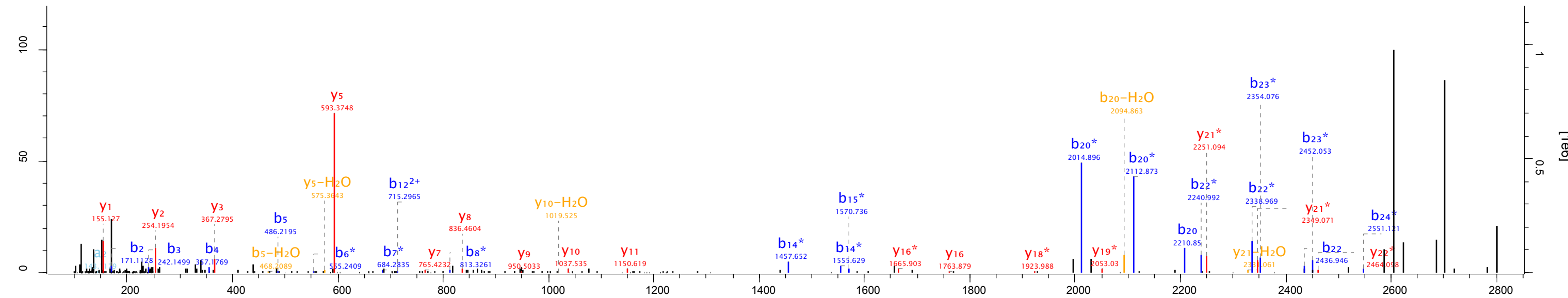
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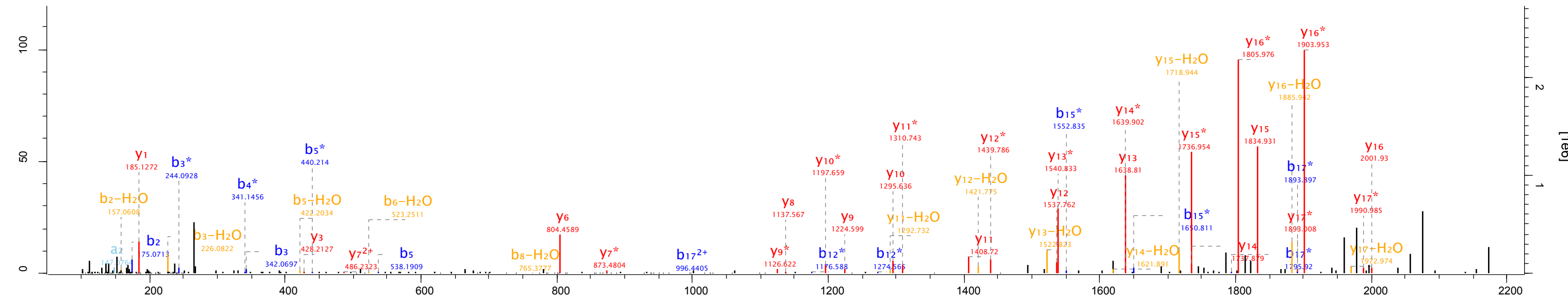


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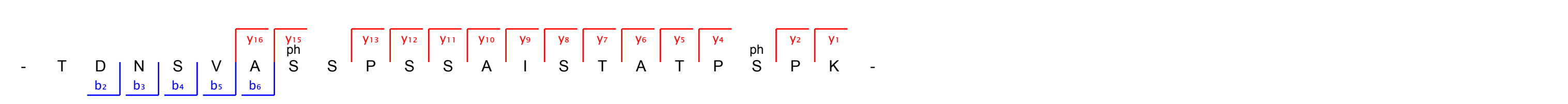
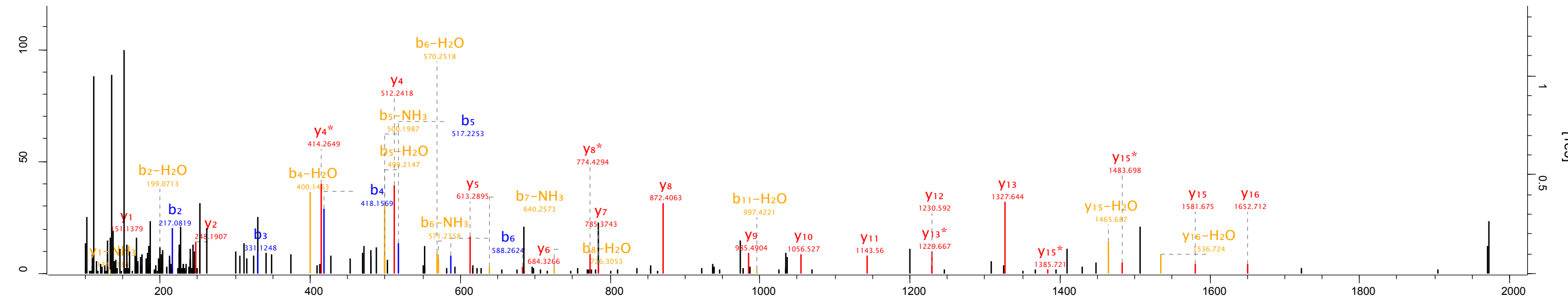


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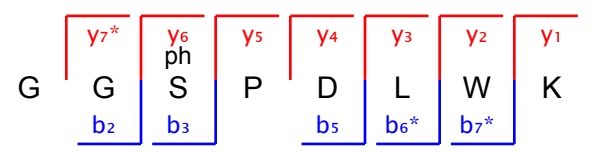
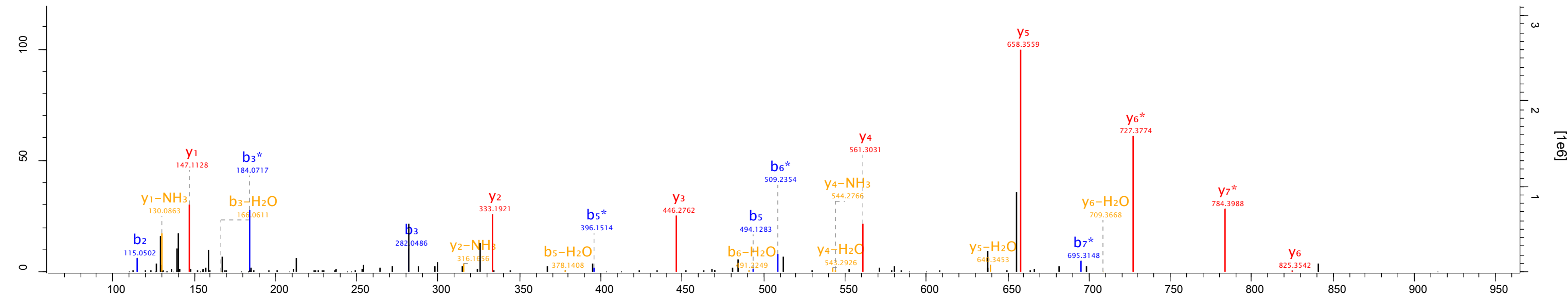
Fragmentation scheme showing amino acid residues and their corresponding b and y ion series:

- S: b₂, y₁₇*
- S: b₃, y₁₆ph
- P: b₄*
- V: b₅, y₁₄
- T: y₁₃
- E: y₁₂
- L: y₁₁
- A: y₁₀
- S: y₉
- R: y₈
- S: b₁₂*
- P: y₆
- I: b₁₅*
- R: y₃
- Q: b₁₇*
- D: b₁₇*
- R: y₁

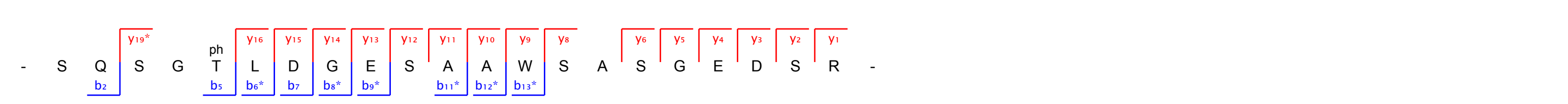
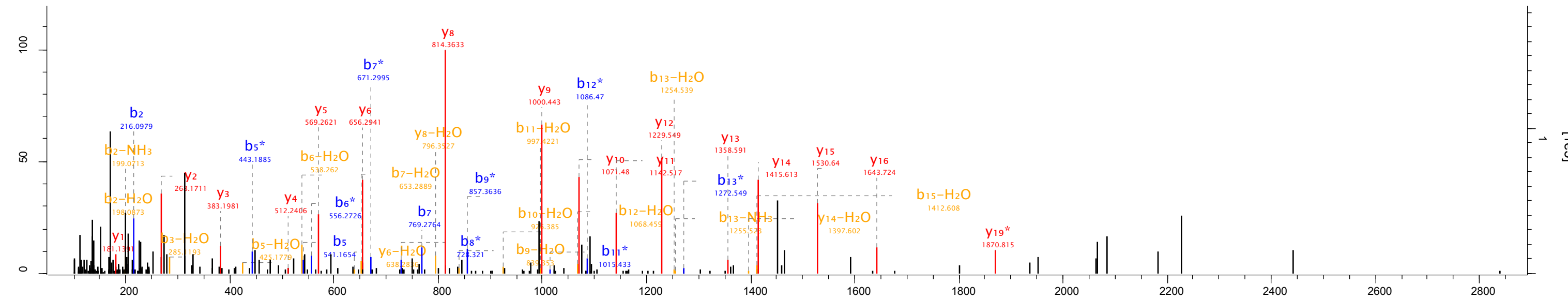
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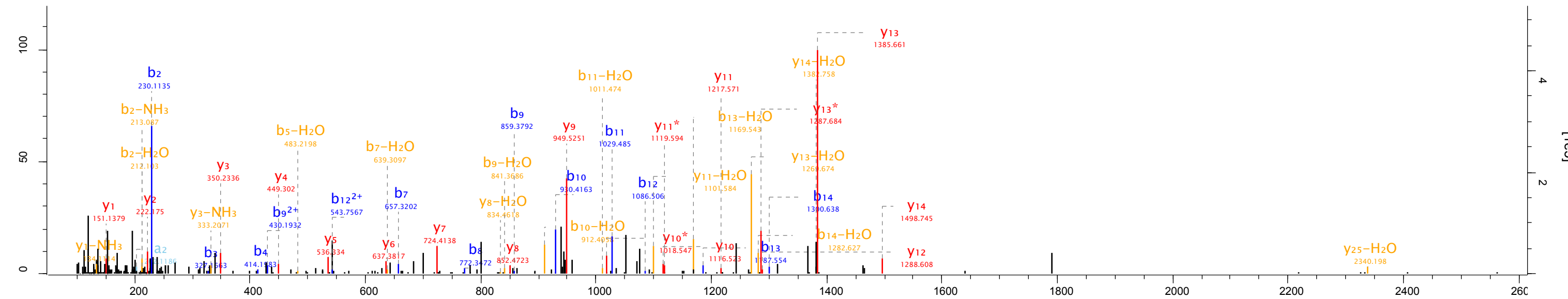
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Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 10878 Method FTMS; HCD Score 114.68 m/z 1092.45 Gene names TSC2



Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 11228 Method FTMS; HCD Score 98.63 m/z 896.1 Gene names TCOF1

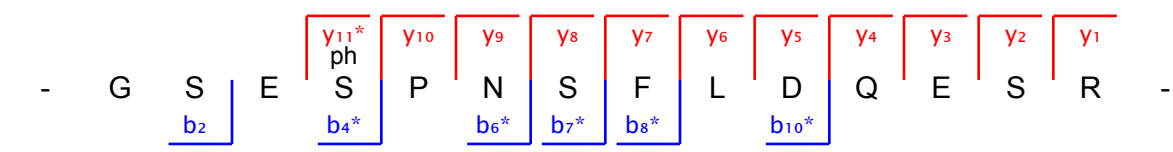
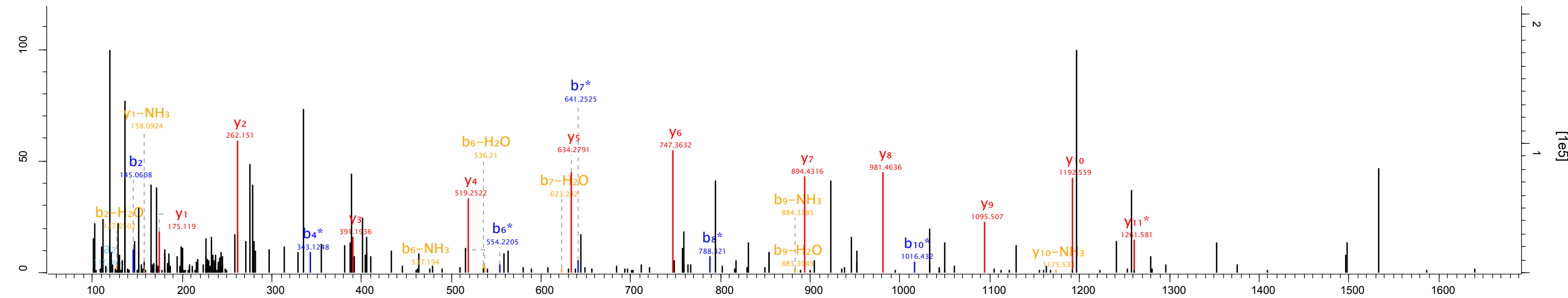


- T Q P S S G V D S A V G T L P A T S_{ph} P Q S T S V Q A K -

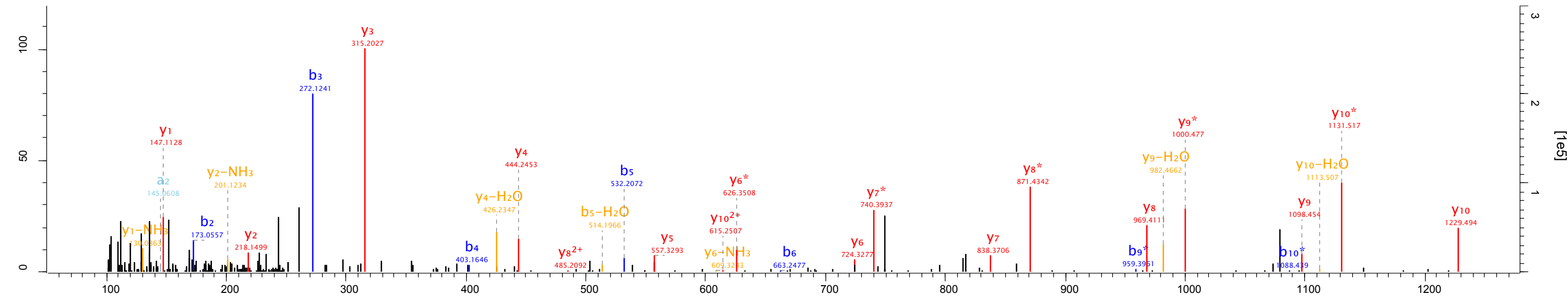
Labels below the sequence indicate the b and y ions corresponding to the peaks in the mass spectrum:

- Blue boxes under Q, P, S, V, D, S, A, V, G, T, L: b₂, b₃, b₄, b₇, b₈, b₉, b₁₀, b₁₁, b₁₂, b₁₃, b₁₄
- Red boxes under L, P, A, T, S, P, Q, S, T, S, V, Q, A, K: y₁₄, y₁₃, y₁₂, y₁₁, y₁₀, y₉, y₈, y₇, y₆, y₅, y₄, y₃, y₂, y₁

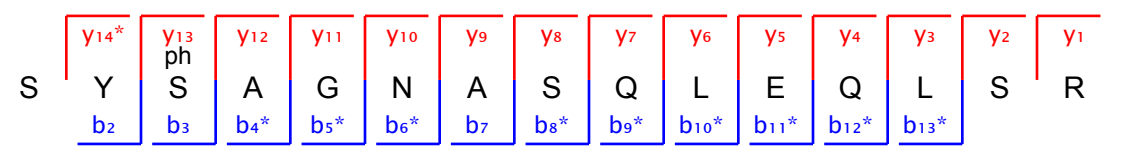
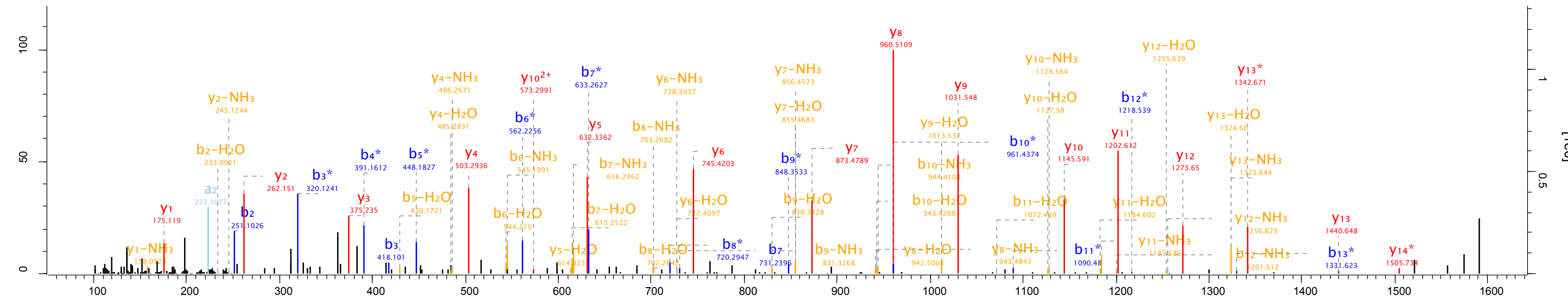
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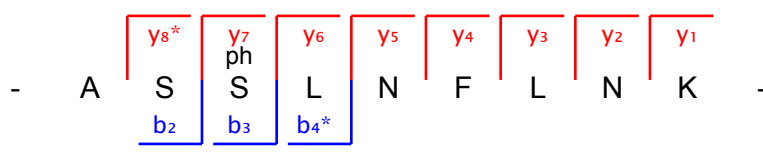
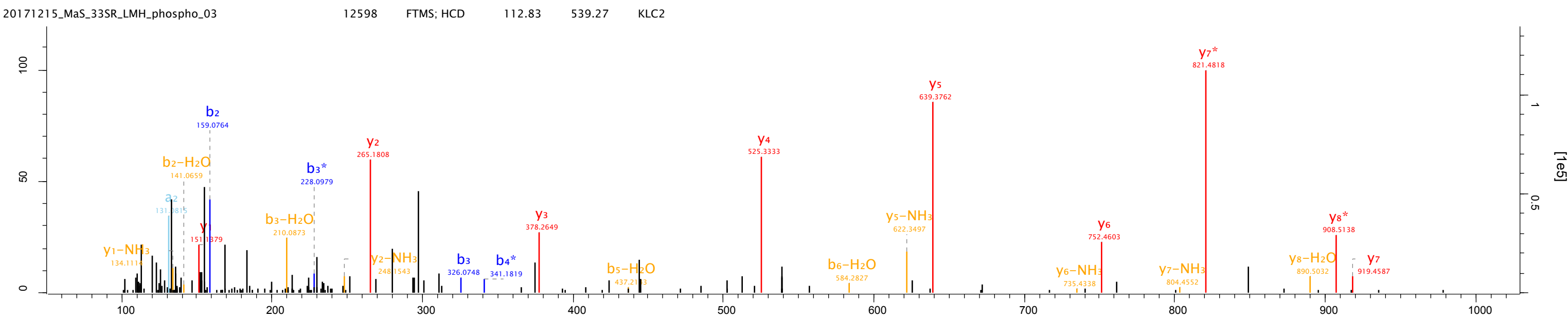


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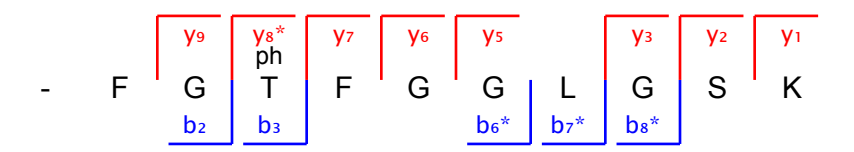
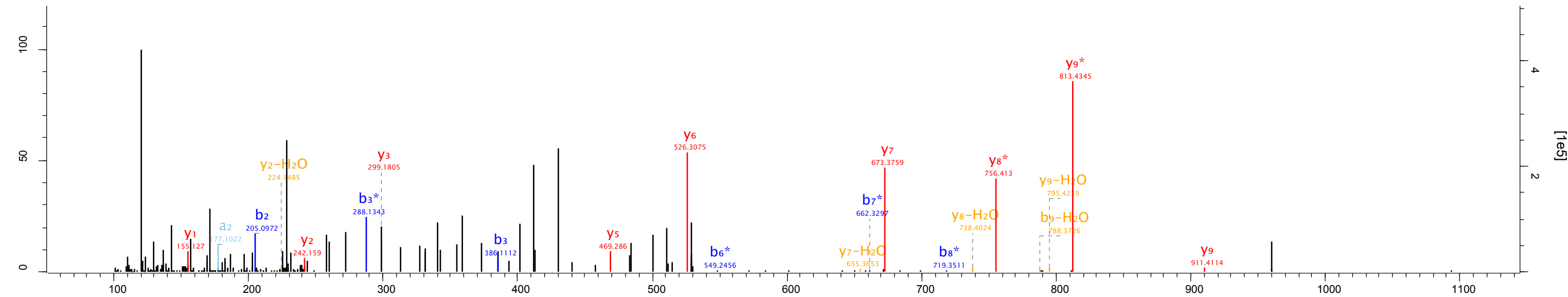


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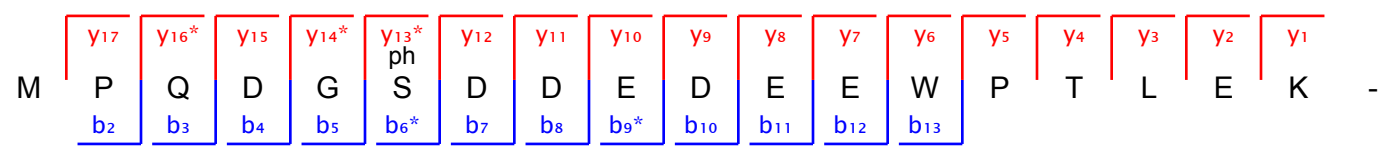
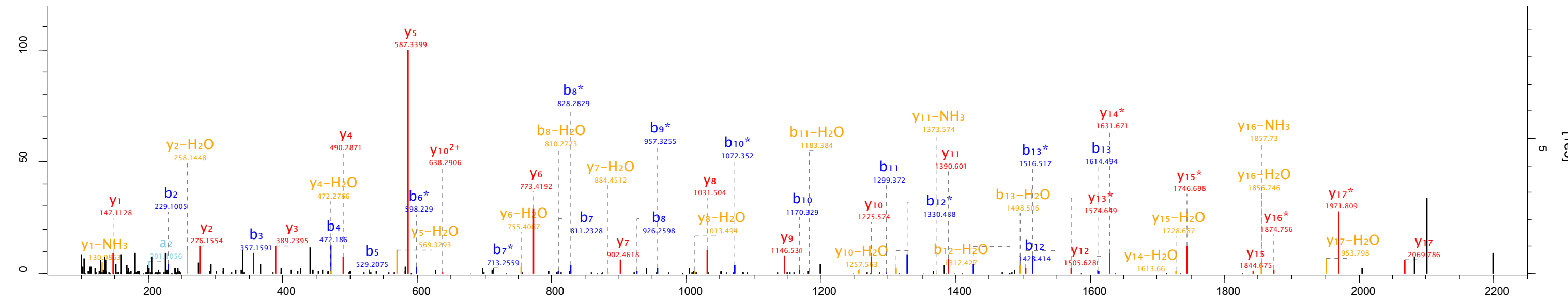




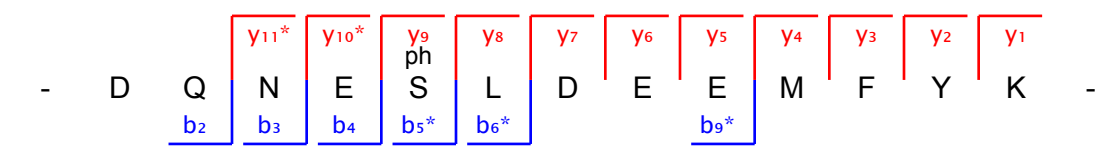
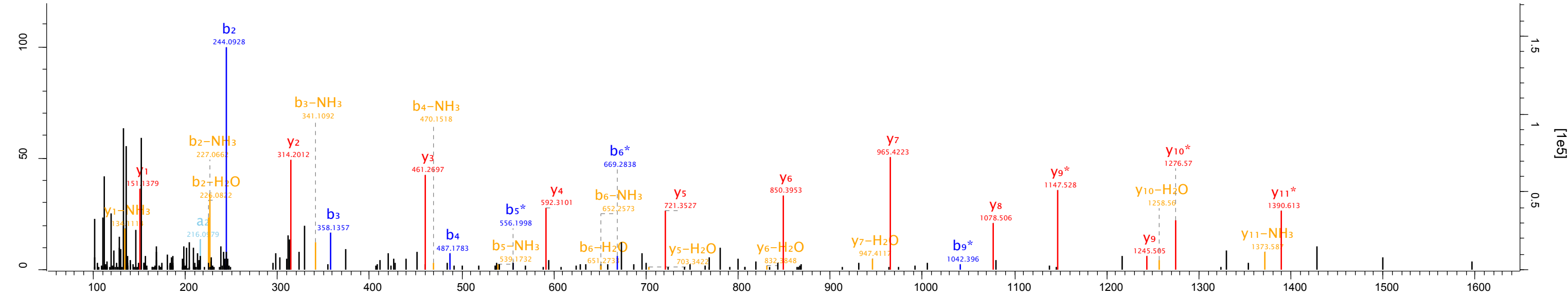
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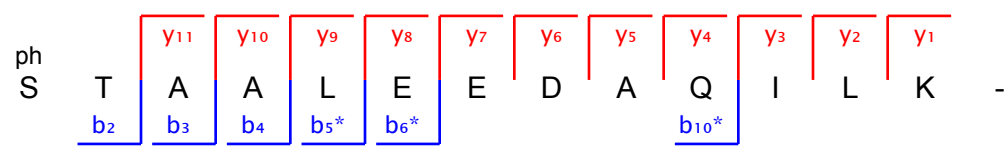
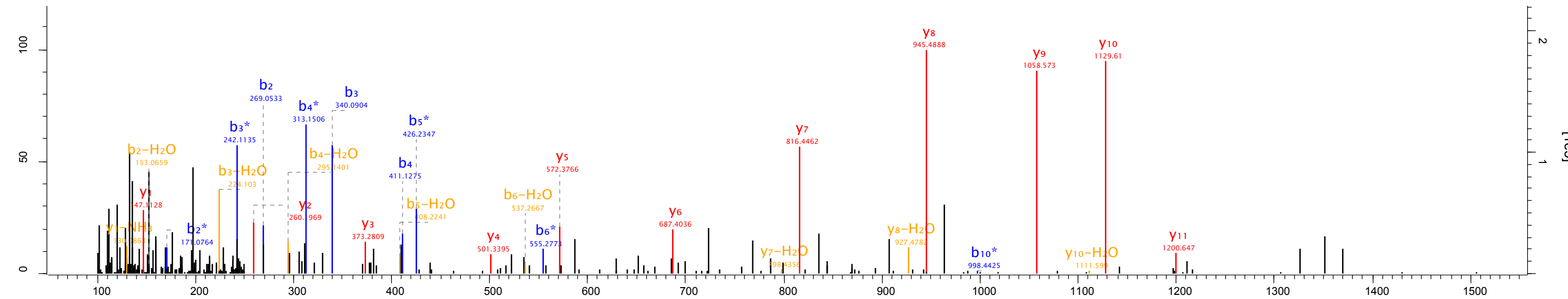
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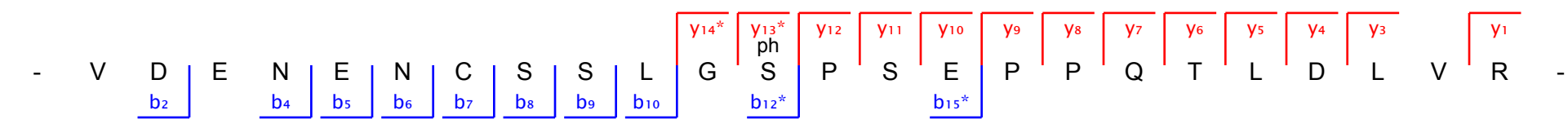
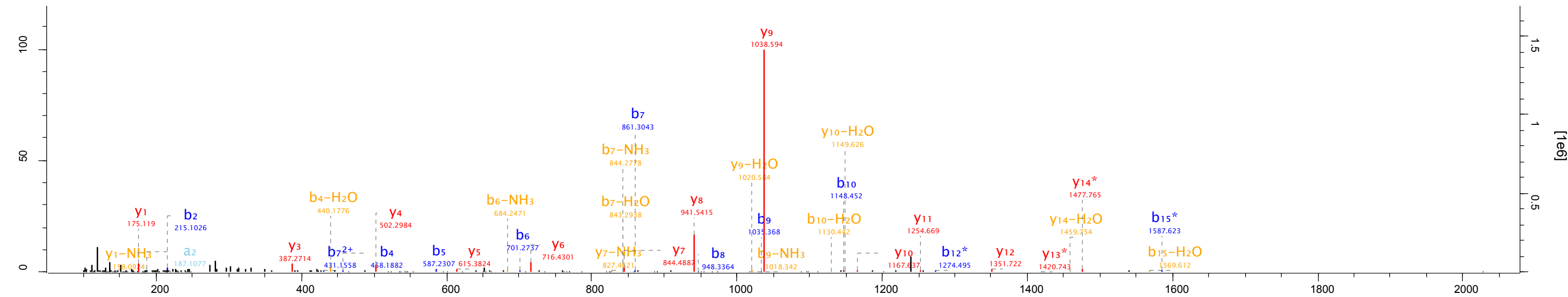
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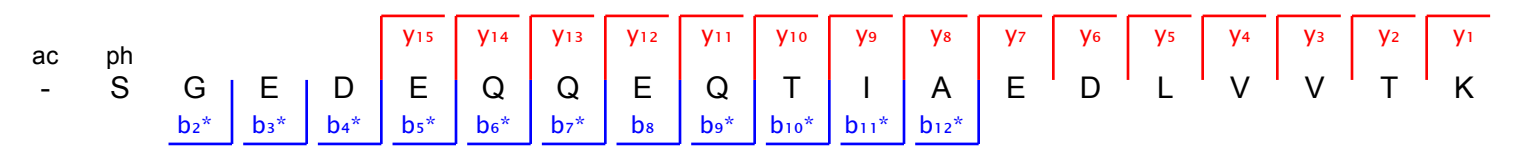
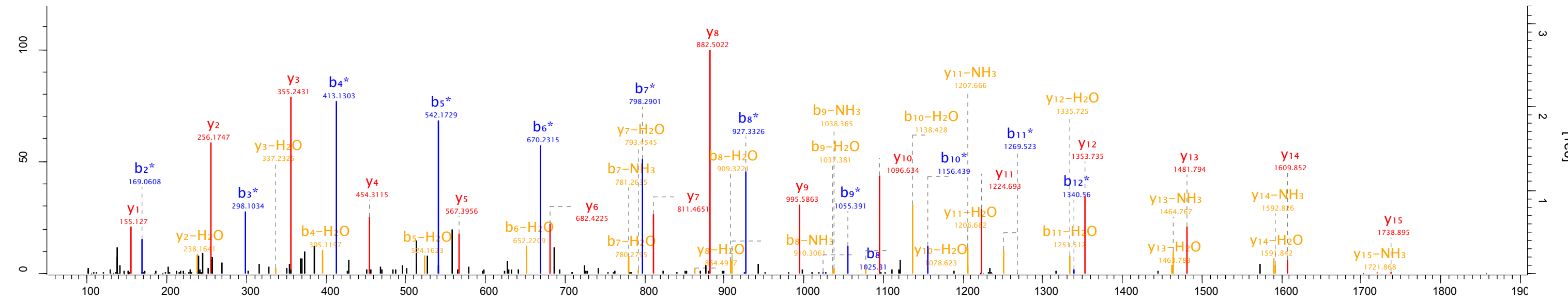
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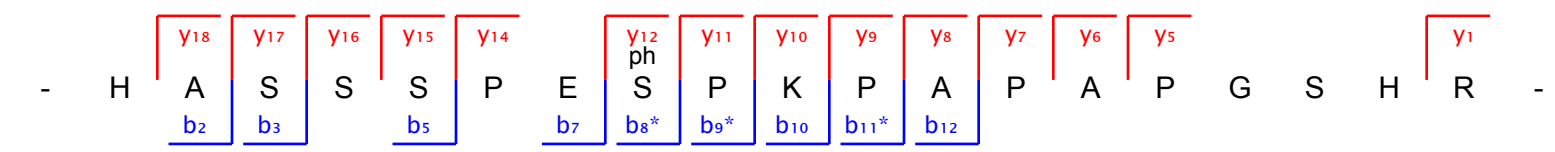
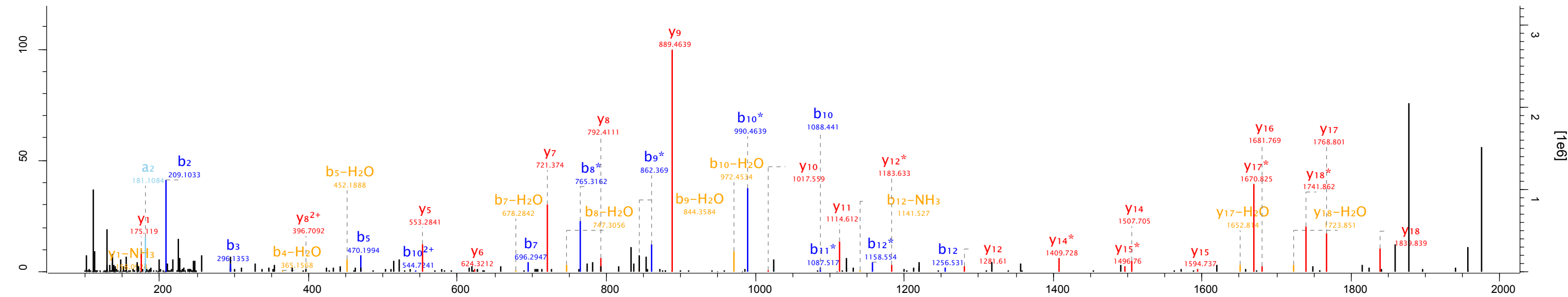
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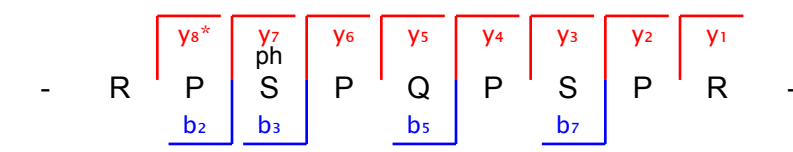
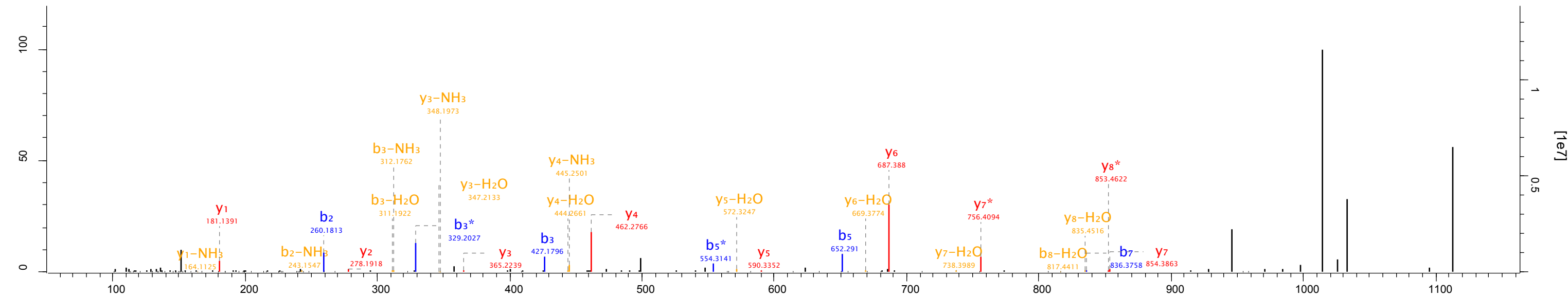
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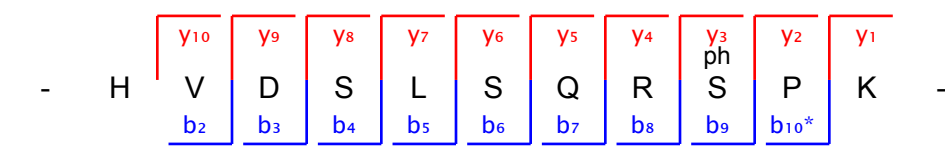
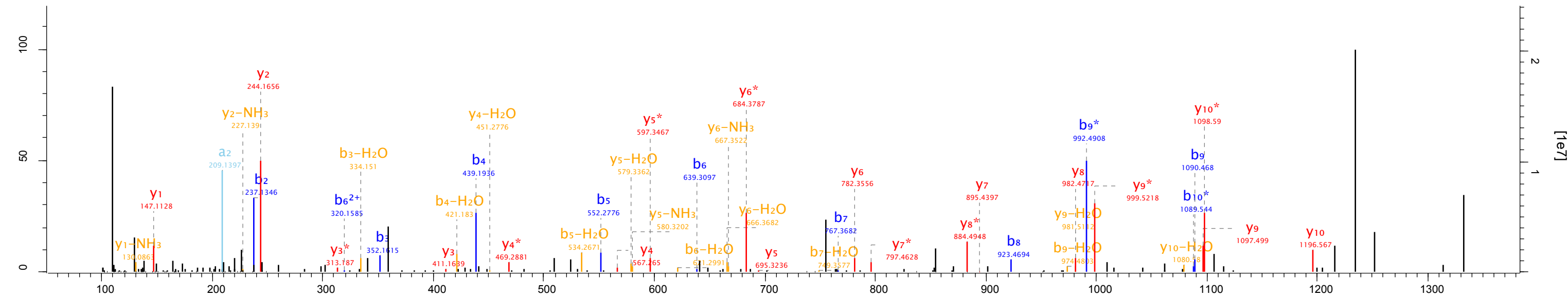
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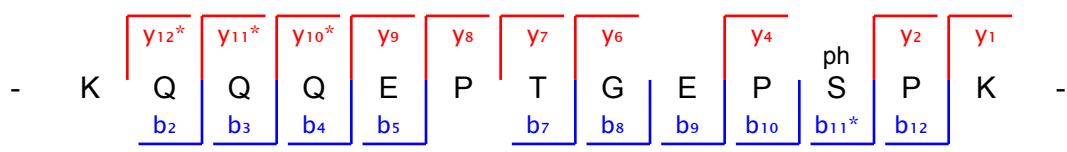
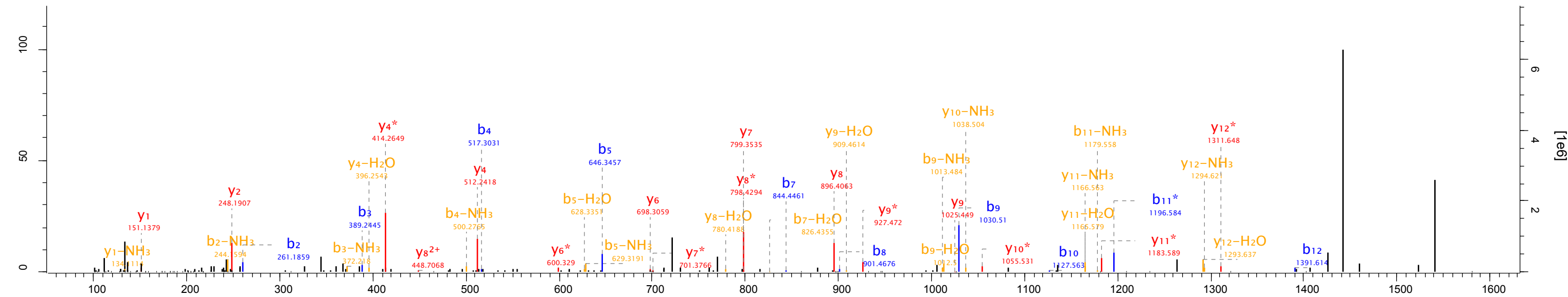
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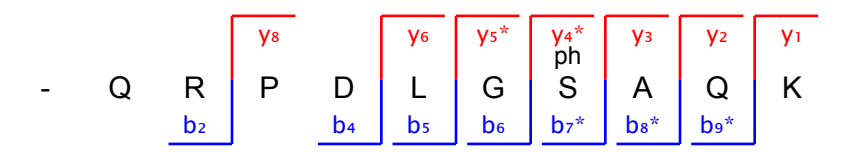
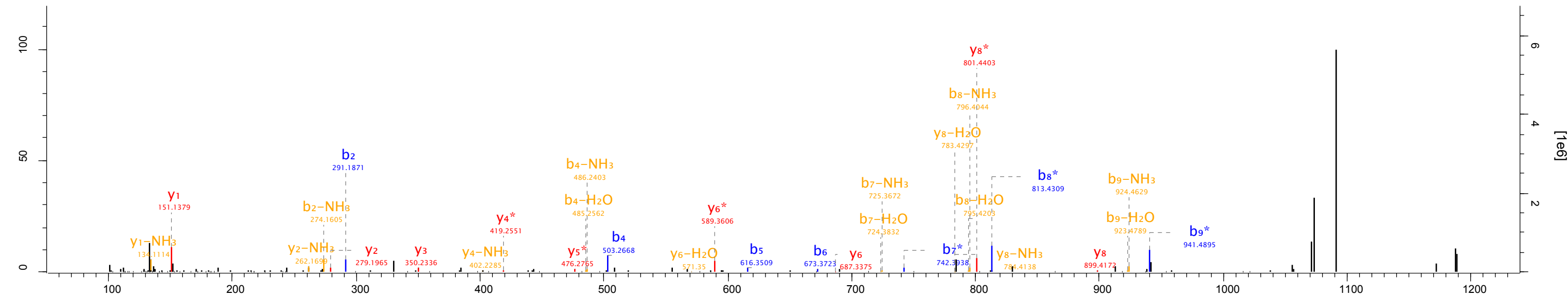
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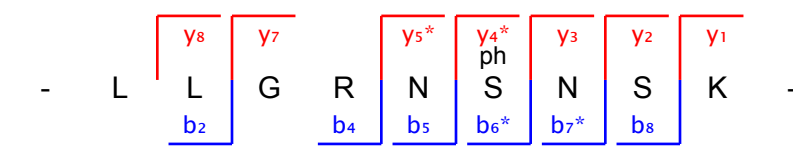
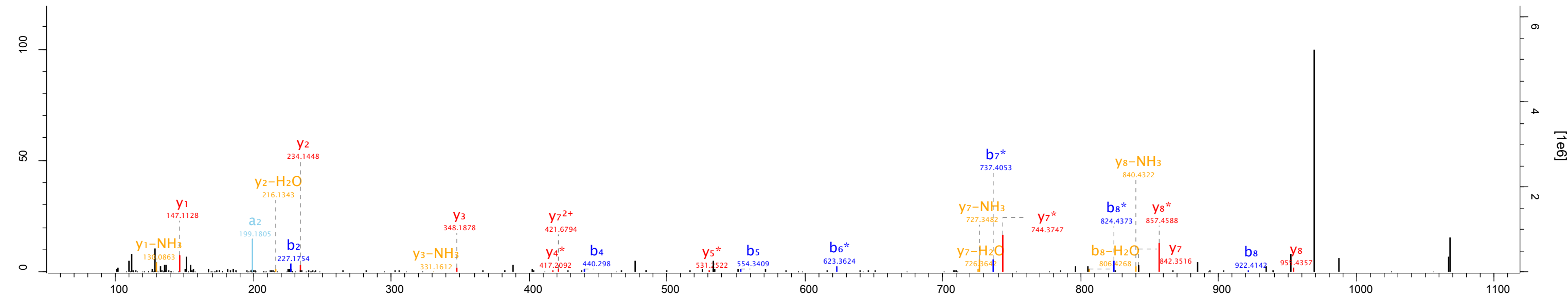
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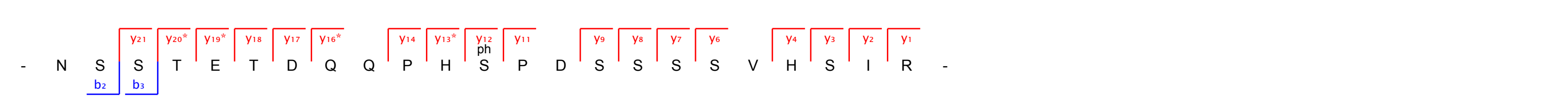
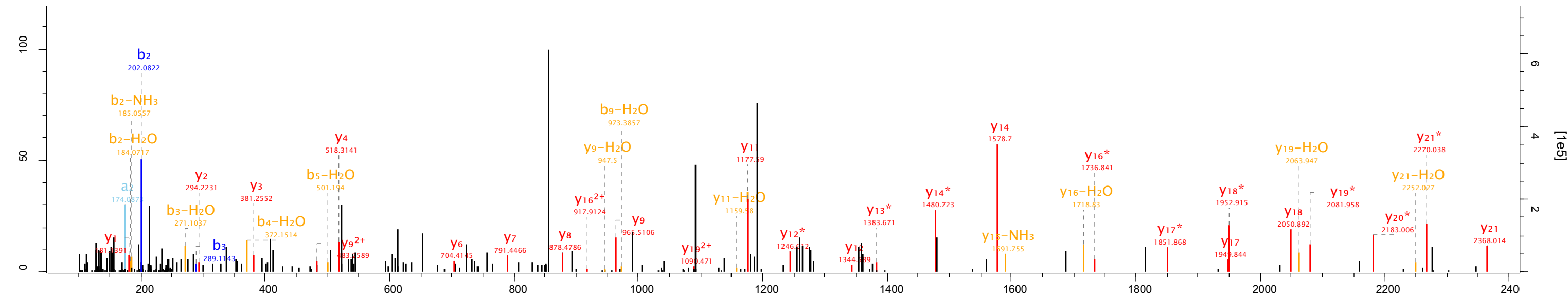
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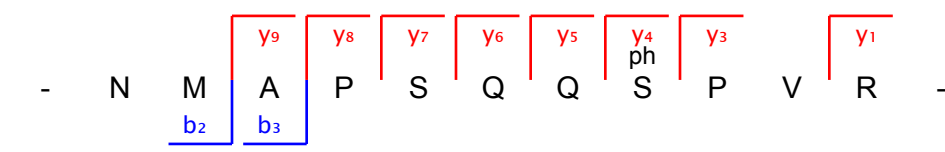
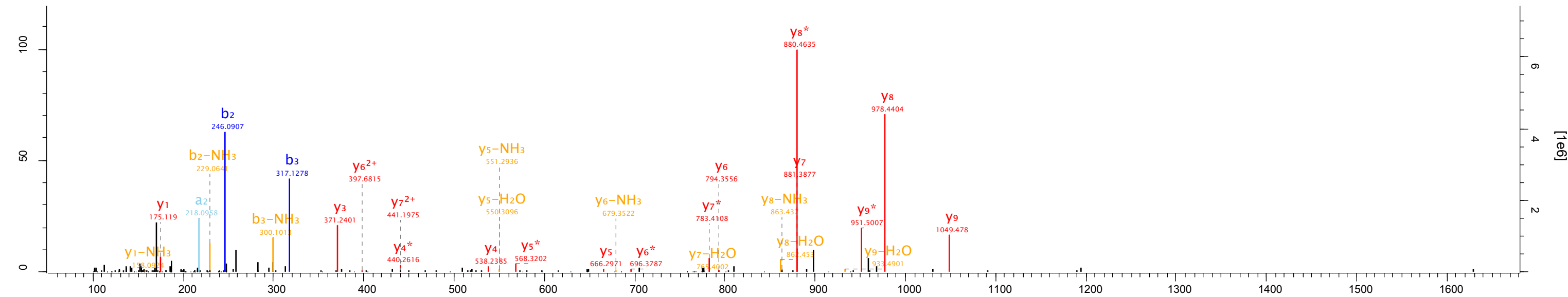
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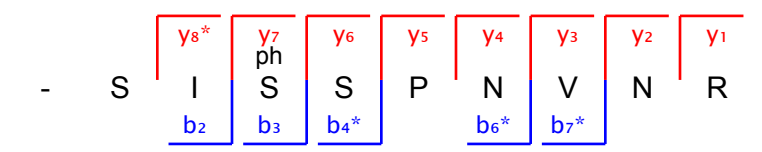
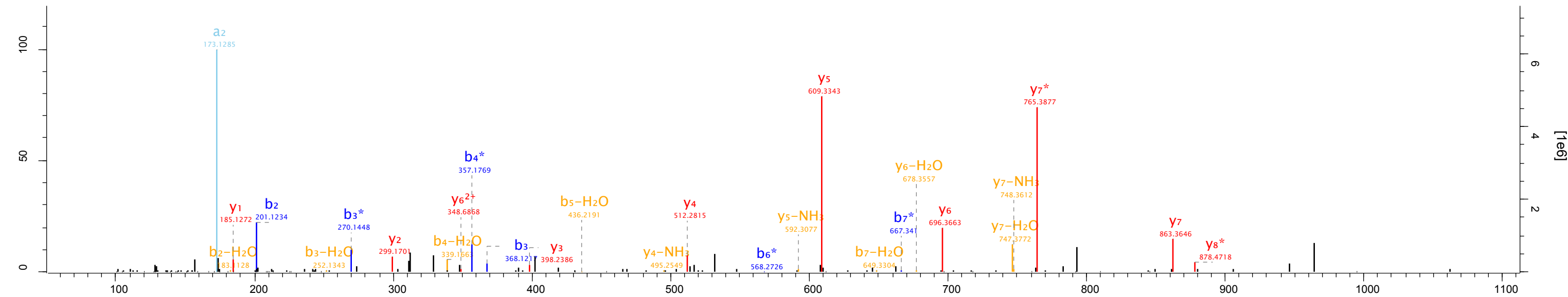
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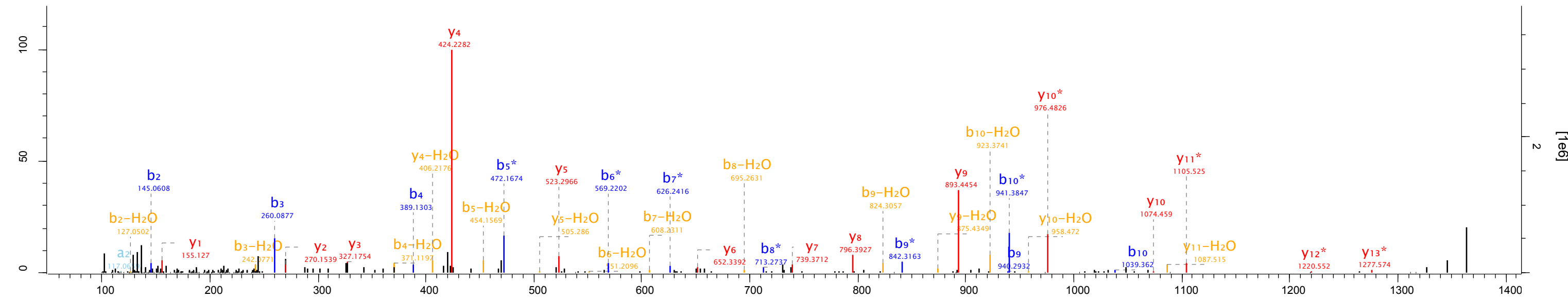


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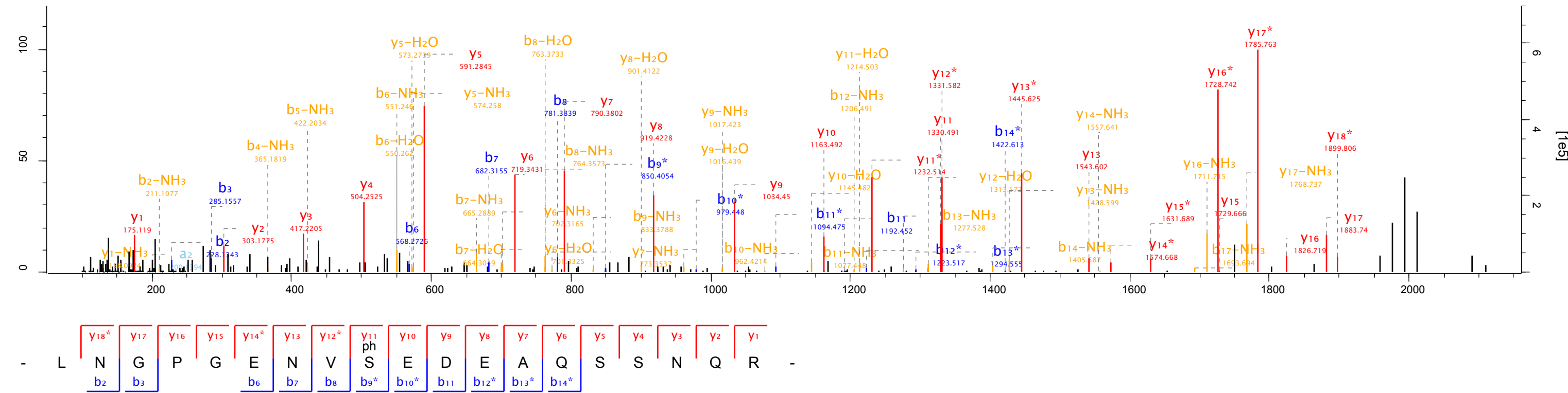


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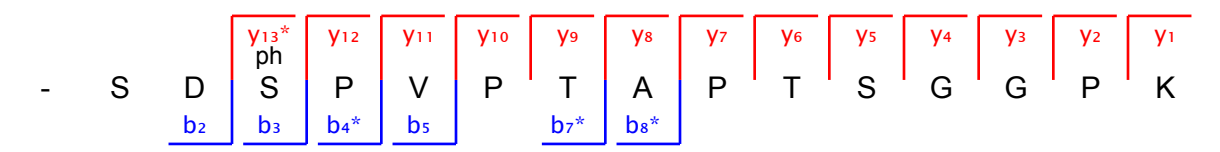
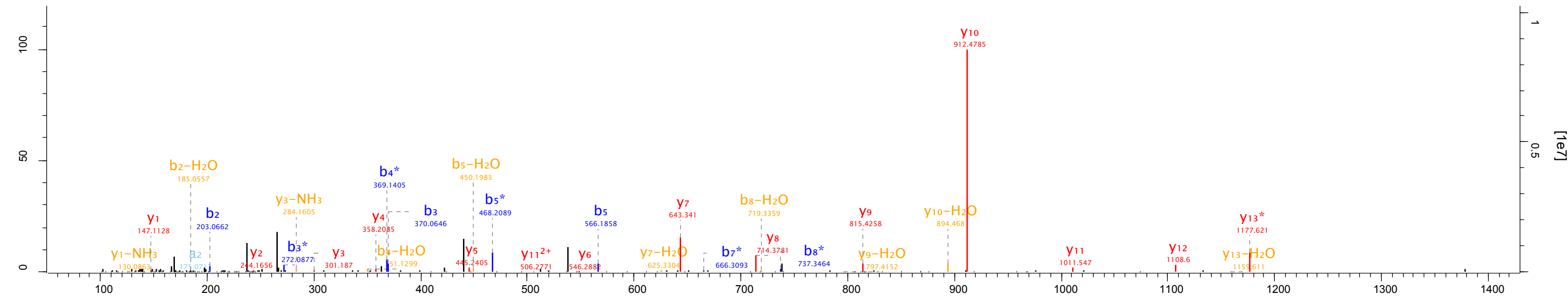


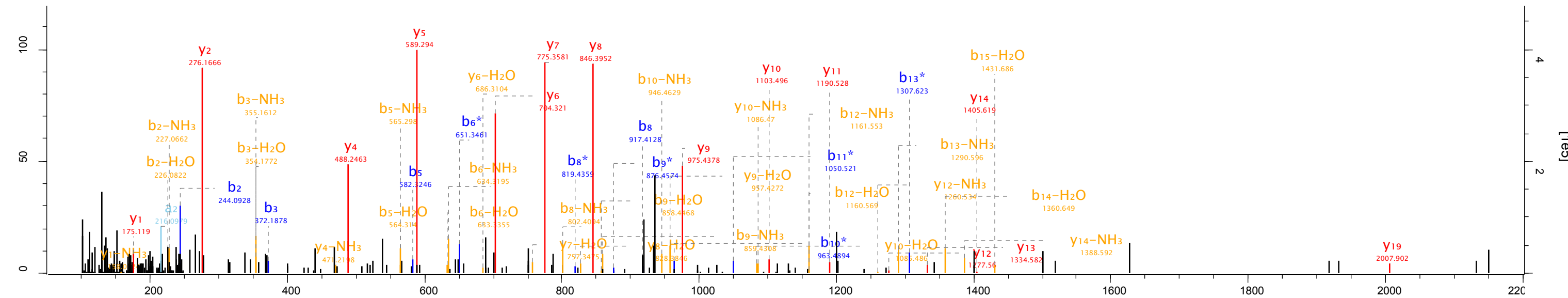


- S y₁₃* y₁₂* y₁₁* y₁₀ph y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁ -
b₂ b₃ b₄ b₅* b₆* b₇* b₈* b₉ b₁₀ P G D K -



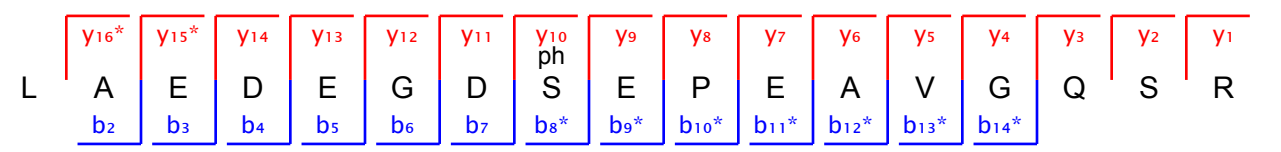
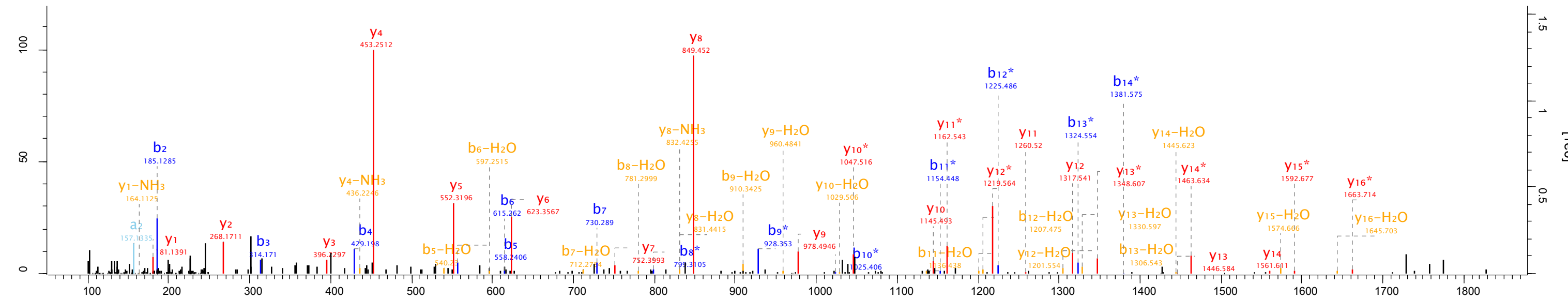
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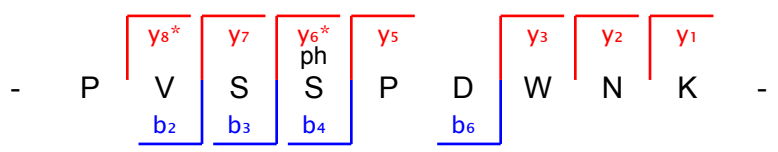
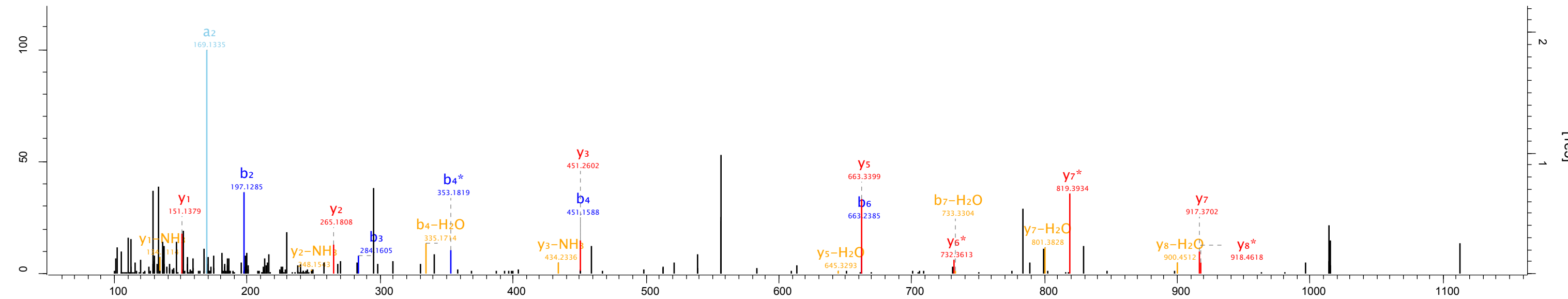


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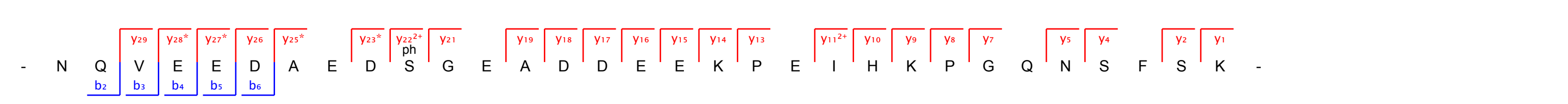
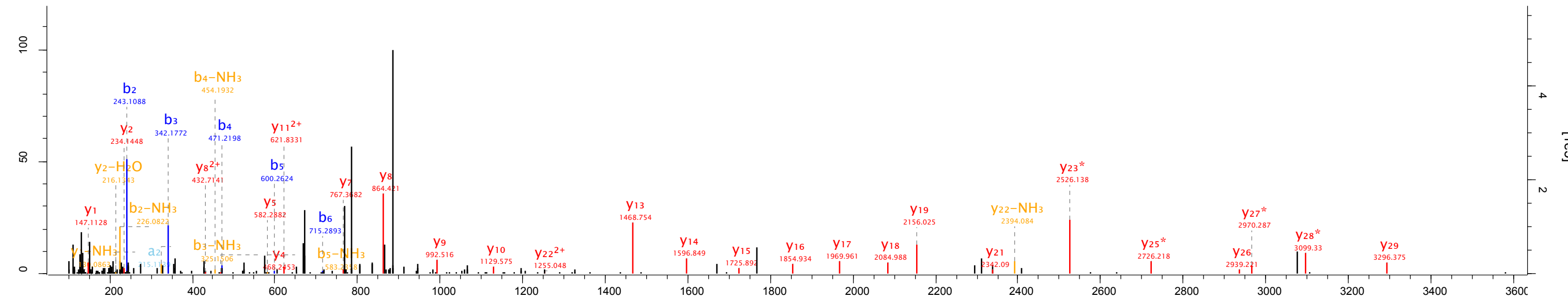
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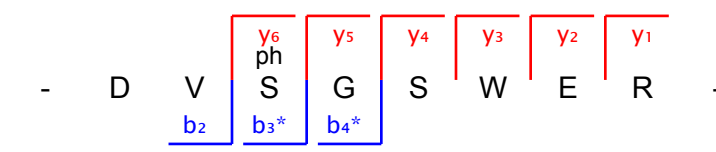
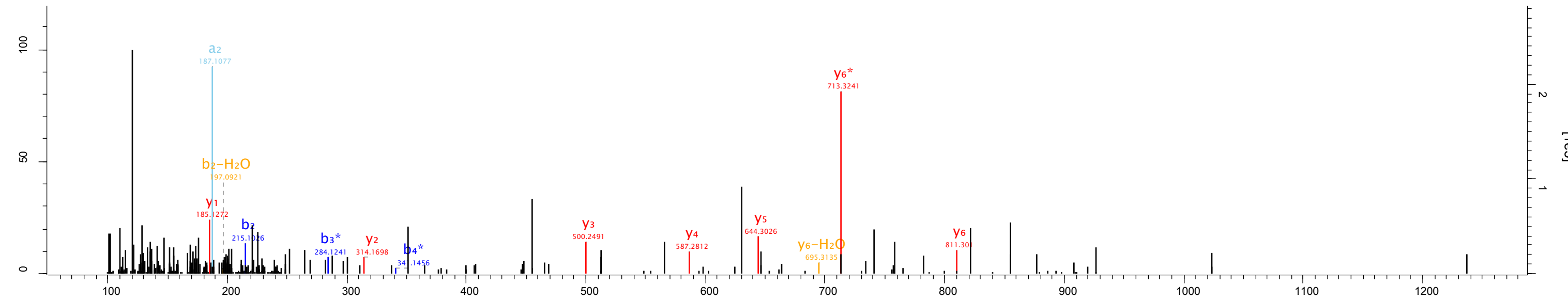
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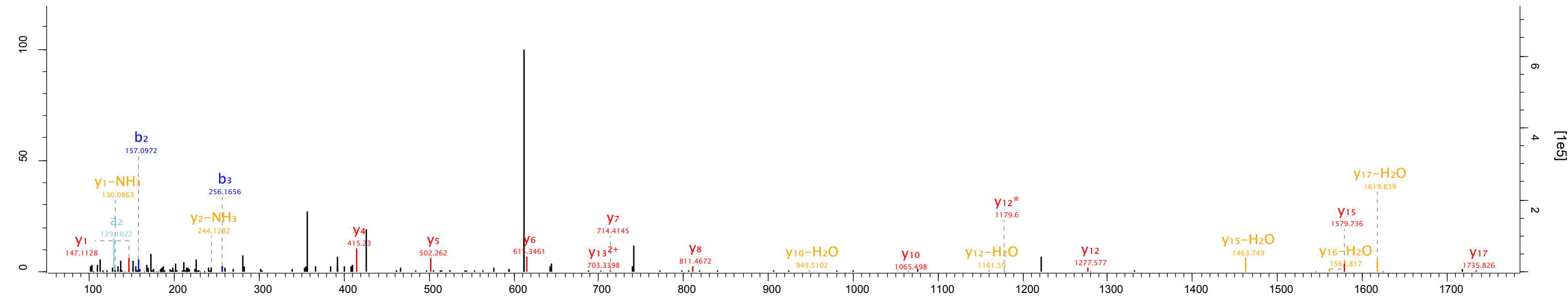
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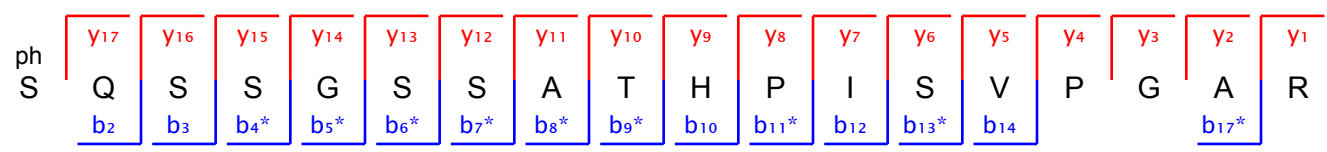
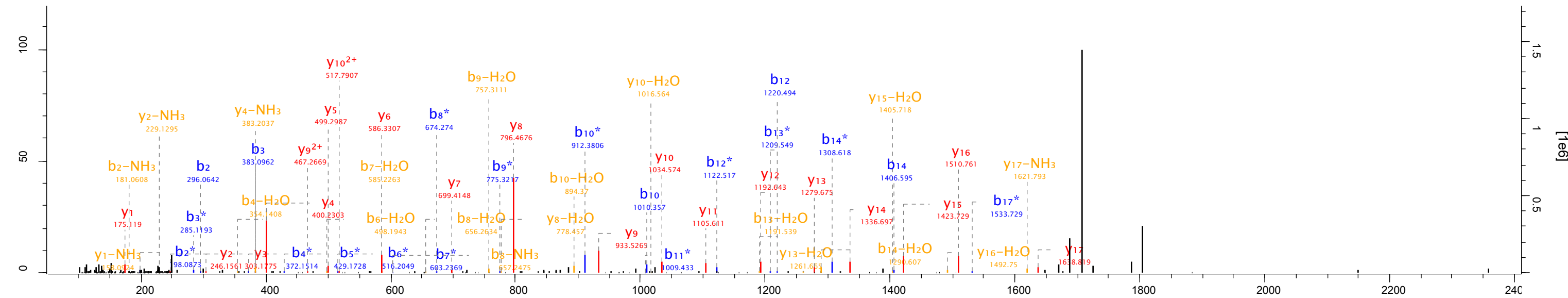
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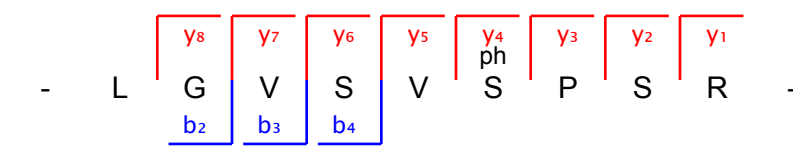
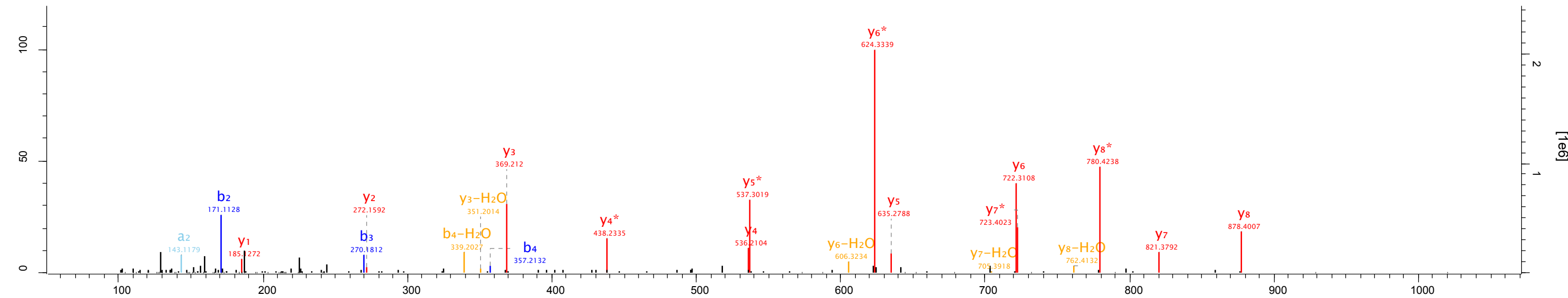
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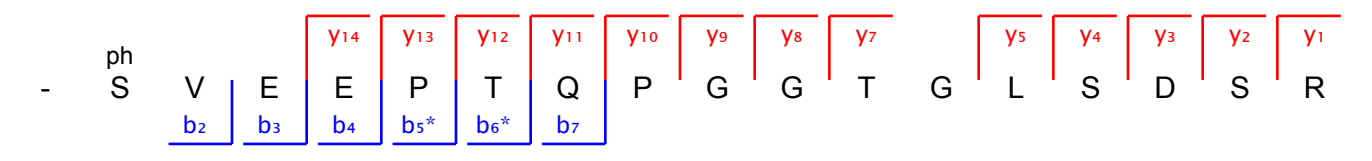
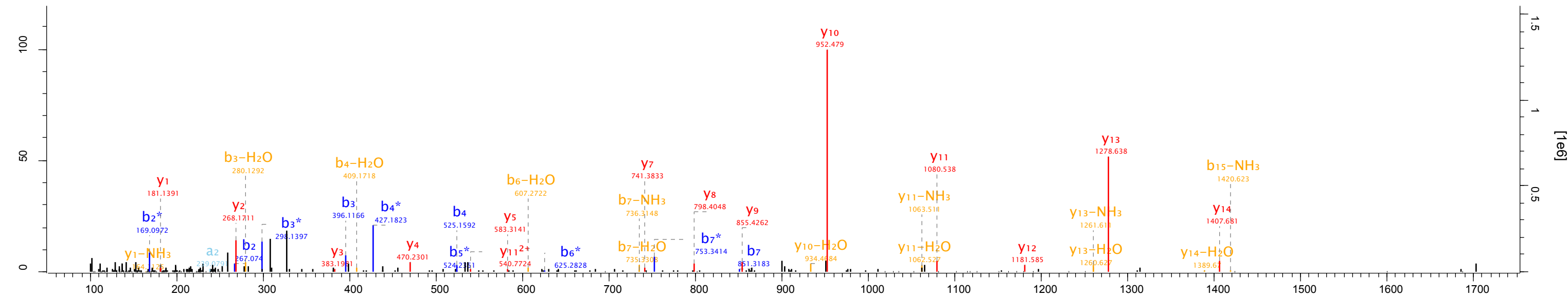
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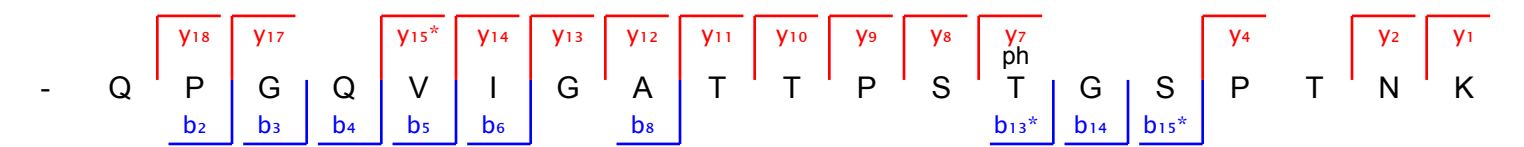
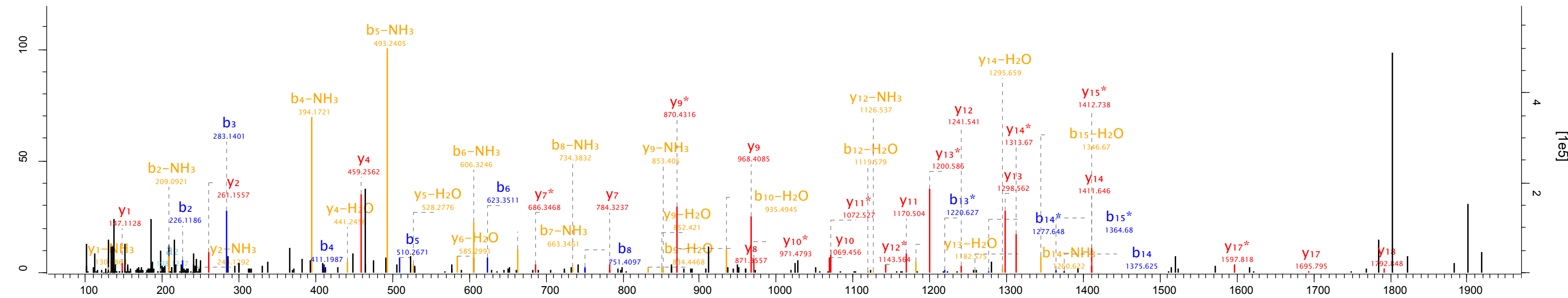


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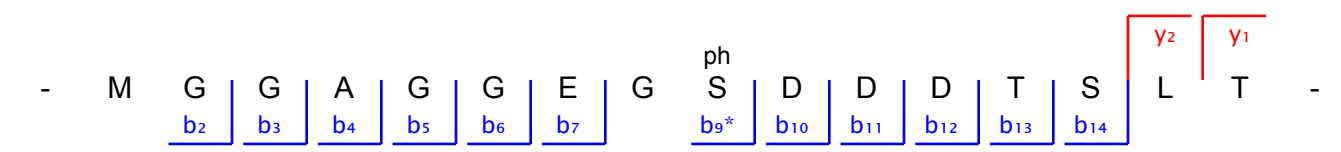
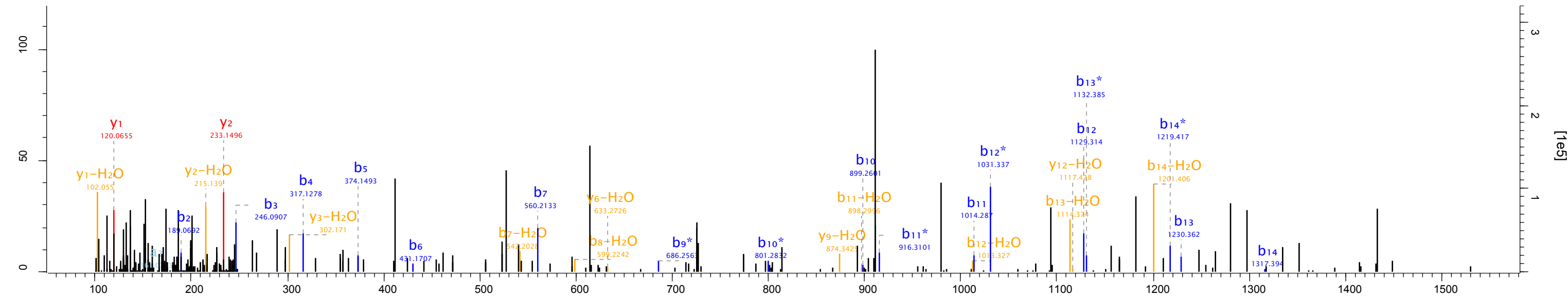


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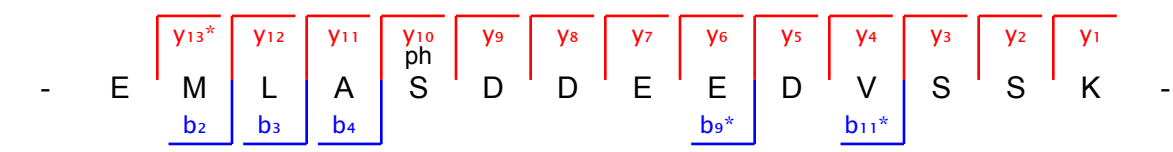
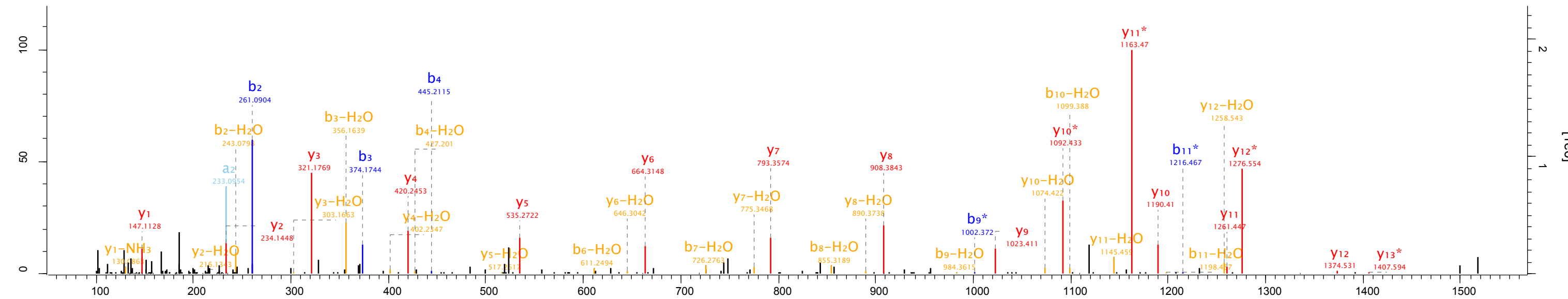




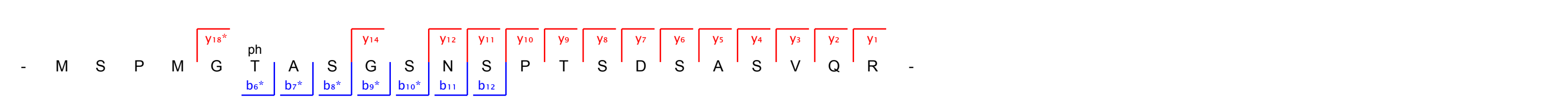
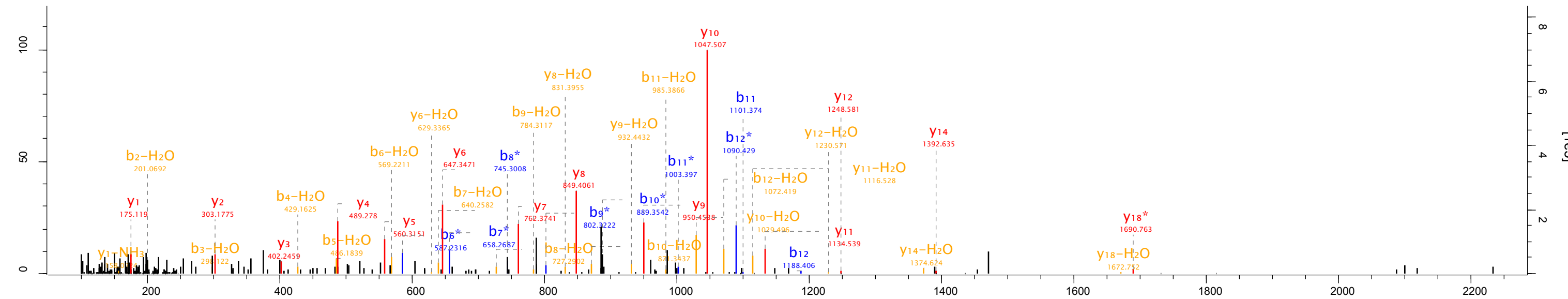
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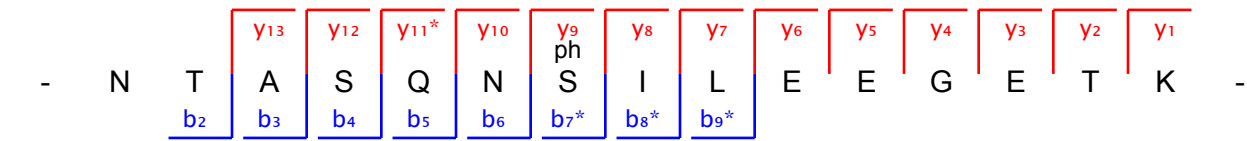
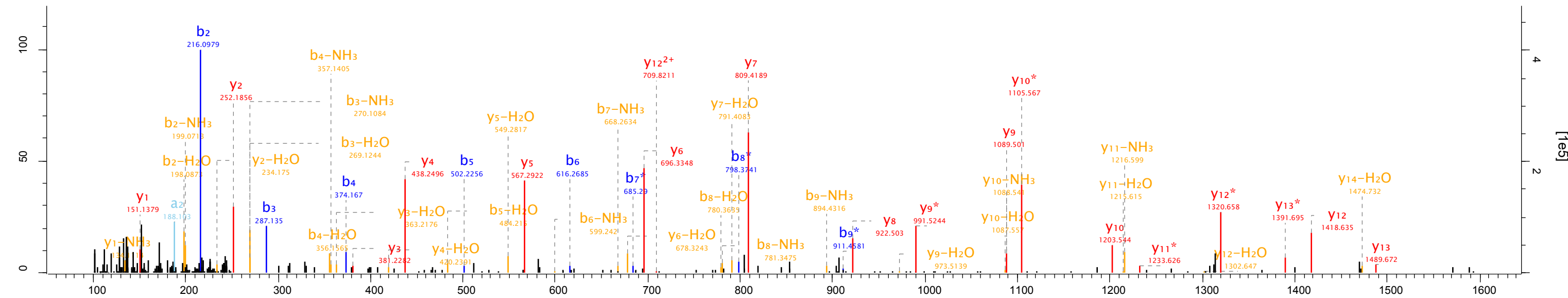


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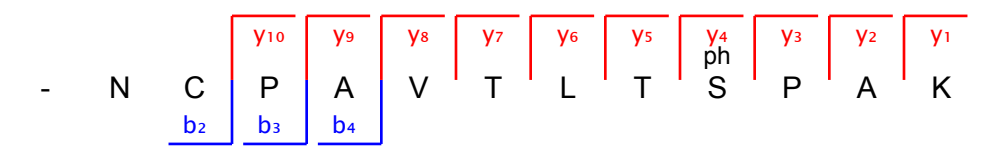
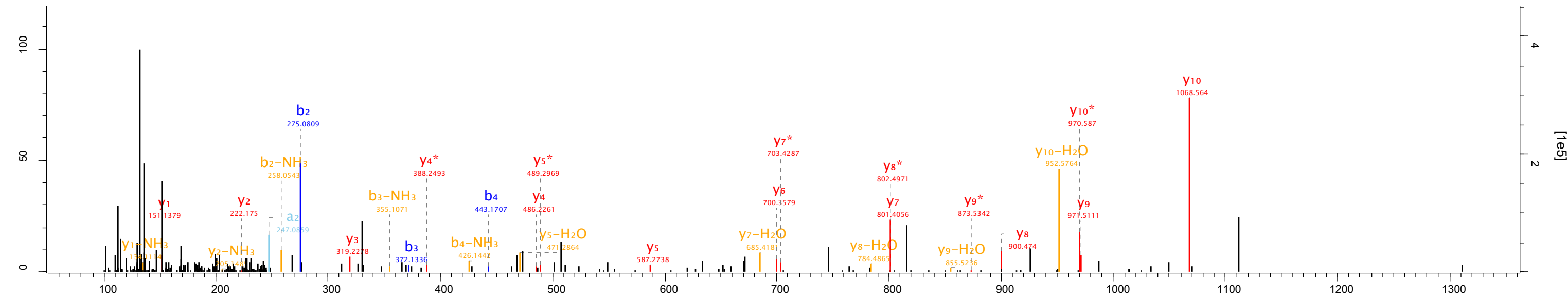


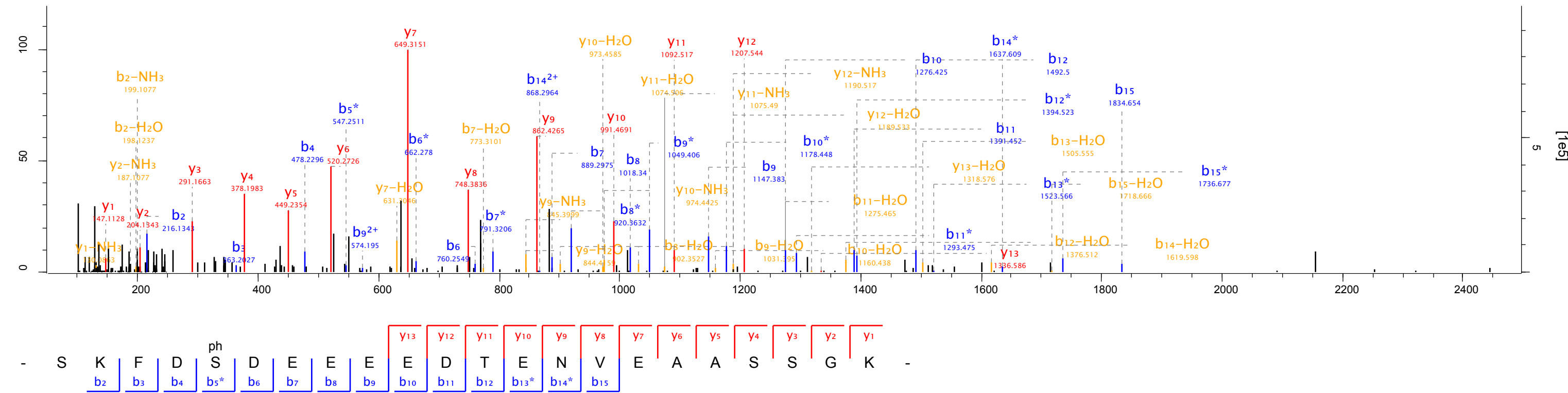
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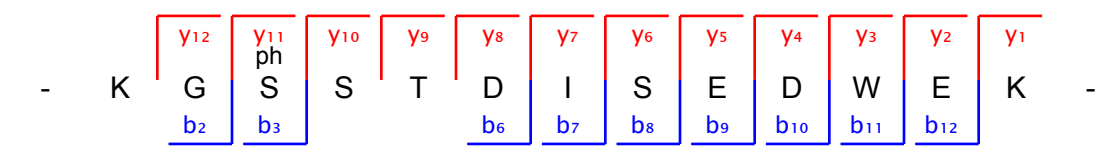
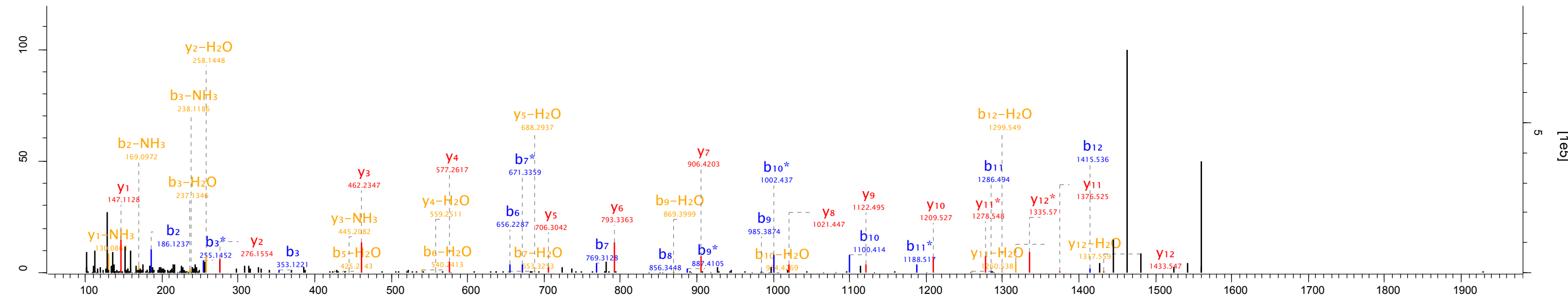


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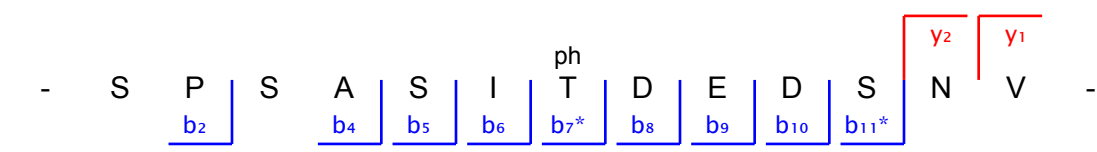
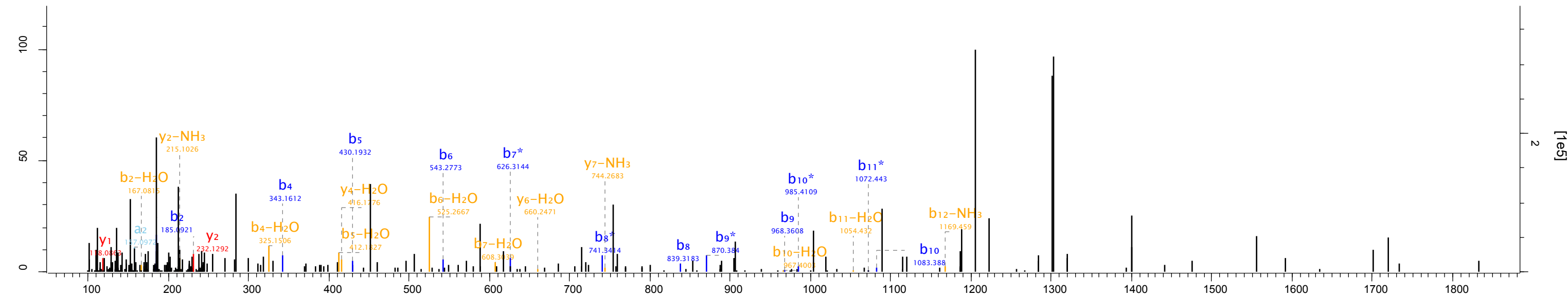




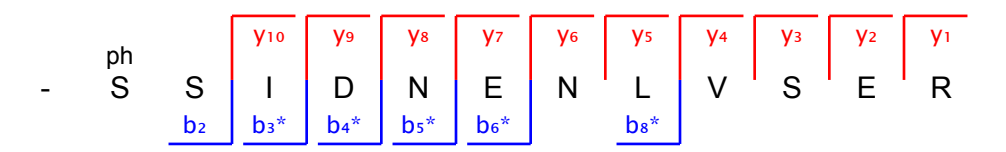
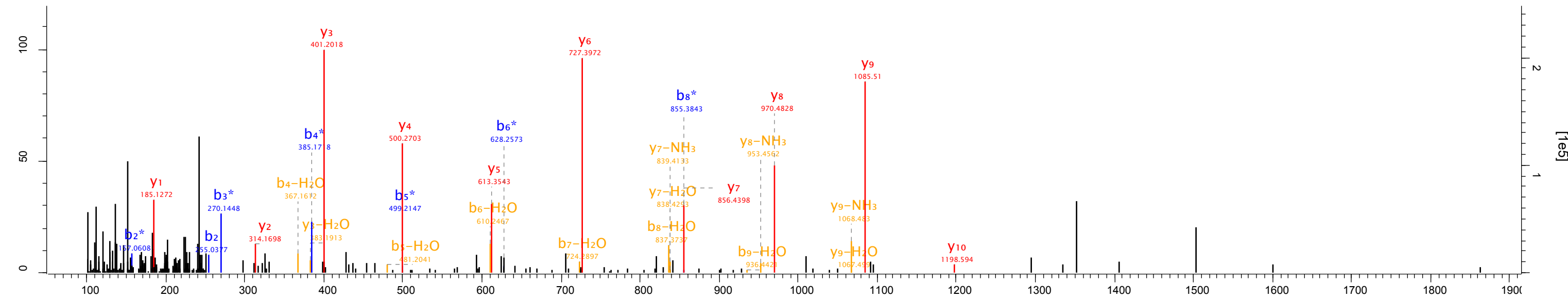
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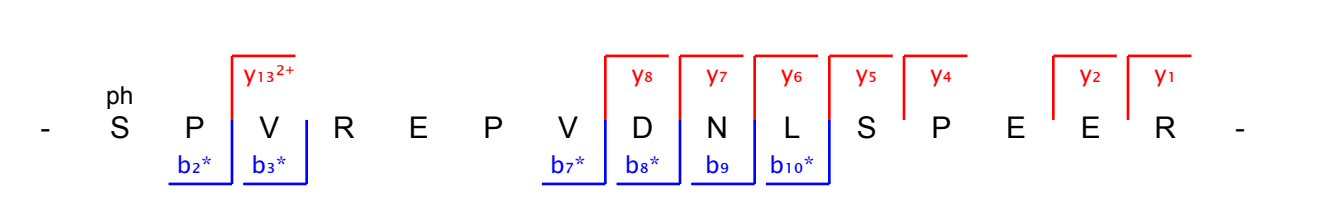
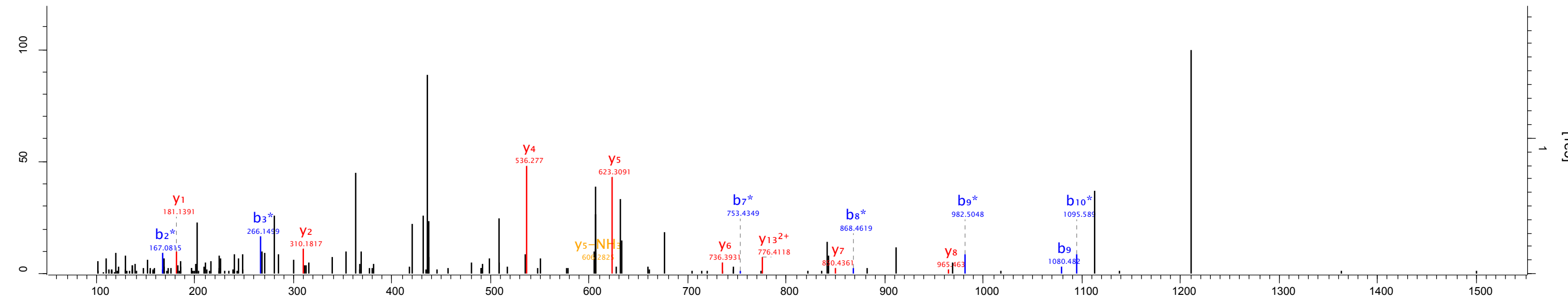
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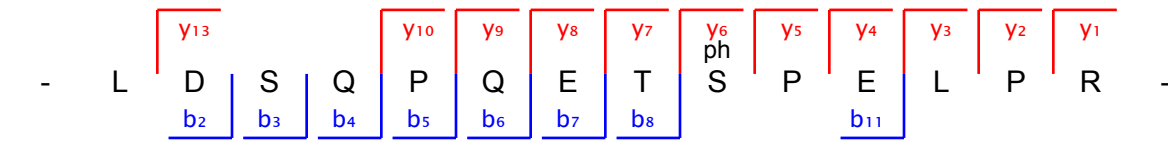
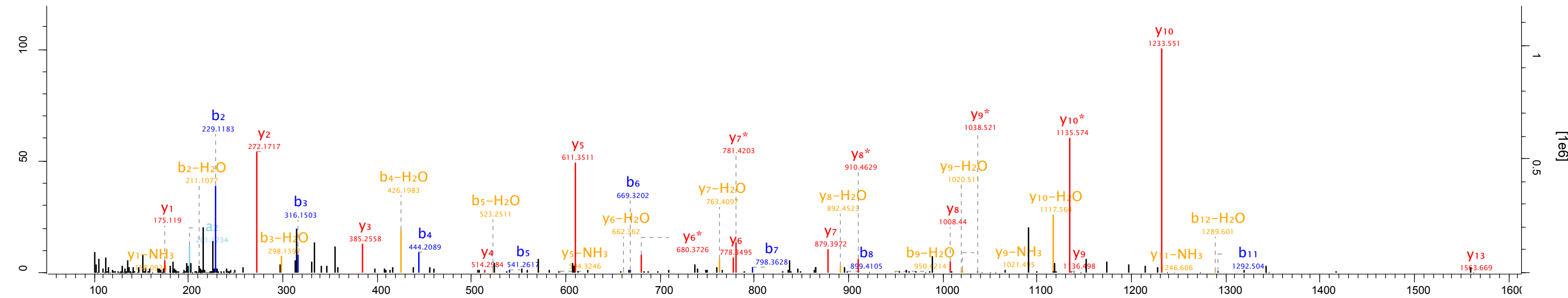


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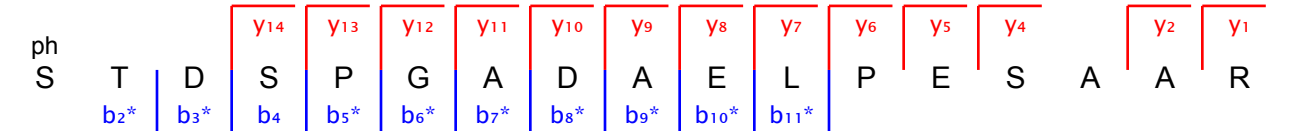
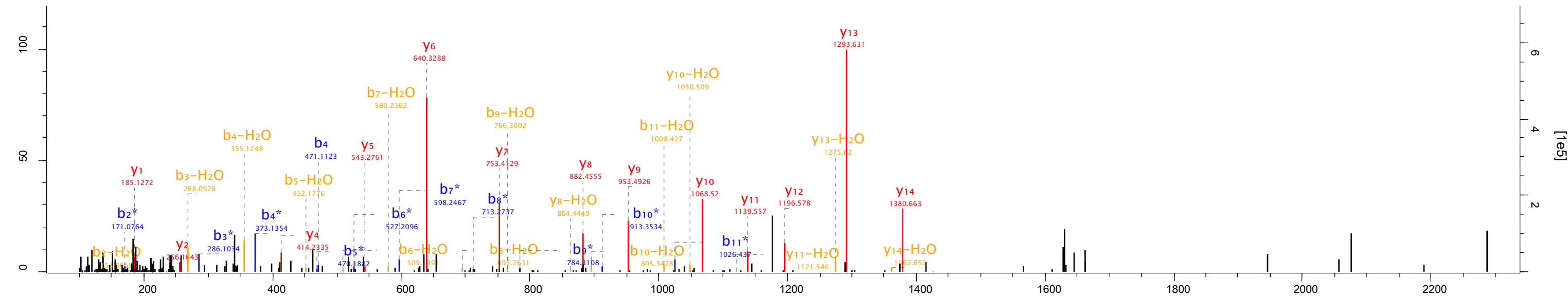


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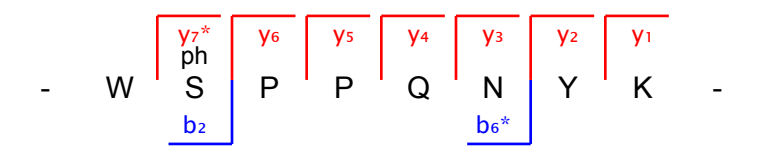
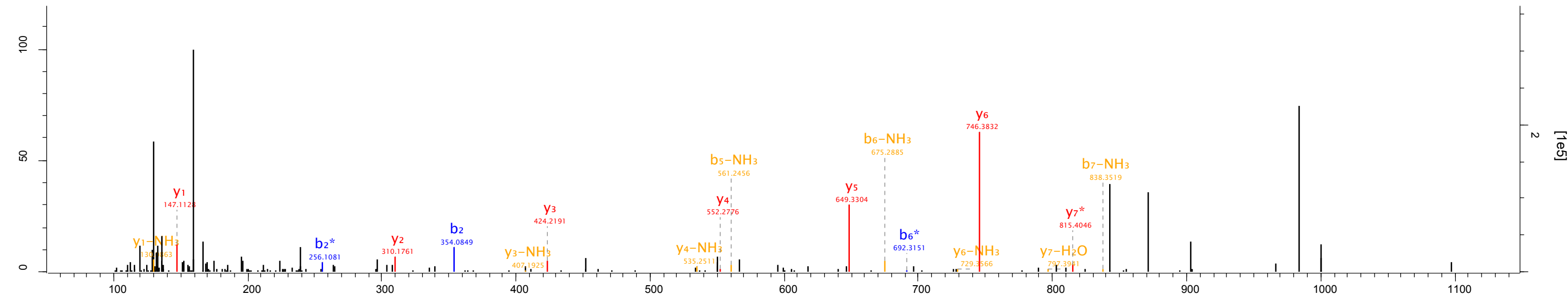




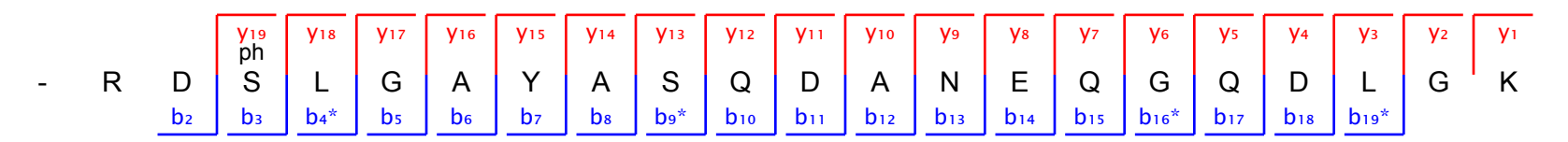
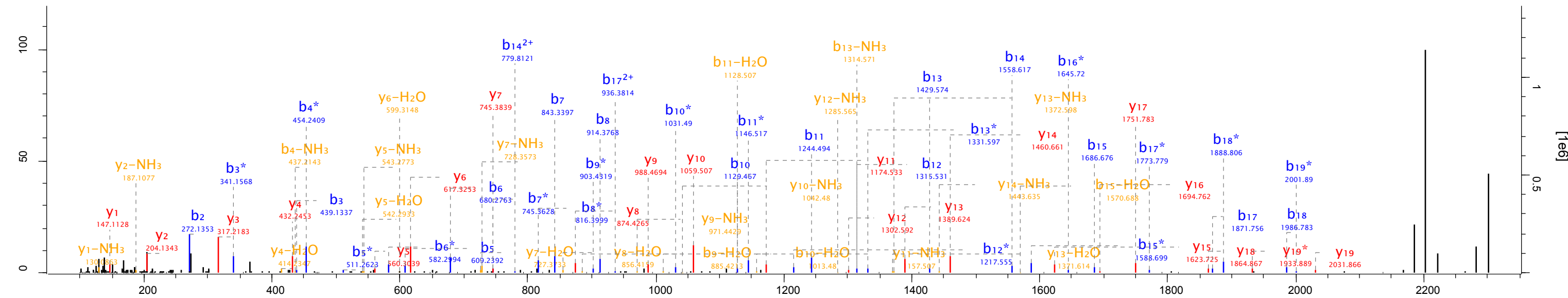
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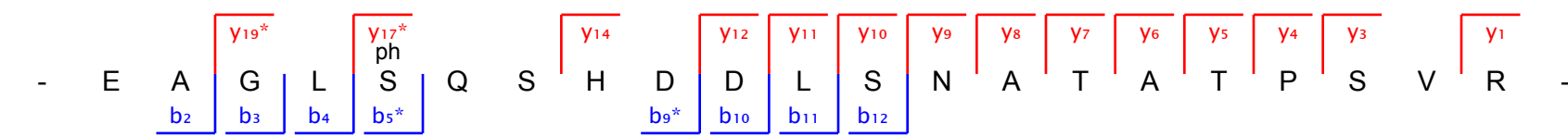
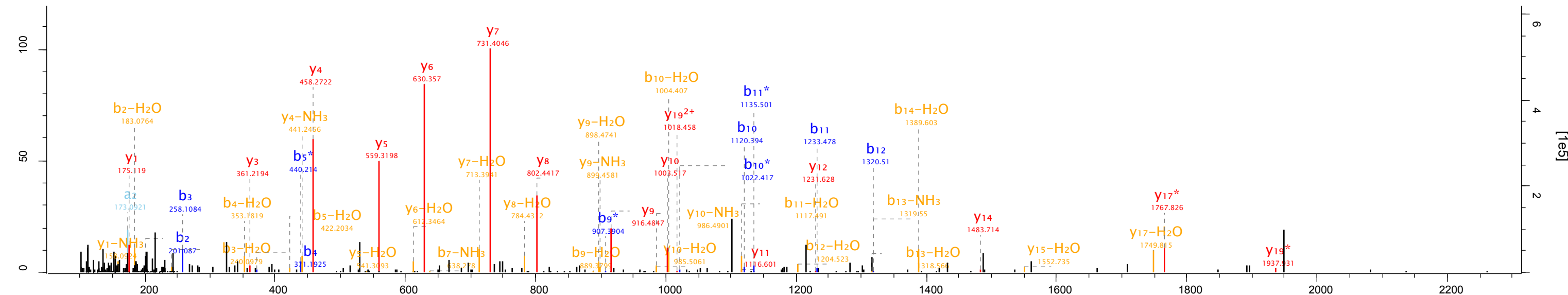


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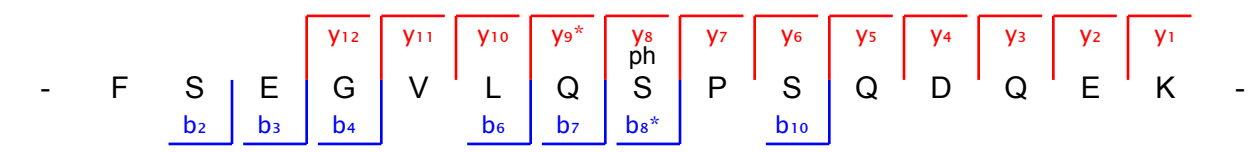
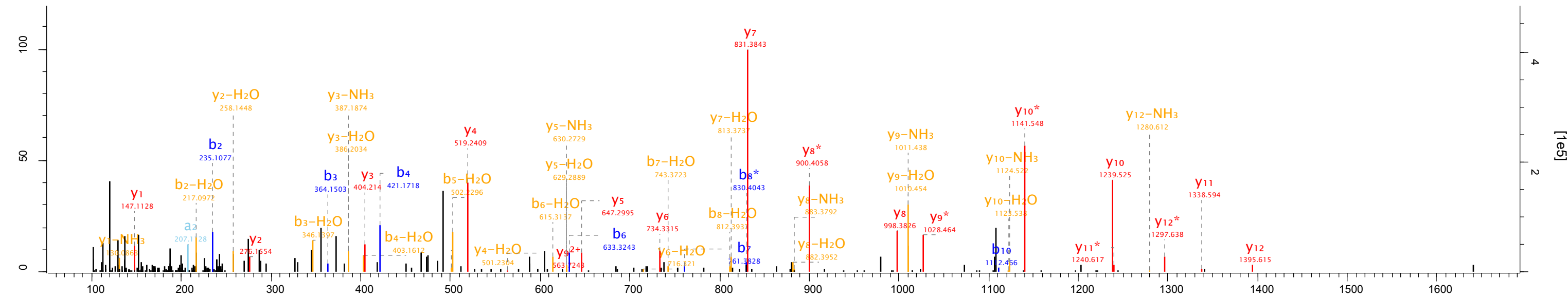


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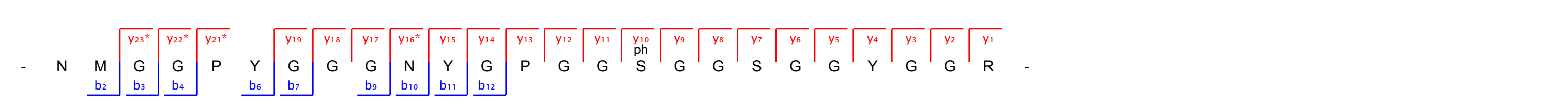
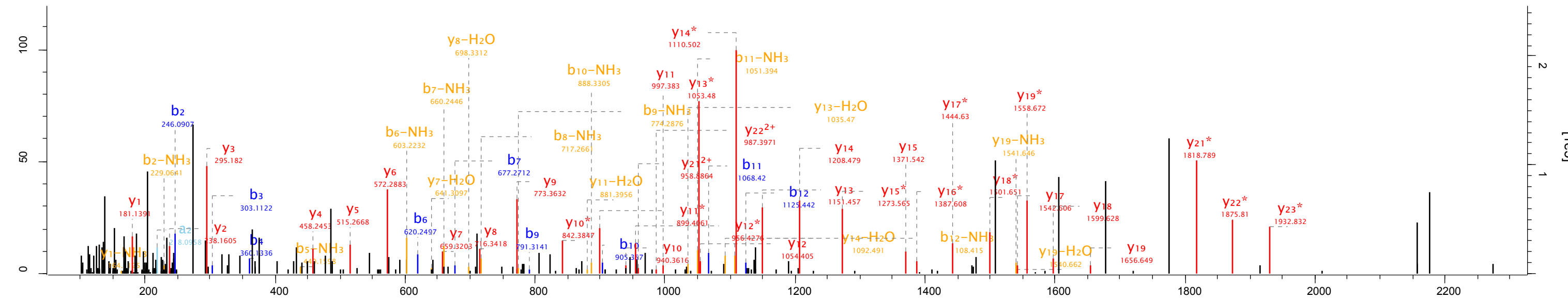




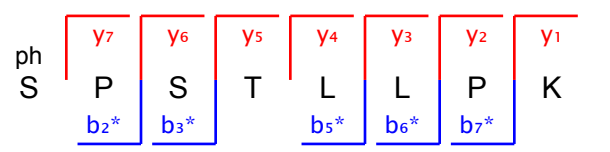
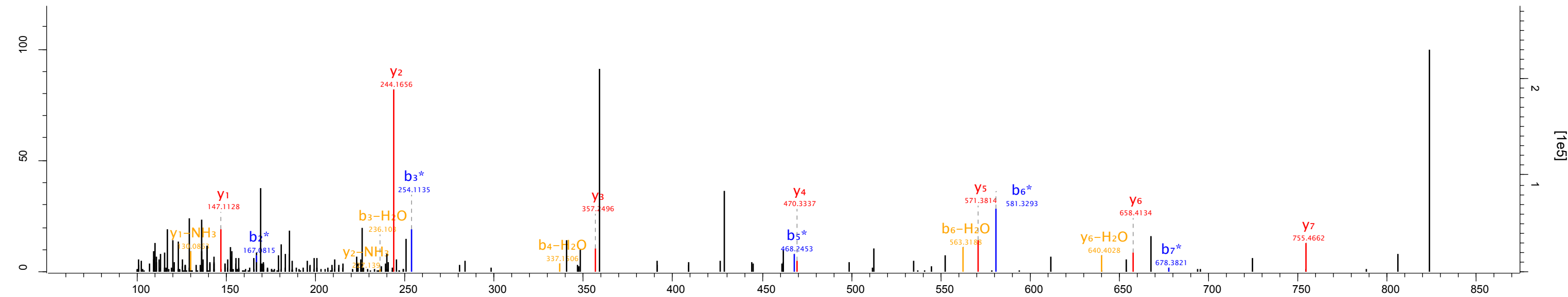
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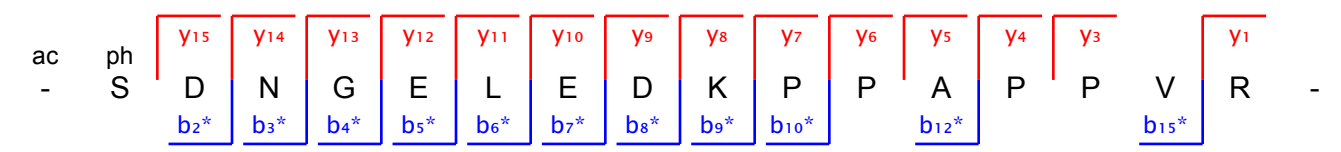
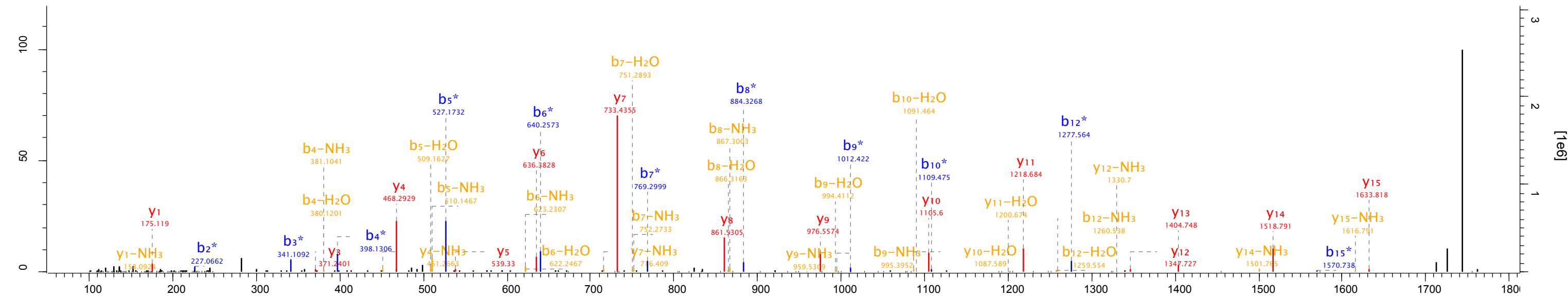
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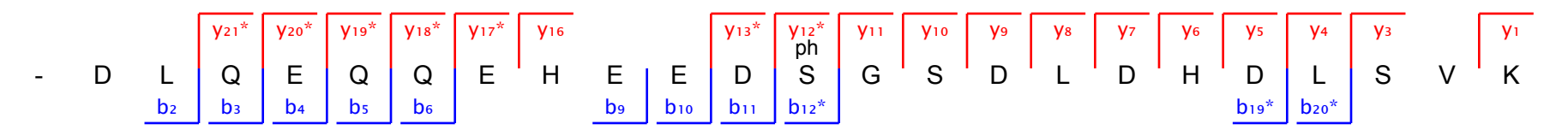
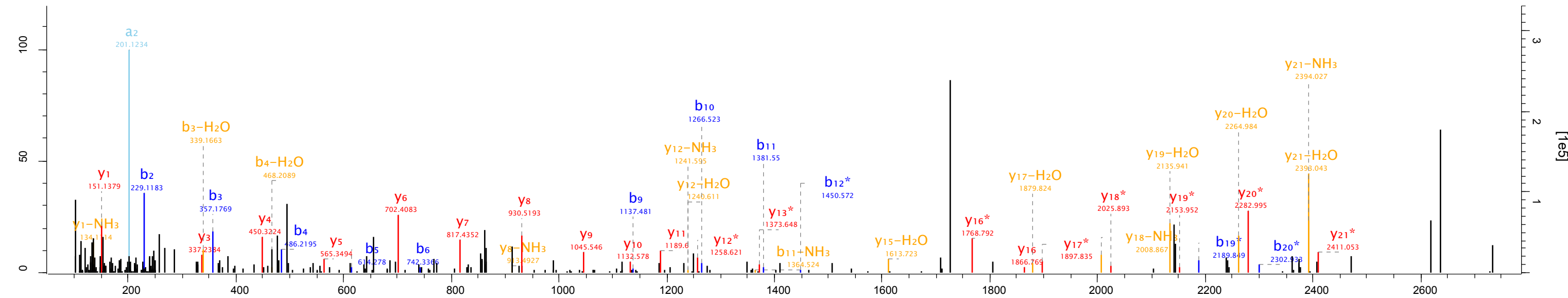
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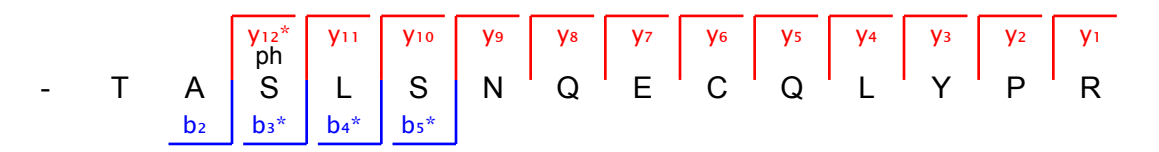
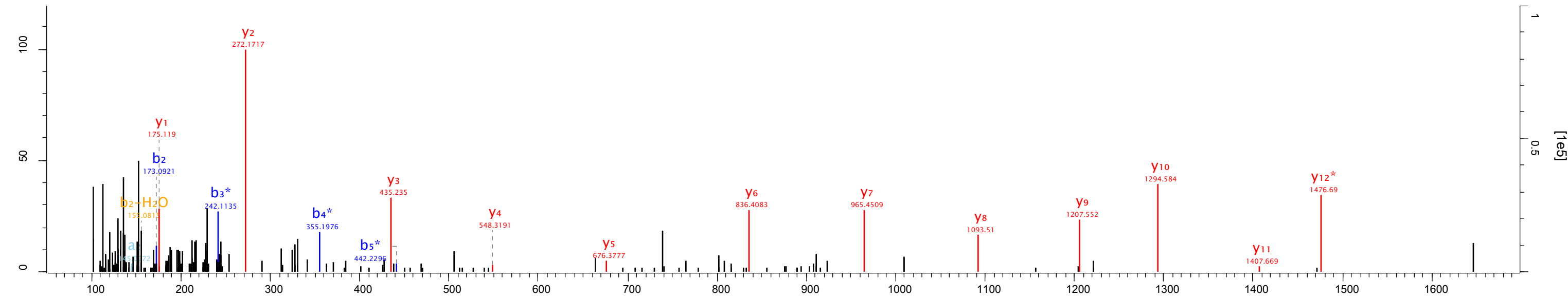
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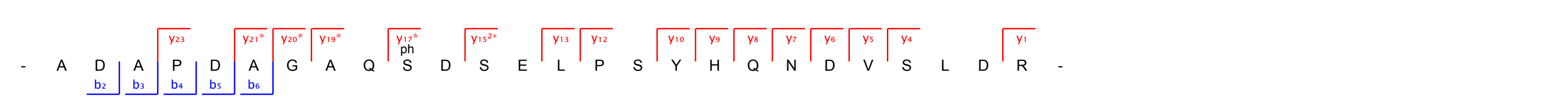
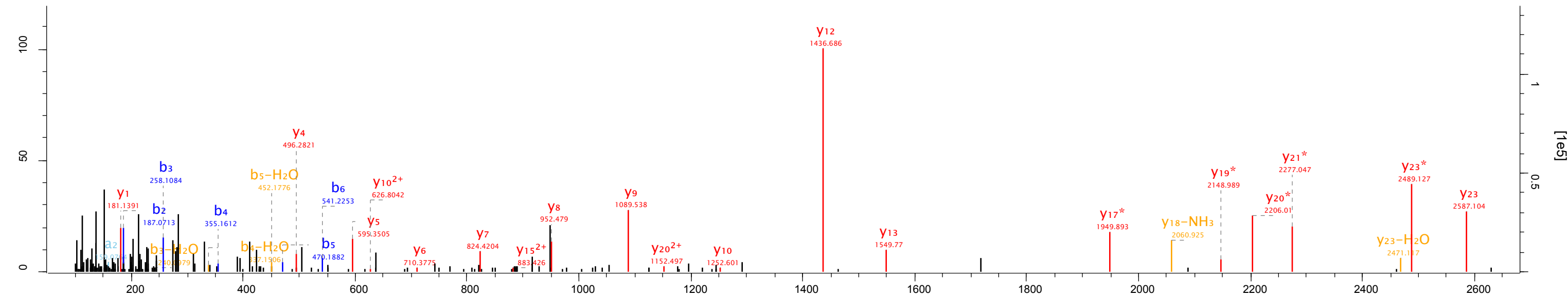
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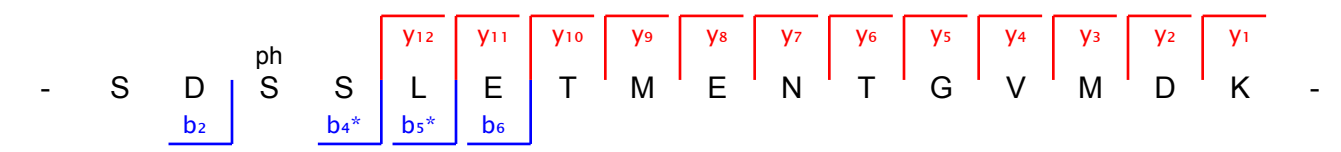
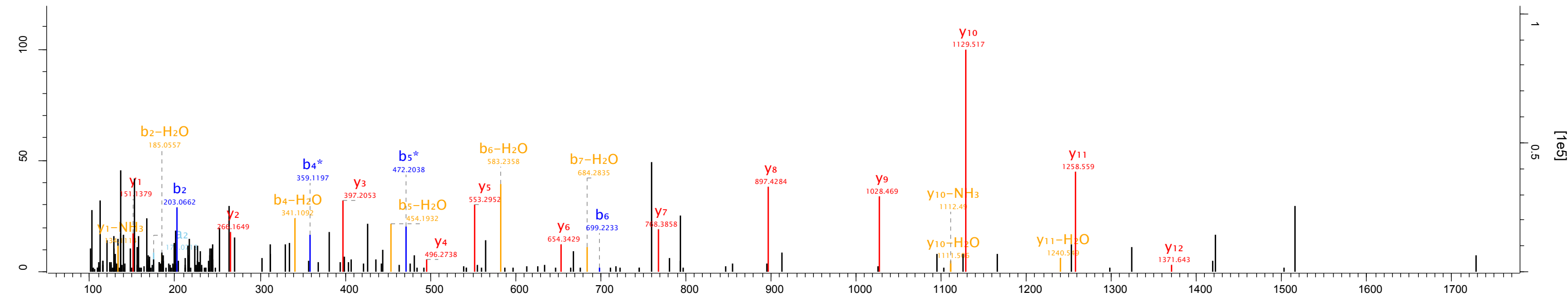
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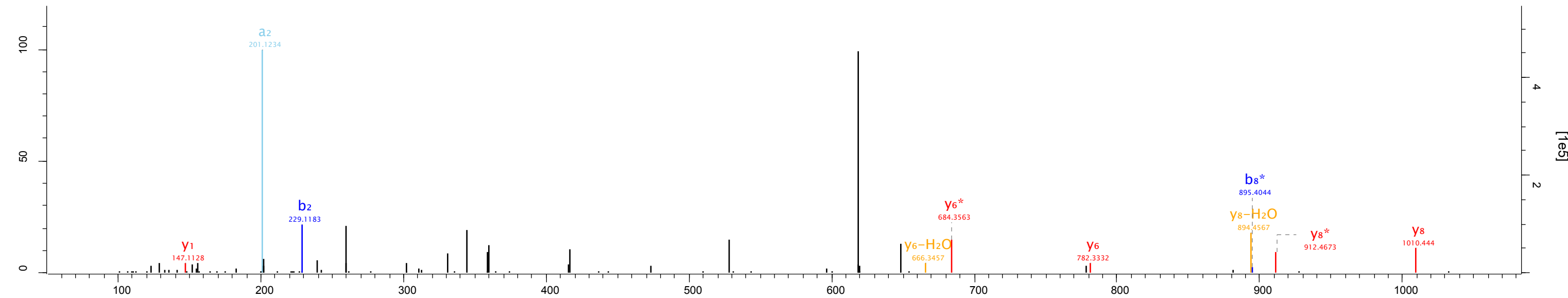
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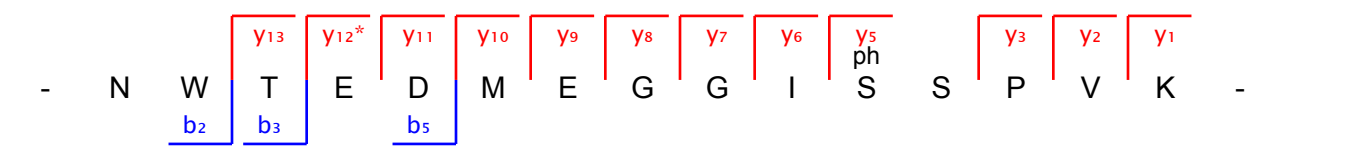
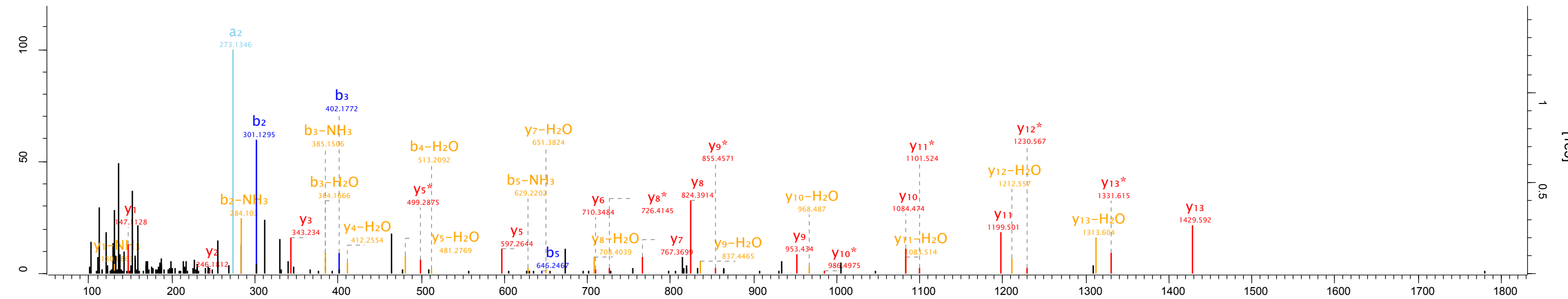
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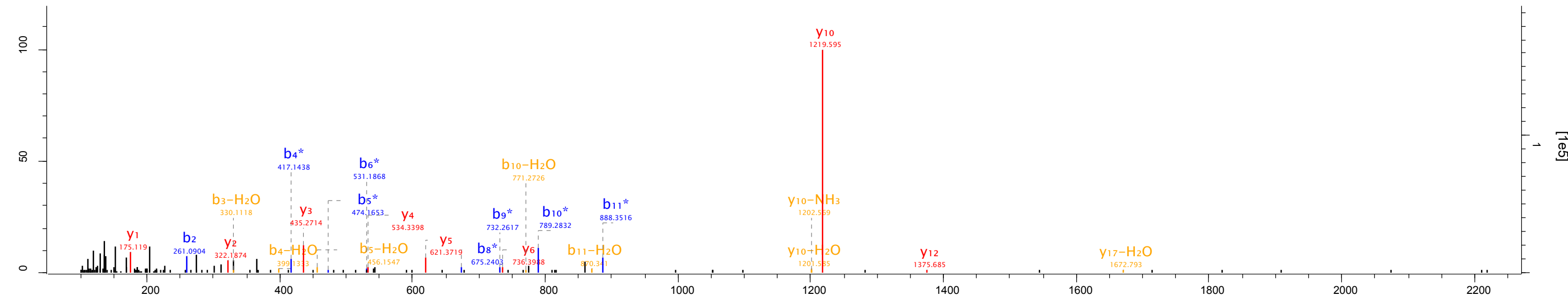
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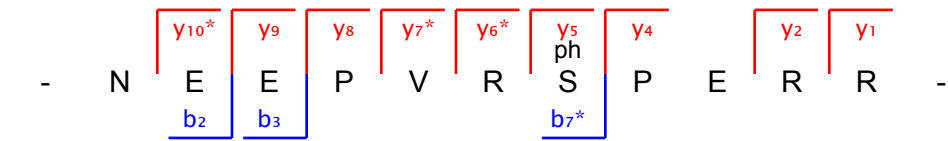
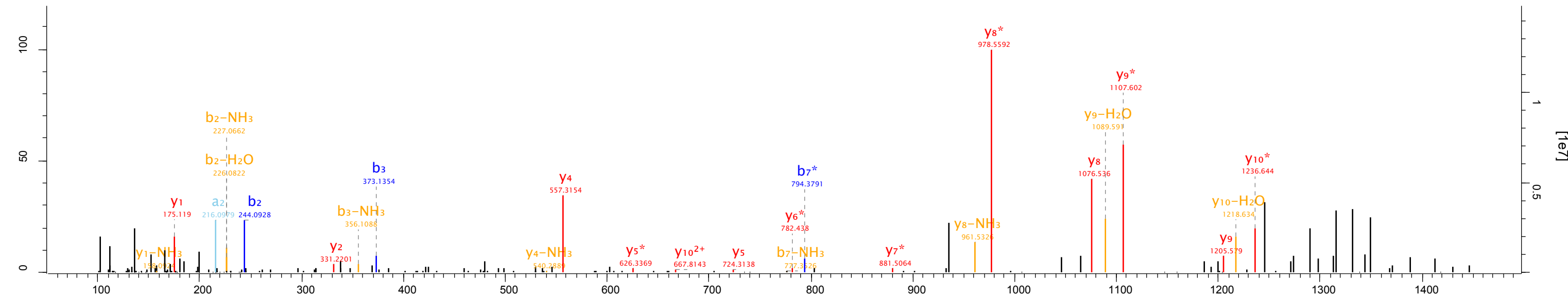
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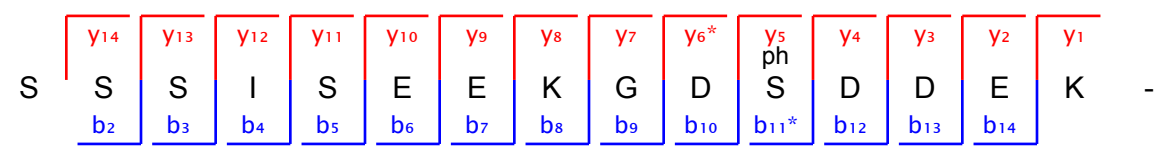
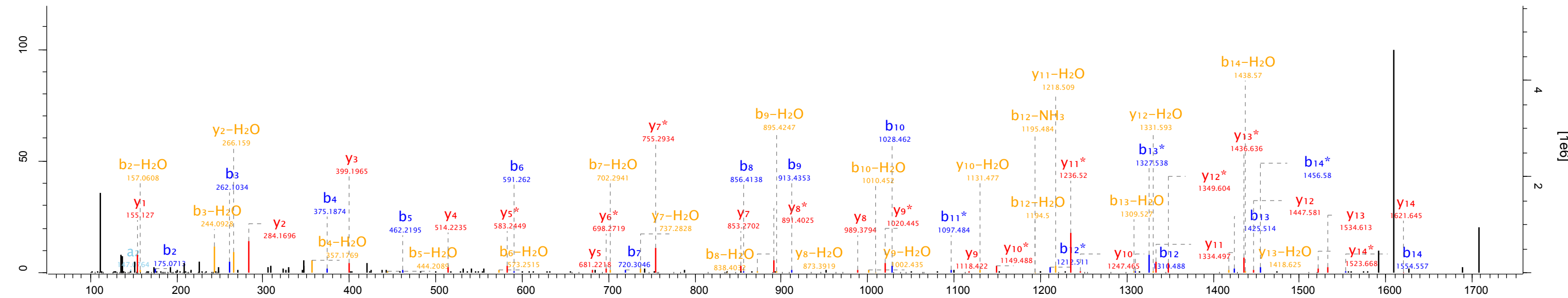
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Fragmentation mapping: b2 (M), b4* (S), b5* (G), b6* (G), b8* (G), b9* (G), b10* (G), b11* (V), y12 (G), y10 (V), y6 (D), y5 (S), y4 (V), y3 (L), y2 (F), y1 (R).

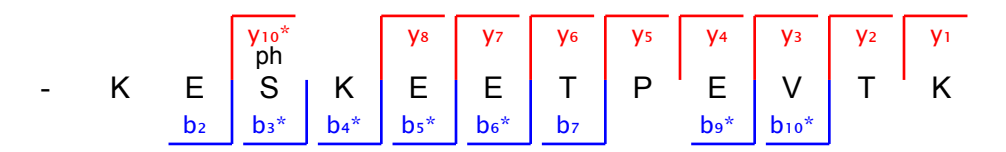
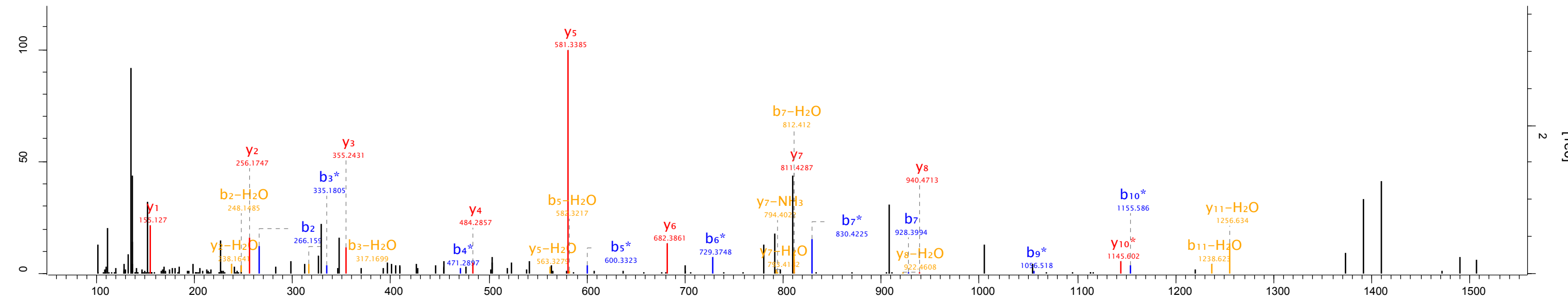
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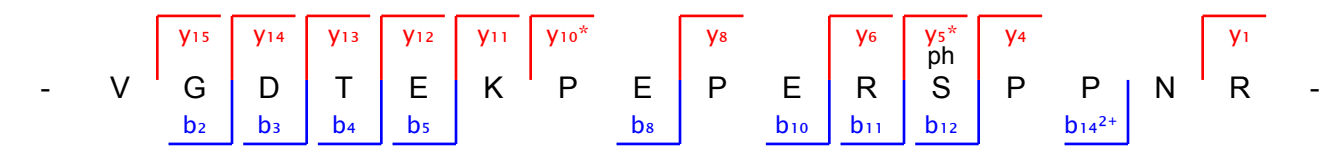
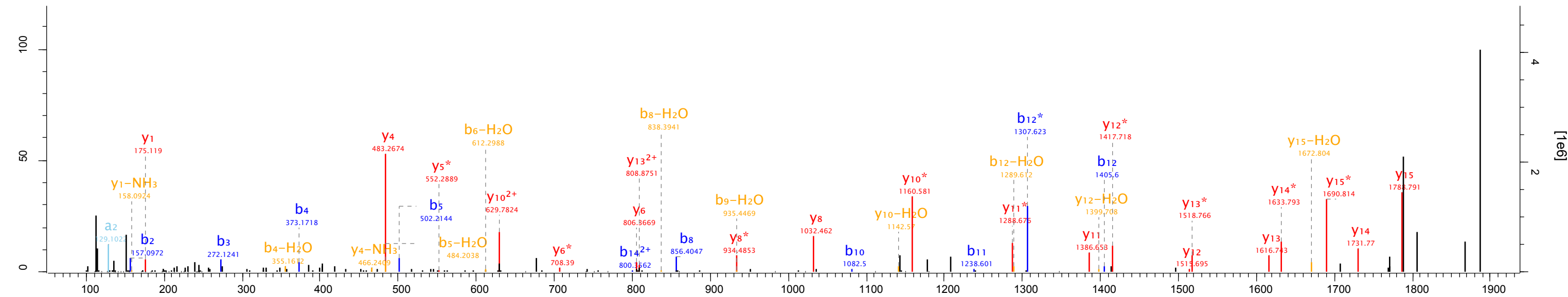
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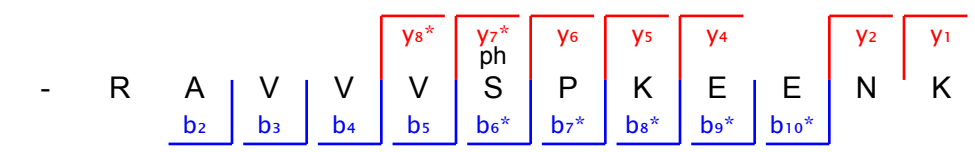
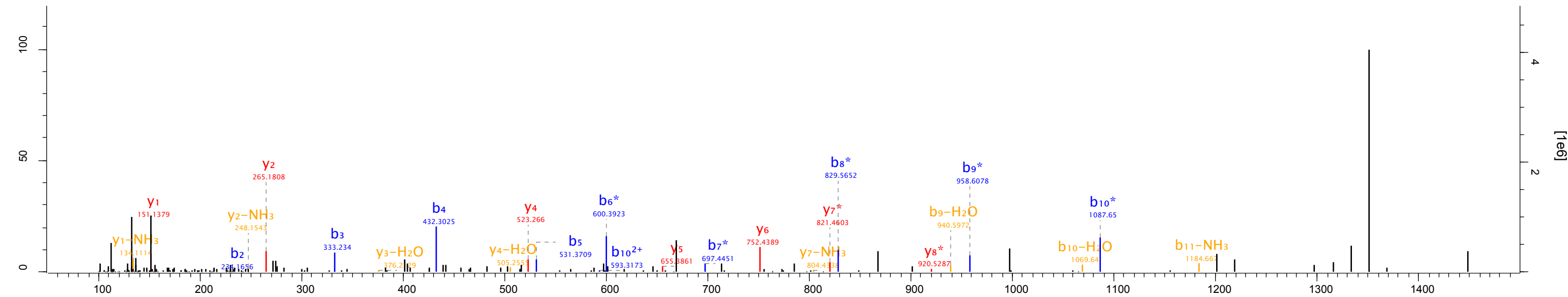
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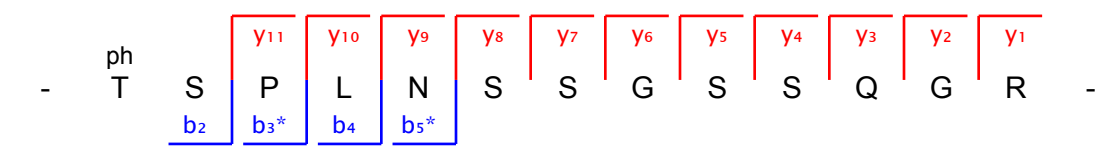
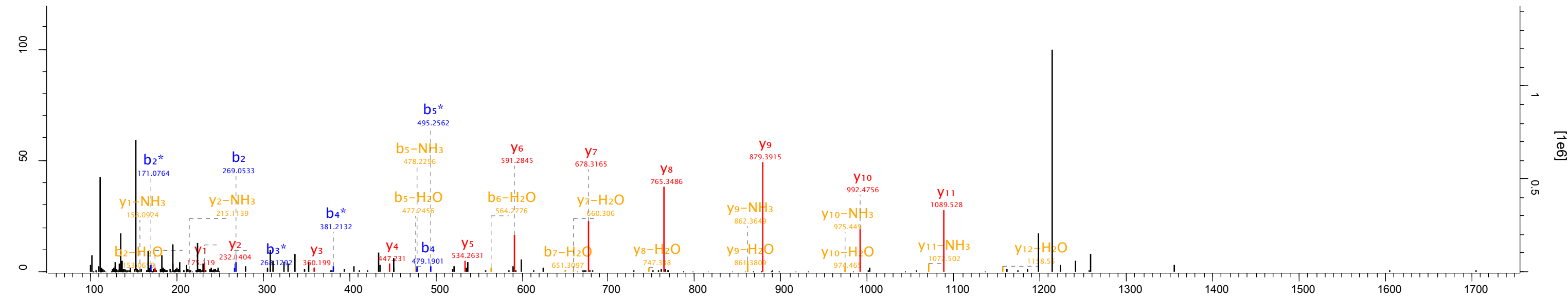
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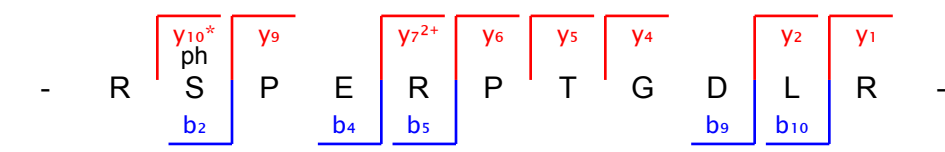
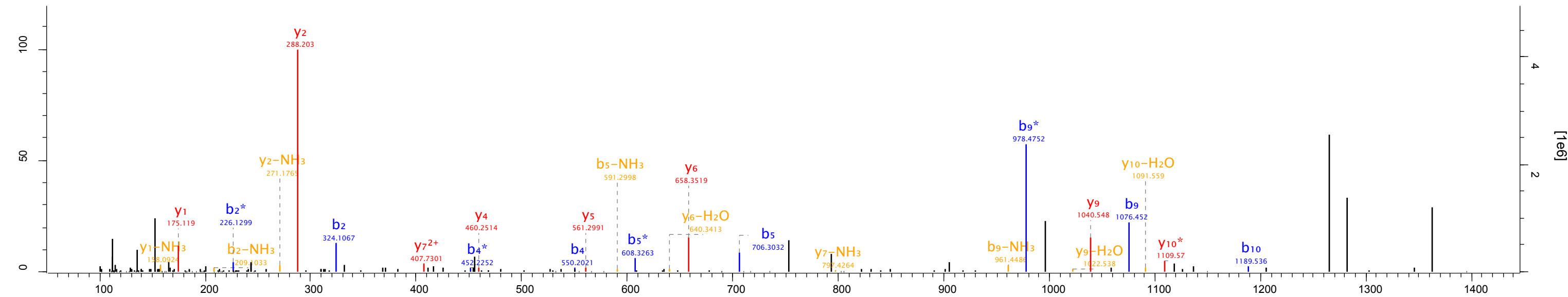
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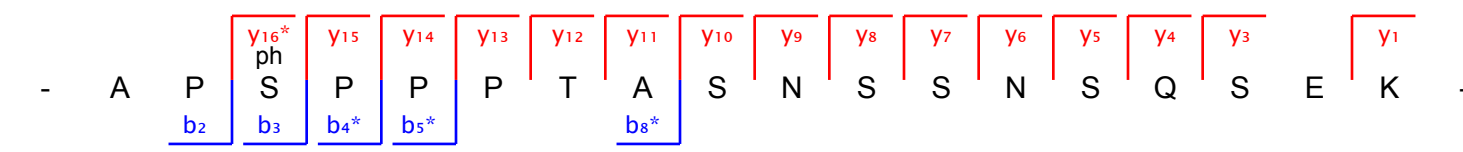
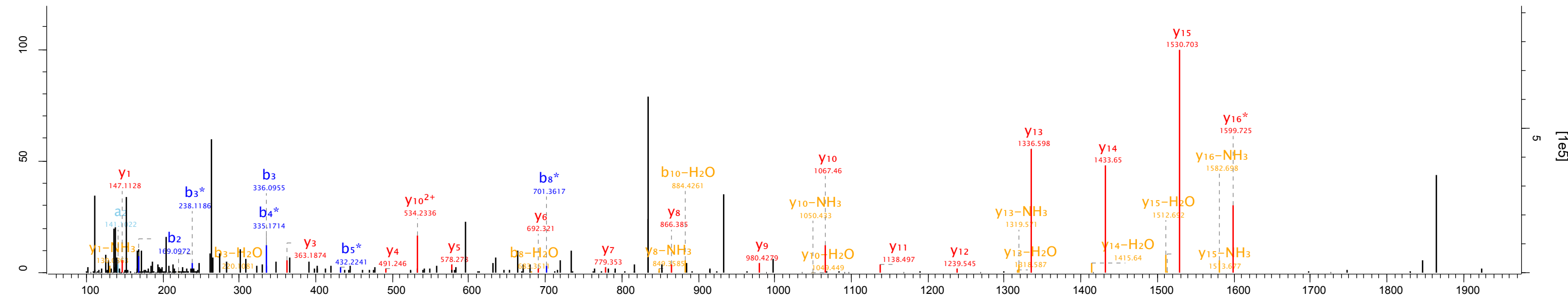
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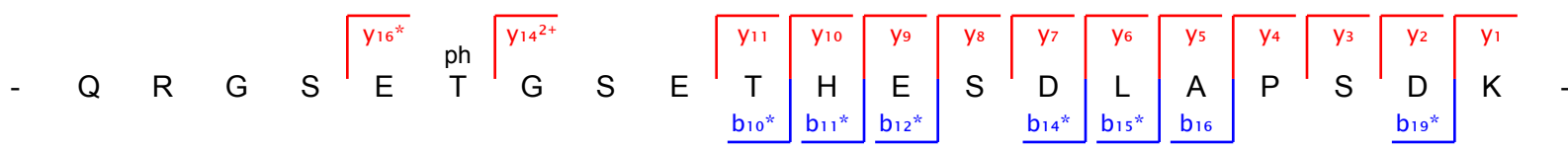
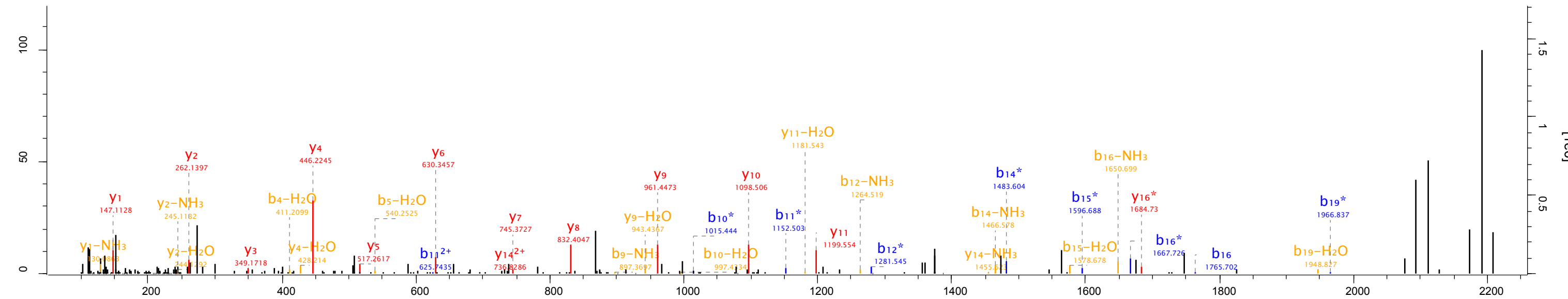
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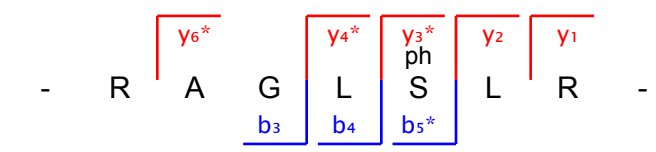
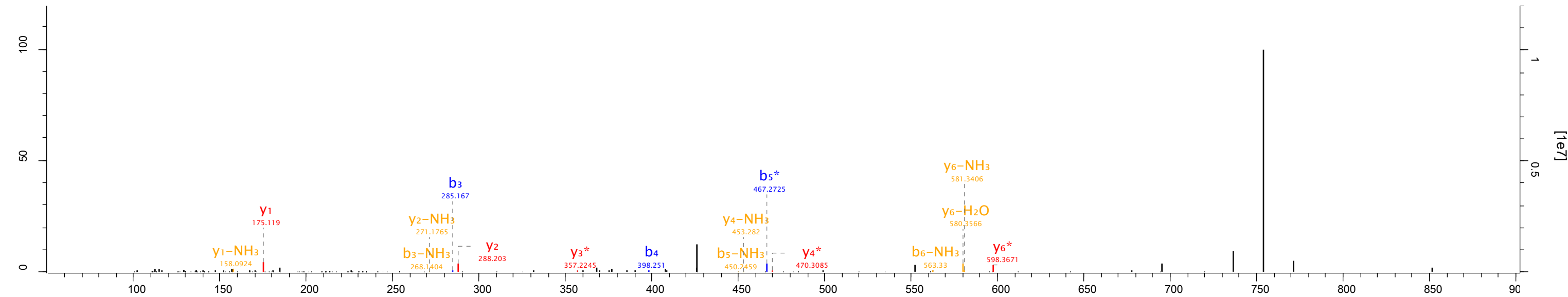
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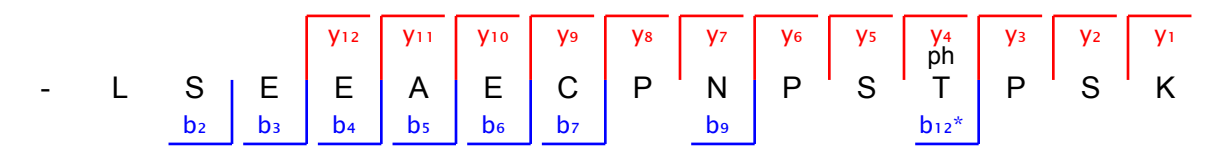
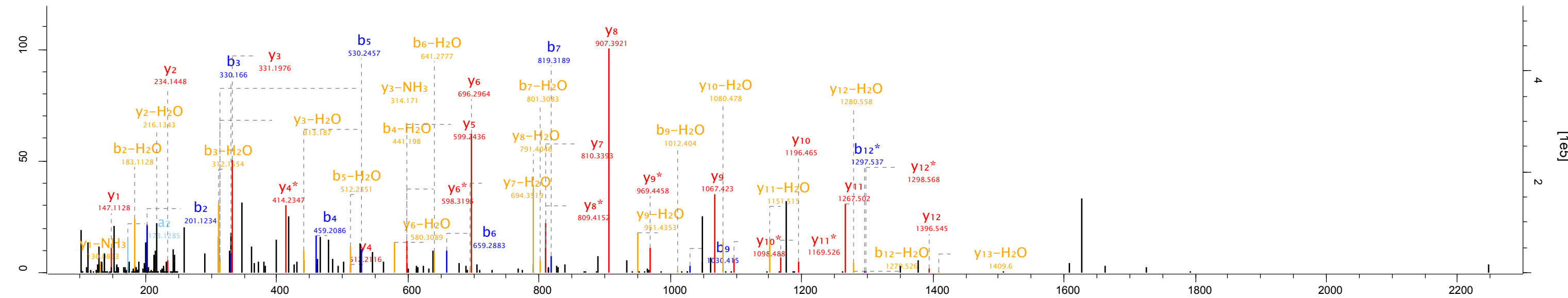
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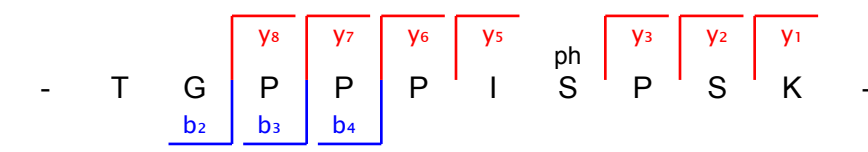
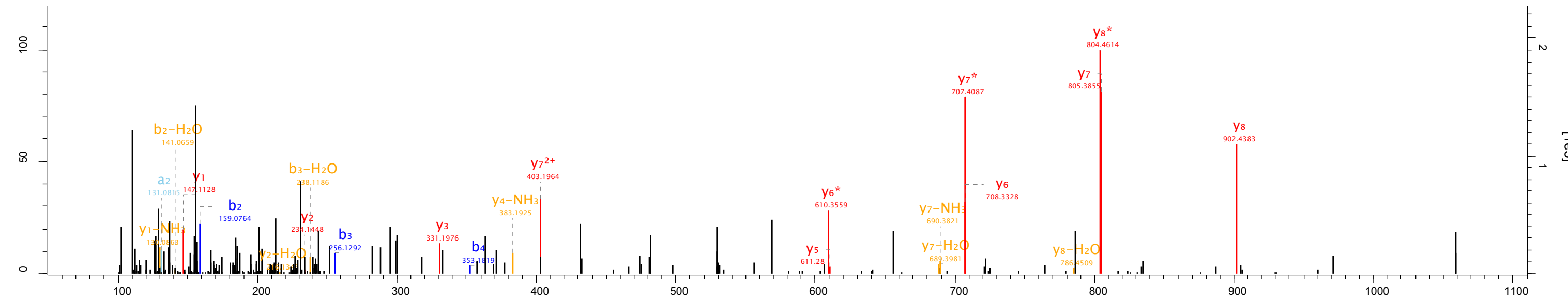
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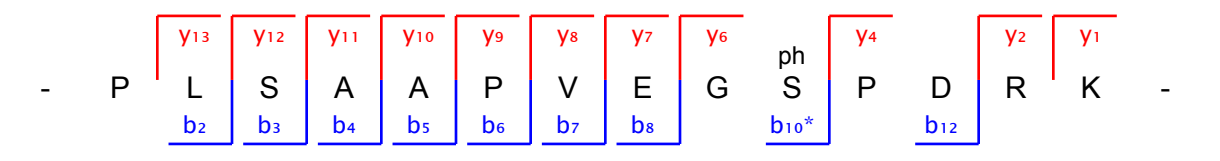
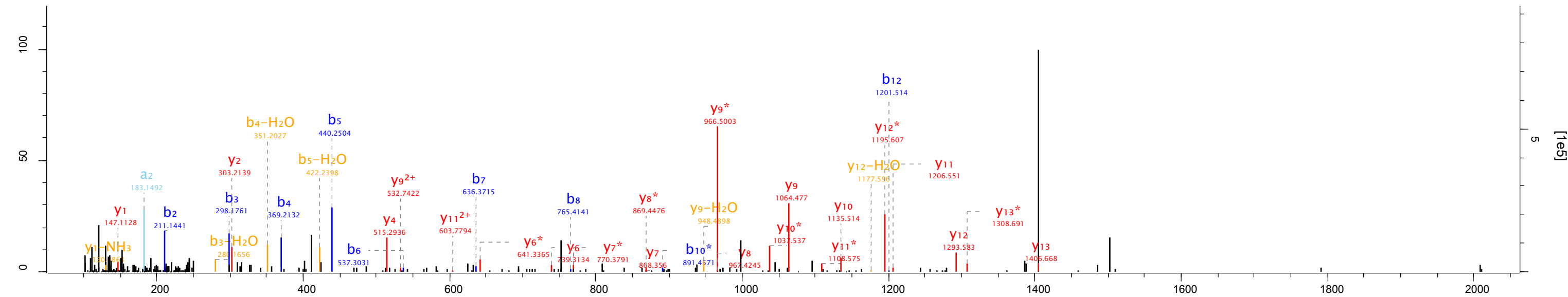
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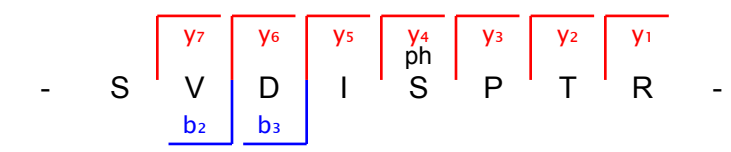
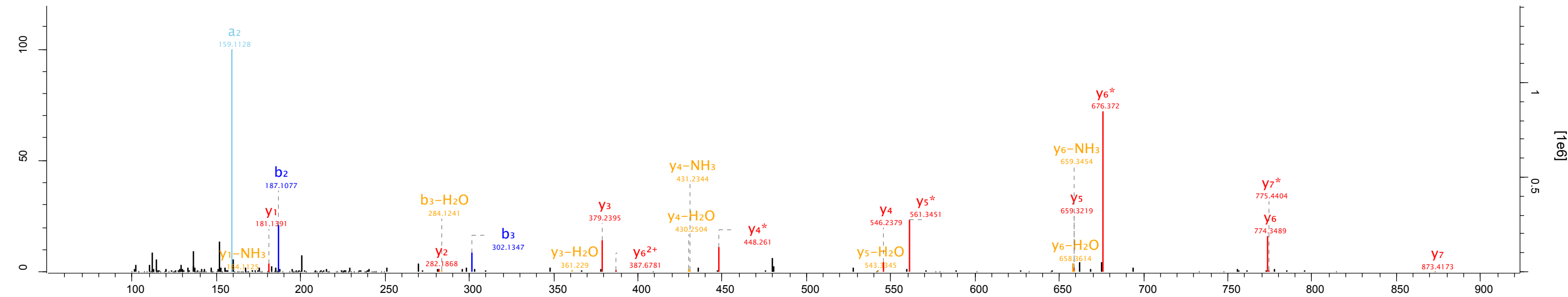
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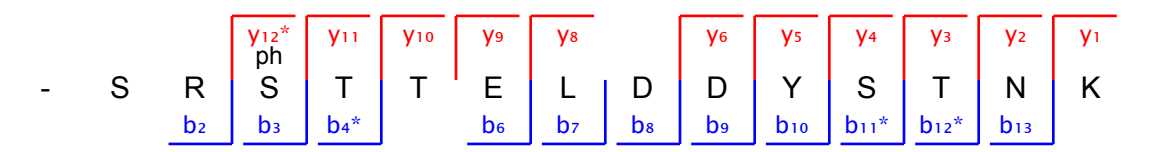
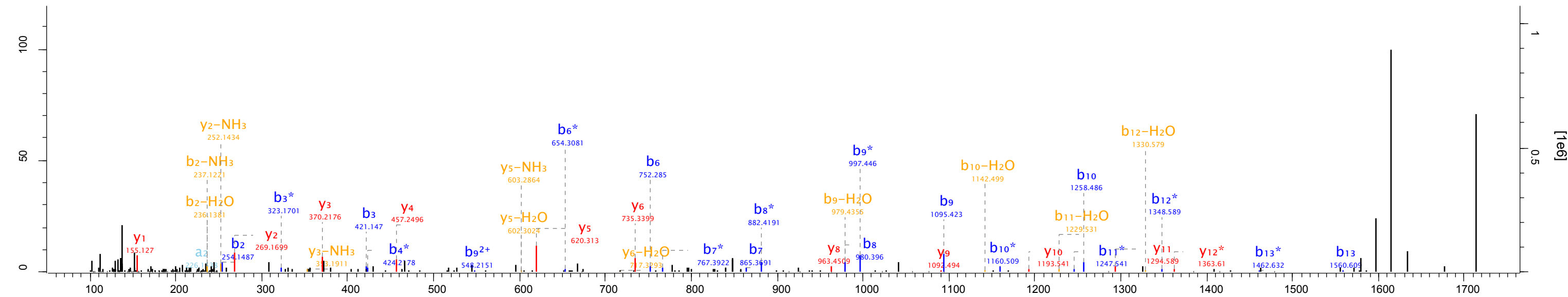
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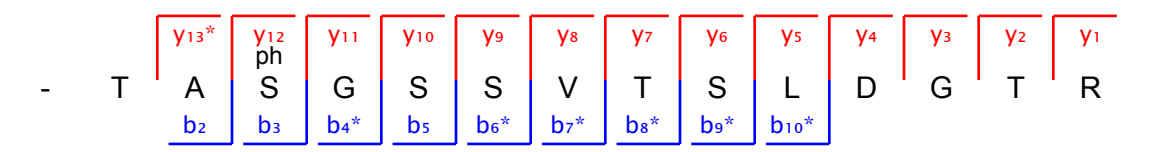
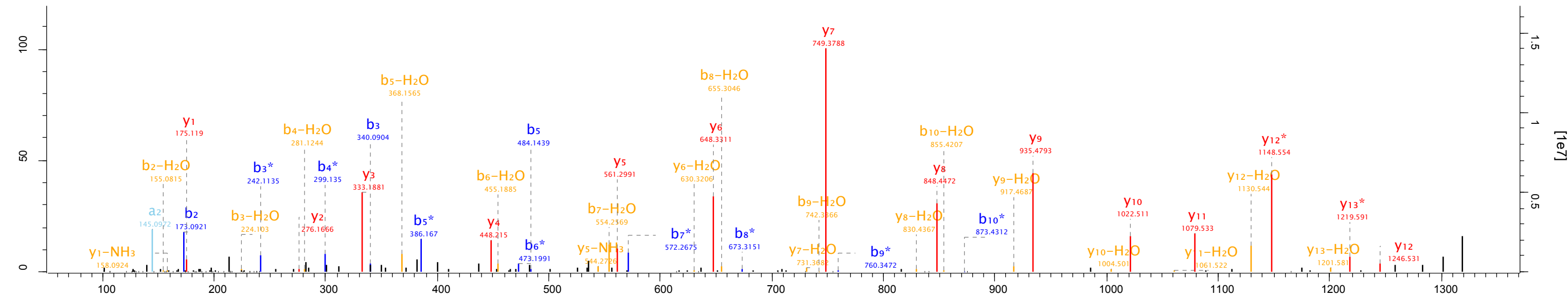
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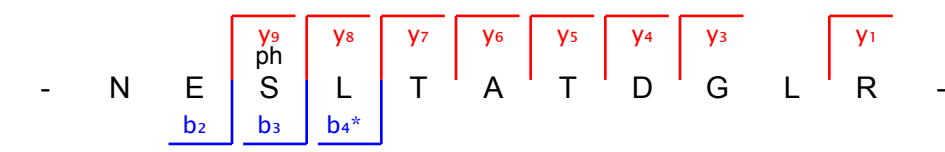
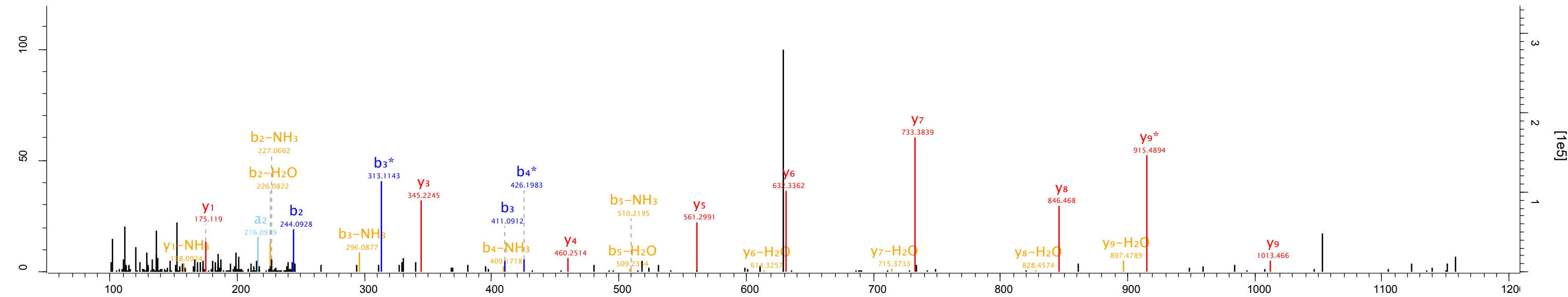
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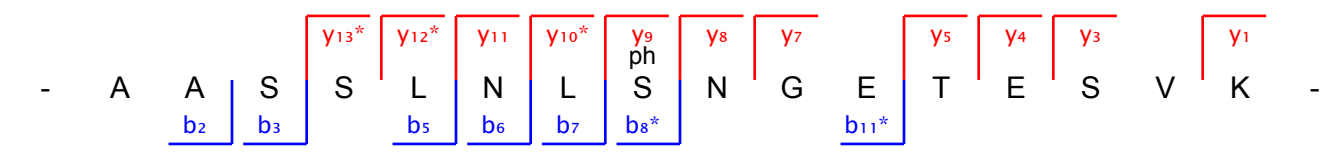
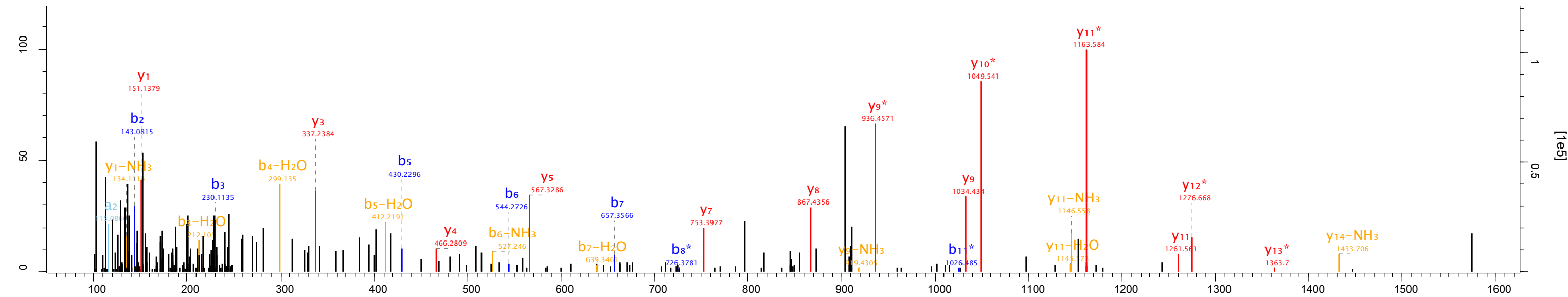
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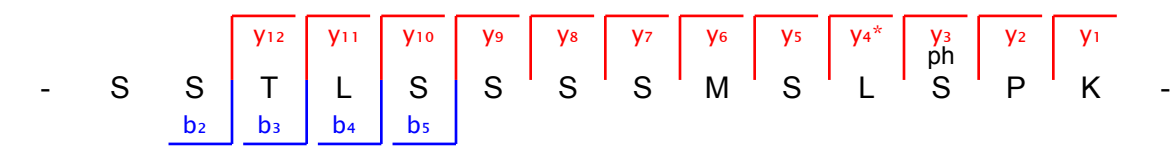
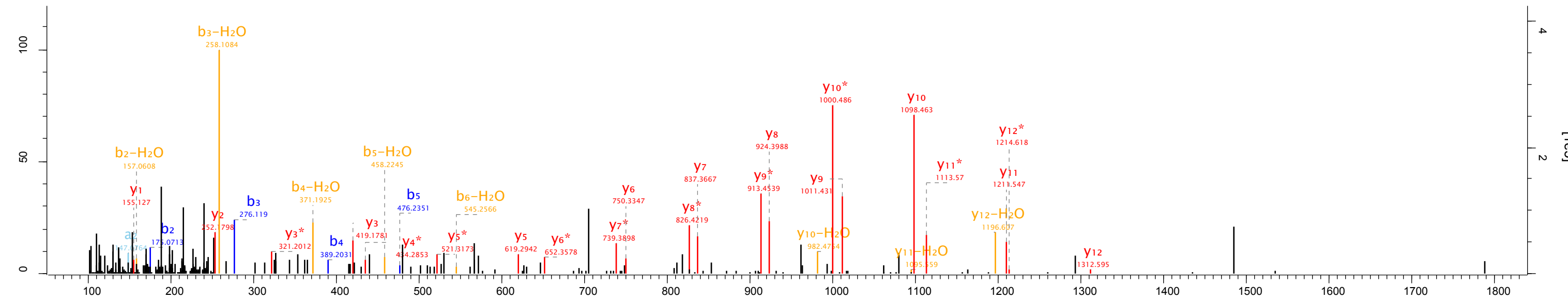
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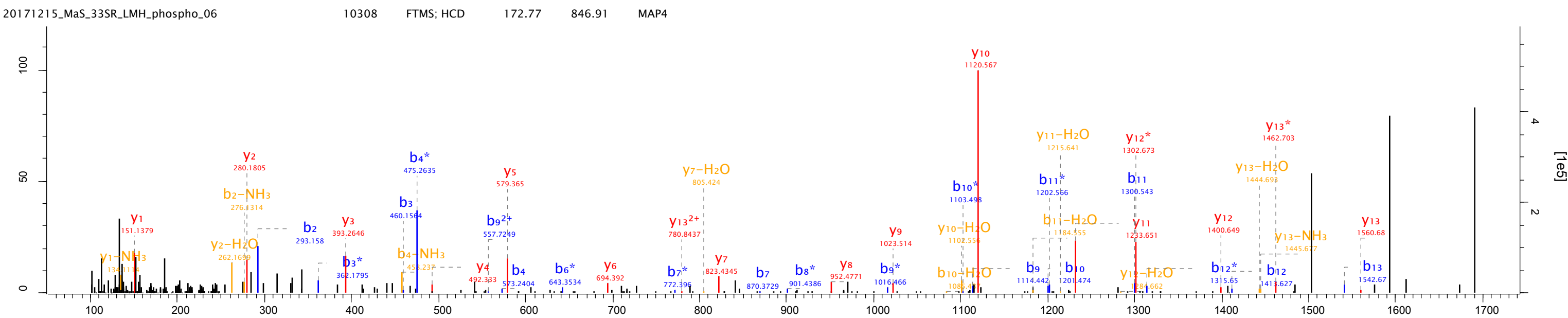
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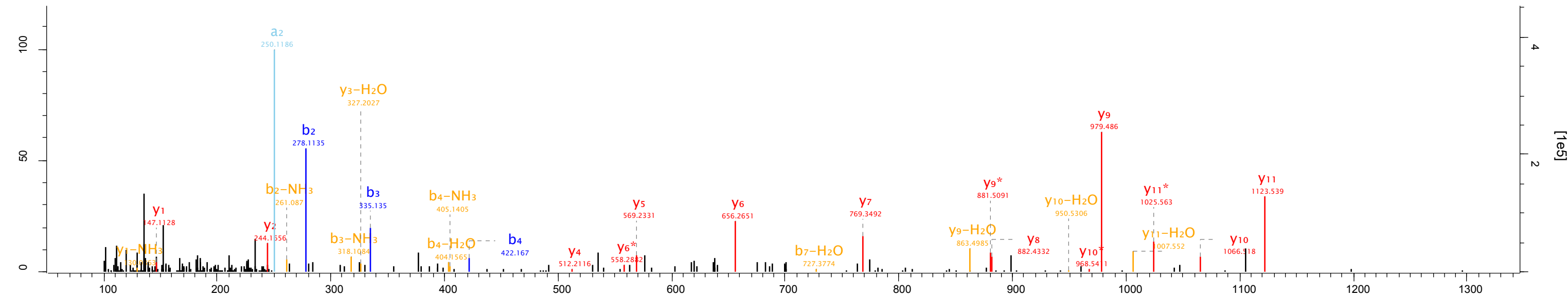
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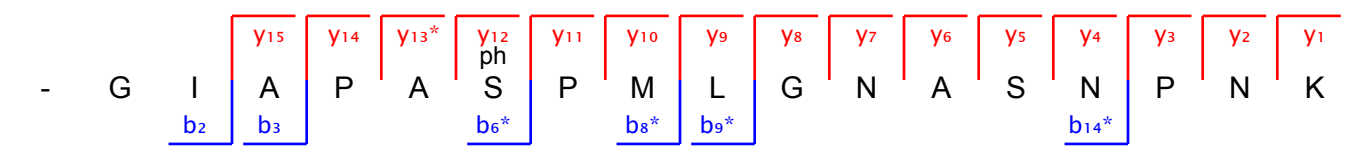
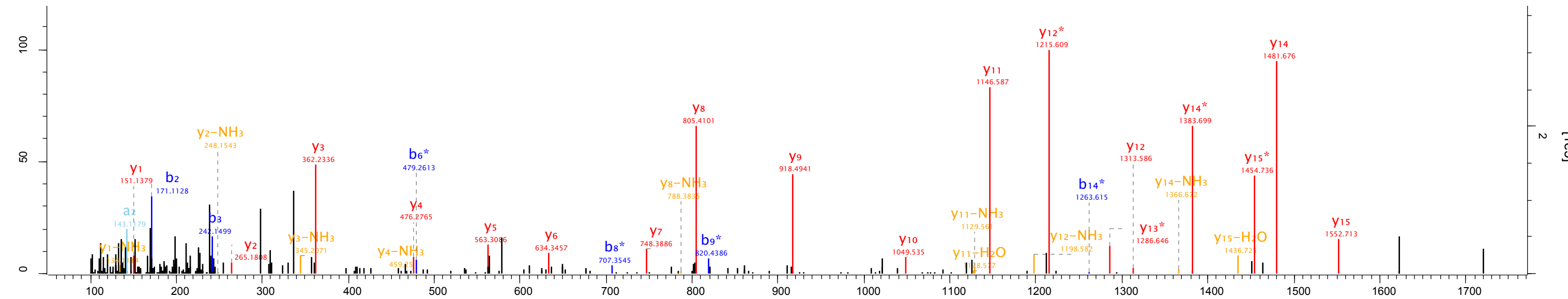
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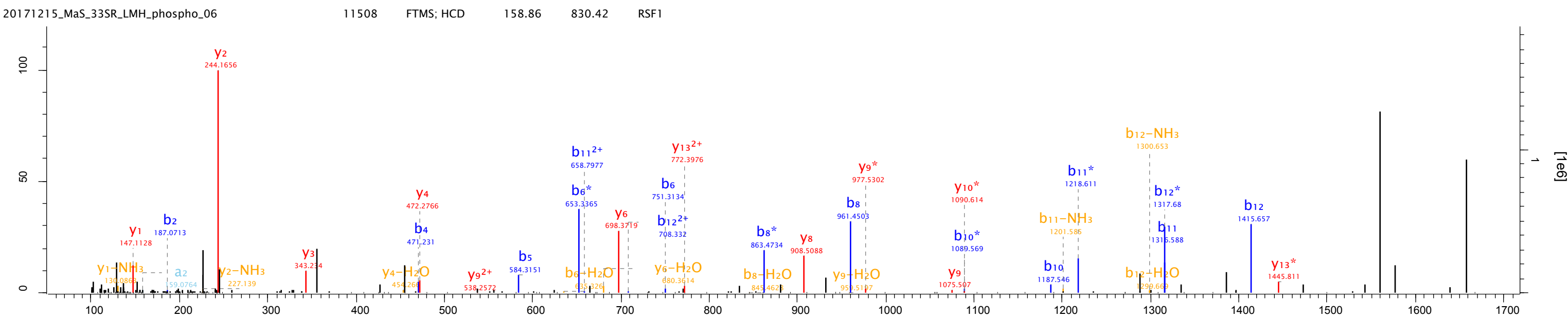
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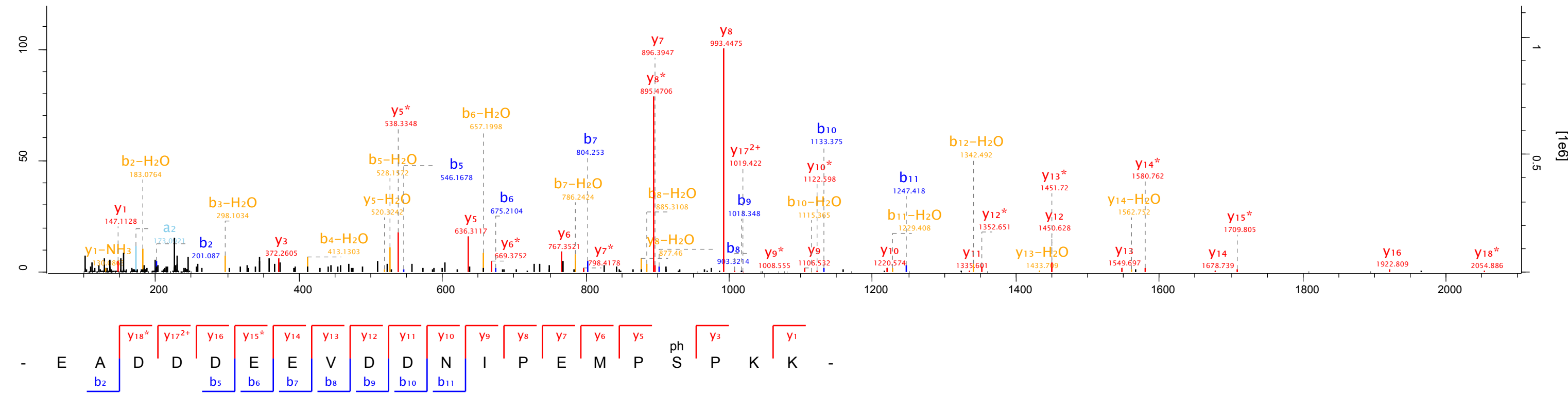


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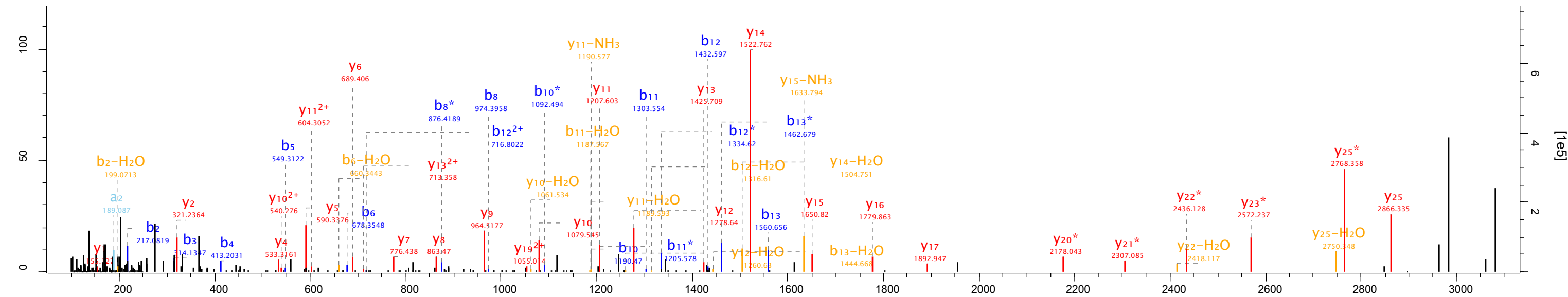


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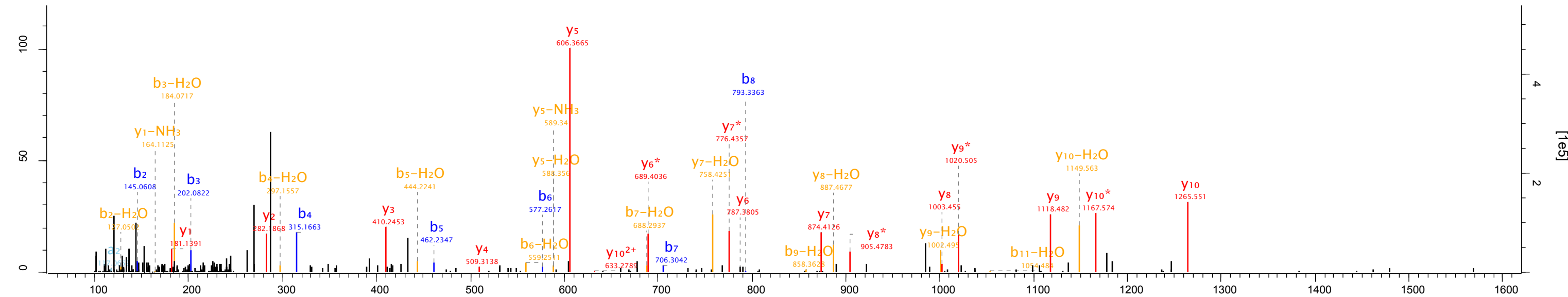
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- S E P V K E E S S E L E Q P F A Q D T S S V G P D R K -

Fragmentation mapping below the sequence:

- Peptide: S E P V K E E S S E L E Q P F A Q D T S S V G P D R K
- Fragmentation sites (b-ions): b2 (E), b3 (P), b4 (V), b5 (K), b6 (E), b8 (S), b10 (E), b11 (L), b12 (E), b13 (Q)
- Fragmentation sites (y-ions): y25 (P), y23* (V), y22* (K), y21* (E), y20* (E), y192+ (S), y17 (E), y16 (L), y15 (E), y14 (P), y13 (F), y12 (A), y11 (Q), y10 (D), y9 (T), y8 (S), y7 (S), y6 (V), y5 (G), y4 (P)

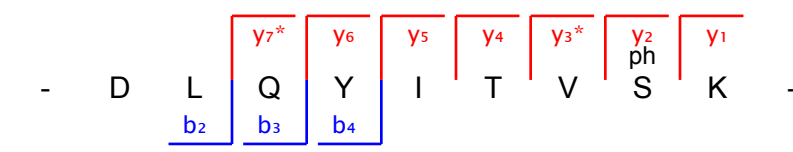
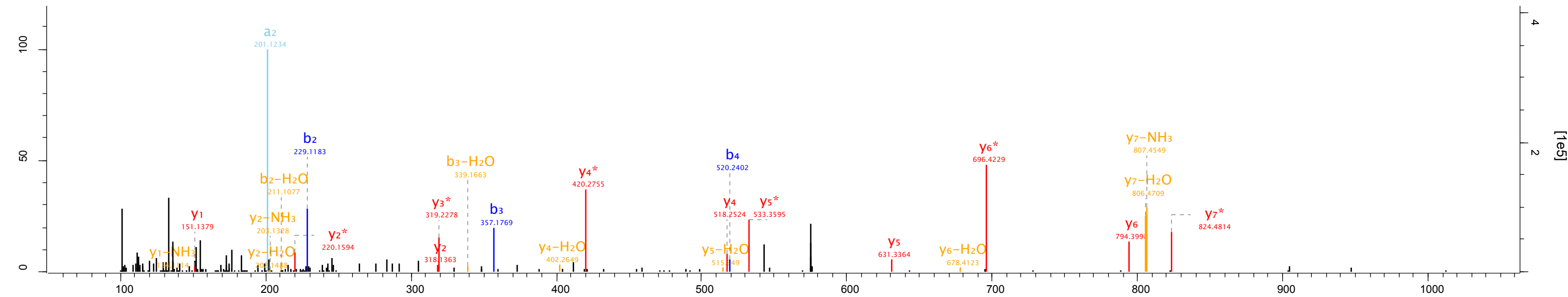


- G S G I F D E S T P V Q T R -

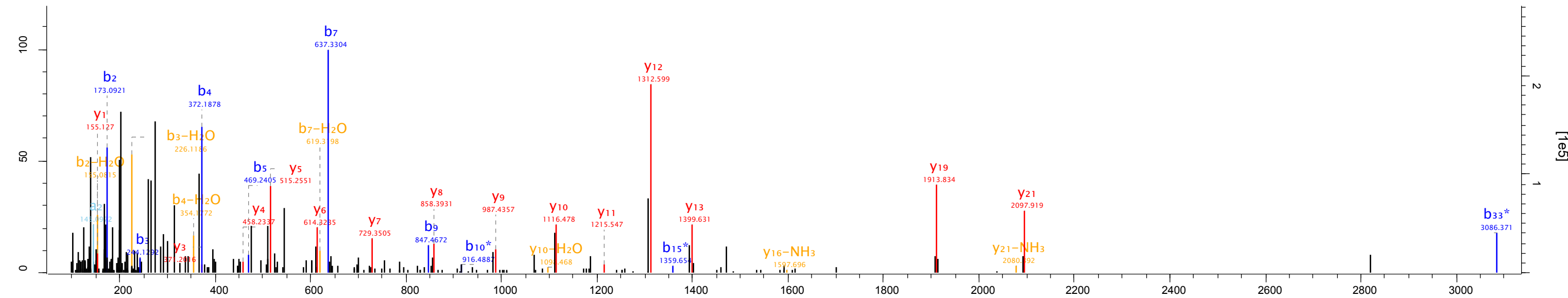
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ph

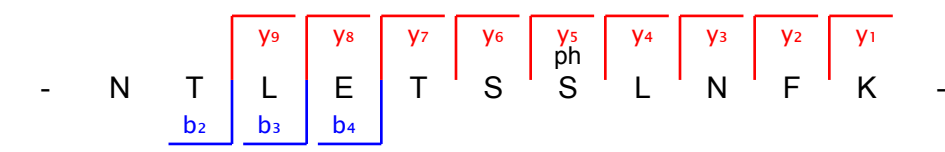
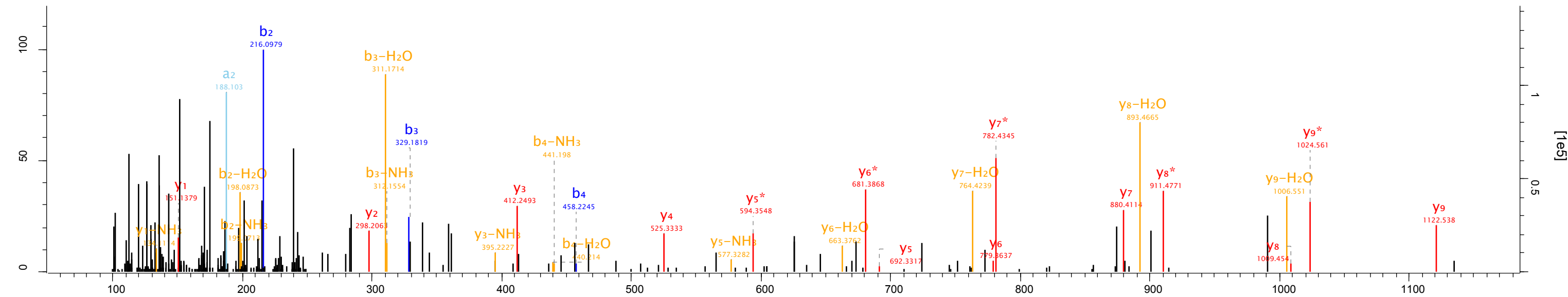
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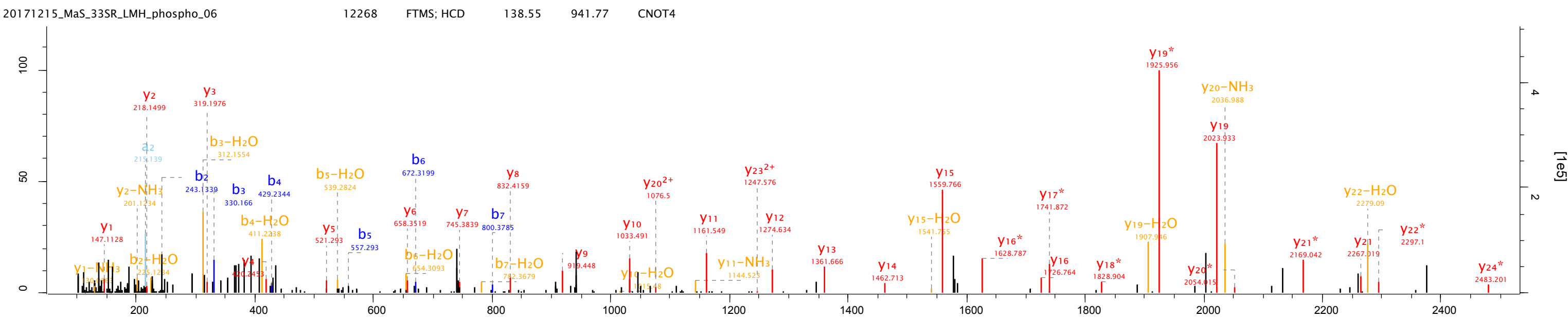
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Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12098 Method FTMS; HCD Score 127.3 m/z 669.82 Gene names SAFB2



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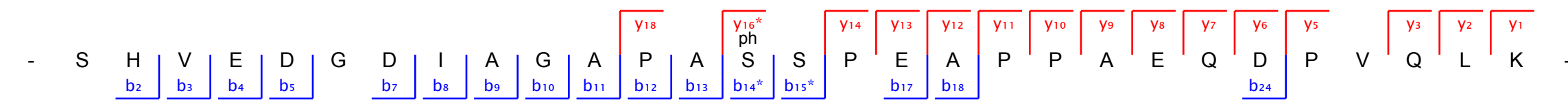
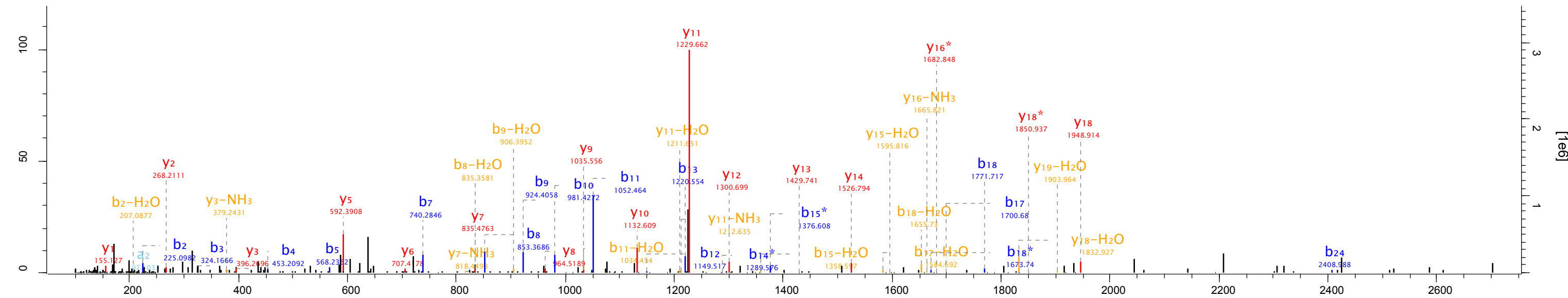


- E L S V Q D Q P S L S P T S L Q N S S H T T T A K -

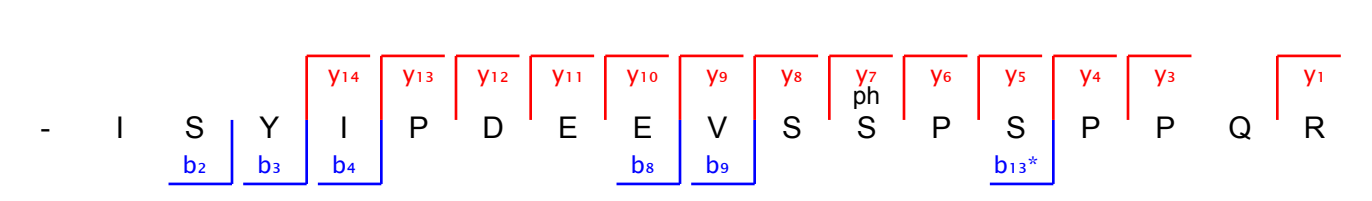
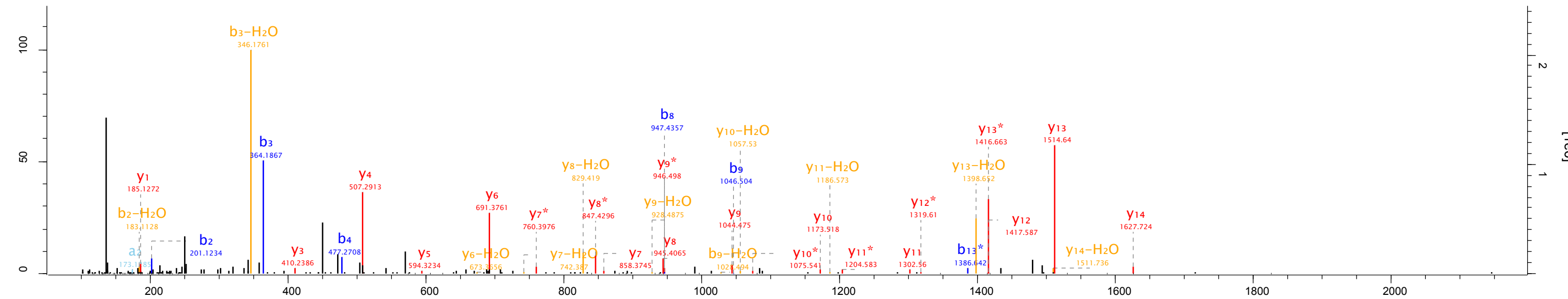
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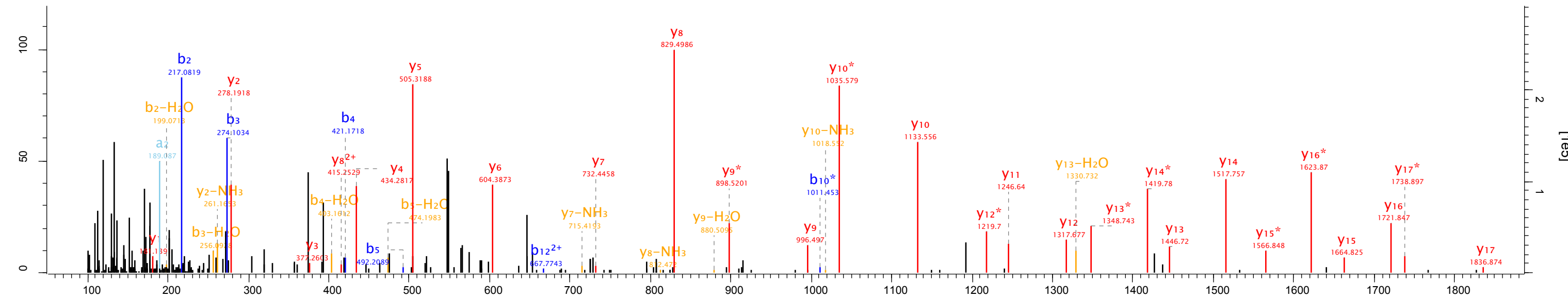
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- Blue boxes: b2, b3, b4, b5, b6, b7

Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12428 Method FTMS; HCD Score 102.4 m/z 1001.47 Gene names RRBP1



Raw file: 20171215_MaS_33SR_LMH_phospho_06
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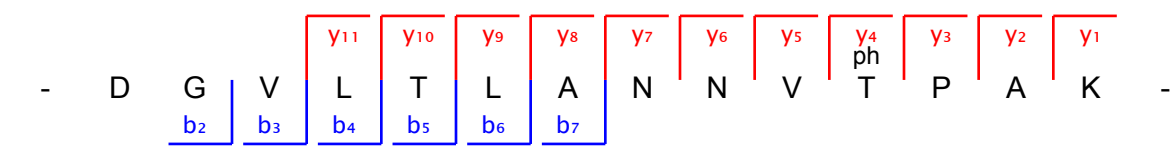
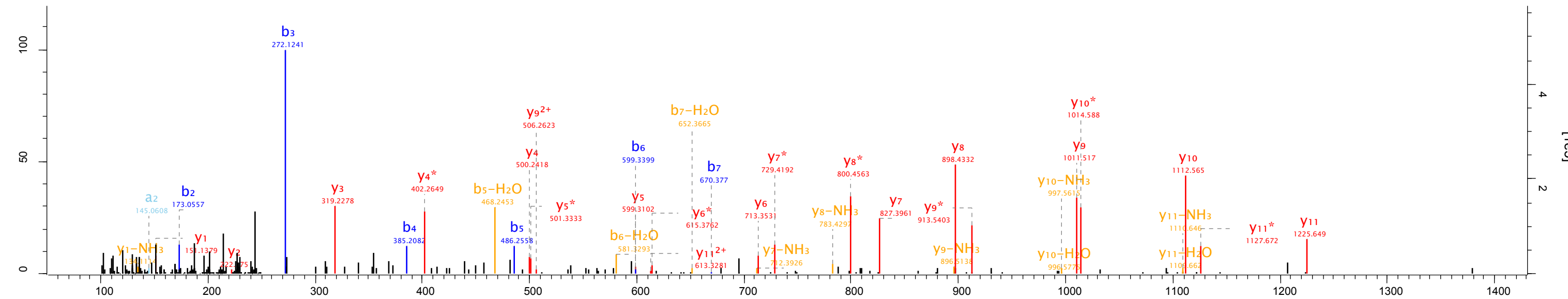




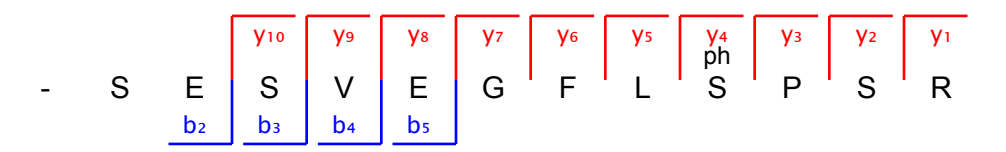
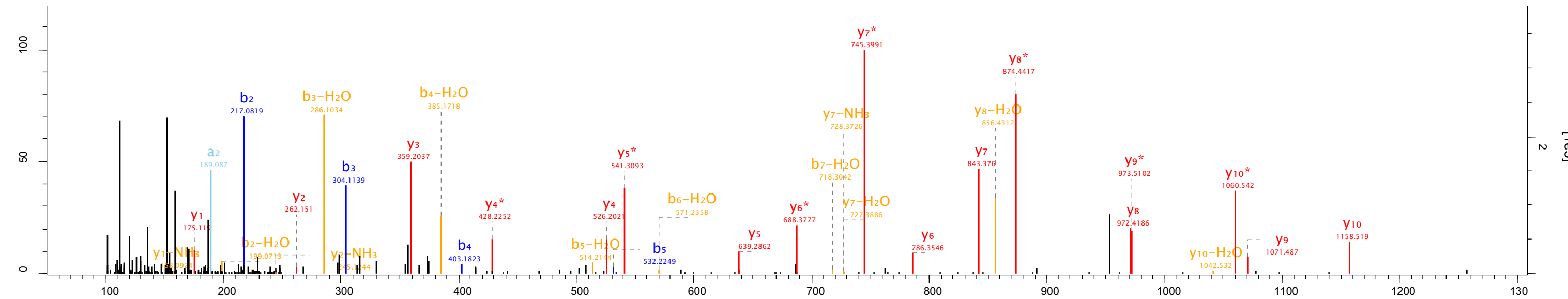
- T D R G F A E A I H S P Q V A G V P R -

b₂
b₃
b₄
b₅
y₁₇
y₁₆
y₁₅
y₁₄
y₁₃
y₁₂
y₁₁
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y₁

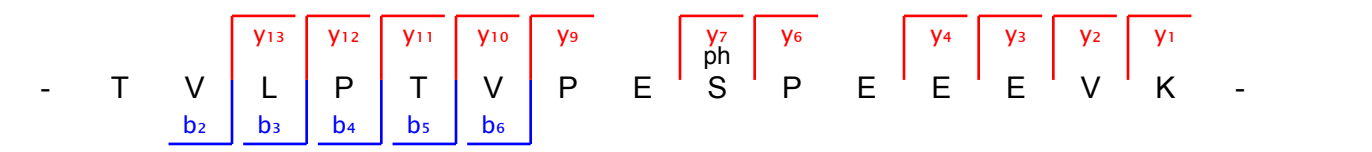
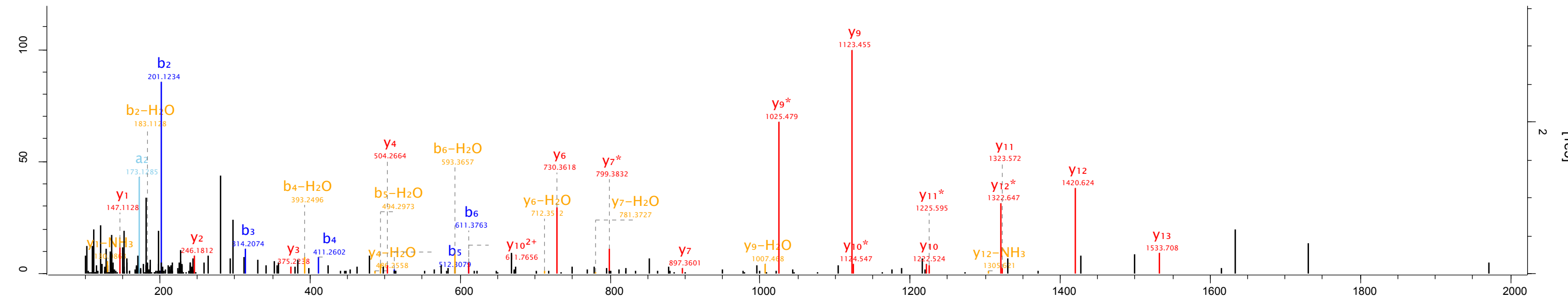
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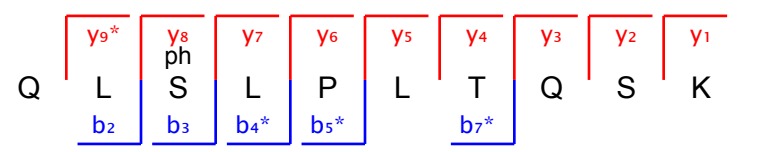
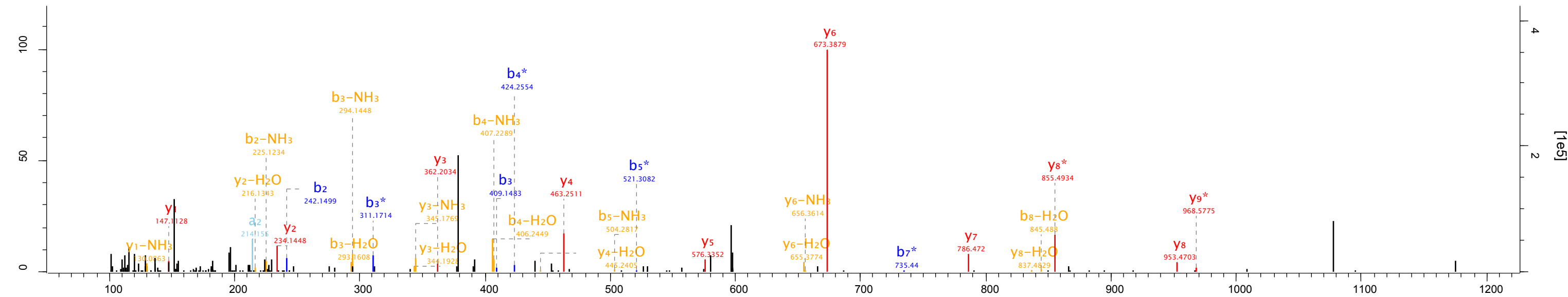
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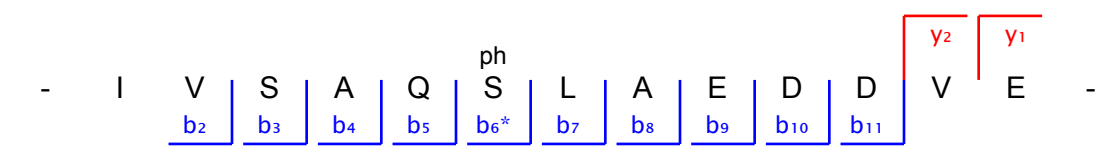
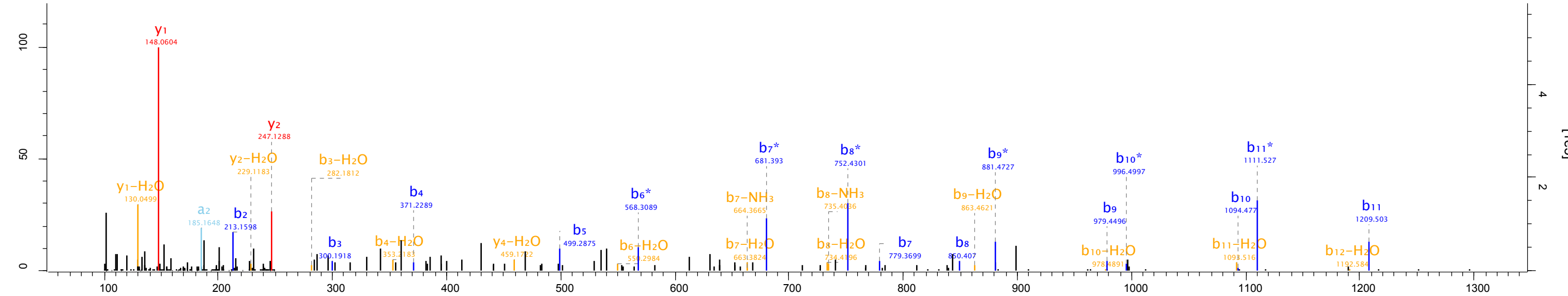
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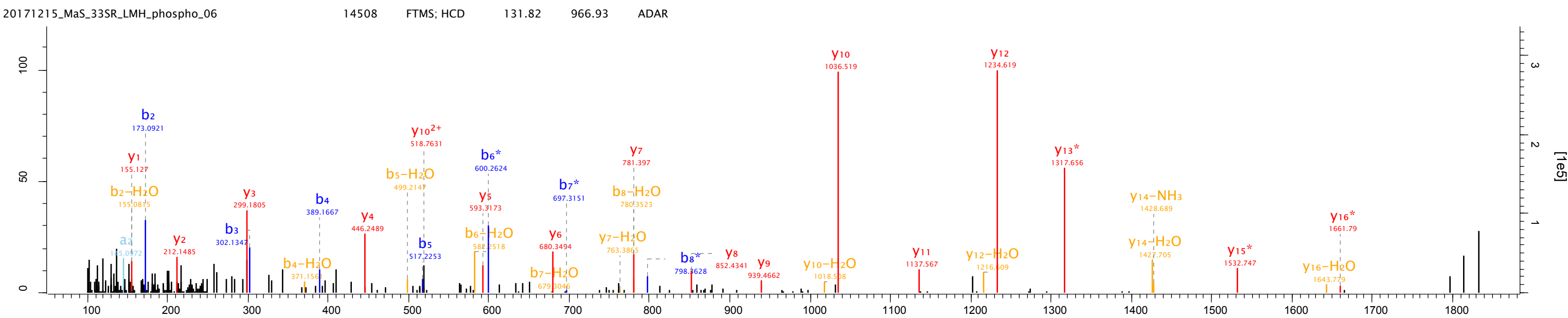
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20171215_MaS_33SR_LMH_phospho_06

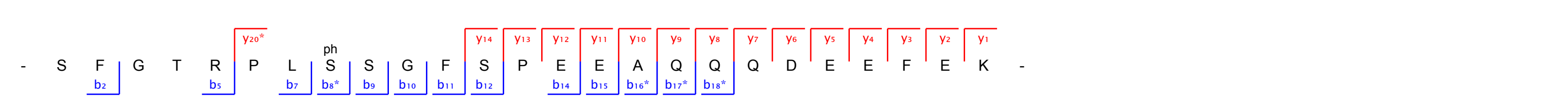
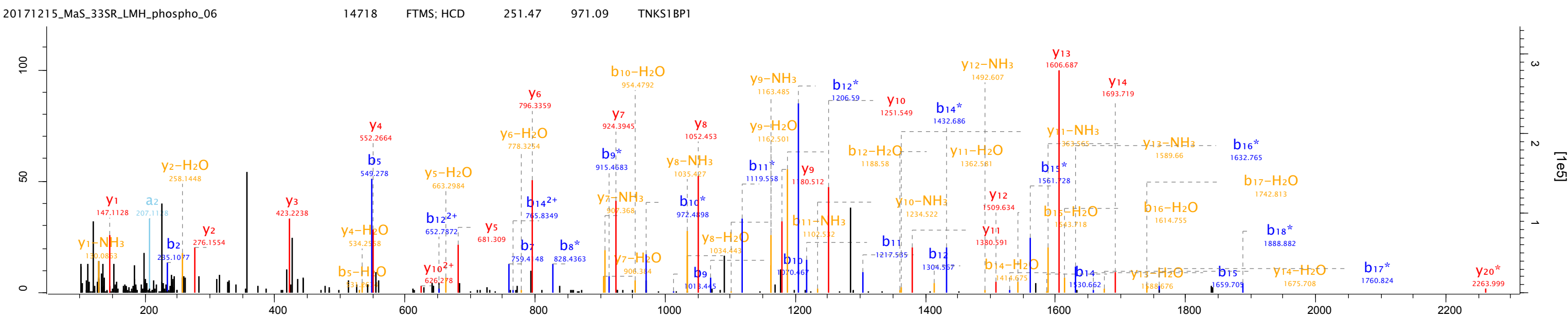
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 m/z: 728.31
 Gene names: TOMM20



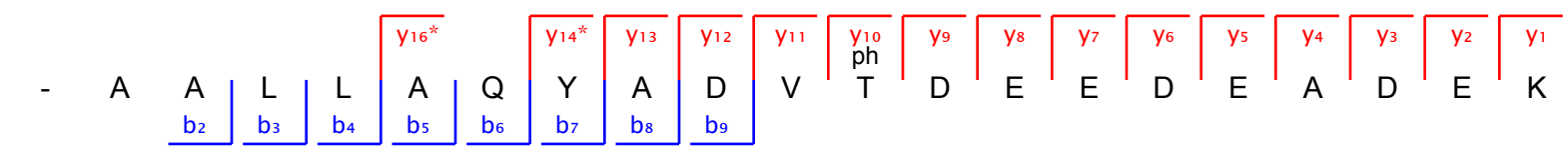
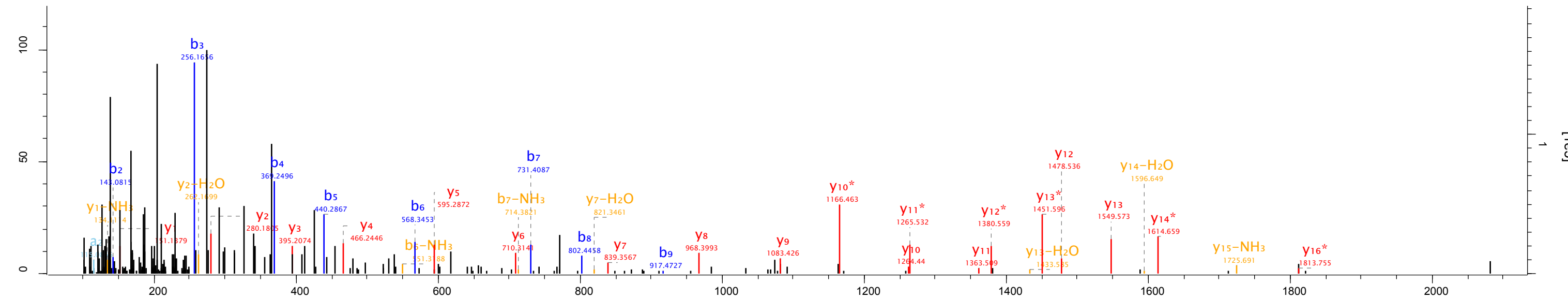
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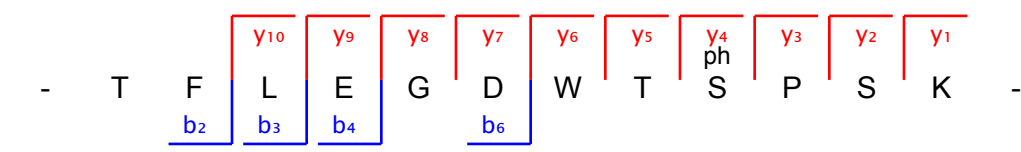
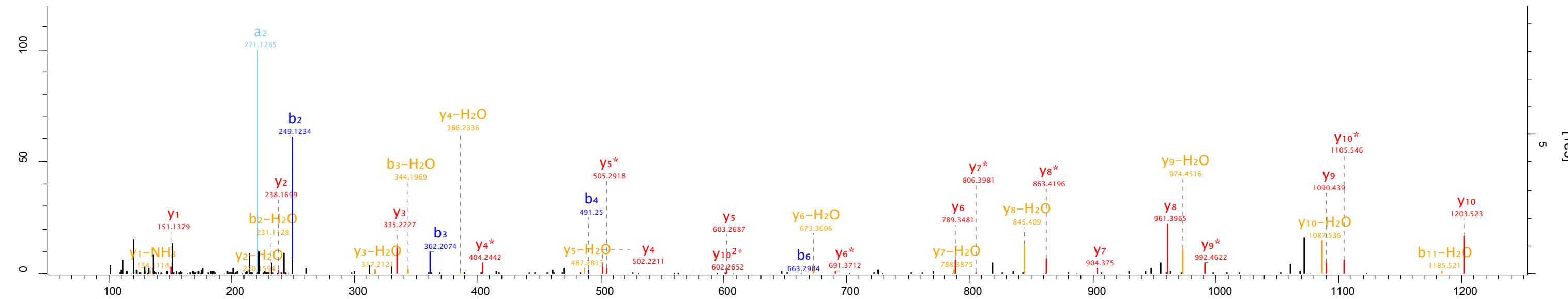
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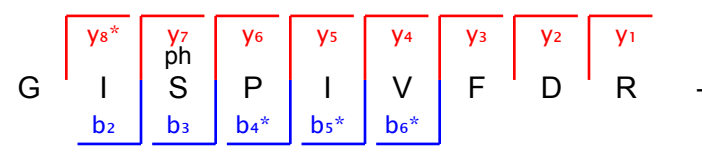
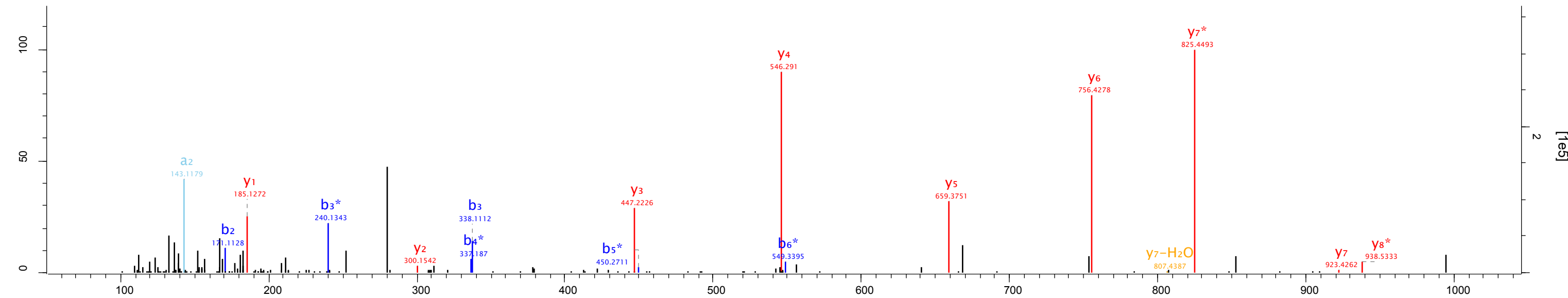
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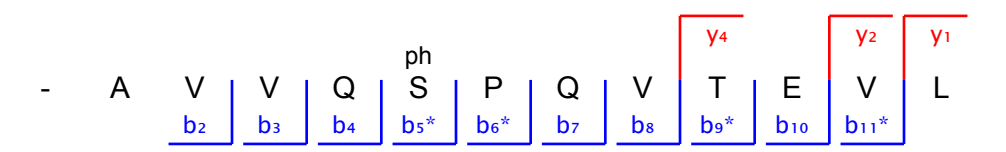
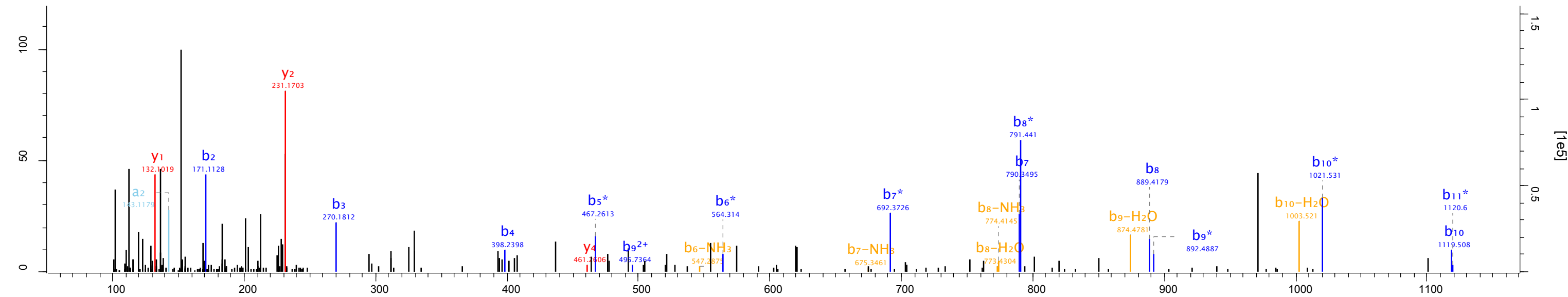
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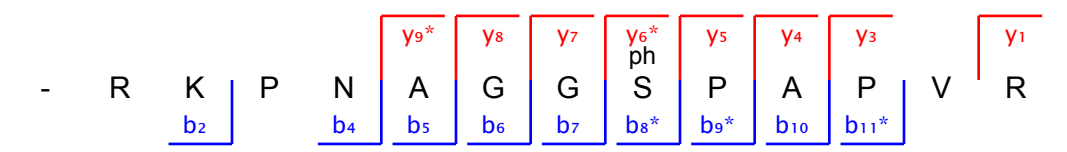
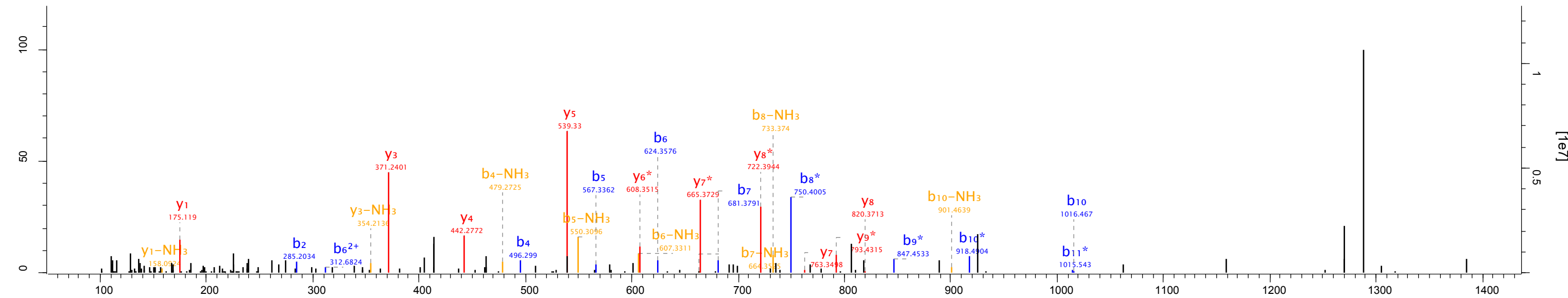
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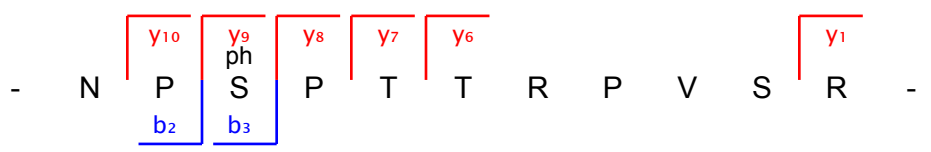
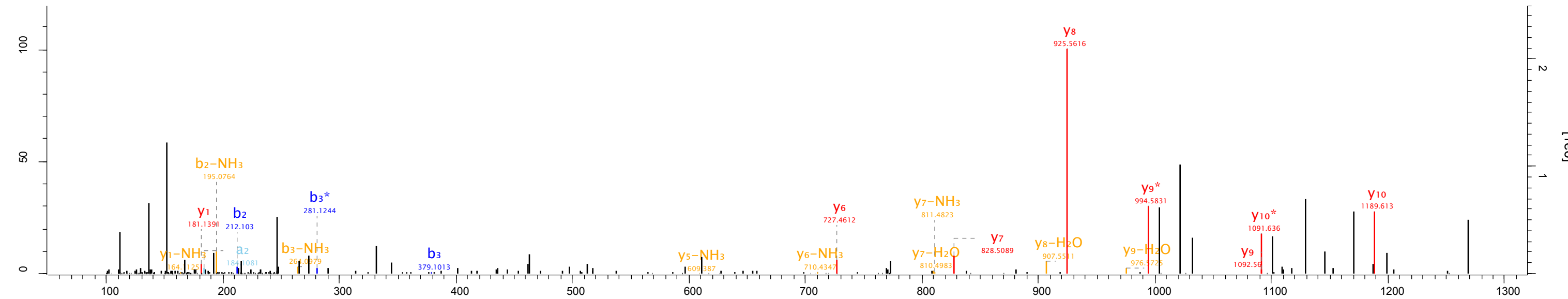
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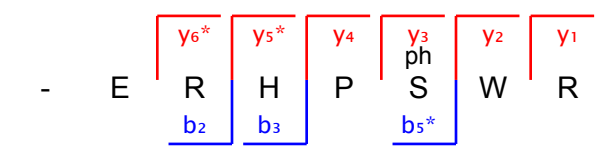
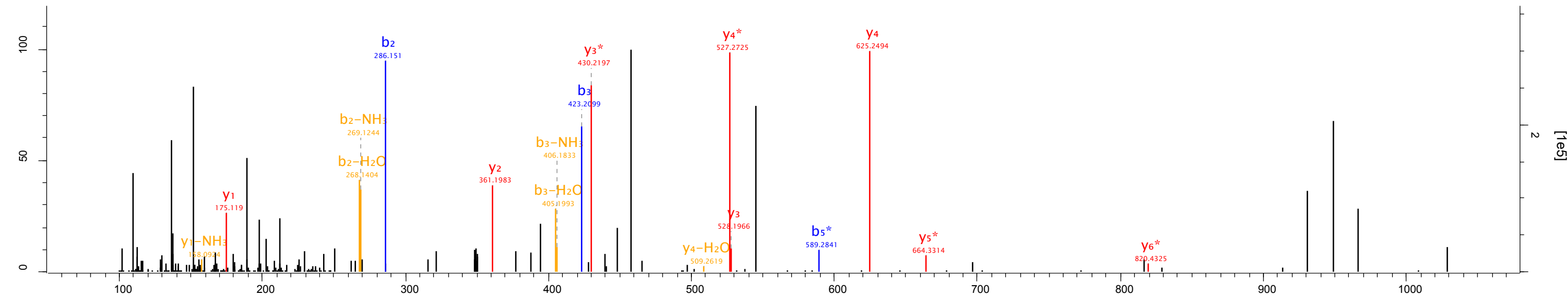
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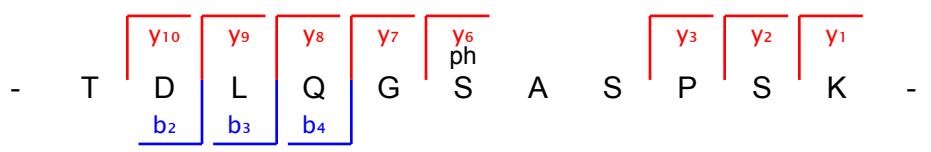
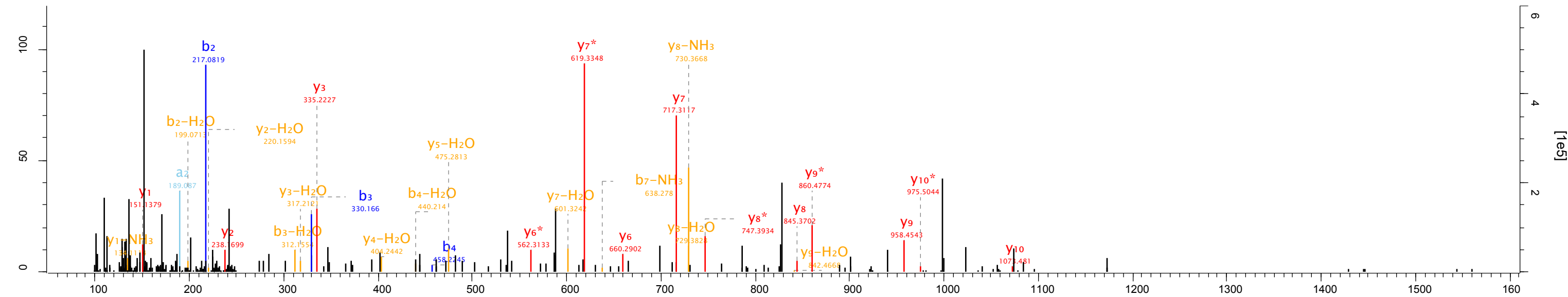
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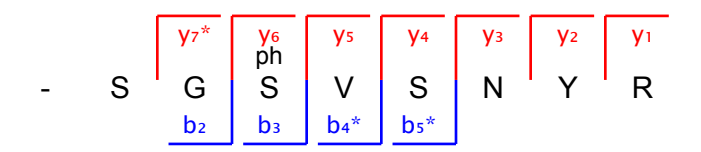
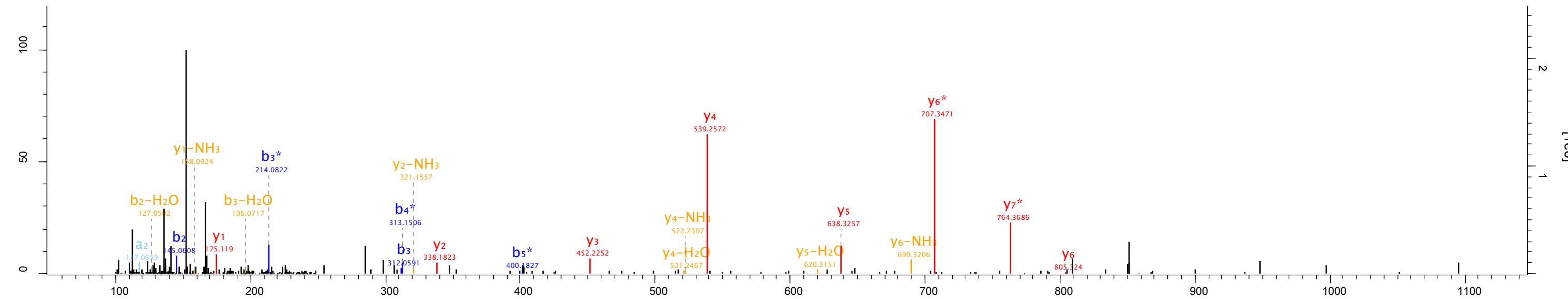
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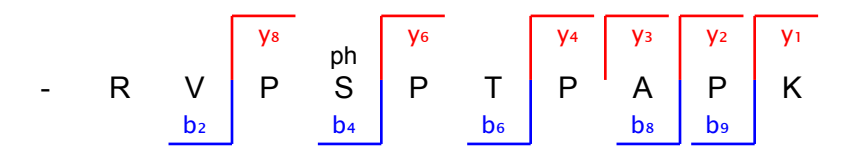
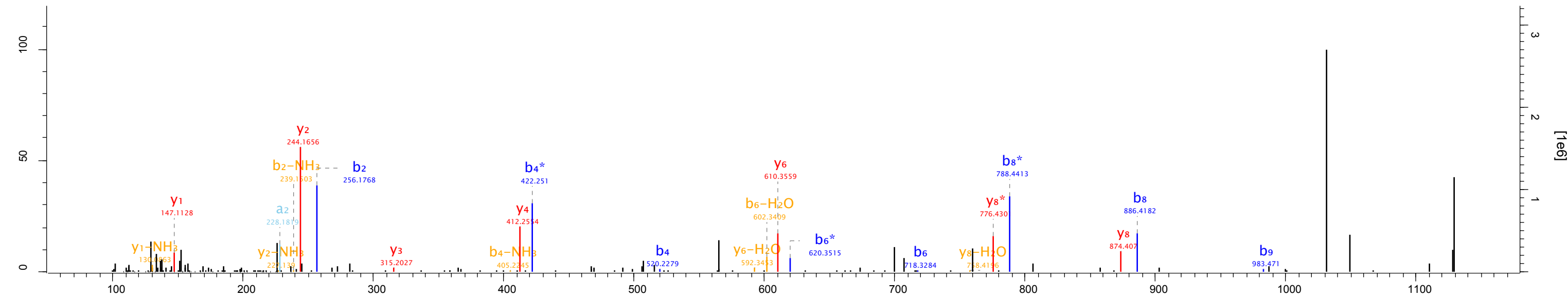
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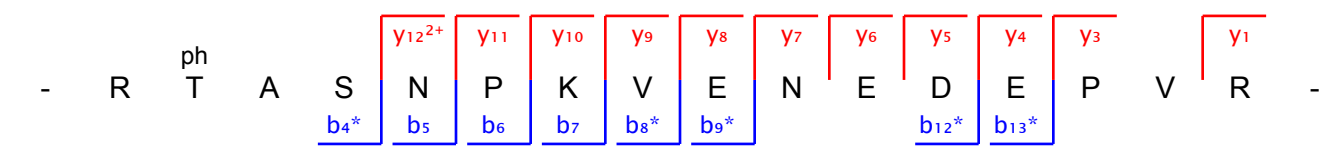
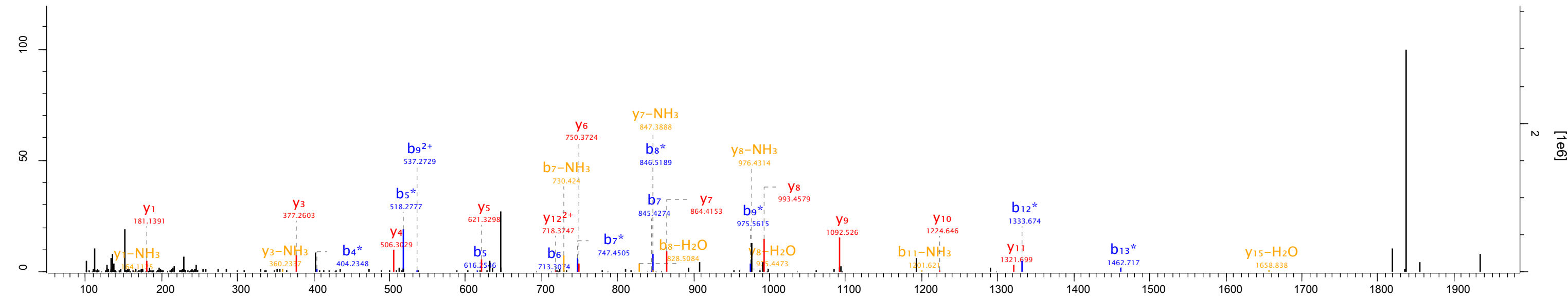
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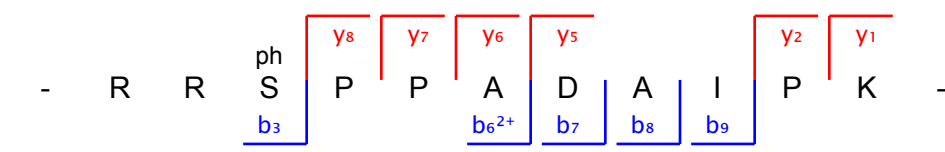
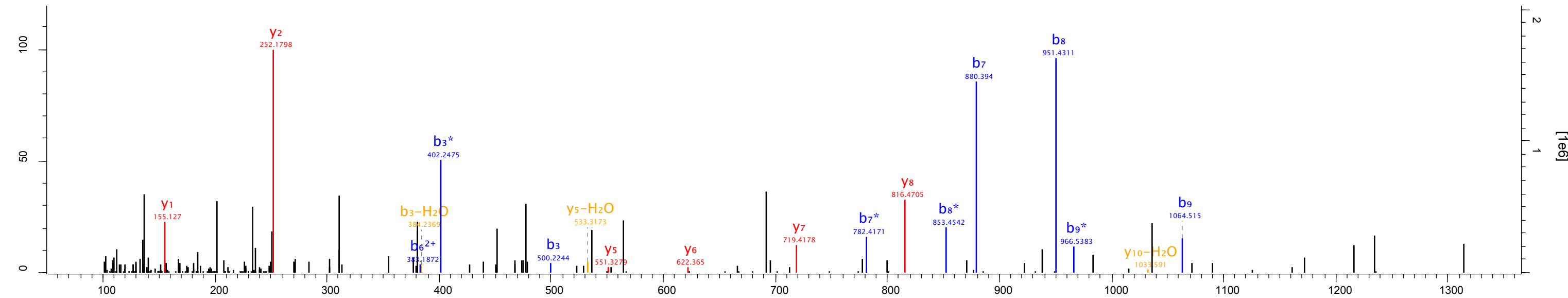
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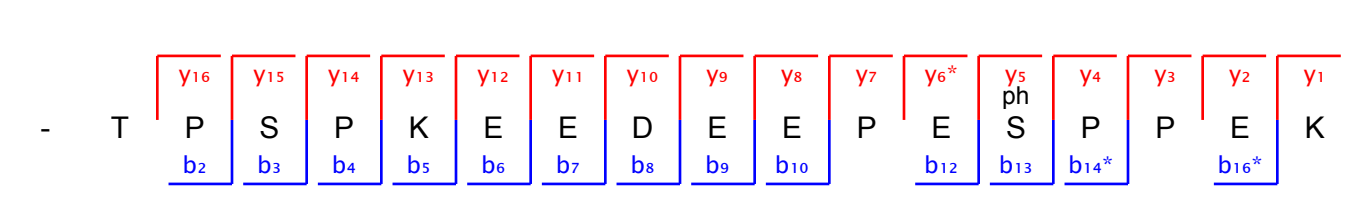
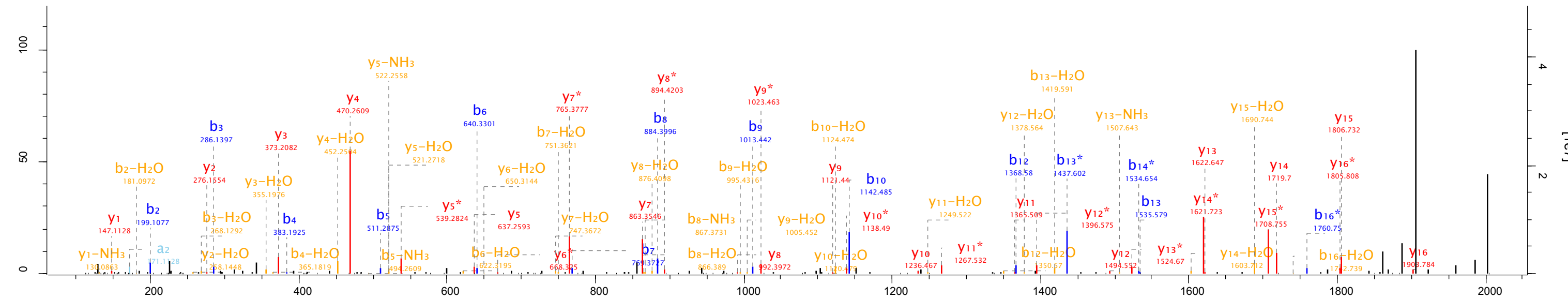
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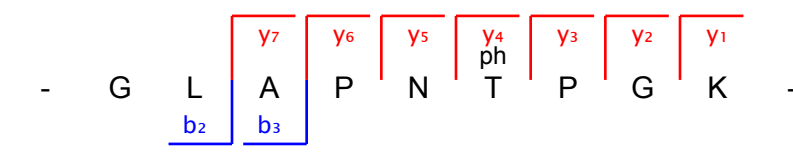
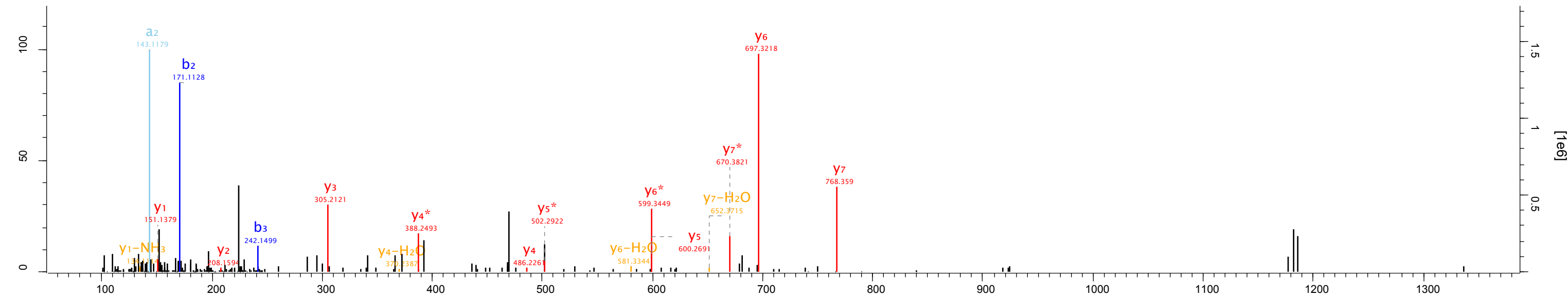
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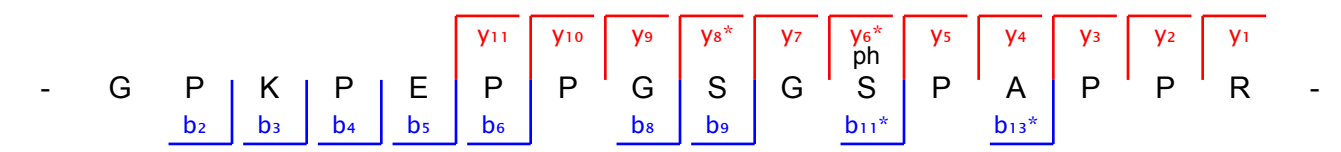
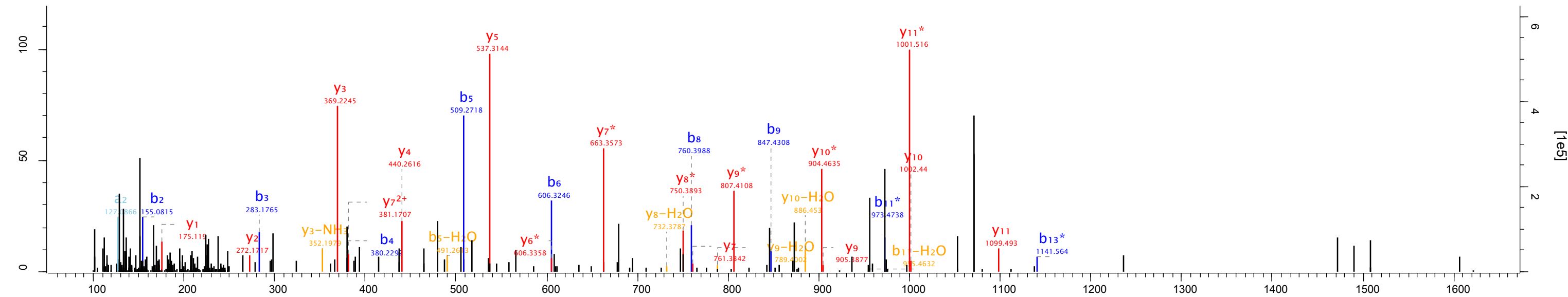
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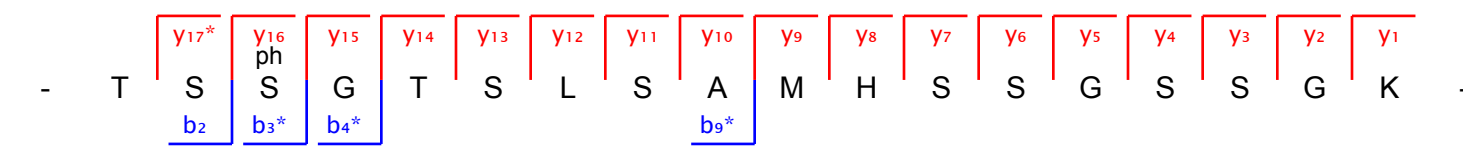
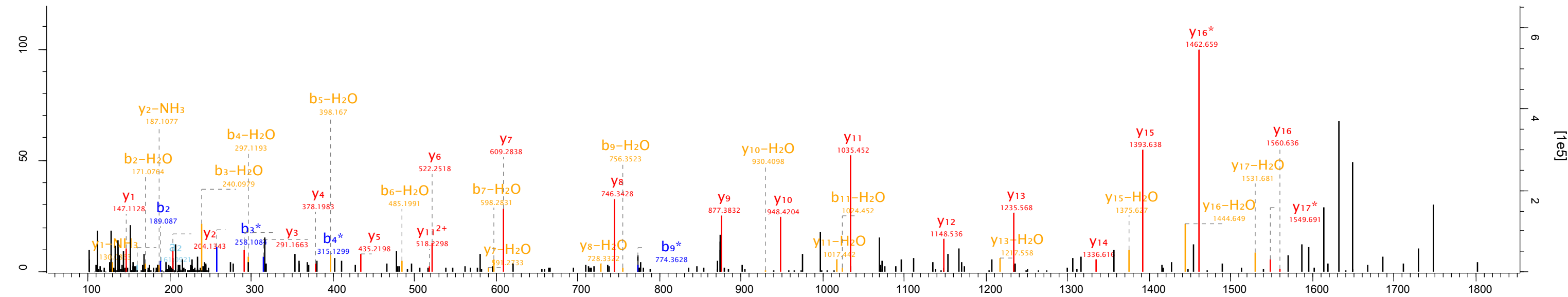
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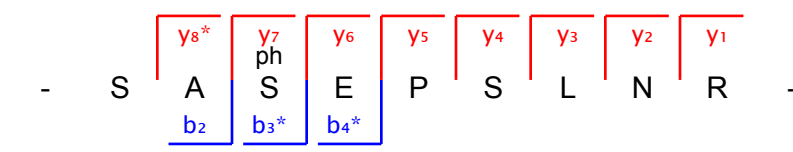
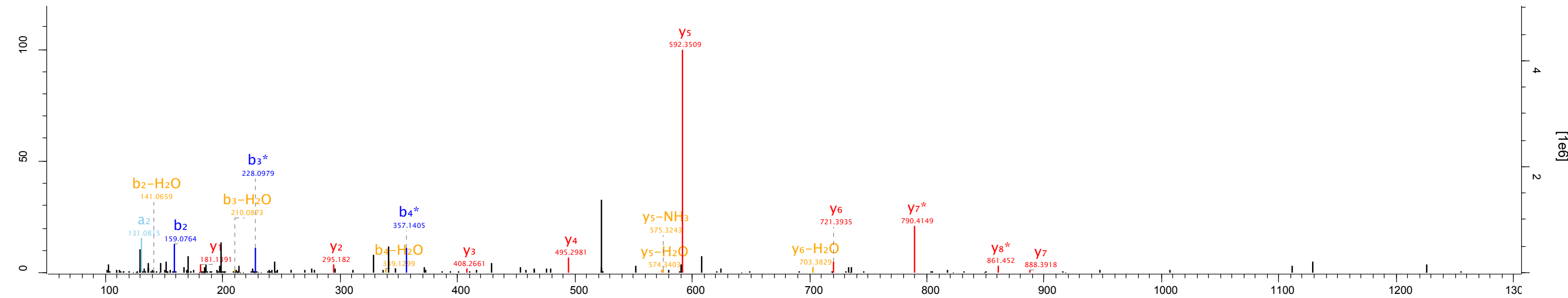
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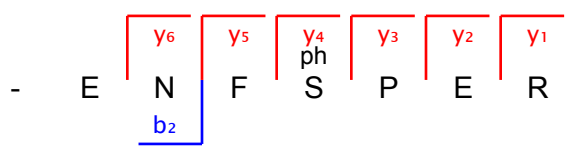
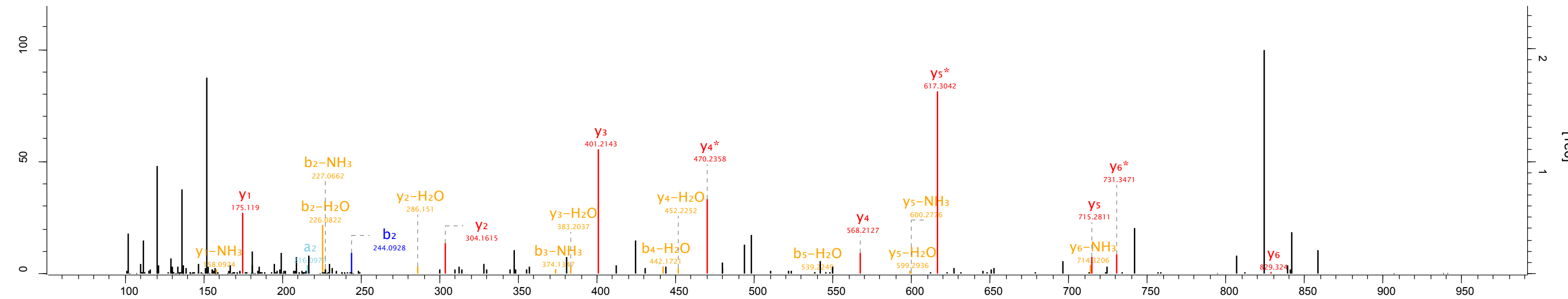
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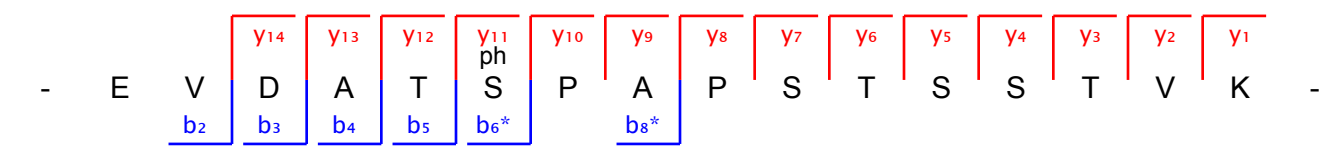
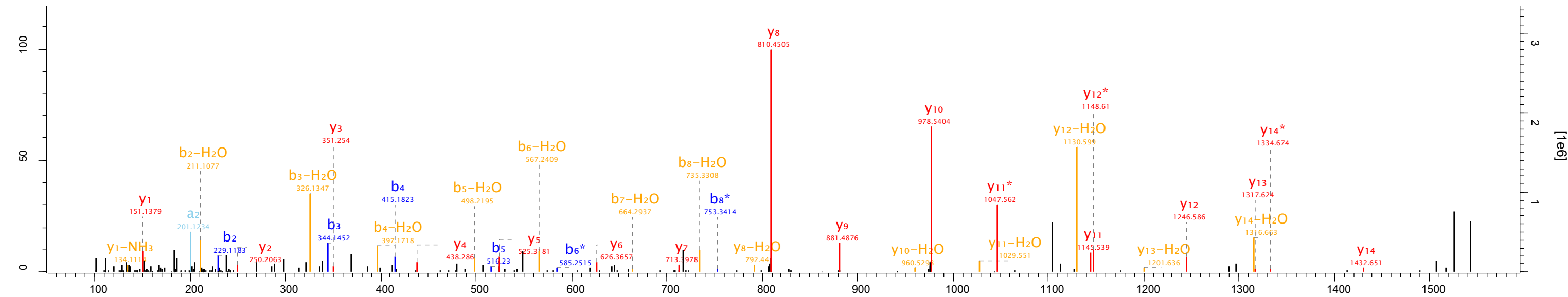
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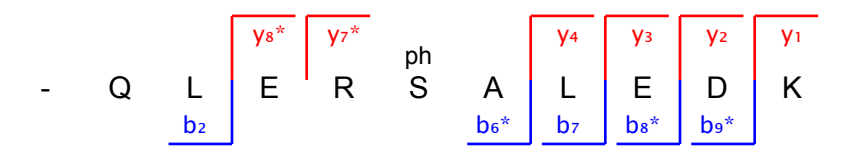
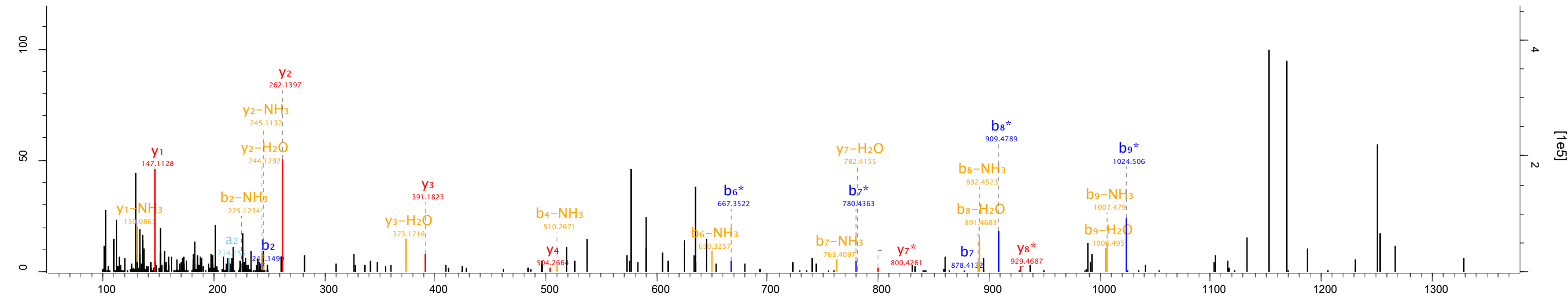
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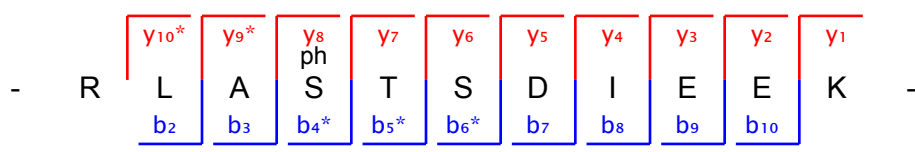
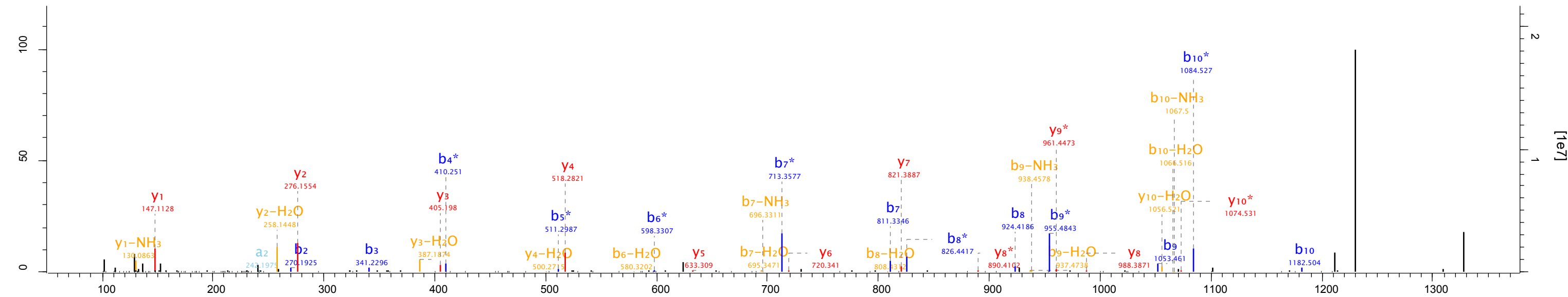
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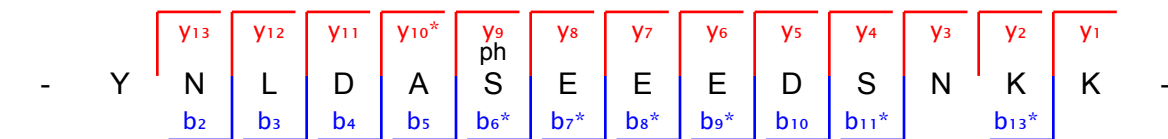
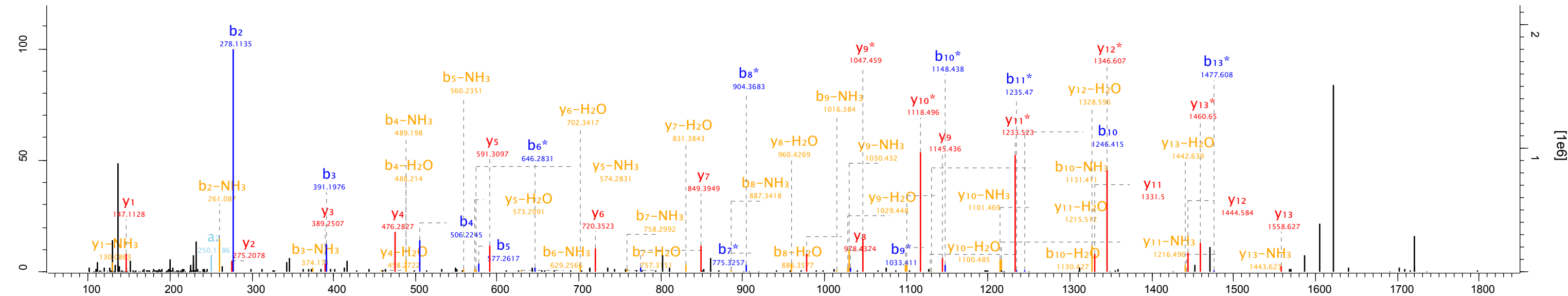


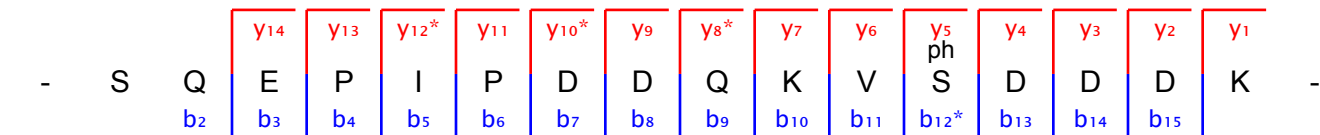
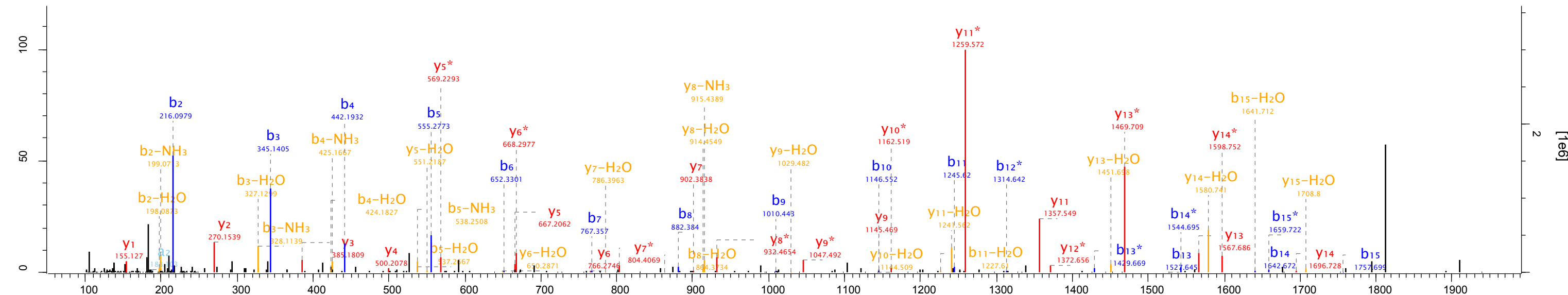
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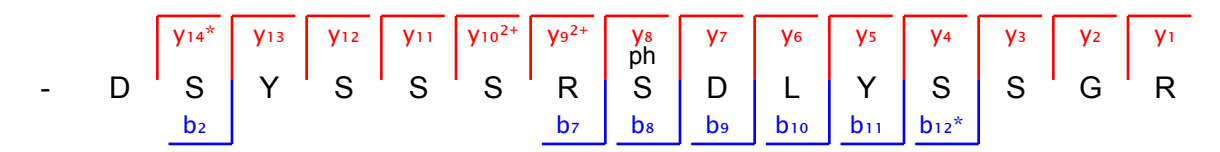
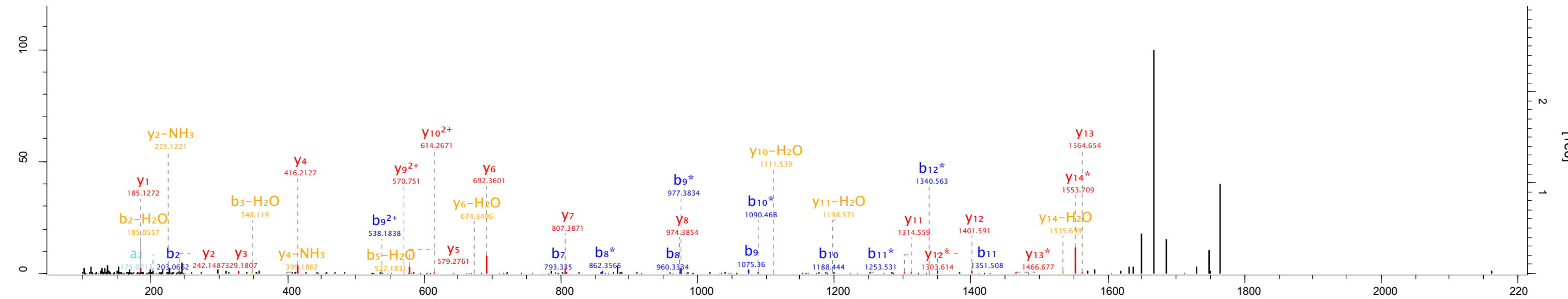
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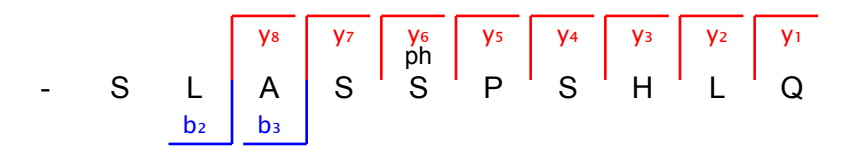
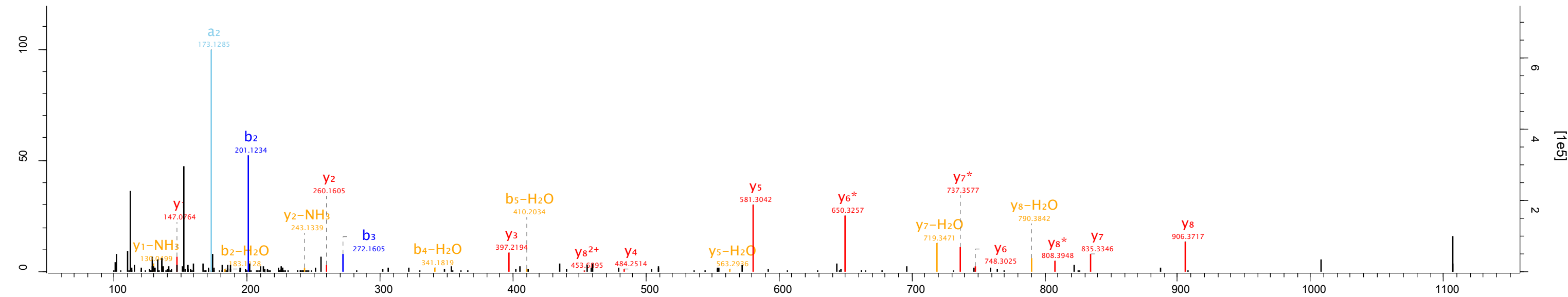




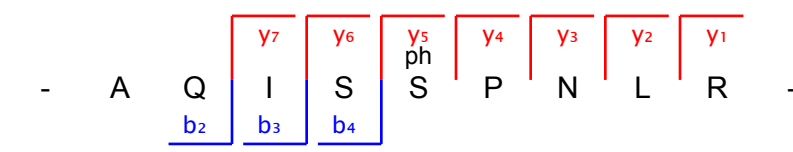
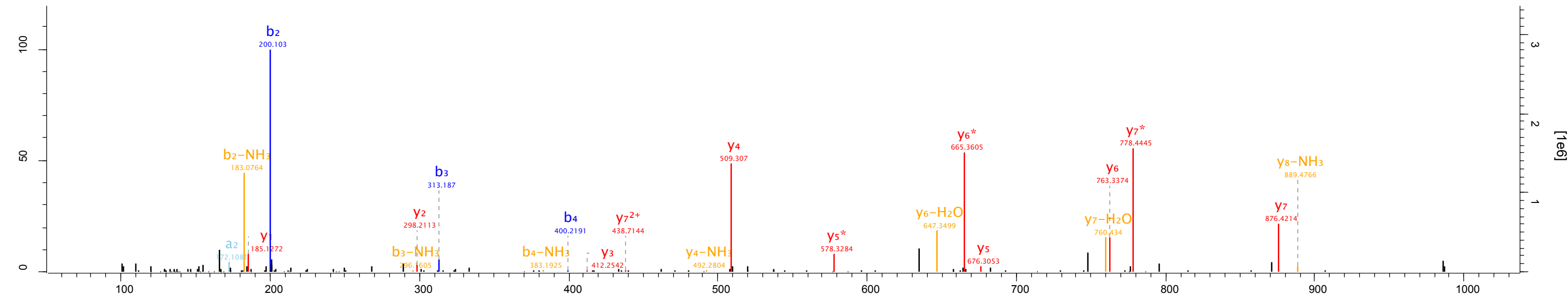
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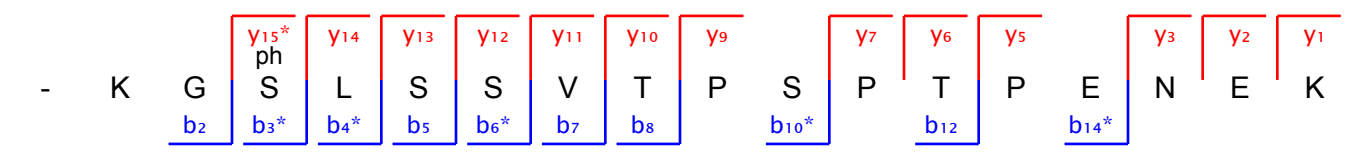
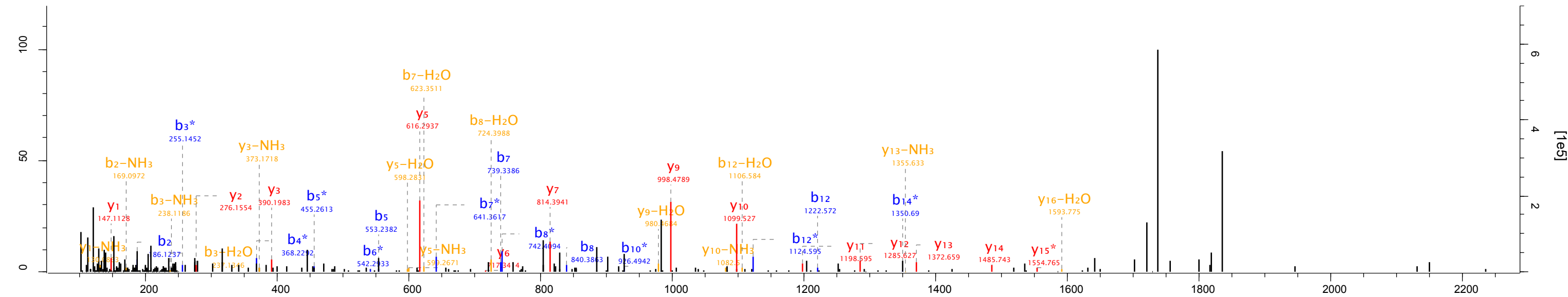
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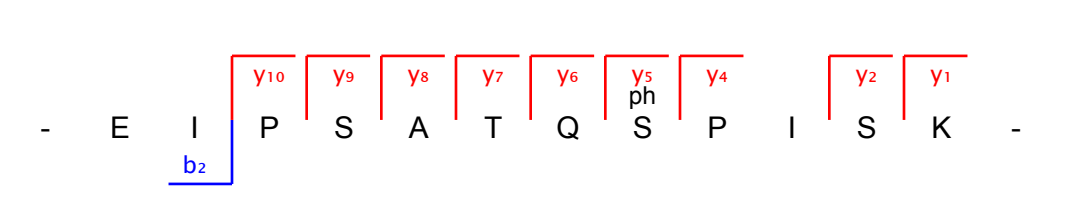
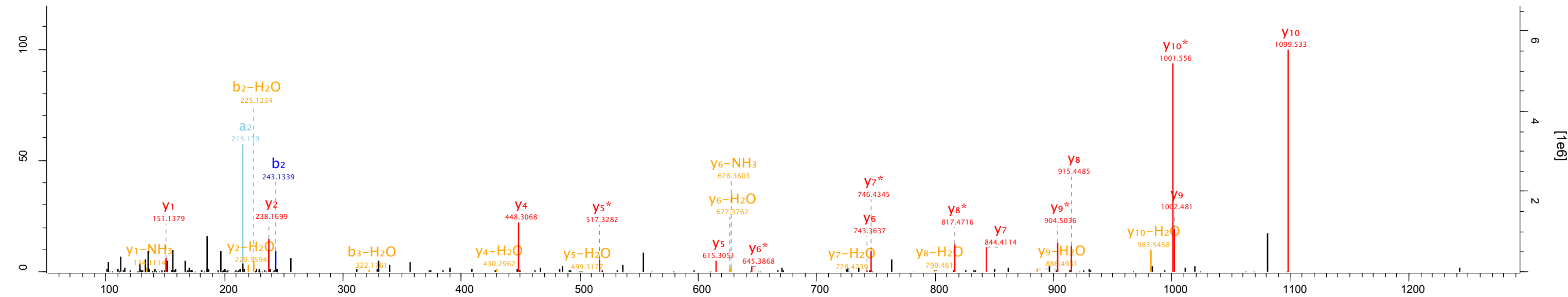
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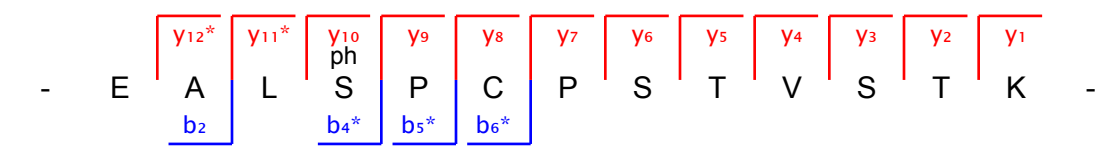
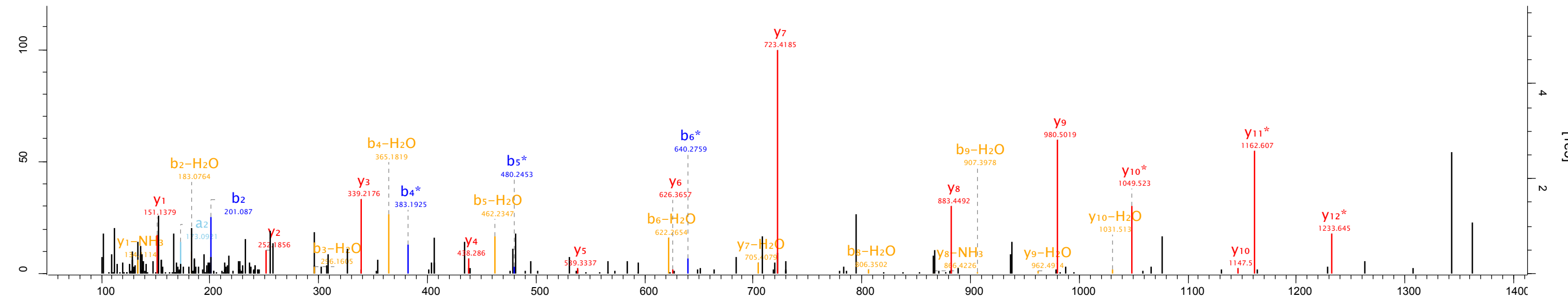
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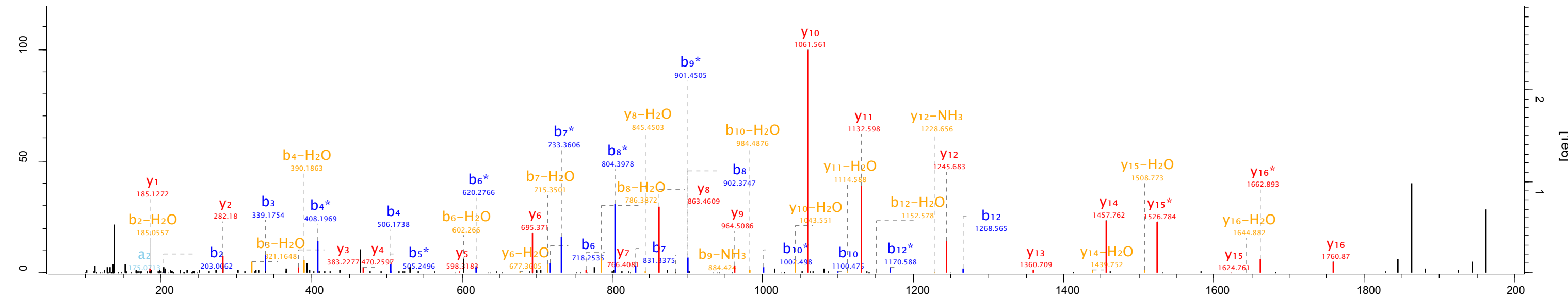


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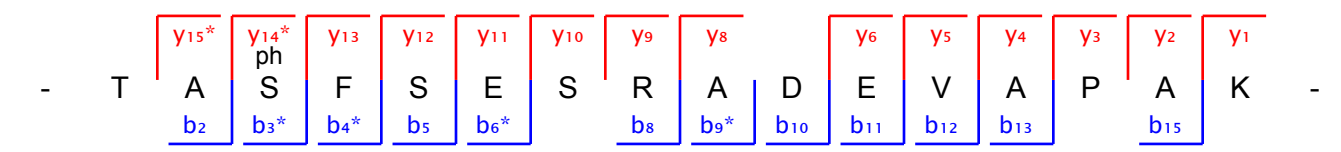
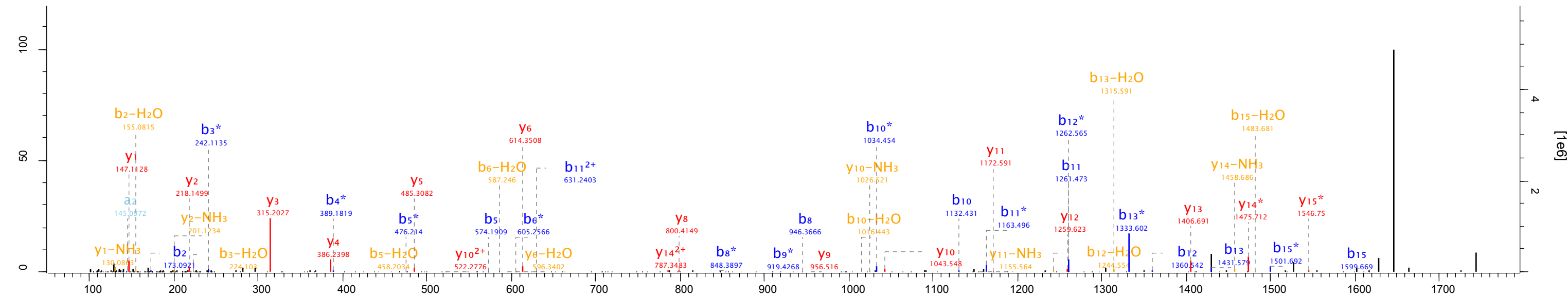
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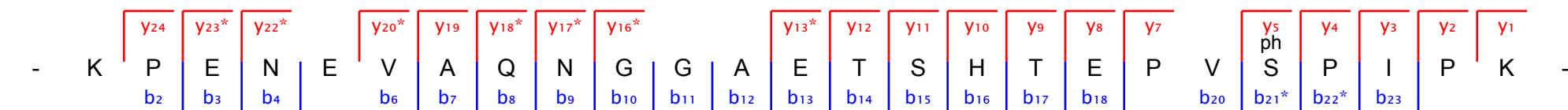
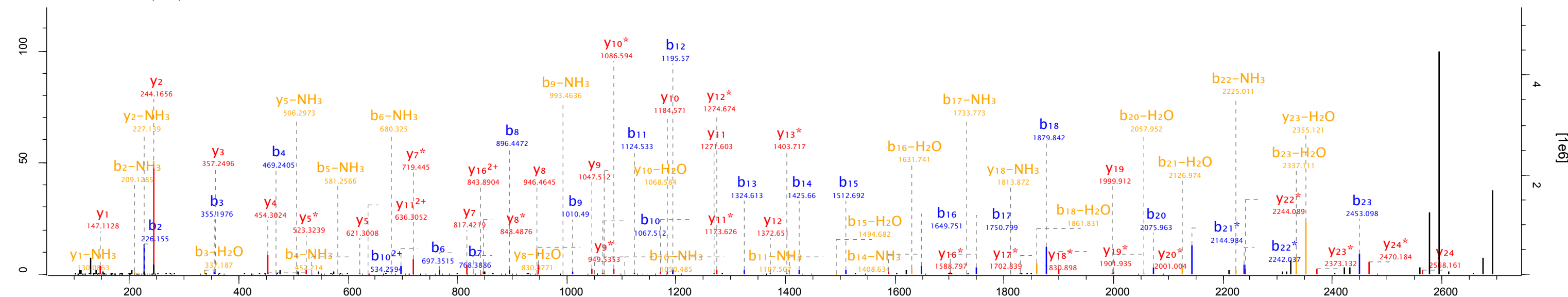




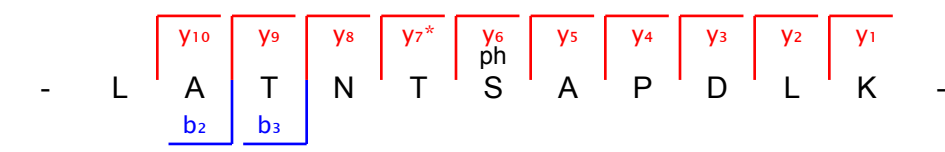
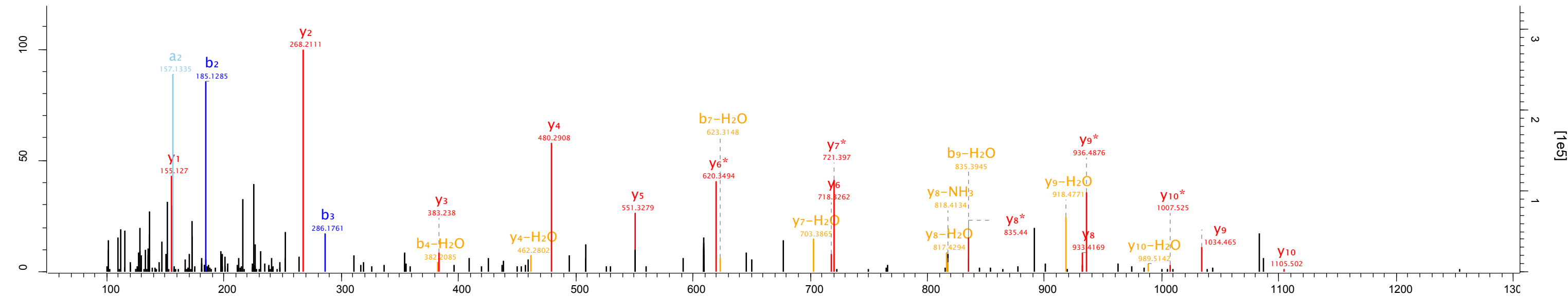
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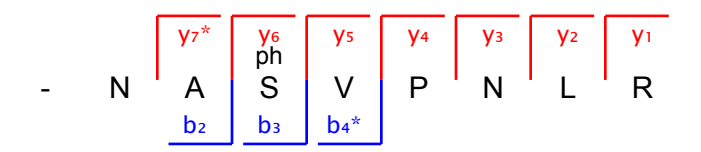
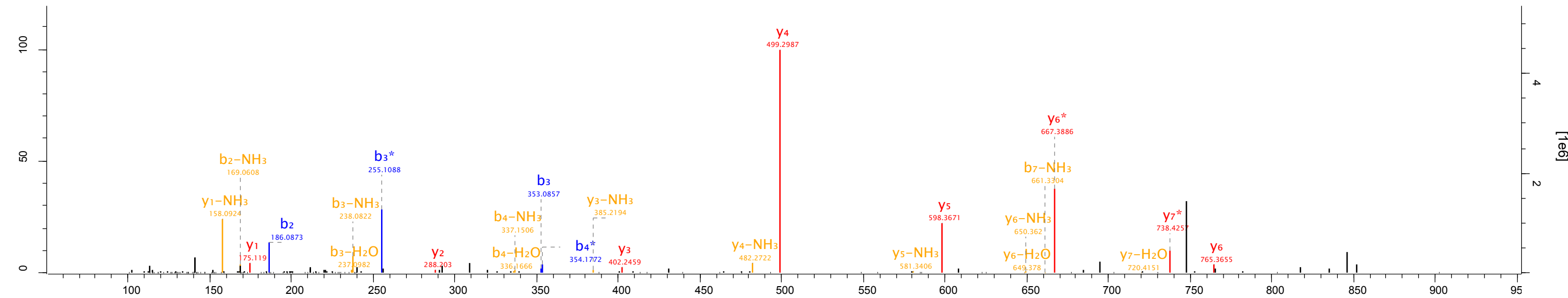




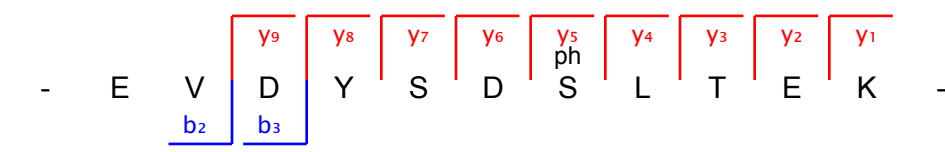
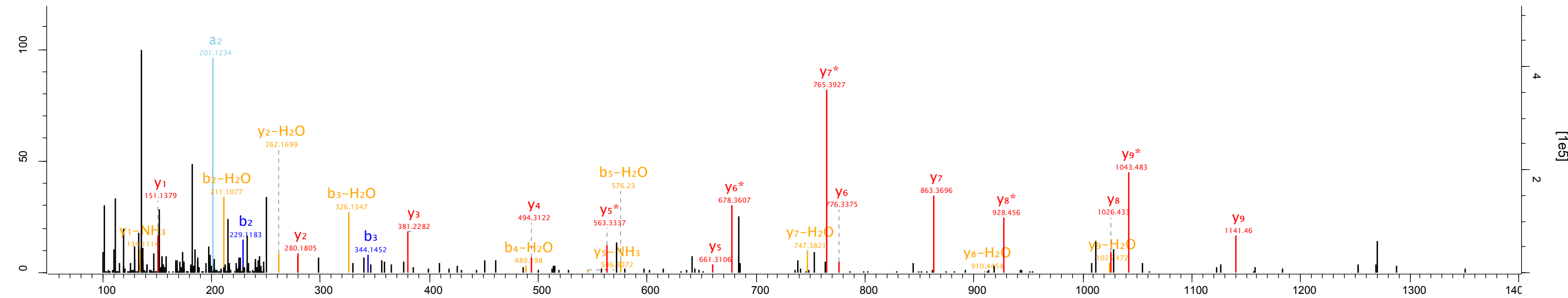
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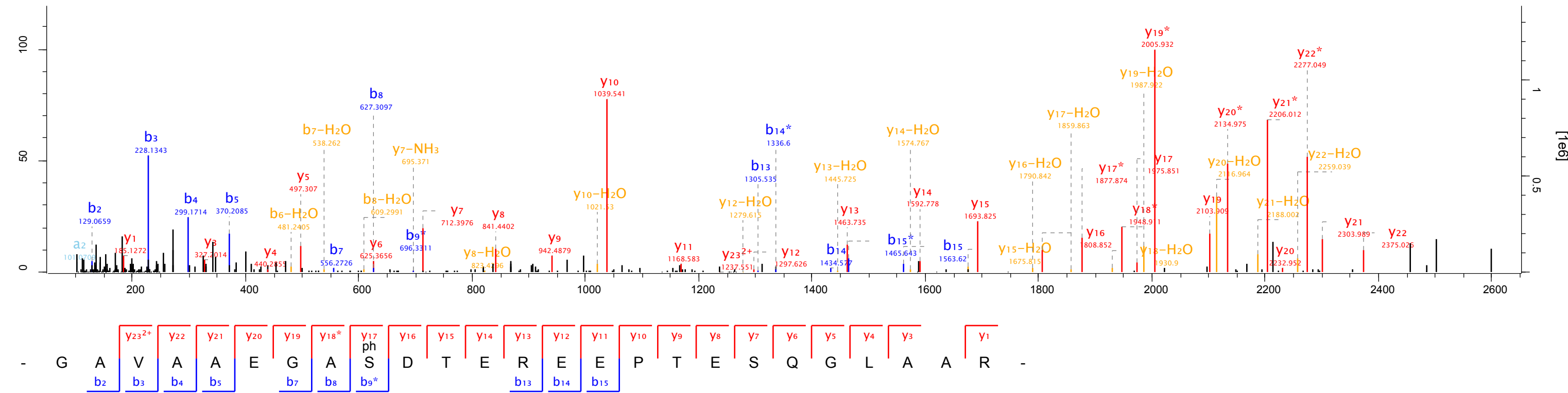
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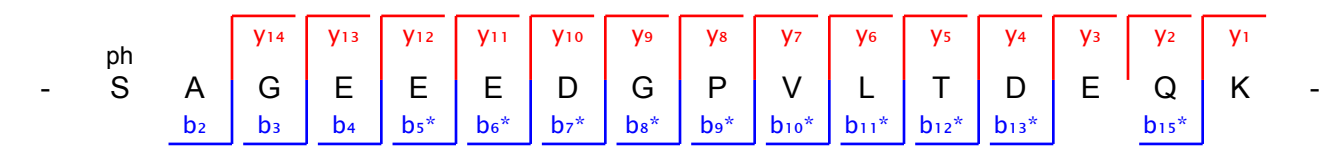
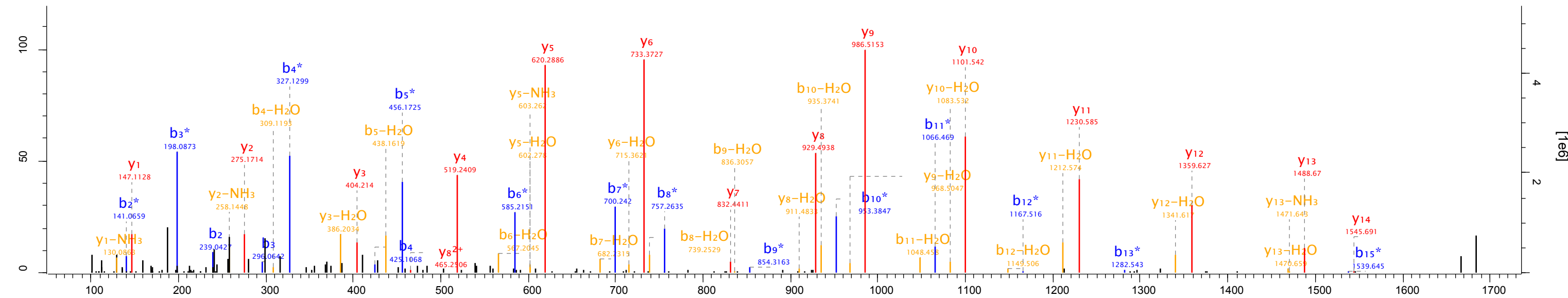
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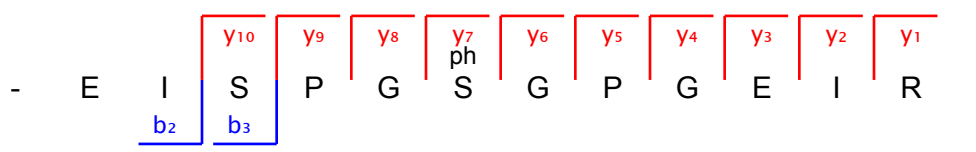
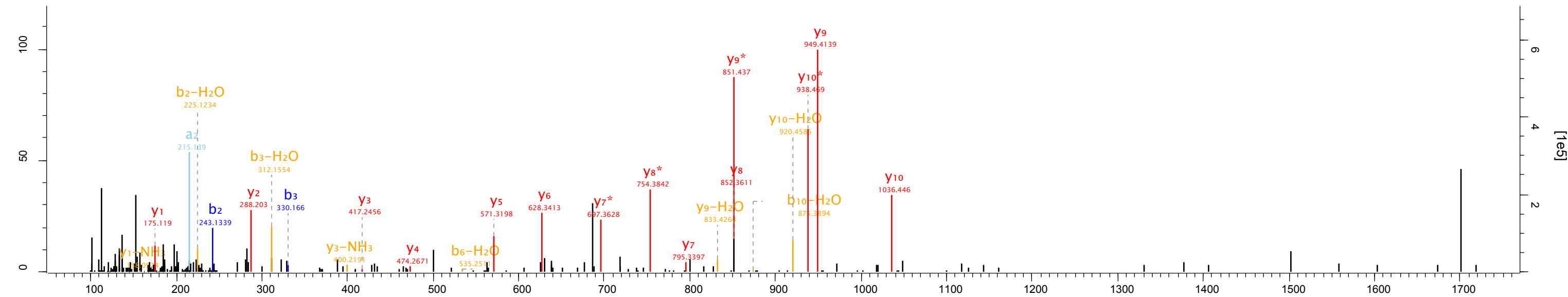
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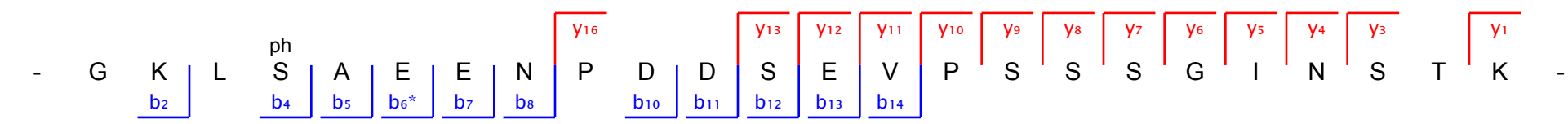
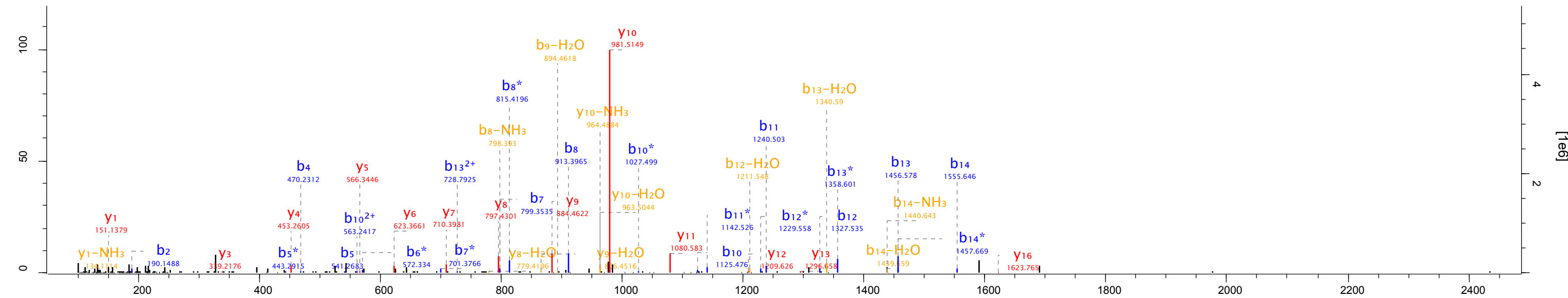
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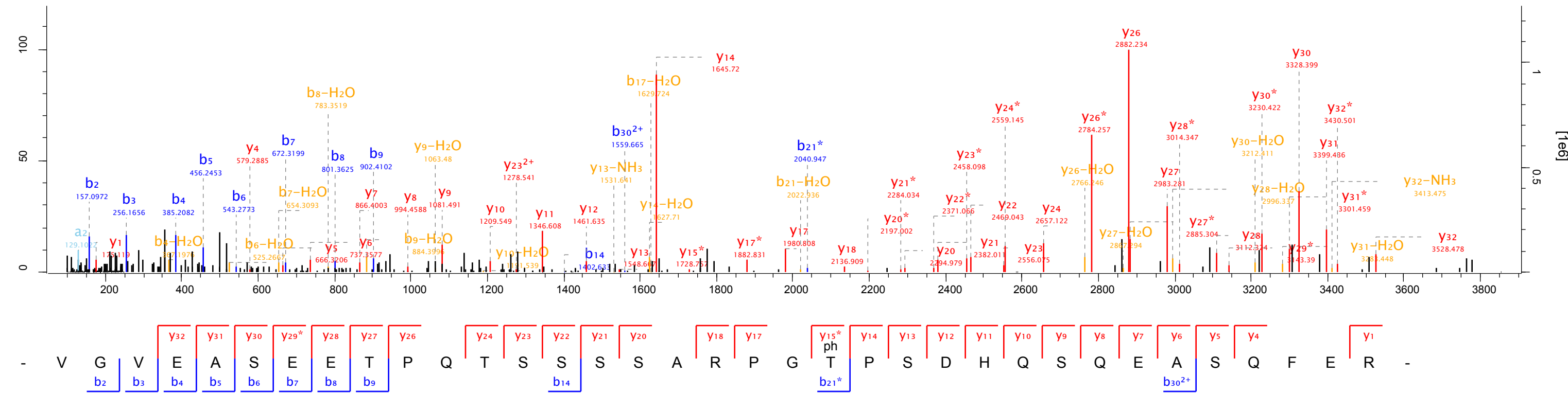
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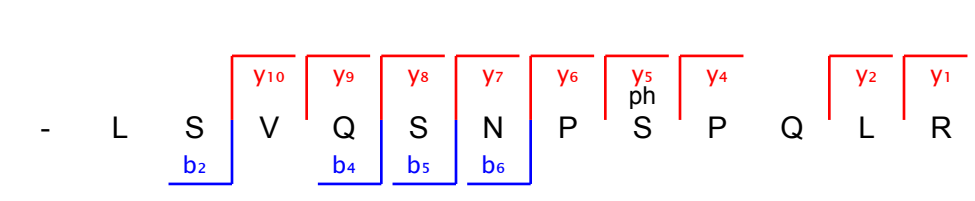
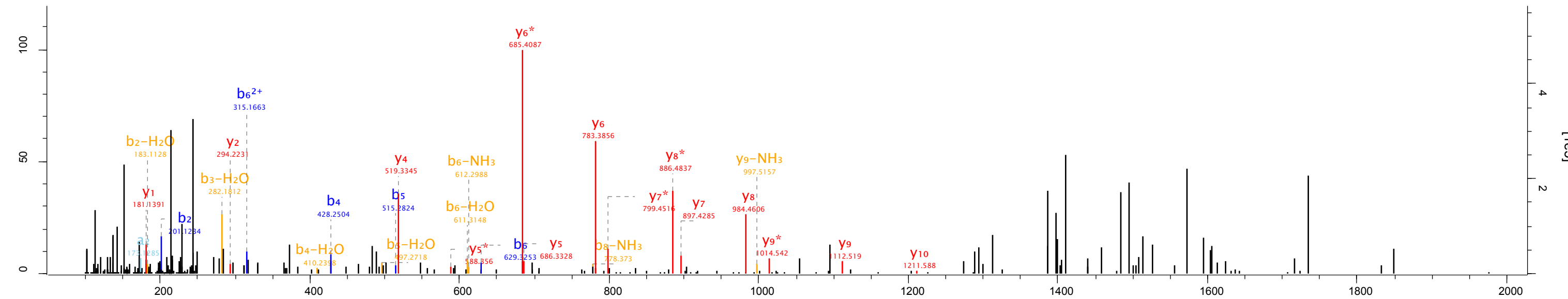
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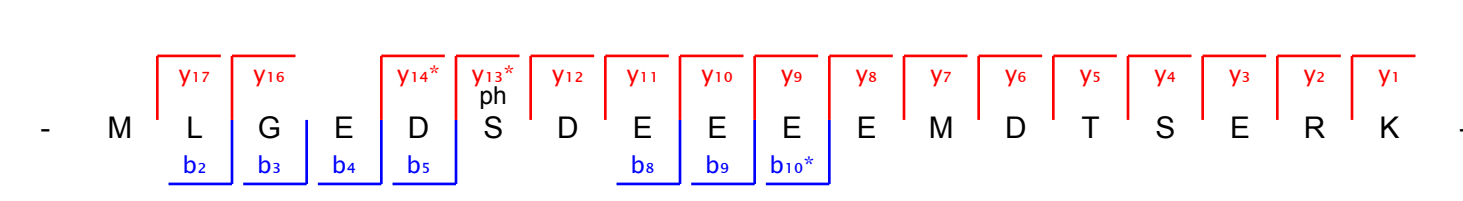
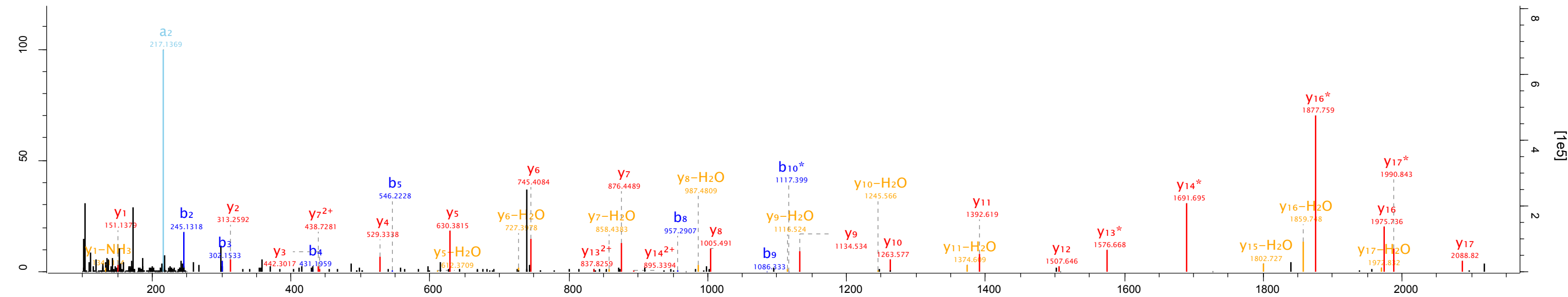
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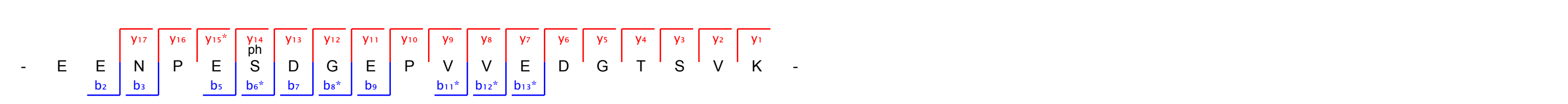
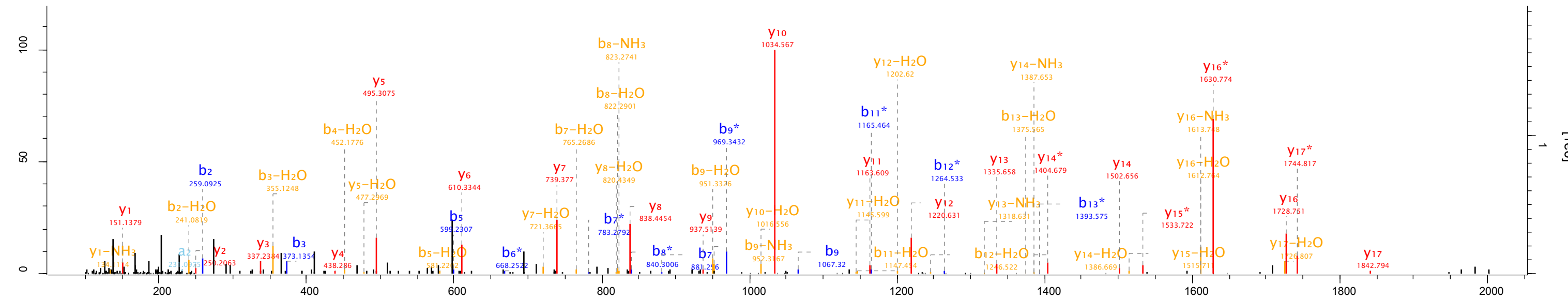
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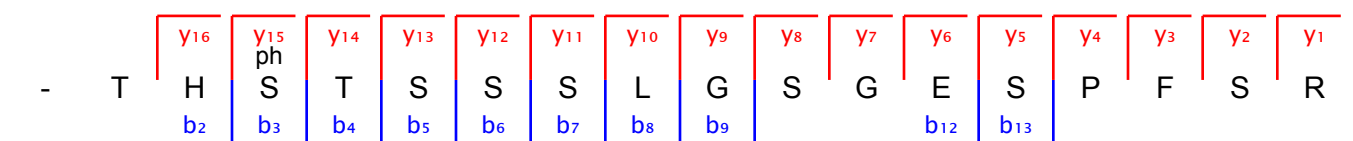
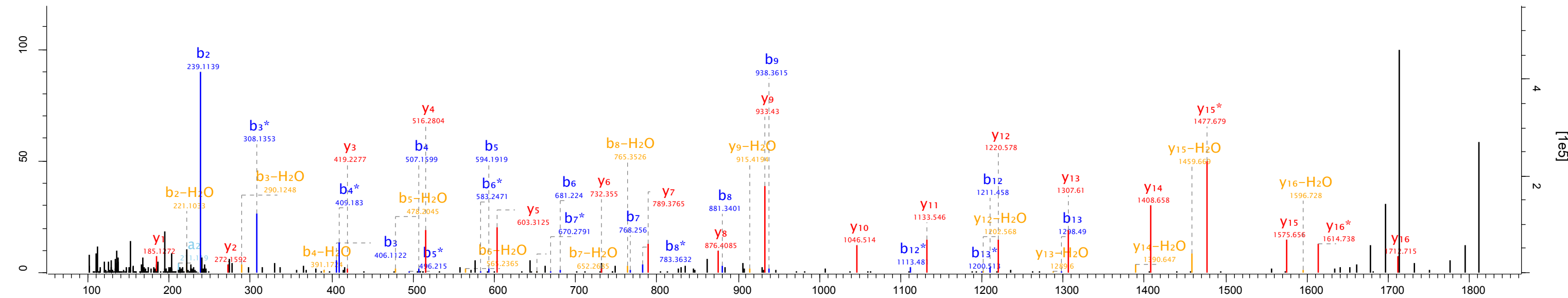
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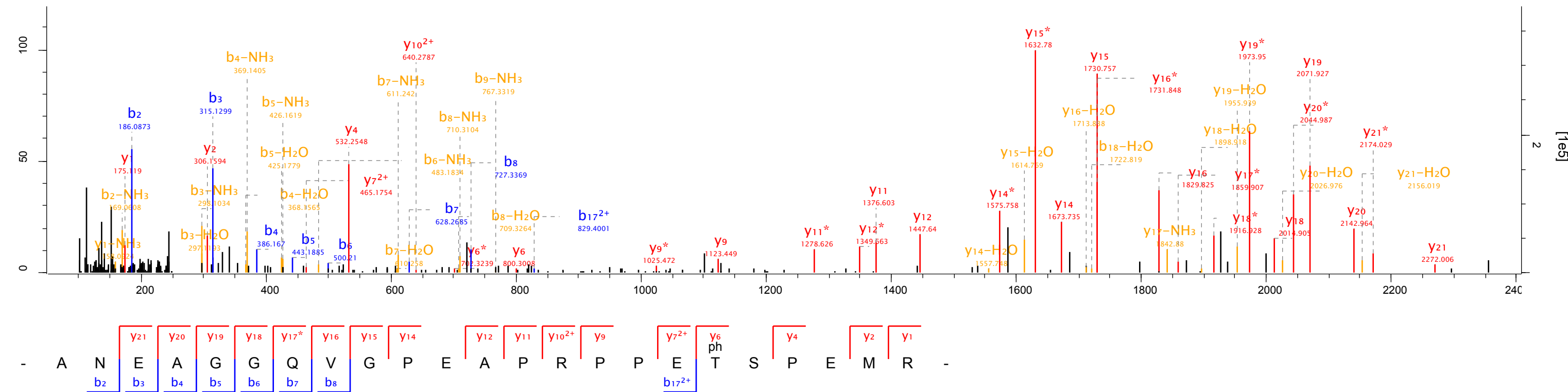
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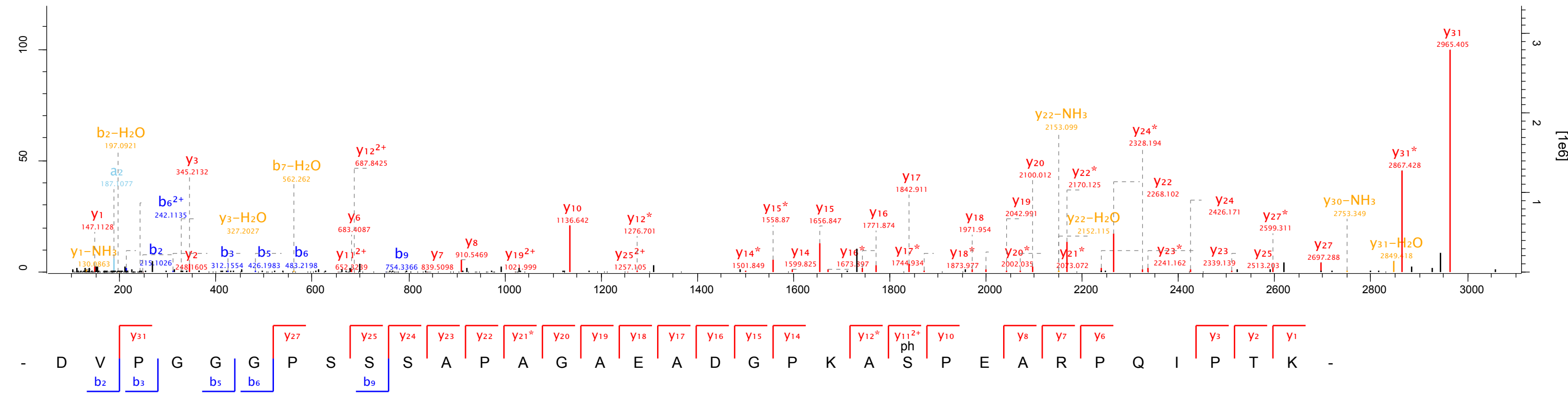
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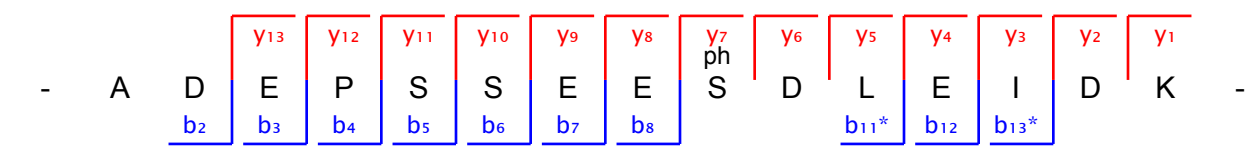
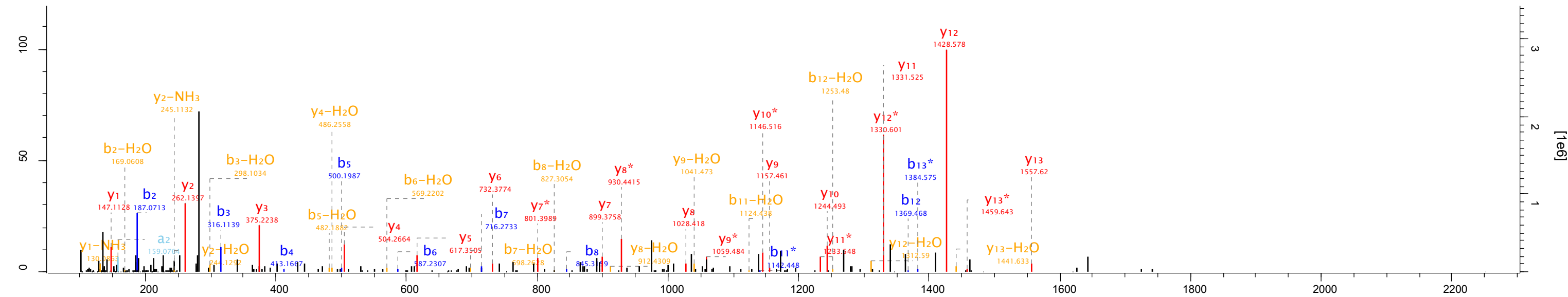
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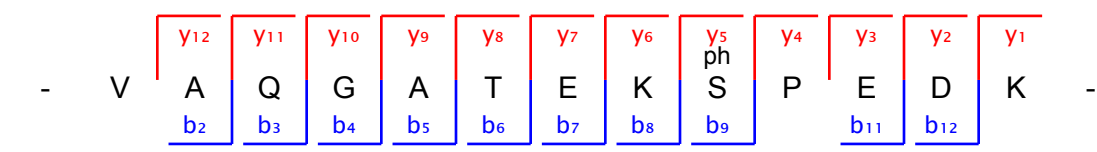
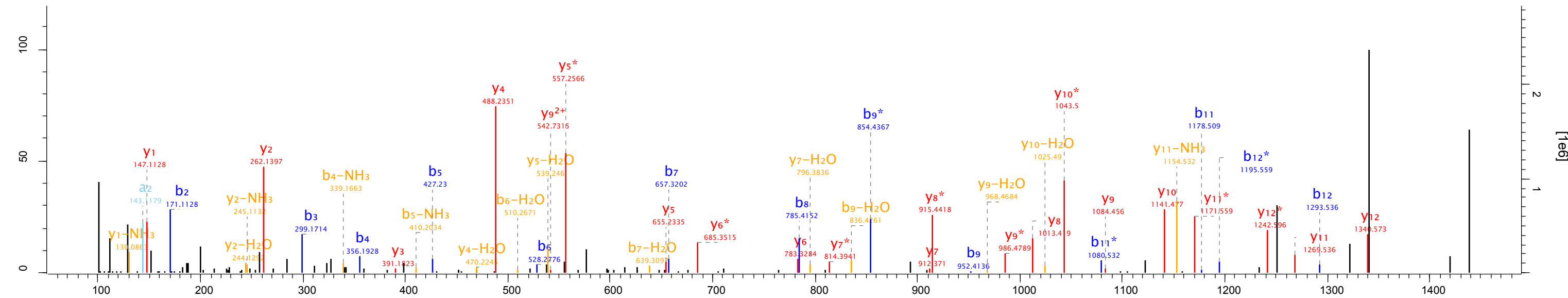
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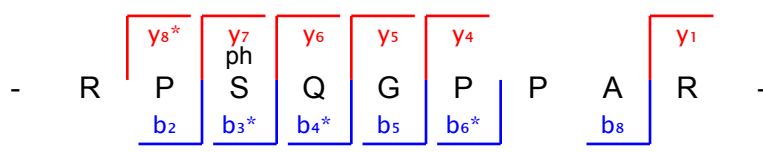
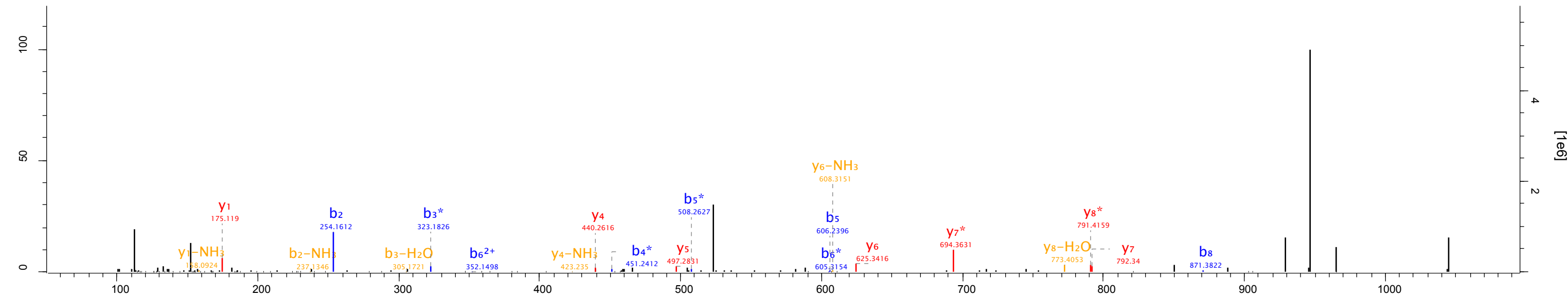
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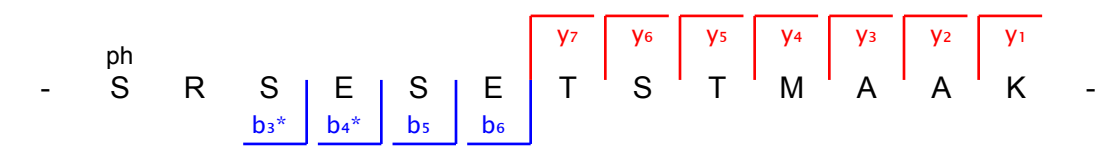
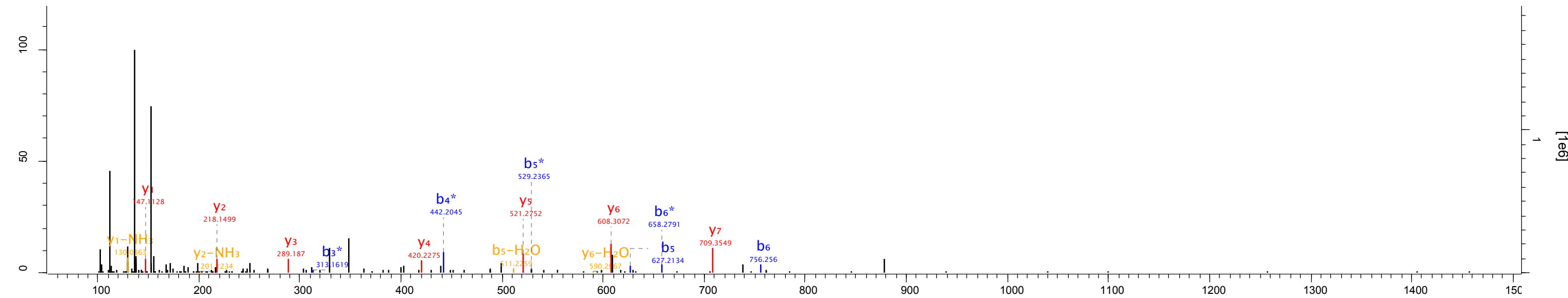
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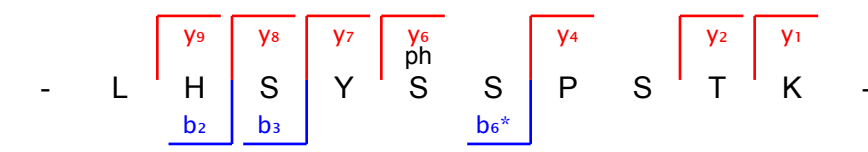
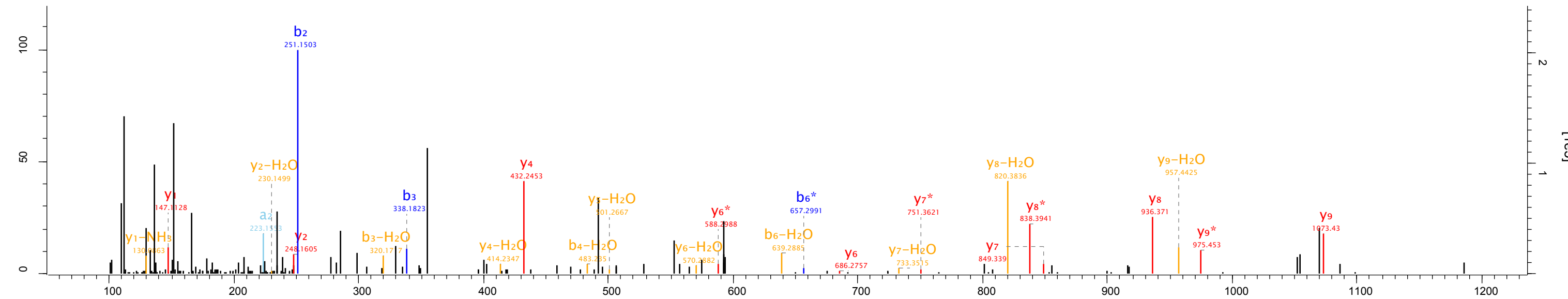
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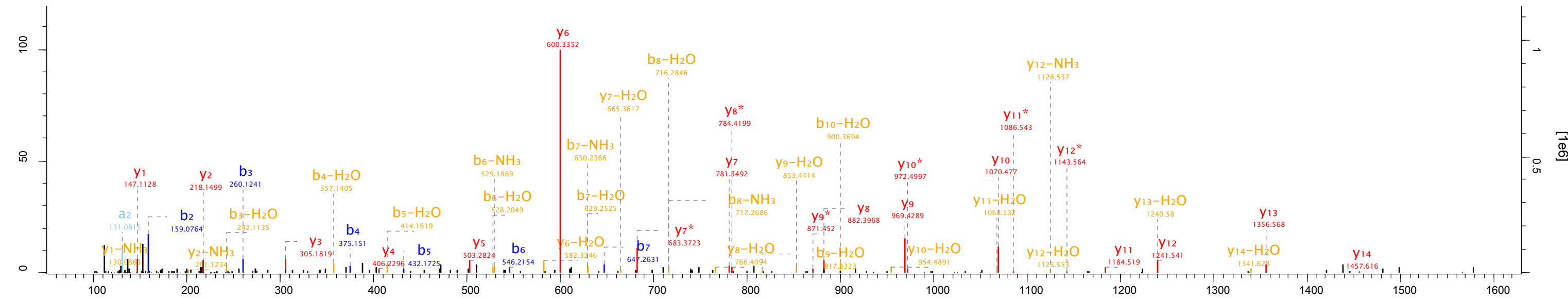
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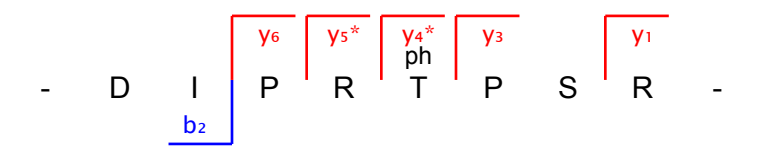
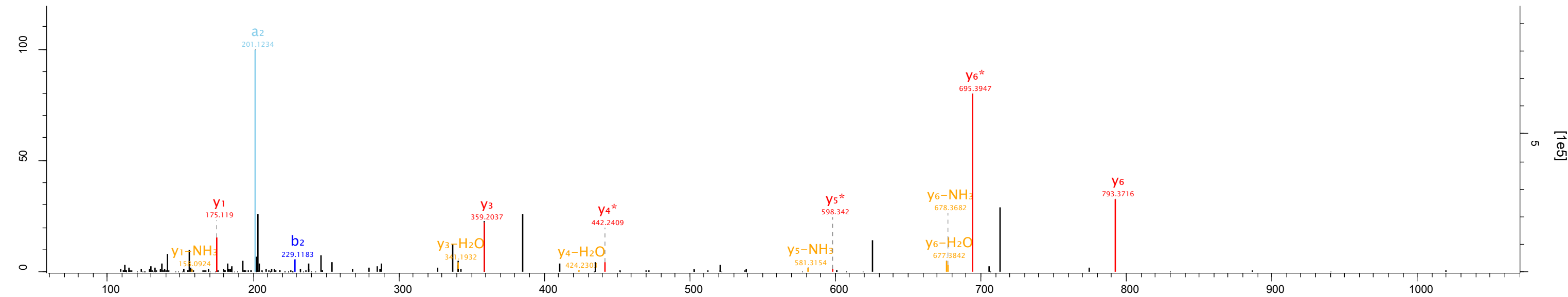


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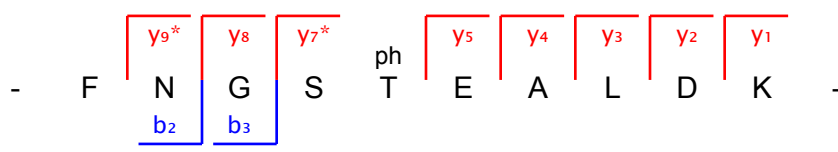
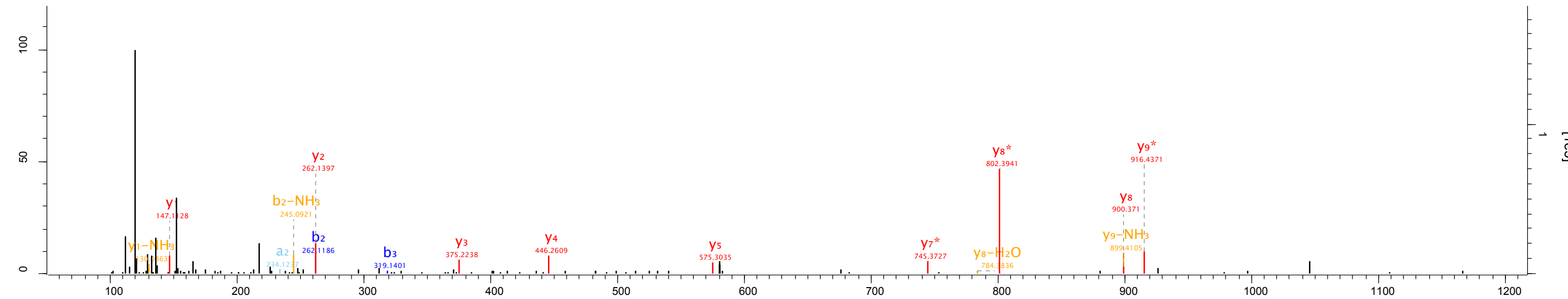
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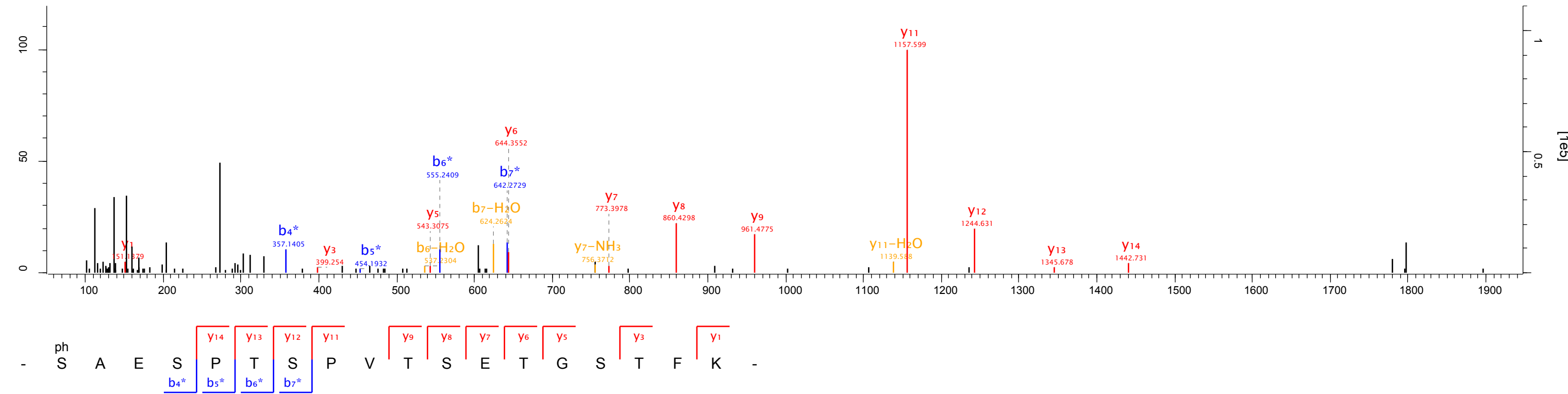
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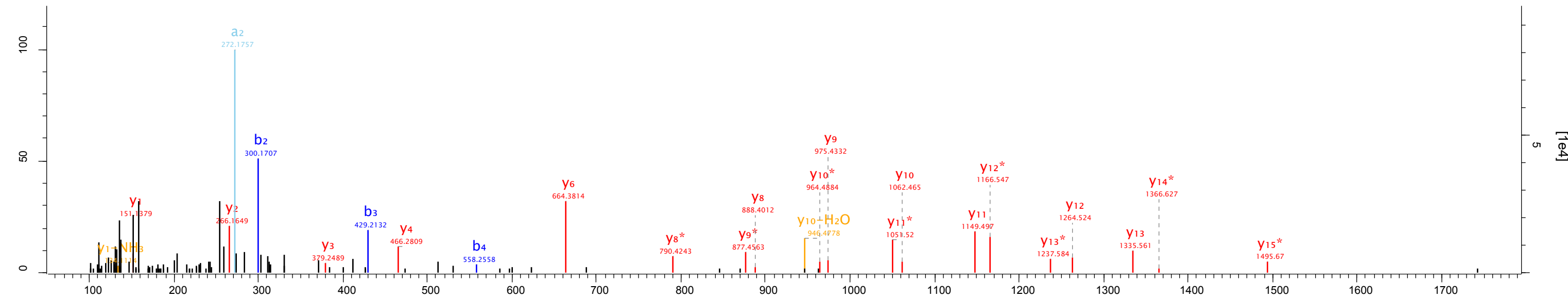
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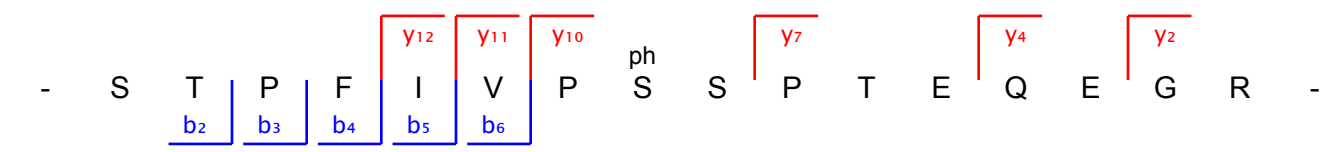
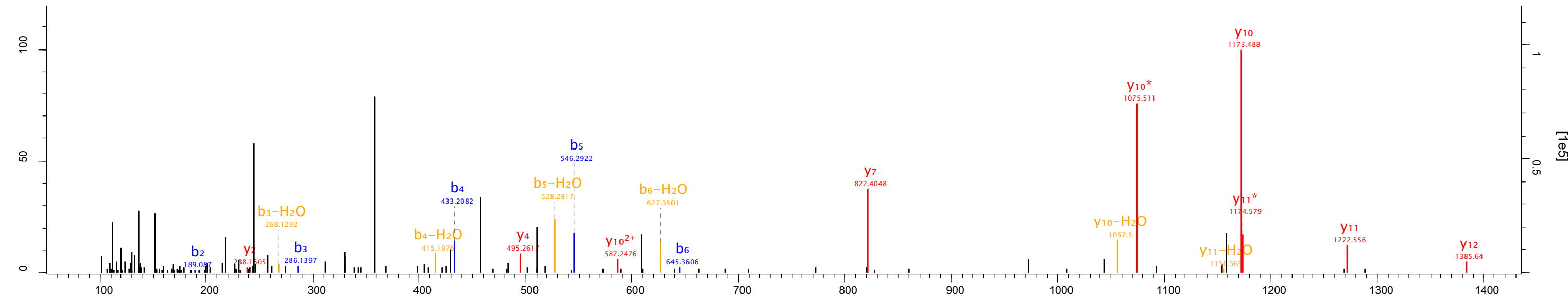


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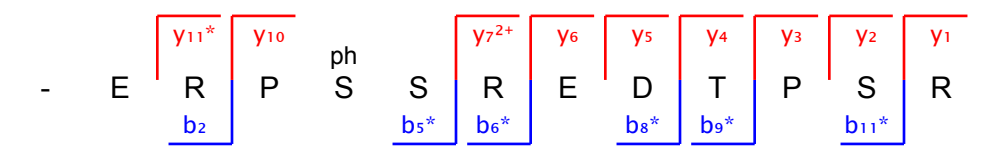
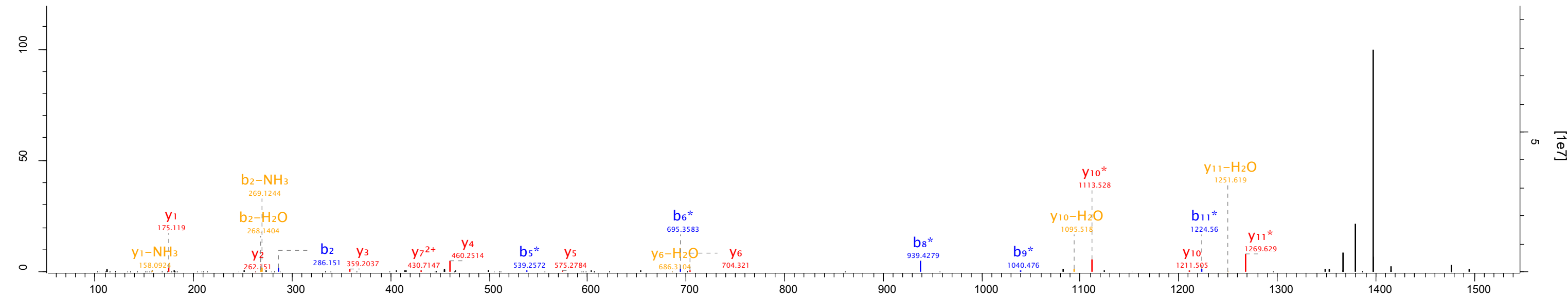
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- b2: L
- b3: E
- b4: E
- y1: K
- y2: D
- y3: I
- y4: S
- y6: P
- y8: G
- y9: S
- y10: S
- y11: S
- y12: A
- y13: E
- y14: E
- y15: L

Raw file 20171215_MaS_33SR_LMH_phospho_08 Scan 12108 Method FTMS; HCD Score 60.33 m/z 909.42 Gene names TP53BP1

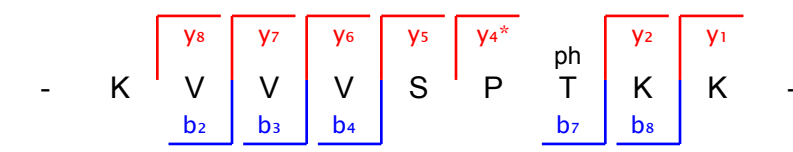
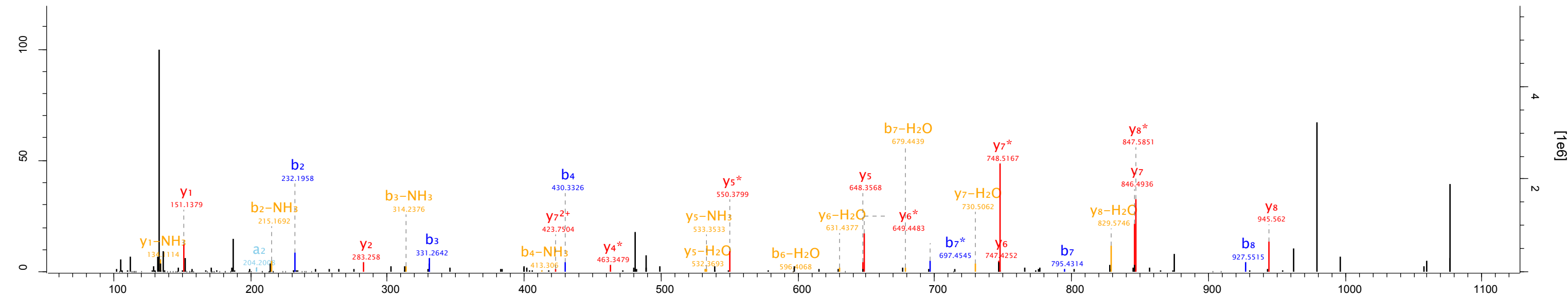


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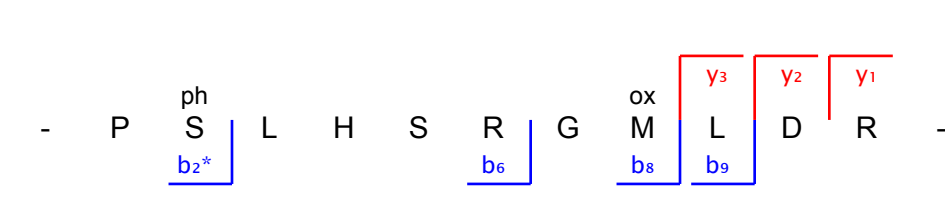
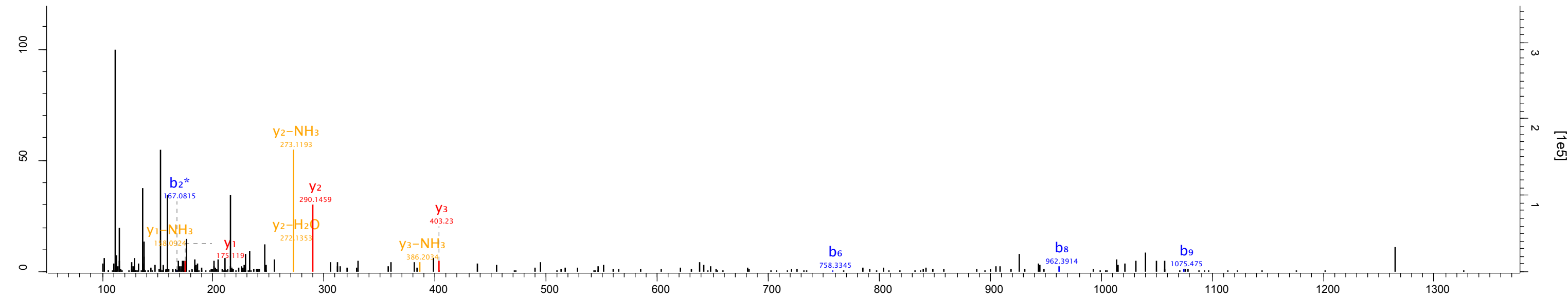


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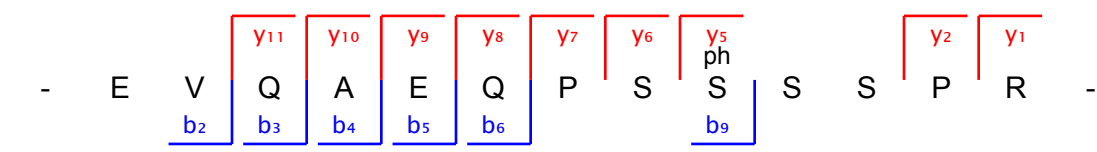
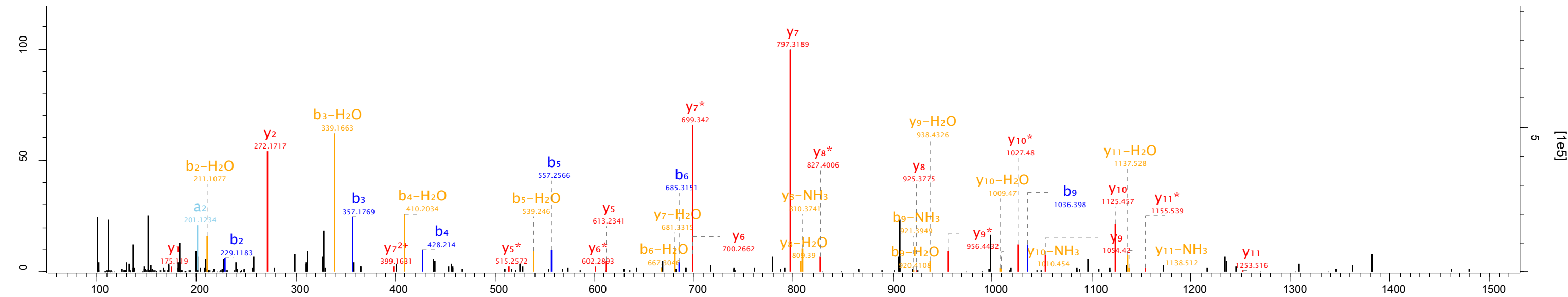
Scan Method Score m/z Gene names
2028 FTMS; HCD 142.51 539.34 NCL

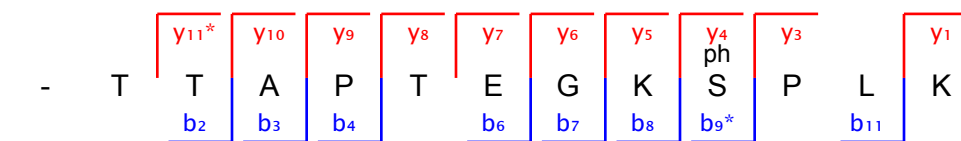
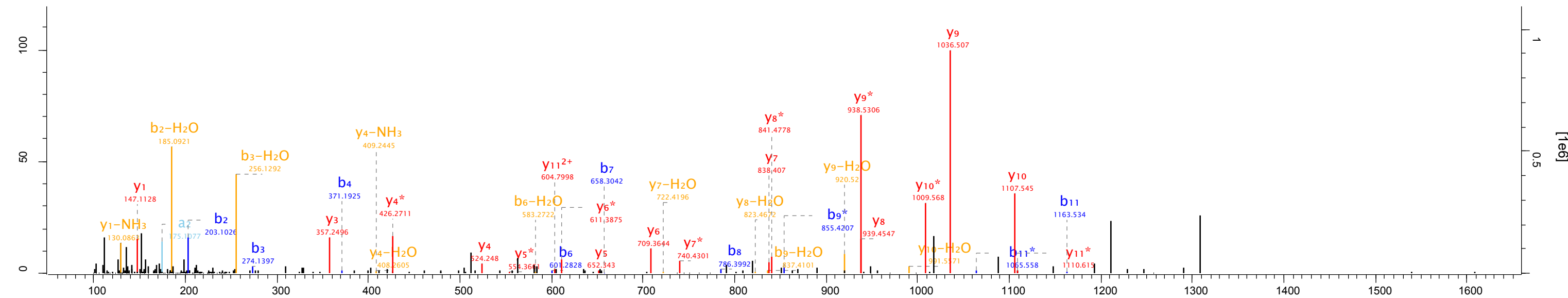


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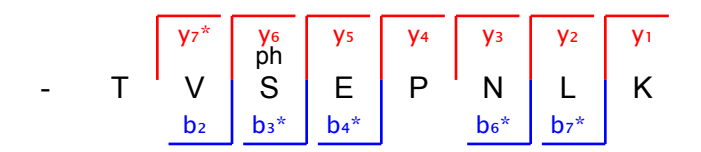
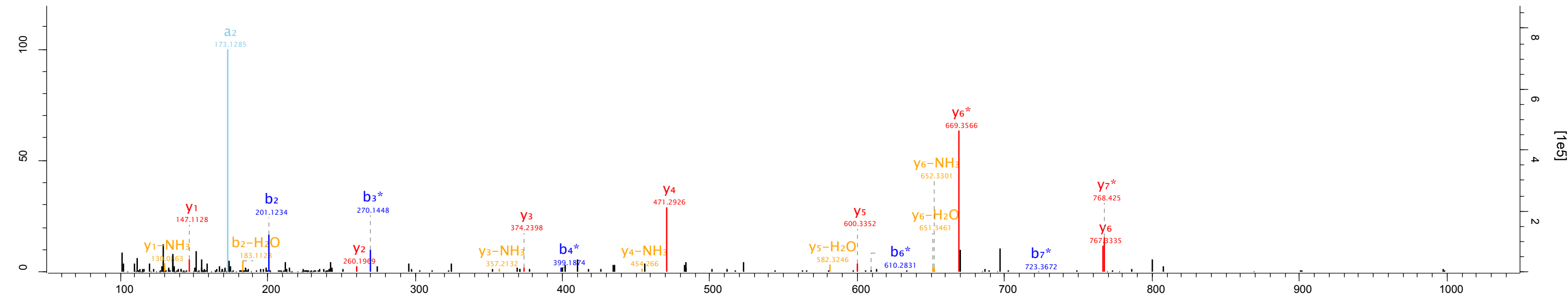


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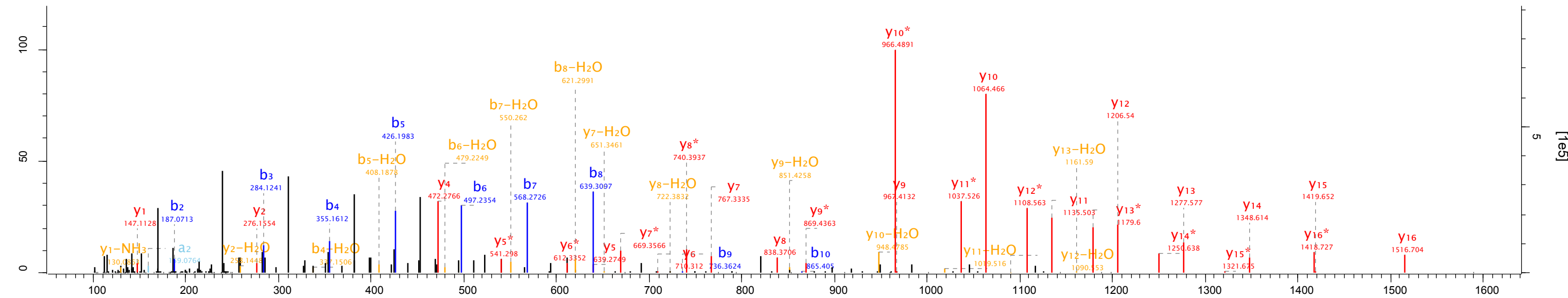




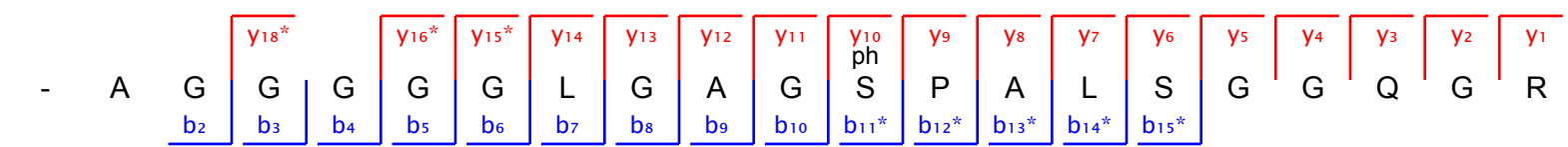
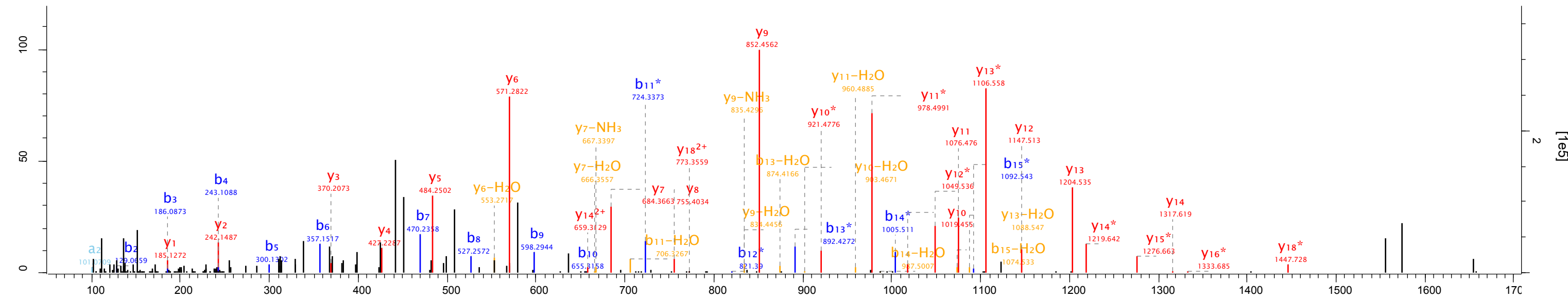
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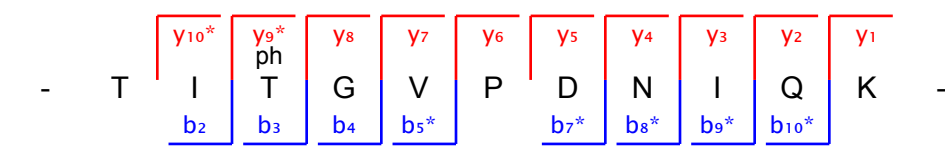
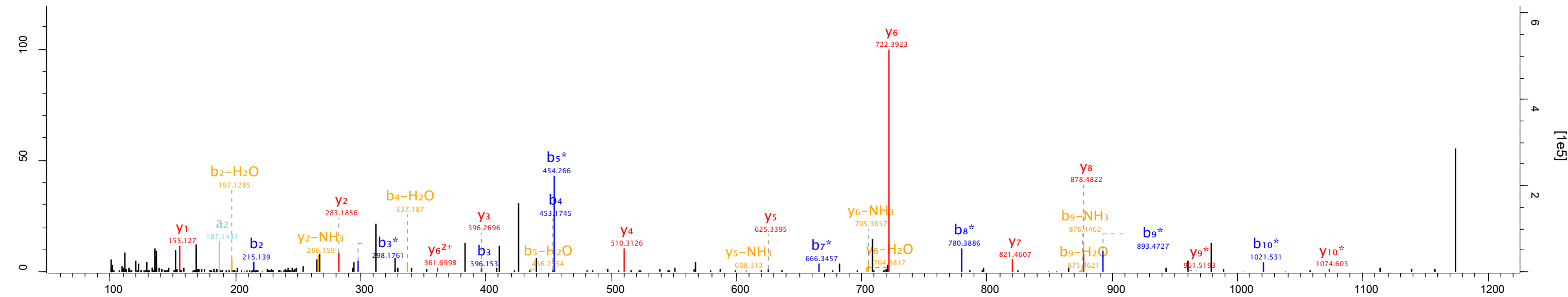
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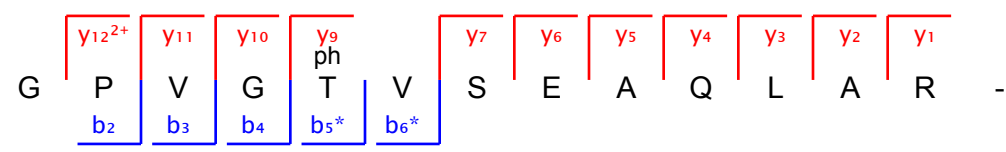
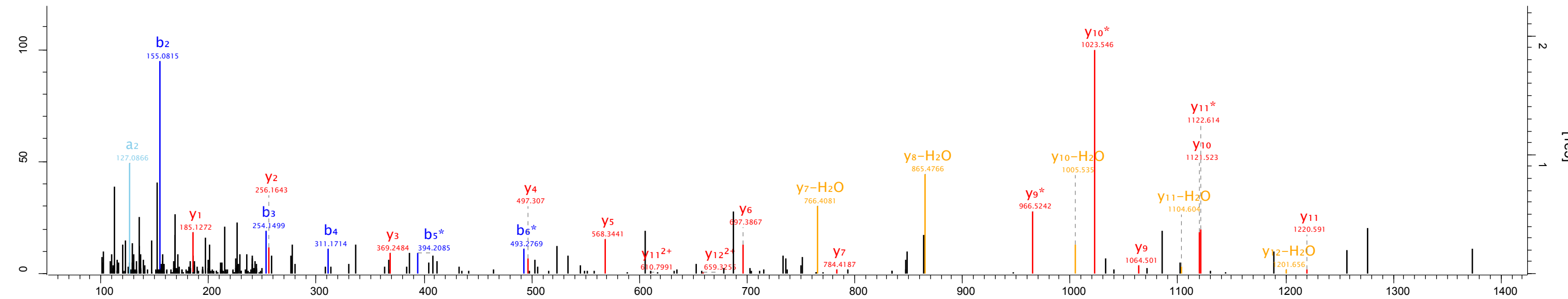
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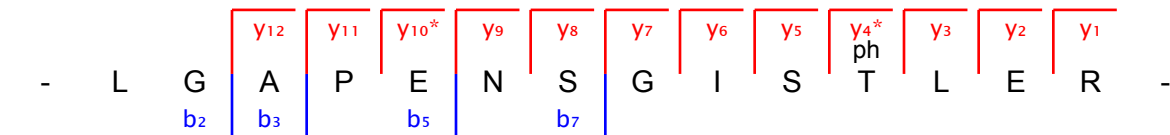
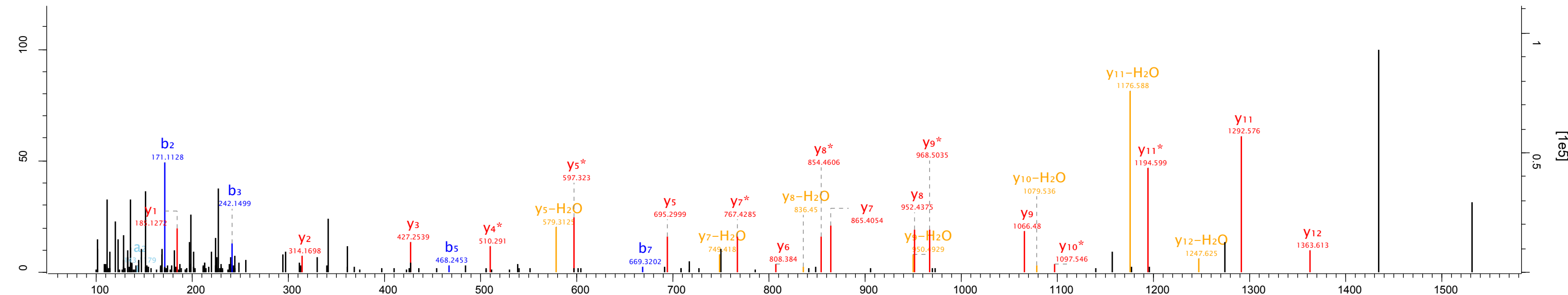


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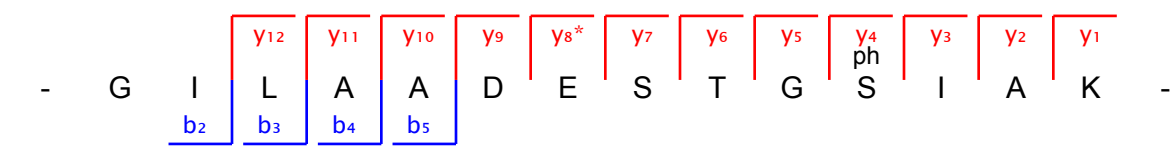
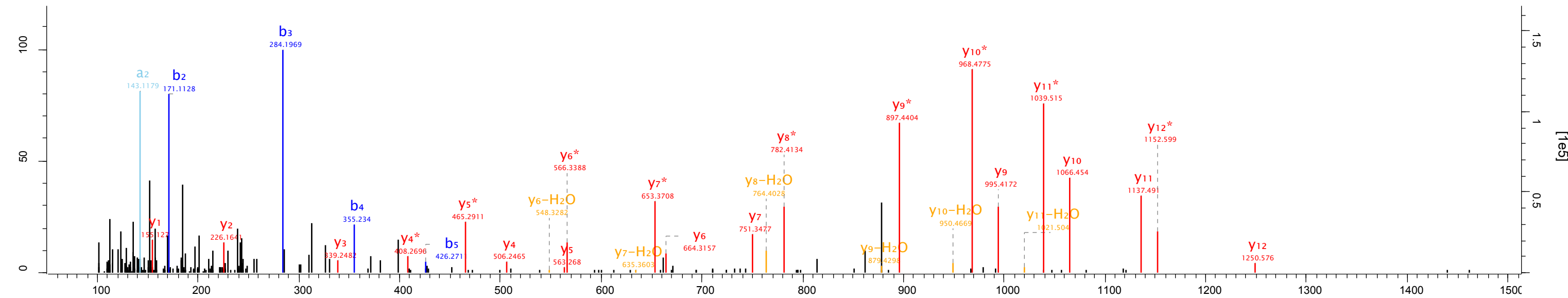


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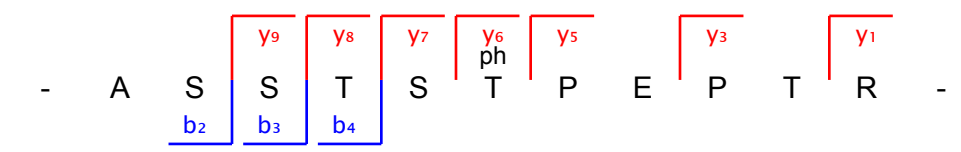
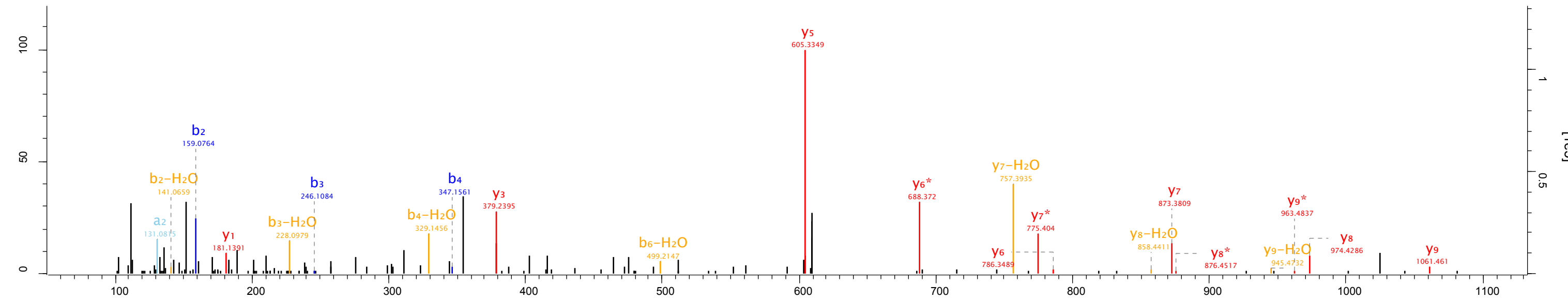




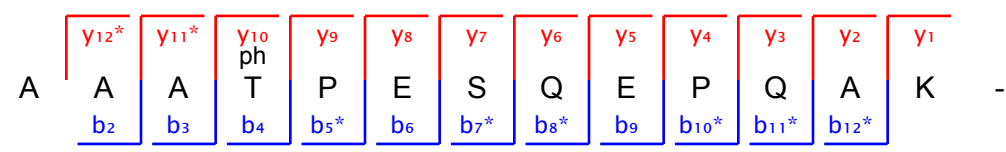
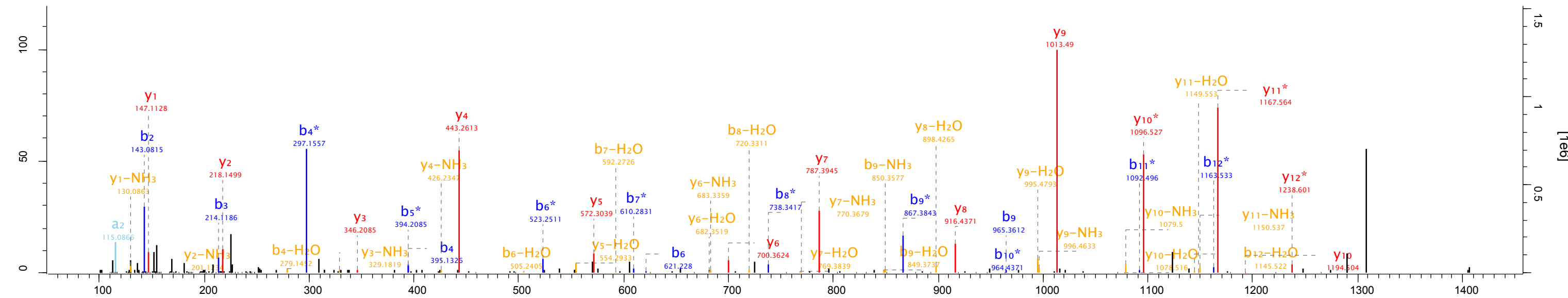
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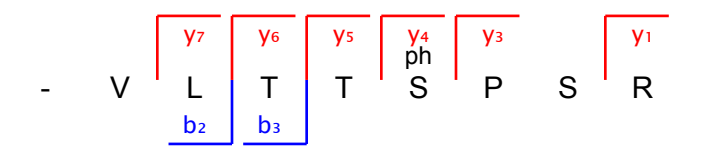
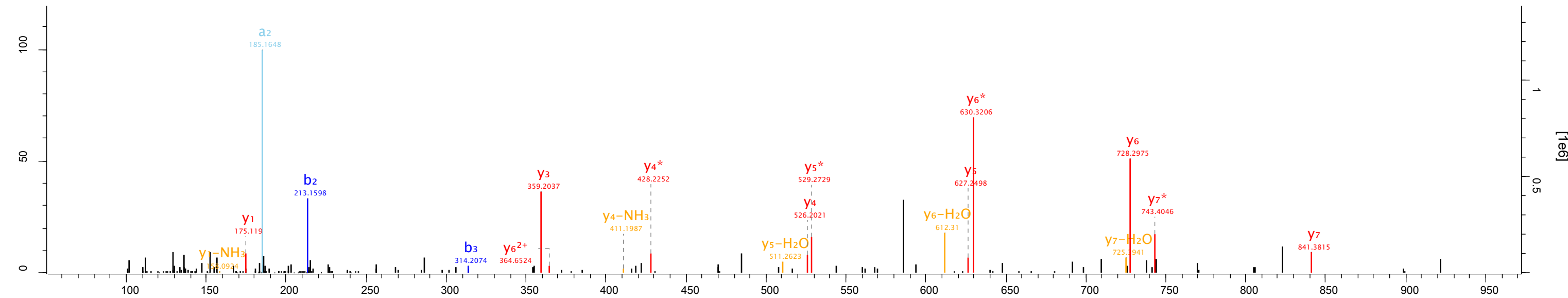
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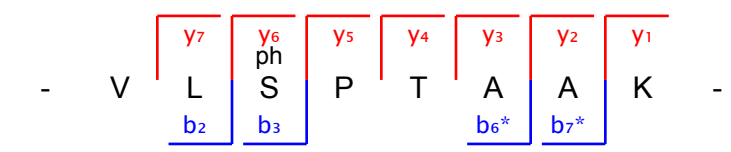
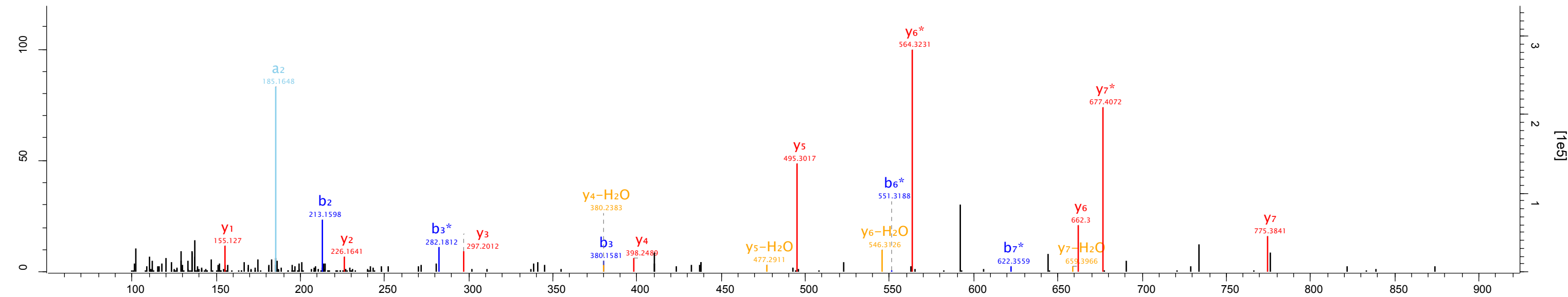
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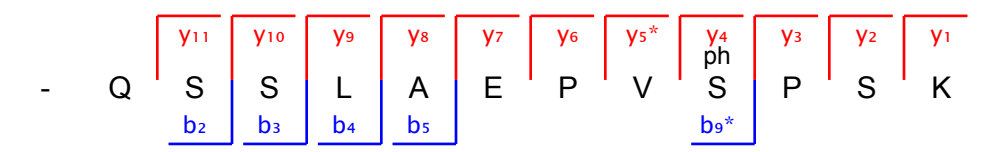
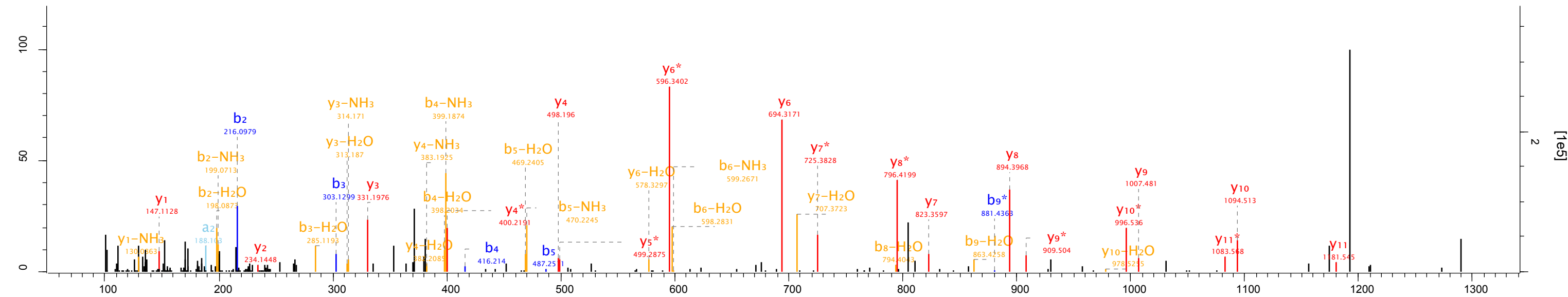
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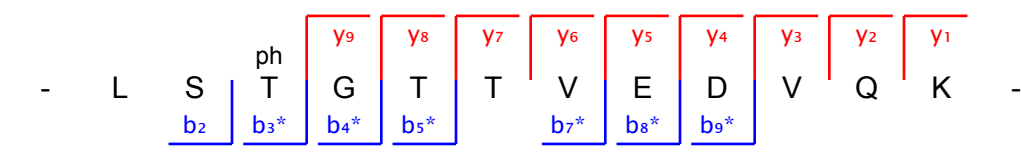
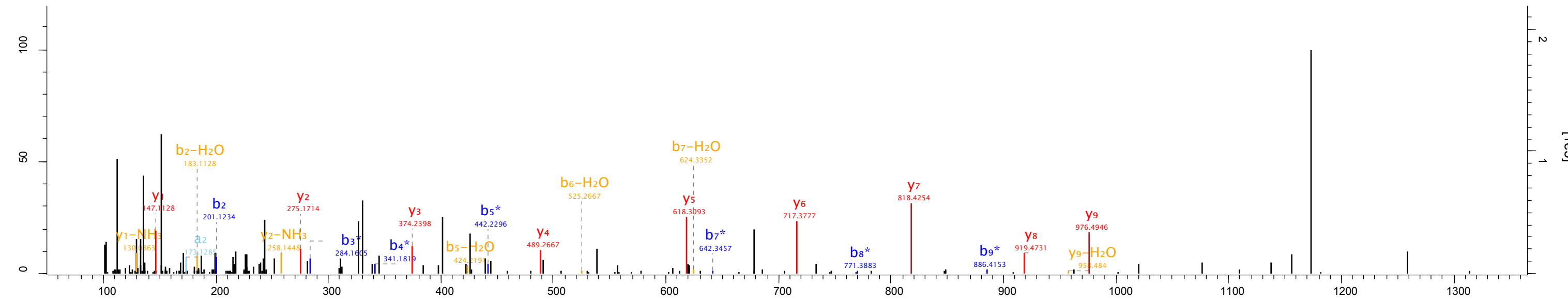
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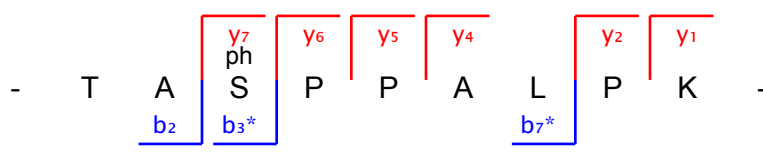
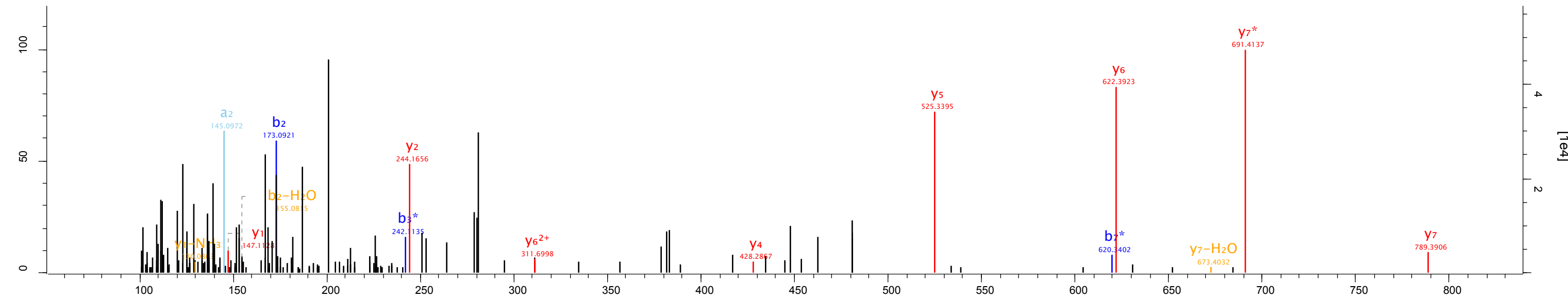
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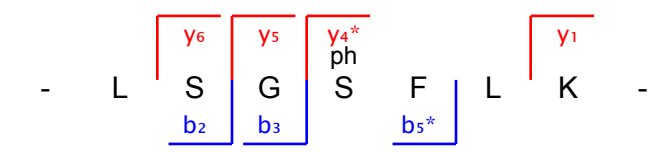
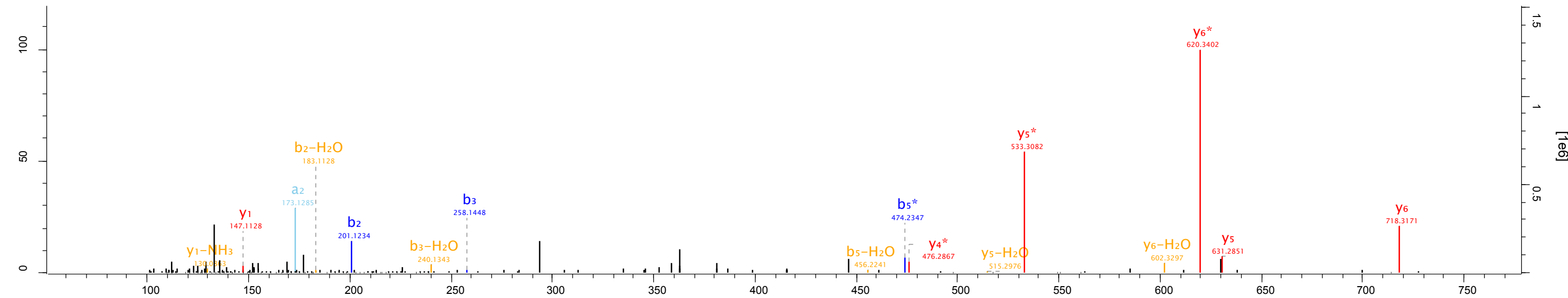
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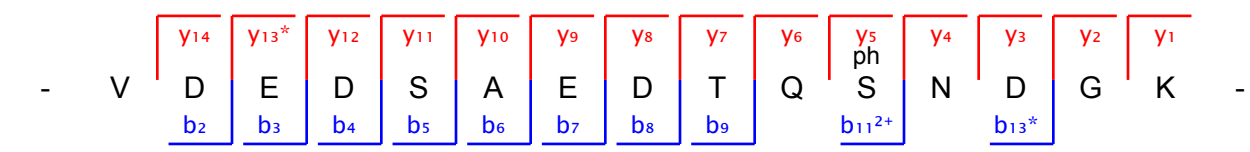
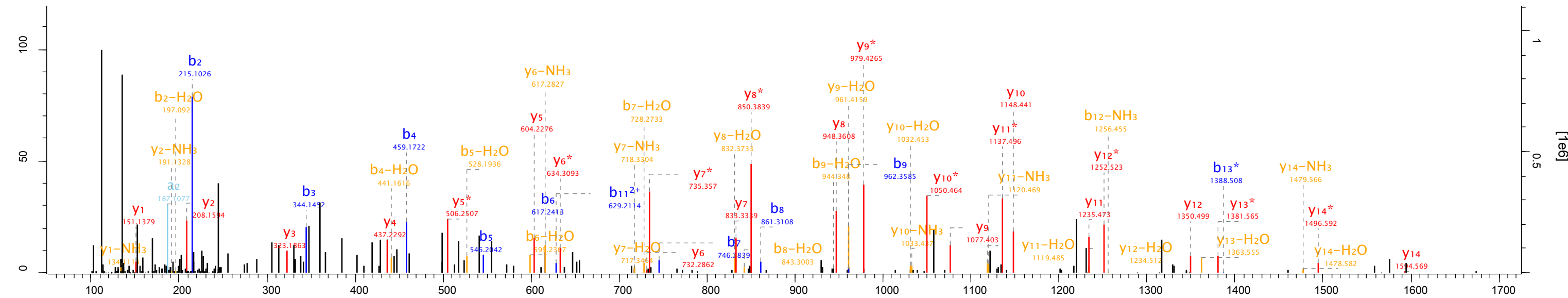


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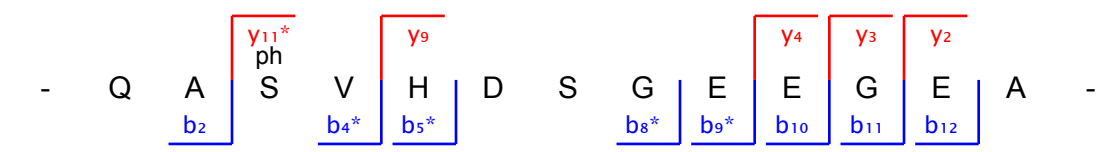
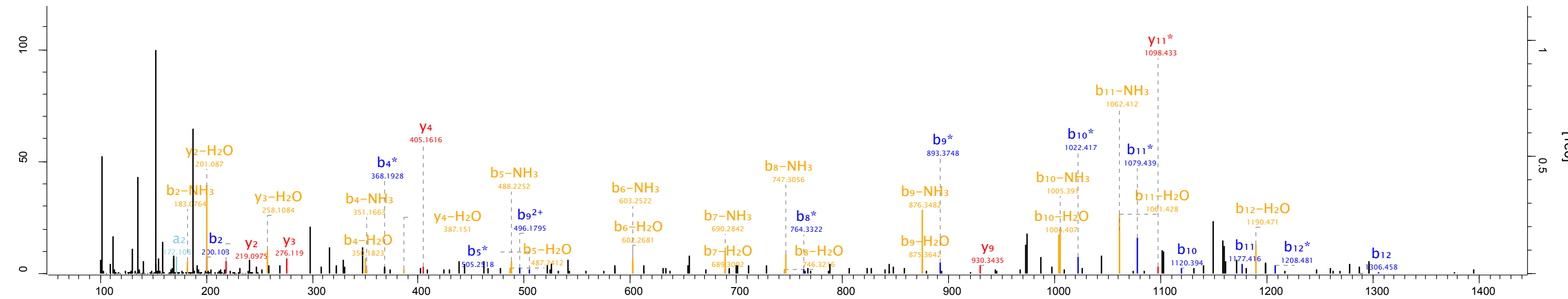


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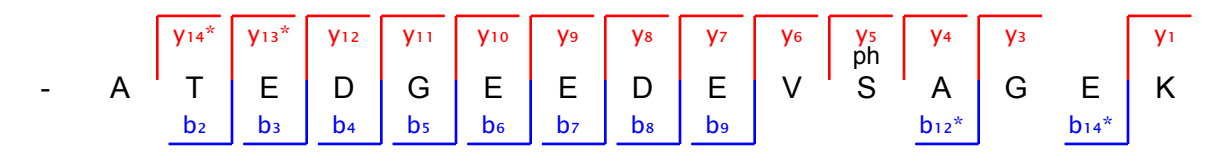
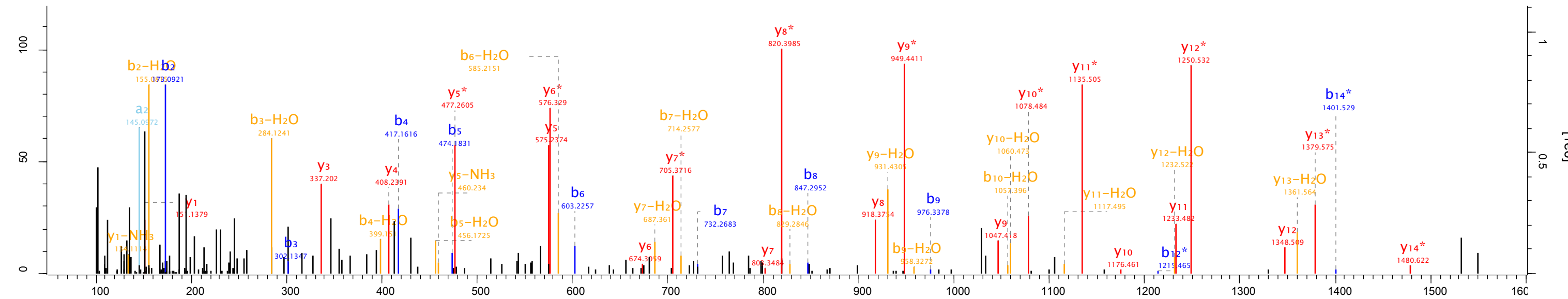


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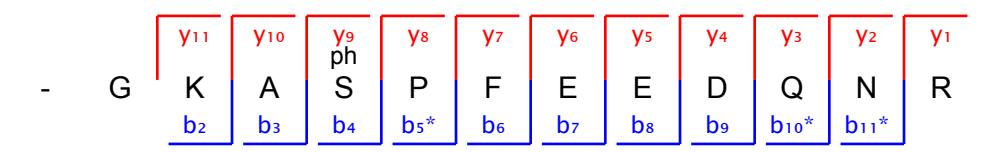
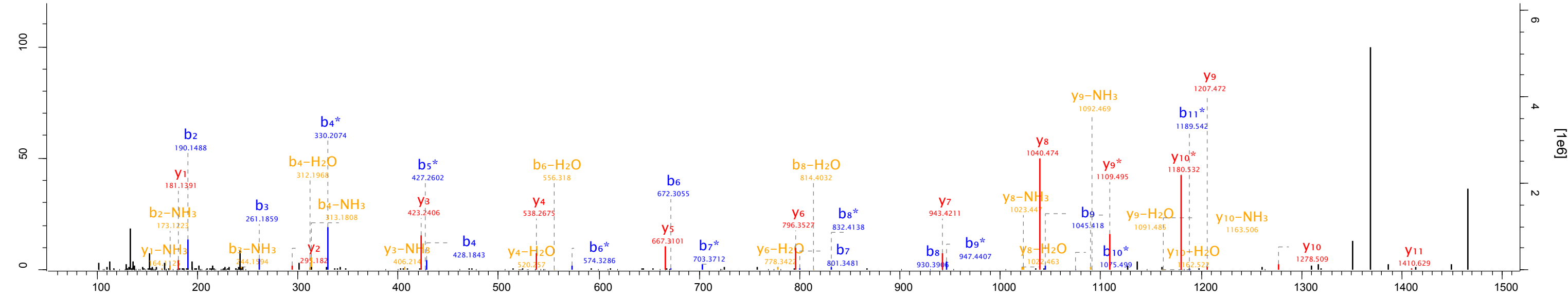


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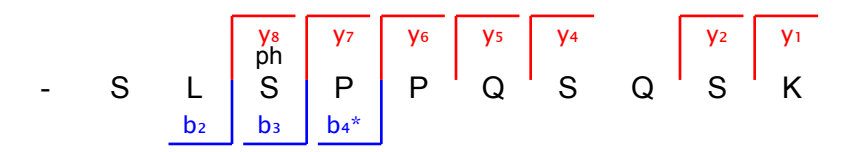
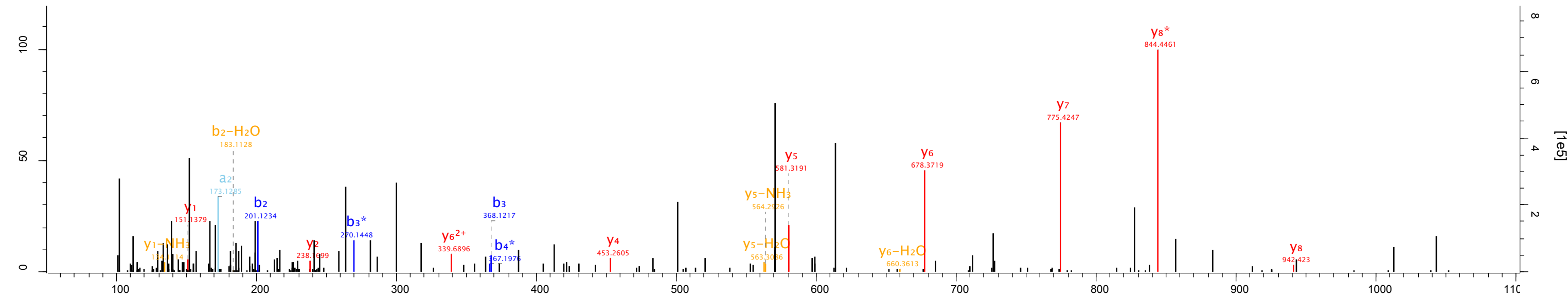
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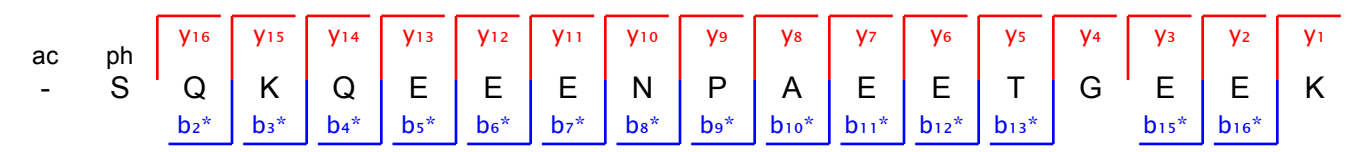
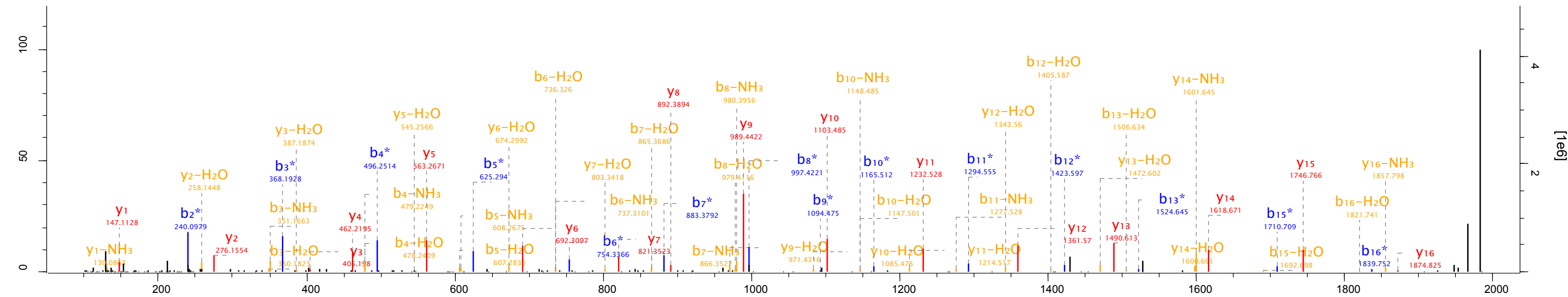
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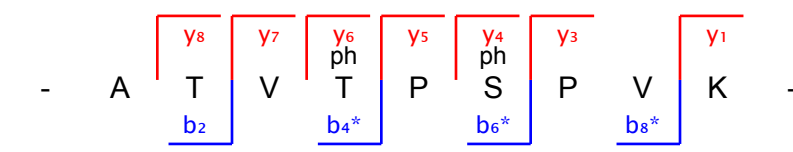
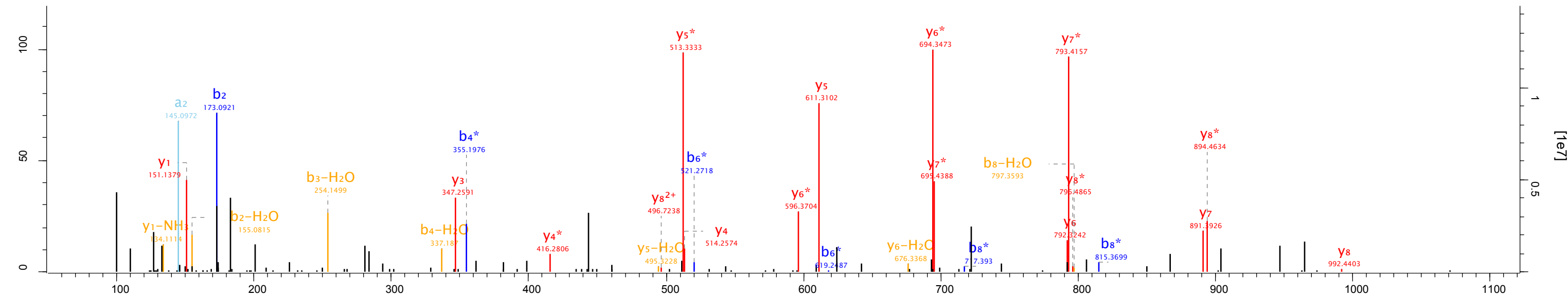
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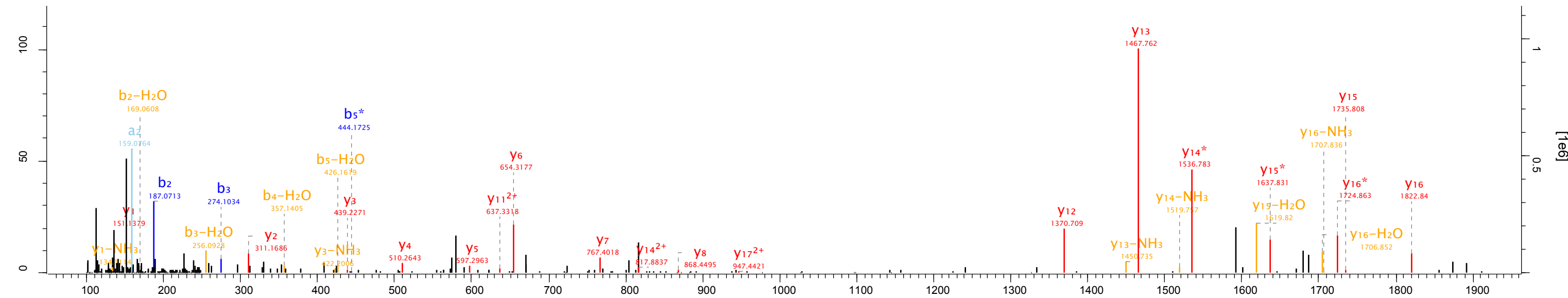
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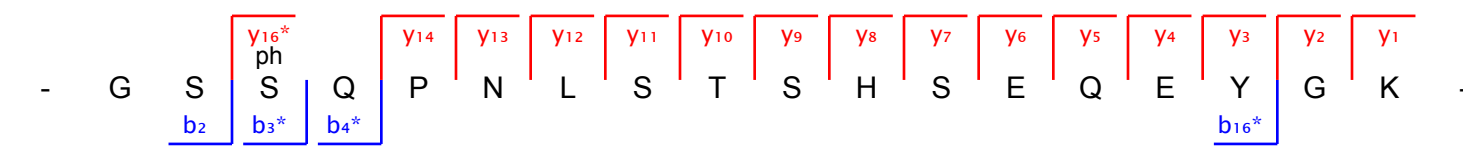
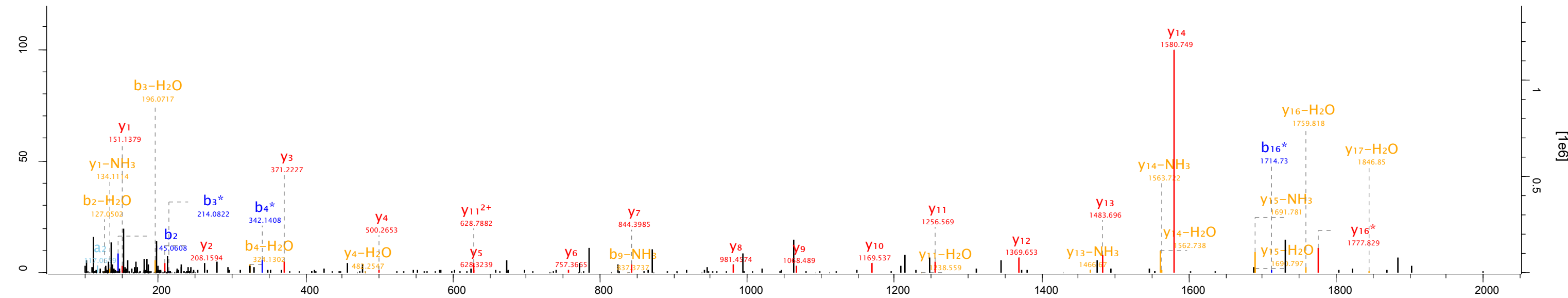


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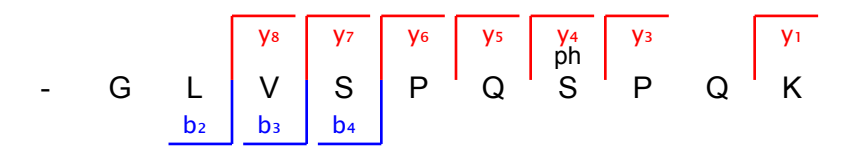
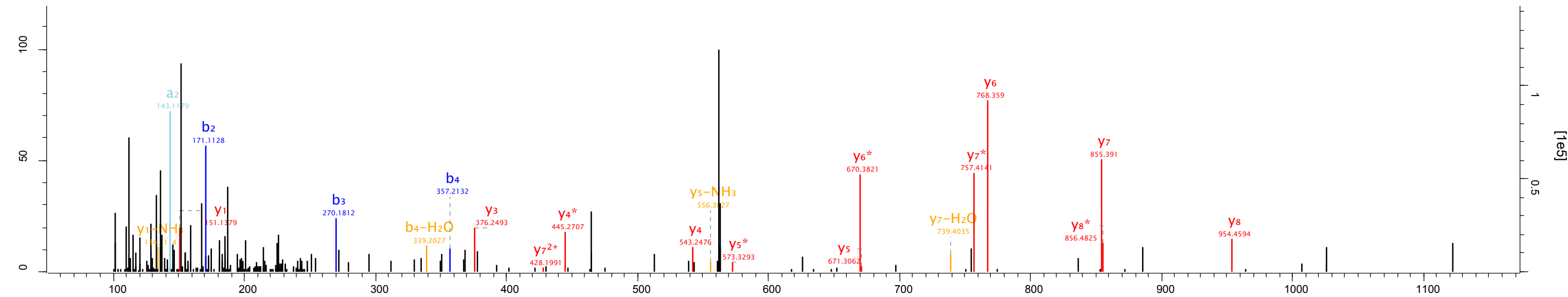


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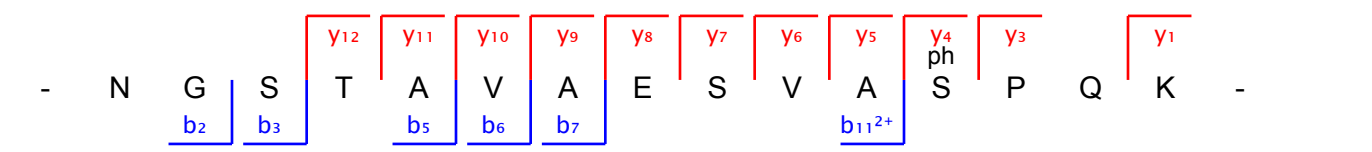
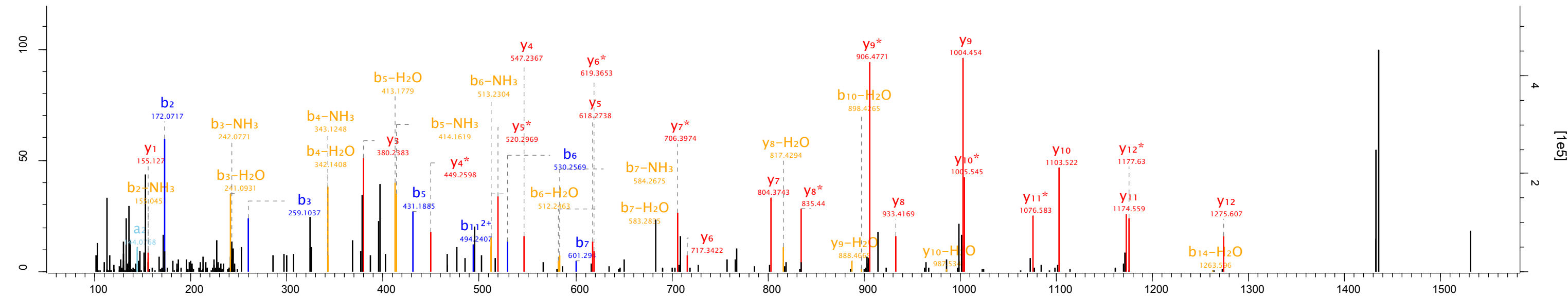
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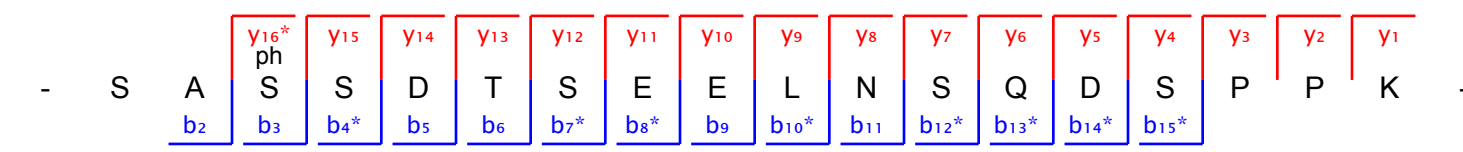
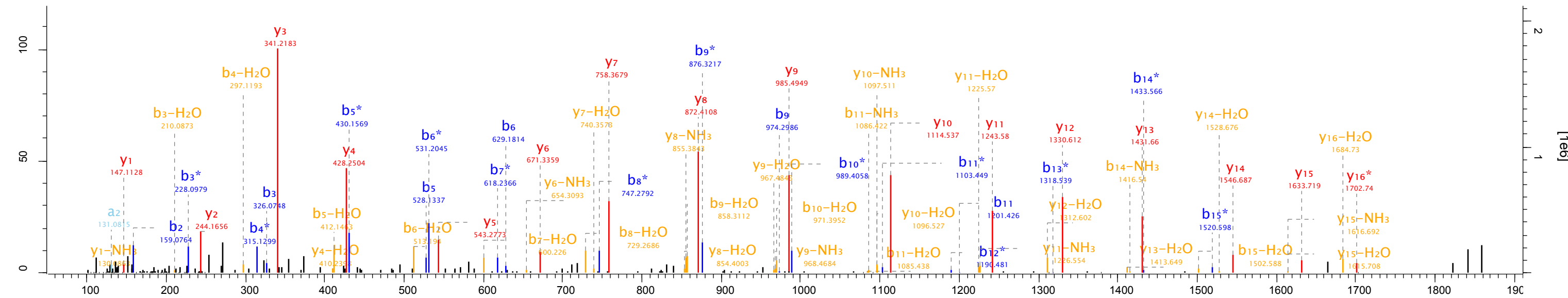
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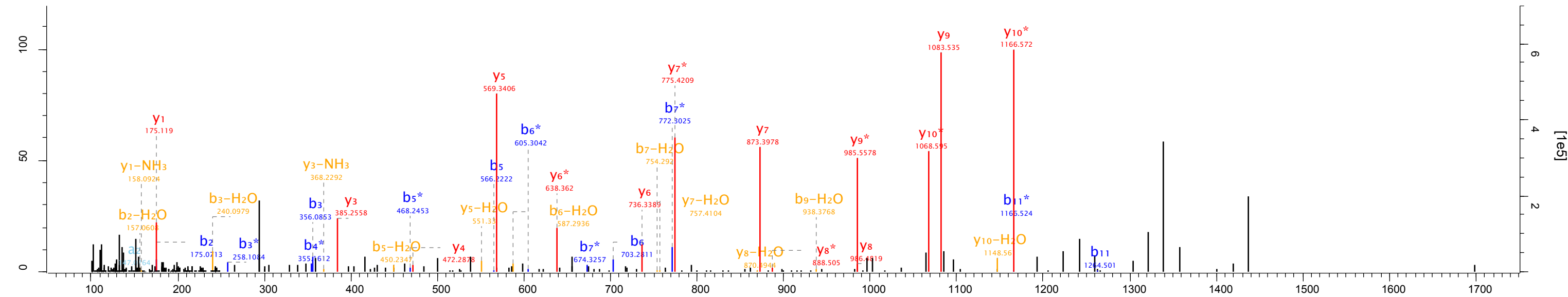
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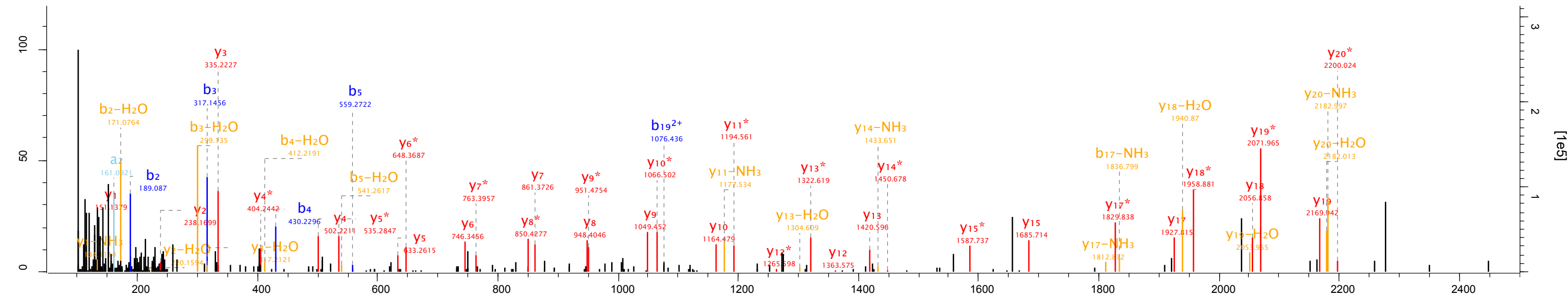
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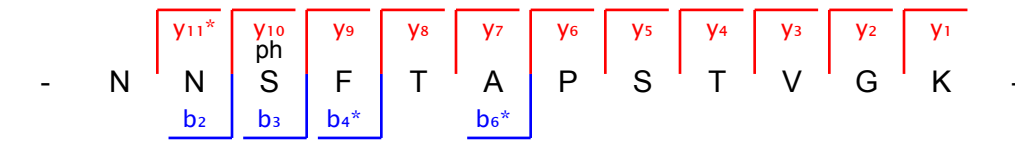
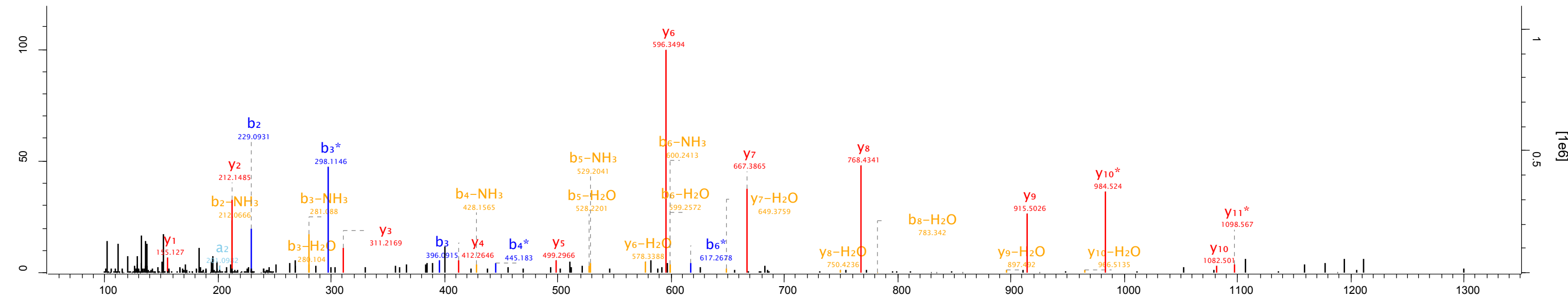


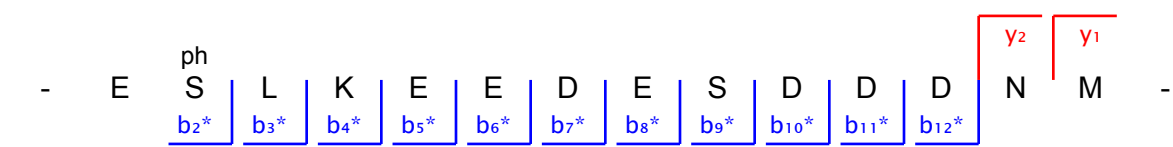
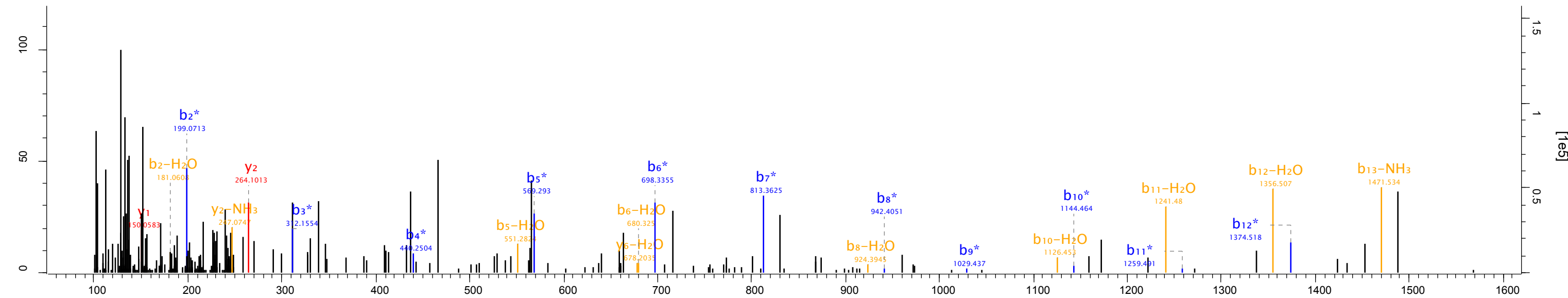
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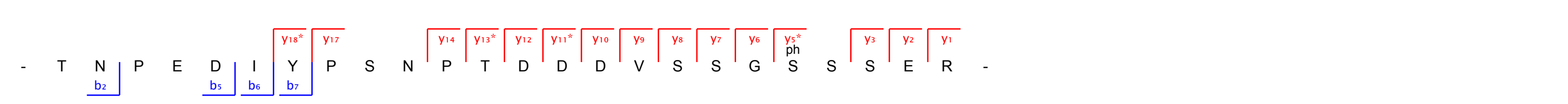
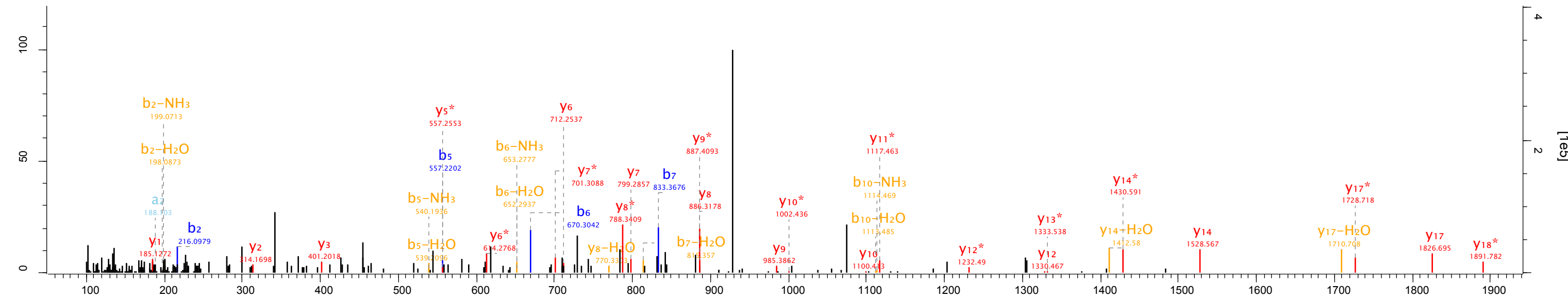
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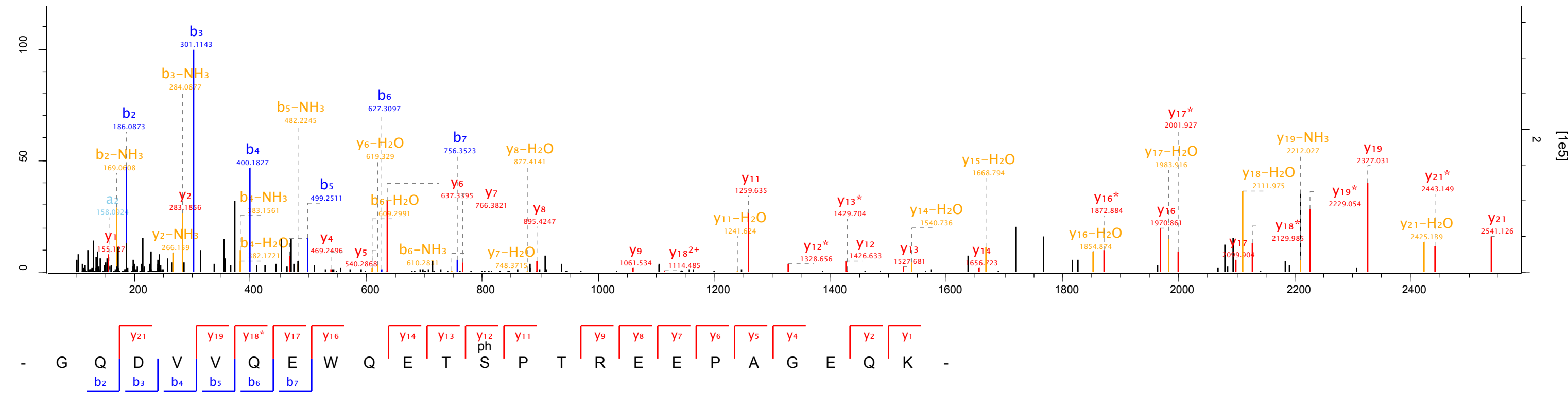
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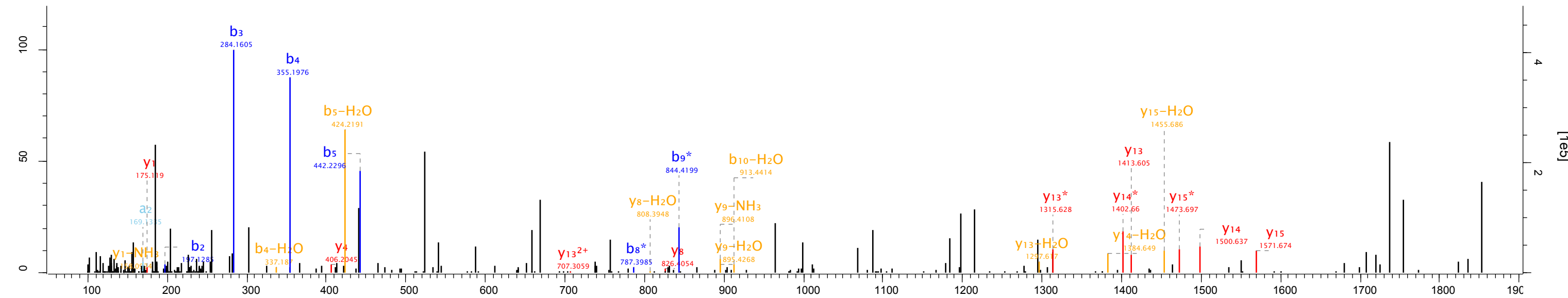


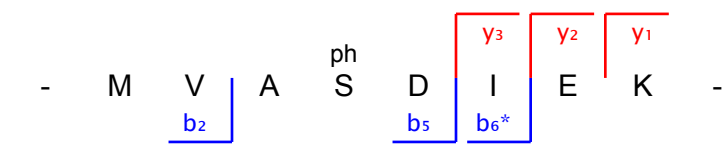
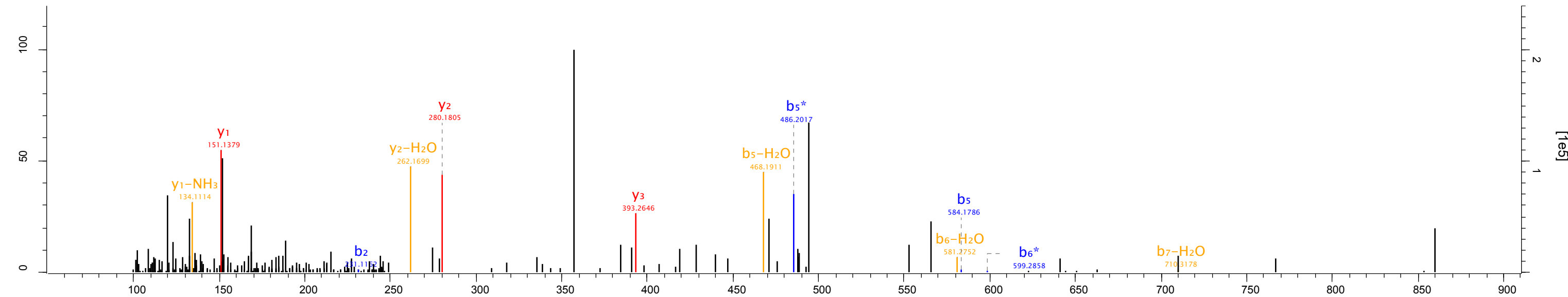
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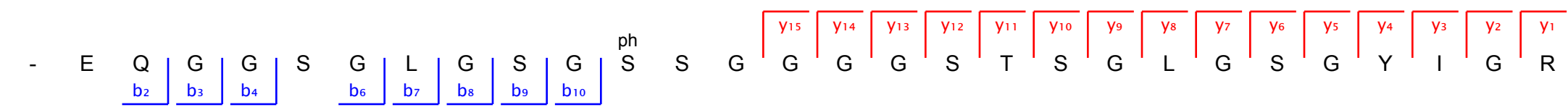
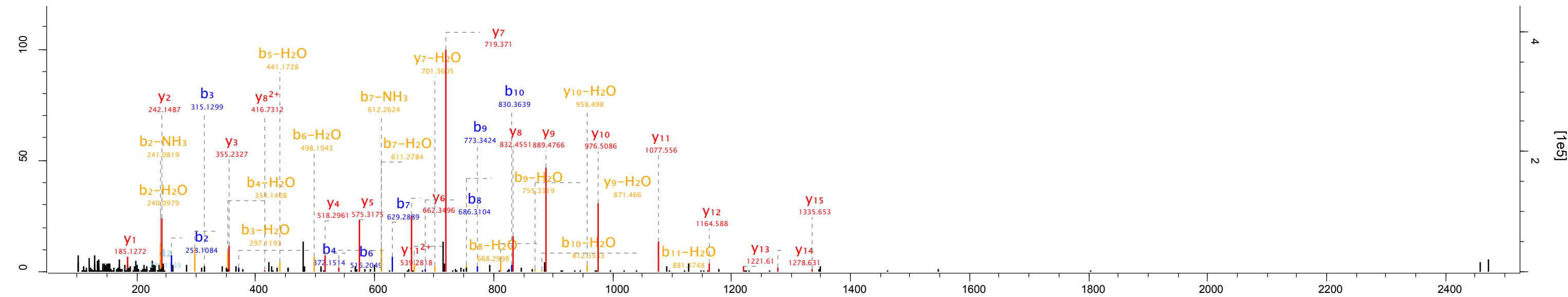


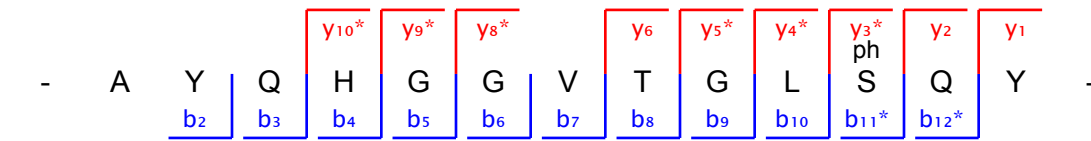
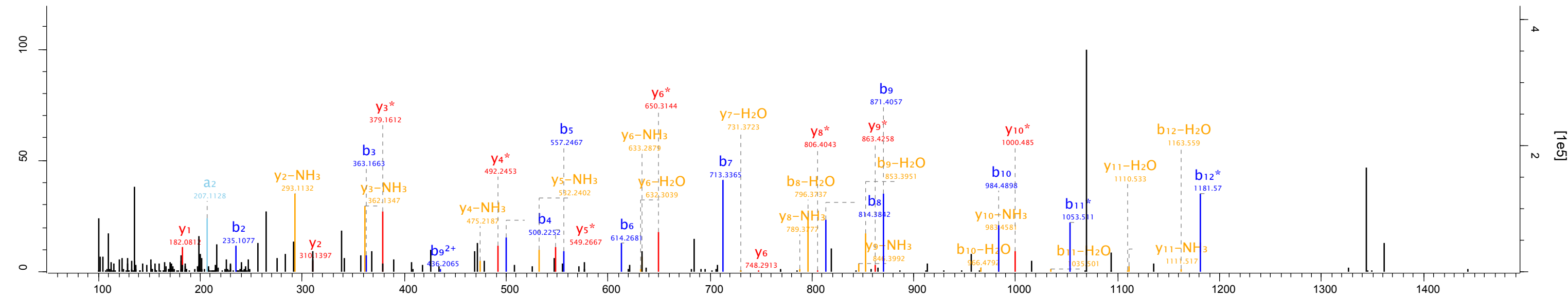
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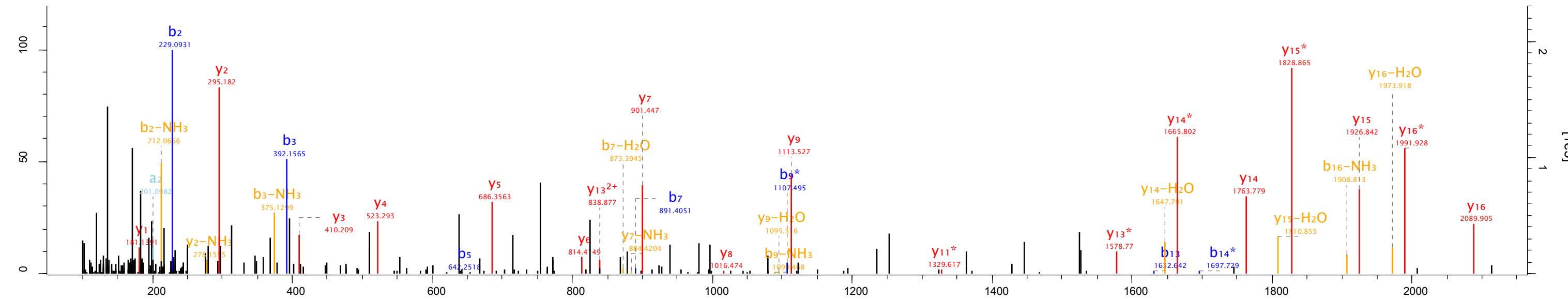


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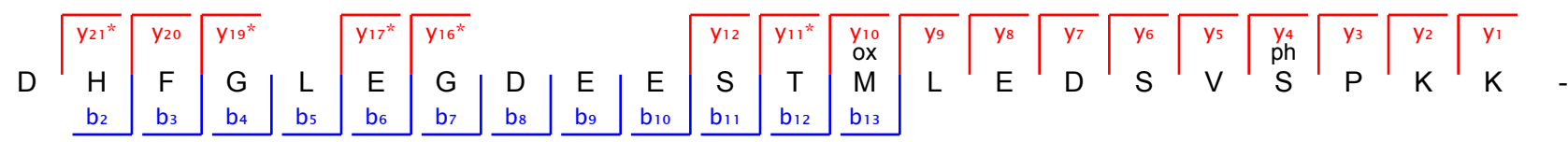
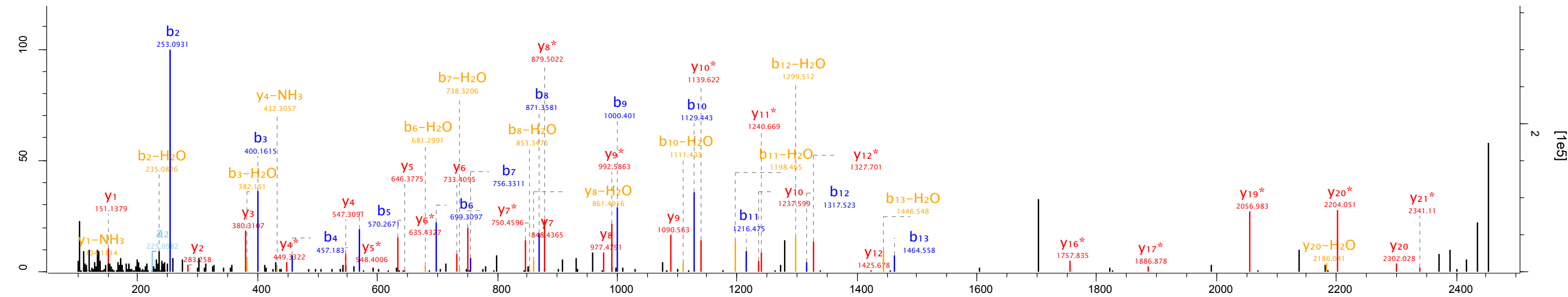


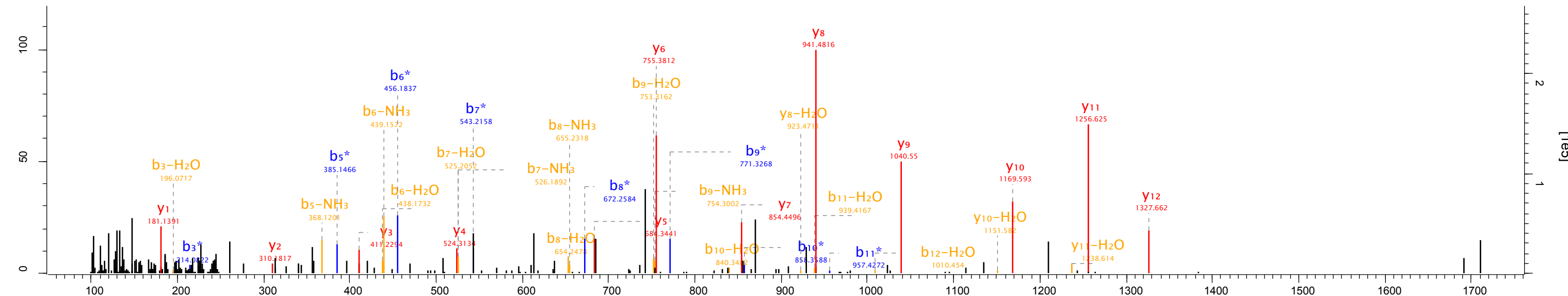


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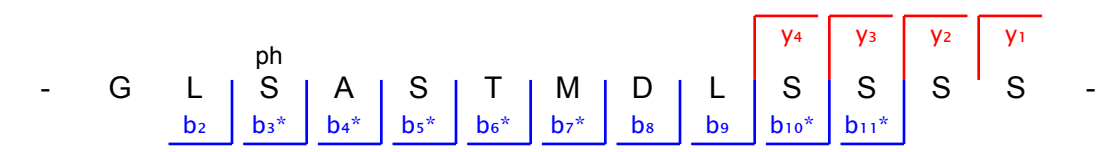
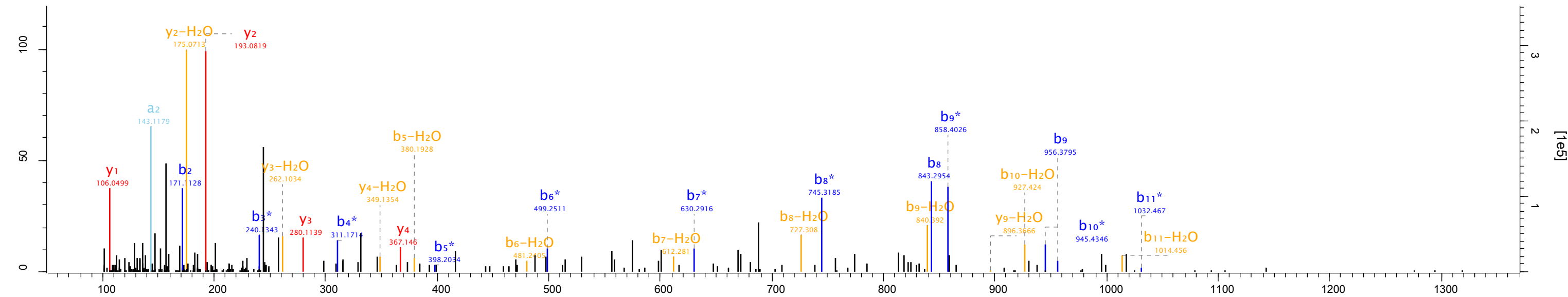
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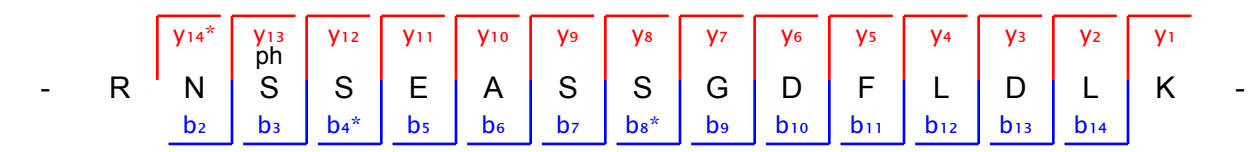
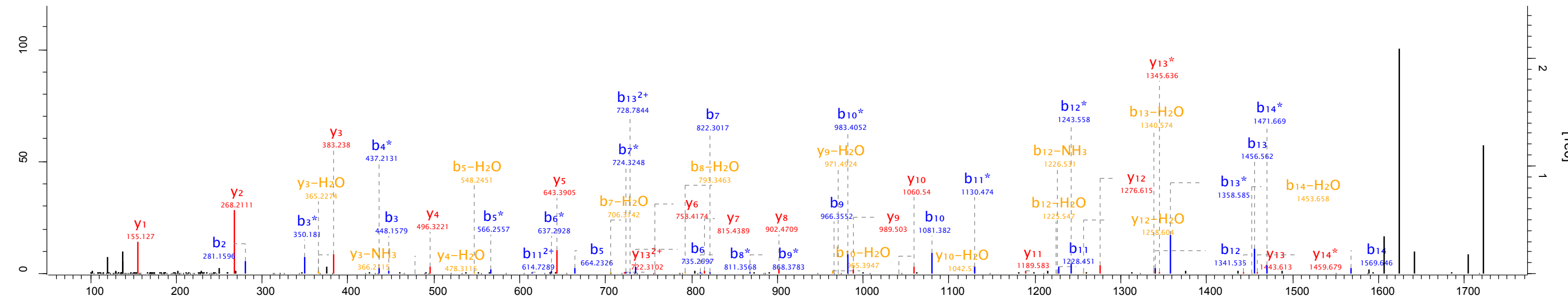


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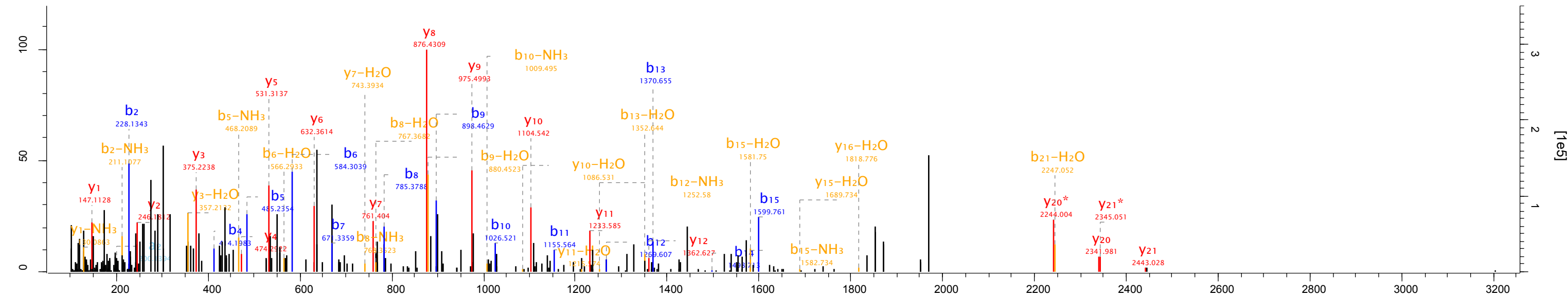
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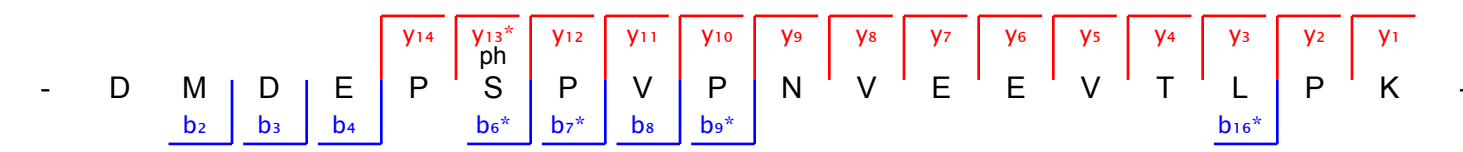
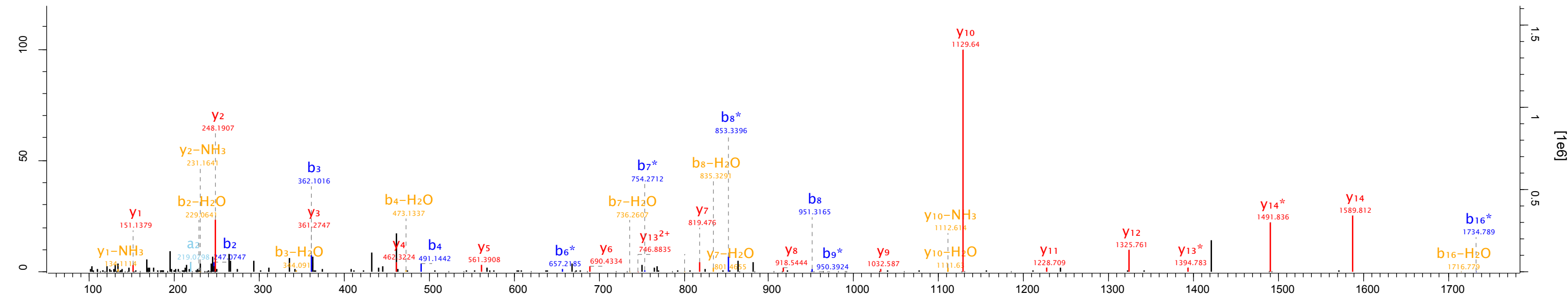
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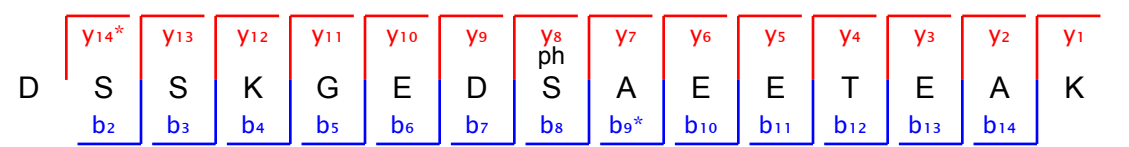
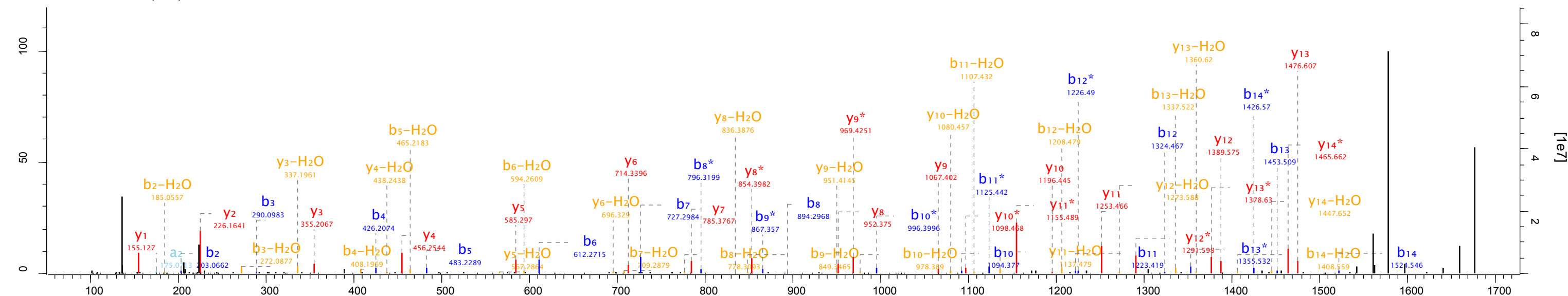


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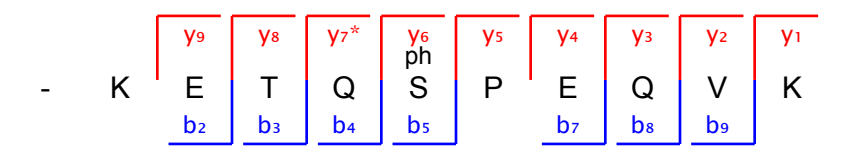
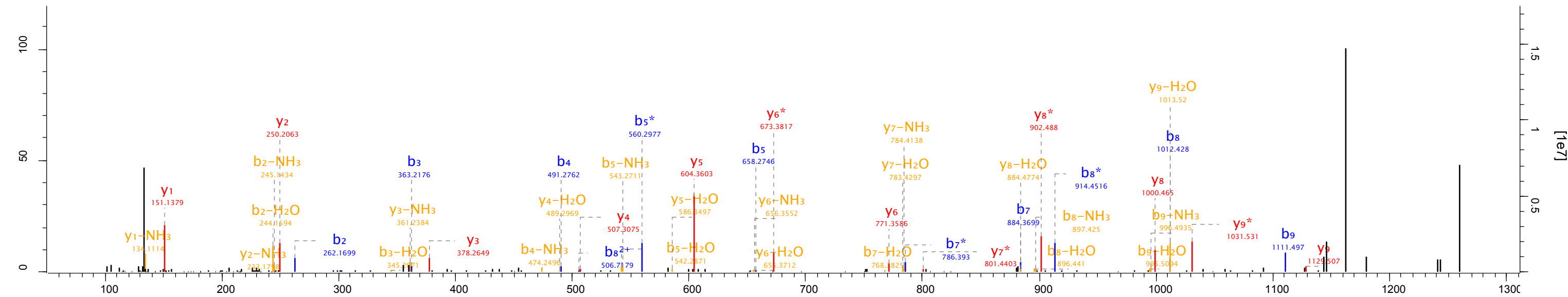


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20171215_MaS_33SR_LMH_phospho2_02

Scan 1978 Method FTMS; HCD Score 346.07 m/z 839.84 Gene names ILF3



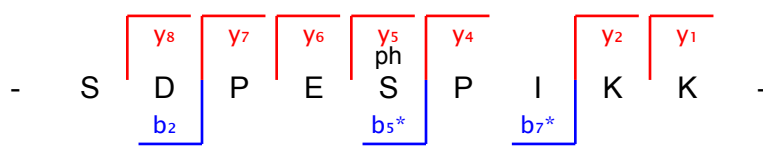
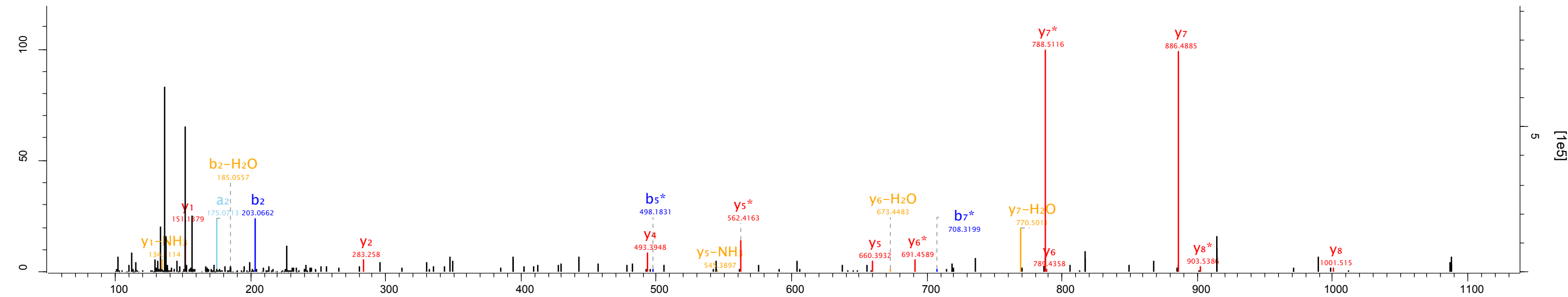
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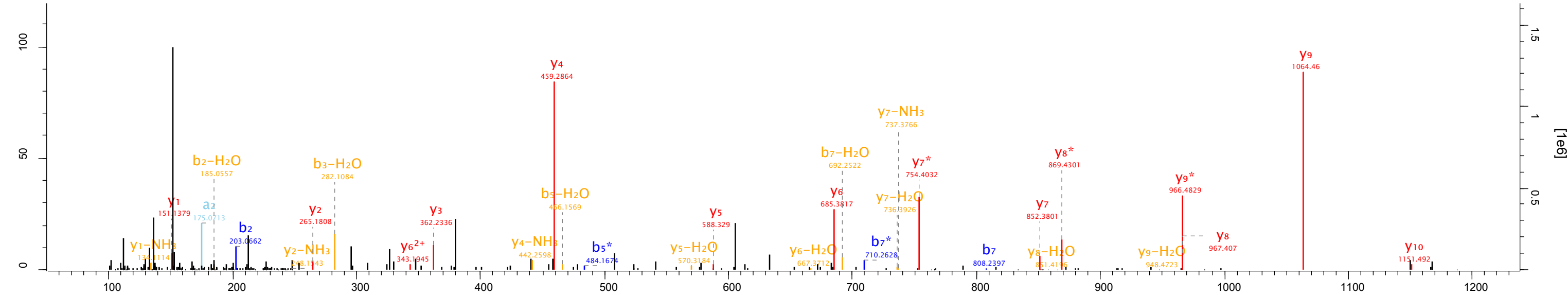


Raw file

20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
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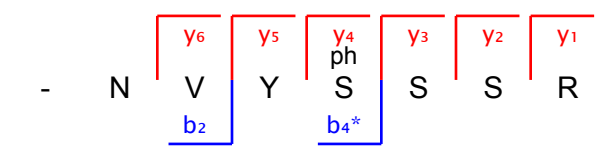
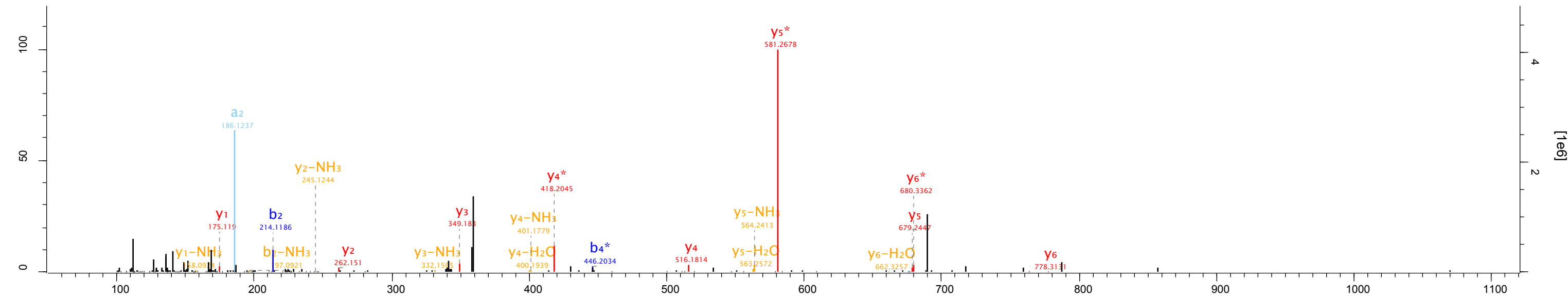




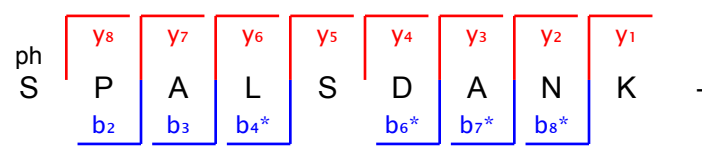
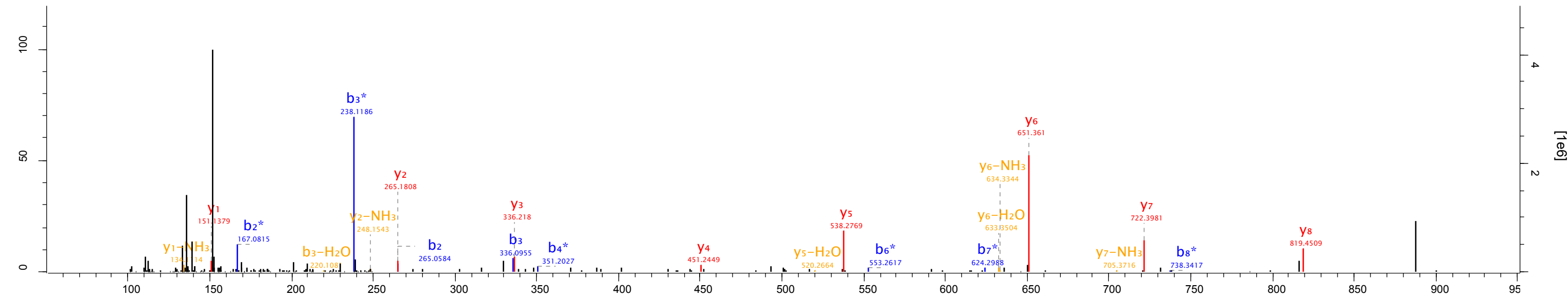
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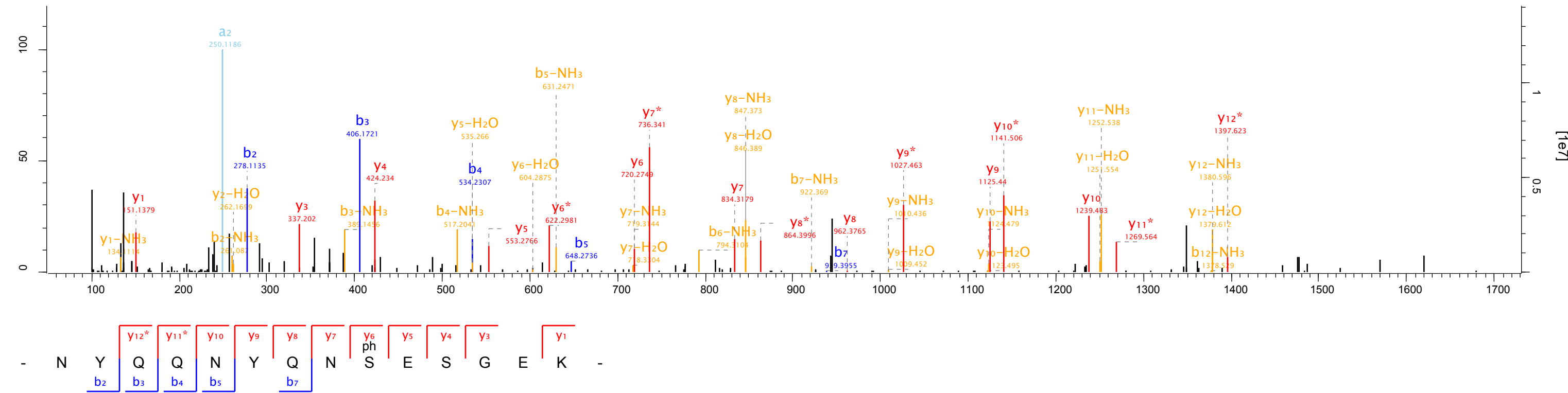
20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
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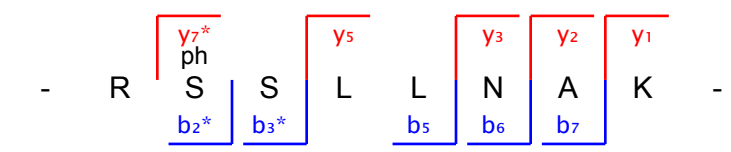
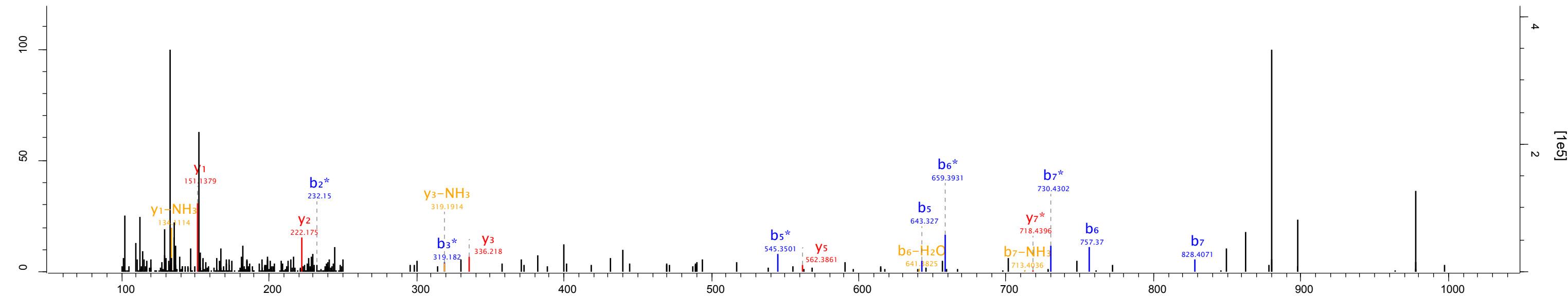


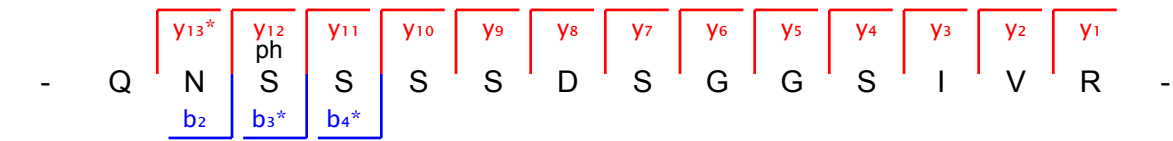
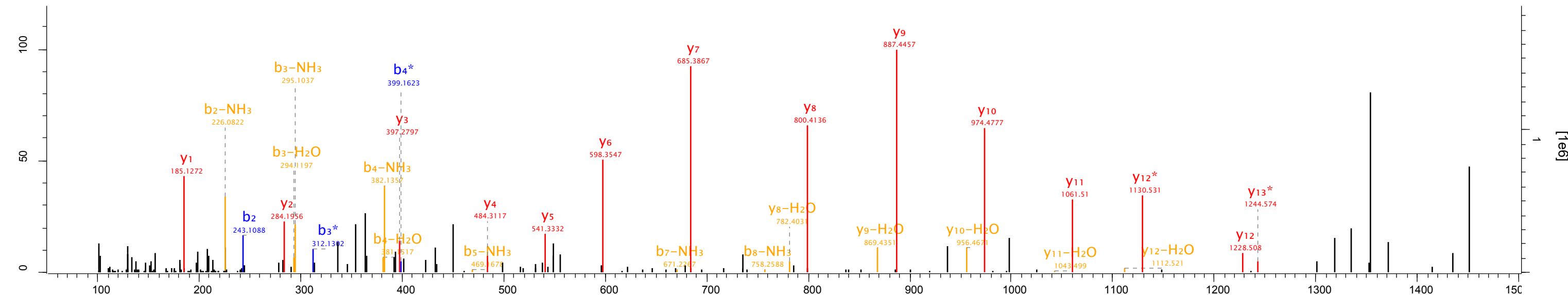
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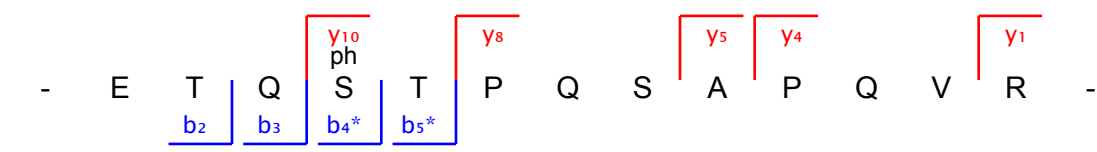
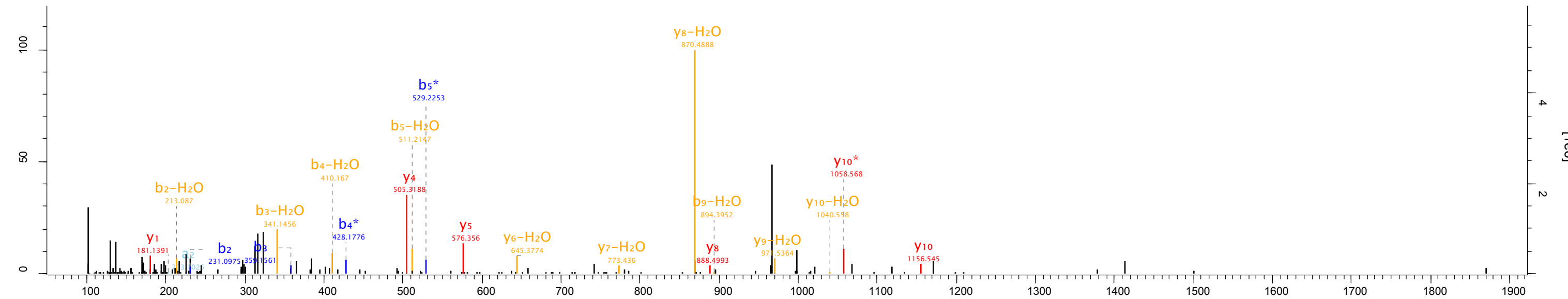
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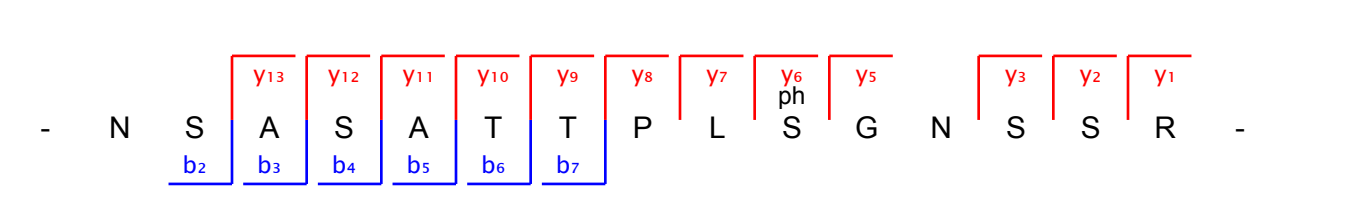
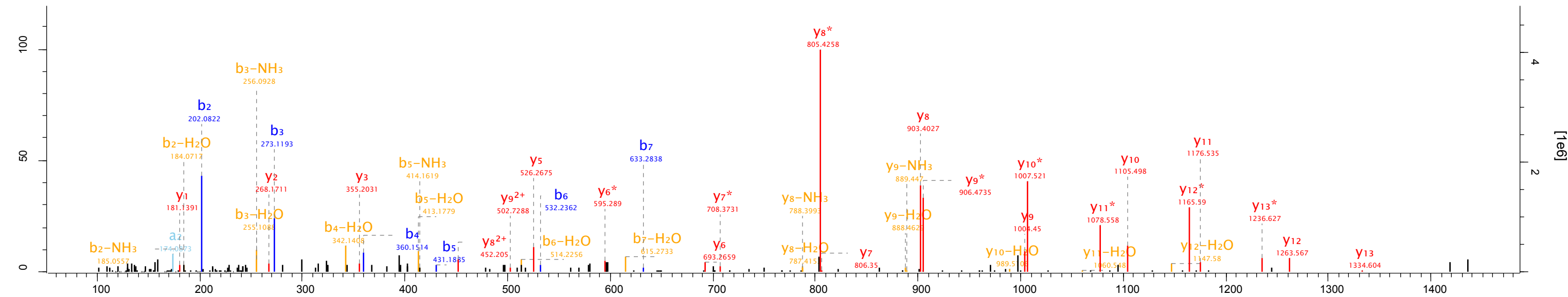


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20171215_MaS_33SR_LMH_phospho2_02

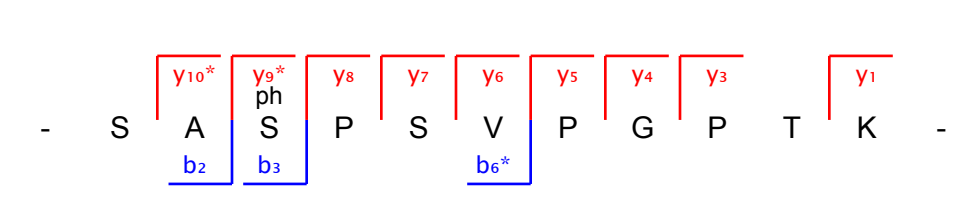
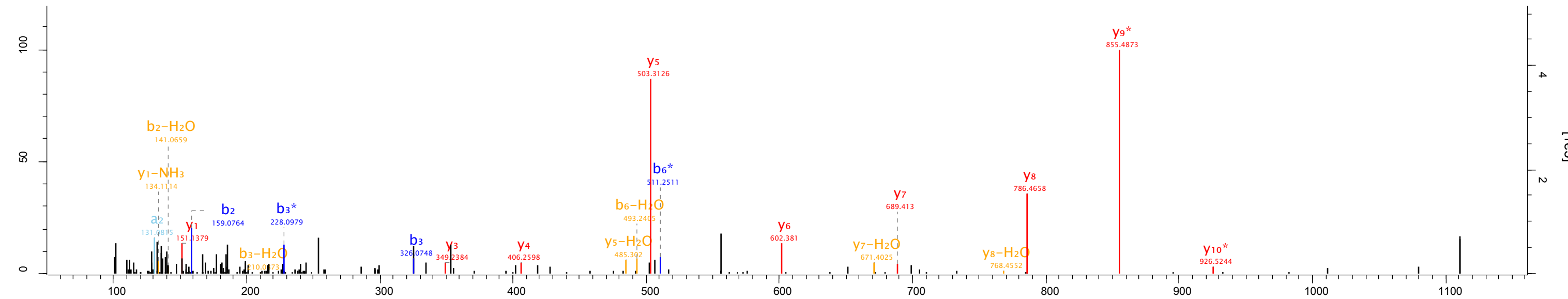
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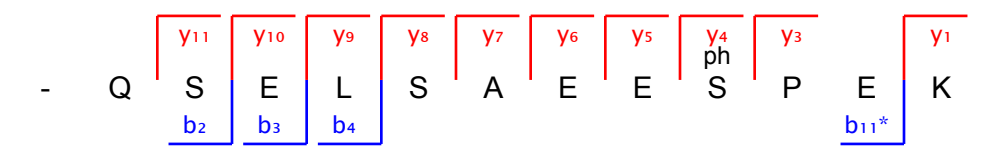
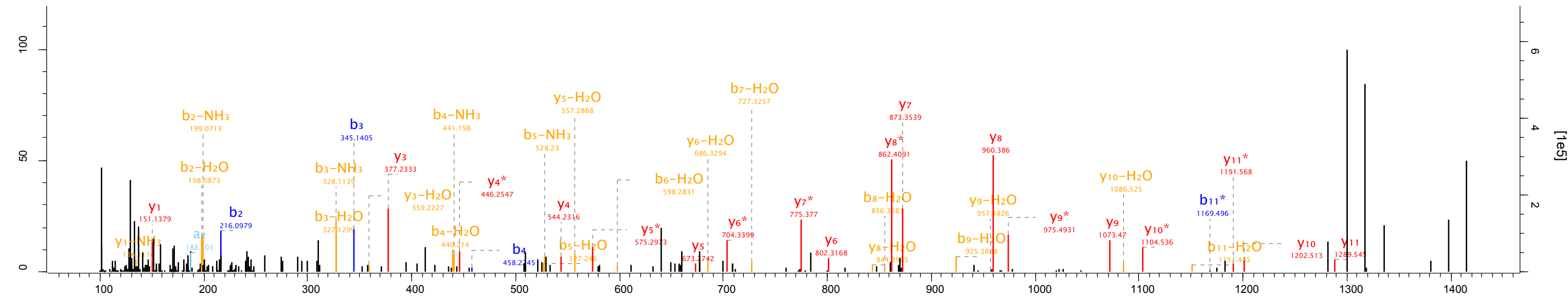
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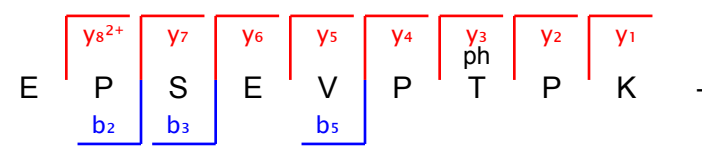
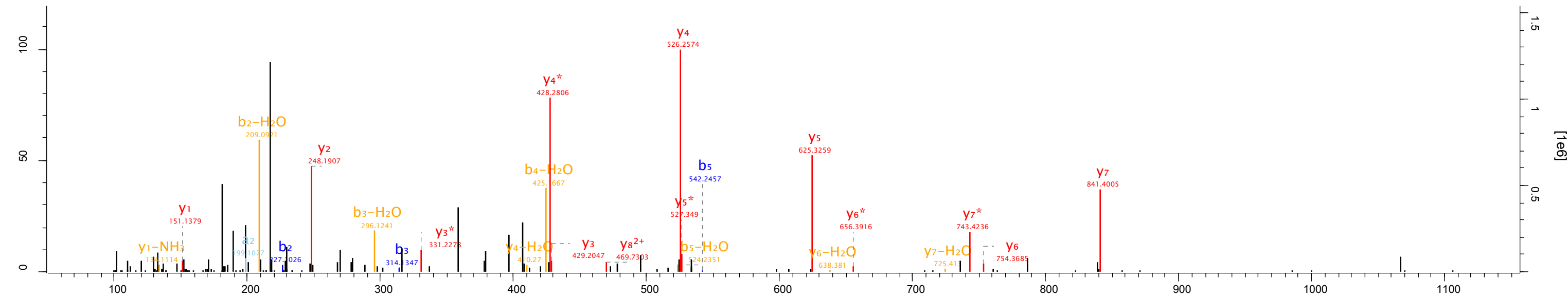
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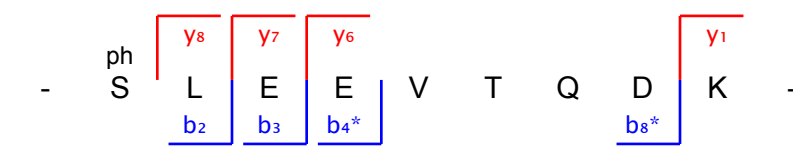
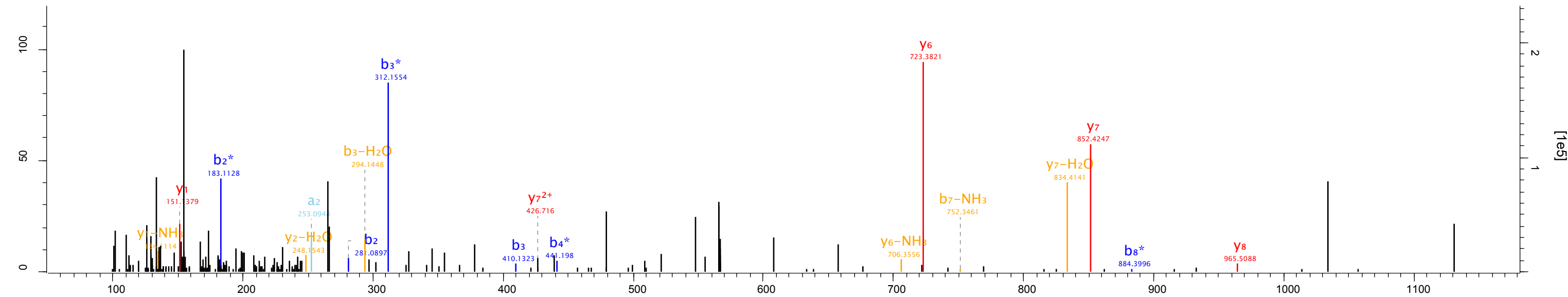
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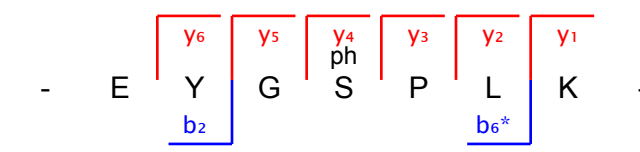
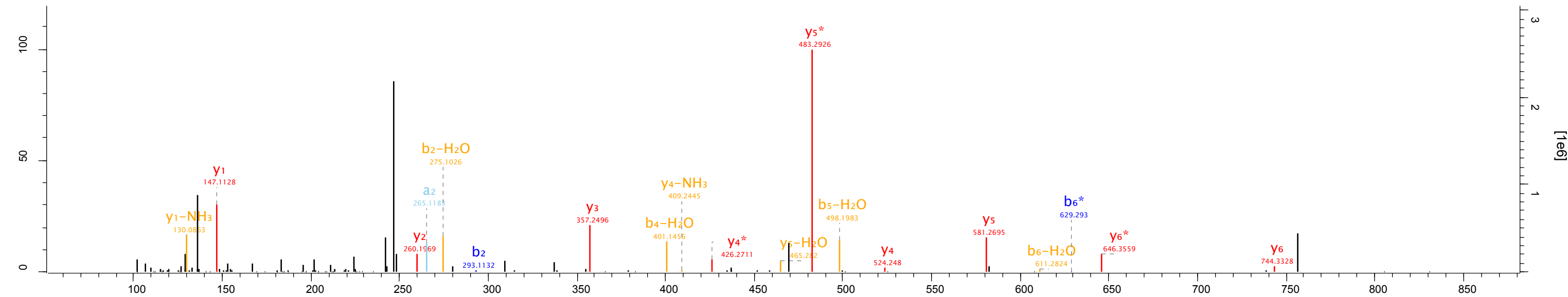
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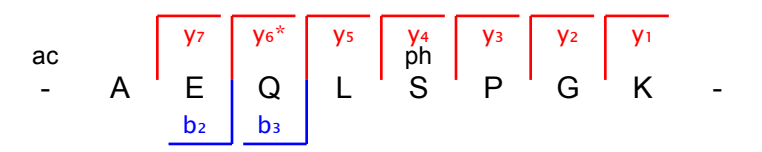
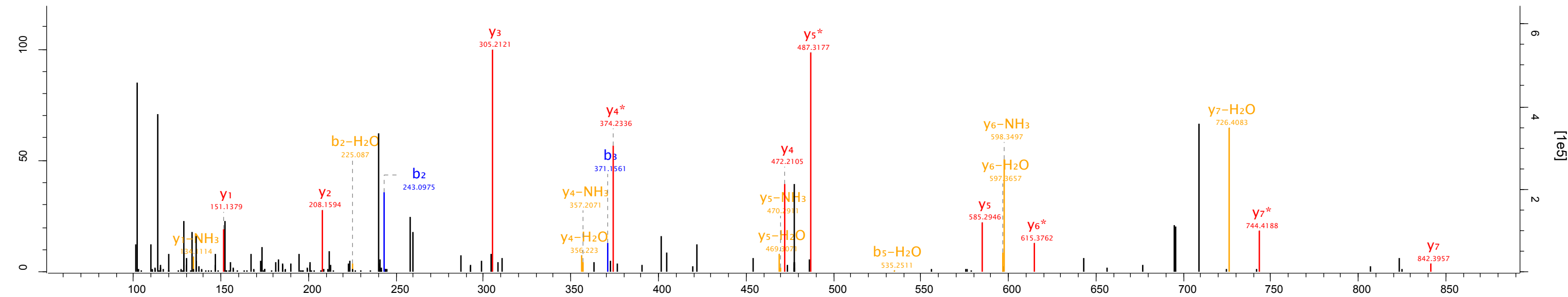
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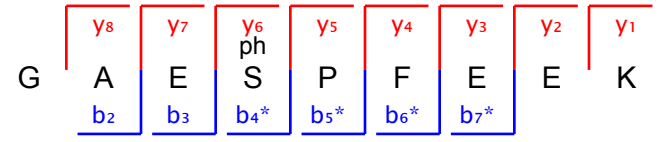
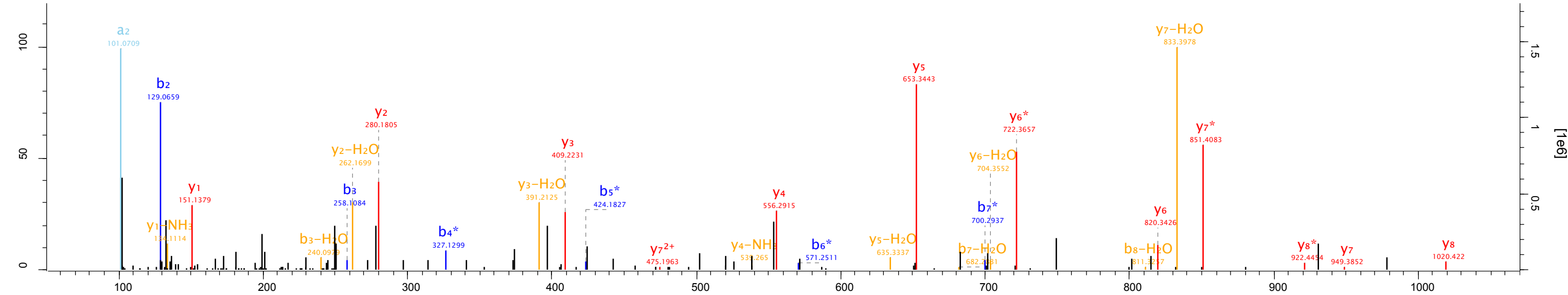


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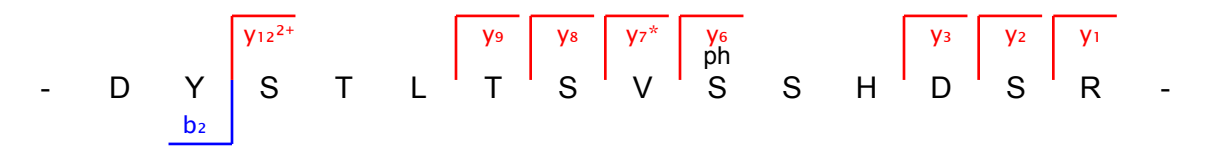
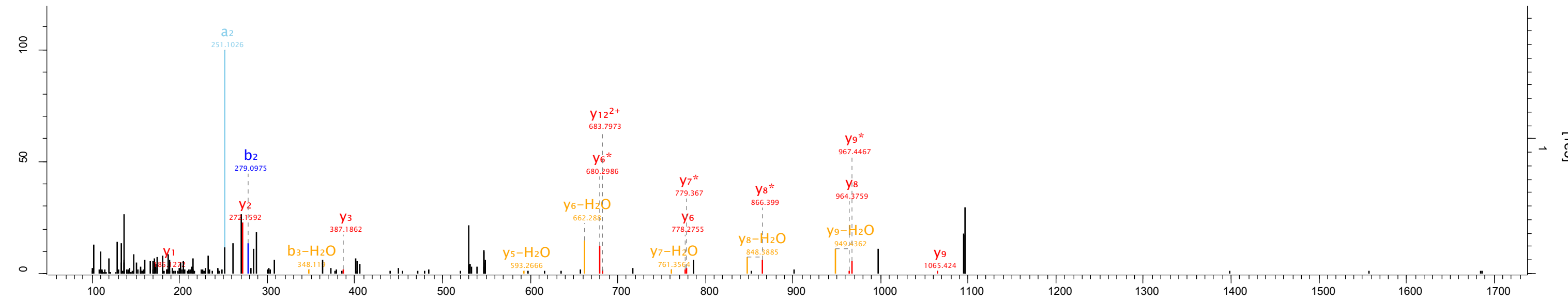


Raw file Scan Method Score m/z Gene names

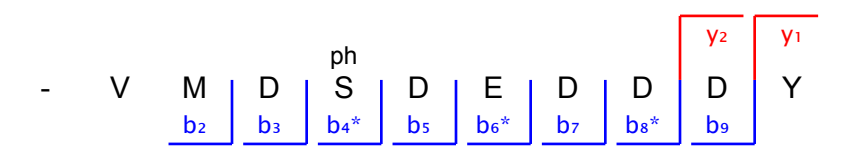
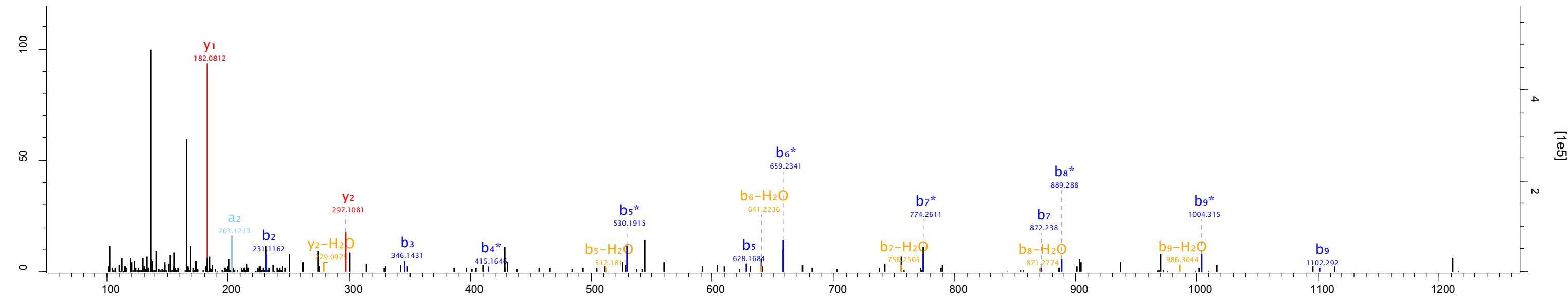
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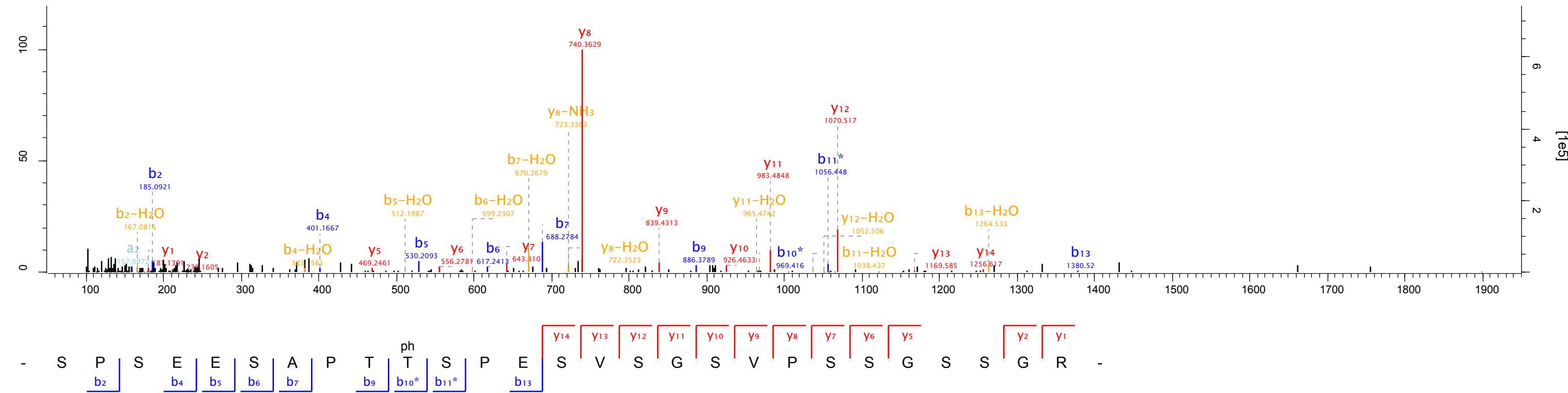


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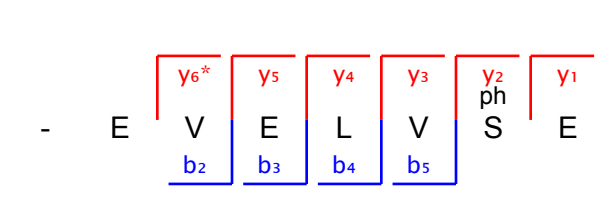
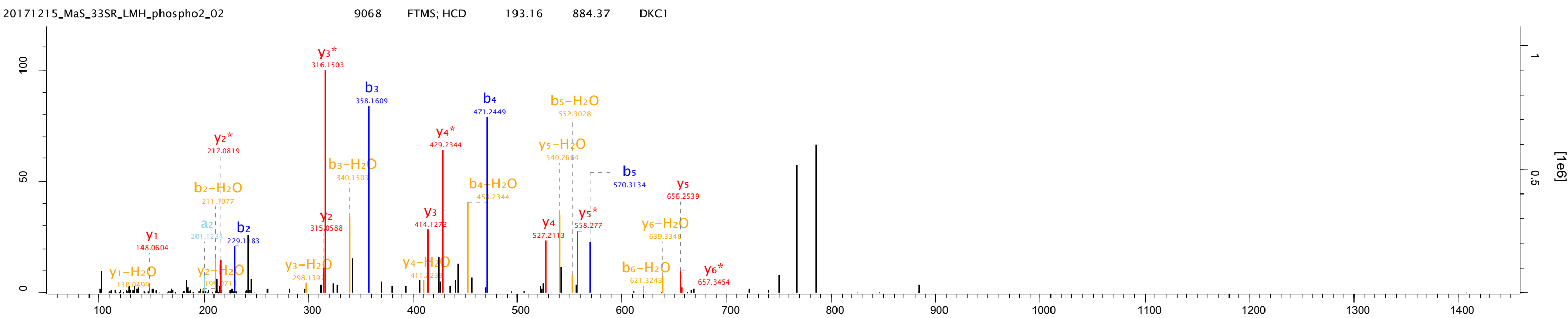
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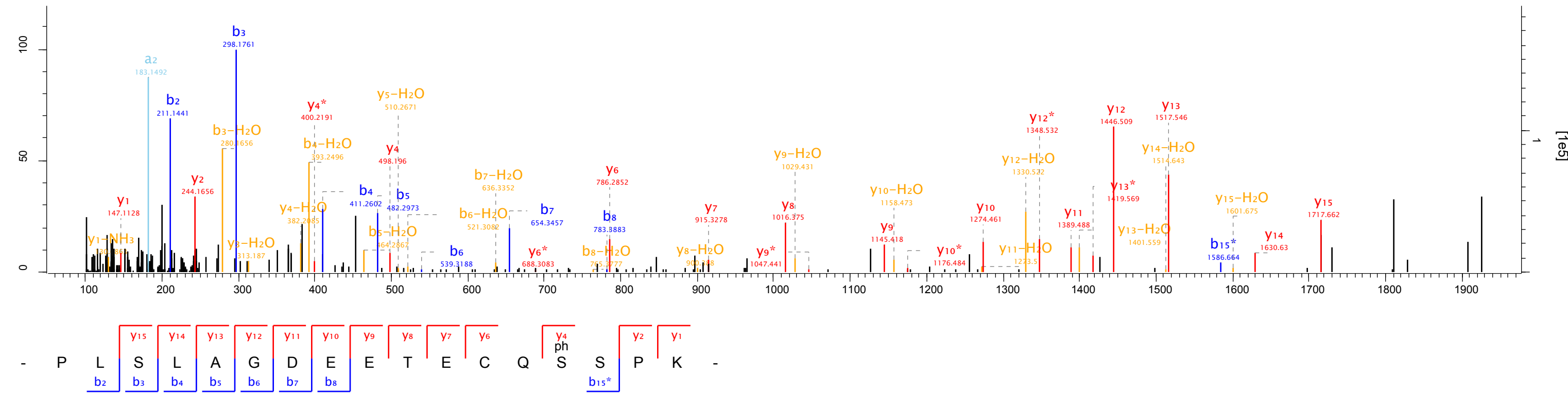




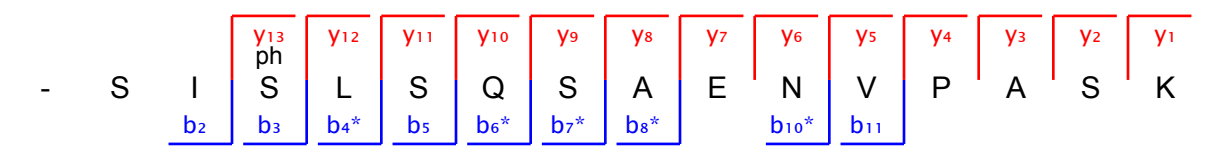
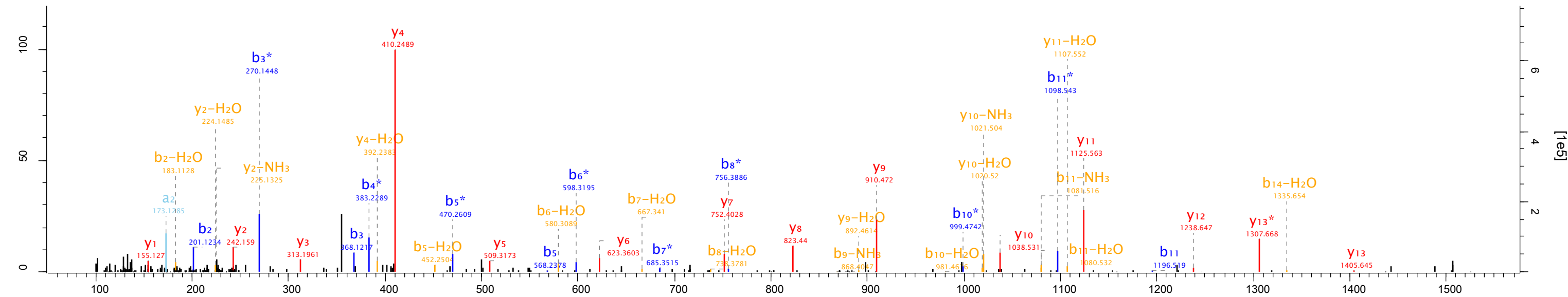
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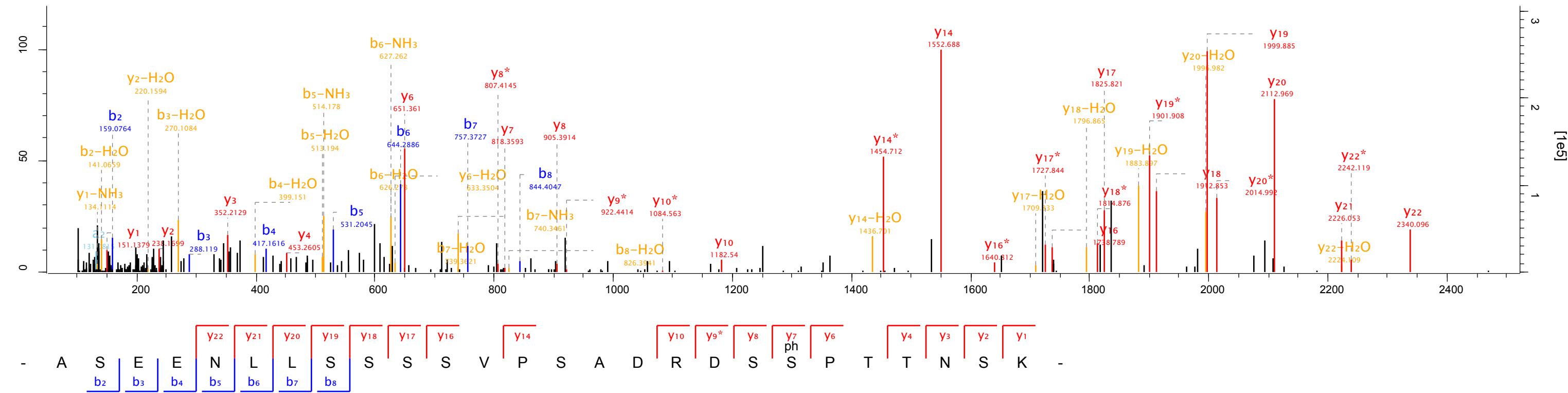




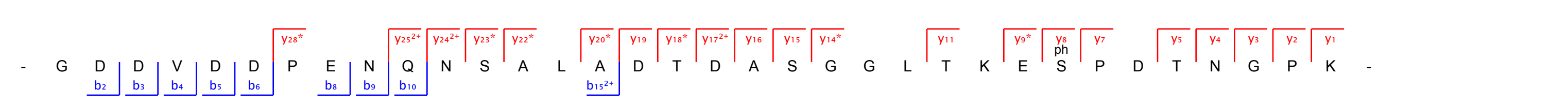
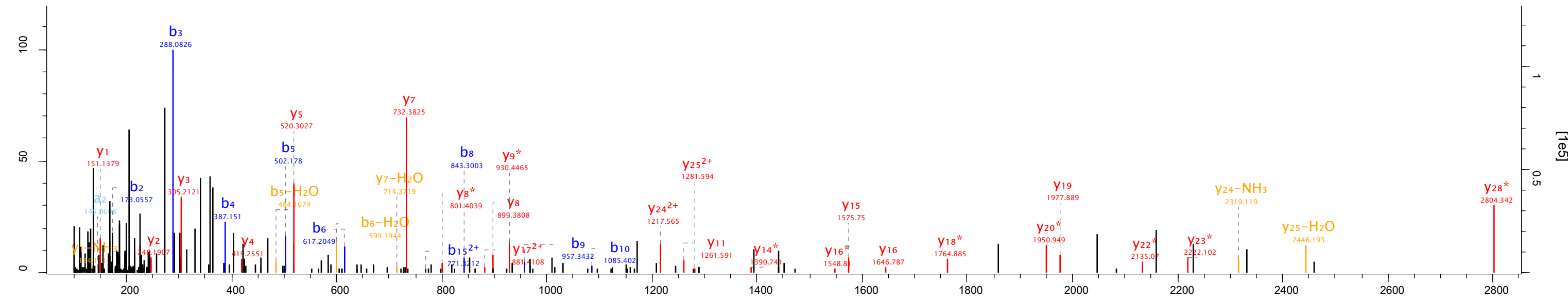
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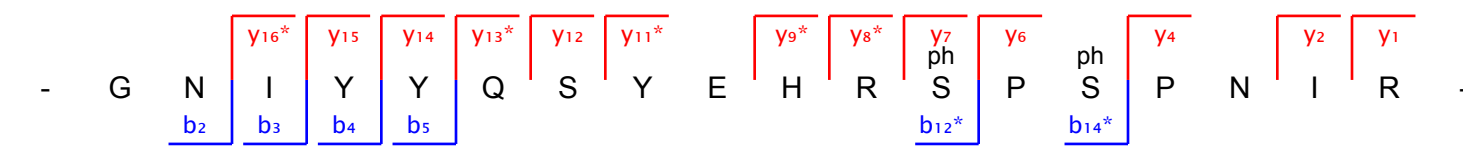
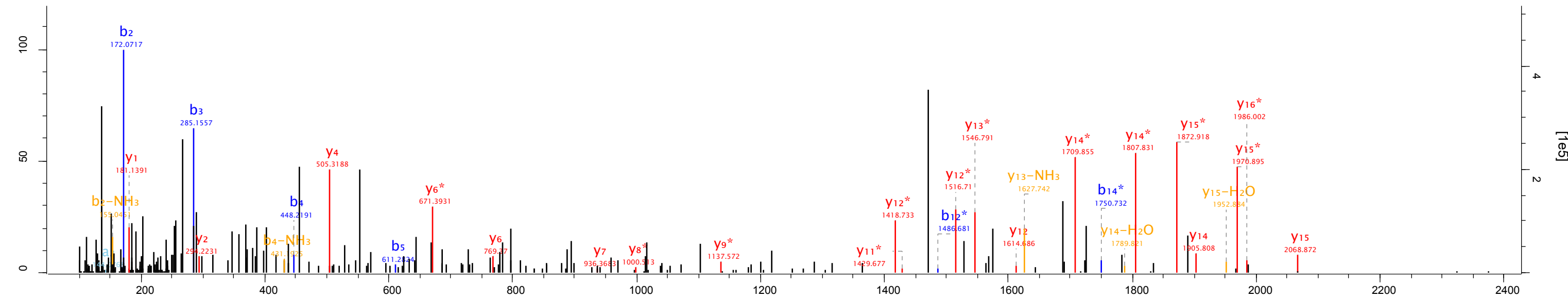
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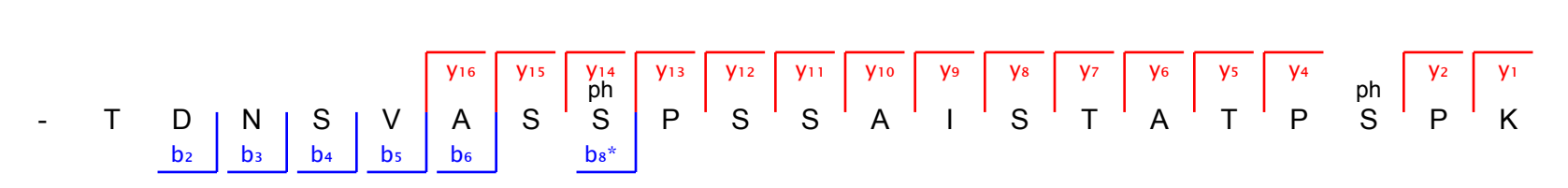
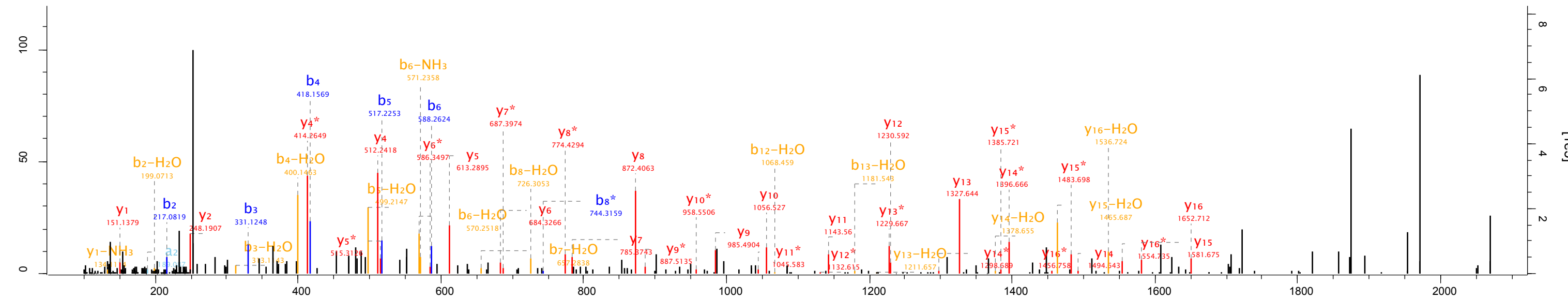
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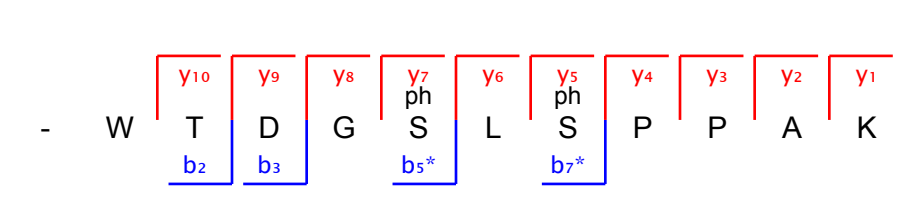
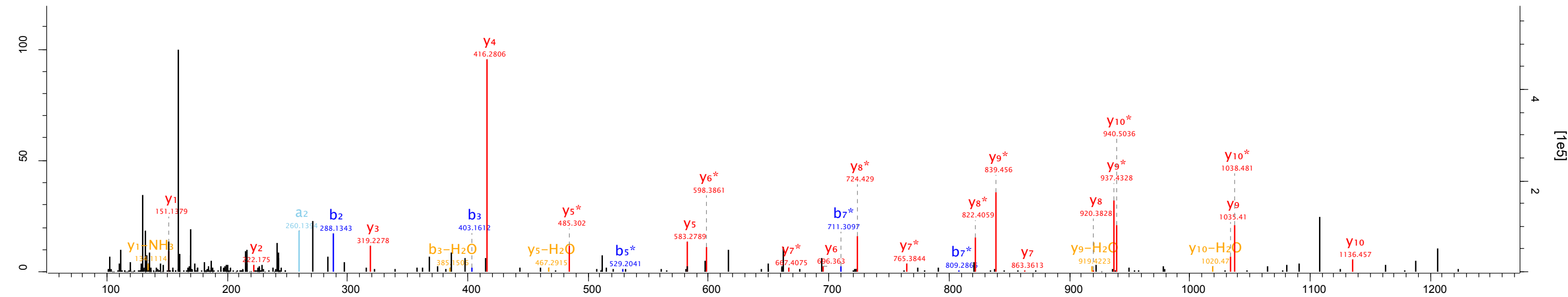
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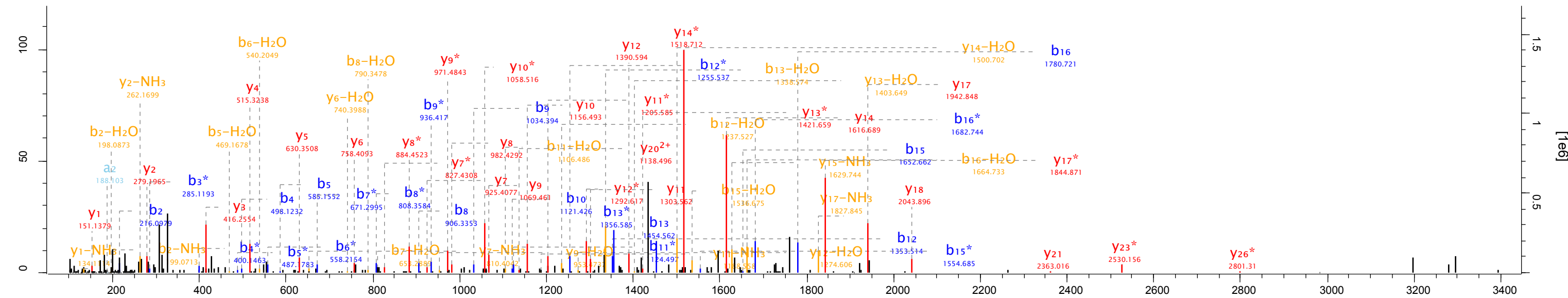
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10048 Method: FTMS; HCD Score: 127.95 m/z: 1085.47 Gene names: KDM6A



20171215_MaS_33SR_LMH_phospho2_03 10218 FTMS; HCD 102.08 661.77 ARHGEF11



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10228 Method FTMS; HCD Score 198.21 m/z 1133.47 Gene names CRTCI

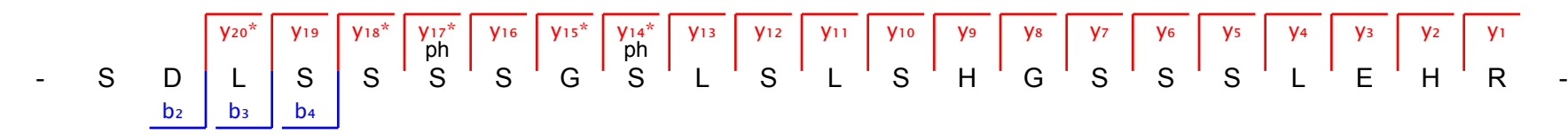
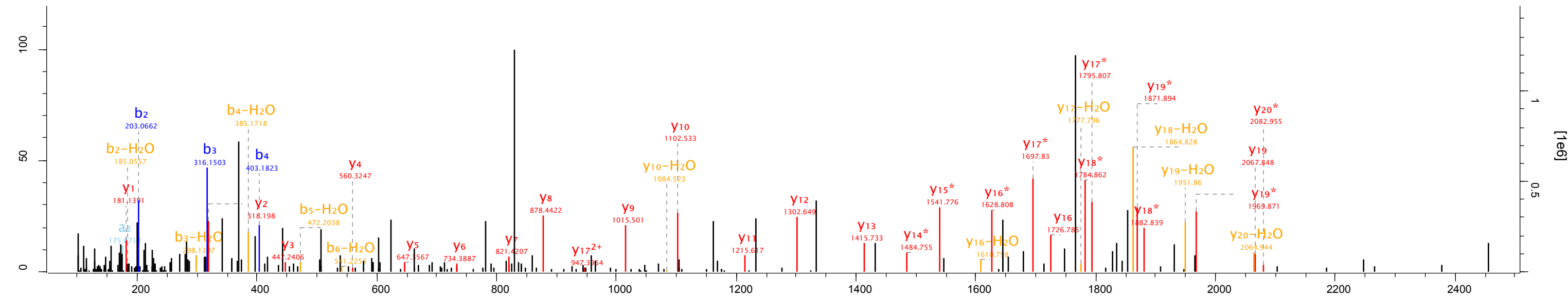


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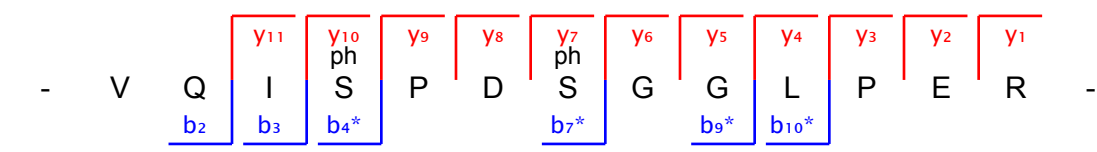
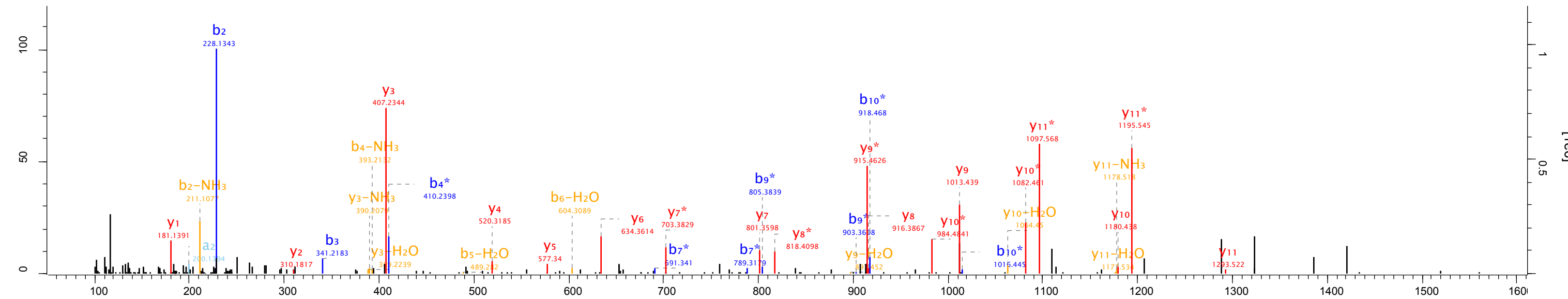
ph

b₂ b₃* b₄ b₅ b₆* b₇* b₈ b₉ b₁₀ b₁₁* b₁₂ b₁₃ b₁₅ b₁₆ y₁₄ y₁₃* y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁ y₂₆* y₂₃* y₂₁ y₂₀²⁺ y₁₈ y₁₇

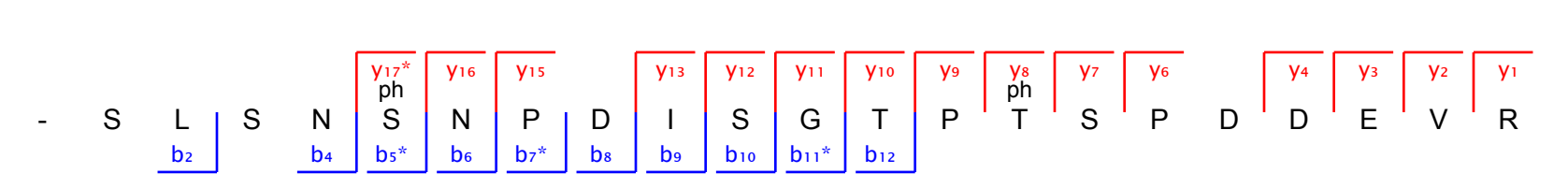
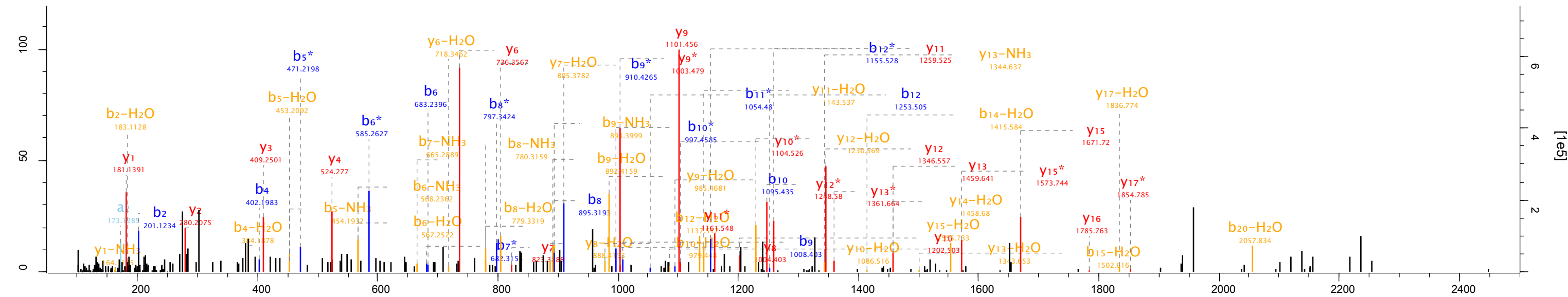
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 Scan: 10378 Method: FTMS; HCD Score: 99.11 m/z: 795 Gene names: ARHGEF10

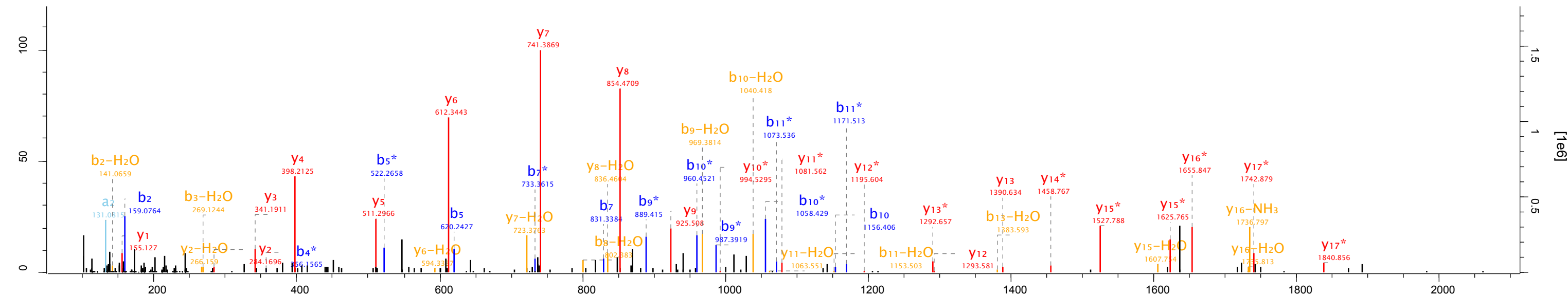


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 Scan: 10388 Method: FTMS; HCD Score: 126.25 m/z: 760.83 Gene names: KHSRP



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10508 Method FTMS; HCD Score 228.55 m/z 1177.48 Gene names DOCK7



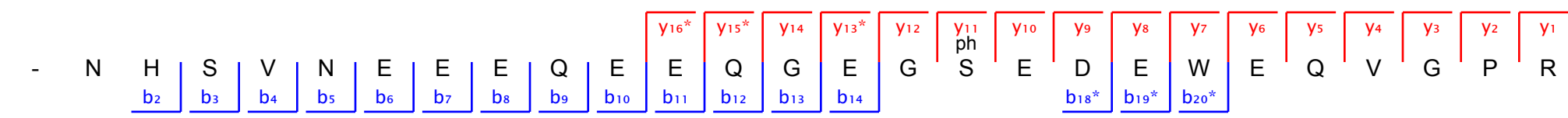
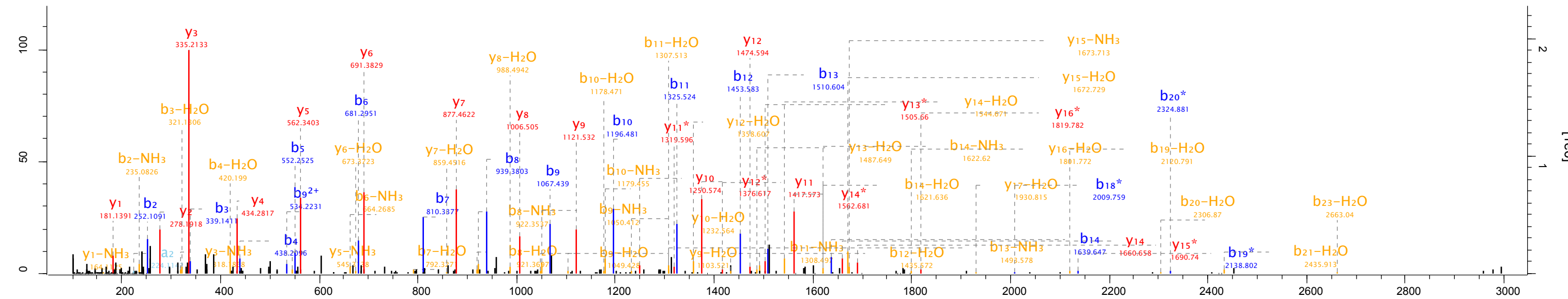


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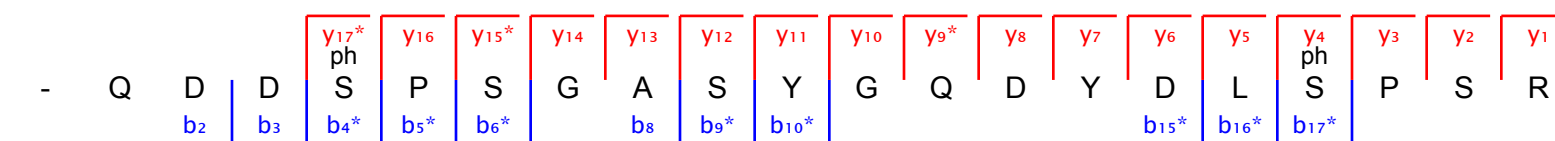
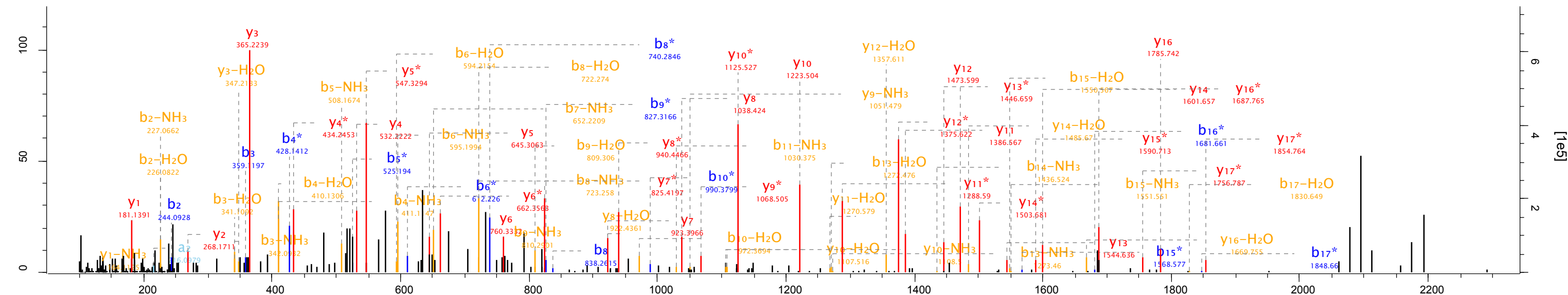
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b₄*
b₅
b₇
b₉*
b₁₀
b₁₁*

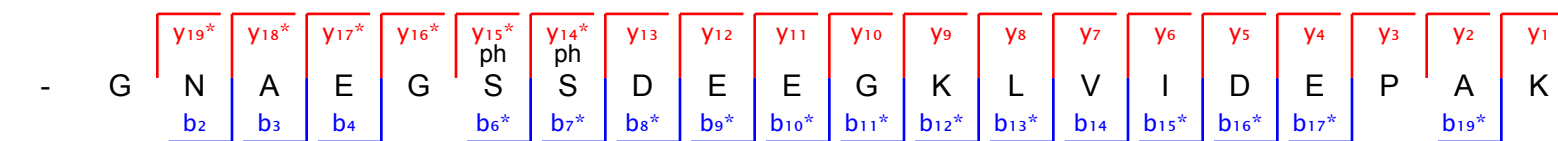
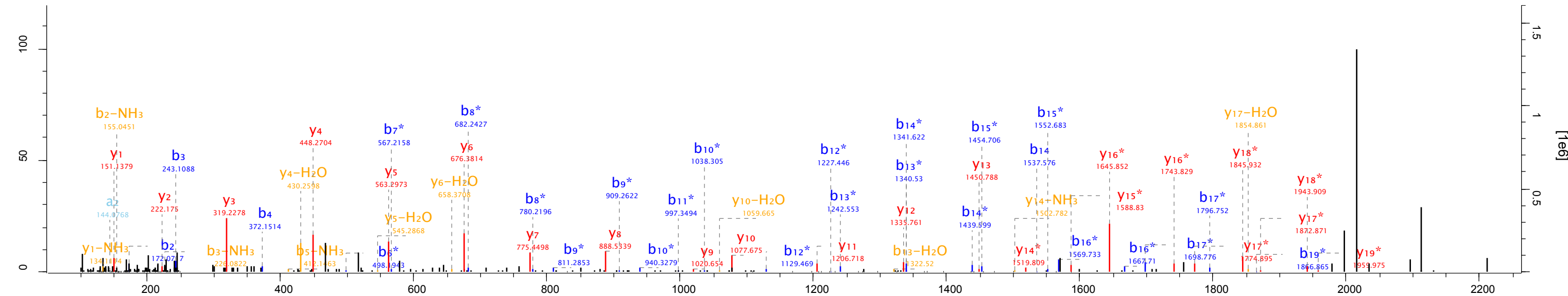
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y₁₆*
y₁₅*
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y₁₃
y₁₂
y₁₁*
y₁₀*
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10748 Method FTMS; HCD Score 221.3 m/z 1038.75 Gene names USP10

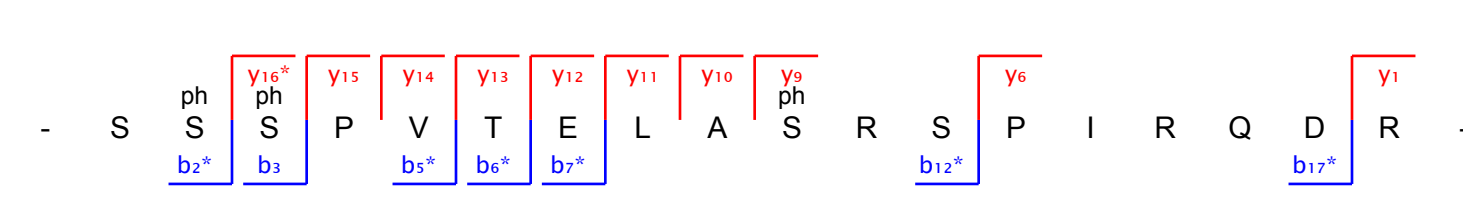
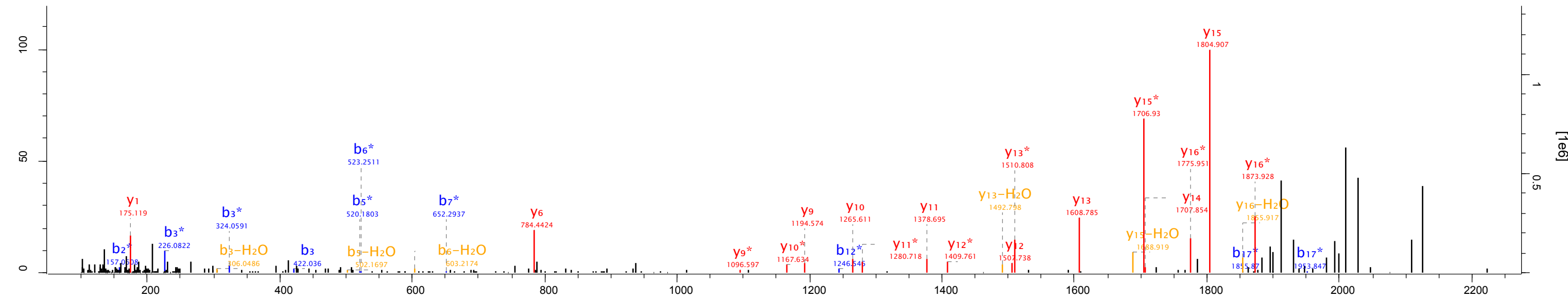


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11048 Method FTMS; HCD Score 234.88 m/z 1155.93 Gene names CDK12

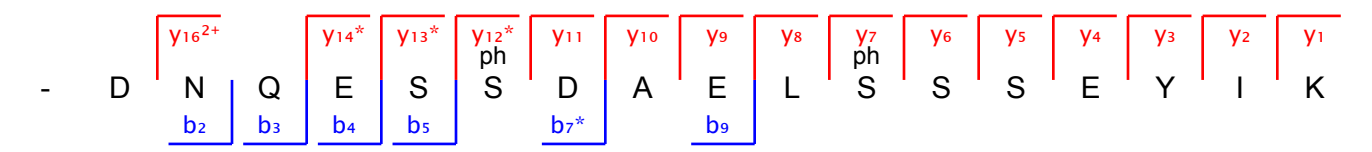
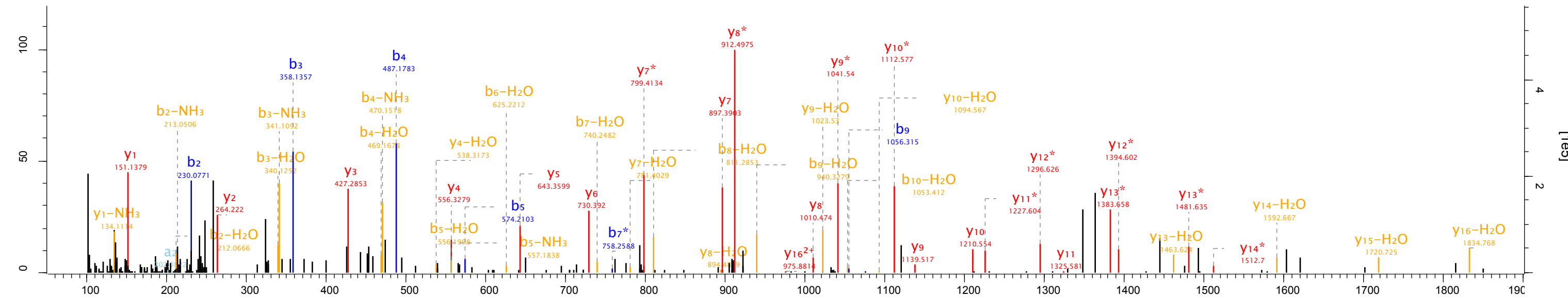




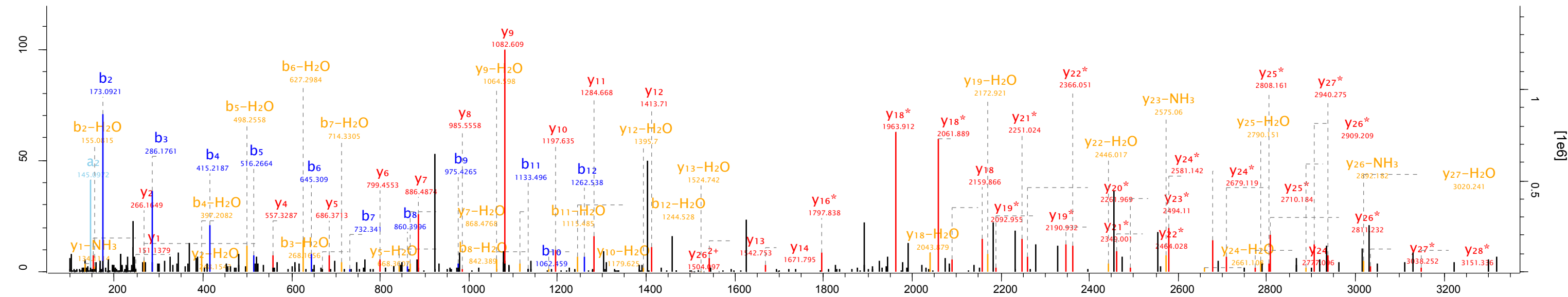
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11328 Method FTMS; HCD Score 96.35 m/z 742.98 Gene names SRRM2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11428 Method FTMS; HCD Score 158.94 m/z 1033.4 Gene names CHAMP1

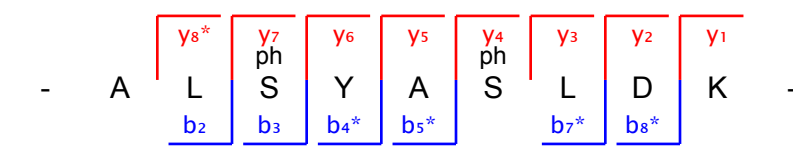
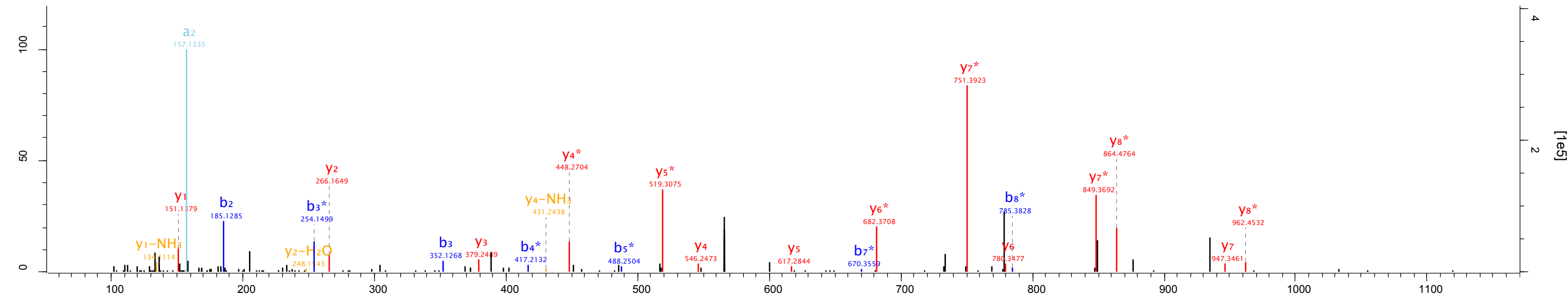


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 Scan: 11778 Method: FTMS; HCD Score: 190.2 m/z: 1141.46 Gene names: NES

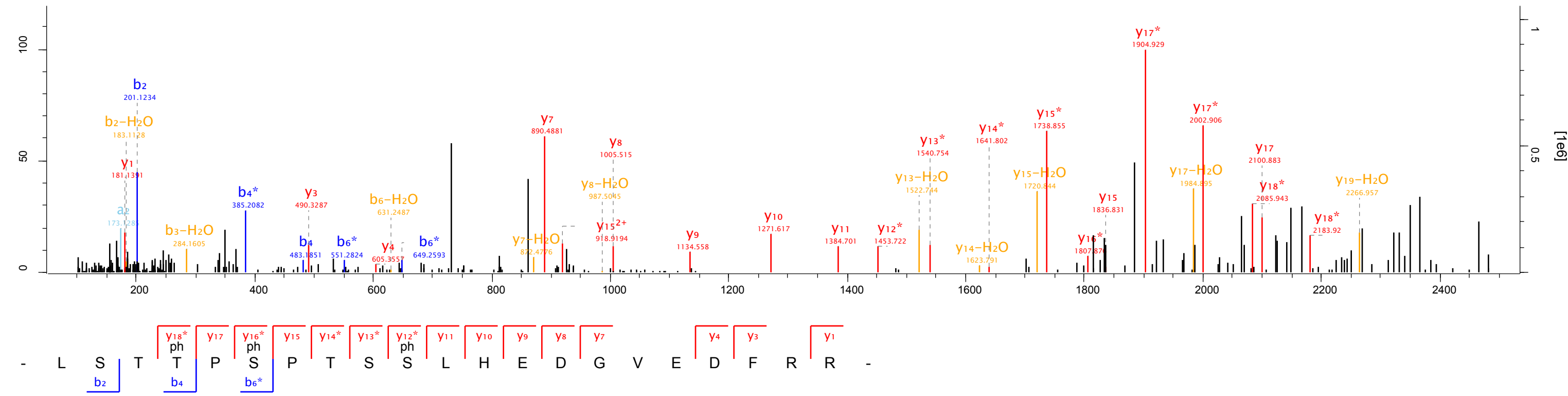


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 b2 b3 b4 b5 b6 b7 b8 b9 b10 b11 b12 y1 y2 y3 y4 y5 y6 y7 y8 y9 y10 y11 y12 y13 y14 y16* y18* y18* y19* y20* y21* y22* y23* y24* y25* y26* y27* y28*

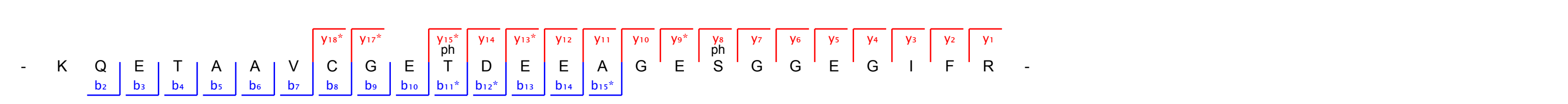
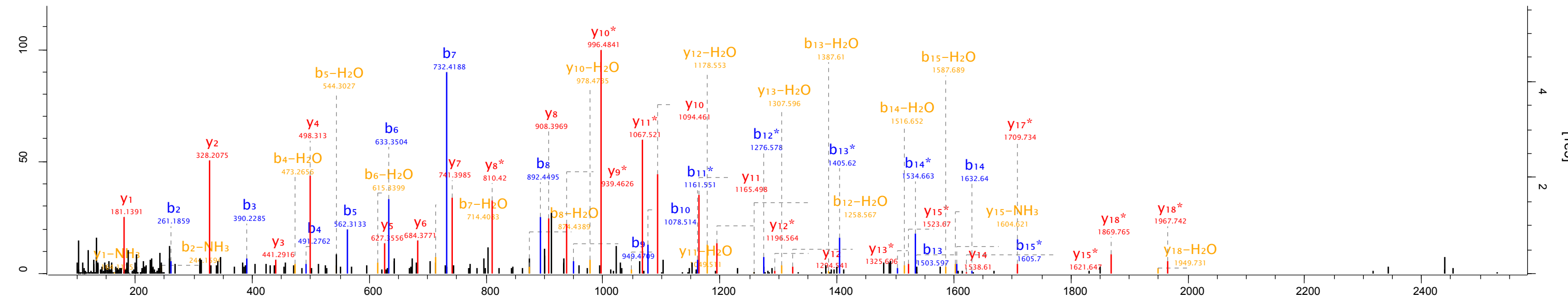
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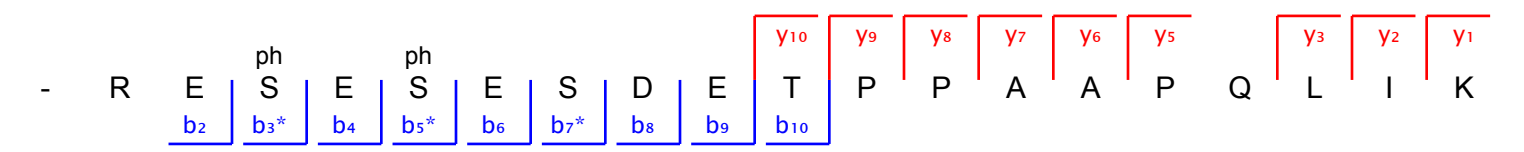
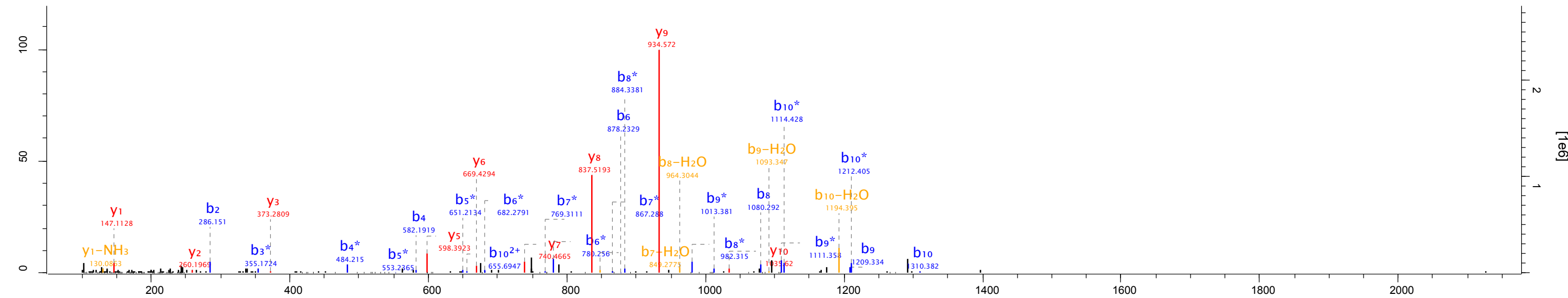
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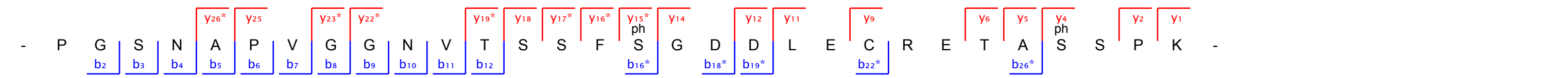
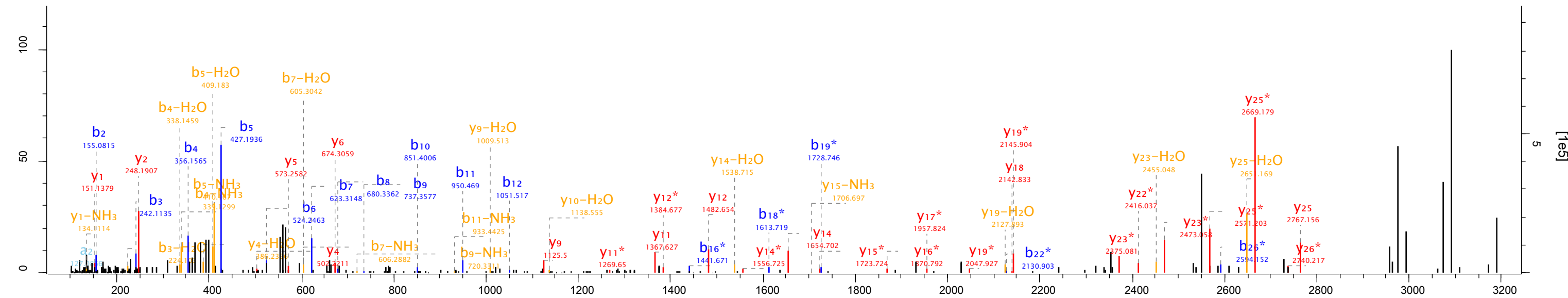
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12398 Method FTMS; HCD Score 99.72 m/z 748.99 Gene names DKC1

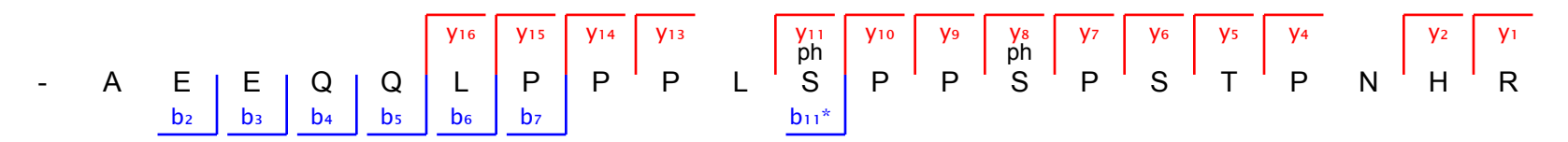
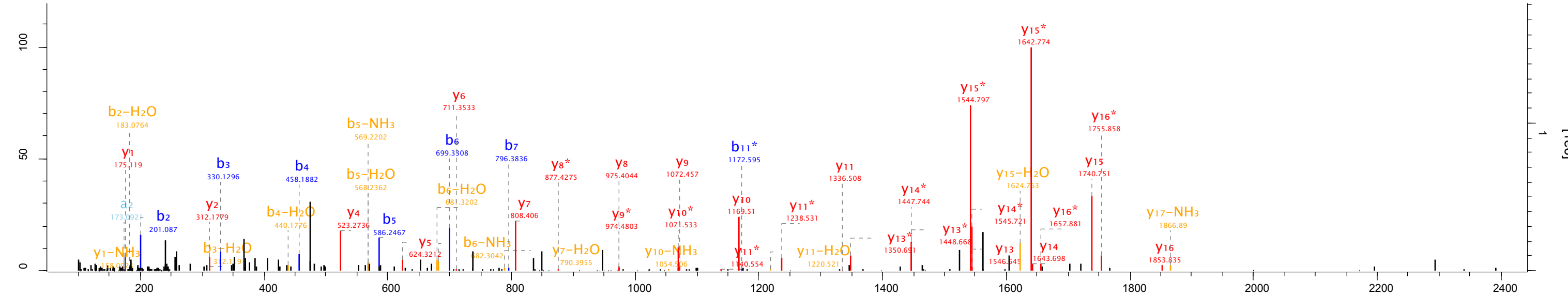


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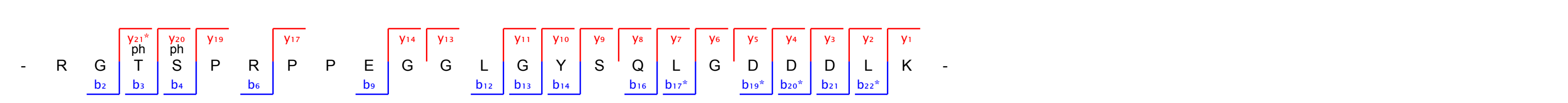
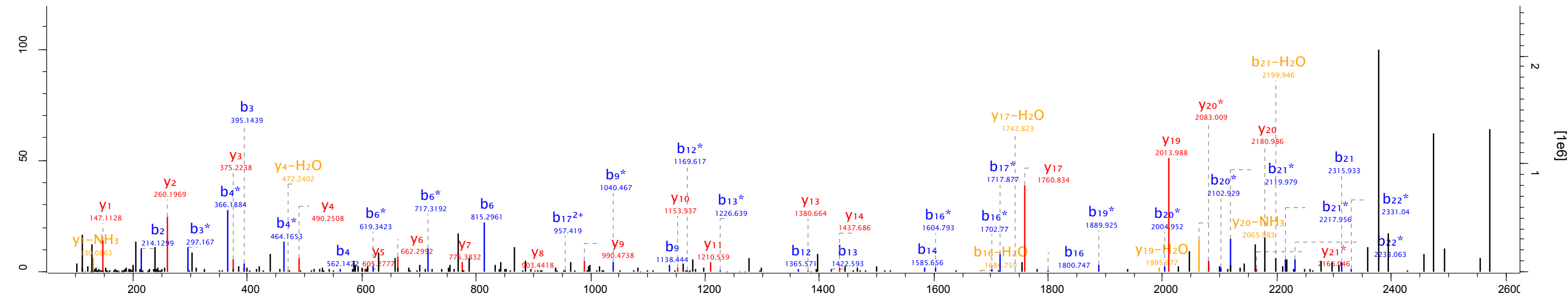


Raw file Scan Method Score m/z Gene names

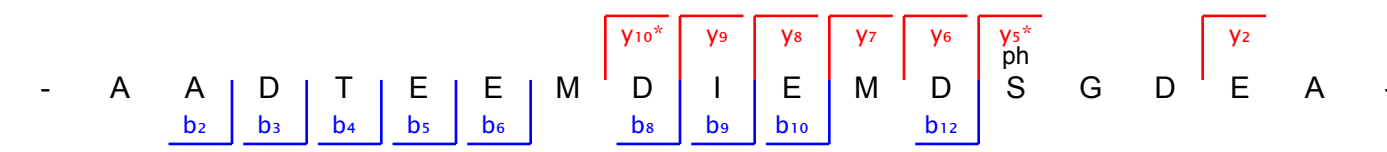
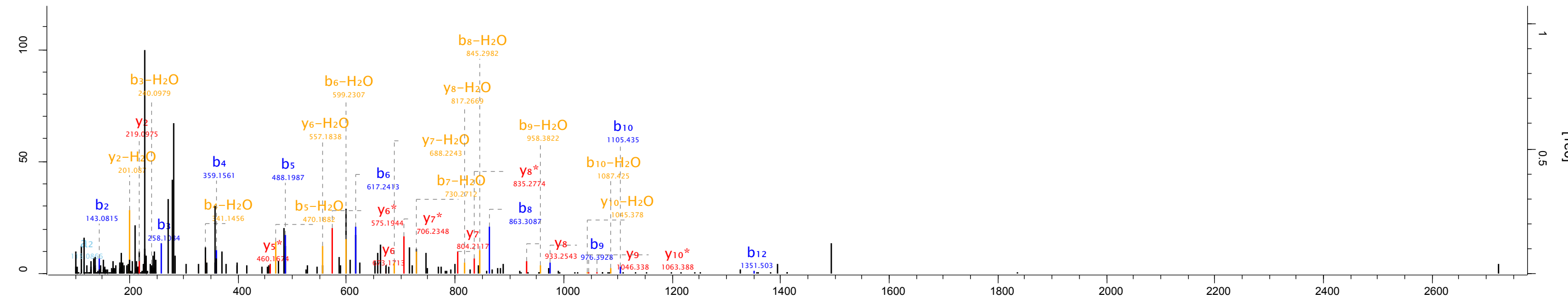
20171215_MaS_33SR_LMH_phospho2_03 12828 FTMS; HCD 148.35 813.7 MPRIP



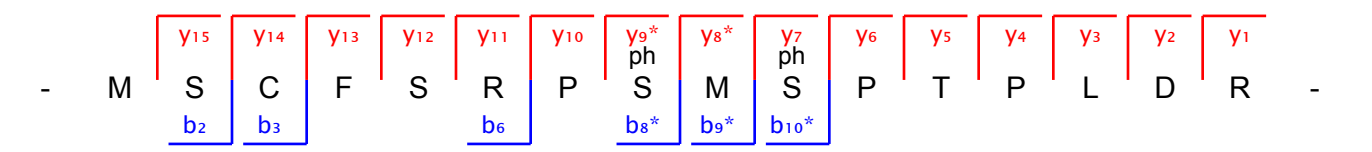
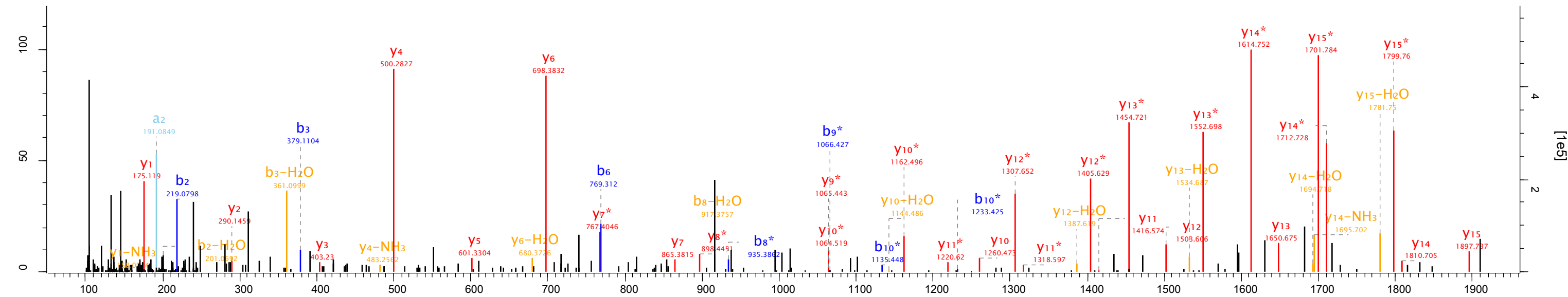
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13188 Method: FTMS; HCD Score: 141.82 m/z: 859.38 Gene names: CDK11A;CDK11B;CDC2L1



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 13348 Method: FTMS; HCD Score: 105.02 m/z: 954.82 Gene names: MBD2

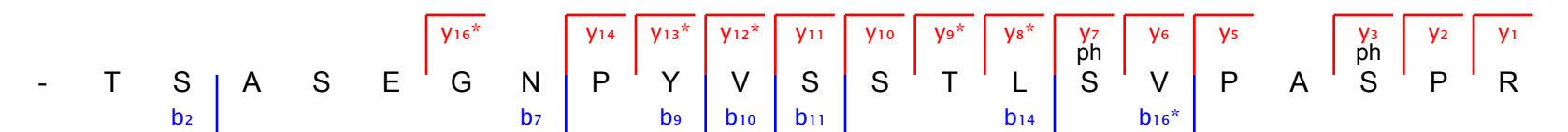
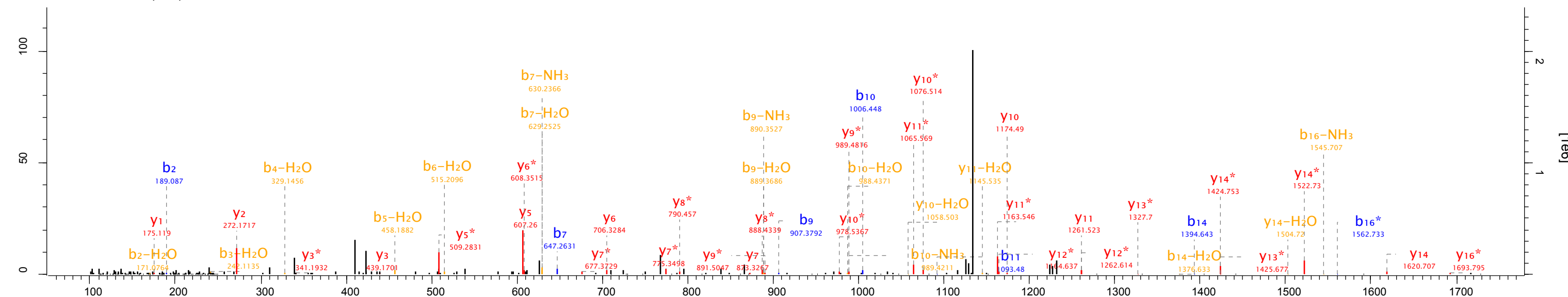


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 Scan: 13518 Method: FTMS; HCD Score: 171.08 m/z: 676.93 Gene names: SRRM2

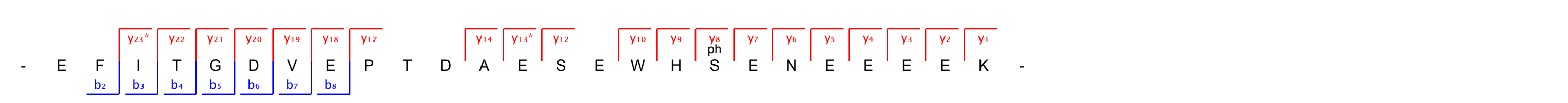
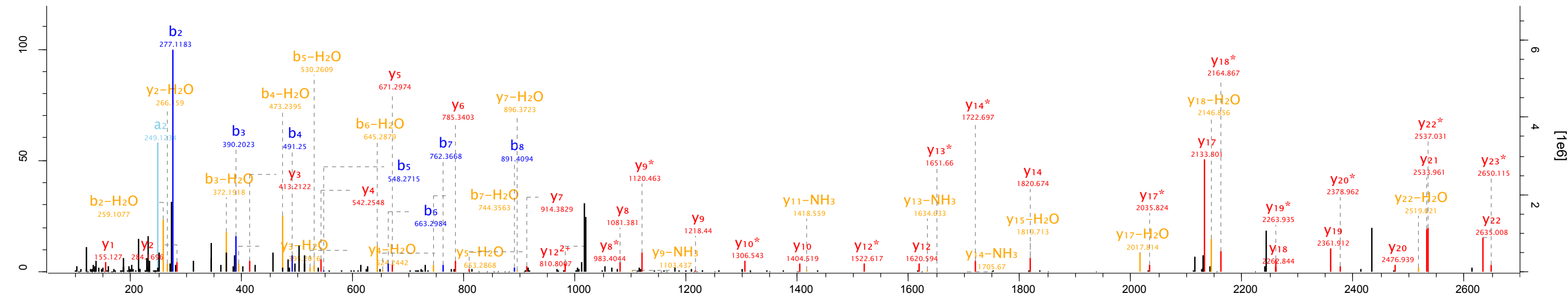


Raw file
20171215_MaS_33SR_LMH_phospho2_03

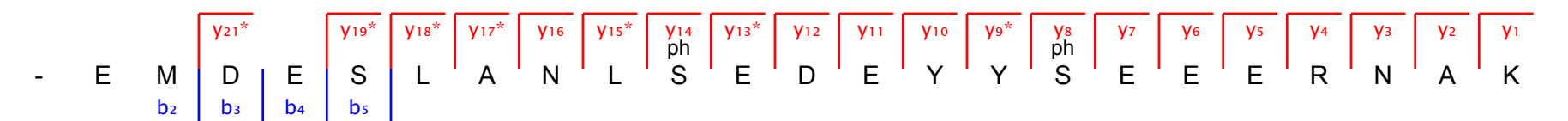
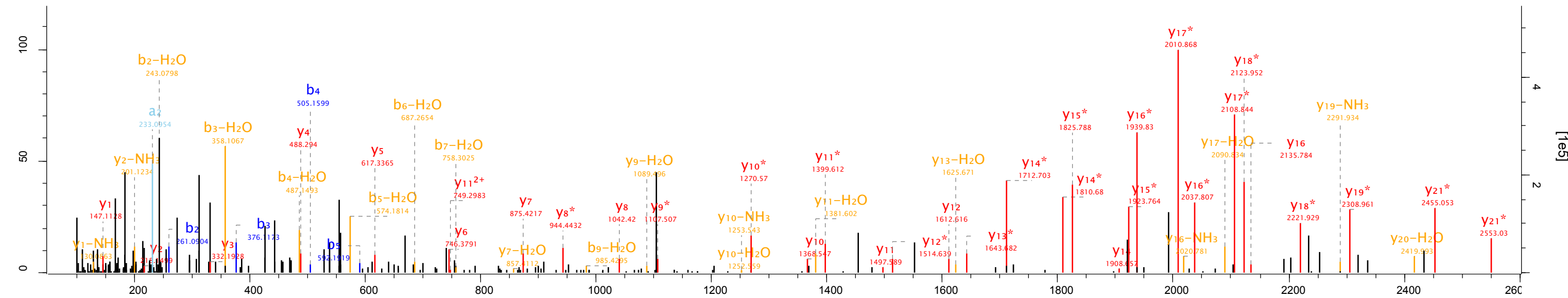
Scan 13578 Method FTMS; HCD Score 97.91 m/z 1133.99 Gene names PHLDB2



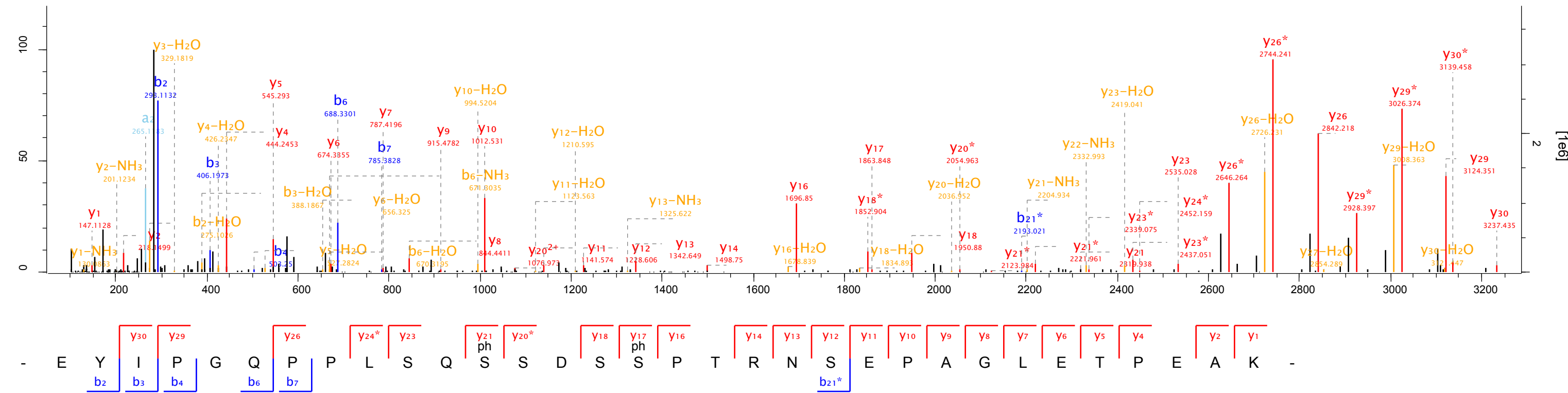
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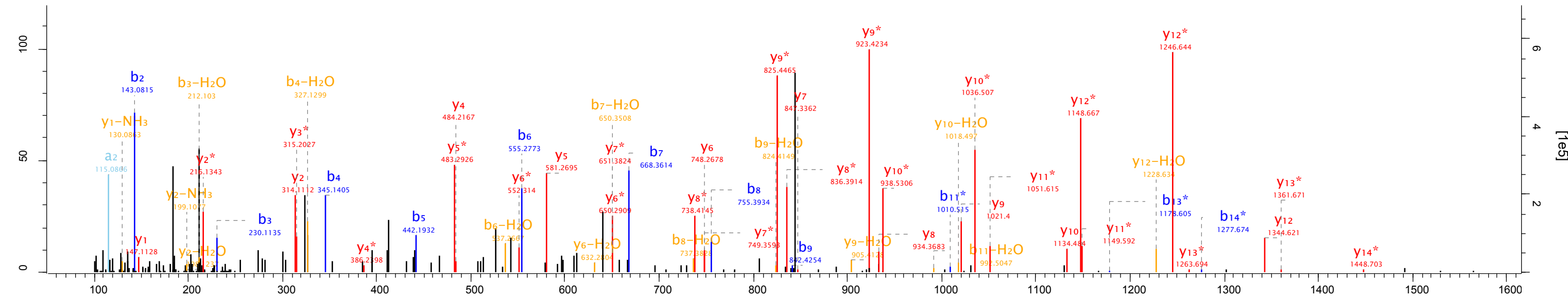


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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14828 Method FTMS; HCD Score 185.65 m/z 1177.52 Gene names EPRS



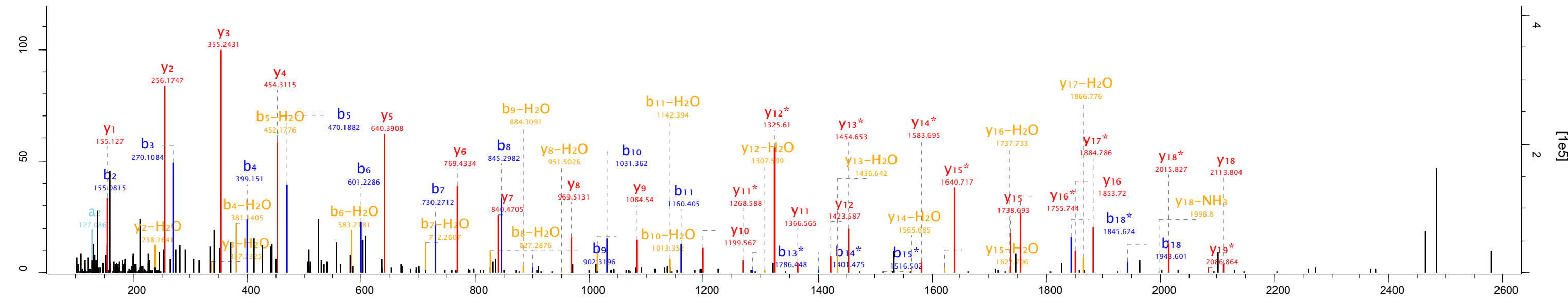


- A A S D P L L S S V S P A V S K -

b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ b₁₁* b₁₃* b₁₄*

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

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14888 Method FTMS; HCD Score 286.42 m/z 1292.49 Gene names EHD2

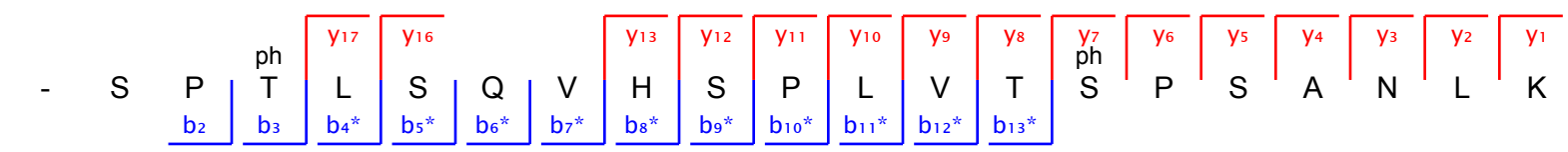
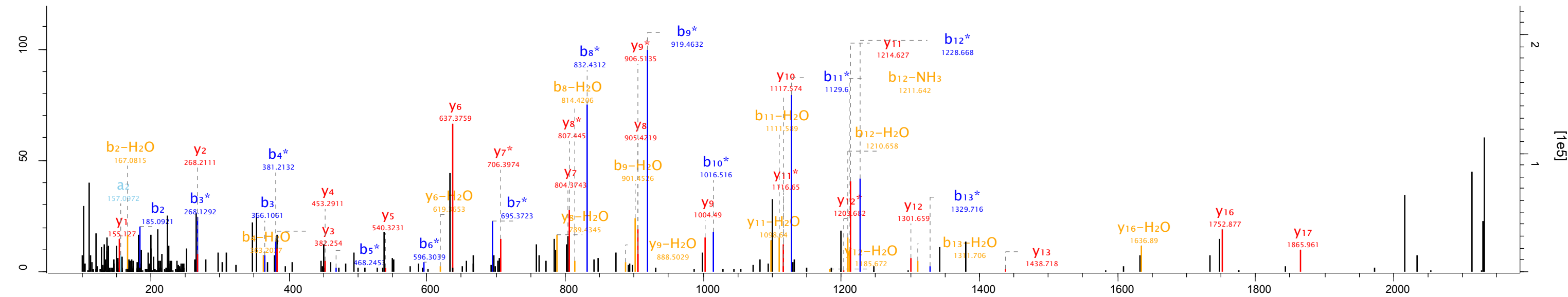


- G P D E A M E D G E E G S D D E A E W V V T K -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
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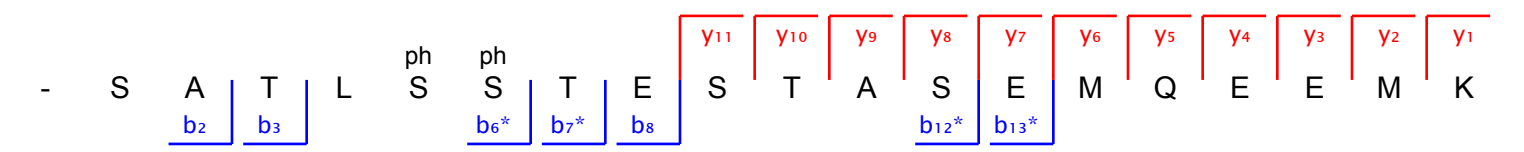
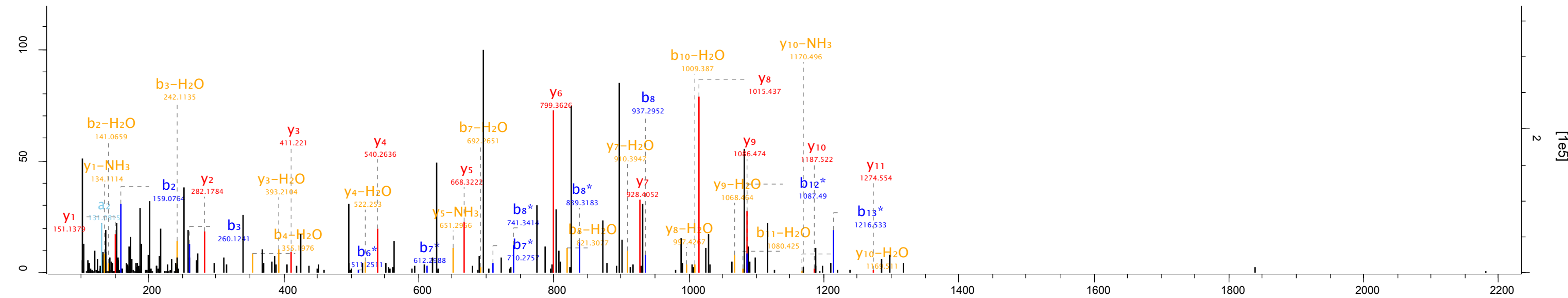
y₁₉*
y₁₈
y₁₇*
y₁₆
y₁₅
y₁₄*
y₁₃*
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
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Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15068 Method FTMS; HCD Score 119.8 m/z 744.36 Gene names BCL9L

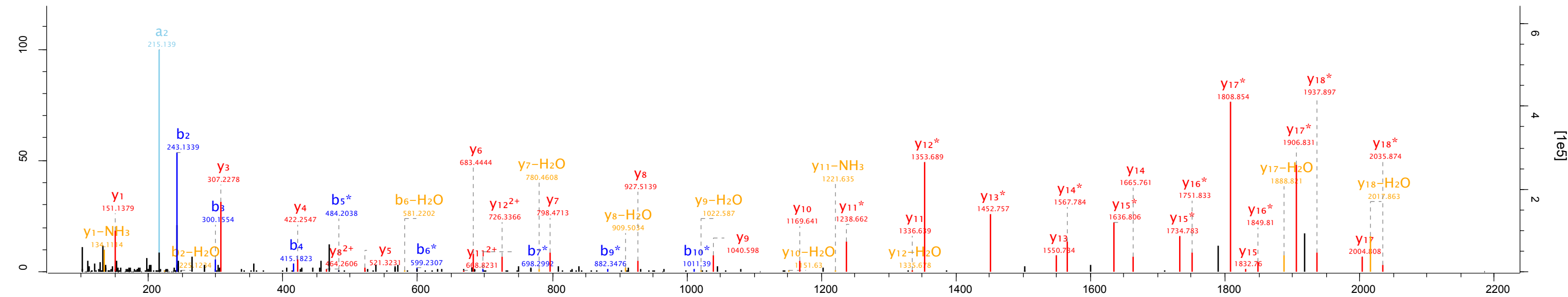


Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 15218 Method FTMS; HCD Score 59.72 m/z 737.95 Gene names AKAP12



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 15318 Method: FTMS; HCD Score: 173.86 m/z: 749.98 Gene names: MYO18A

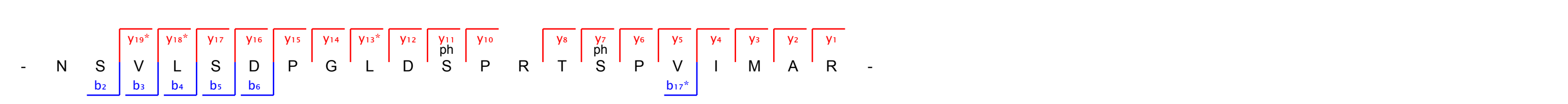
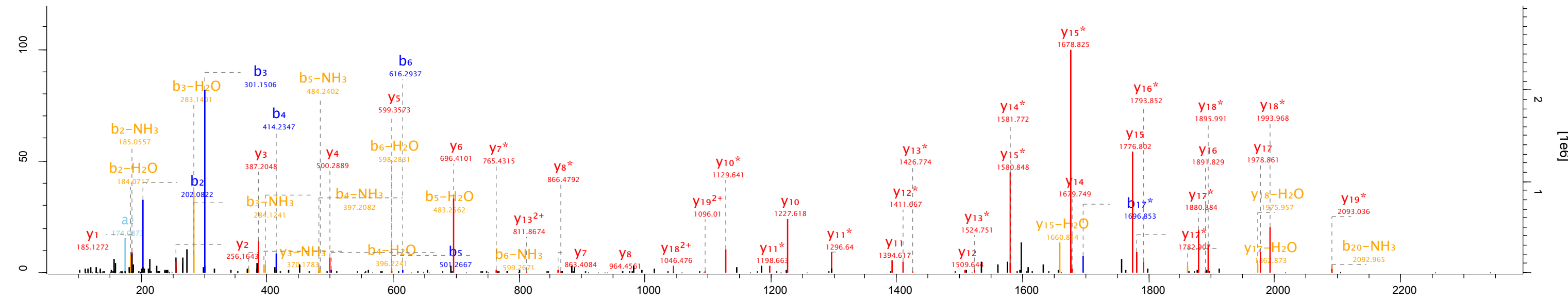


- L E G D S D V D S E L E D R V D G V K -

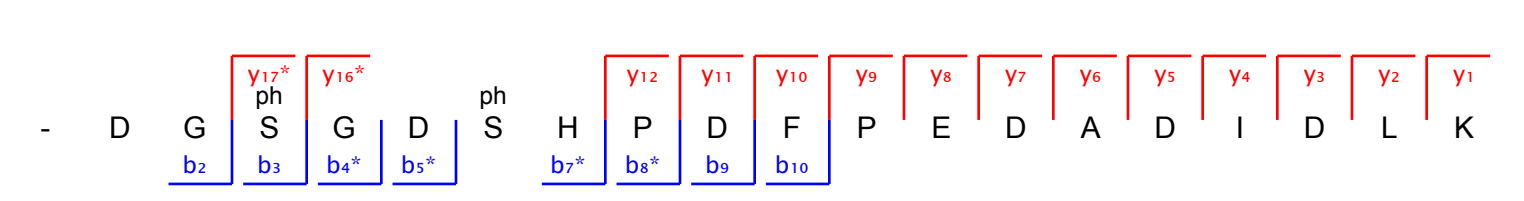
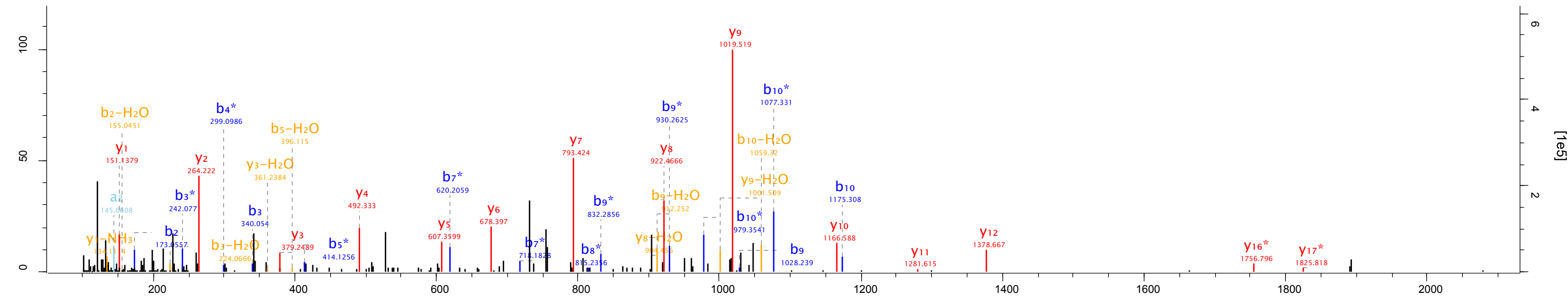
Fragmentation mapping (b and y ions) is shown below the sequence:

- b2 (E), b3 (G), b4 (D), b5* (S), b6* (D), b7* (V), b9* (S), b10* (E)
- y1 (K), y3 (G), y4 (D), y5 (V), y6 (R), y7 (D), y8 (E), y9 (L), y10 (E), y11 (S), y12* (D), y13 (V), y14 (D), y15 (S), y16* (D), y17 (S), y18* (E)

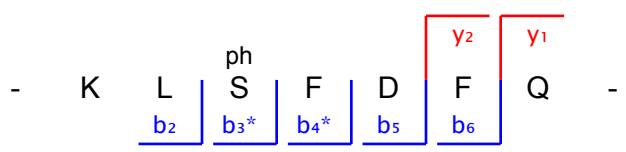
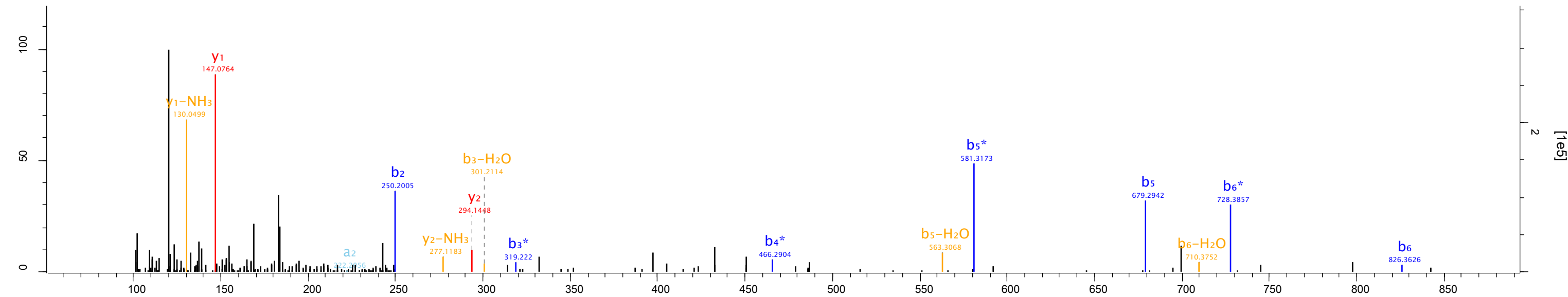
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15878 Method FTMS; HCD Score 217.01 m/z 798.37 Gene names ARHGEF11



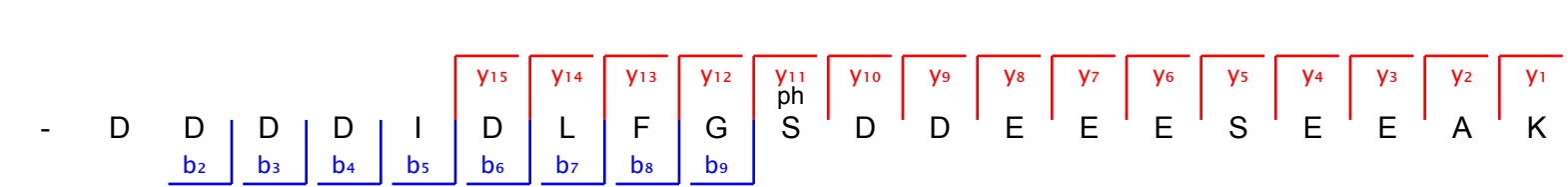
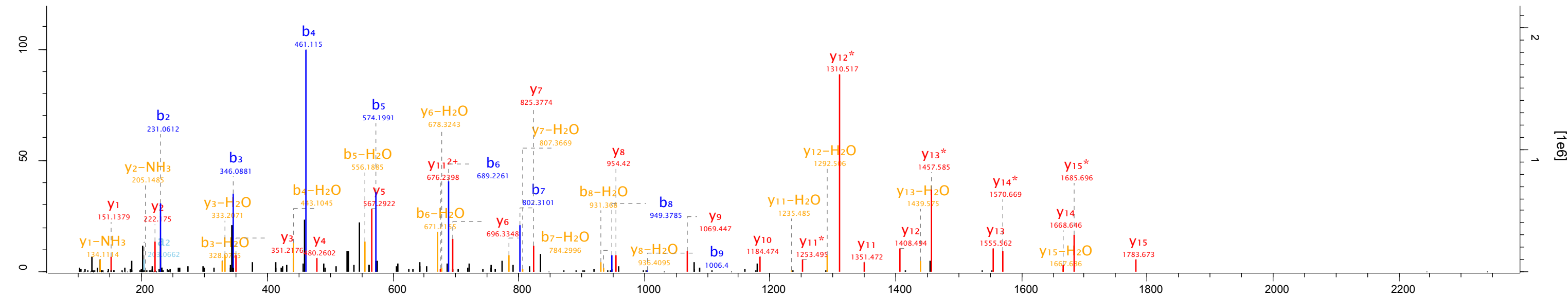
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15918 Method FTMS; HCD Score 107.47 m/z 731.94 Gene names PPID



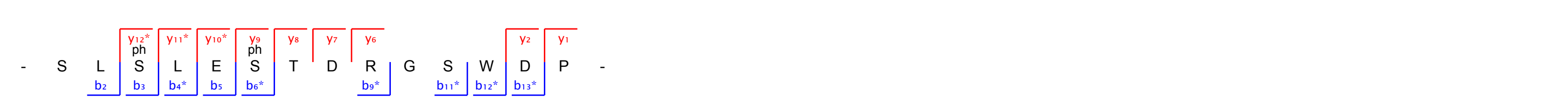
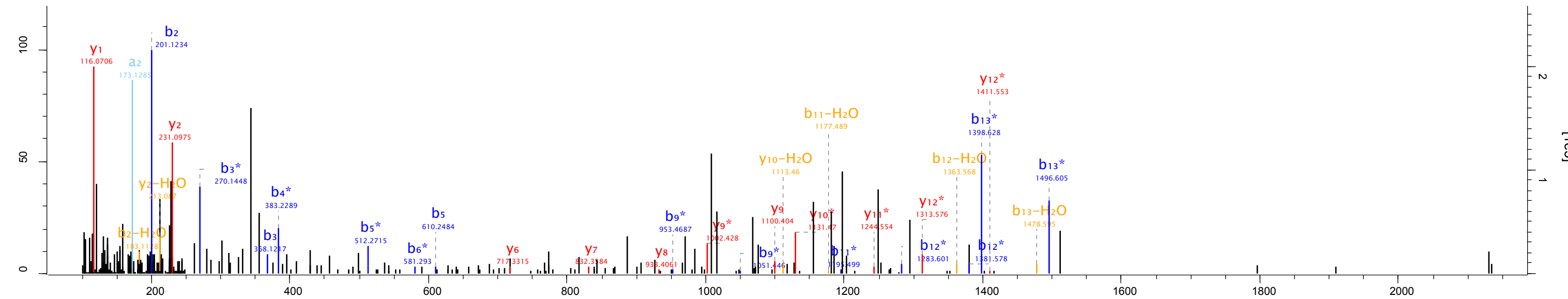
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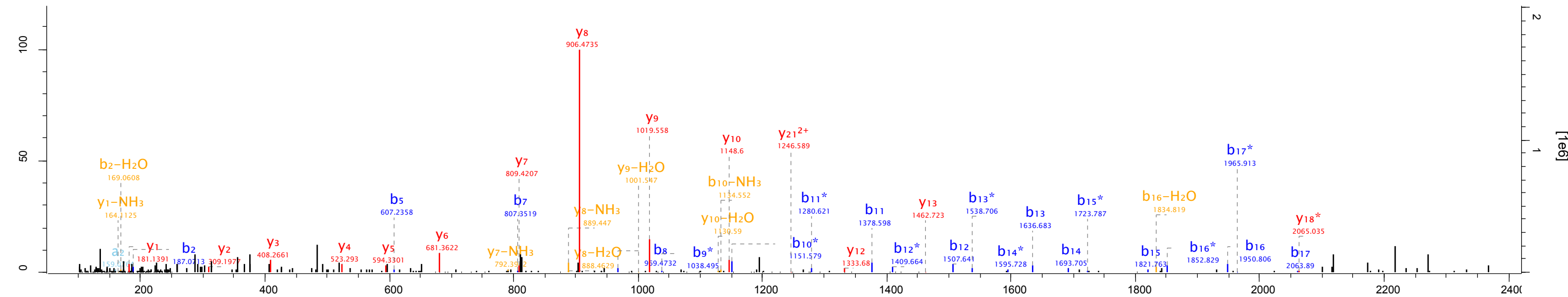


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16278 Method FTMS; HCD Score 205.9 m/z 1178.93 Gene names EEF1B2



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16358 Method FTMS; HCD Score 78.42 m/z 855.33 Gene names CDC42BPA

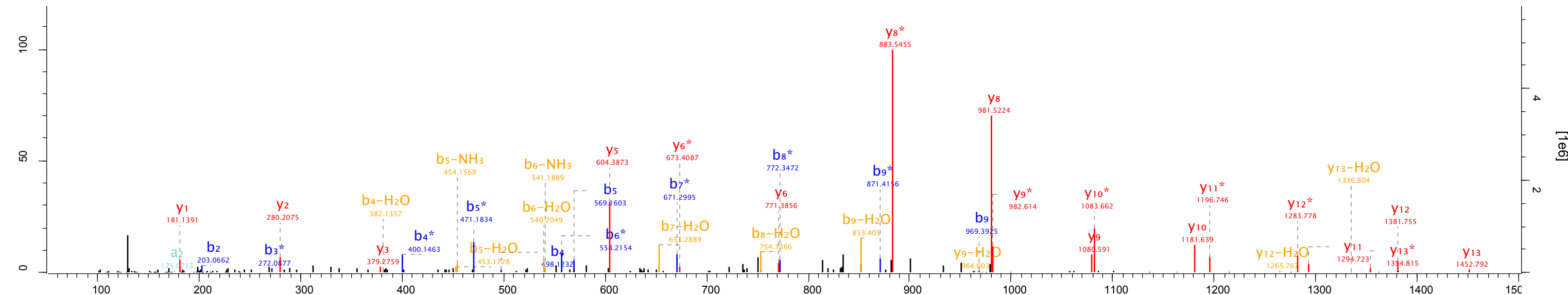




- G E Y Q E S L R S L E E E G Q E L P Q S A D V Q R -

Annotations below the sequence:

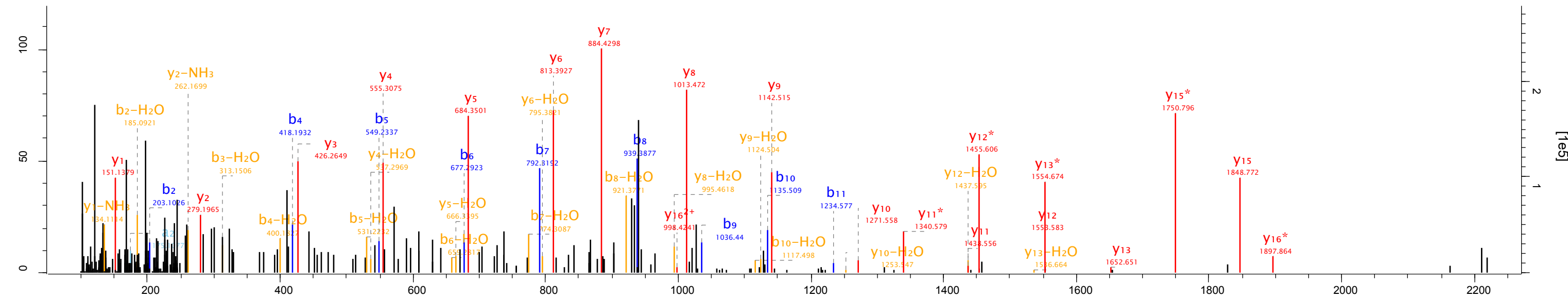
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- y_{18}^* above R (position 6)
- b_2 below E (position 2)
- b_5 below E (position 5)
- b_7 below L (position 7)
- b_8 below R (position 6)
- b_9^* below S (position 8)
- b_{10}^* below L (position 9)
- b_{11} below E (position 10)
- b_{12} below E (position 11)
- b_{13} below E (position 12)
- b_{14} below G (position 13)
- b_{15} below Q (position 14)
- b_{16} below E (position 15)
- b_{17} below L (position 16)
- y_{13} above E (position 12)
- y_{12} above G (position 13)
- y_{10} above E (position 15)
- y_9 above L (position 16)
- y_8 above P (position 17)
- y_7 above Q (position 18)
- y_6 above S (position 19)
- y_5 above A (position 20)
- y_4 above D (position 21)
- y_3 above V (position 22)
- y_2 above Q (position 23)
- y_1 above R (position 24)



- S D S ph Q A S L T V P L S ph P Q V V R -

b₂ b₃* b₄ b₅ b₆* b₇* b₈* b₉ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₆ y₅ y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16888 Method FTMS; HCD Score 147.41 m/z 930.39 Gene names TFIP11

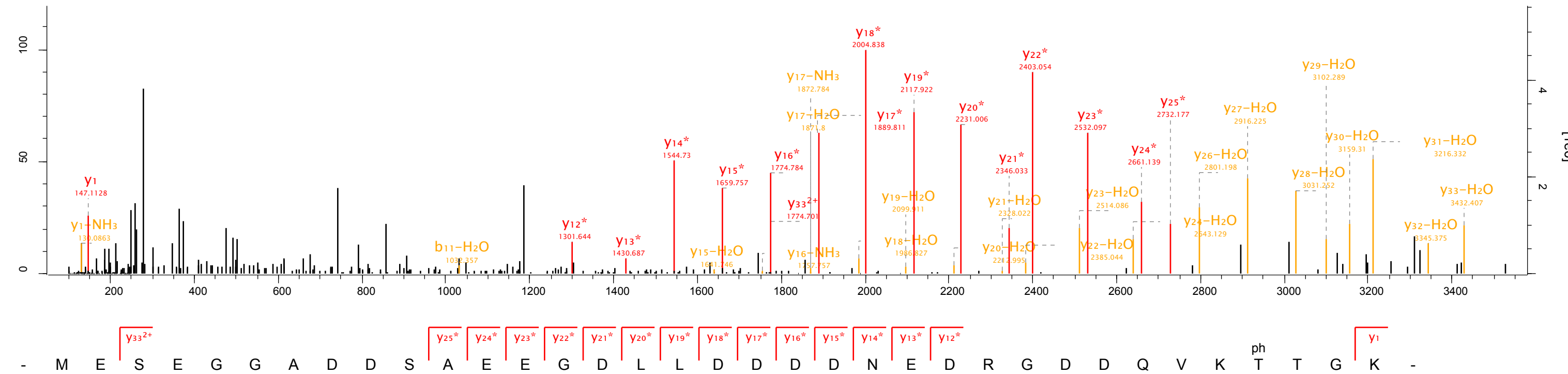


- T T Q S M Q D F P V V D S E E E A E E E F Q K -

b₂
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀
b₁₁
y₁₆*
y₁₅
y₁₃
y₁₂
y₁₁
ph
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

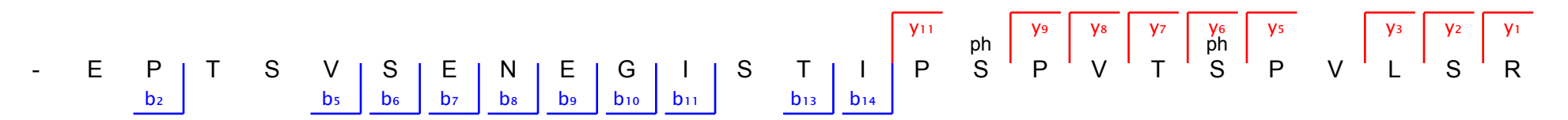
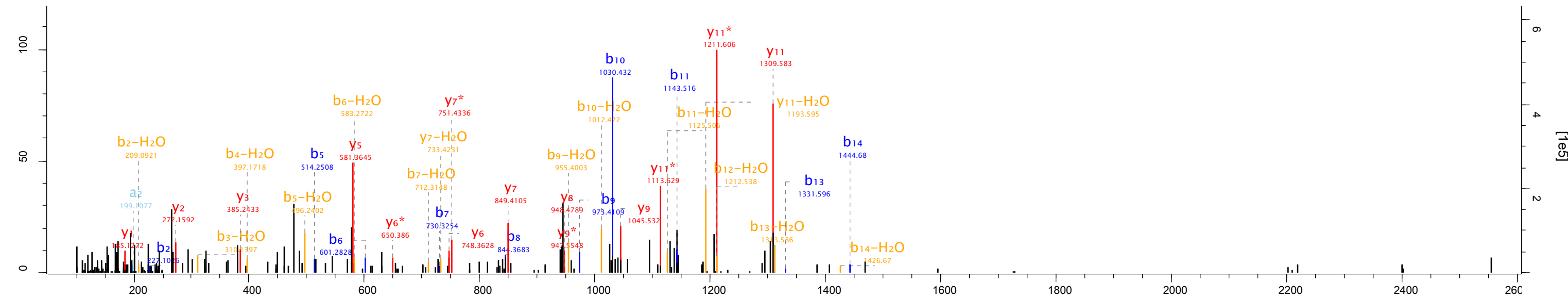
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 16918 Method FTMS; HCD Score 61.59 m/z 1270.17 Gene names HNRNPC

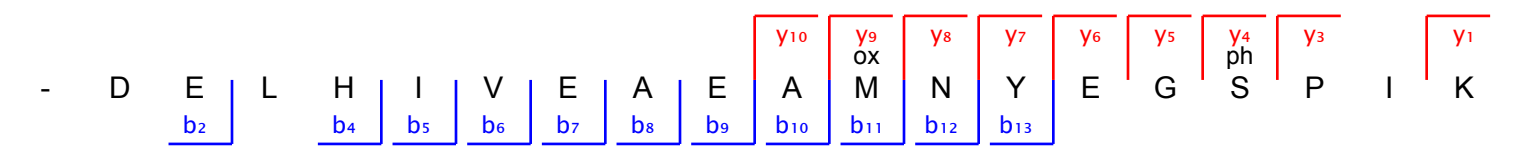
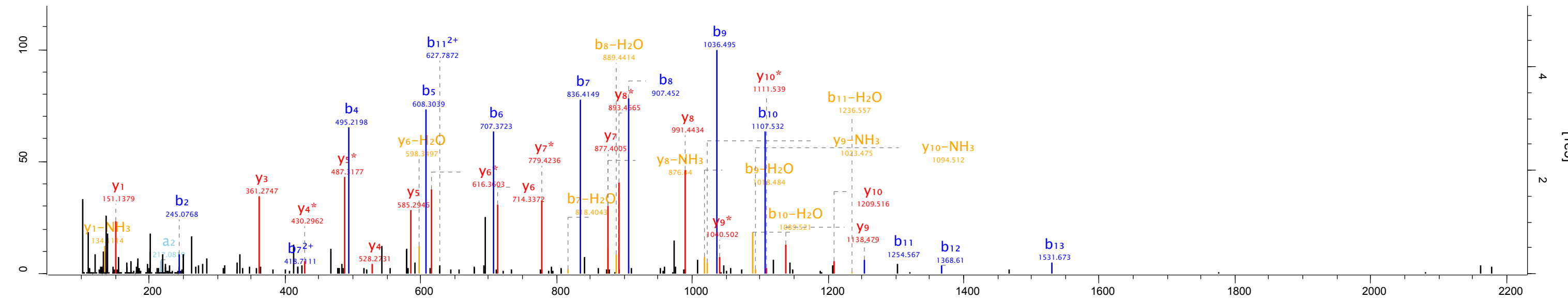


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20171215_MaS_33SR_LMH_phospho2_03

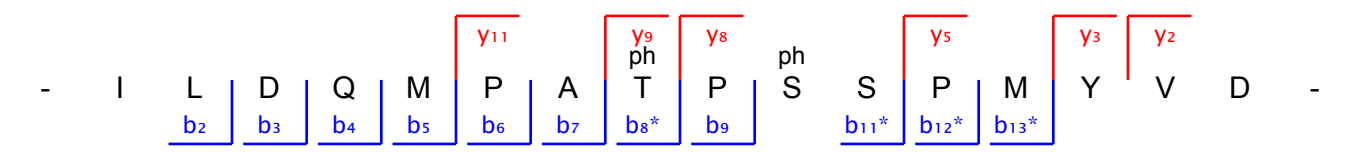
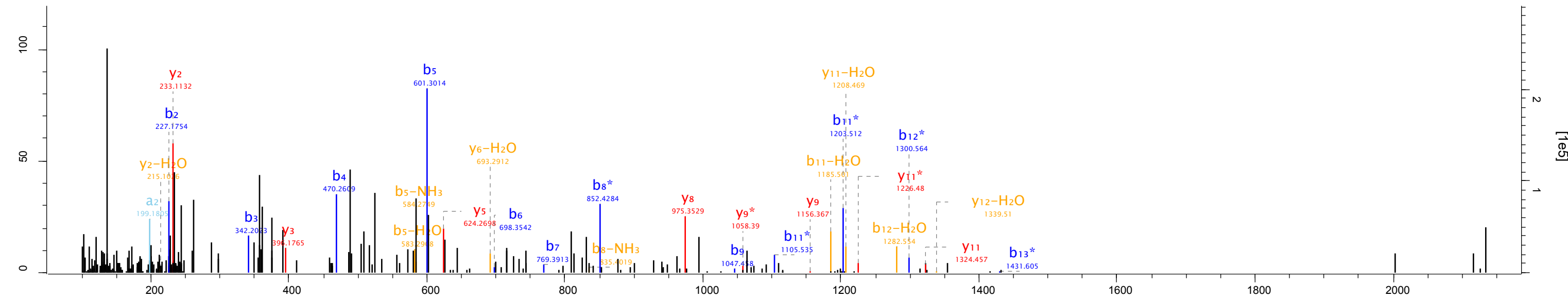
Scan 16928 Method FTMS; HCD Score 58.43 m/z 919.09 Gene names DDHD1



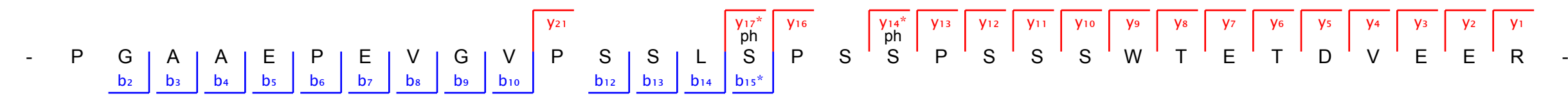
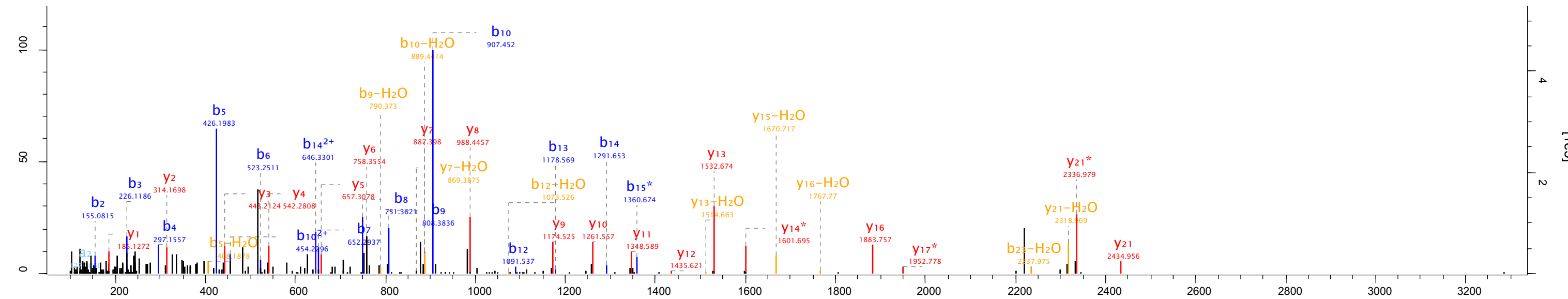
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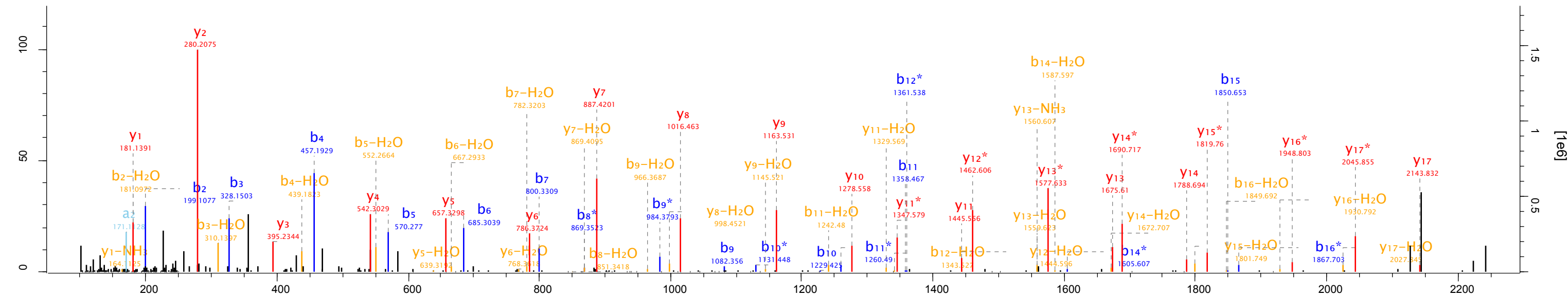
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 17238 Method FTMS; HCD Score 53.03 m/z 963.38 Gene names MAP2K4



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 17348 Method FTMS; HCD Score 112.68 m/z 1114.8 Gene names PDE12



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 17478 Method FTMS; HCD Score 397.8 m/z 1123.44 Gene names CTNNA1

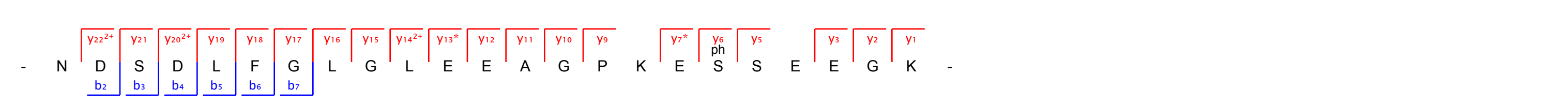
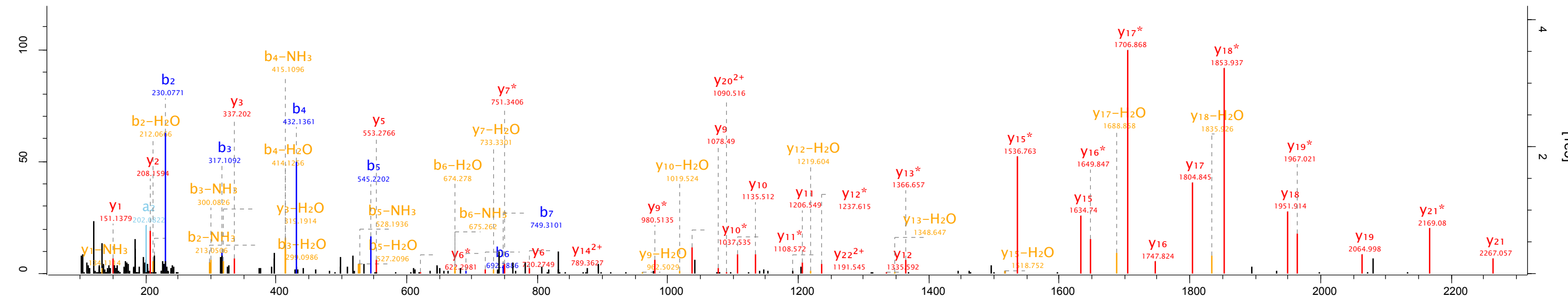


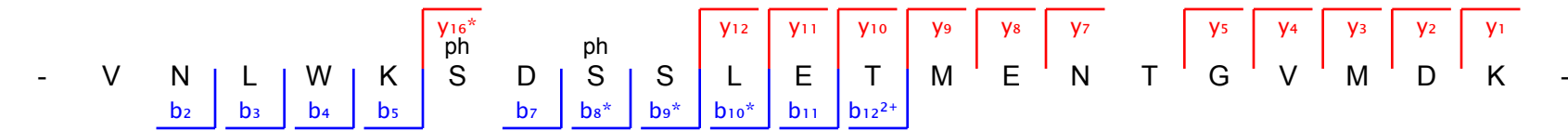
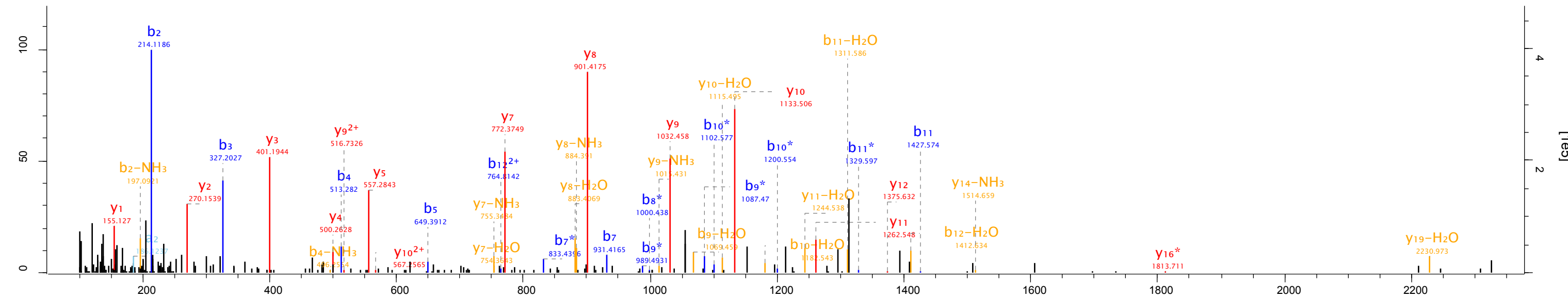
T P E E L D D S D F E T E D F D V R

b₂ b₃ b₄ b₅ b₆ b₇ b₈* b₉ b₁₀ b₁₁ b₁₂* b₁₄* b₁₅ b₁₆*

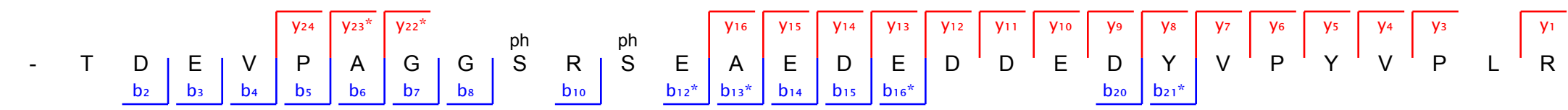
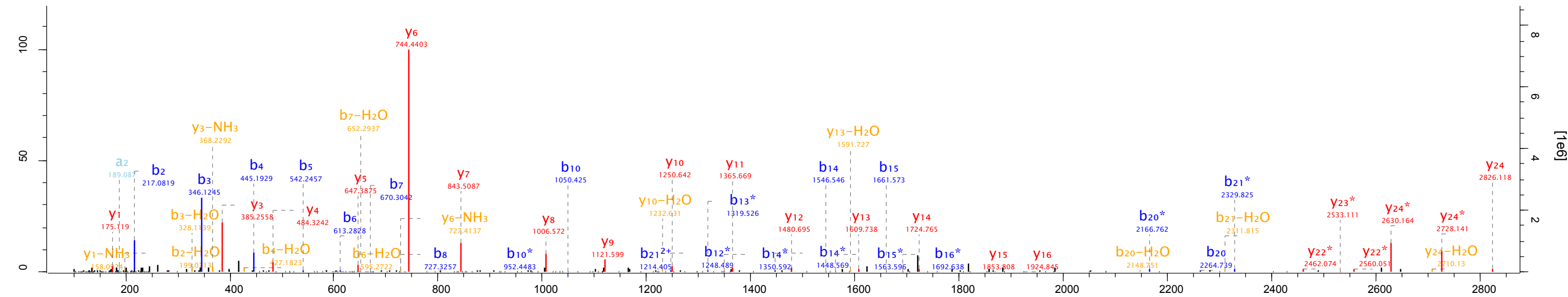
y₁₇ y₁₆* y₁₅* y₁₄ y₁₃ y₁₂* y₁₁ph y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 17608 Method: FTMS; HCD Score: 185.27 m/z: 833.05 Gene names: RABL6

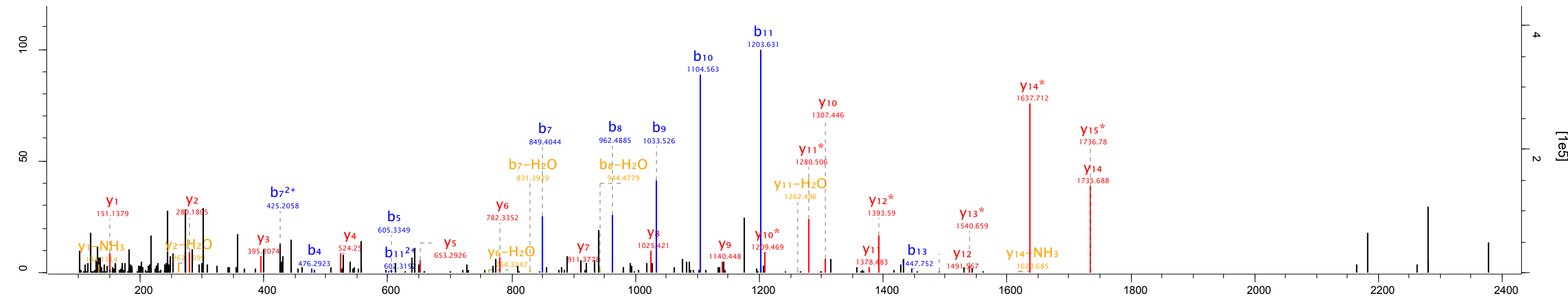




Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 17998 Method: FTMS; HCD Score: 125.43 m/z: 1091.11 Gene names: DDX41



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18228 Method FTMS; HCD Score 50.22 m/z 980.44 Gene names HERC2

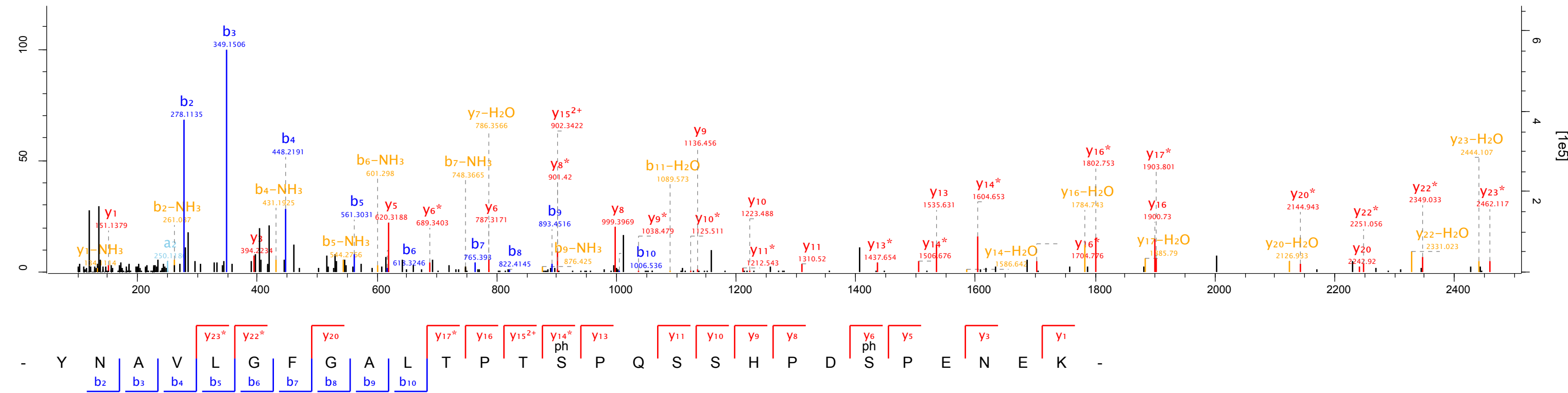


- I R A E E E D L A A V P F L A S D N E E E E D E K -

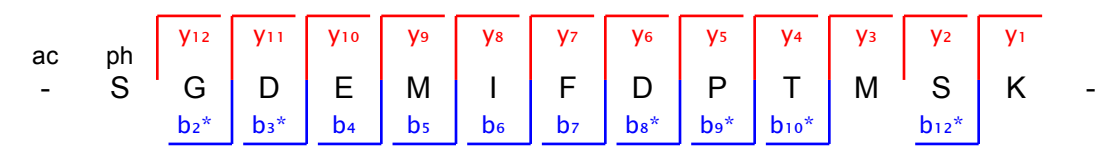
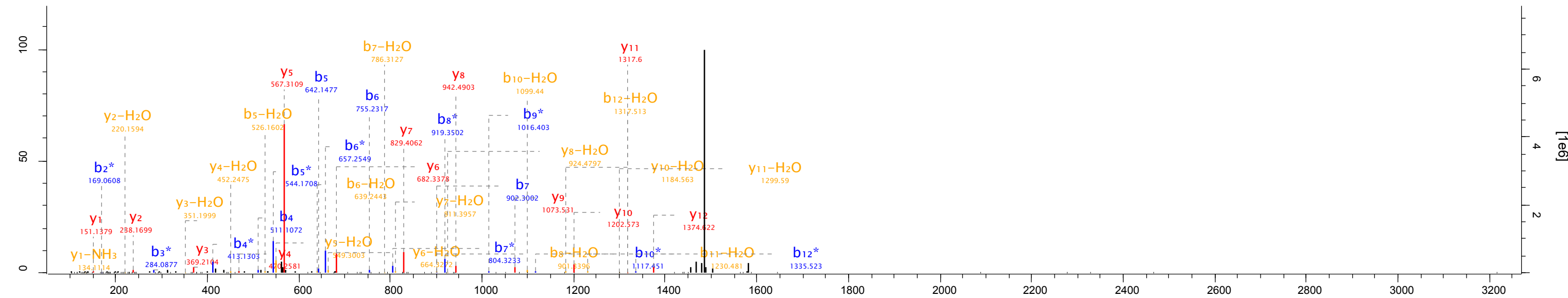
Fragmentation mapping (b and y ions) is shown below the sequence:

- b4: E
- b5: E
- b7: D
- b8: L
- b9: A
- b10: A
- b11: V
- b13: F
- y1: K
- y2: D
- y3: E
- y4: E
- y5: E
- y6: E
- y7: N
- y8: D
- y9: S
- y10: A
- y11: L
- y12: F
- y13: P
- y14: V
- y15: I

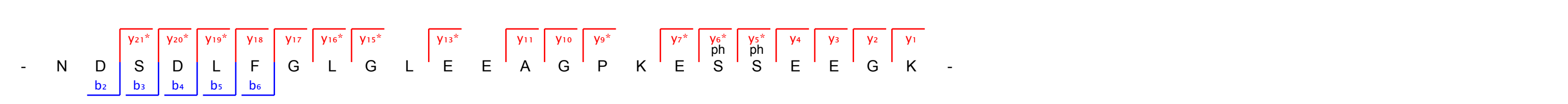
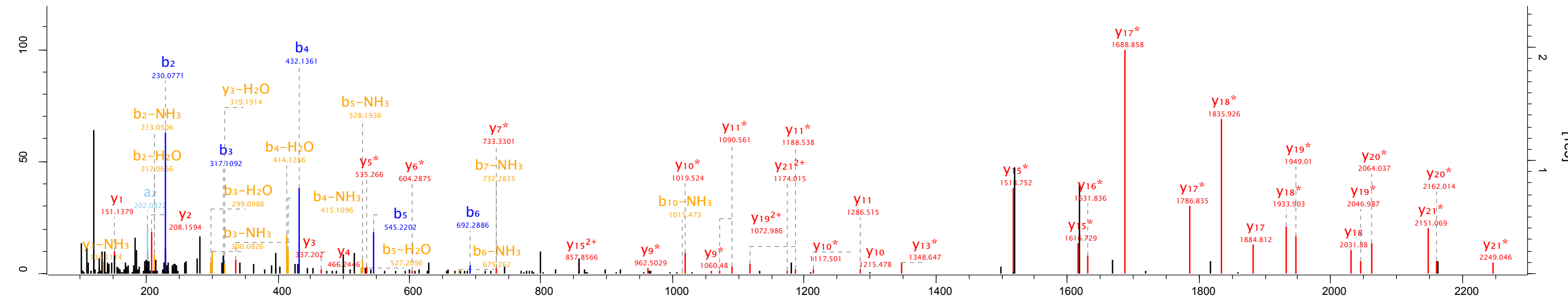
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18568 Method FTMS; HCD Score 126.33 m/z 1003.44 Gene names PHF21A



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 19038 Method: FTMS; HCD Score: 210.14 m/z: 1583.63 Gene names: EIF2S2



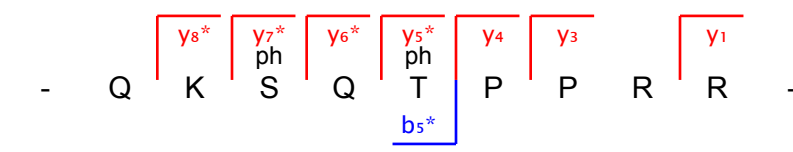
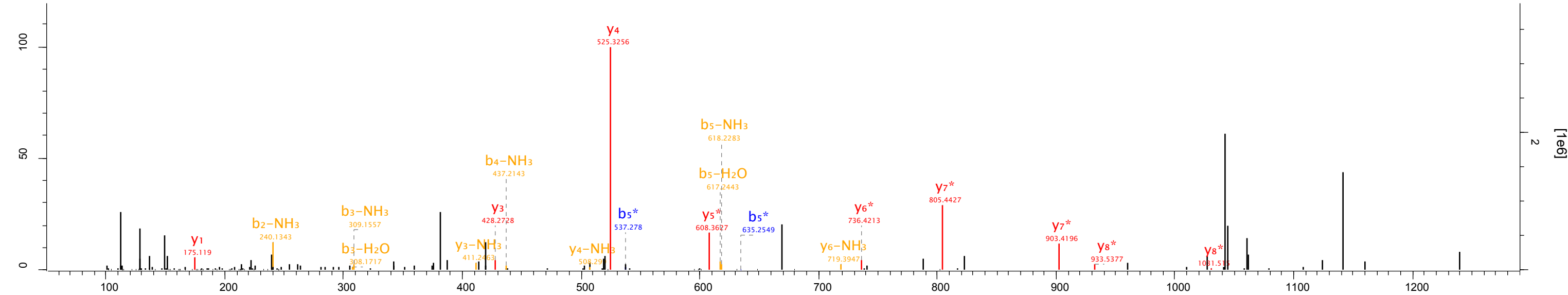
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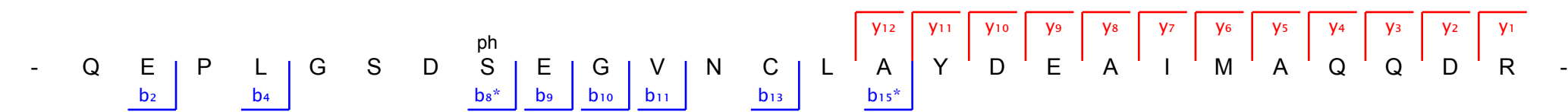
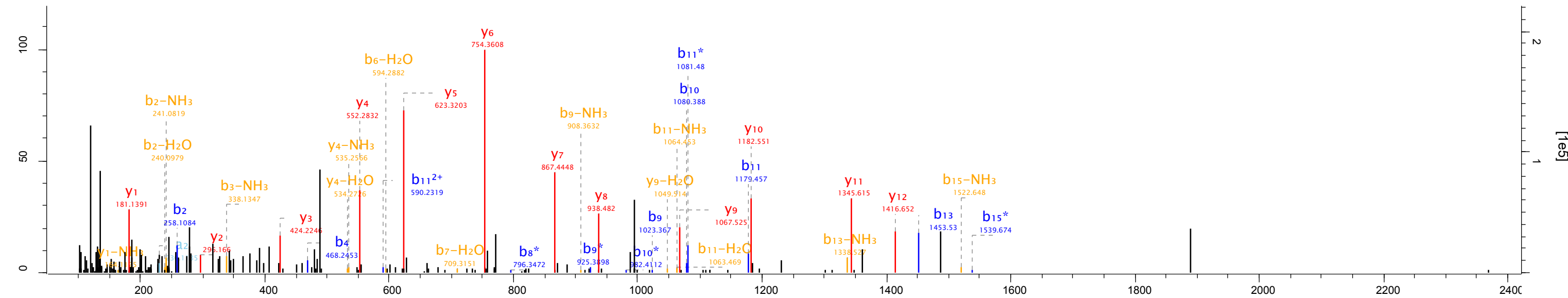


Raw file

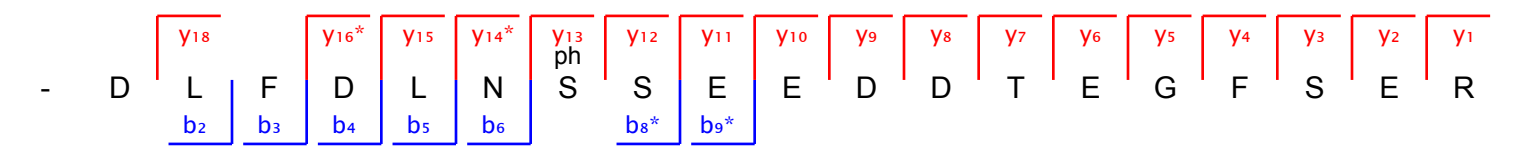
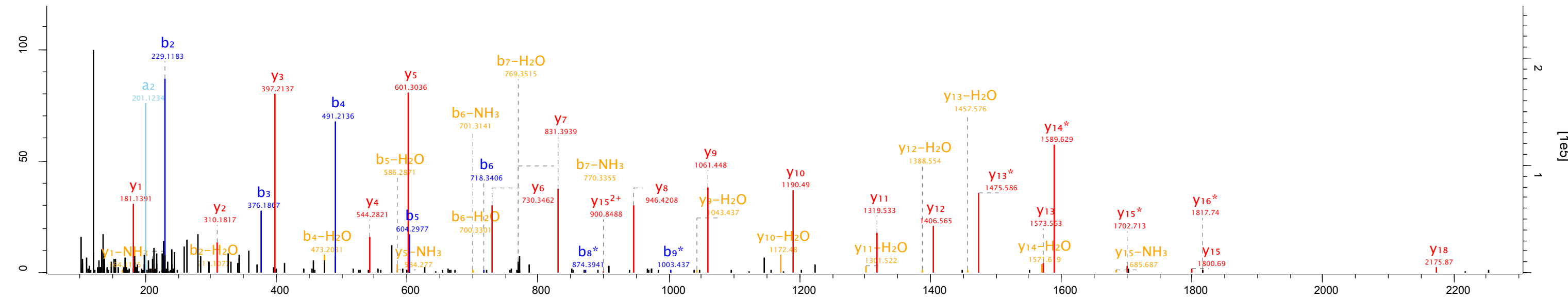
20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
1938	FTMS; HCD	59.16	419.85	SRRM2

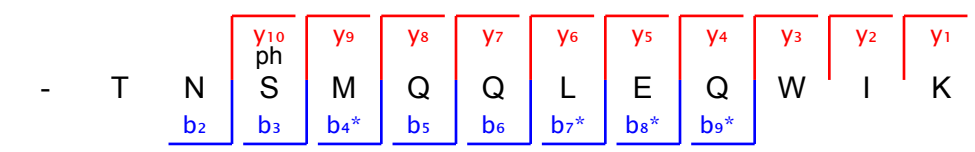
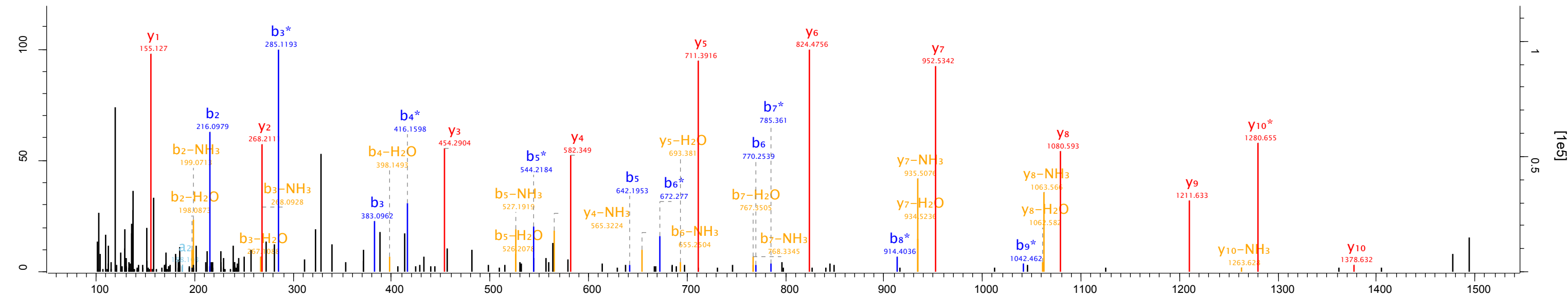




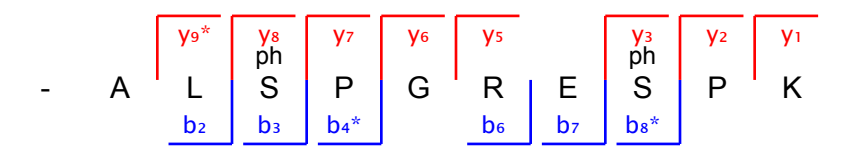
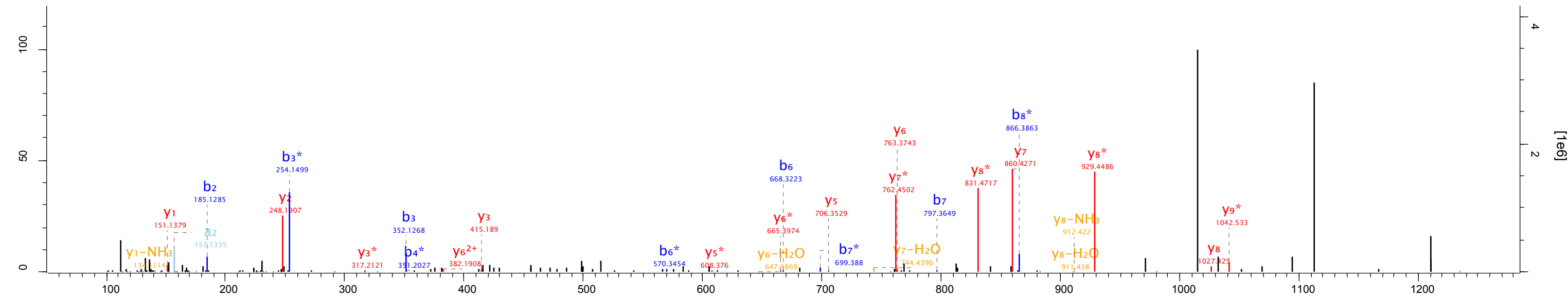
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 19568 Method: FTMS; HCD Score: 172.42 m/z: 1146.44 Gene names: NOC2L



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 19848 Method FTMS; HCD Score 199.58 m/z 797.87 Gene names PLEKHA5

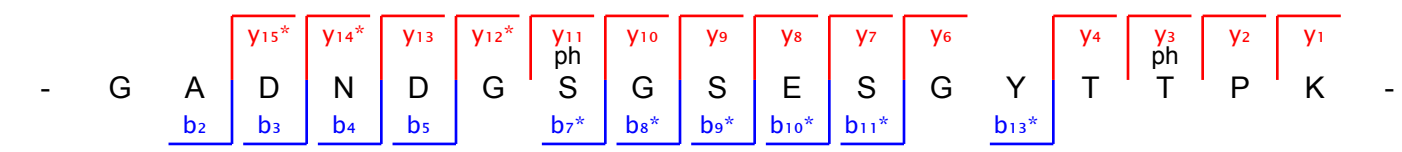
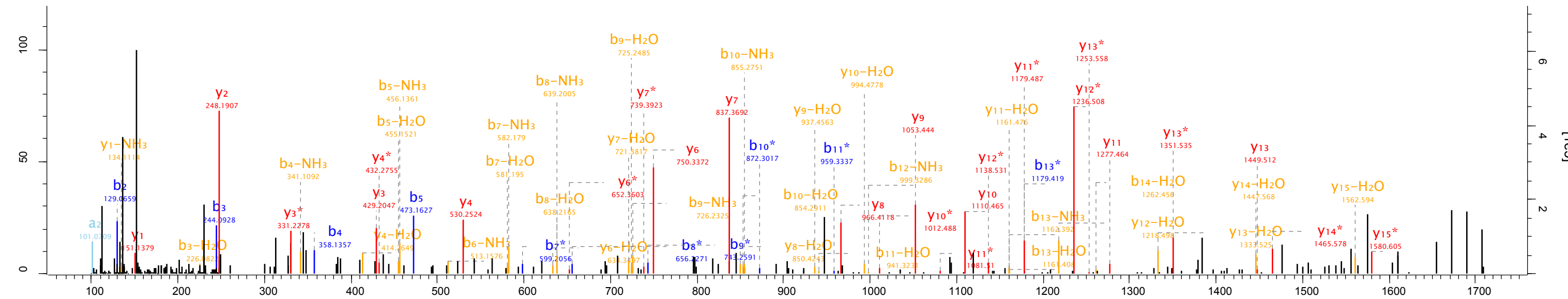


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3318 Method FTMS; HCD Score 76.05 m/z 606.28 Gene names TBX2



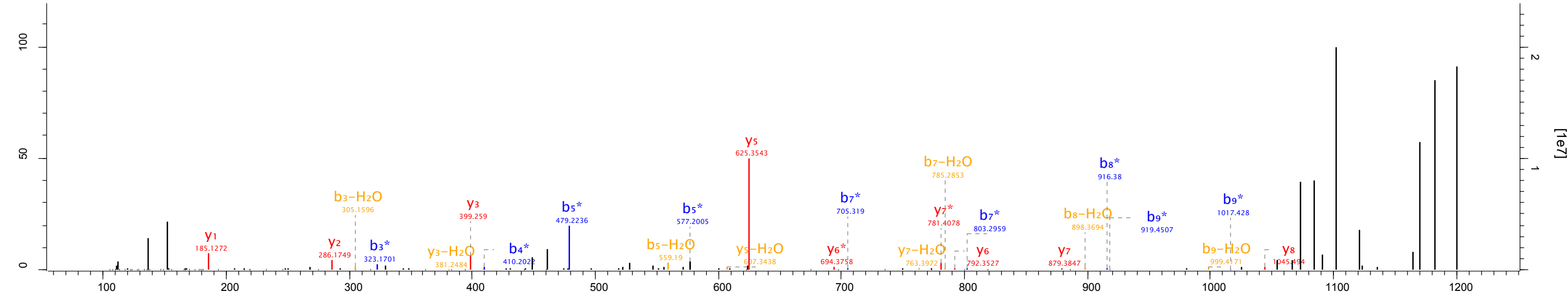
Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 3518 Method FTMS; HCD Score 198.04 m/z 904.32 Gene names NUFIP2

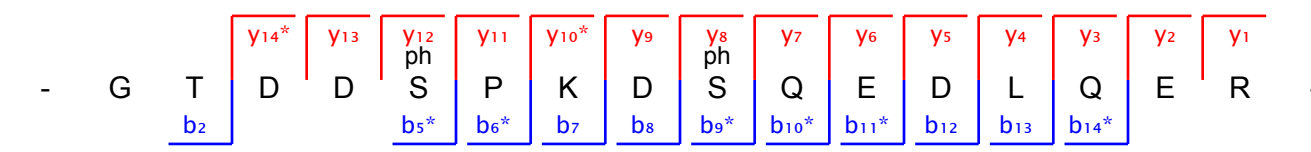
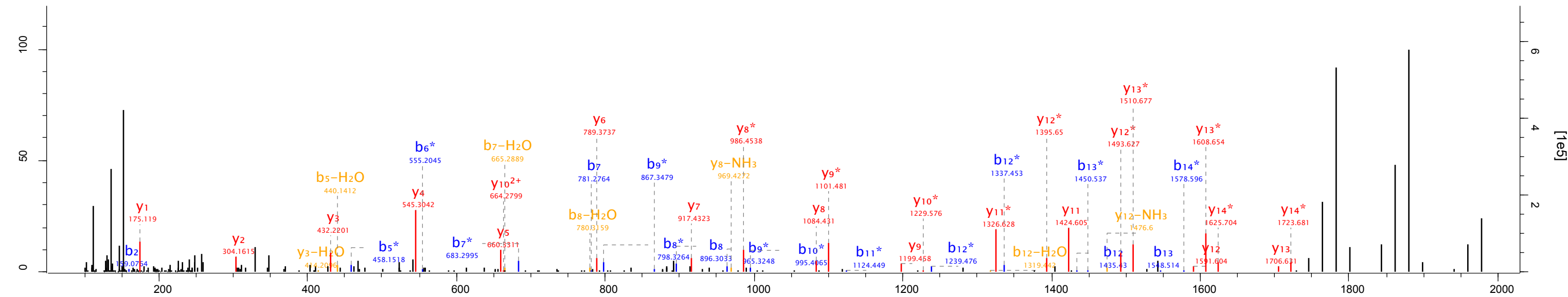


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 3628 Method FTMS; HCD Score 112.96 m/z 650.27 Gene names SRRM2

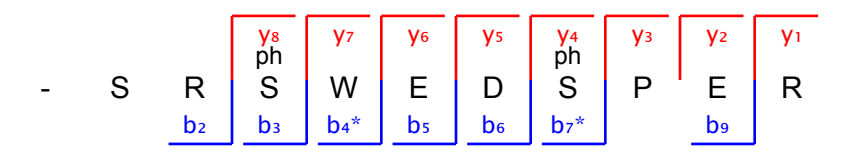
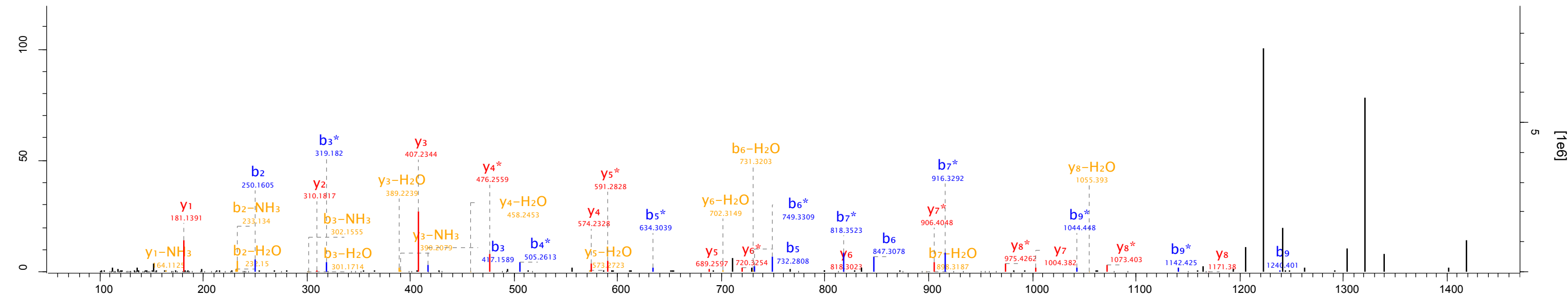
20171215_MaS_33SR_LMH_phospho2_03



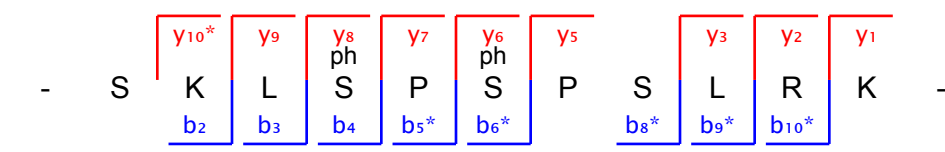
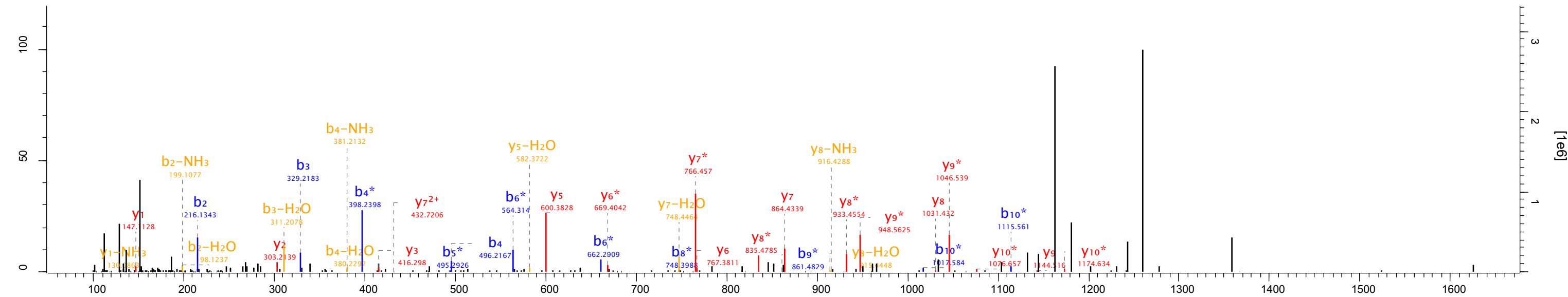
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 4058 Method: FTMS; HCD Score: 142.23 m/z: 990.37 Gene names: TCEAL3;TCEAL6;TCEAL5



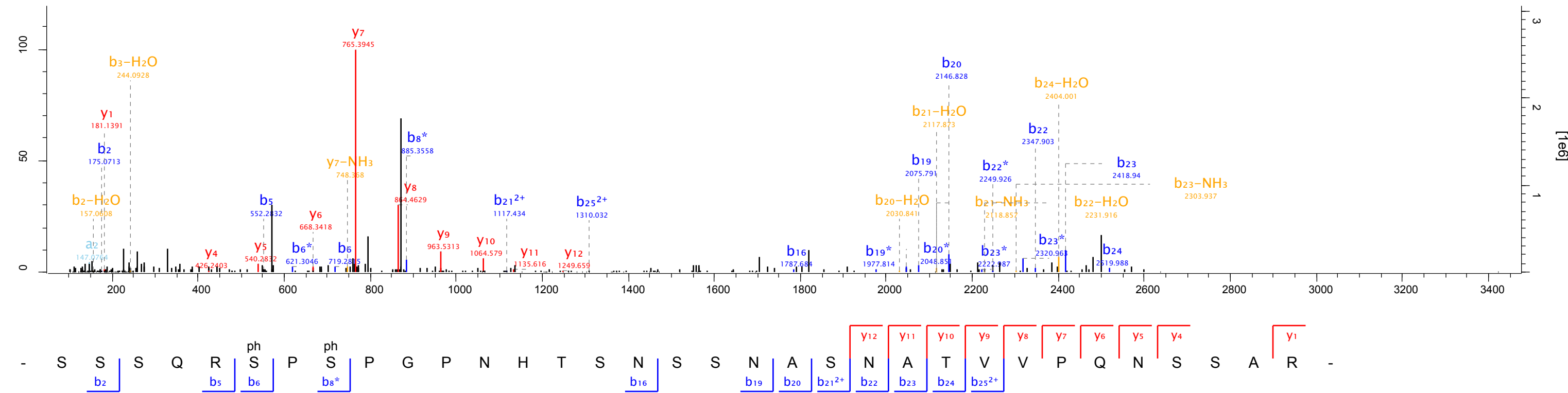
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 Scan: 4618 Method: FTMS; HCD Score: 173.31 m/z: 711.27 Gene names: TJP2



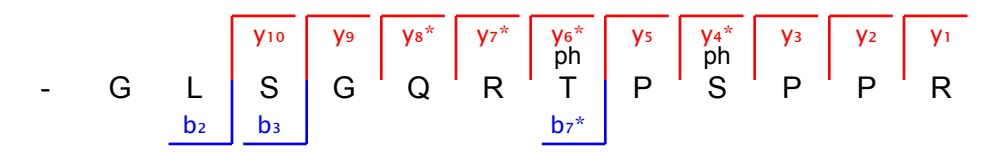
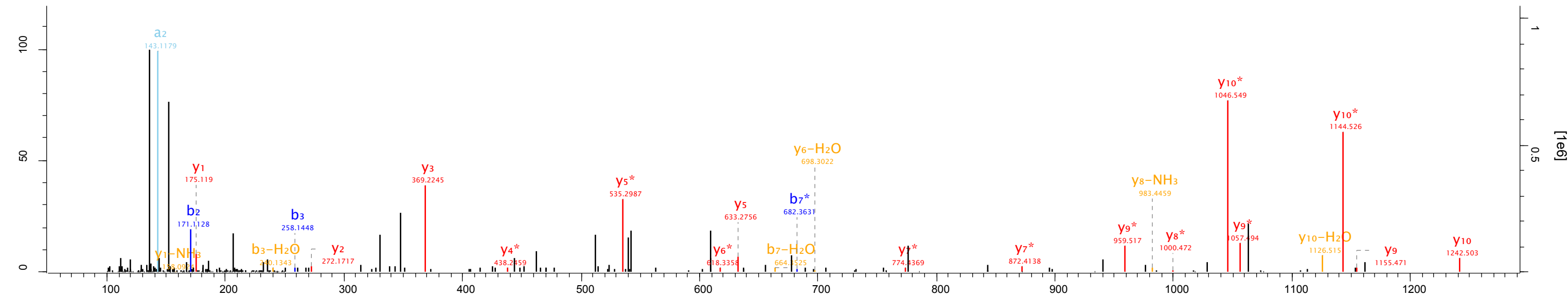
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 Scan: 4628 Method: FTMS; HCD Score: 136.99 m/z: 680.33 Gene names: ZC3H13



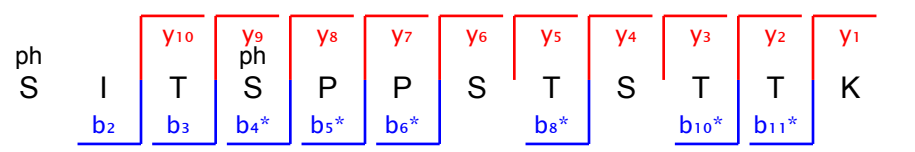
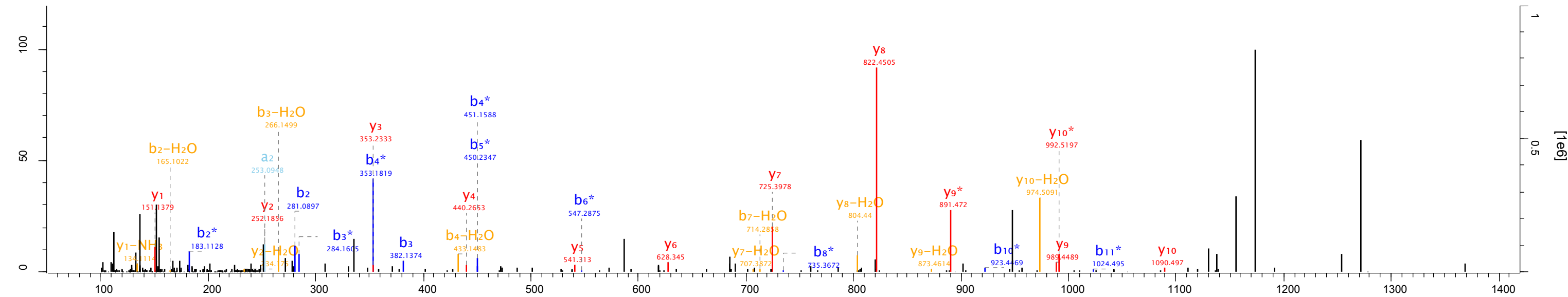
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4738 Method FTMS; HCD Score 41.35 m/z 871.64 Gene names WAC

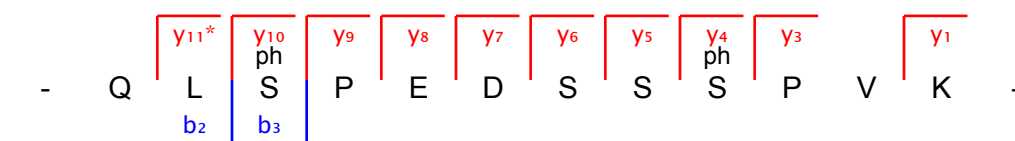
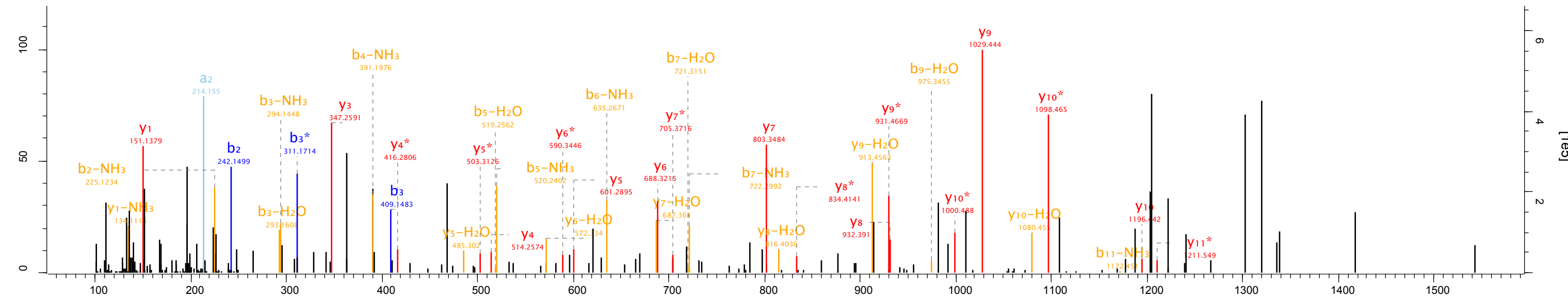


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4998 Method FTMS; HCD Score 66.98 m/z 471.54 Gene names CROCC



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5458 Method FTMS; HCD Score 108.77 m/z 685.79 Gene names NFIX

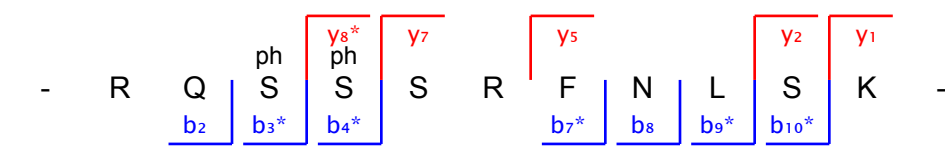
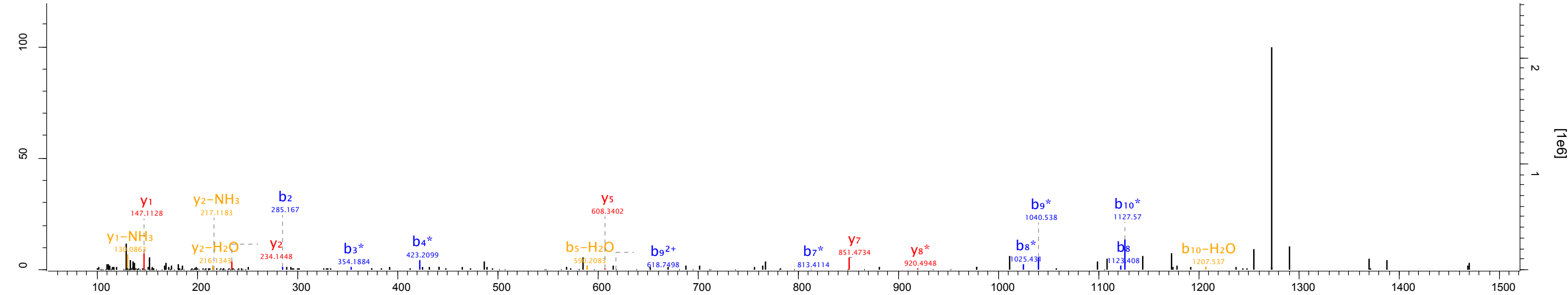




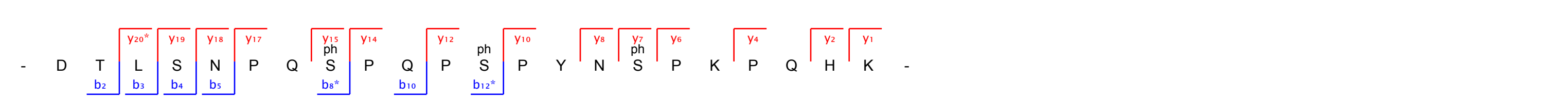
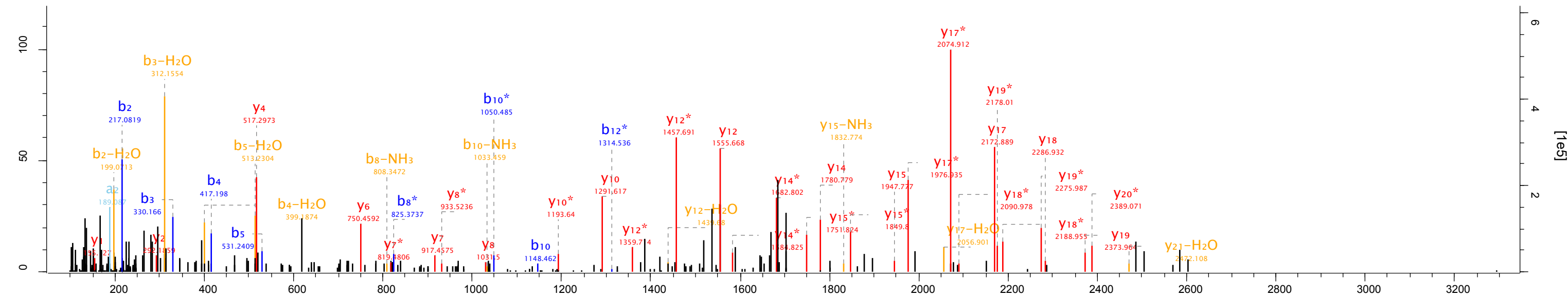
Raw file

20171215_MaS_33SR_LMH_phospho2_03

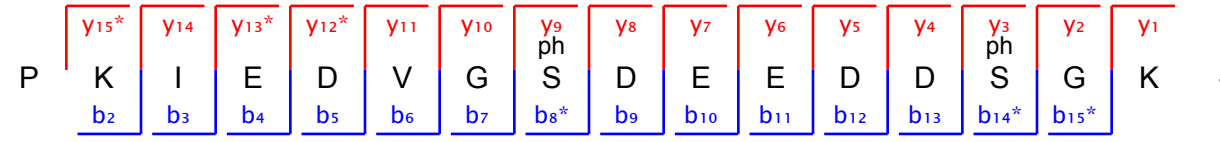
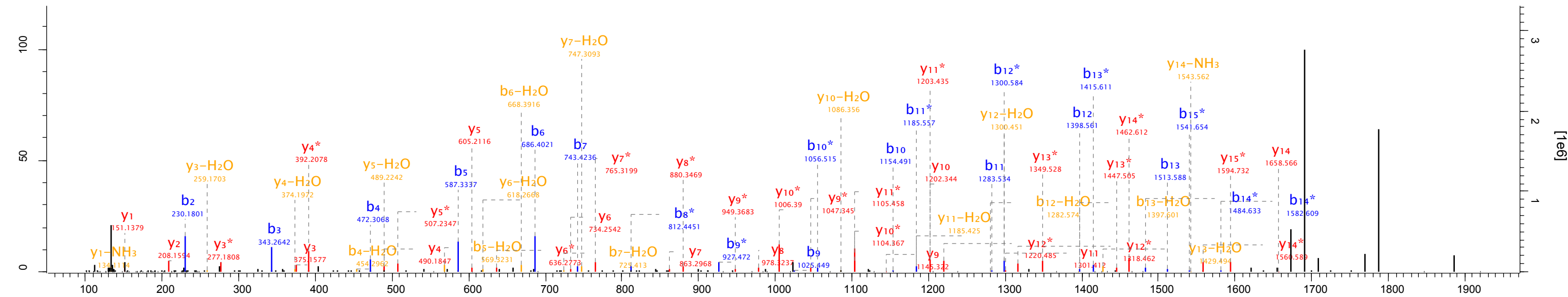
Scan	Method	Score	m/z	Gene names
5538	FTMS; HCD	51.73	490.55	PPP2R5D

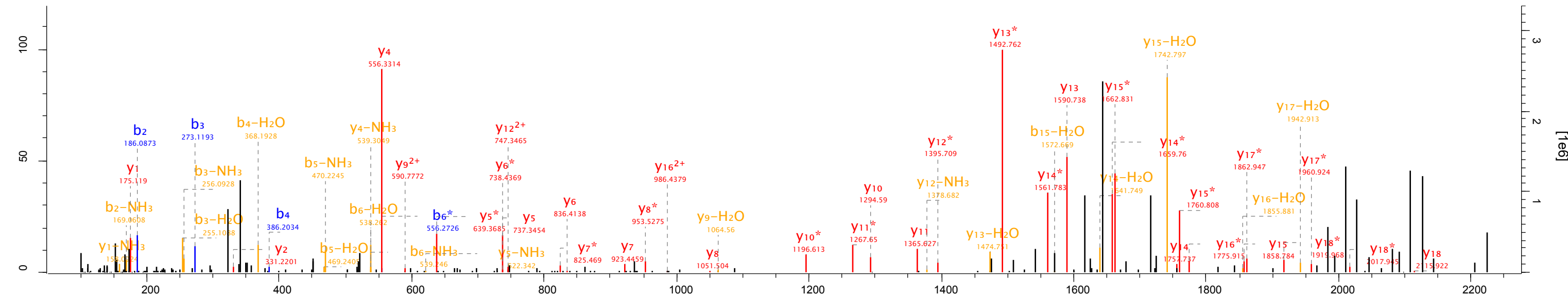


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5628 Method FTMS; HCD Score 181.63 m/z 902.05 Gene names NEDD4L



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5658 Method FTMS; HCD Score 285.16 m/z 944.37 Gene names HSP90AB2P;HSP90AB1



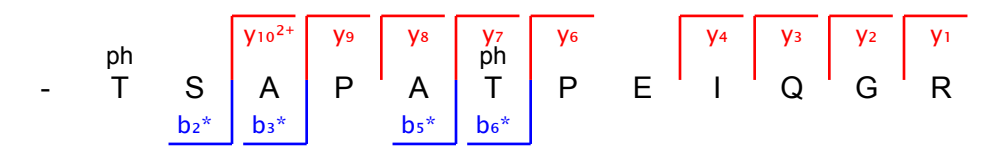
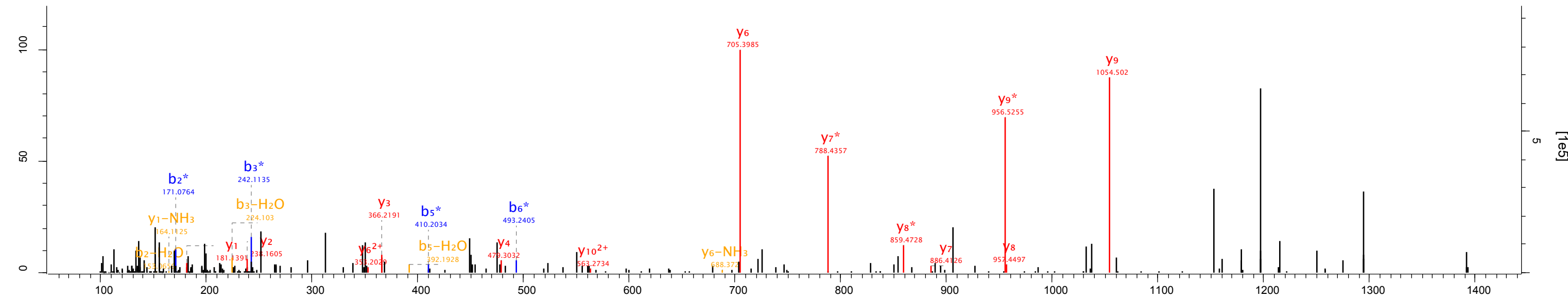


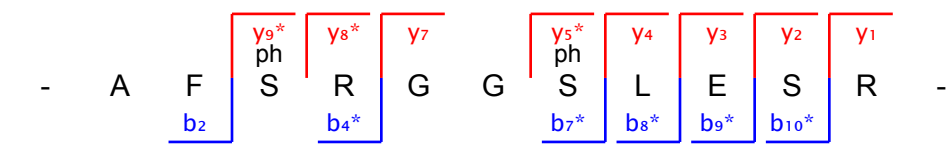
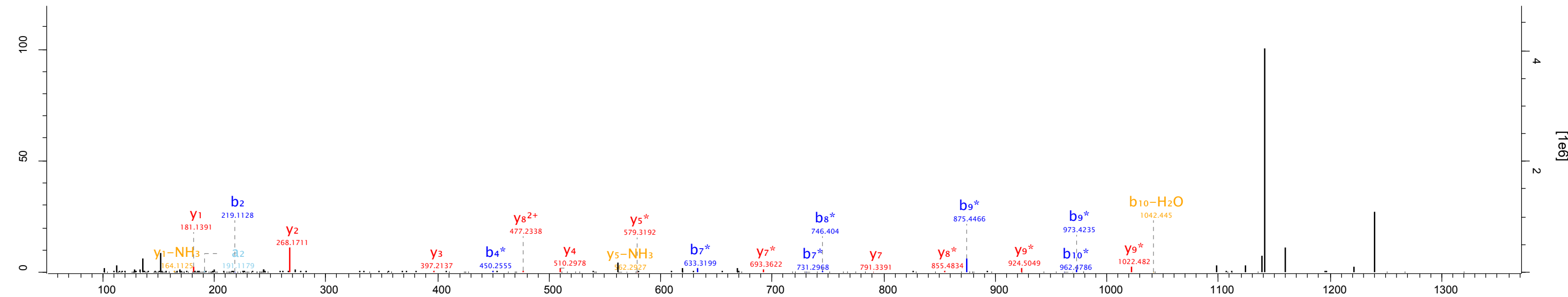
- Q G S I T S P Q A N E Q S V T P Q R R -

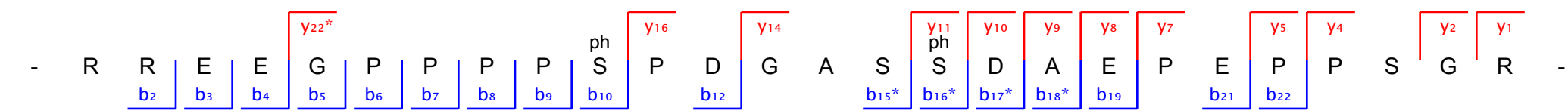
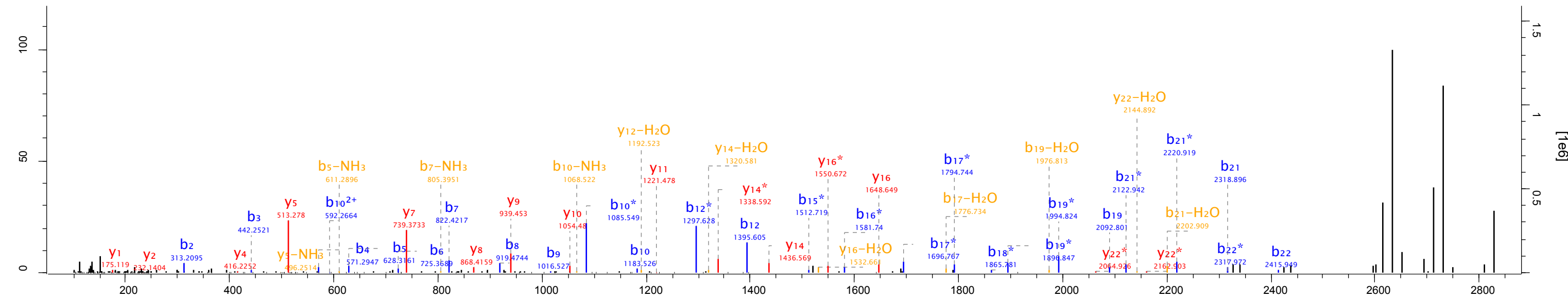
Fragmentation sites are indicated by brackets above the sequence:

- Red brackets above: y18, y17*, y16*, y15, y14 ph, y13, y12*, y11, y10, y9²⁺, y8, y7, y6, y5 ph, y4, y2, y1
- Blue brackets below: b2, b3, b4, b6*

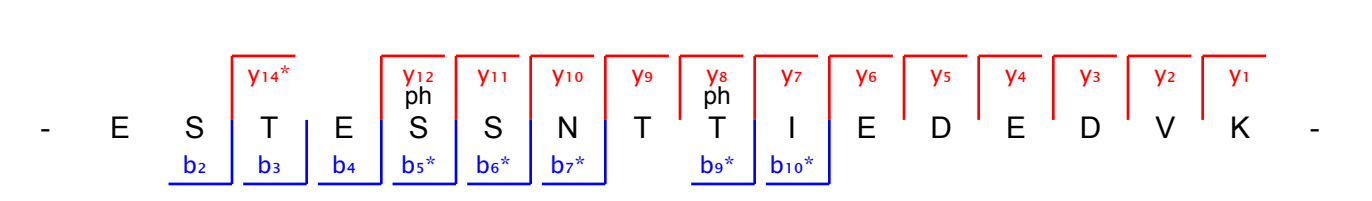
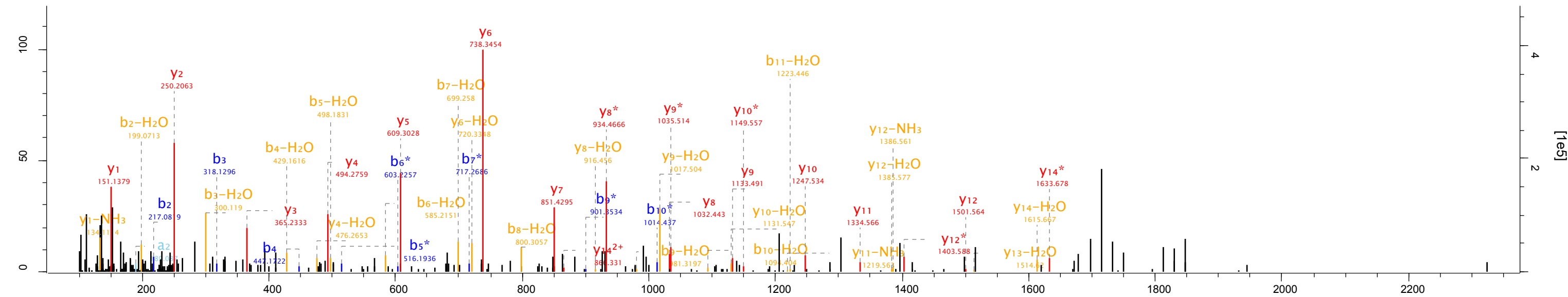
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 5938 Method FTMS; HCD Score 52.52 m/z 697.3 Gene names C1orf106



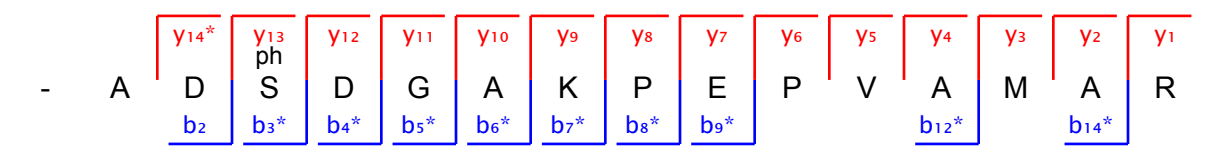
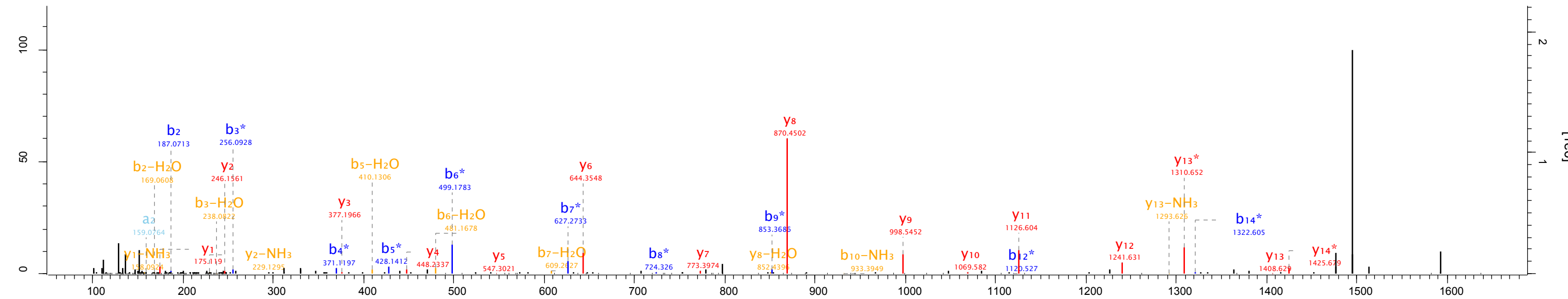




Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 6108 Method FTMS; HCD Score 133.92 m/z 974.37 Gene names CAMK2D

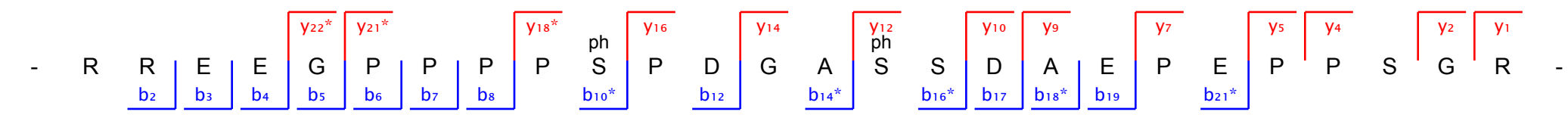
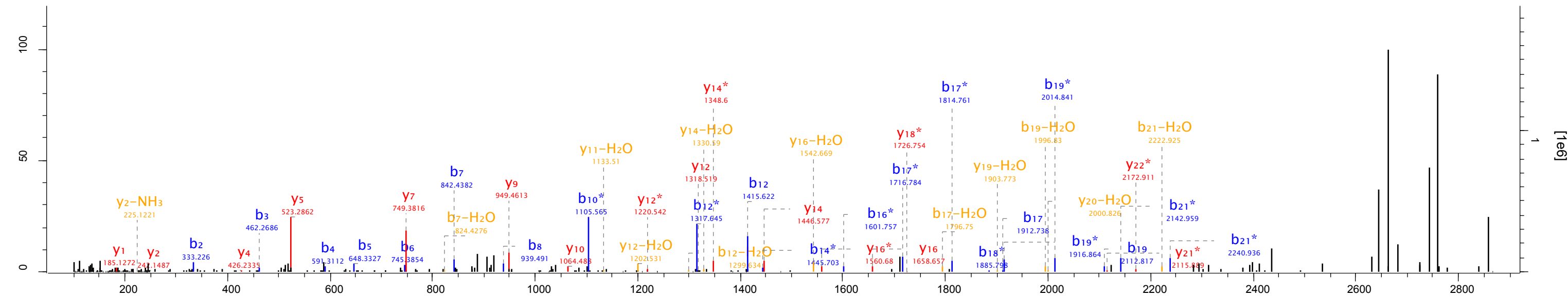


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 Scan: 6118 Method: FTMS; HCD Score: 100.39 m/z: 798.35 Gene names: HDGFRP2

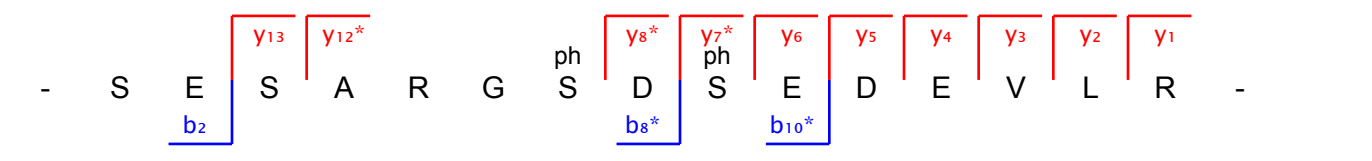
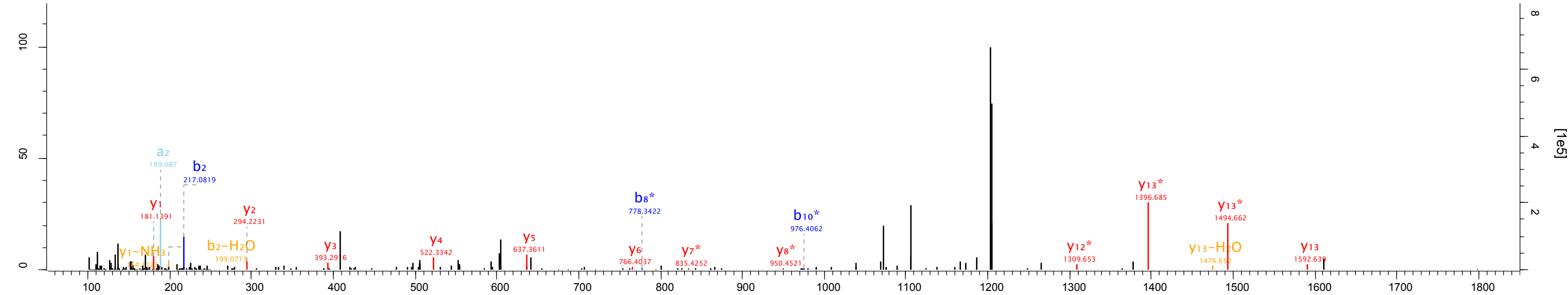


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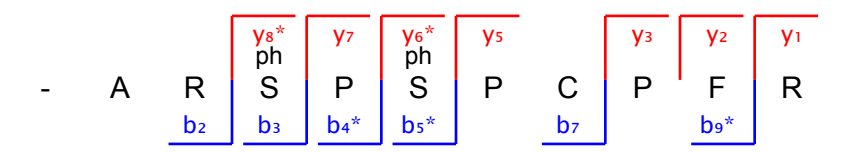
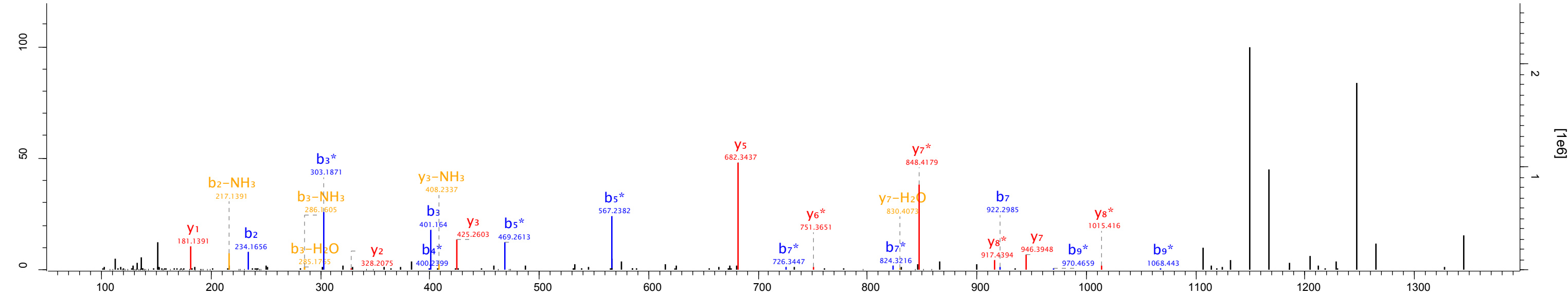
Scan 6138 Method FTMS; HCD Score 125.48 m/z 954.74 Gene names SMC4

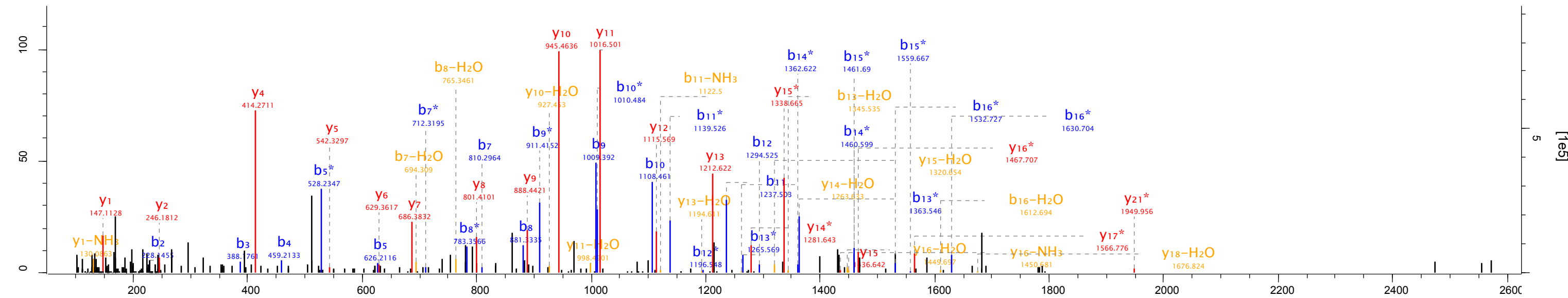


20171215_MaS_33SR_LMH_phospho2_03 6418 FTMS; HCD 46.49 603.58 LEO1



20171215_MaS_33SR_LMH_phospho2_03 6518 FTMS; HCD 97.45 673.78 ITPKB



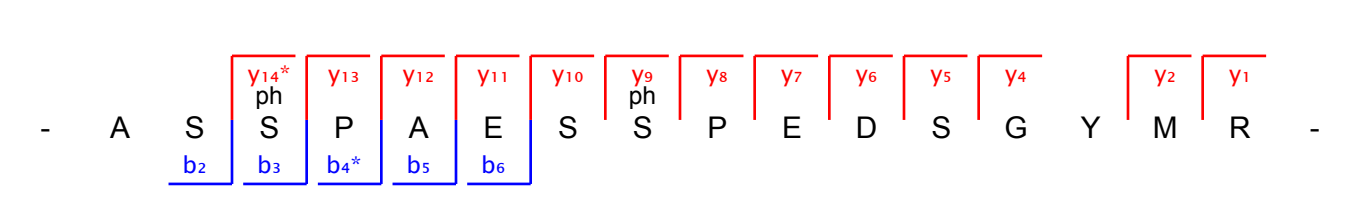
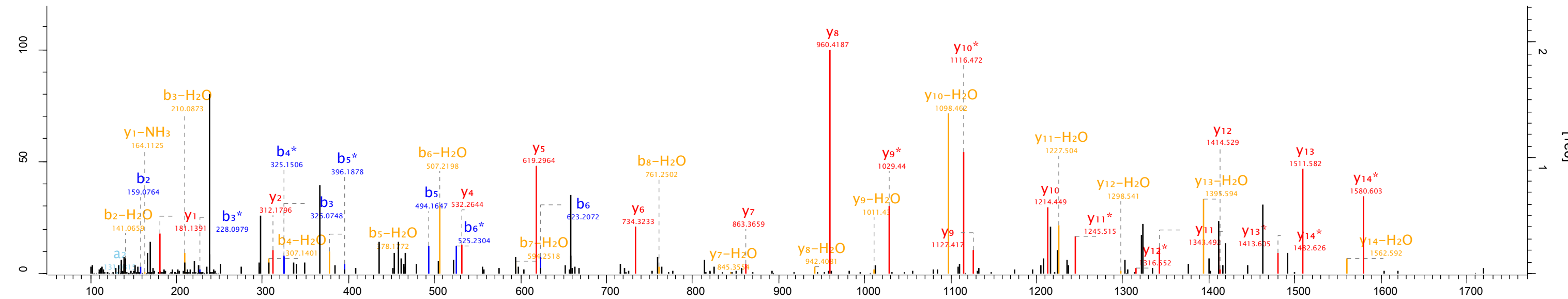


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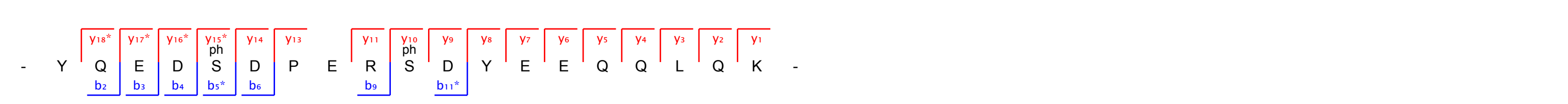
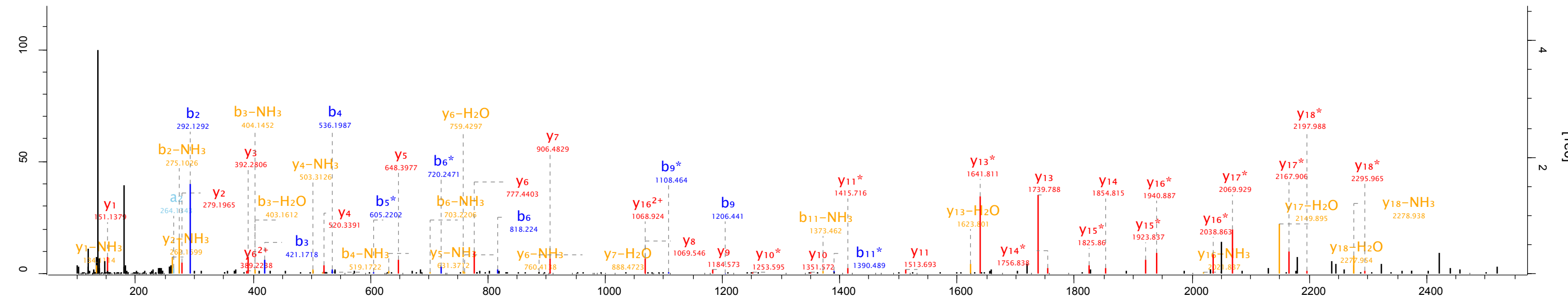
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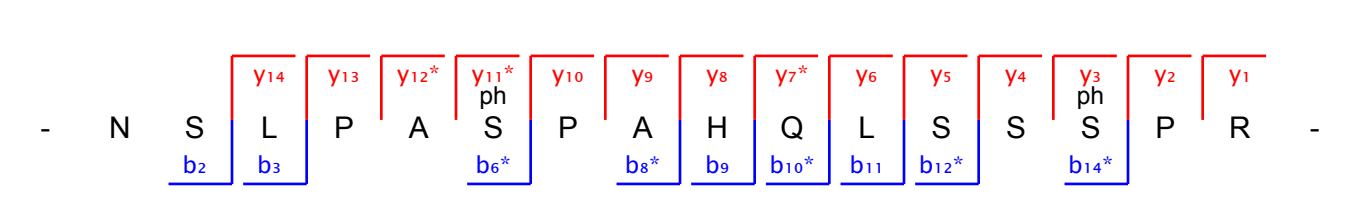
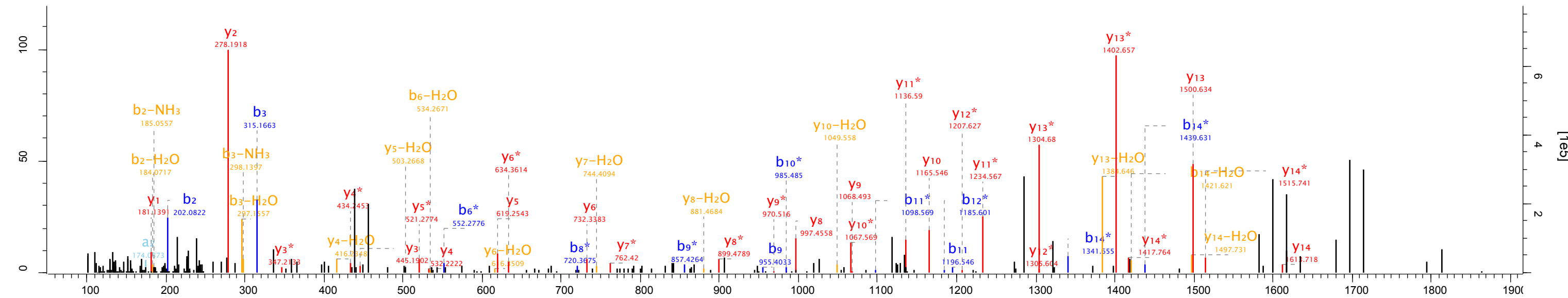
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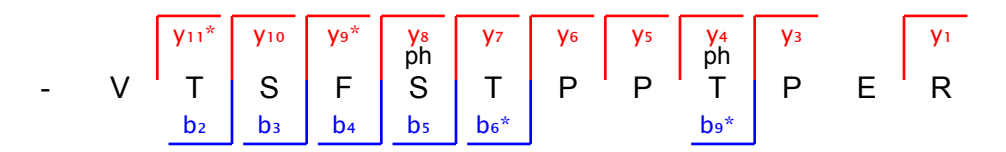
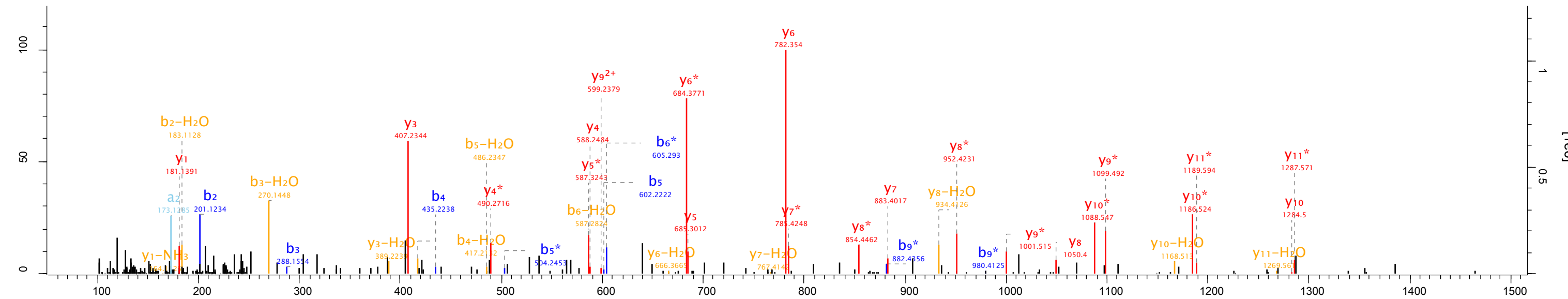


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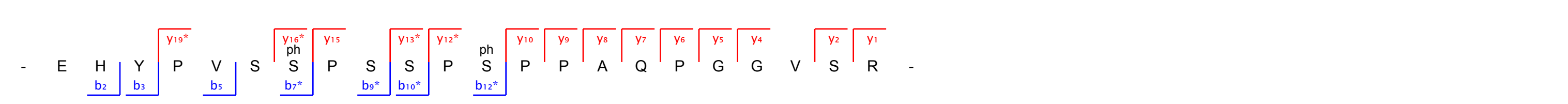
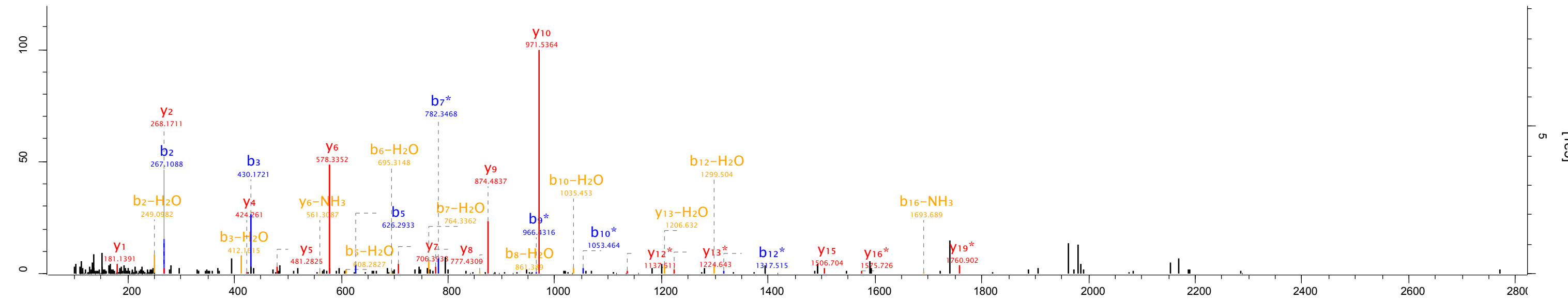


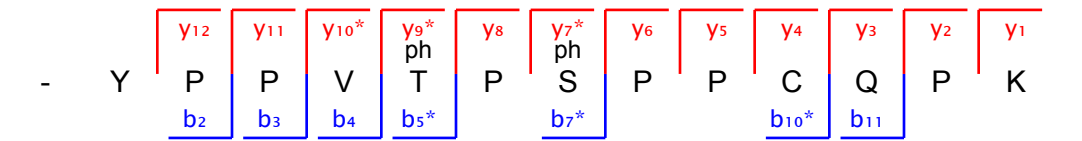
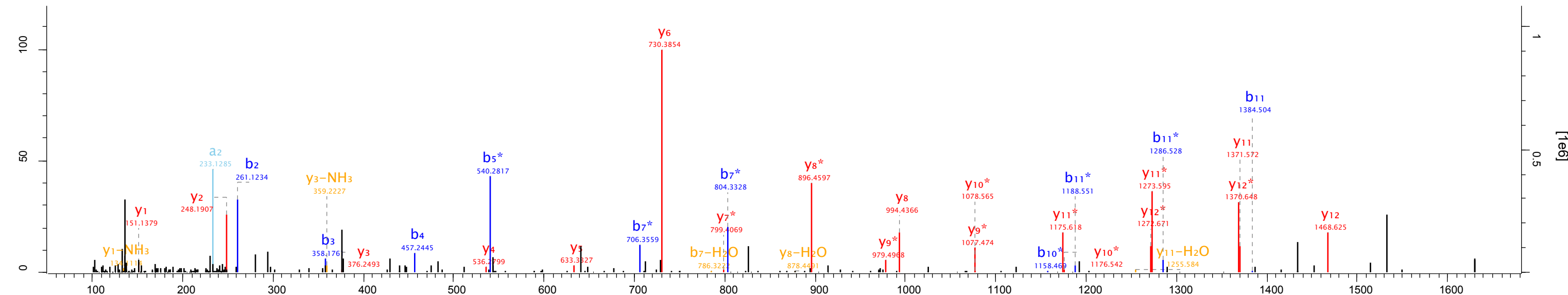
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20171215_MaS_33SR_LMH_phospho2_03

Scan 9028 Method FTMS; HCD Score 158.41 m/z 743.31 Gene names KIAA0930

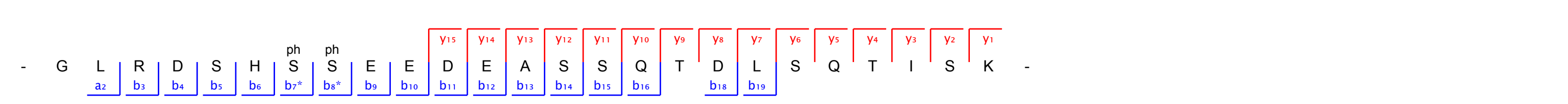
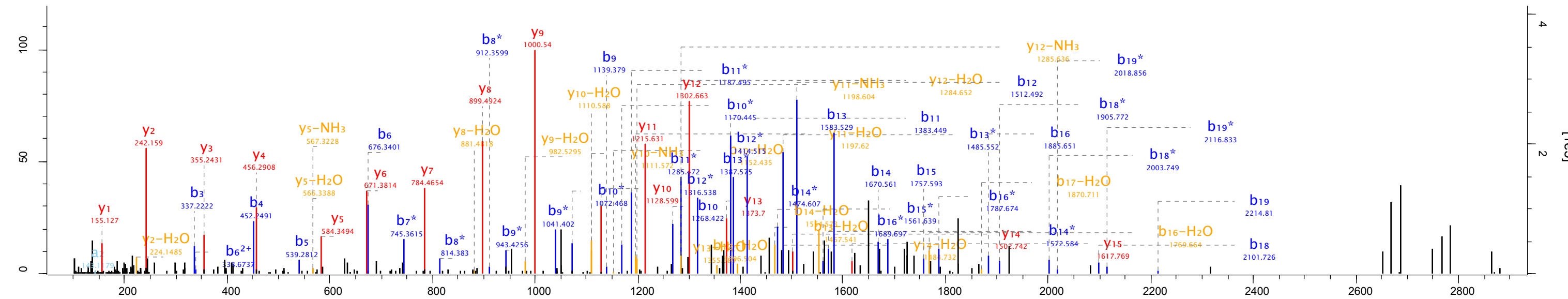


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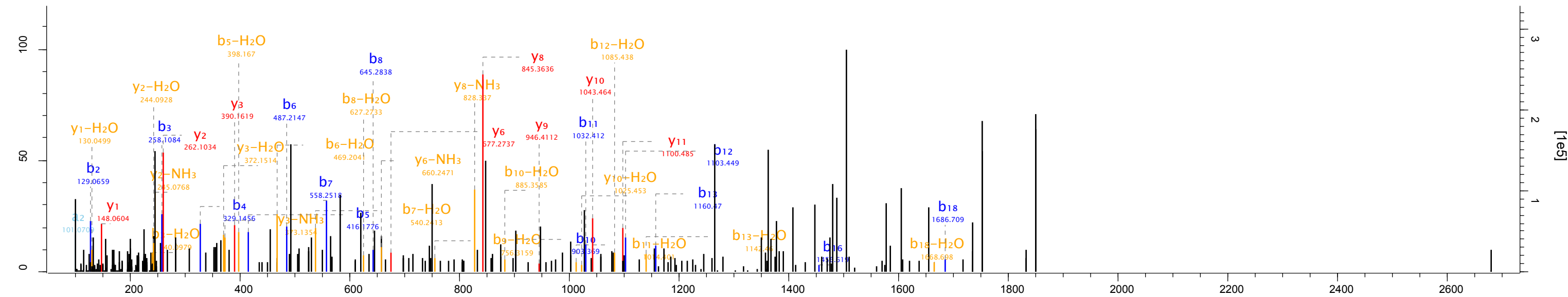




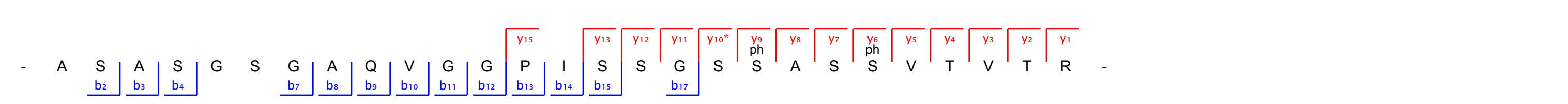
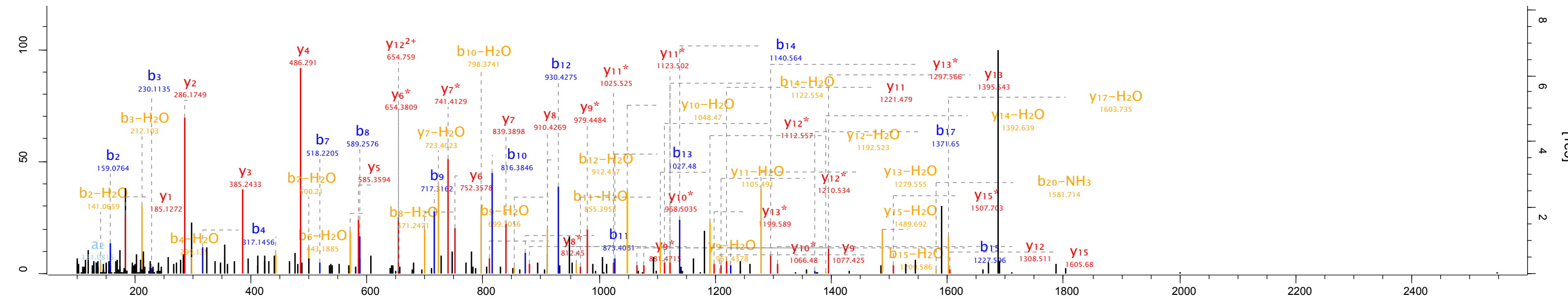
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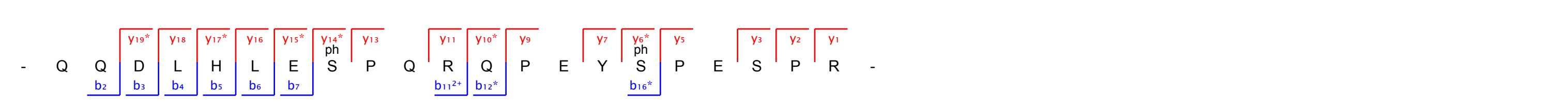
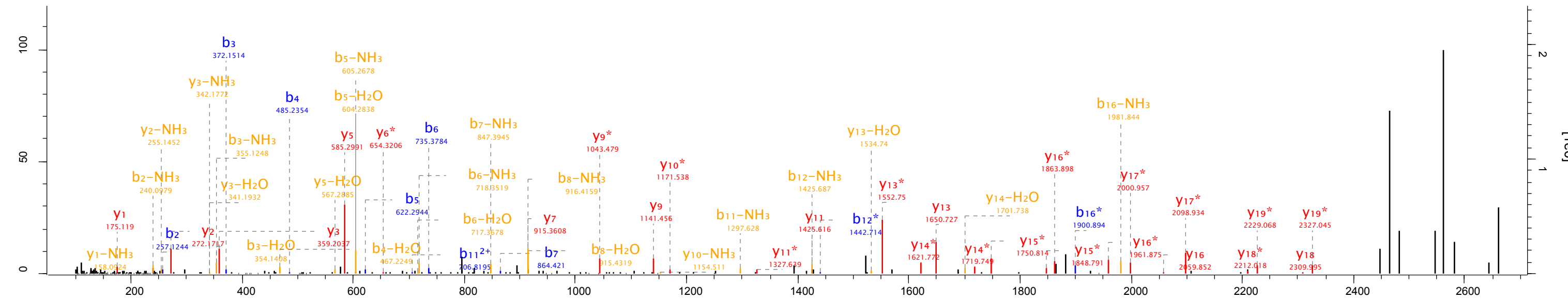
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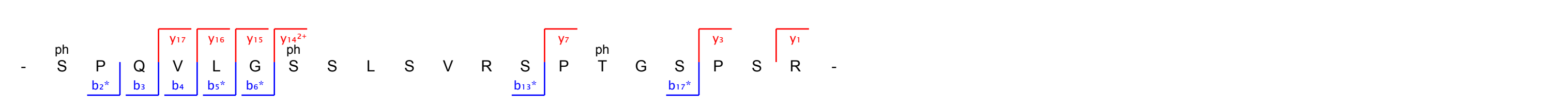
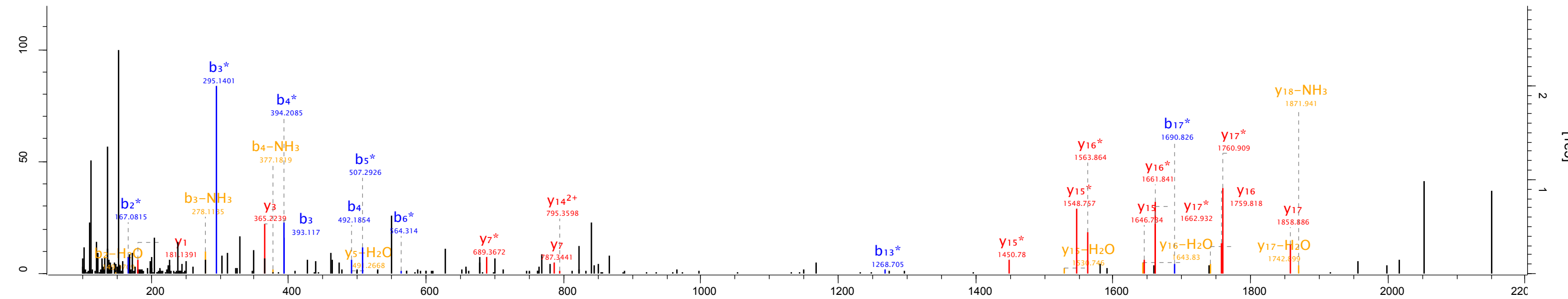
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 9848 FTMS; HCD 135.04 846.04 LMNA



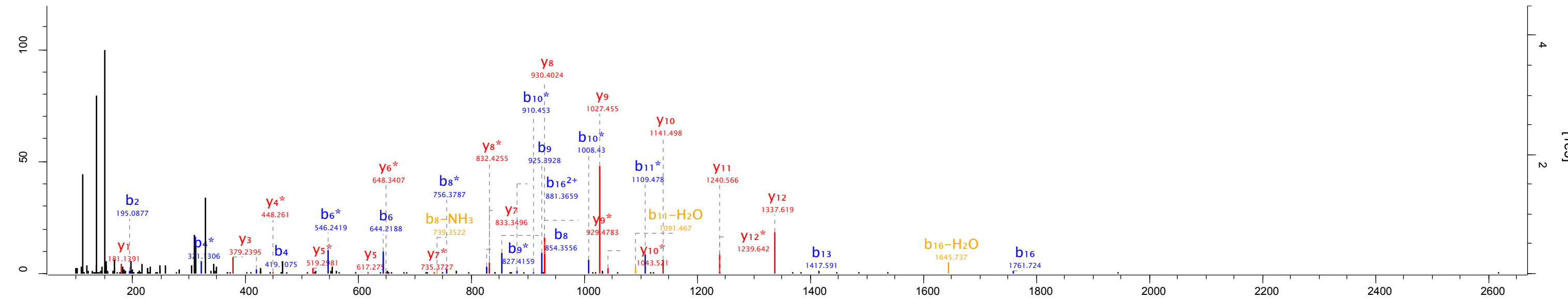
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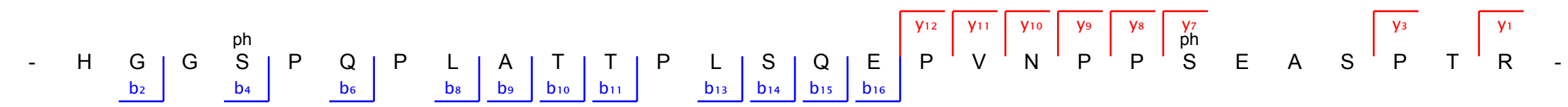
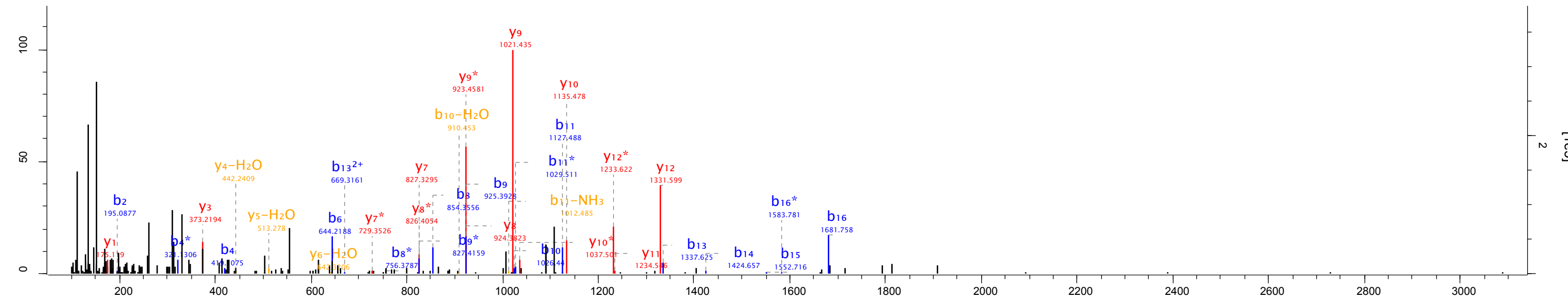
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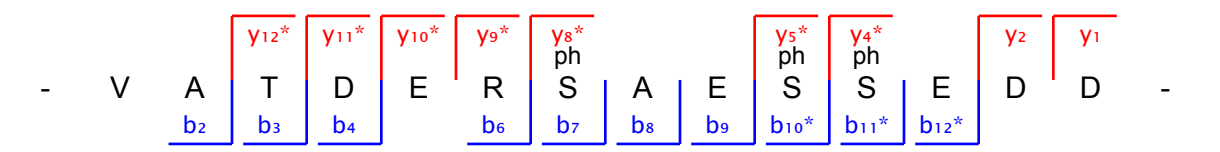
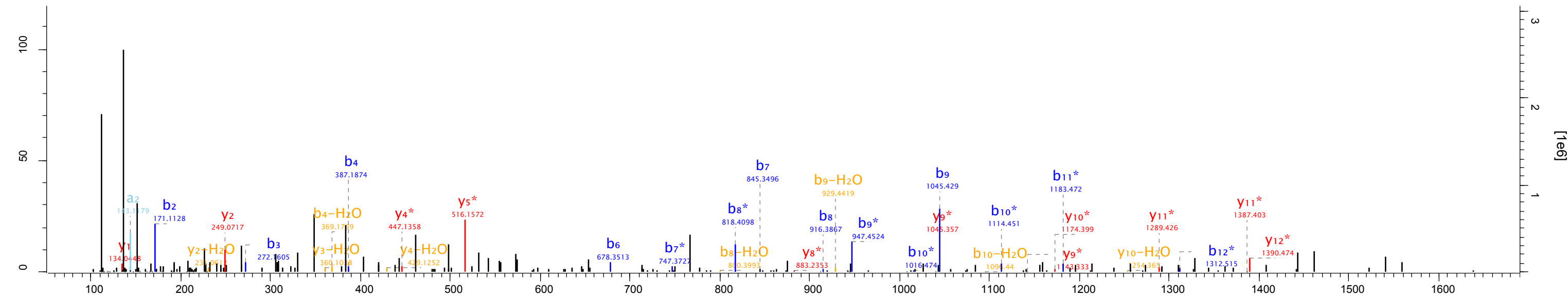
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 20171215_MaS_33SR_LMH_phospho2_04
 Scan 11418 Method FTMS; HCD Score 56.01 m/z 1033.45 Gene names SRRM2



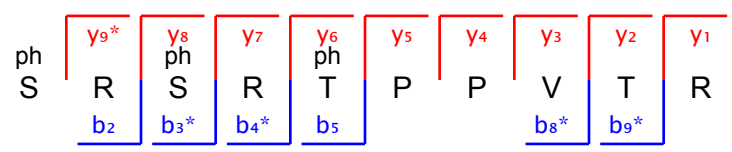
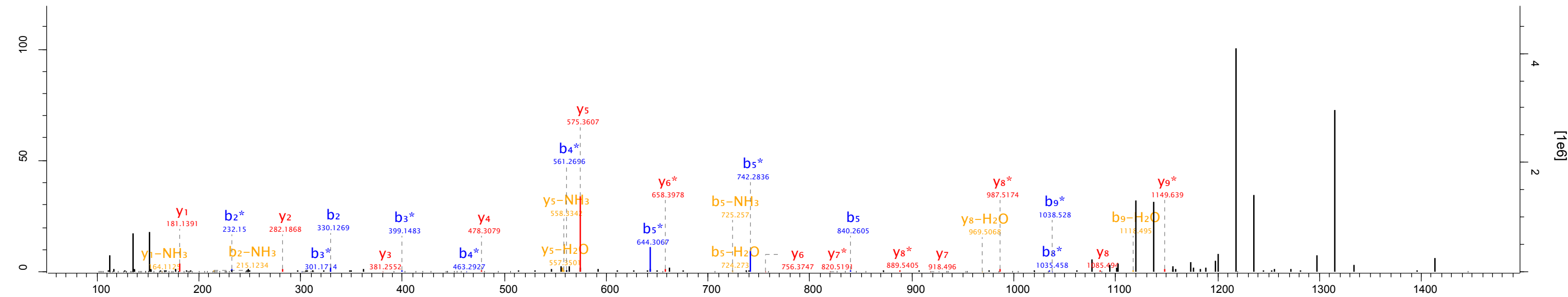
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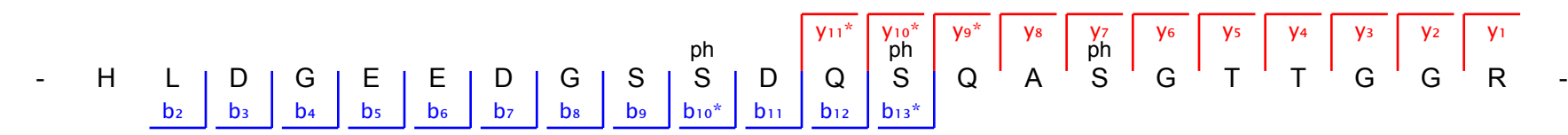
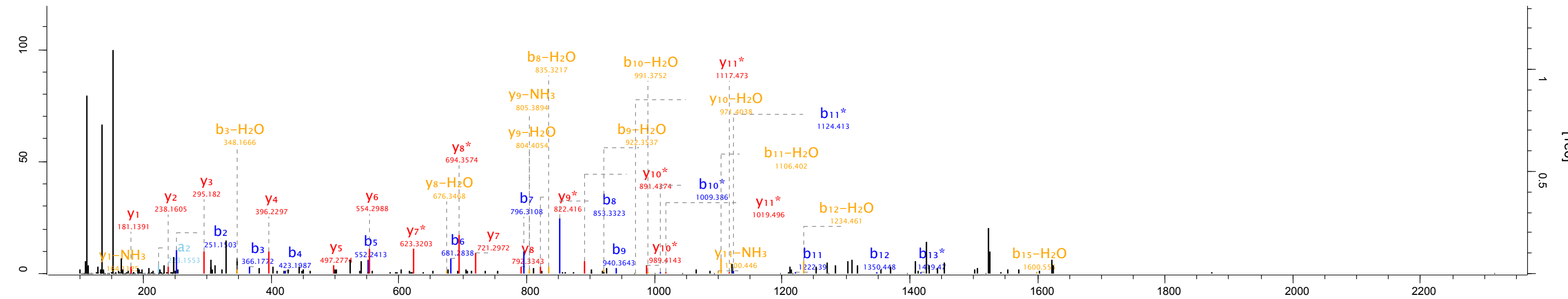
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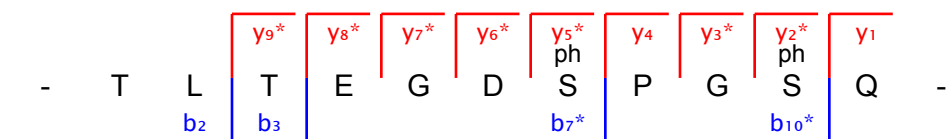
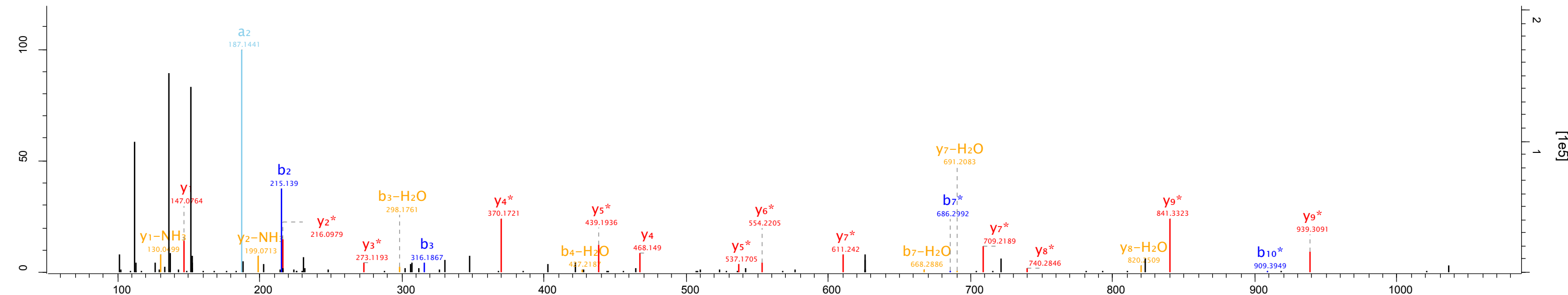


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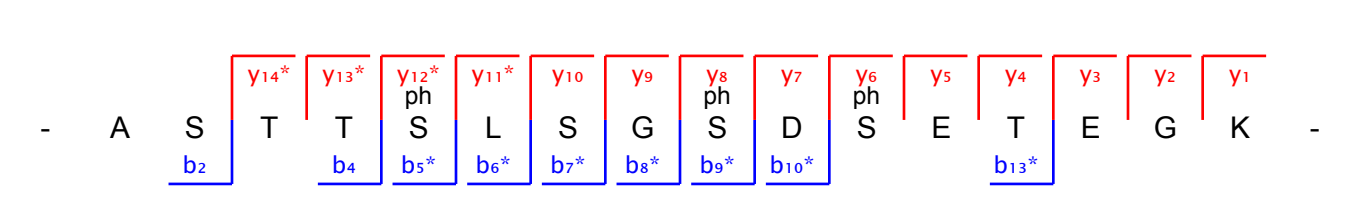
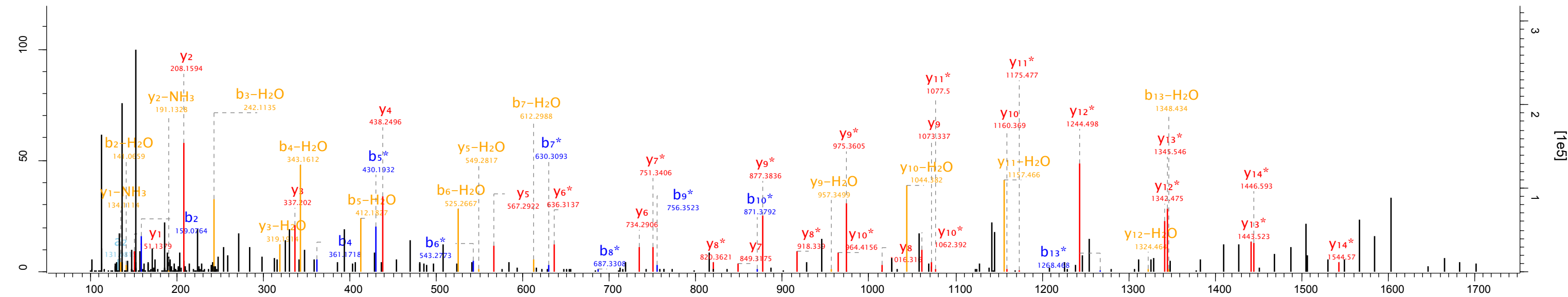


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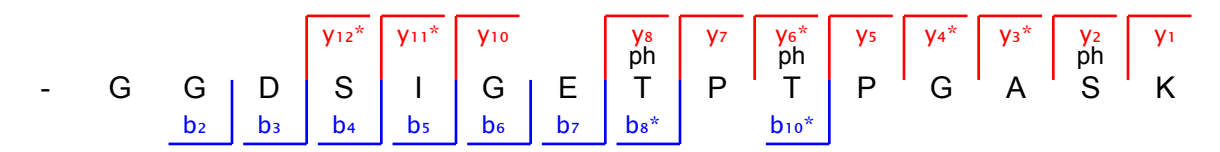
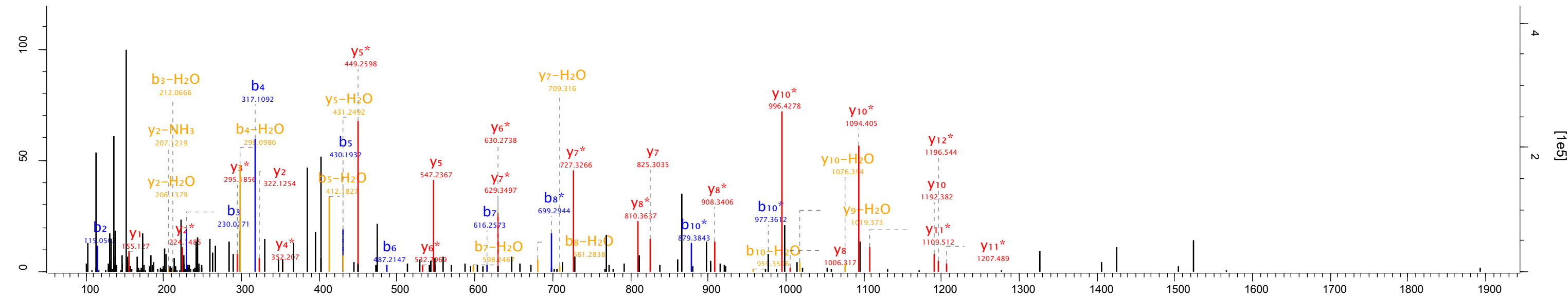




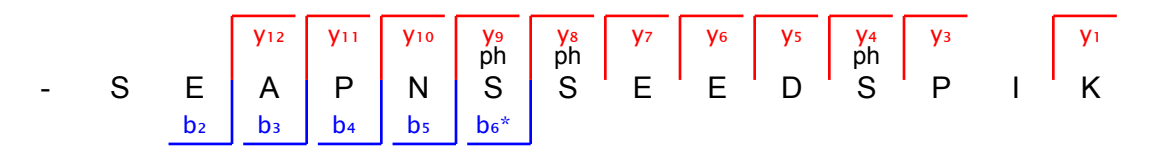
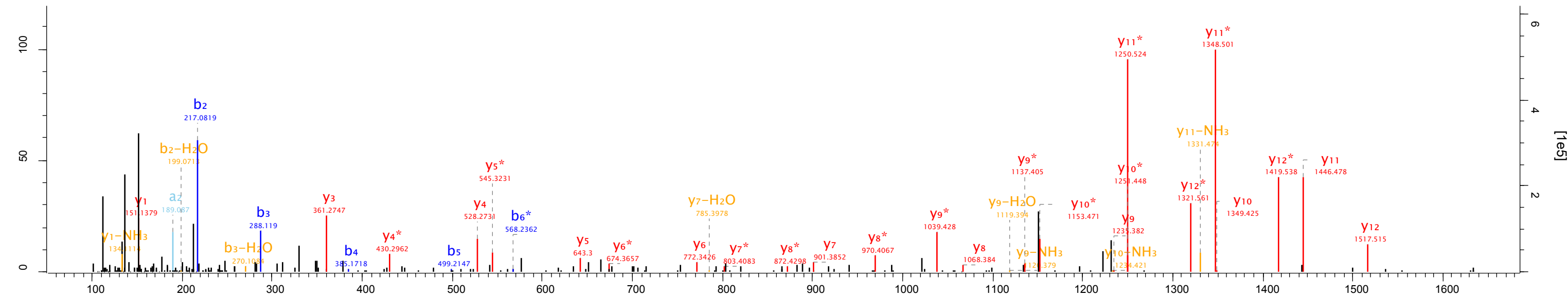
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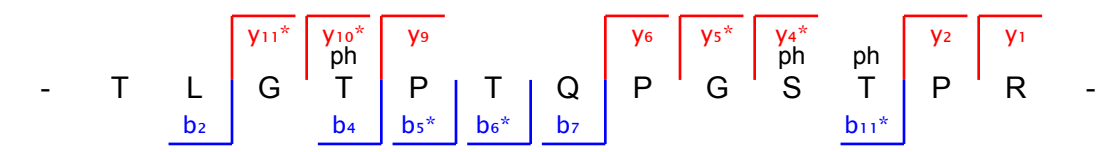
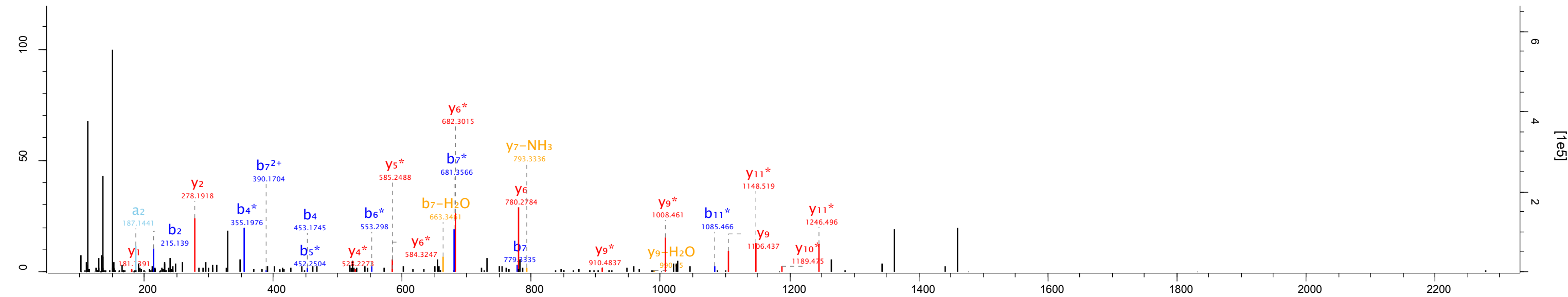
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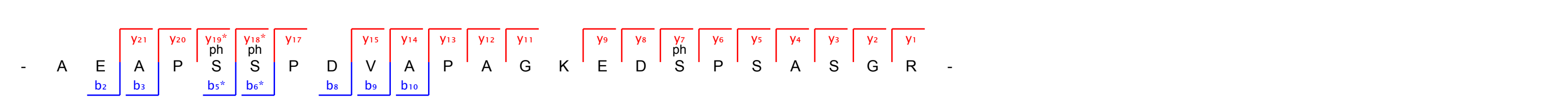
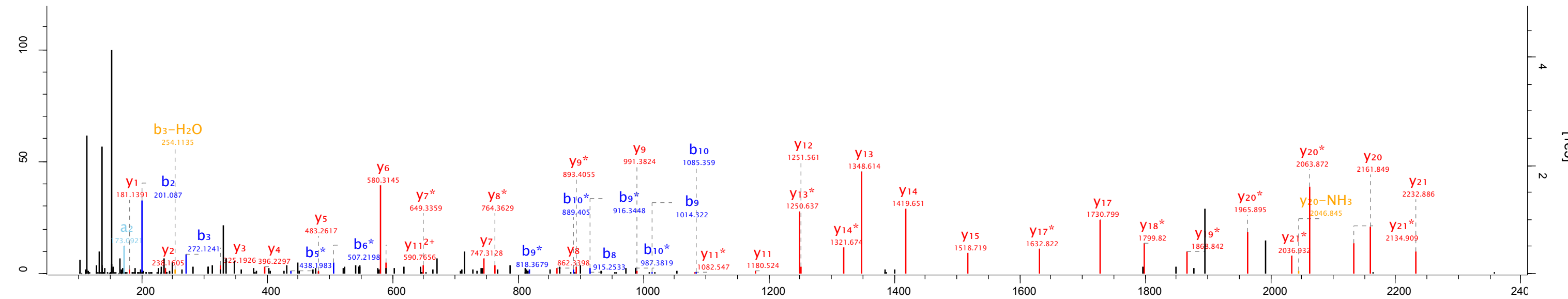
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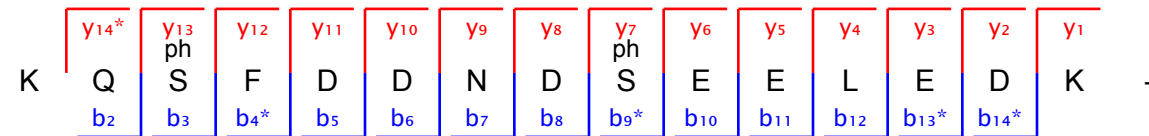
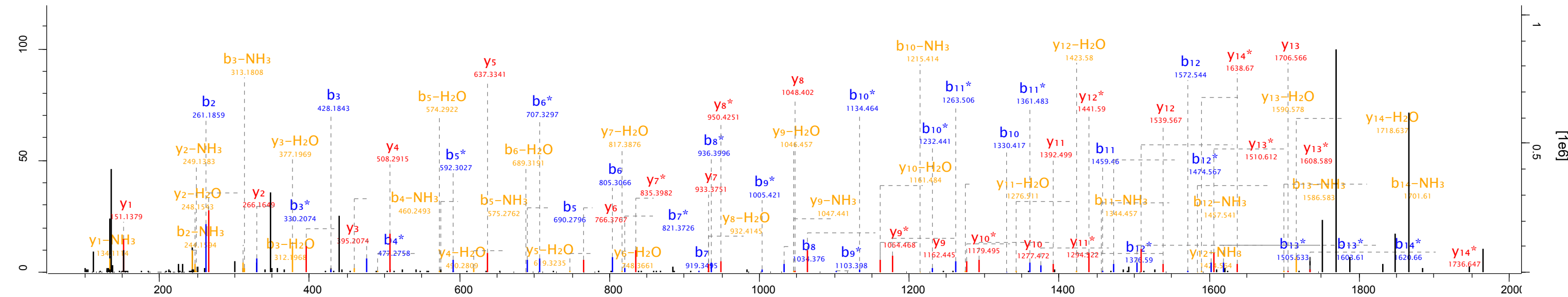


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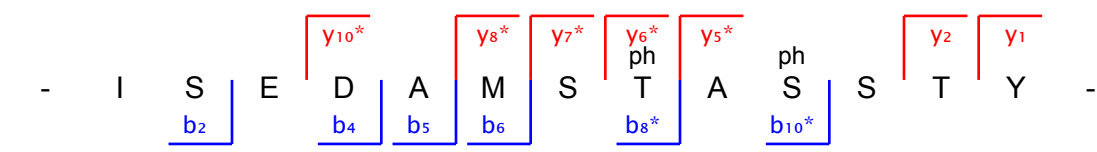
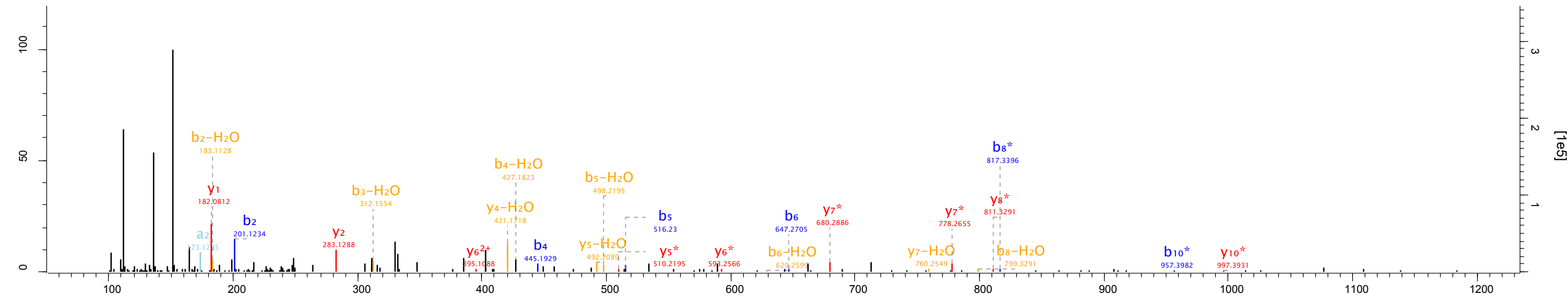


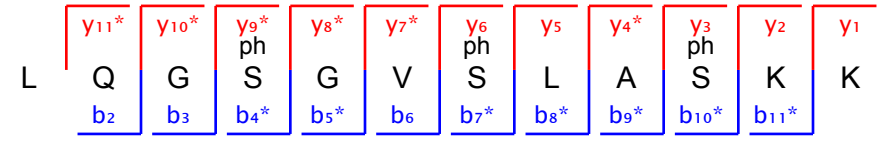
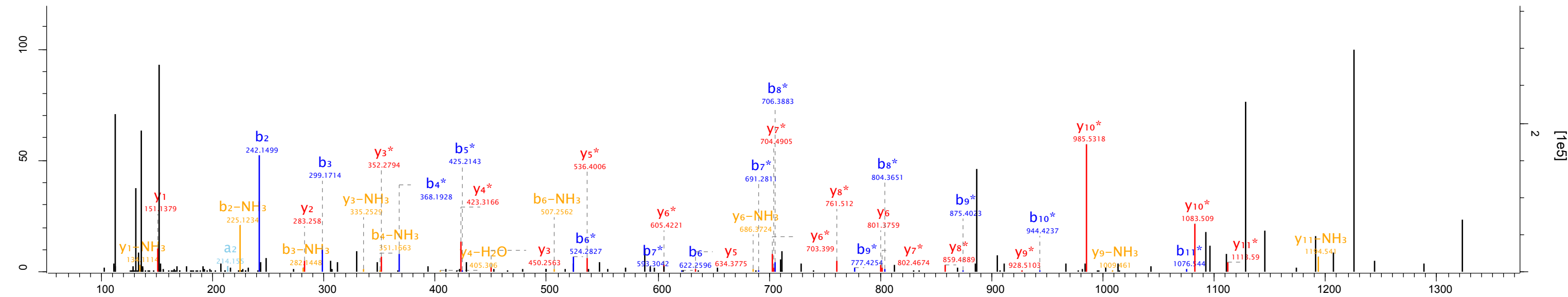
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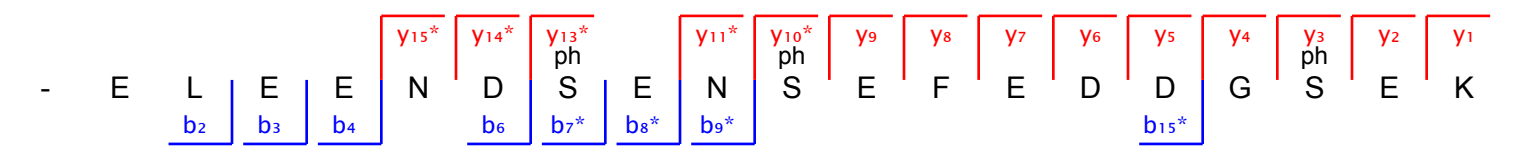
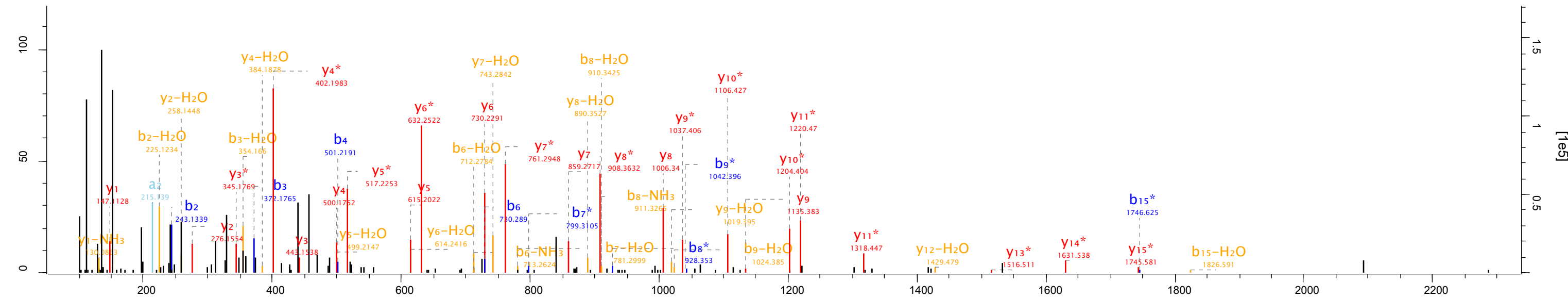


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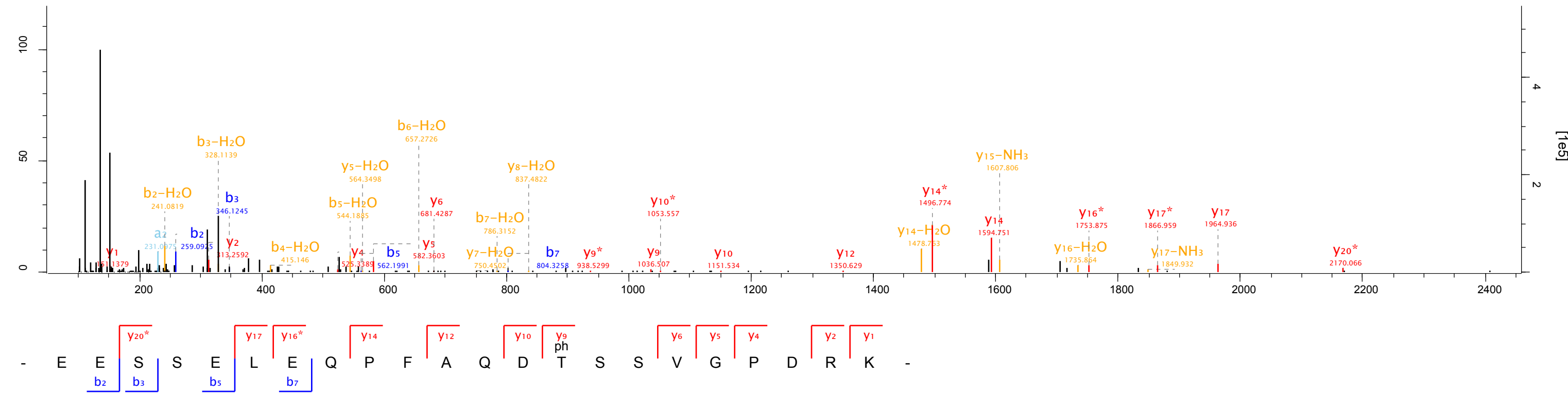


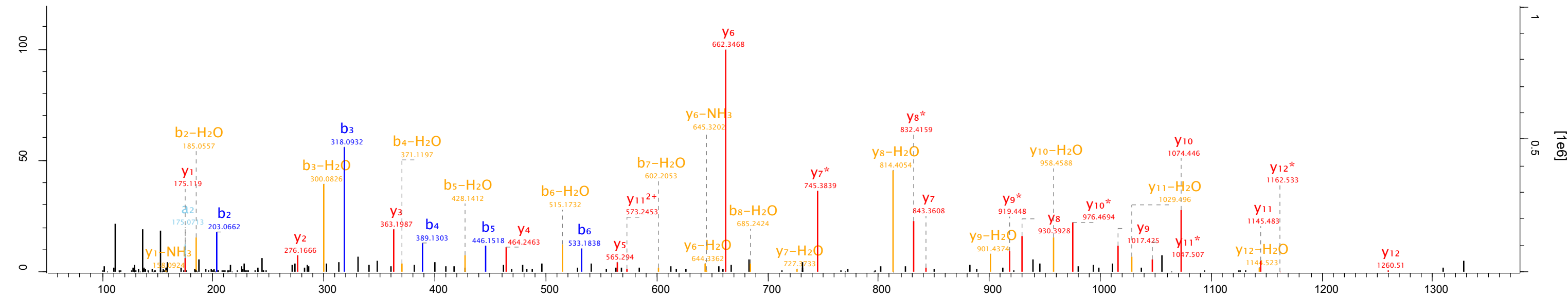


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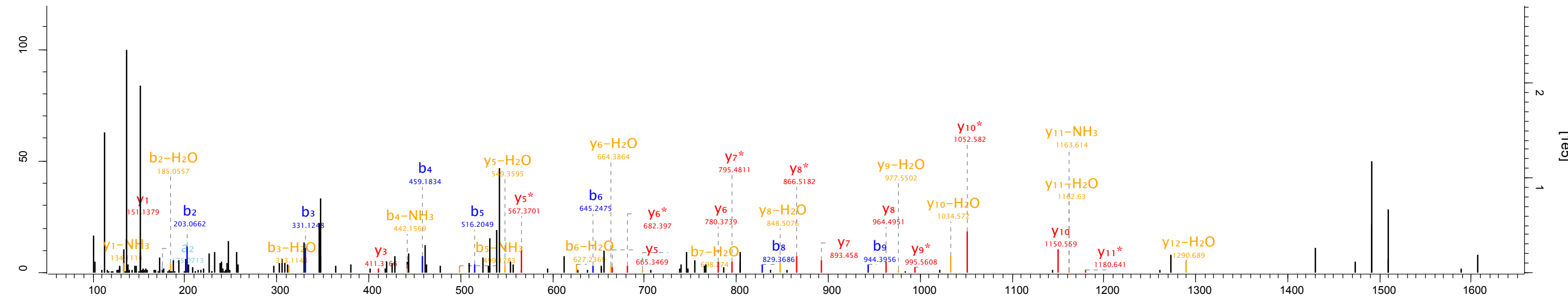




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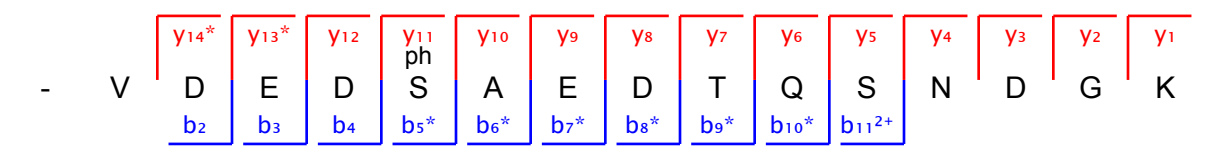
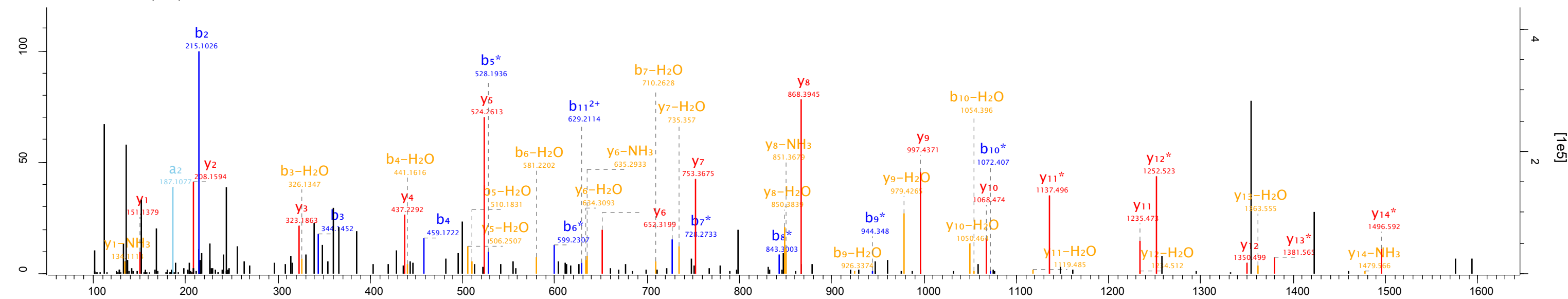


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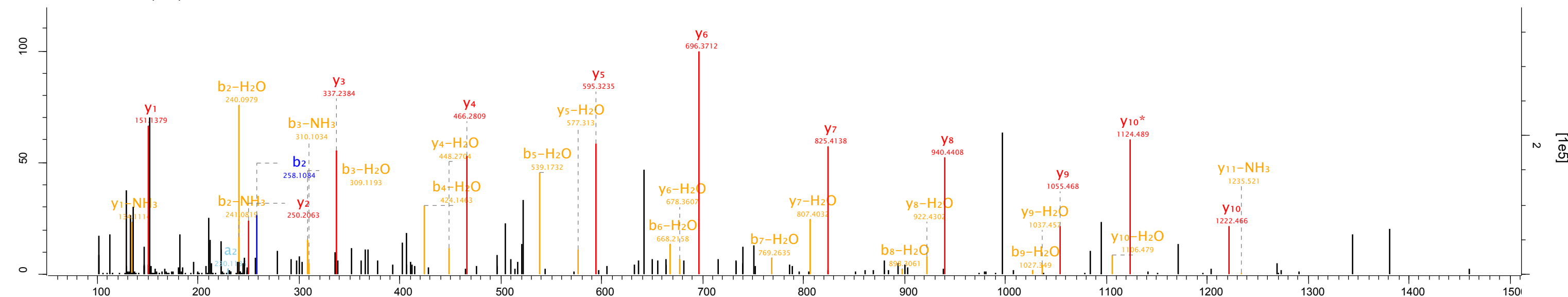
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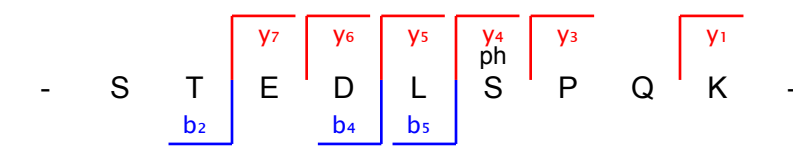
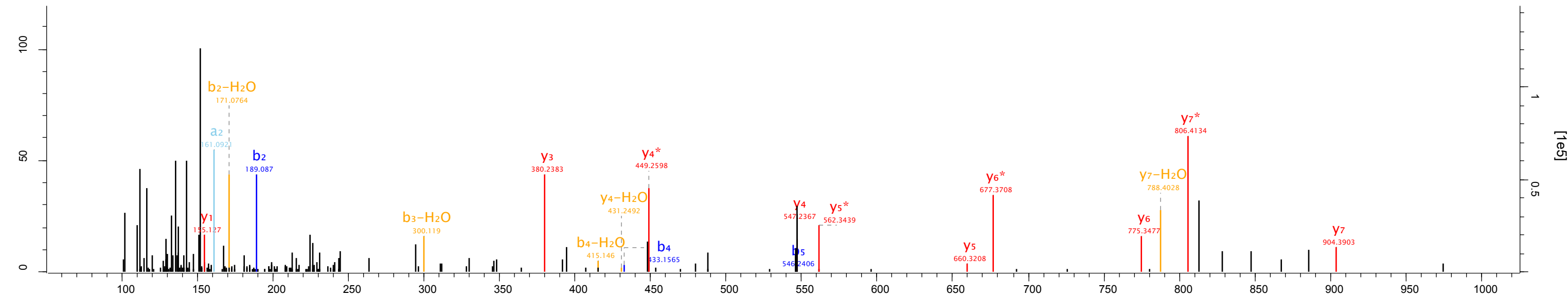
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Scan 2778 Method FTMS; HCD Score 122.33 m/z 740.29 Gene names SASH1

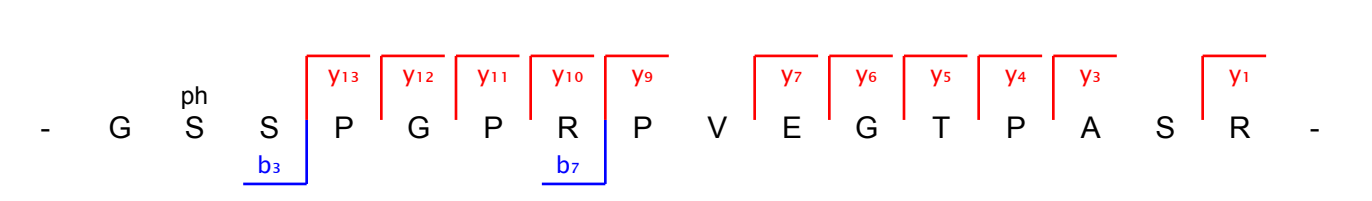
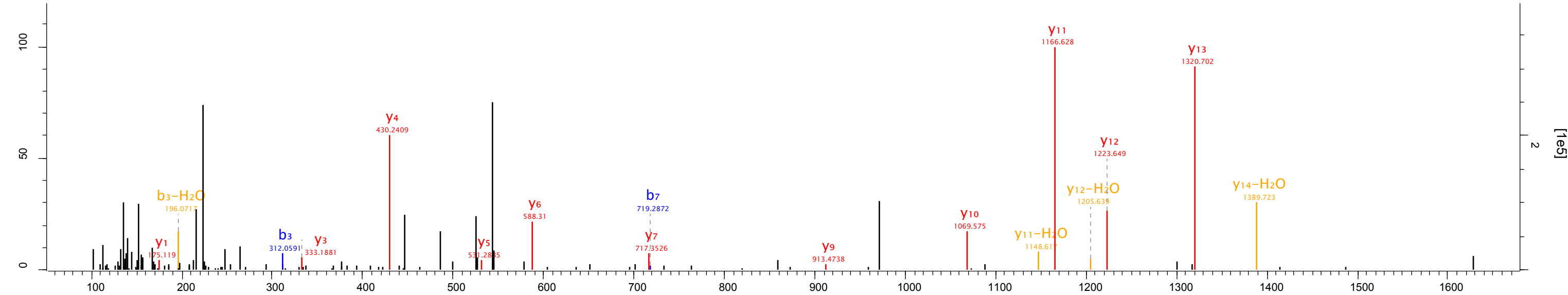


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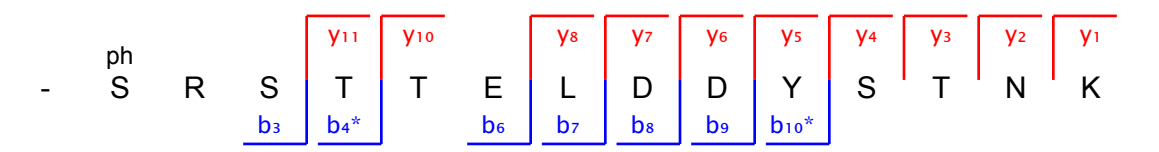
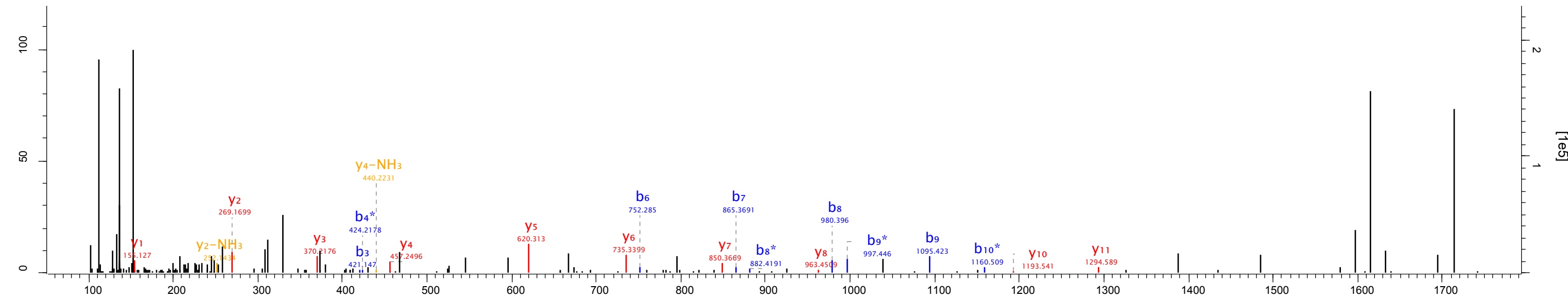
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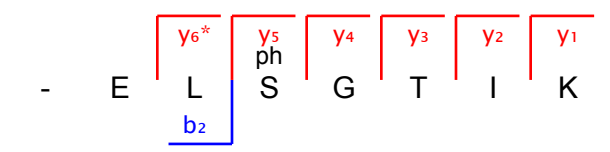
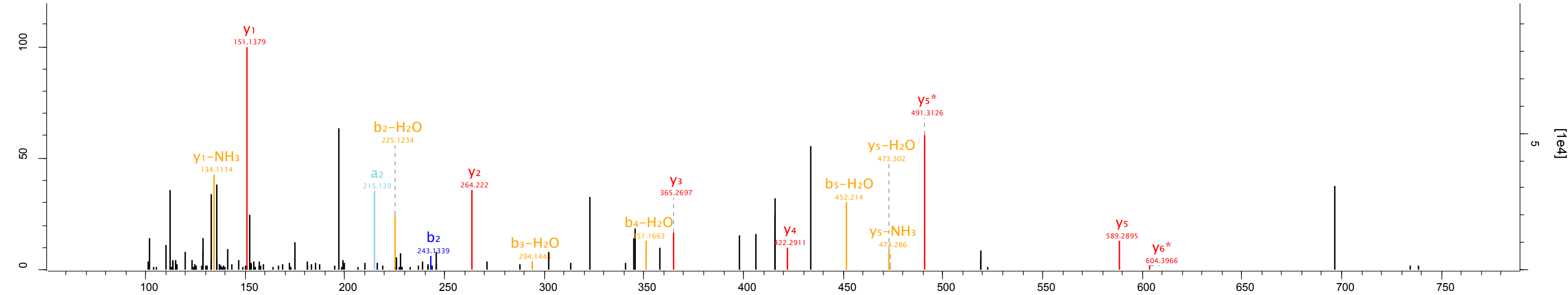
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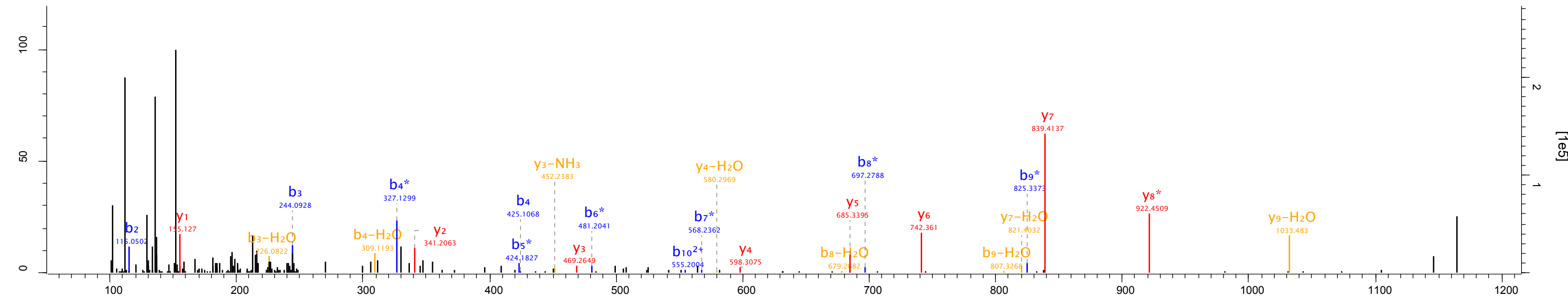


Raw file

20171215_MaS_33SR_LMH_phospho2_06

Scan	Method	Score	m/z	Gene names
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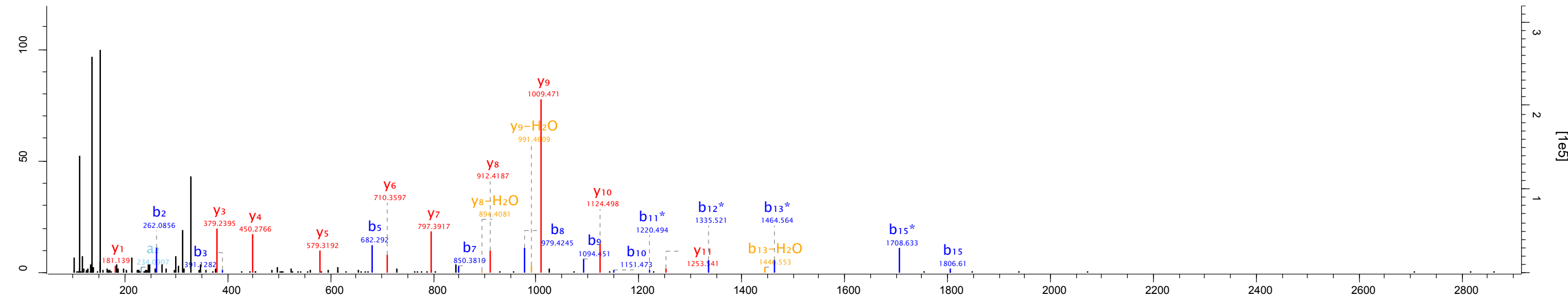


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y₁

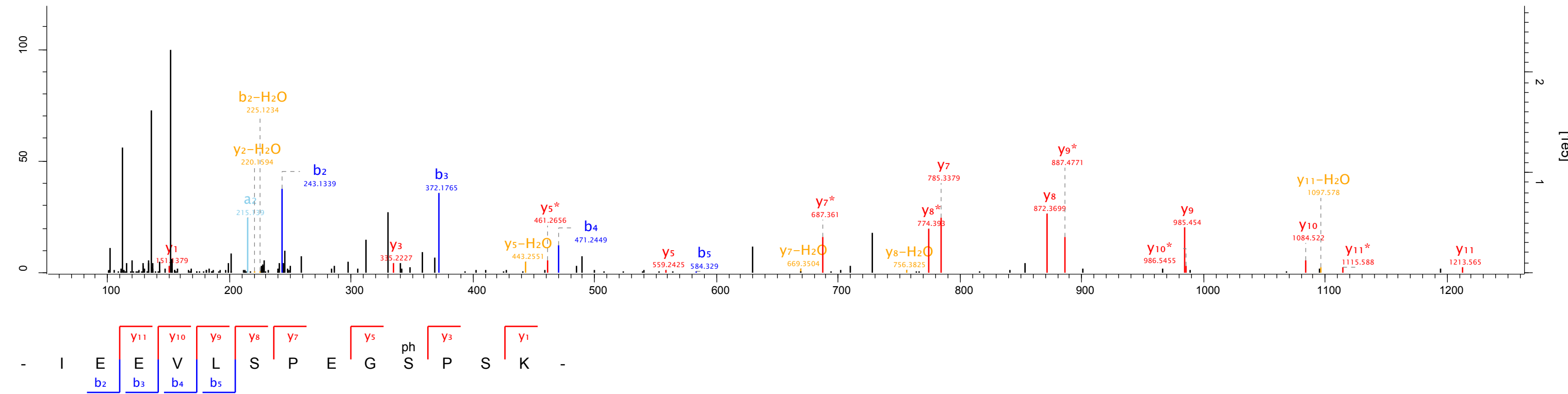
ph

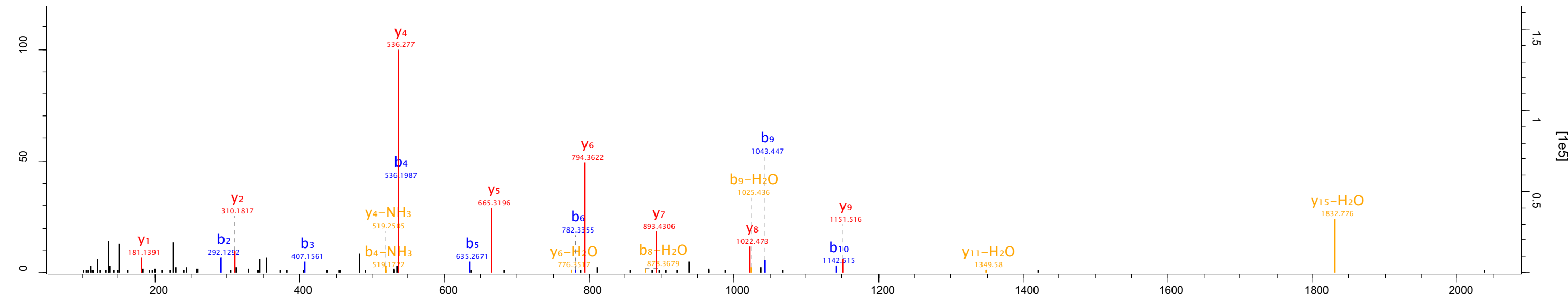


- T C E E R P A E D G S D E E D P D S M E A P T R -

ph

b2 b3 b5 b7 b8 b9 b10 b11* b12* b13* b15 y11 y10 y9 y8 y7 y6 y5 y4 y3 y1



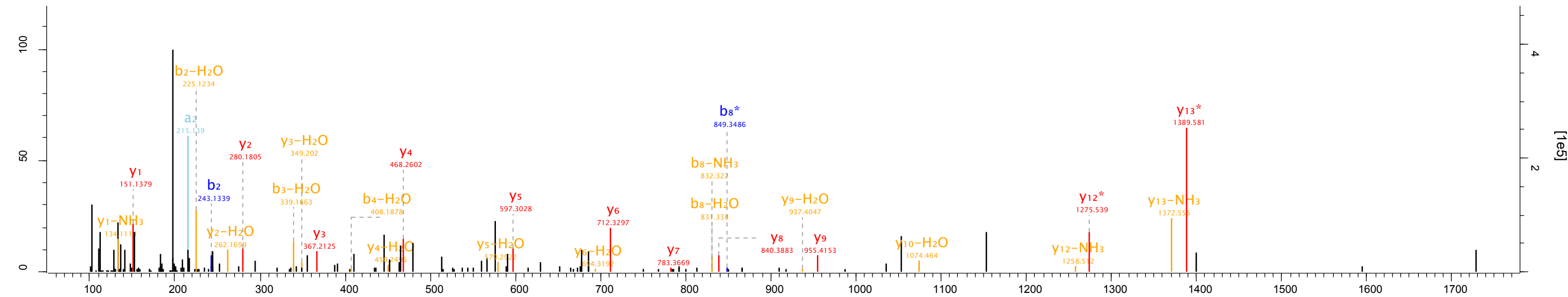


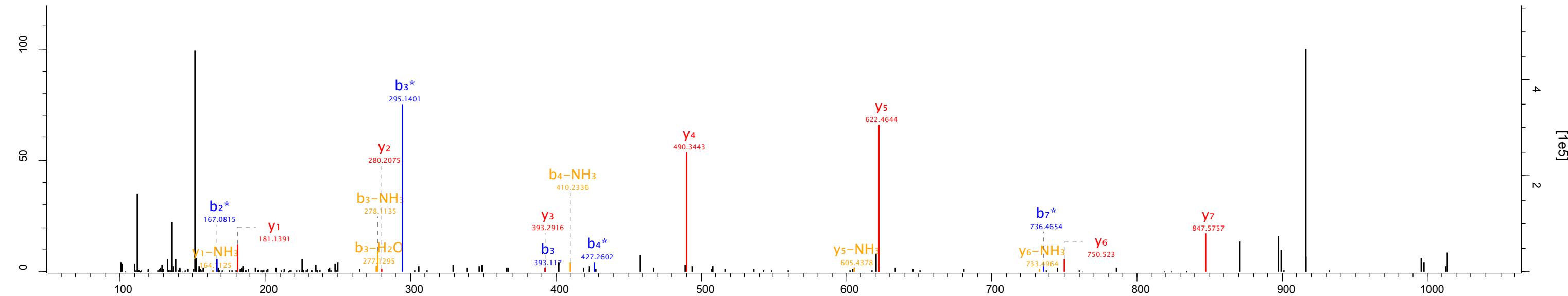
- Y Q D E V F G G F V T E P Q E E S E E E V E E P E E R -

b₂
b₃
b₄
b₅
b₆
b₉
b₁₀
ph
y₉
y₈
y₇
y₆
y₅
y₄
y₂
y₁

Raw file
20171215_MaS_33SR_LMH_phospho2_08

Scan 2208 Method FTMS; HCD Score 75.91 m/z 577.23 Gene names SET



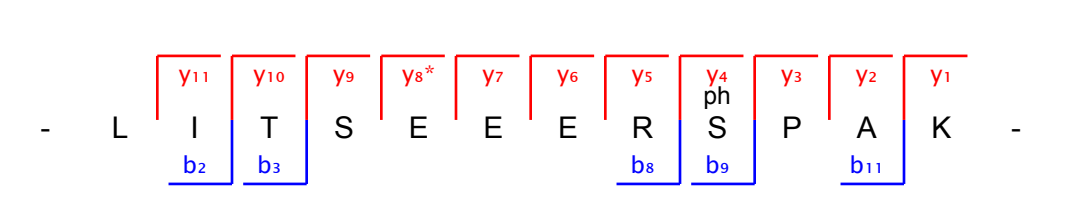
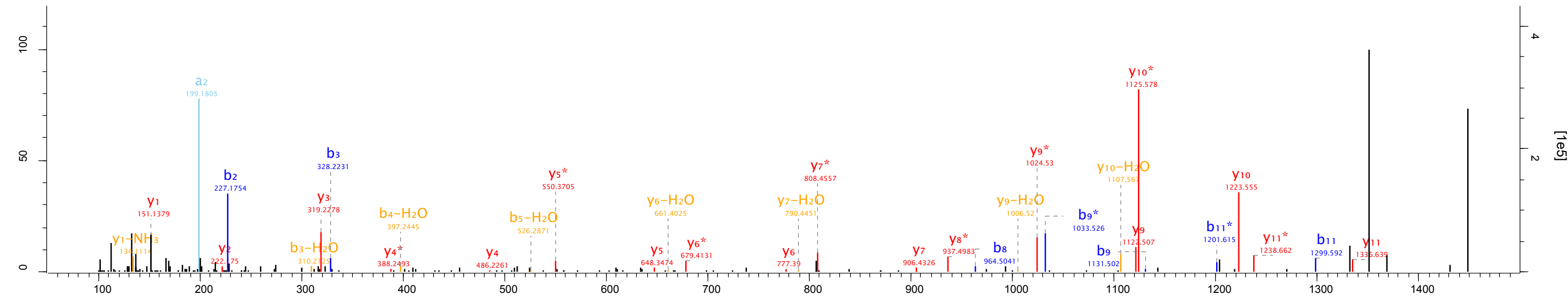


ph S -

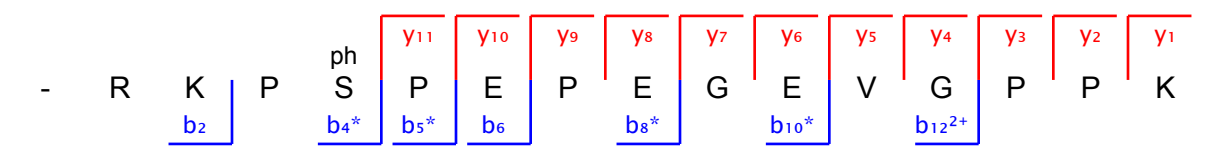
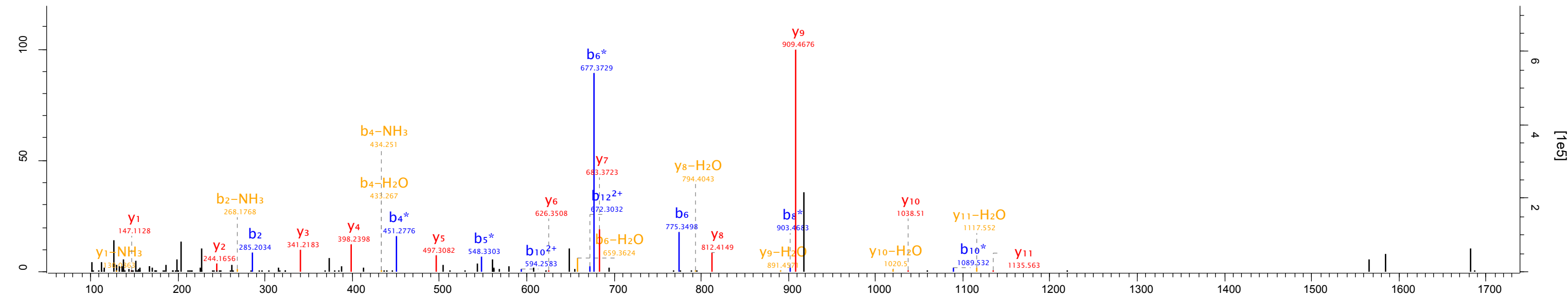
y ₇	y ₆	y ₅	y ₄	y ₃	y ₂	y ₁
P	Q	K	P	I	V	R
b ₂ *	b ₃	b ₄ *			b ₇ *	

-

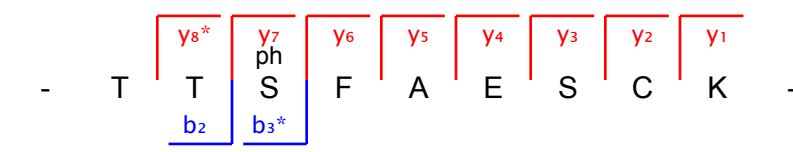
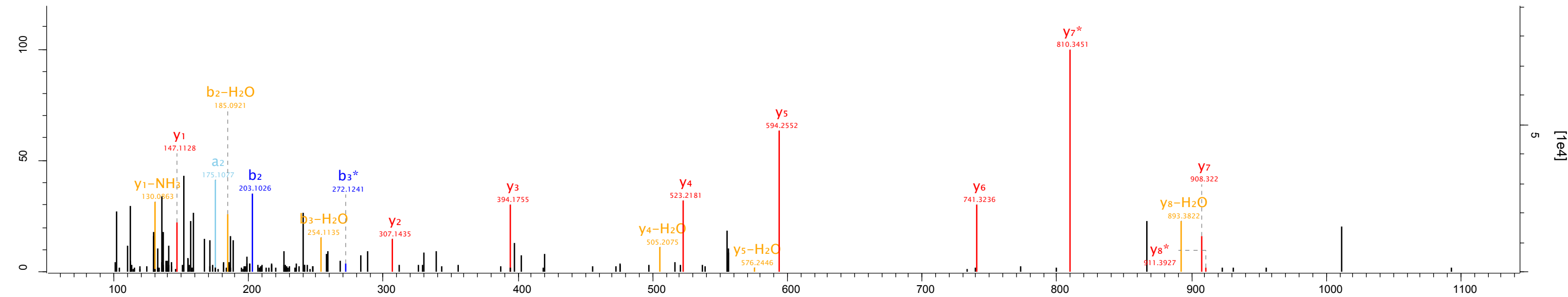
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 Scan: 3458 Method: FTMS; HCD Score: 163.02 m/z: 725.37 Gene names: TP53BP1

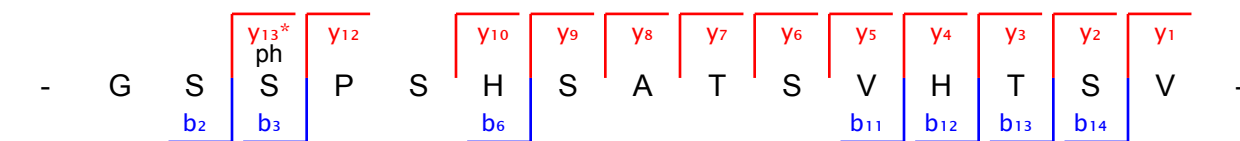
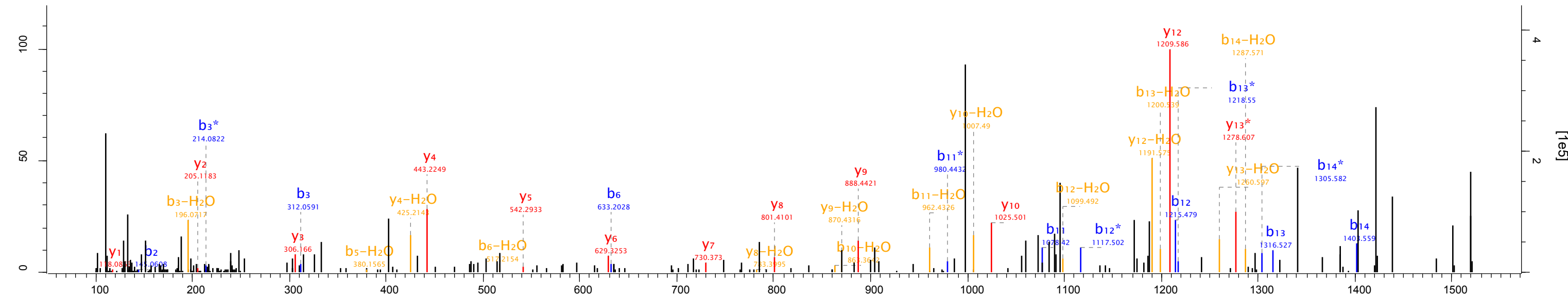


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 Scan: 3568 Method: FTMS; HCD Score: 111.77 m/z: 561.94 Gene names: IRF2BP2

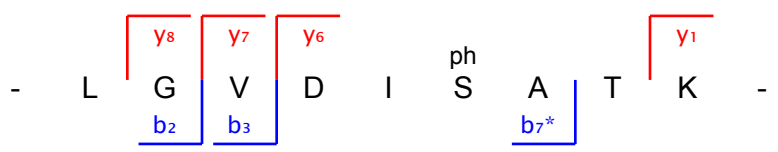
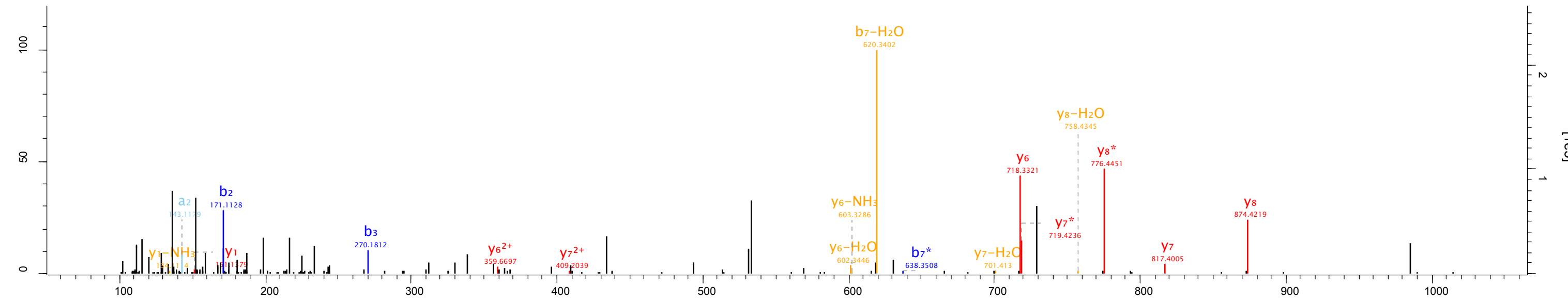


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 Scan: 3668 Method: FTMS; HCD Score: 84.48 m/z: 555.71 Gene names: GSK3B

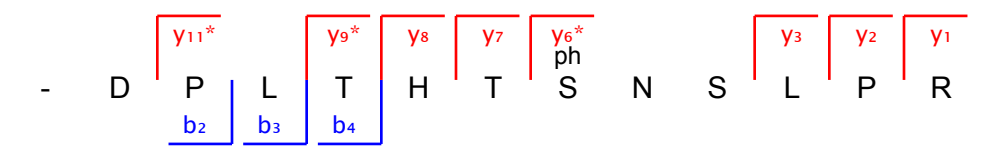
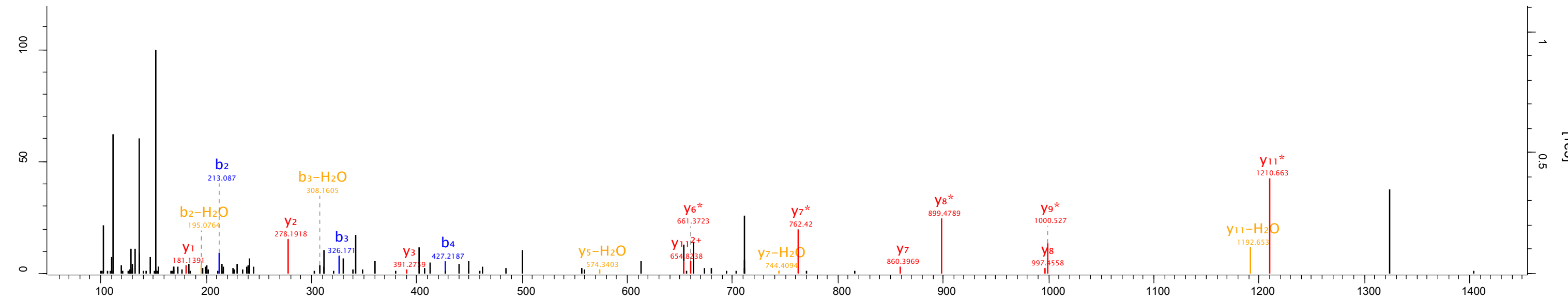




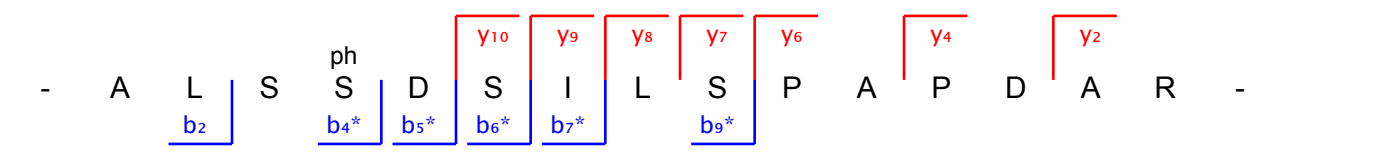
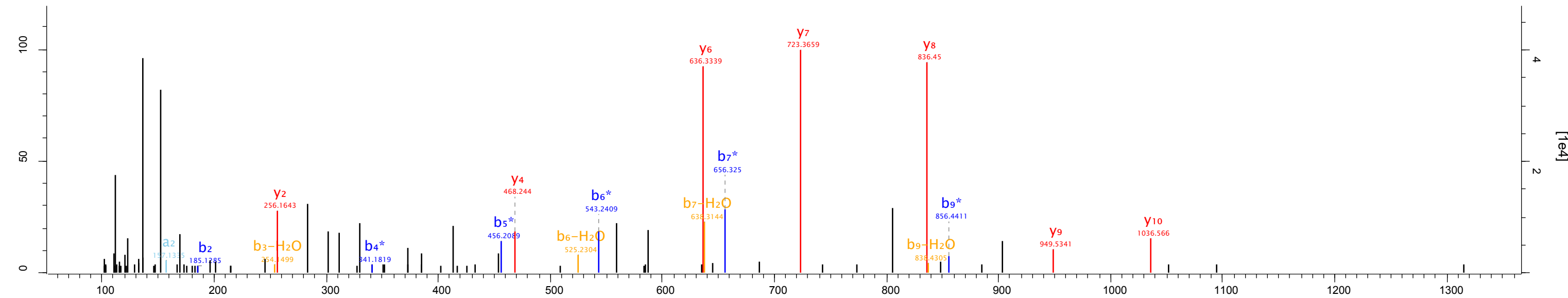
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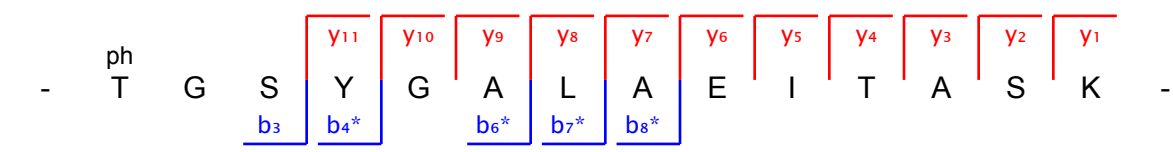
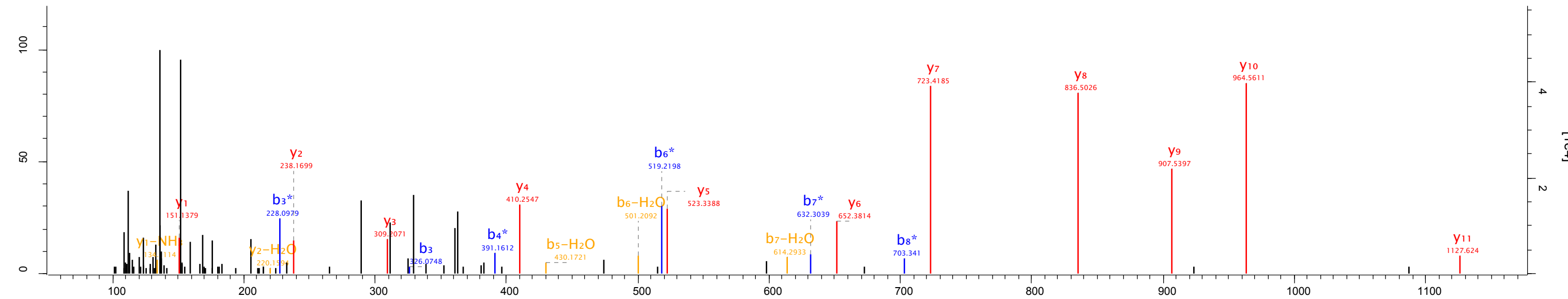
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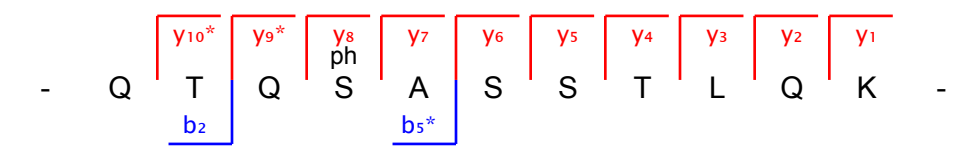
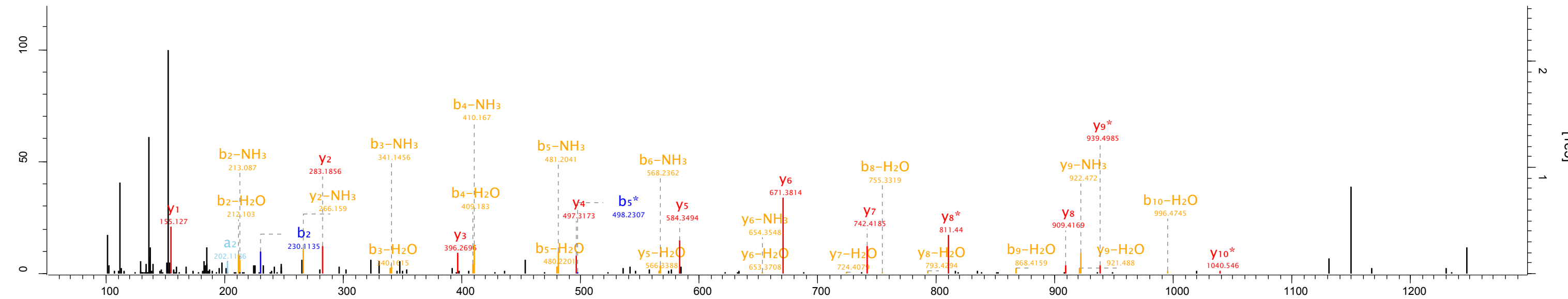
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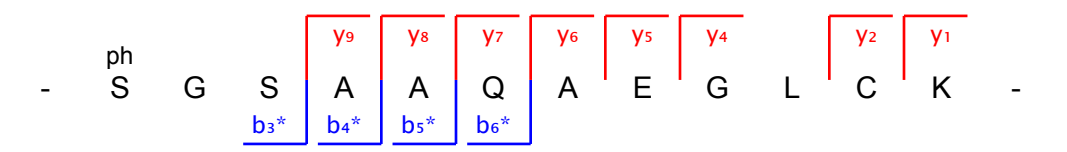
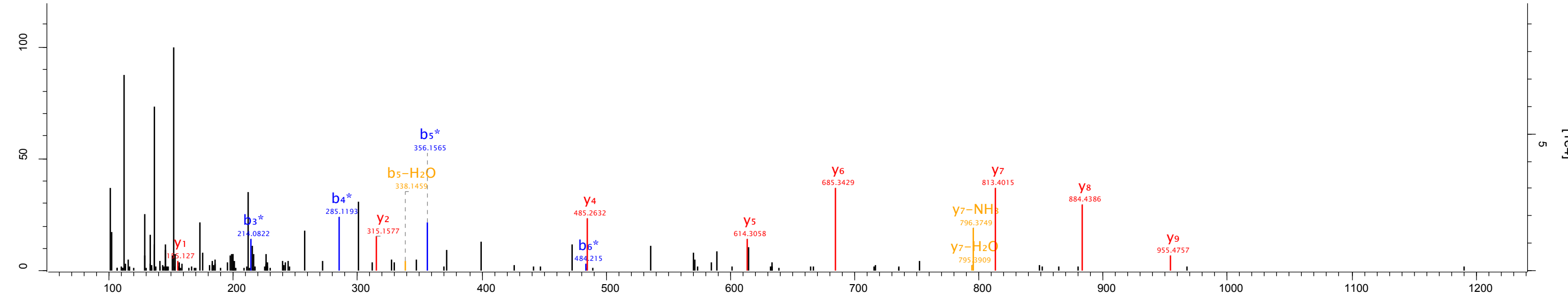
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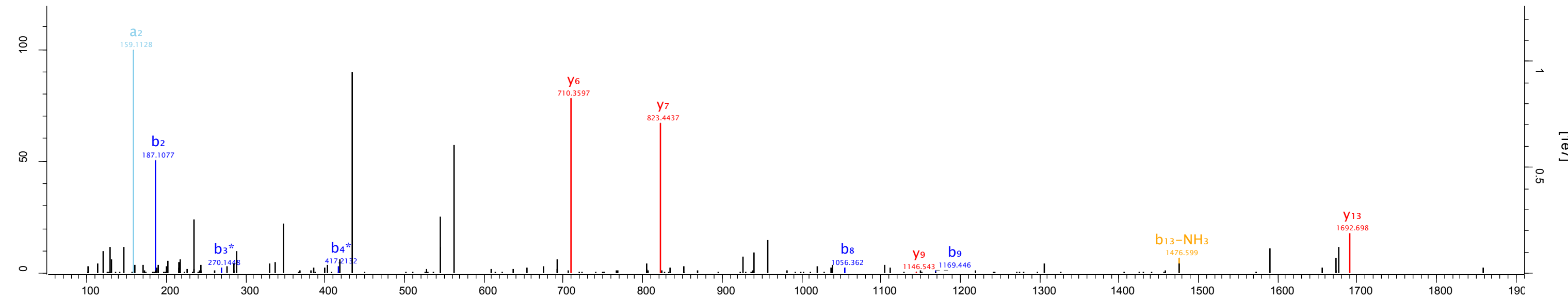
Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 2668 Method FTMS; HCD Score 115.12 m/z 633.79 Gene names MAP4K4



20171215_MaS_33SR_LMH_phospho2_09 3858 FTMS; HCD 49.19 633.77 ALG3



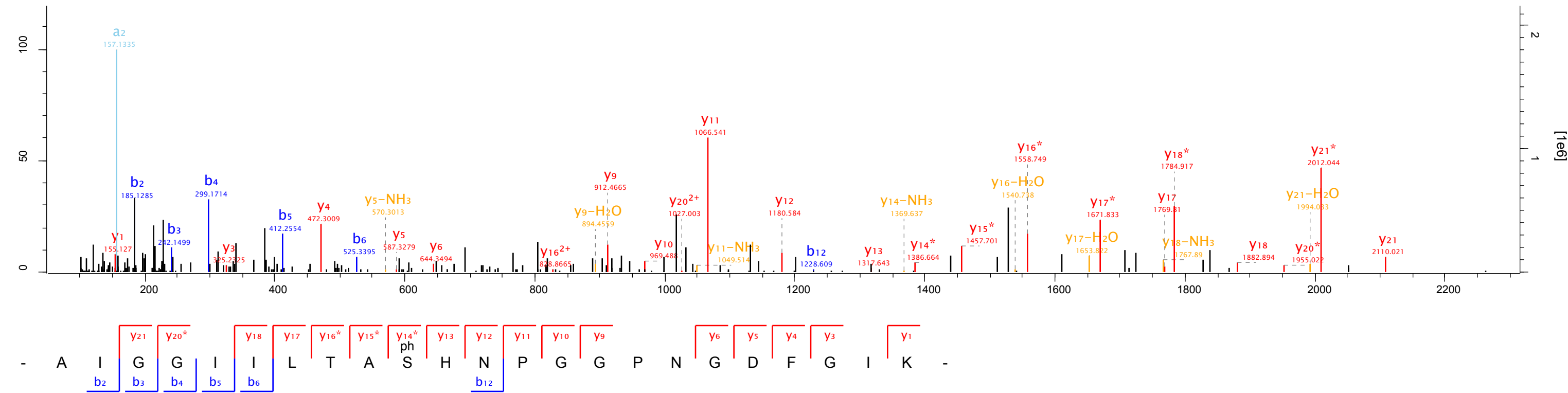
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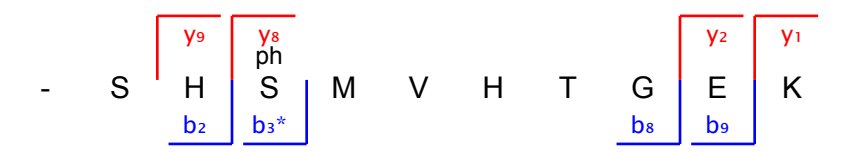
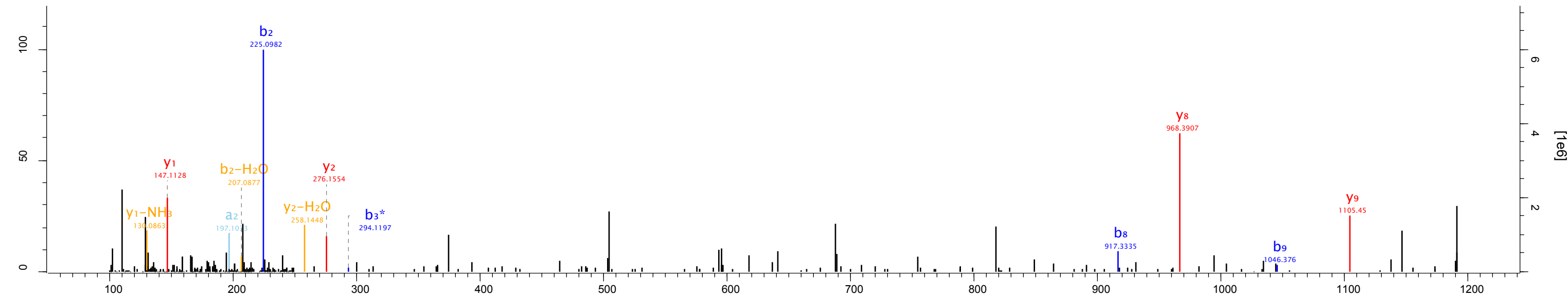
- V S T F A ox M R ph S L A ph S L A L R -

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

- b₂ (under S)
- b₃* (under T)
- b₄* (under F)
- b₈ (under S)
- b₉ (under L)
- y₉ (under R)
- y₇ (under L)
- y₆ (under A)
- y₁₃ (under T)



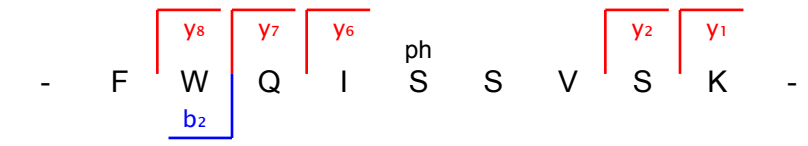
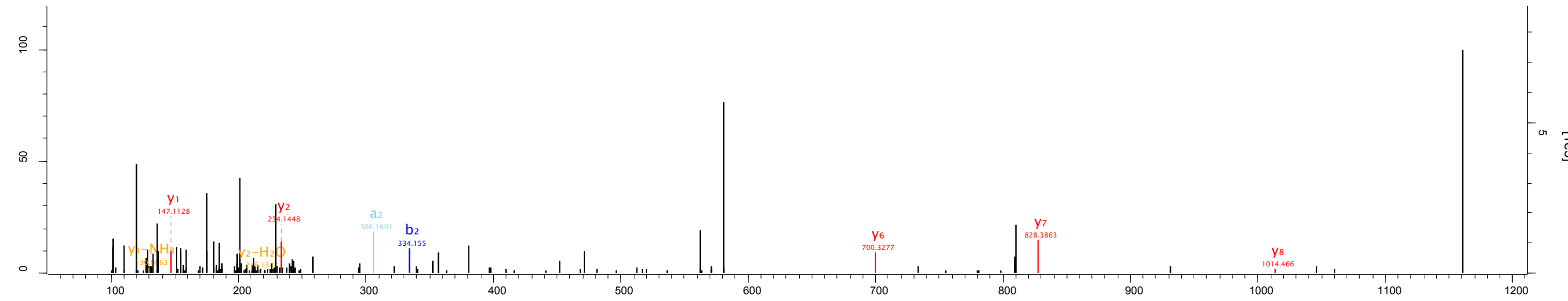
Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 9208 Method FTMS; HCD Score 52.73 m/z 596.74 Gene names ZNF155



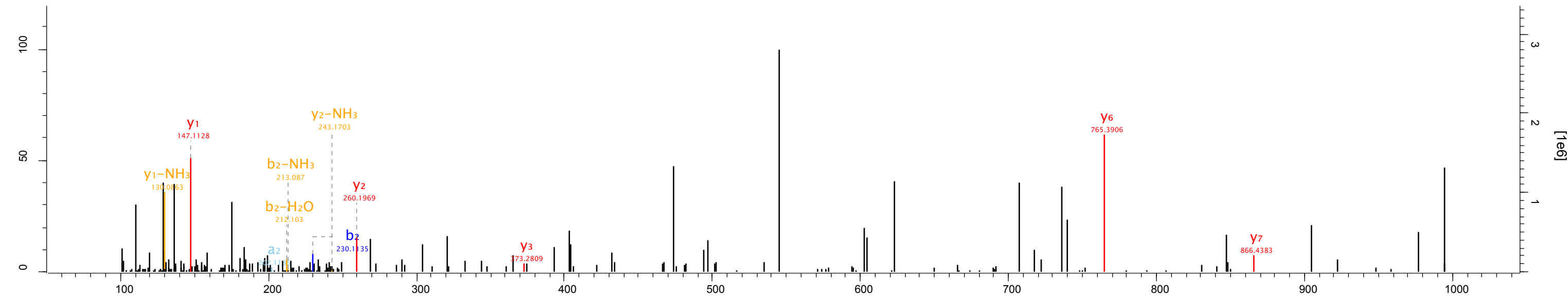
Raw file

20171215_MaS_33SR_LMH_proteome_02

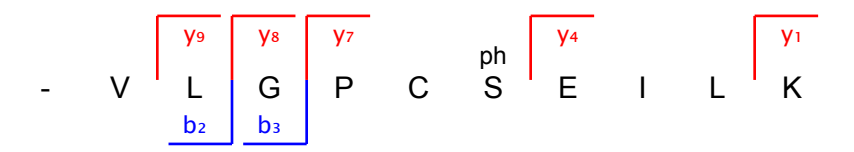
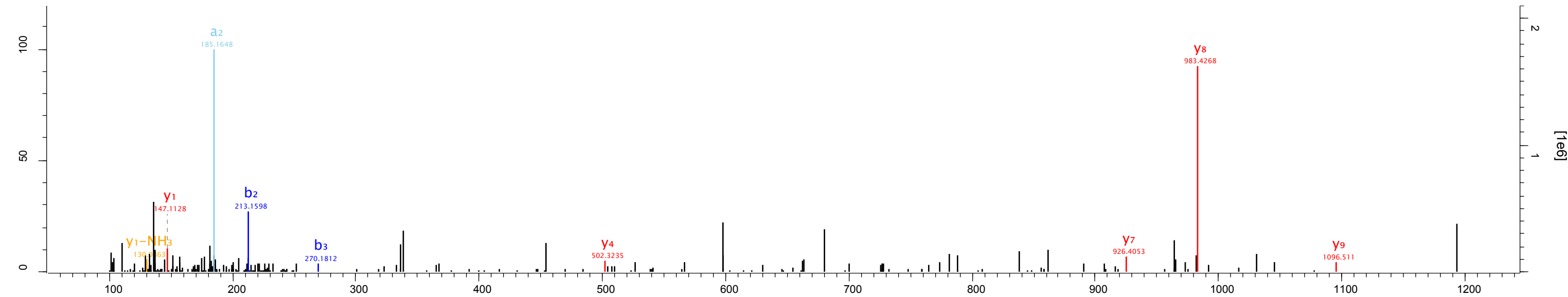
Scan 19638 Method FTMS; HCD Score 46.46 m/z 581.27 Gene names KDM5A



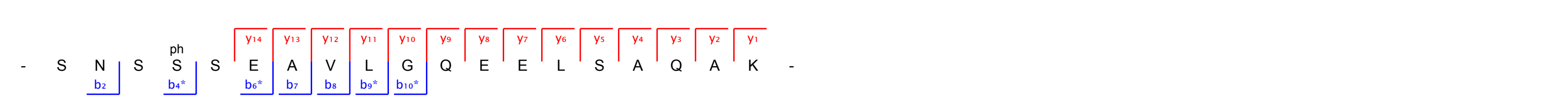
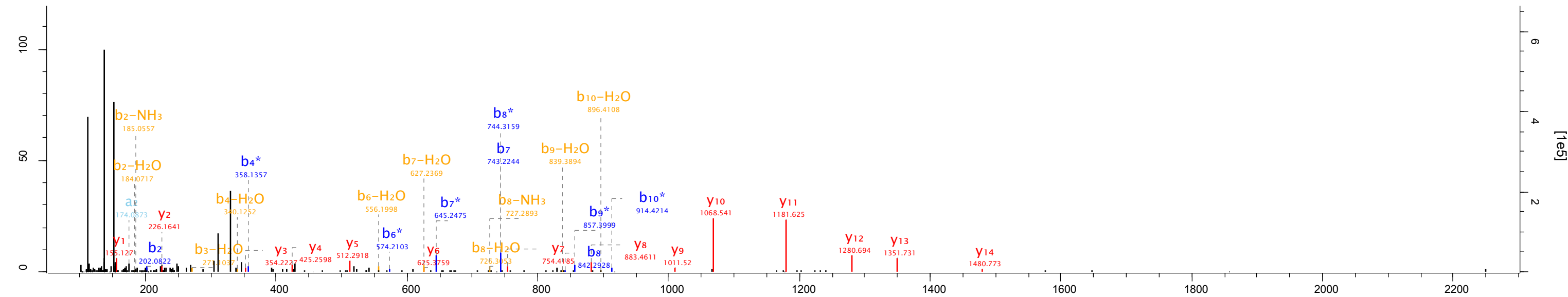
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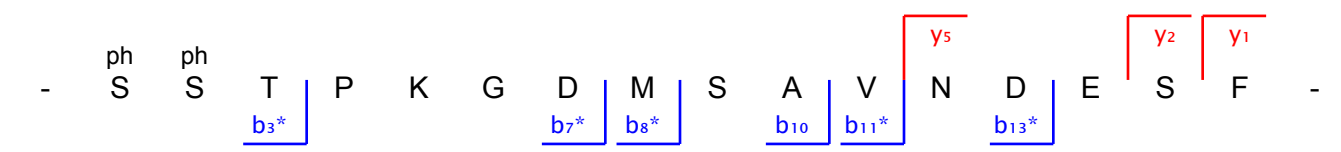
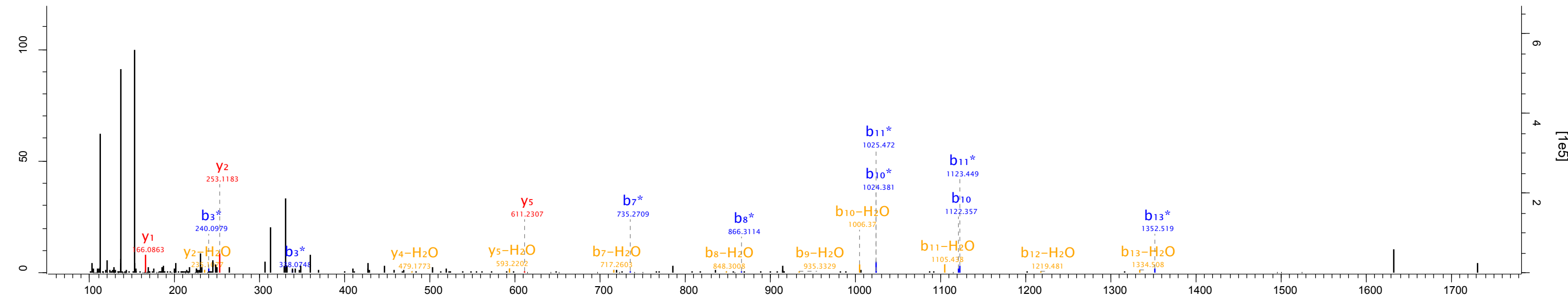
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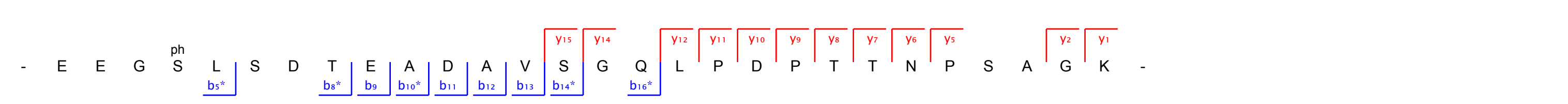
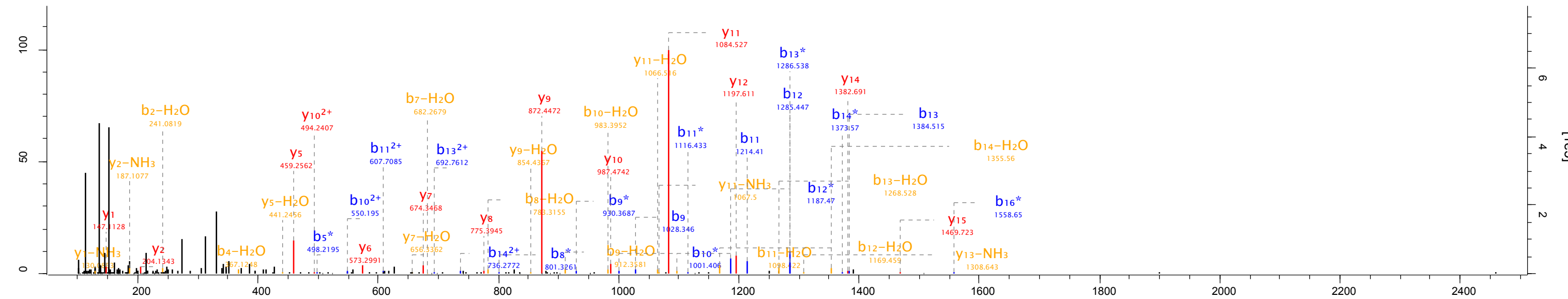
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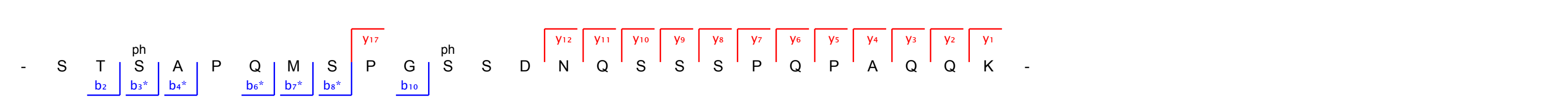
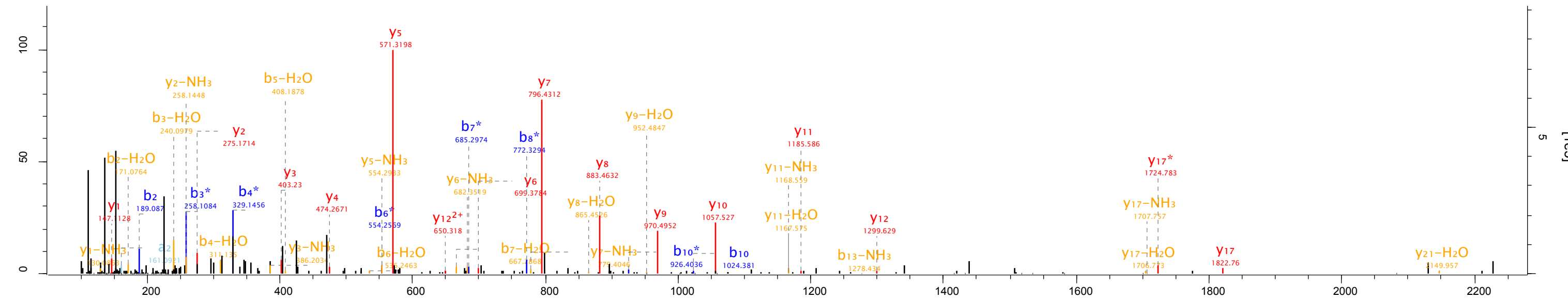
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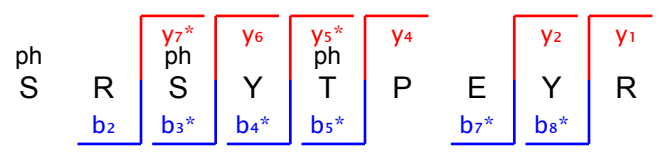
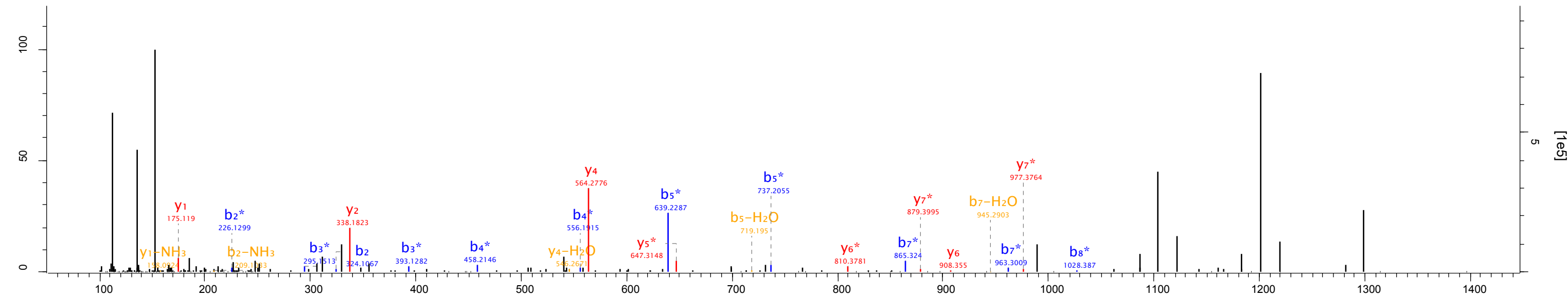
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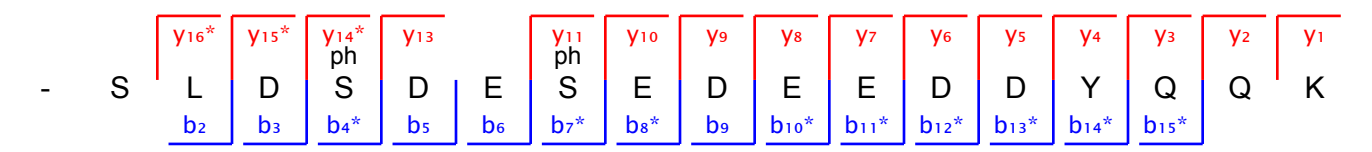
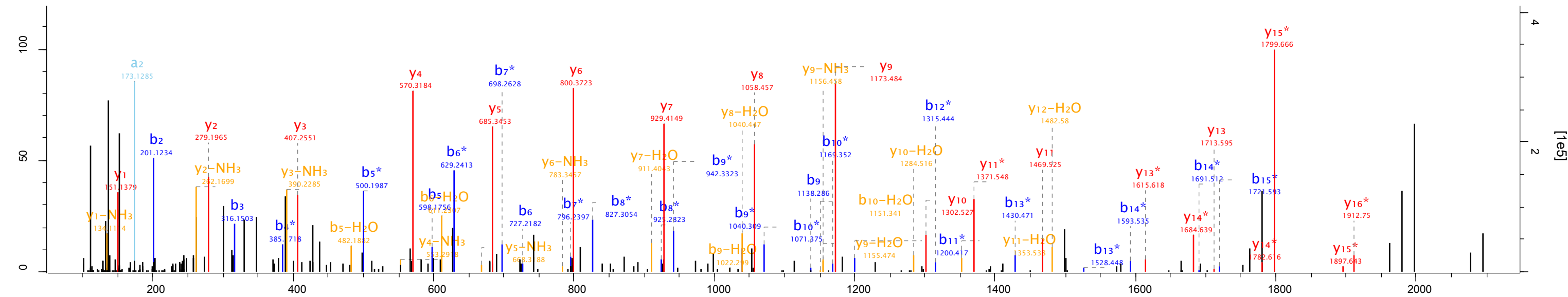
Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 4579 Method FTMS; HCD Score 86.26 m/z 898.02 Gene names UBAP2L



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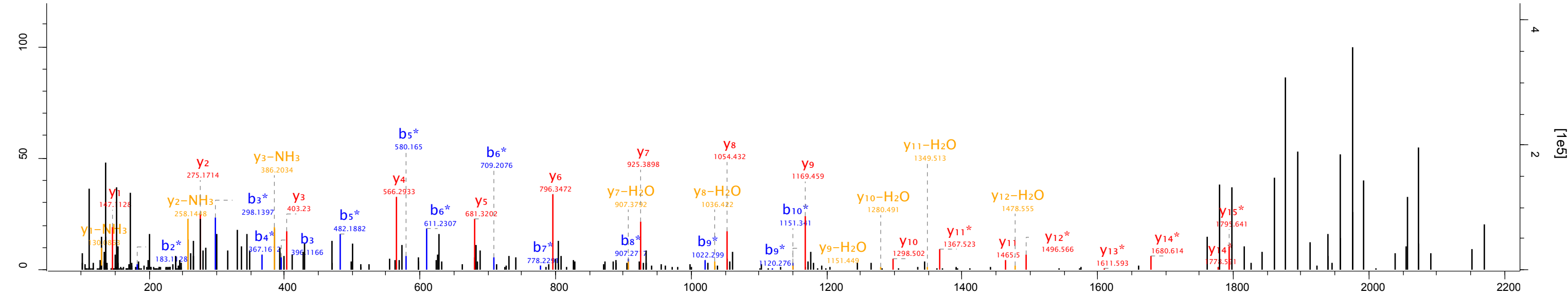


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Raw file Scan Method Score m/z Gene names

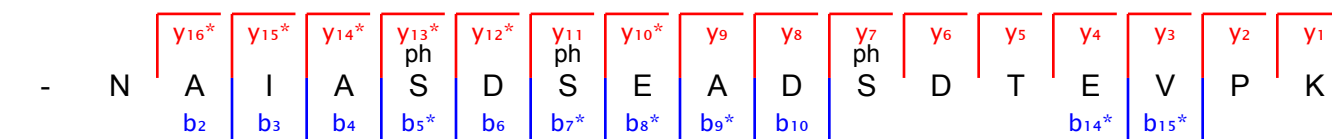
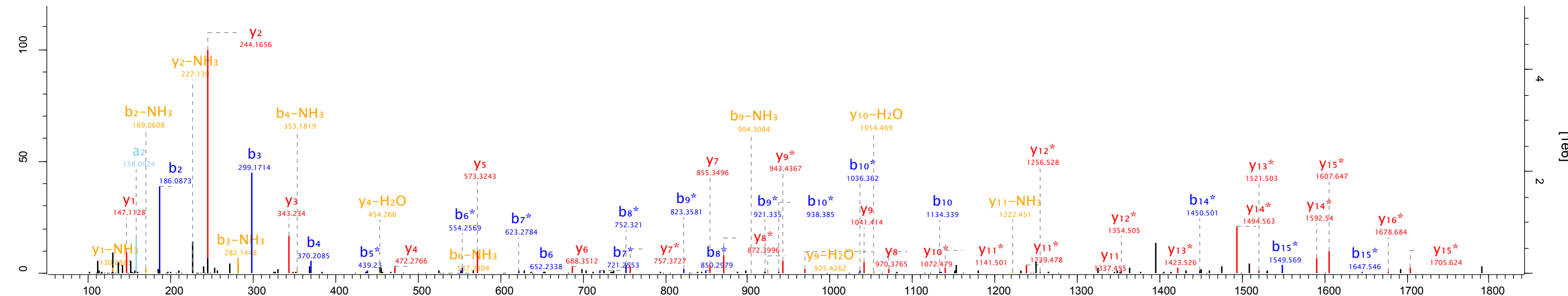
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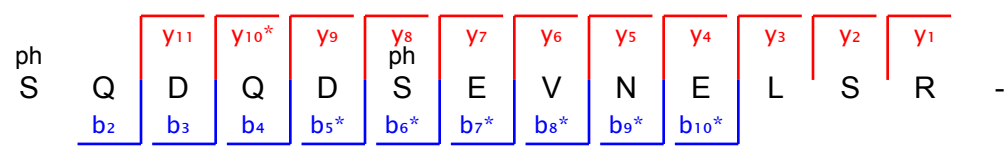
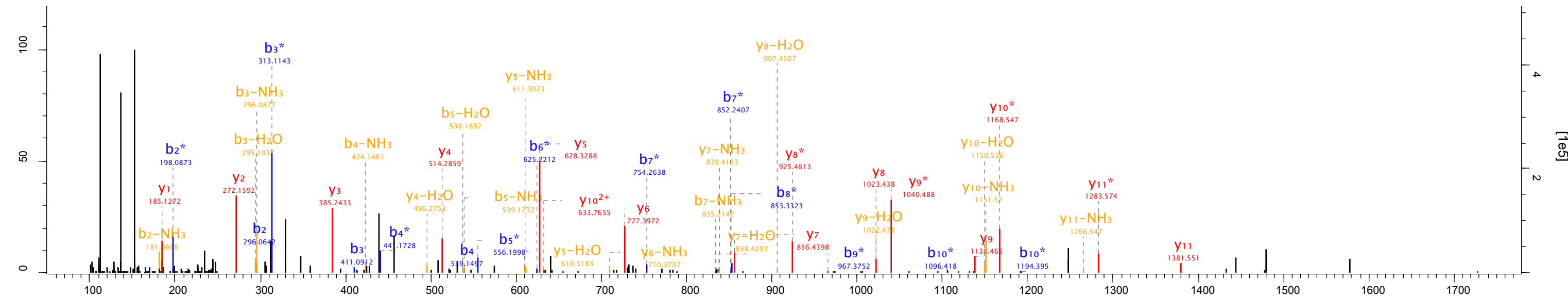
ph S L D S D E S E D E E D D Y Q Q K -

y15*
y14*
ph
y13*
y12*
y11
ph
y10
y9
y8
y7
y6
y5
y4
y3
y2
y1

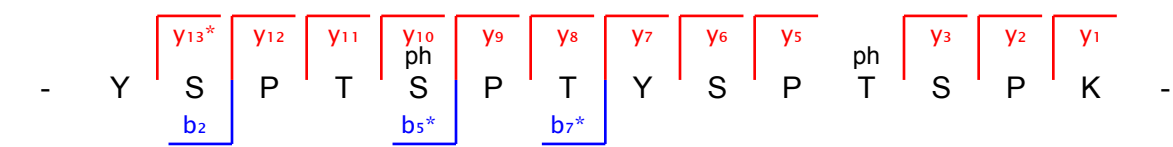
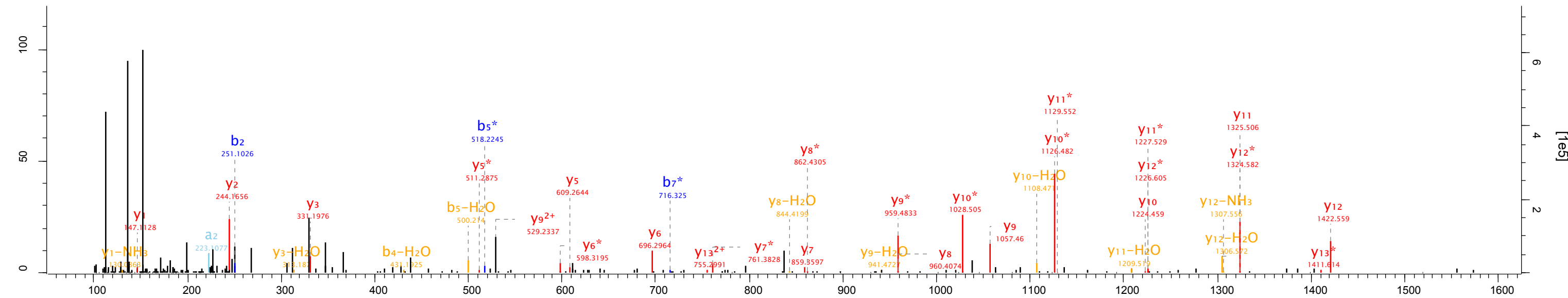
b2*
b3
b4*
b5*
b6*
b7*
b8*
b9*
b10*



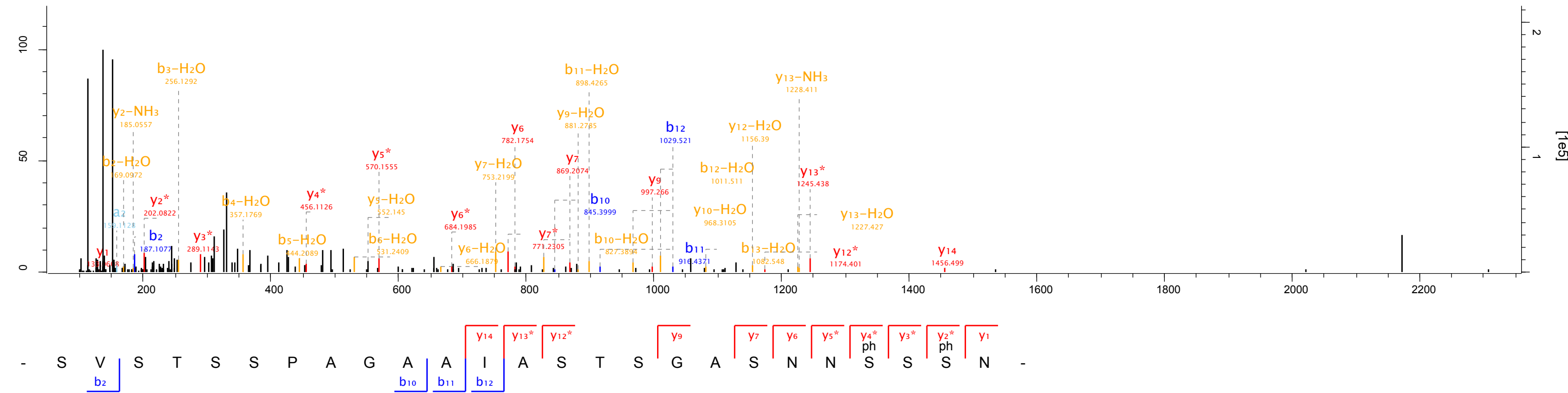
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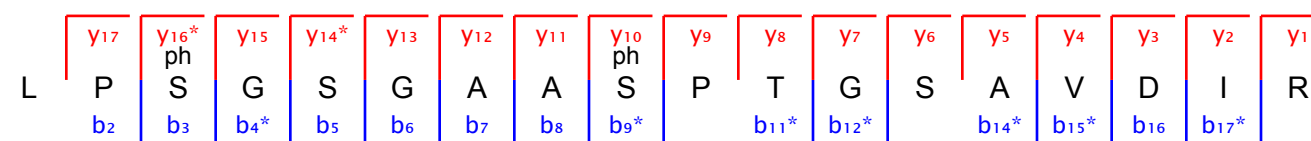
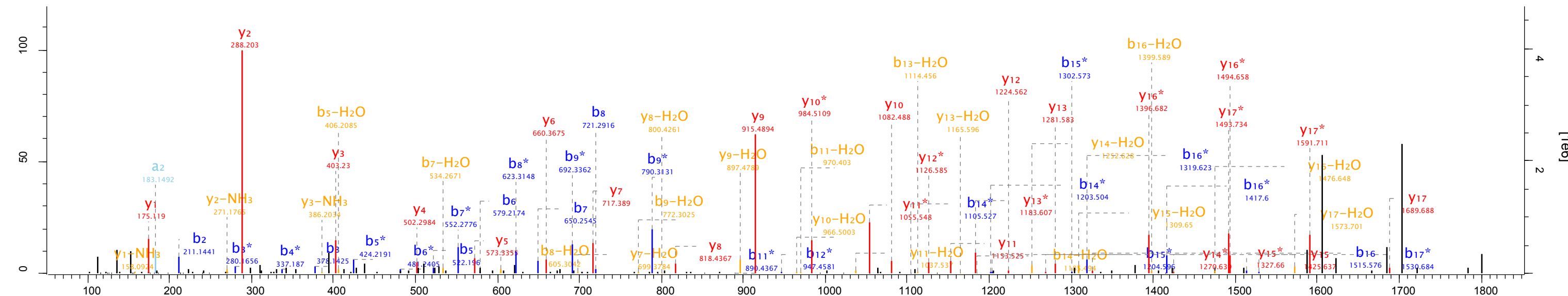
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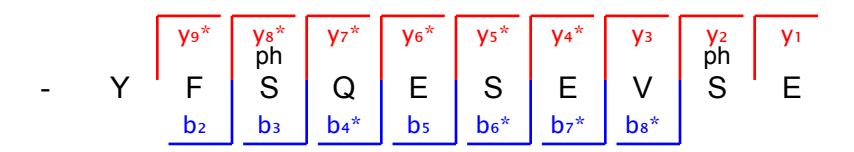
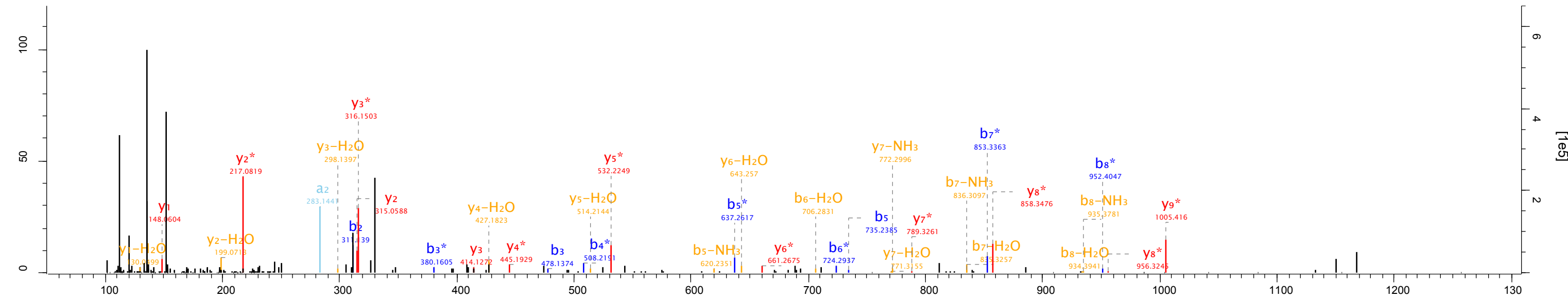


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 20171215_MaS_33SR_LMH_phospho_01
 Scan 9609 FTMS; HCD Score 291.1 m/z 901.89 Gene names AHNAK

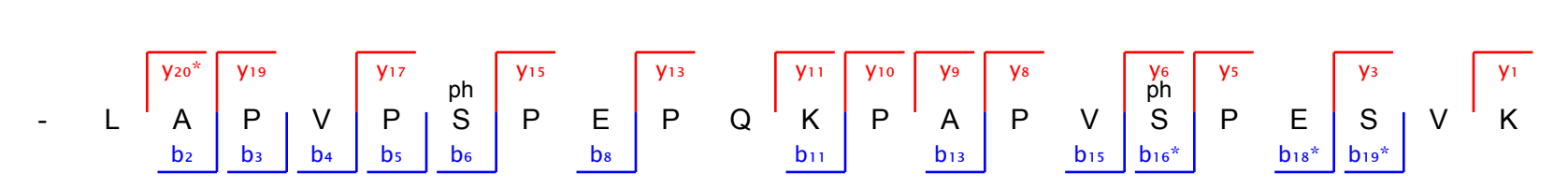
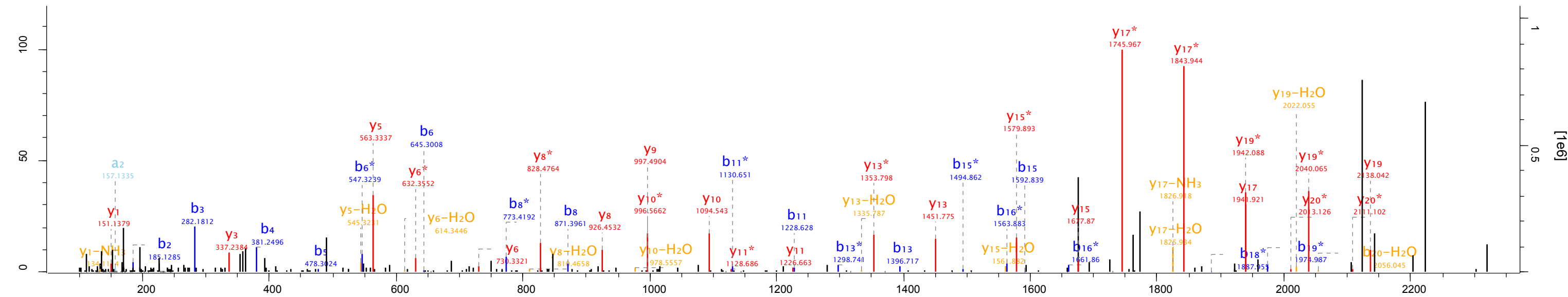


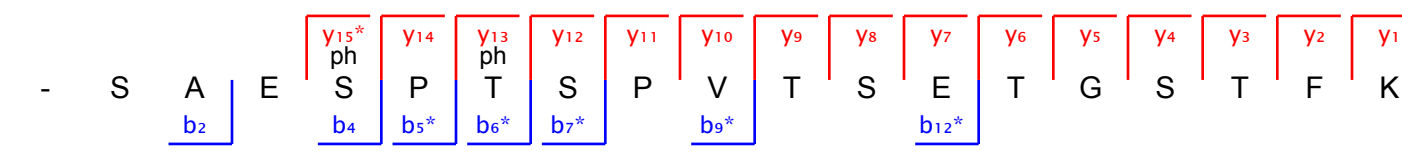
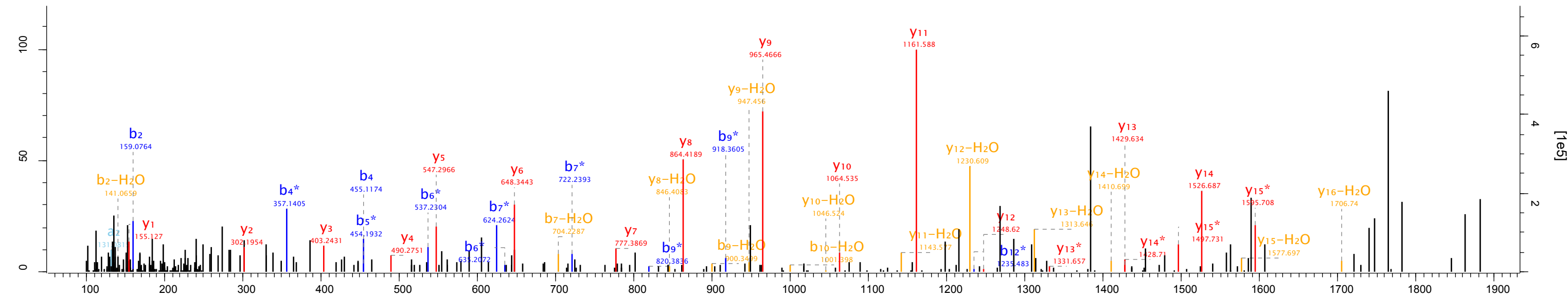
- L P S G S G A A S P T G S A V D I R -
 b2 b3 b4* b5 b6 b7 b8 b9* b11* b12* b14* b15* b16 b17*

Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 9979 Method FTMS; HCD Score 145.61 m/z 682.72 Gene names KRT80

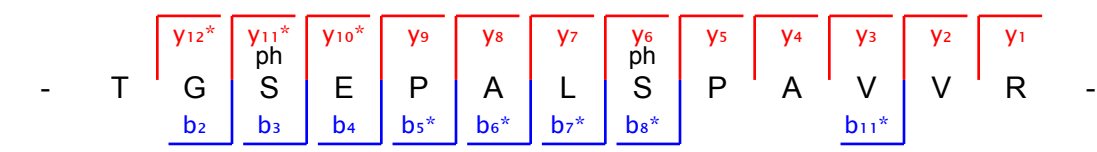
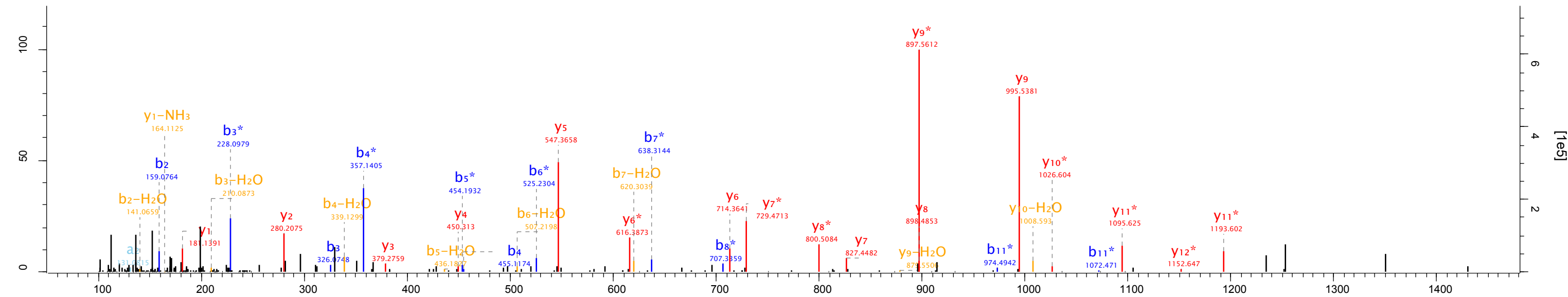


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 Scan: 11029 Method: FTMS; HCD Score: 194.26 m/z: 1162.09 Gene names: CHAMP1





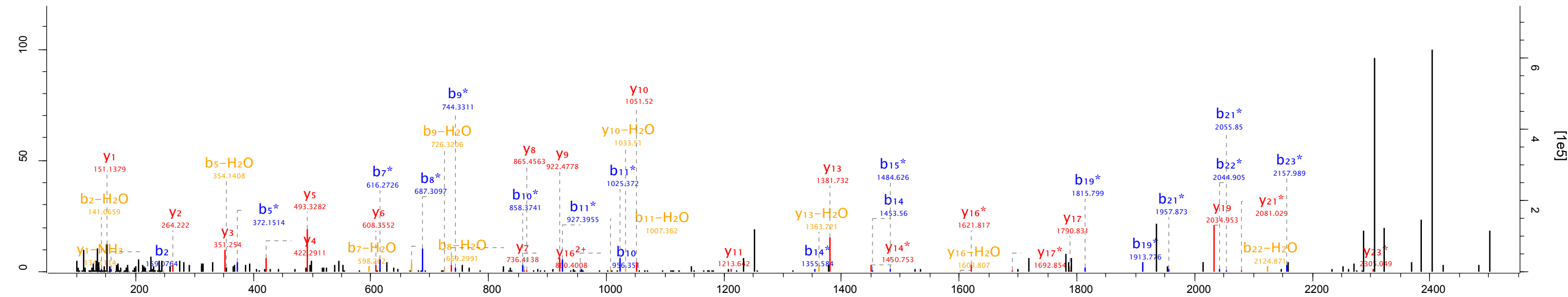
Raw file: 20171215_MaS_33SR_LMH_phospho_02
 Scan: 11059 Method: FTMS; HCD Score: 142.72 m/z: 725.33 Gene names: BCAR3



Raw file

20171215_MaS_33SR_LMH_phospho_02

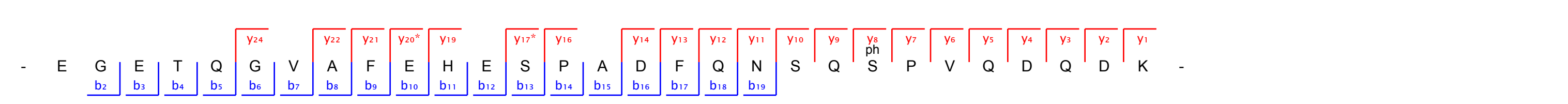
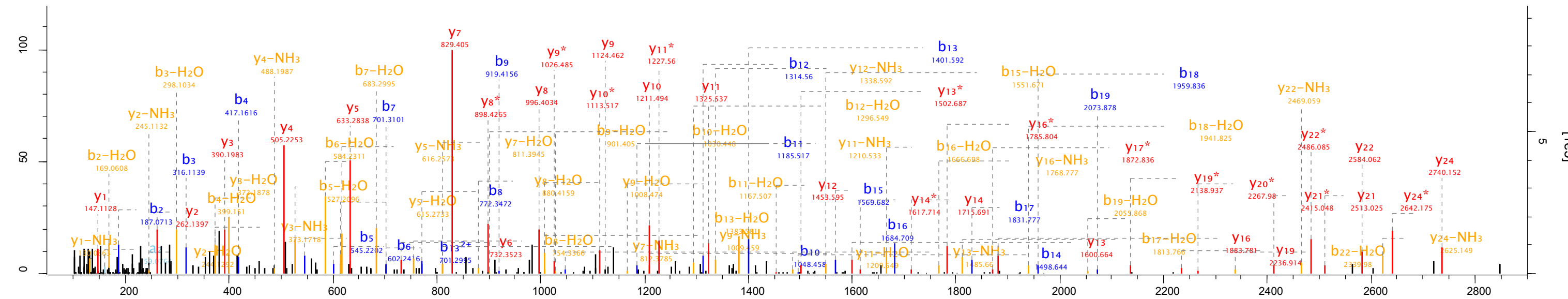
Scan	Method	Score	m/z	Gene names
11209	FTMS; HCD	104.15	1252.54	ZC3H4



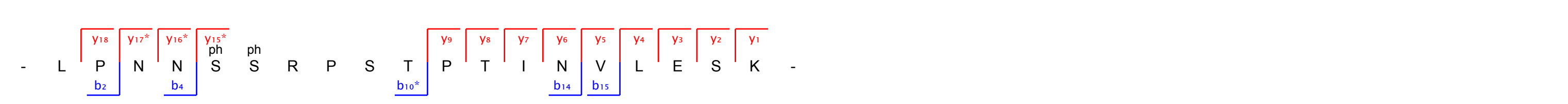
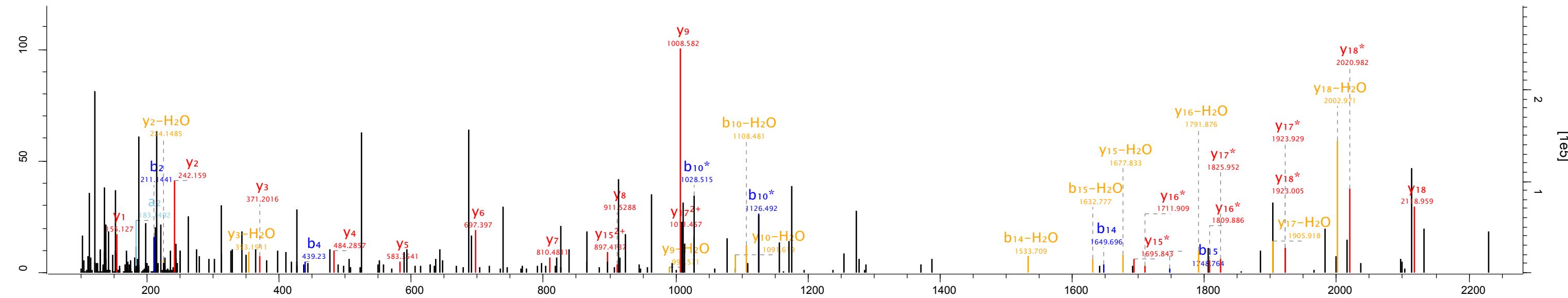
- T G S G S P F A G N S P A R E G E Q D A A S L K -

y₂₃*
y₂₁*
y₁₉
y₁₇
y₁₆*
y₁₄*
y₁₃
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y₇
y₆
y₅
y₄
y₃
y₂
y₁

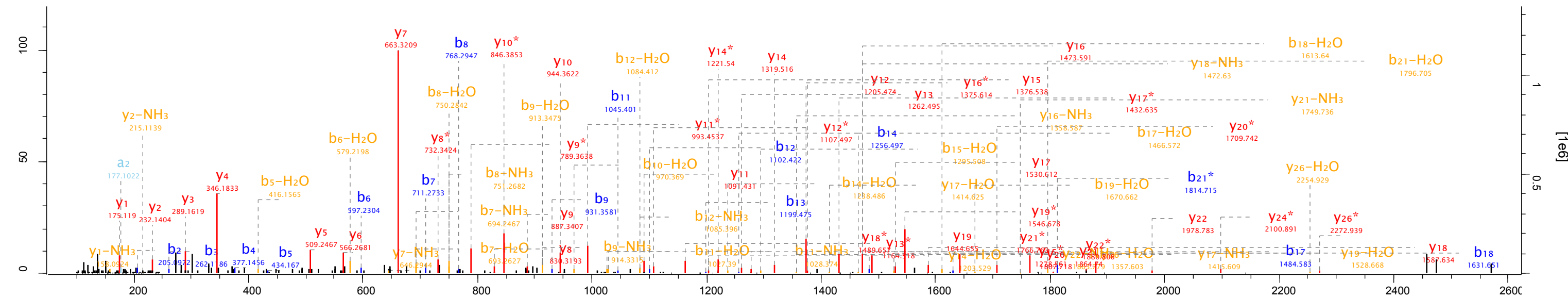
b₂
b₅*
b₇*
b₈*
b₉*
b₁₀
b₁₁*
b₁₄
b₁₅*
b₁₉*
b₂₁*
b₂₂*
b₂₃*



Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 12939 Method FTMS; HCD Score 68.15 m/z 744.69 Gene names EZH2



Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 12979 Method FTMS; HCD Score 307.19 m/z 1288.01 Gene names HNRNPA2B1



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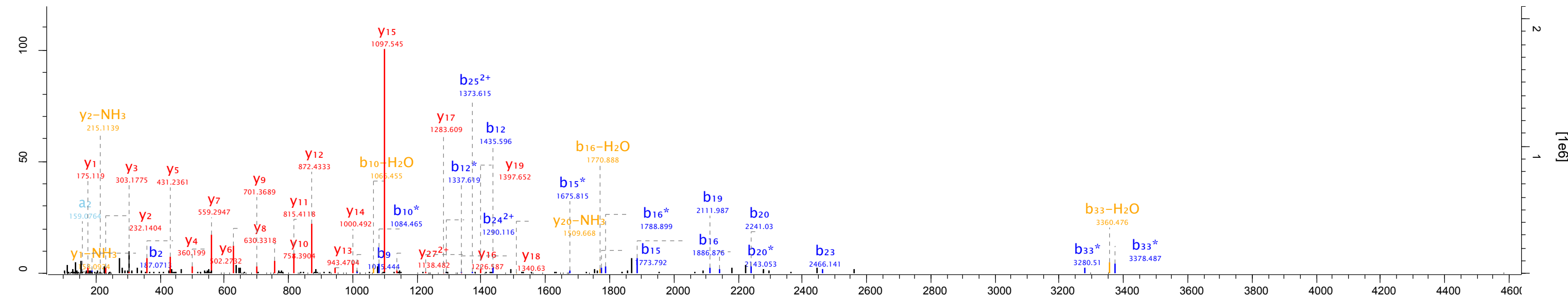
Fragmentation labels below the sequence:

- b₂ (under F)
- b₃ (under G)
- b₄ (under D)
- b₅ (under G)
- b₆ (under Y)
- b₇ (under N)
- b₈ (under G)
- b₉ (under Y)
- b₁₁ (under G)
- b₁₂ (under G)
- b₁₃ (under P)
- b₁₄ (under G)
- b₁₇ (under N)
- b₁₈ (under F)
- b₂₁* (under S)

Fragmentation labels above the sequence:

- y₂₆* (above G)
- y₂₄* (above D)
- y₂₂ (above N)
- y₂₁ (above G)
- y₂₀ (above Y)
- y₁₉ (above G)
- y₁₈ (above G)
- y₁₇ (above G)
- y₁₆ (above P)
- y₁₅ (above G)
- y₁₄ (above G)
- y₁₃ (above G)
- y₁₂ (above N)
- y₁₁ (above F)
- y₁₀ (above G)
- y₉ (above G)
- y₈ (above S)
- y₇ (above P)
- y₆ (above G)
- y₅ (above Y)
- y₄ (above G)
- y₃ (above G)
- y₂ (above G)
- y₁ (above R)

Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 13059 Method FTMS; HCD Score 85.93 m/z 1144.76 Gene names LARP1



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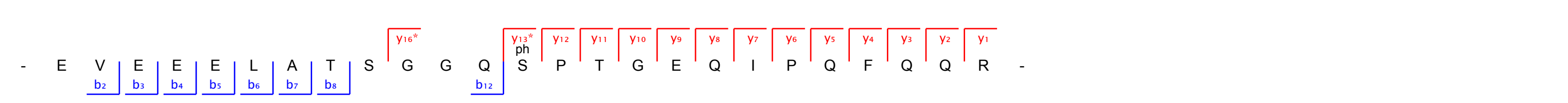
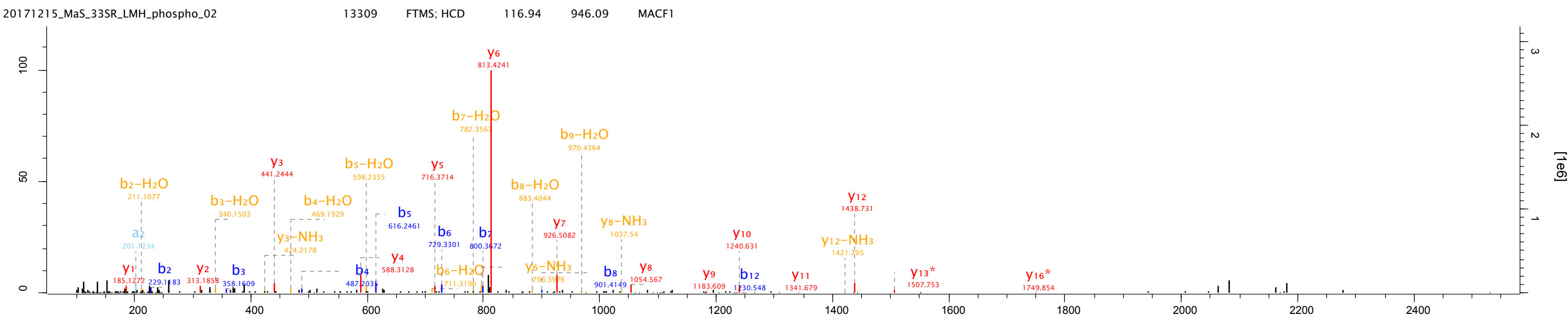
ph ph

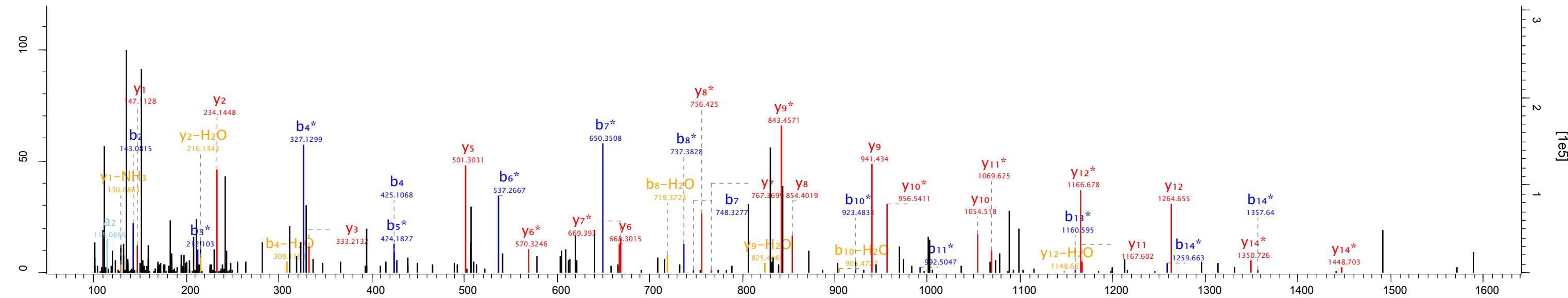
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y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁ y₁₉ y₁₈ y₁₇ y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁

G A A G A A G A G R -

Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 13309 Method FTMS; HCD Score 116.94 m/z 946.09 Gene names MACF1



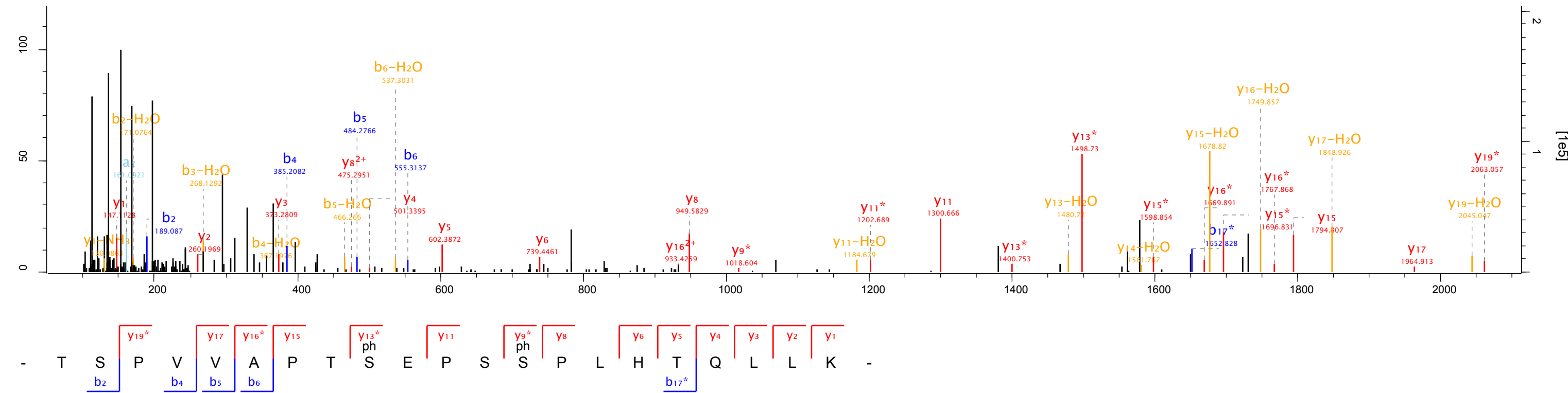


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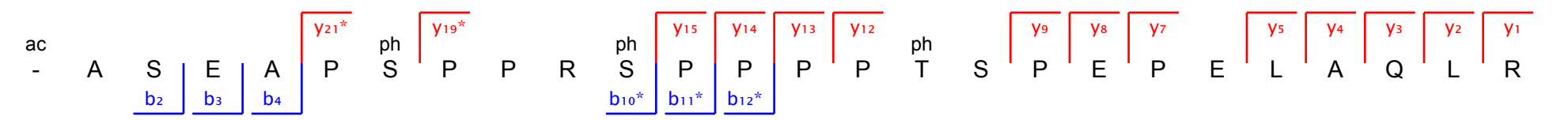
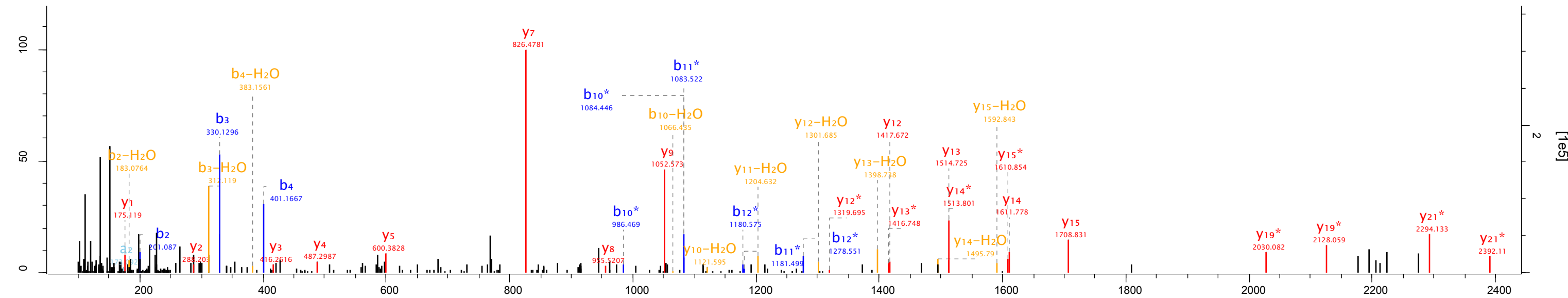
y₁₄^{*}
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y₁₀
y₉
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y₇
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ph
y₅
y₃
y₂
y₁

b₂
b₃^{*}
b₄
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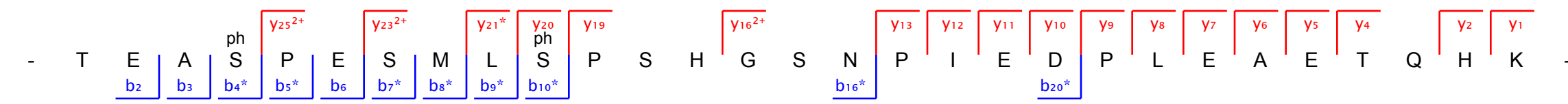
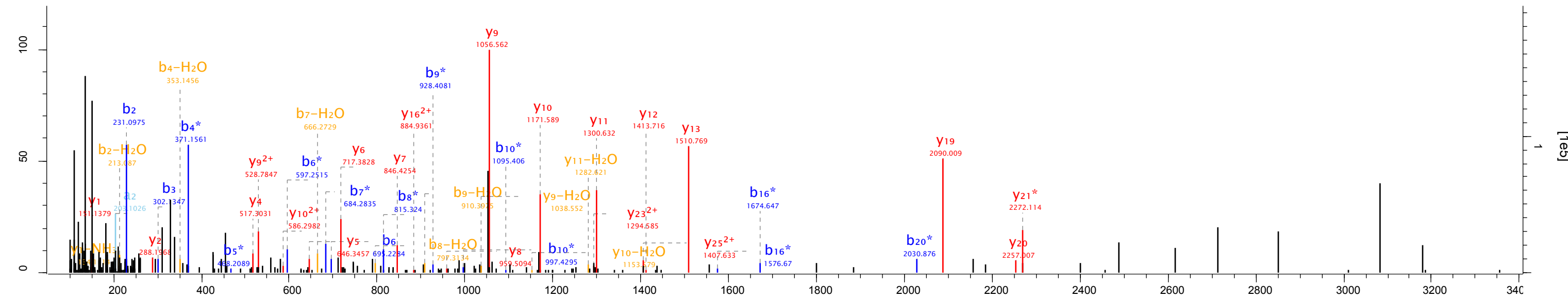
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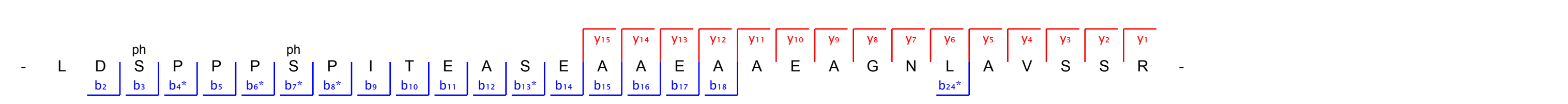
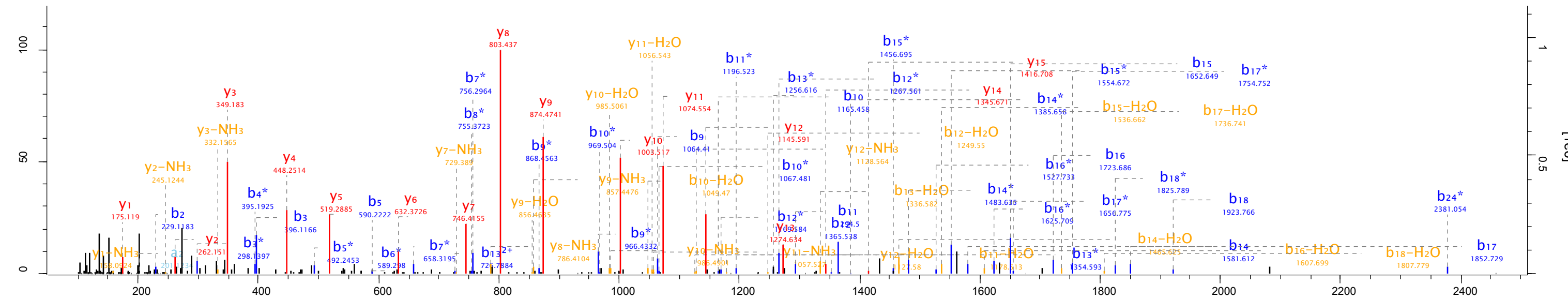
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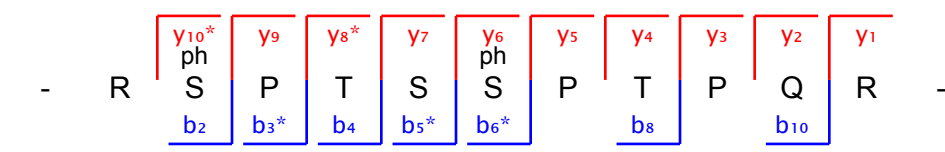
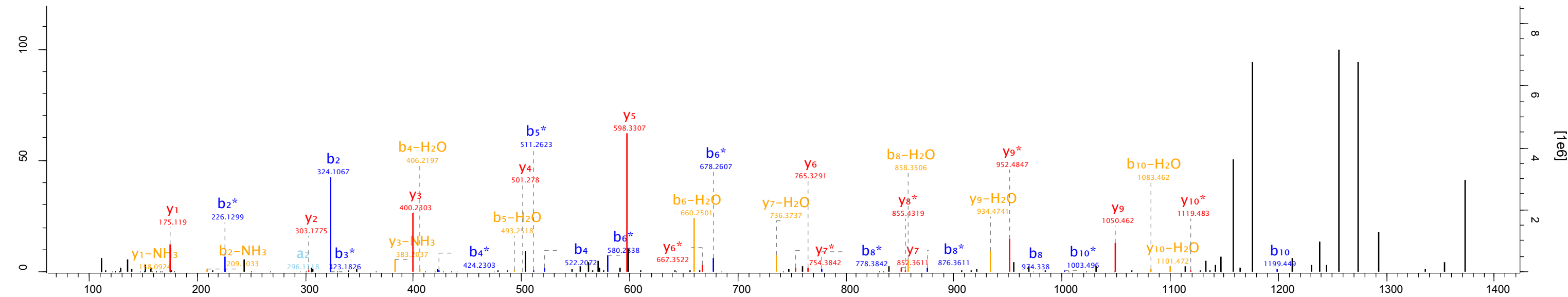
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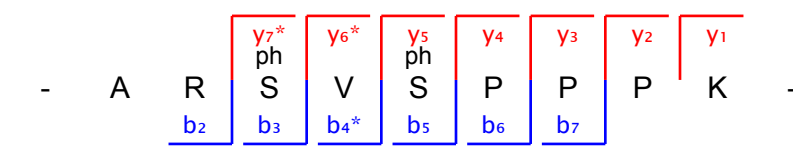
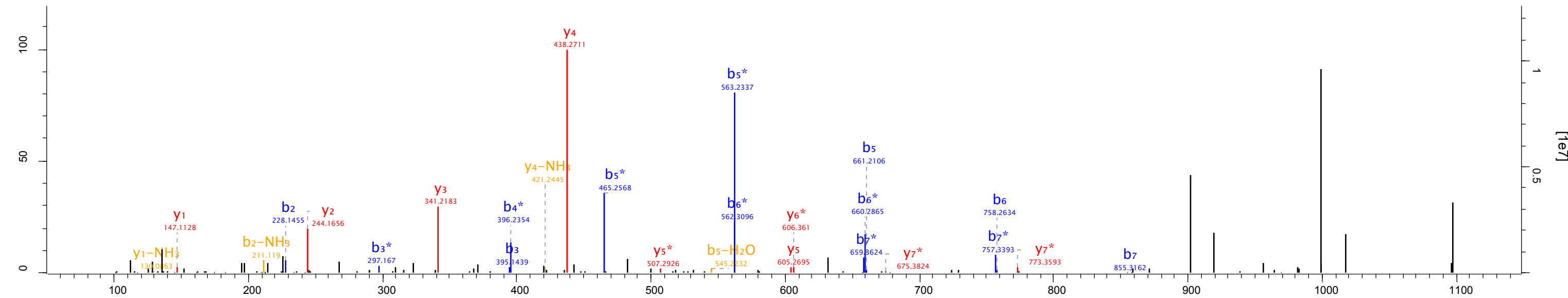
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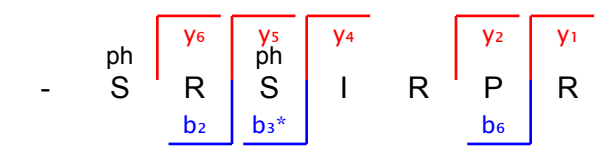
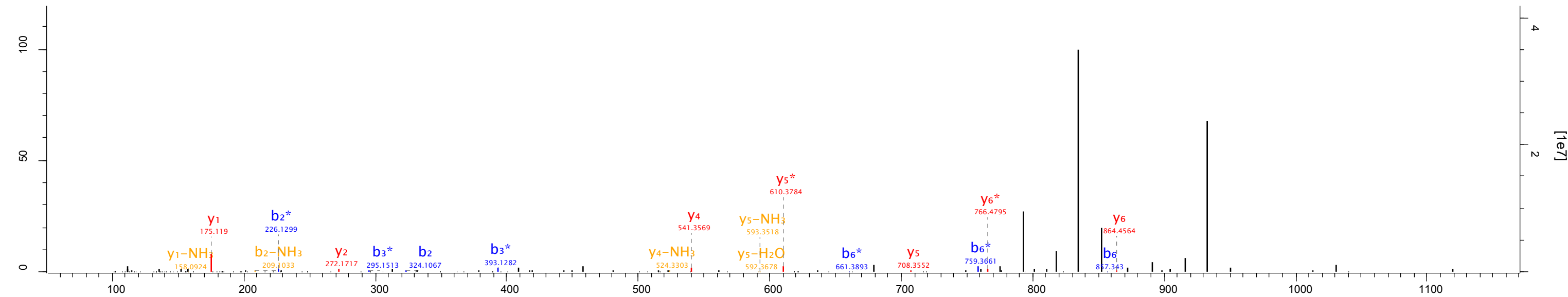
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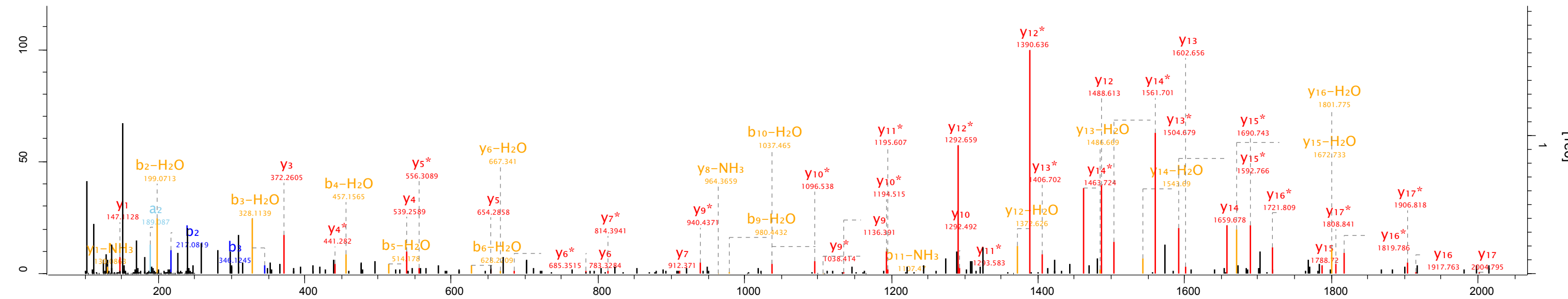
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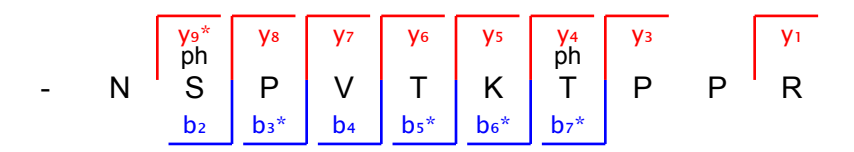
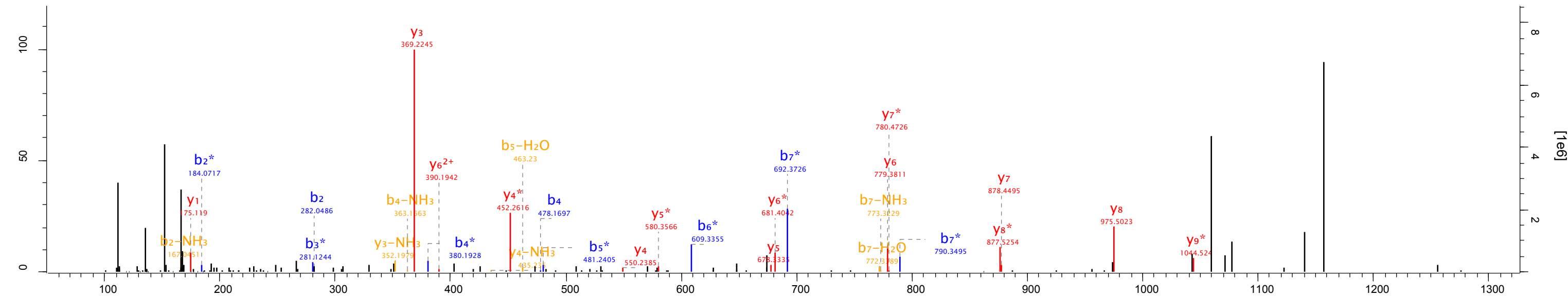
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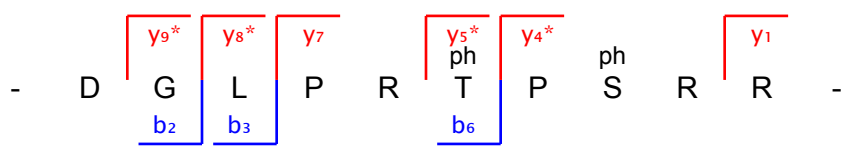
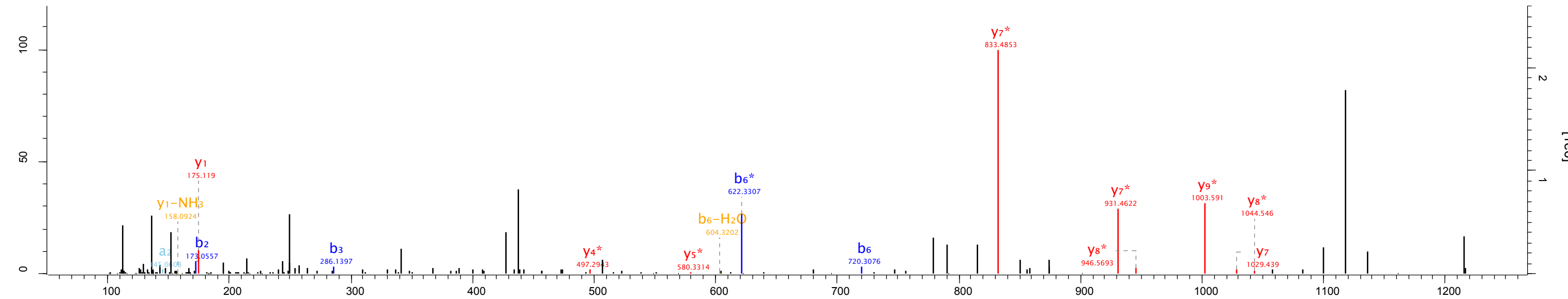
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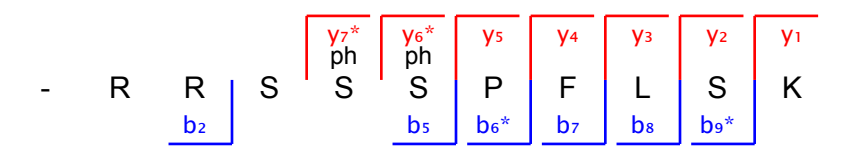
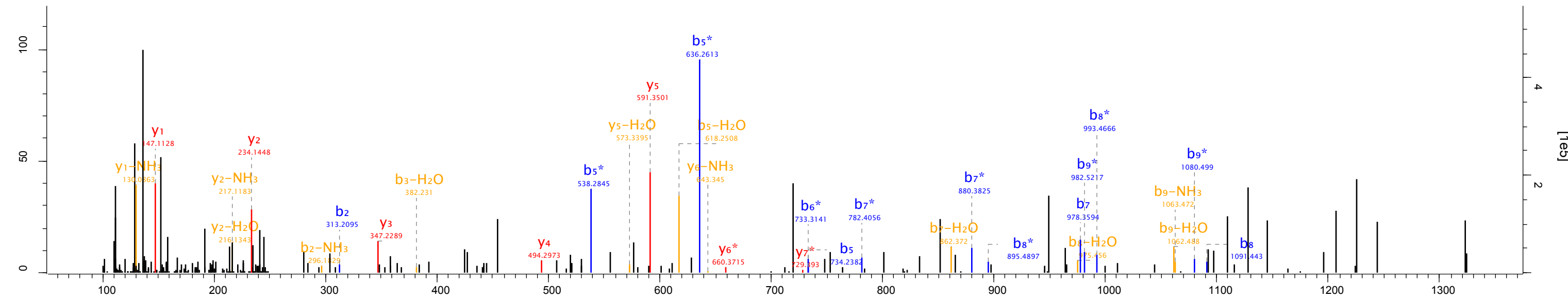
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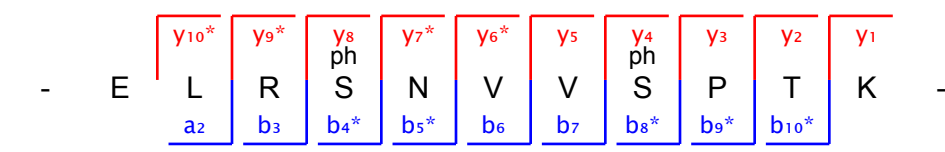
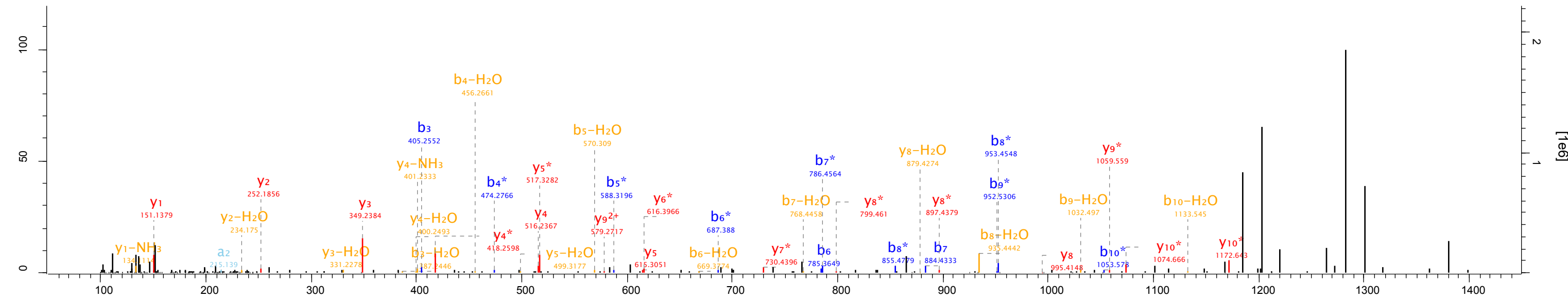
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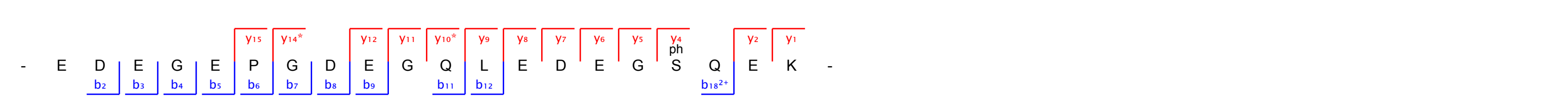
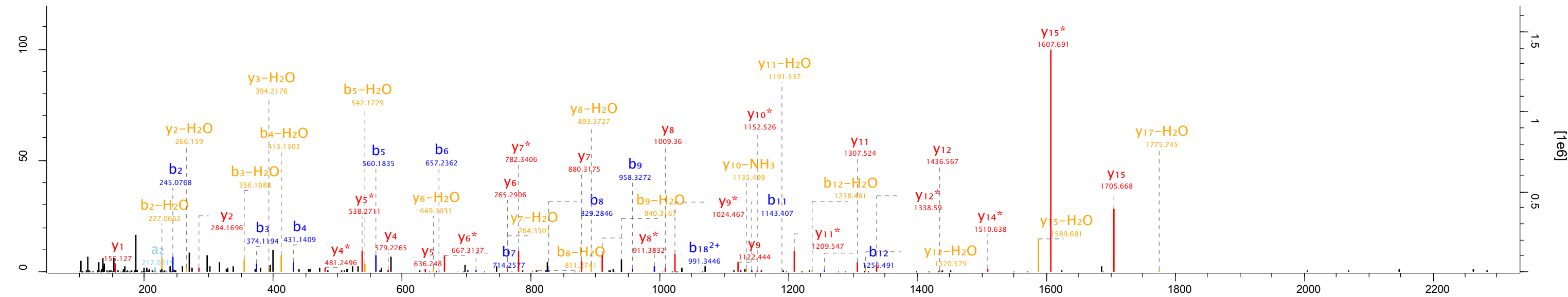
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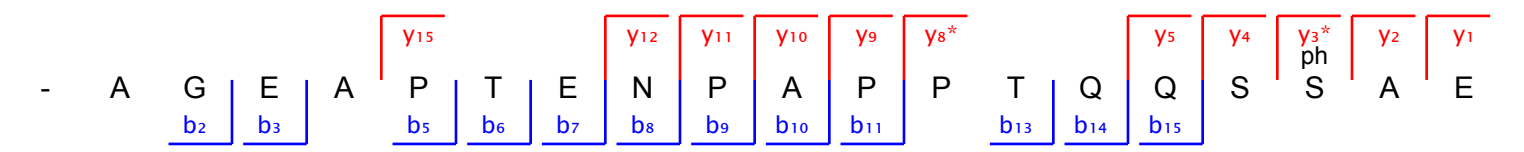
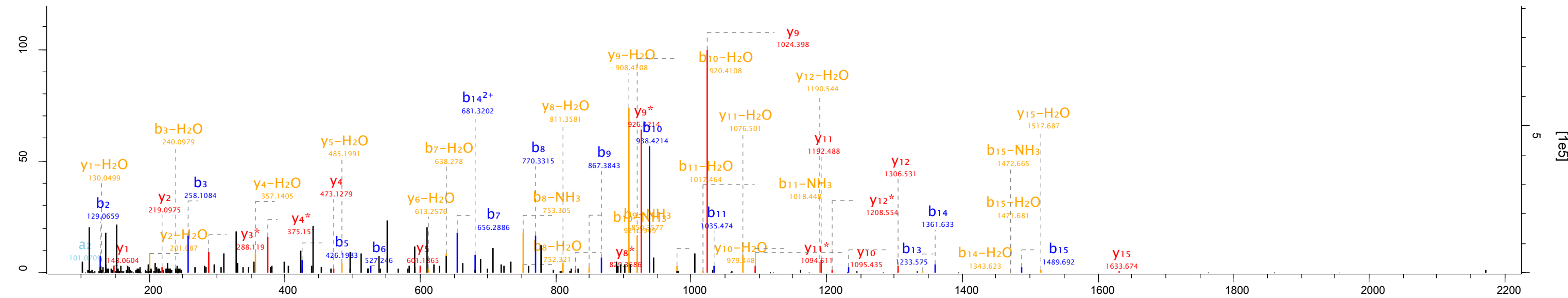
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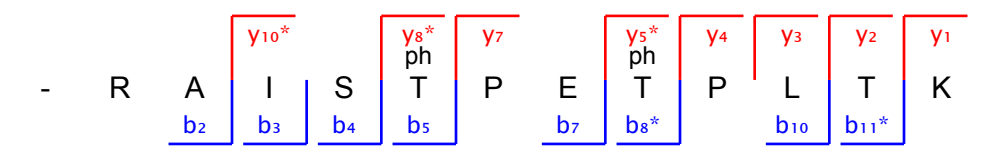
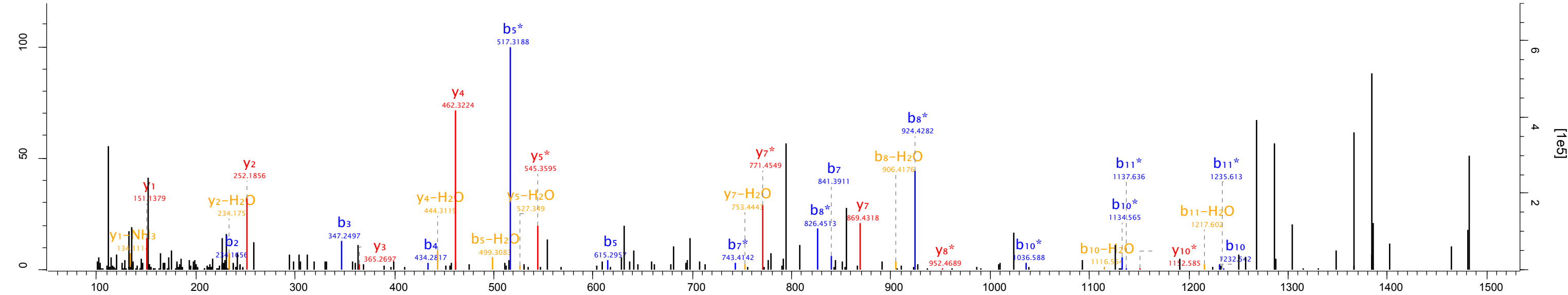


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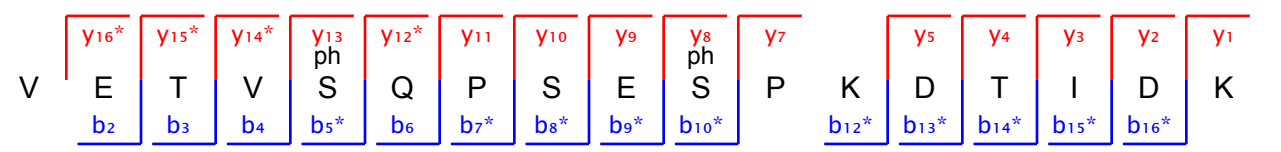
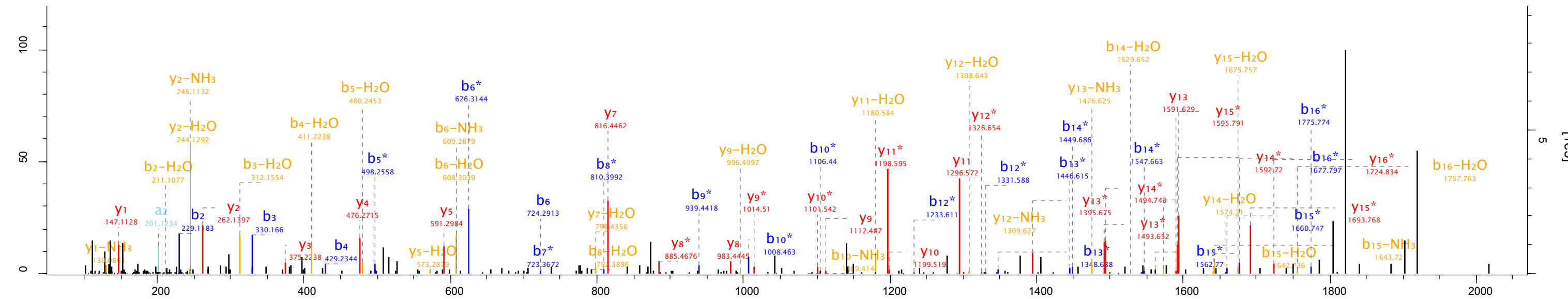


20171215_MaS_33SR_LMH_phospho_02

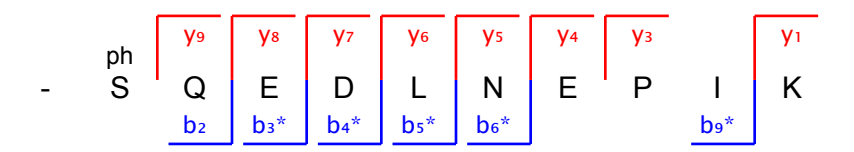
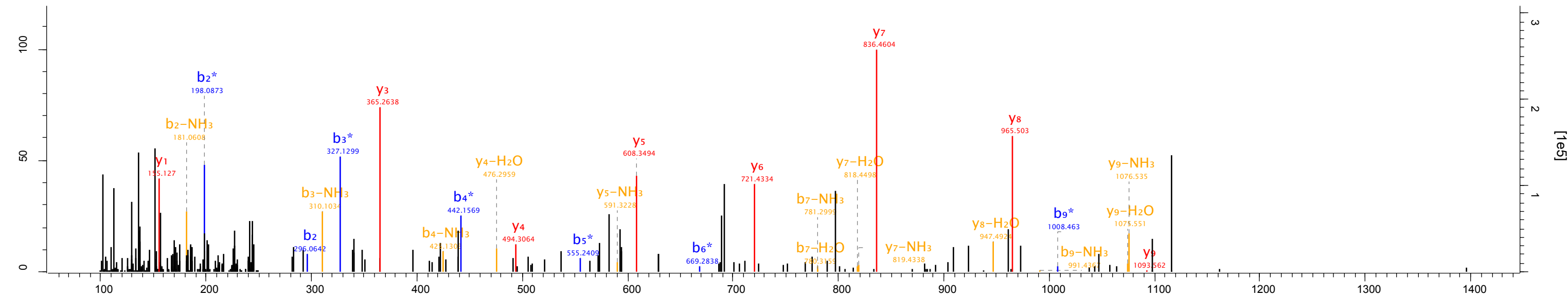
6089 FTMS; HCD 77.91 742.36 POLA2



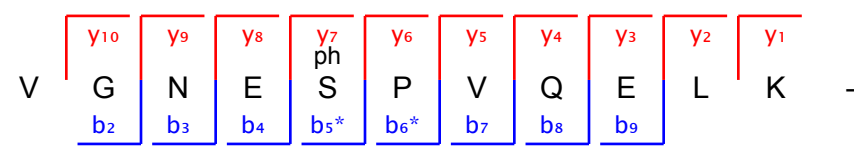
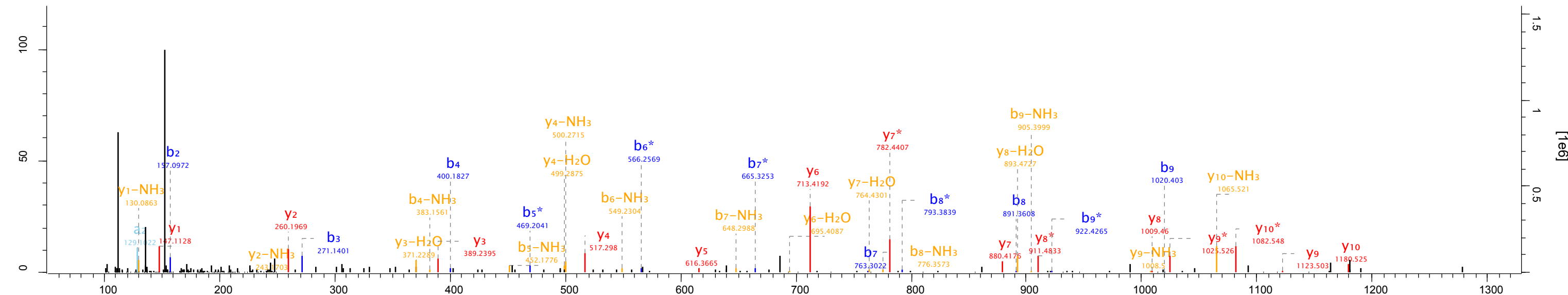
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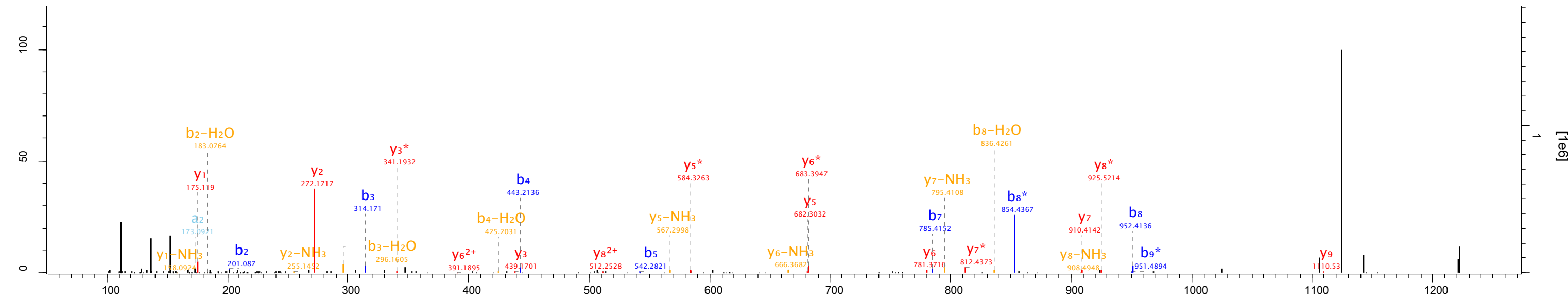


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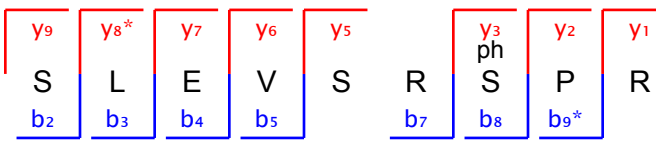




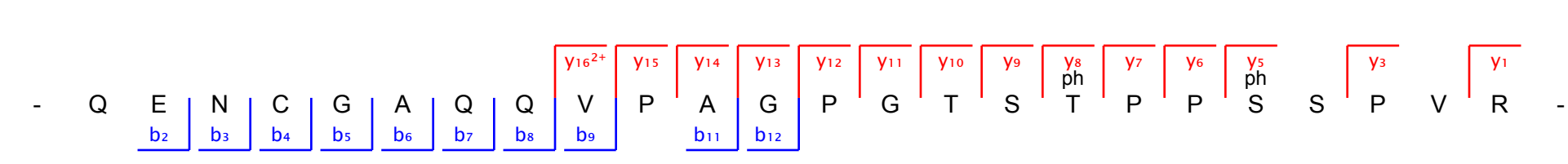
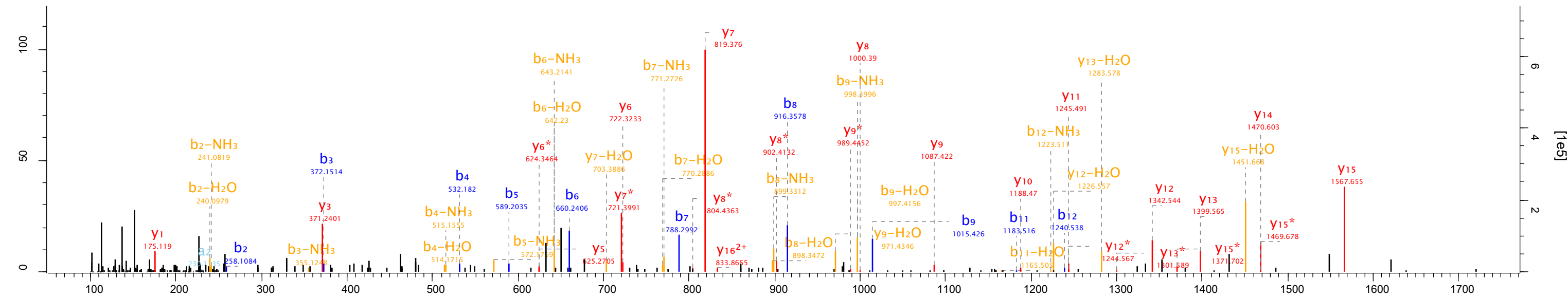
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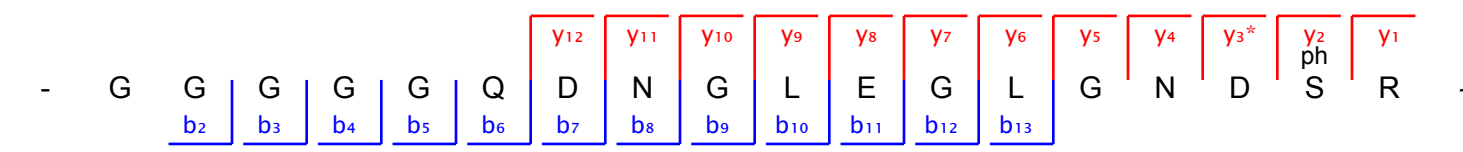
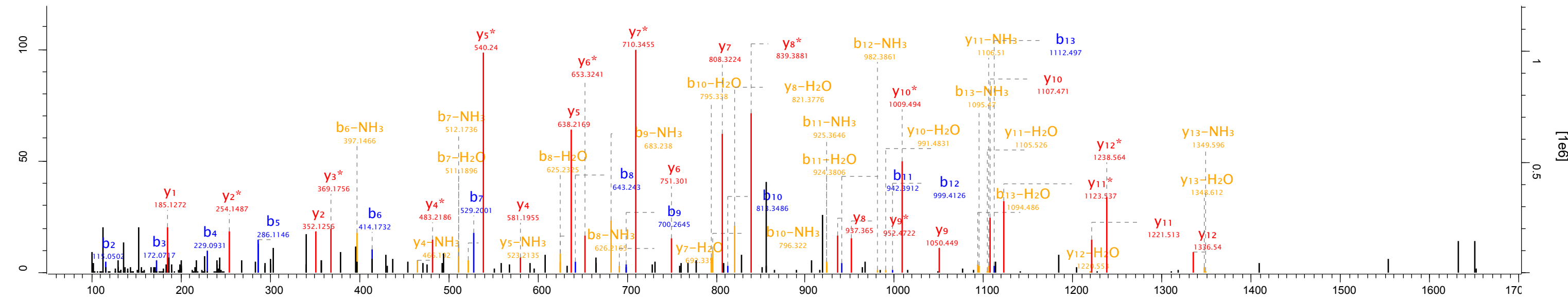
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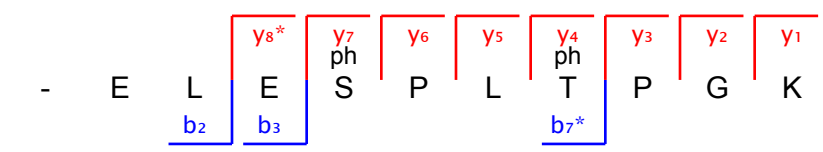
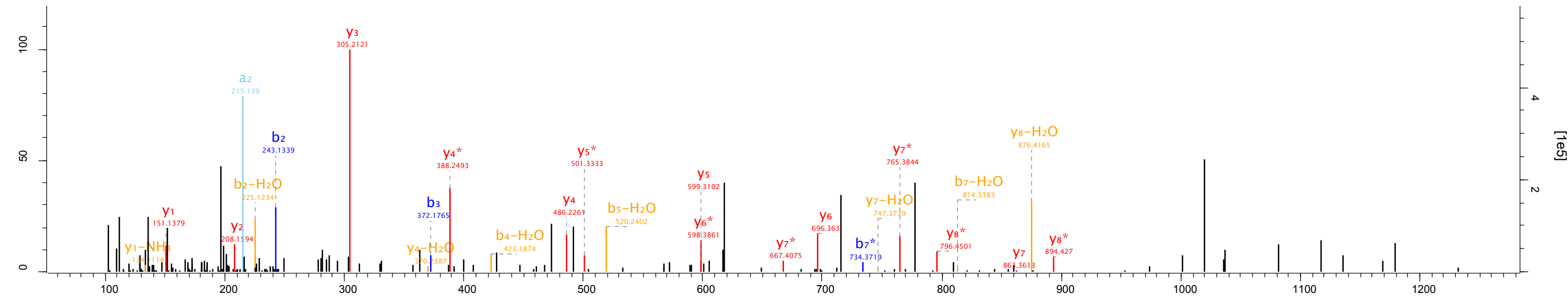
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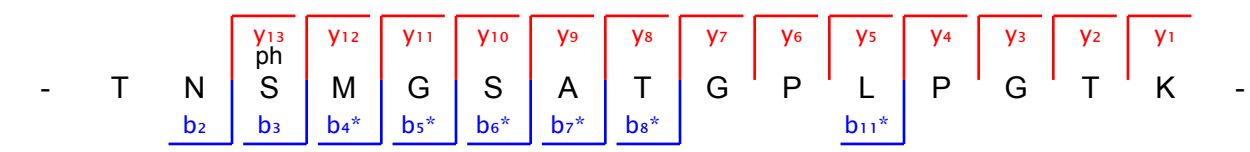
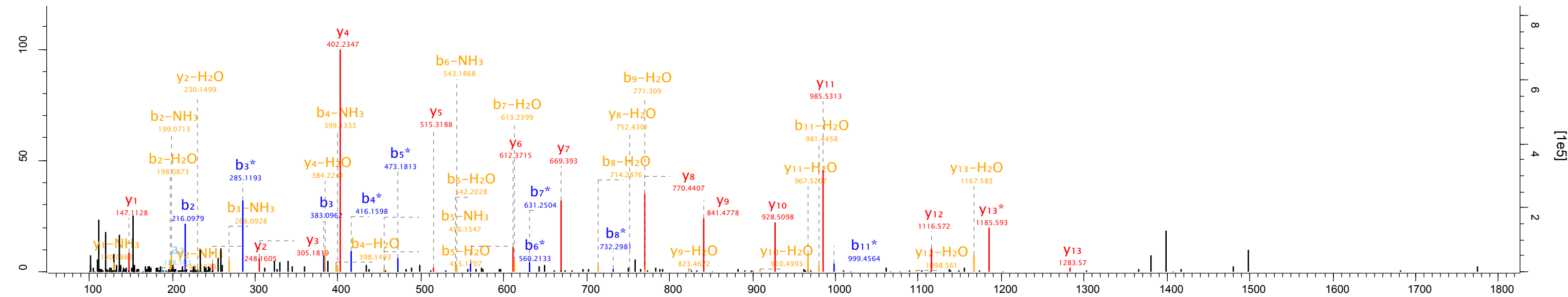
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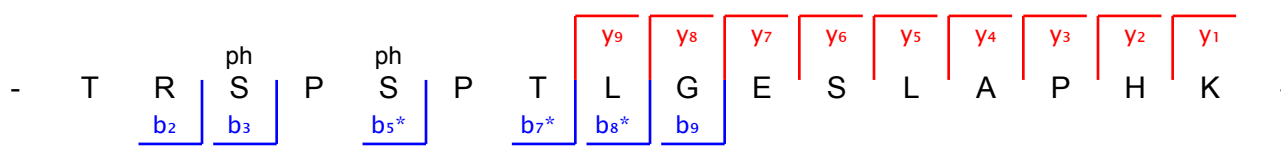
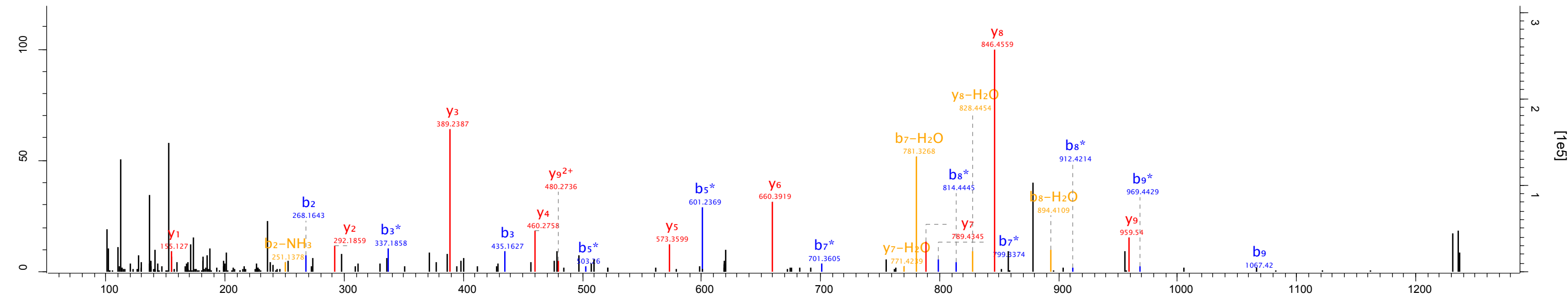
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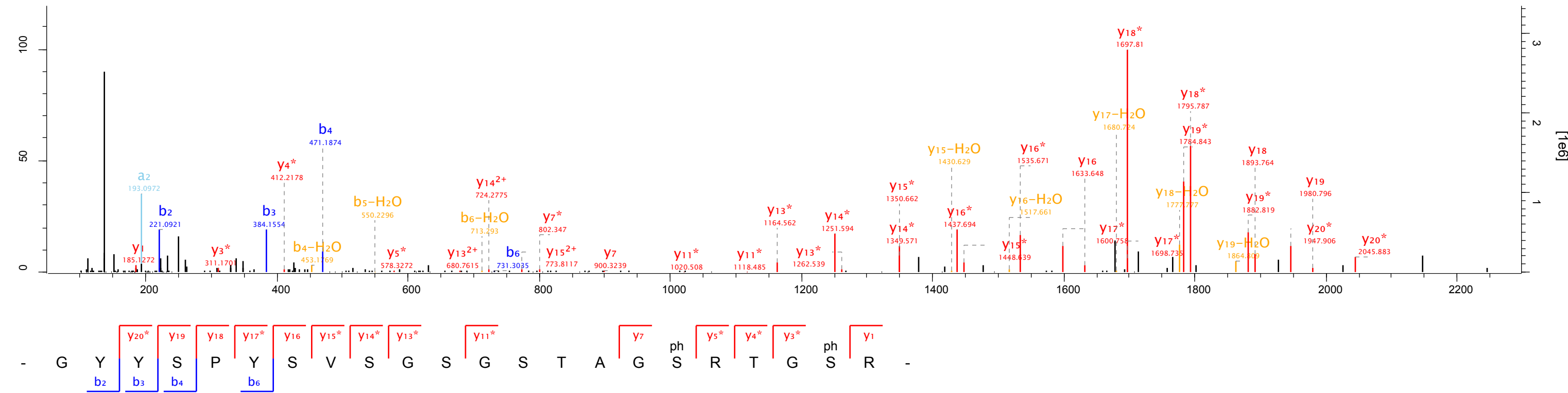


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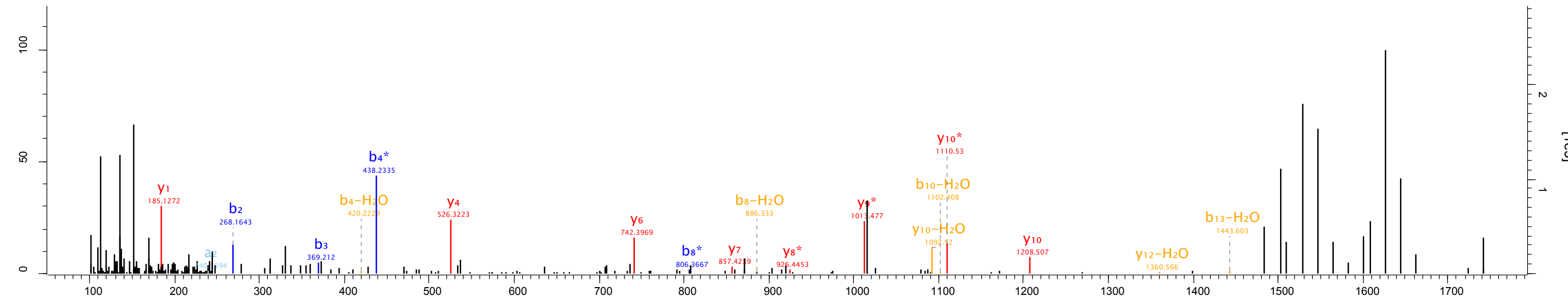


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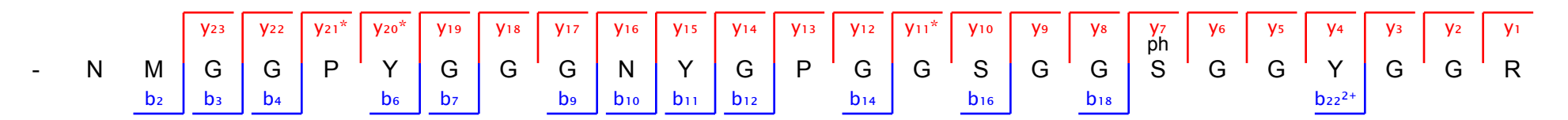
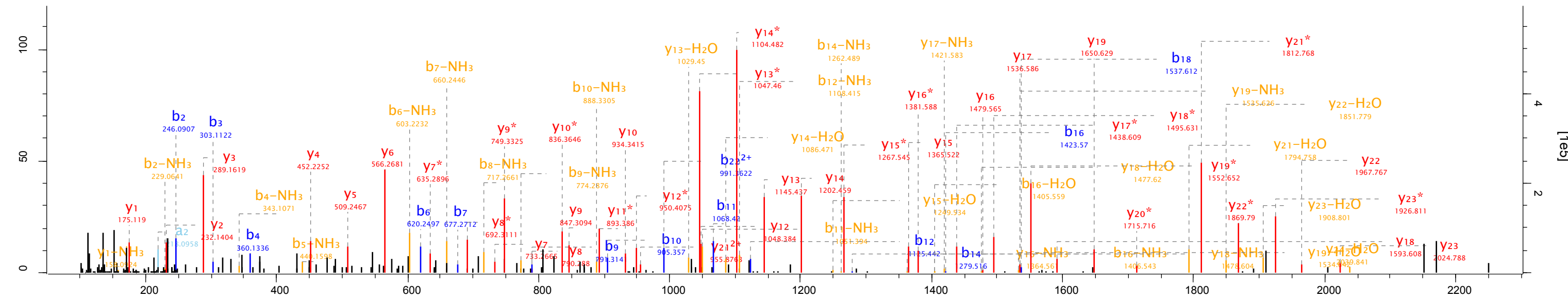




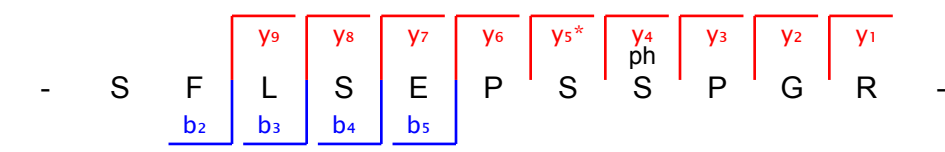
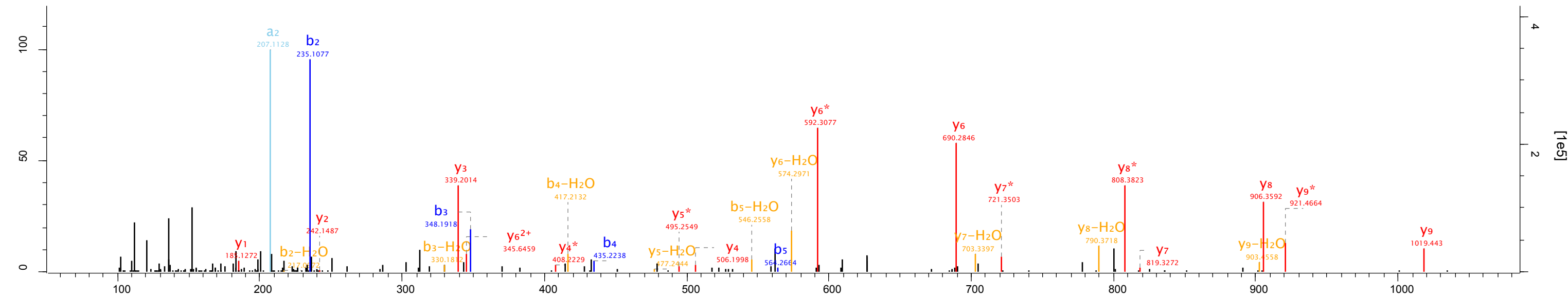
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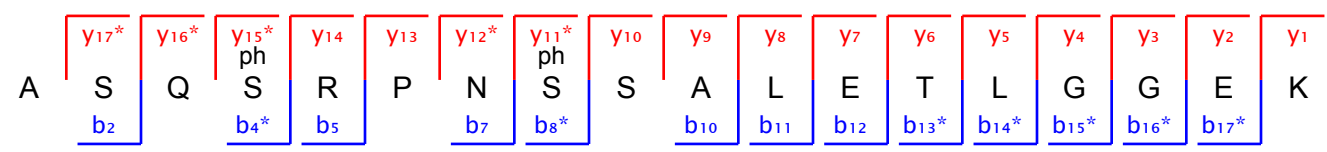
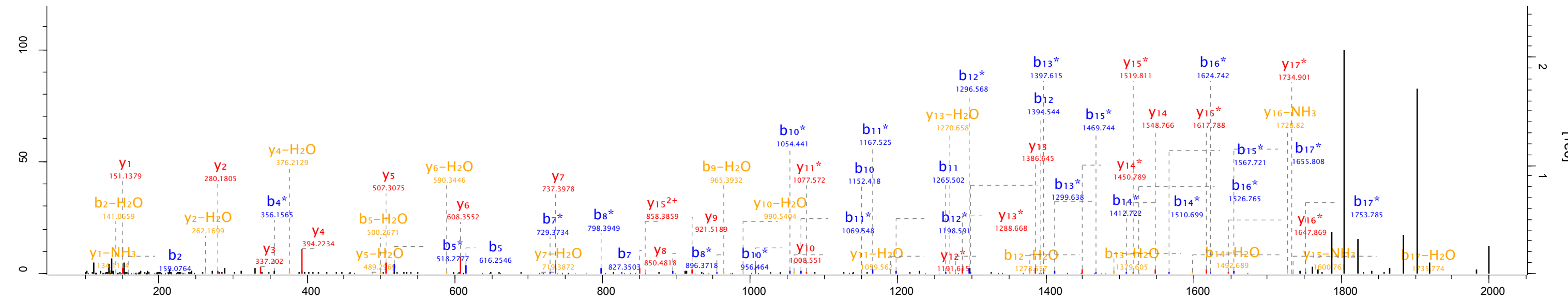
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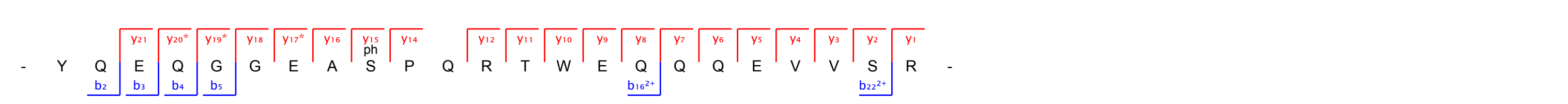
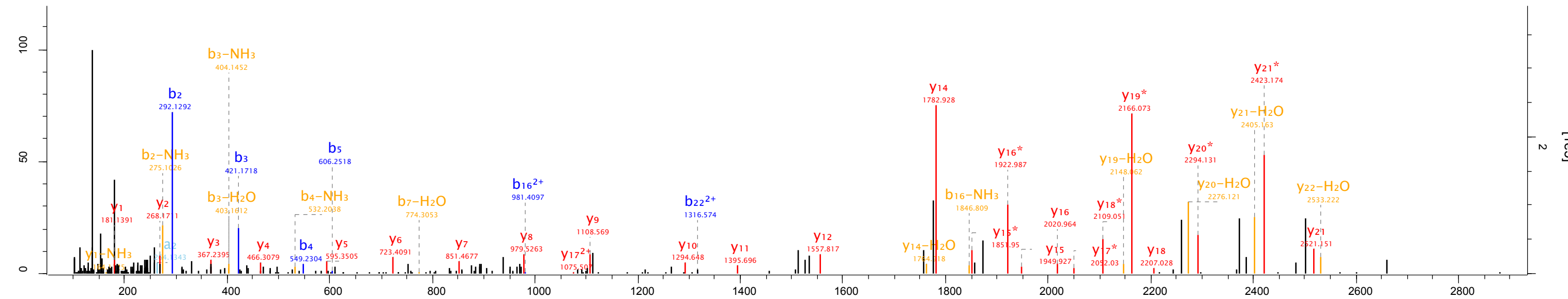
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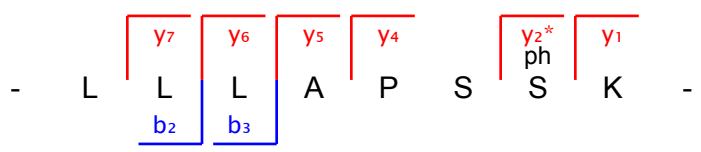
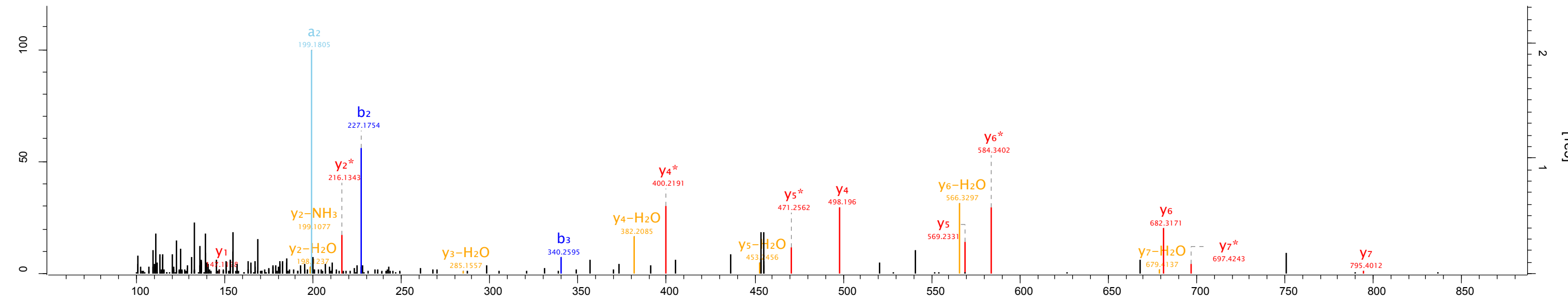
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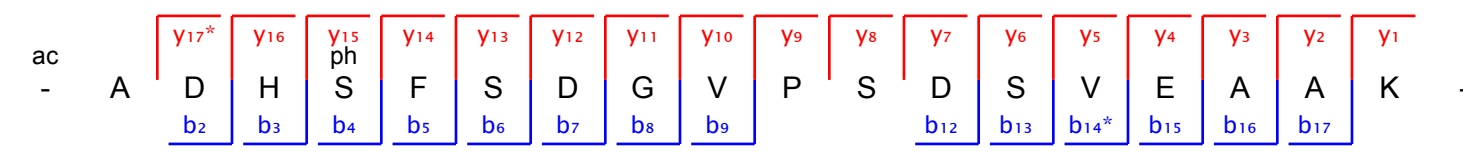
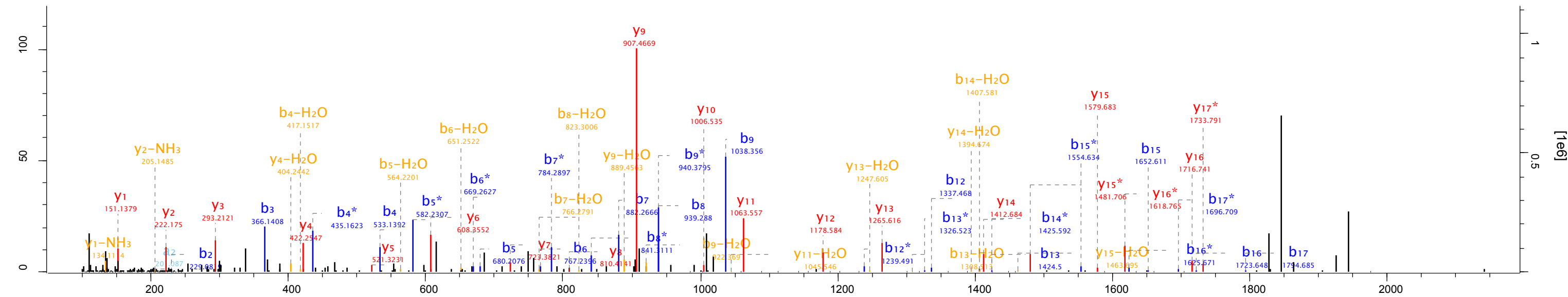
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20171215_MaS_33SR_LMH_phospho_03

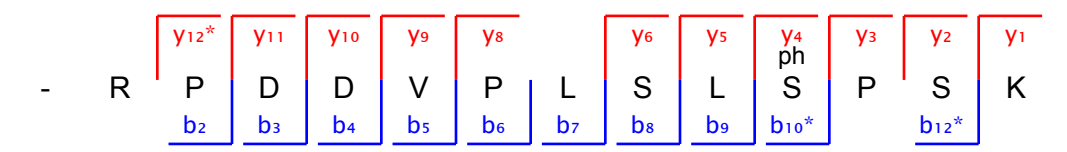
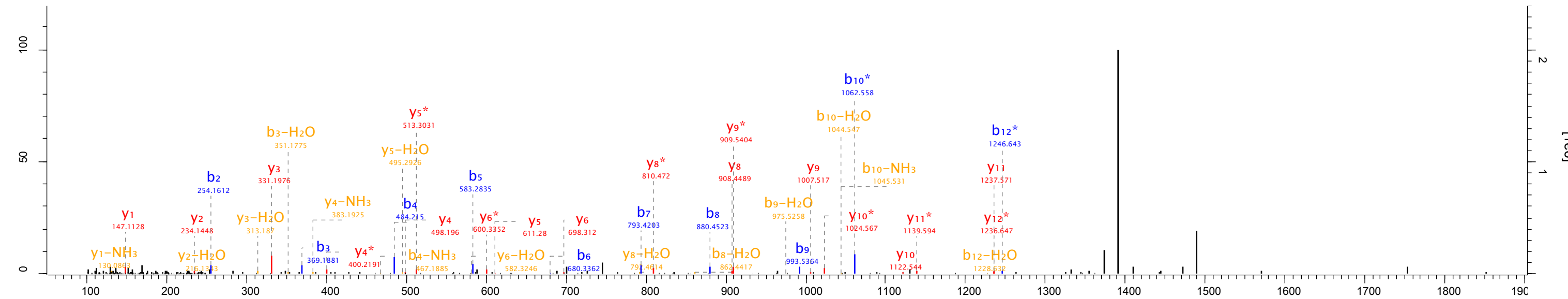
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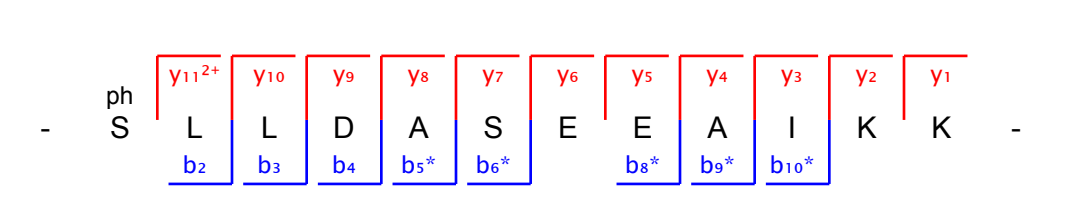
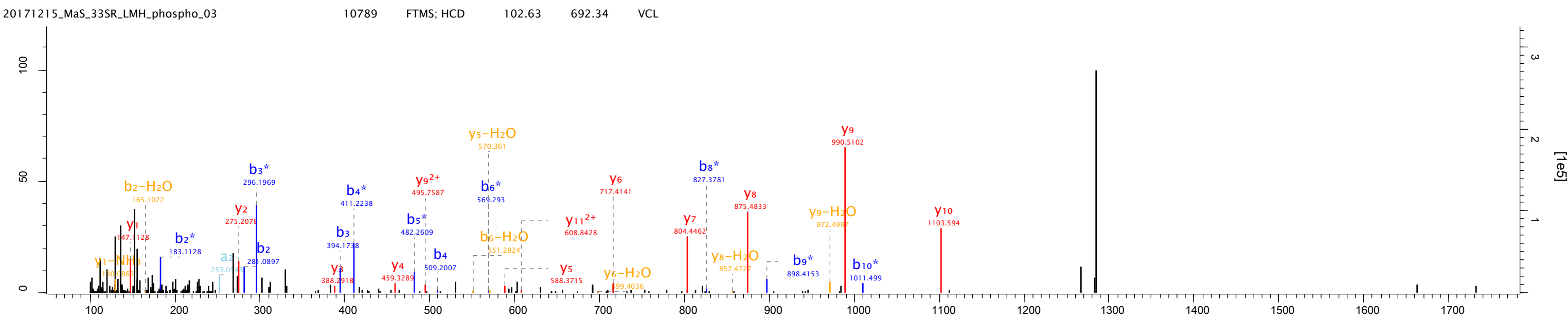
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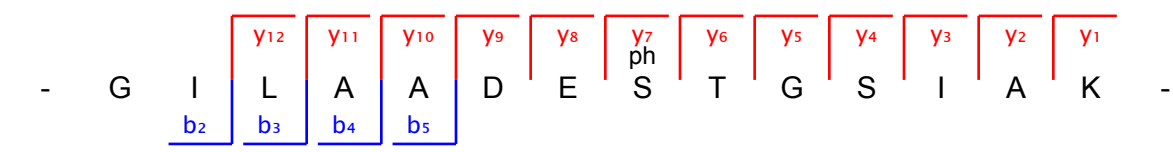
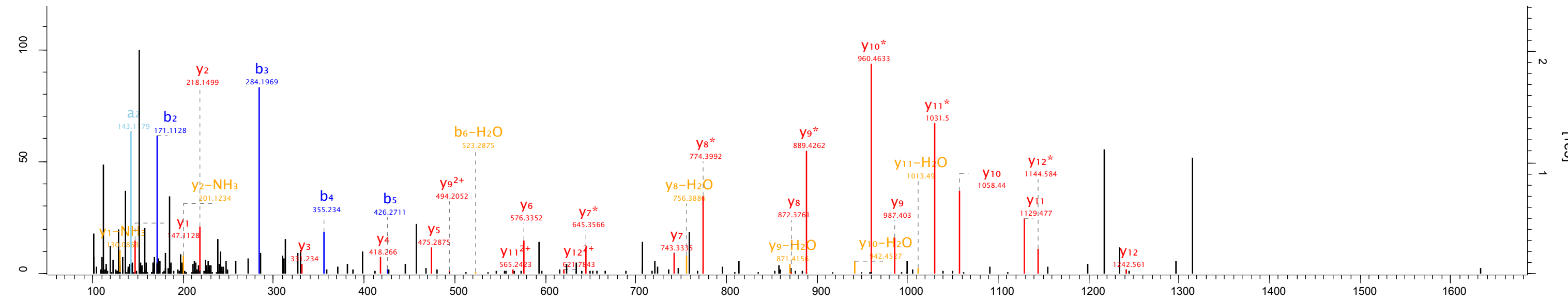
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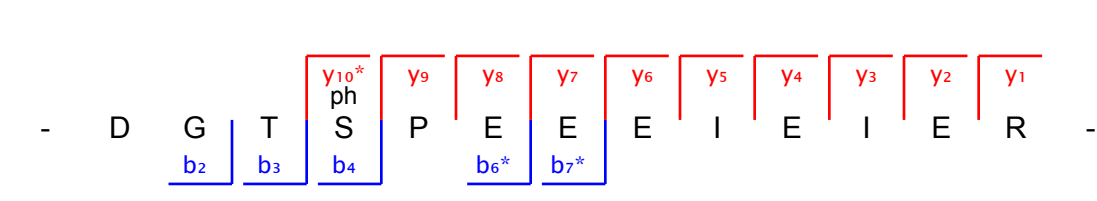
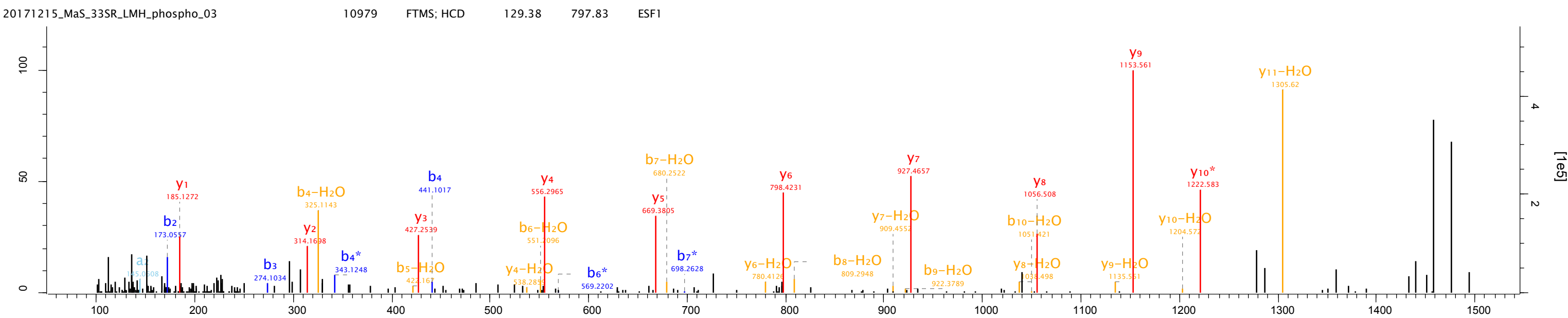


Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 10789 Method FTMS; HCD Score 102.63 m/z 692.34 Gene names VCL



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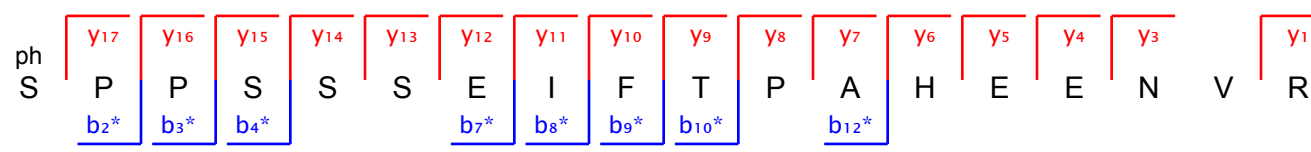
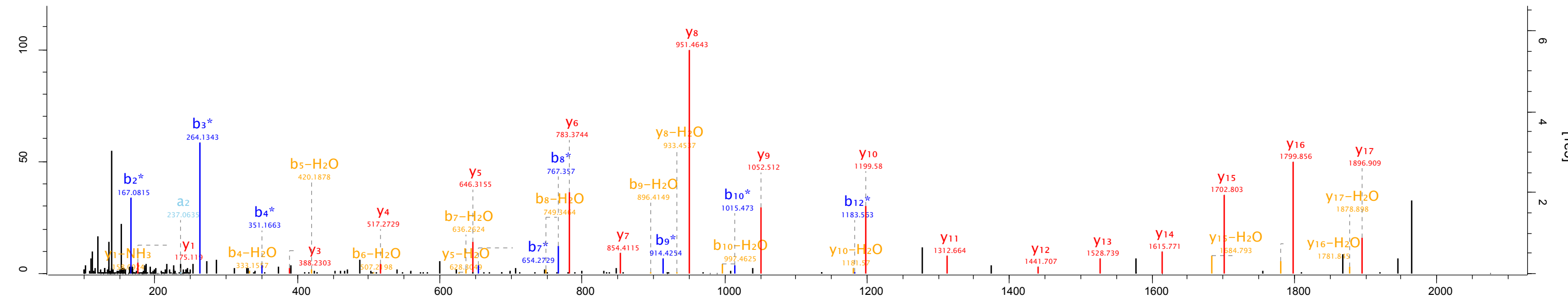




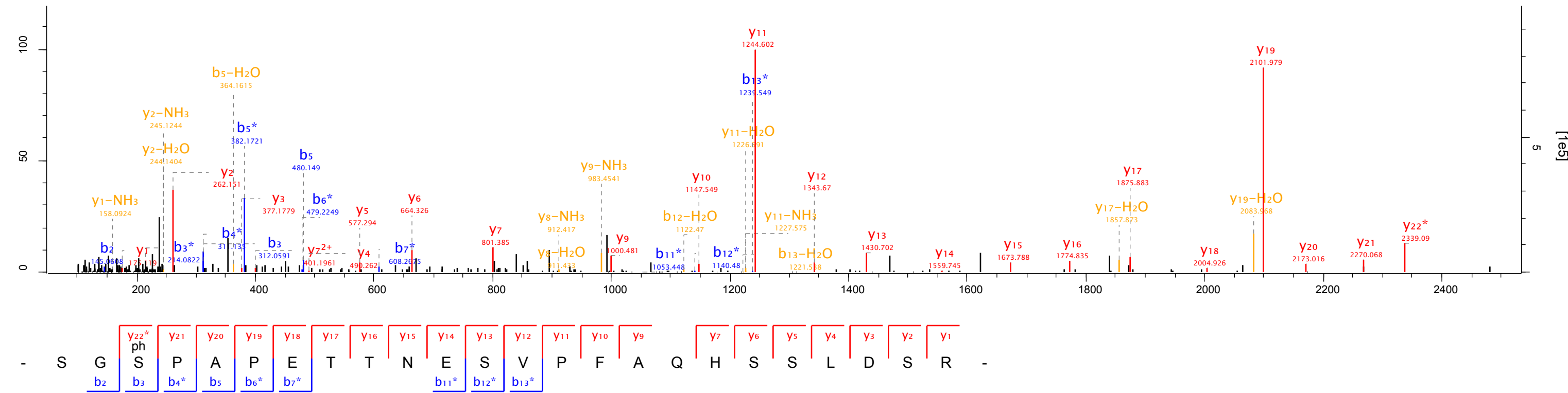
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20171215_MaS_33SR_LMH_phospho_03

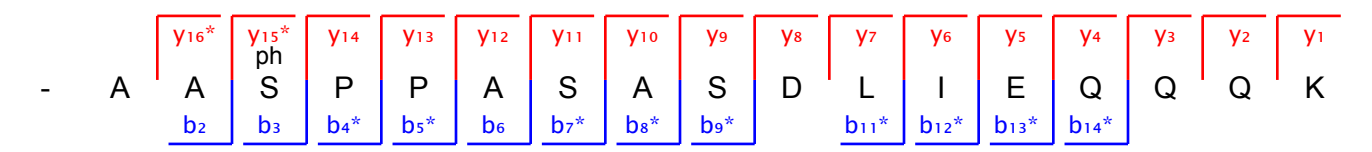
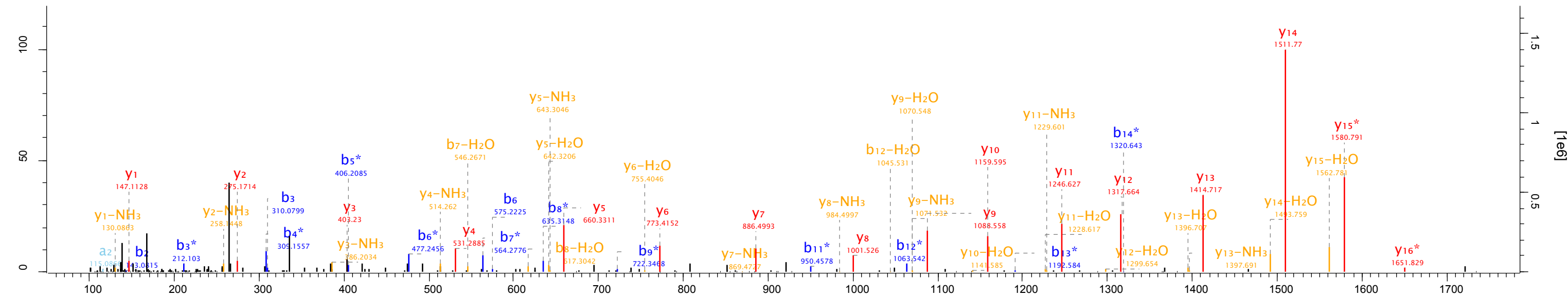
Scan 11049 Method FTMS; HCD Score 132.83 m/z 688.64 Gene names FAM195B



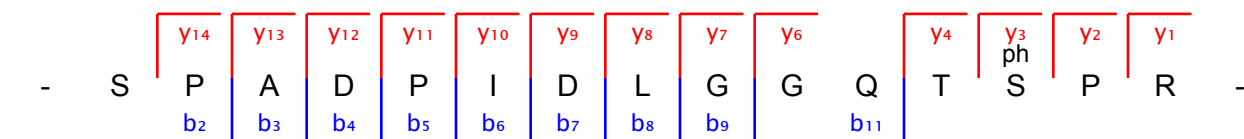
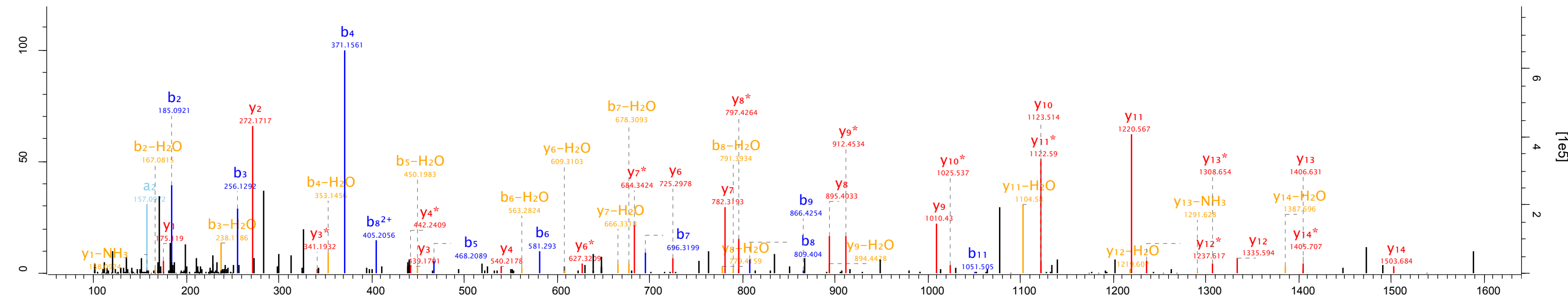
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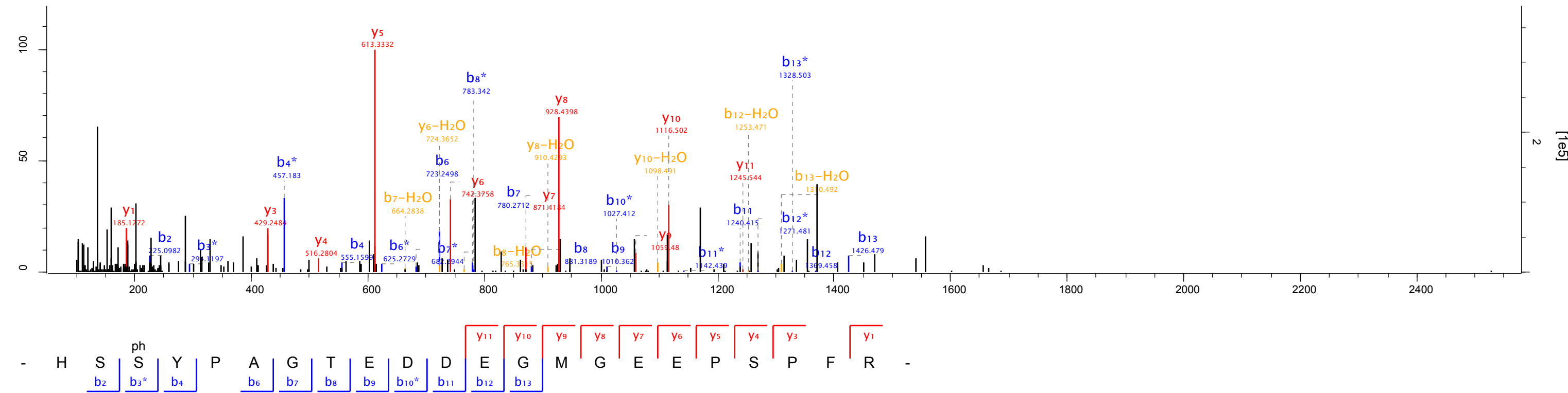


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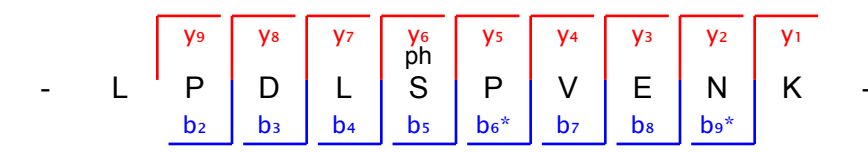
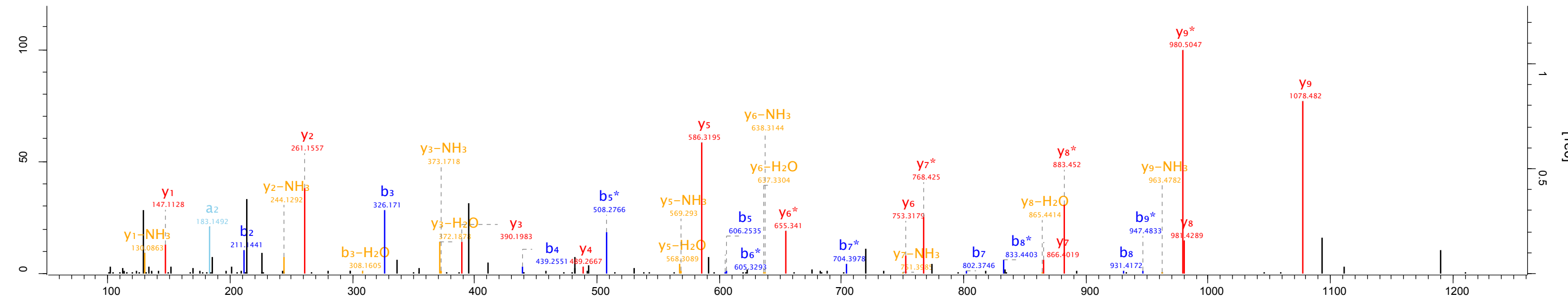


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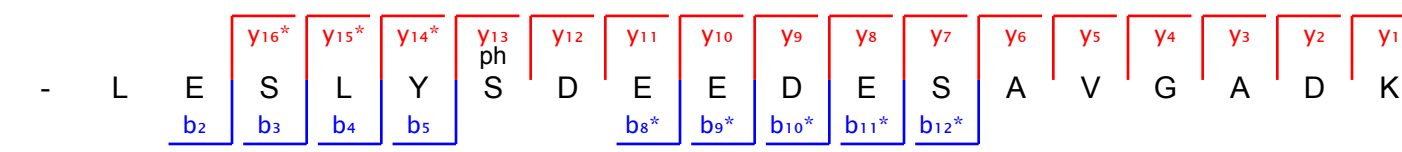
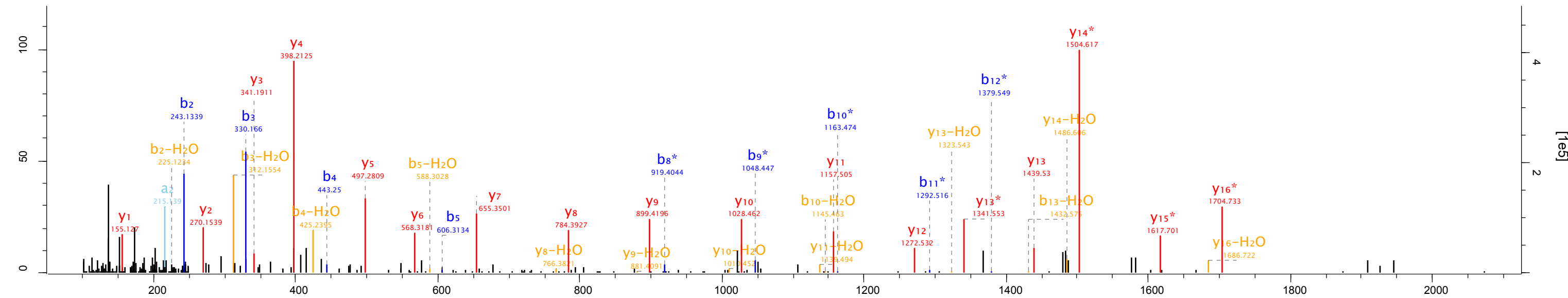




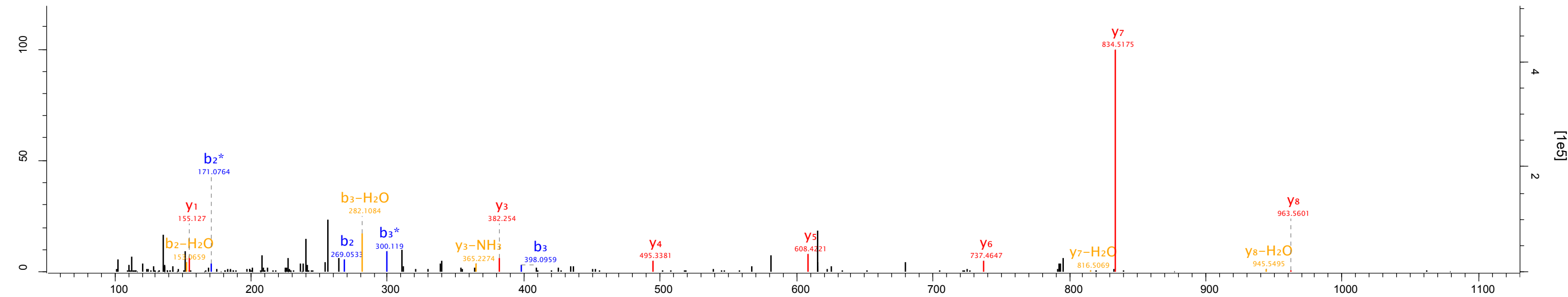
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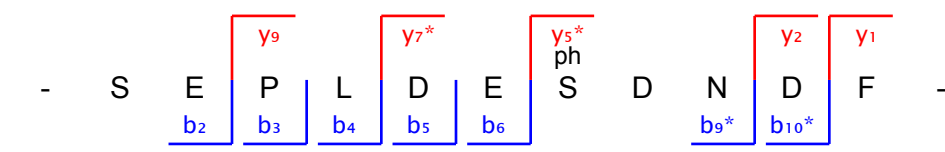
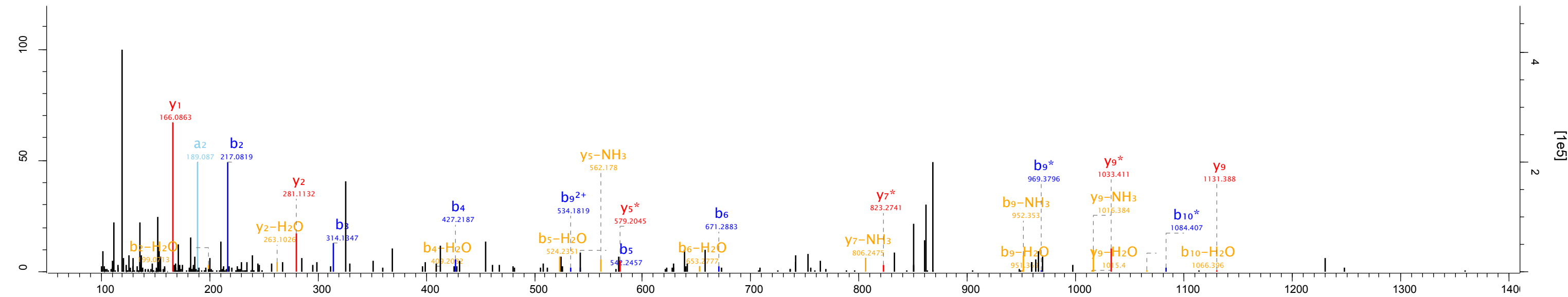
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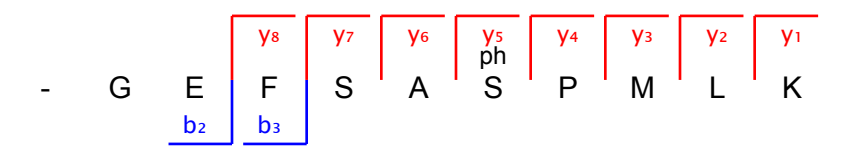
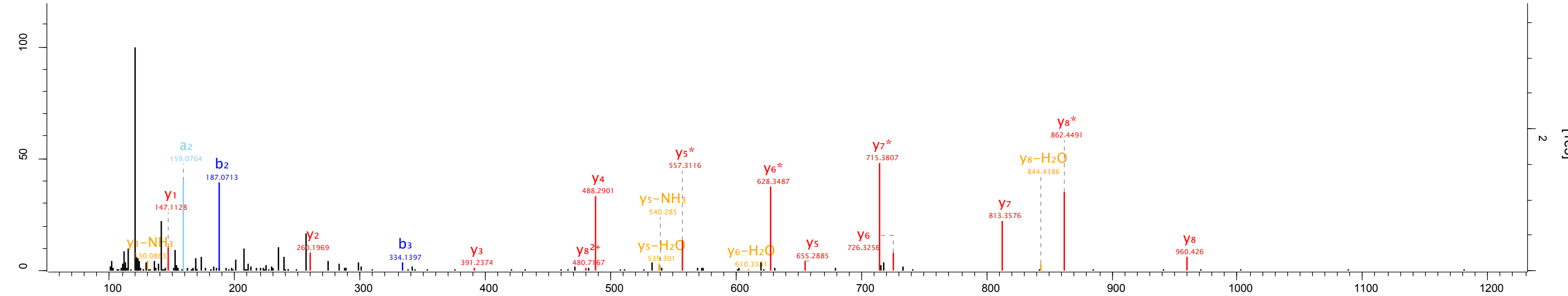
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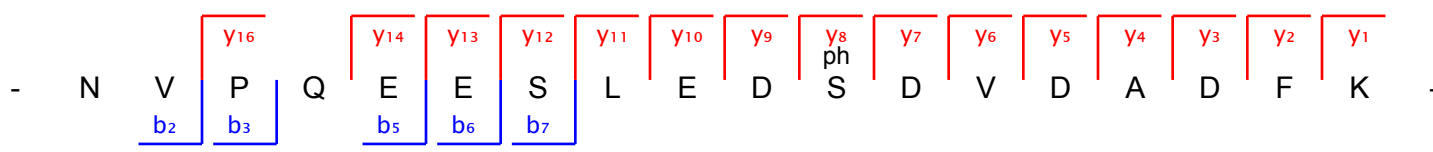
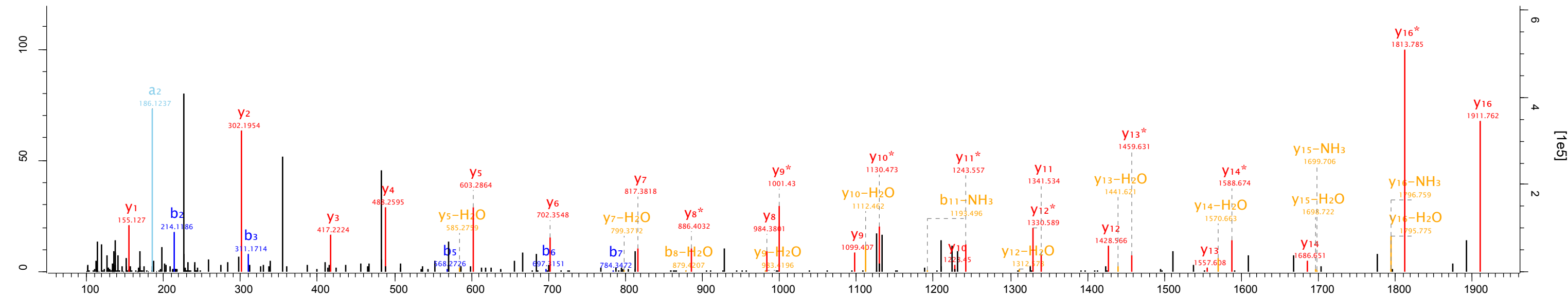
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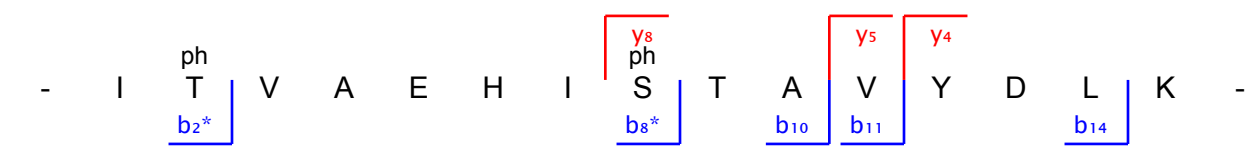
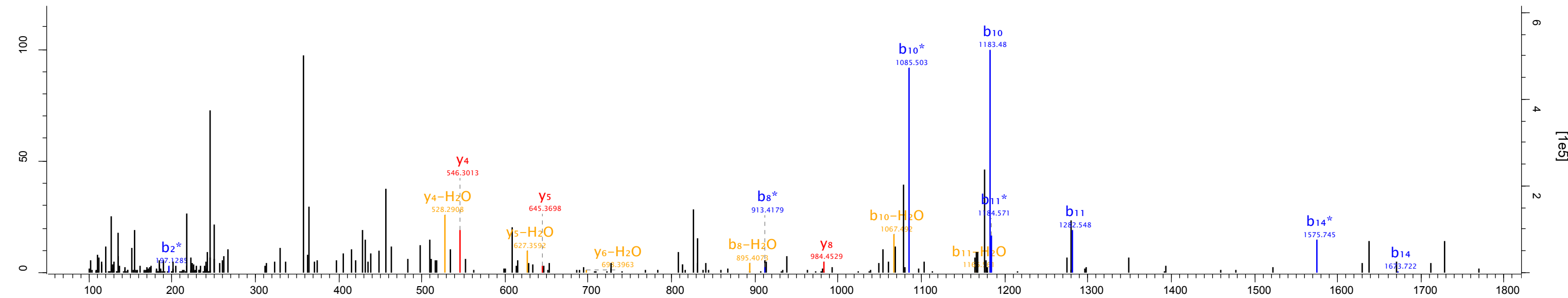
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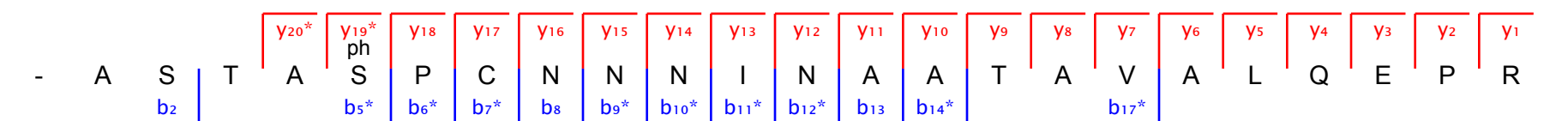
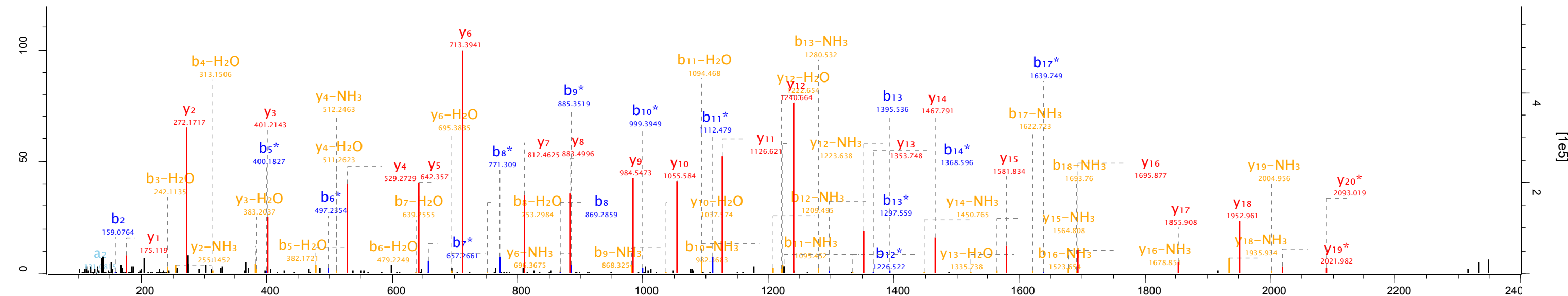
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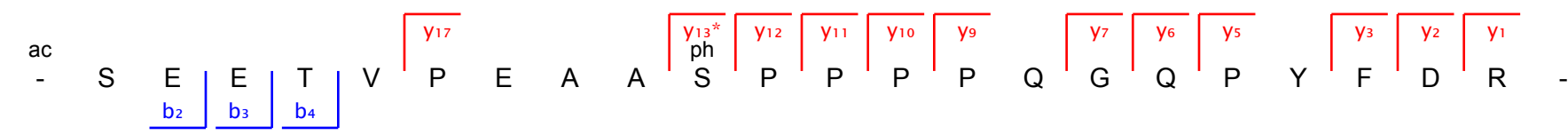
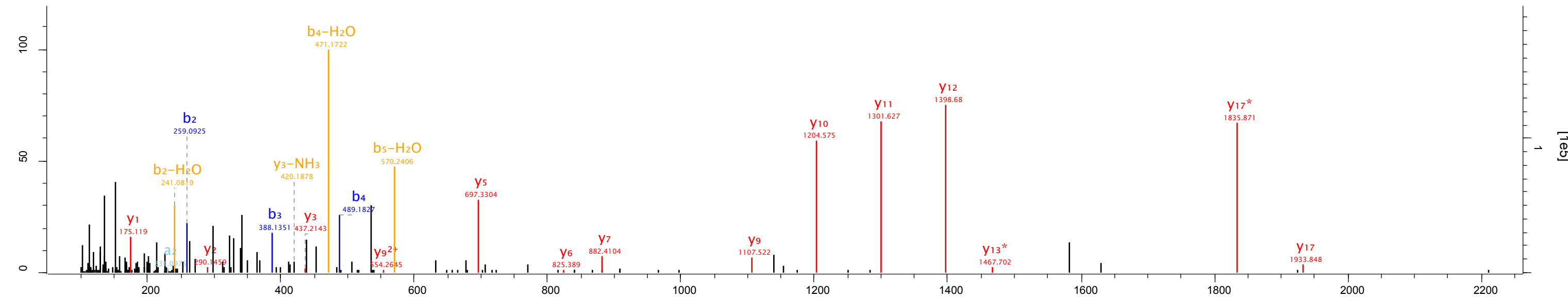
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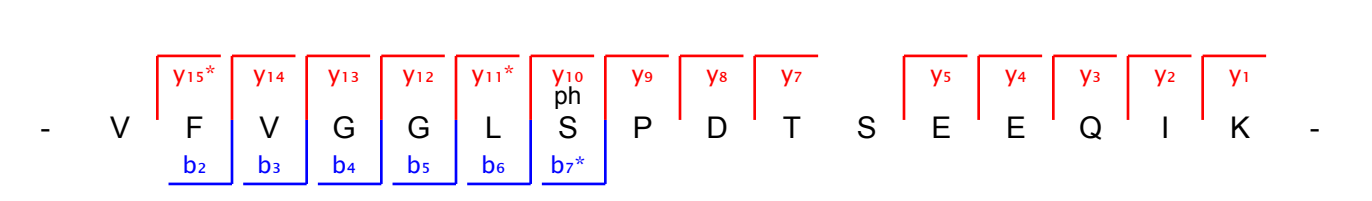
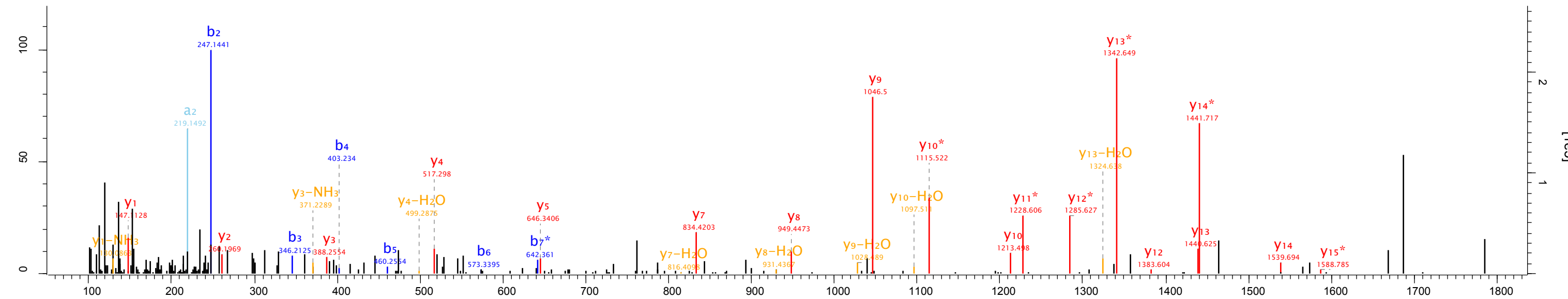
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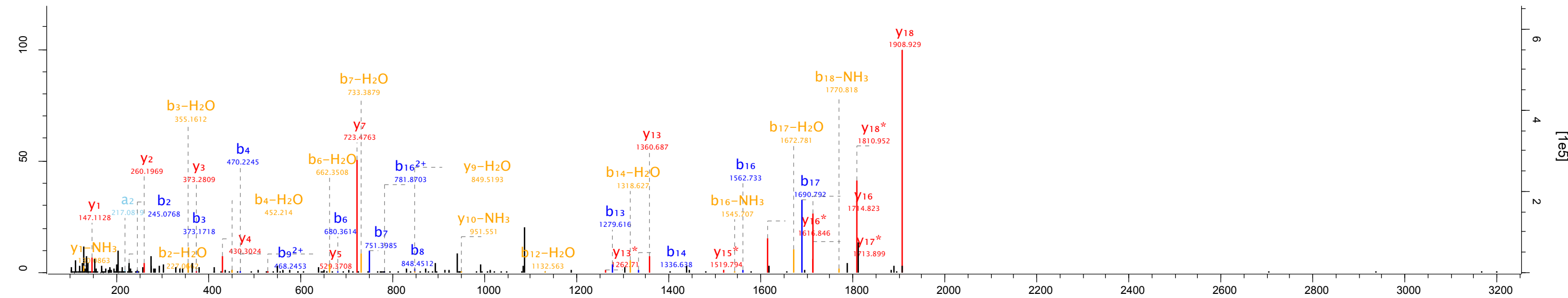
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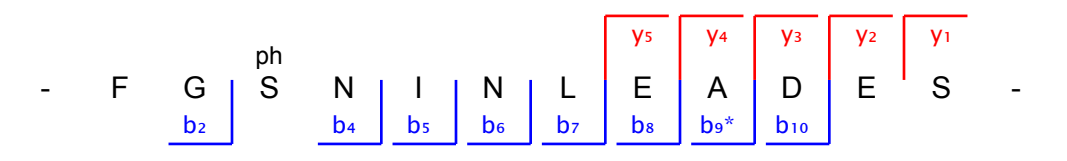
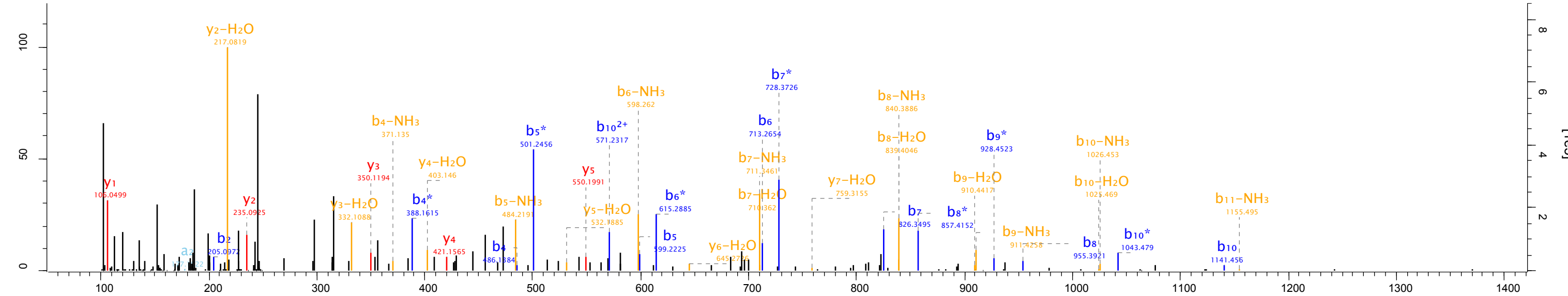
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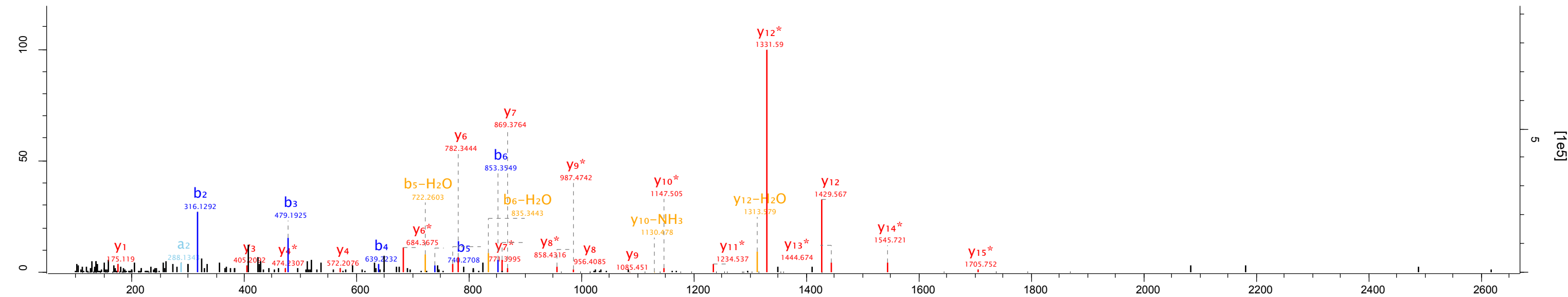


- E D K P P L A P S G G T E G P E Q P P P P C P S Q T G S P P V G L I K -

b₂
b₃
b₄
b₆
b₇
b₈
b₉²⁺
b₁₃
b₁₄
b₁₆
b₁₇
y₁₈
y₁₇^{*}
y₁₆
y₁₅^{*}
y₇
y₅
y₄
y₃
y₂
y₁

20171215_MaS_33SR_LMH_phospho_03 14579 FTMS; HCD 199.03 688.27 PFDN4



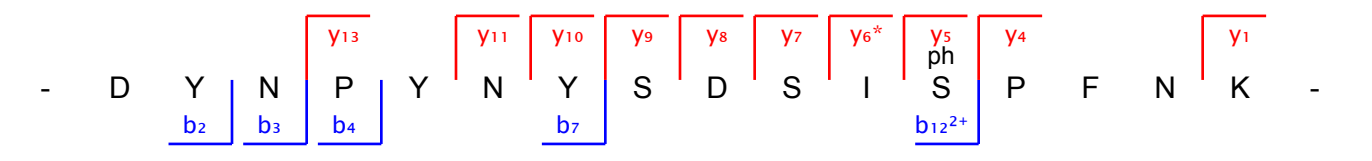
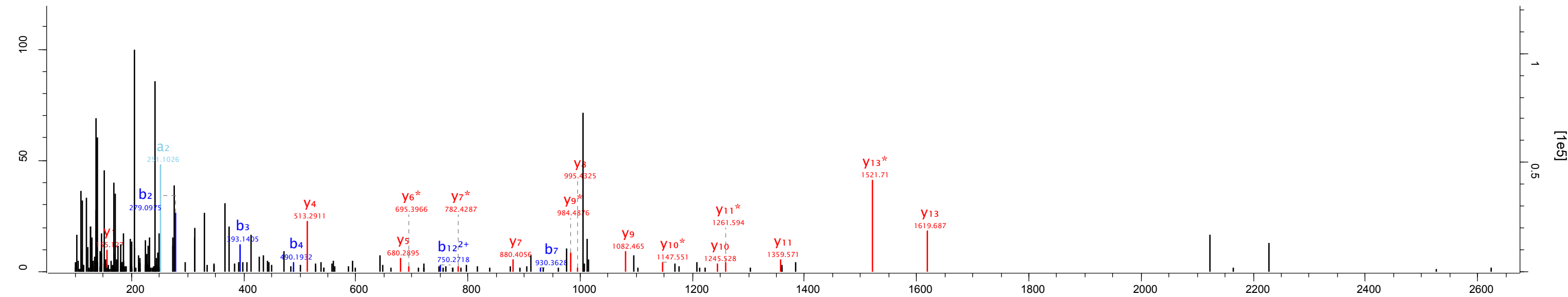


- W E Y C T I P S C E S S P L S T E R -

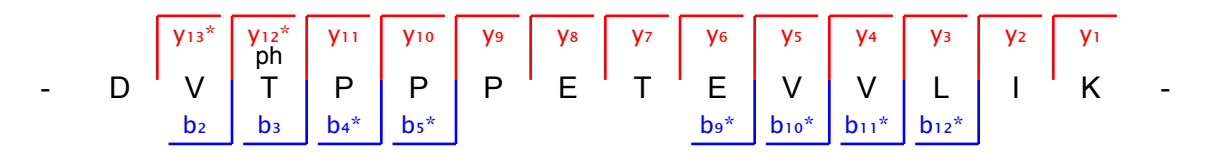
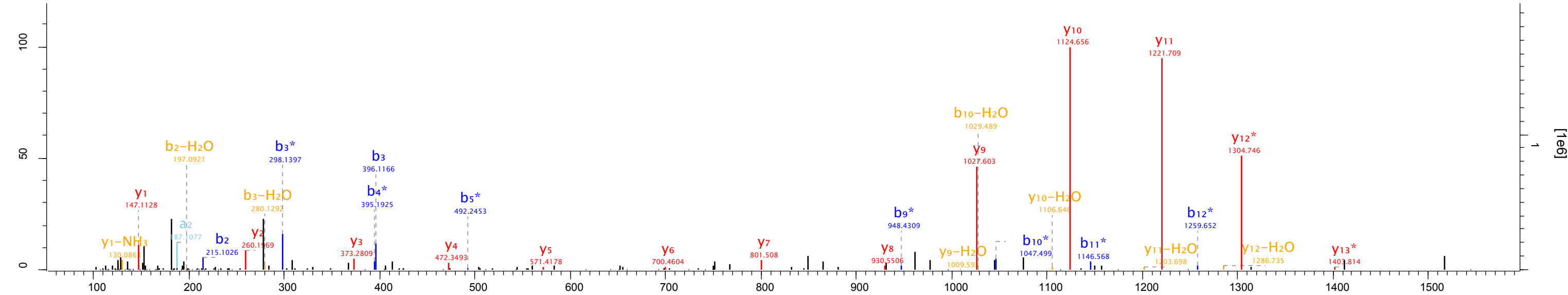
Fragmentation sites are indicated by brackets below the sequence:

- W E Y C T I P S C E S S P L S T E R
- b2 (under E)
- b3 (under Y)
- b4 (under C)
- b5 (under T)
- b6 (under I)
- y15* (under T)
- y14* (under I)
- y13* (under P)
- y12 (under S)
- y11* (under C)
- y10* (under E)
- y9 (under S)
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- y7 (under P)
- y6 (under L)
- y4 ph (under S)
- y3 (under T)
- y1 (under E)

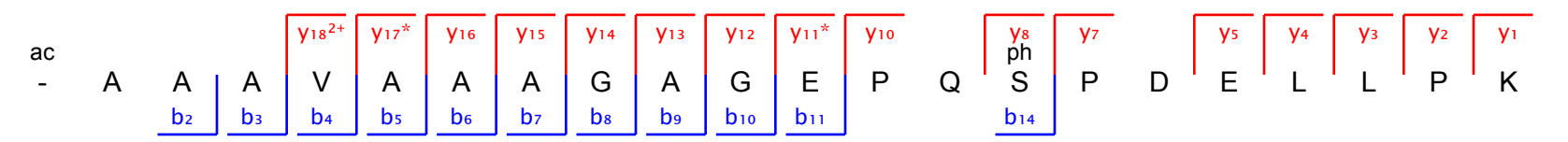
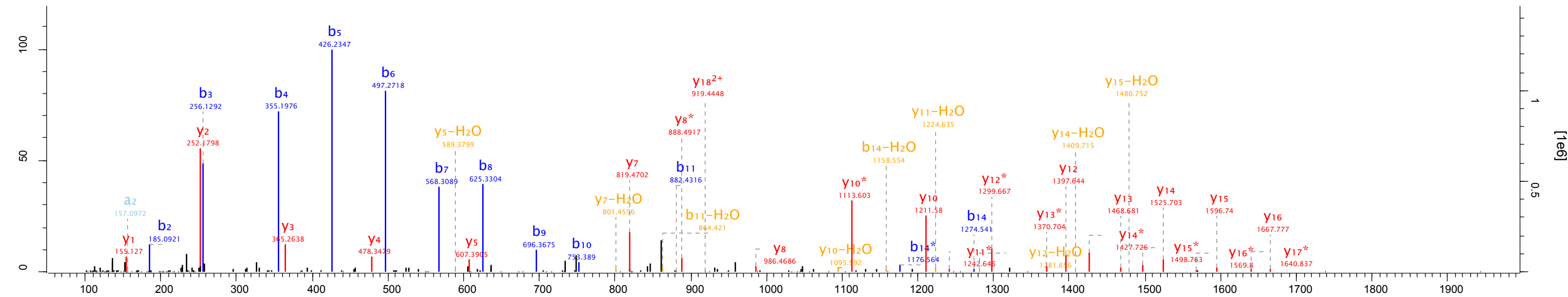
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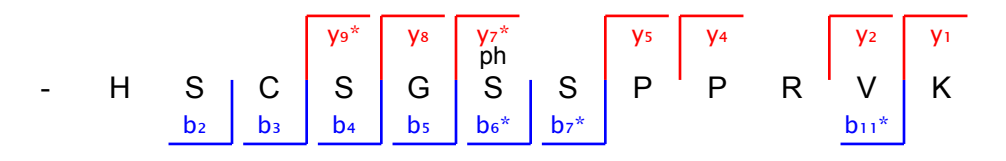
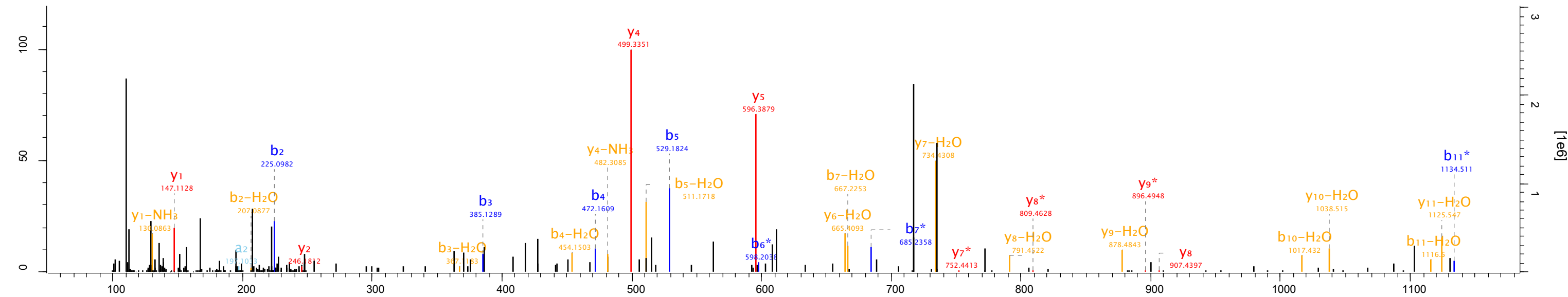
20171215_MaS_33SR_LMH_phospho_03 15839 FTMS; HCD 133.28 808.91 MAP4



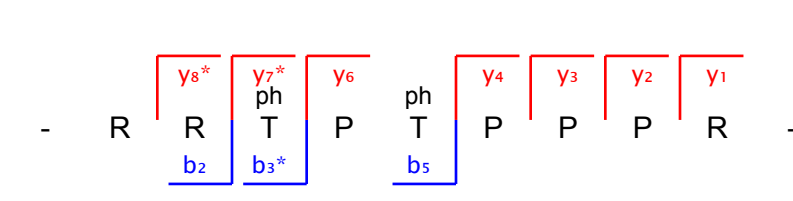
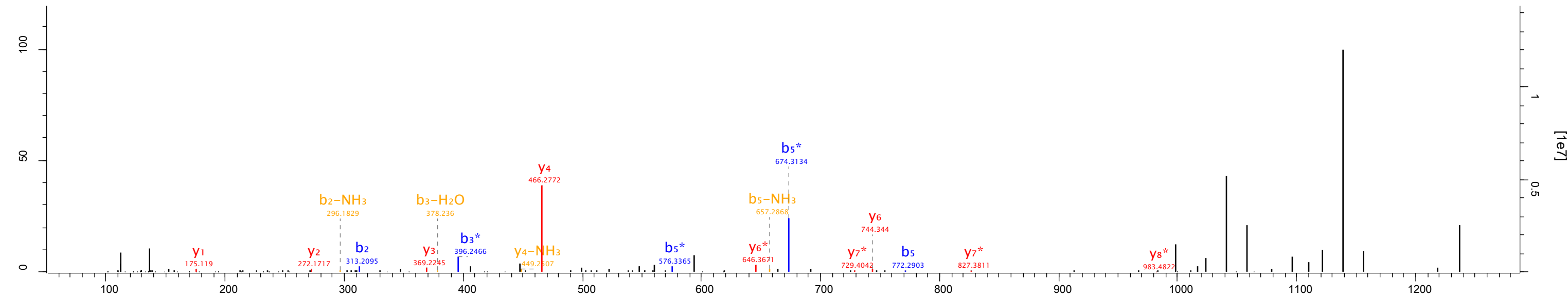
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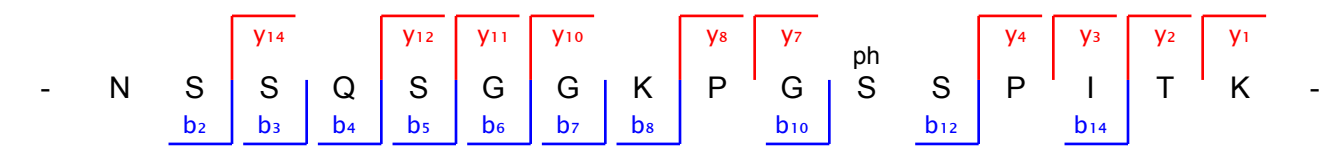
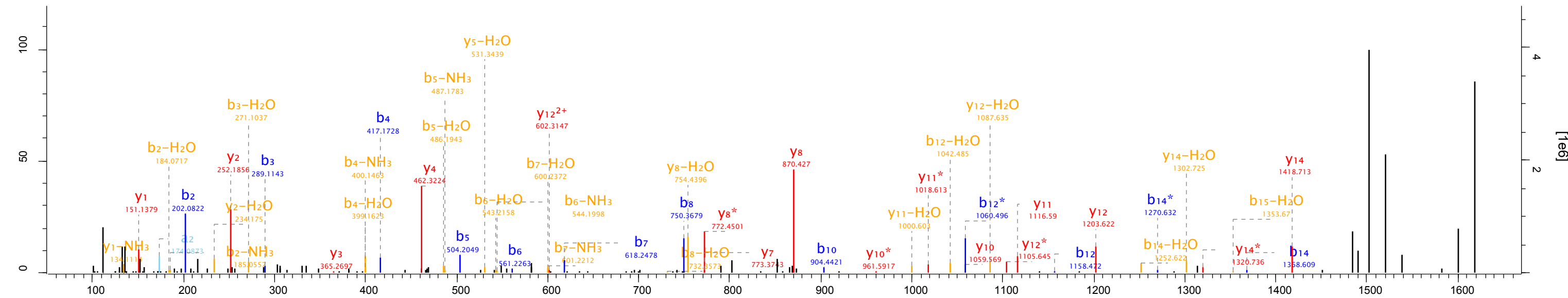
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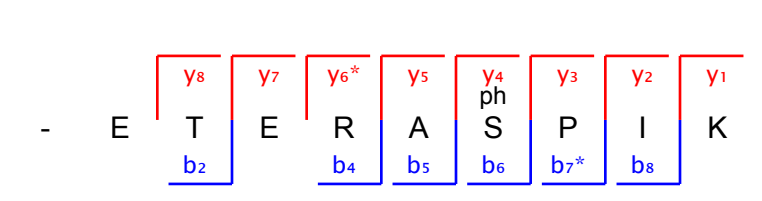
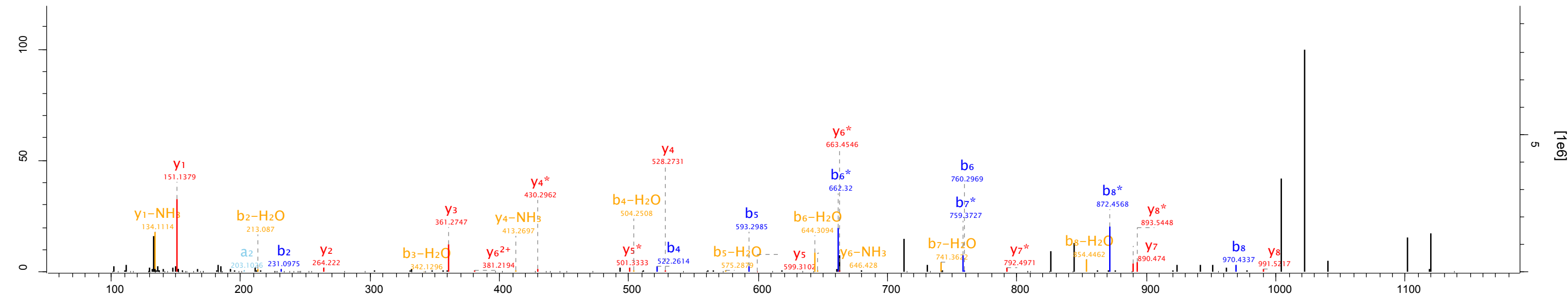
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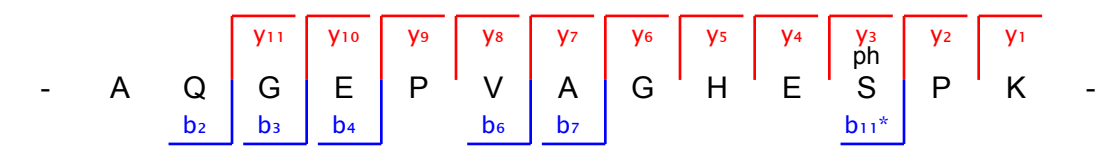
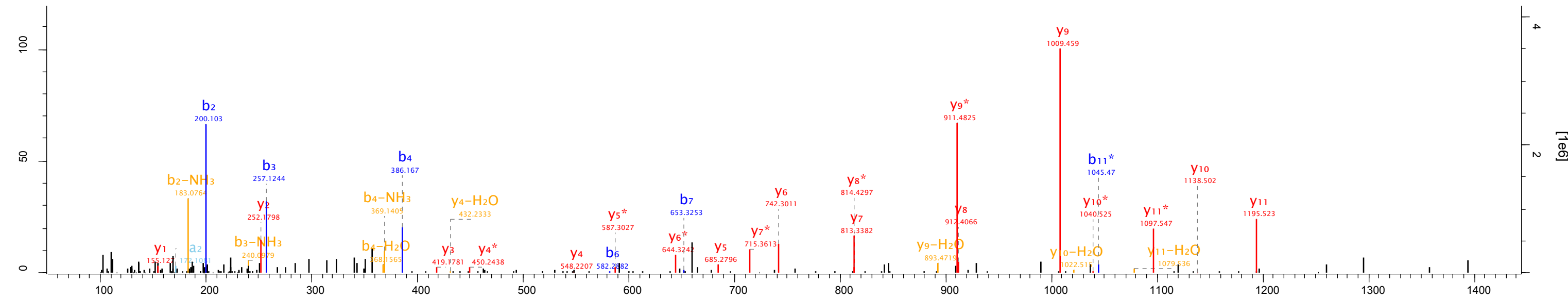
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 Scan 2179 Method FTMS; HCD Score 192.09 m/z 810.4 Gene names MED1



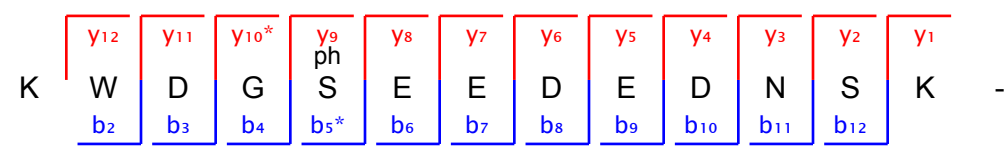
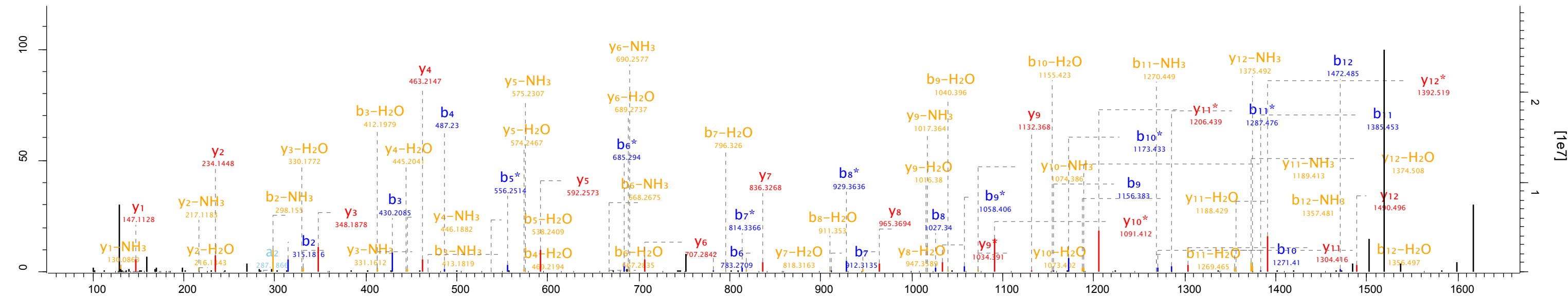
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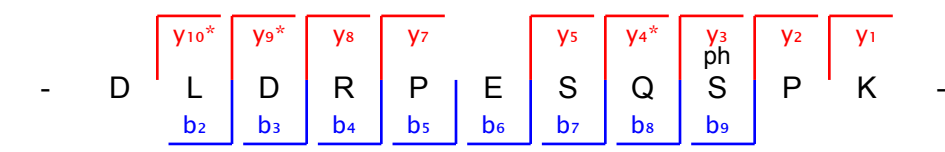
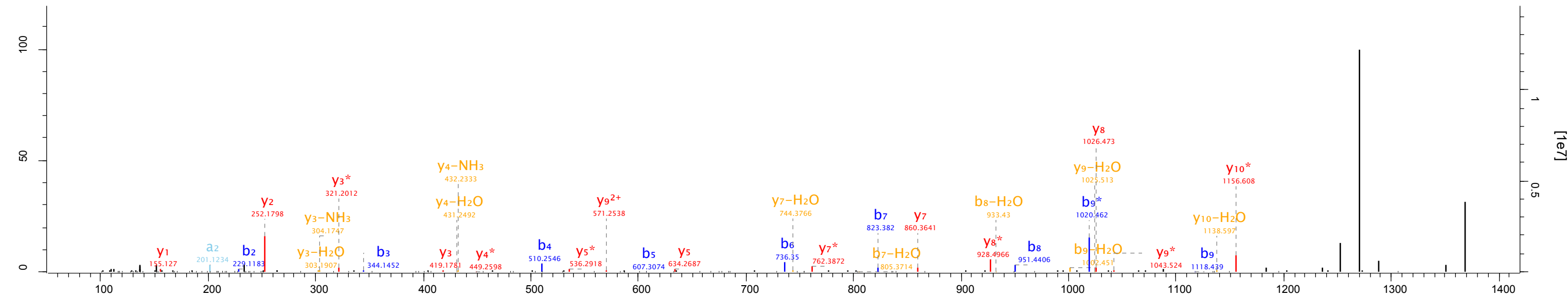
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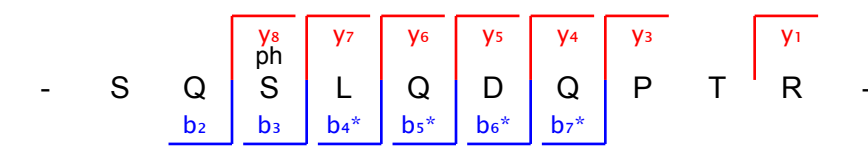
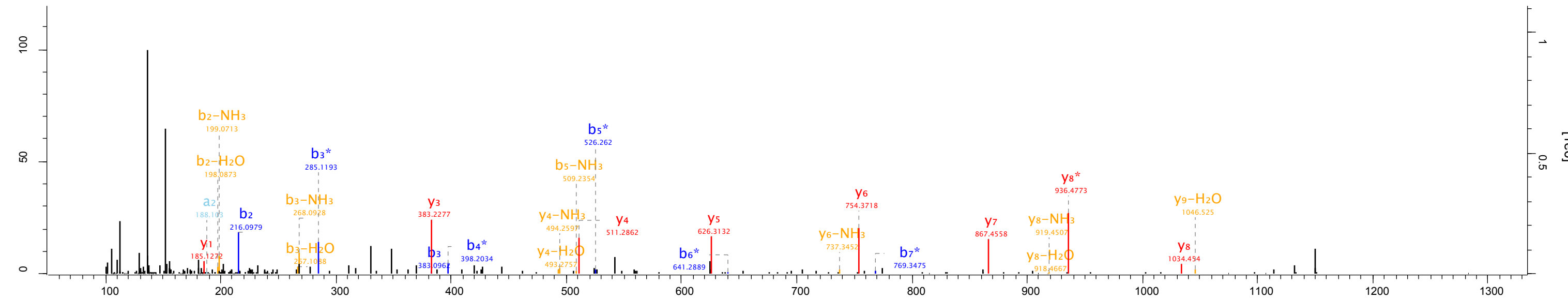
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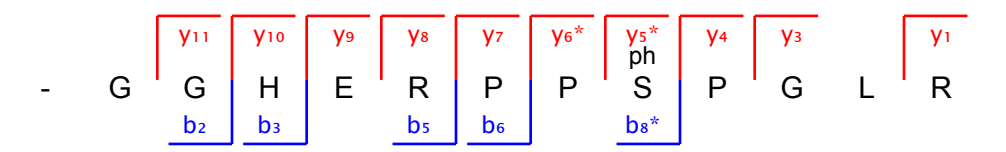
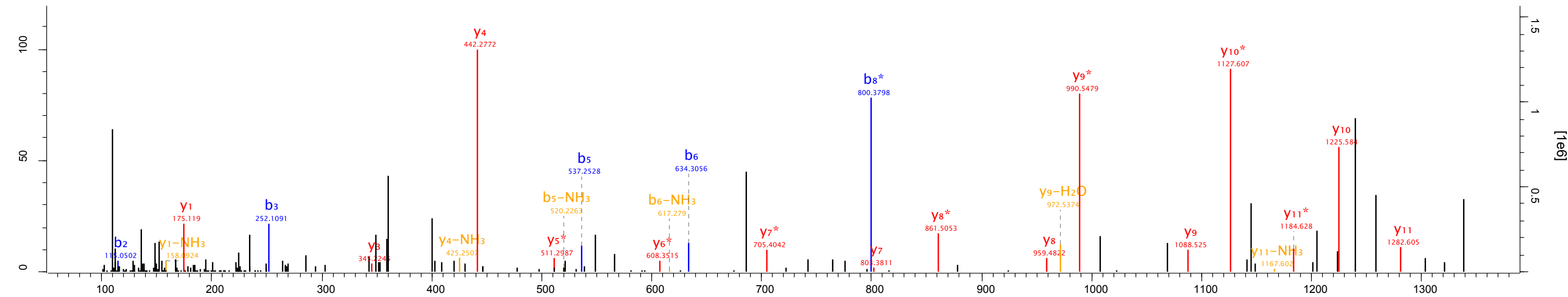
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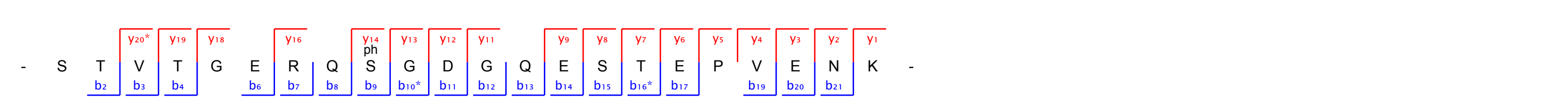
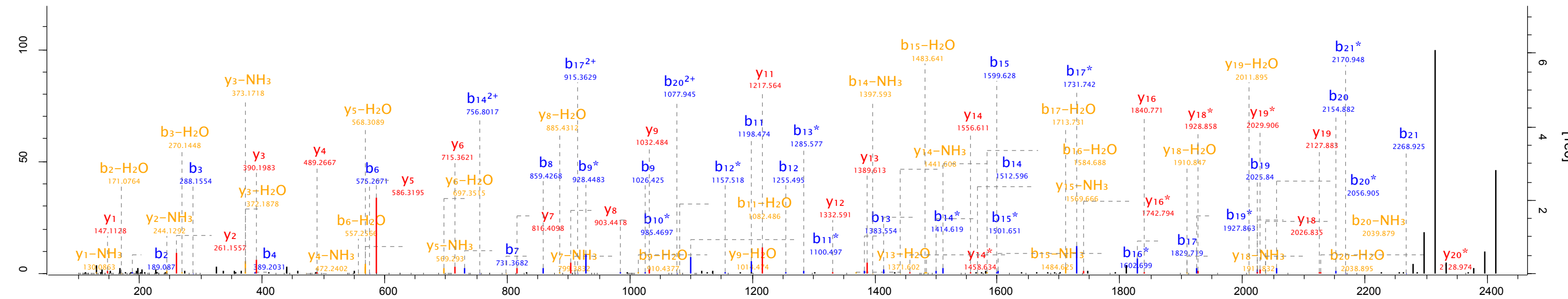
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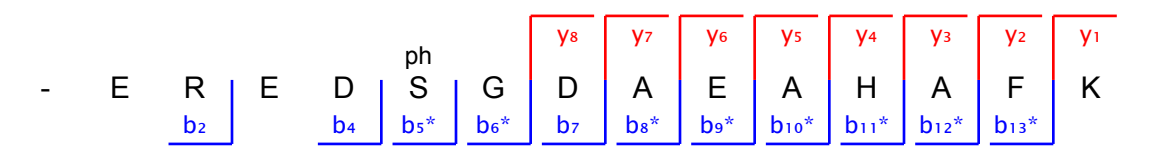
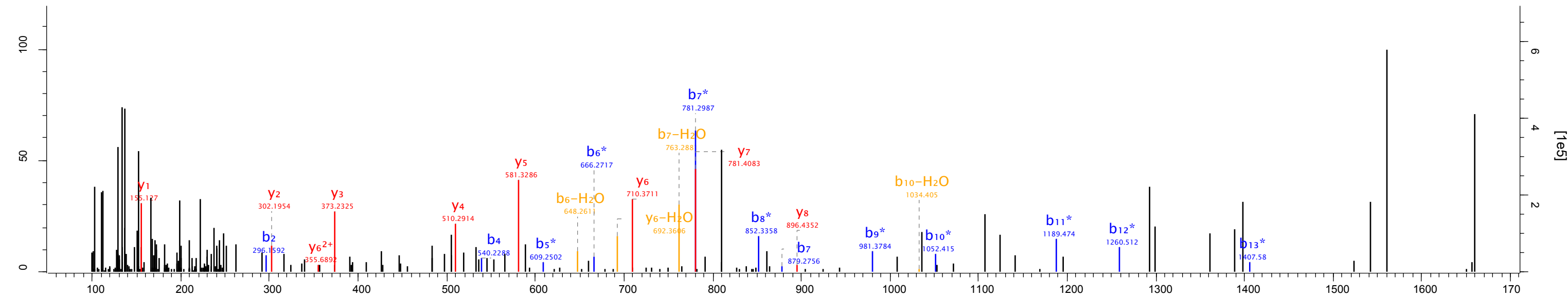
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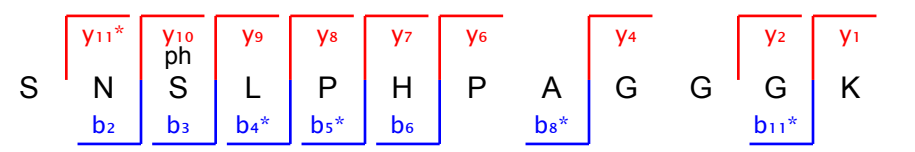
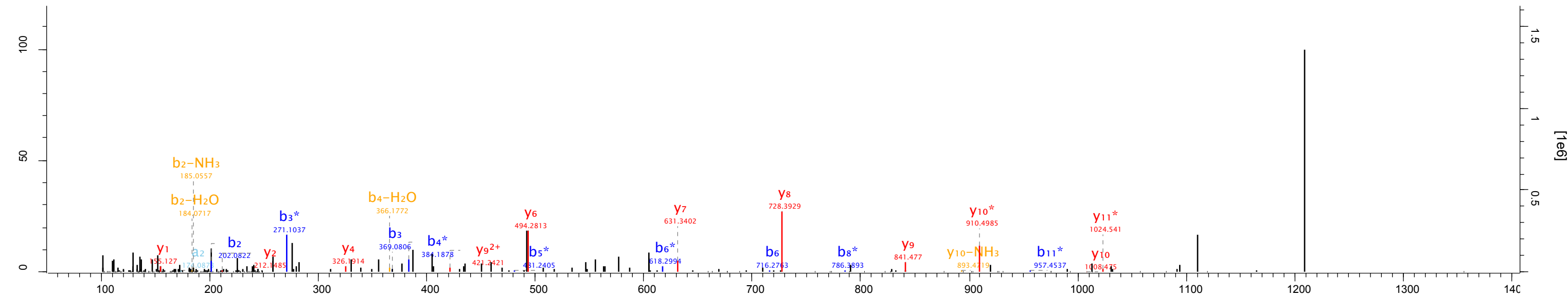
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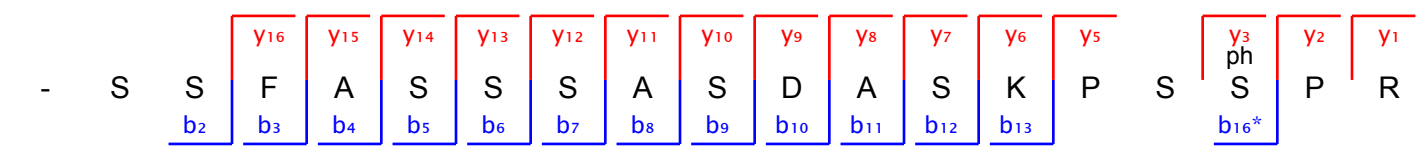
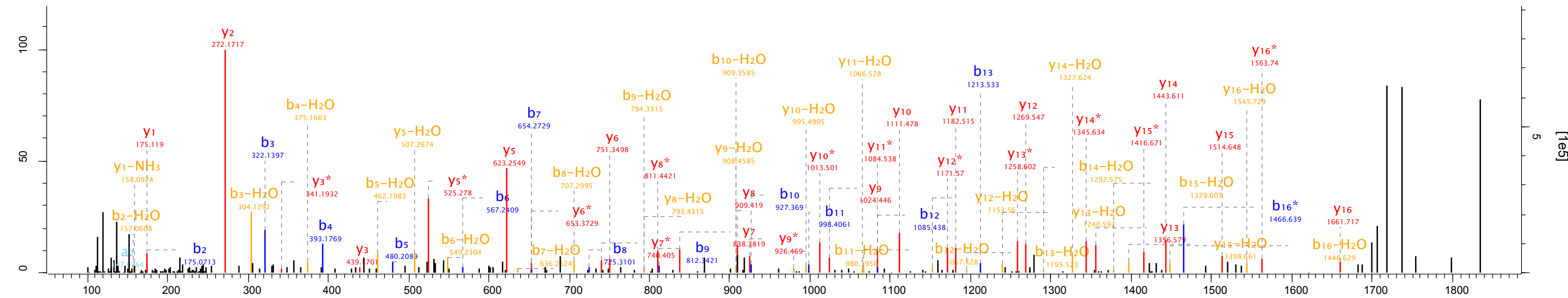
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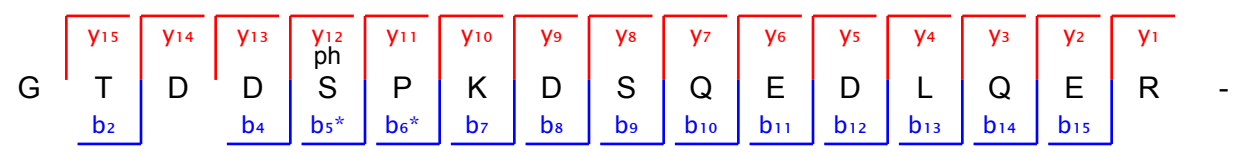
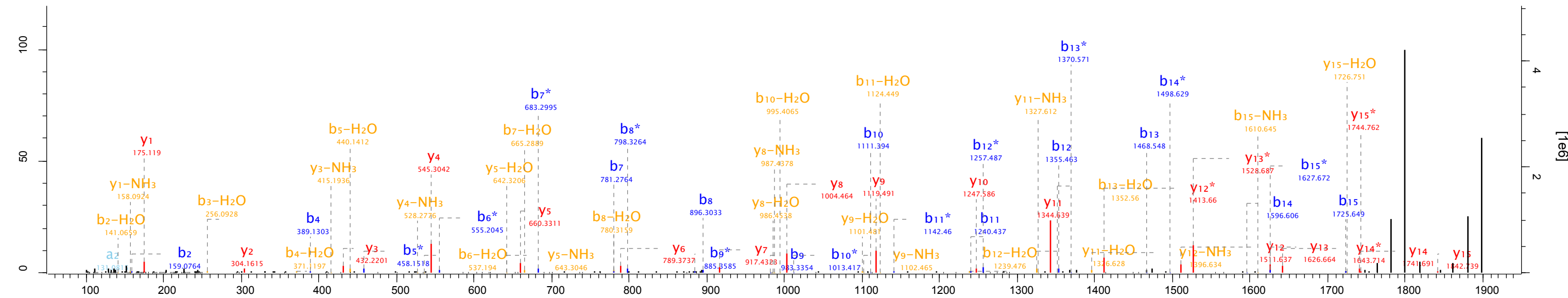
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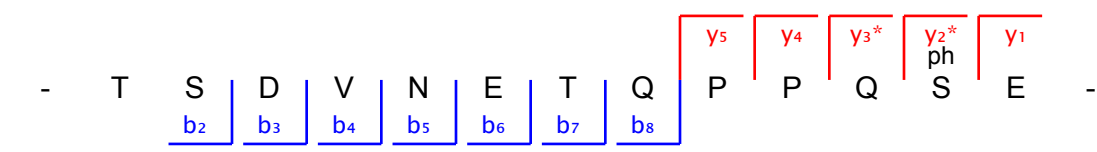
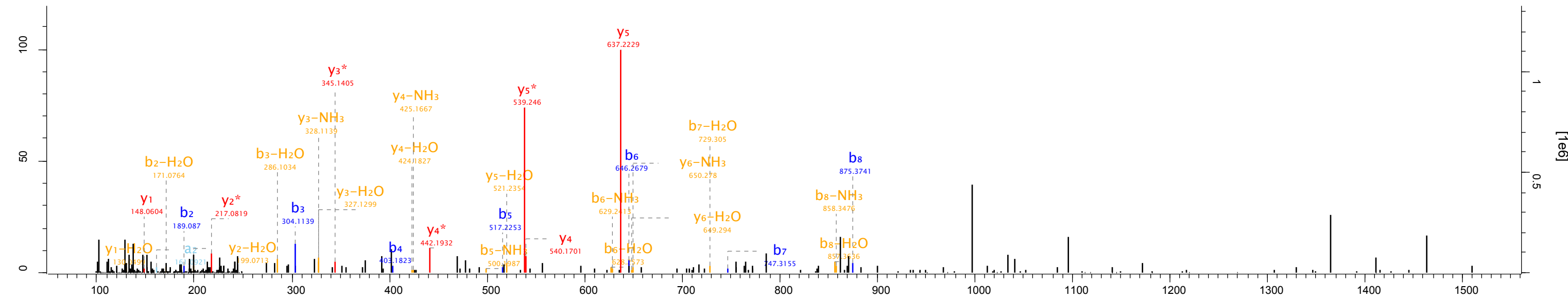
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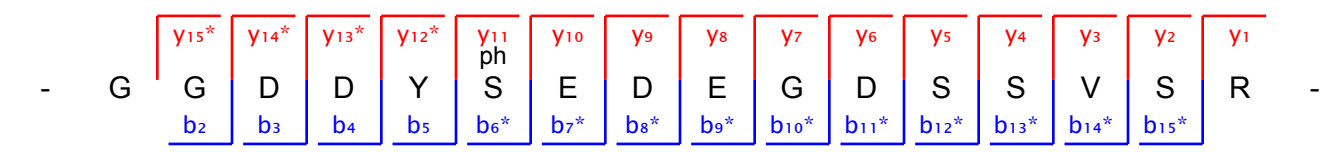
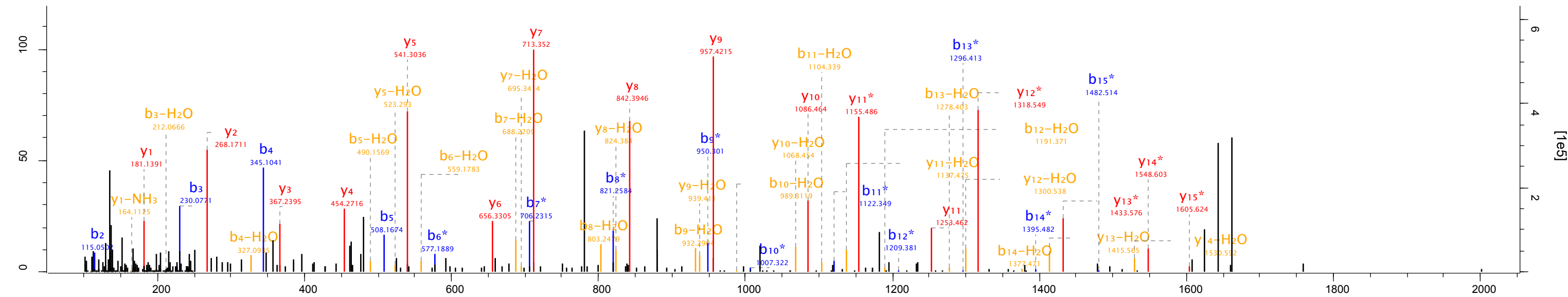
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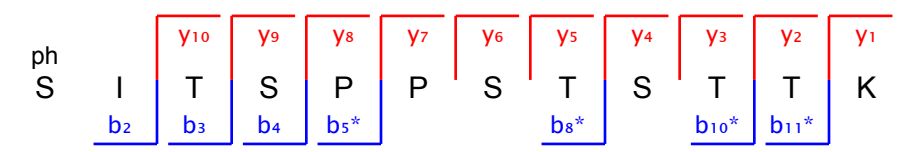
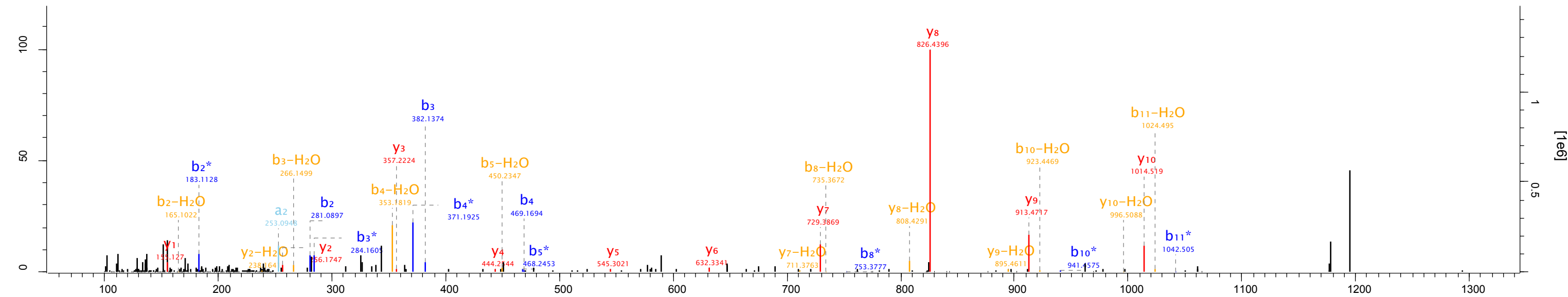
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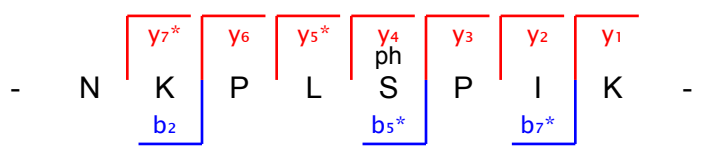
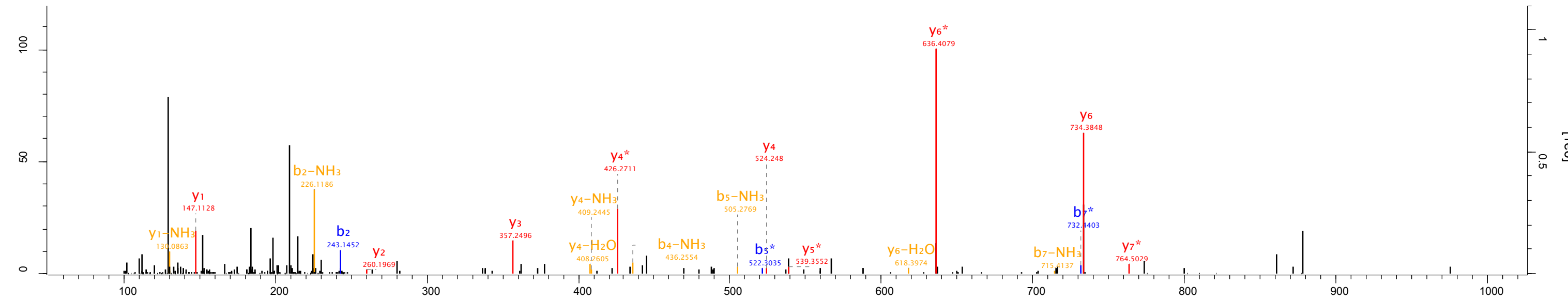
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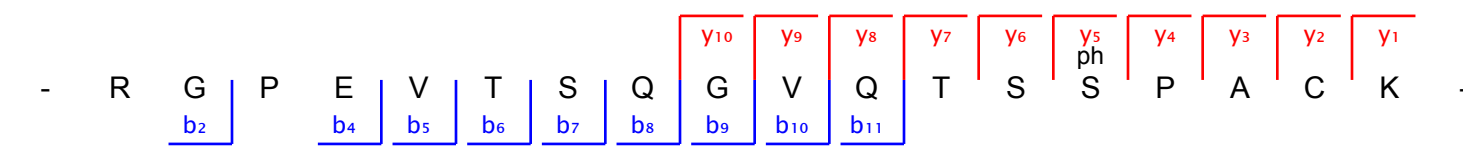
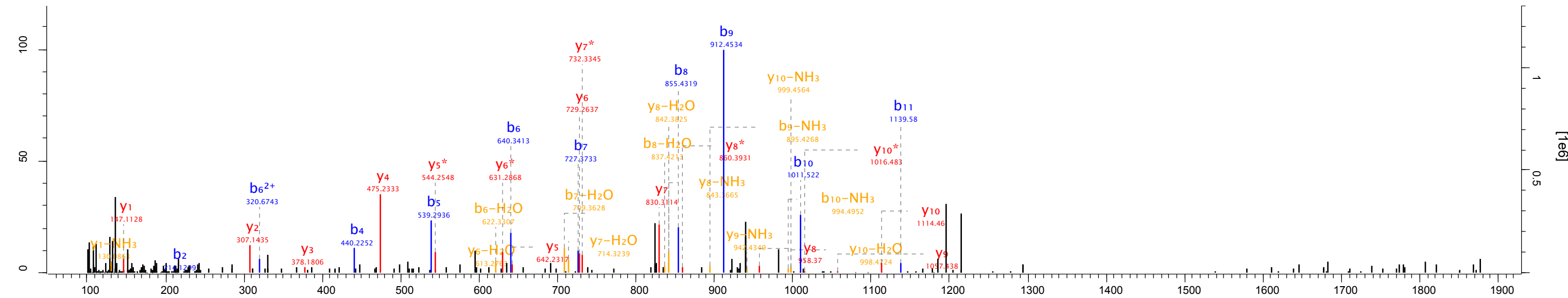
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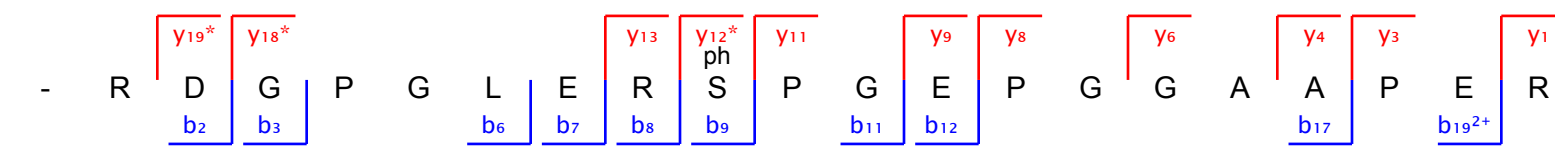
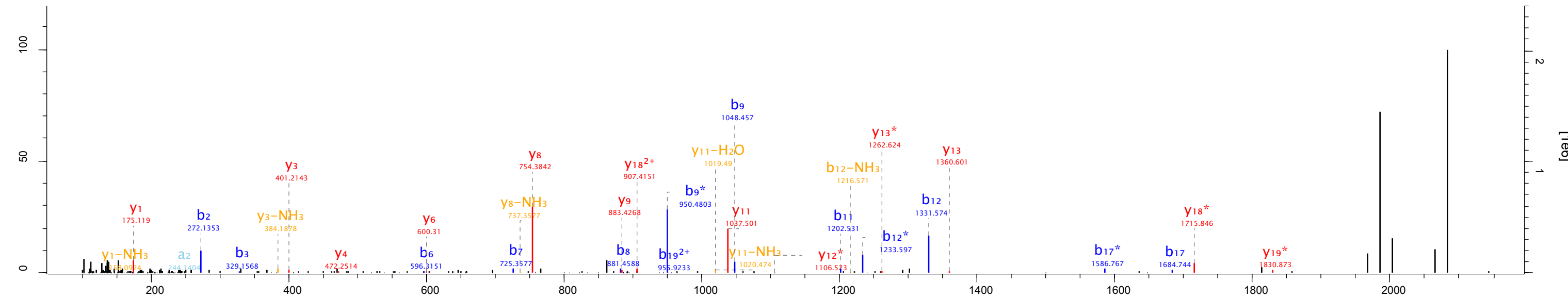
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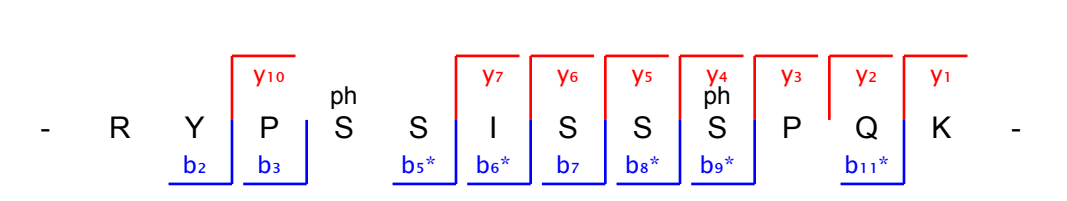
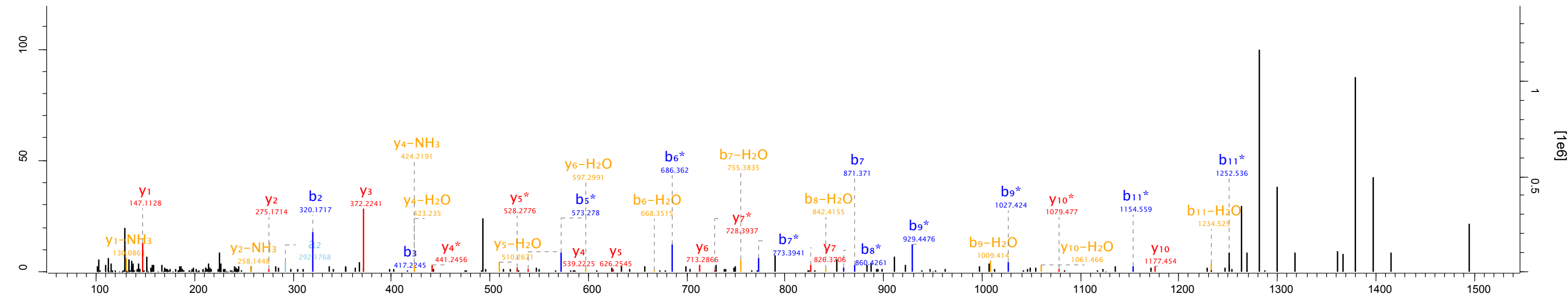
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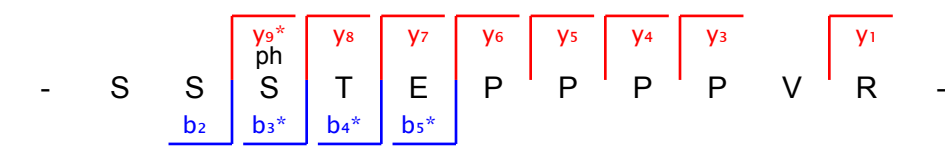
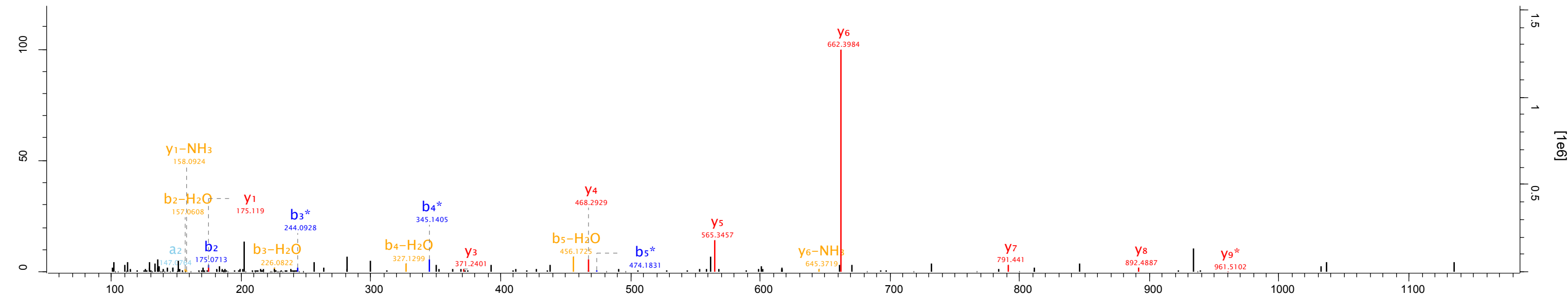
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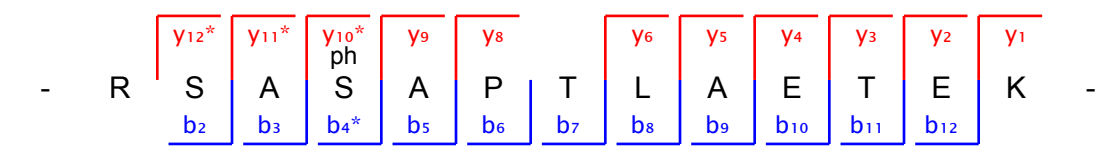
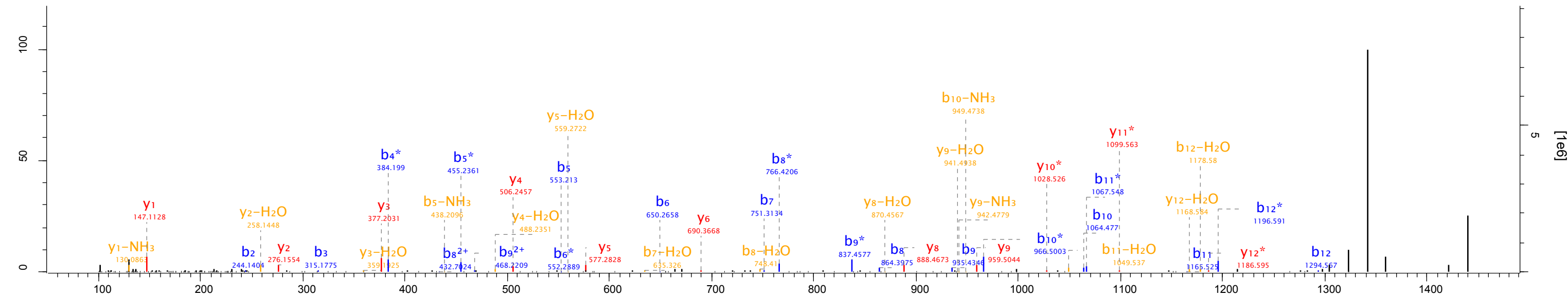
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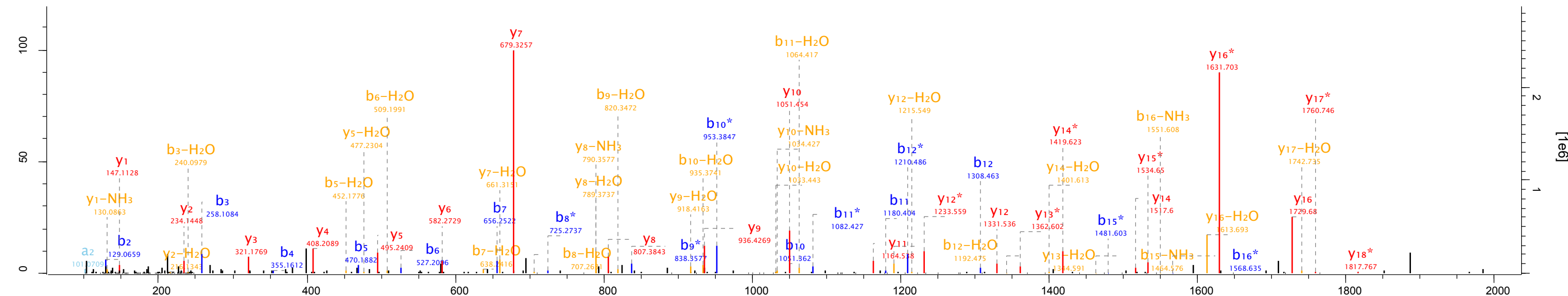
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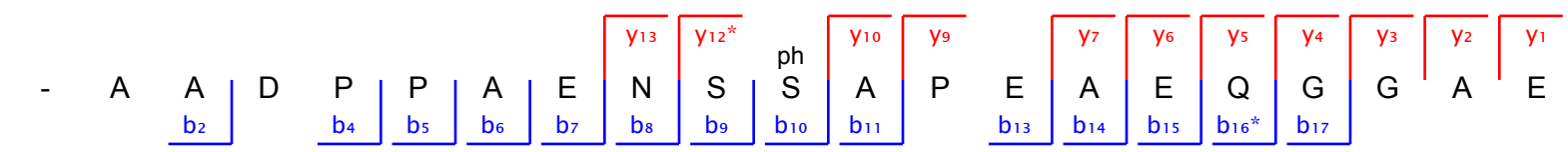
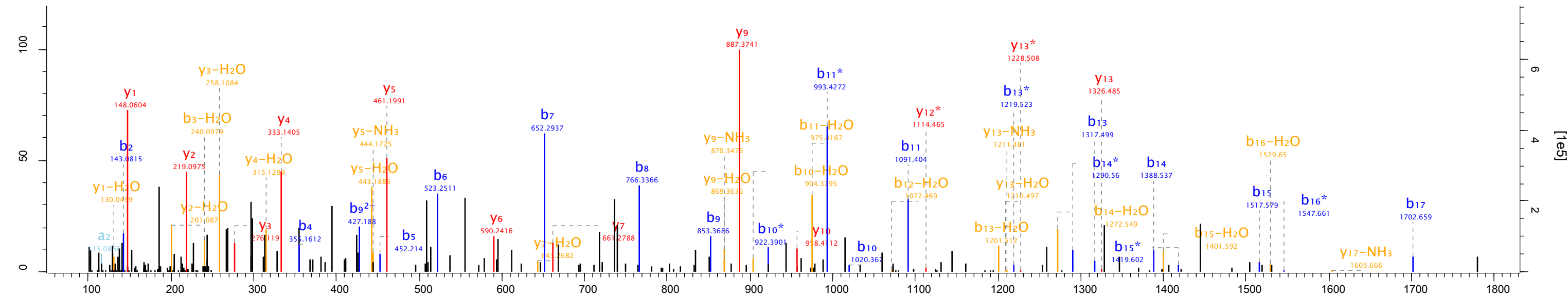
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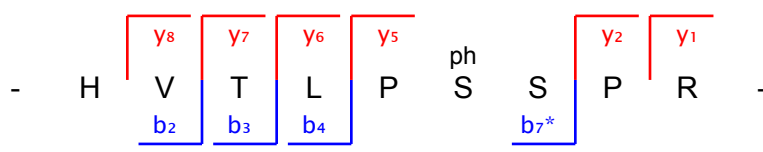
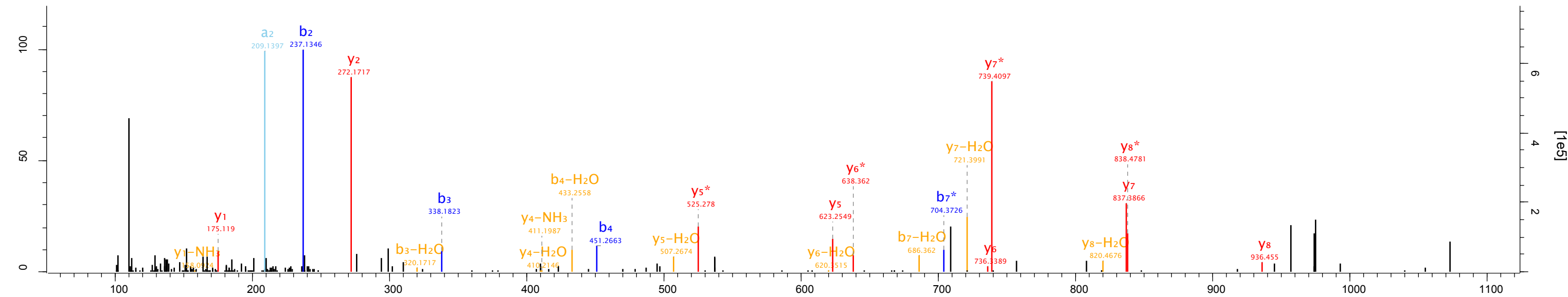
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y18*	y17*	y16	y15*	y14	y13*	y12 ph	y11	y10	y9	y8	y7	y6	y5	y4	y3	y2	y1
G	E	P	D	G	E	S	L	D	E	Q	P	S	S	S	S	S	K
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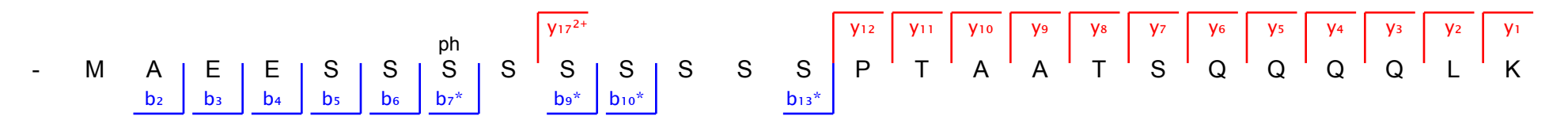
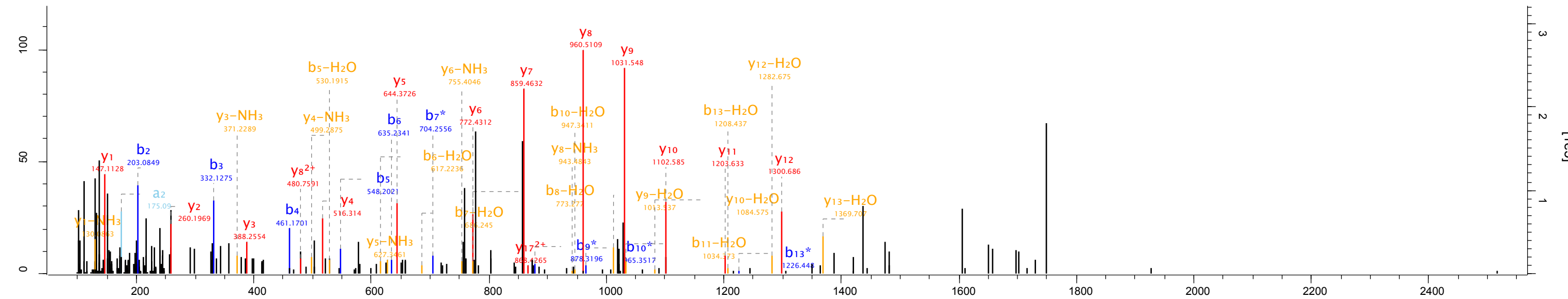
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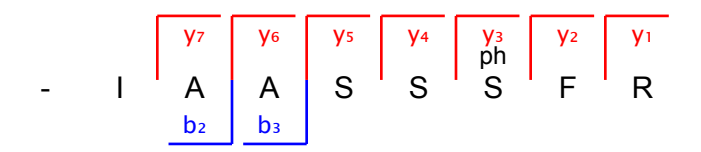
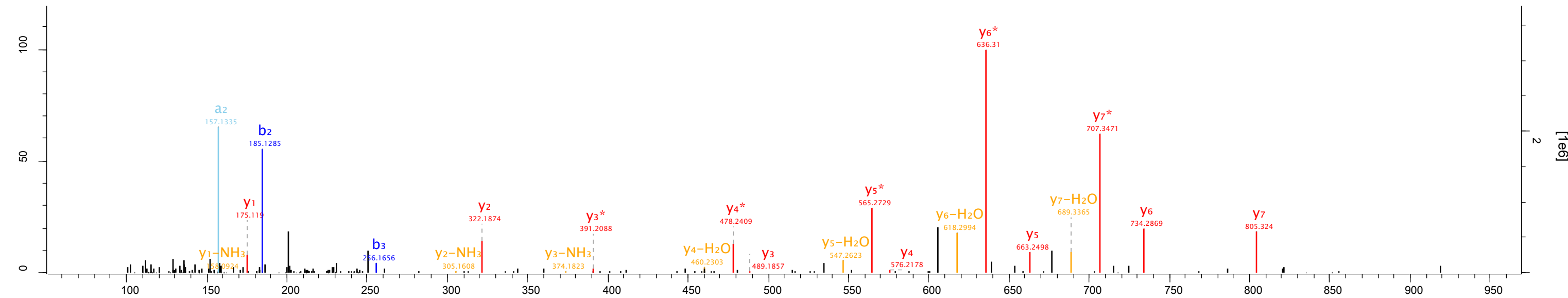
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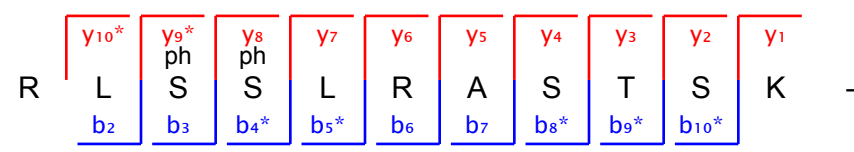
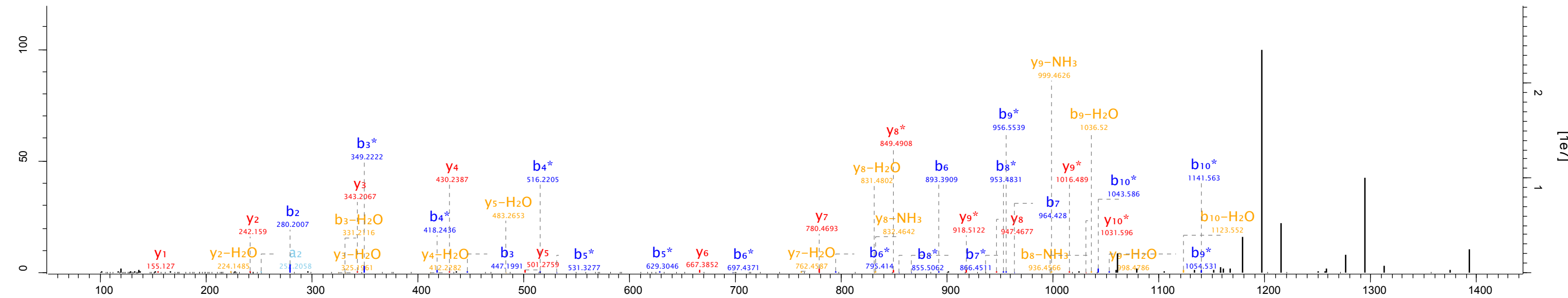
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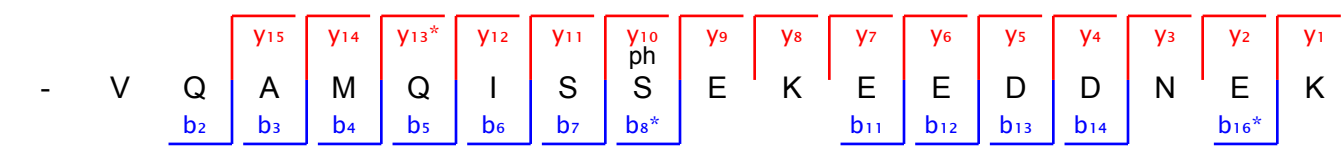
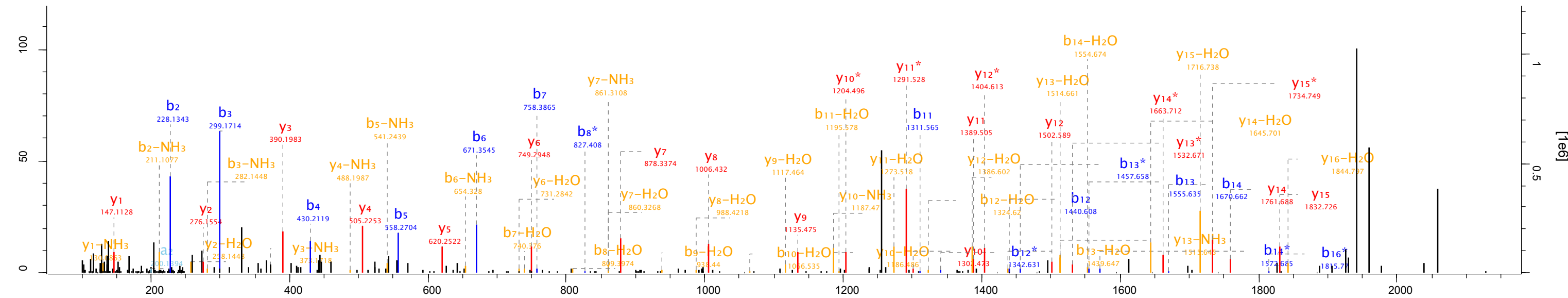
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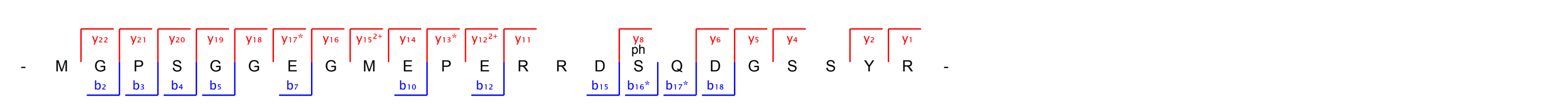
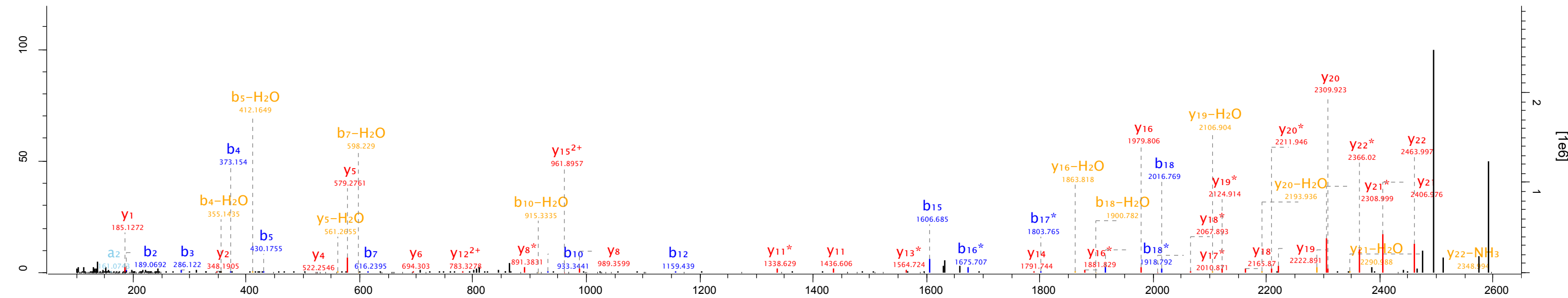
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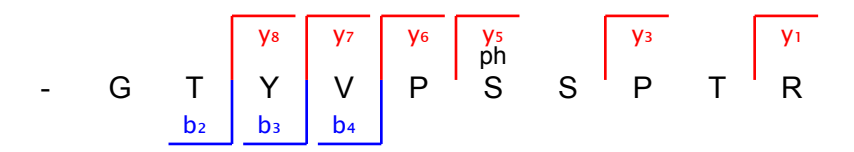
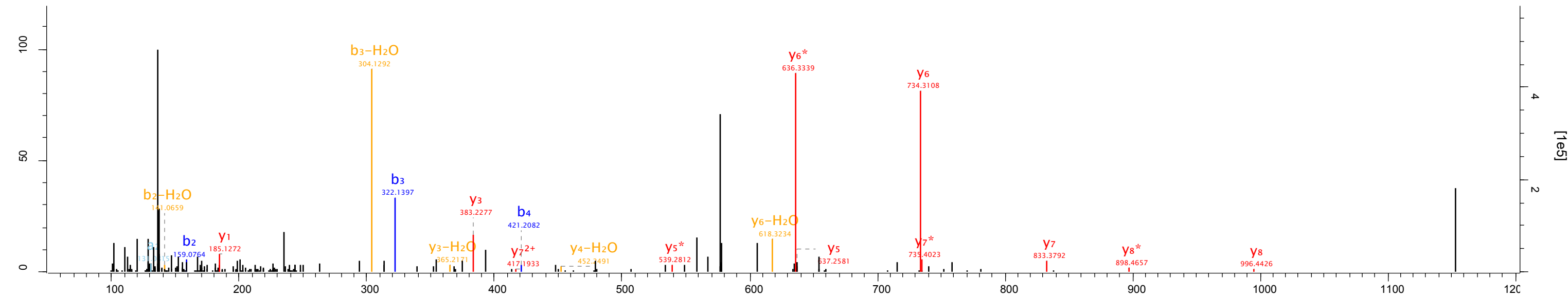
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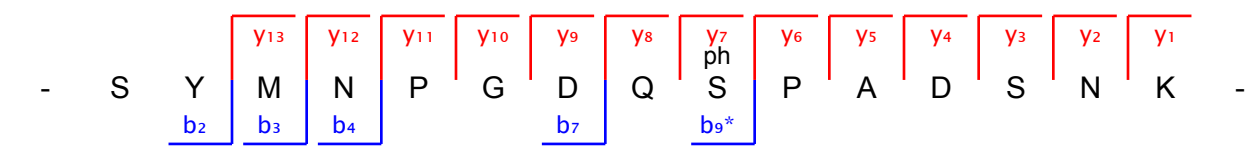
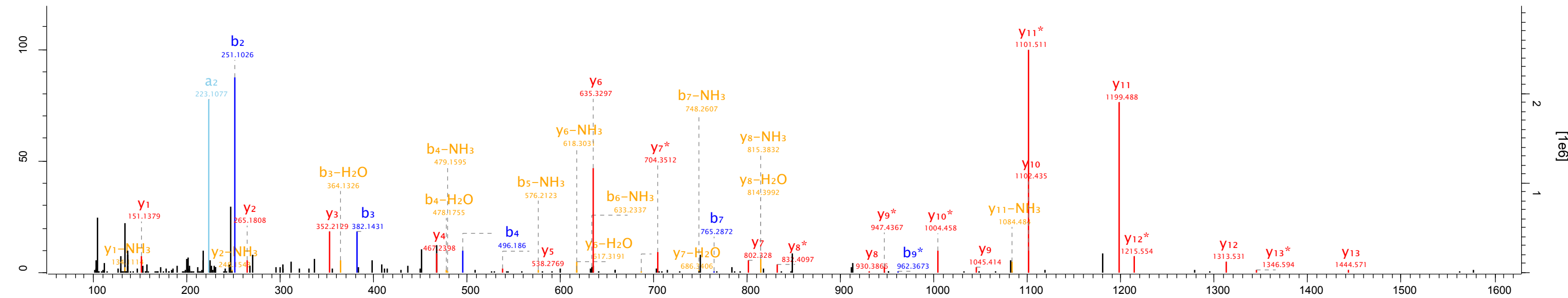
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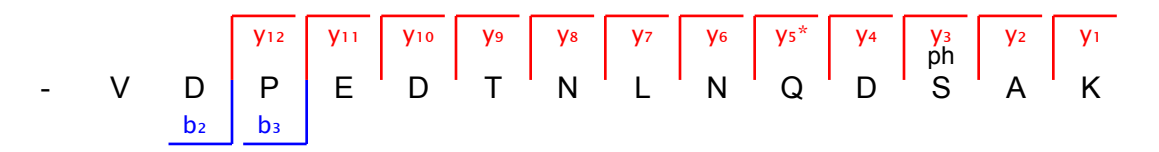
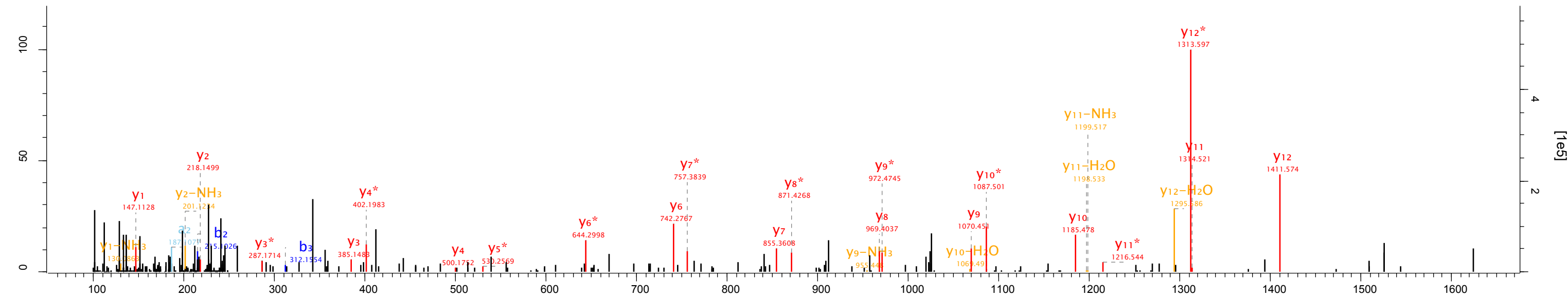
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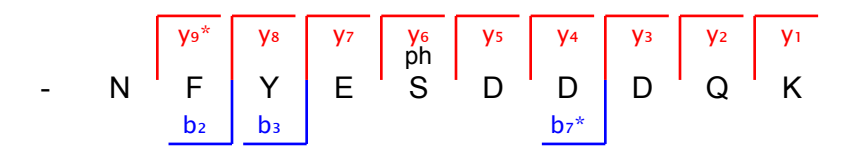
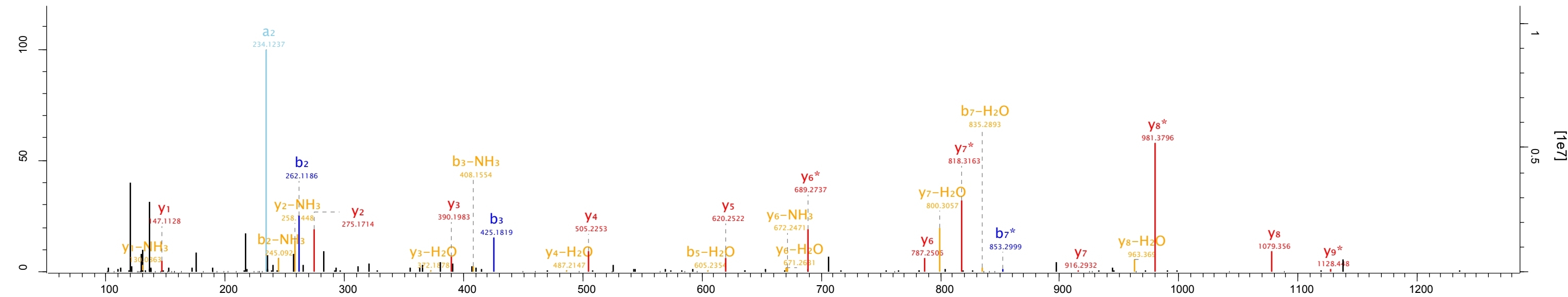
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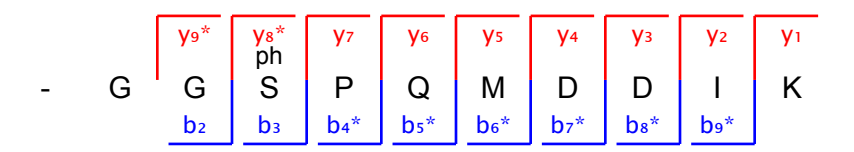
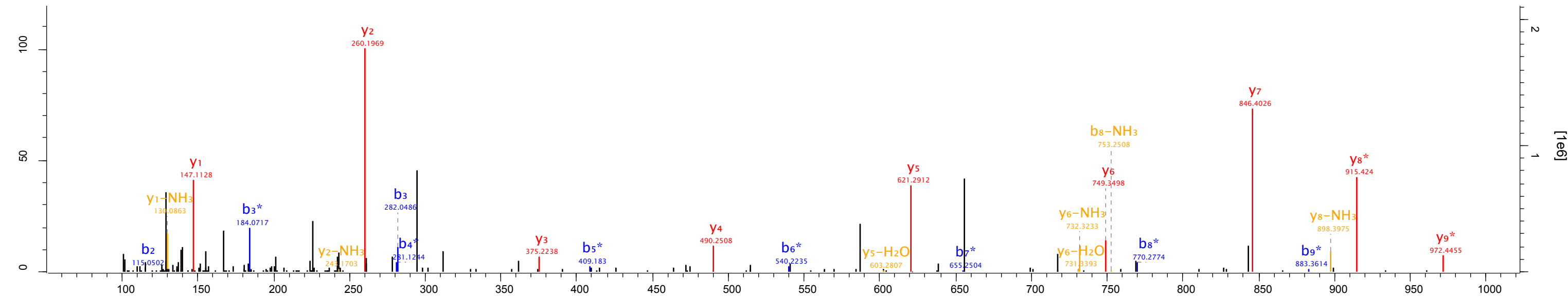


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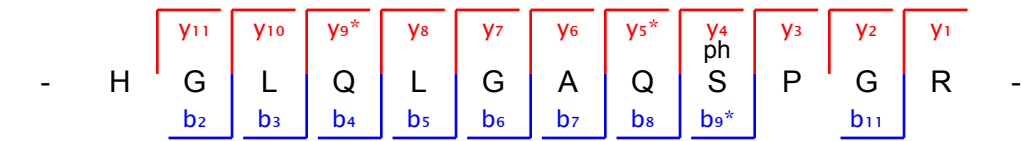
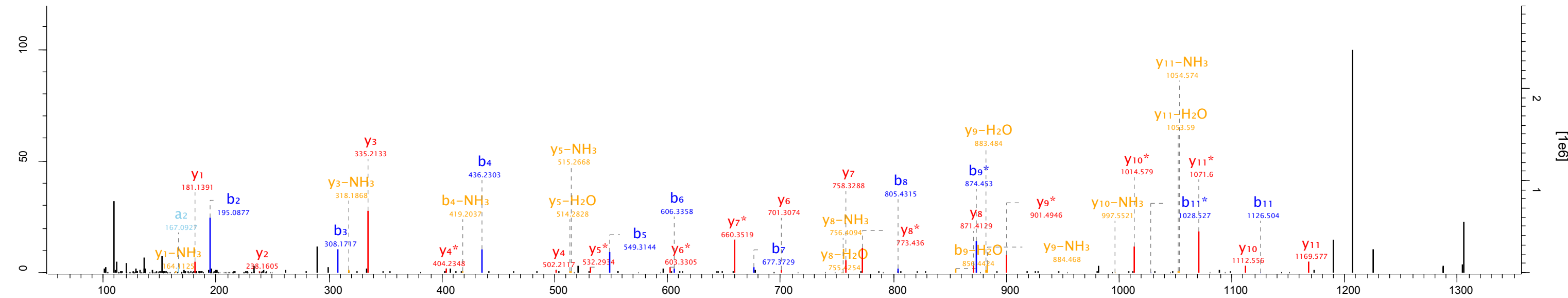


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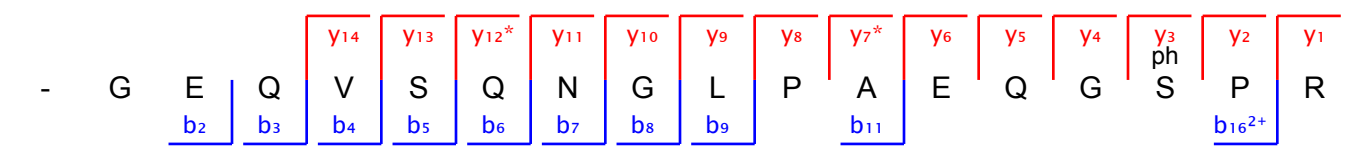
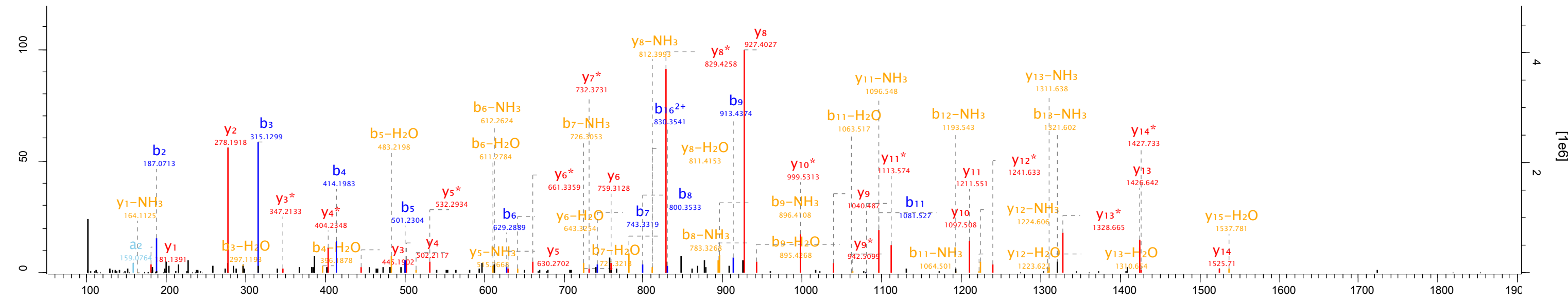
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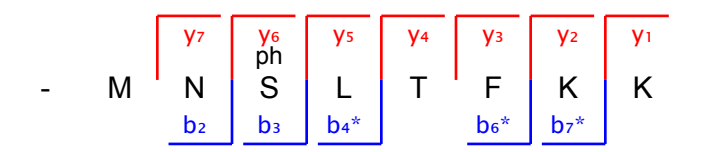
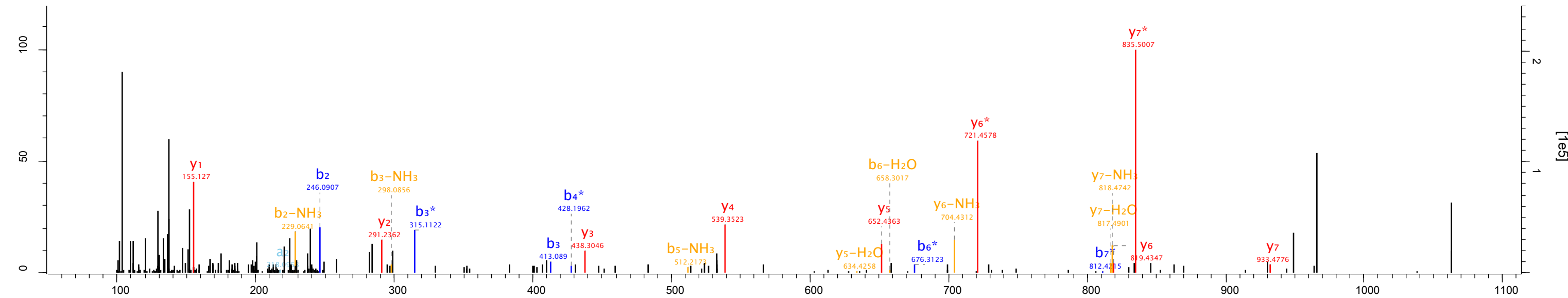
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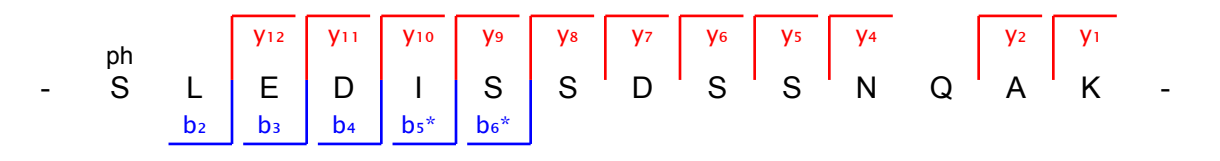
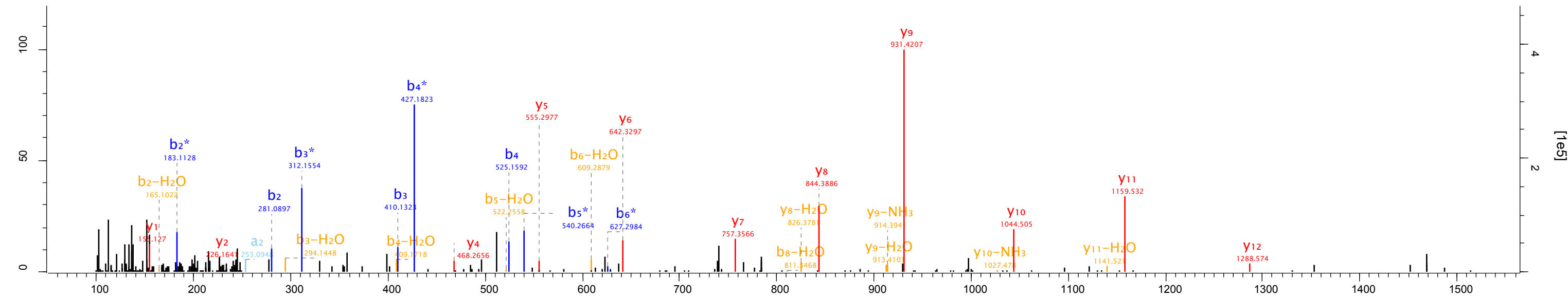
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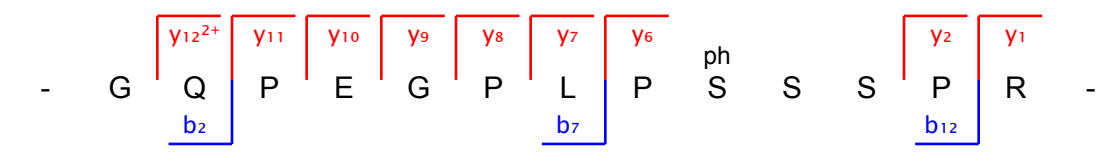
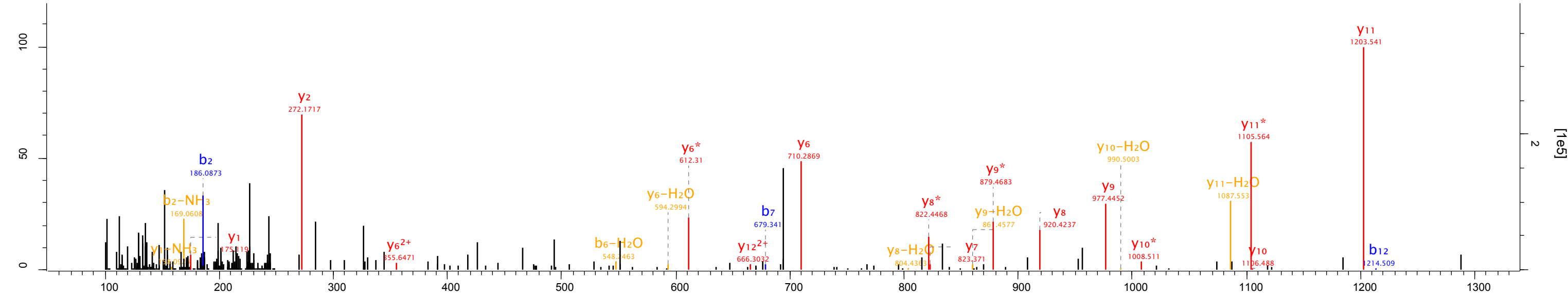
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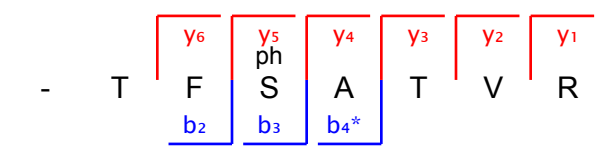
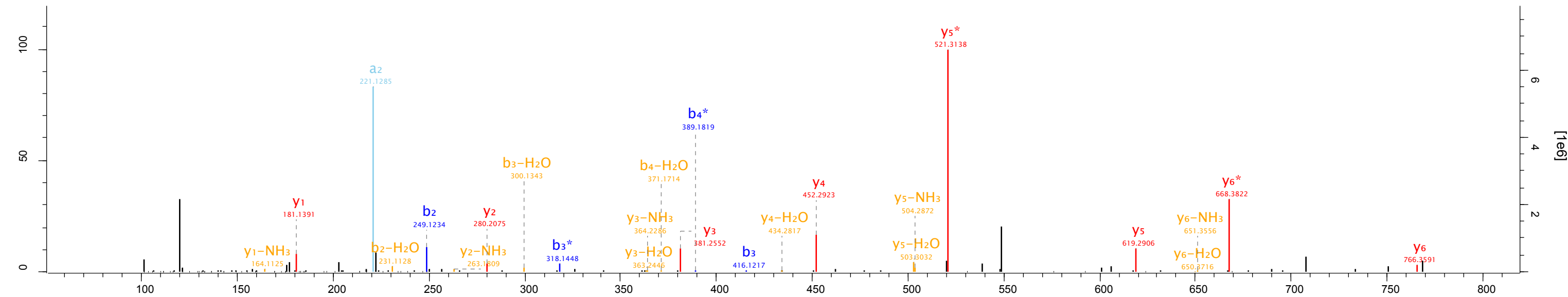
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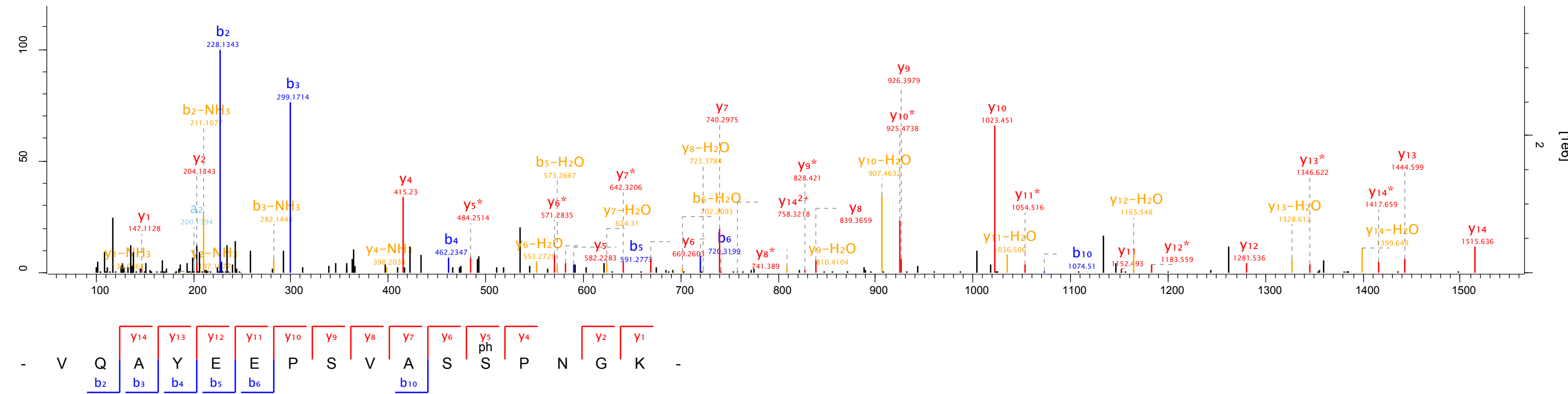


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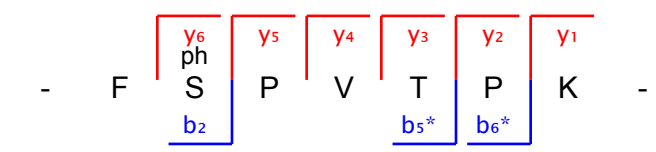
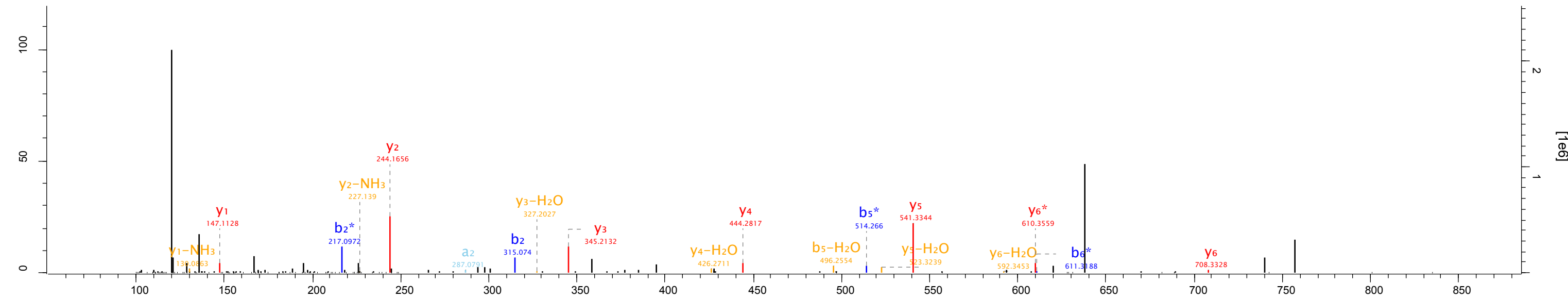


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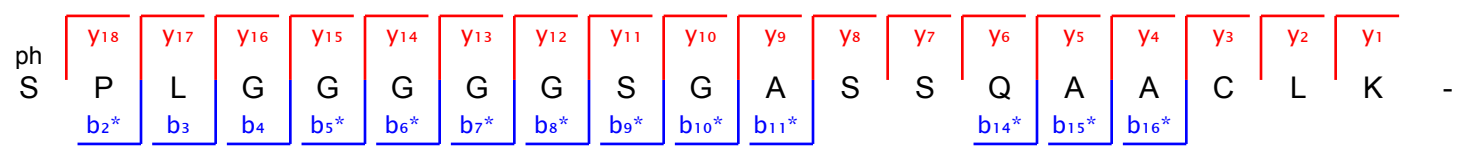
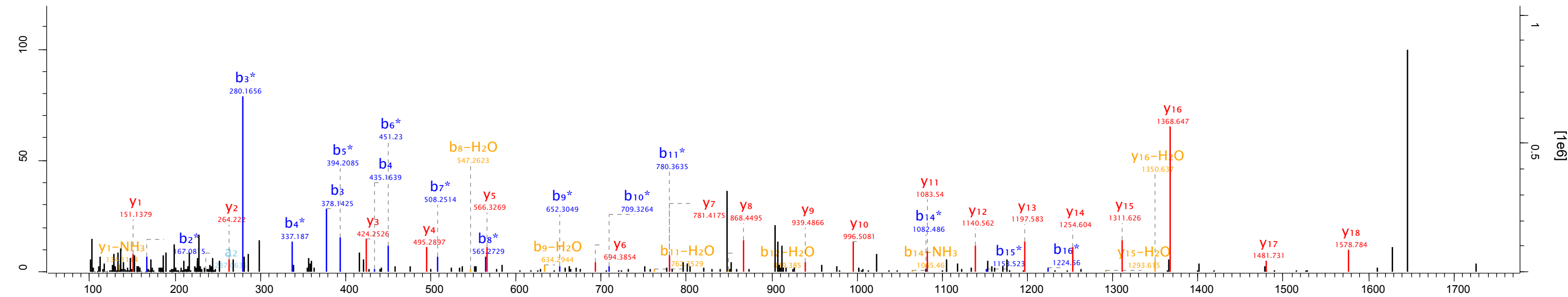




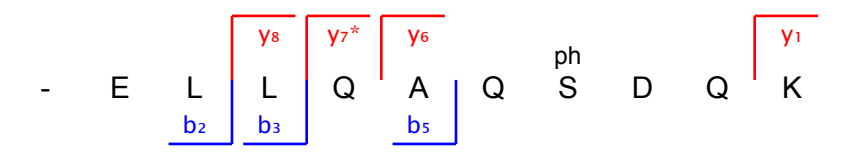
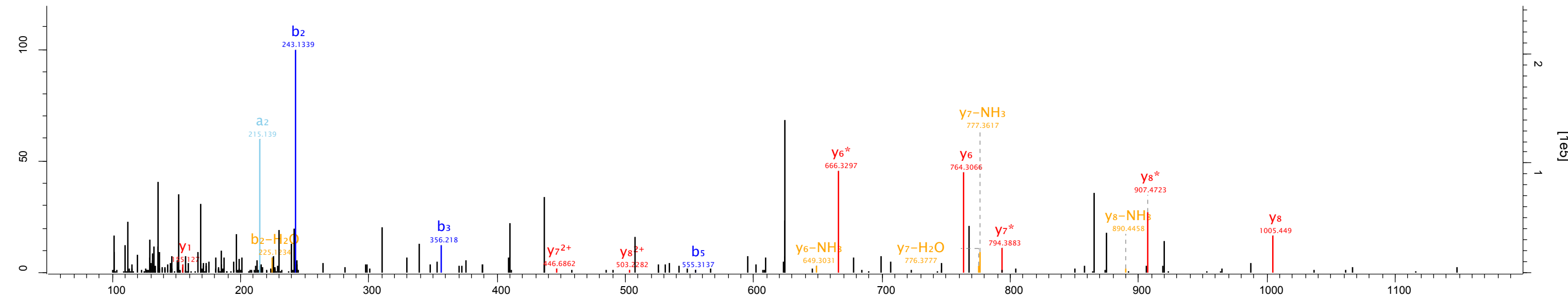
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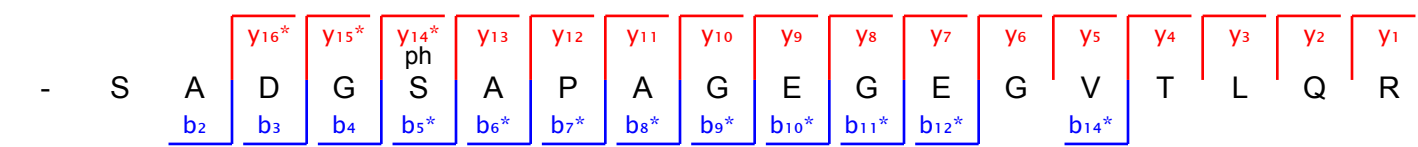
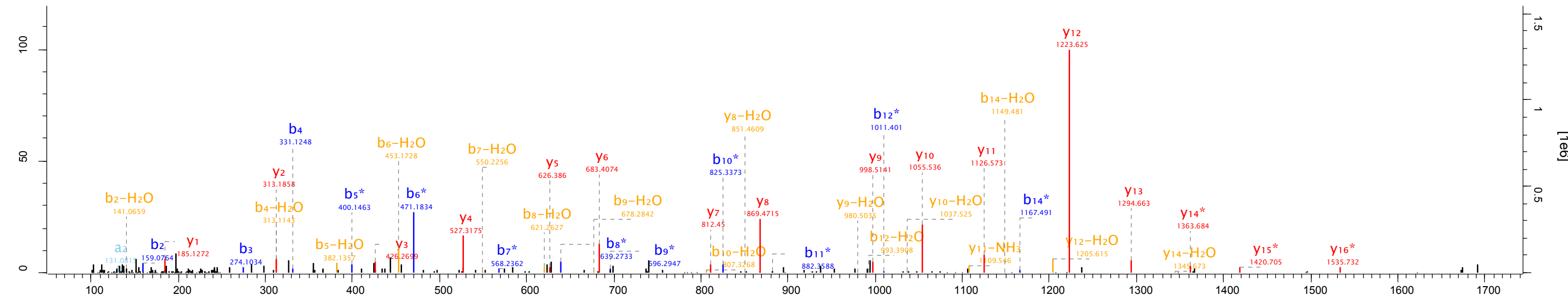
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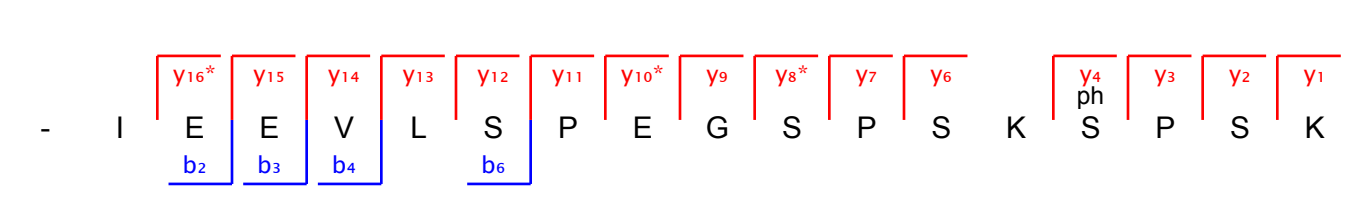
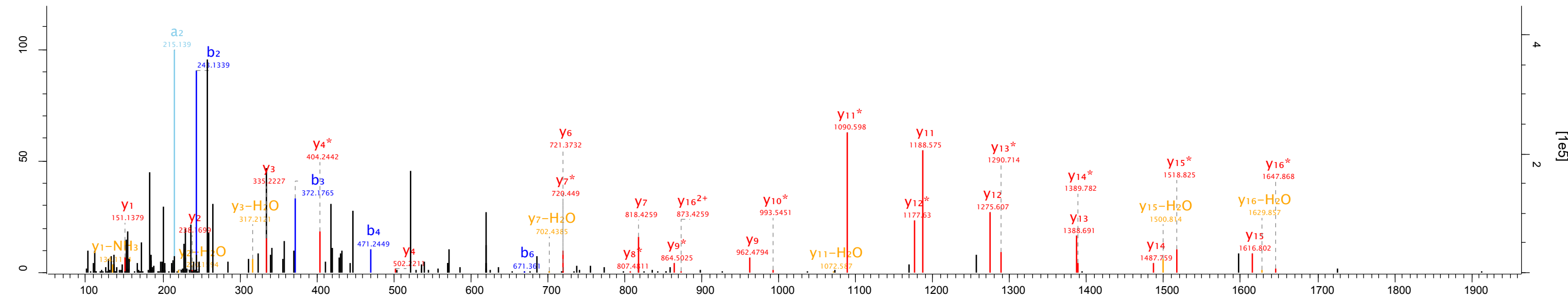
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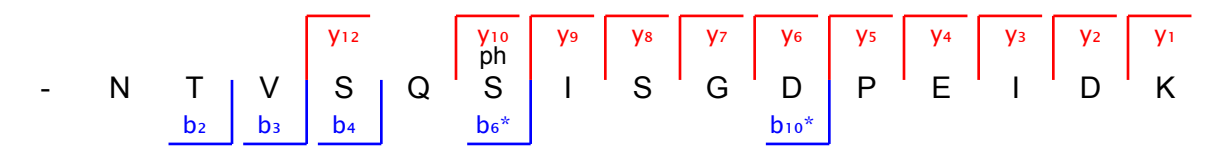
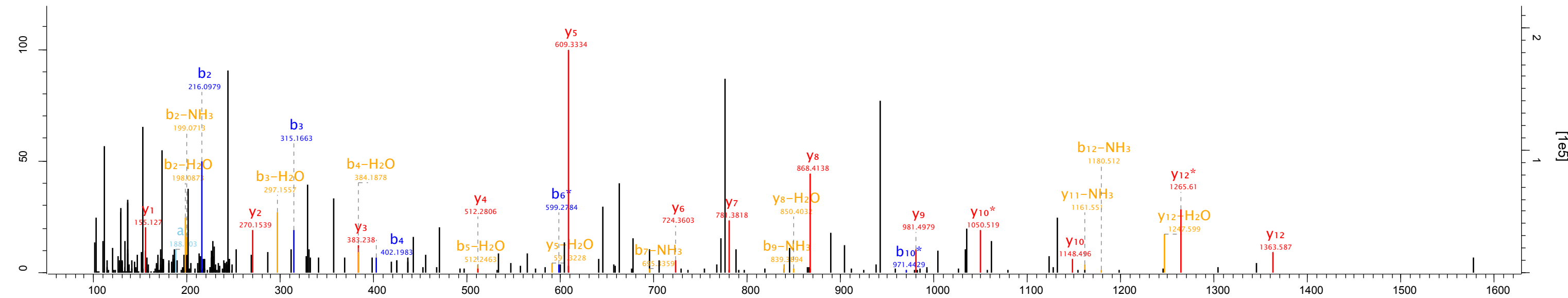
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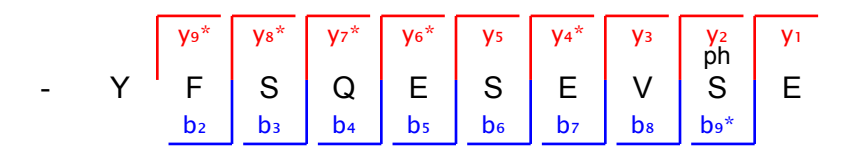
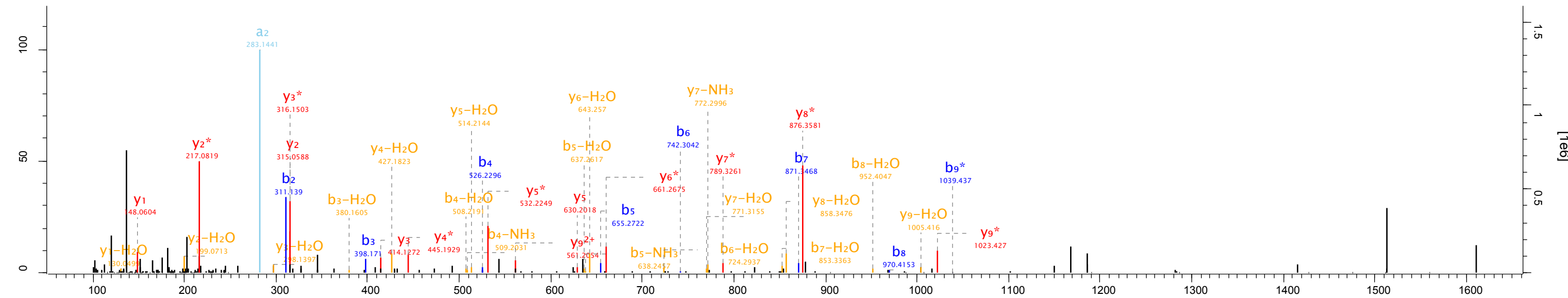
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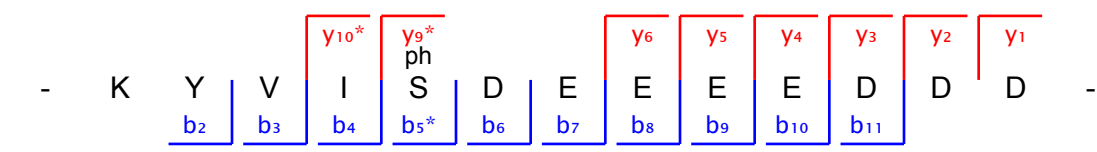
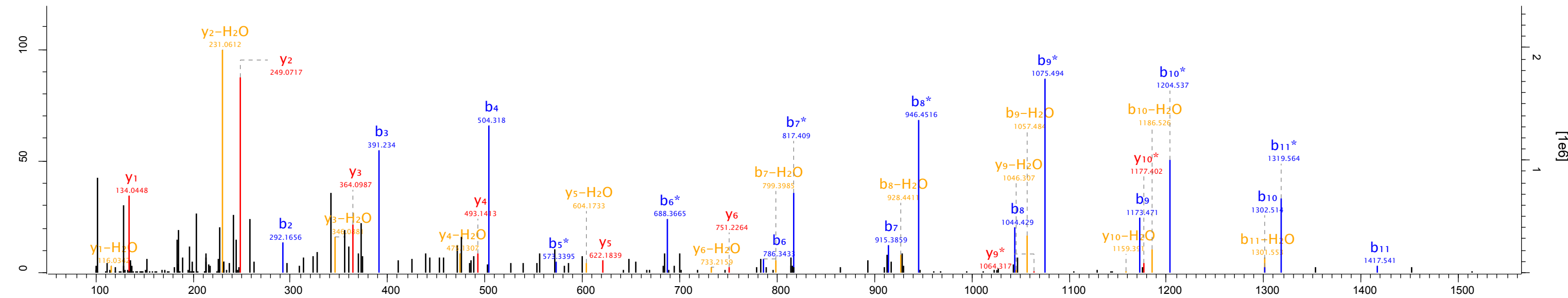
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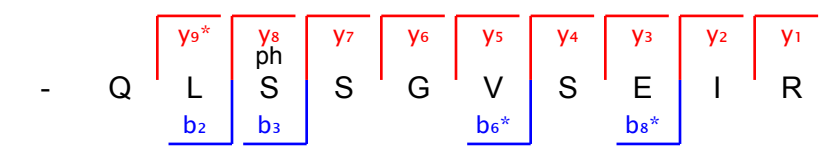
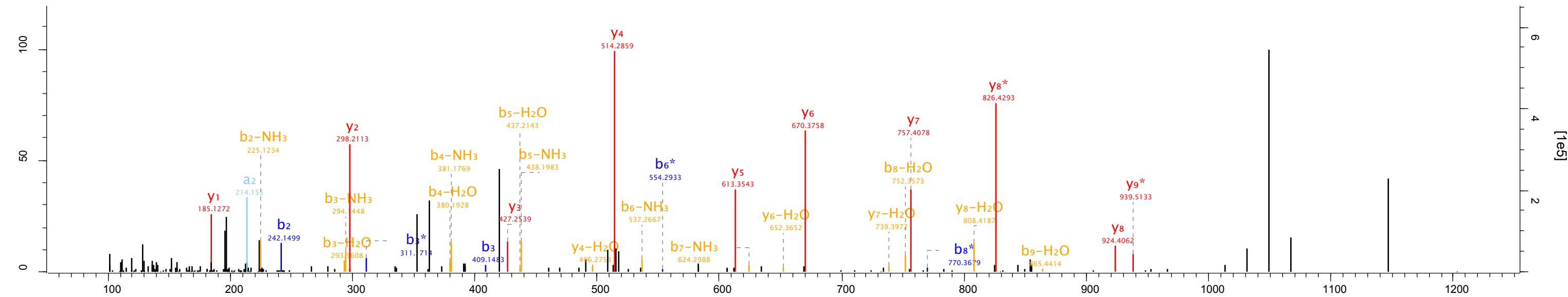
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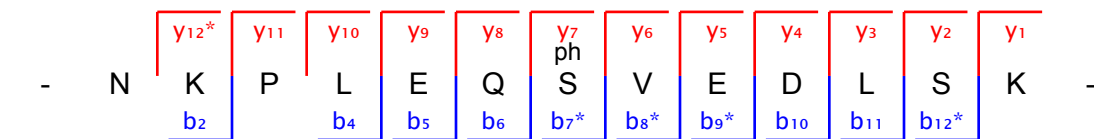
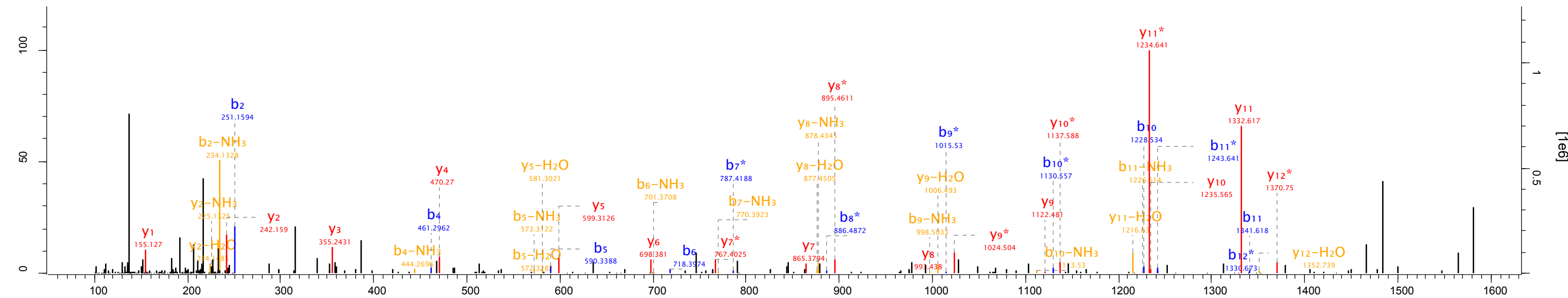


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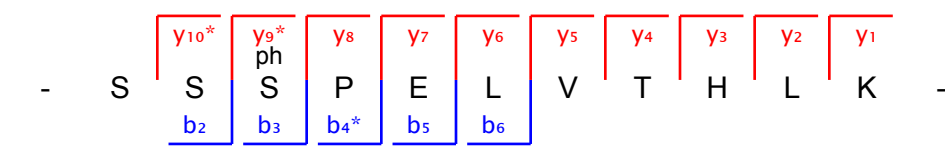
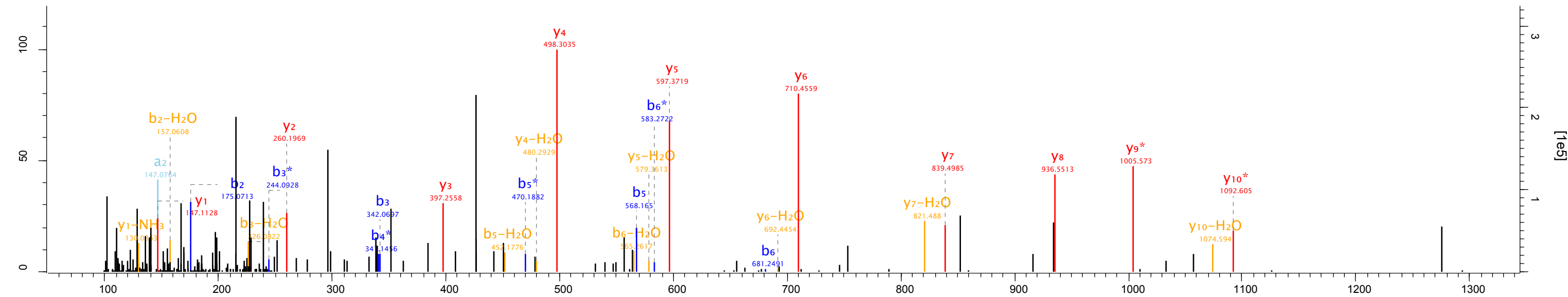


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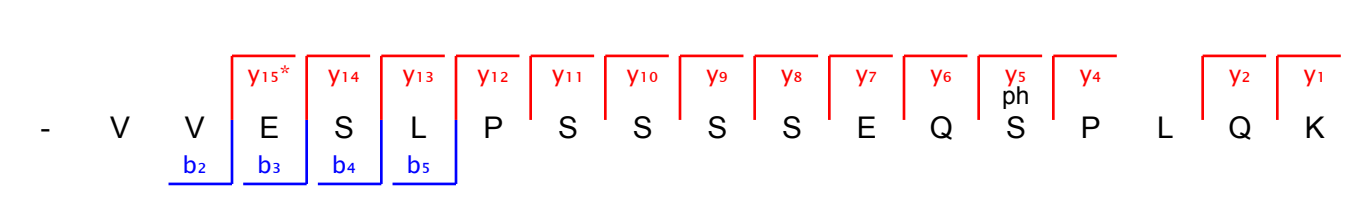
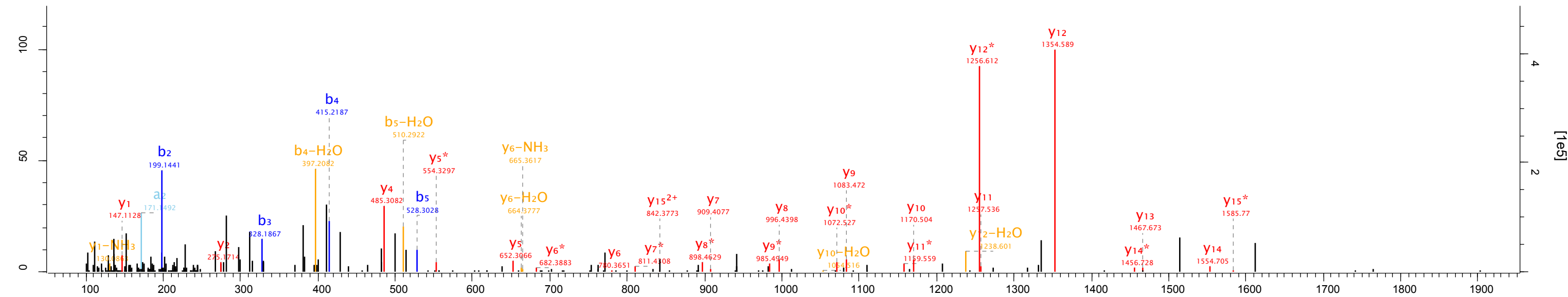




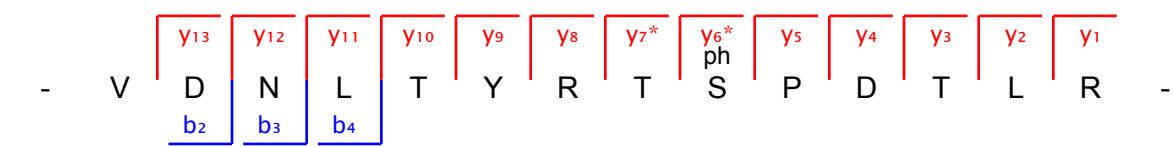
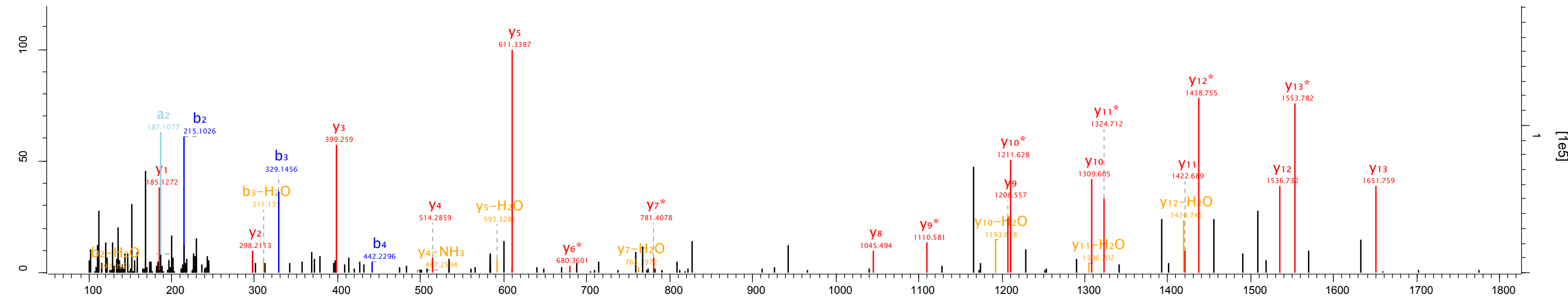
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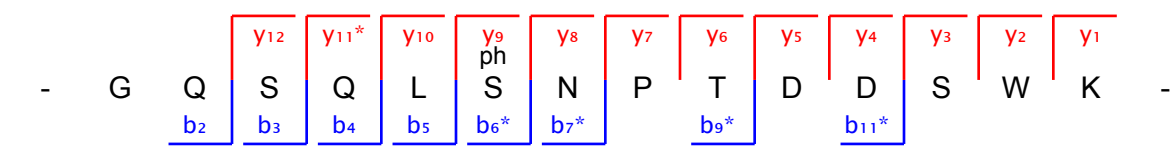
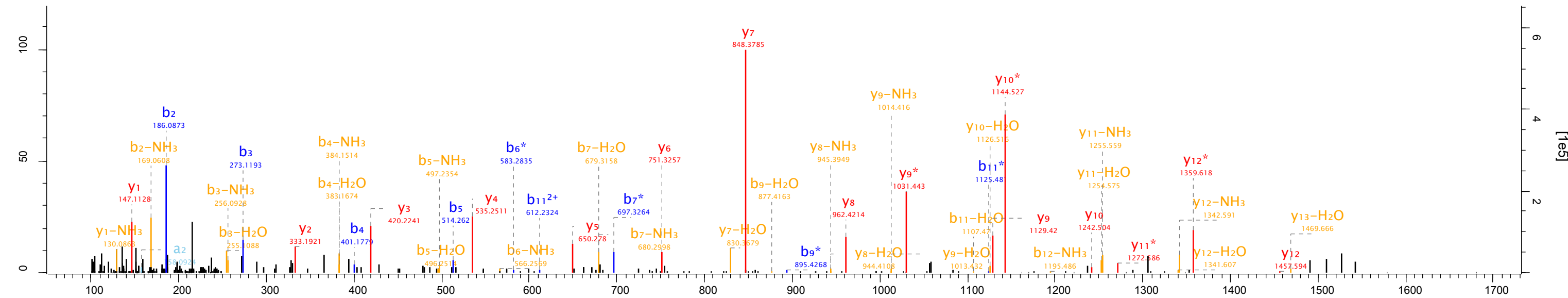
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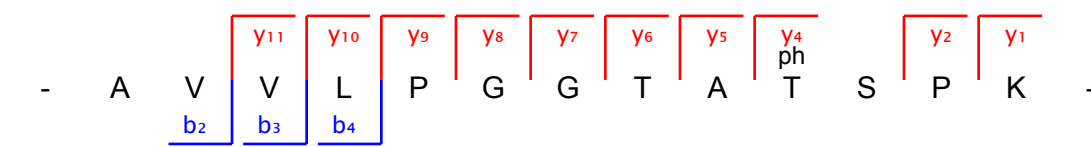
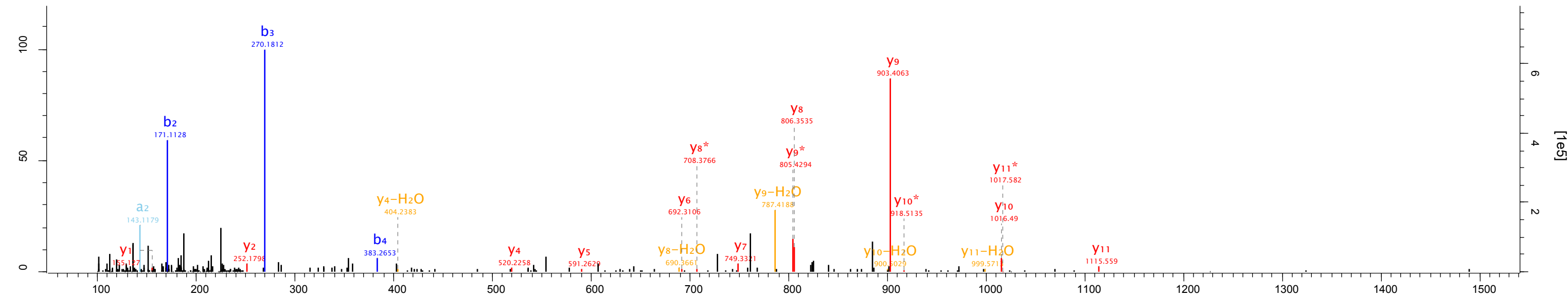


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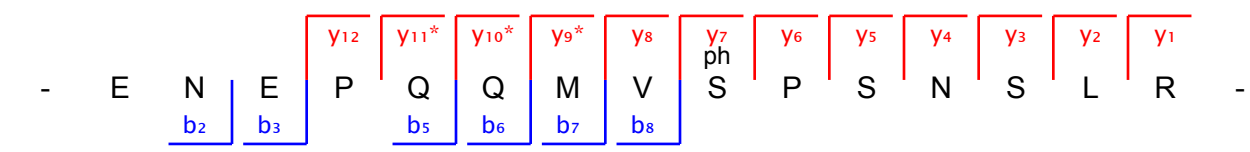
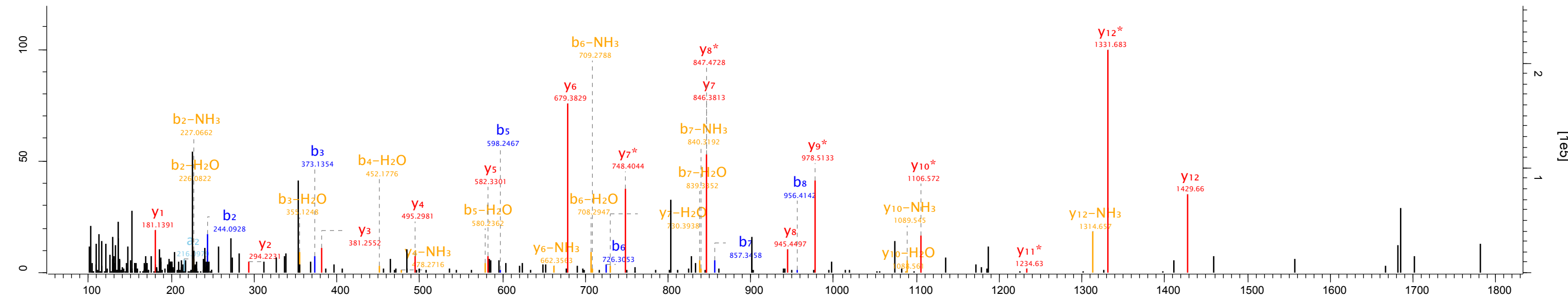


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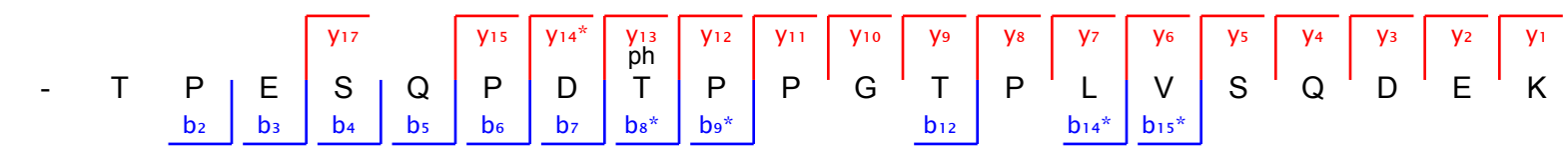
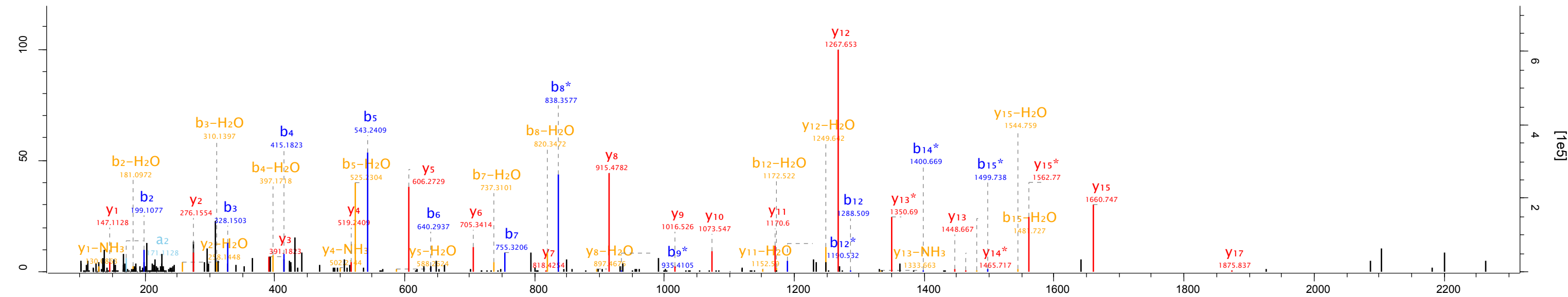


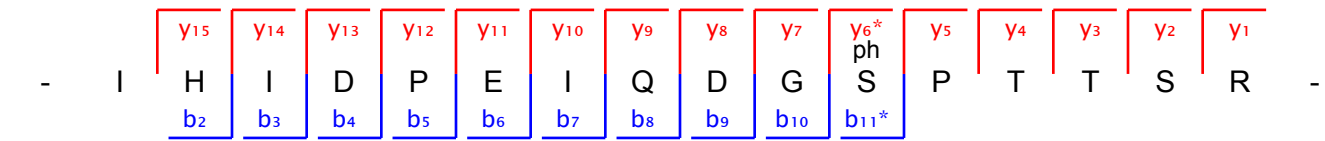
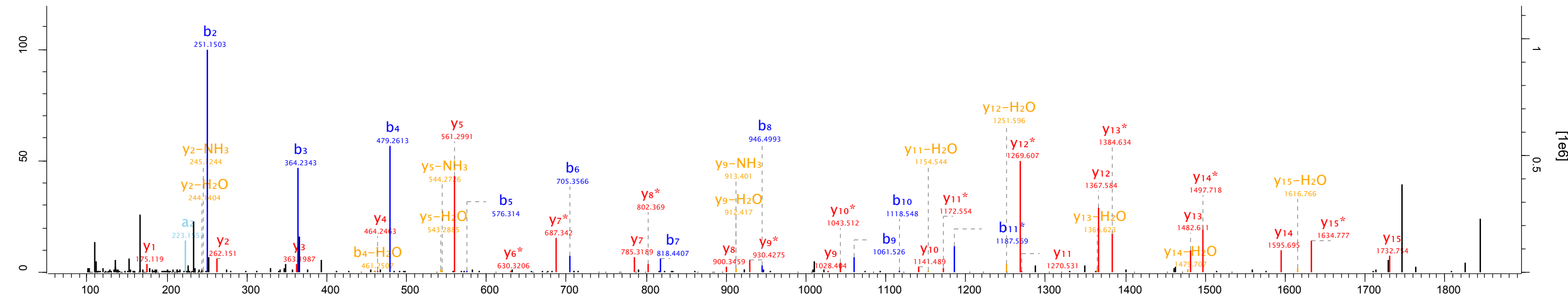


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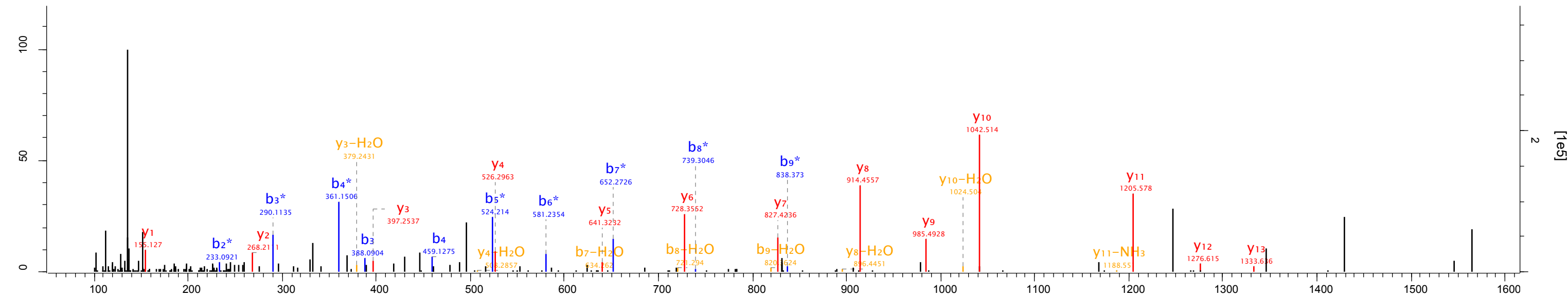


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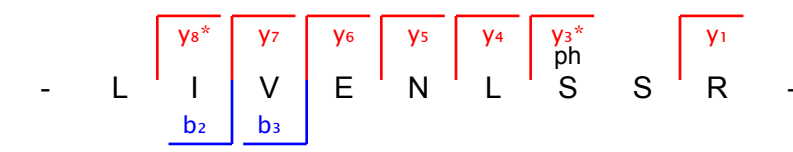
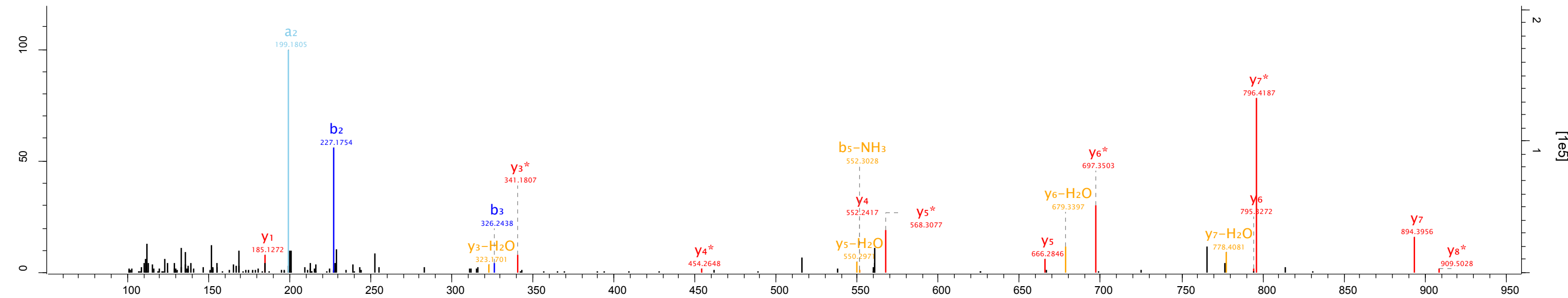


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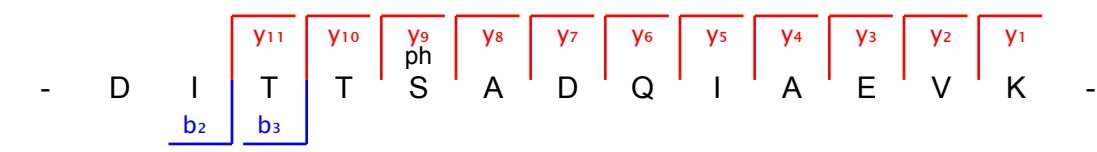
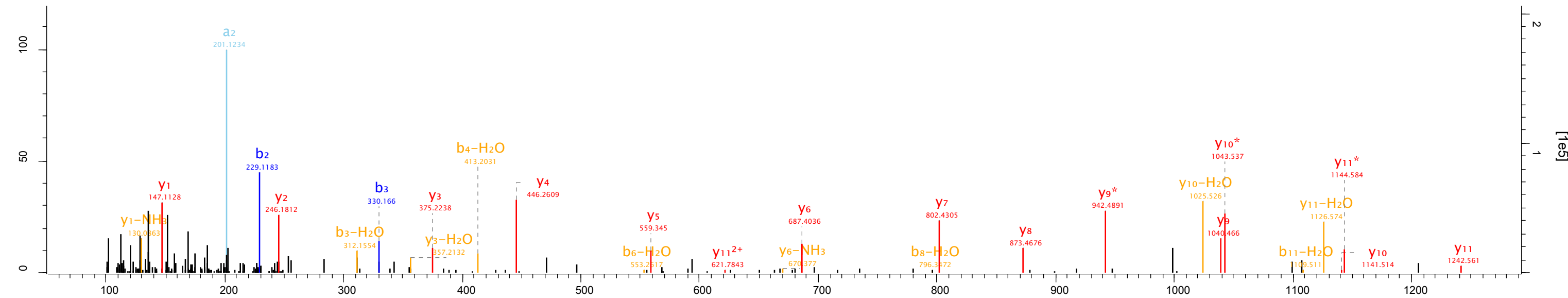
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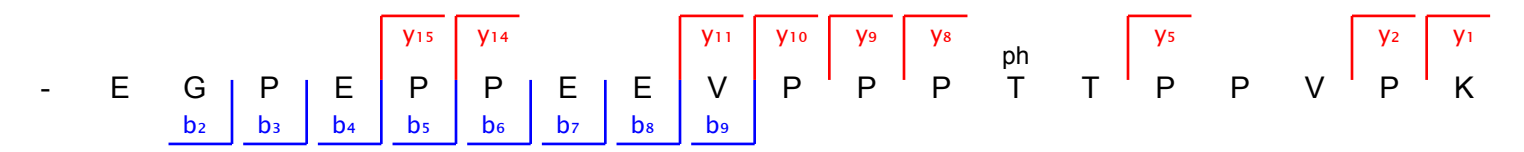
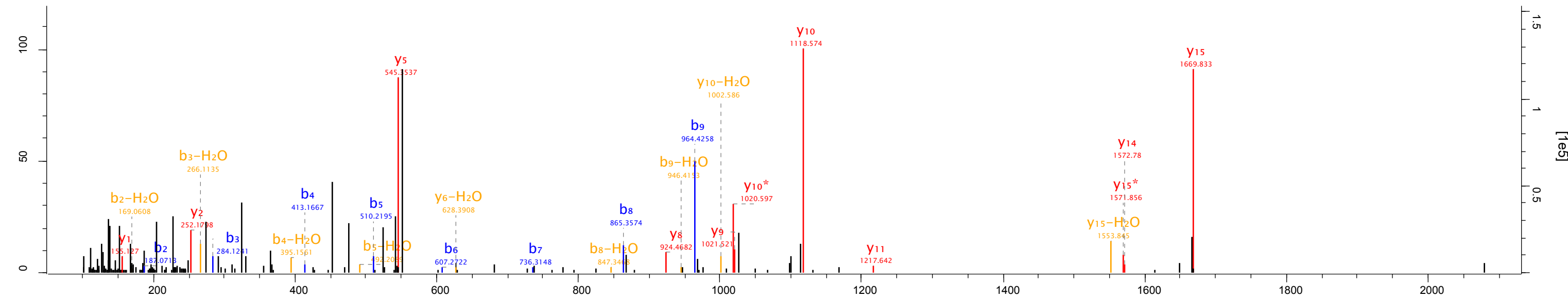
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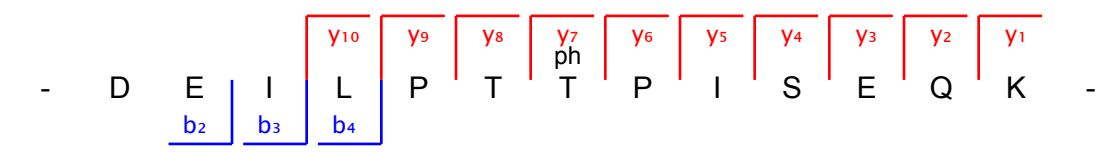
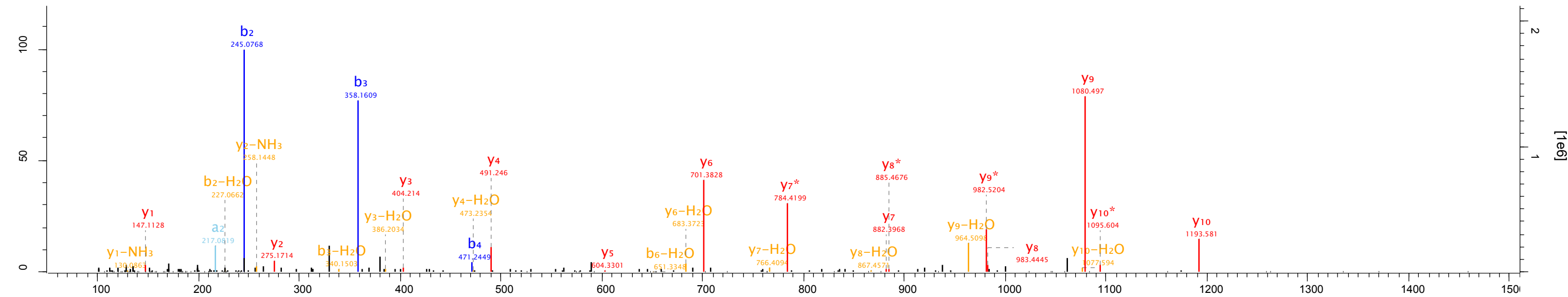
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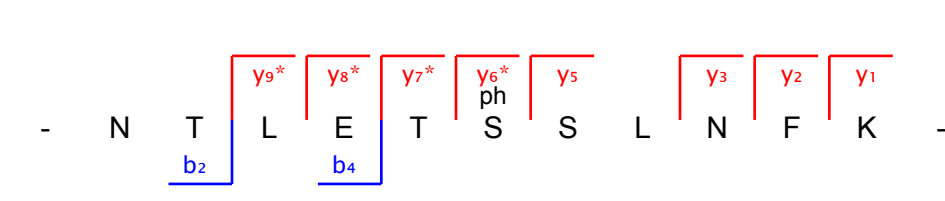
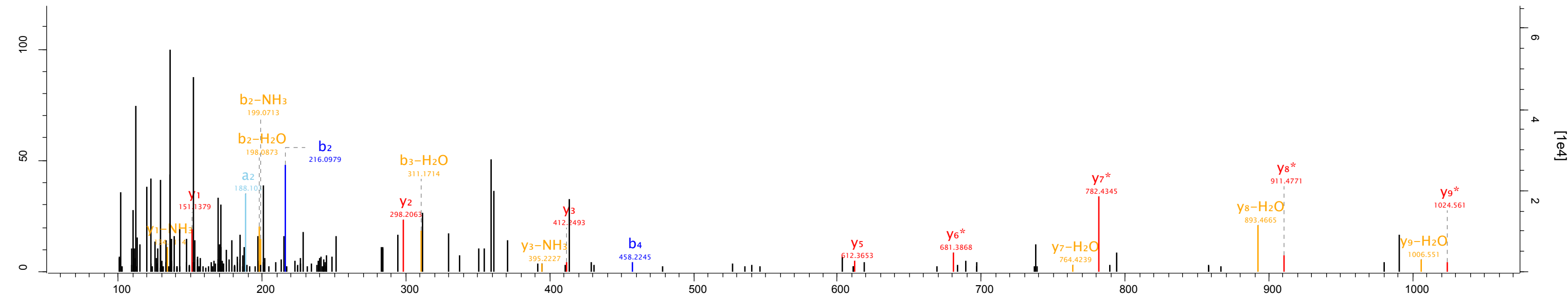
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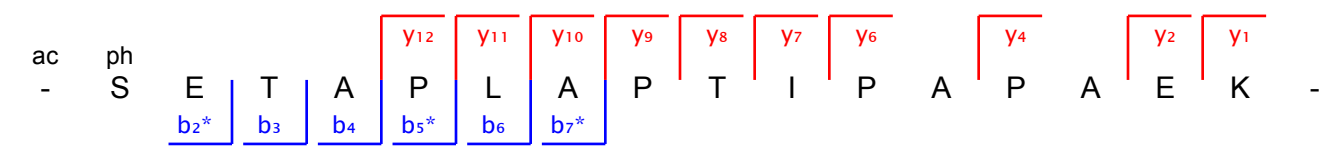
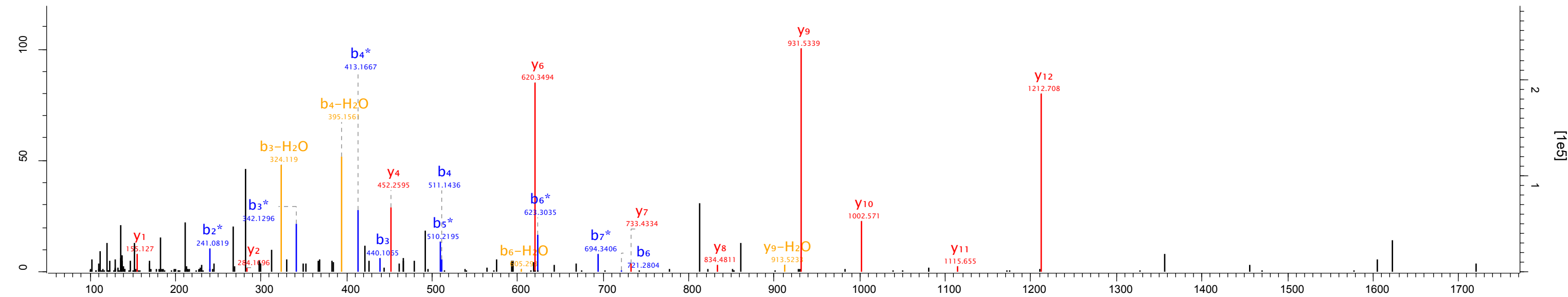
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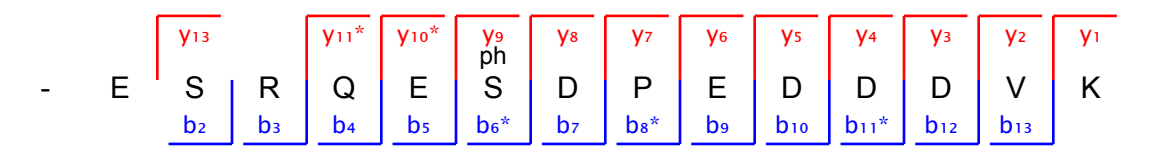
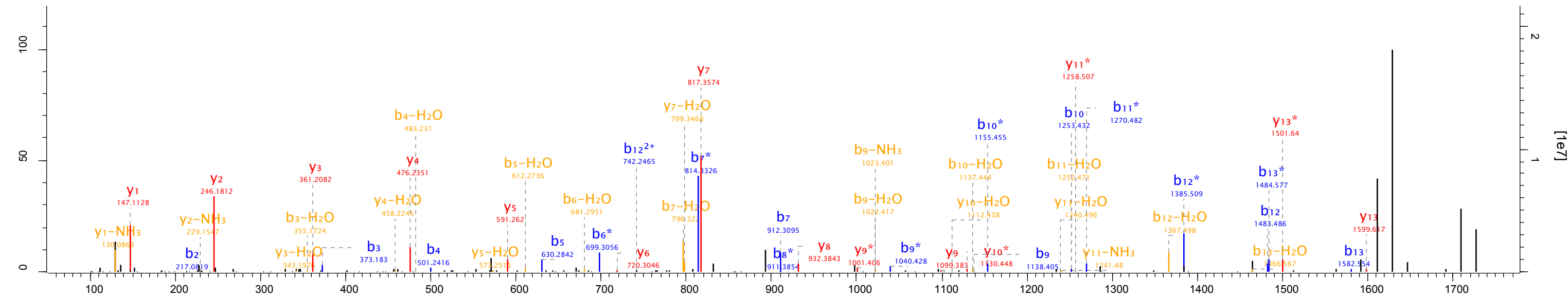
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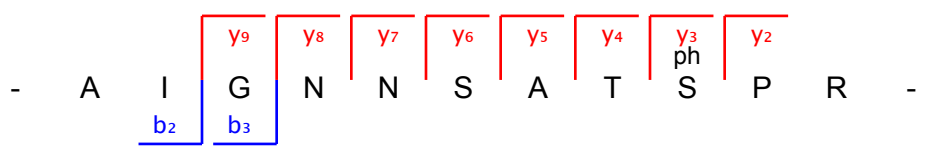
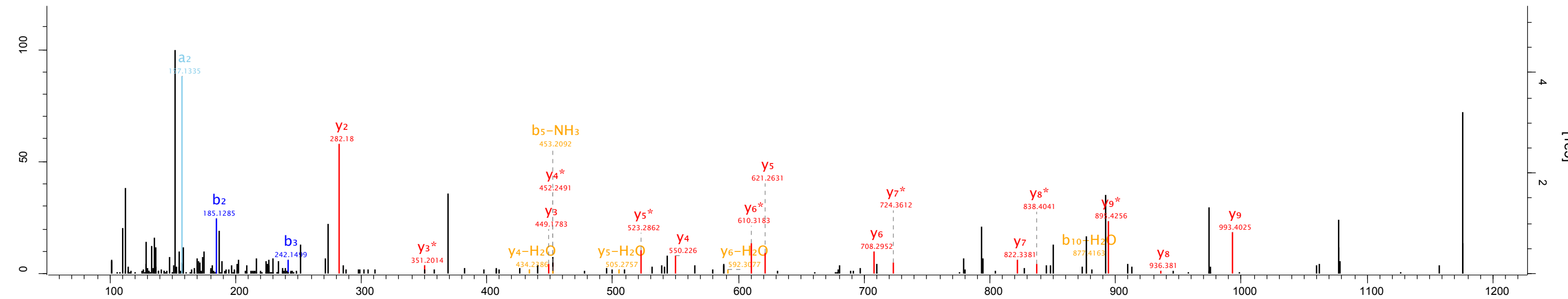
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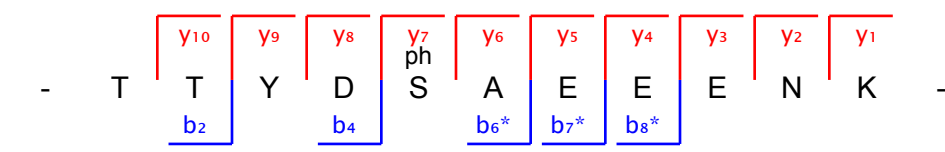
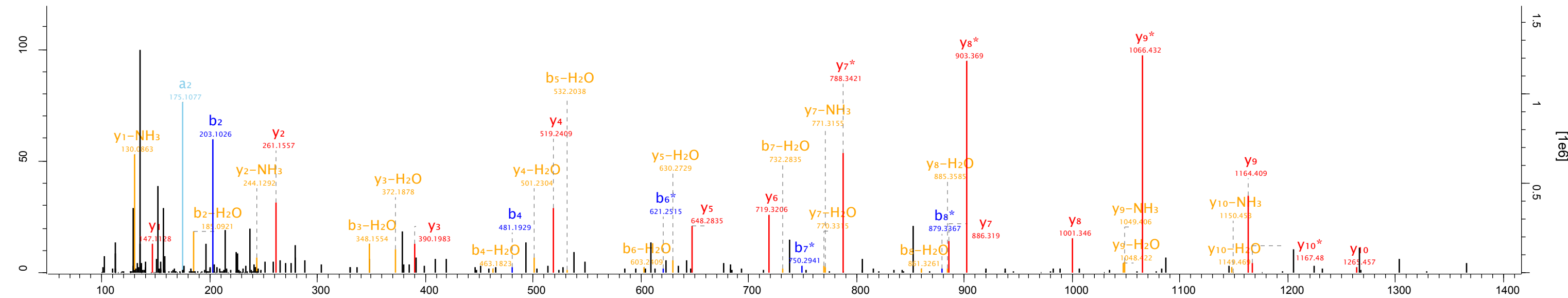
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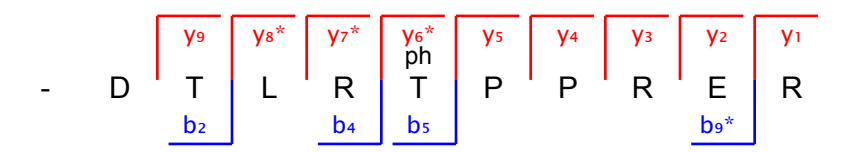
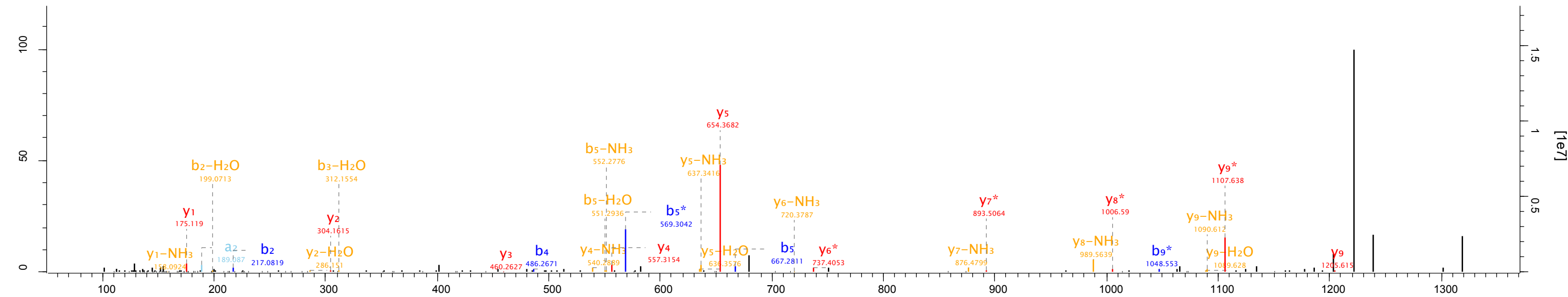
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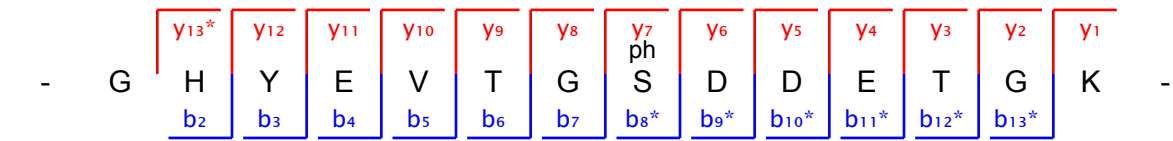
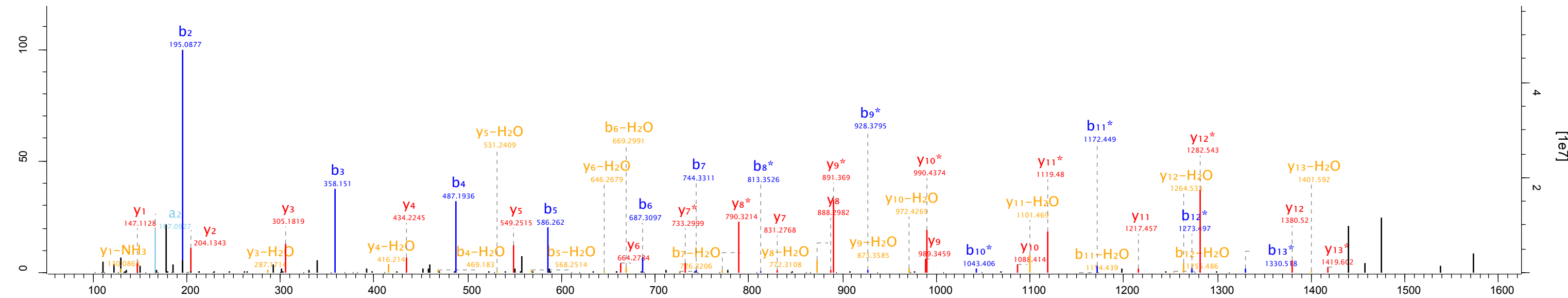


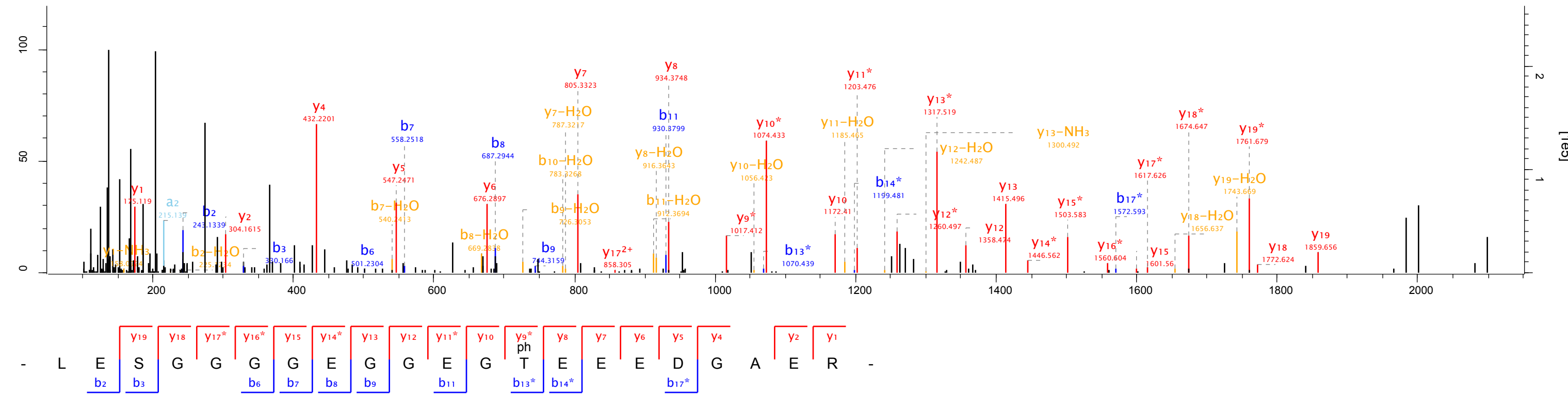
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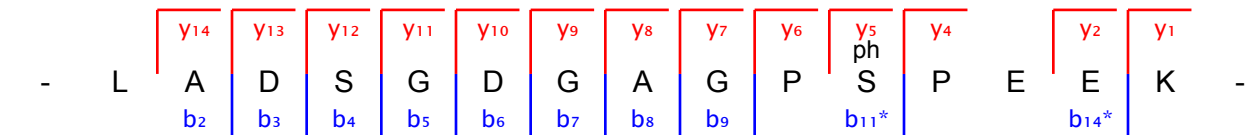
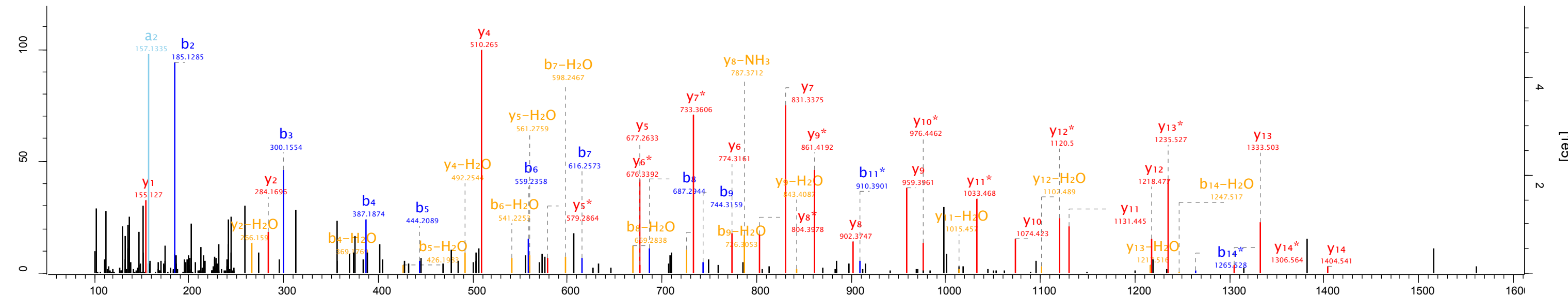


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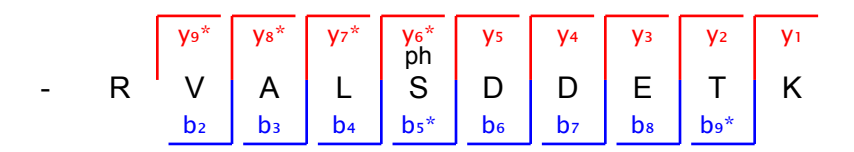
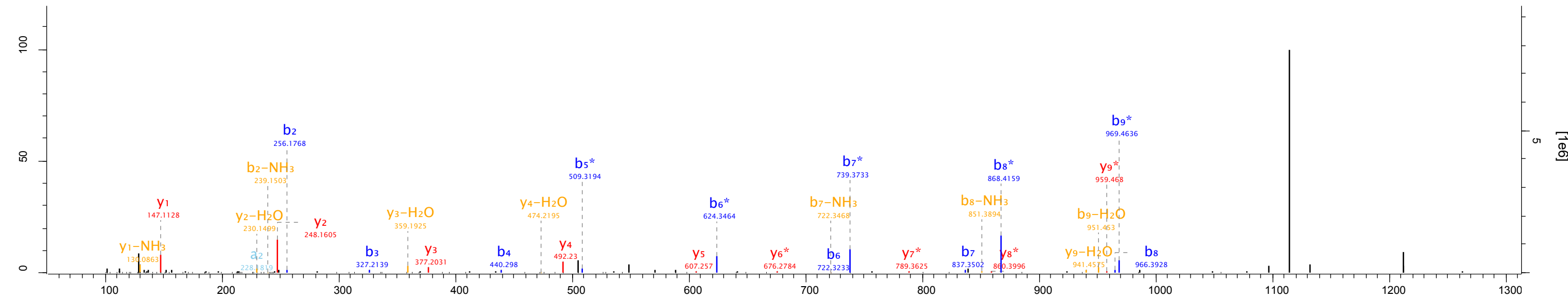




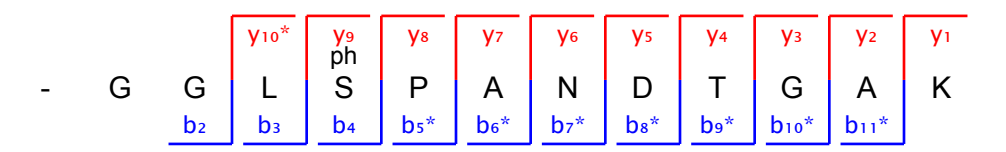
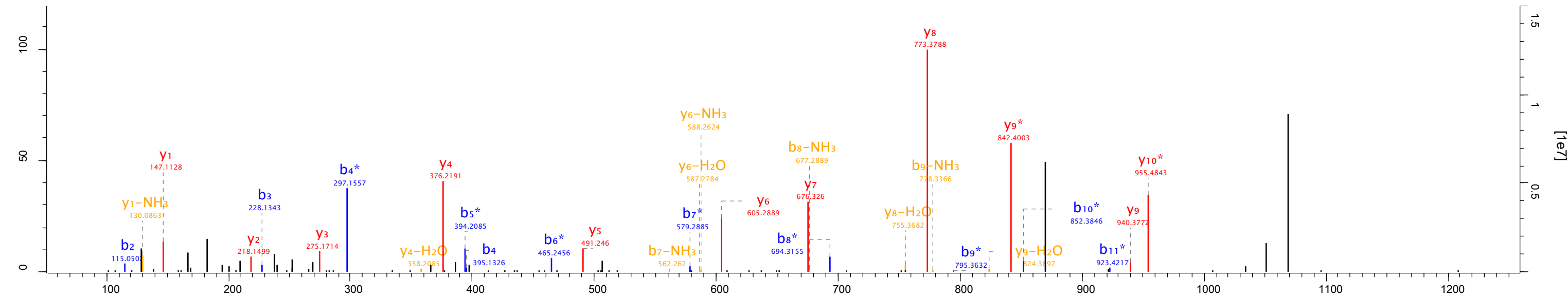




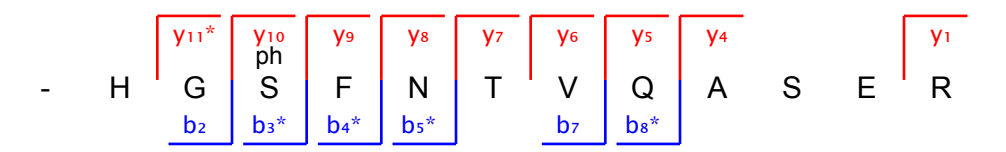
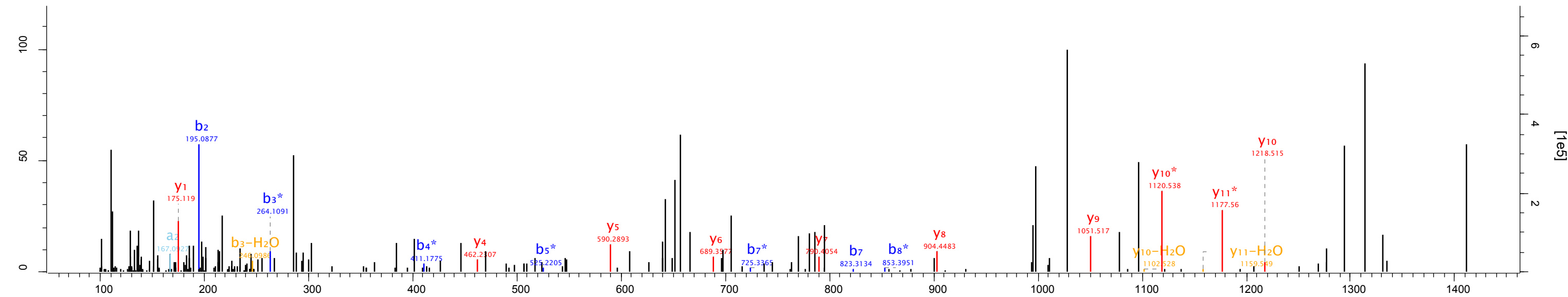
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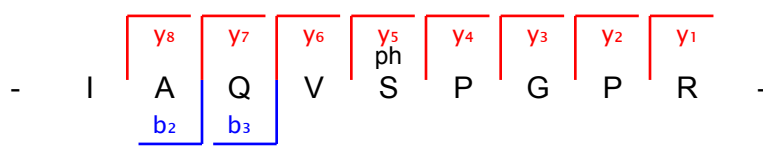
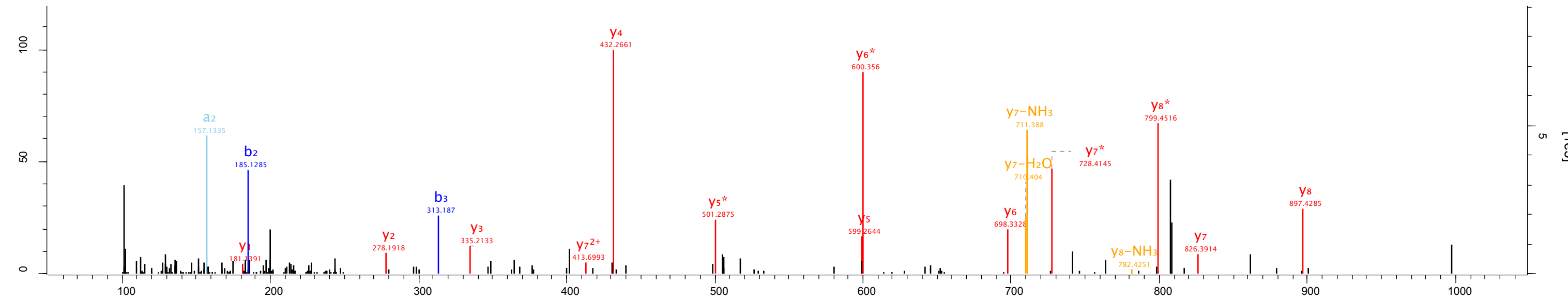
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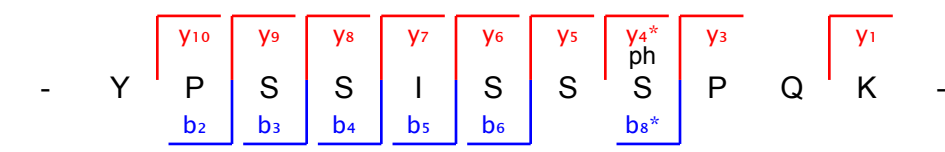
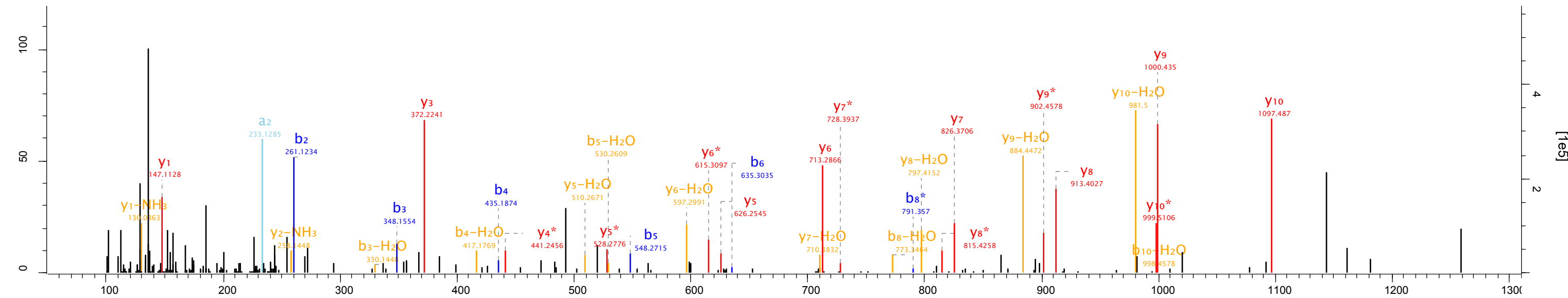
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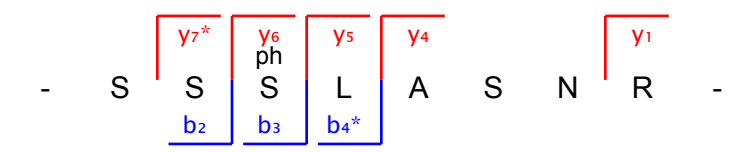
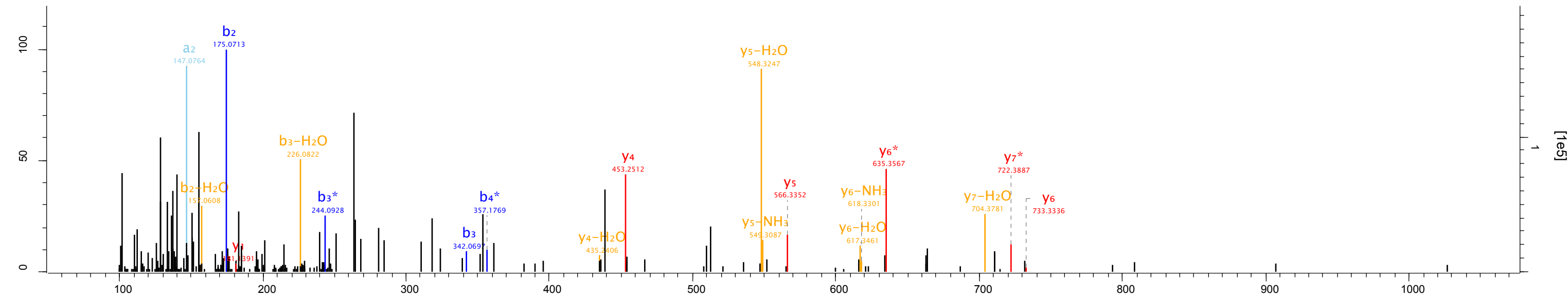
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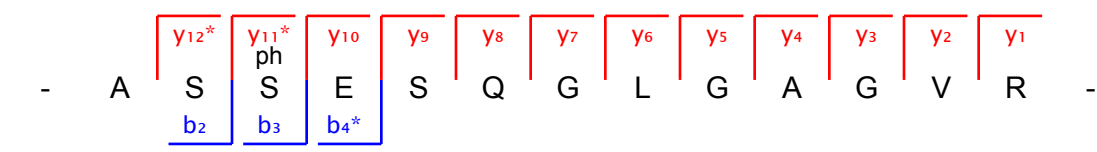
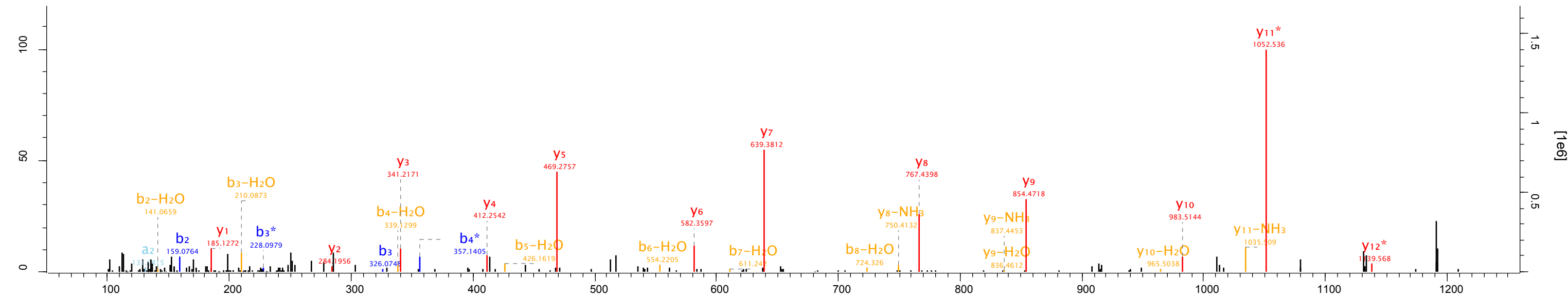
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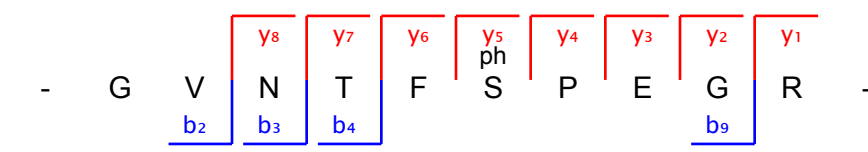
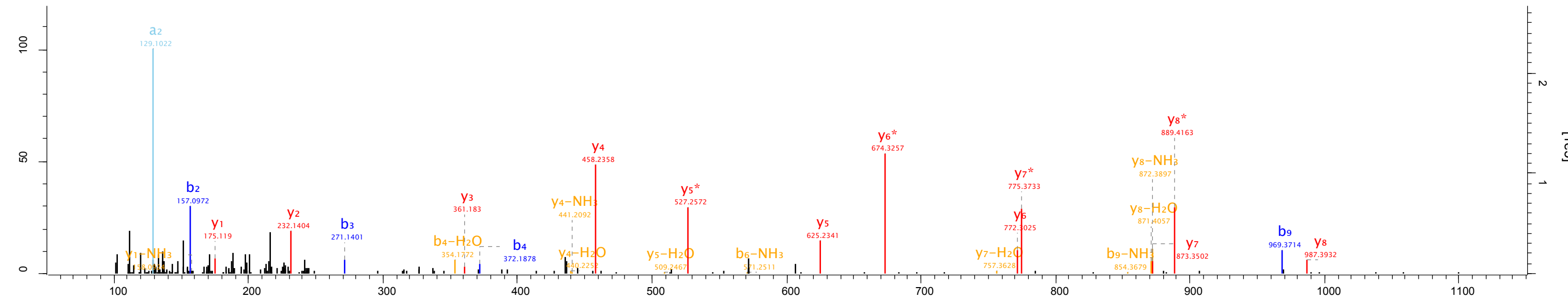
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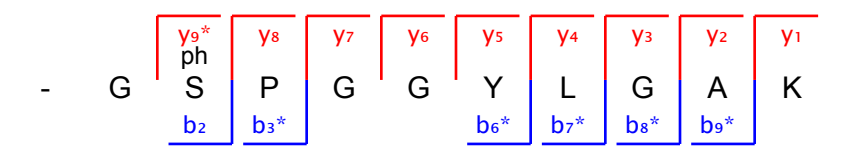
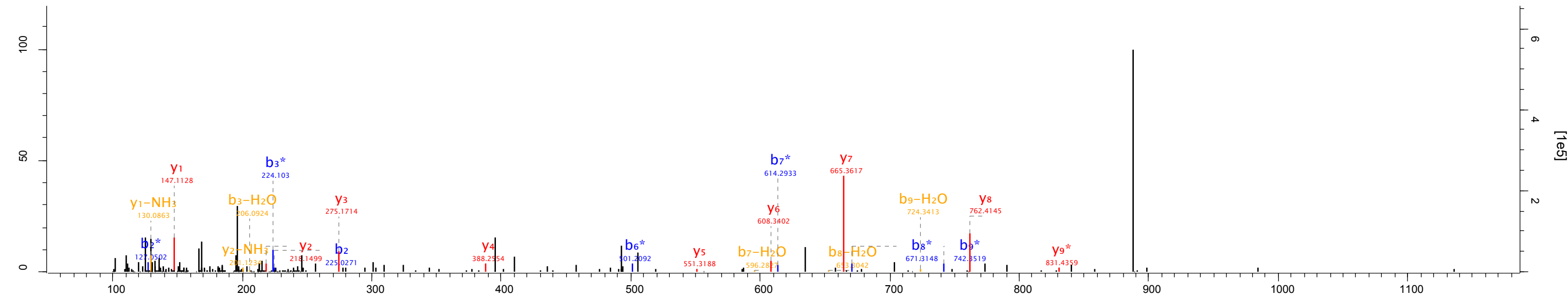
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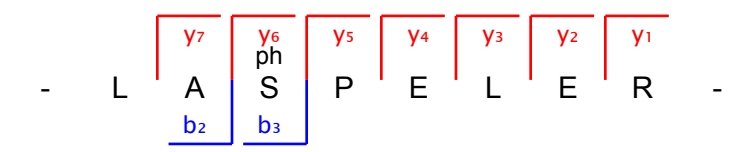
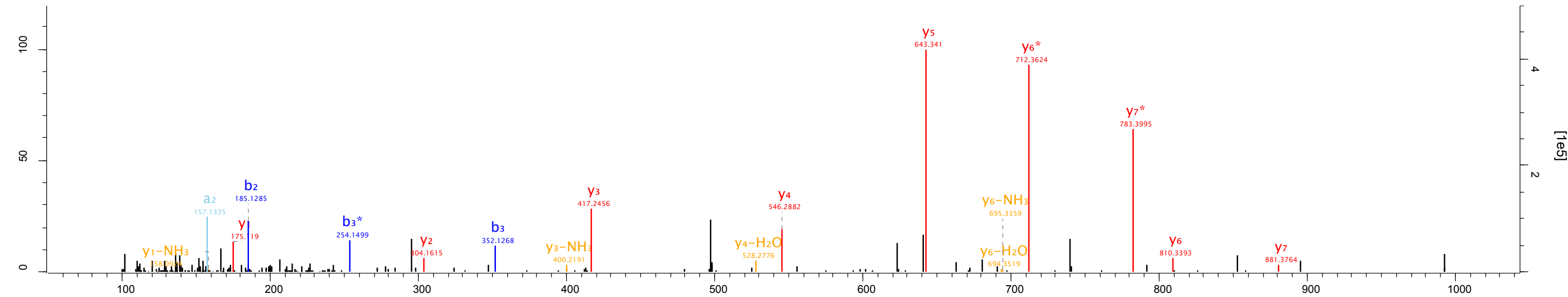
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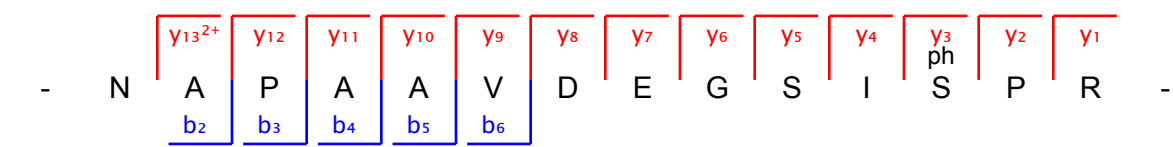
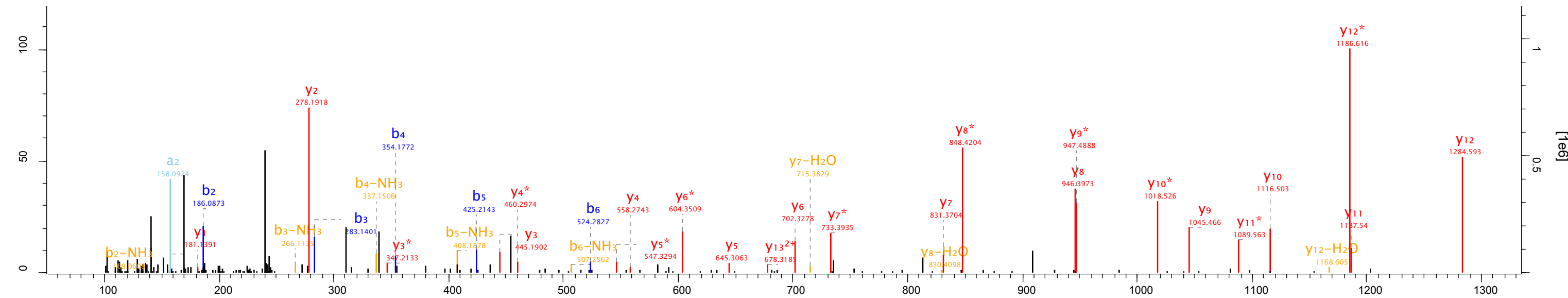
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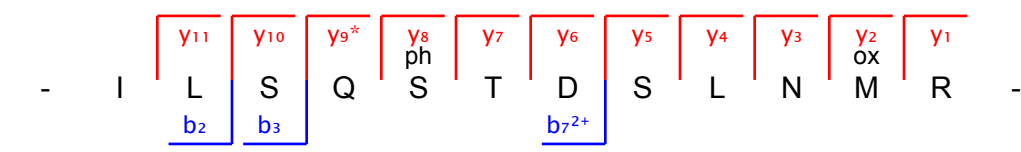
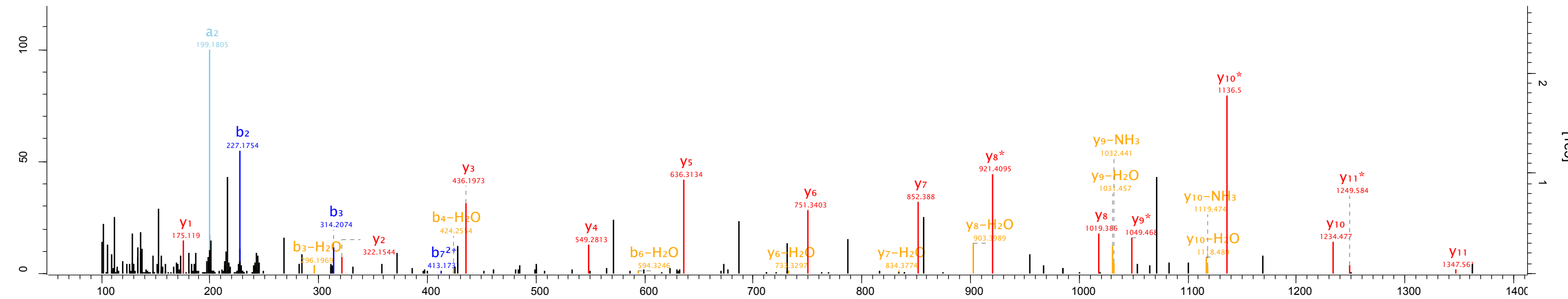
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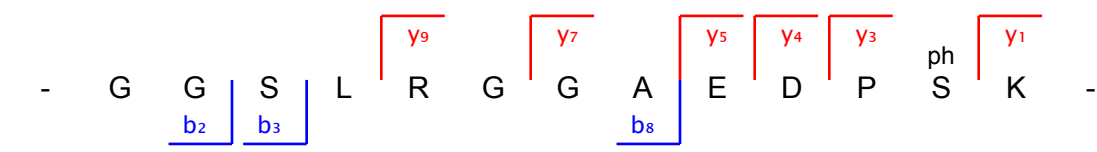
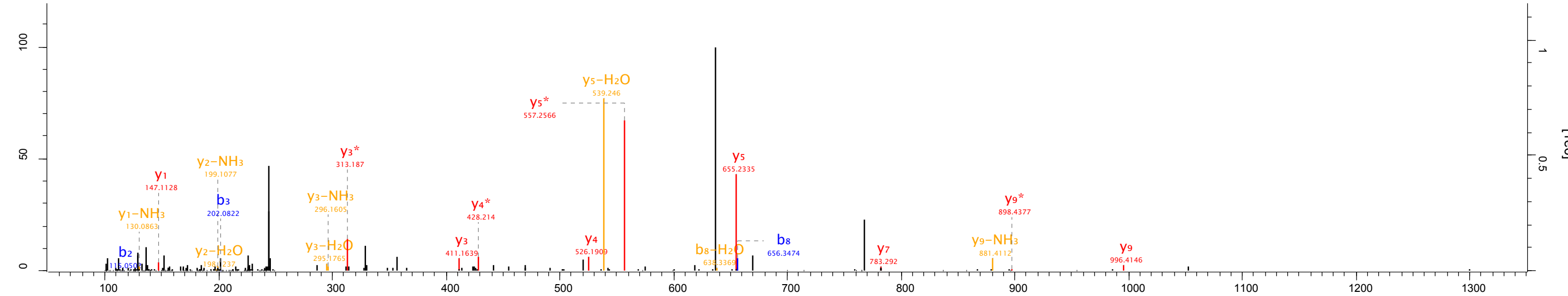
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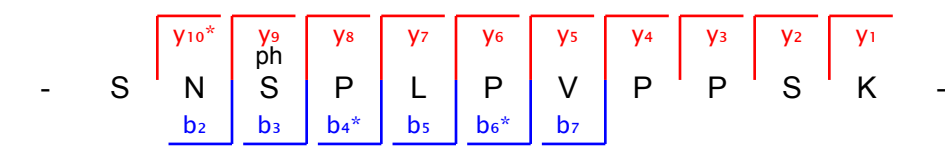
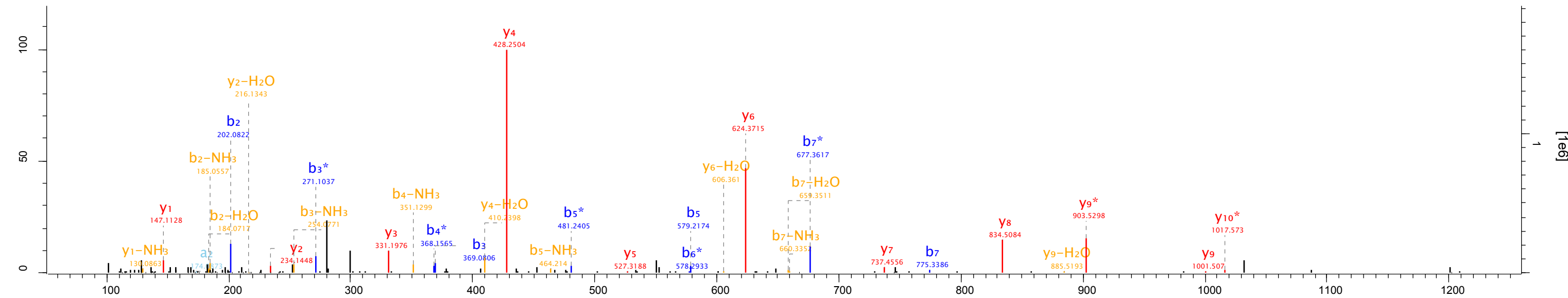
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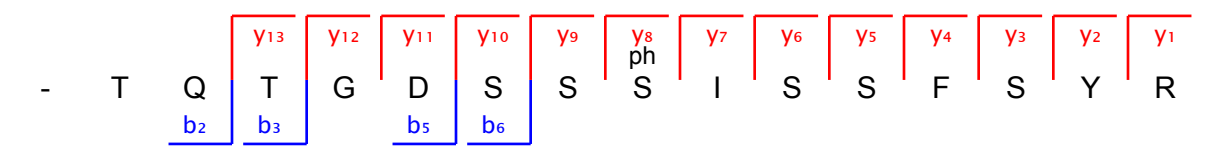
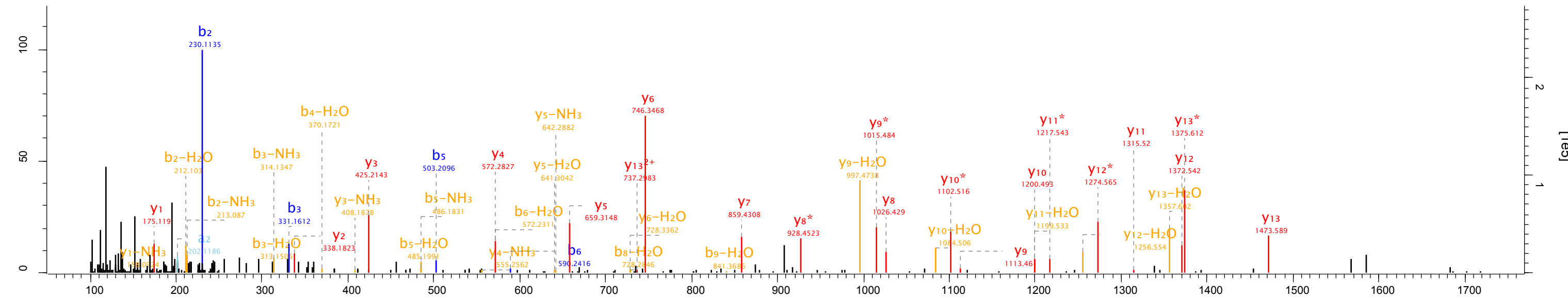
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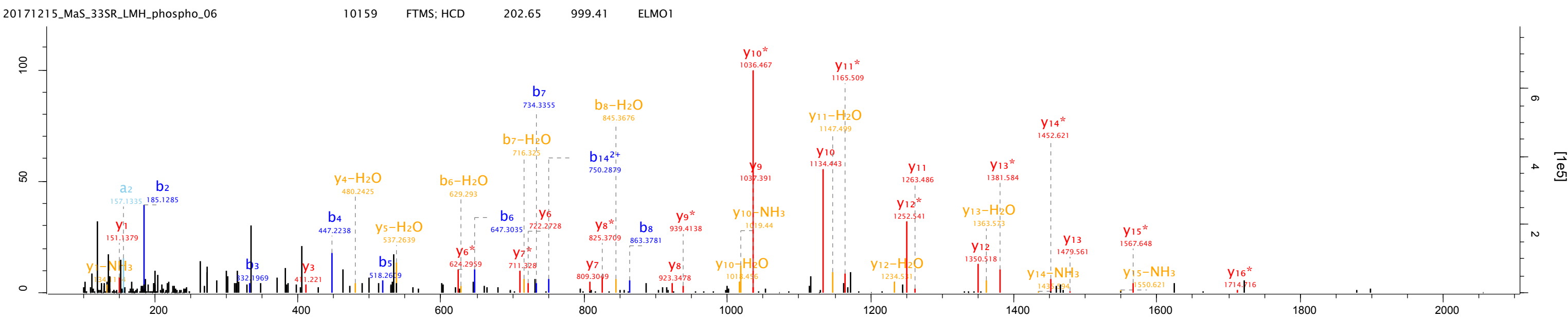
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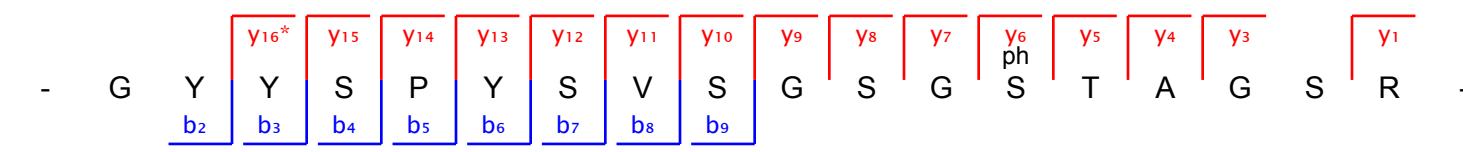
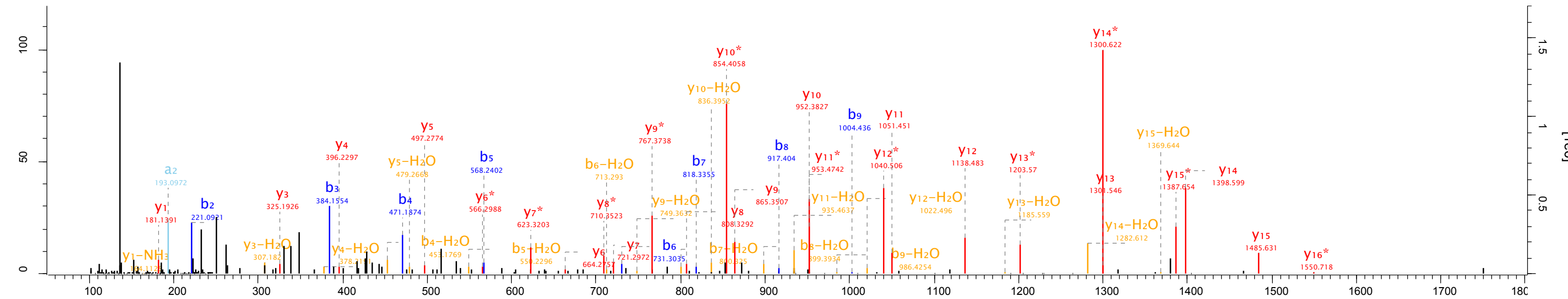
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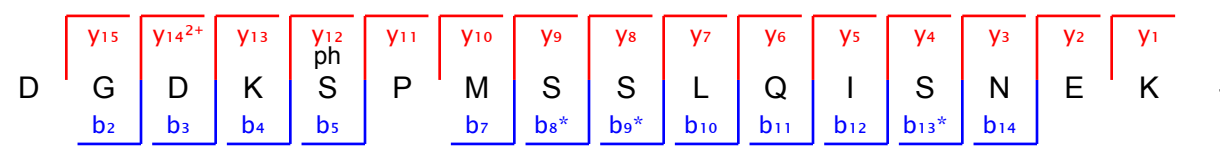
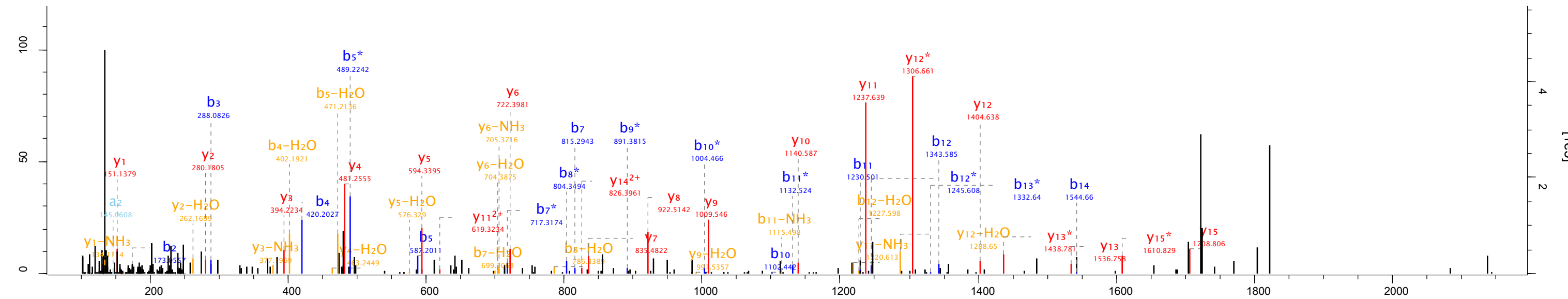
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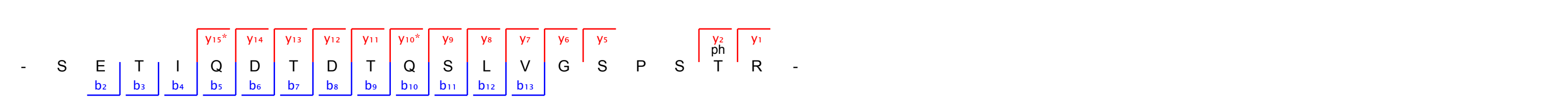
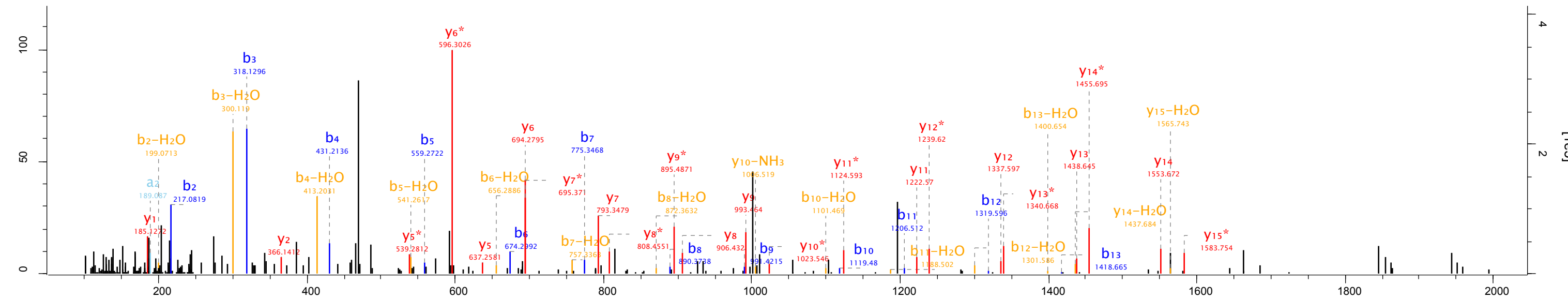
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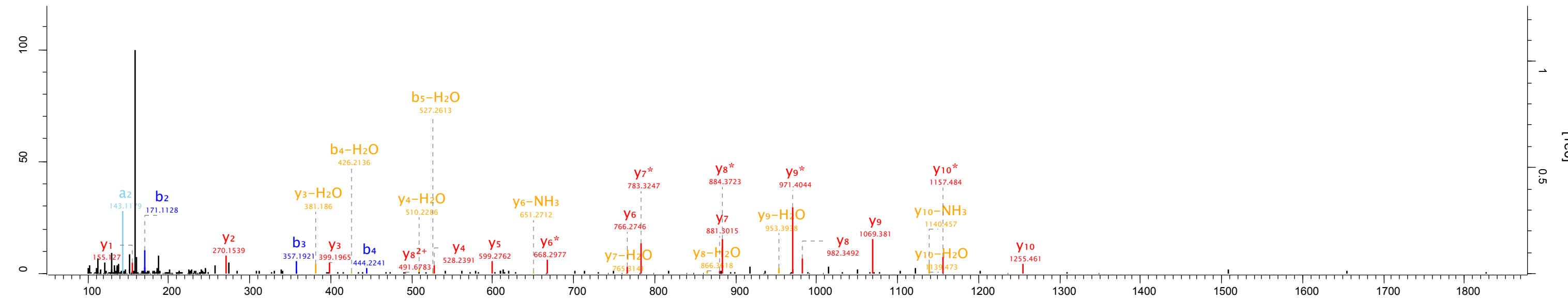
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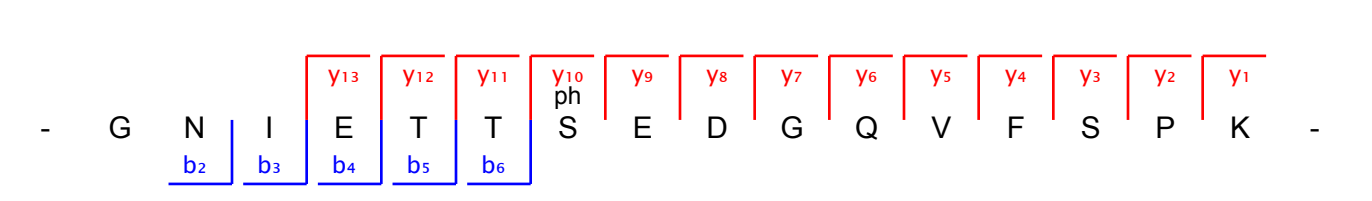
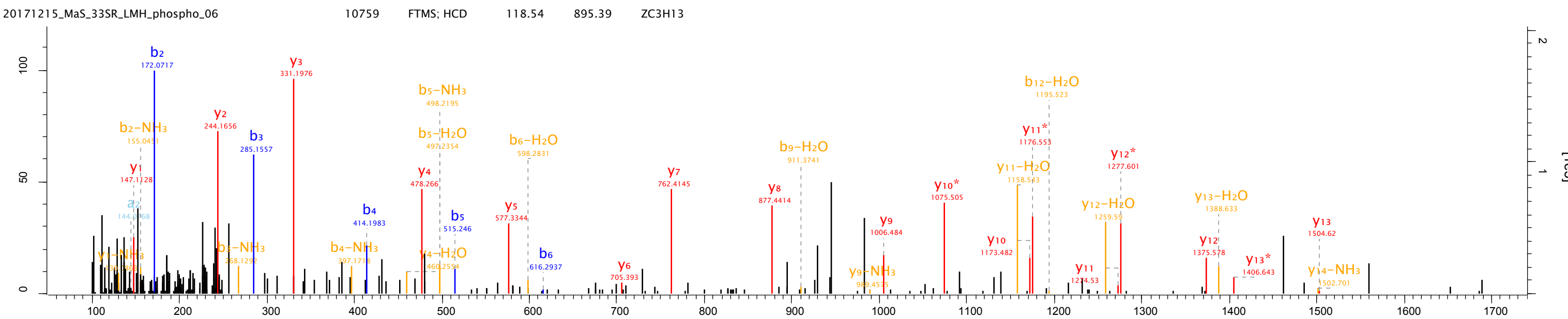
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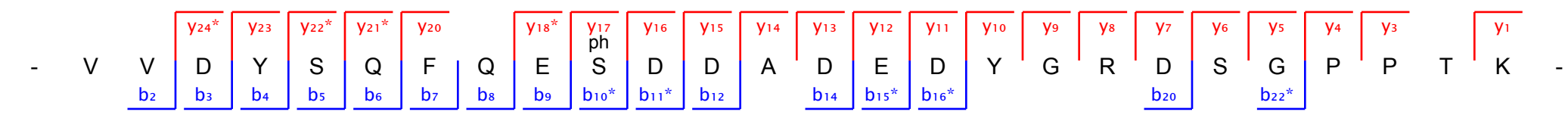
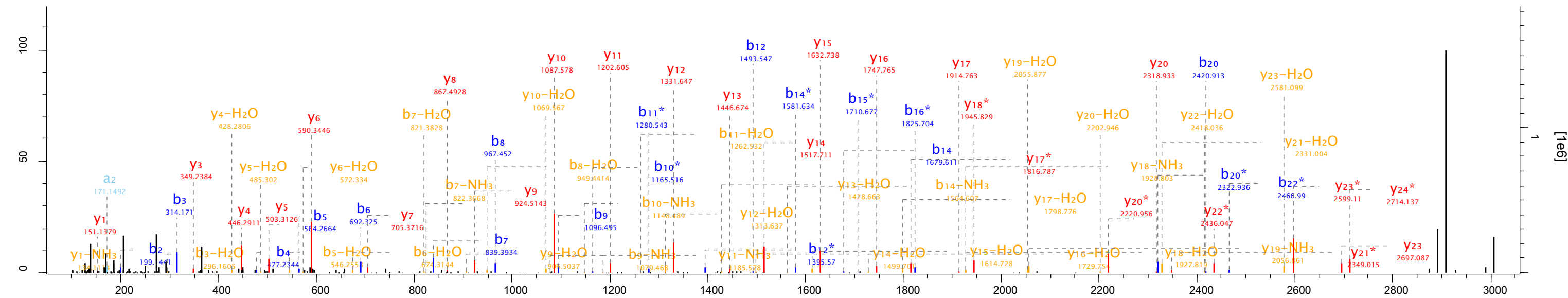
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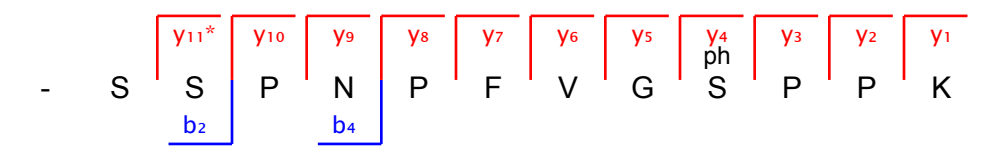
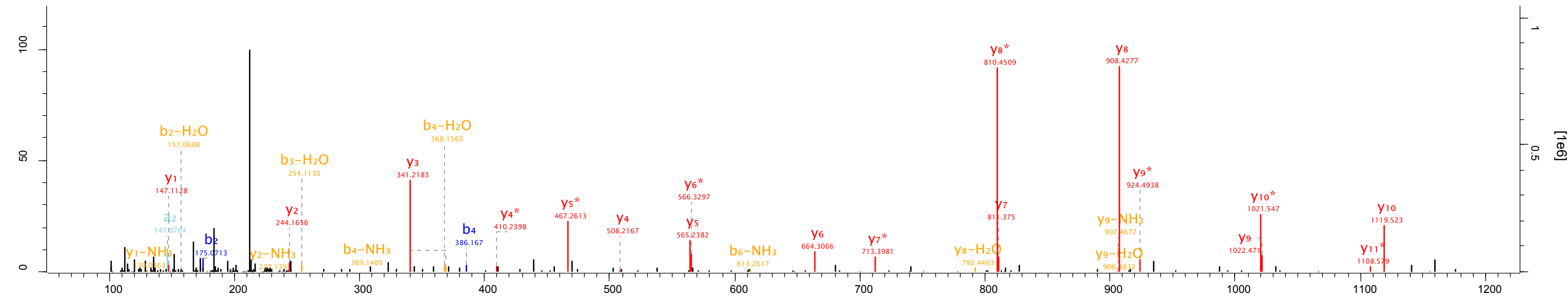
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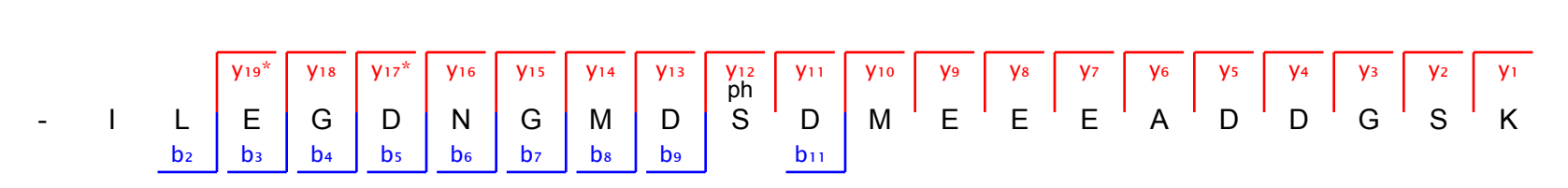
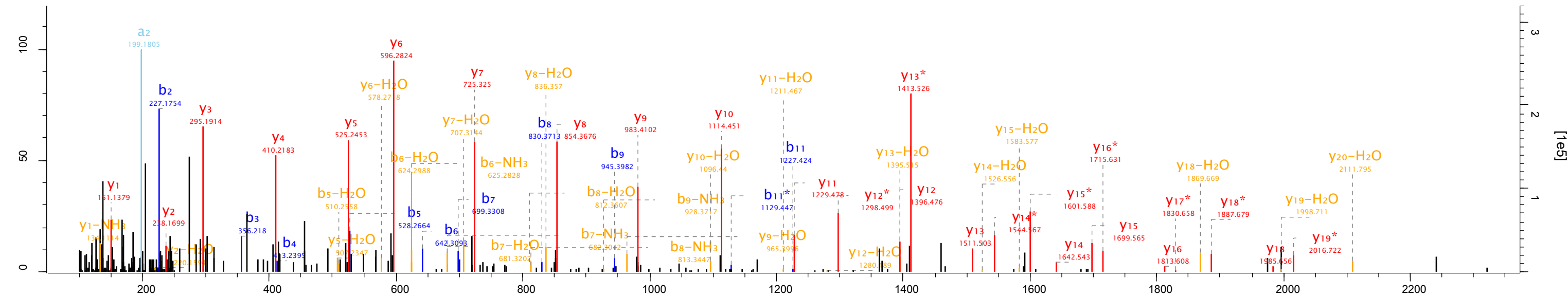
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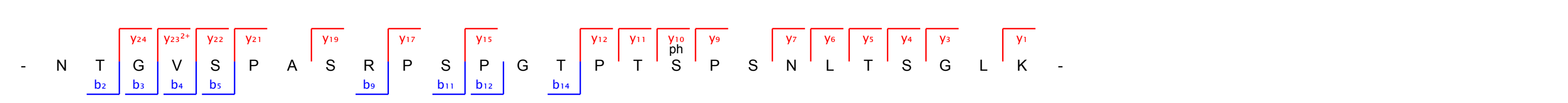
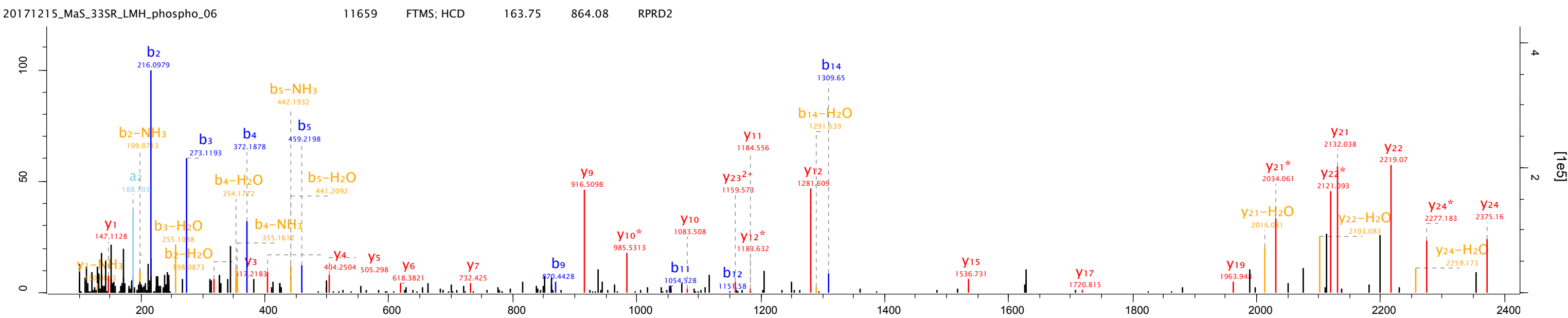
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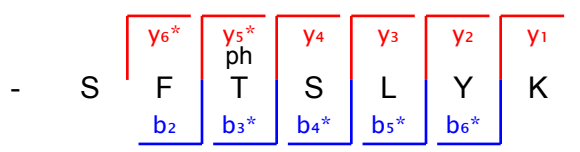
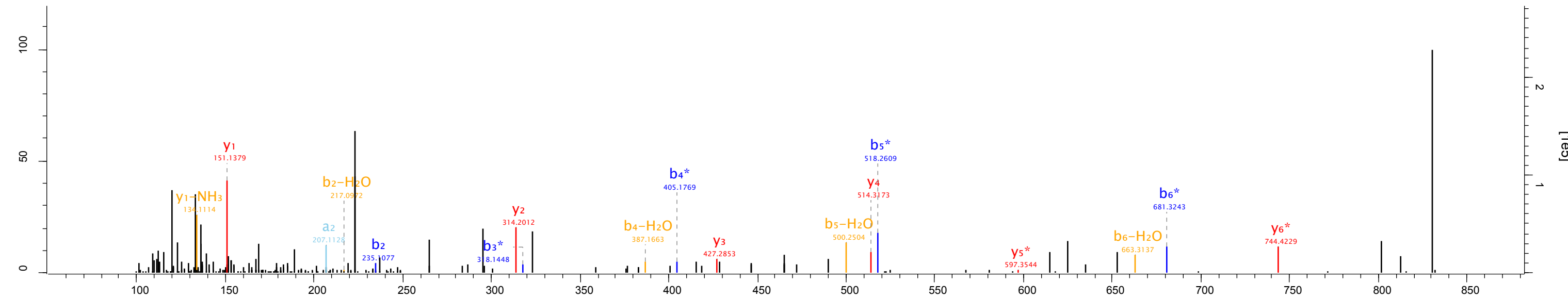
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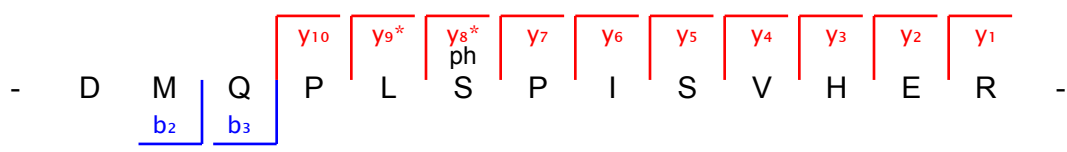
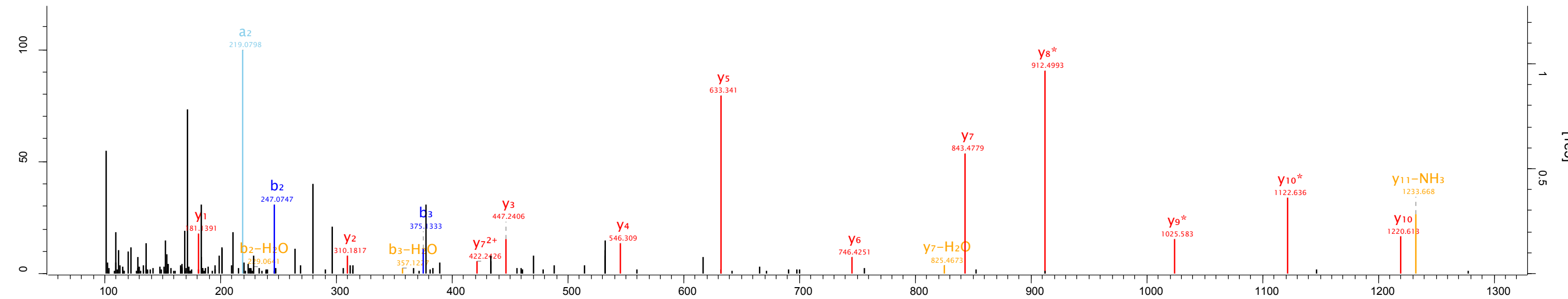
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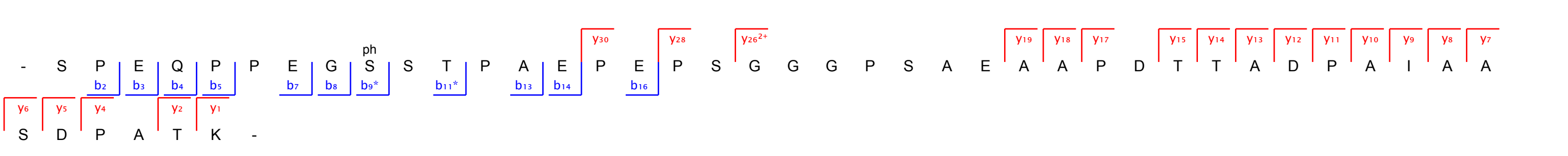
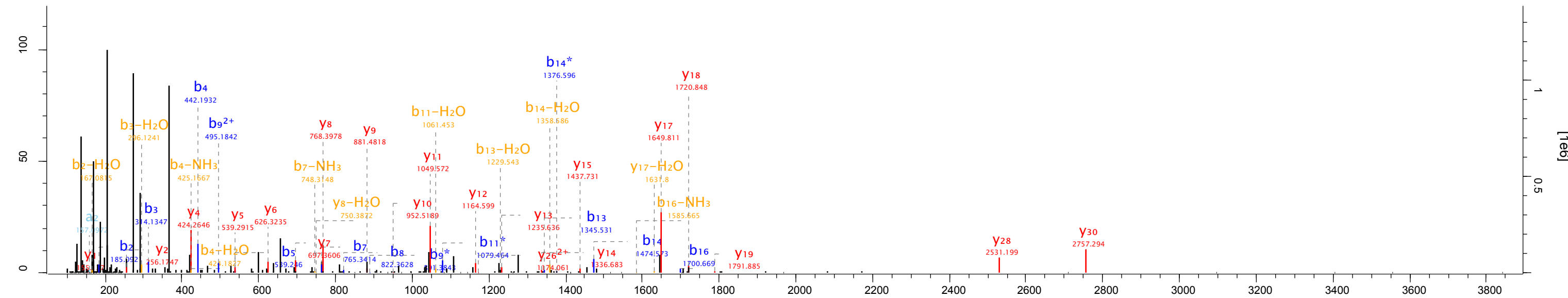
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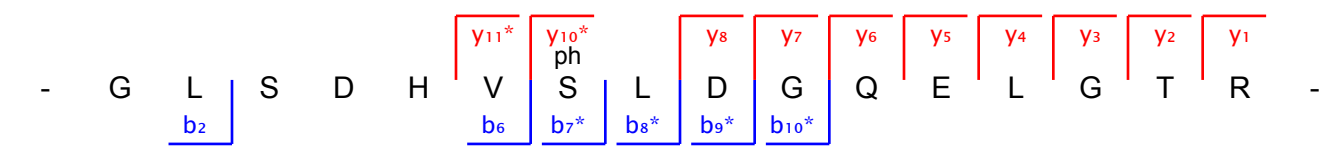
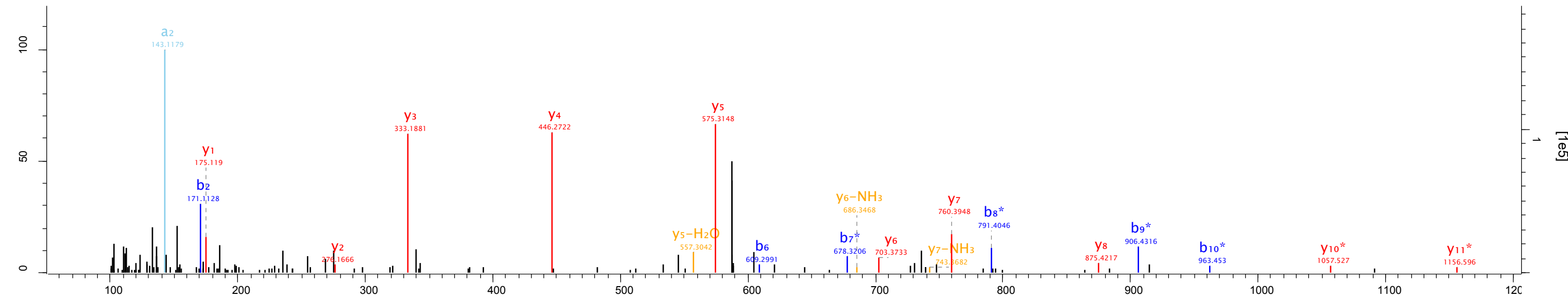


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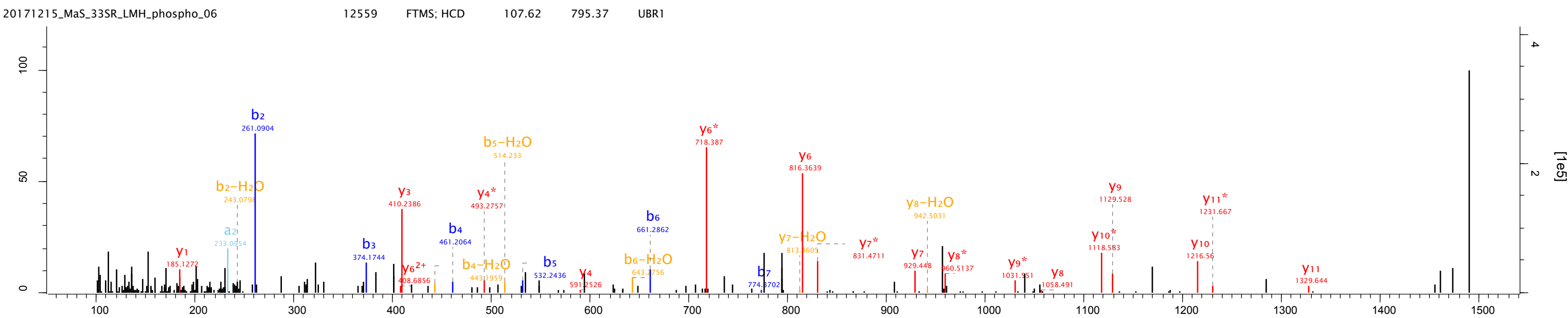


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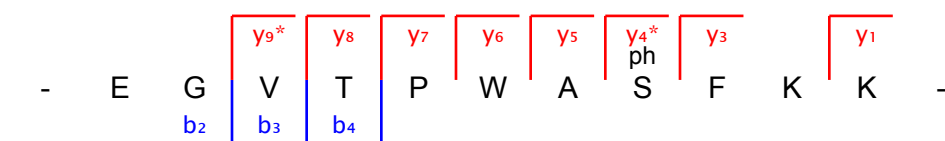
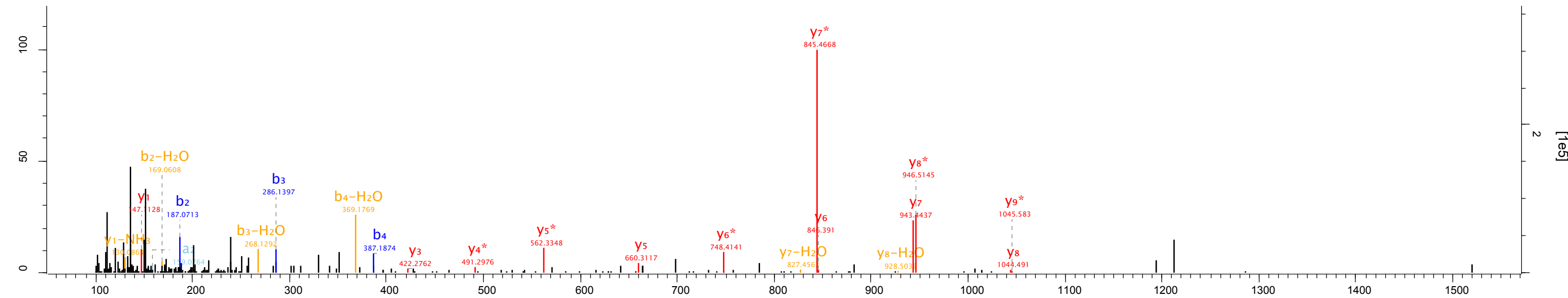




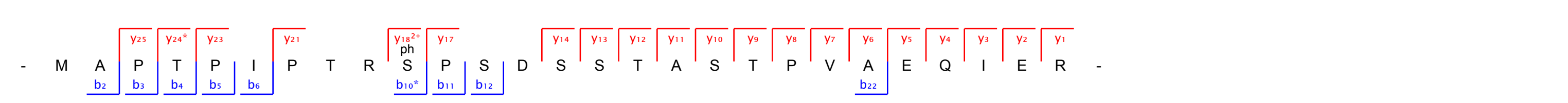
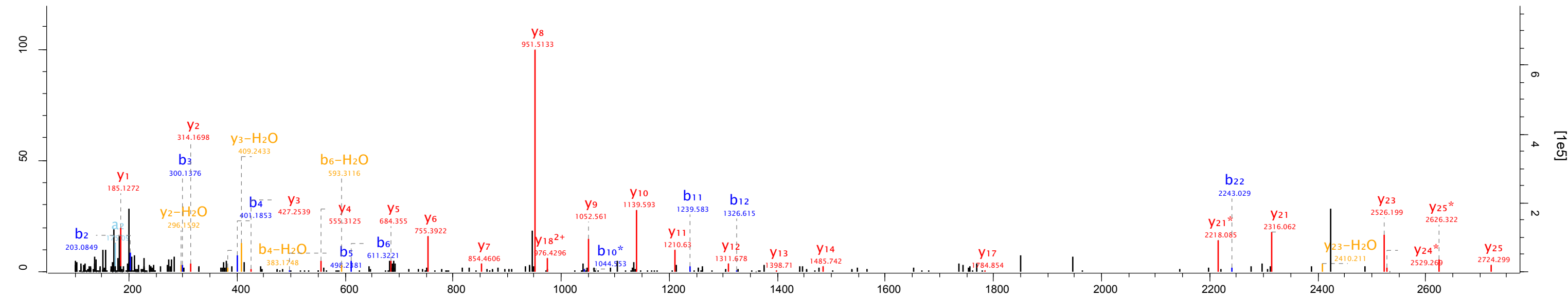
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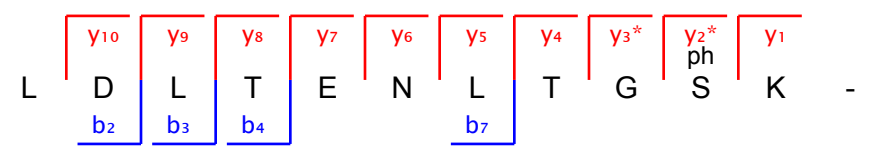
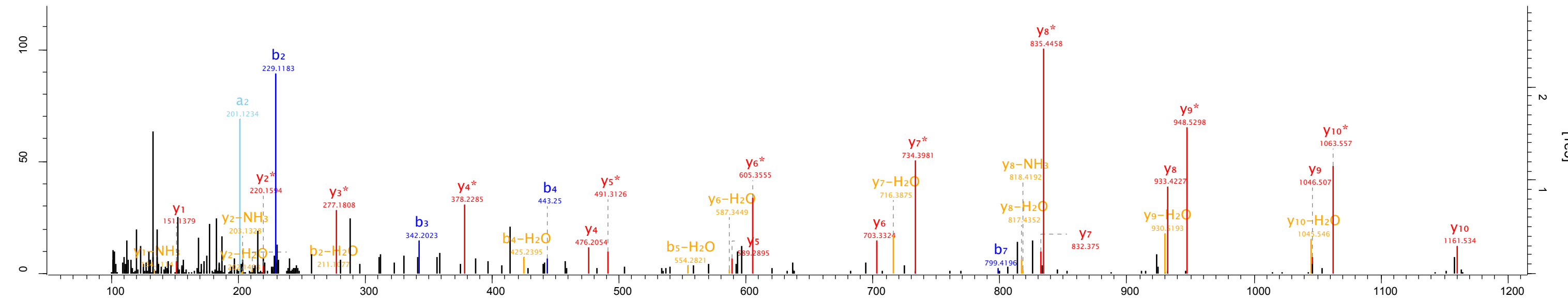
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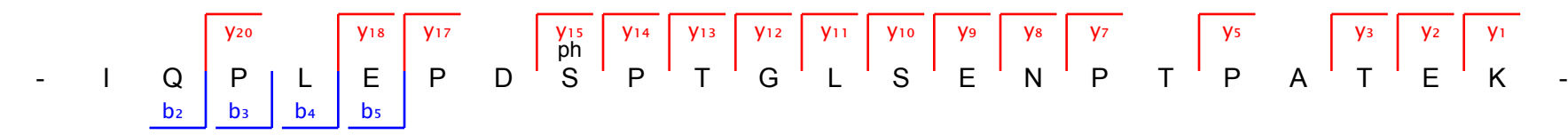
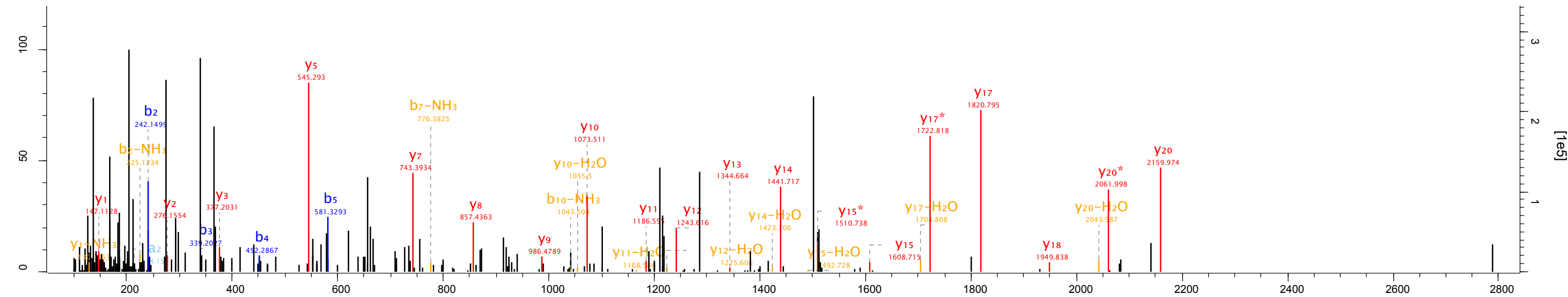
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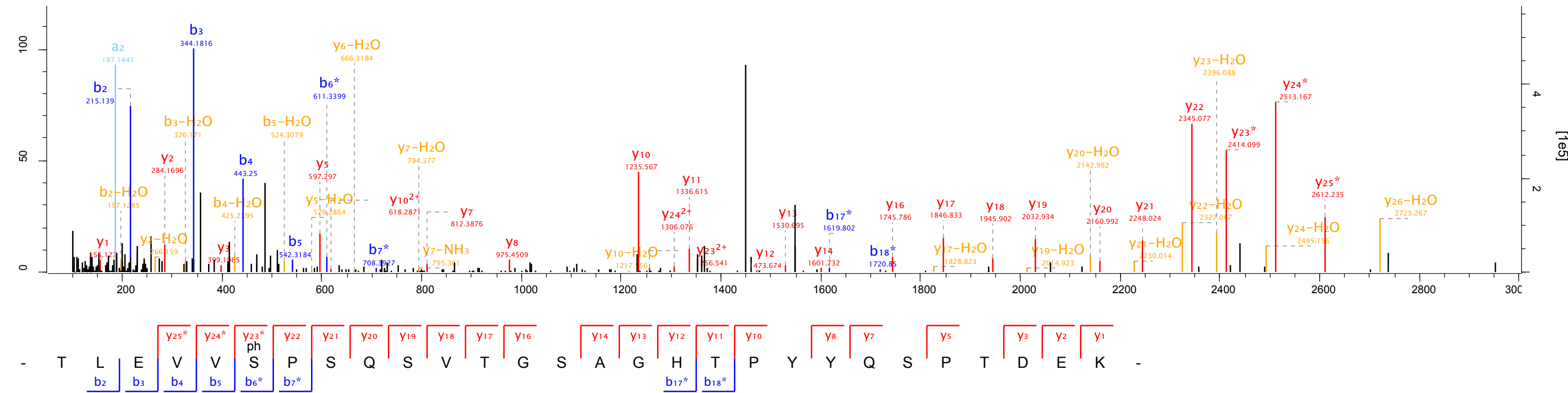
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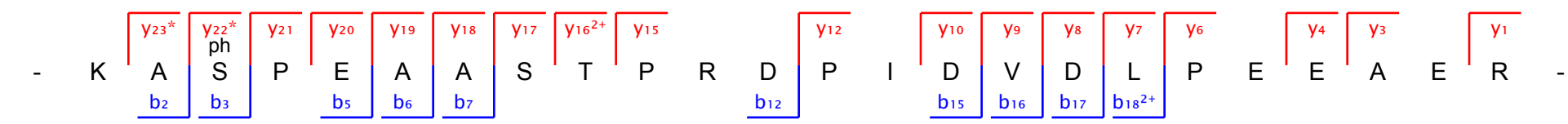
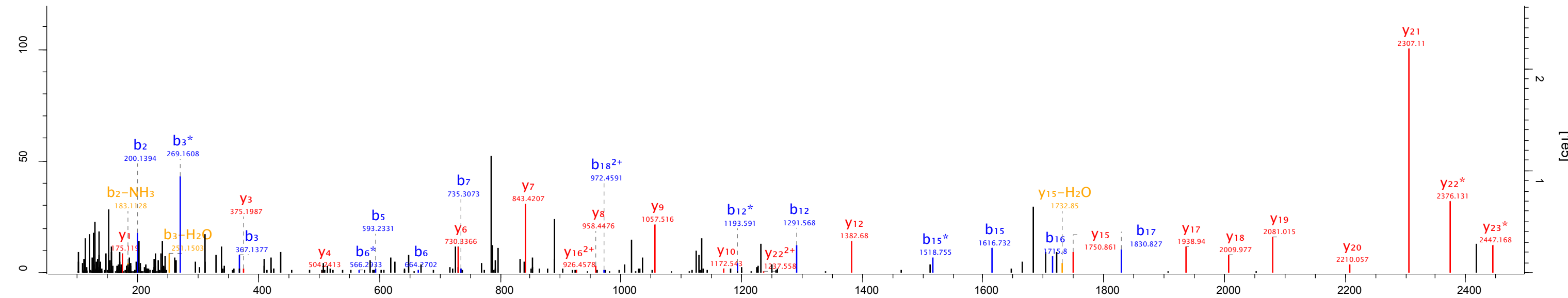
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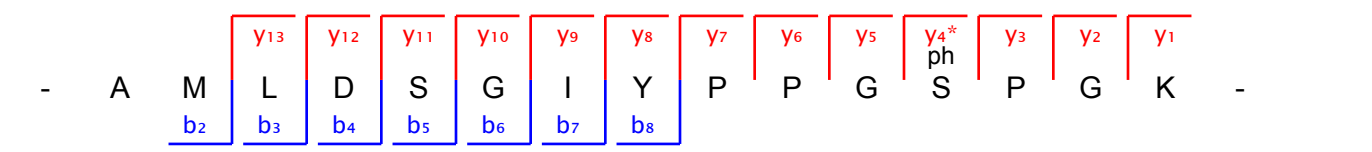
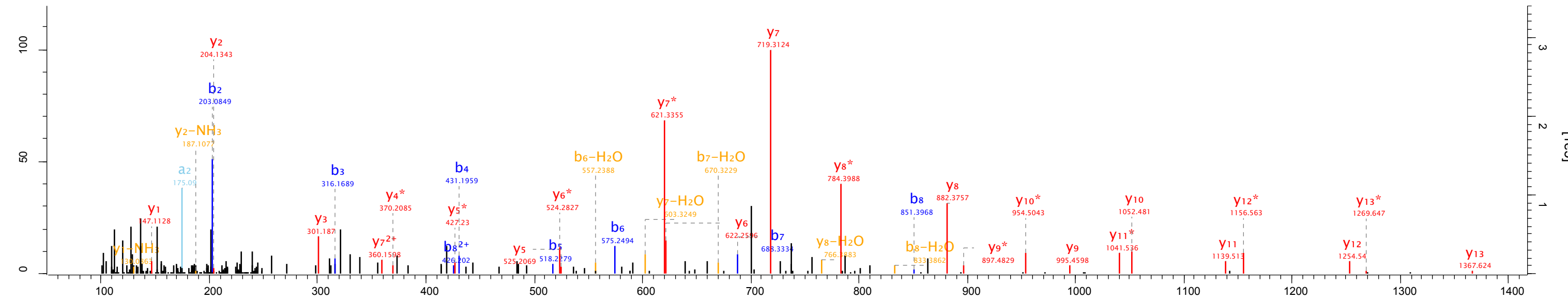
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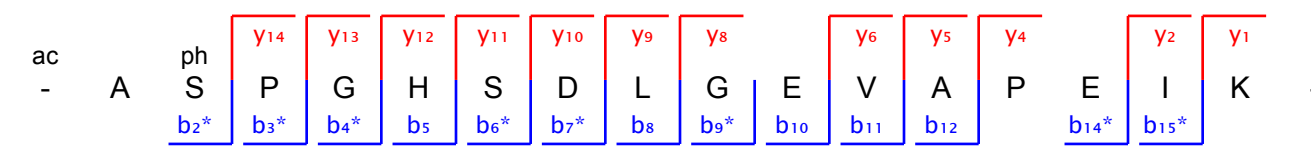
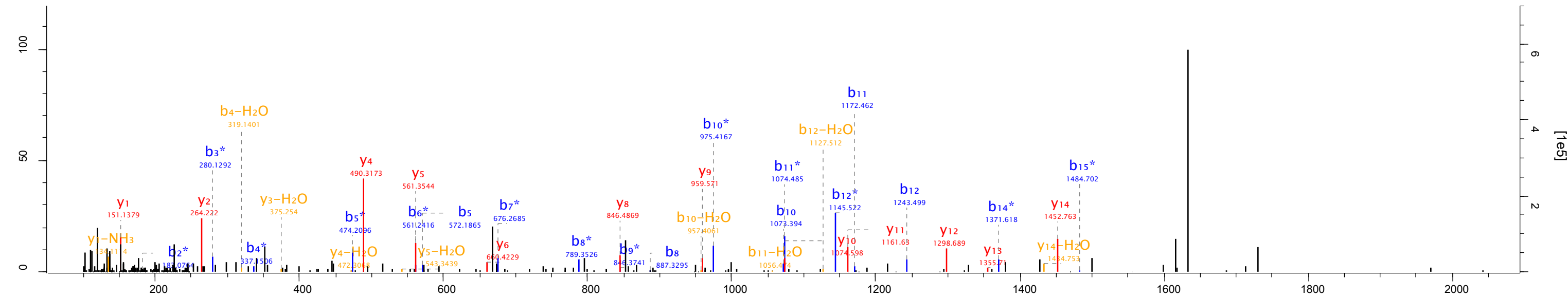
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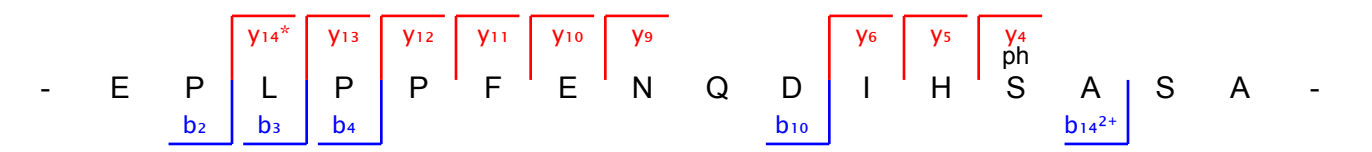
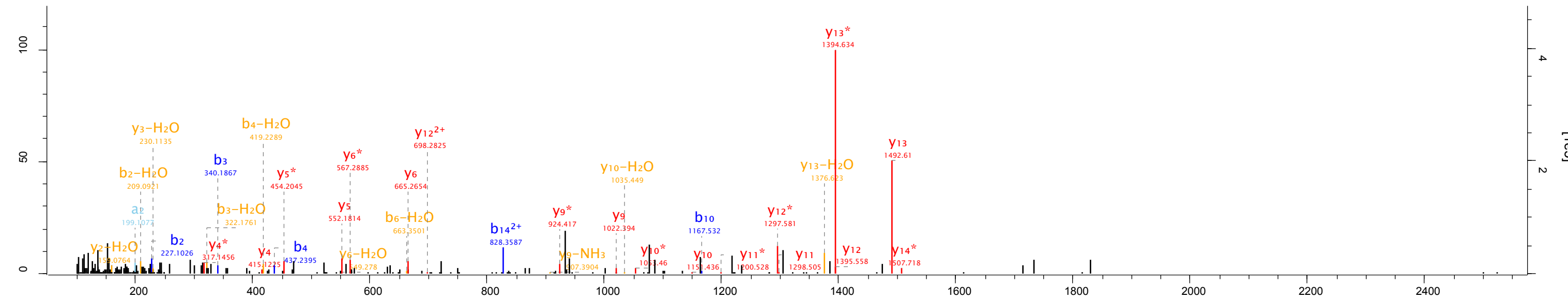
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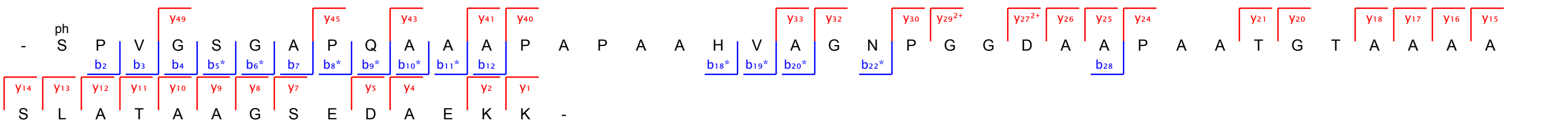
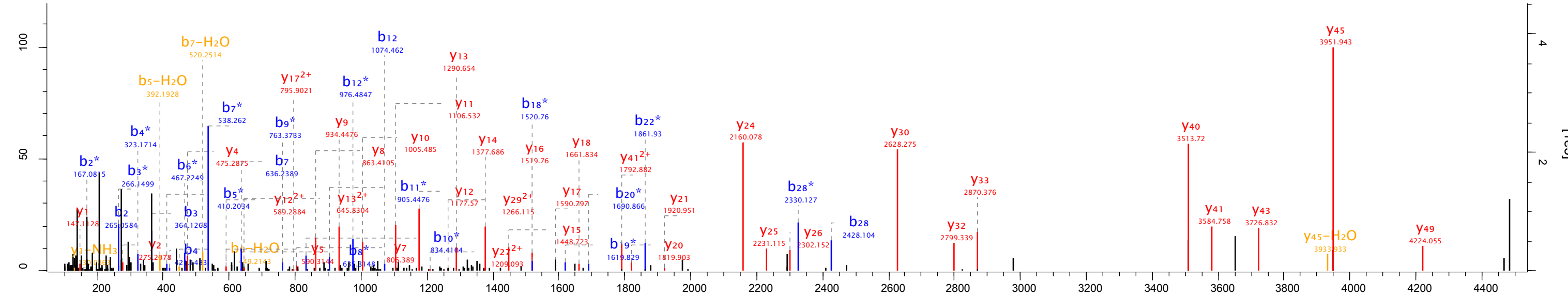


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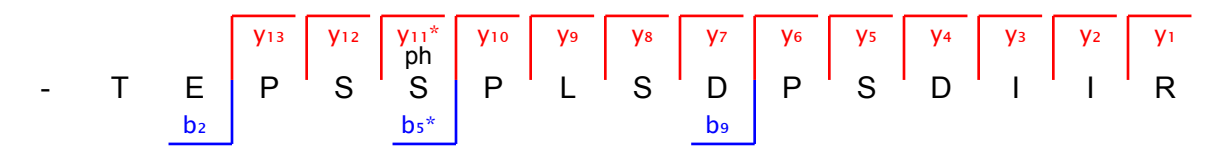
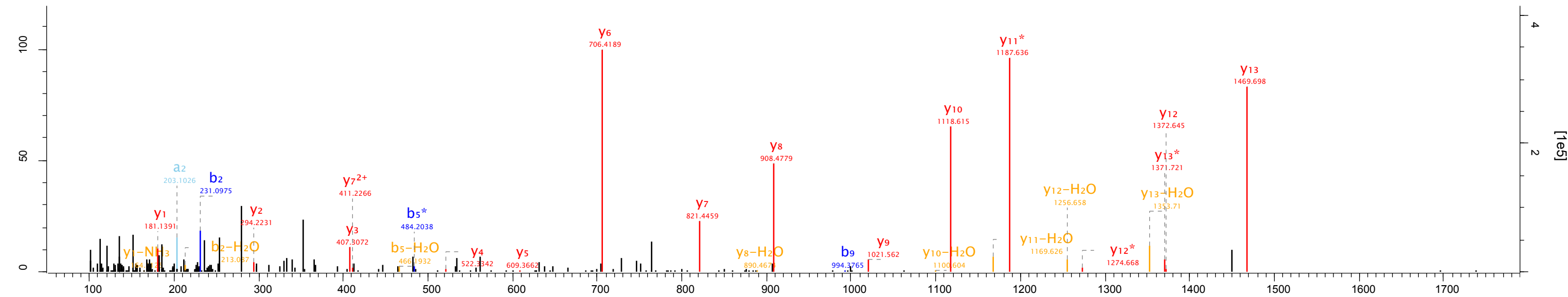


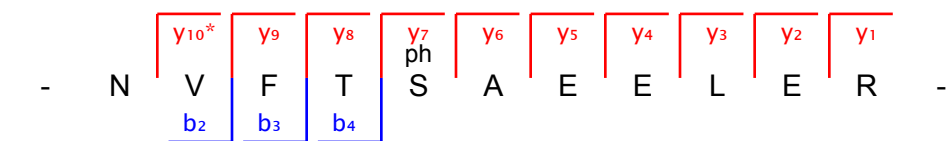
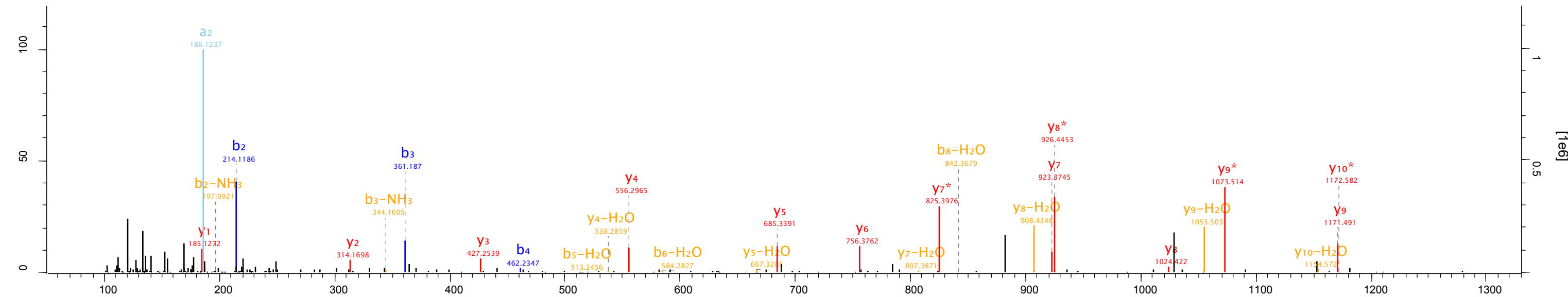
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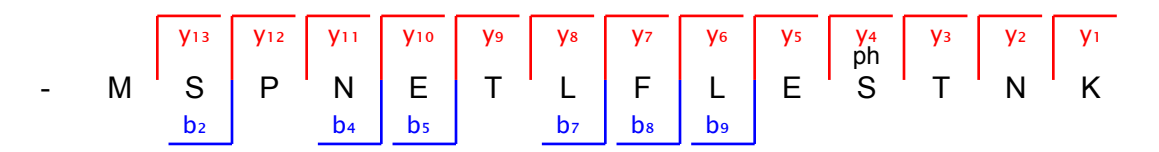
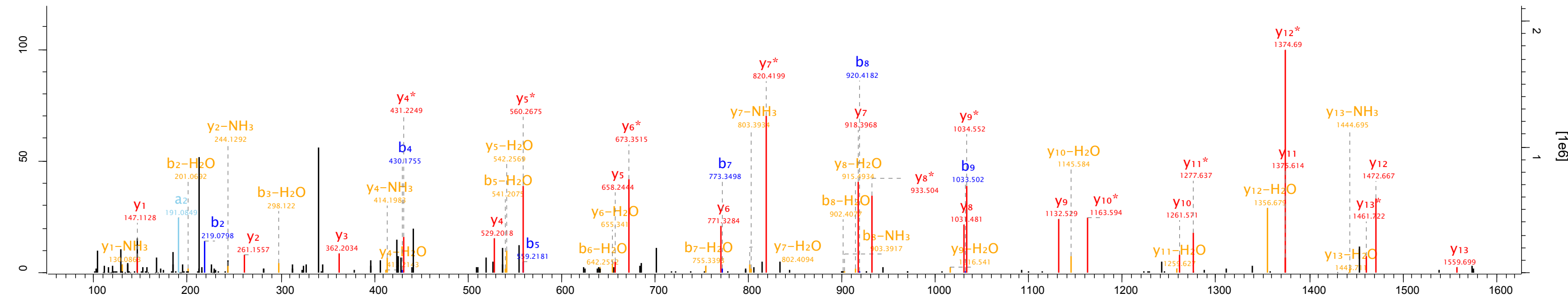


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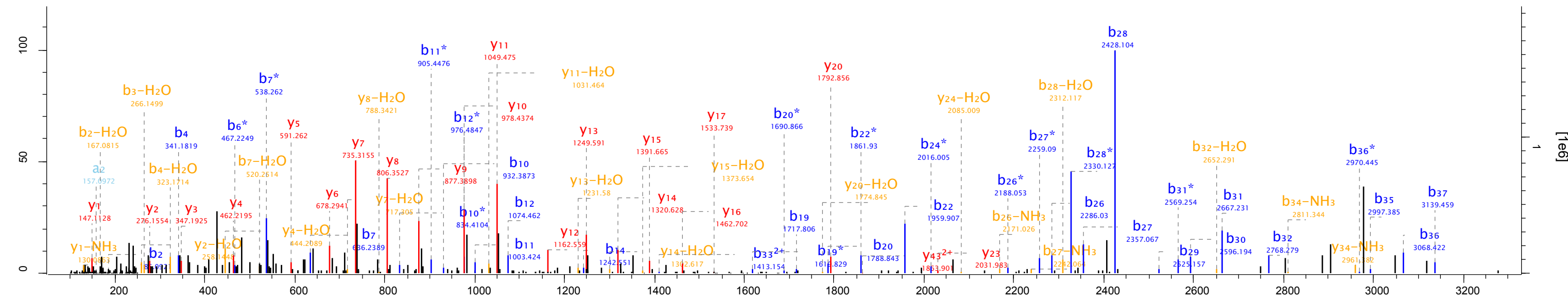




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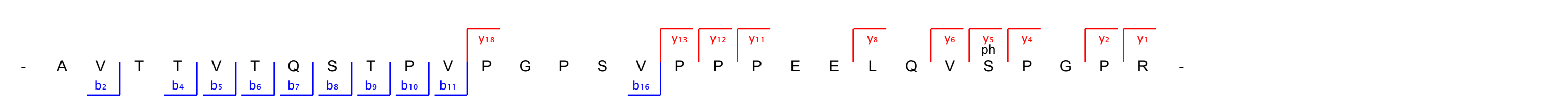
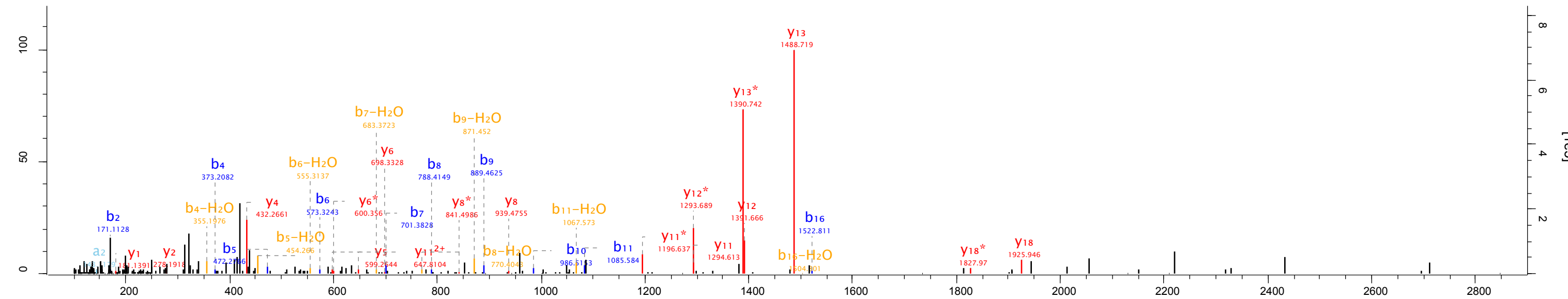


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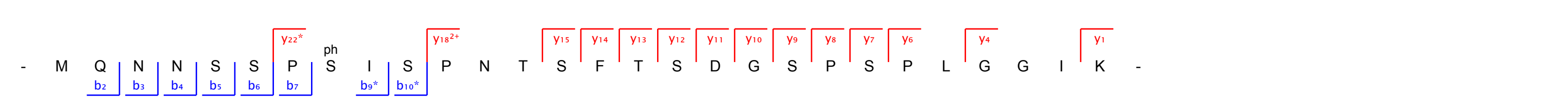
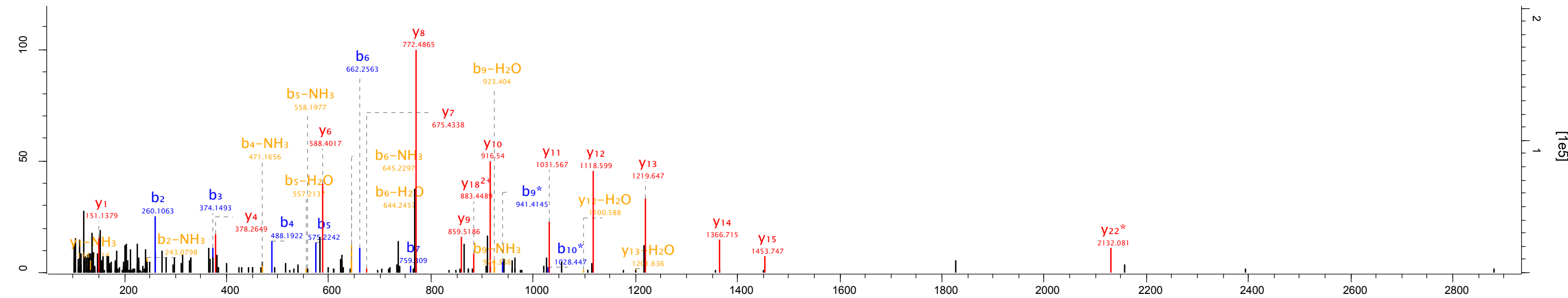


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 y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁ y₄₃²⁺ y₂₃ y₂₀ y₁₇ y₁₆ y₁₅ y₁₄
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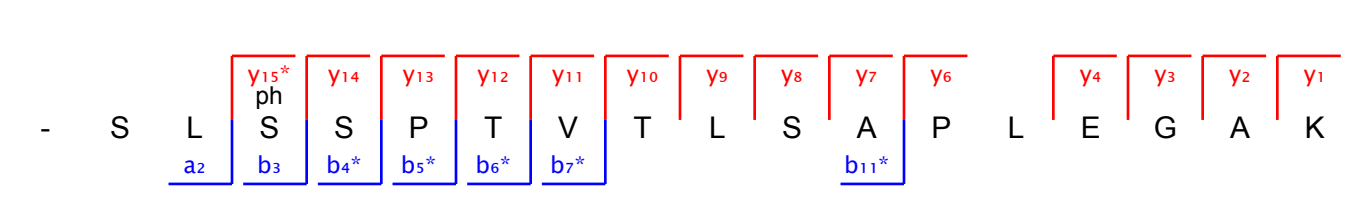
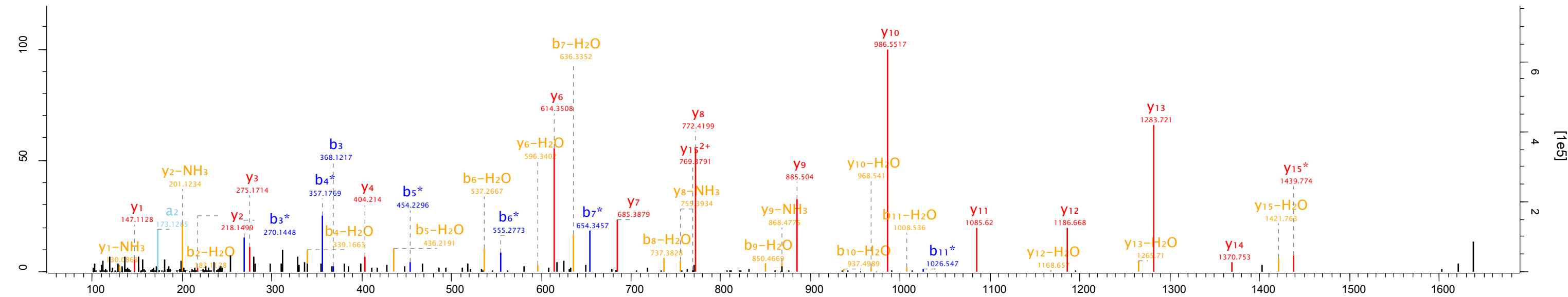
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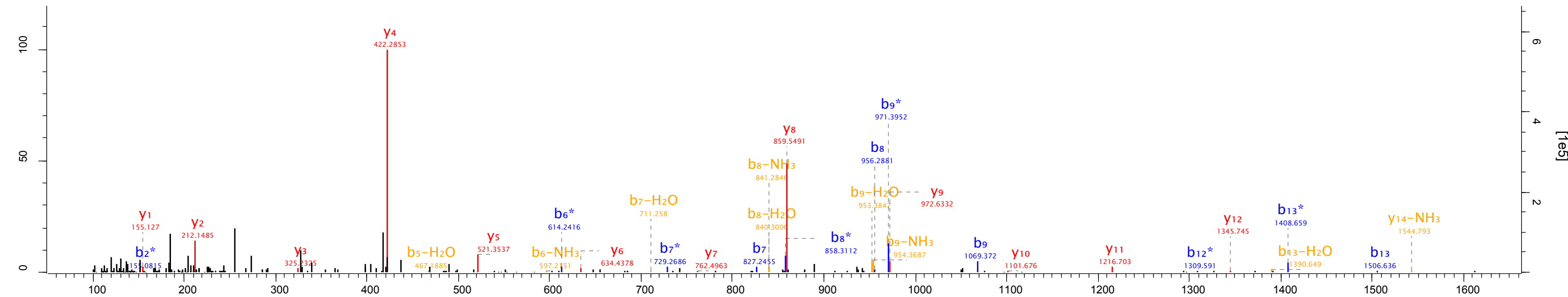


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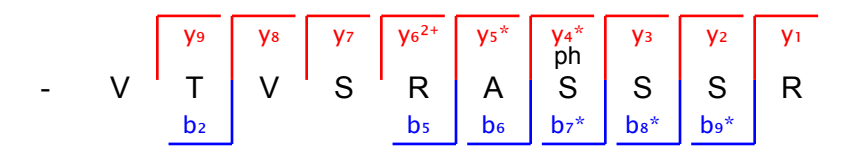
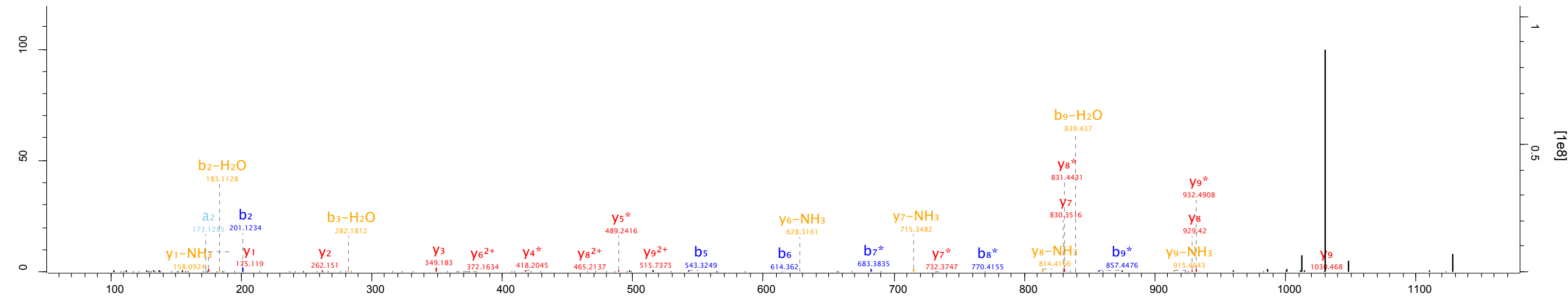




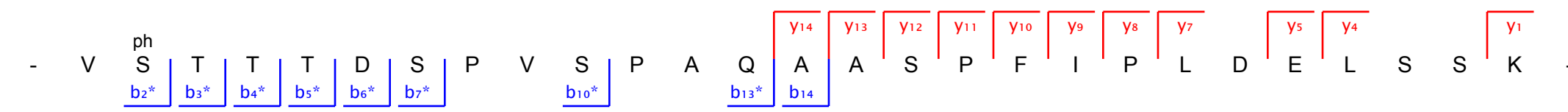
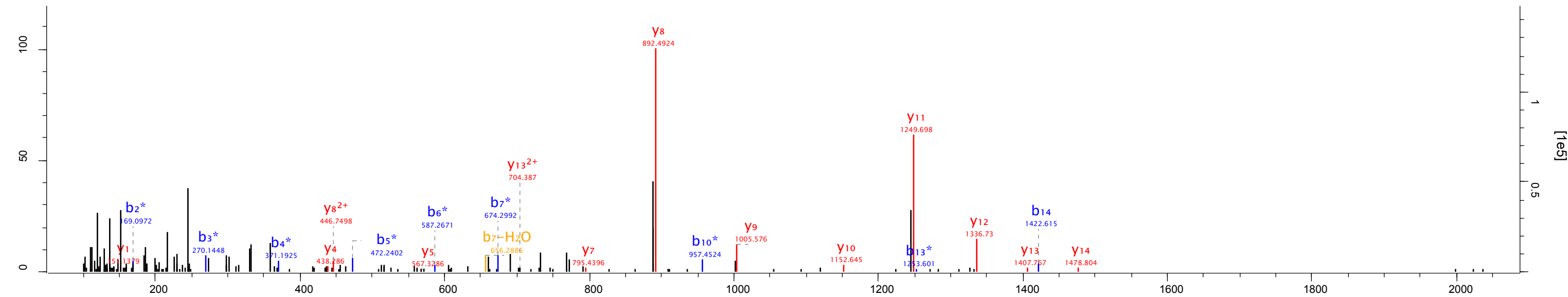
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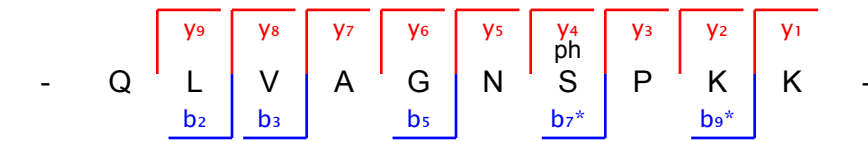
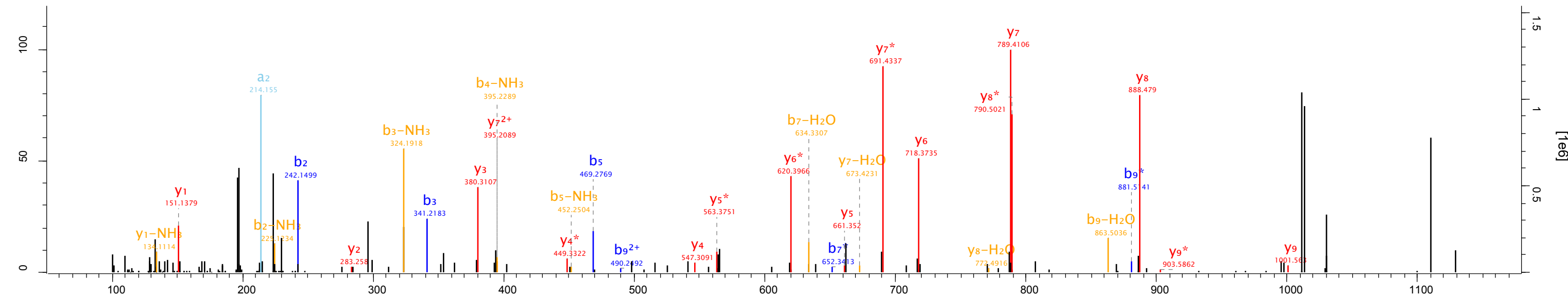
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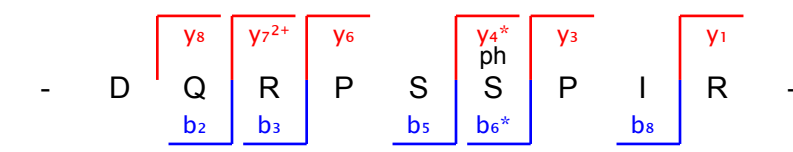
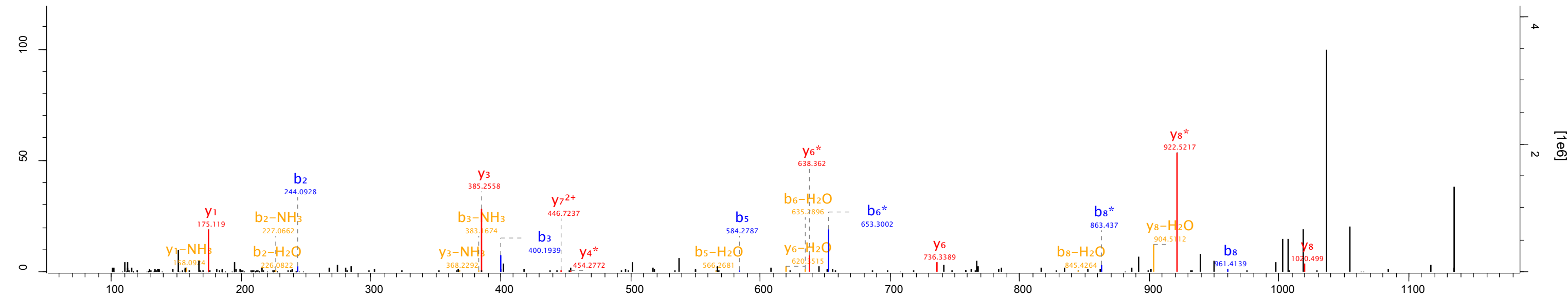
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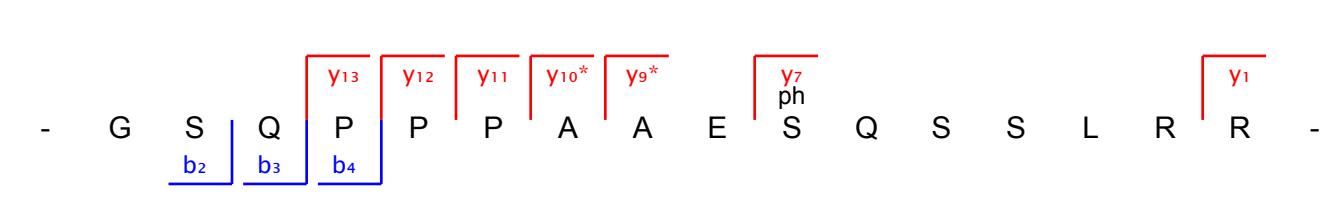
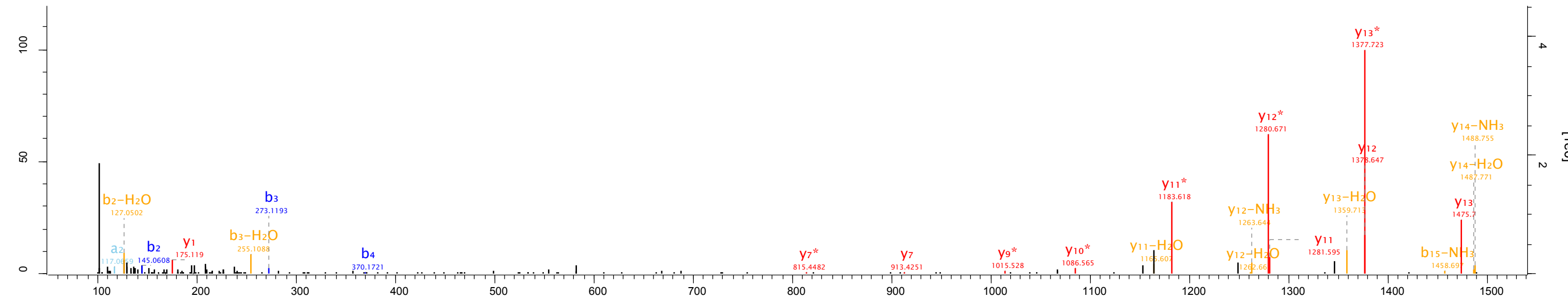
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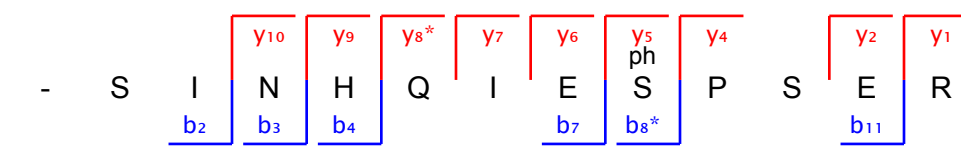
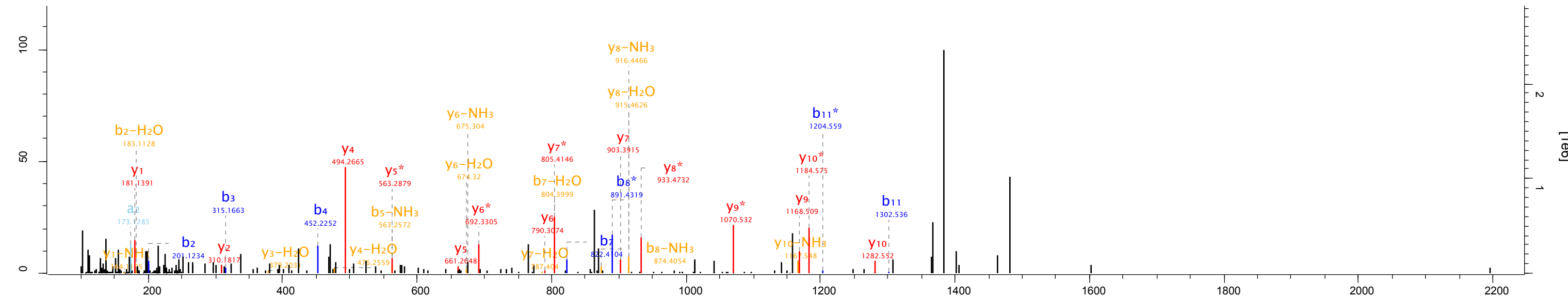
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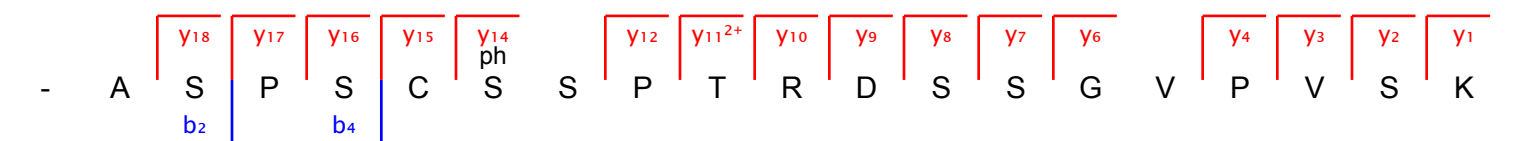
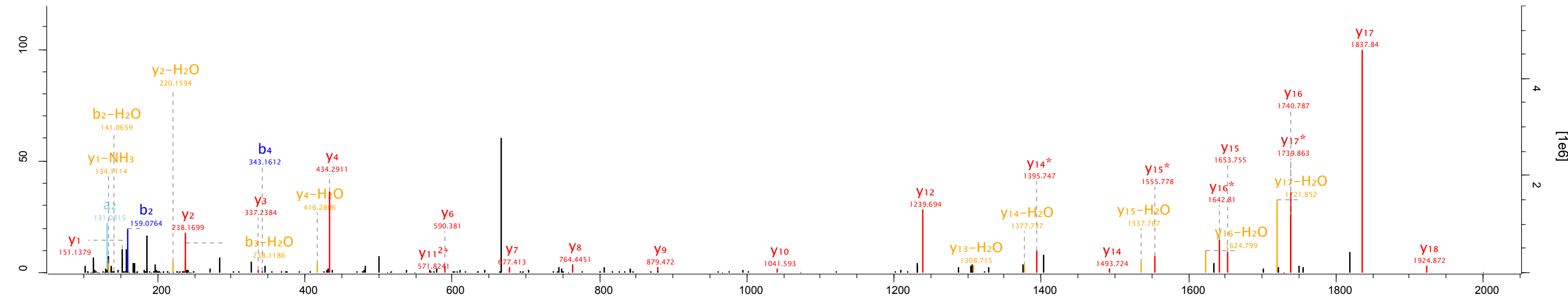
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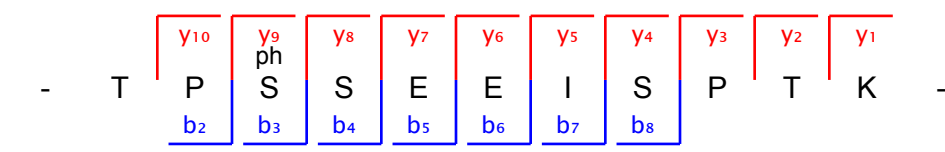
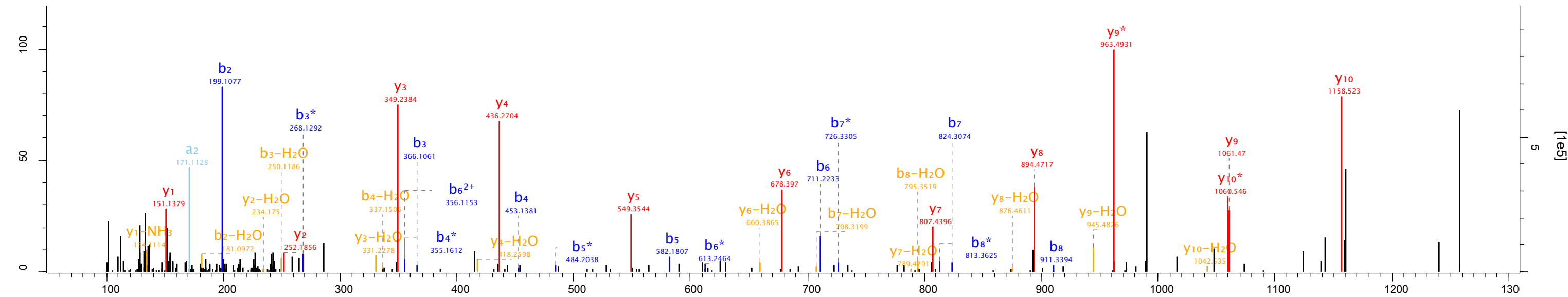
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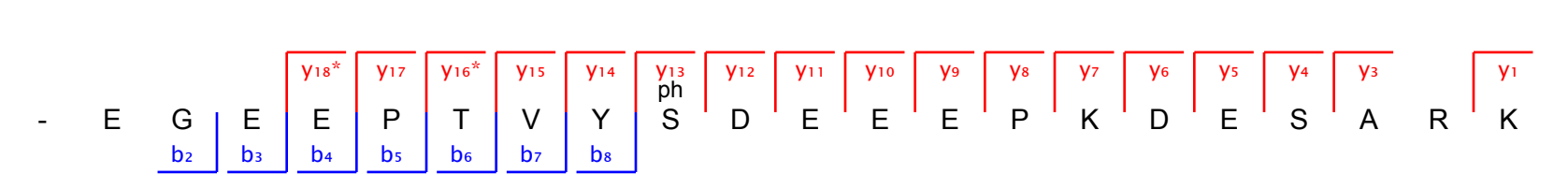
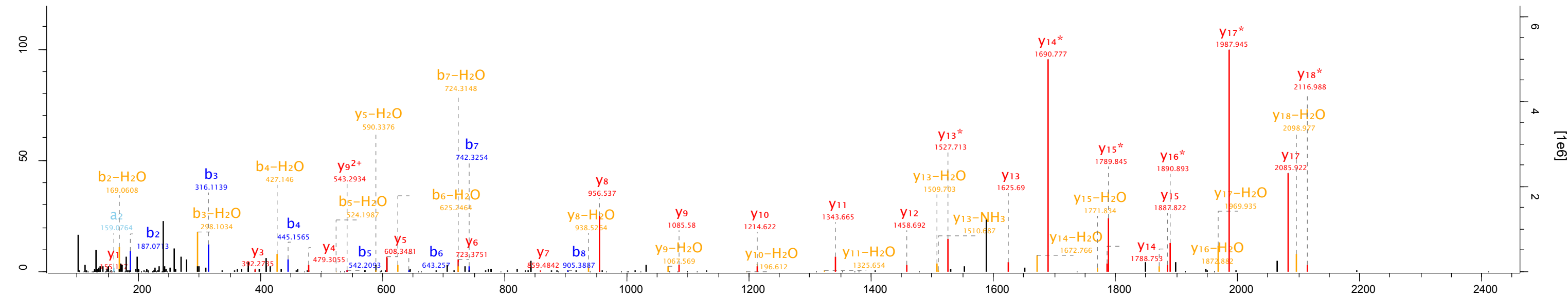
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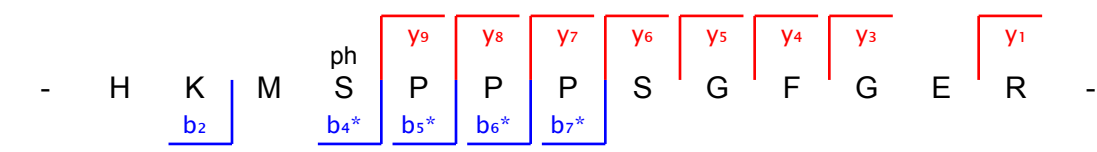
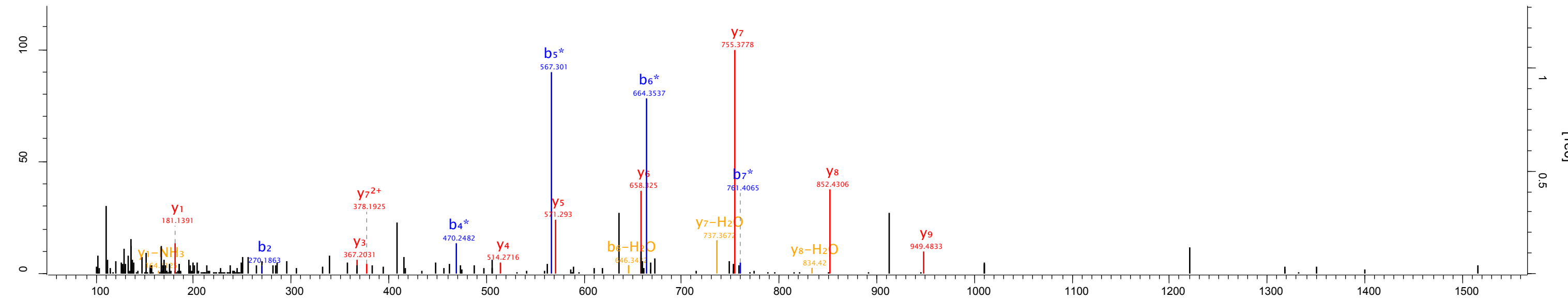
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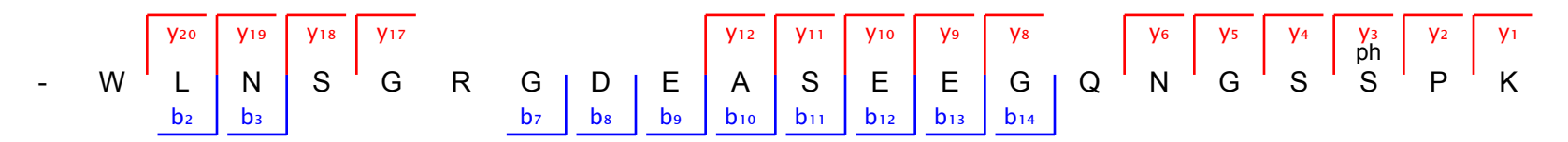
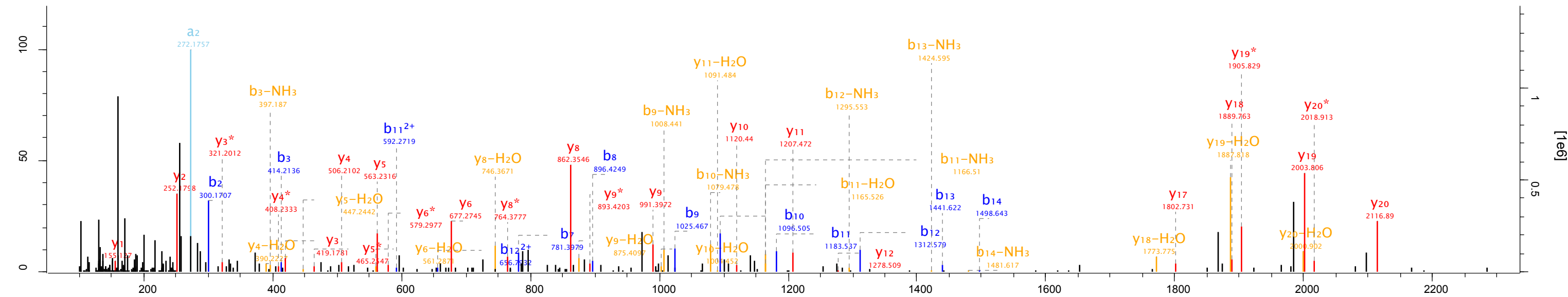
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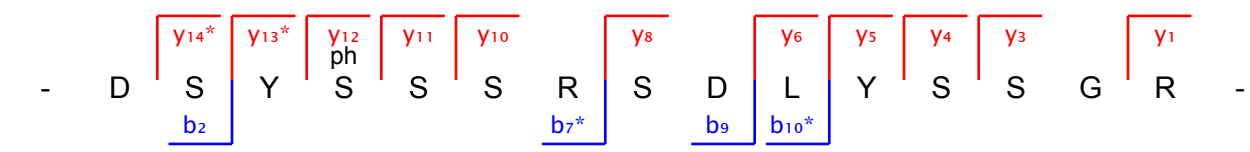
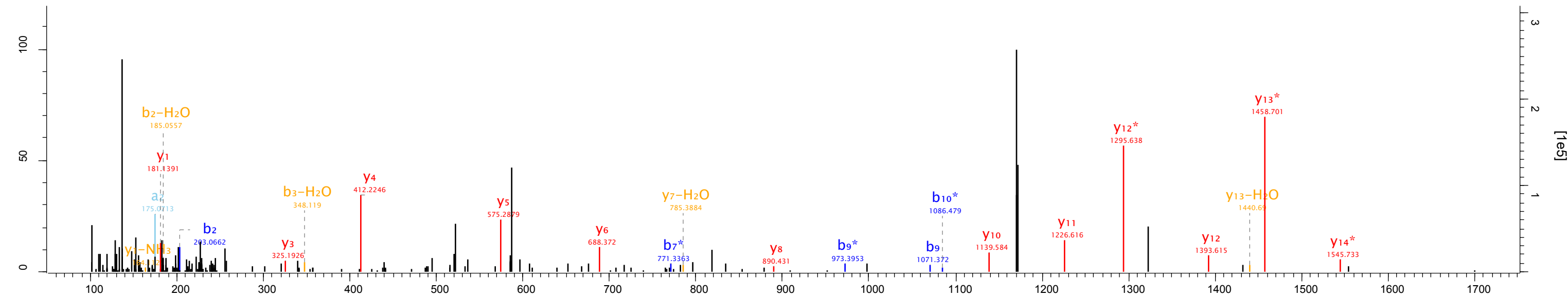
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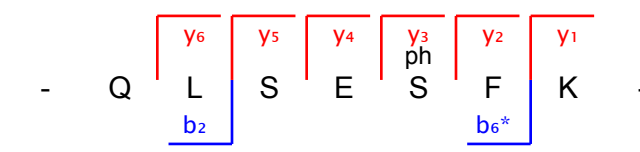
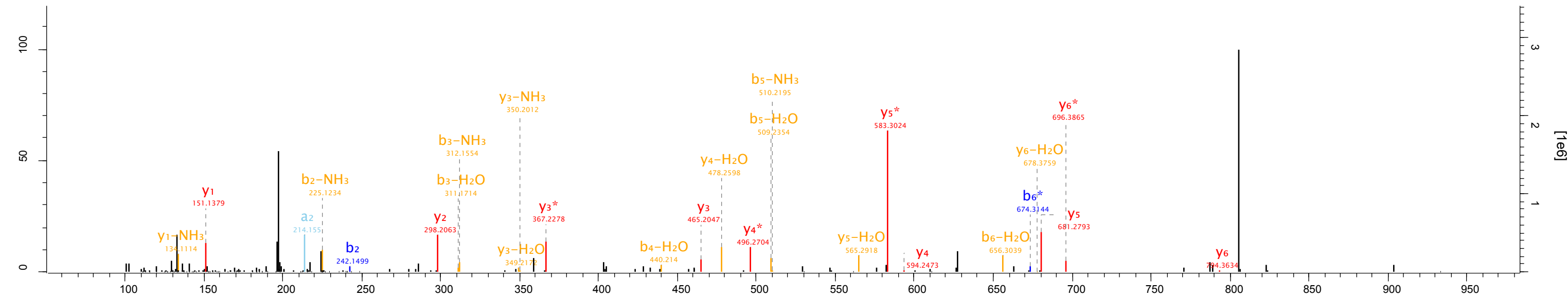
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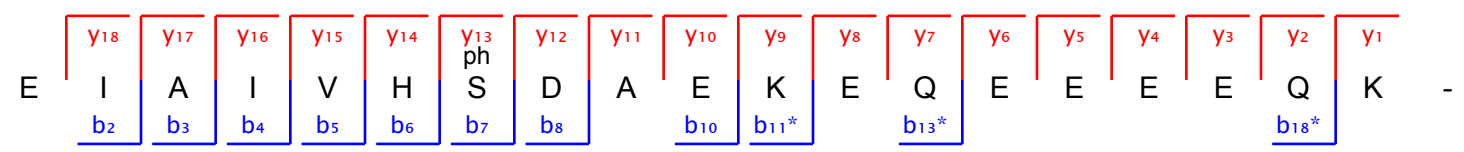
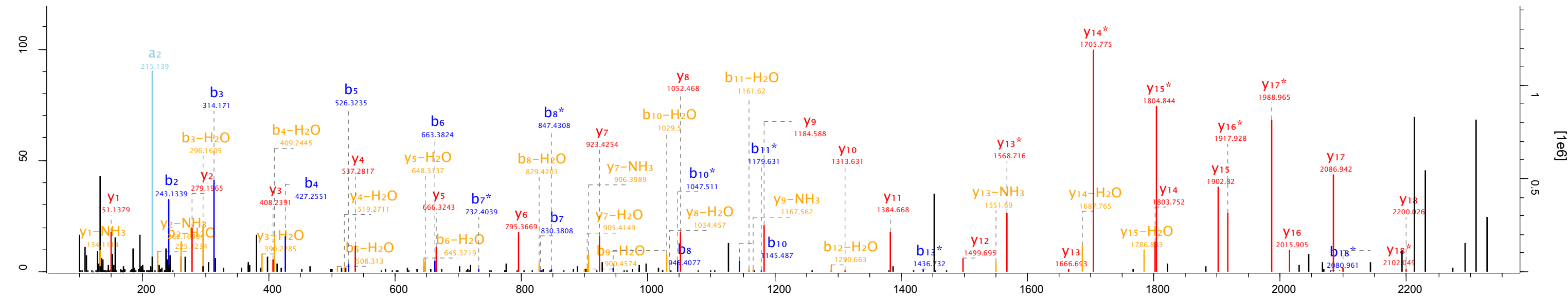
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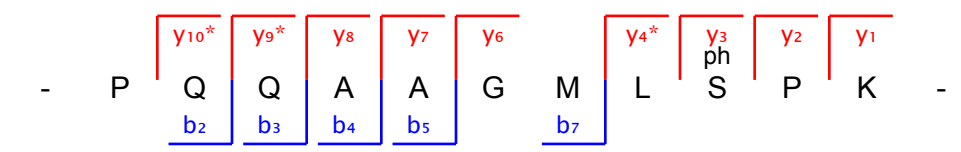
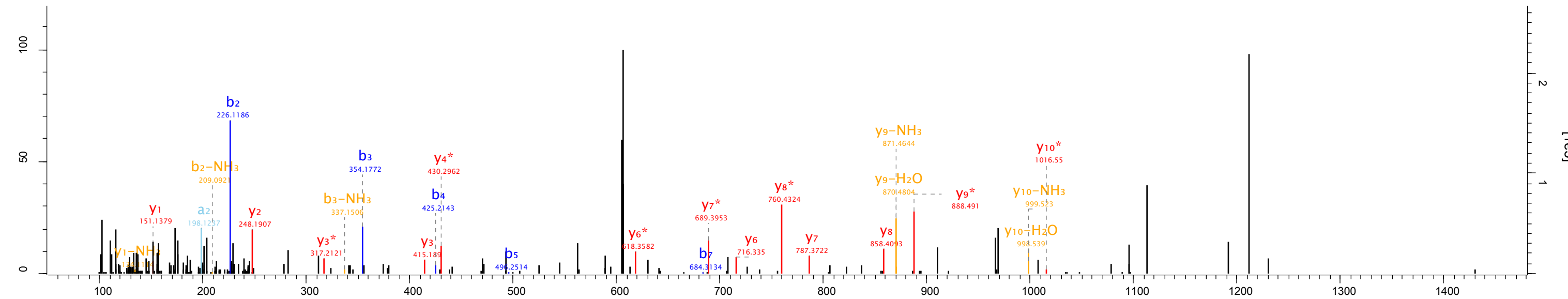
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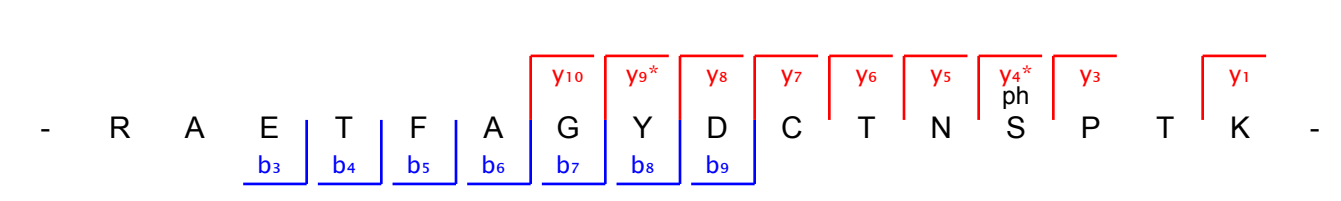
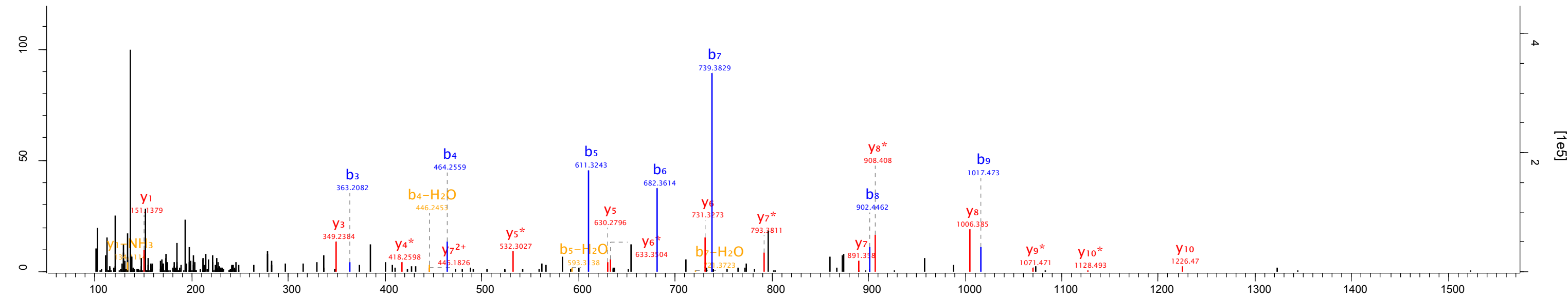
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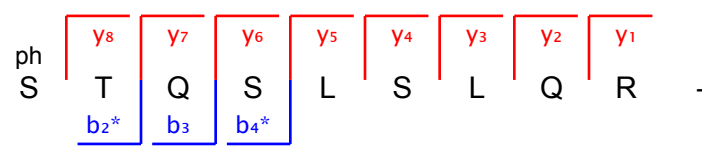
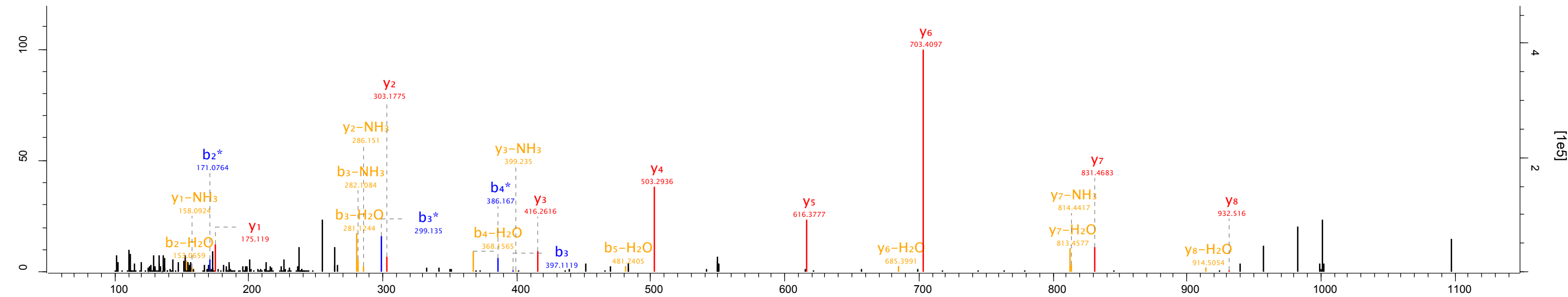
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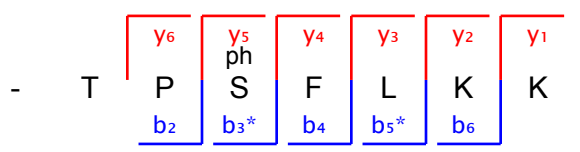
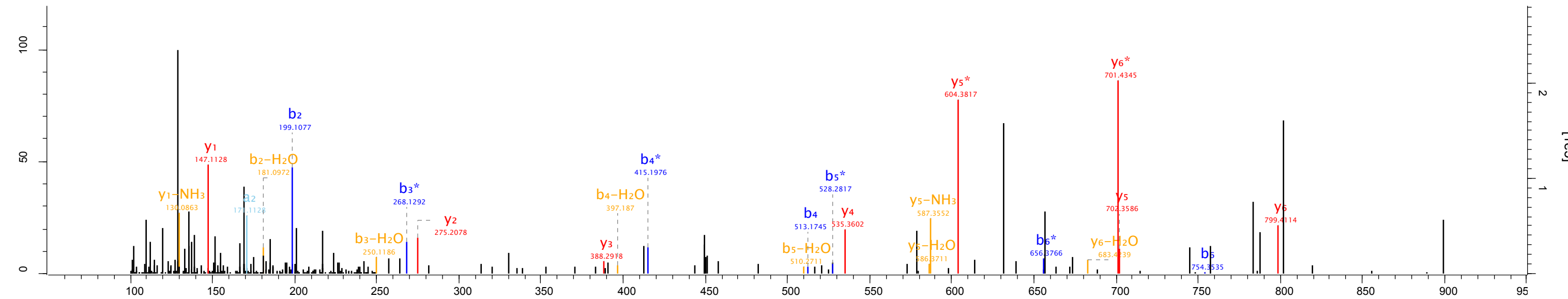
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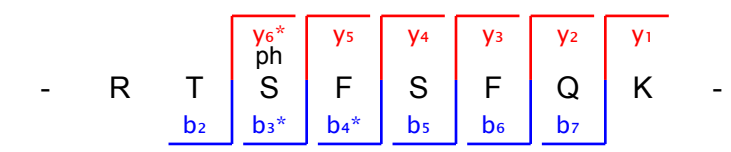
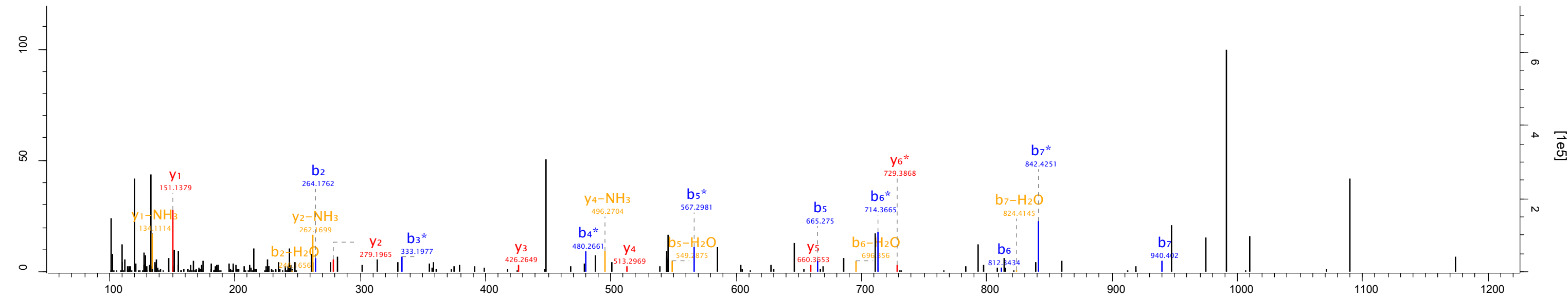
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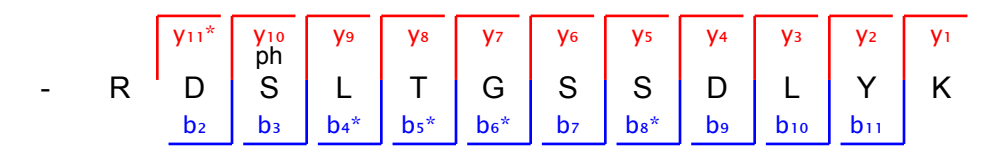
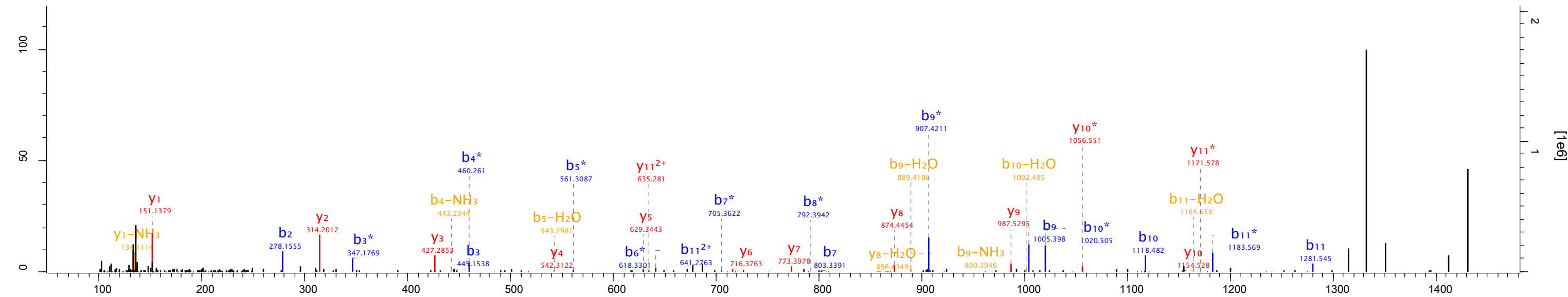
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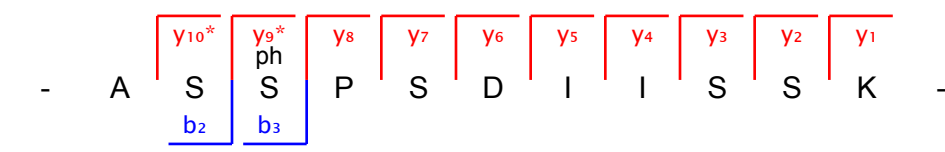
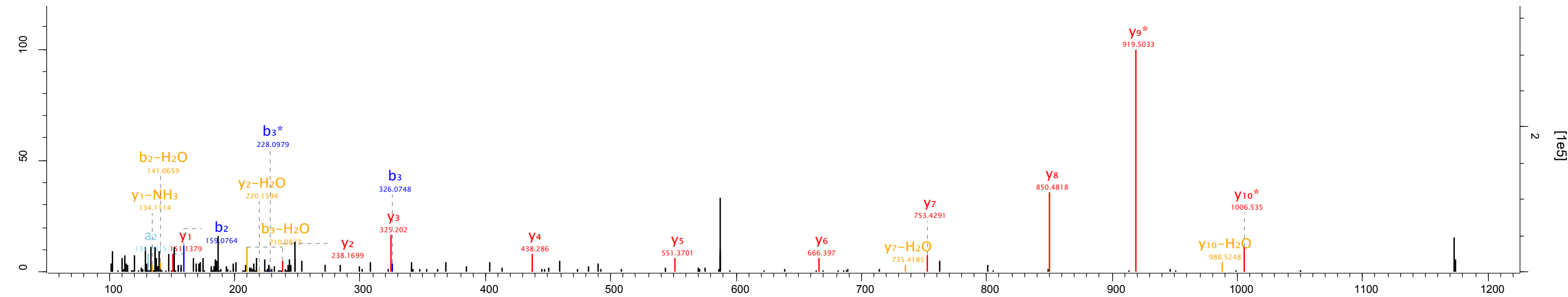
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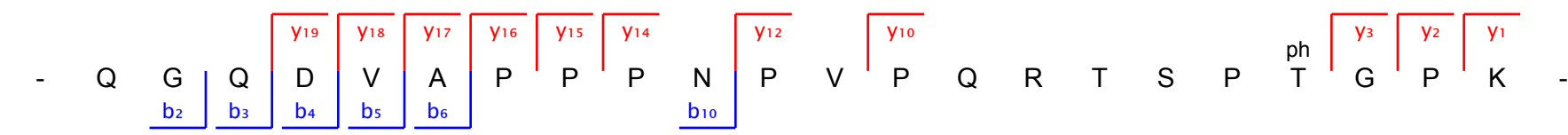
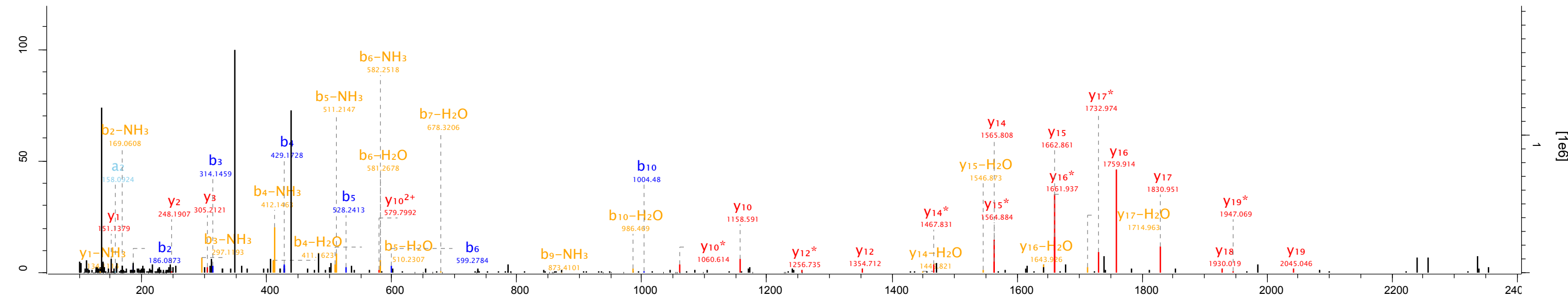
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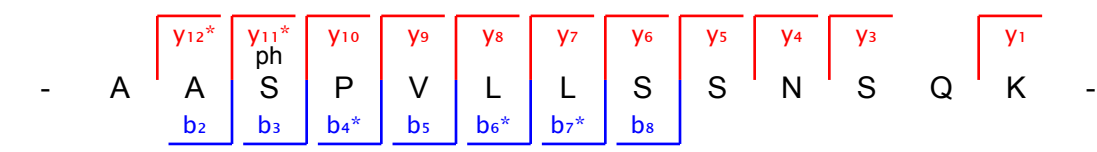
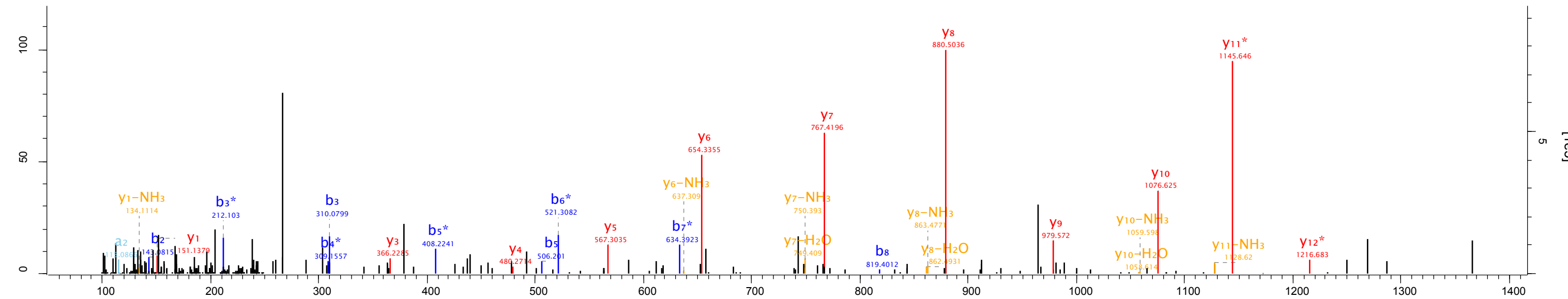
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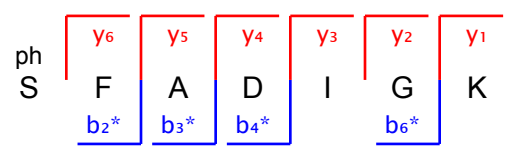
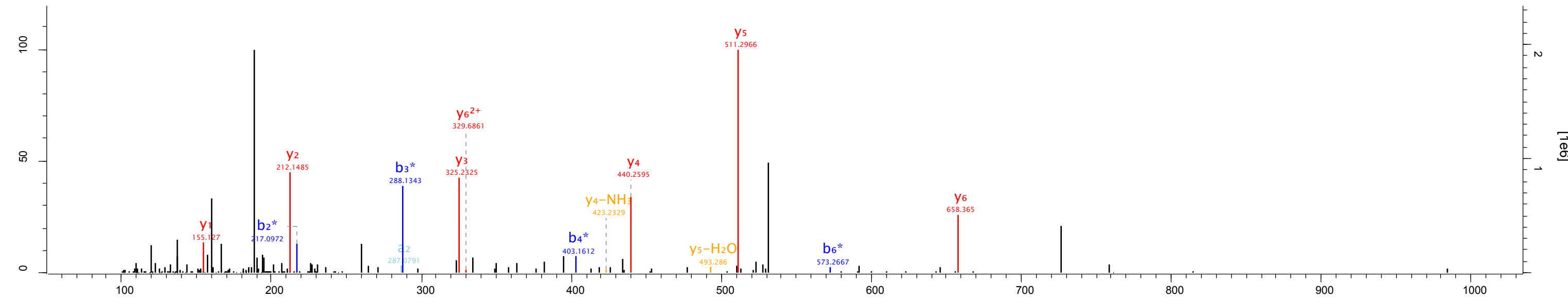
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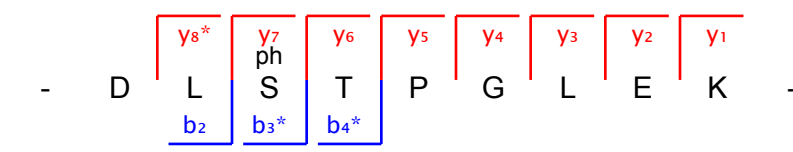
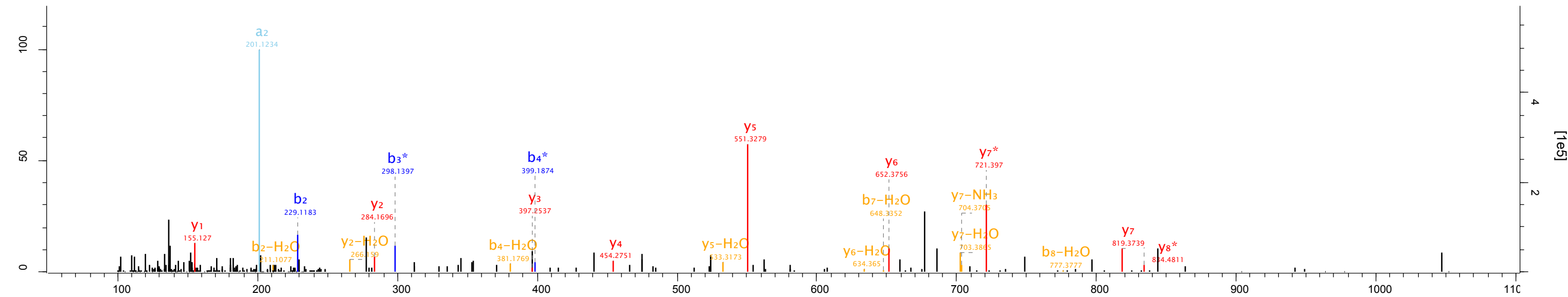
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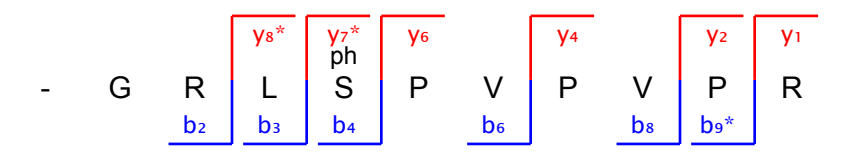
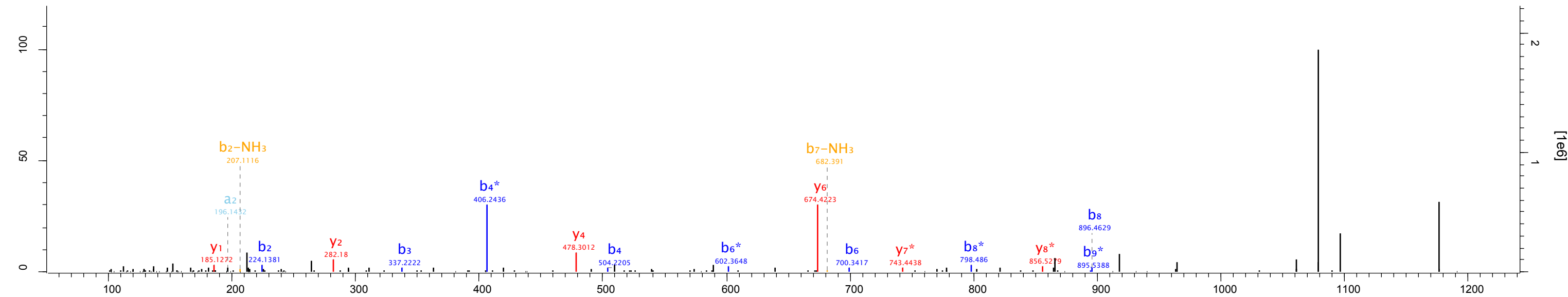
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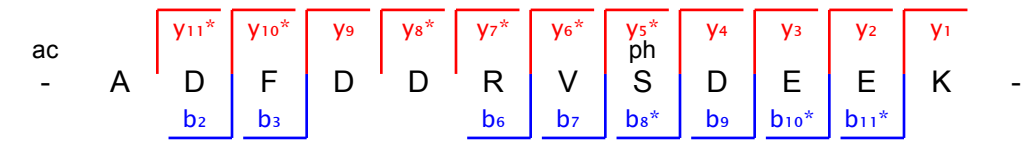
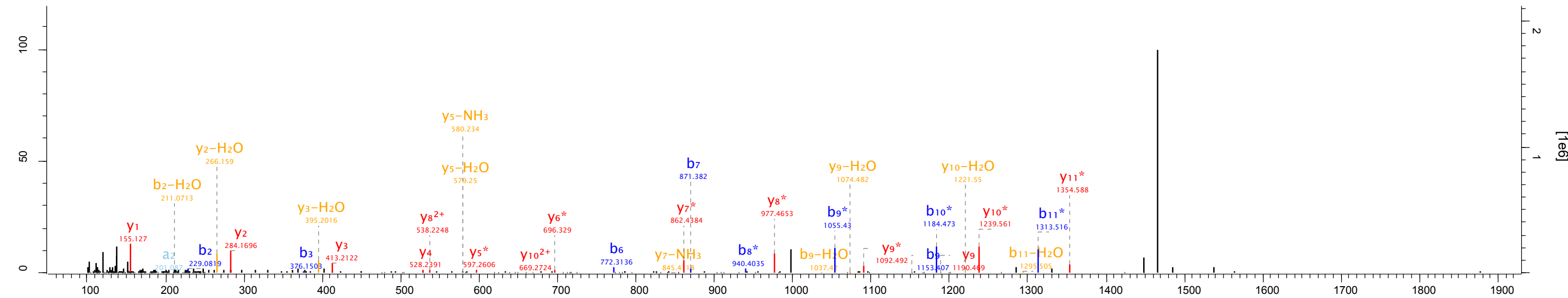
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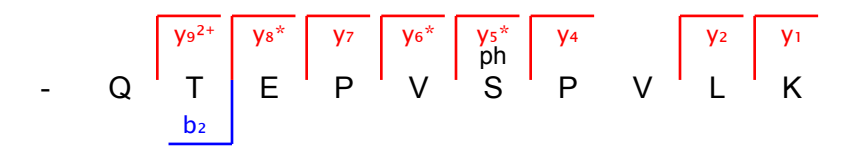
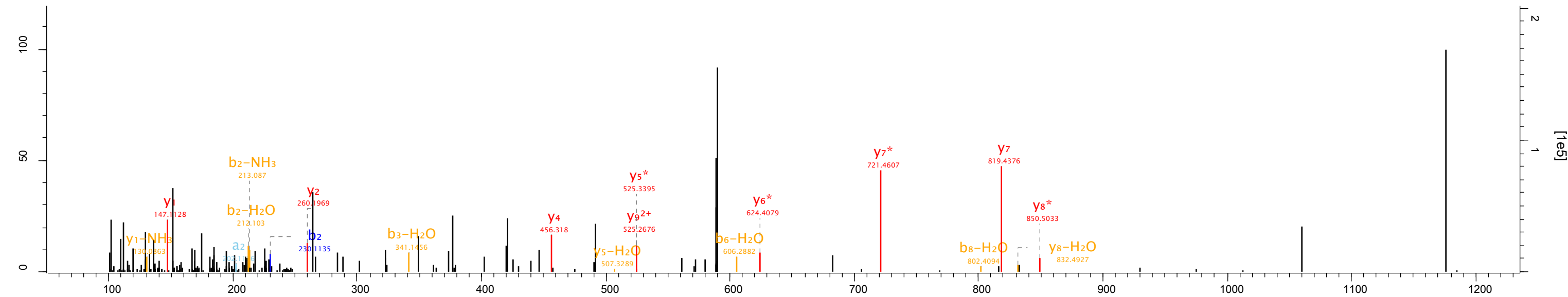
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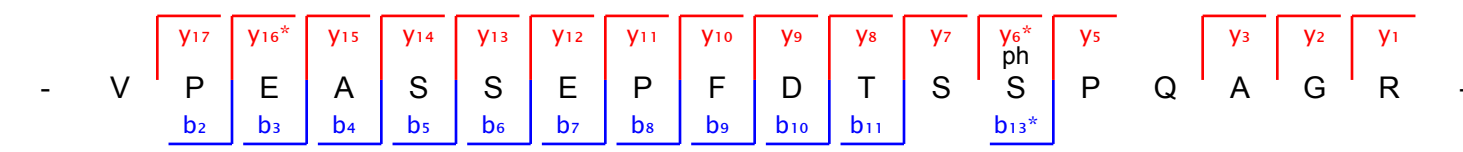
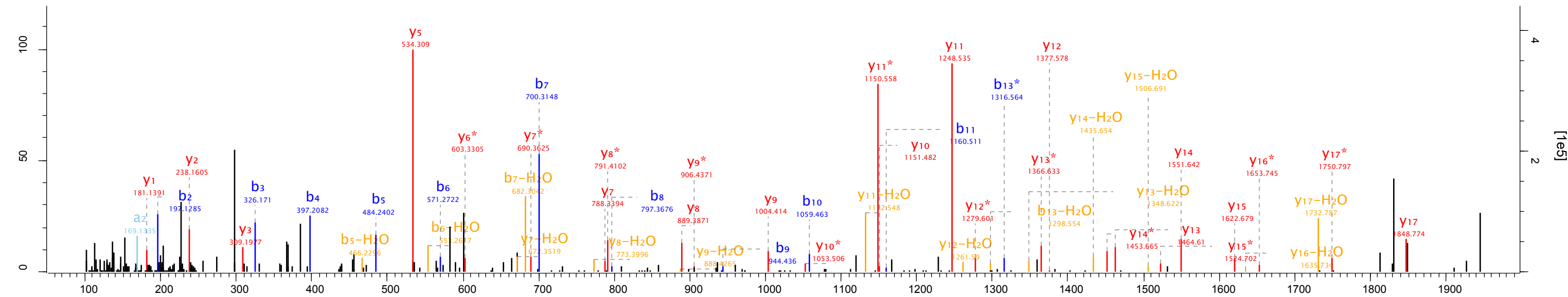
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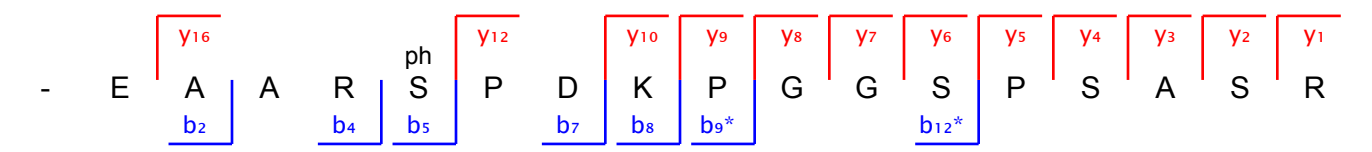
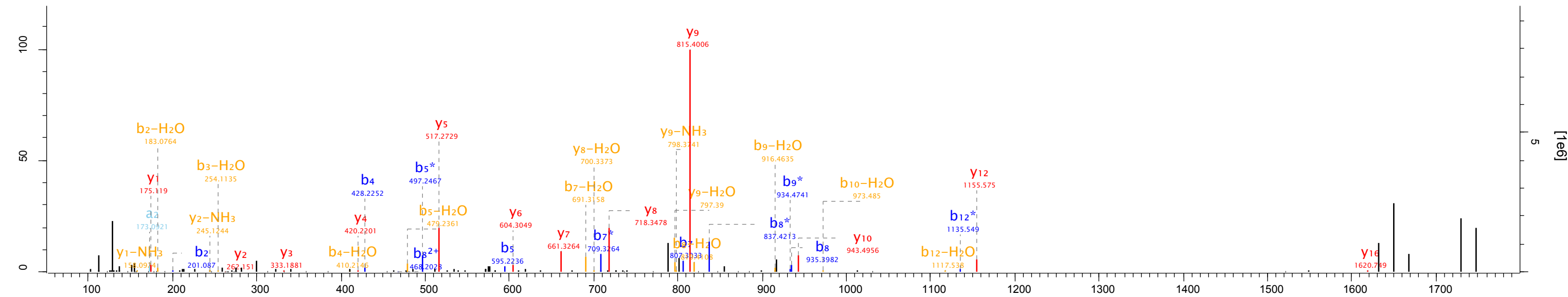
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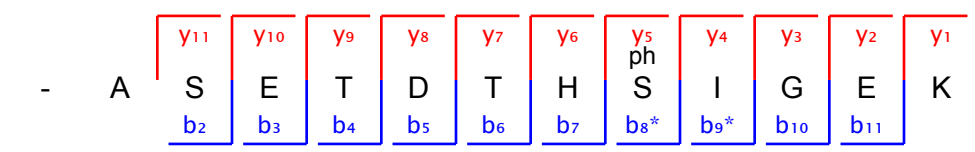
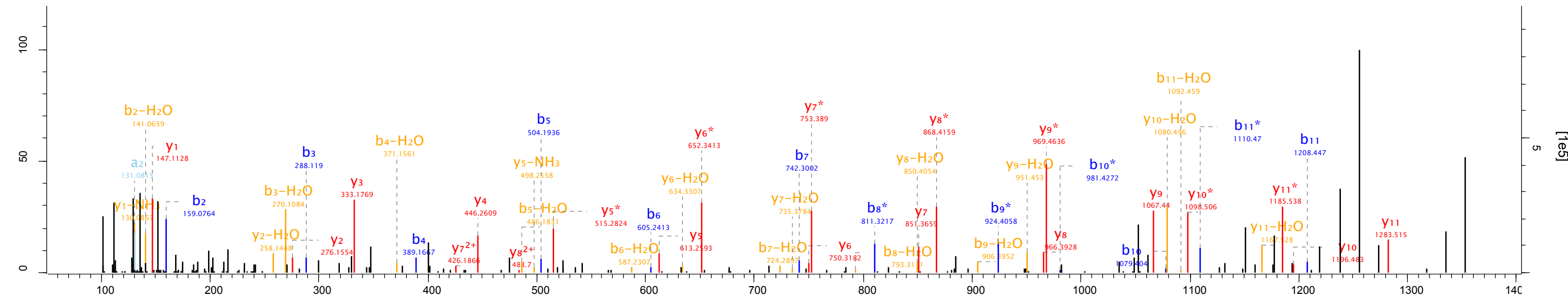
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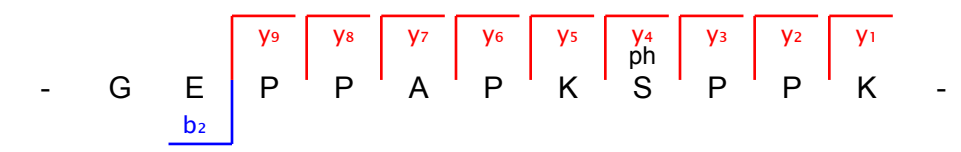
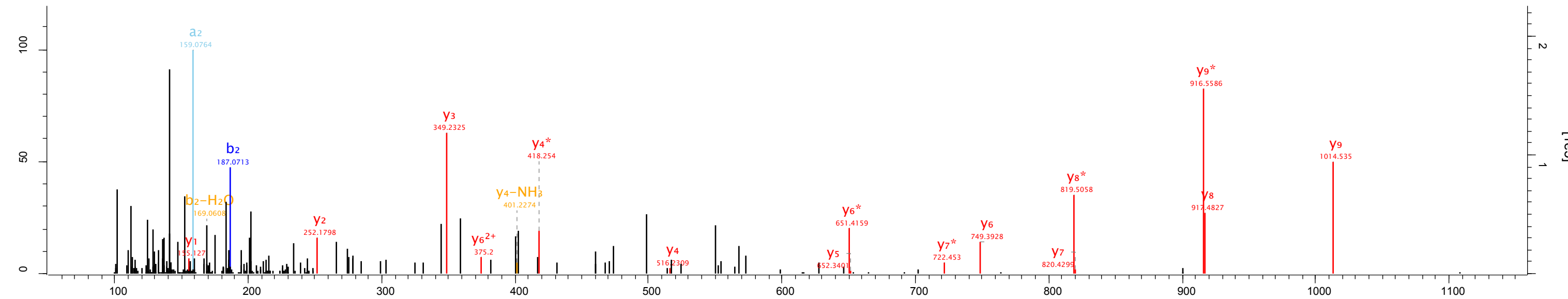
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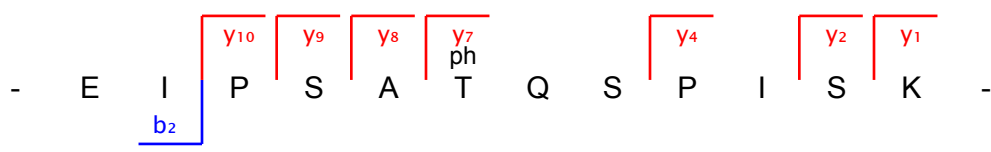
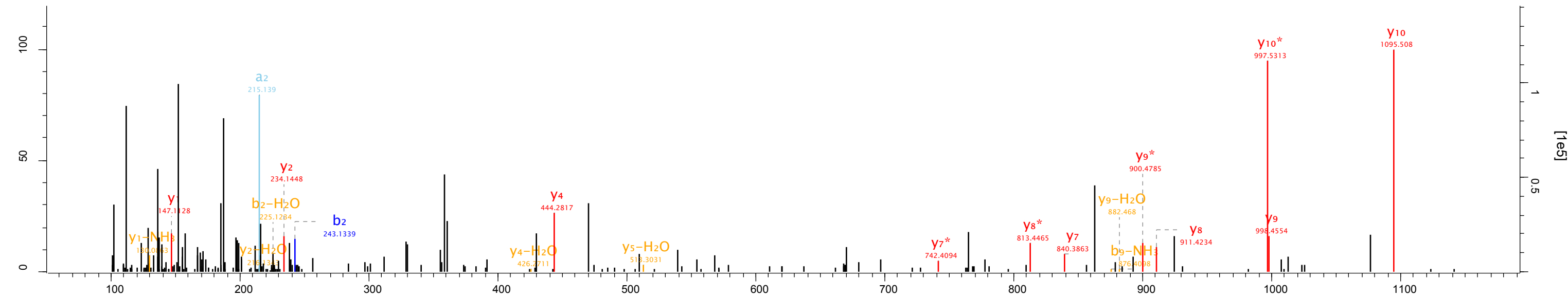
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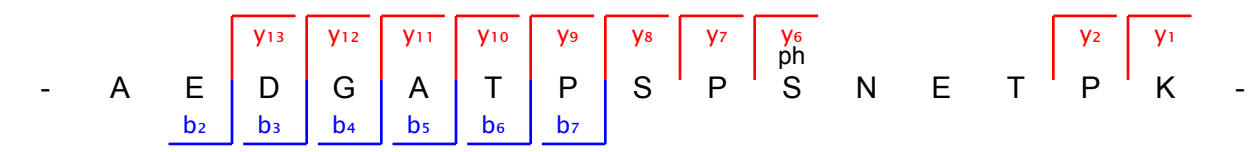
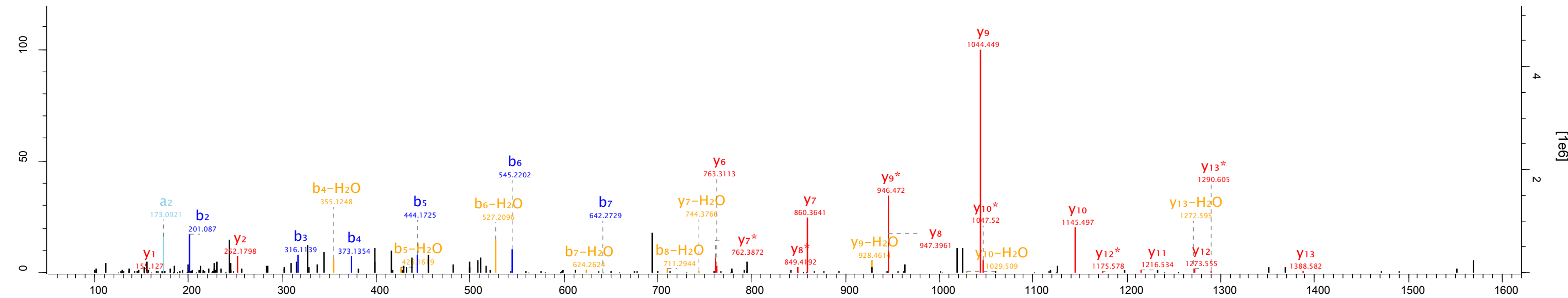
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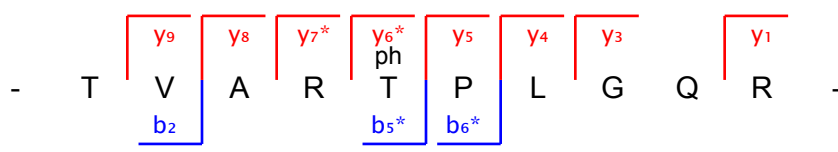
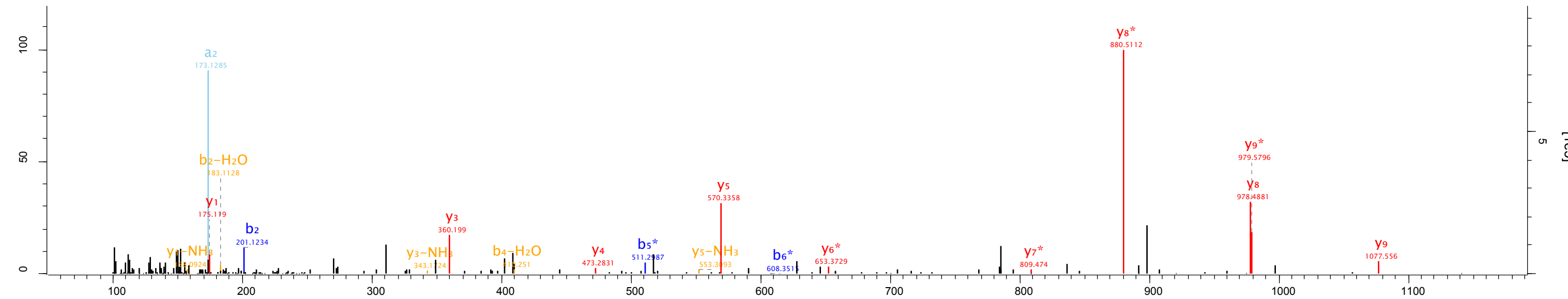
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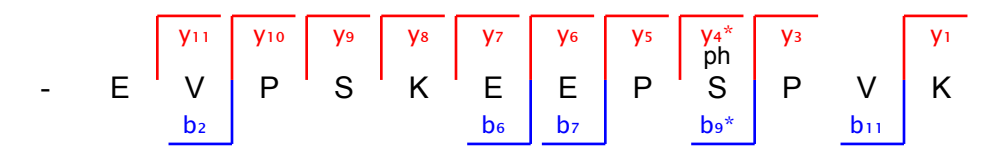
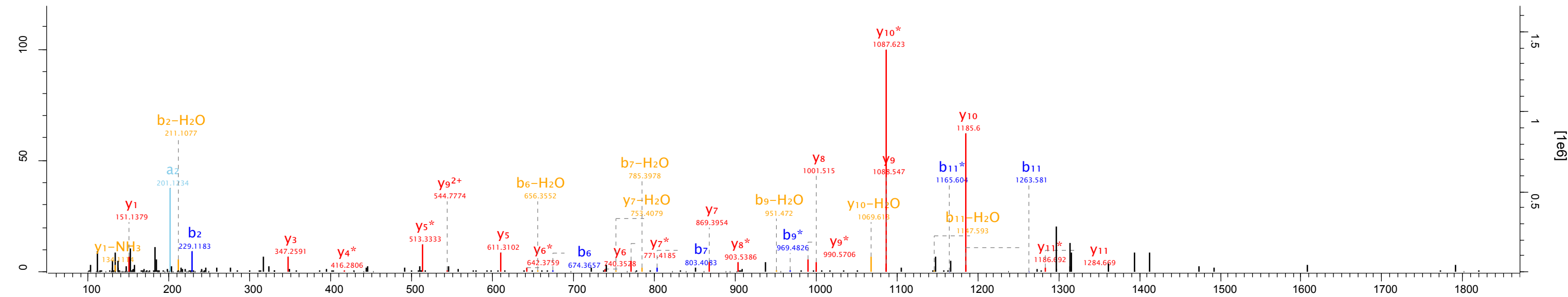
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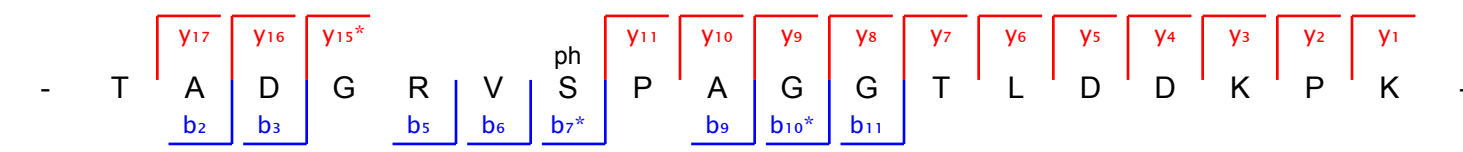
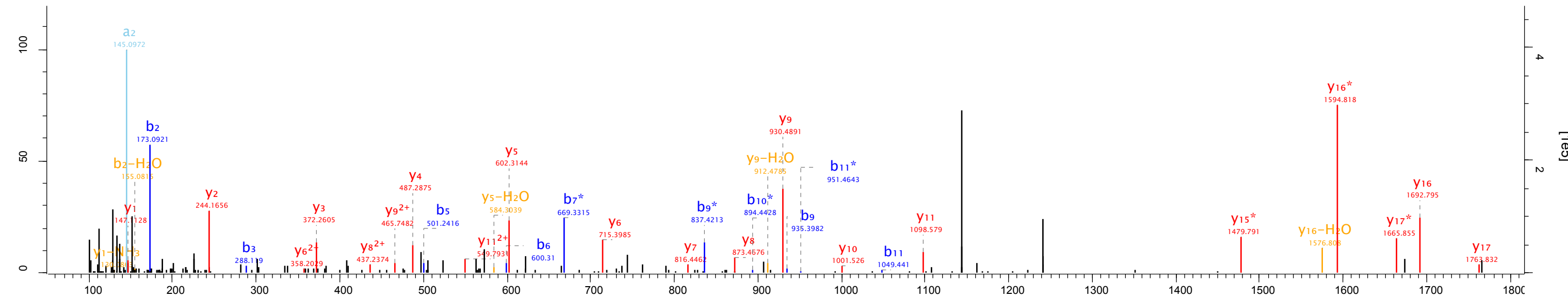
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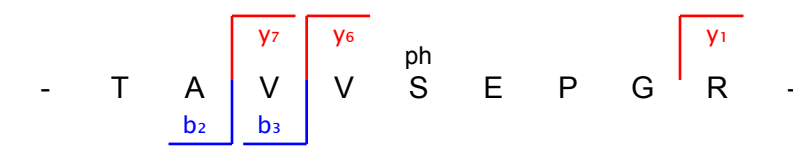
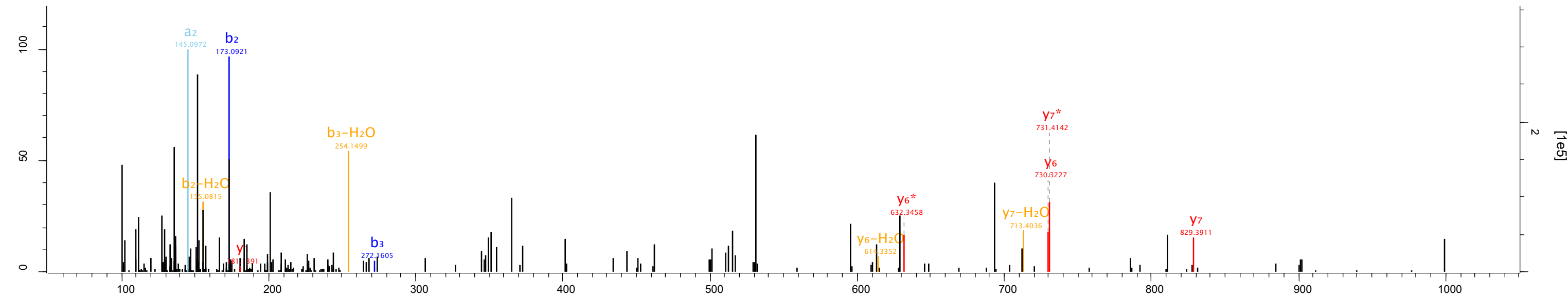
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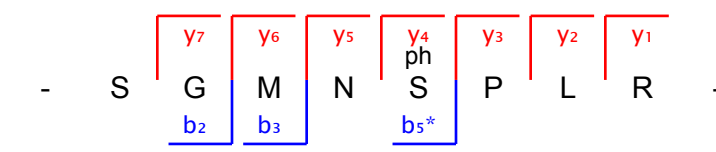
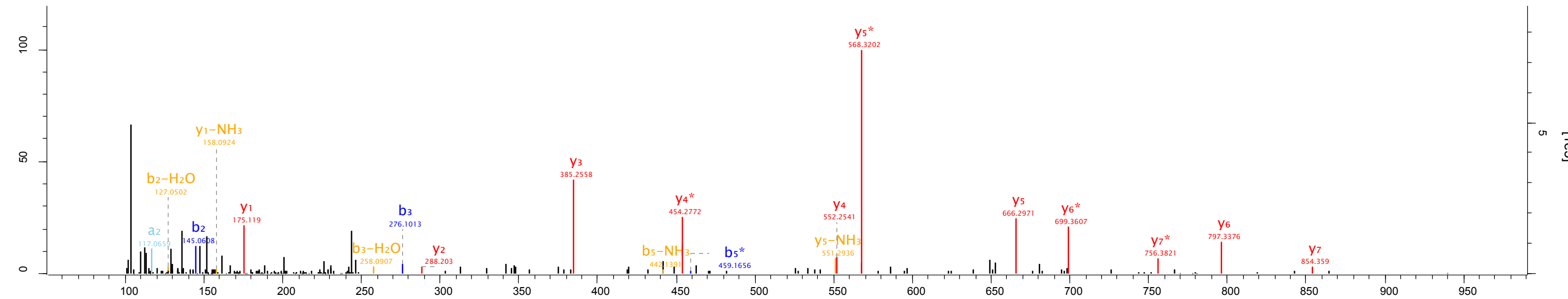
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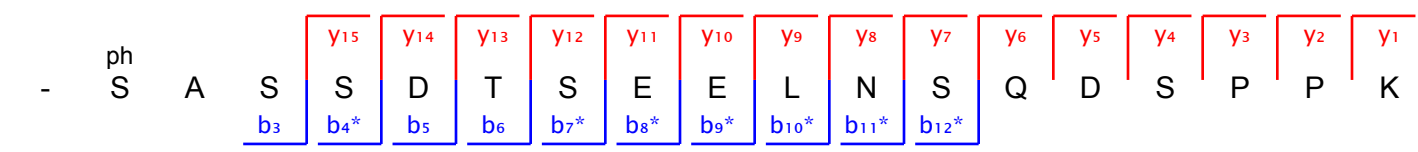
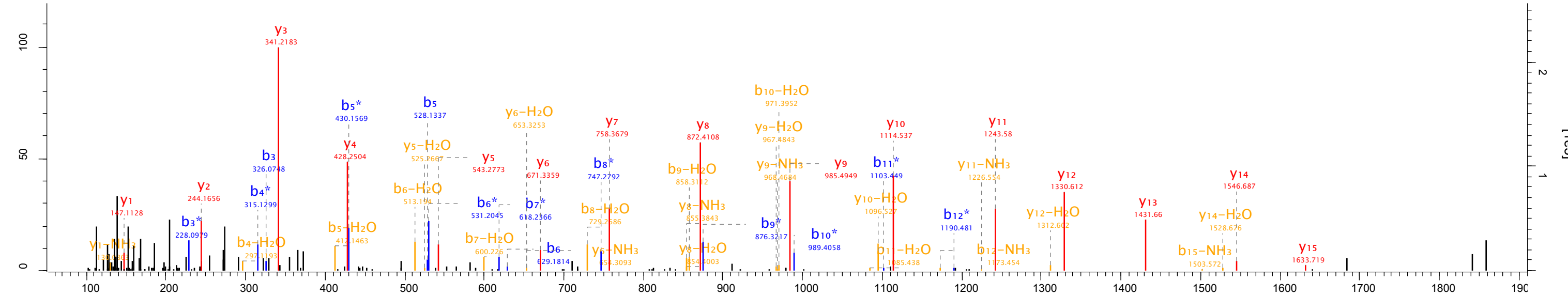


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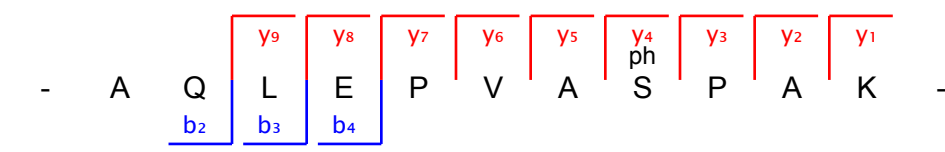
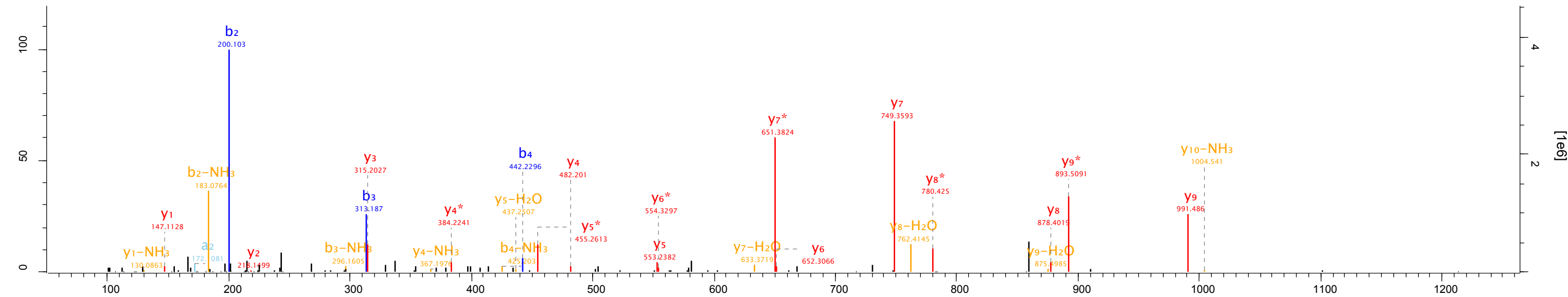


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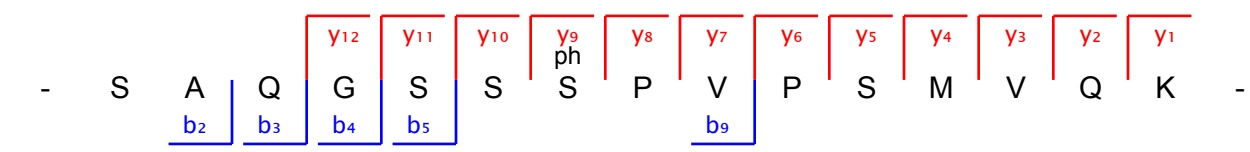
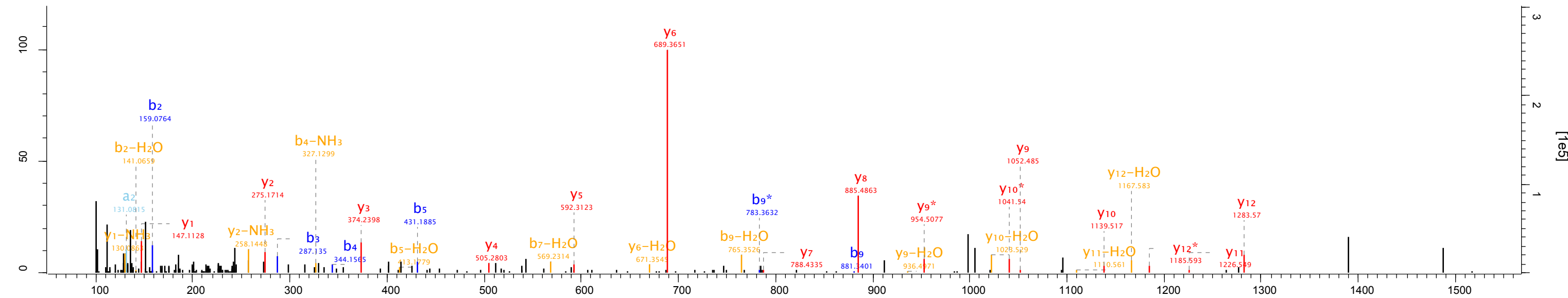


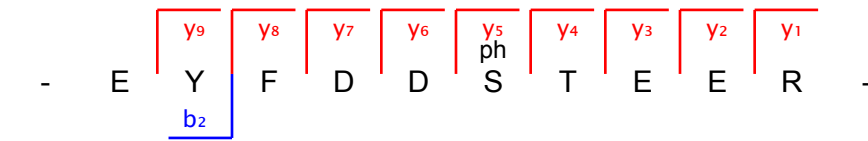
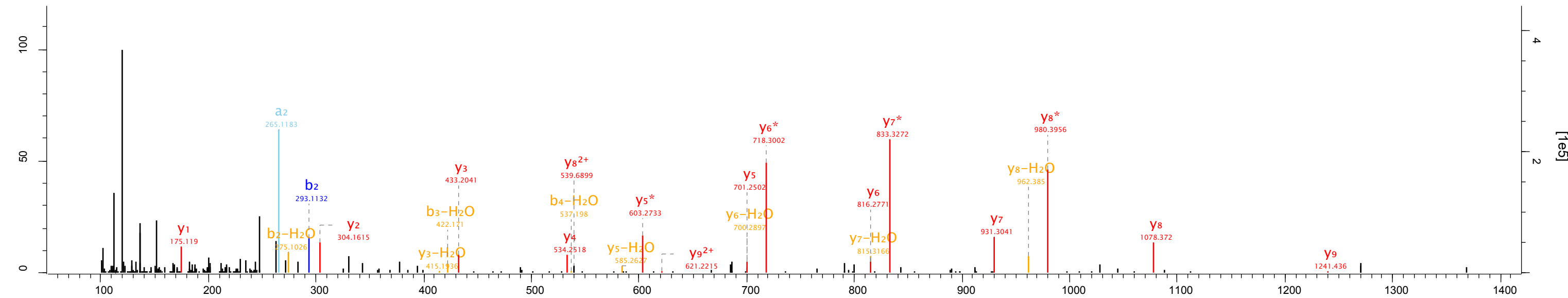


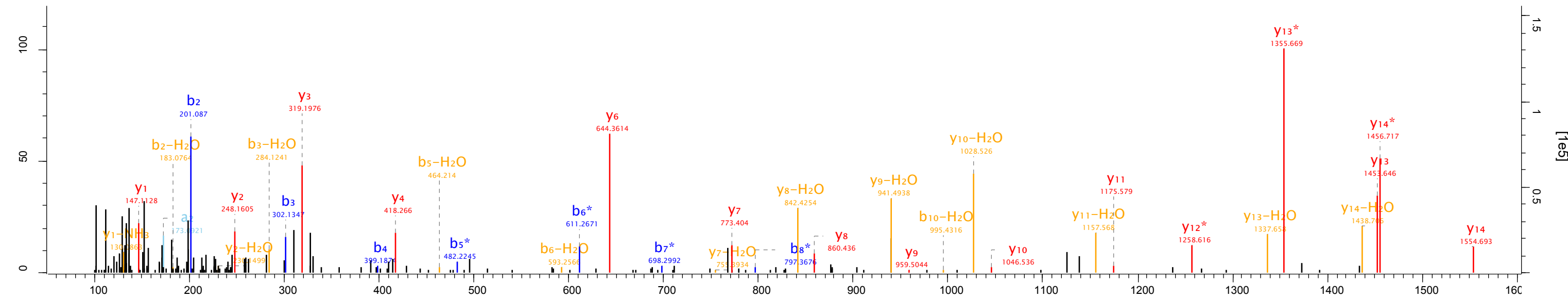
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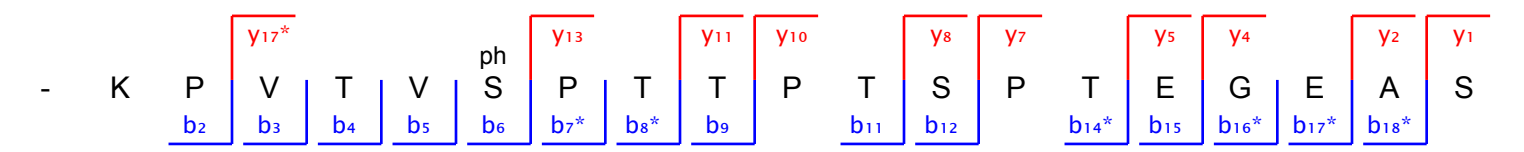
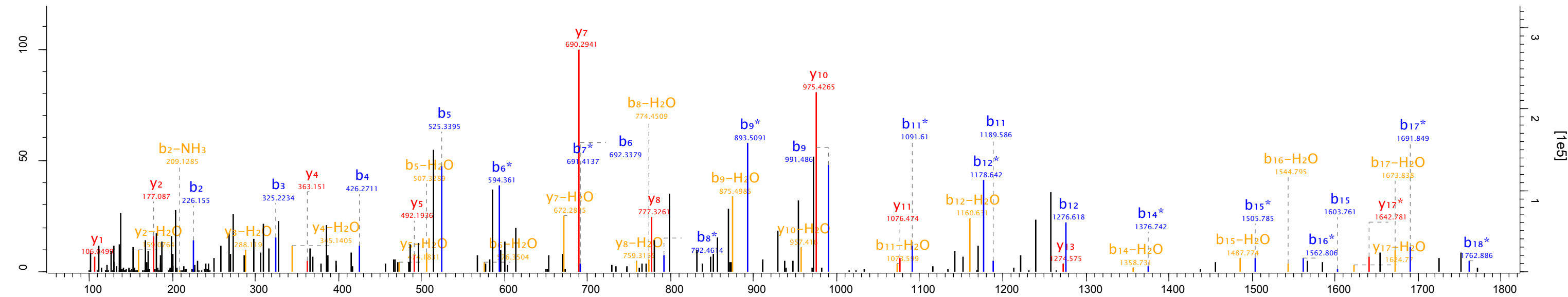
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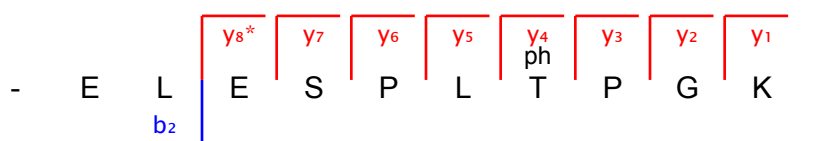
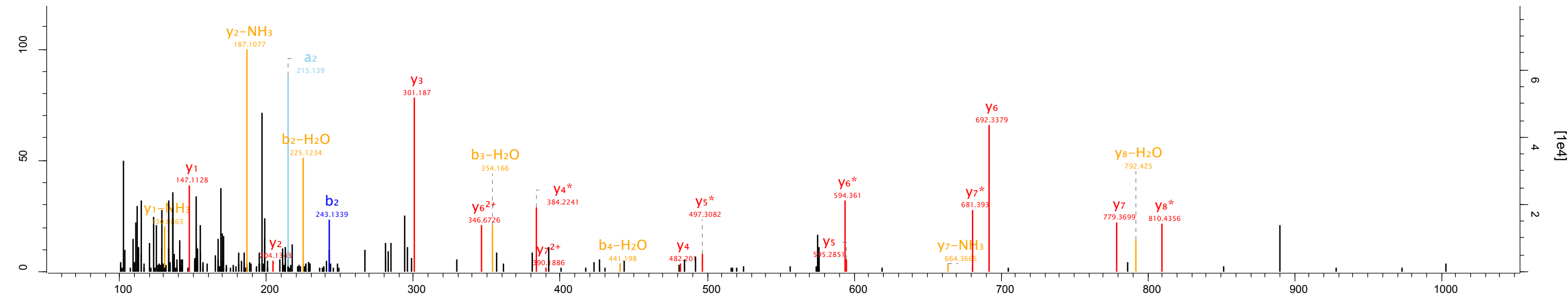
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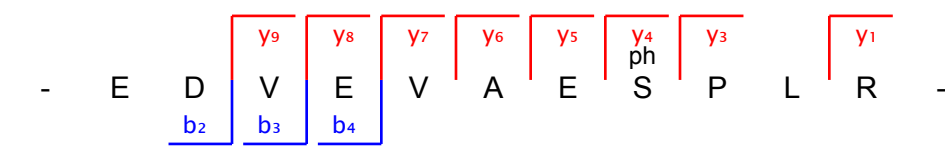
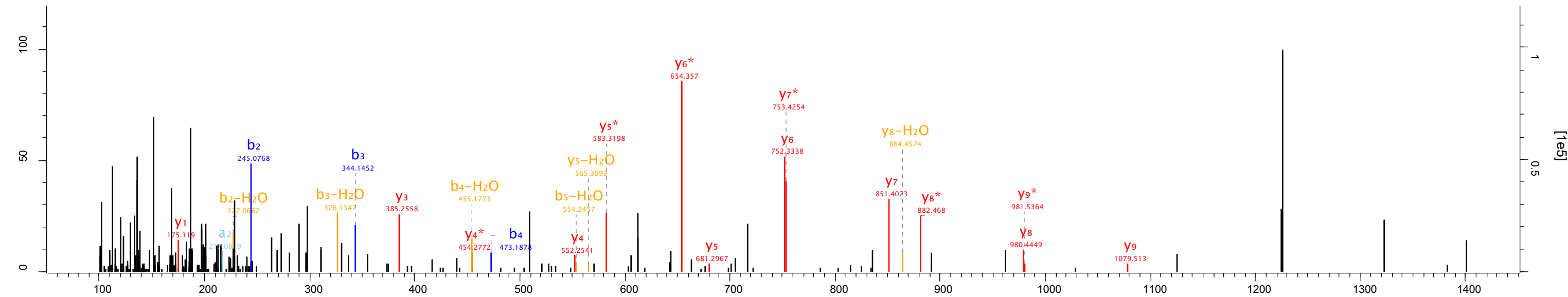
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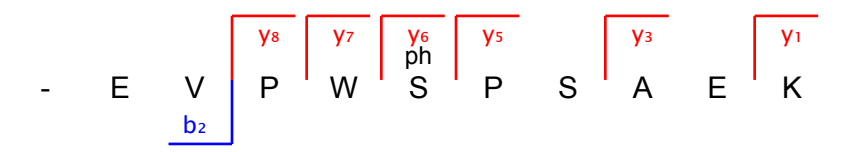
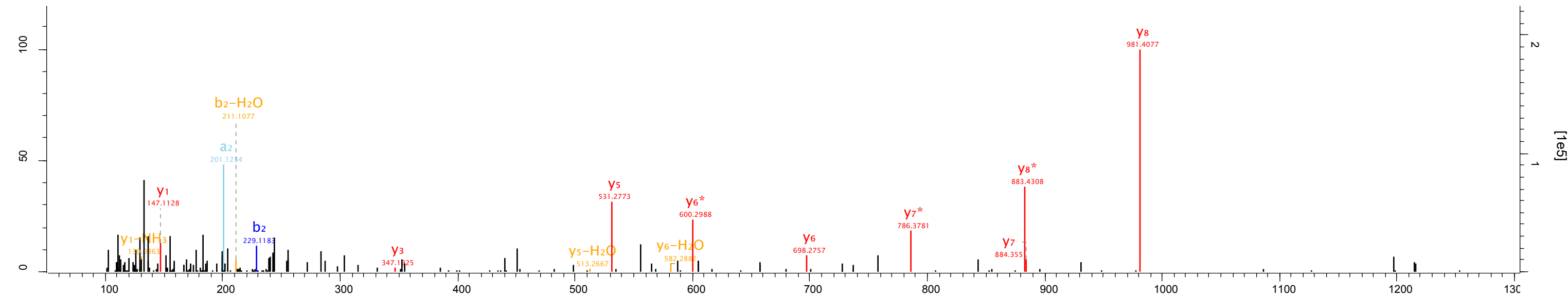
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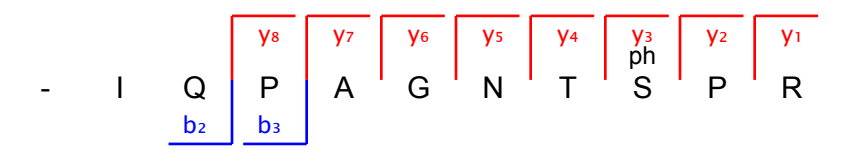
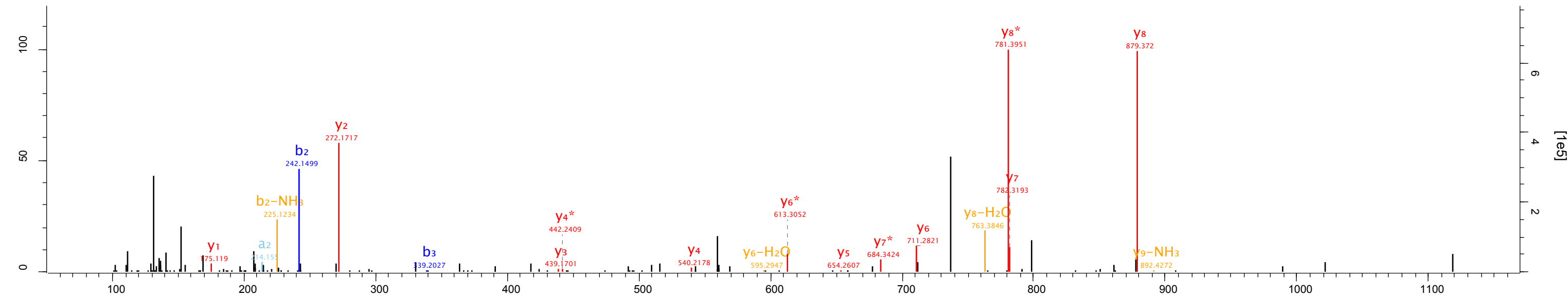
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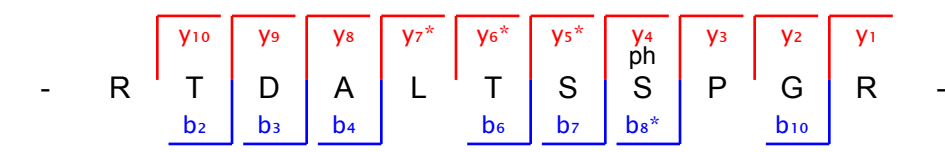
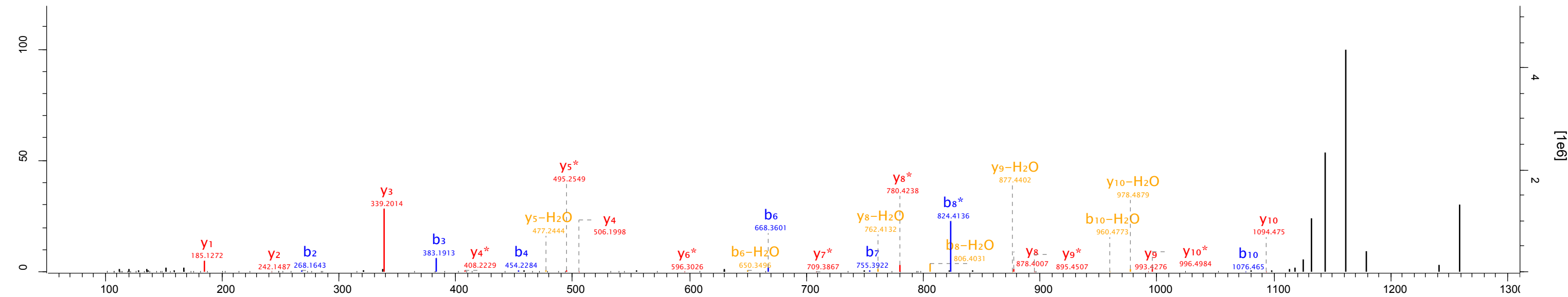
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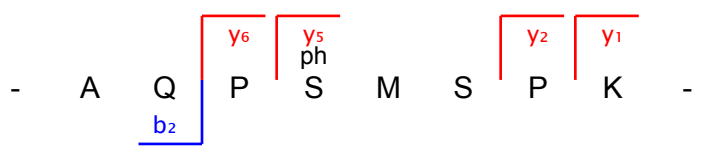
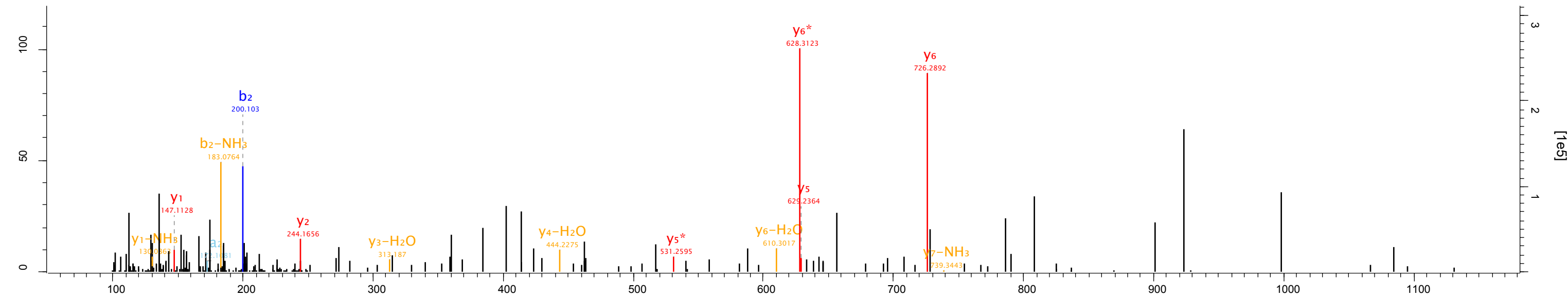
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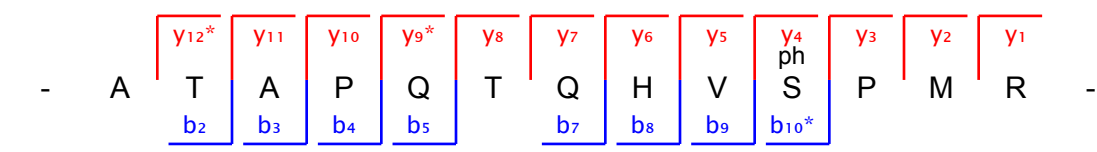
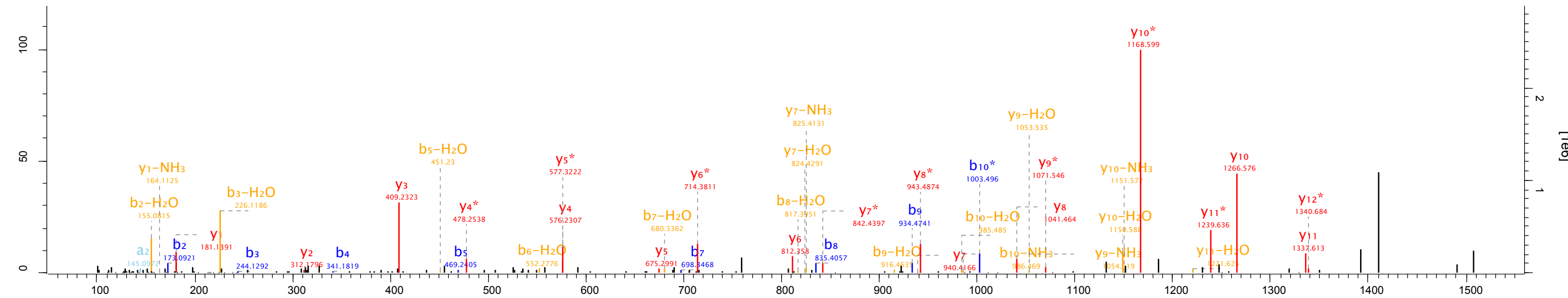
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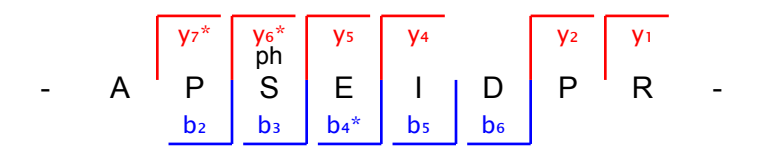
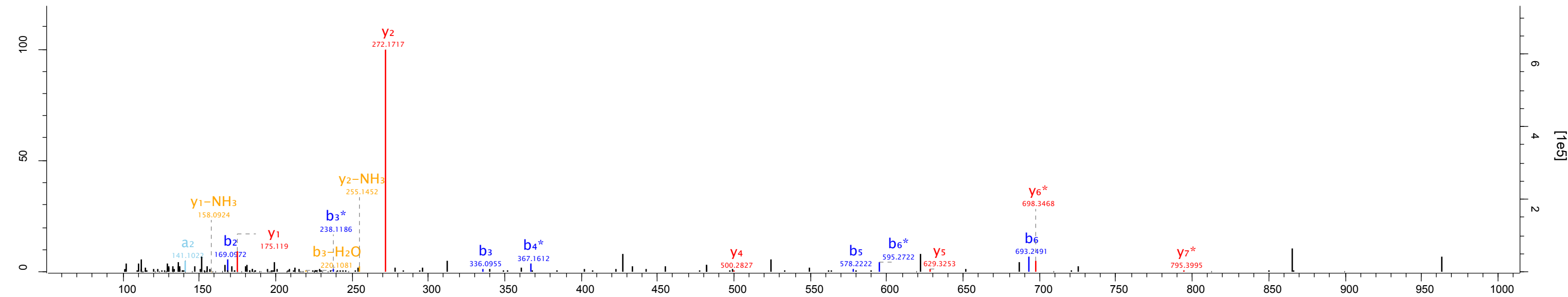
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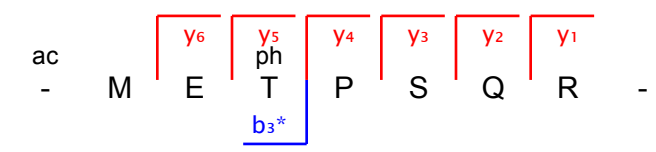
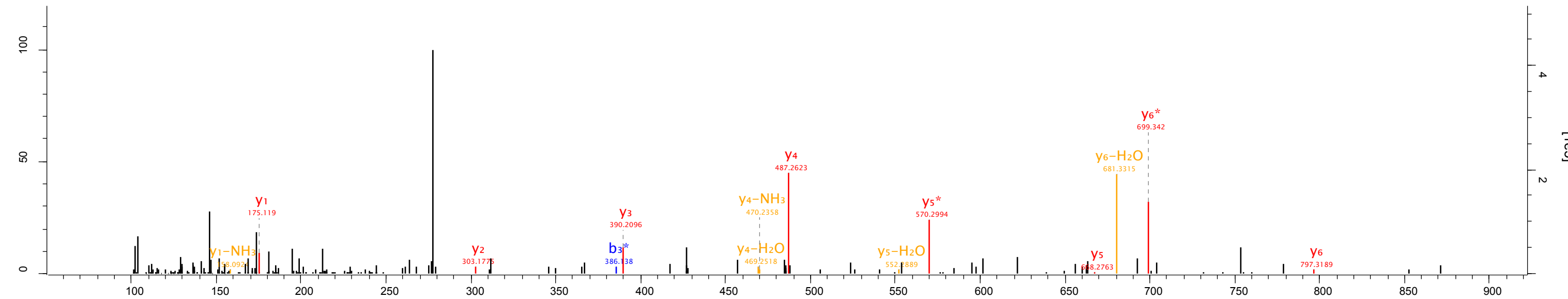
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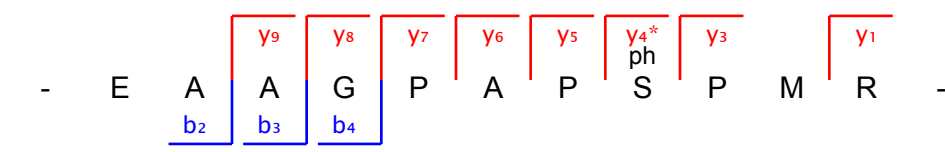
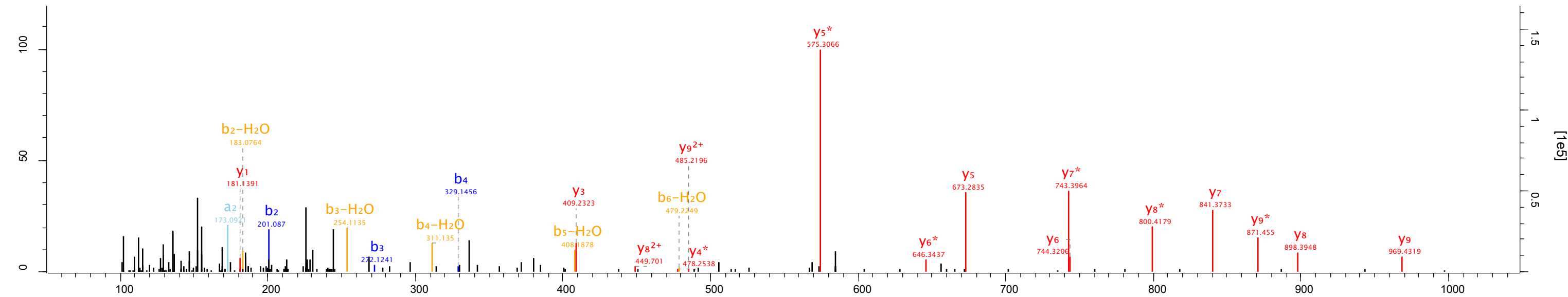
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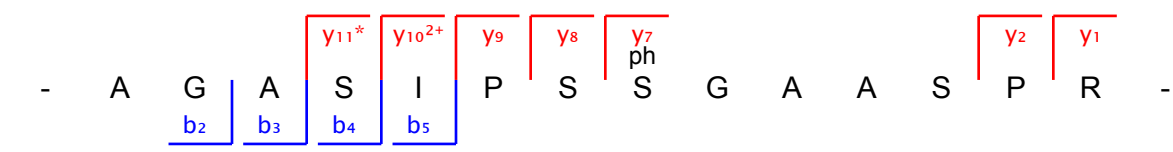
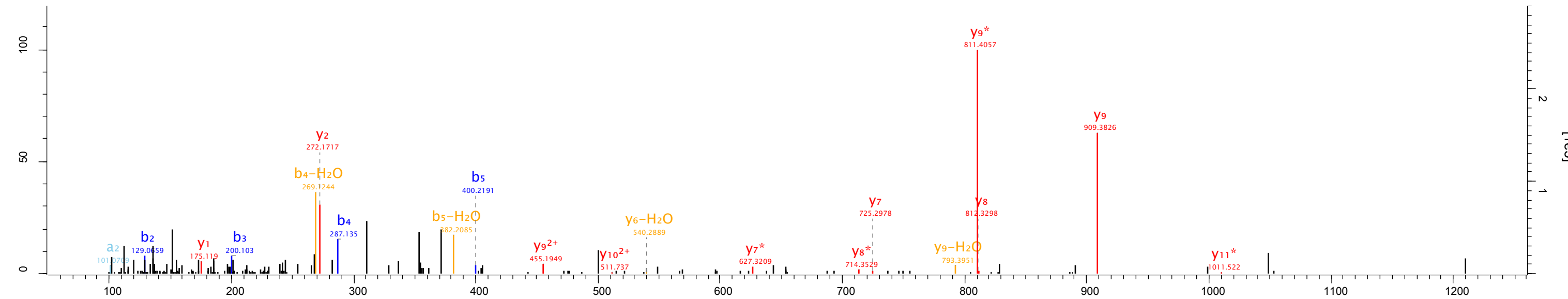
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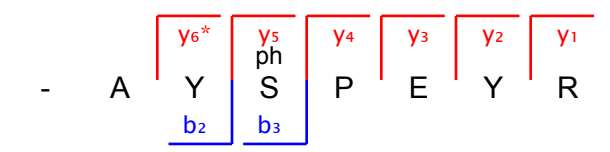
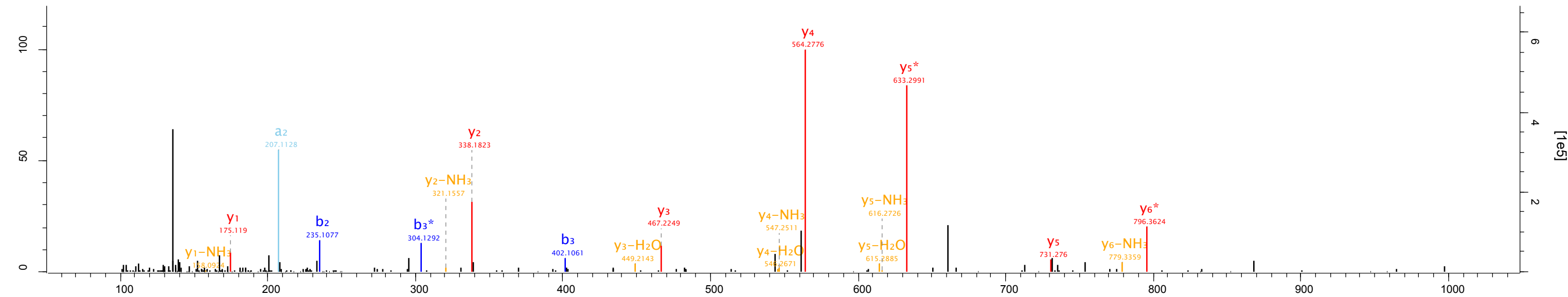
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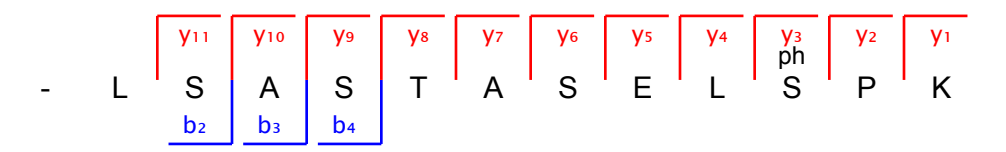
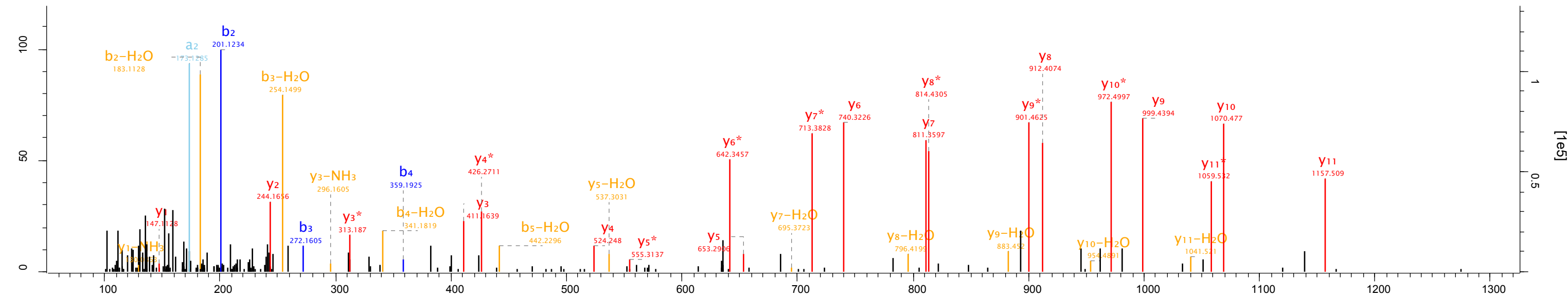
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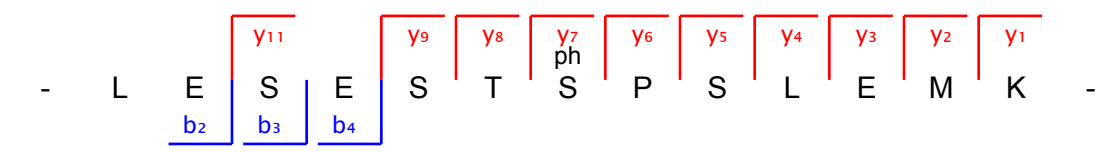
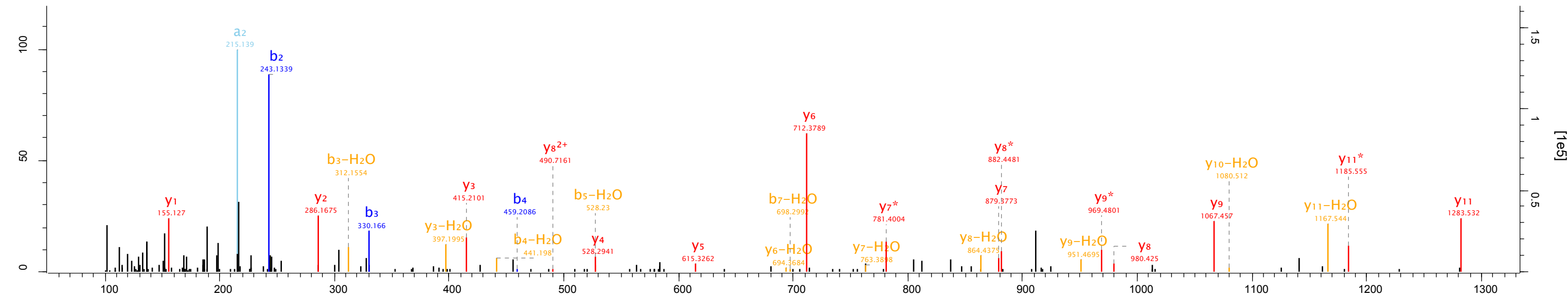
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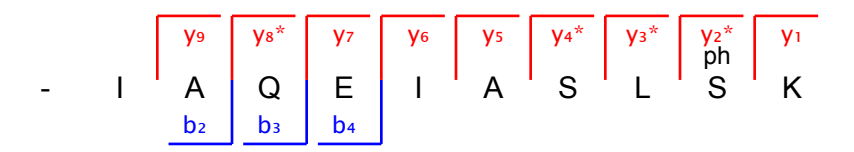
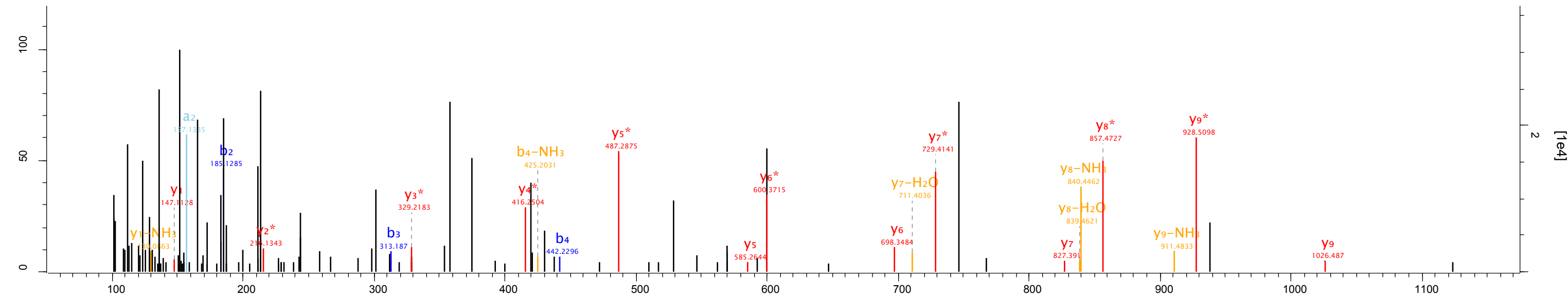
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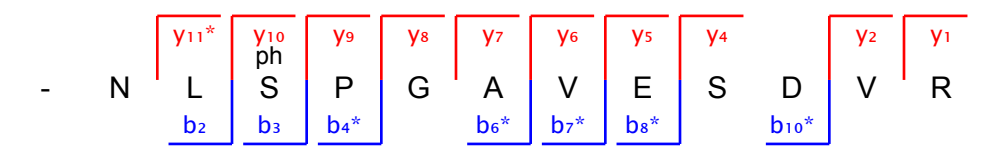
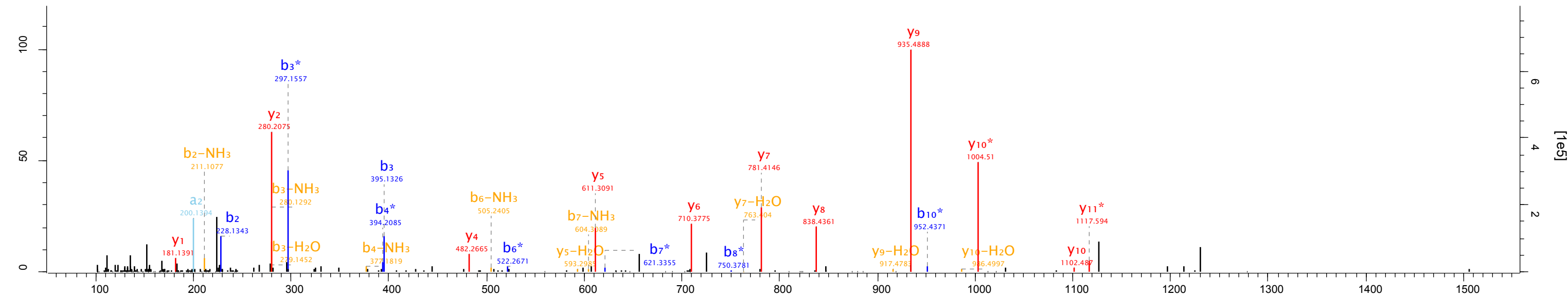
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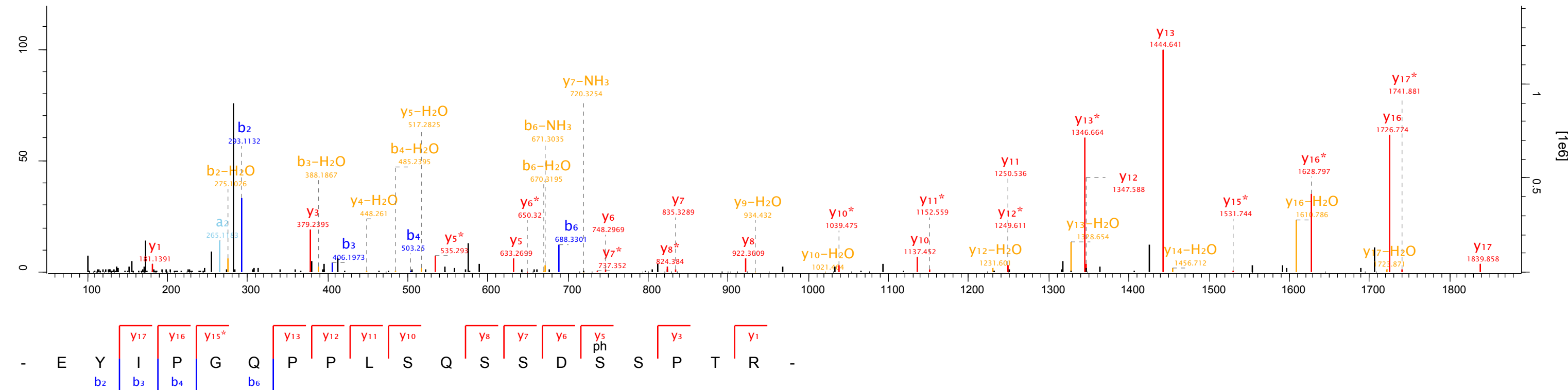


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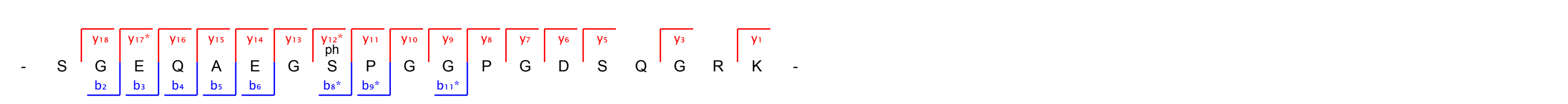
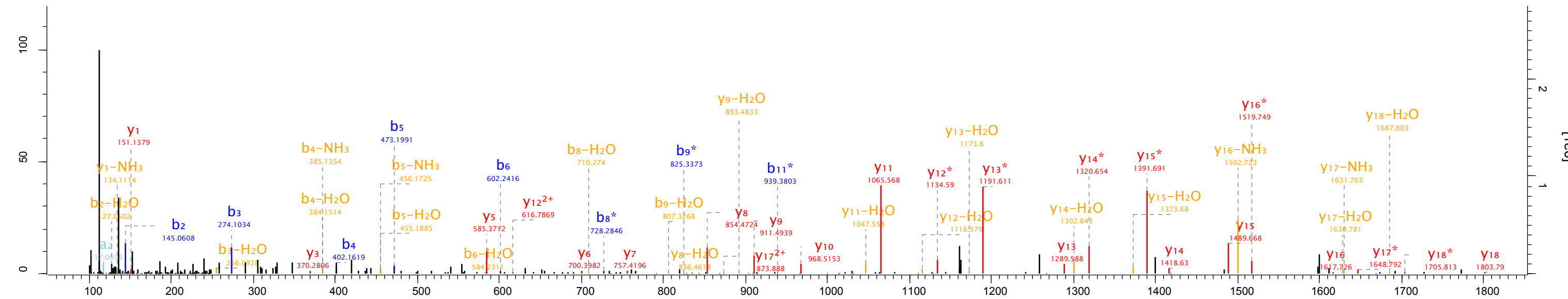


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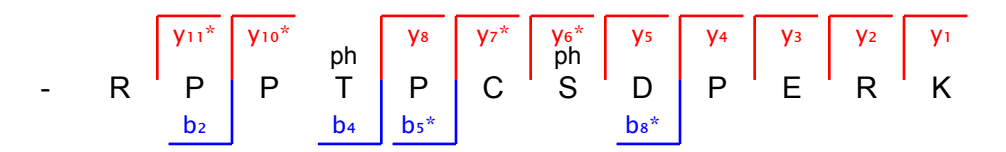
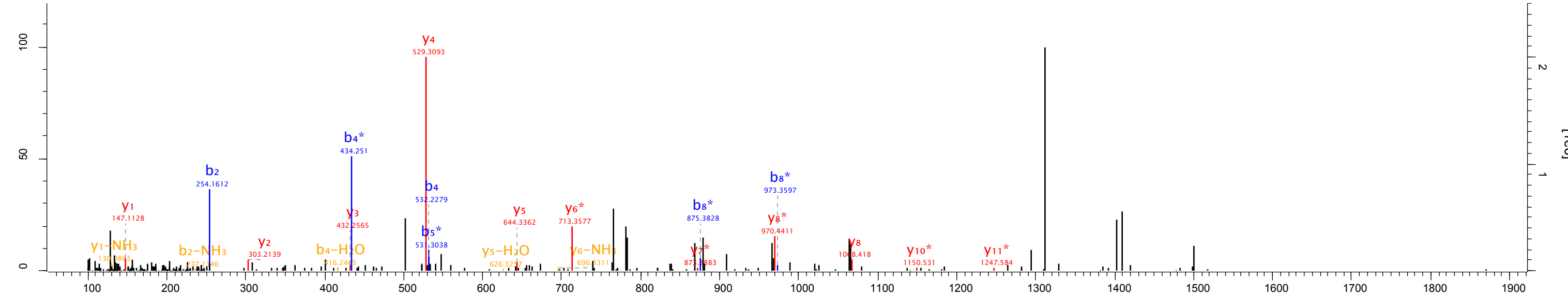




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 Scan: 1999 Method: FTMS; HCD Score: 154.92 m/z: 631.28 Gene names: CDKN1A



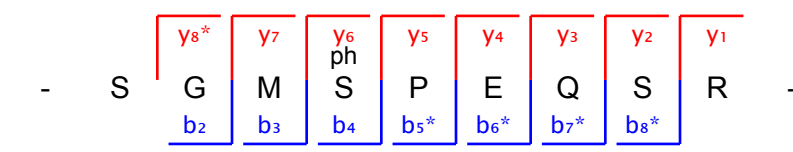
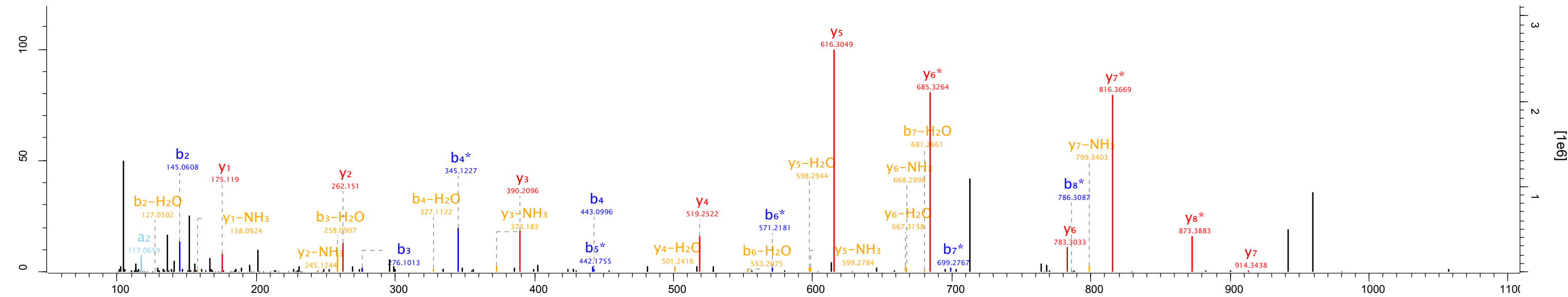
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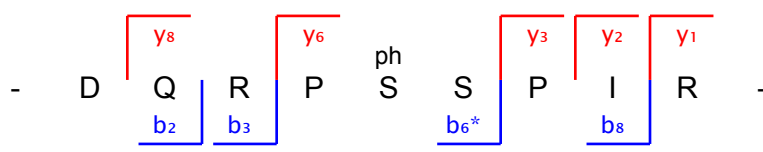
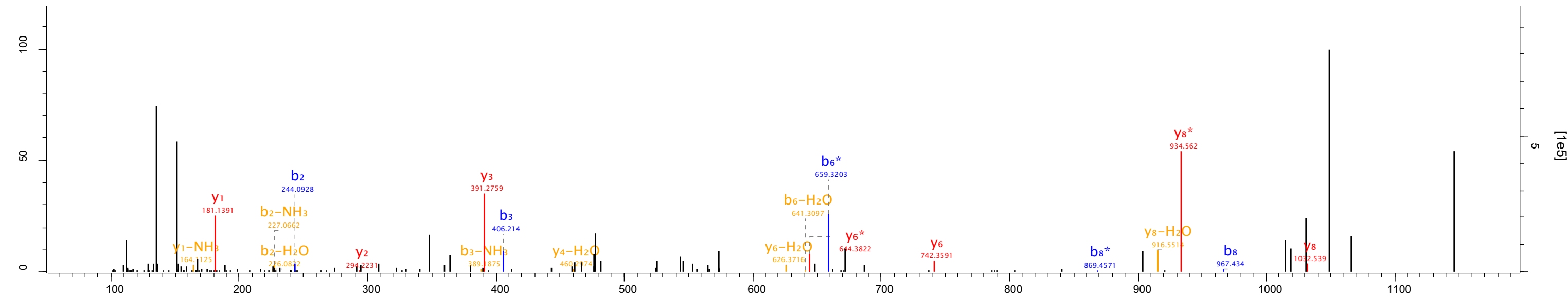
[1e6]

Raw file
20171215_MaS_33SR_LMH_phospho2_01

Scan 2659 Method FTMS; HCD Score 165.35 m/z 529.7 Gene names SRRM2

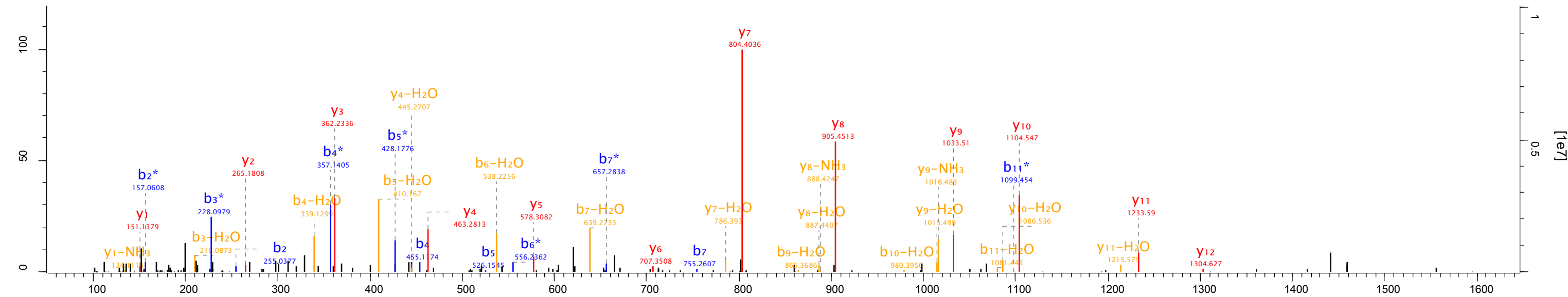


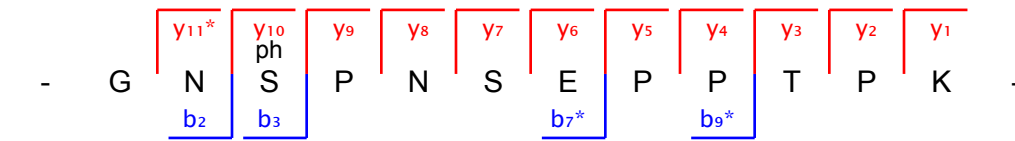
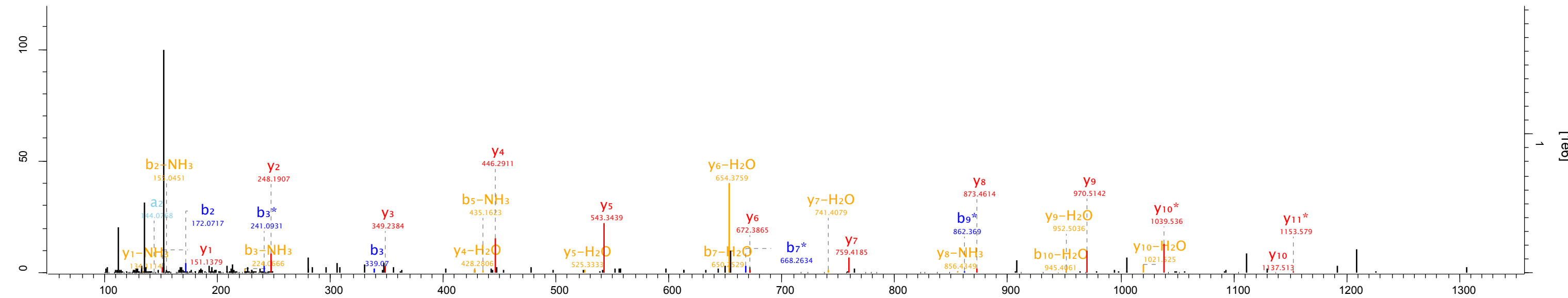
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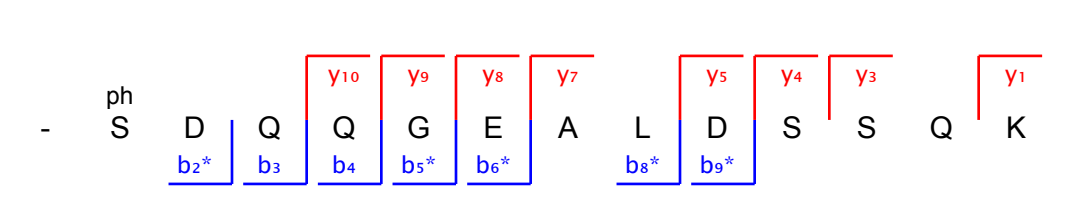
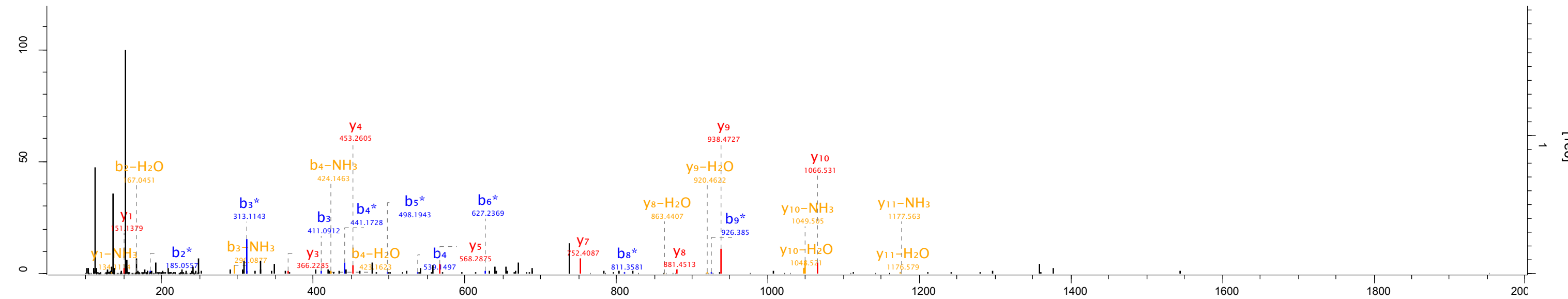
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20171215_MaS_33SR_LMH_phospho2_01

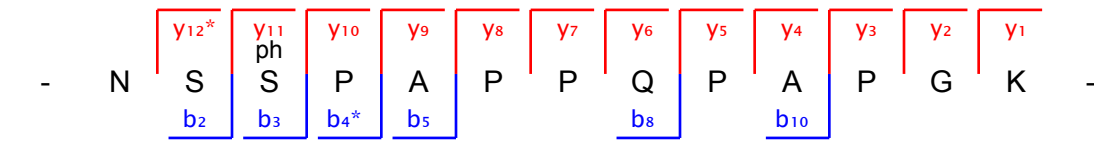
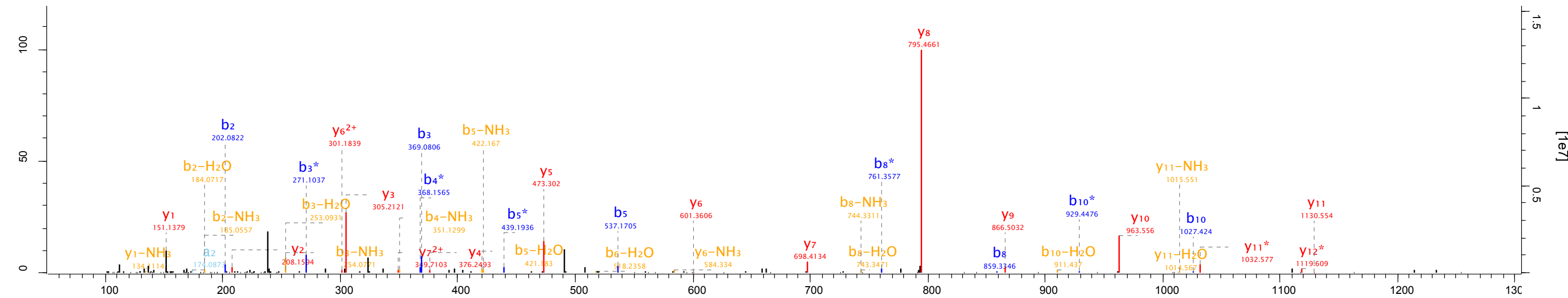
Scan Method Score m/z Gene names
2969 FTMS; HCD 148.44 779.83 TGOLN2

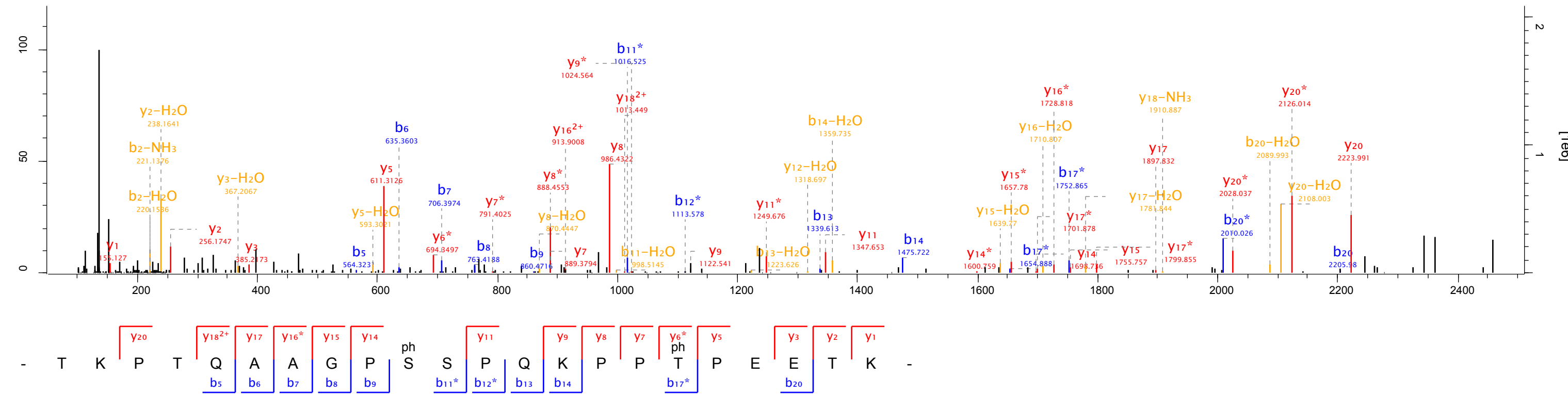




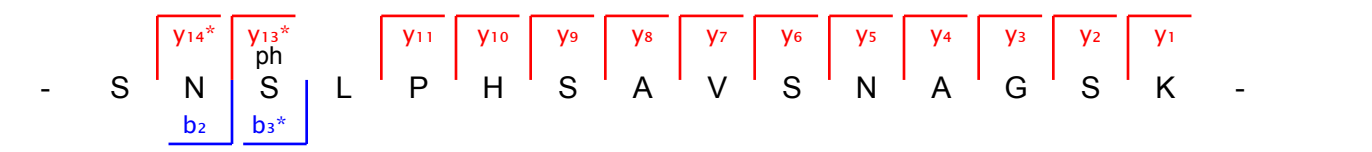
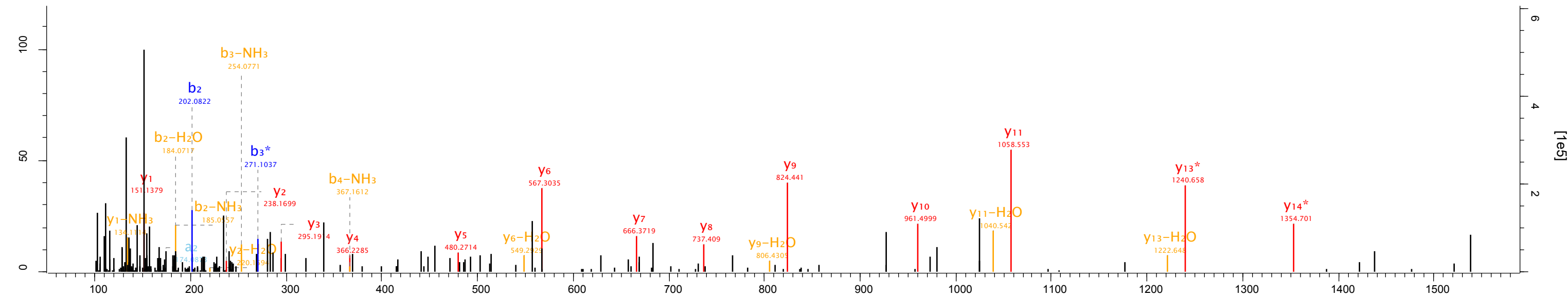
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 Scan: 3309 Method: FTMS; HCD Score: 45.82 m/z: 738.81 Gene names: LRRFIP1

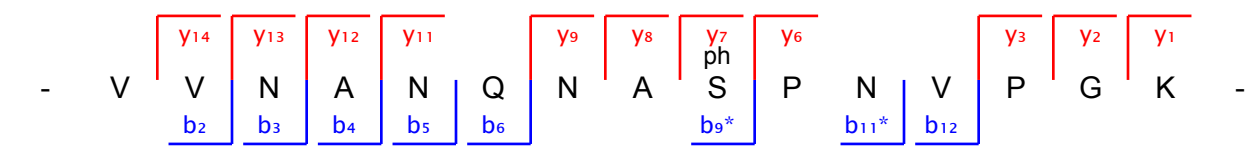
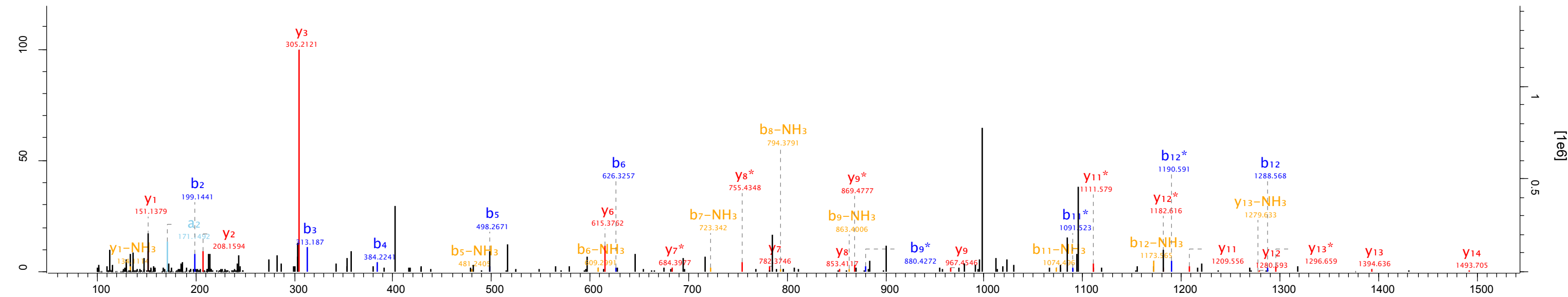




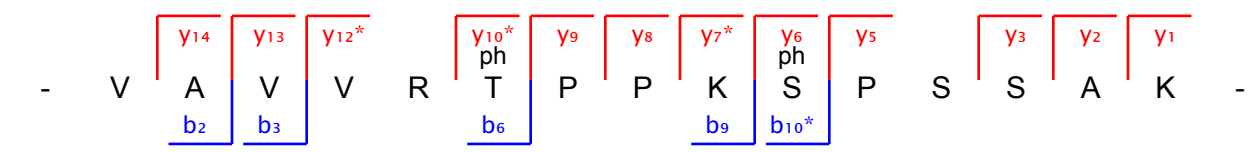
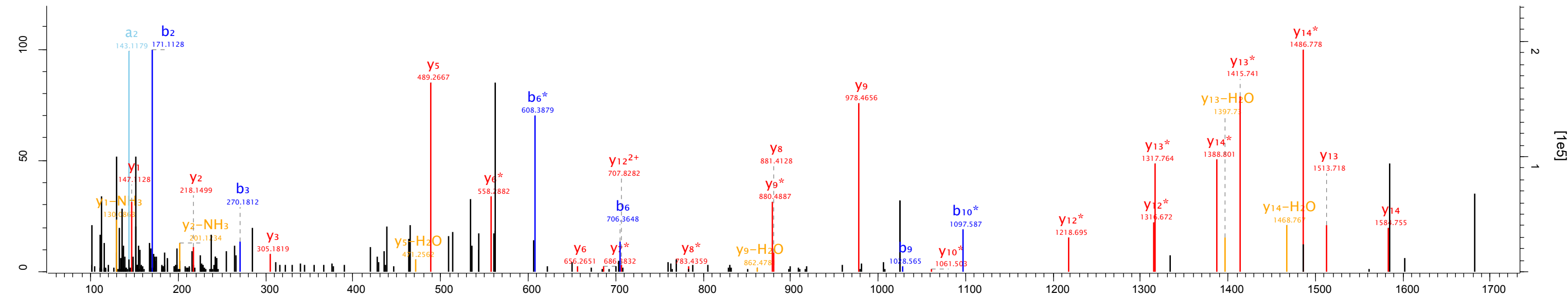


Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 4239 Method FTMS; HCD Score 63.3 m/z 513.91 Gene names WDR20

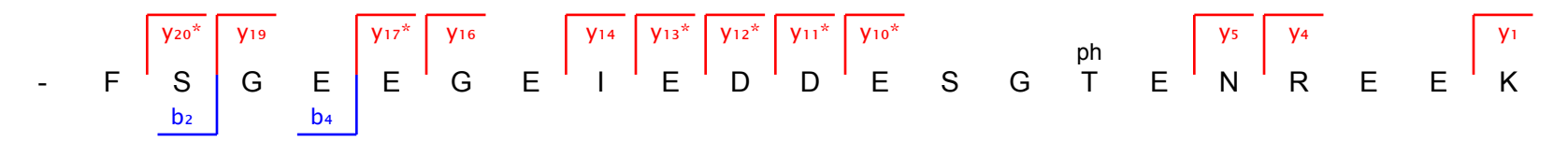
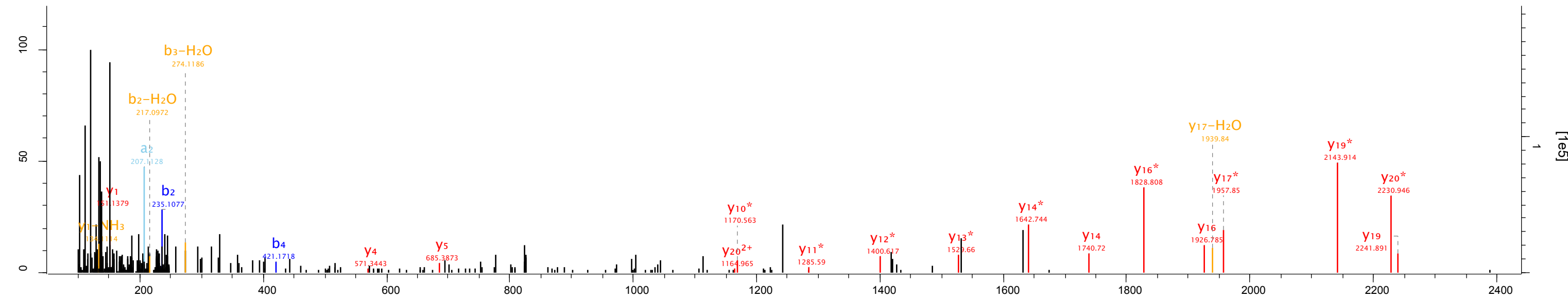


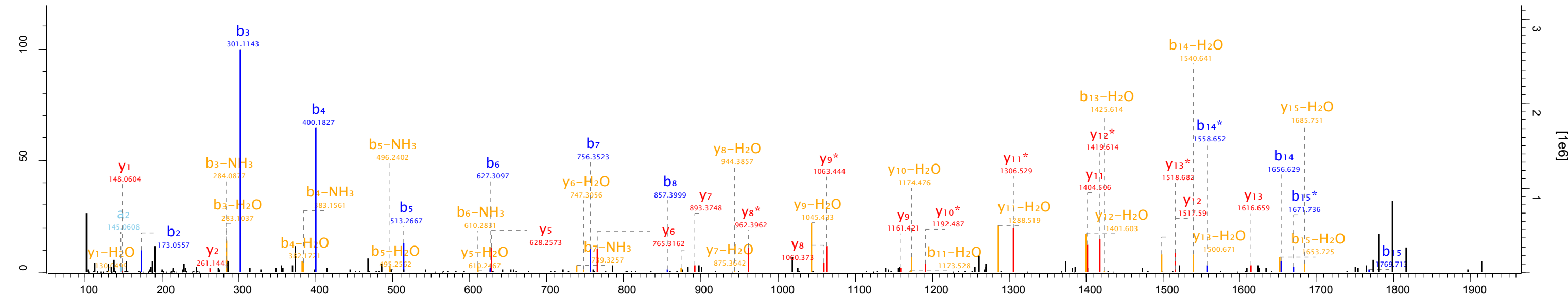


Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 4519 Method FTMS; HCD Score 98.96 m/z 562.28 Gene names MAPT



Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 6329 Method FTMS; HCD Score 45.49 m/z 826 Gene names THRAP3



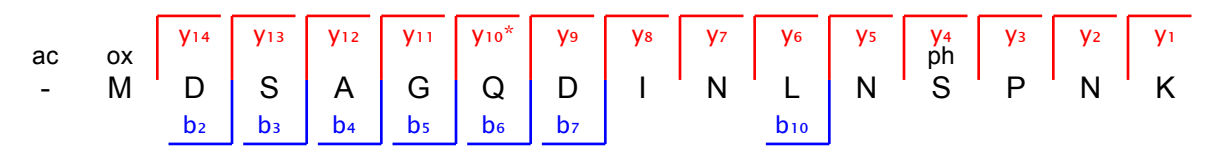
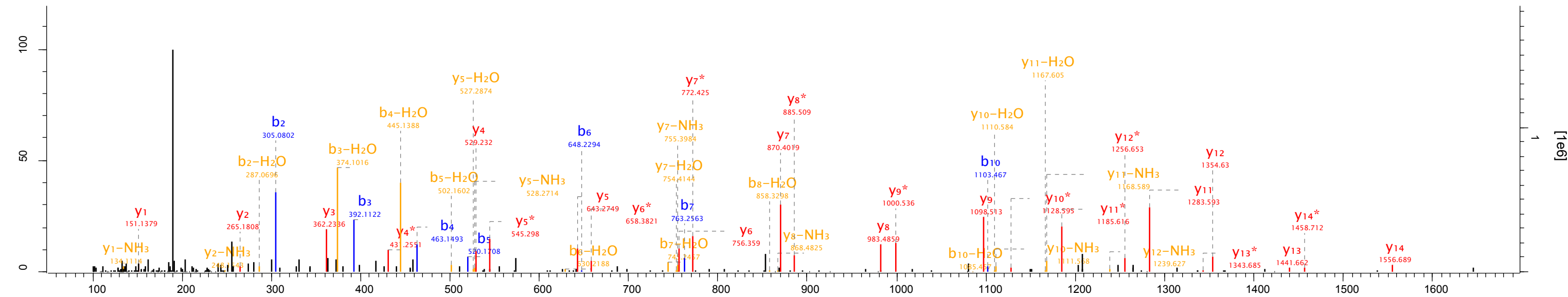


- D G Q V I N E T S_{ph} Q H H D D L E -

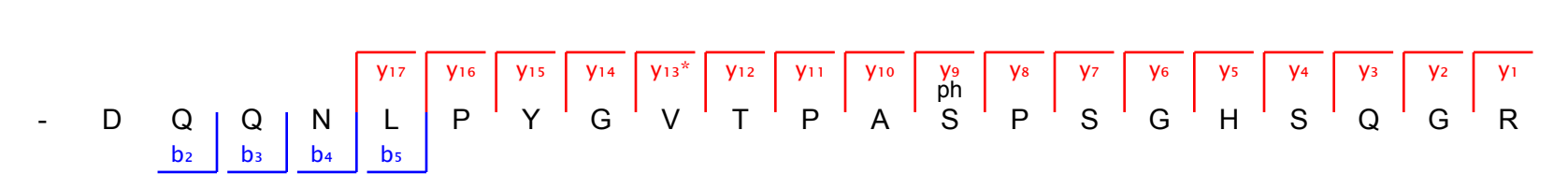
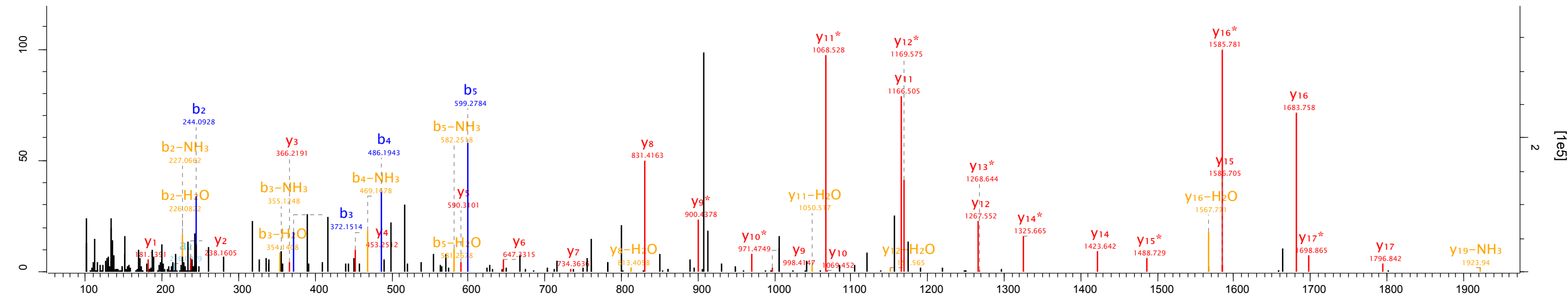
Fragmentation mapping (b and y ions) is shown below the sequence:

- b₂ (under G)
- b₃ (under Q)
- b₄ (under V)
- b₅ (under I)
- b₆ (under N)
- b₇ (under E)
- b₈ (under T)
- b₁₄ (under D)
- b₁₅ (under L)
- y₁ (under E)
- y₅ (under H)
- y₆ (under H)
- y₇ (under Q)
- y₈ (under S_{ph})
- y₉ (under T)
- y₁₀^{*} (under E)
- y₁₁ (under N)
- y₁₂ (under I)
- y₁₃ (under V)
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Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 8649 Method FTMS; HCD Score 261.16 m/z 873.37 Gene names TPD52L2

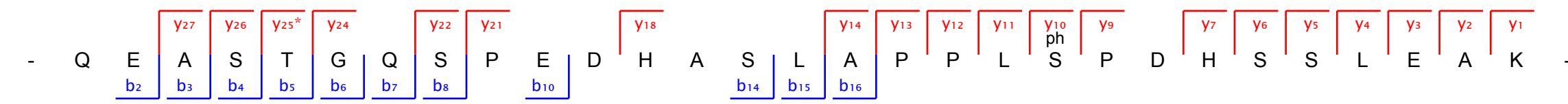
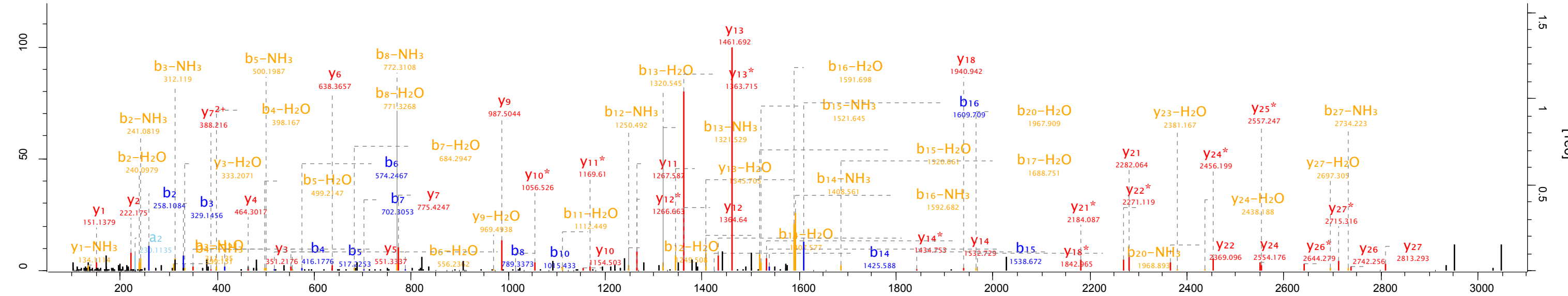


Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 8739 Method FTMS; HCD Score 105.58 m/z 761.68 Gene names MARK2

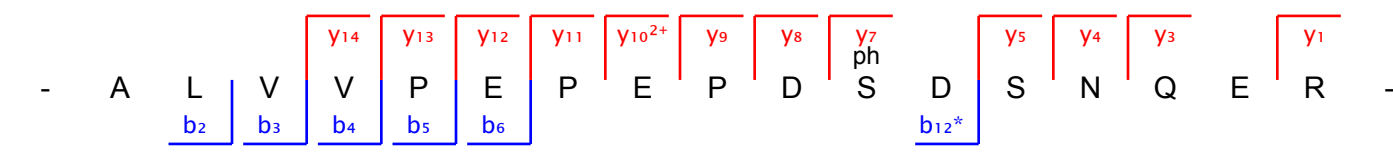
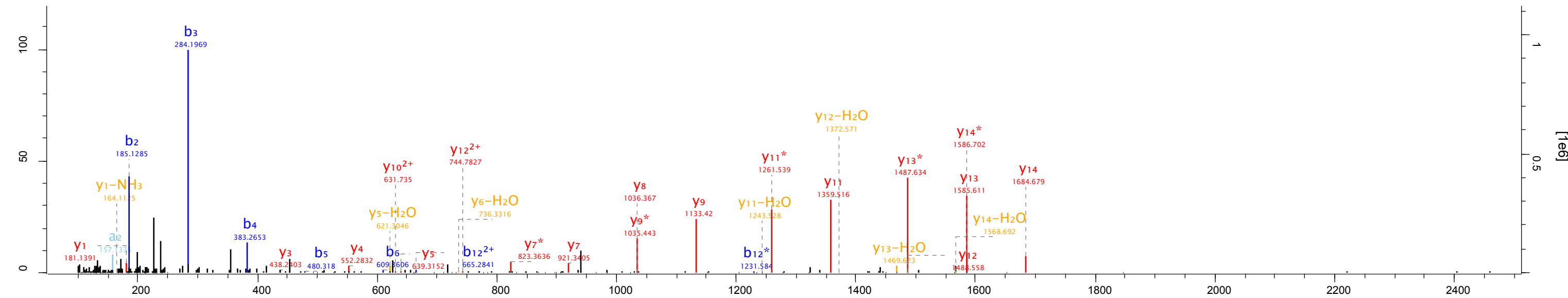


Raw file
20171215_MaS_33SR_LMH_phospho2_02

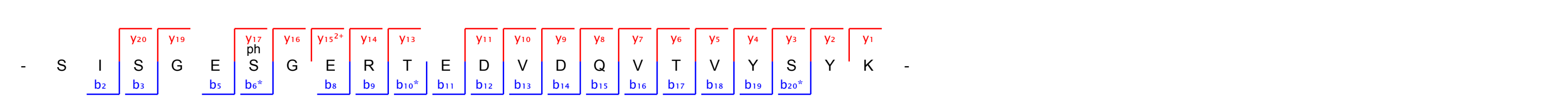
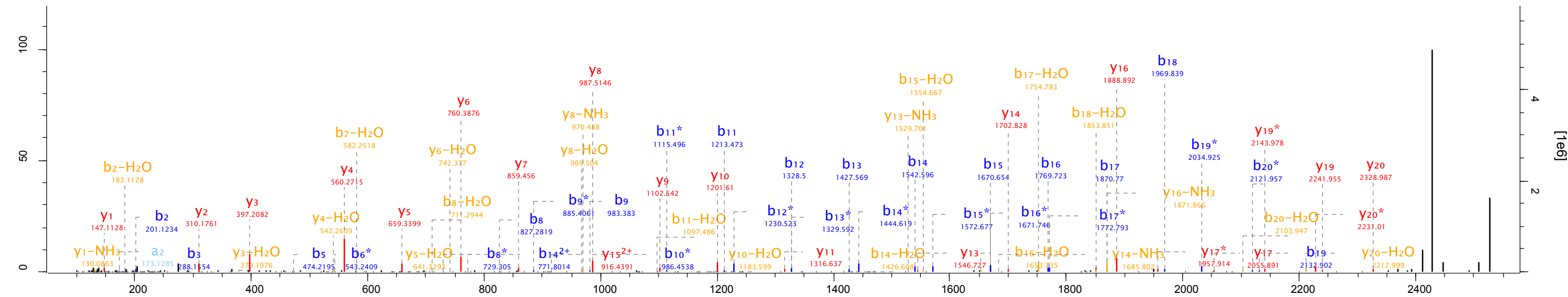
Scan Method Score m/z Gene names
10589 FTMS; HCD 179.55 1024.47 NES



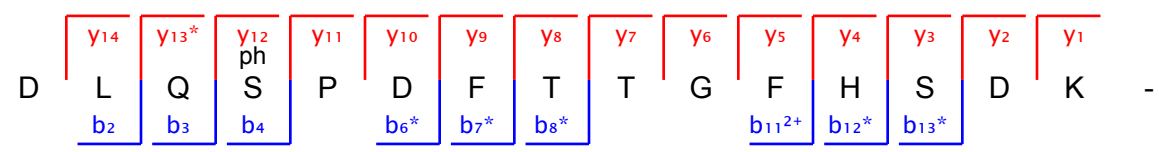
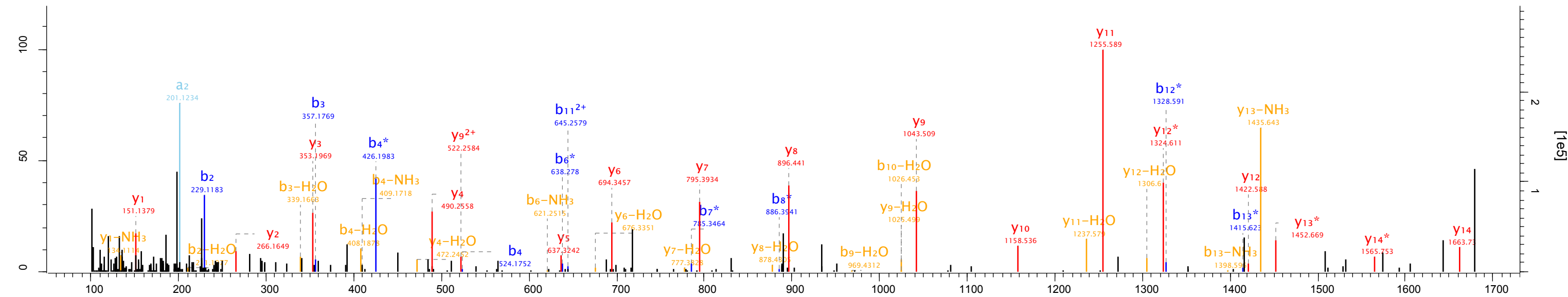
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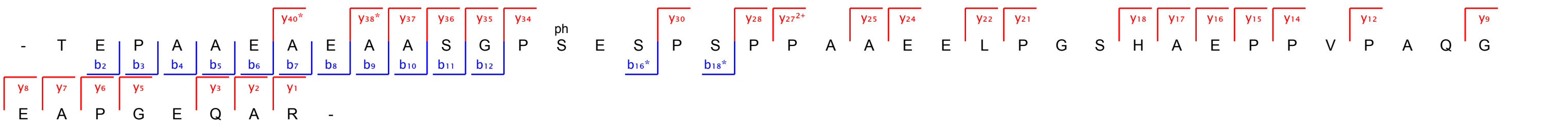
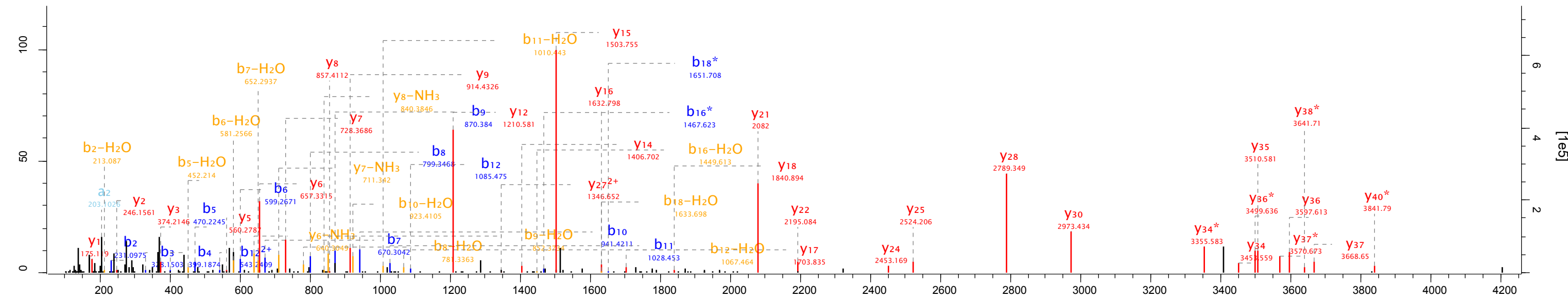
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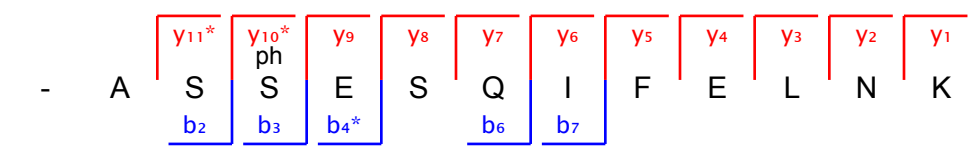
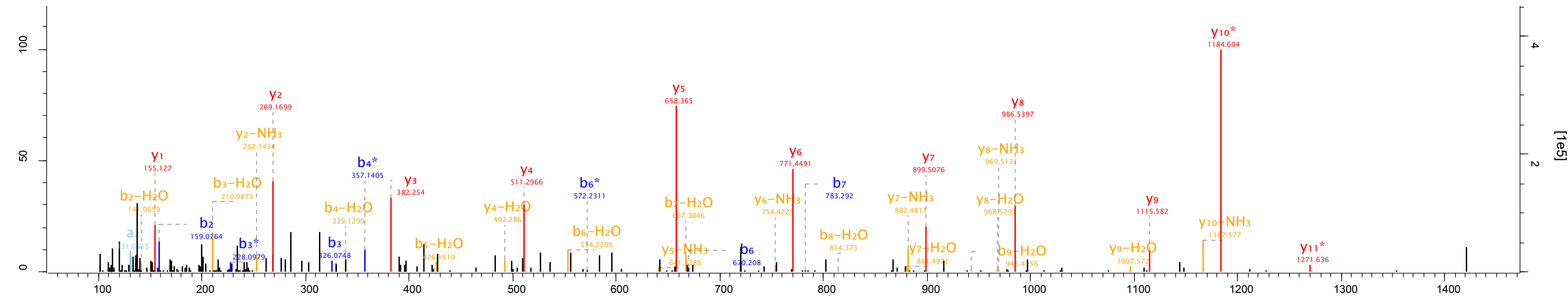
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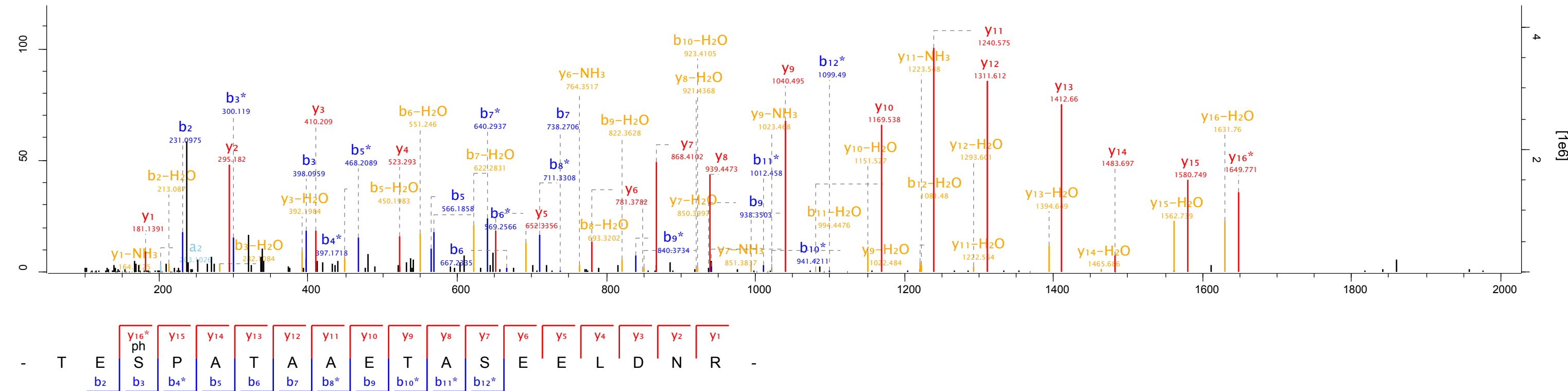


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 Scan: 12249 Method: FTMS; HCD Score: 143.75 m/z: 1513.68 Gene names: EIF3B

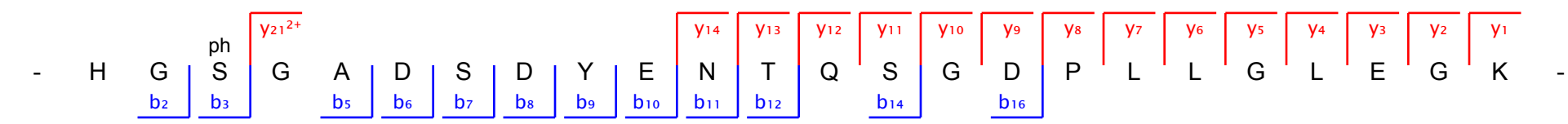
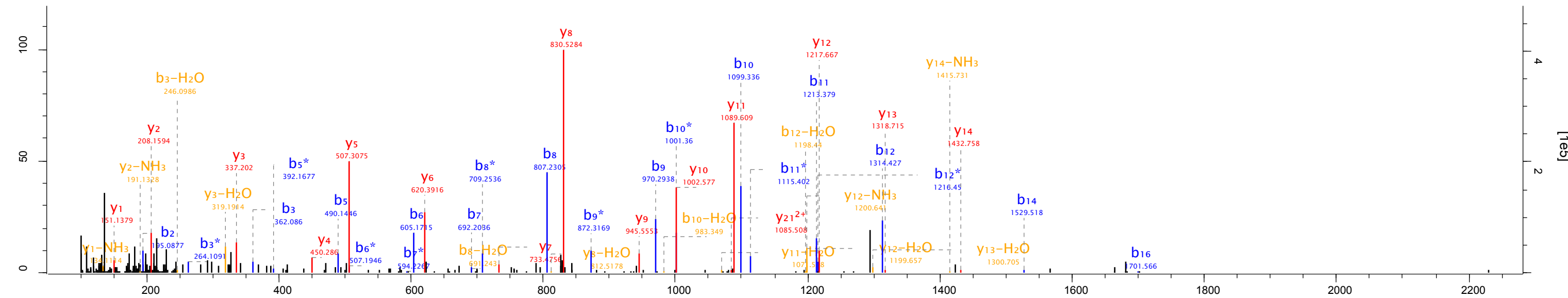


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 12849 Method FTMS; HCD Score 125.36 m/z 720.83 Gene names MLPH

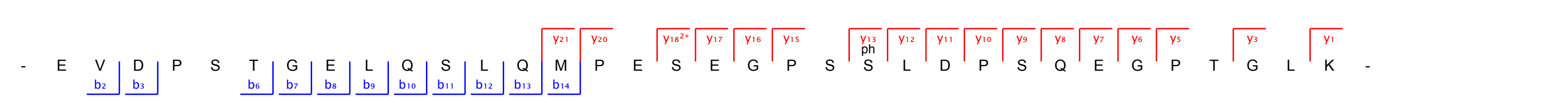
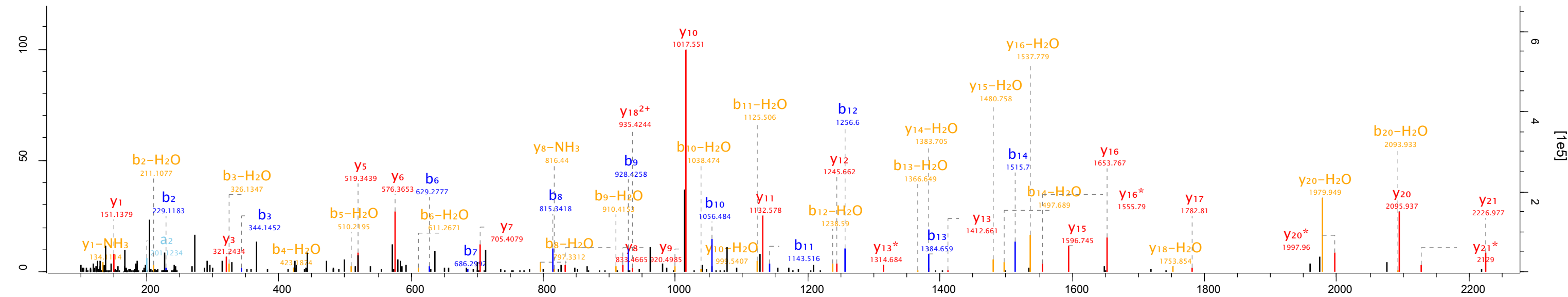




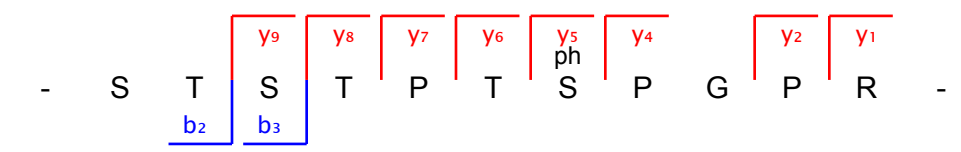
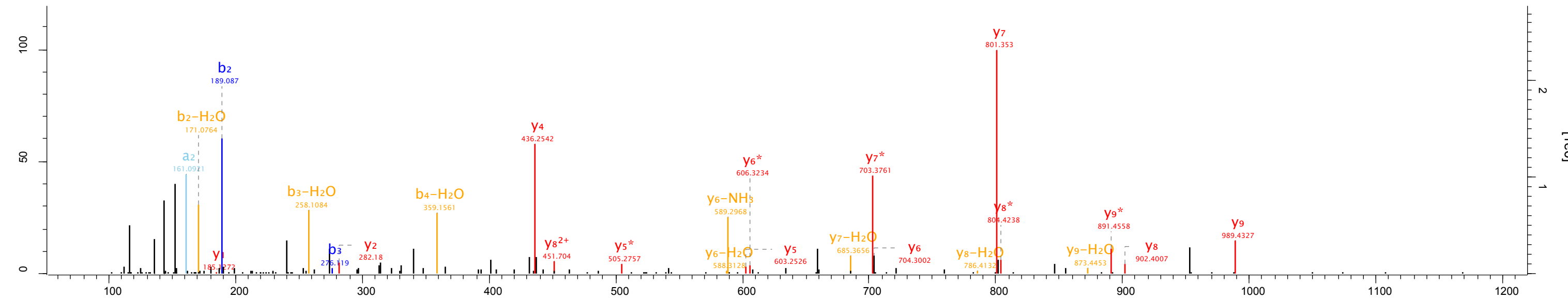
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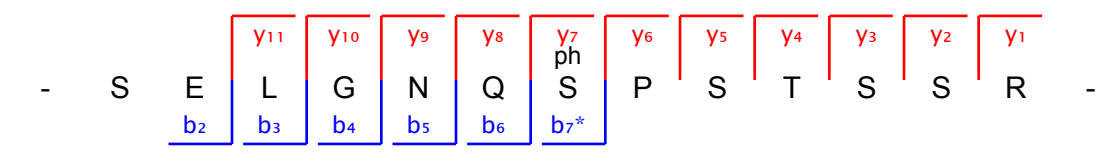
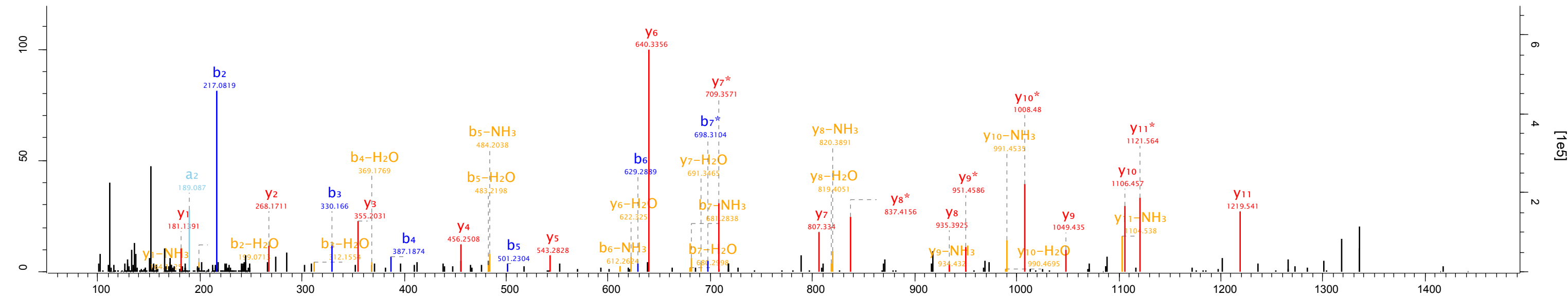
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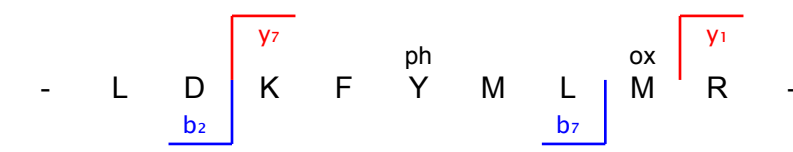
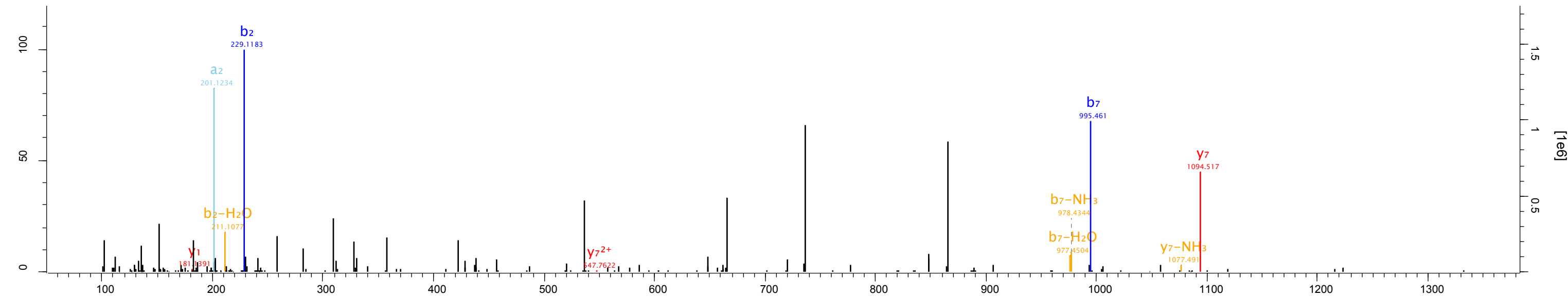
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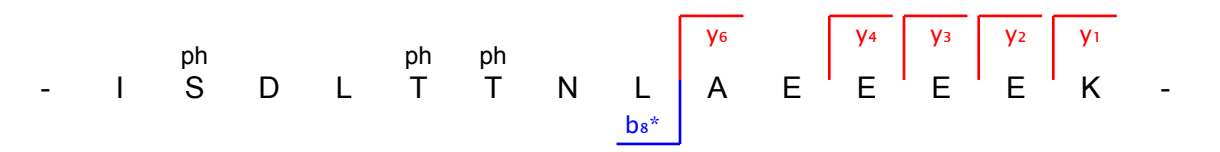
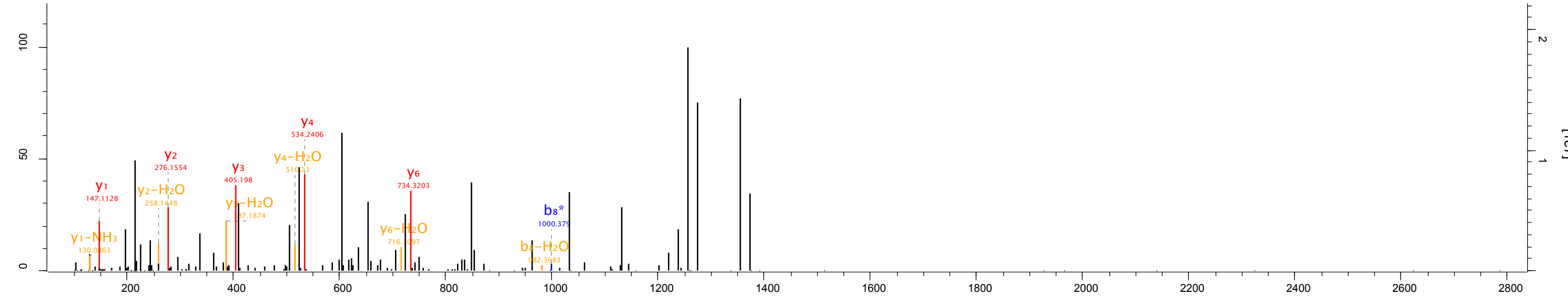
Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3379 Method FTMS; HCD Score 208.66 m/z 718.31 Gene names TOR1AIP1

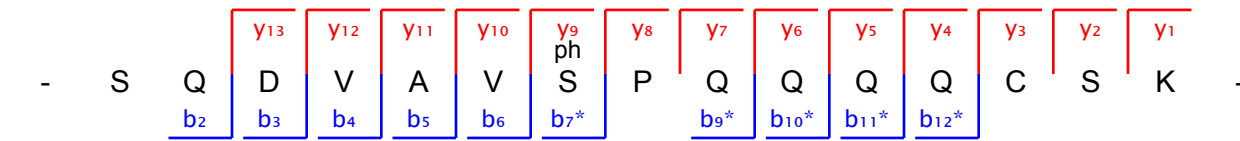
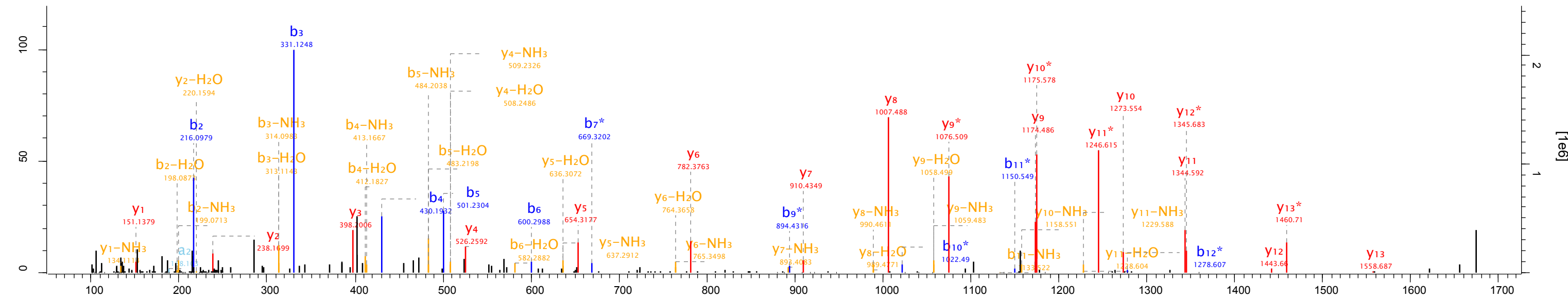


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3519 Method FTMS; HCD Score 50.04 m/z 661.82 Gene names RRP1



20171215_MaS_33SR_LMH_phospho2_02 3629 FTMS; HCD 45.28 916.33 MYH11

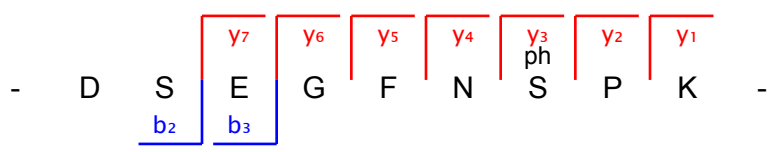
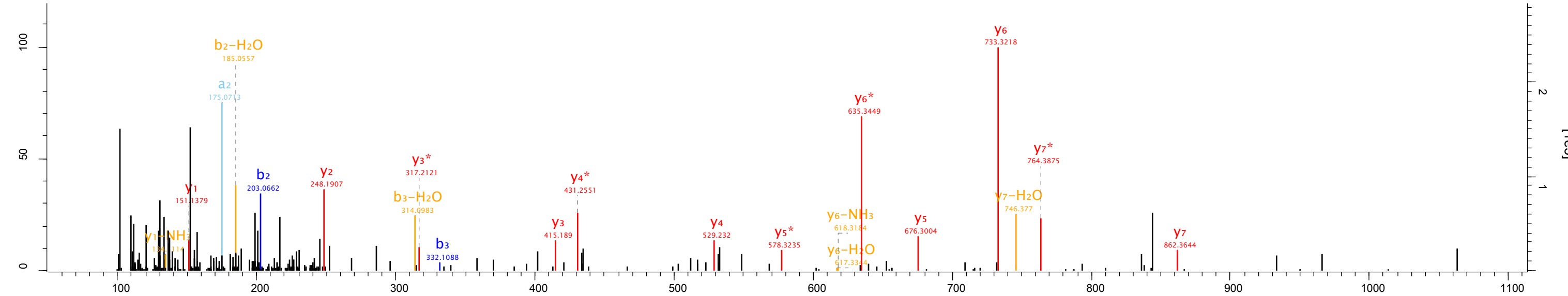




Raw file

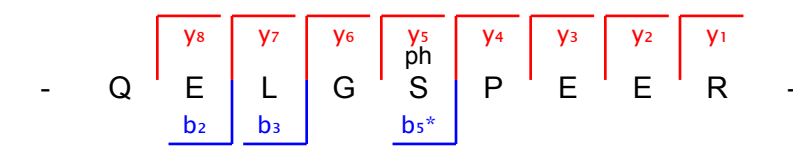
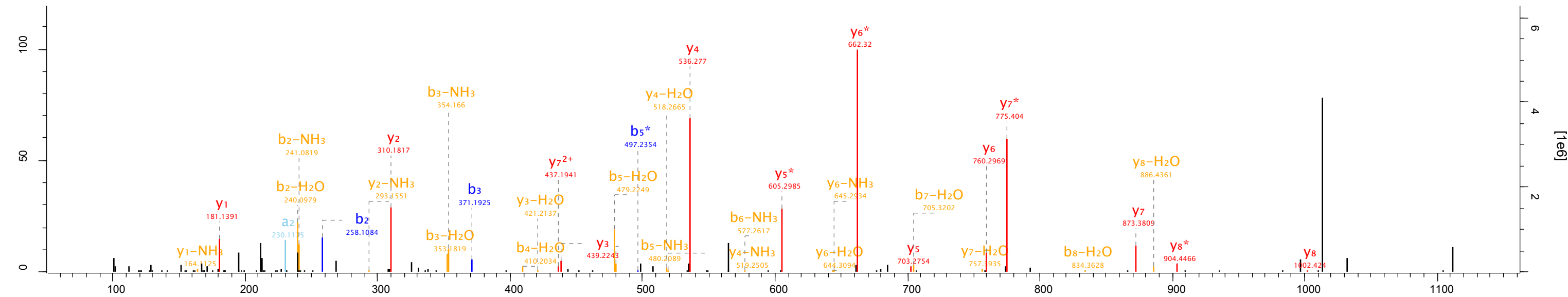
20171215_MaS_33SR_LMH_phospho2_02

Scan	Method	Score	m/z	Gene names
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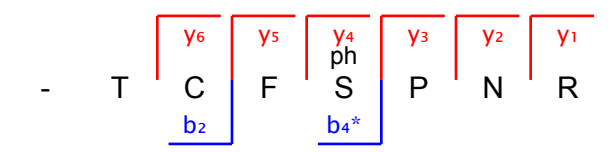
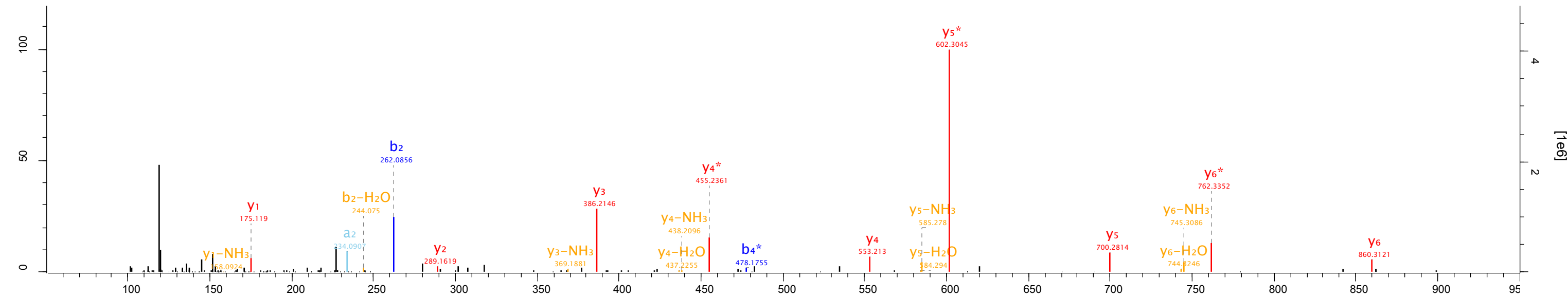


Raw file
20171215_MaS_33SR_LMH_phospho2_02

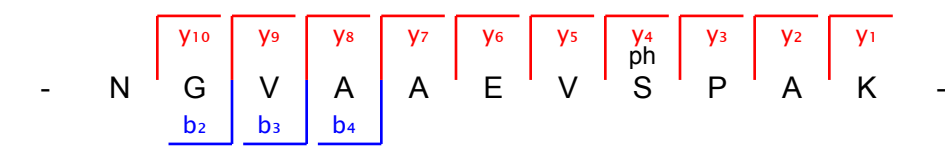
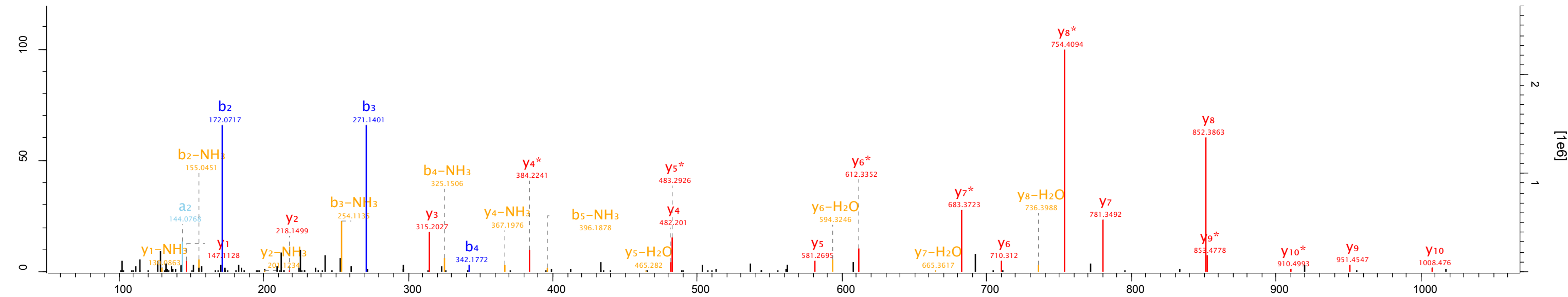
Scan 3889 Method FTMS; HCD Score 167.71 m/z 565.74 Gene names ARHGEF2



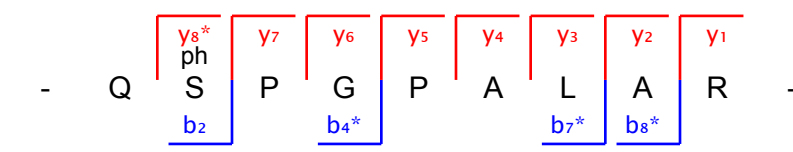
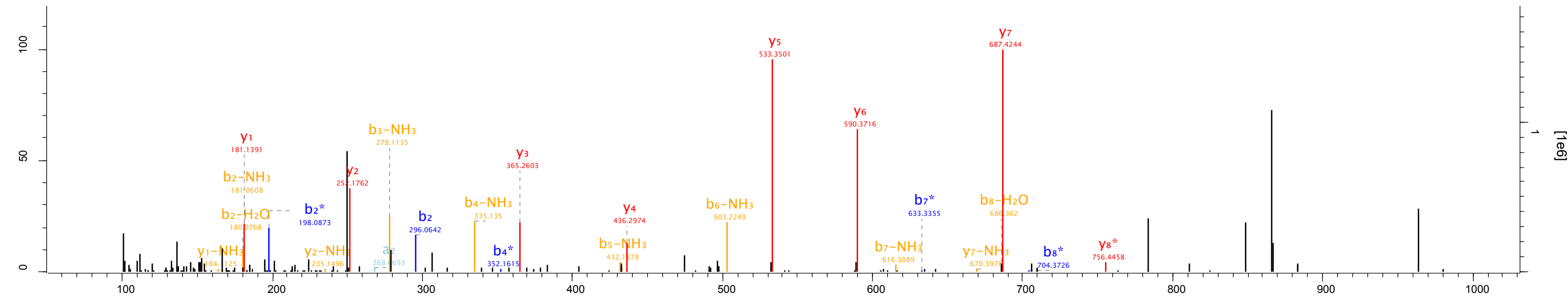
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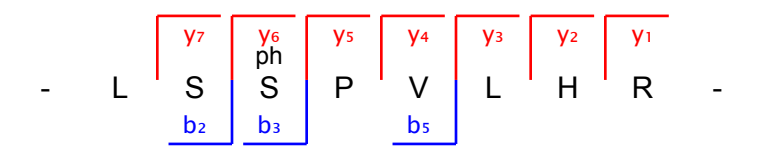
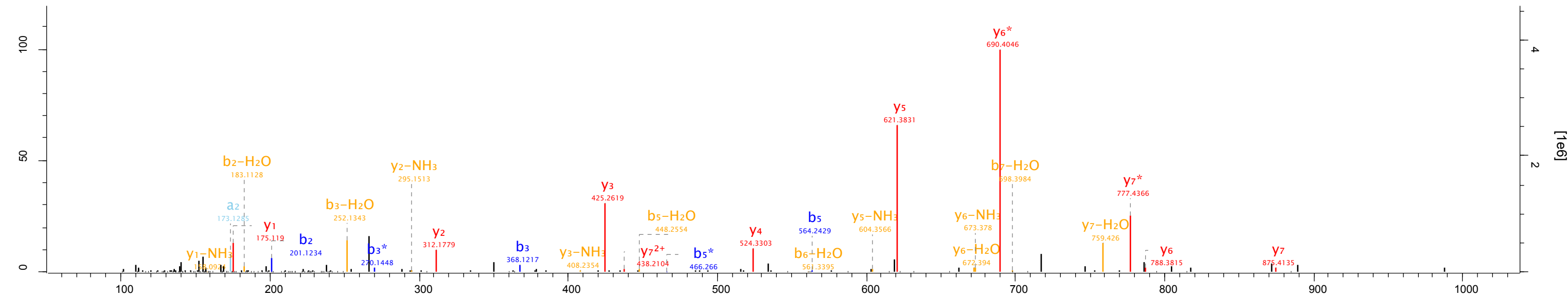
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 Scan: 4459 Method: FTMS; HCD Score: 141.34 m/z: 561.76 Gene names: HIRIP3

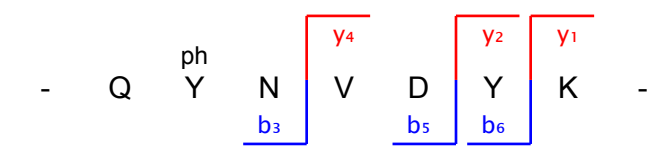
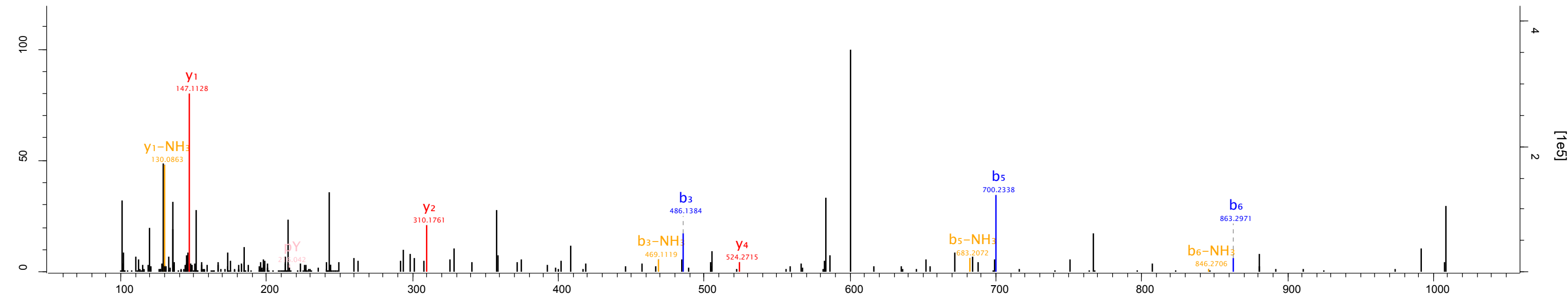


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 Scan: 4849 Method: FTMS; HCD Score: 78.04 m/z: 491.74 Gene names: FOXK1



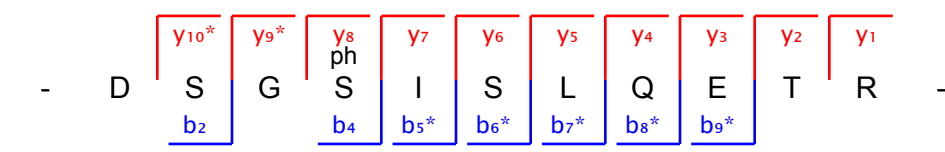
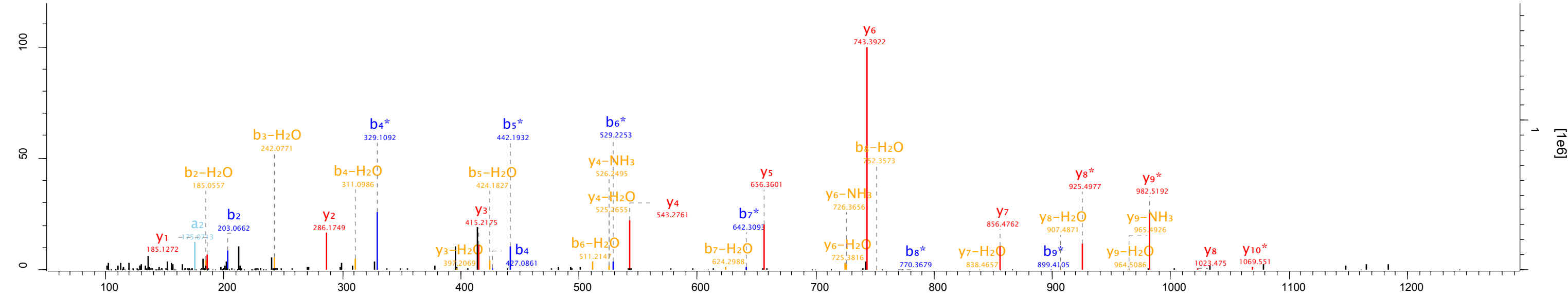
Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 4929 Method: FTMS; HCD Score: 151.22 m/z: 494.75 Gene names: DBN1



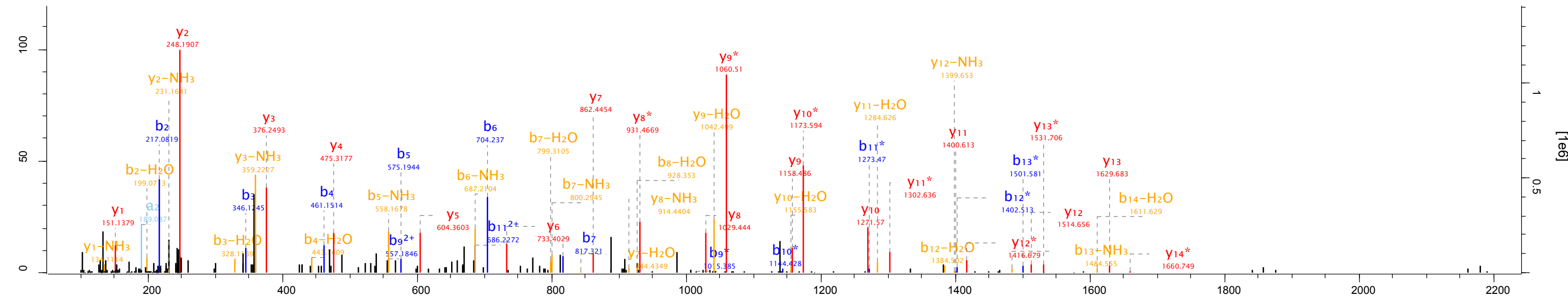


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_02 6939 FTMS; HCD 199.31 641.78 SLK



Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 7069 Method FTMS; HCD Score 275.23 m/z 987.9 Gene names MSH6

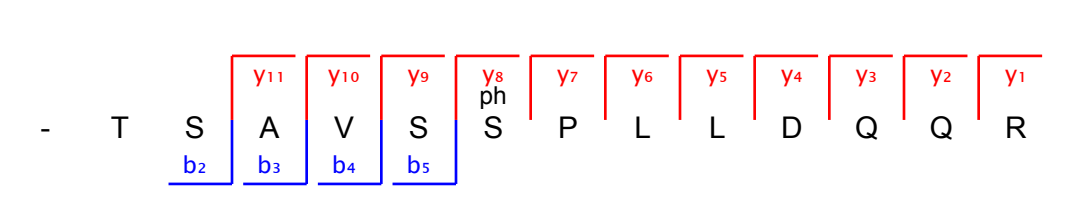
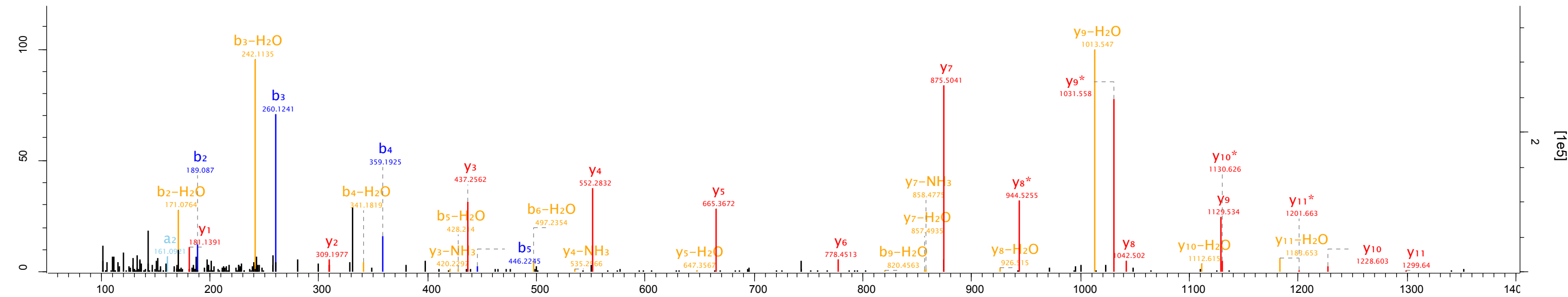


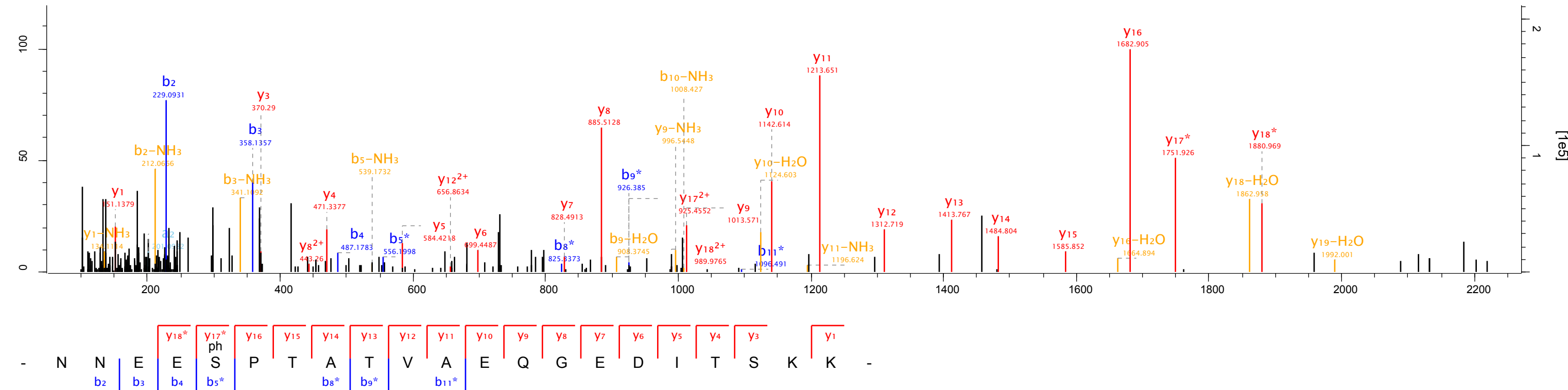
- S E E E D N E I E E S E E E V Q P K -

b2 b3 b4 b5 b6 b7 b9* b10* b11* b12* b13*

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

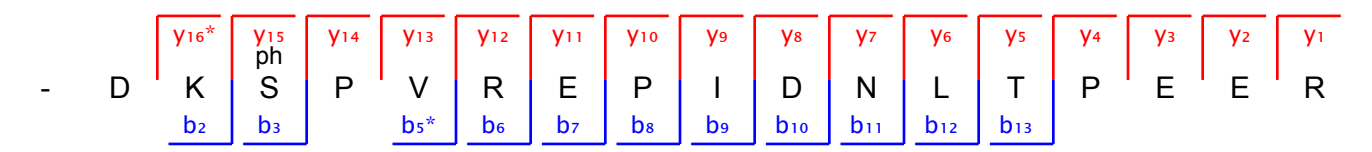
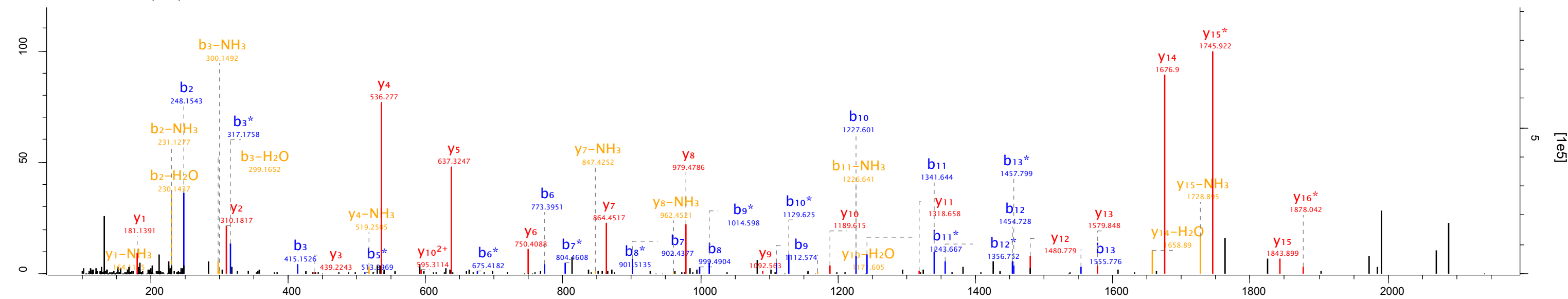
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 Scan: 9049 Method: FTMS; HCD Score: 178.14 m/z: 744.36 Gene names: ZC3H13



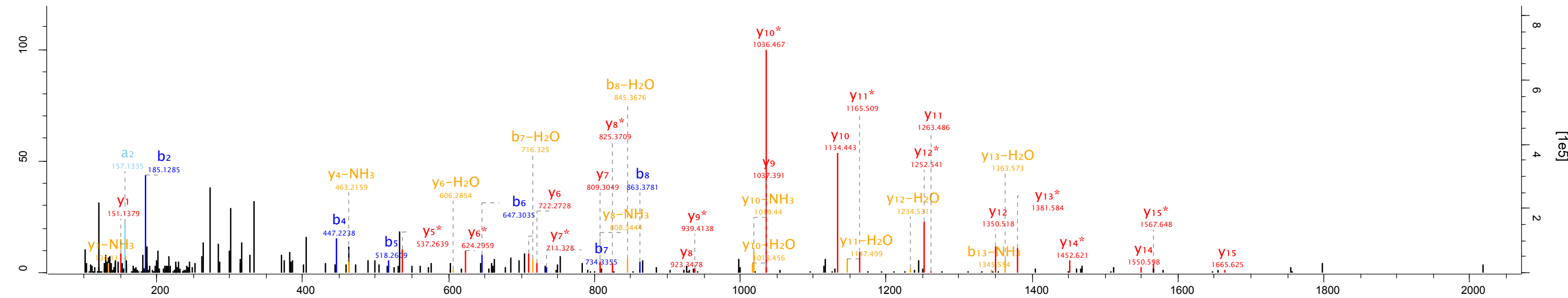


Raw file
20171215_MaS_33SR_LMH_phospho2_02

Scan Method Score m/z Gene names
9359 FTMS; HCD 260.41 698.02 RBM39



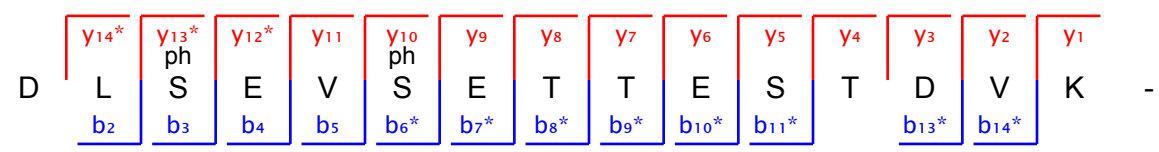
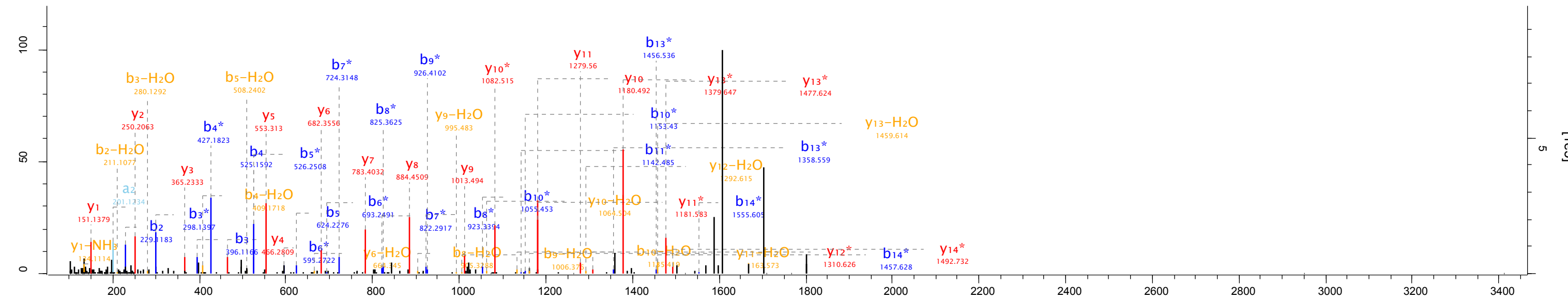
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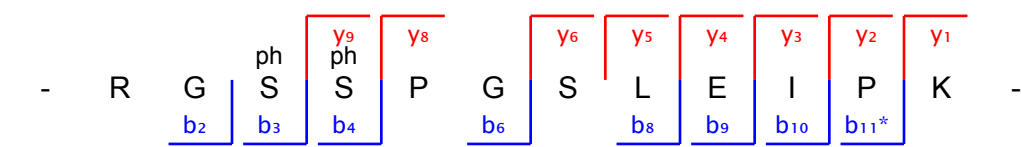
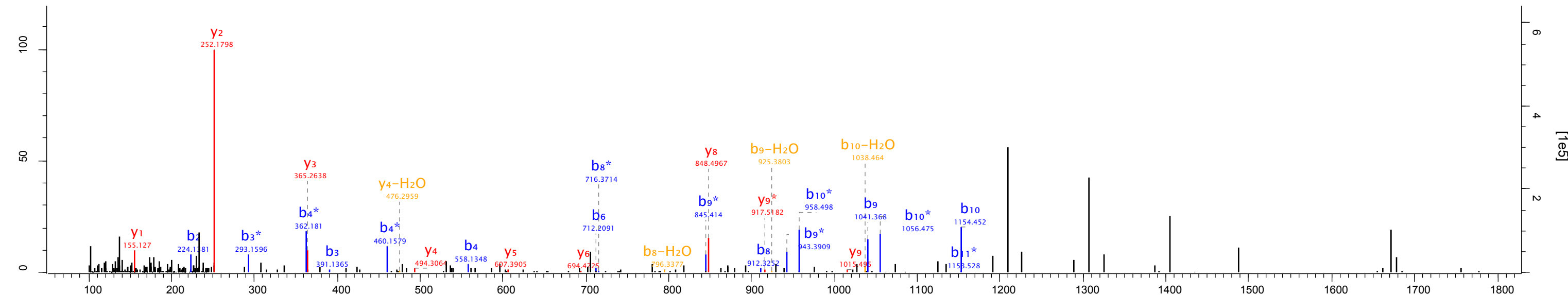


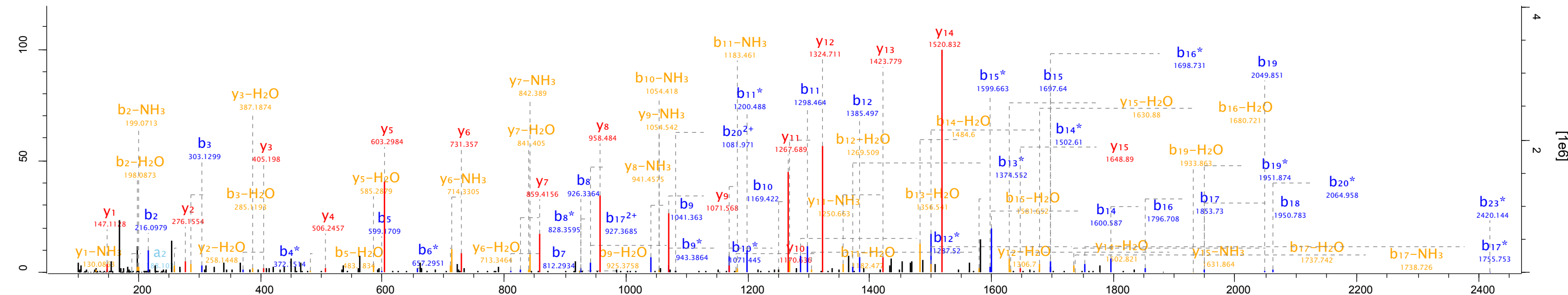
- I A F D A E S E P N N S S G ph S M E K -

b2
b4
b5
b6
b7
b8
y15
y14
y13*
y12
y11
y10
y9
y8
y7
y6
y5*
y1

Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10229 Method: FTMS; HCD Score: 227.57 m/z: 902.36 Gene names: NAA10







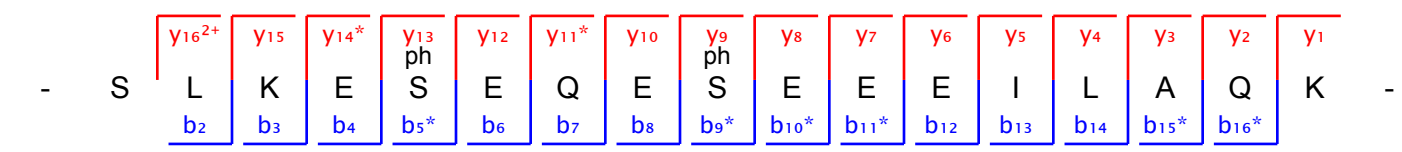
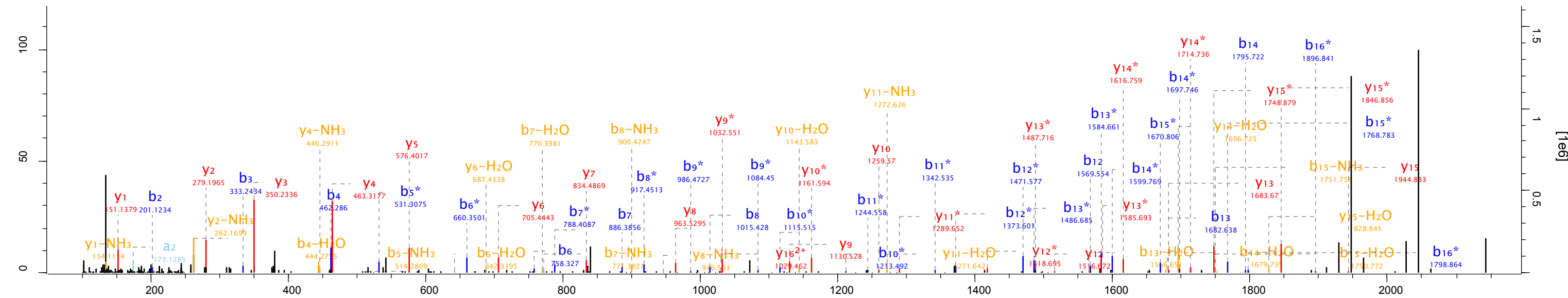
- S Q S S E R G N D Q E S S Q P V G P V I V Q Q P T E E K -

ph

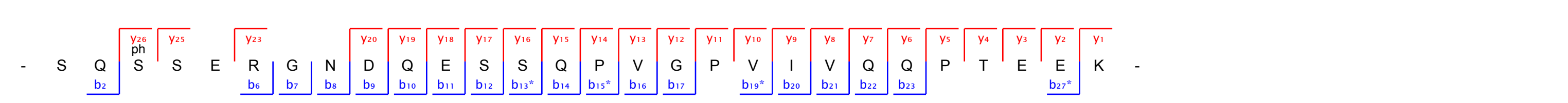
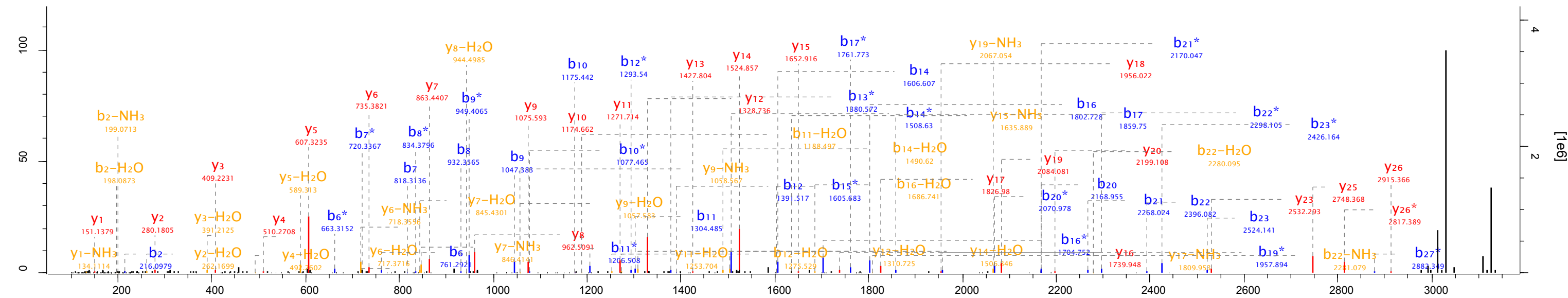
b₂ b₃ b₄^{*} b₅ b₆^{*} b₇ b₈ b₉ b₁₀ b₁₁ b₁₂ b₁₃^{*} b₁₄ b₁₅ b₁₆ b₁₇ b₁₈ b₁₉ b₂₀^{*} b₂₃^{*}

y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

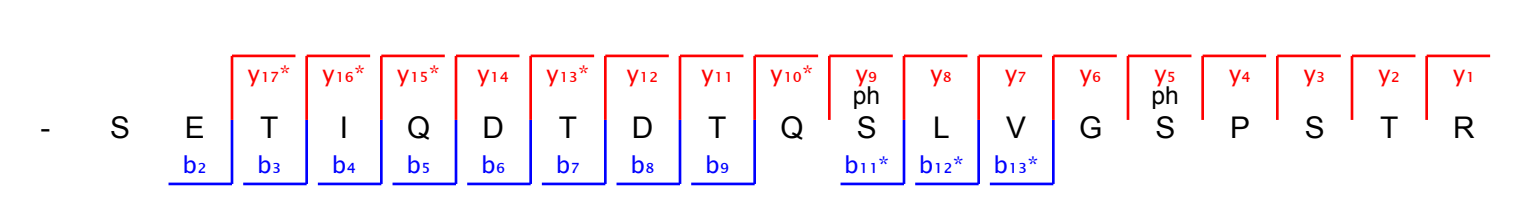
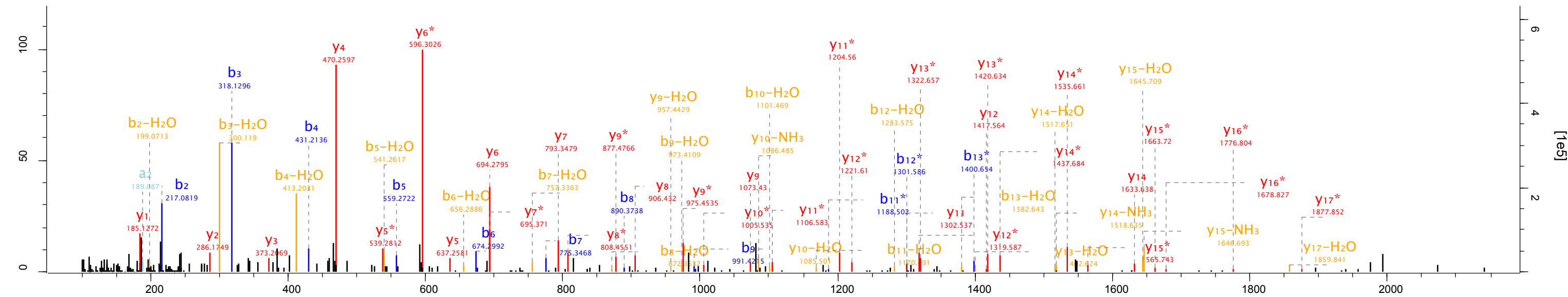
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 Scan: 10349 Method: FTMS; HCD Score: 357.94 m/z: 1072.98 Gene names: HIRIP3



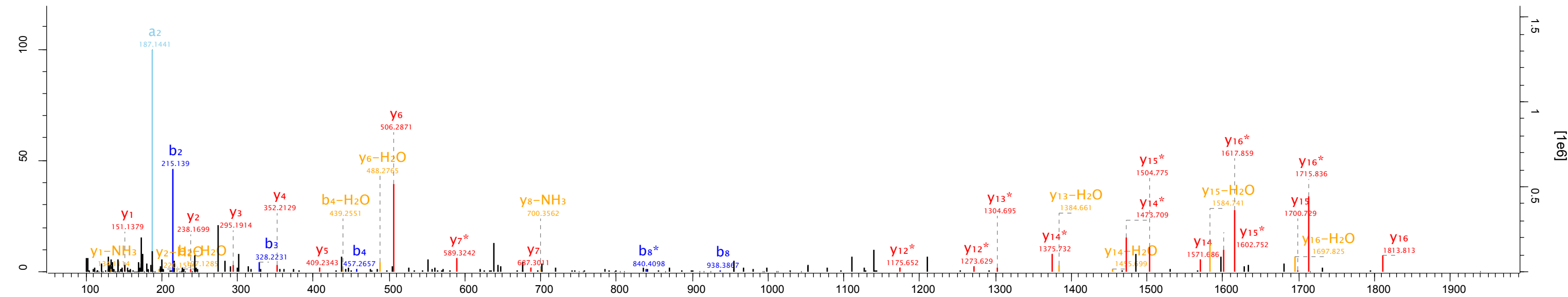
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10369 Method: FTMS; HCD Score: 281.37 m/z: 1566.23 Gene names: PAGE5

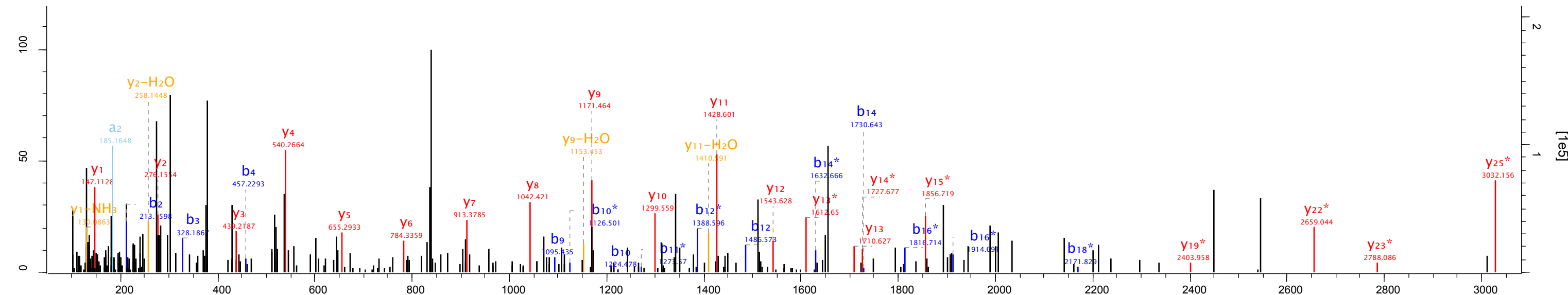


Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10399 Method: FTMS; HCD Score: 264.21 m/z: 1096.46 Gene names: ARHGEF12



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 10539 Method: FTMS; HCD Score: 102.97 m/z: 676.99 Gene names: NES

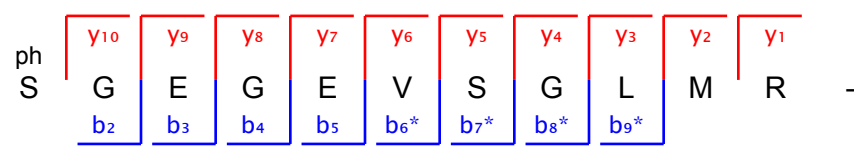
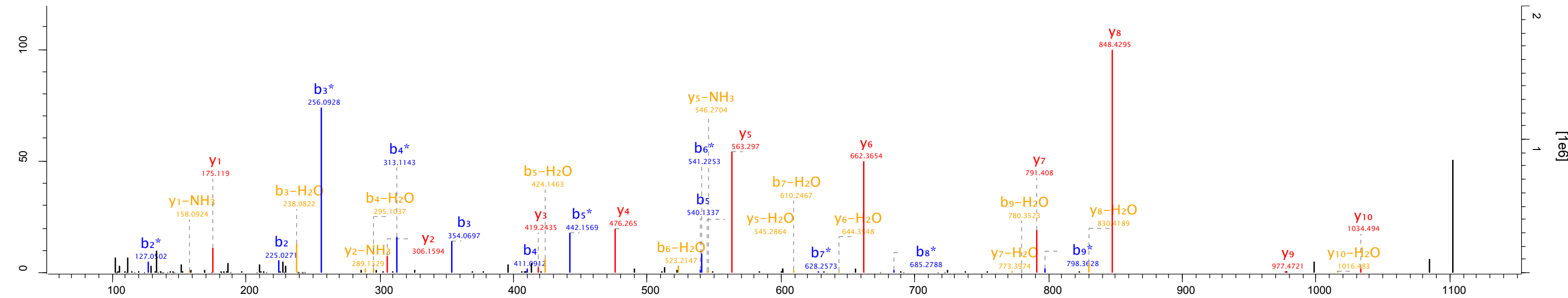




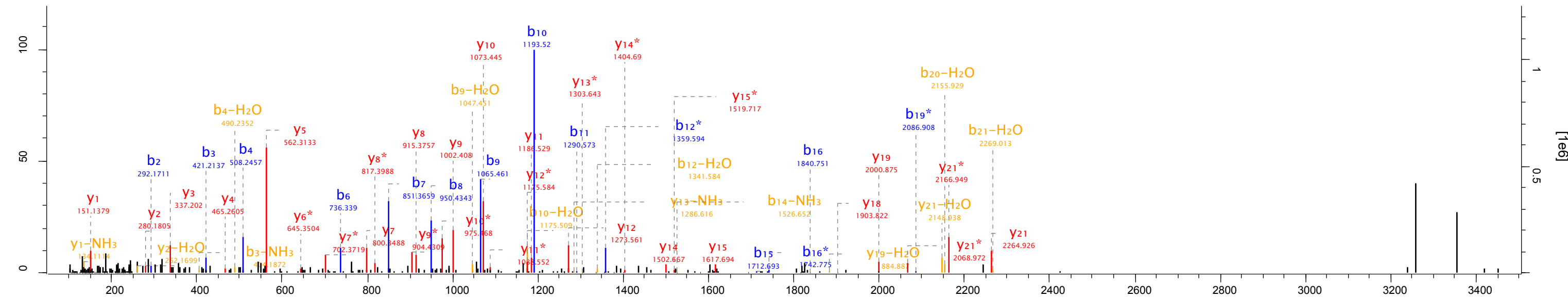
- V L D E E G S E R E F D E D S D E K E E E E D T Y E K -

b₂ b₃ b₄ y₂₅* y₂₃* y₂₂* ph y₁₉* b₉ b₁₀ b₁₁* b₁₂ y₁₅* y₁₄* b₁₄ b₁₃ y₁₃ y₁₂ y₁₁ b₁₆* b₁₈* y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10649 Method FTMS; HCD Score 164.56 m/z 601.25 Gene names TRIM28



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10659 Method FTMS; HCD Score 105.45 m/z 1153.49 Gene names HUWE1

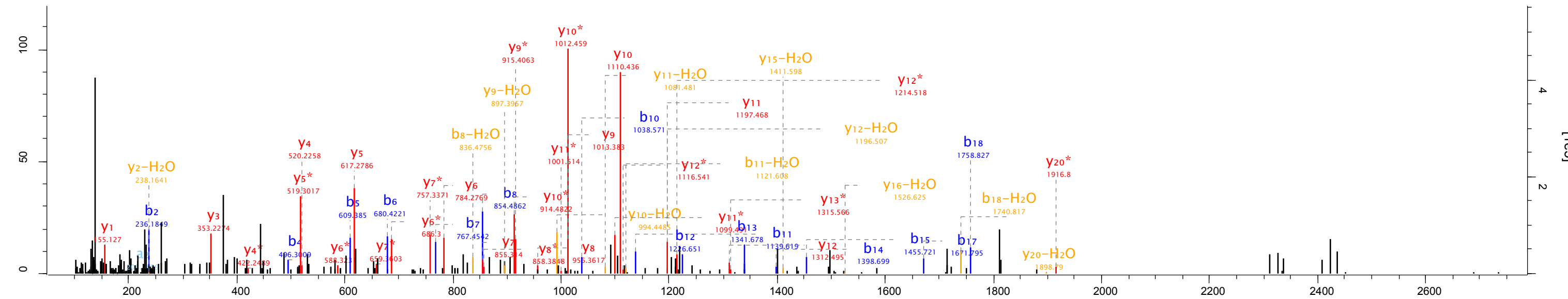


- R E E S P M D V D Q P S ph y19 y18 A Q D T Q S I A S D G T ph y5 y4 y3 y2 y1 -

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

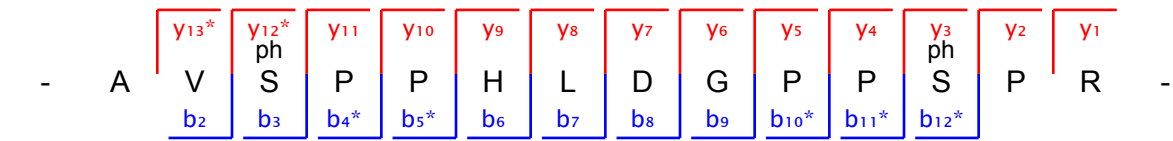
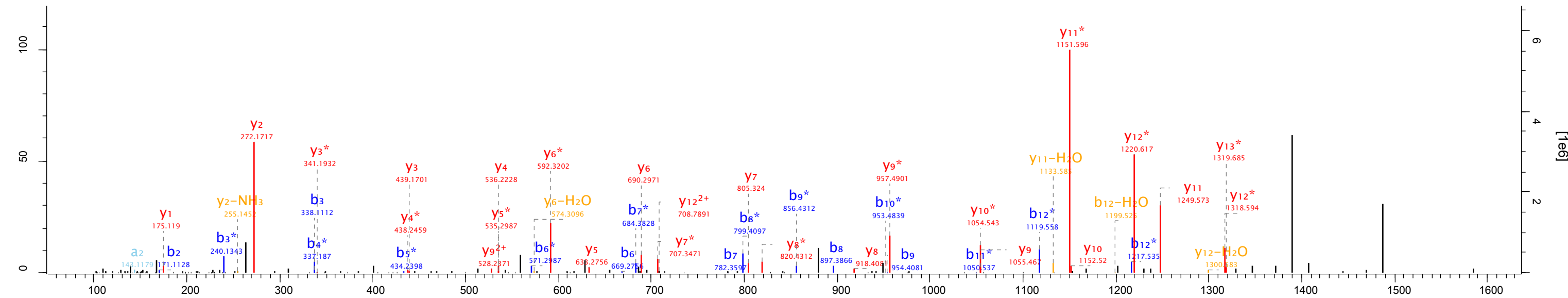
- b2 (E), b3 (E), b4 (S)
- b6 (M), b7 (D), b8 (V), b9 (D), b10 (Q), b11 (P), b12* (S)
- b15 (A), b16 (Q)
- b19* (Q)

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10749 Method FTMS; HCD Score 108.94 m/z 957.09 Gene names KCTD3

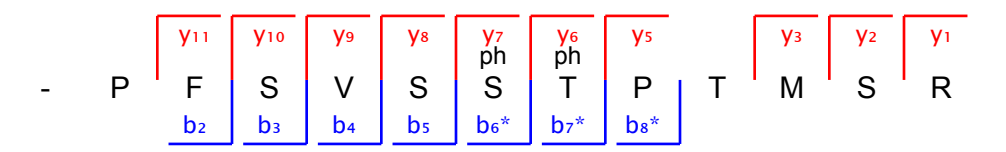
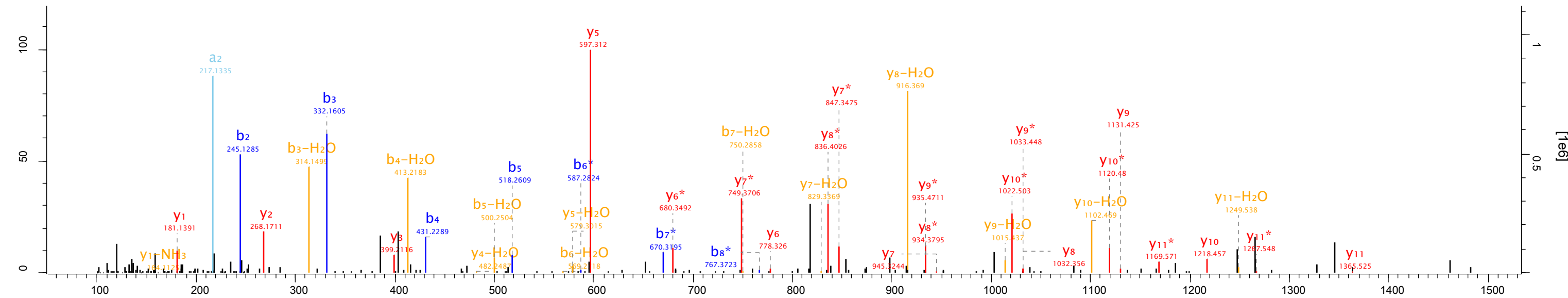


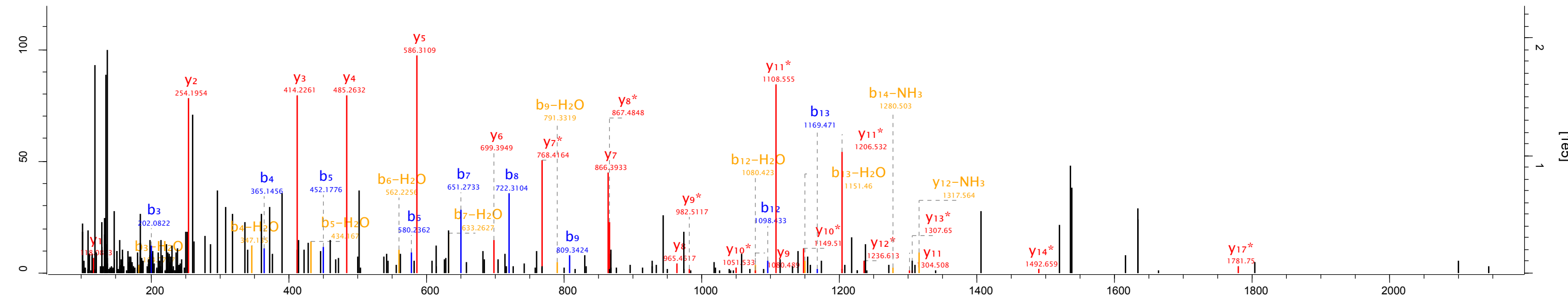
- K V P Y L A S S P S T S D G G T D S P G T A S P S P T K -

Fragmentation mapping: b2 (V), b4 (Y), b5 (L), b6 (A), b7 (S), b8 (S), y20* (P), b10 (S), b11 (T), b12 (S), b13 (D), b14 (G), b15 (G), y13* (T), y12 (D), y11 (S), y10 (P), y9 (G), y8 (T), y7 (A), y6-ph (S), y5 (P), y4-ph (S), y3 (P), y1 (K)



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11019 Method FTMS; HCD Score 173.77 m/z 731.79 Gene names TMF1

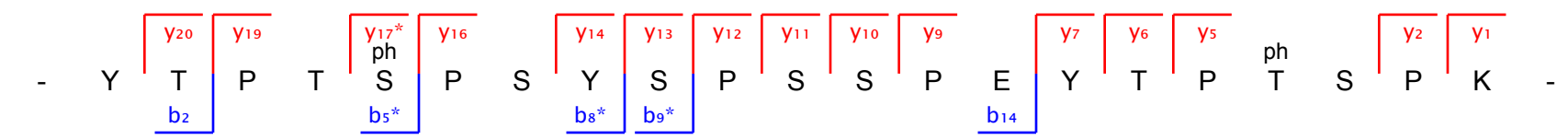
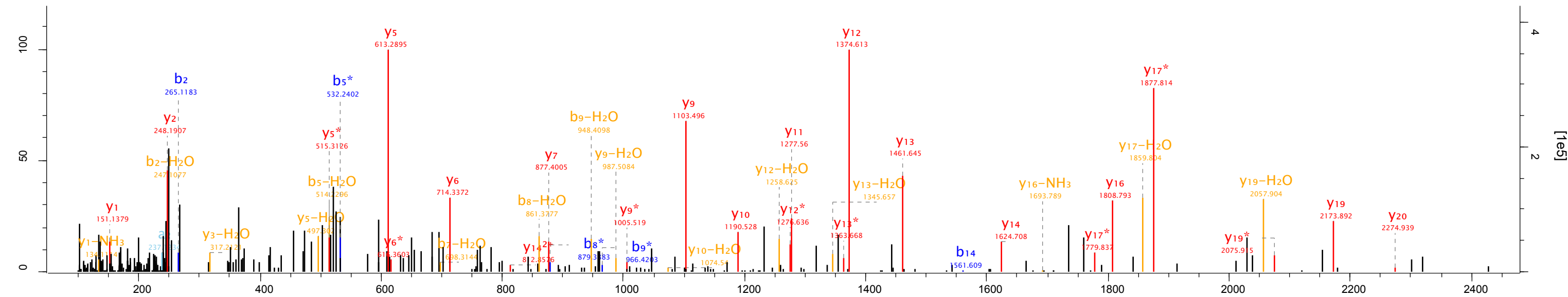




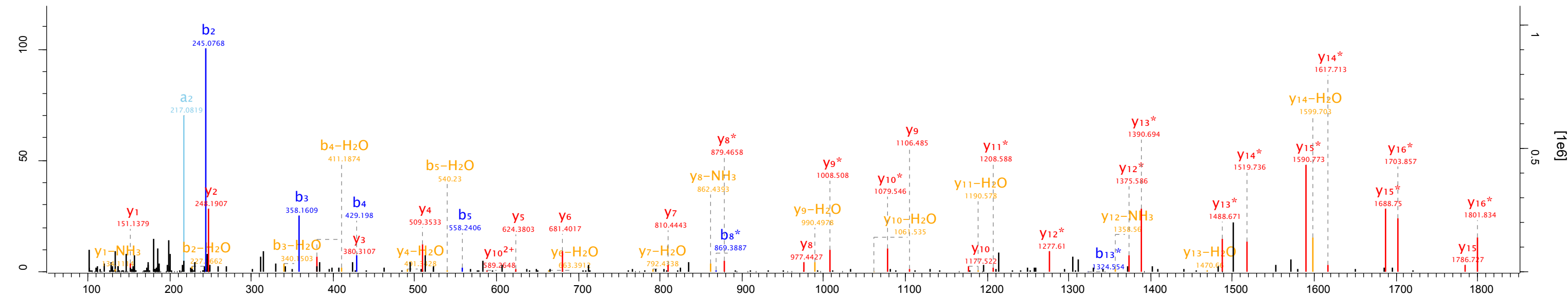
- G G S Y S Q A A S S D S A Q G S D V S L T A C K V -

b₃
b₄
b₅
b₆
b₇
b₈
b₉
y₁₇*
y₁₄*
y₁₃*
y₁₂*
y₁₁
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y₇
y₆
y₅
y₄
y₃
y₂
y₁

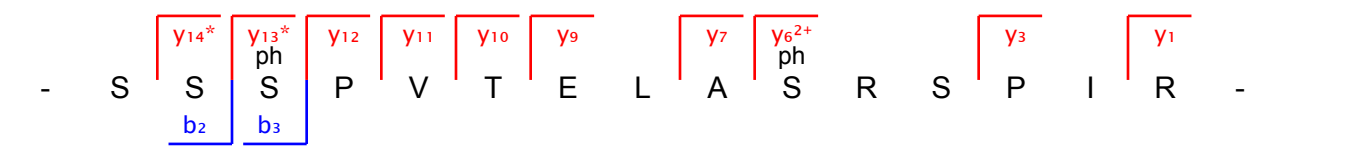
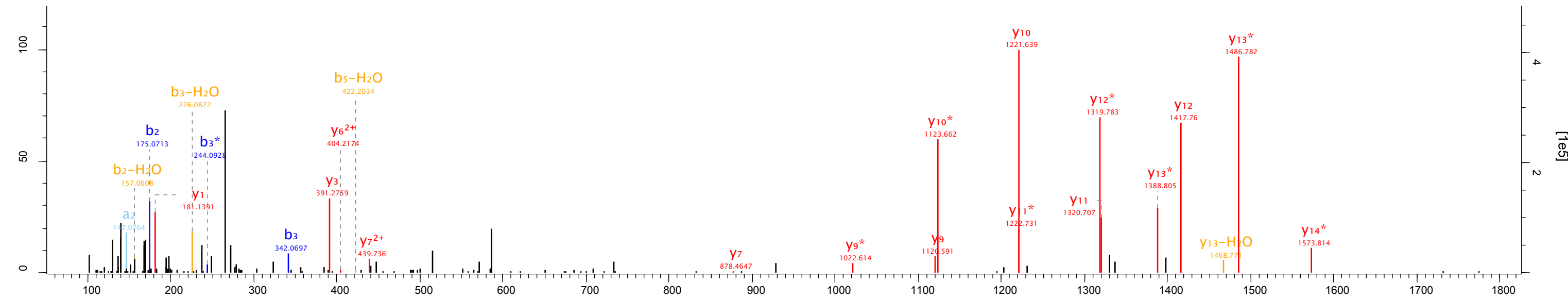
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11349 Method FTMS; HCD Score 161.5 m/z 1220 Gene names POLR2A



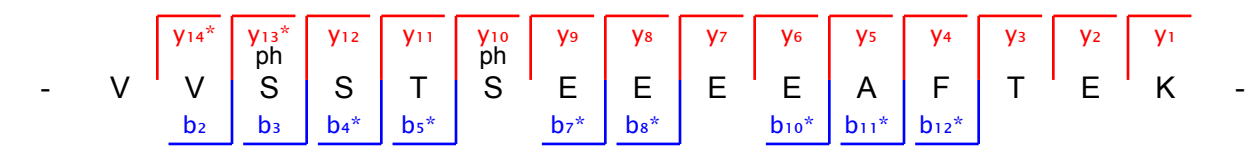
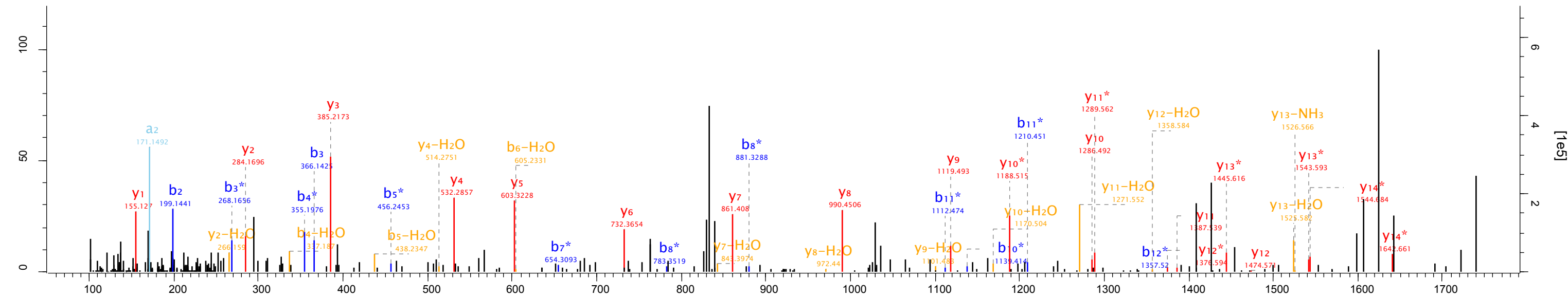
Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 11379 Method: FTMS; HCD Score: 147.11 m/z: 715.3 Gene names: CHD9



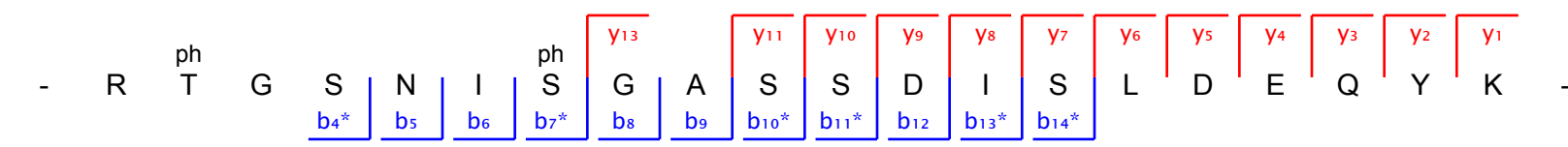
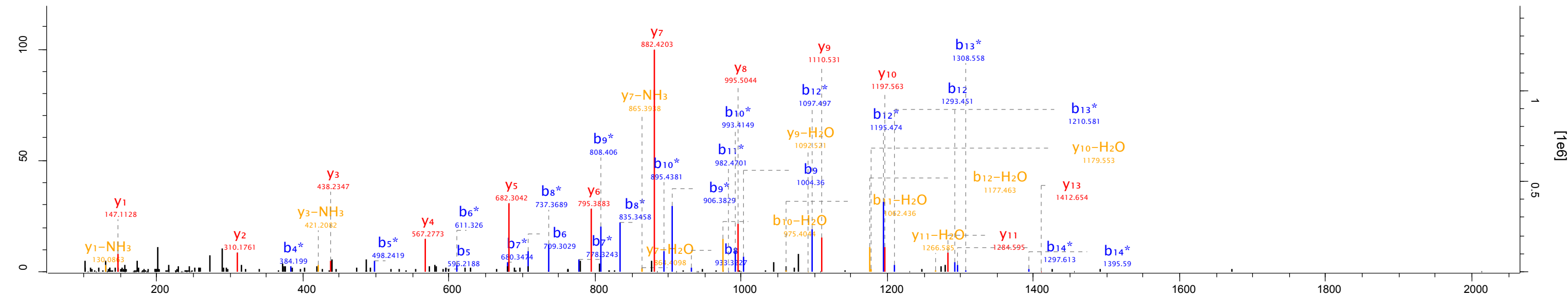
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11459 Method FTMS; HCD Score 101.17 m/z 587.28 Gene names SRRM2



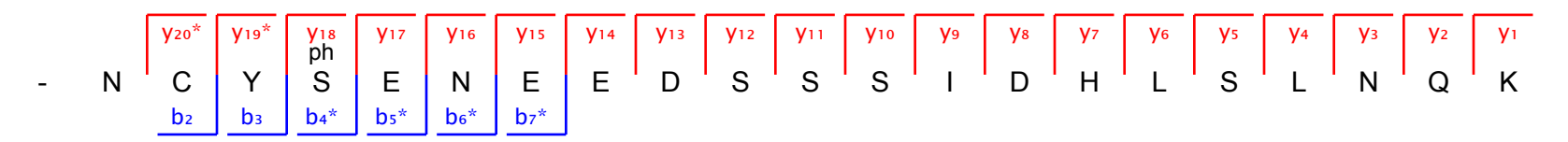
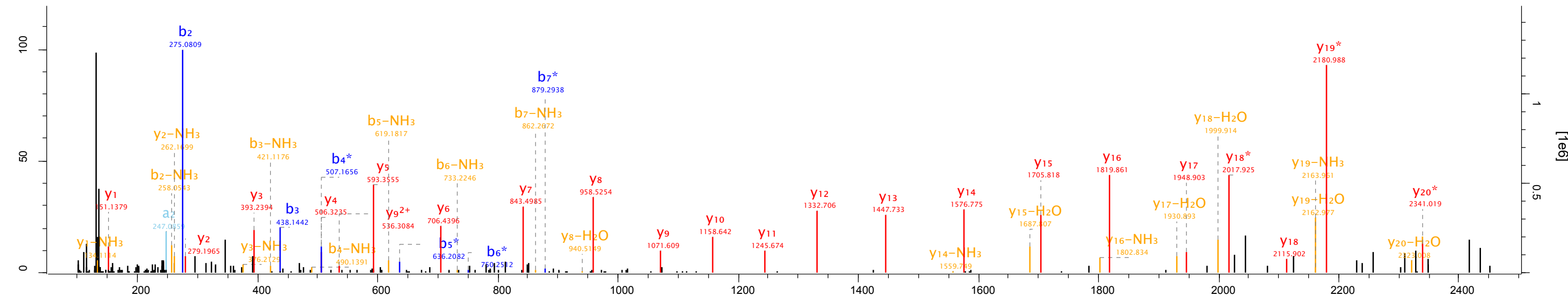
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11649 Method FTMS; HCD Score 135.82 m/z 920.86 Gene names OXR1



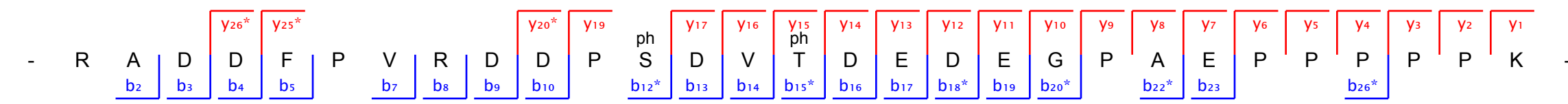
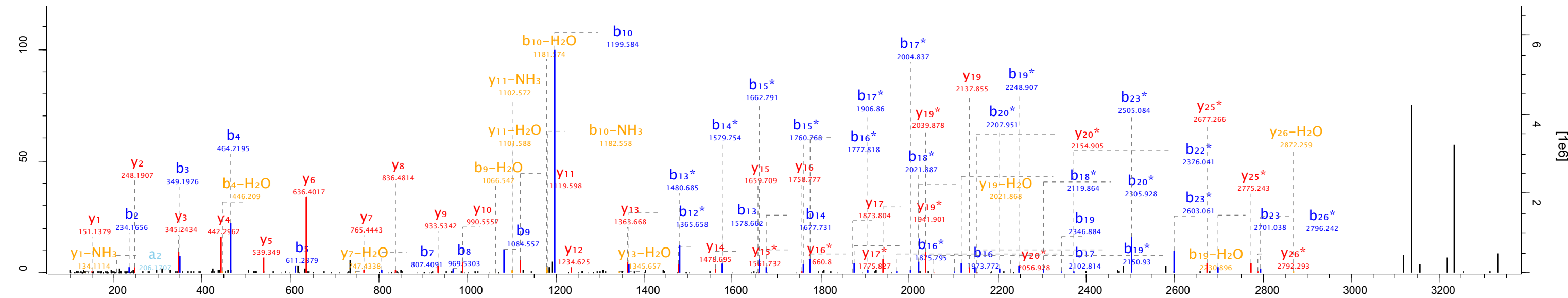
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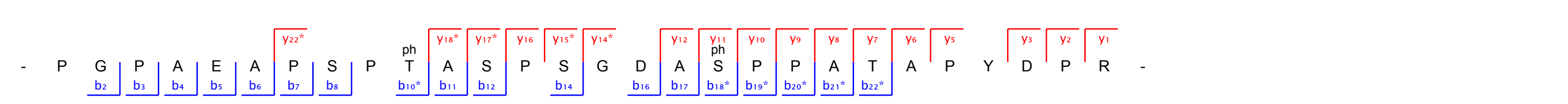
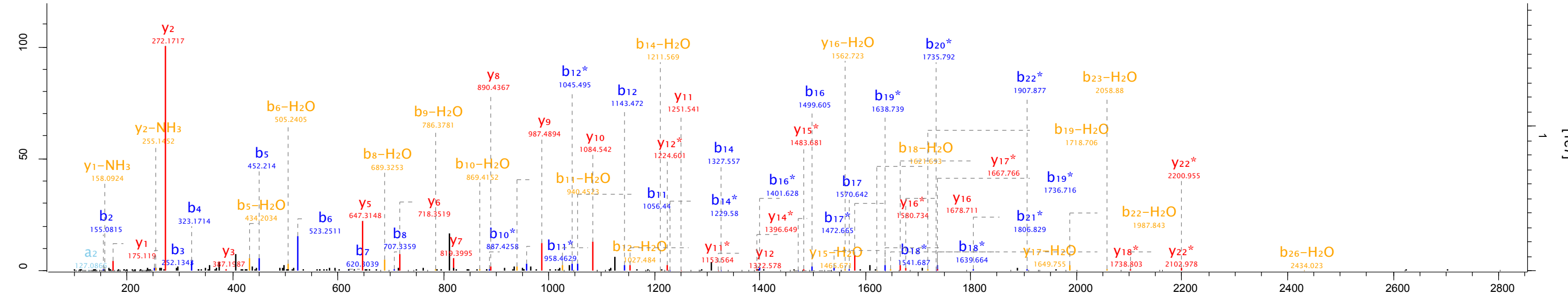
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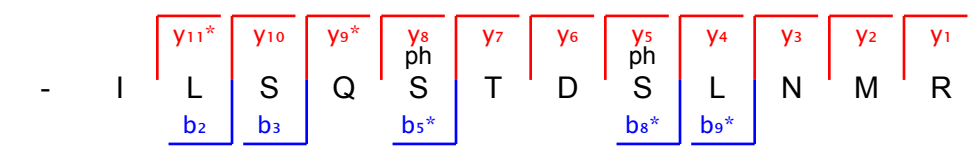
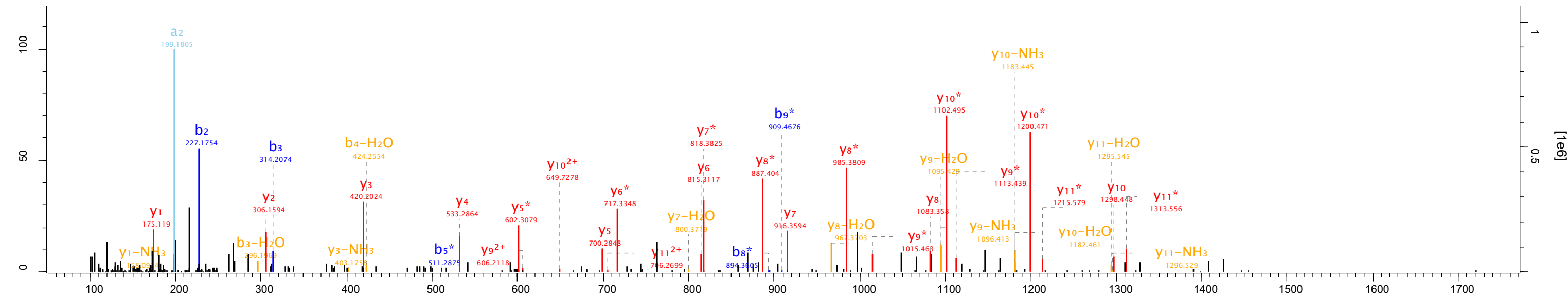
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11849 Method FTMS; HCD Score 247.01 m/z 1112.82 Gene names RABL6



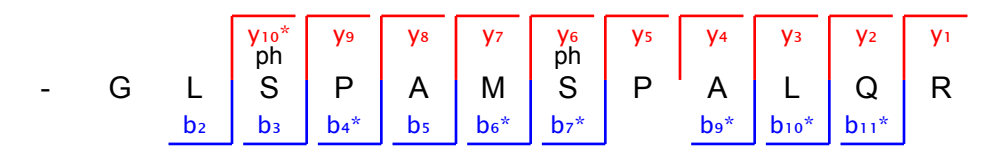
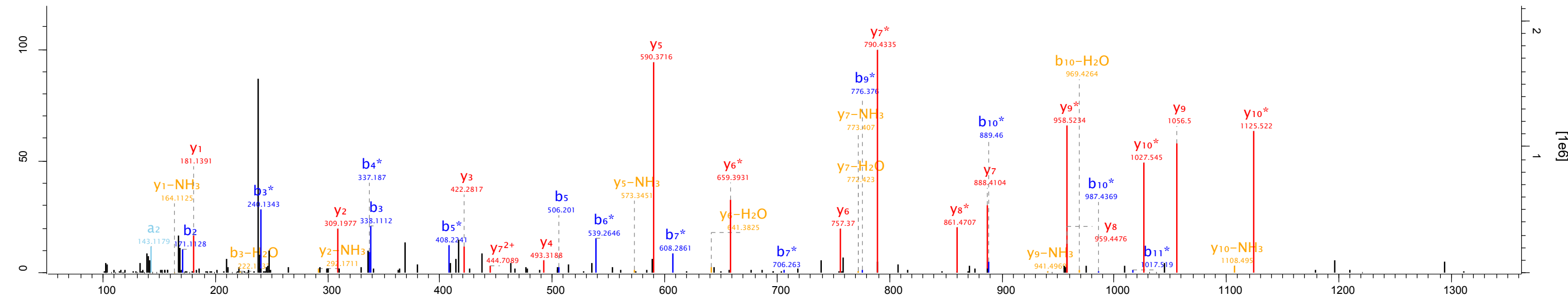
20171215_MaS_33SR_LMH_phospho2_03 11879 FTMS; HCD 169.05 941.4 ZC3H4



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 11899 Method FTMS; HCD Score 156.67 m/z 762.81 Gene names ARHGEF2

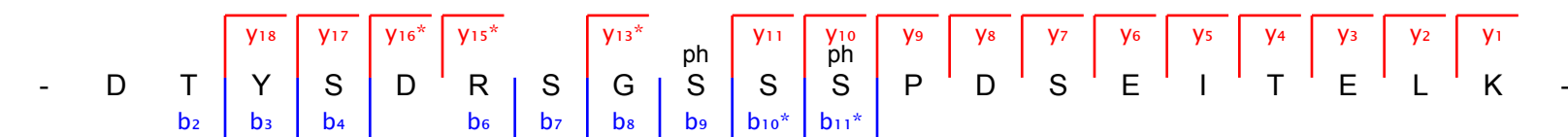
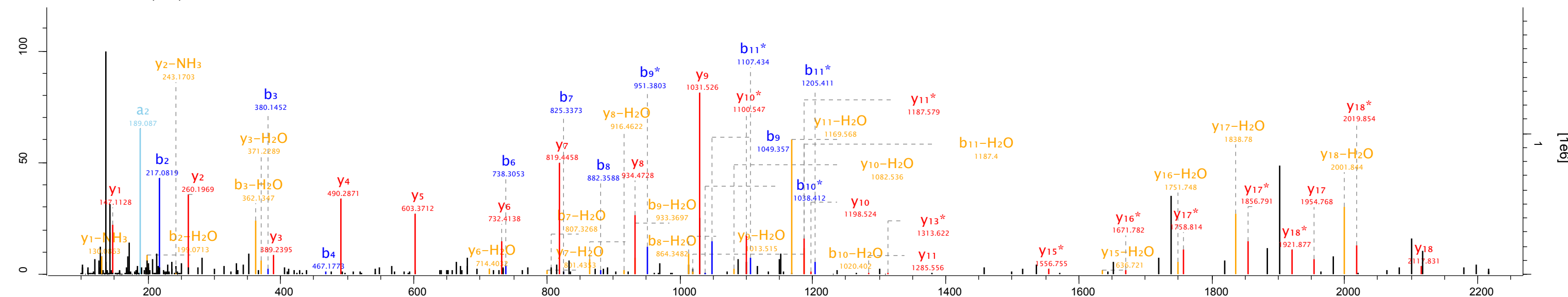


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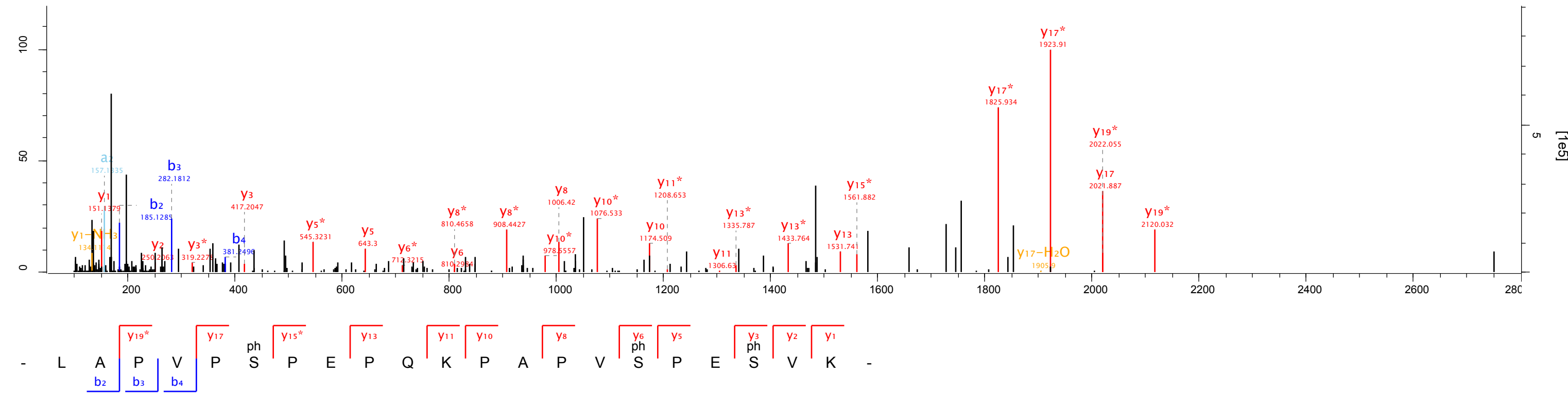


Raw file
20171215_MaS_33SR_LMH_phospho2_03

Scan 12009 Method FTMS; HCD Score 163.39 m/z 778.64 Gene names CTPS1

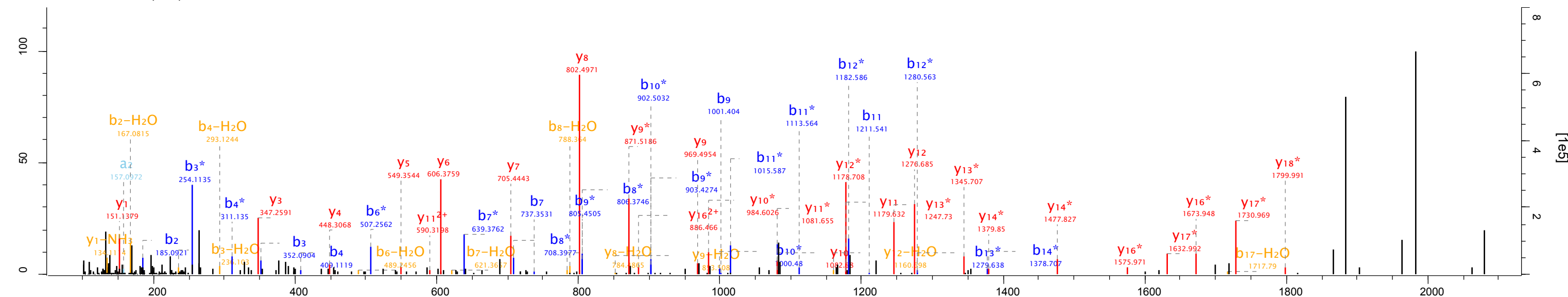


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12269 Method FTMS; HCD Score 57.53 m/z 801.71 Gene names CHAMP1



20171215_MaS_33SR_LMH_phospho2_03

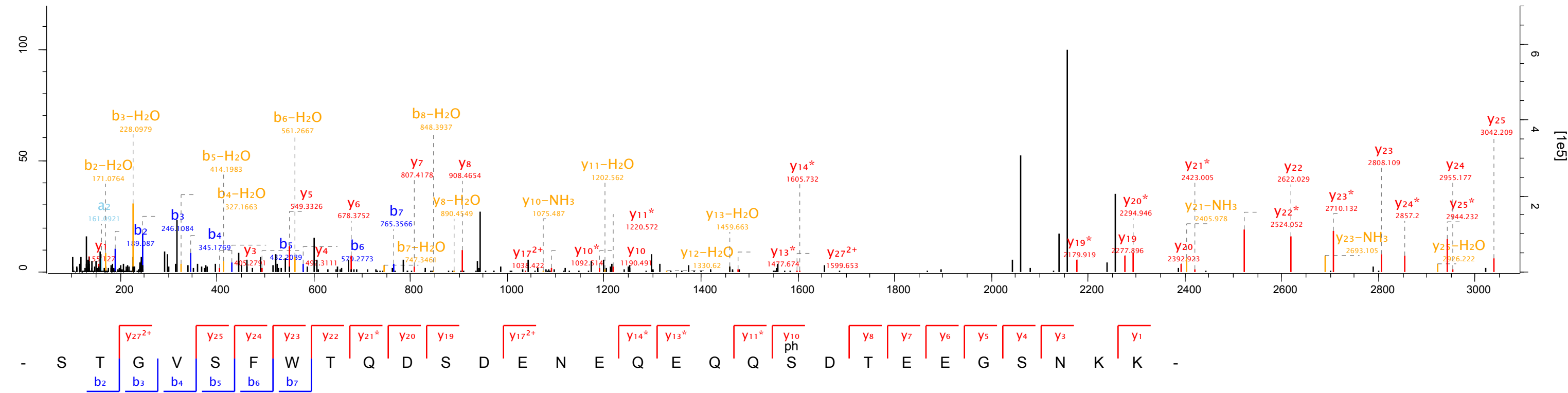
12299 FTMS; HCD 171.4 727.68 C2orf49

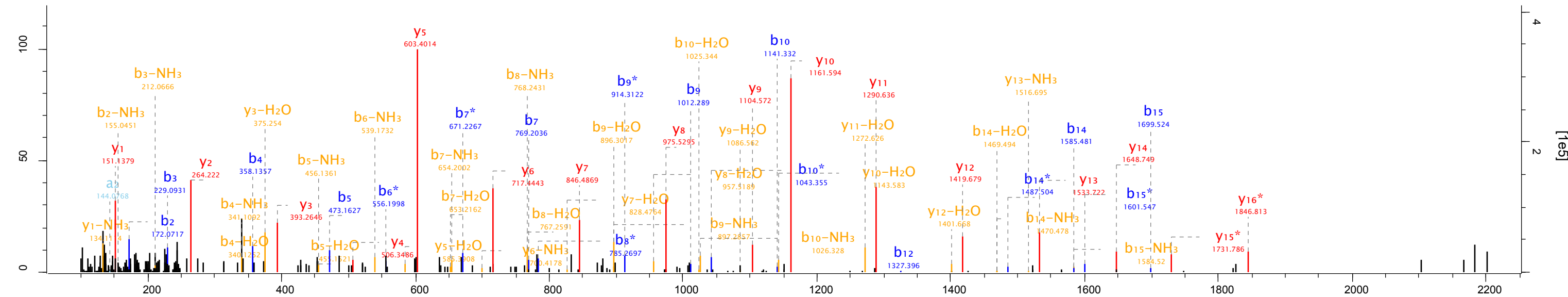


- S P S G P V K S P P L S P V G T T P V K -

b₂
b₃
b₄
b₆*
b₇
b₈*
b₉
b₁₀*
b₁₁
b₁₂*
b₁₃*
b₁₄*
y₁
y₃
y₄
y₅
y₆
y₇
y₈
y₉
y₁₀
y₁₁
y₁₂
y₁₃*
y₁₄*
y₁₆*
y₁₇*
y₁₈*

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 Scan: 12389 Method: FTMS; HCD Score: 145.01 m/z: 1130.12 Gene names: PPP1R12A

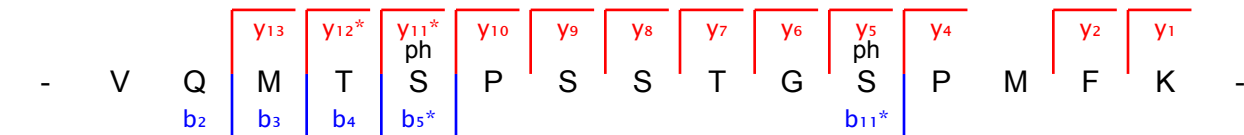
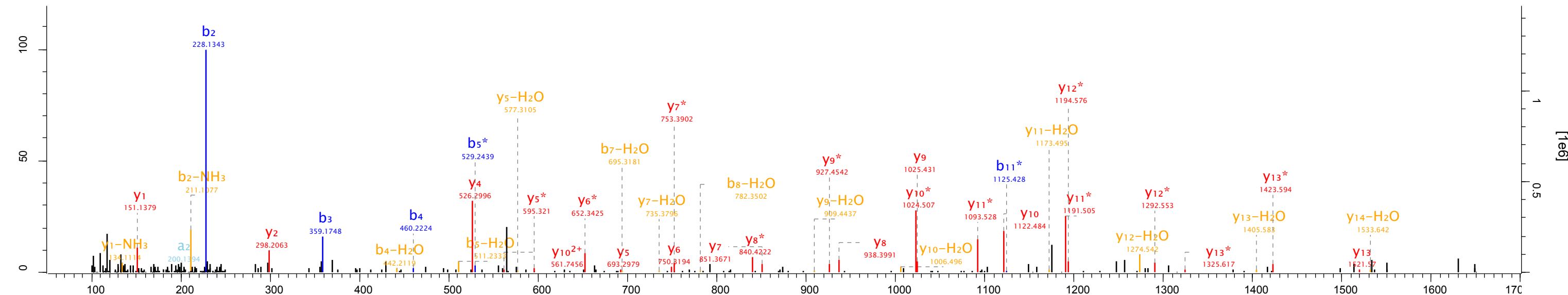


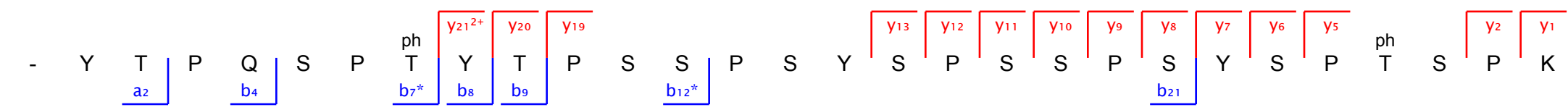
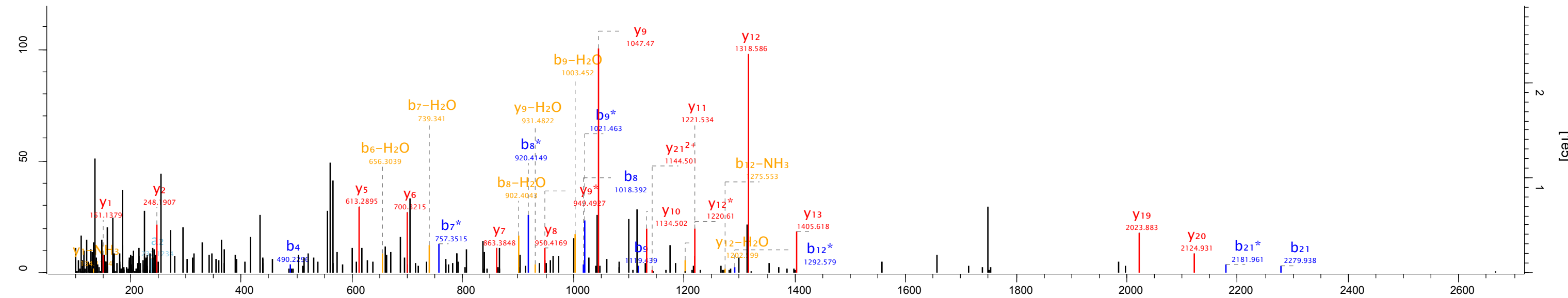


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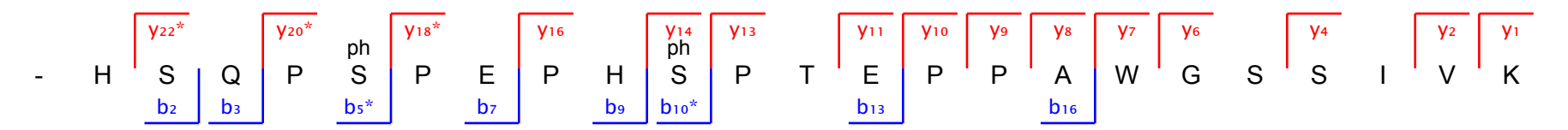
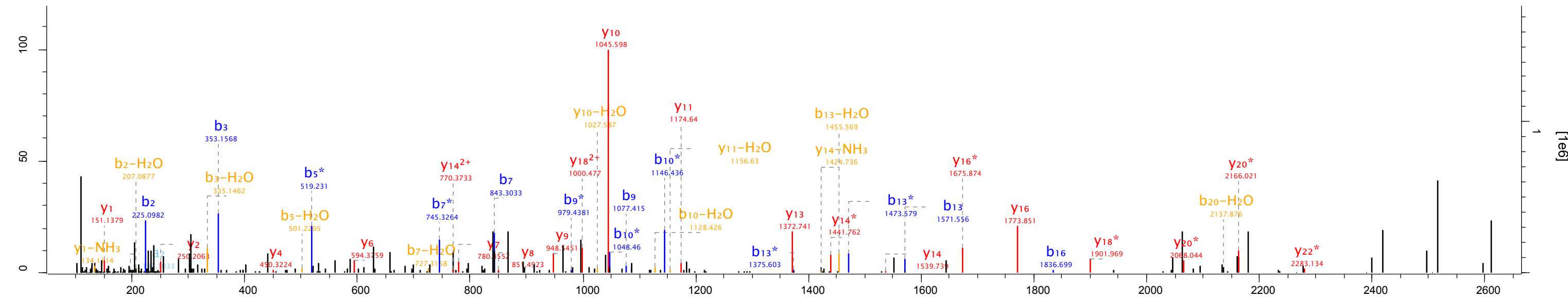
Fragmentation mapping (b and y ions) is shown below the sequence:

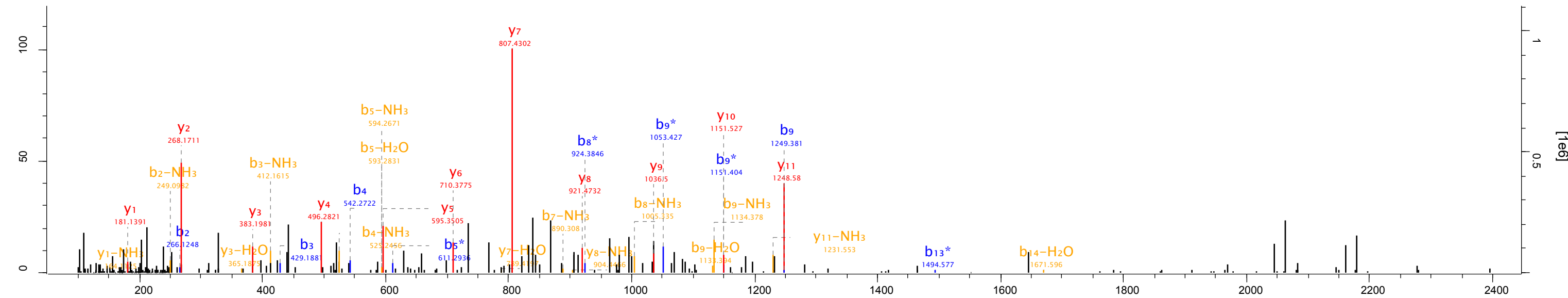
- b₂ (under G), b₃ (under G), b₄ (under E), b₅ (under D), b₆* (under T), b₇ (under D), b₈* (under N), b₉ (under E), b₁₀ (under E), b₁₂ (under G), b₁₄ (under E), b₁₅ (under N)
- y₁ (under K), y₂ (under I), y₃ (under L), y₄ (under P), y₅ (under E), y₆ (under N), y₇ (under E), y₈ (under E), y₉ (under G), y₁₀ (under G), y₁₁ (under E), y₁₂ (under E), y₁₃ (under D), y₁₄ (under T), y₁₅* (under D), y₁₆* (under G)





Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12949 Method FTMS; HCD Score 115.44 m/z 873.05 Gene names DENND4C

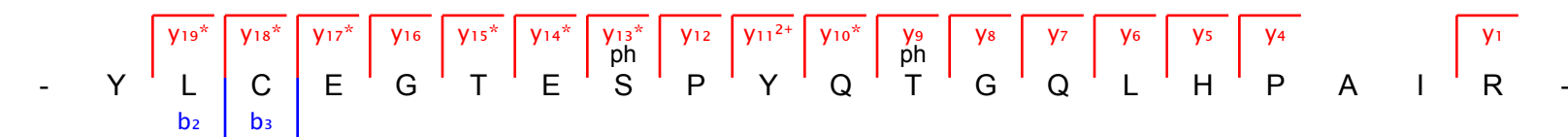
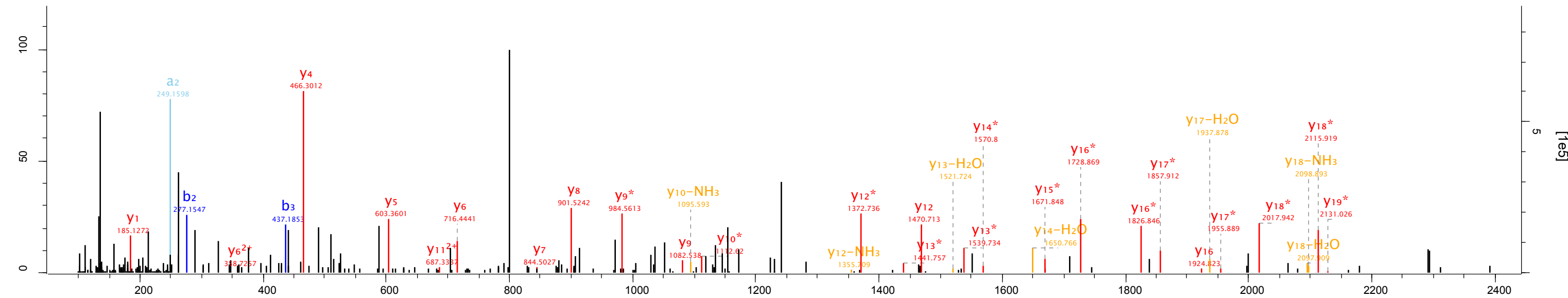


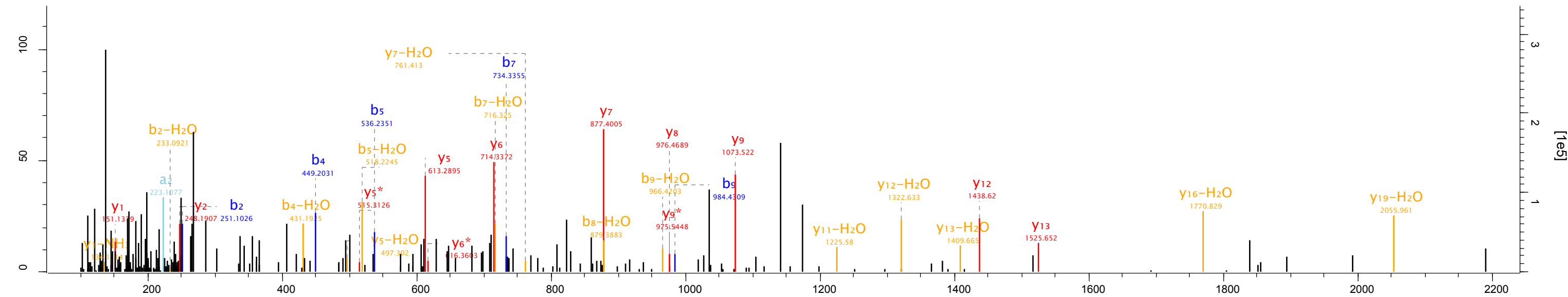


- Q H Y L ph S ph S E D E P D D N P D V L D S R -

b₂
b₃
b₄
b₅*
b₈*
b₉
b₁₃*
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13099 Method FTMS; HCD Score 101.45 m/z 831.02 Gene names PTPRK

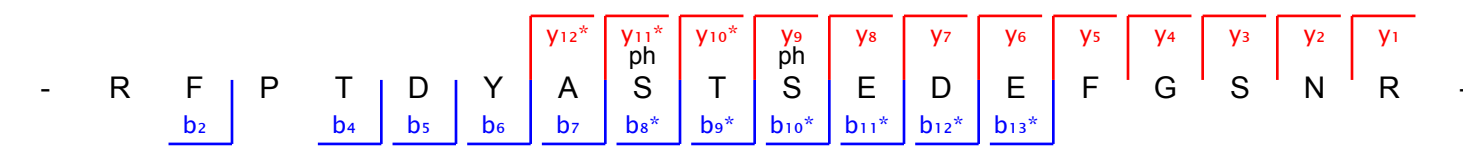
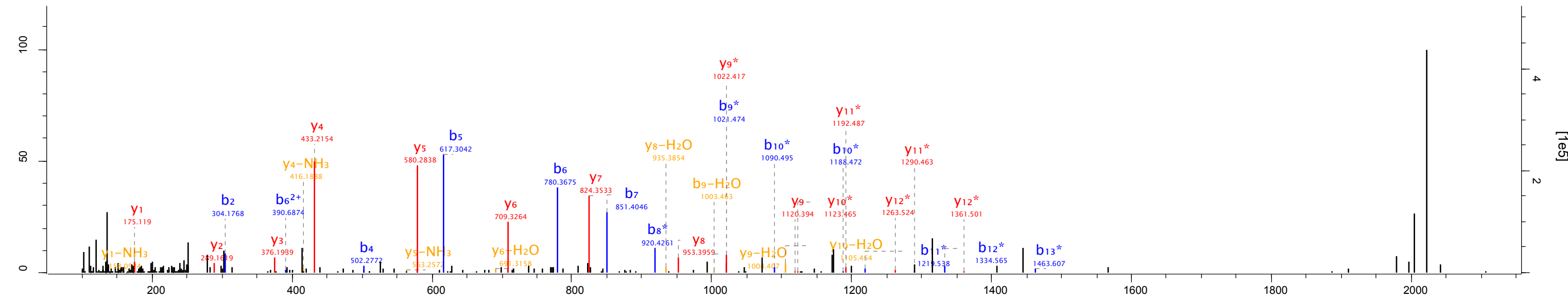




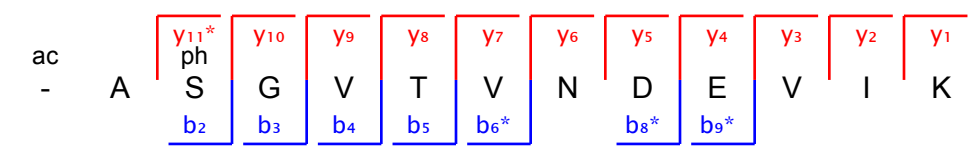
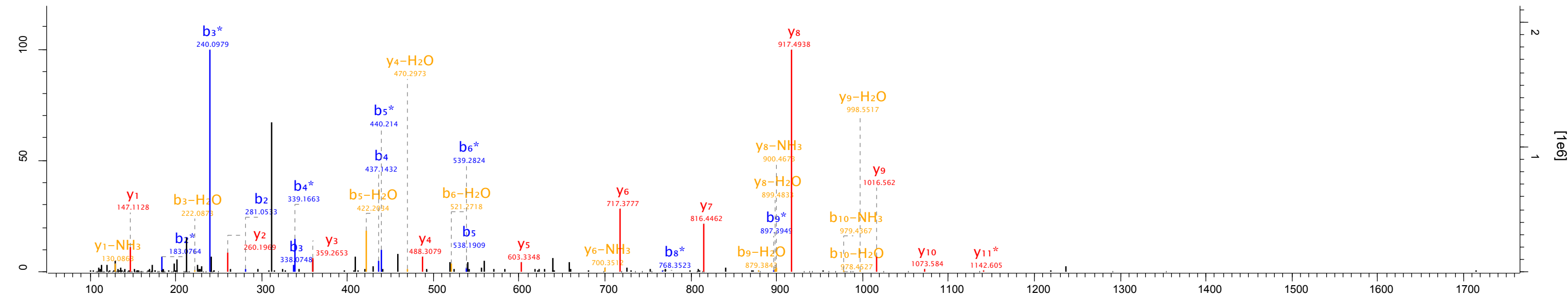
- Y S P T S P T Y S P T S P V Y T P T S P K -

b₂
b₄
b₅
b₇
b₉
y₁₃
y₁₂
y₉
y₈
y₇
y₆
y₅
y₂
y₁

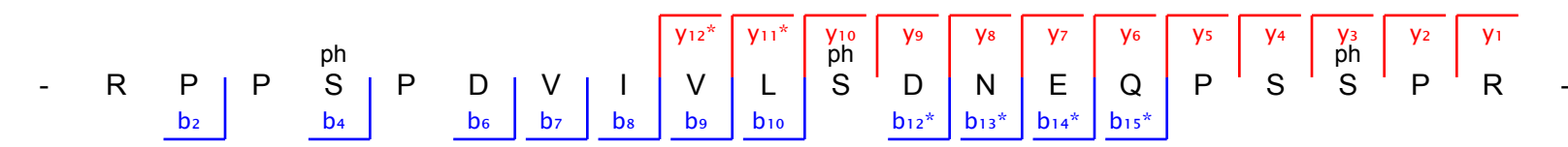
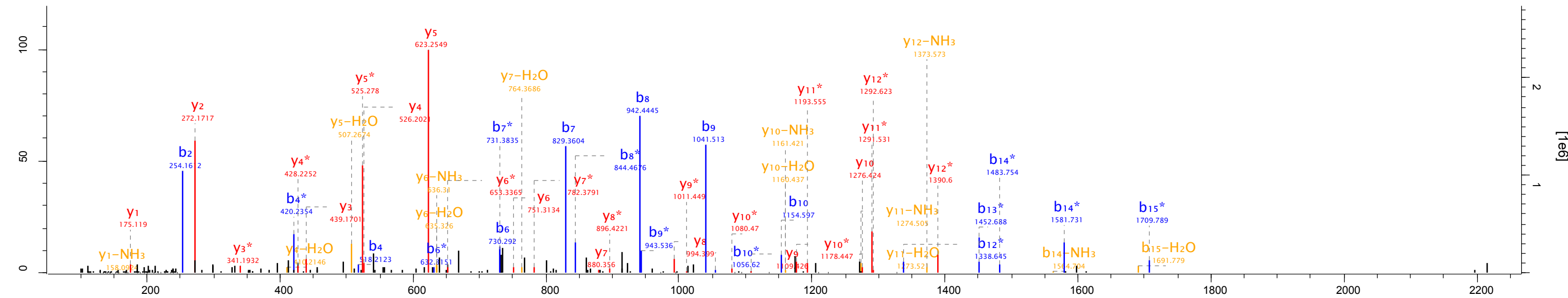
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 Scan: 13349 Method: FTMS; HCD Score: 71.79 m/z: 747.28 Gene names: CEP170



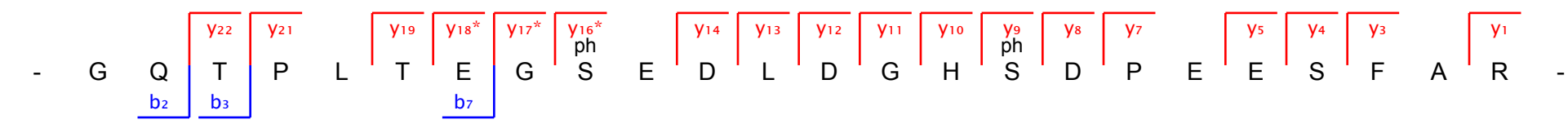
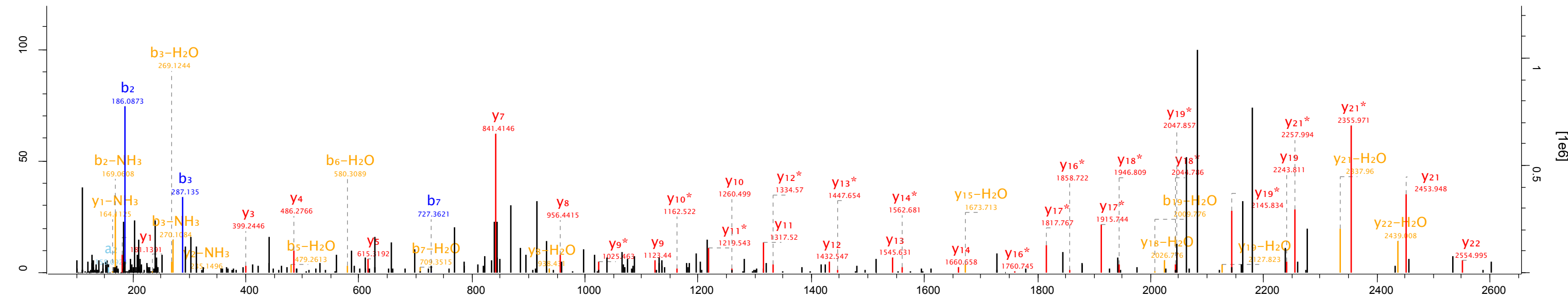
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13429 Method FTMS; HCD Score 138.28 m/z 677.32 Gene names CFL2



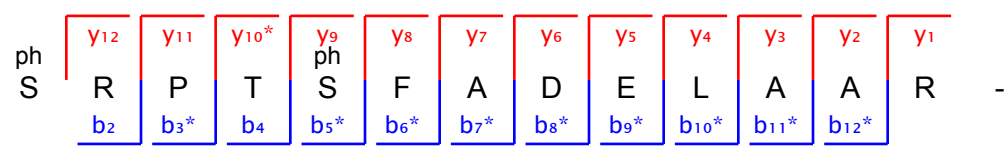
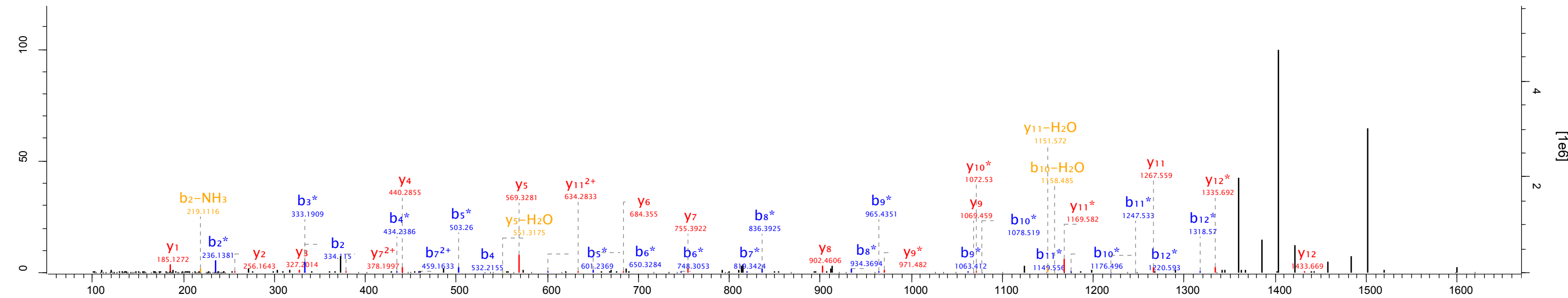
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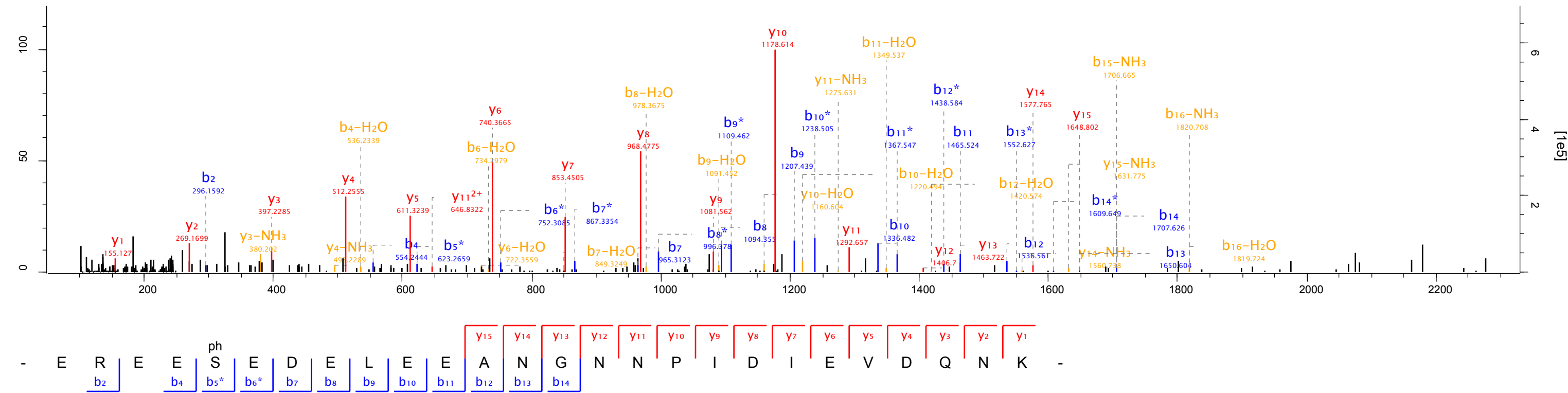


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13799 Method FTMS; HCD Score 95.36 m/z 914.69 Gene names FAM134C

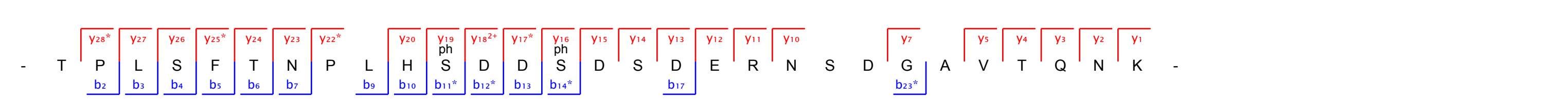
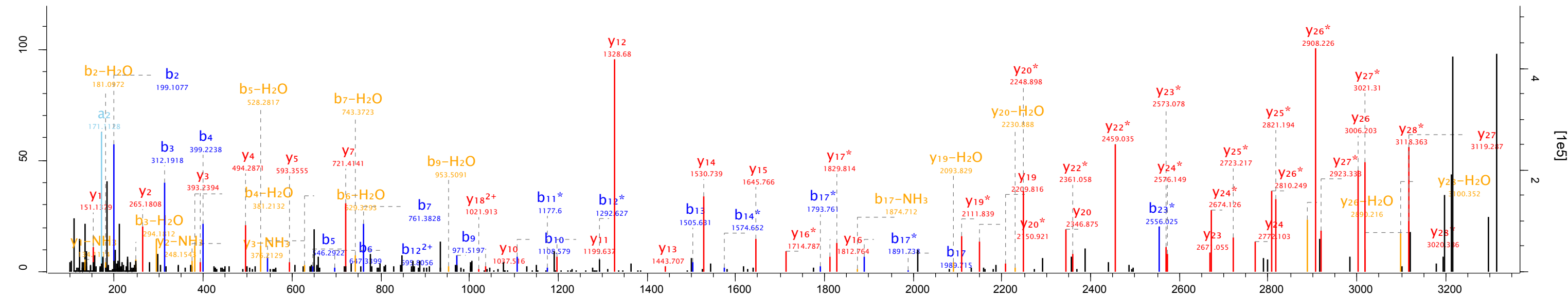


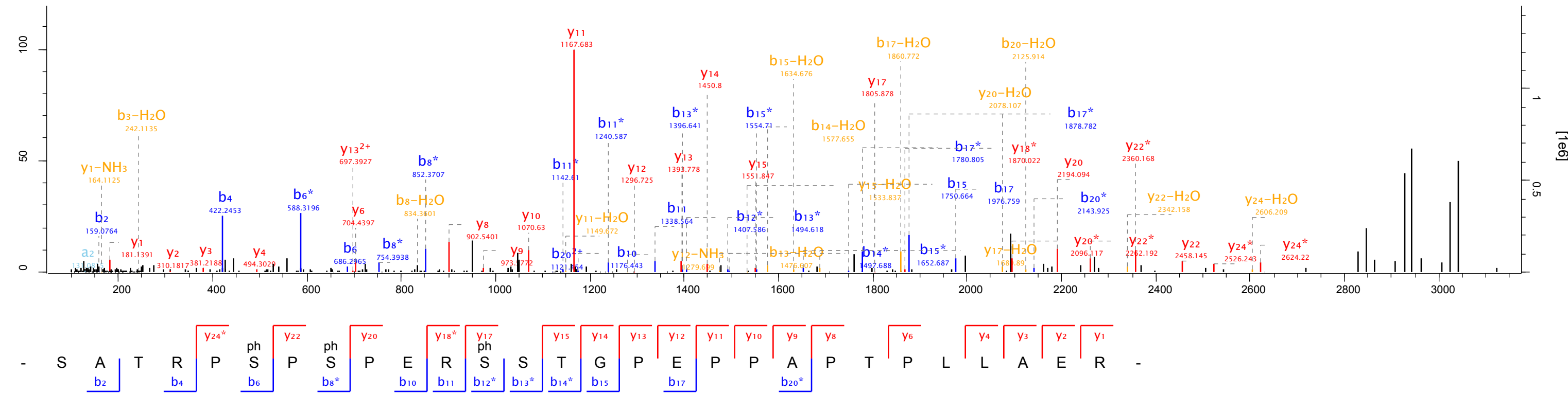
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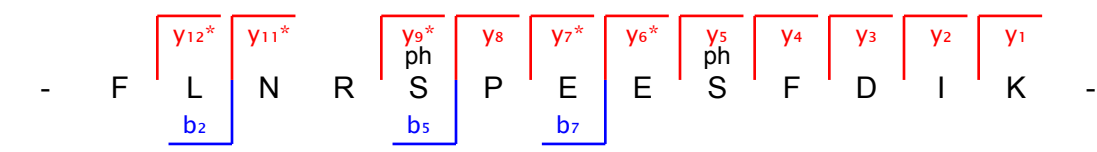
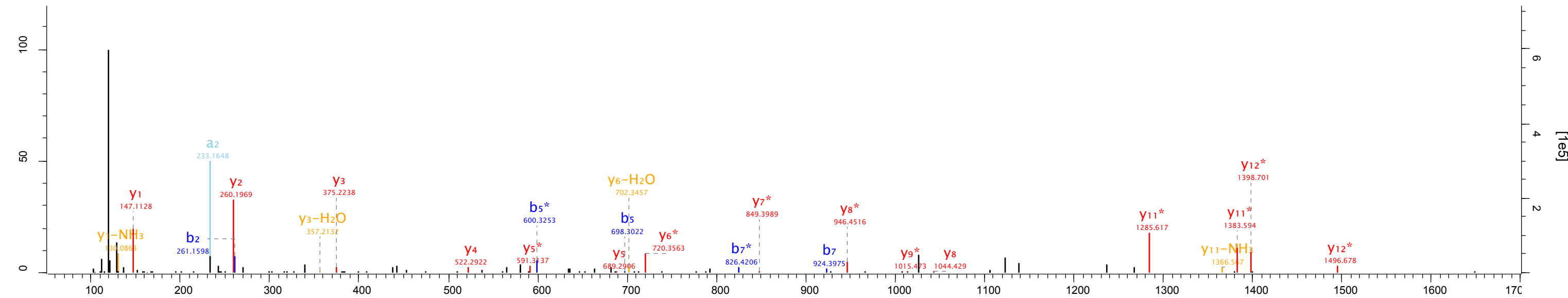


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14249 Method FTMS; HCD Score 246.12 m/z 830.35 Gene names PTPN12

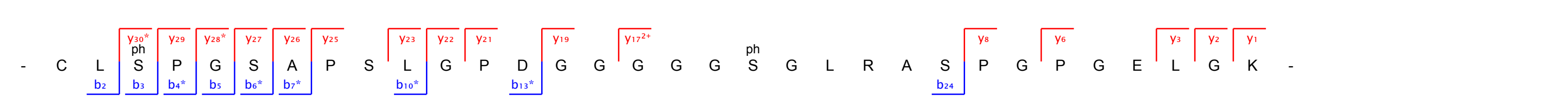
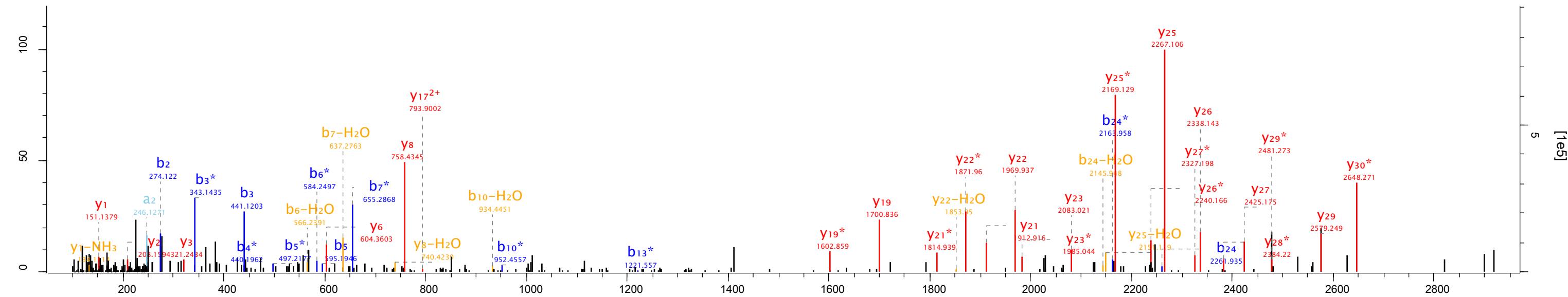




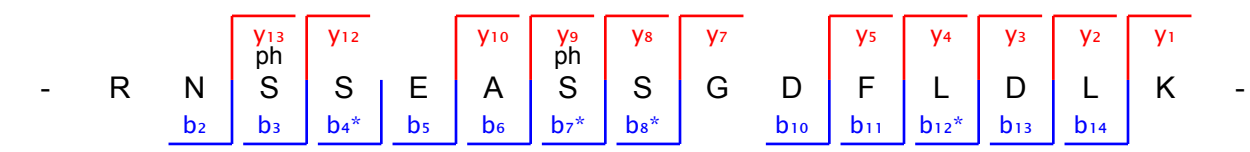
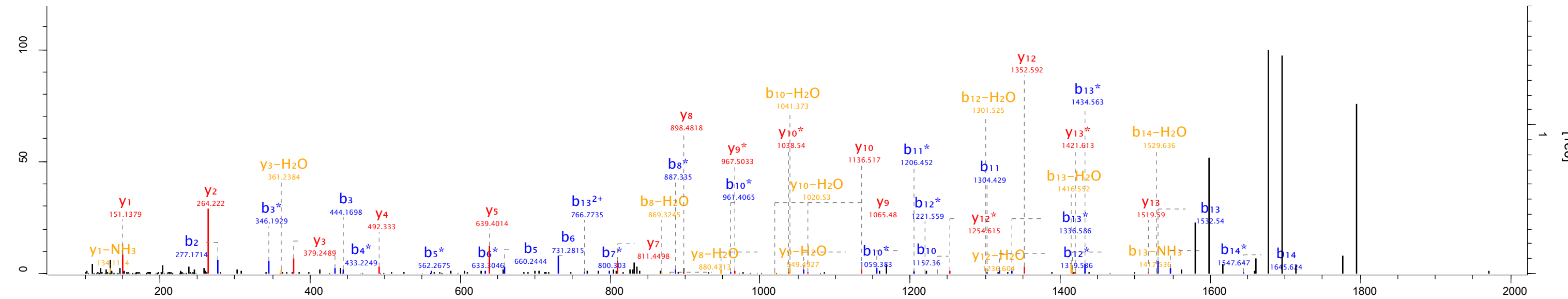
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14509 Method FTMS; HCD Score 118.72 m/z 581.25 Gene names RPS6KC1



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 14639 Method: FTMS; HCD Score: 113.42 m/z: 1007.13 Gene names: SOX10

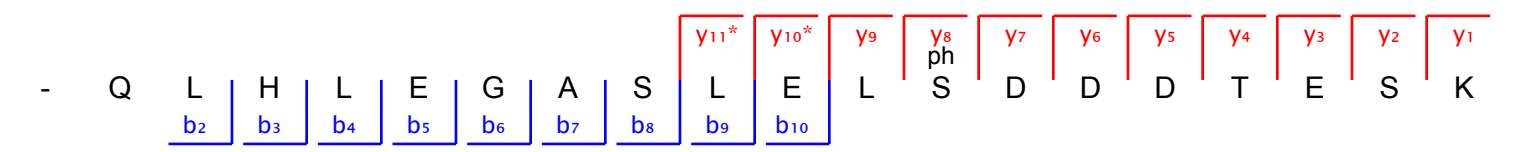
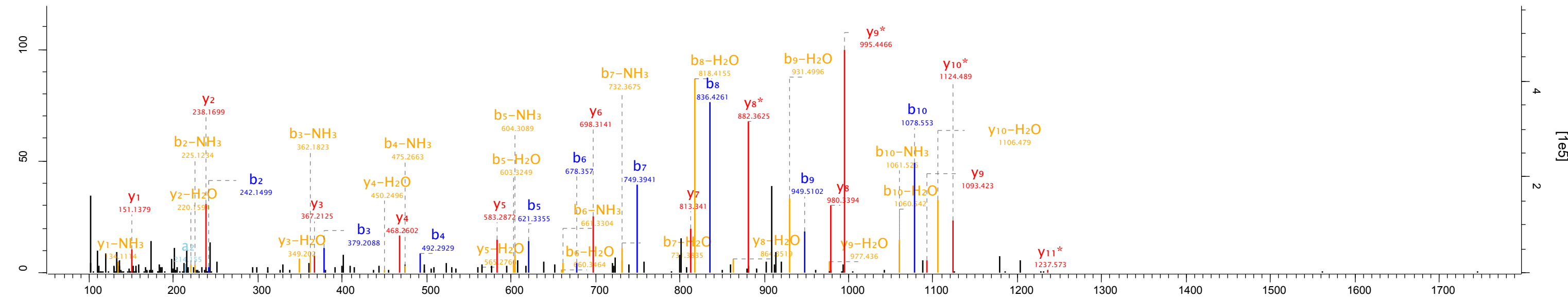


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 Scan: 14689 Method: FTMS; HCD Score: 153.83 m/z: 898.88 Gene names: HN1

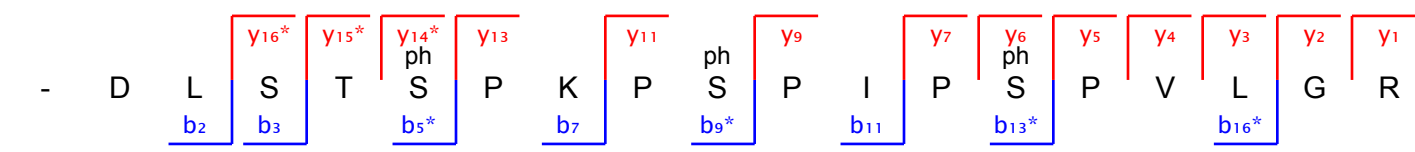
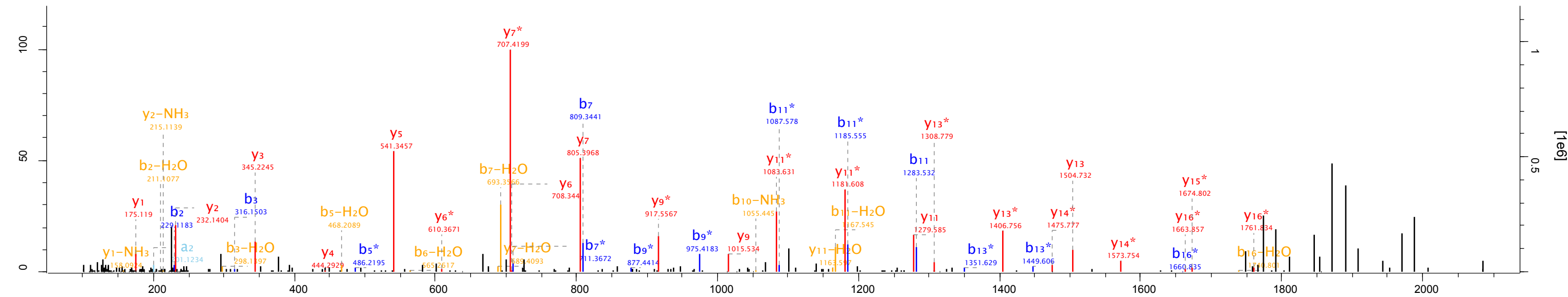


Raw file
20171215_MaS_33SR_LMH_phospho2_03

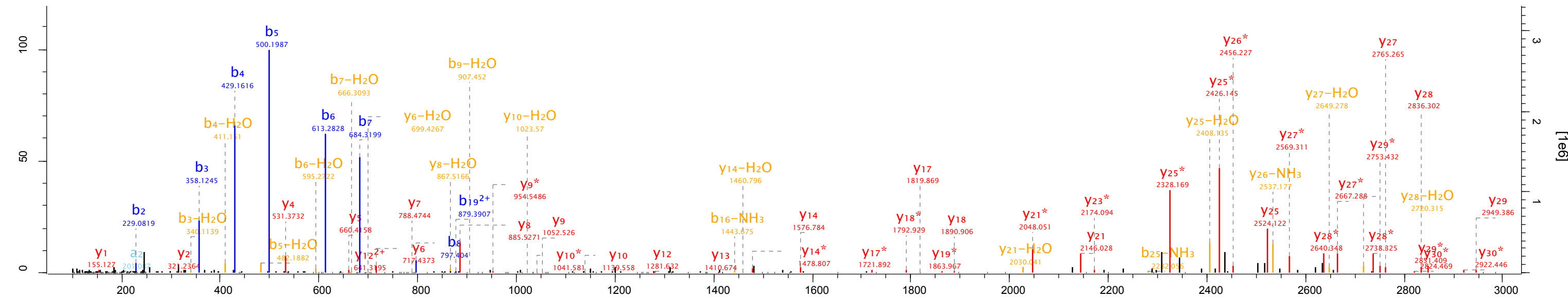
Scan 14799 Method FTMS; HCD Score 131.35 m/z 724.66 Gene names MYH10



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15109 Method FTMS; HCD Score 132.79 m/z 1044.97 Gene names EHBP1



Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 15149 Method: FTMS; HCD Score: 169.09 m/z: 1150.87 Gene names: SIRT1

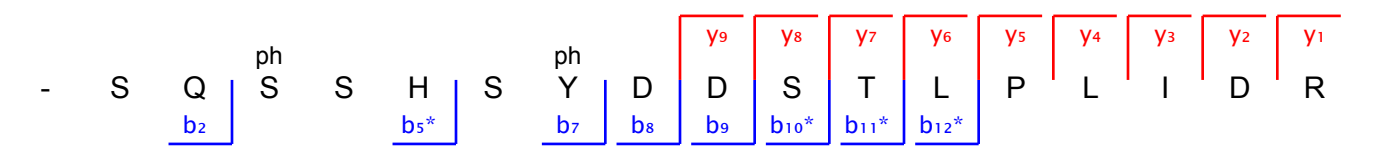
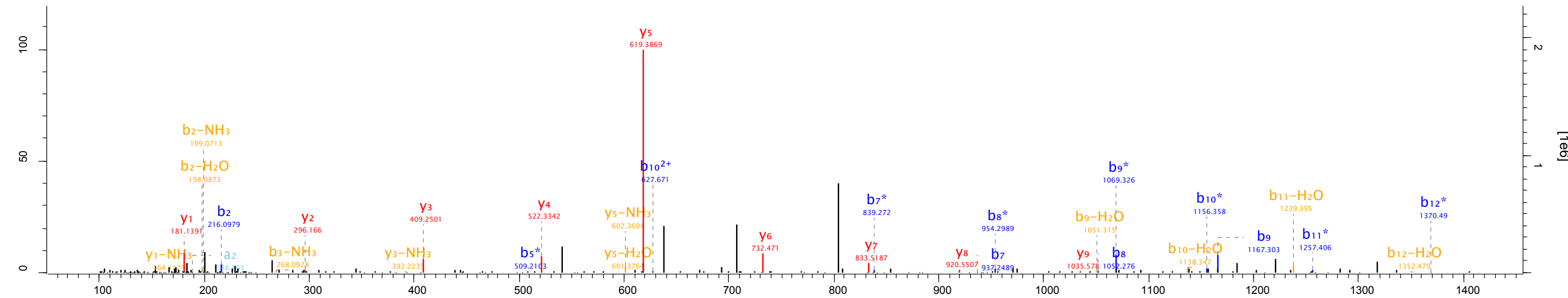


ac - A D E A A L A L Q P G G S P S A A G A D R E A A S S P A G E P L R K -

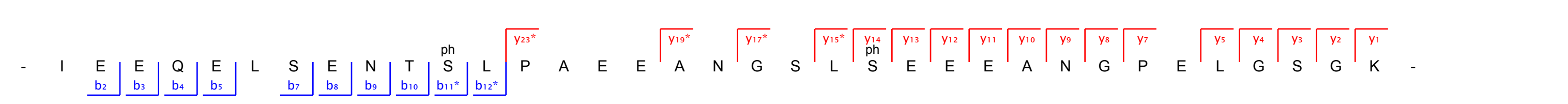
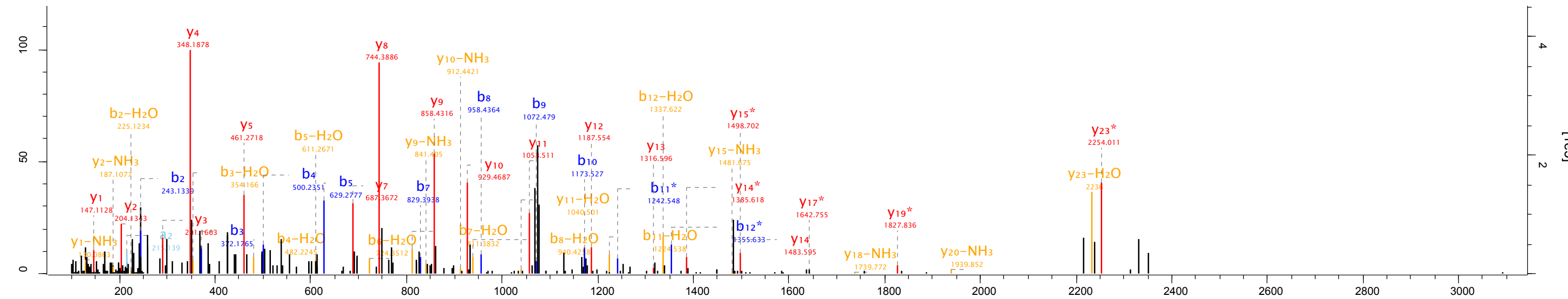
Fragmentation sites are indicated by brackets below the amino acid sequence:

- Blue brackets (b ions): b2 (D-E), b3 (E-A), b4 (A-A), b5 (A-L), b6 (L-A), b7 (A-L), b8 (L-Q), b19²⁺ (A-D).
- Red brackets (y ions): y1 (K), y2 (R), y4 (E), y5 (G), y6 (A), y7 (P), y8 (S), y9 (S), y10 (S), y12 (A), y13 (A), y14 (R), y17 (G), y18 (A), y19 (A), y21 (P), y23 (G), y25 (P), y26 (Q), y27 (L), y28 (A), y29 (L), y30 (A).

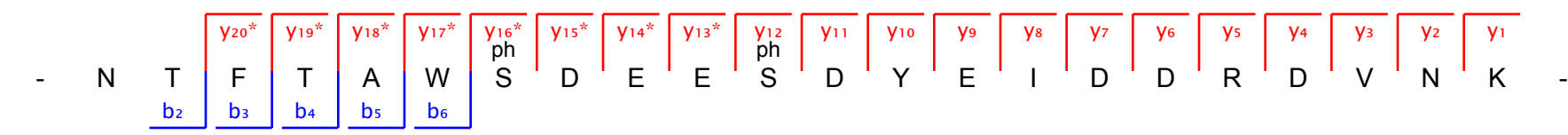
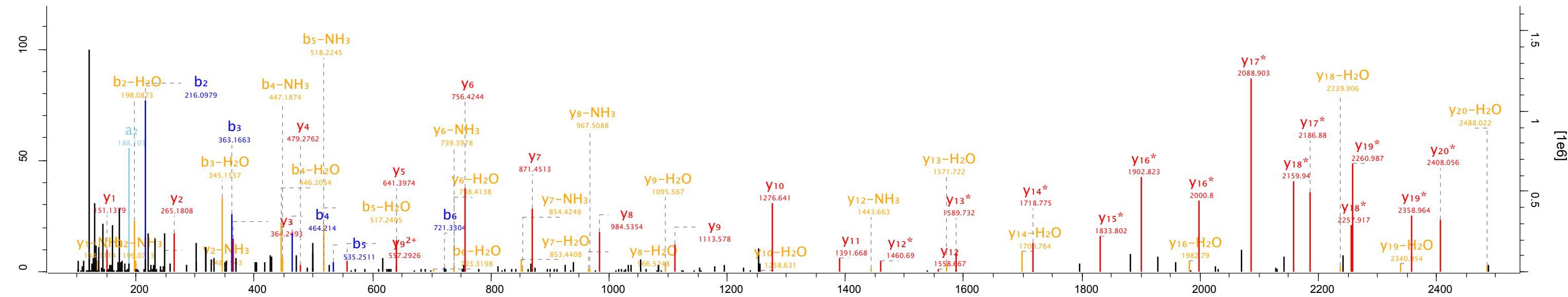
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15199 Method FTMS; HCD Score 52.65 m/z 696.29 Gene names CTNND1



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15479 Method FTMS; HCD Score 64.17 m/z 1269.55 Gene names WRAP53

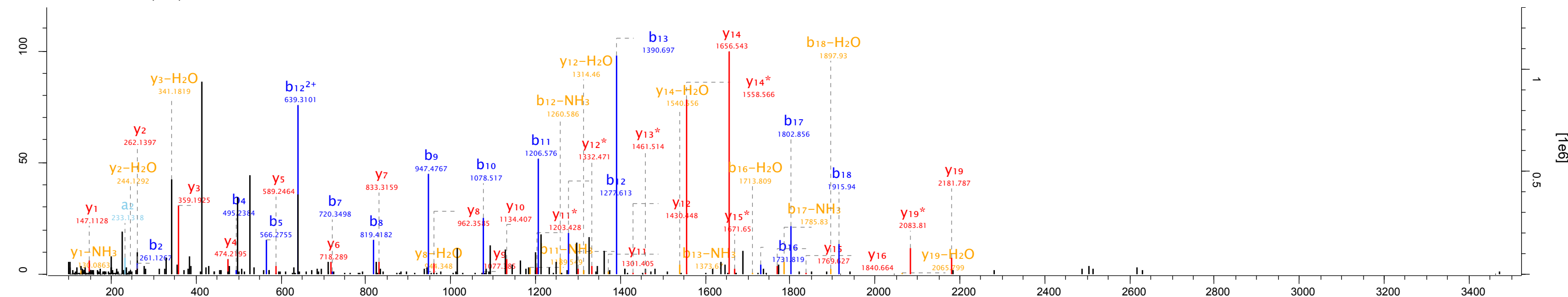


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 15839 Method FTMS; HCD Score 205.59 m/z 940.71 Gene names LARP1



Raw file
20171215_MaS_33SR_LMH_phospho2_03

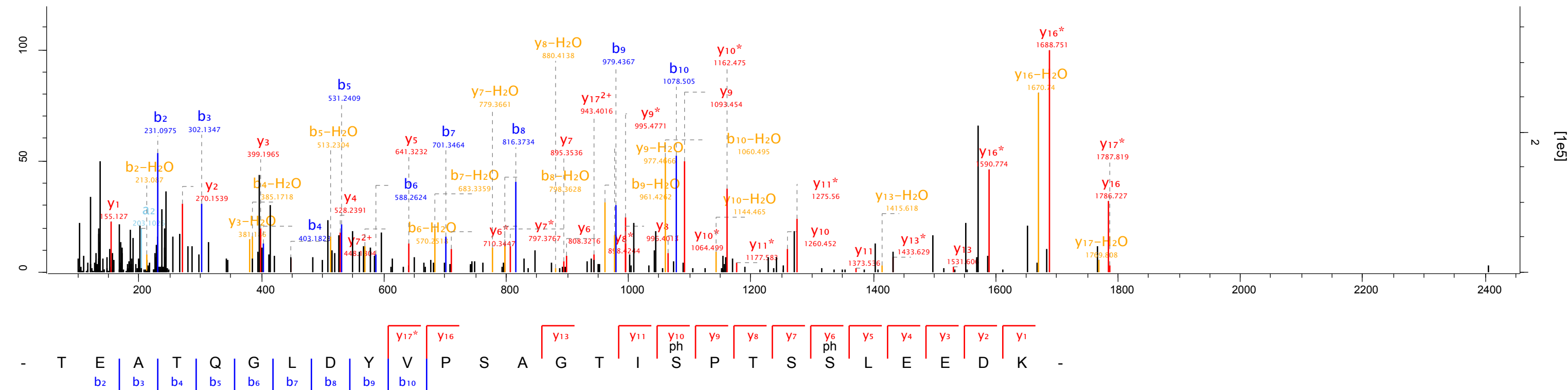
Scan 16239 Method FTMS; HCD Score 105.94 m/z 1191.5 Gene names HDAC1



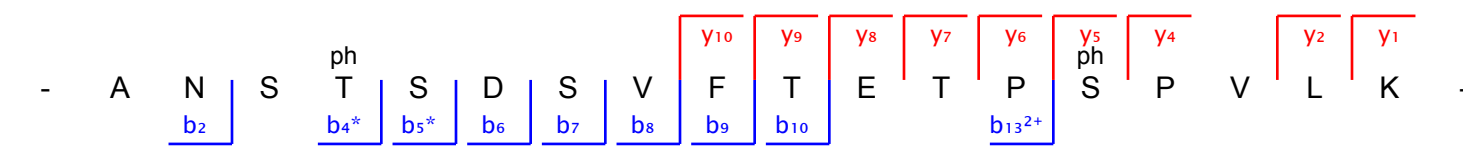
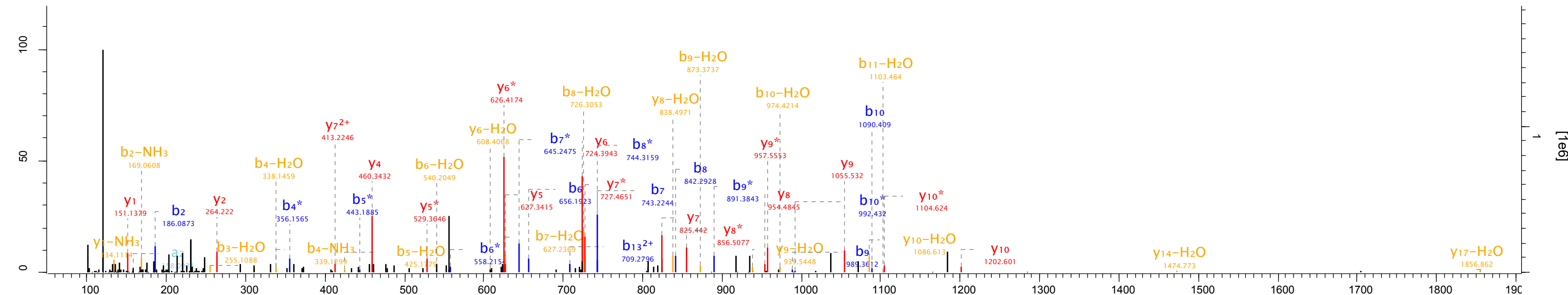
ox
- M L P H A P G V Q M Q A I P E D A I P E E S G D E D D P D K -

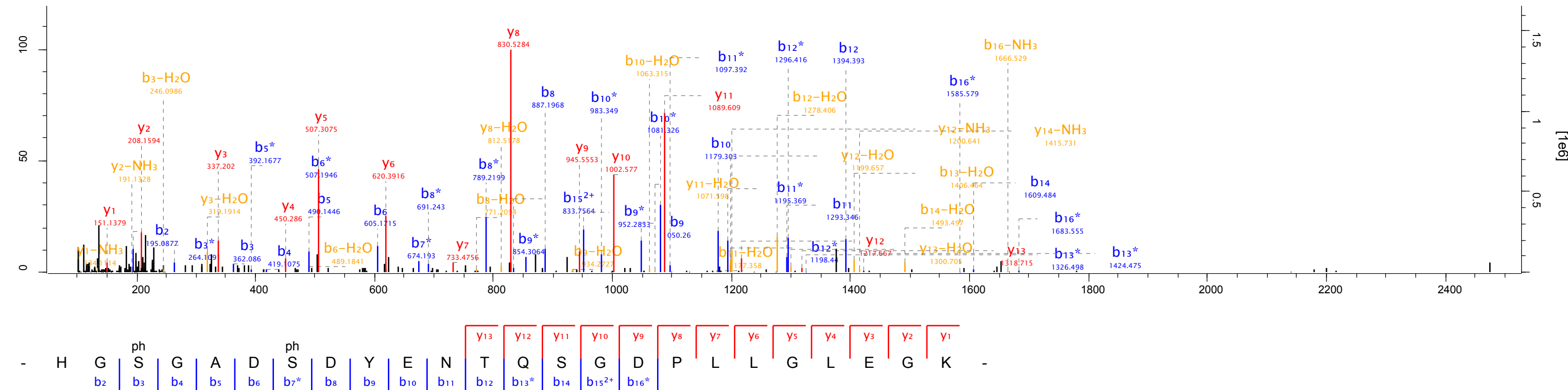
b2 b4 b5 b7 b8 b9 b10 b11 b12 b13 b16 b17 b18 y19 y16 y15 y14 y13* y12 y11 ph y10 y9 y8 y7 y6 y5 y4 y3 y2 y1

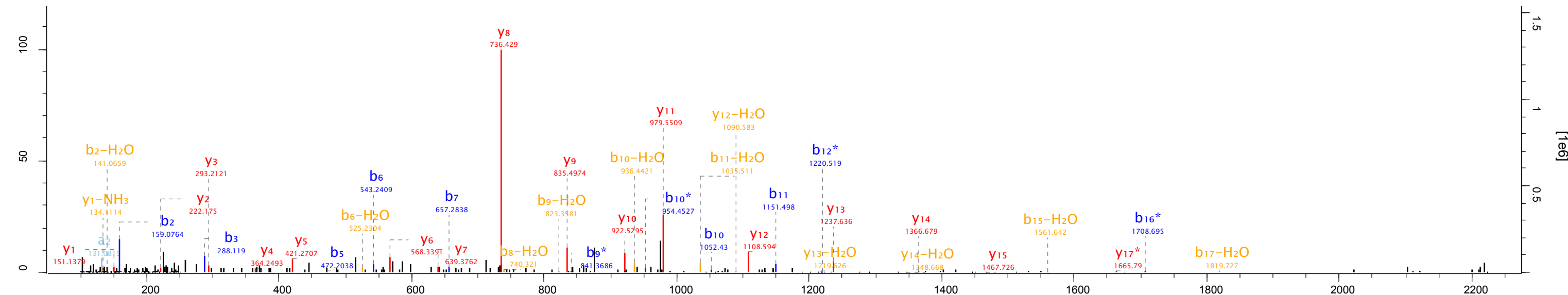
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 16269 Method FTMS; HCD Score 166.74 m/z 955.75 Gene names MAP1A



Raw file
 20171215_MaS_33SR_LMH_phospho2_03
 Scan 16609 Method FTMS; HCD Score 160.83 m/z 681.97 Gene names CDC42EP3



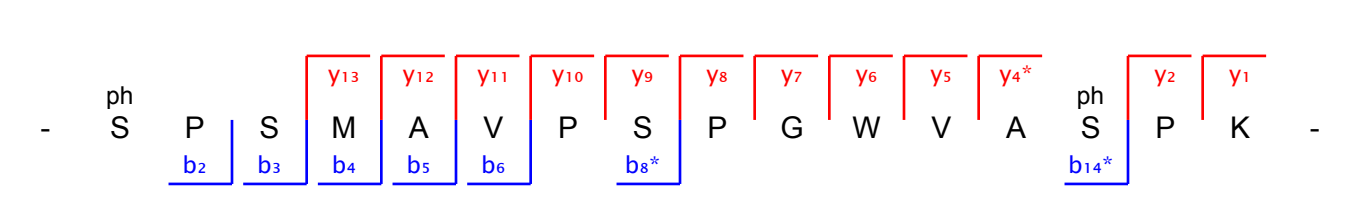
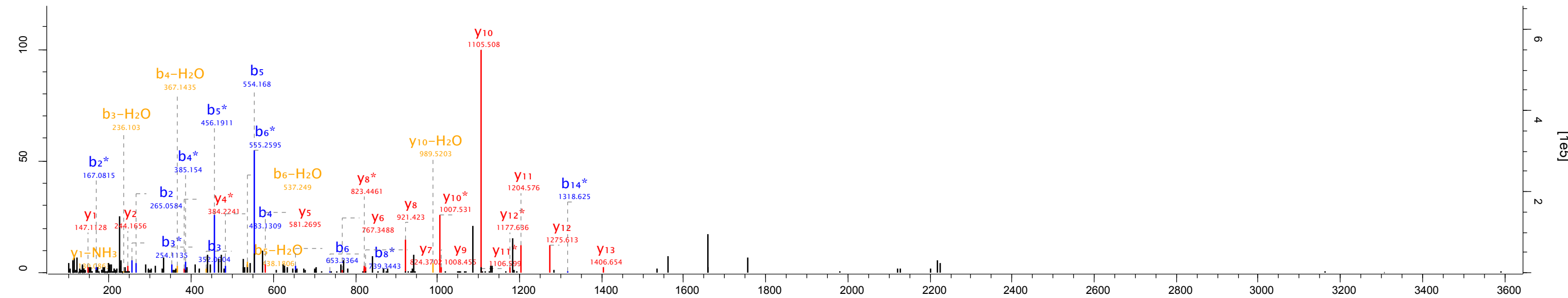


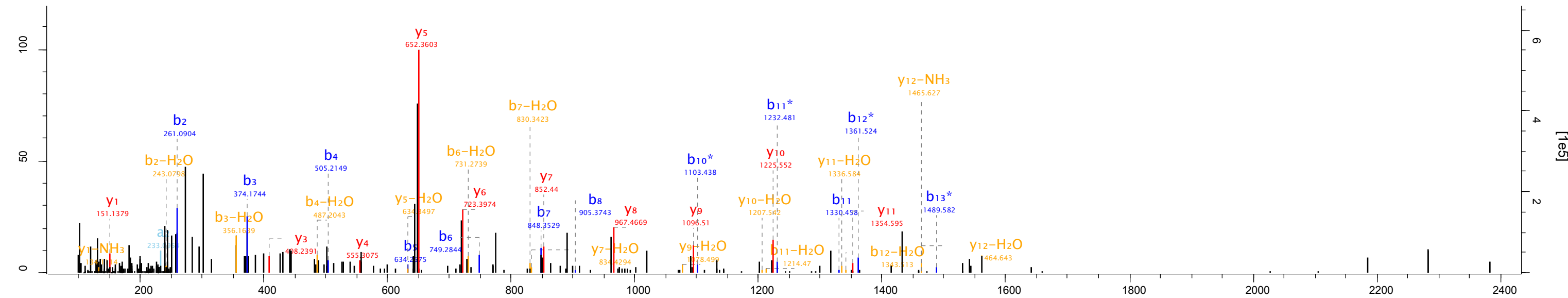


- S A E P S A N T ph T L V S E T E E E G S V P A F G A A A K -

b₂
b₃
b₅
b₆
b₇
b₉*
b₁₀
b₁₁
b₁₂*
b₁₆*
y₁₅
y₁₄
y₁₃
y₁₂
y₁₁
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y₆
y₅
y₄
y₃
y₂
y₁

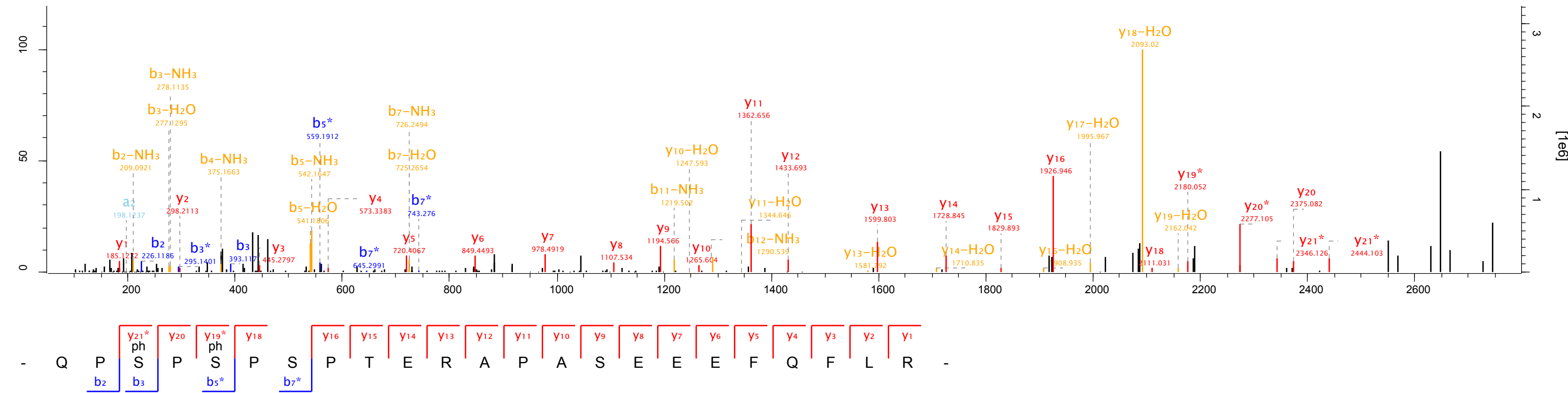
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 Scan: 16979 Method: FTMS; HCD Score: 92.52 m/z: 879.37 Gene names: BCL9L



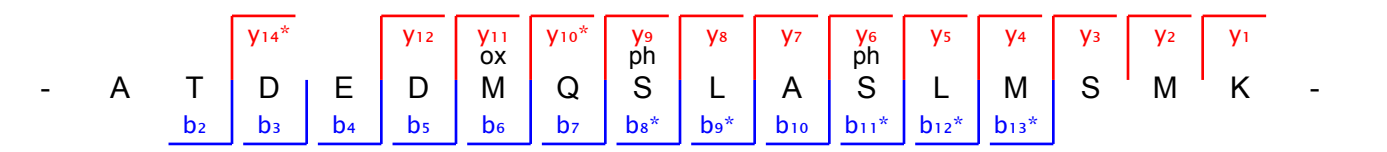
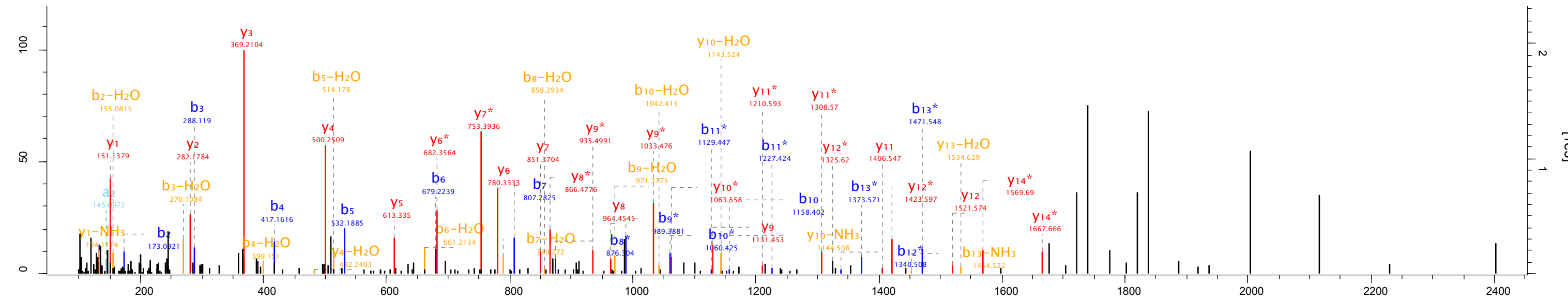


- E M L M E D V G S E E E Q E E E D E A P F Q E K -

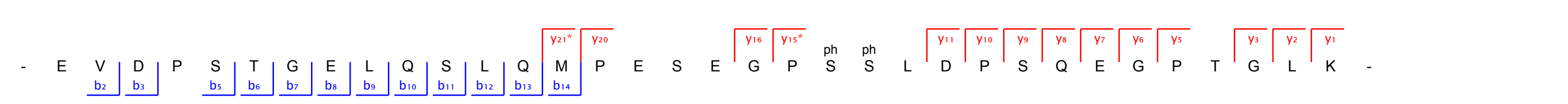
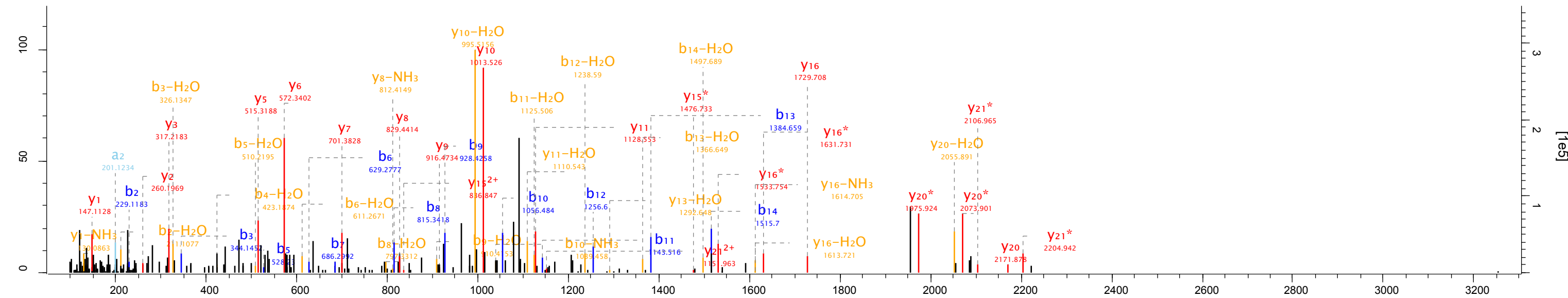
b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₁₀^{*} b₁₁ b₁₂^{*} b₁₃^{*} y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 18479 Method FTMS; HCD Score 171.32 m/z 969.37 Gene names EHBP1

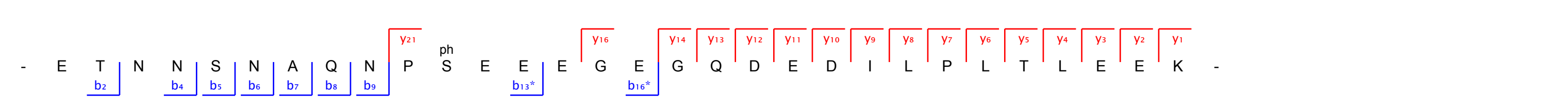
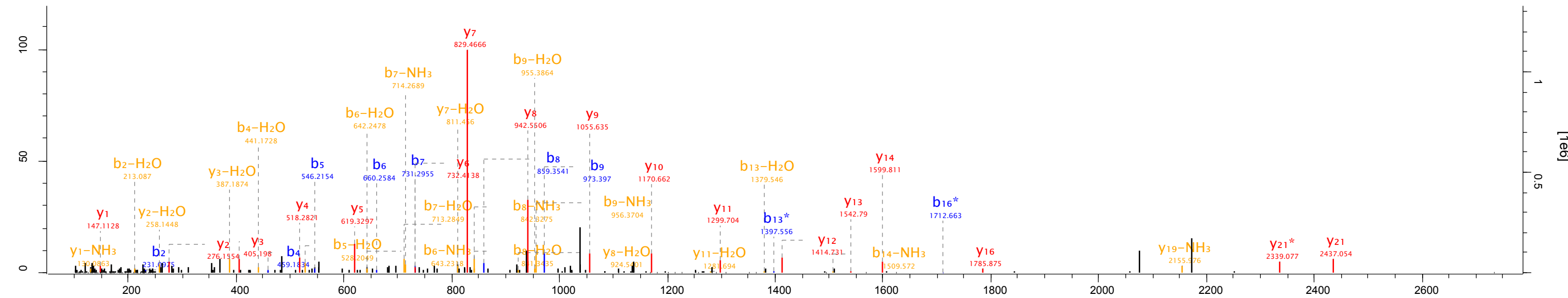


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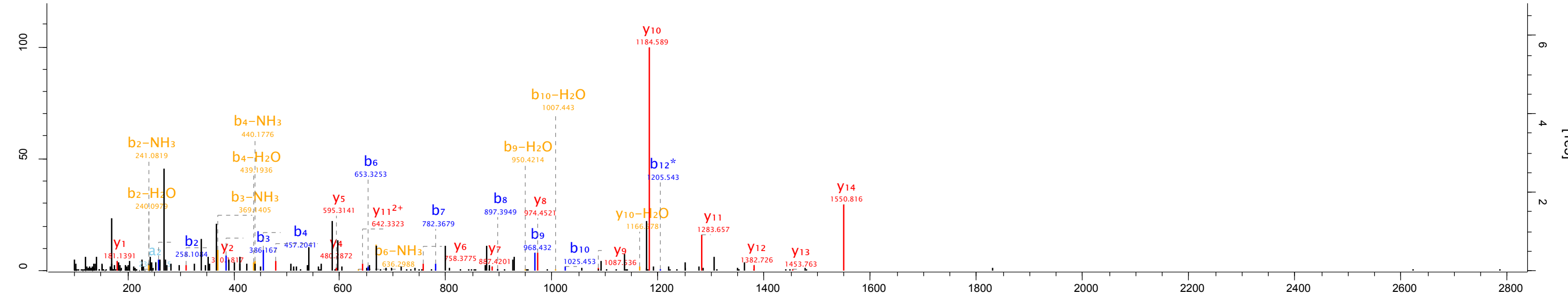
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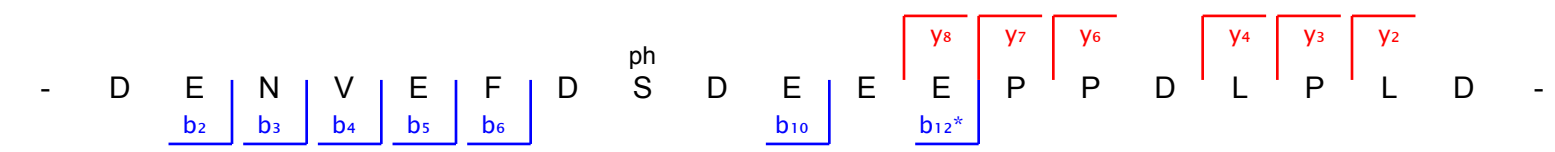
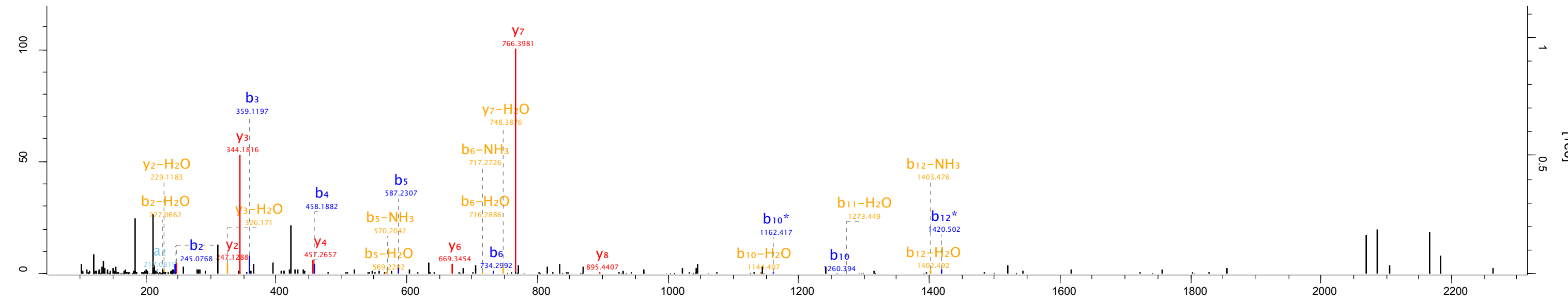


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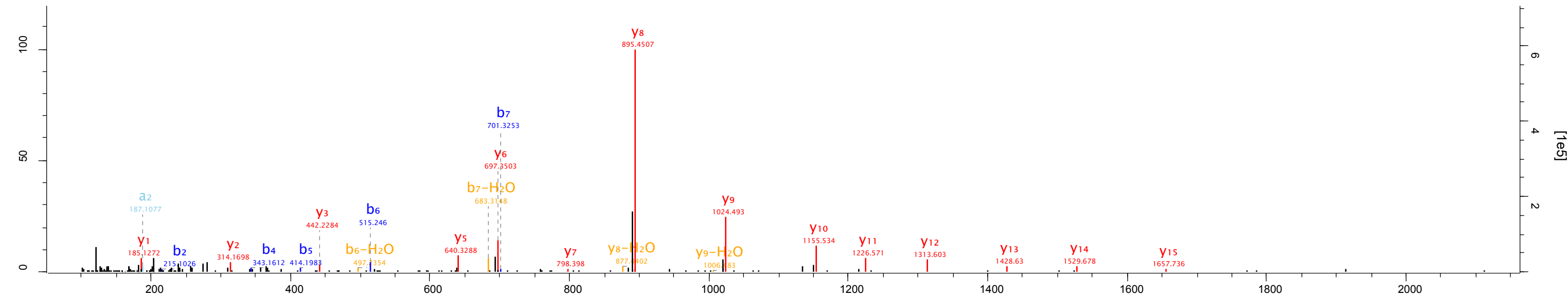


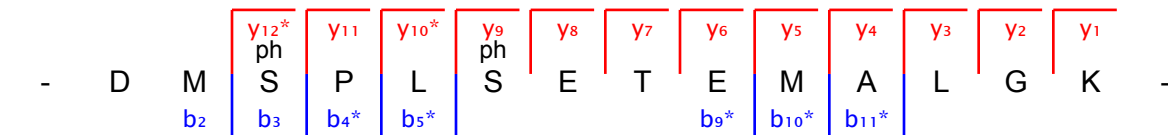
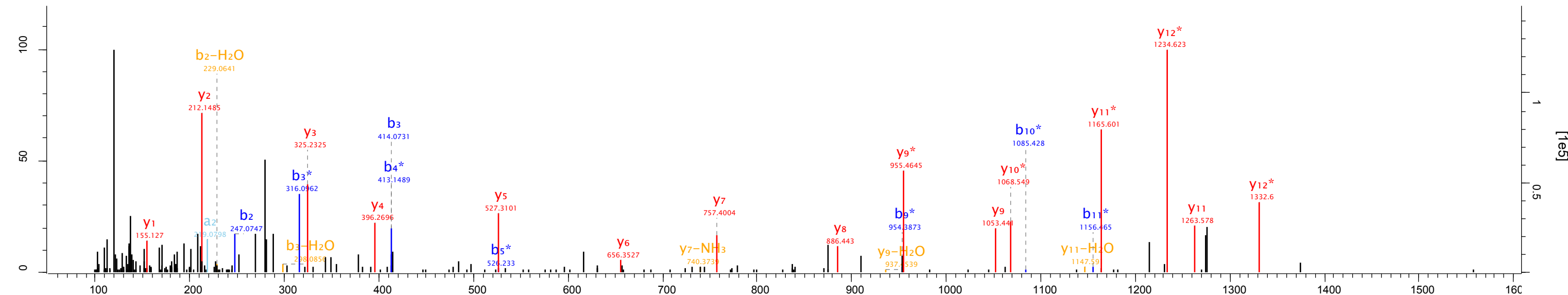
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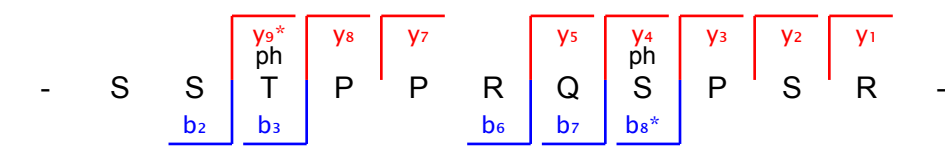
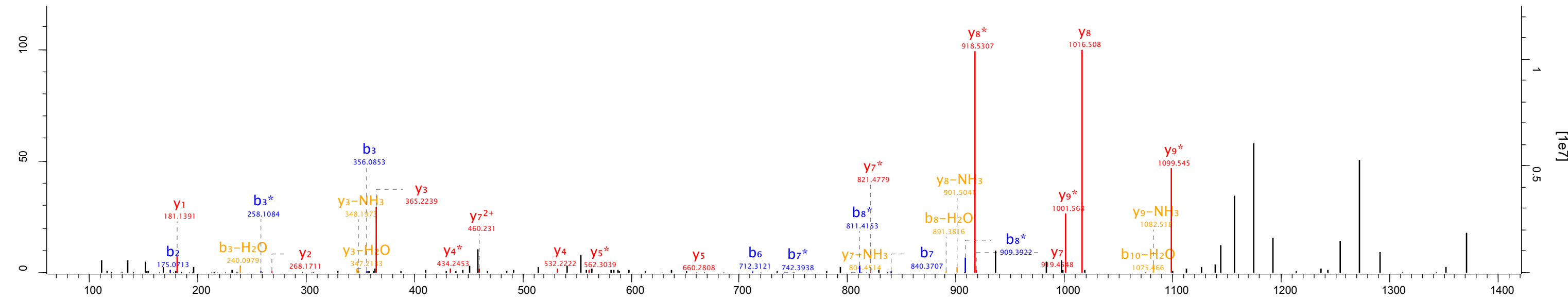
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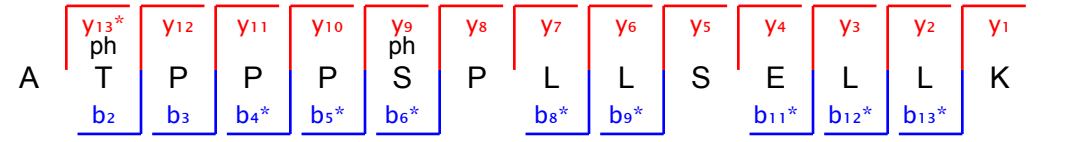
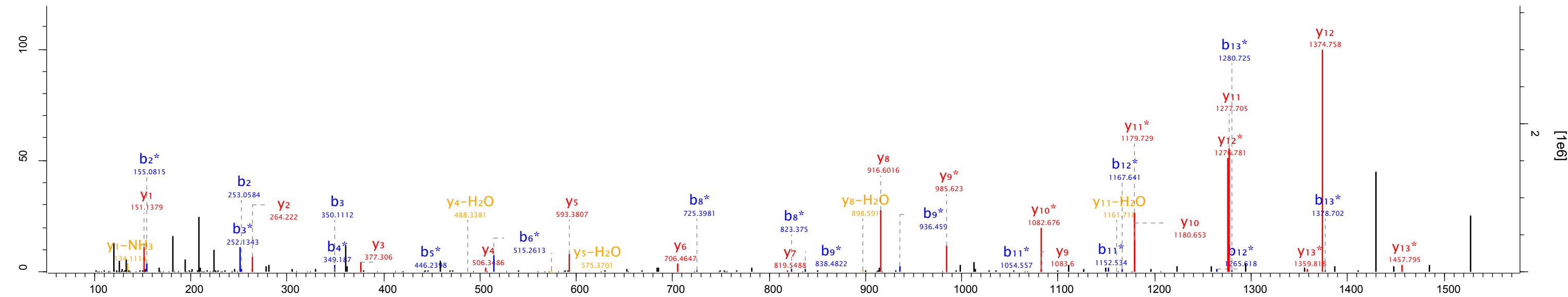




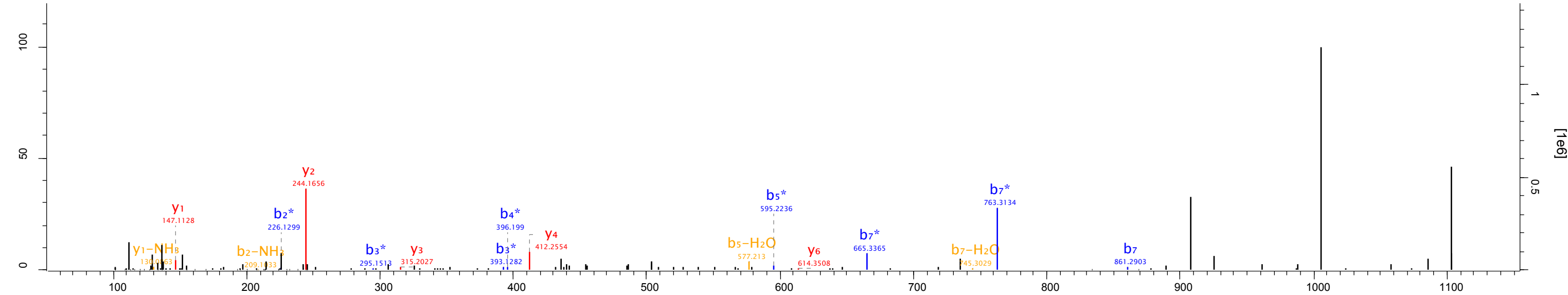
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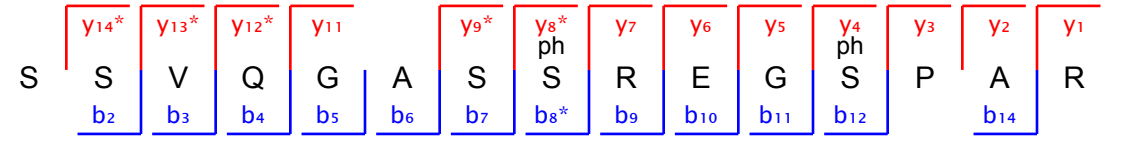
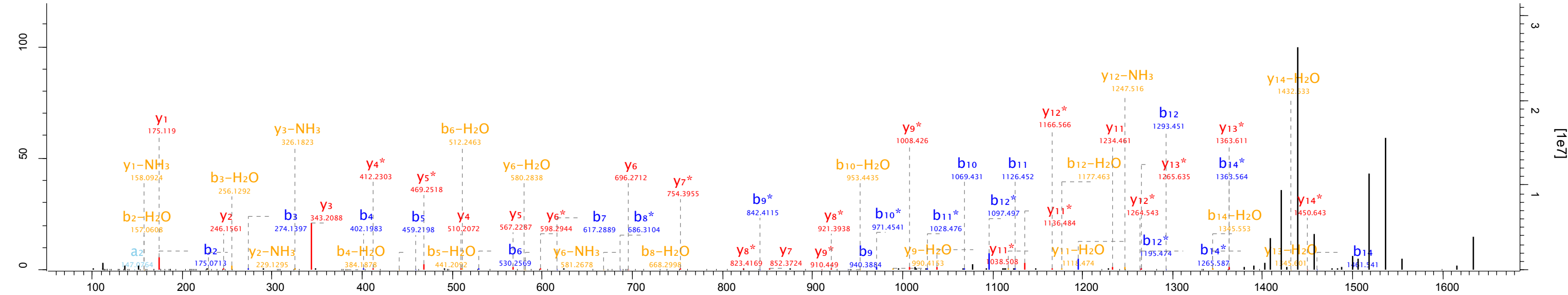
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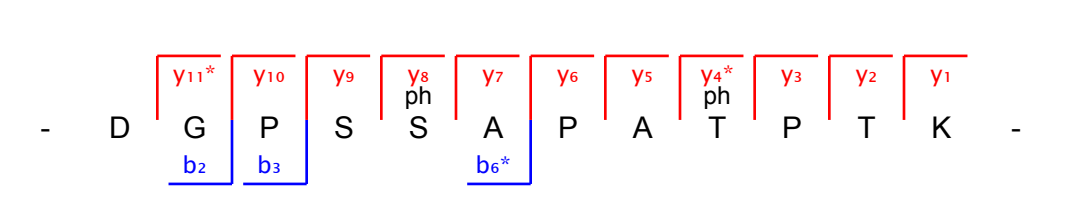
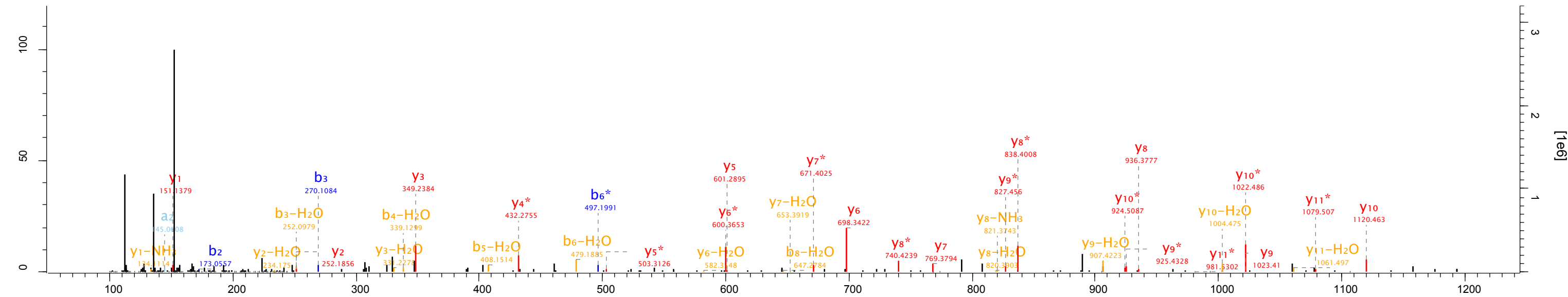
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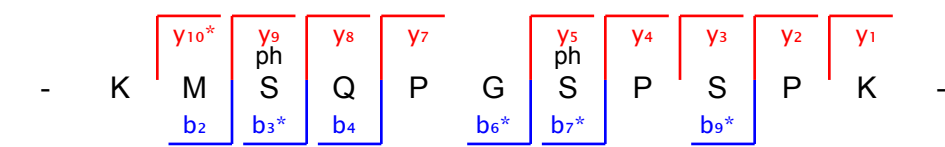
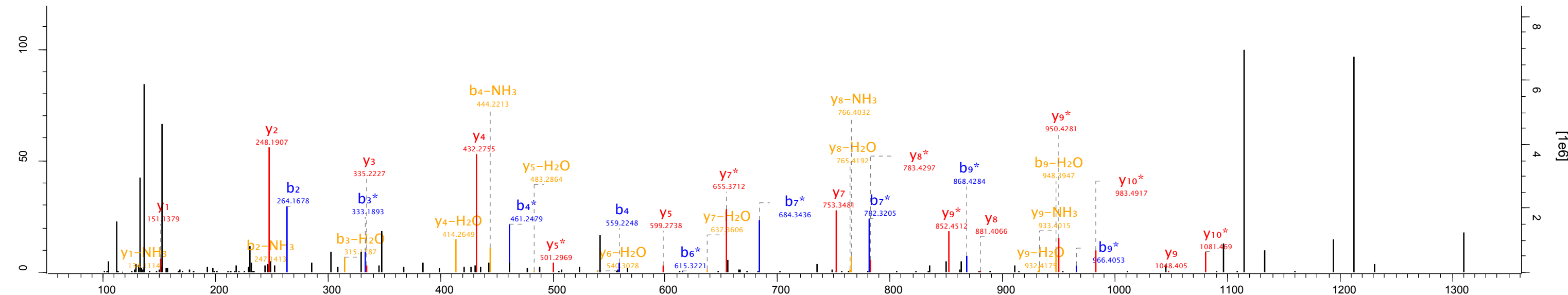


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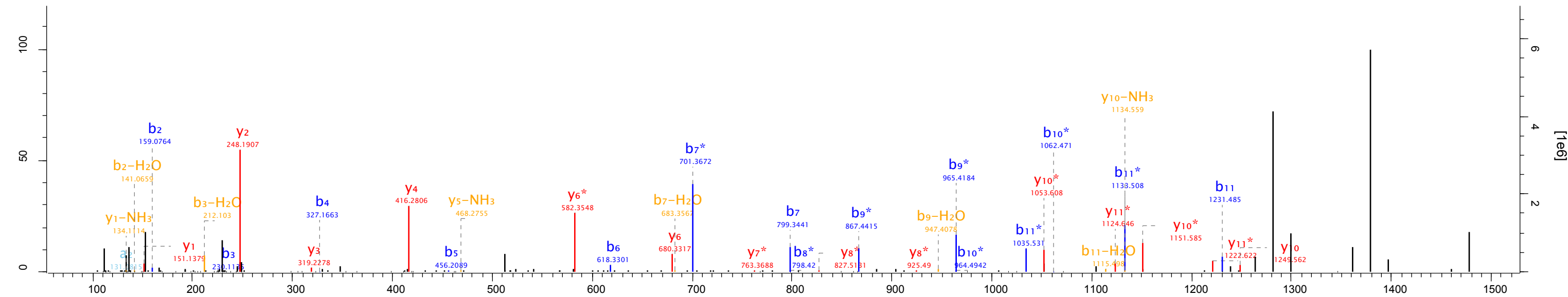


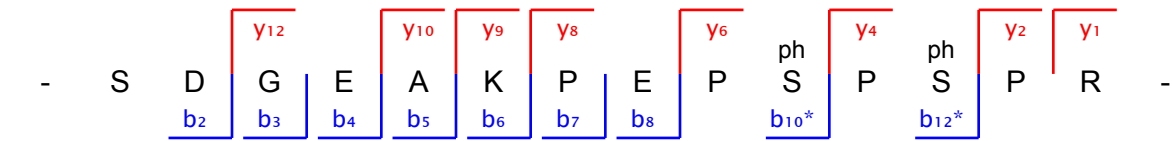
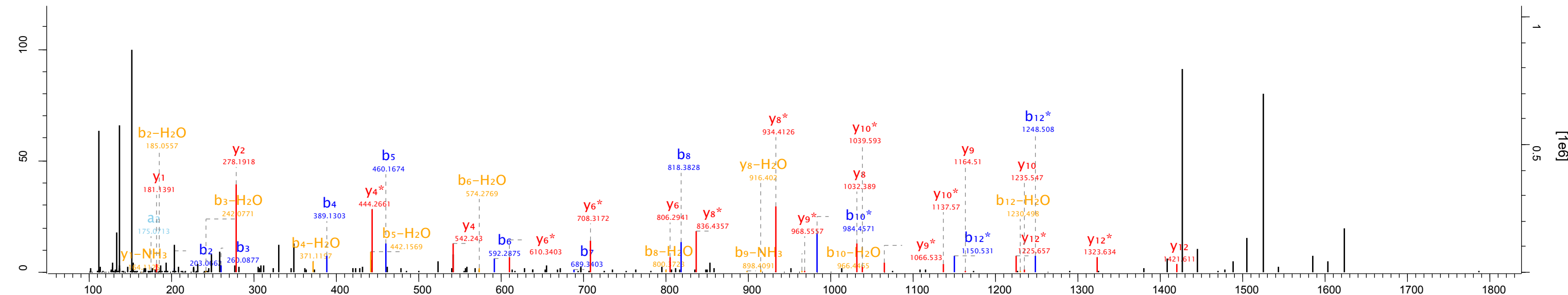
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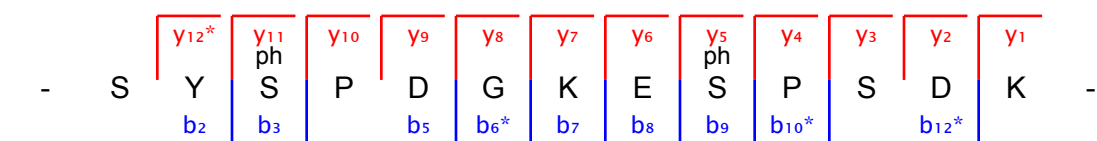
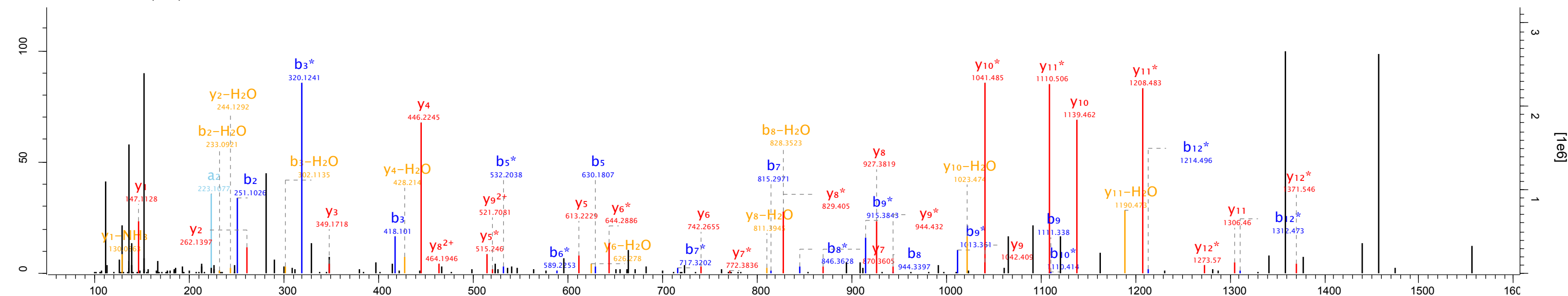
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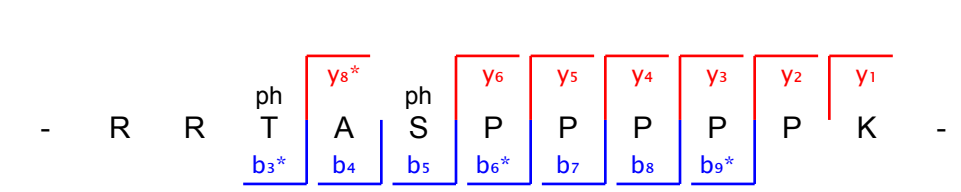
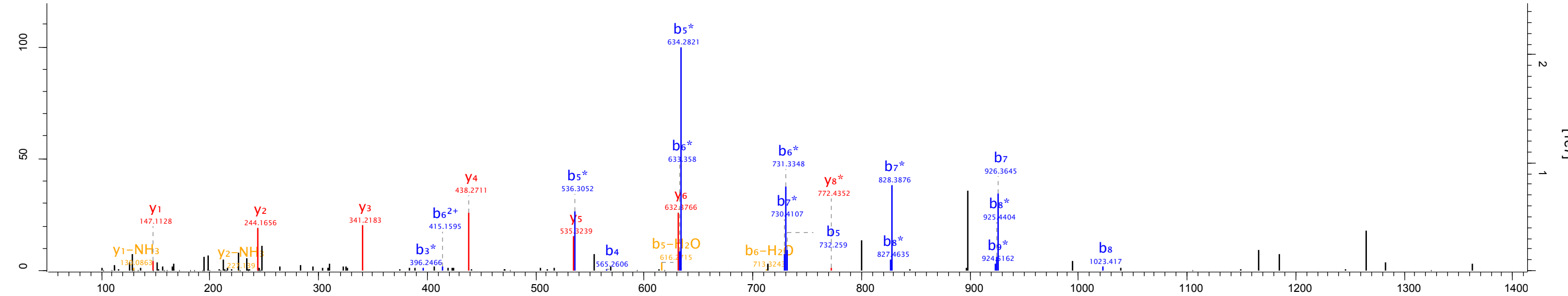
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20171215_MaS_33SR_LMH_phospho2_03

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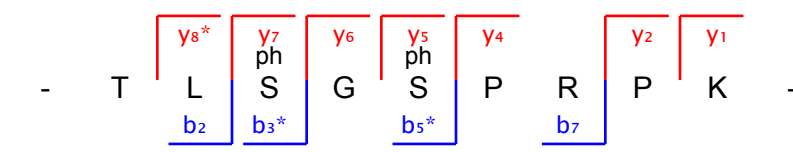
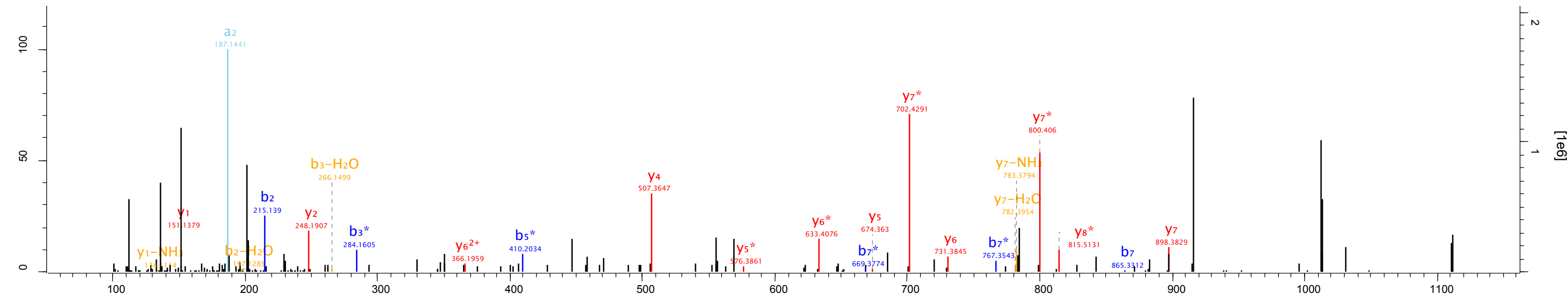


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20171215_MaS_33SR_LMH_phospho2_03

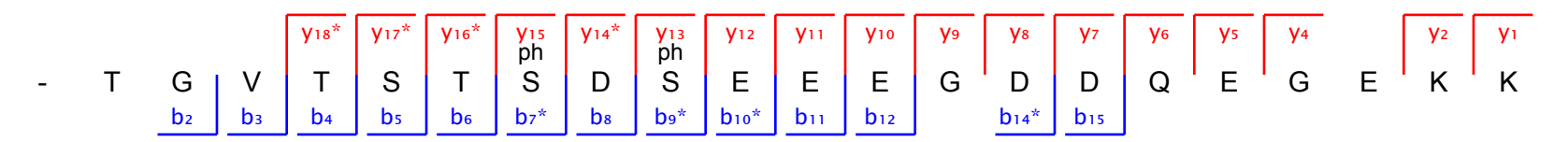
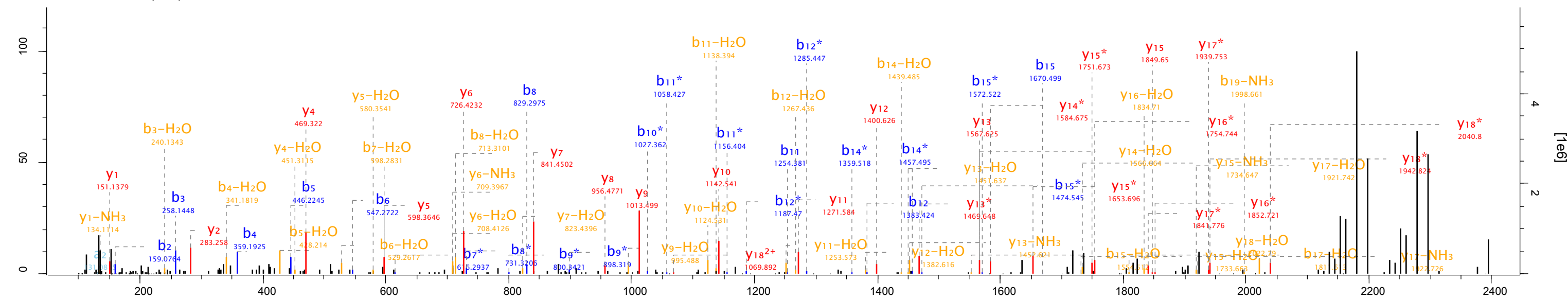


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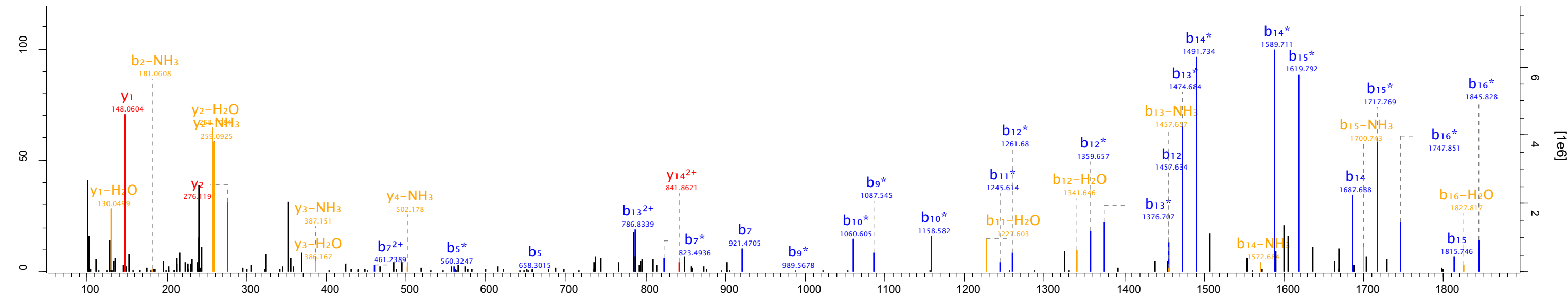


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20171215_MaS_33SR_LMH_phospho2_03

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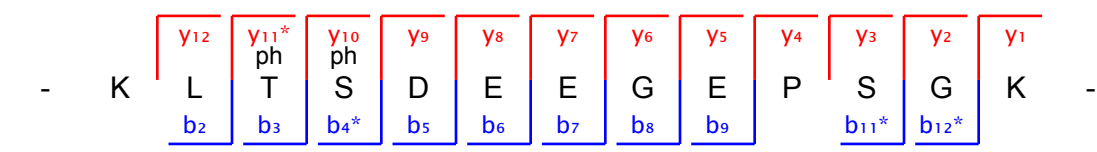
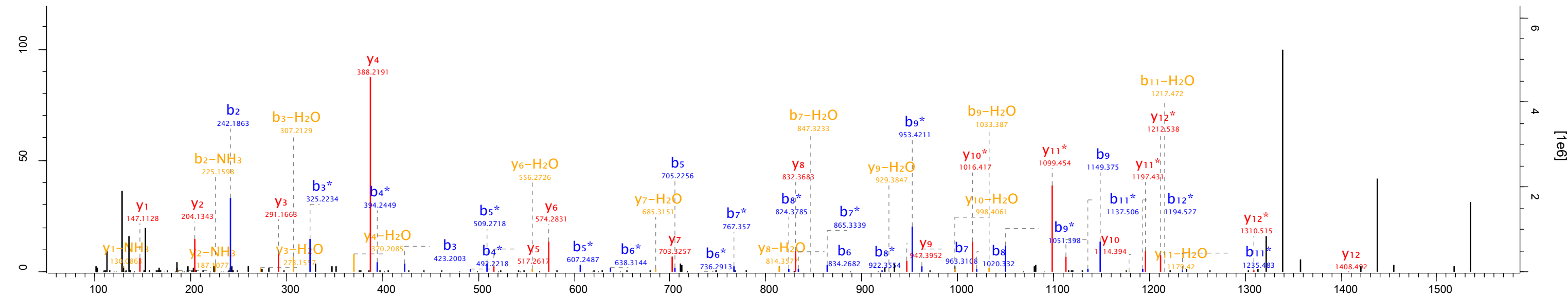


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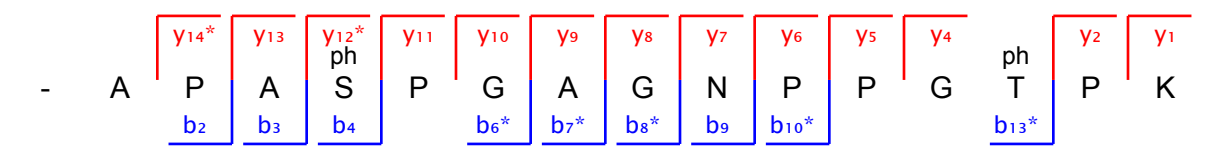
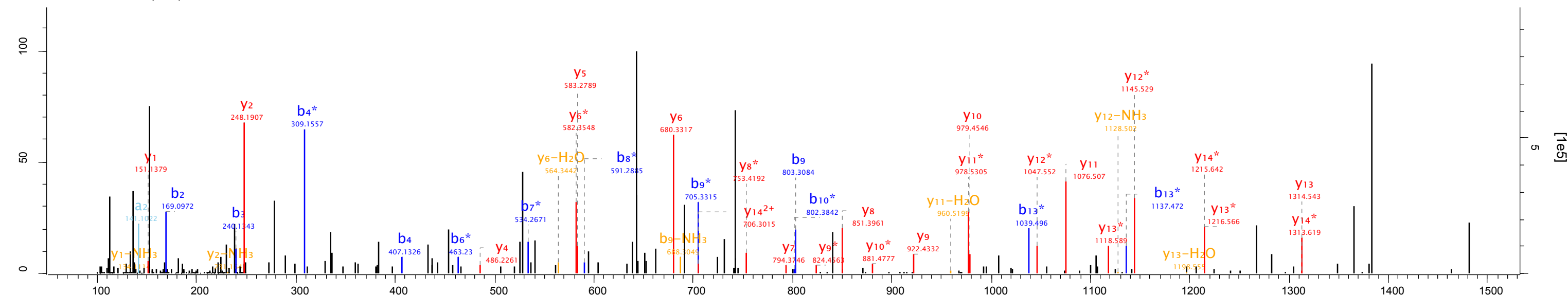
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20171215_MaS_33SR_LMH_phospho2_03

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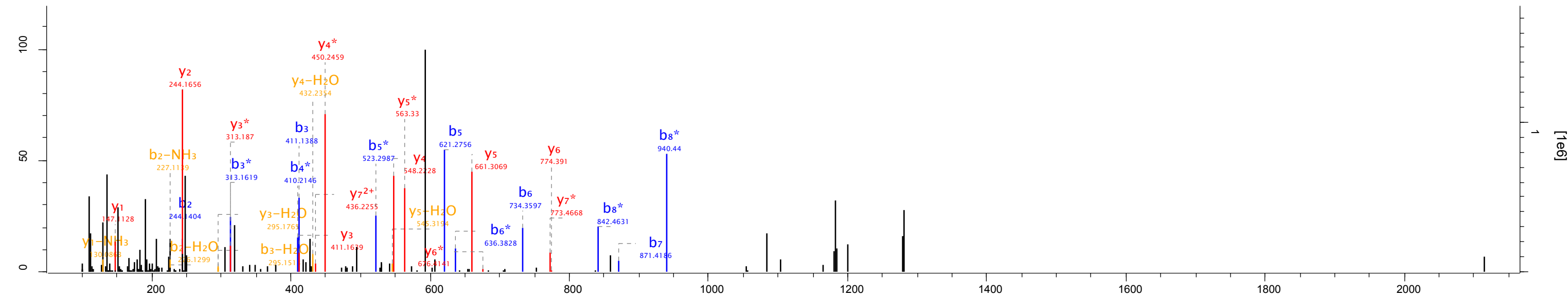


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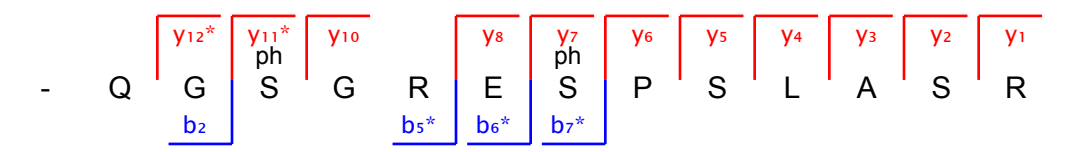
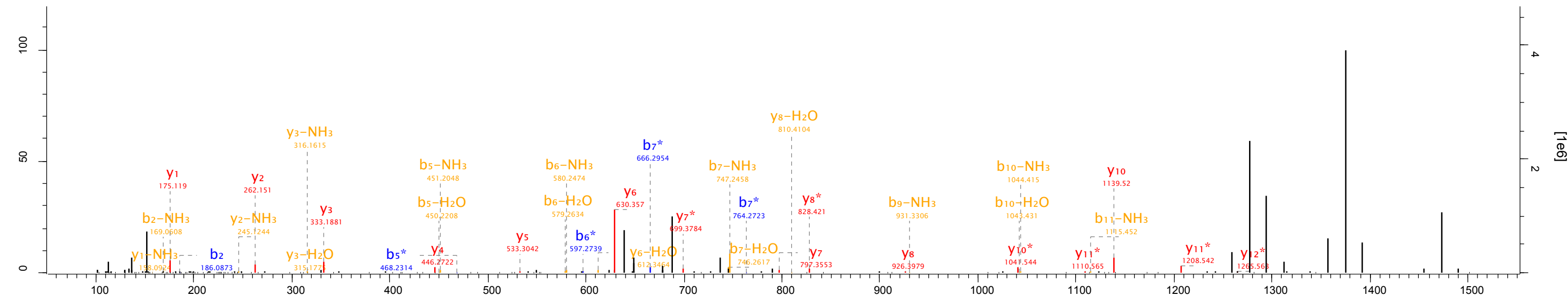


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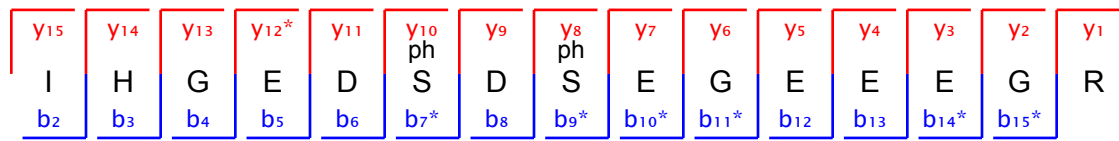
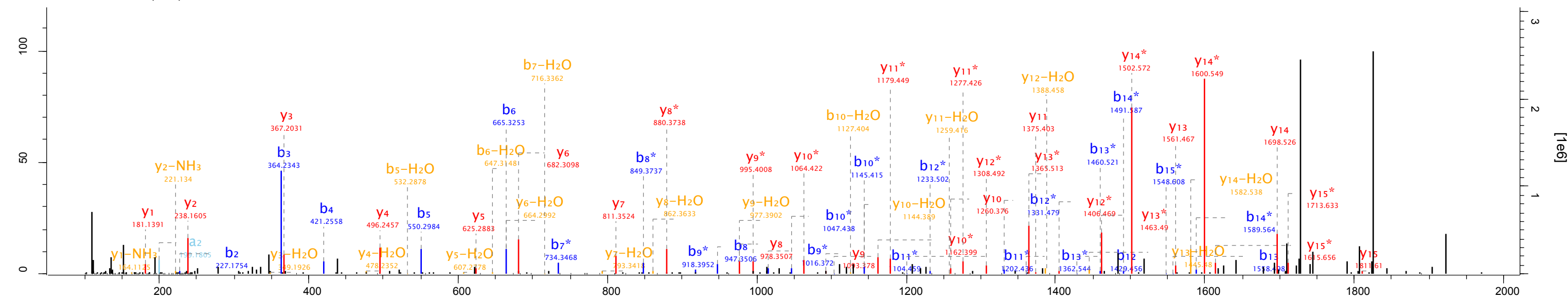
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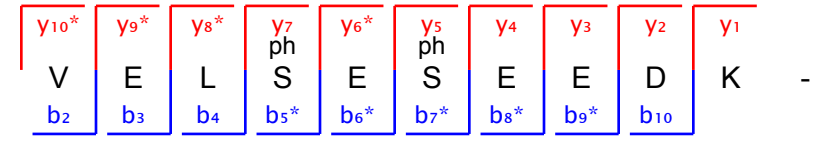
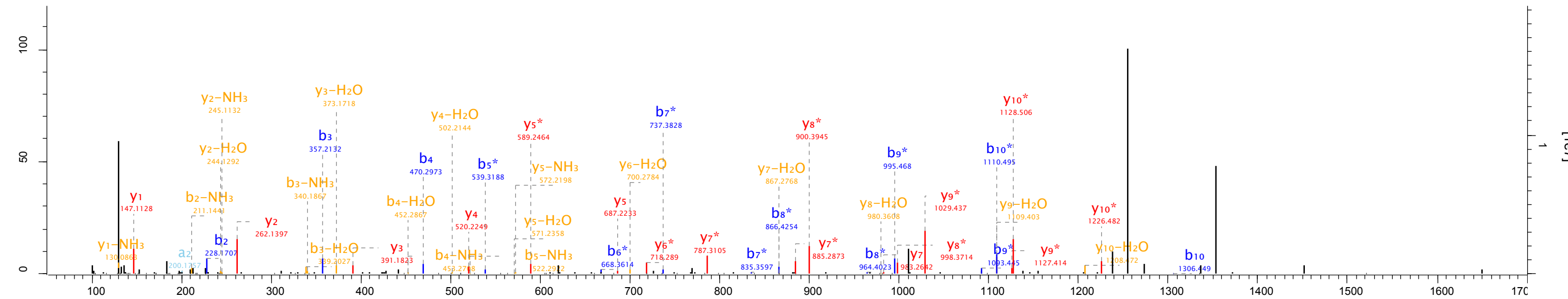


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20171215_MaS_33SR_LMH_phospho2_03

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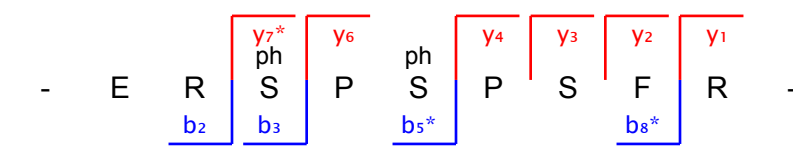
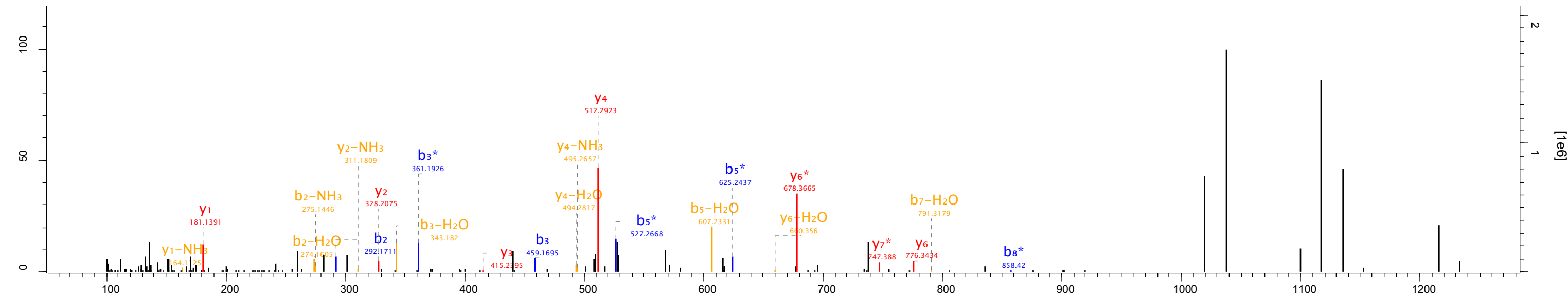


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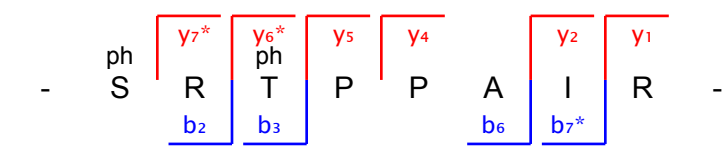
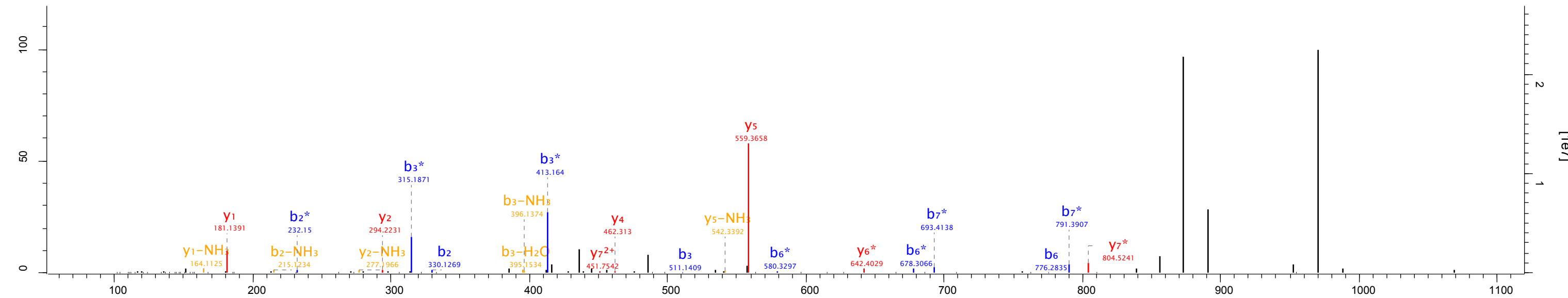
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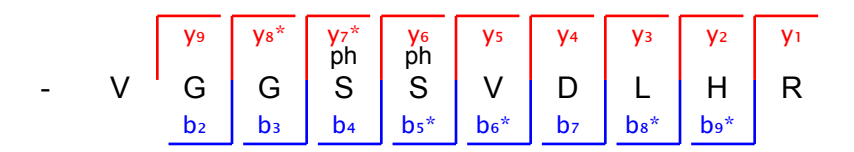
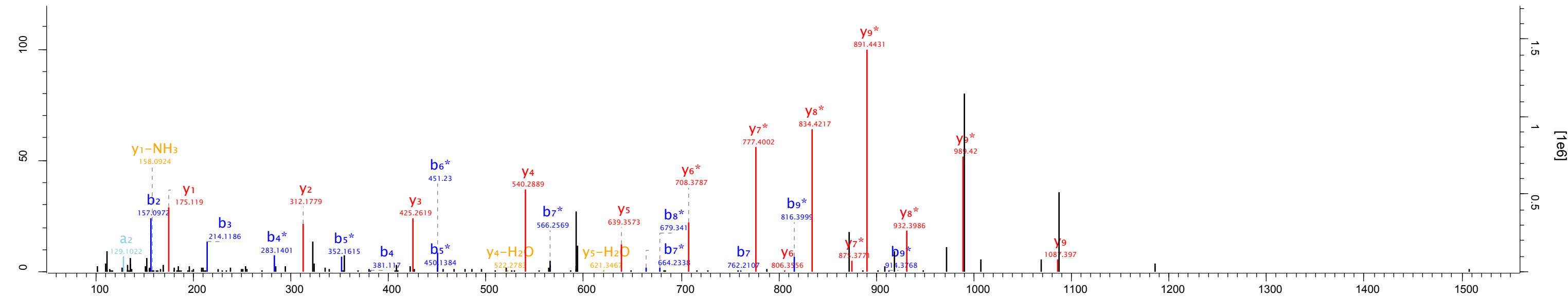
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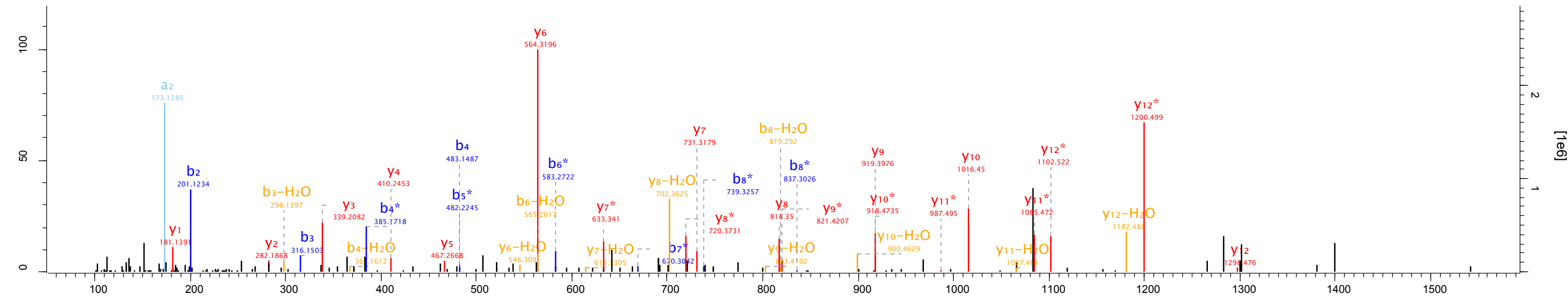
20171215_MaS_33SR_LMH_phospho2_03

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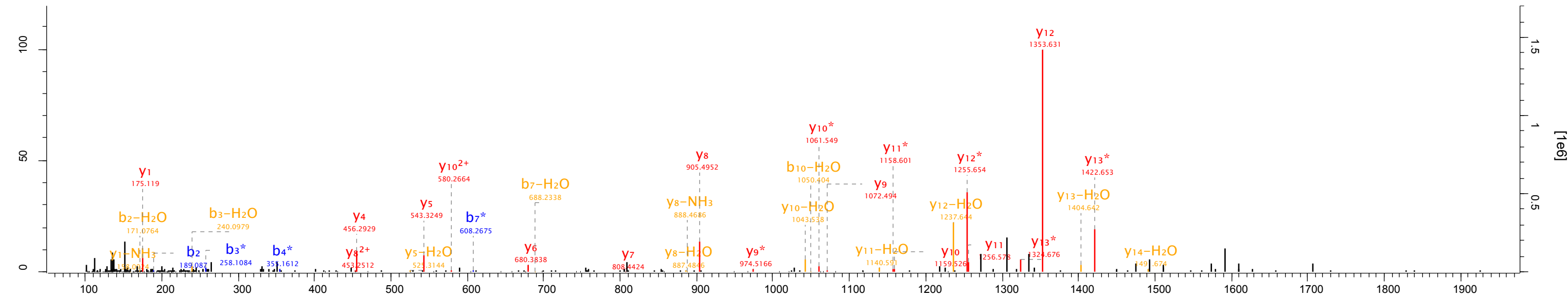


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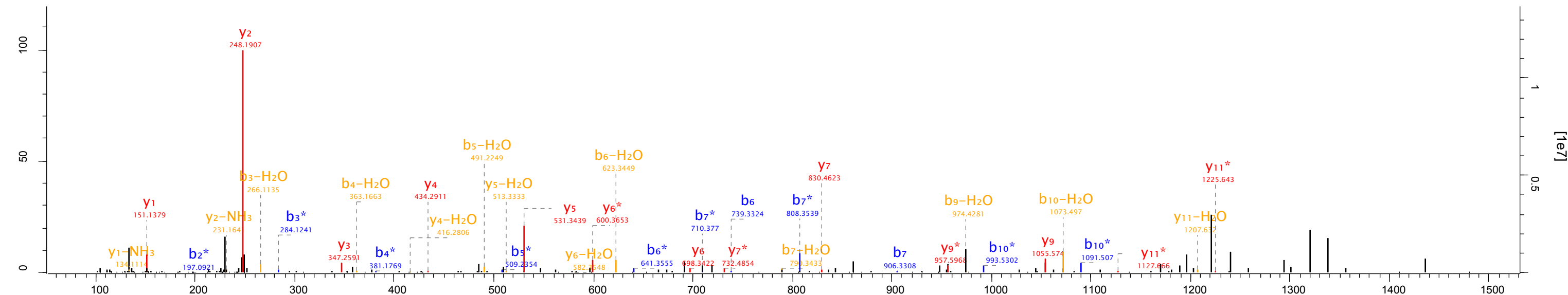


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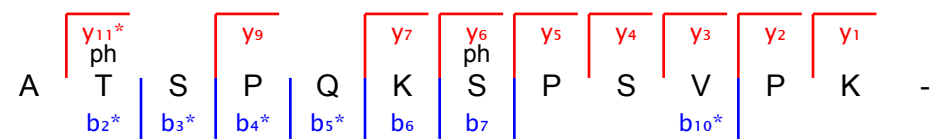
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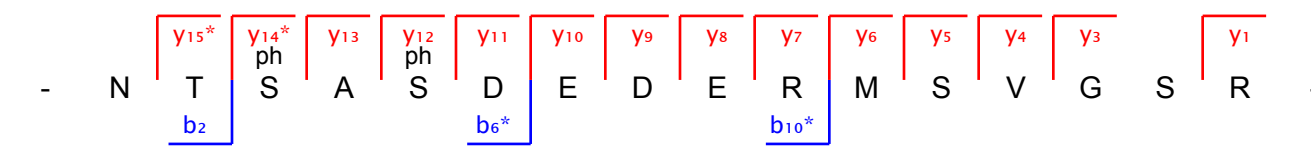
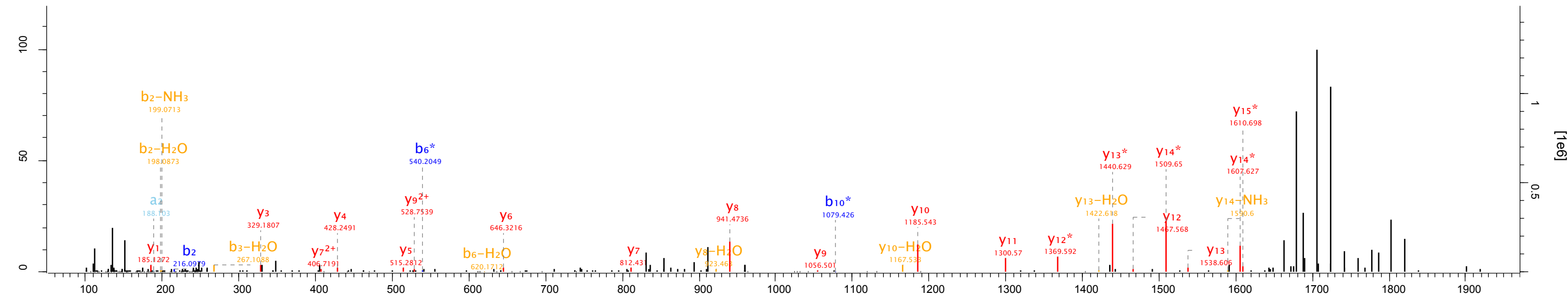


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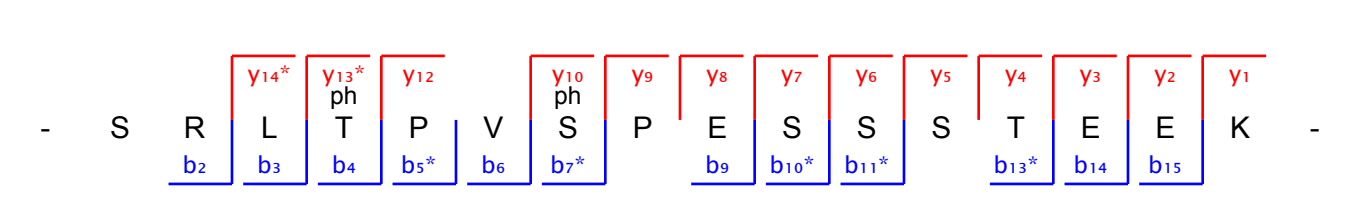
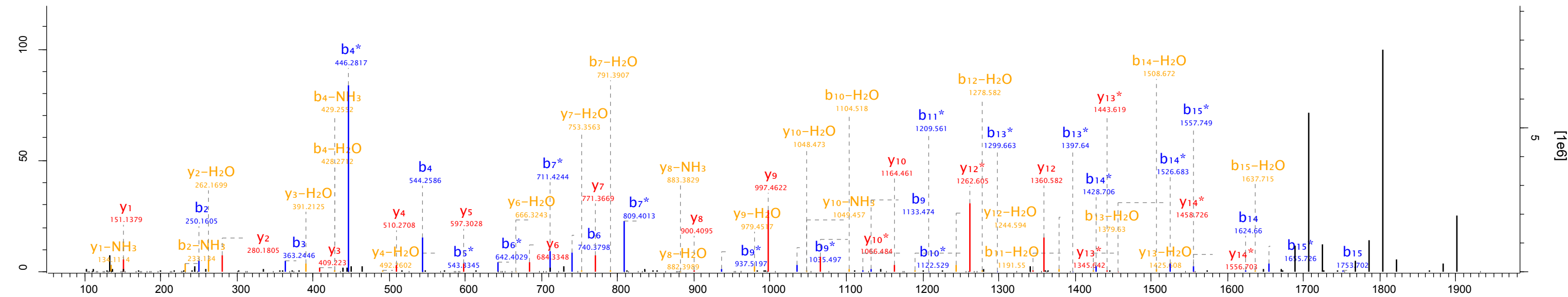
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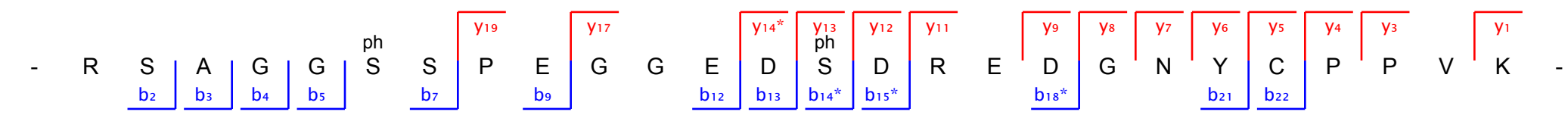
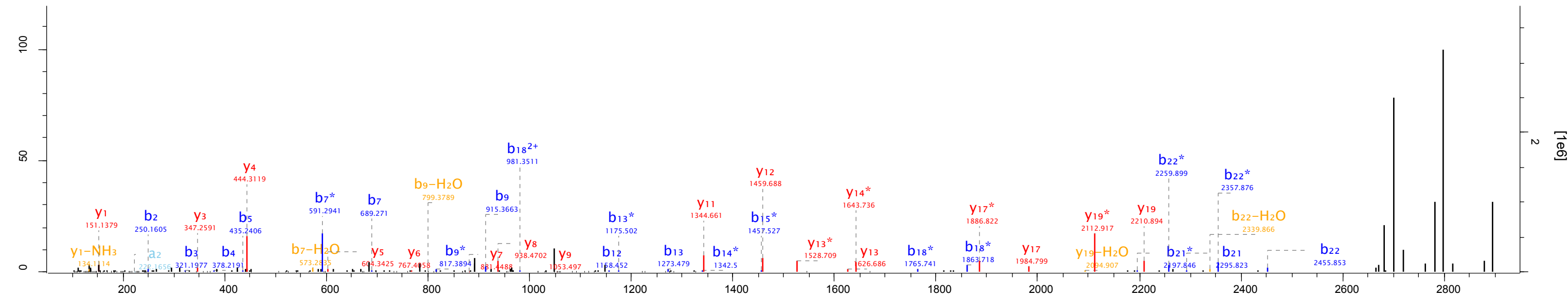


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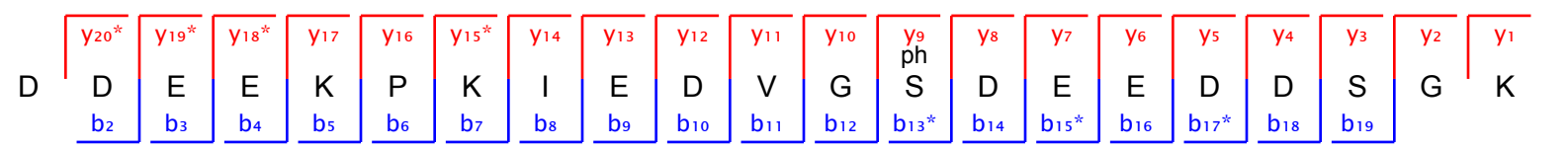
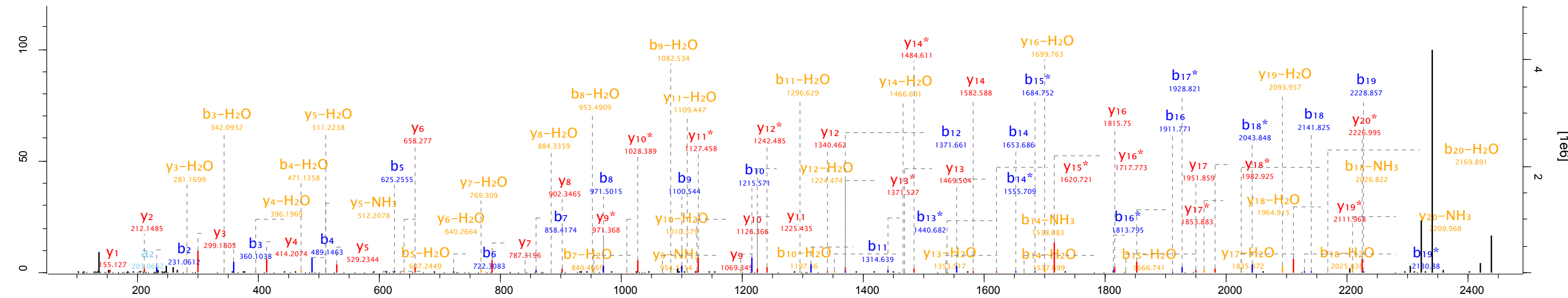


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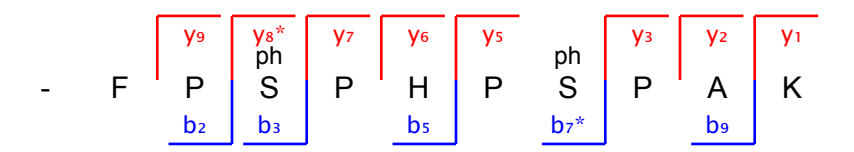
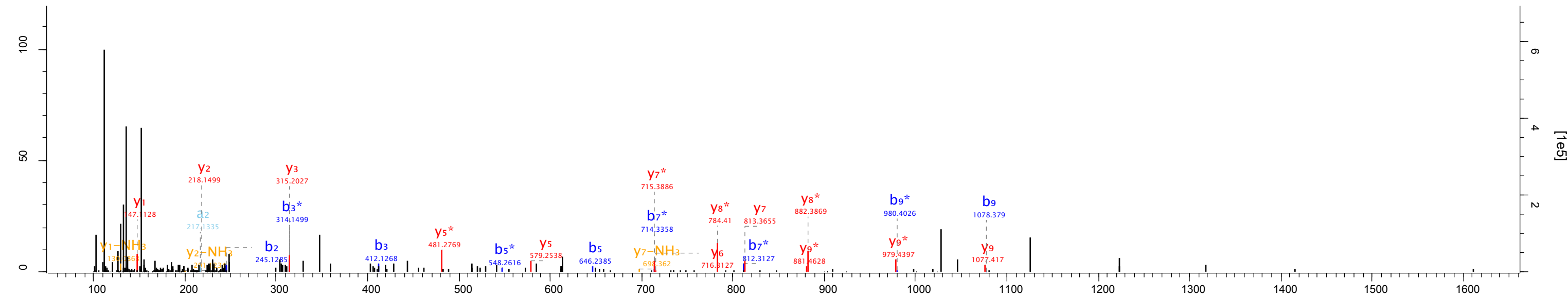
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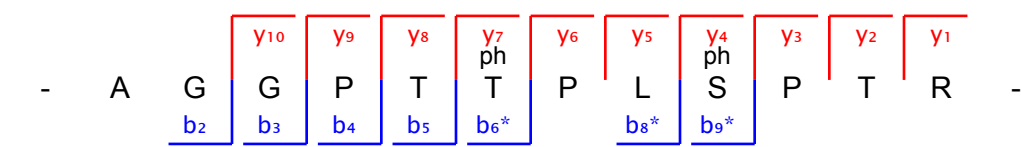
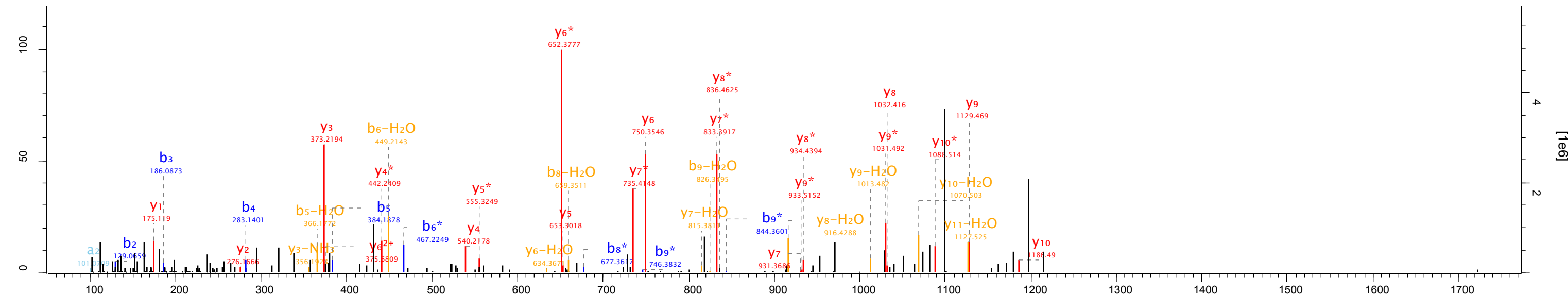


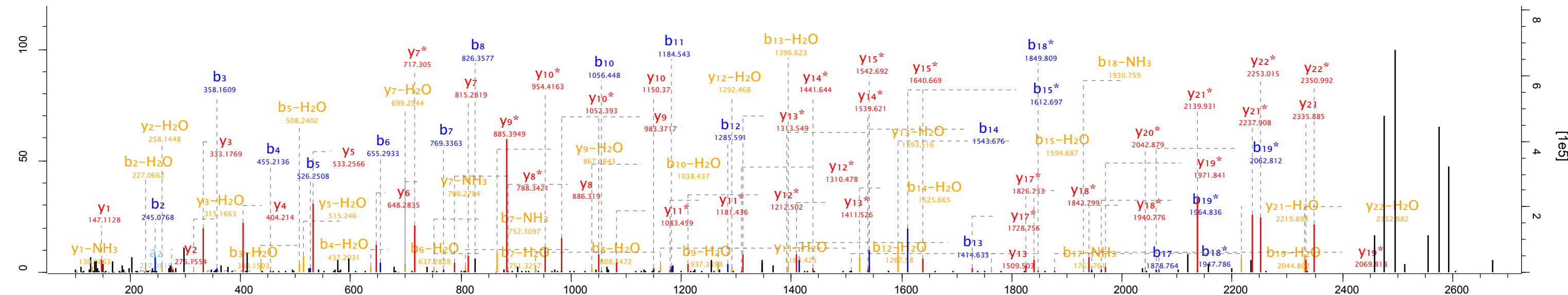
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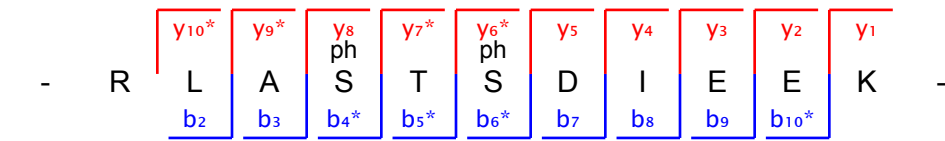
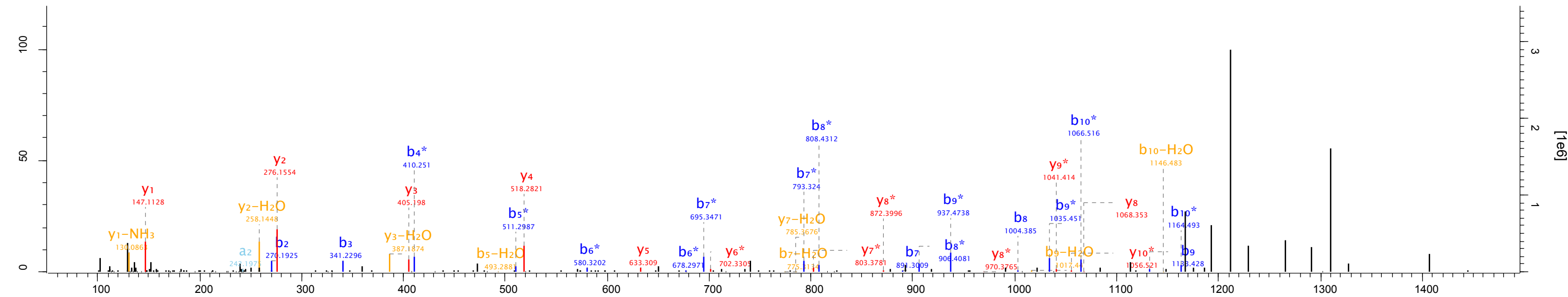




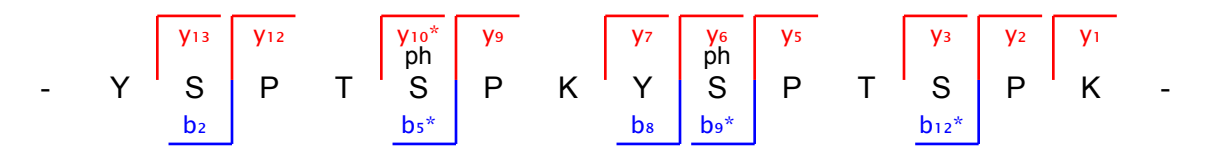
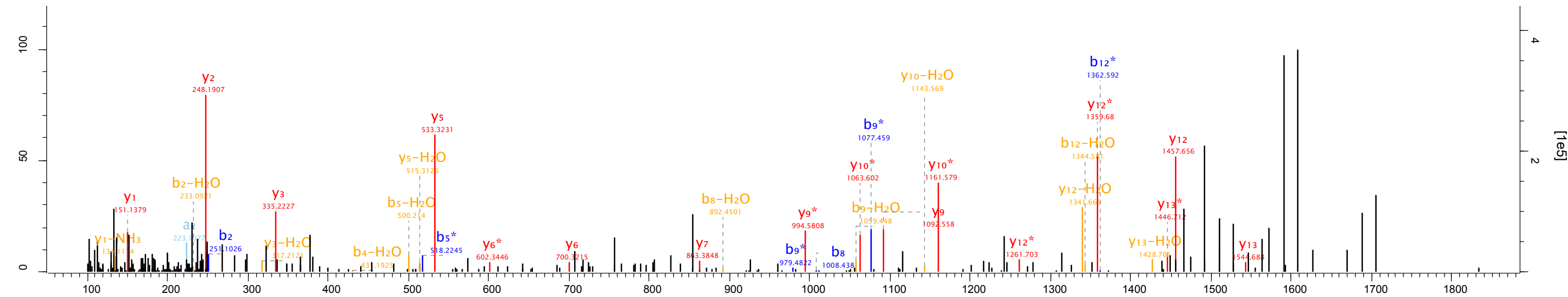


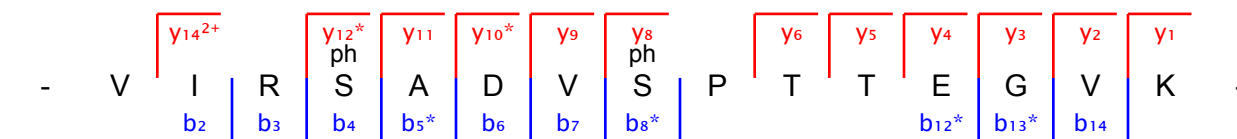
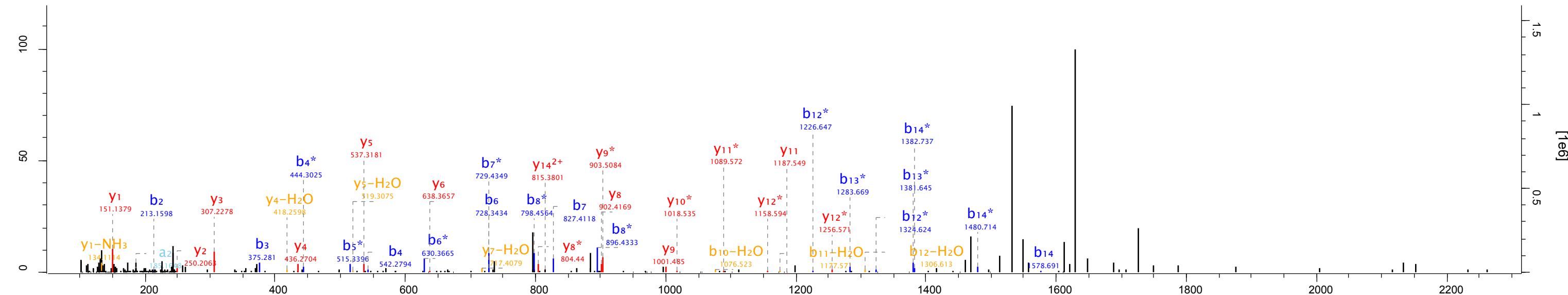
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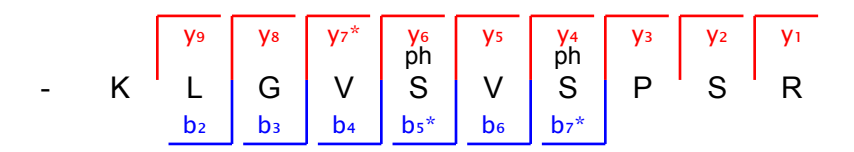
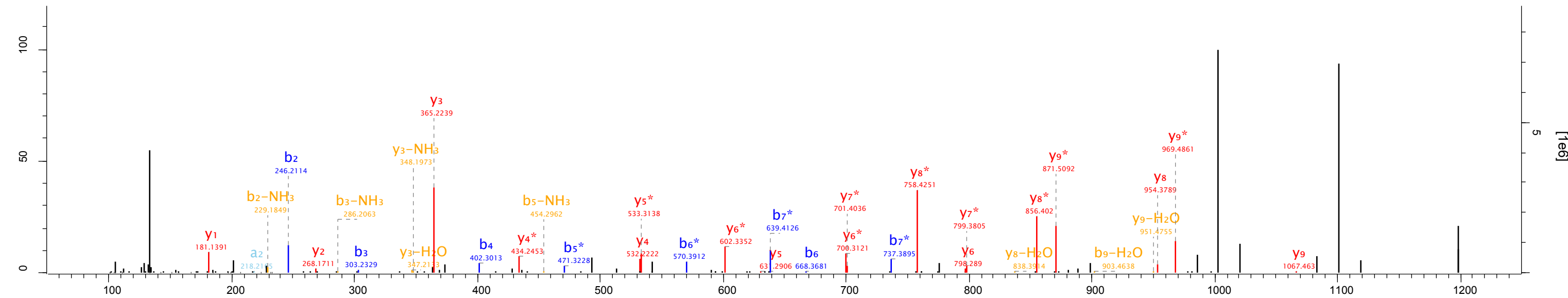


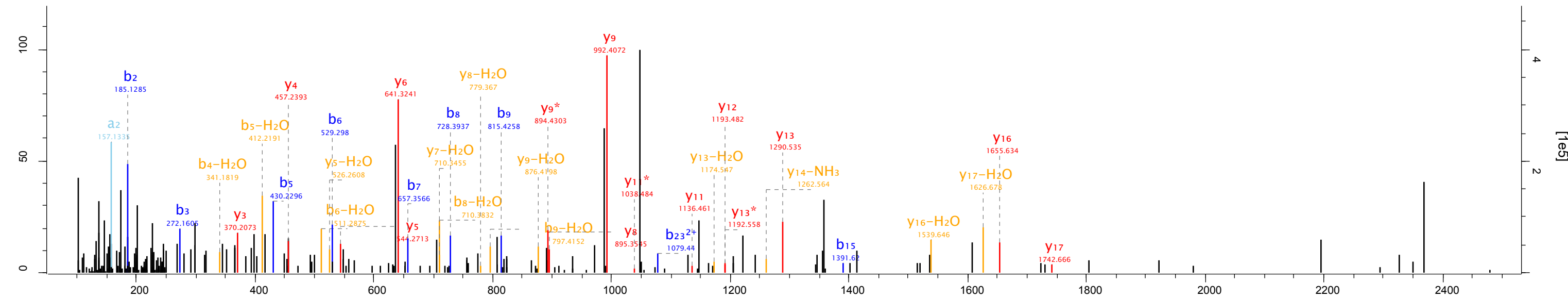
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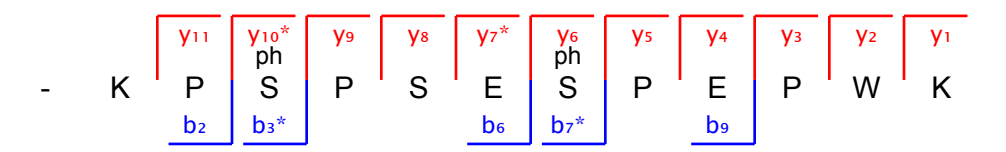
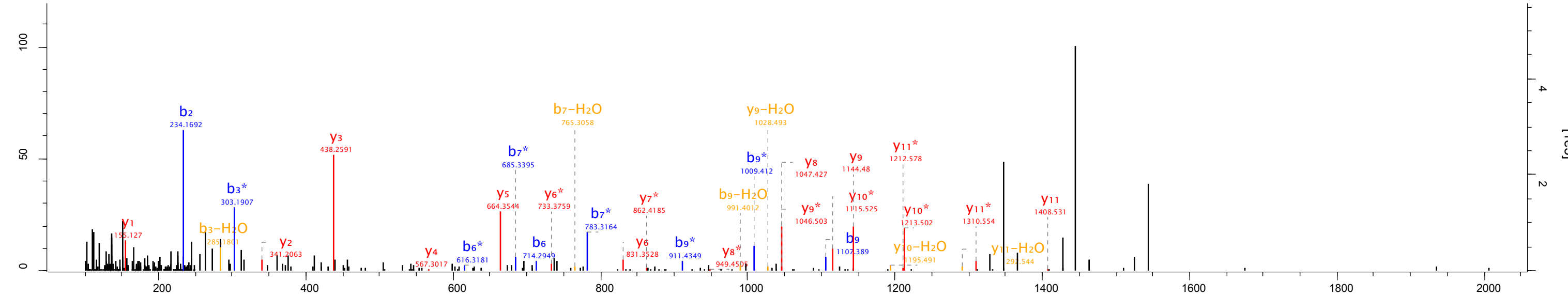
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y₁₆
y₁₇

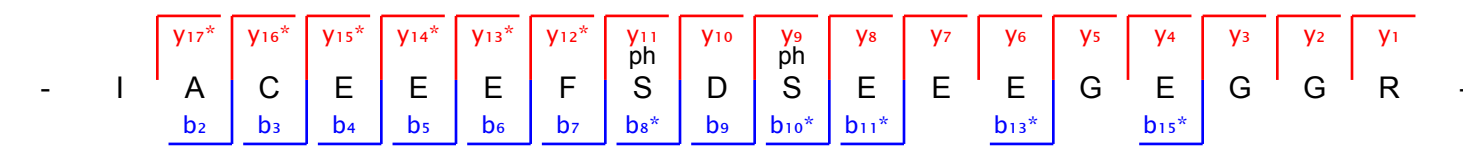
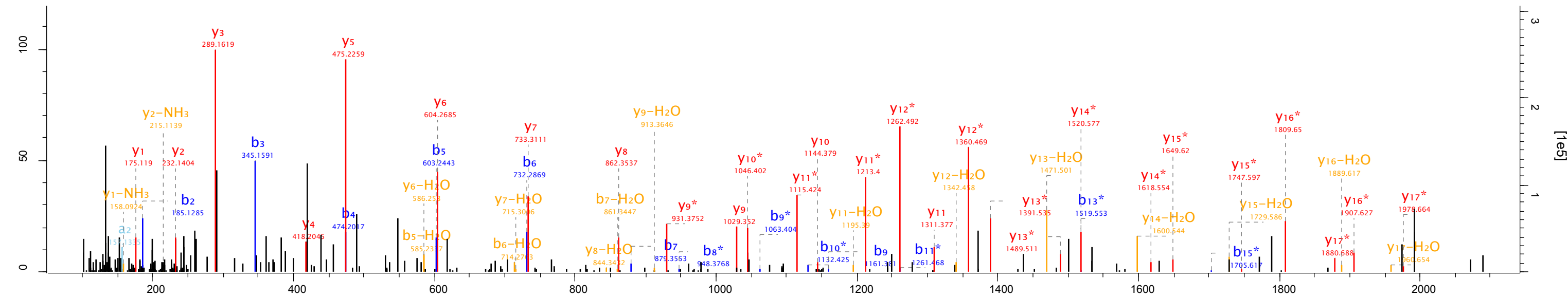
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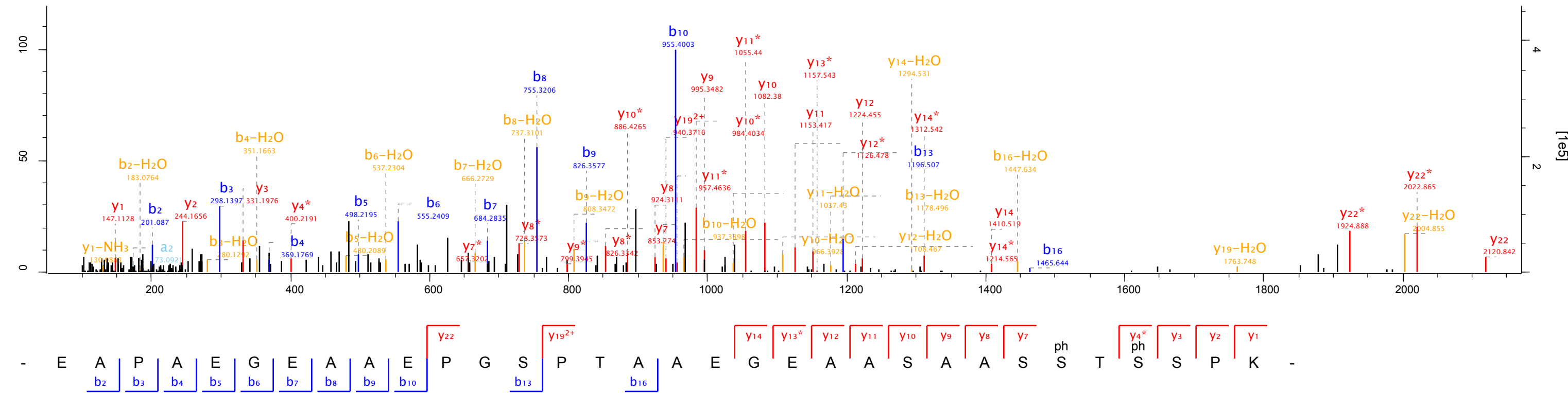
20171215_MaS_33SR_LMH_phospho2_03

Scan 8479 Method FTMS; HCD Score 132.62 m/z 773.32 Gene names CHAMP1

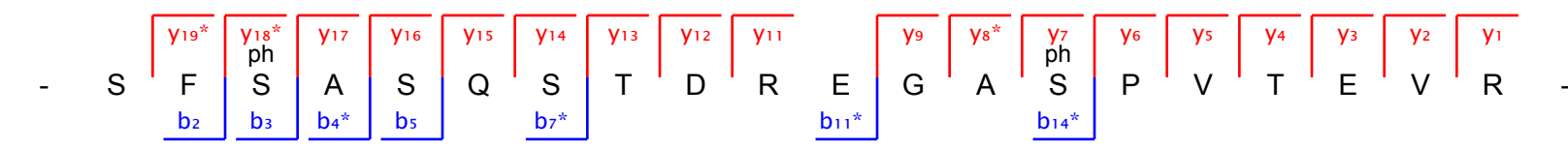
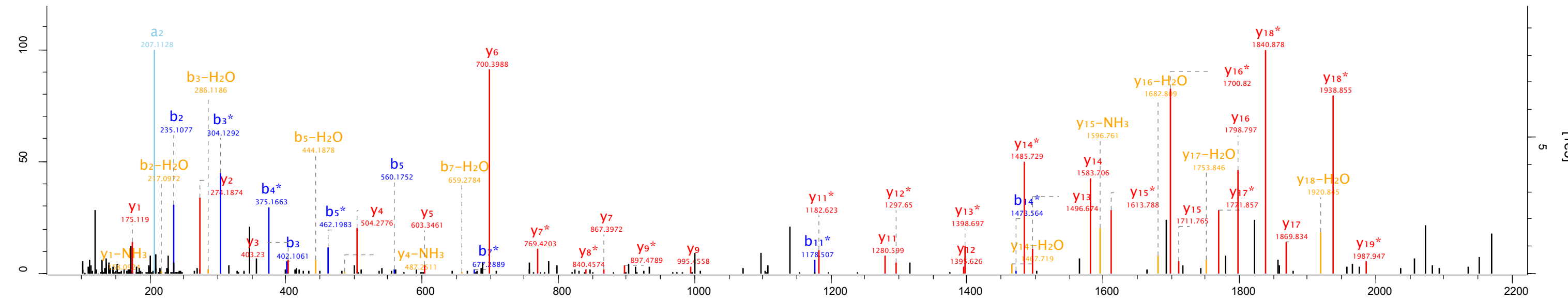


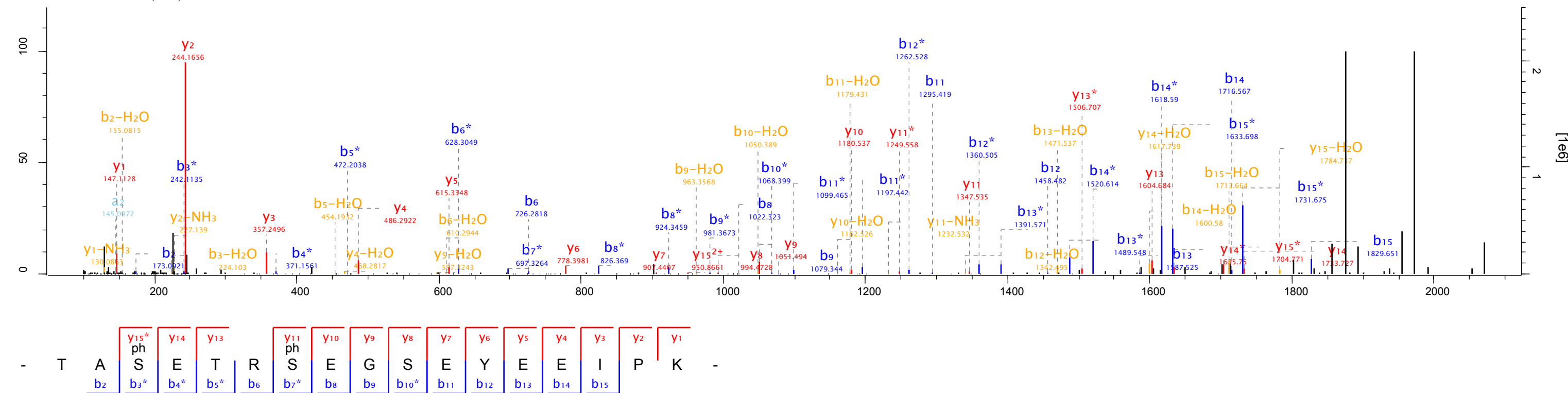
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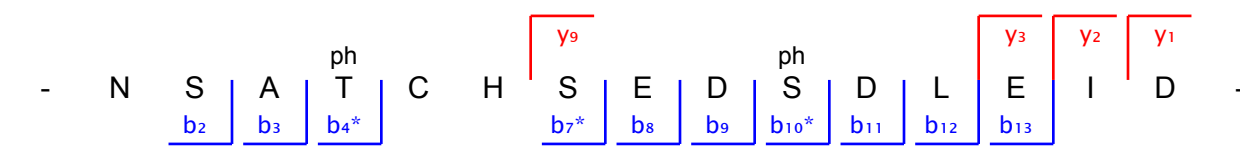
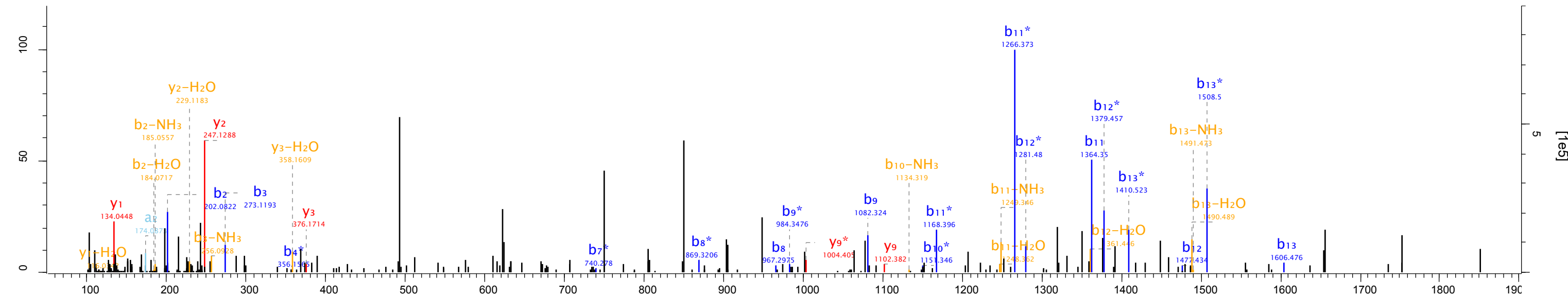




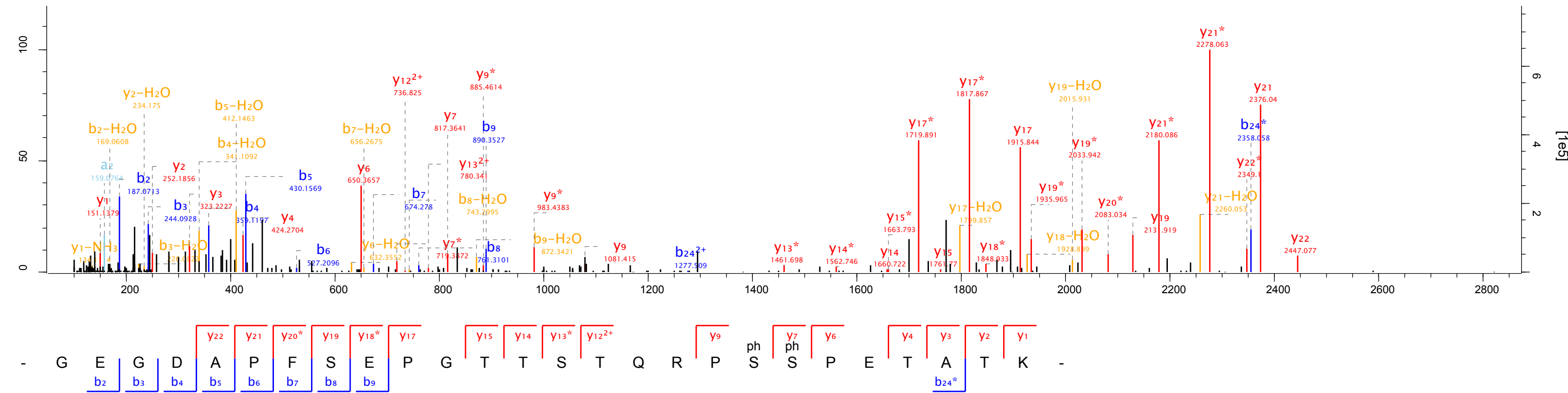
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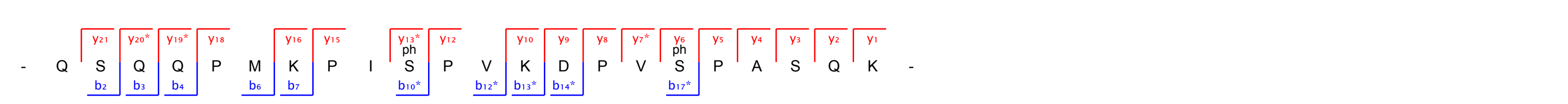
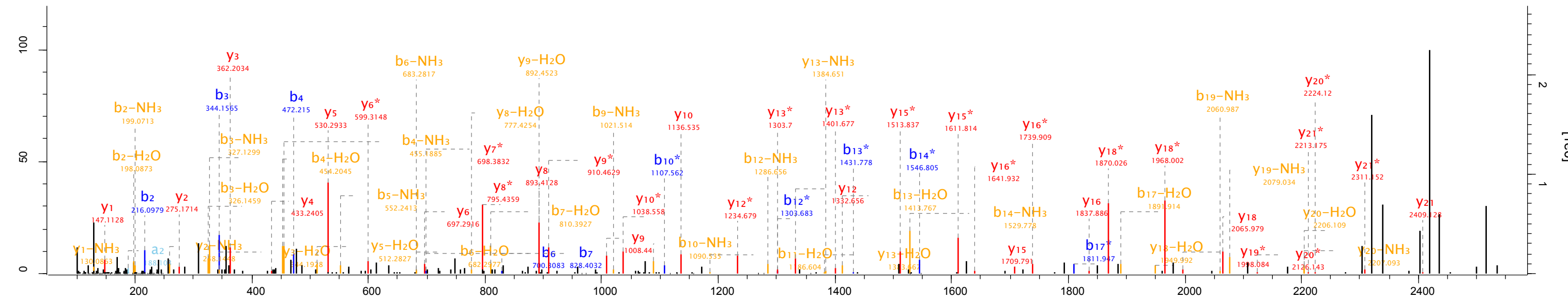




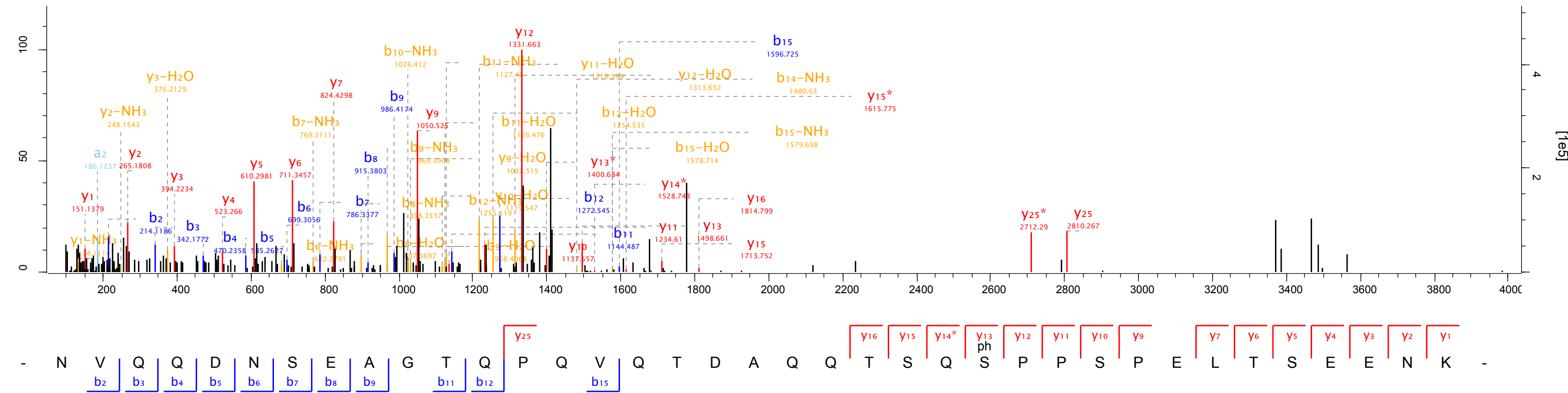
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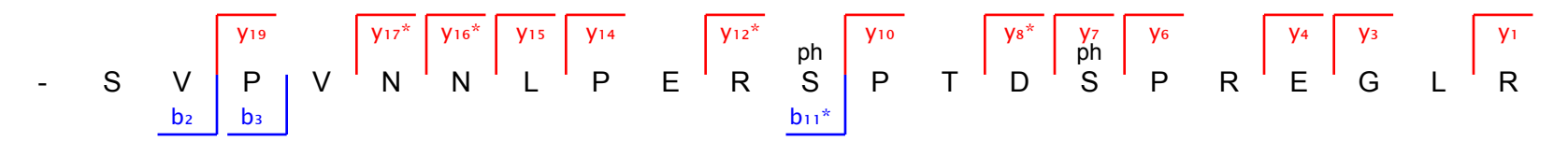
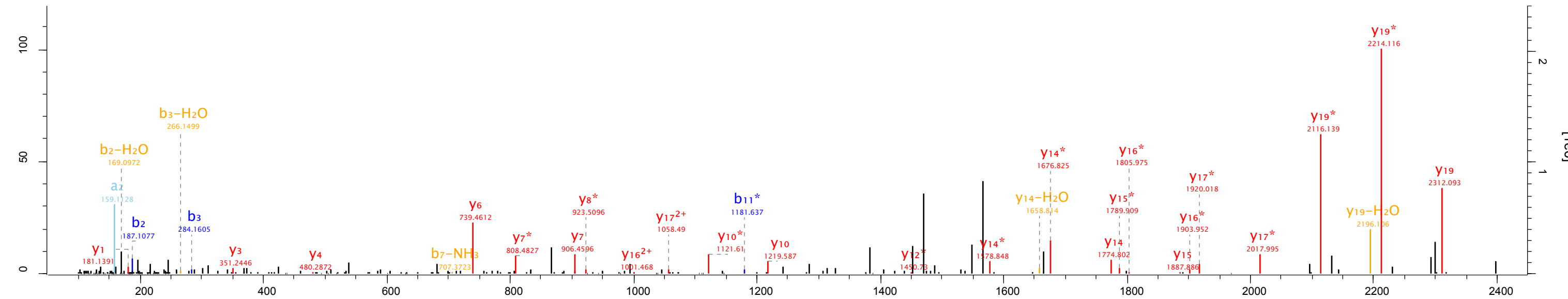


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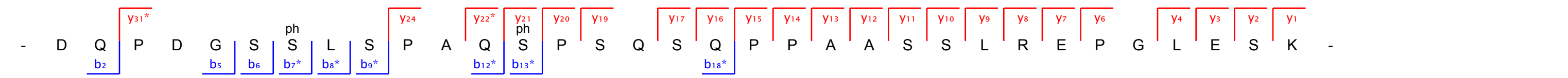
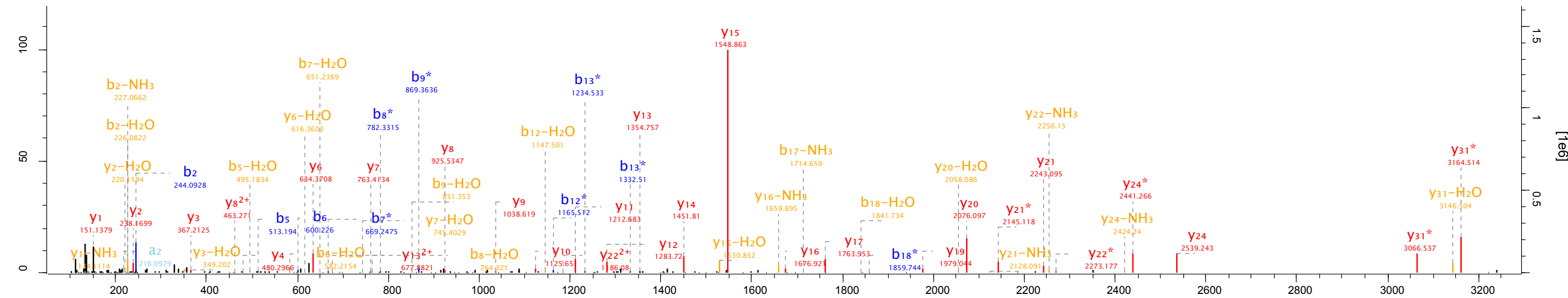


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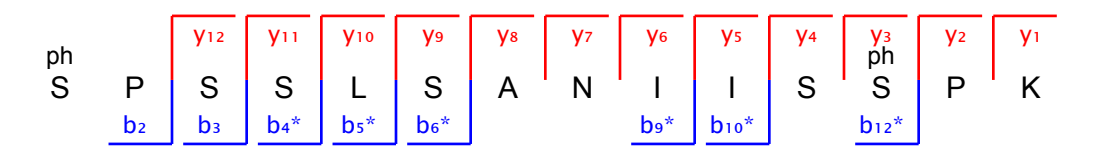
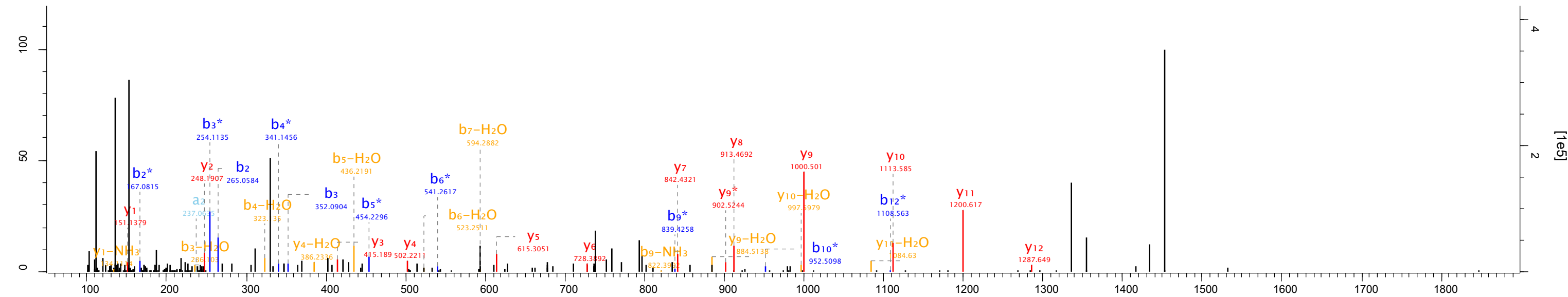


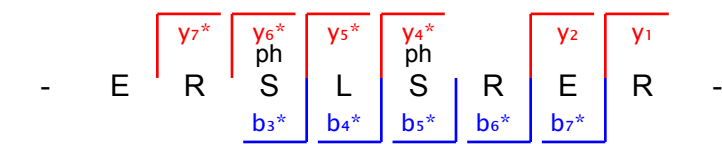
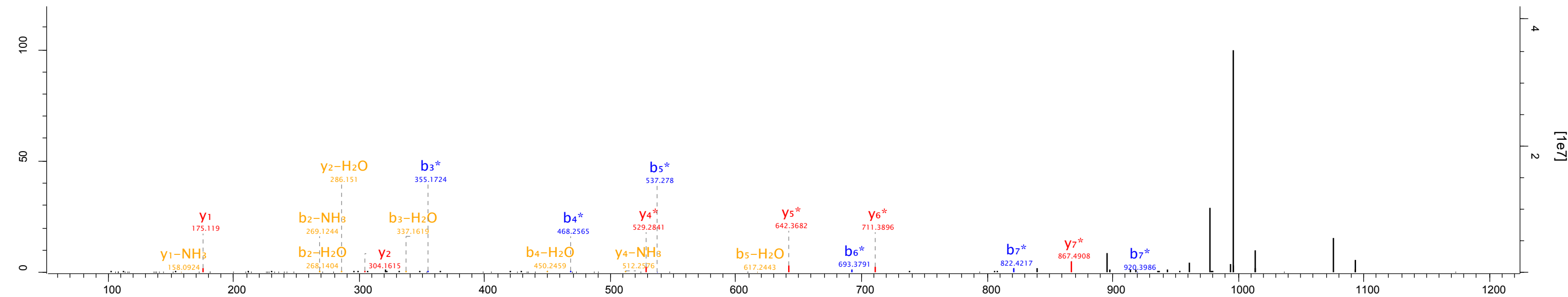


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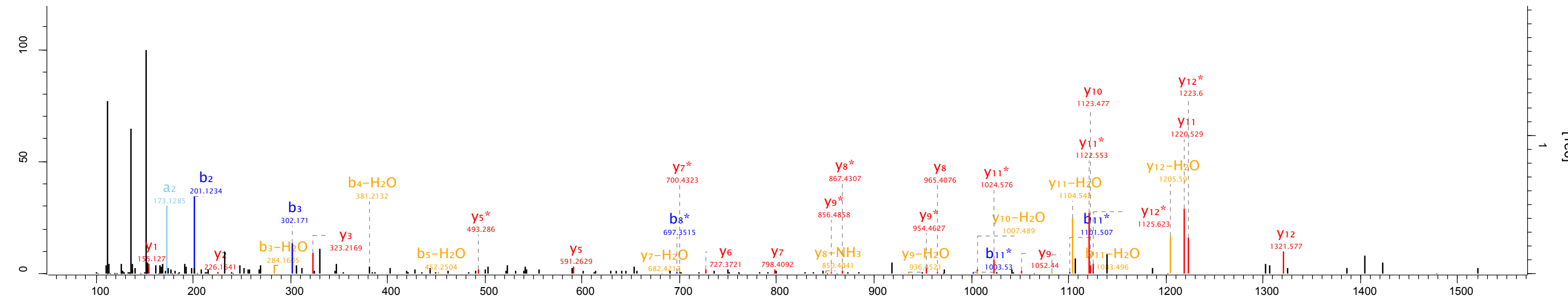


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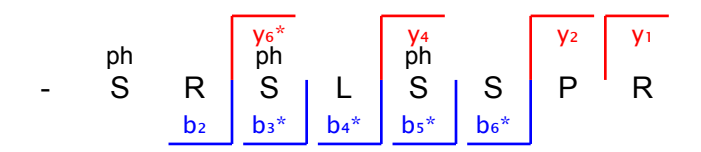
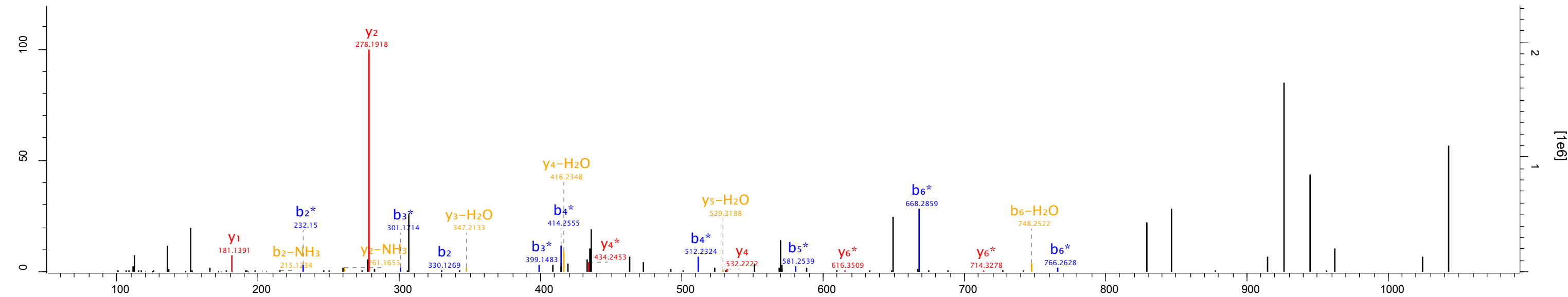


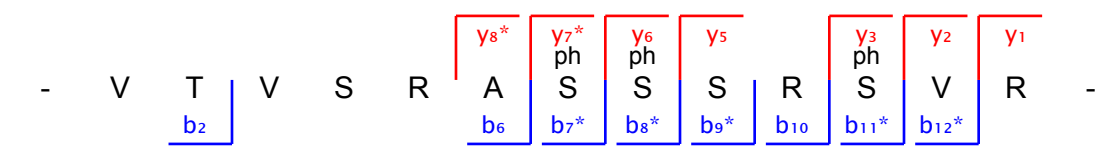
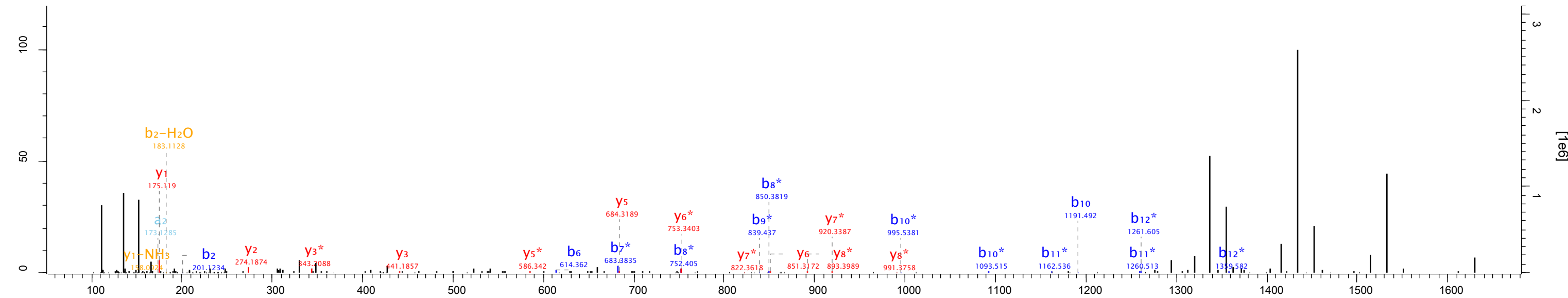


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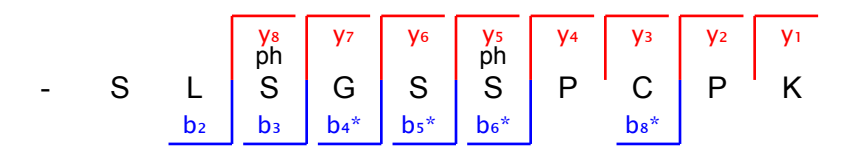
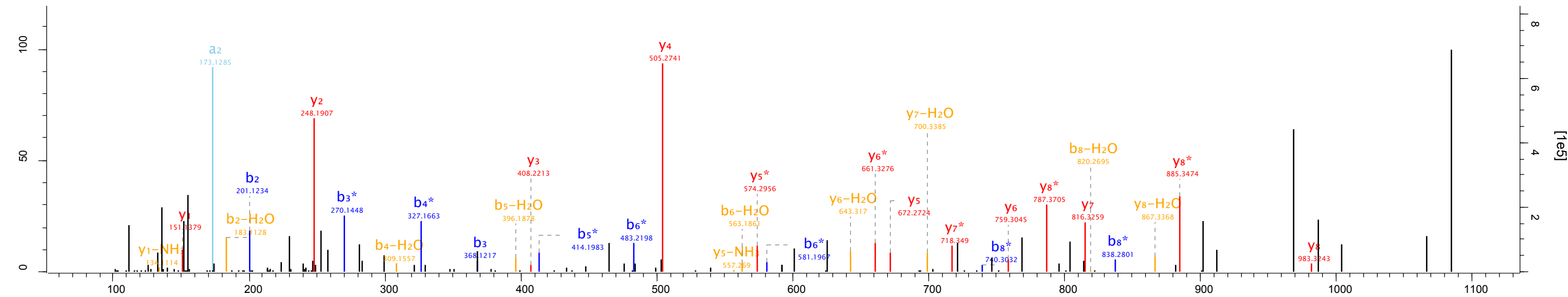


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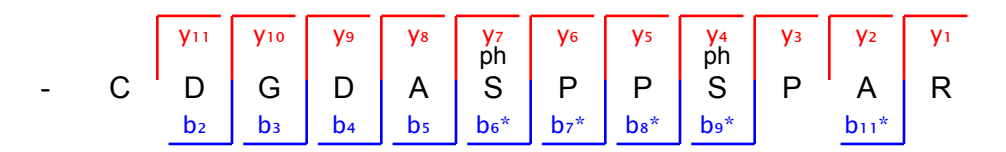
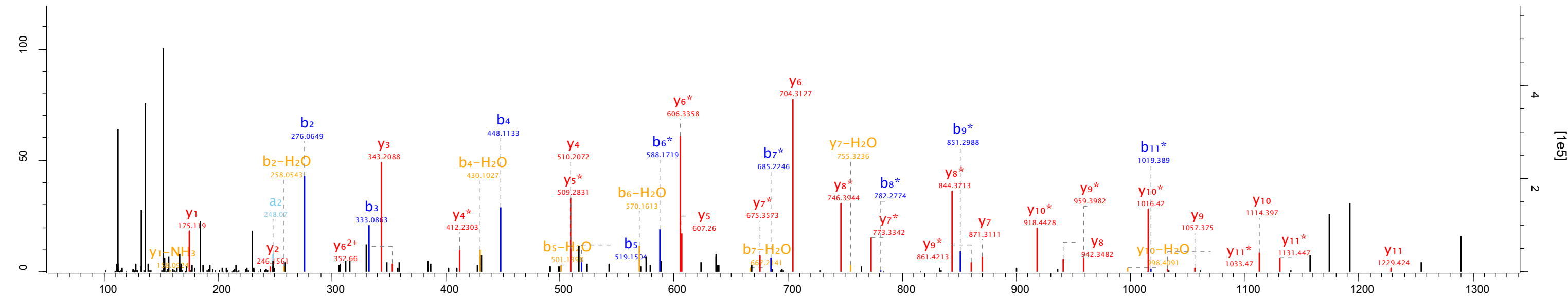


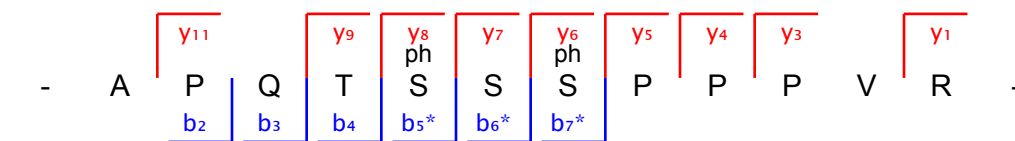
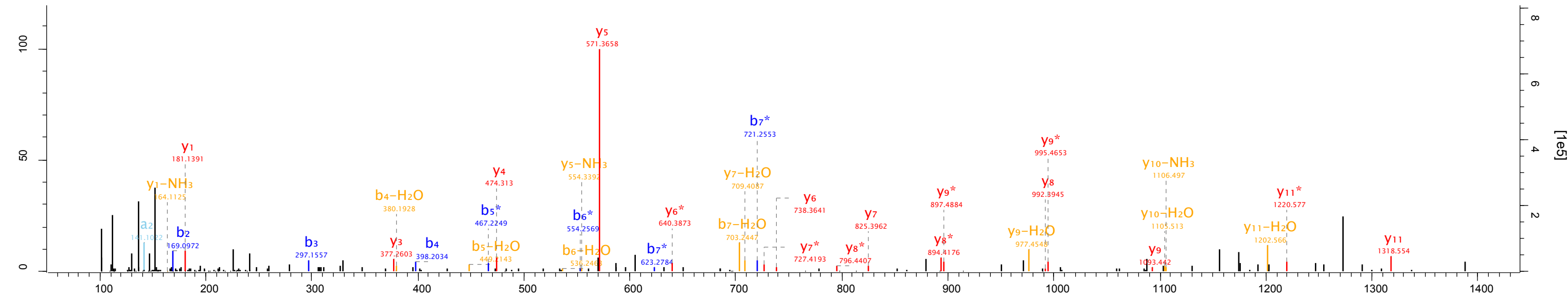


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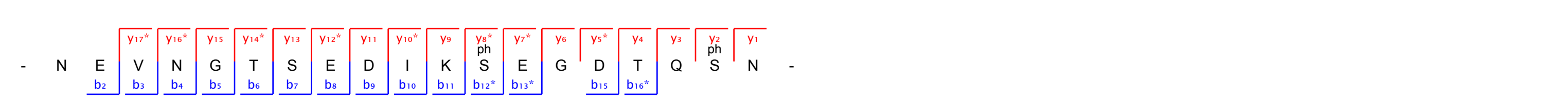
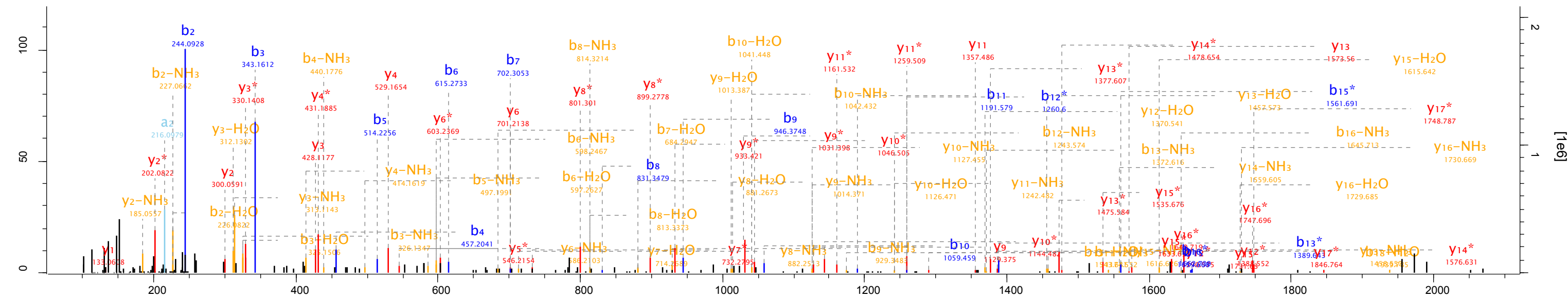


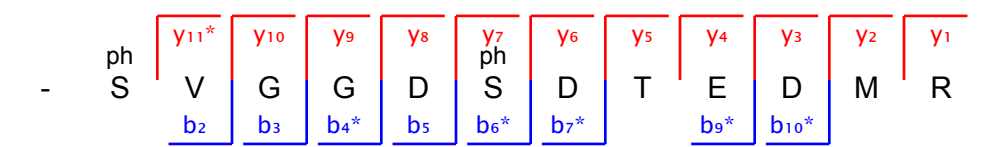
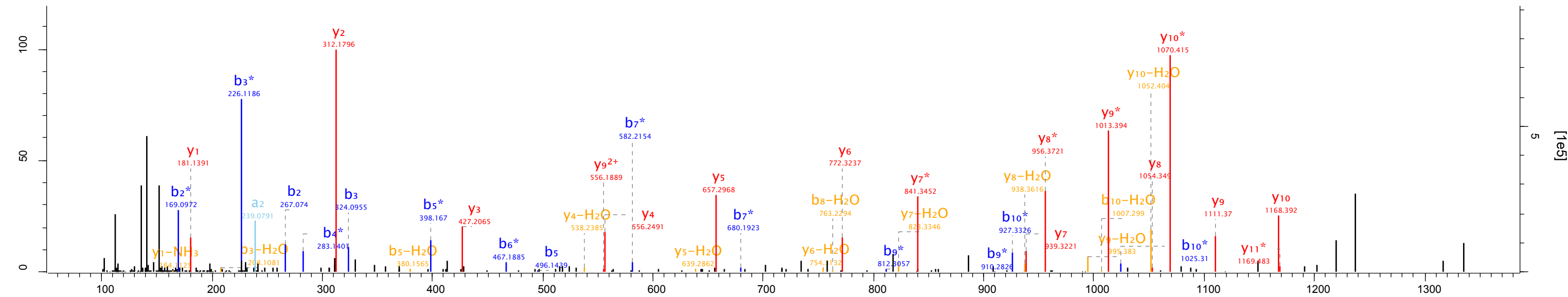
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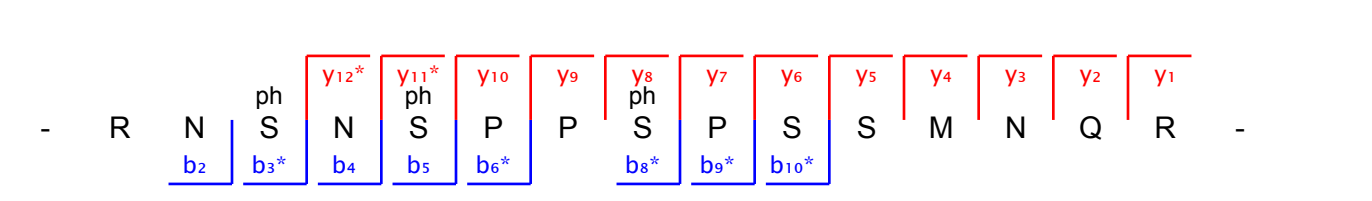
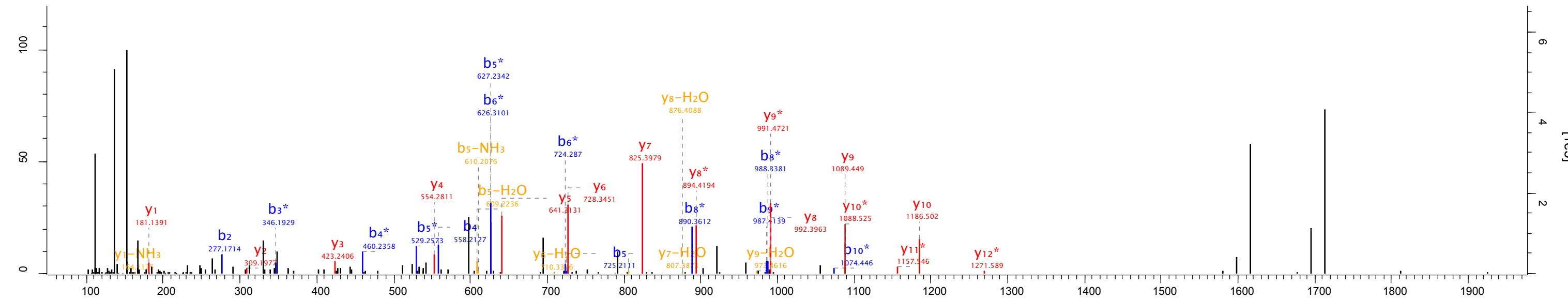


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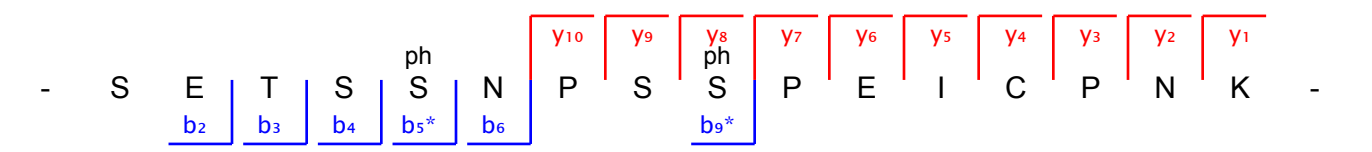
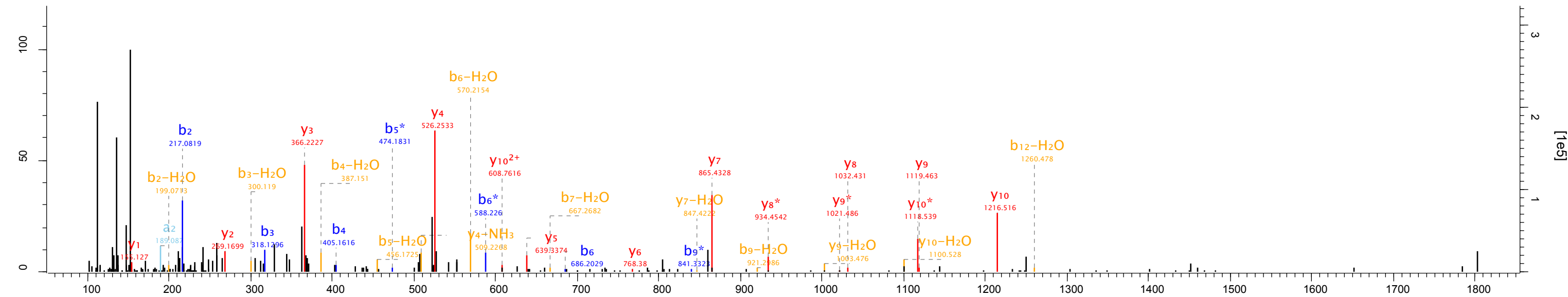




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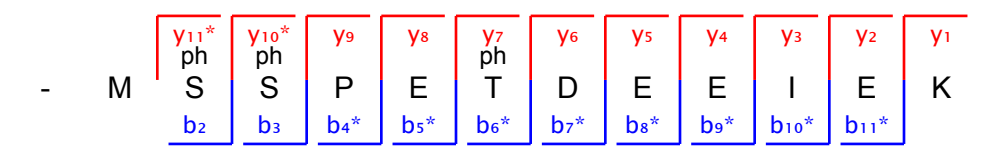
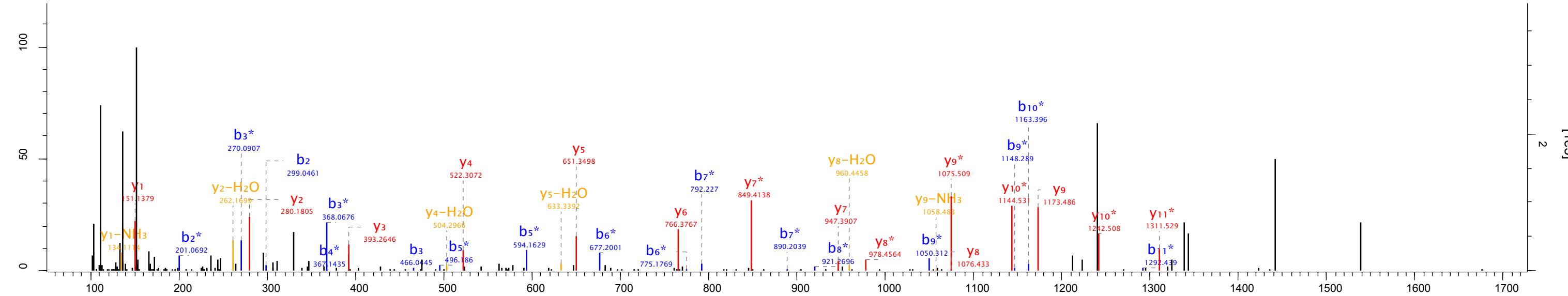


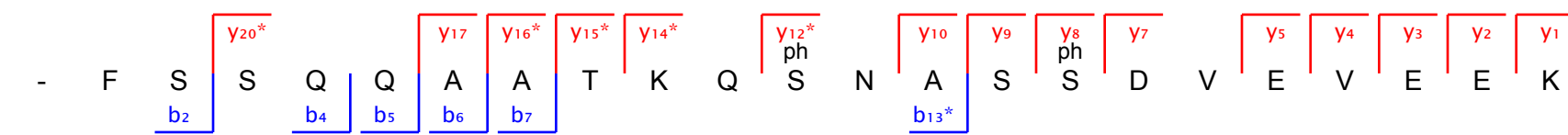
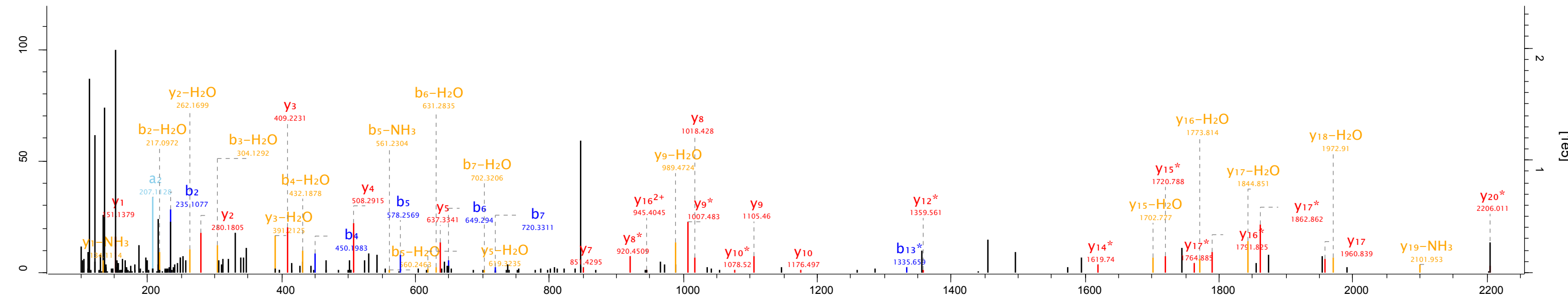
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 Scan: 5019 Method: FTMS; HCD Score: 72.8 m/z: 951.87 Gene names: RAP1GAP2



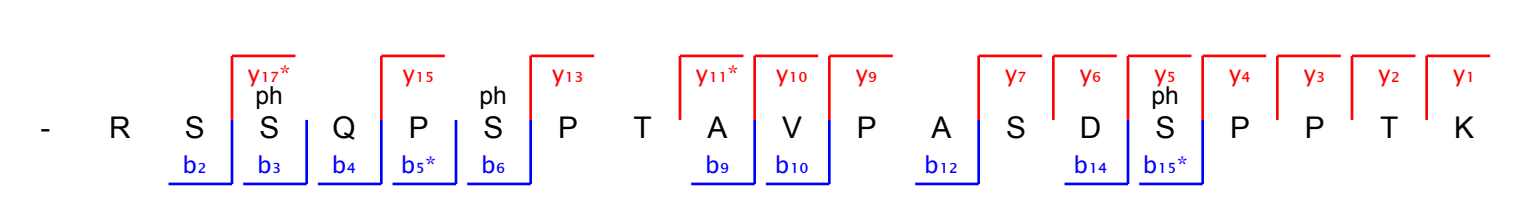
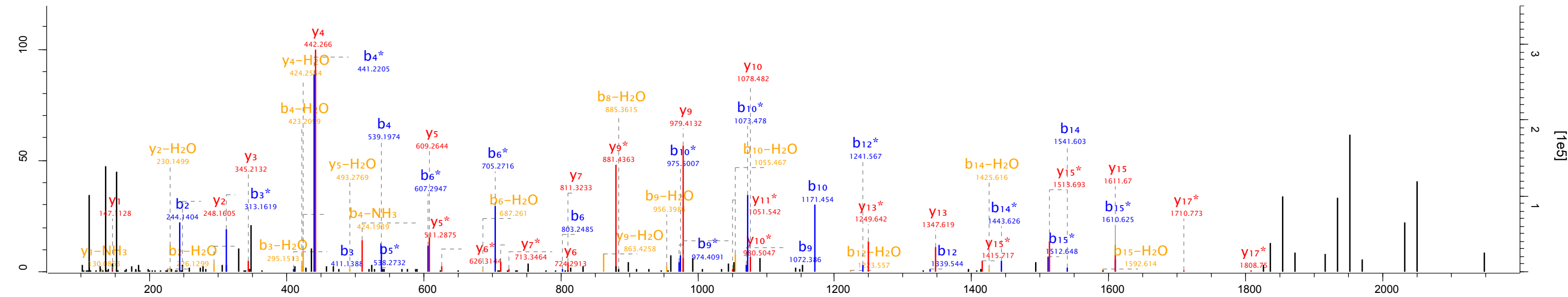
Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_04 5429 FTMS; HCD 145.91 819.76 FAM175A

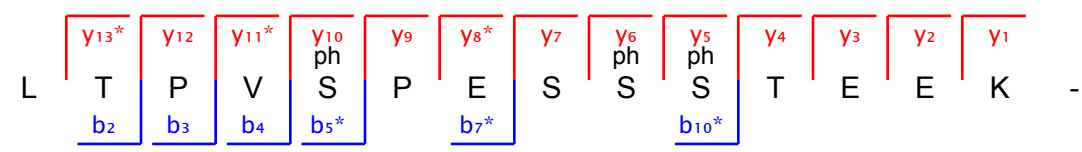
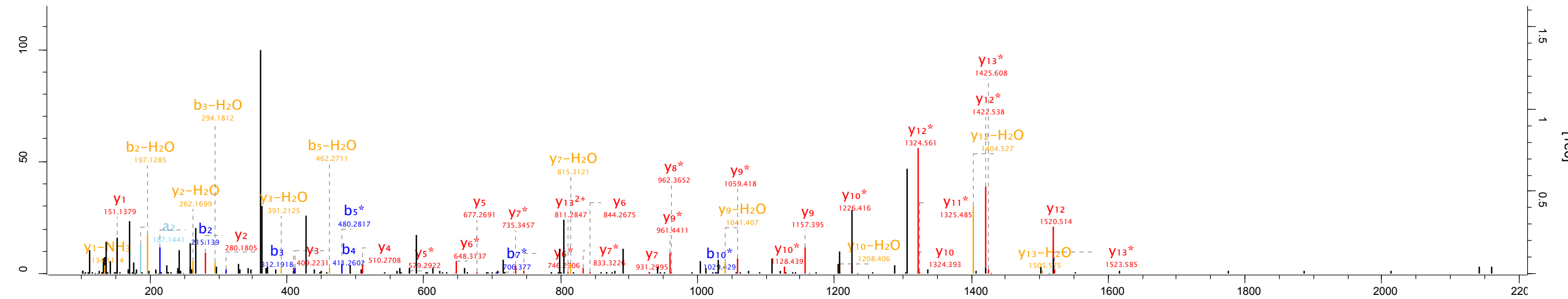


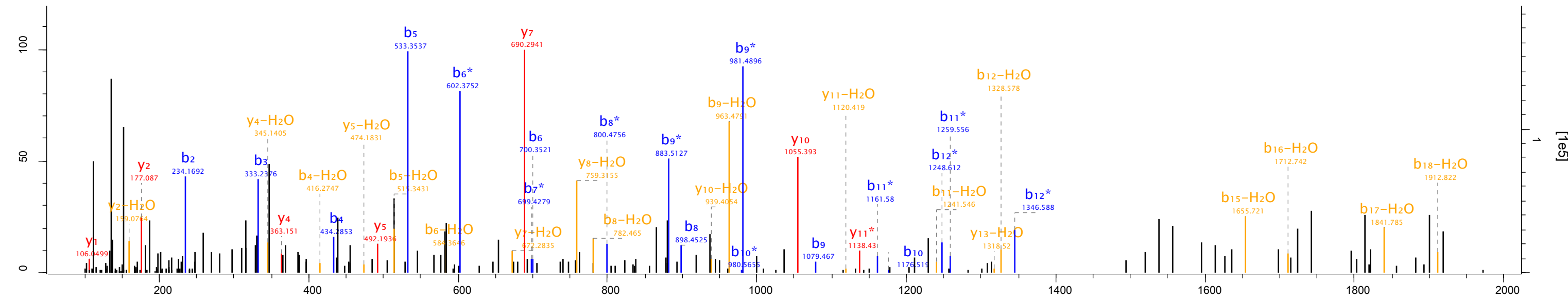


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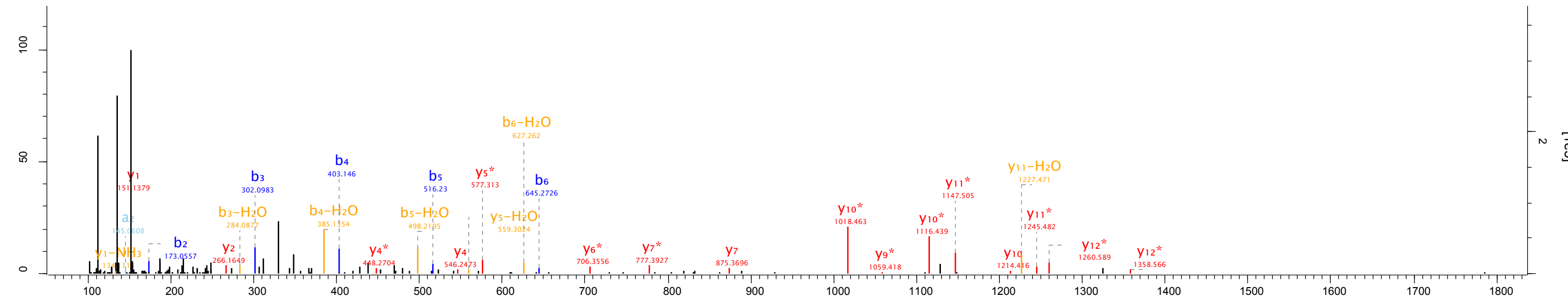
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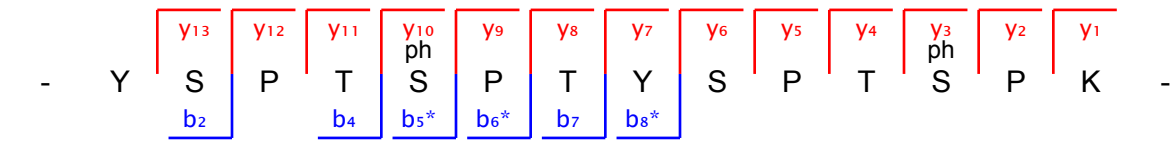
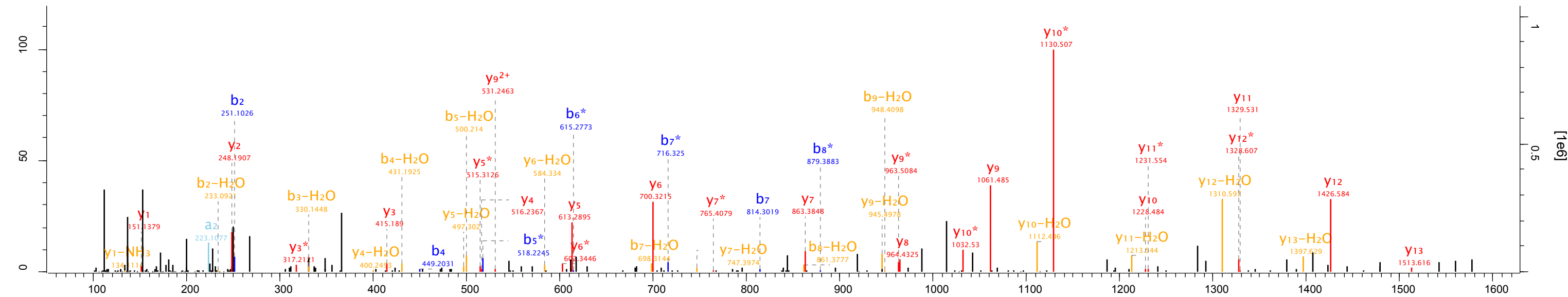
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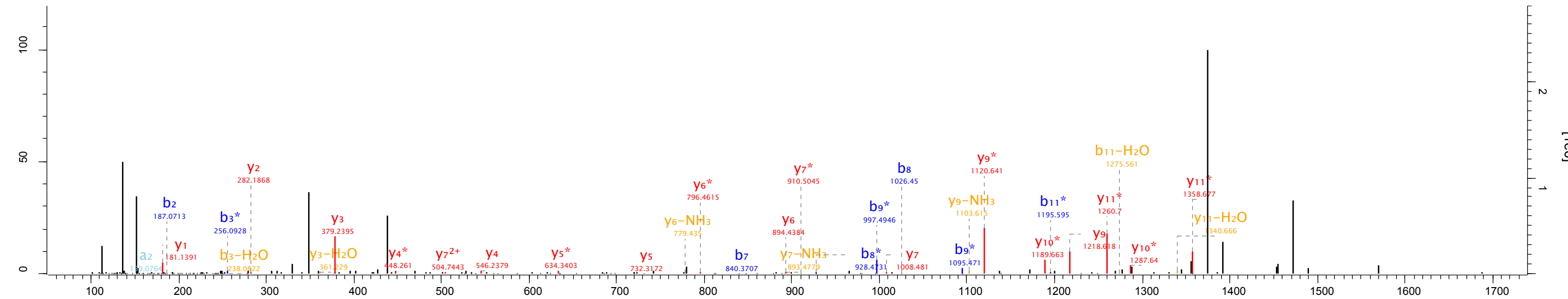


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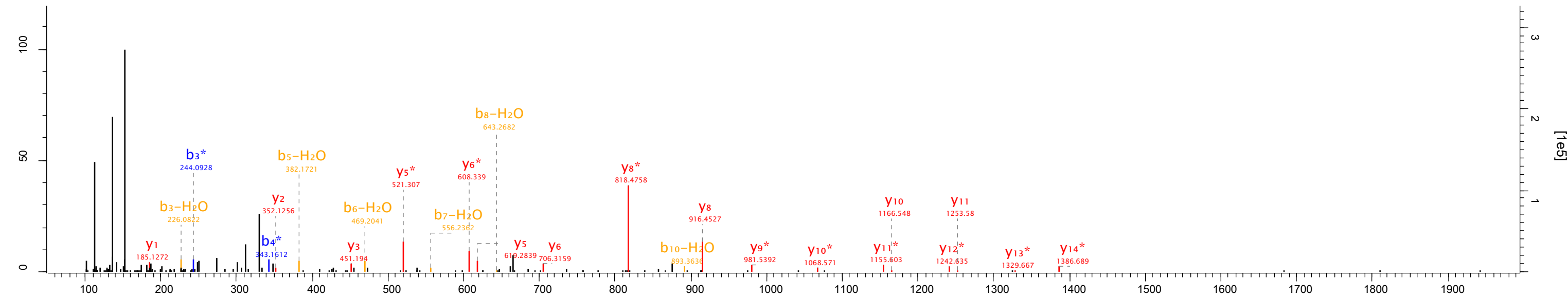
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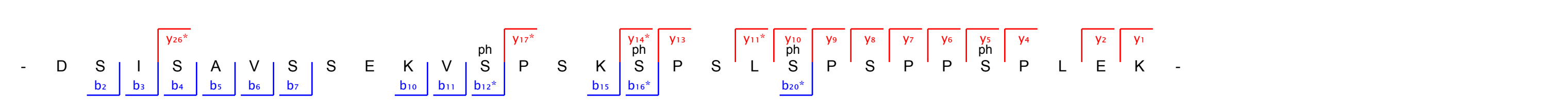
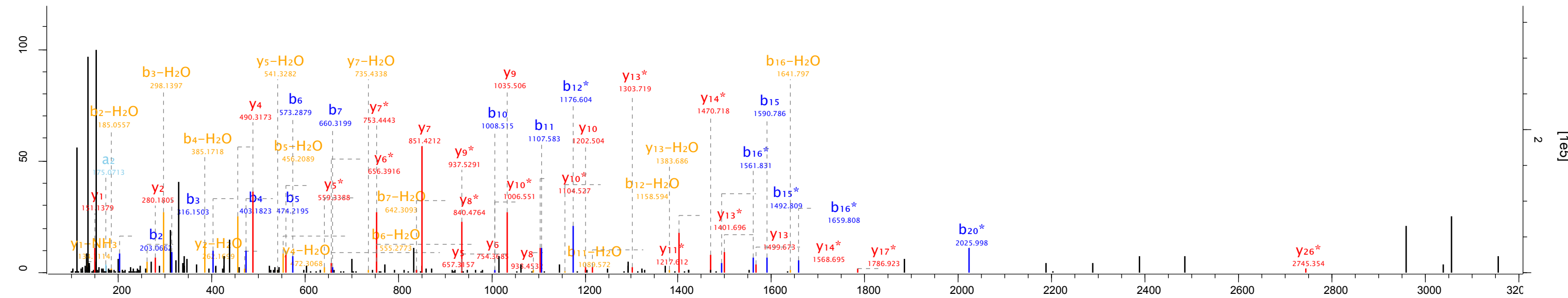
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 Scan 8409 Method FTMS; HCD Score 111.63 m/z 786.34 Gene names PRPF4B



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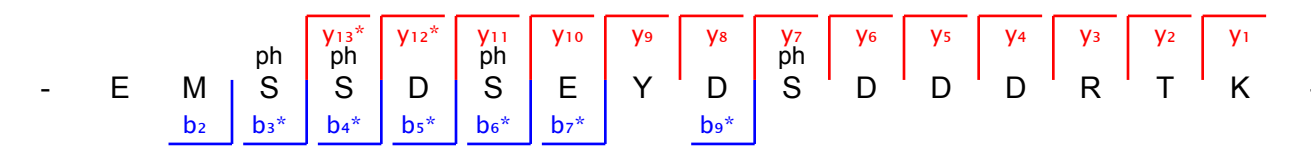
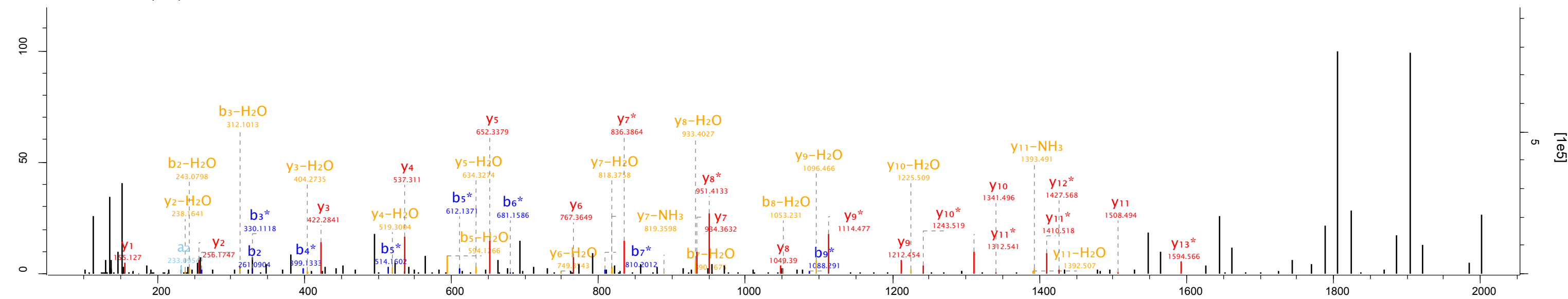


Raw file: 20171215_MaS_33SR_LMH_phospho2_05
 Scan: 11699 Method: FTMS; HCD Score: 121.28 m/z: 1086.49 Gene names: MAP1B



Raw file
20171215_MaS_33SR_LMH_phospho2_05

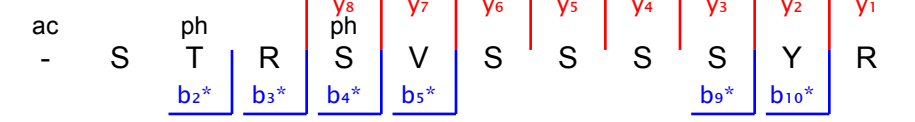
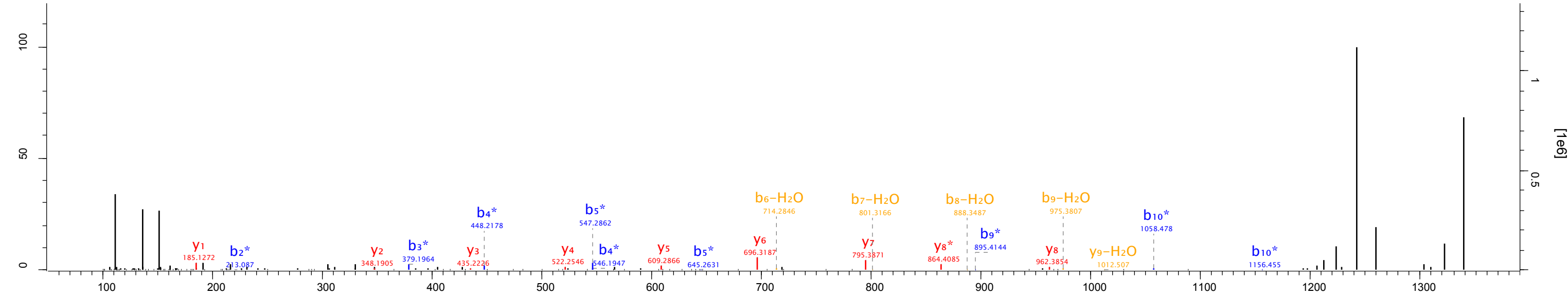
Scan 3739 Method FTMS; HCD Score 149.8 m/z 1109.31 Gene names EIF5B



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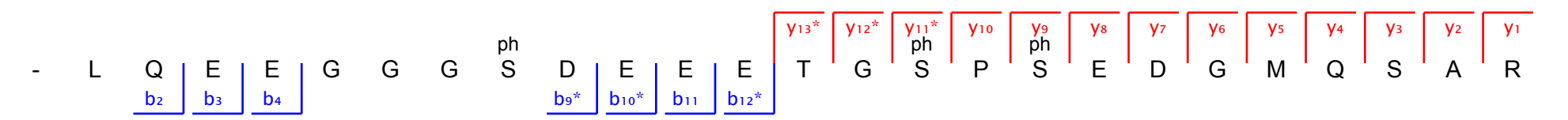
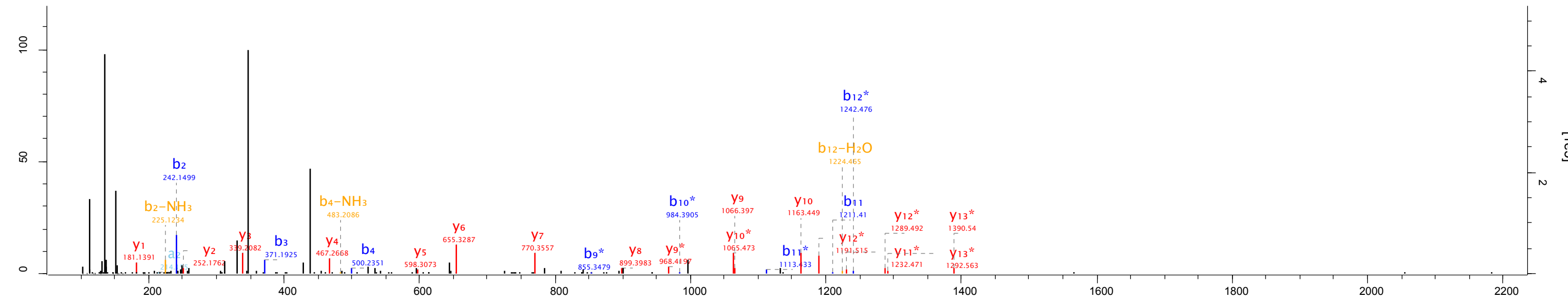
20171215_MaS_33SR_LMH_phospho2_05

Scan	Method	Score	m/z	Gene names
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Raw file
20171215_MaS_33SR_LMH_phospho2_05

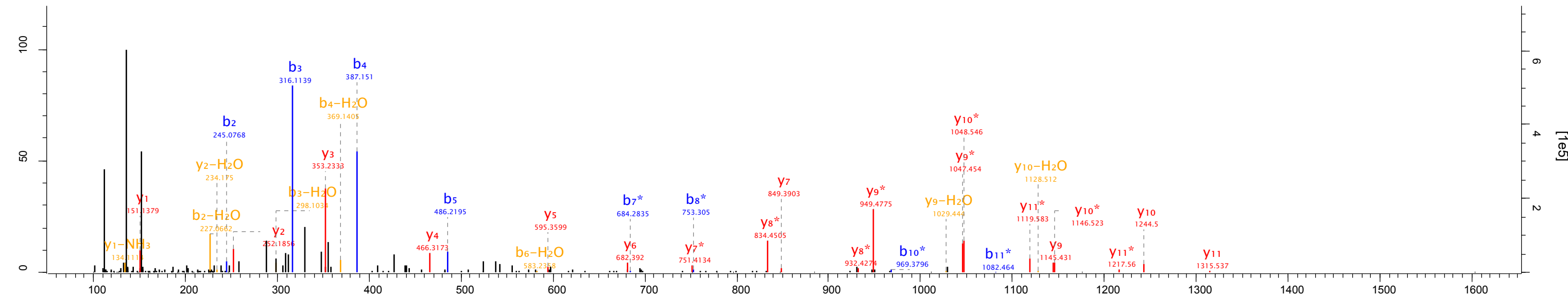
Scan 5919 Method FTMS; HCD Score 45.28 m/z 943.33 Gene names PWP1



Raw file

20171215_MaS_33SR_LMH_phospho2_05

Scan	Method	Score	m/z	Gene names
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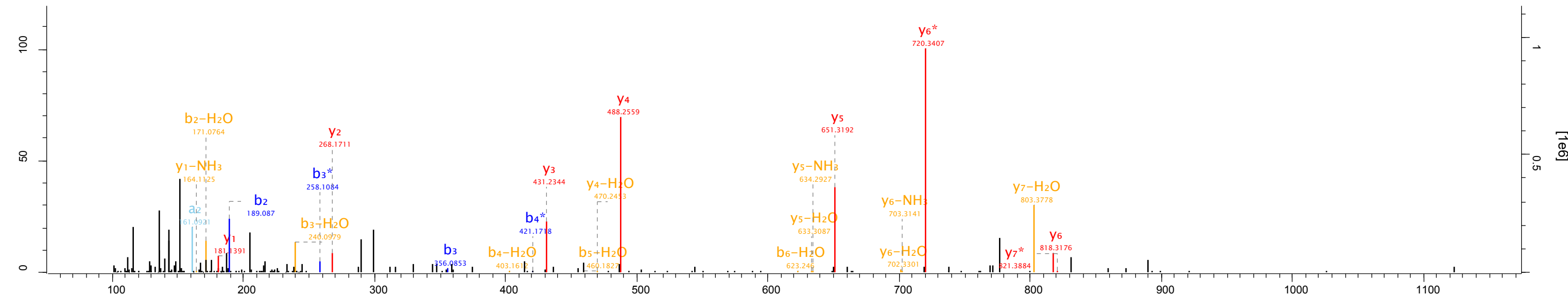


ac

- S D A A V D T ph S E I T T K -

b₂ b₃ b₄ b₅ b₇* b₈* b₁₀* b₁₁*

y₁₁ y₁₀ y₉ y₈* y₇ y₆ y₅ y₄ y₃ y₂ y₁

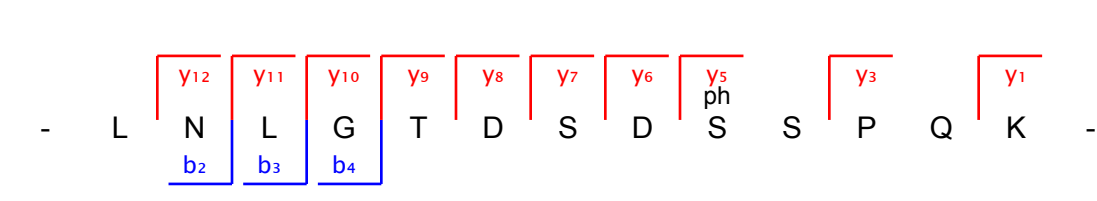
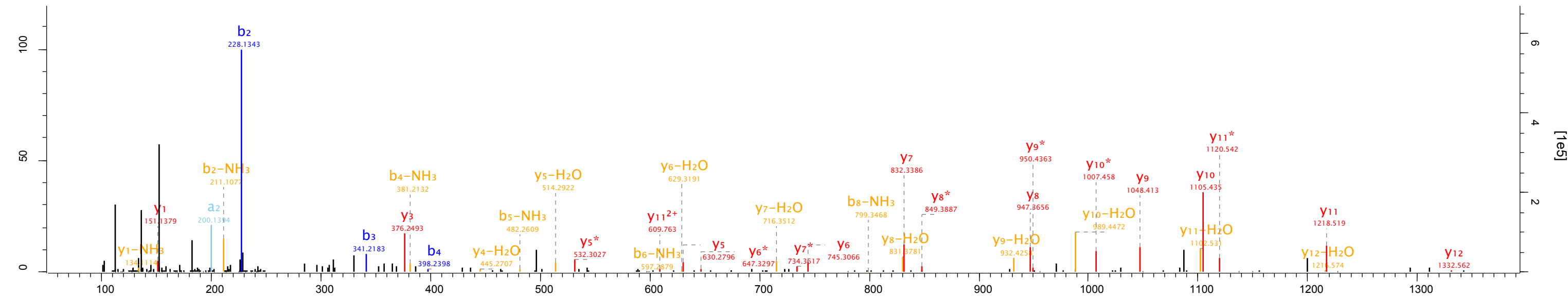


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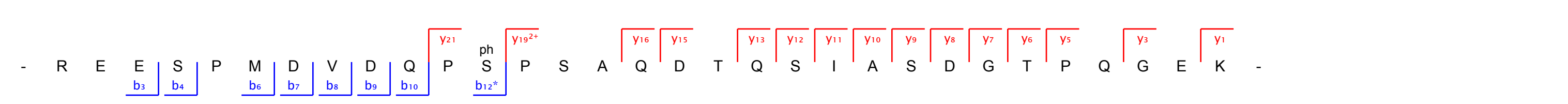
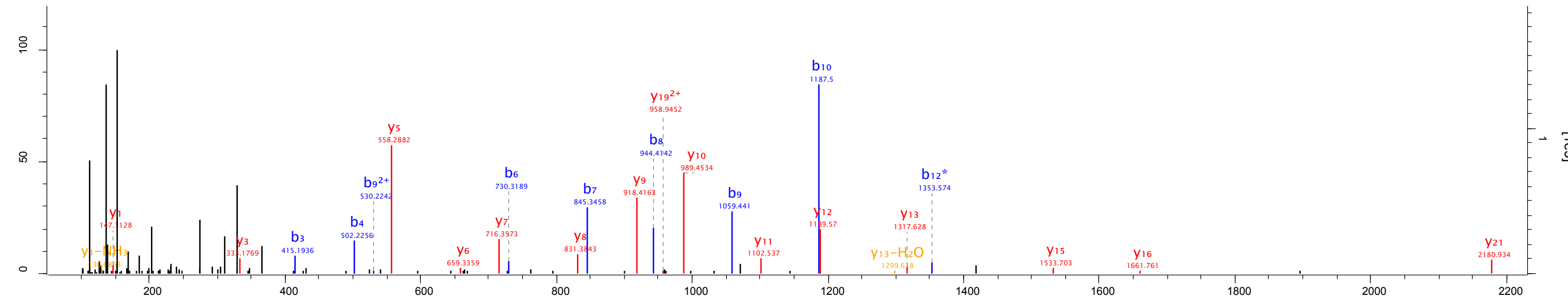
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b2	b3	b4*	G	Y	S	R

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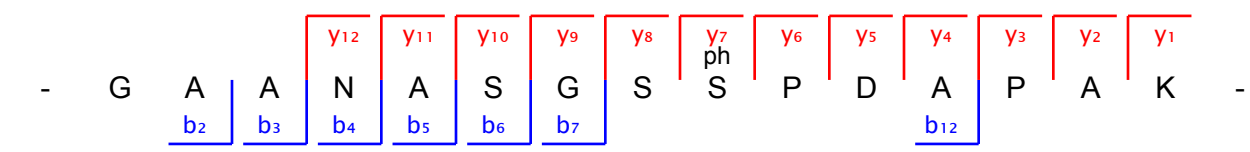
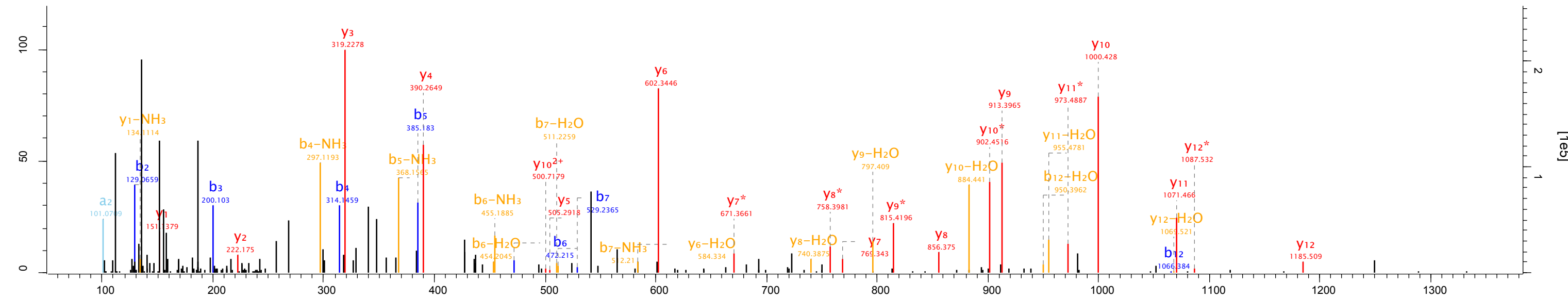
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Raw file 20171215_MaS_33SR_LMH_phospho2_06
 Scan 9009 Method FTMS; HCD Score 67.4 m/z 1123.48 Gene names HUWE1

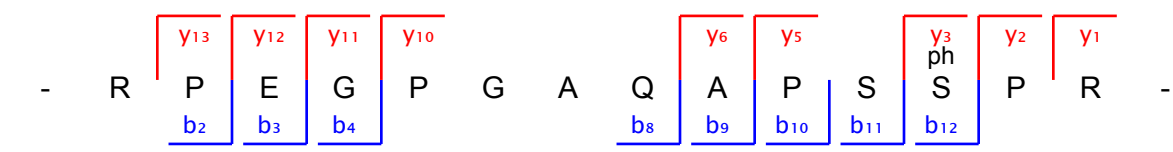
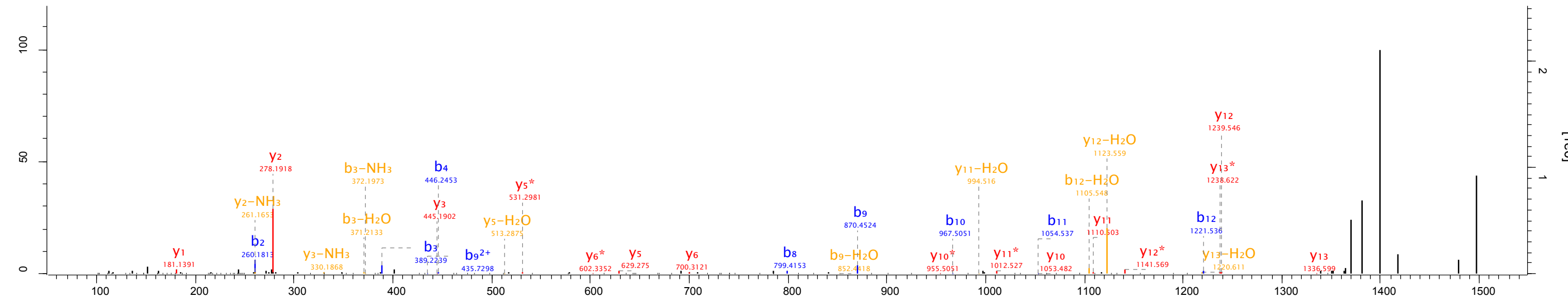


Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 2209 Method FTMS; HCD Score 164.97 m/z 692.8 Gene names TRIO



Raw file
20171215_MaS_33SR_LMH_phospho2_08

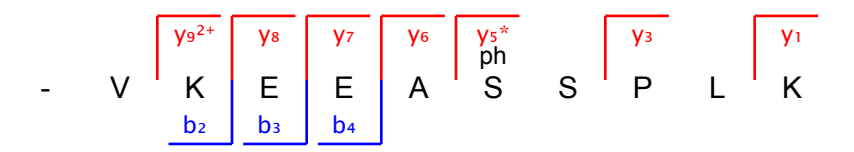
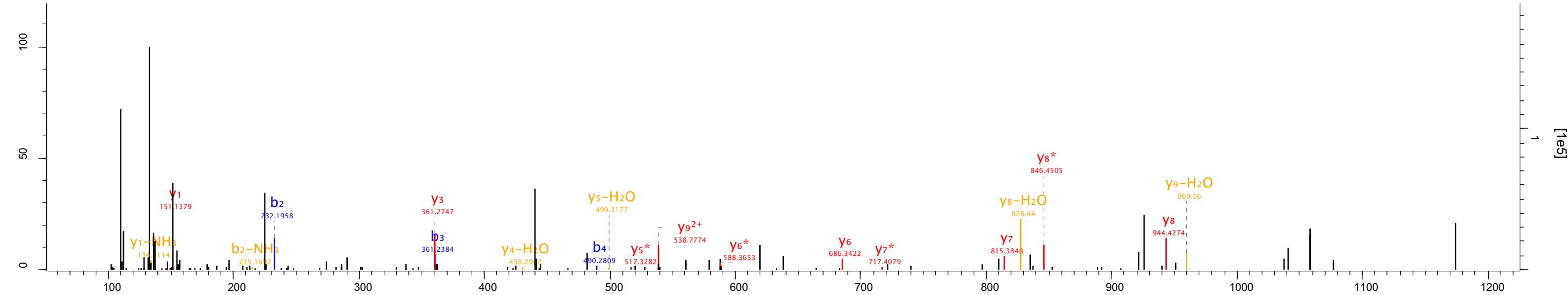
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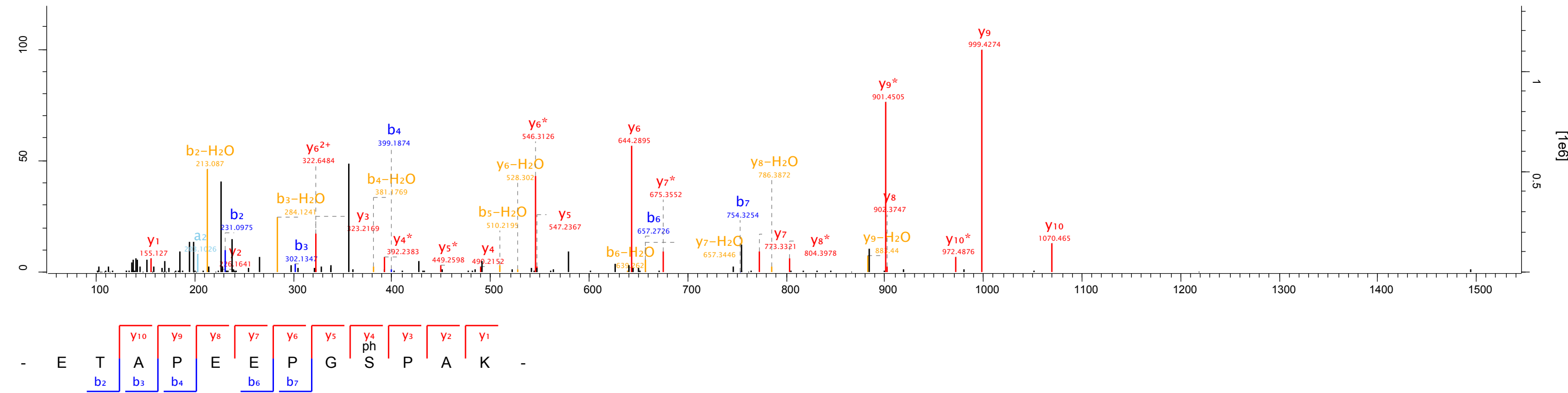


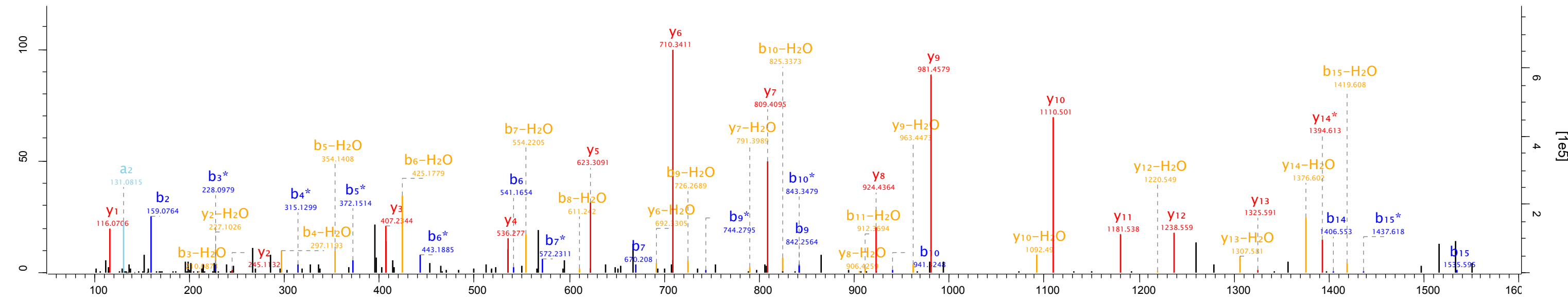
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20171215_MaS_33SR_LMH_phospho2_08

Scan 2609 Method FTMS; HCD Score 55.2 m/z 588.31 Gene names RERE







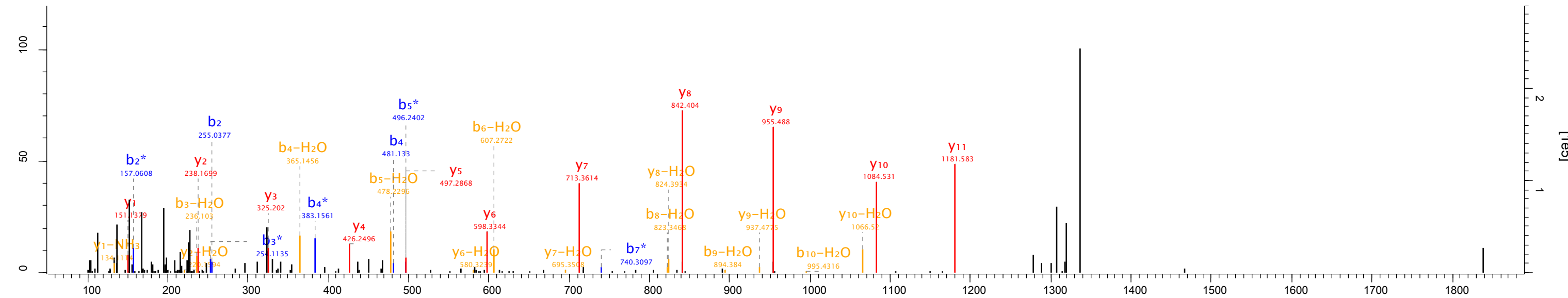
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b2 b3* b4* b5* b6 b7 b9 b10 b14 b15

Raw file

20171215_MaS_33SR_LMH_phospho2_08

Scan	Method	Score	m/z	Gene names
4369	FTMS; HCD	94.45	718.31	MKI67



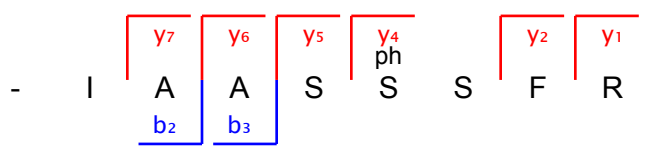
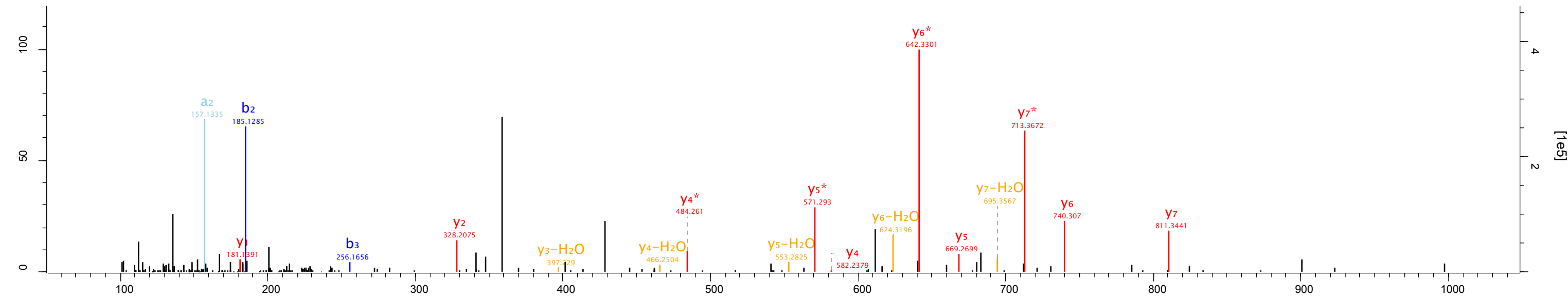
ph S - S P E L E D T A T S S K -

b₂ b₃^{*} b₄ b₅^{*} b₇^{*} y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

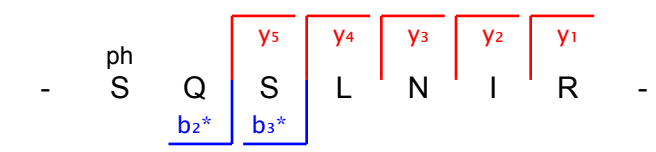
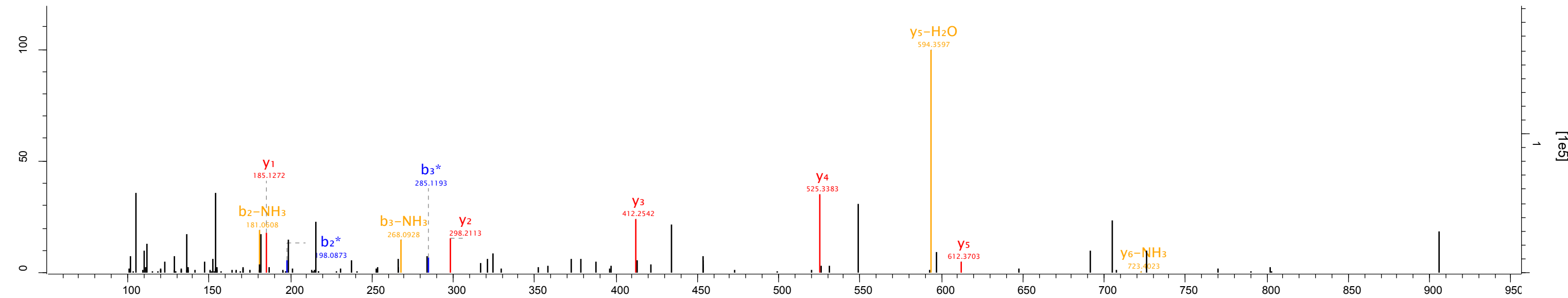
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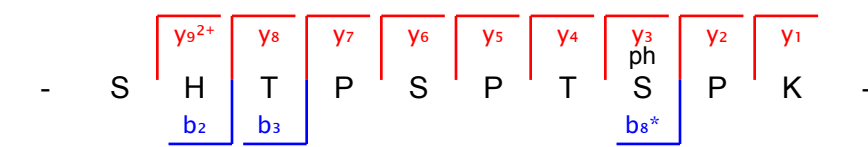
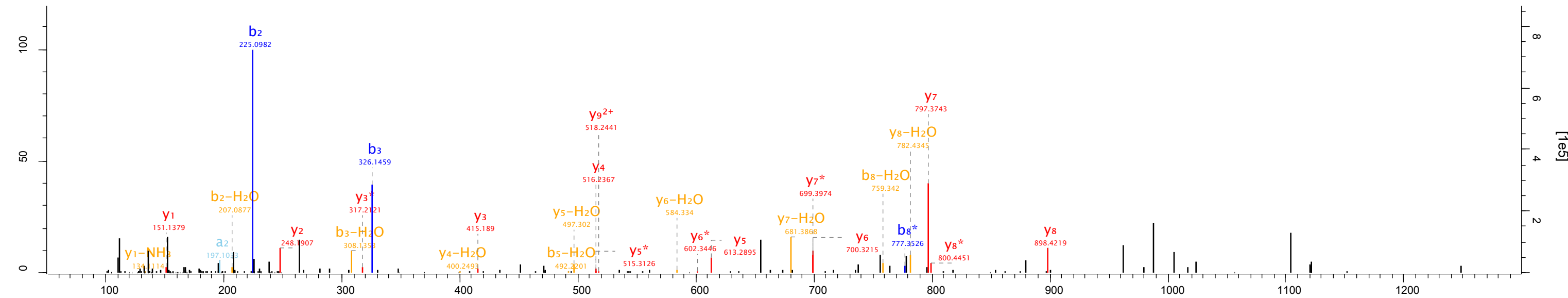
20171215_MaS_33SR_LMH_phospho2_08

Scan	Method	Score	m/z	Gene names
4619	FTMS; HCD	102.52	462.72	SH3GL1

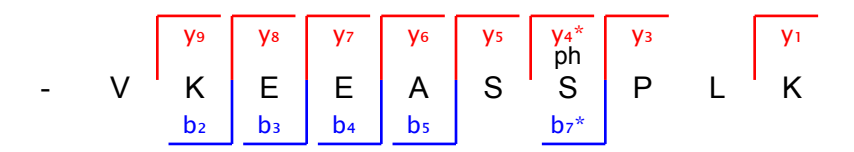
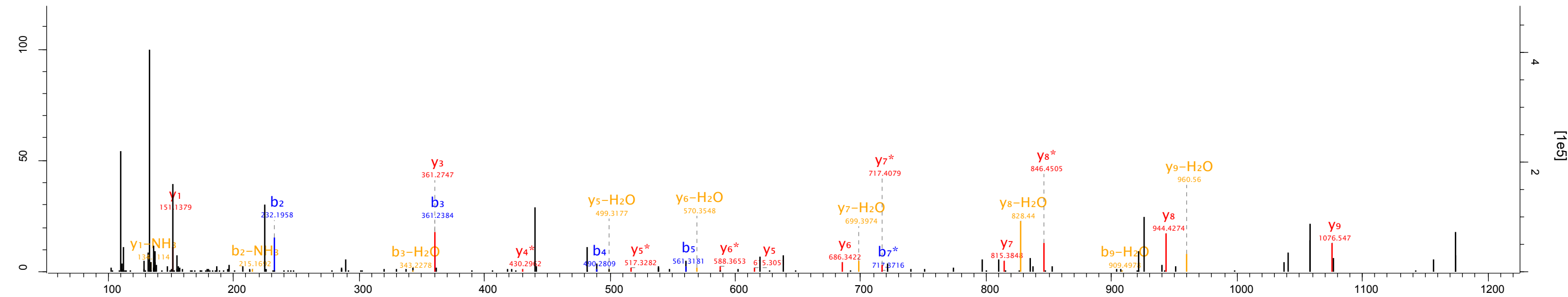


Raw file 20171215_MaS_33SR_LMH_phospho2_08 Scan 5379 Method FTMS; HCD Score 49.72 m/z 454.22 Gene names PIK3C2A

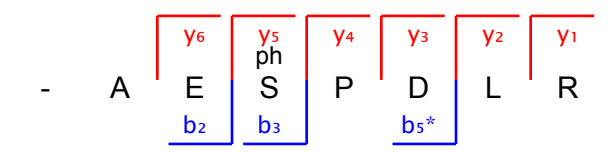
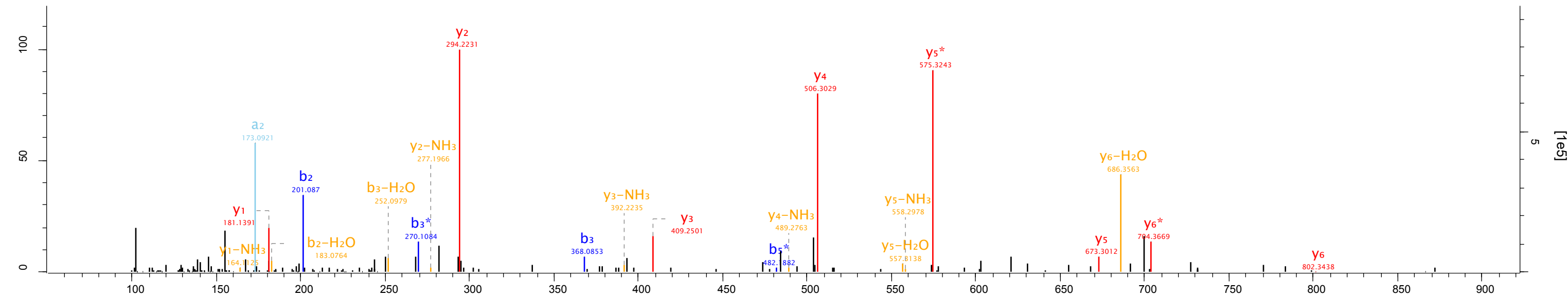




Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 2629 Method FTMS; HCD Score 89.45 m/z 588.31 Gene names RERE

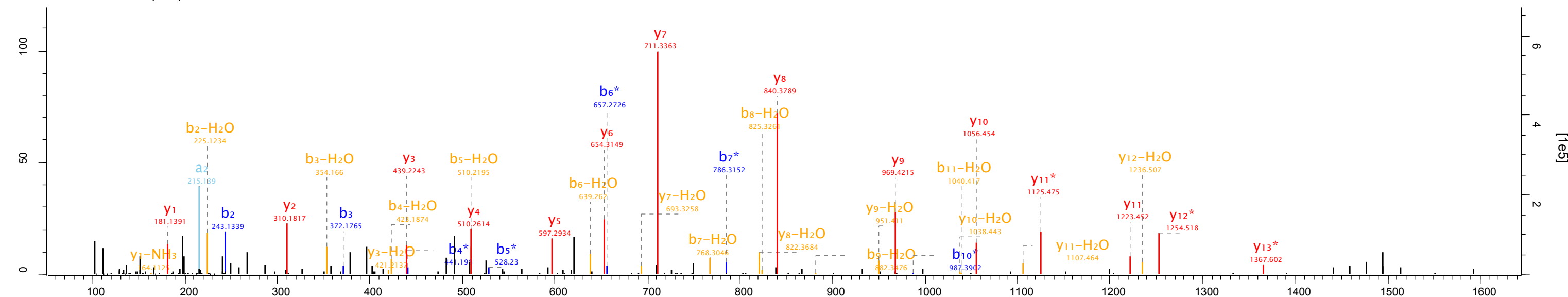


Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 3349 Method FTMS; HCD Score 117.84 m/z 437.19 Gene names FIP1L1



Raw file
20171215_MaS_33SR_LMH_phospho2_09

Scan 3479 Method FTMS; HCD Score 173.51 m/z 797.81 Gene names C17orf75



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

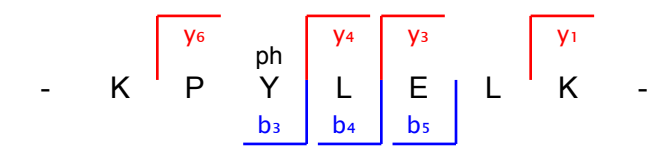
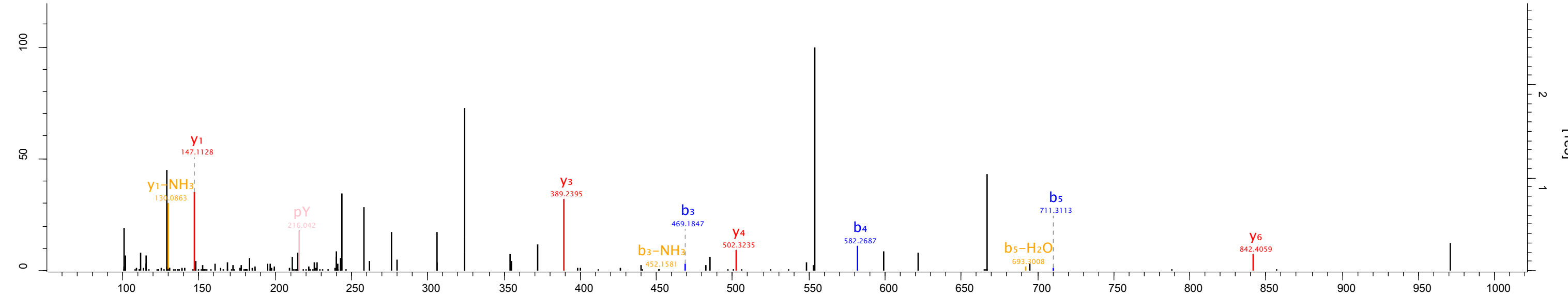
Phosphorylation sites (y ions) are indicated by red boxes above the sequence: y13*, y12*, y11-ph, y10, y9, y8, y7, y6, y5, y4, y3, y2, y1.

Other labeled ions (b ions) are indicated by blue boxes below the sequence: b2, b3, b4*, b5*, b6*, b7*, b10*.

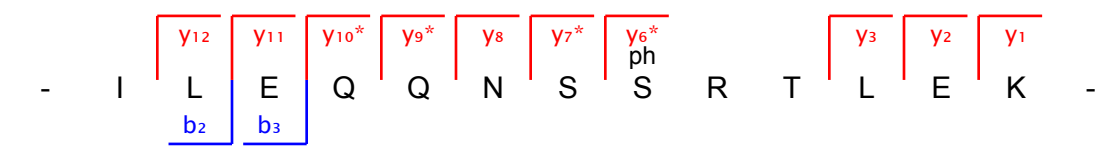
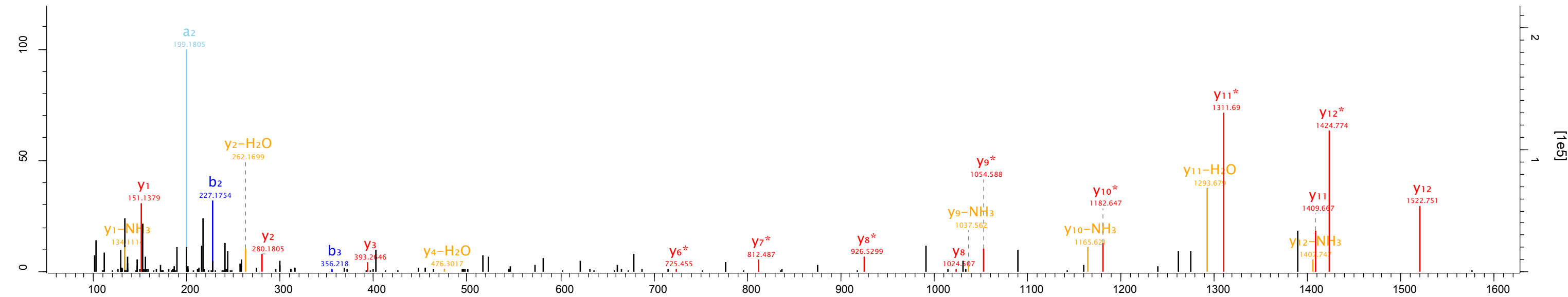
Raw file

20171215_MaS_33SR_LMH_phospho2_09

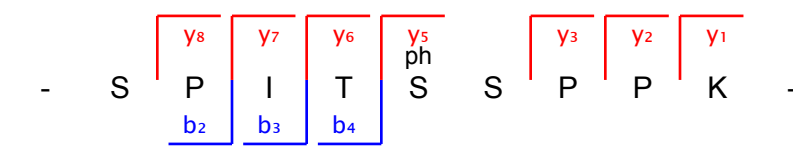
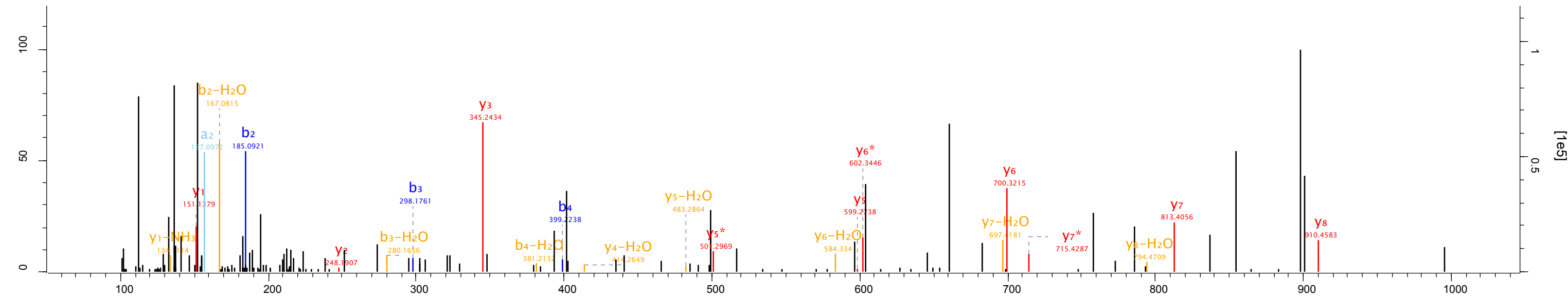
Scan	Method	Score	m/z	Gene names
3529	FTMS; HCD	75.11	324.17	USP4



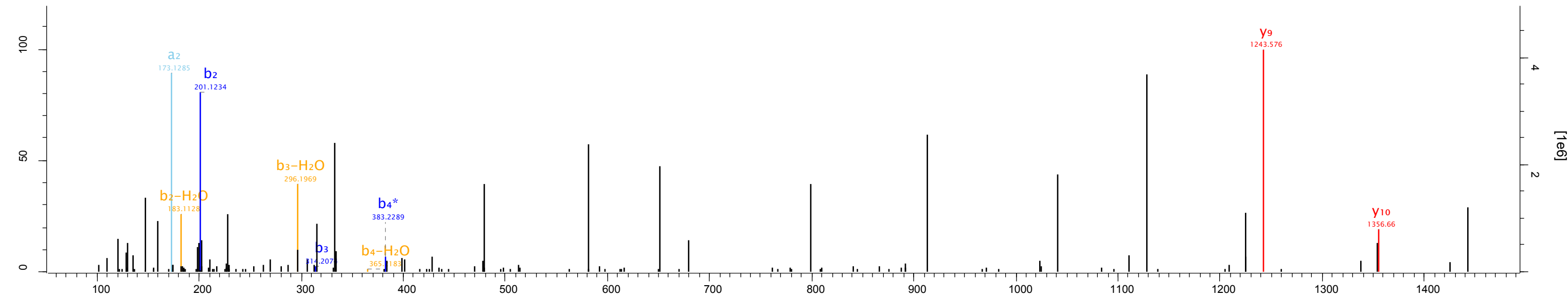
Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 3999 Method FTMS; HCD Score 91.66 m/z 546.28 Gene names SEPT7;DKFZp586I031



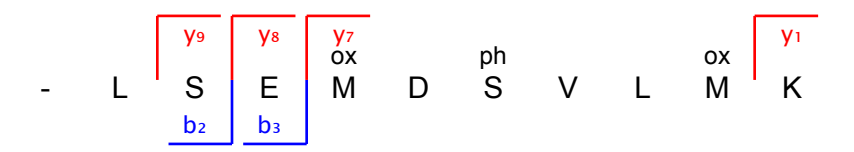
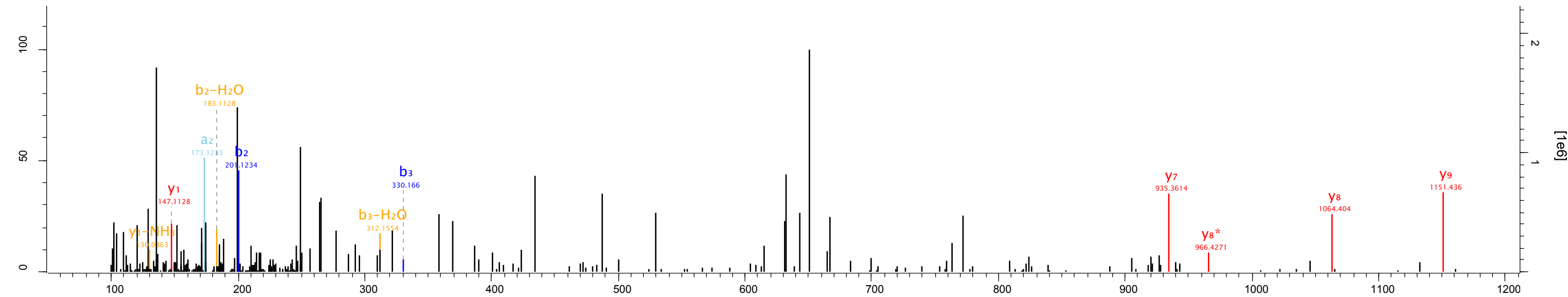
Raw file 20171215_MaS_33SR_LMH_phospho2_09 Scan 4189 Method FTMS; HCD Score 60.51 m/z 499.25 Gene names LIN52



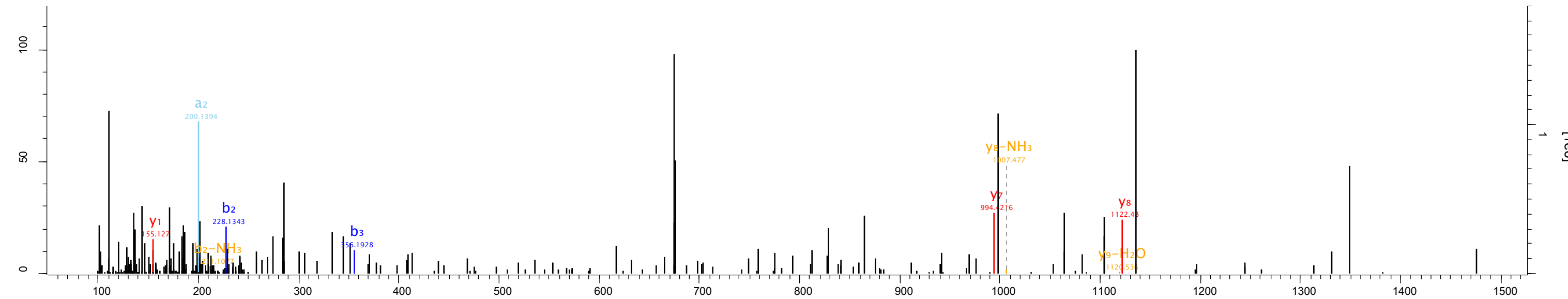
Raw file: 20171215_MaS_33SR_LMH_proteome_01
 Scan: 102919 Method: FTMS; HCD Score: 46.35 m/z: 778.89 Gene names: FMN2



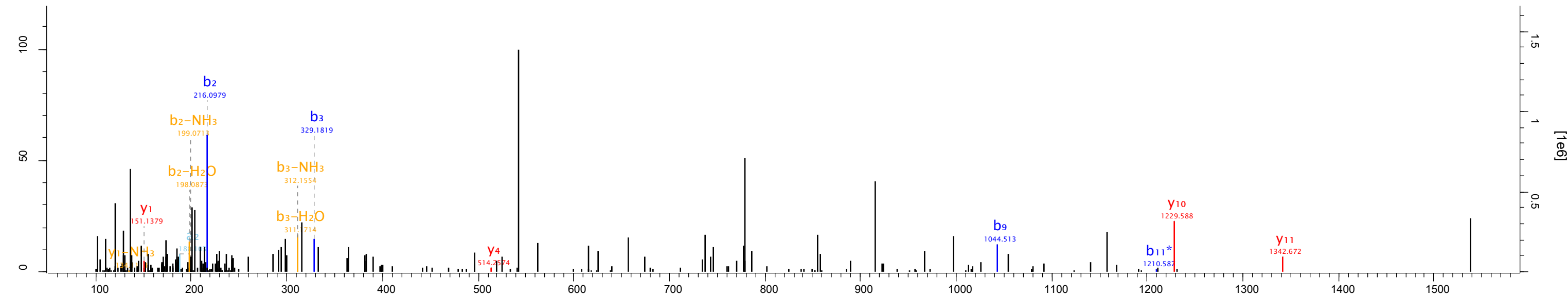
Raw file: 20171215_MaS_33SR_LMH_proteome_01
 Scan: 23919 Method: FTMS; HCD Score: 42.34 m/z: 632.77 Gene names: PIGG



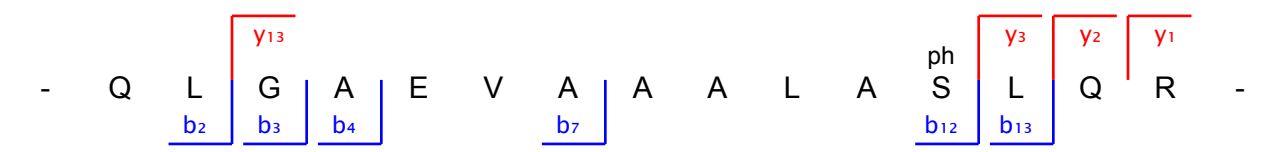
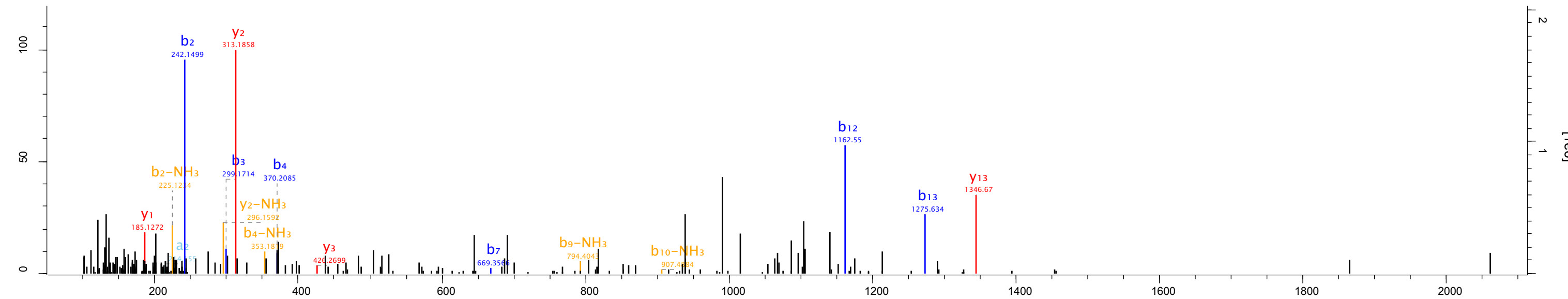
Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 32189 Method FTMS; HCD Score 44.32 m/z 675.81 Gene names AKAP8



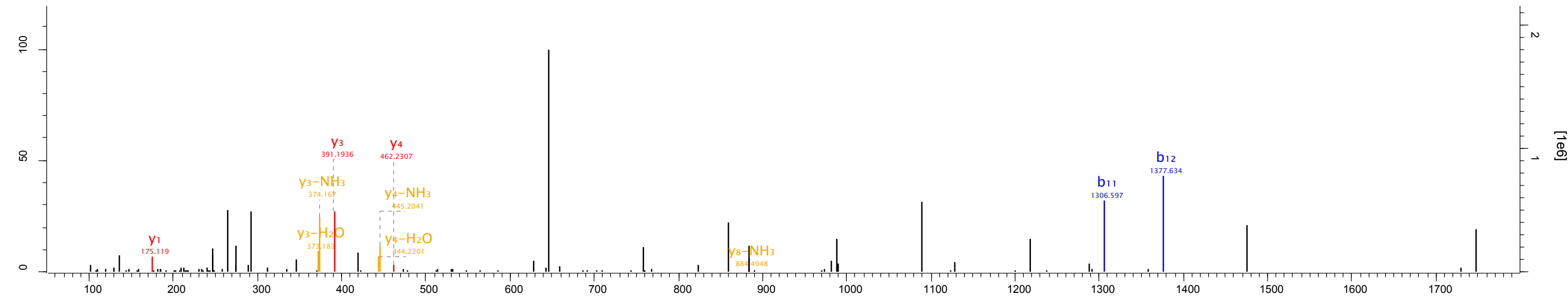
Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 42869 Method FTMS; HCD Score 45.28 m/z 779.38 Gene names WDR72



Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 72519 Method FTMS; HCD Score 50.1 m/z 794.4 Gene names TRIM68



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 38489 Method FTMS; HCD Score 41.23 m/z 884.92 Gene names C17orf97



ac ox ph
 - M E T R G P G L A V R A E S R -
 b11 b12 y4 y3 y1

Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 6979 Method FTMS; HCD Score 46 m/z 398.2

