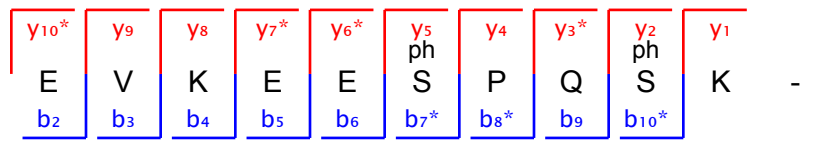
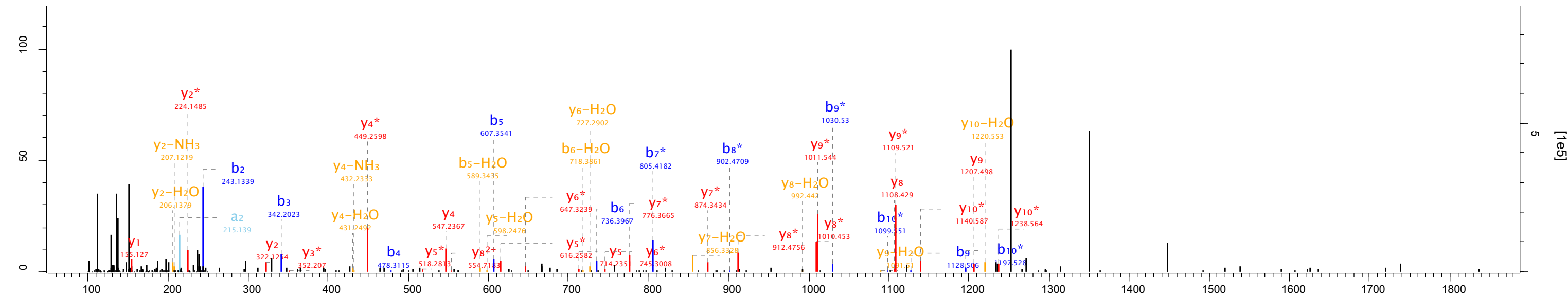
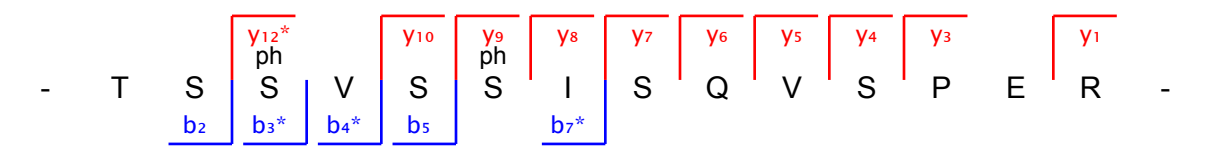
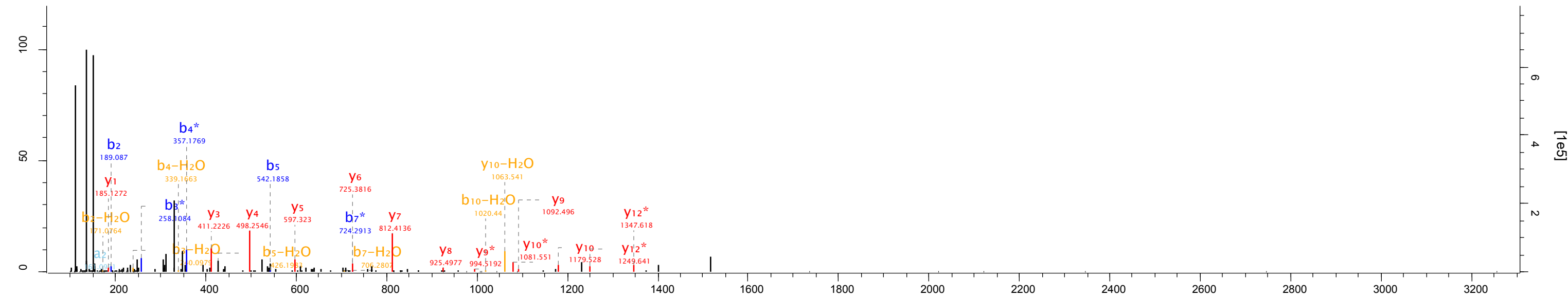


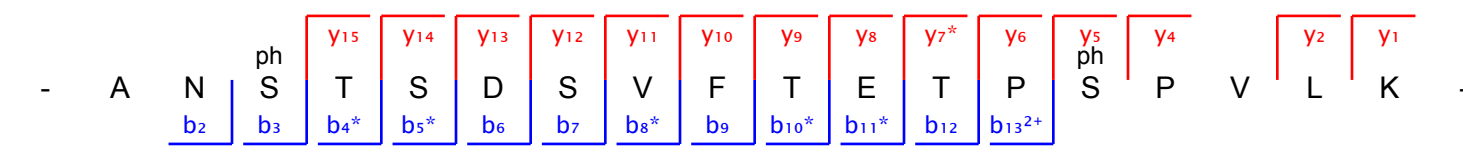
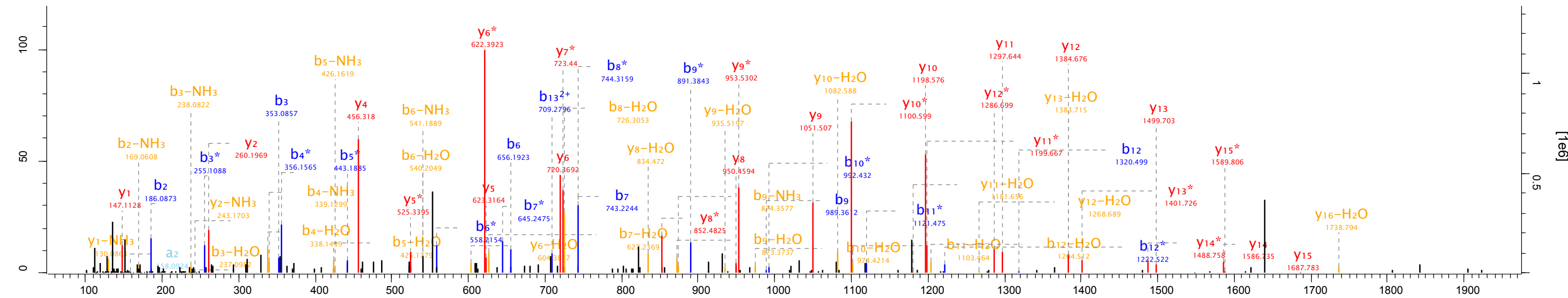
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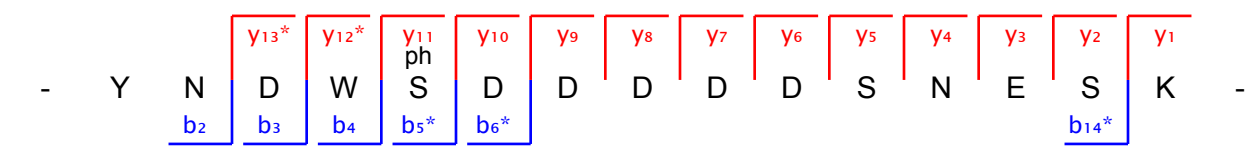
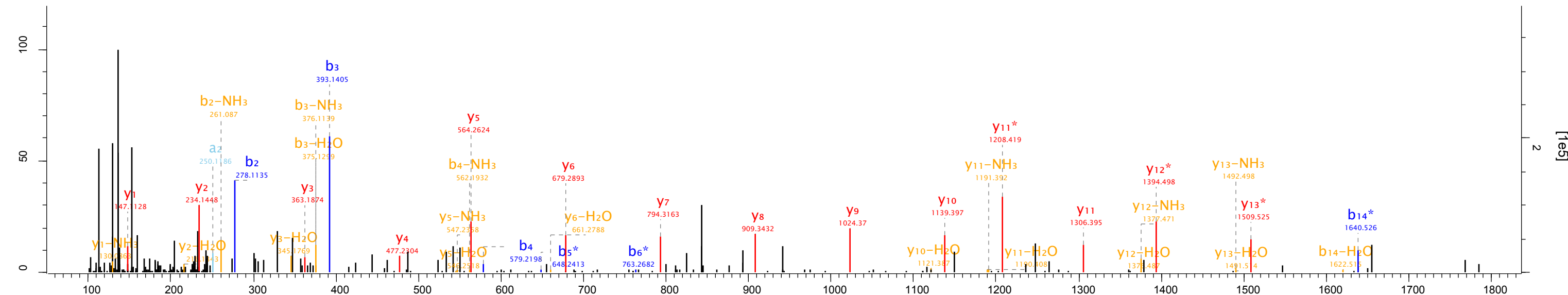
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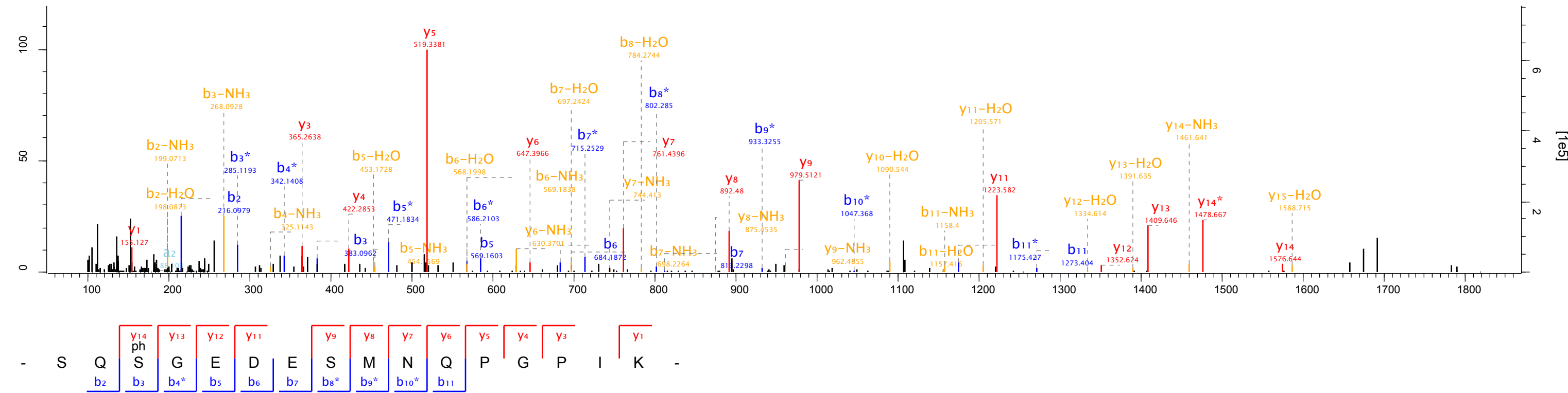


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 Scan: 15430
 Method: FTMS; HCD
 Score: 259.44
 m/z: 1020.93
 Gene names: CDC42EP3

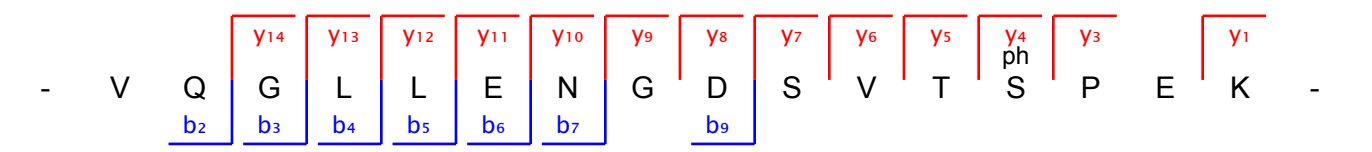
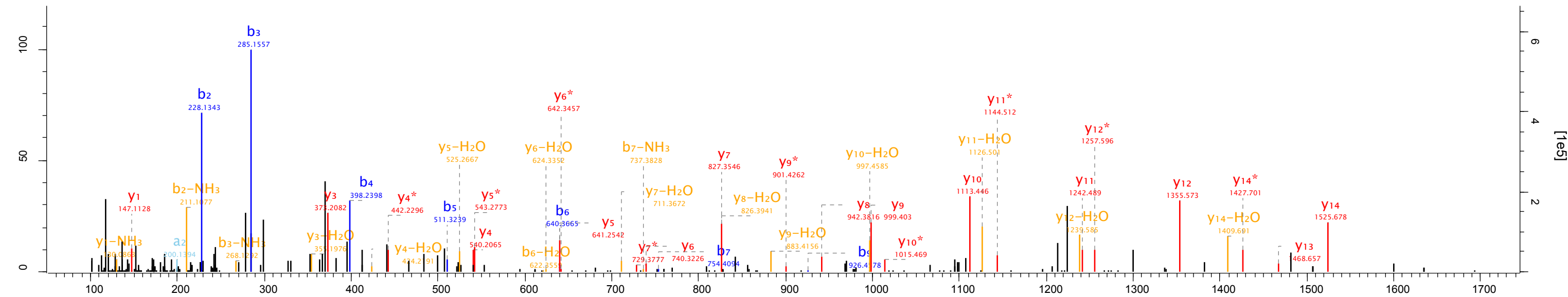


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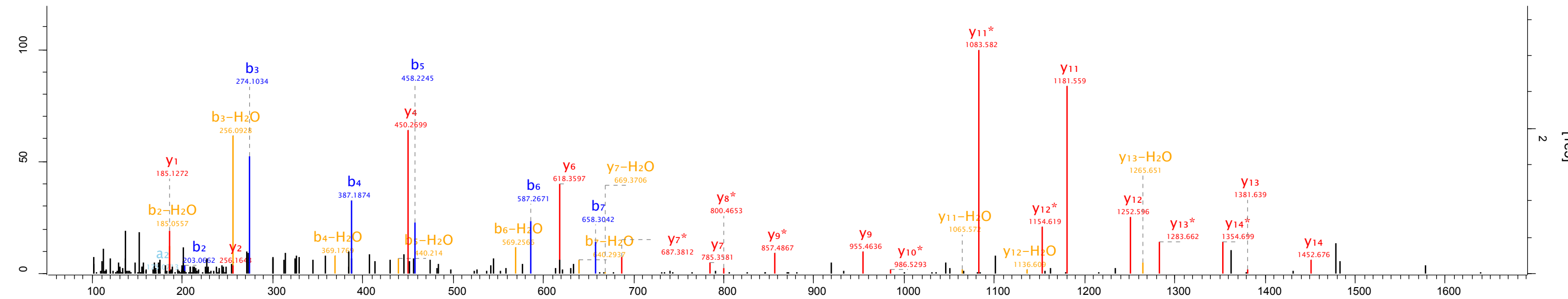




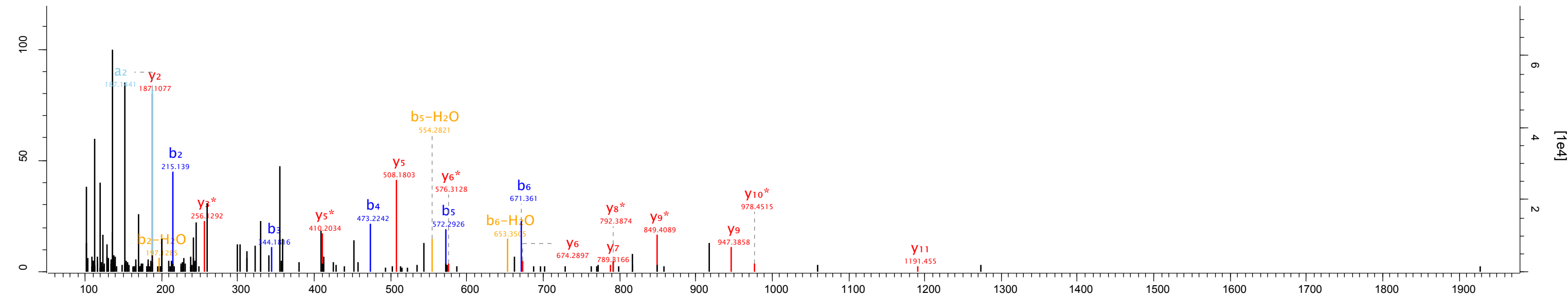
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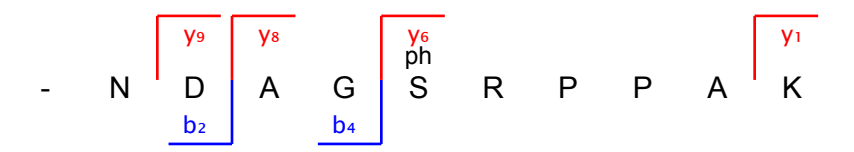
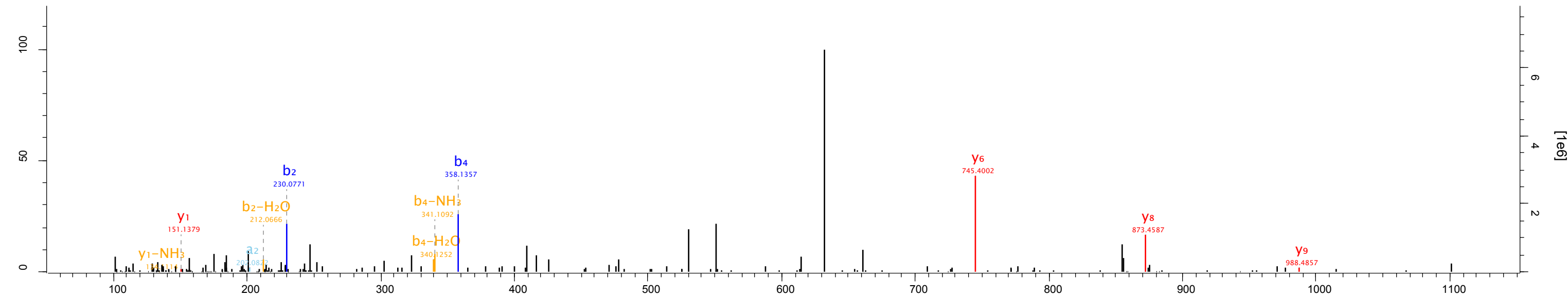
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 Scan: 11800 Method: FTMS; HCD Score: 150.94 m/z: 920.44 Gene names: USP42



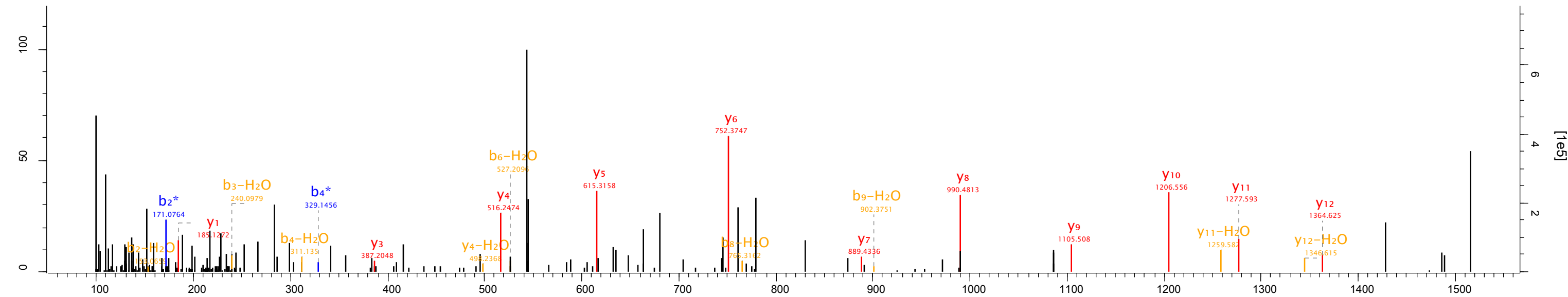
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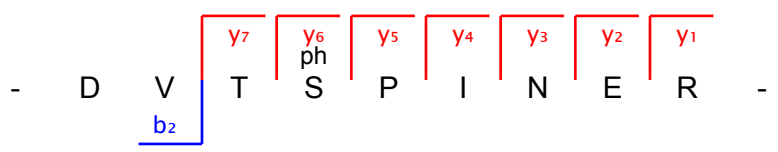
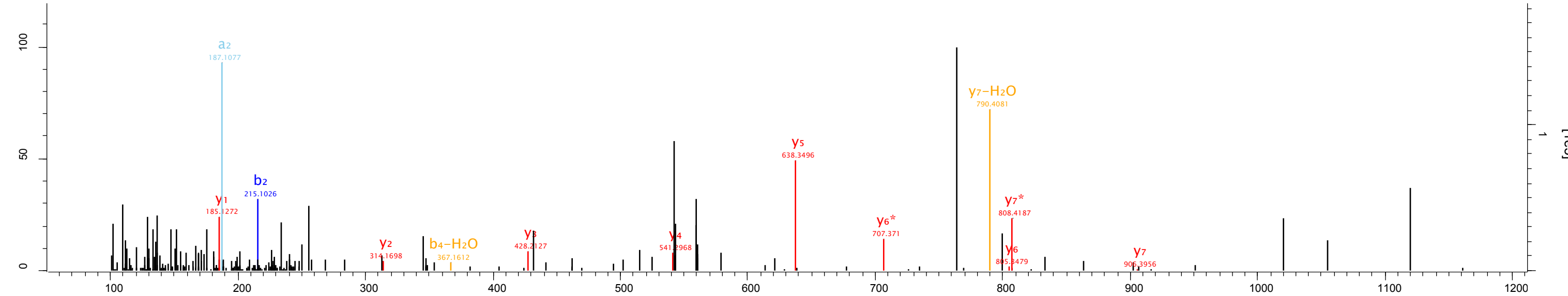
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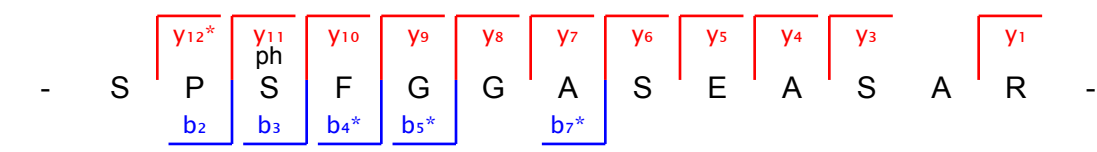
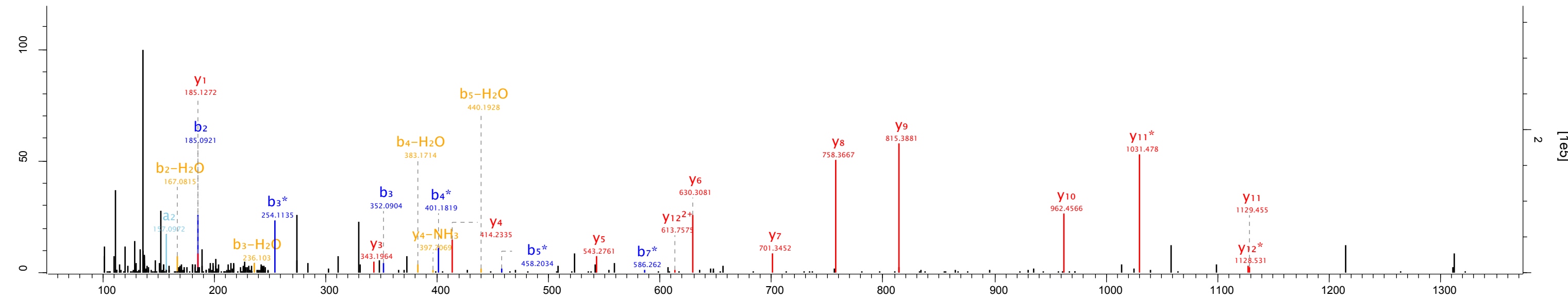
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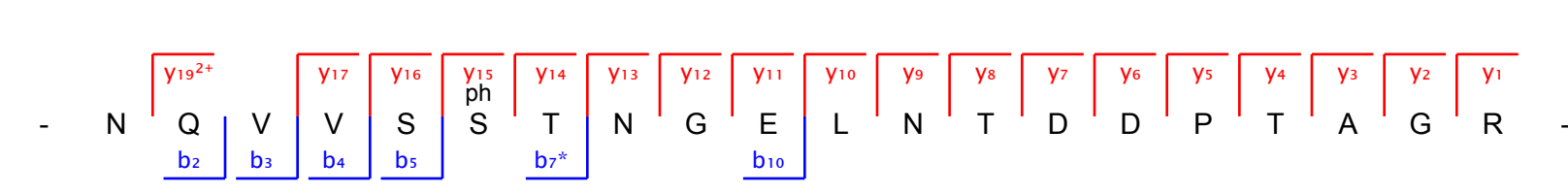
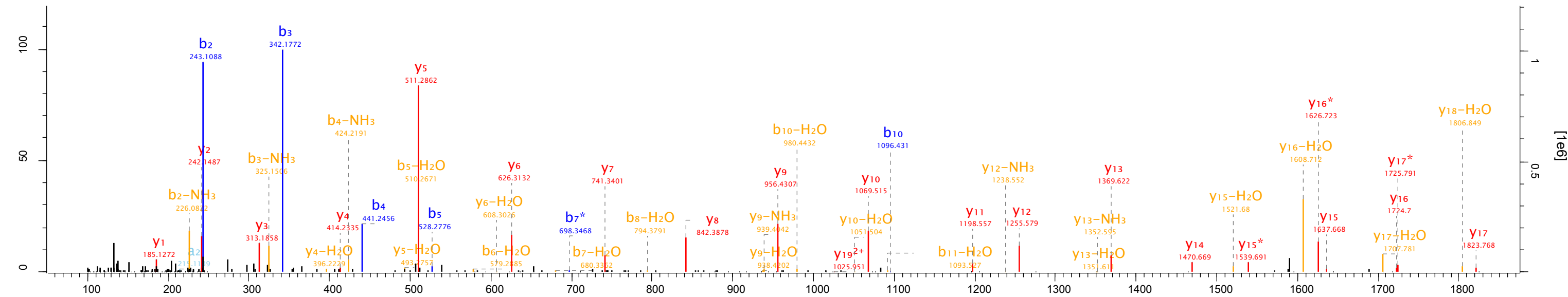
20171215_MaS_33SR_LMH_phospho_03 5960 FTMS; HCD 47.04 560.75 ANKS3



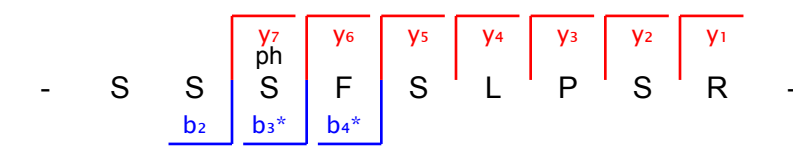
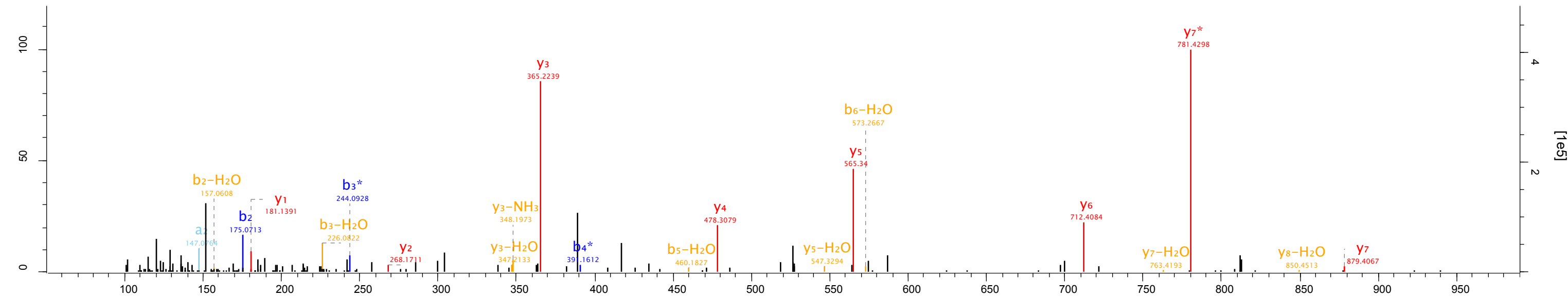
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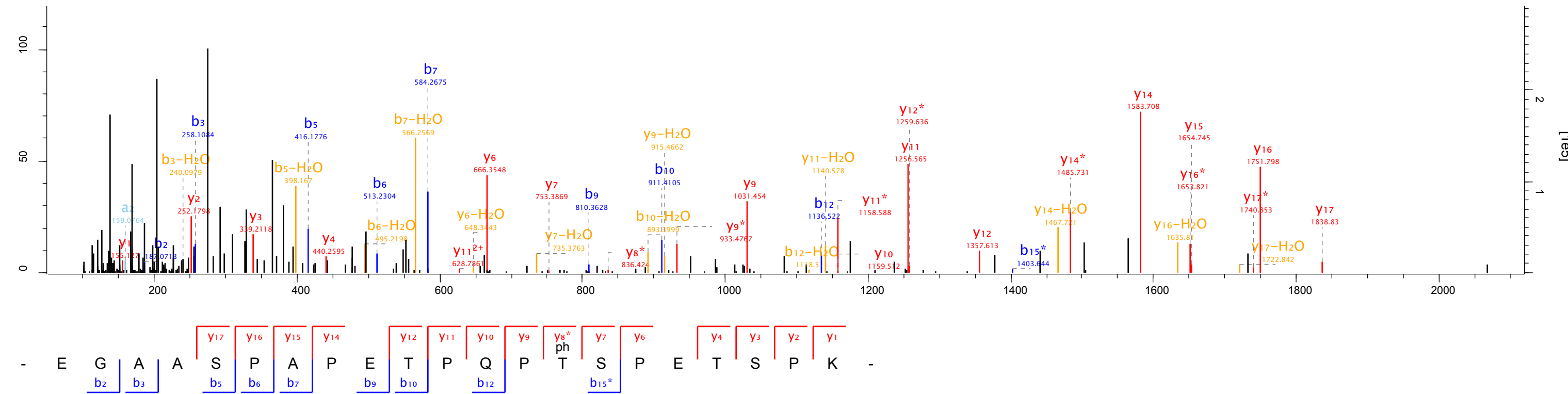


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 Scan: 8460 Method: FTMS; HCD Score: 157.12 m/z: 1083.47 Gene names: CSNK1G3

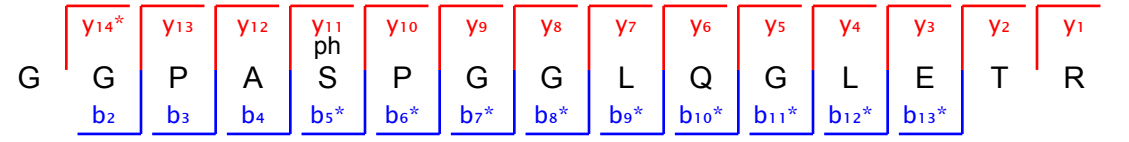
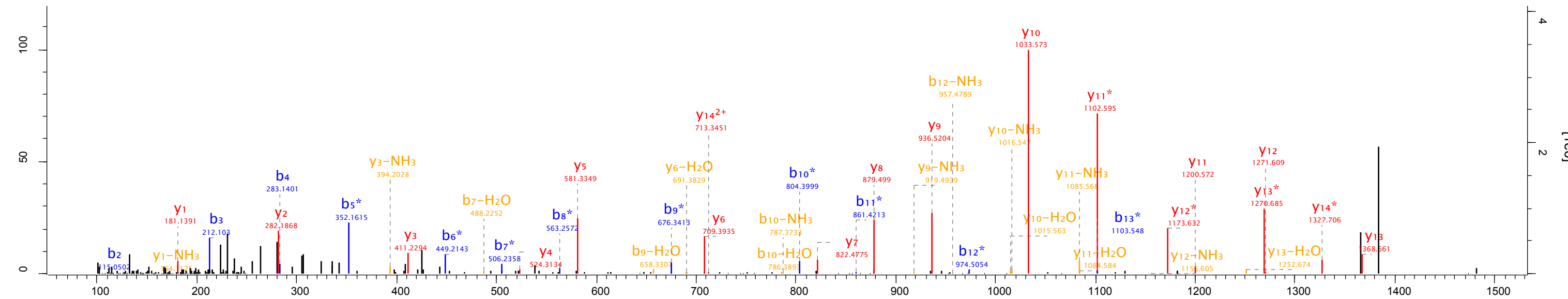


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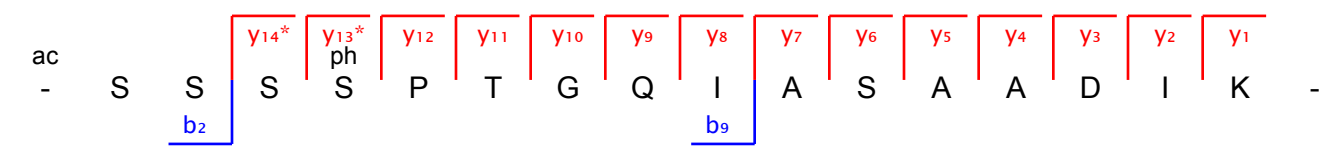
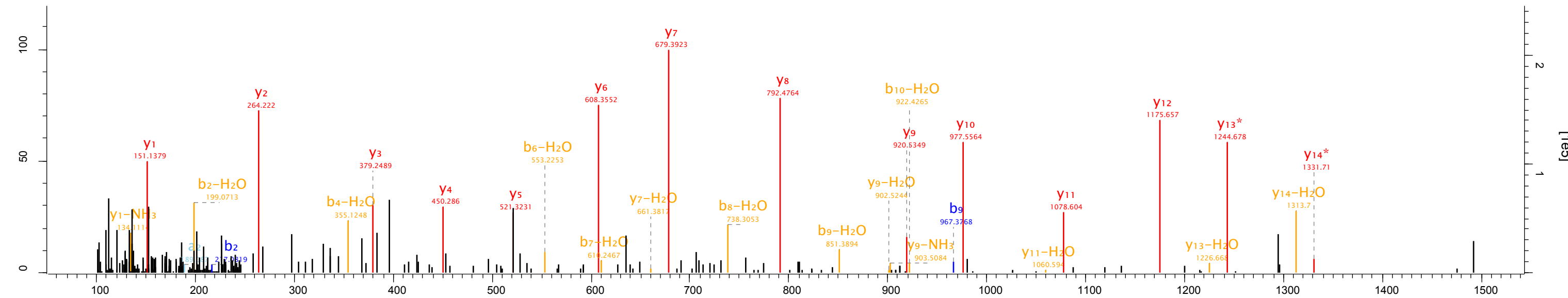




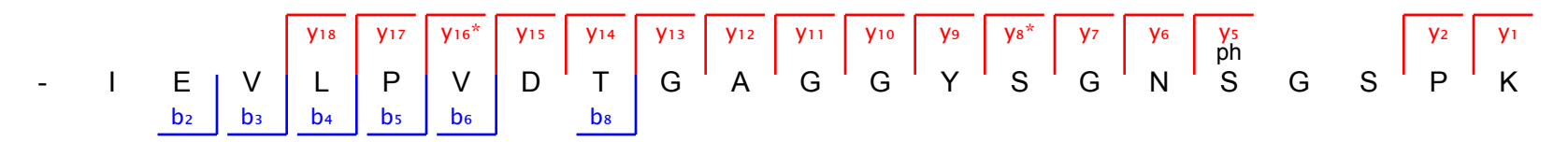
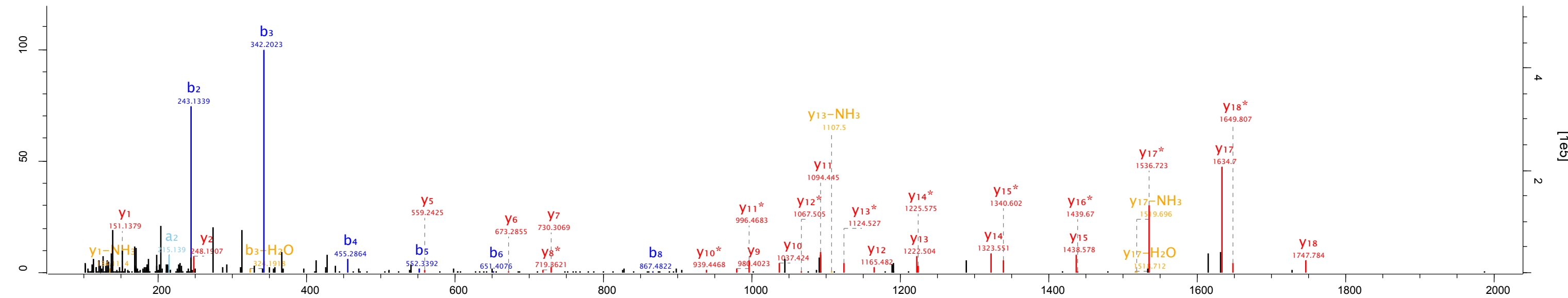
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 Scan: 11810 Method: FTMS; HCD Score: 189.55 m/z: 741.85 Gene names: HJURP



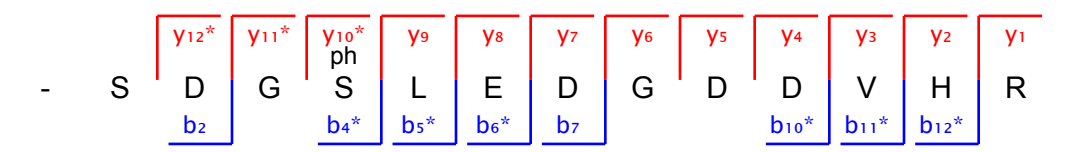
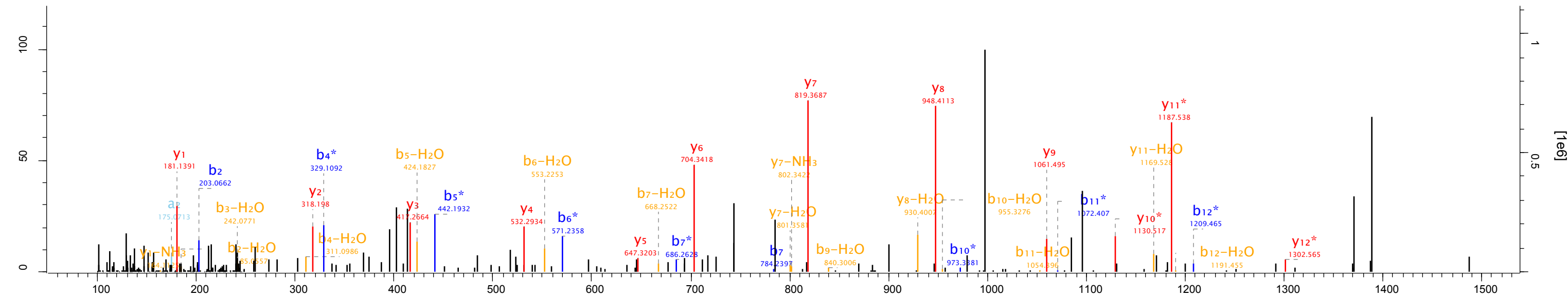
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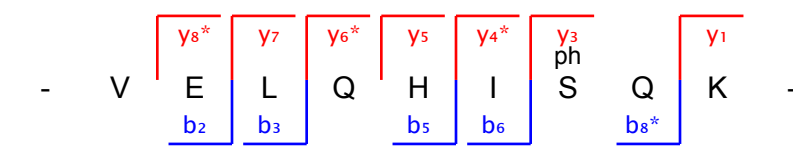
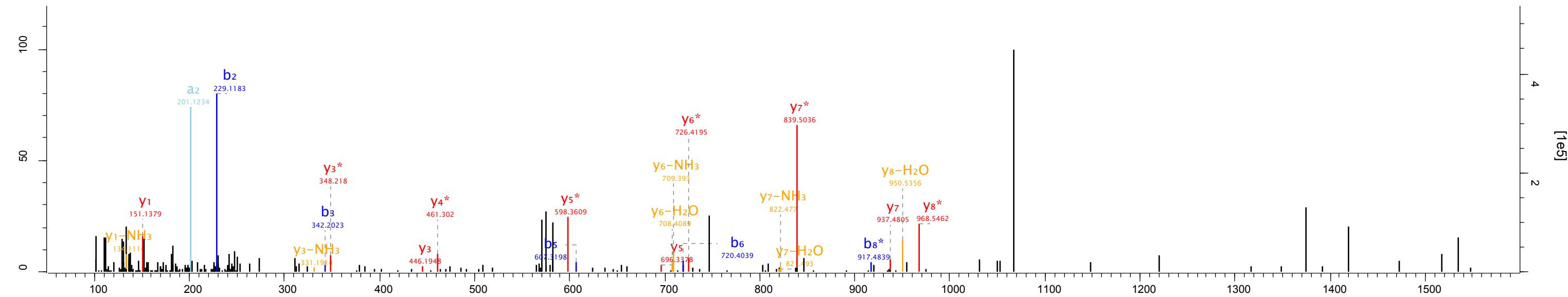
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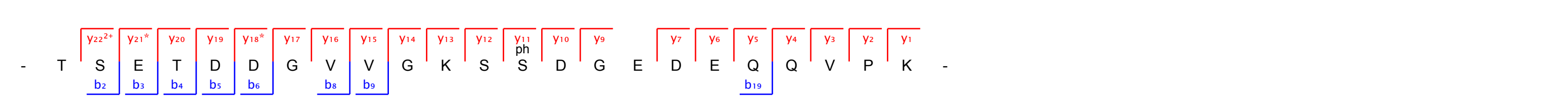
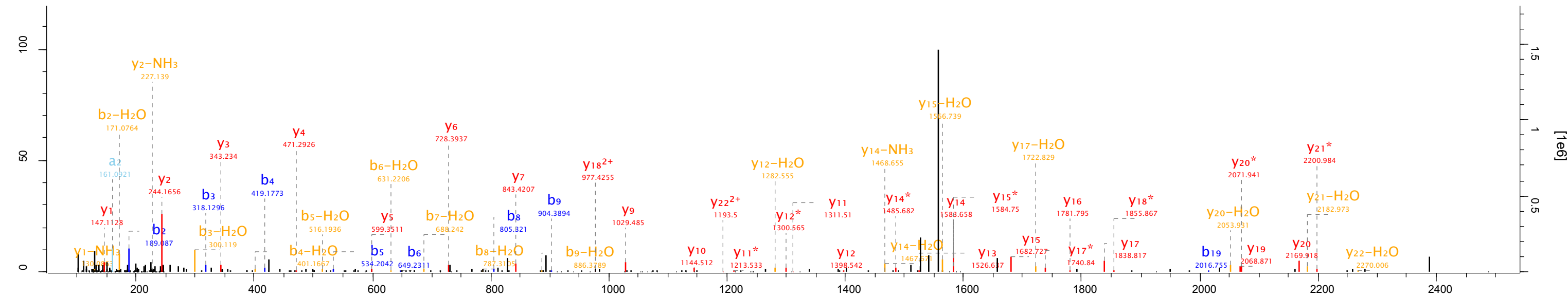
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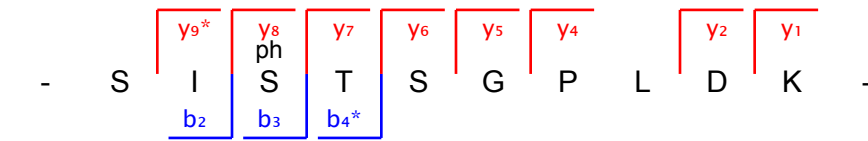
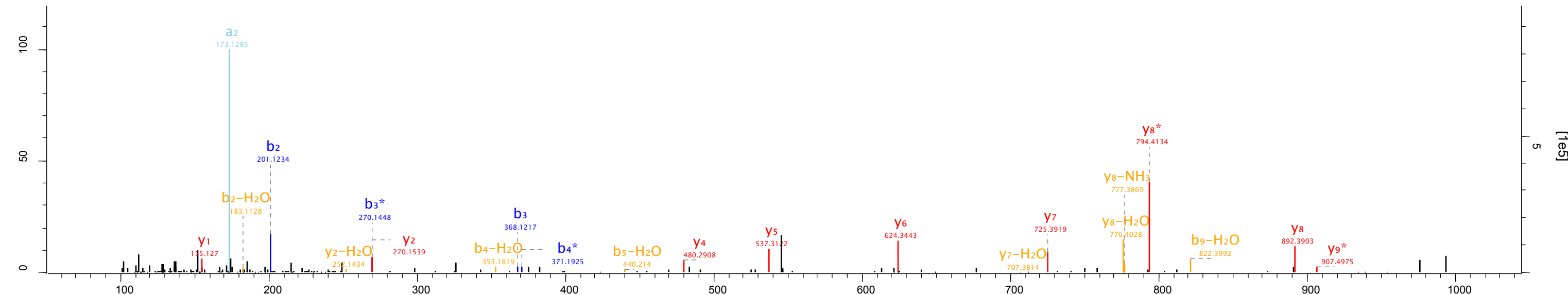


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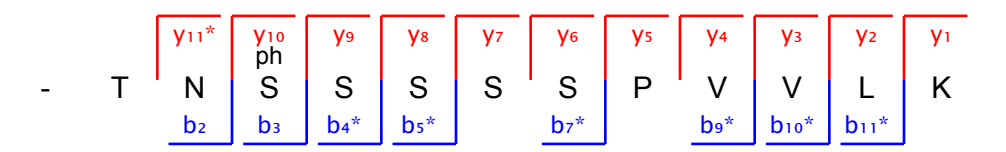
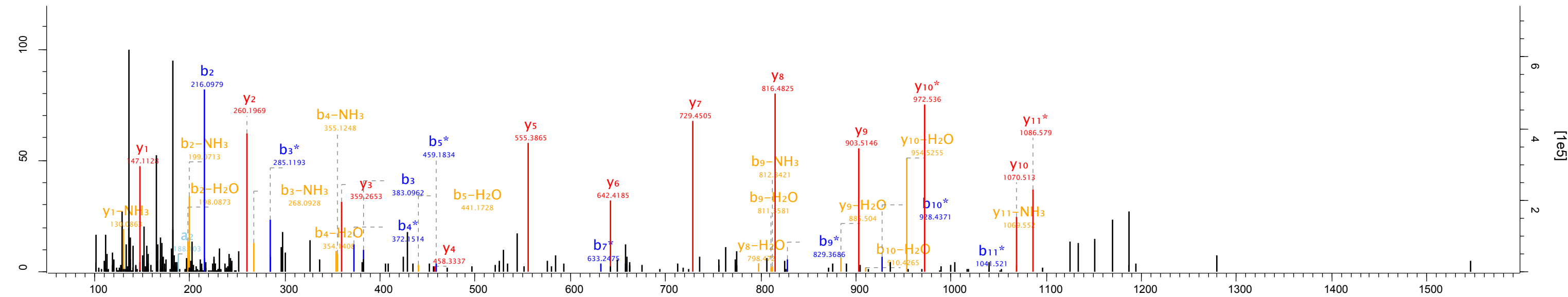


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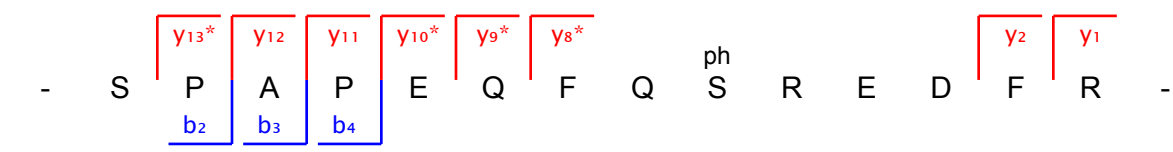
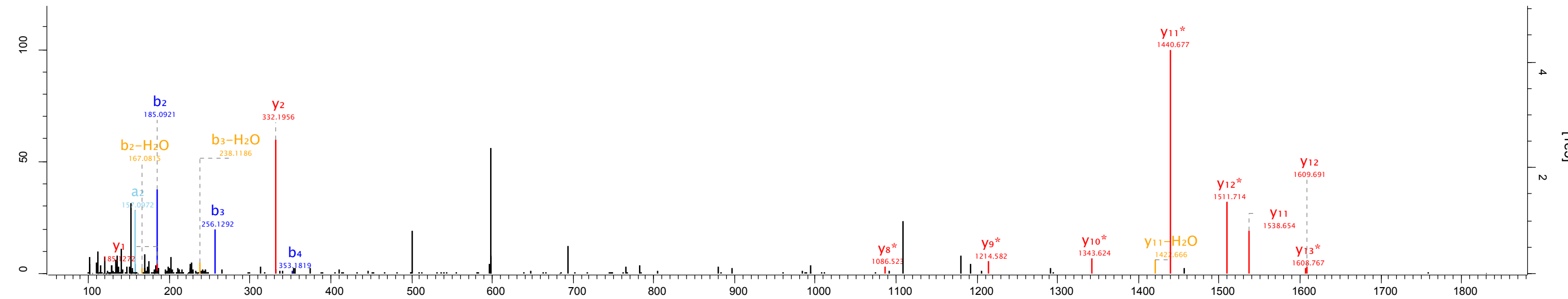


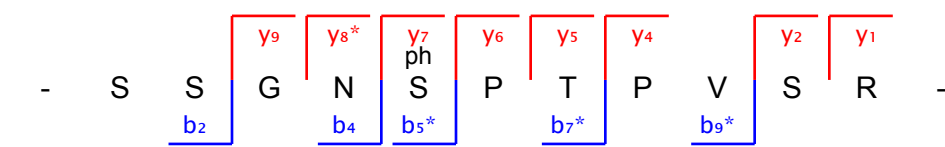
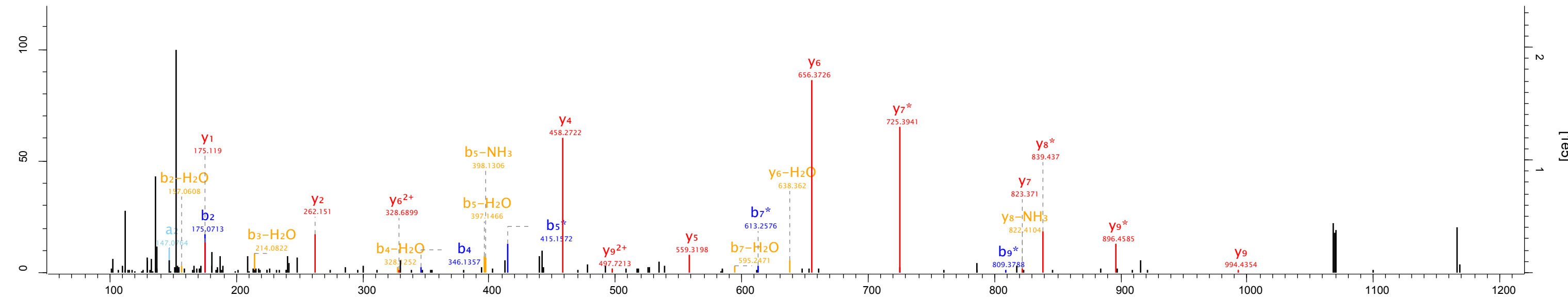


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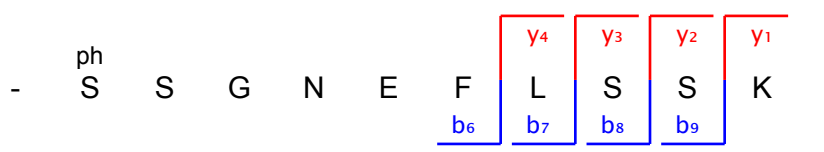
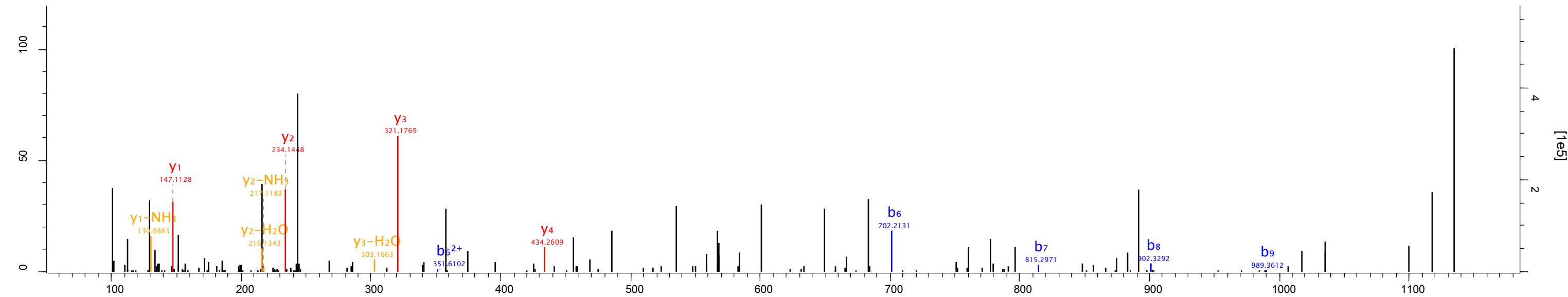


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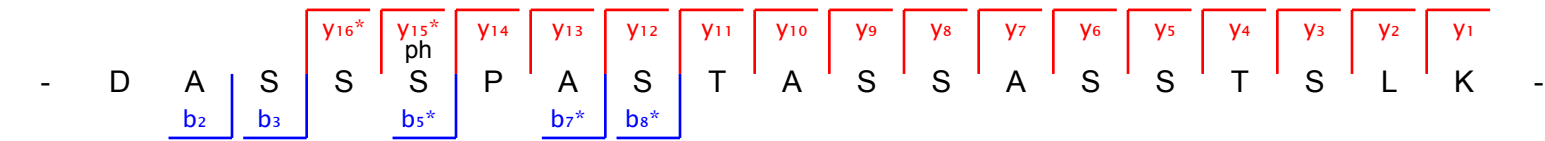
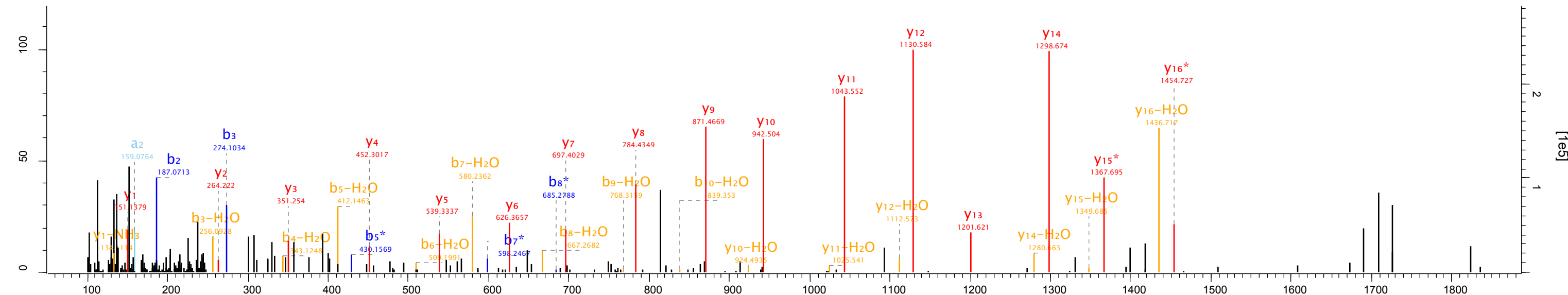


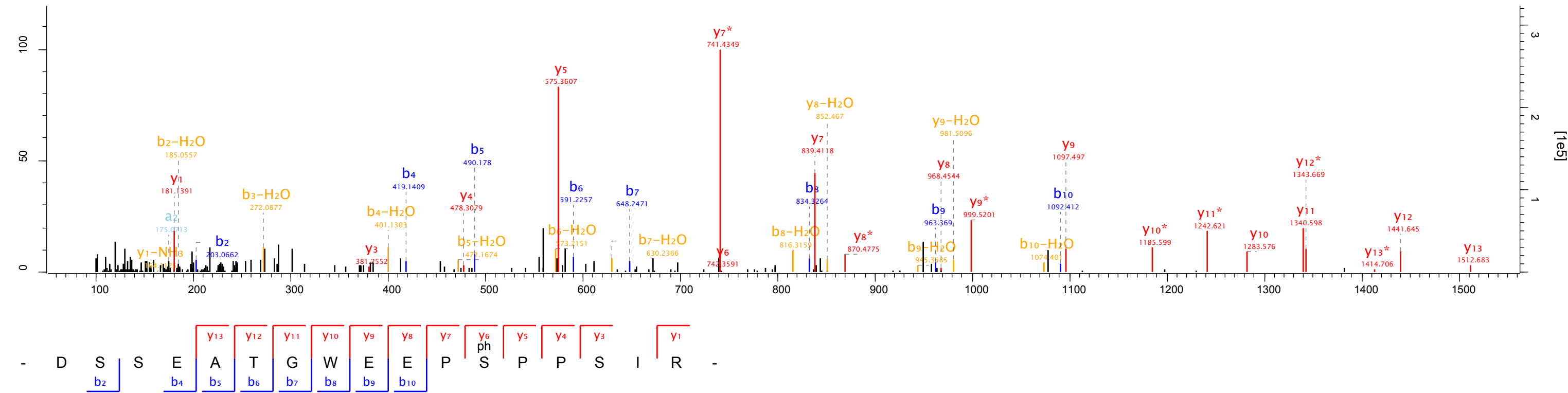


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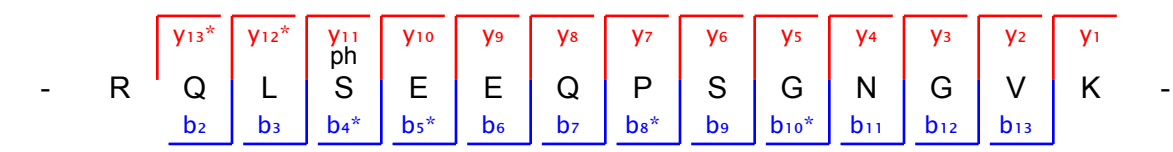
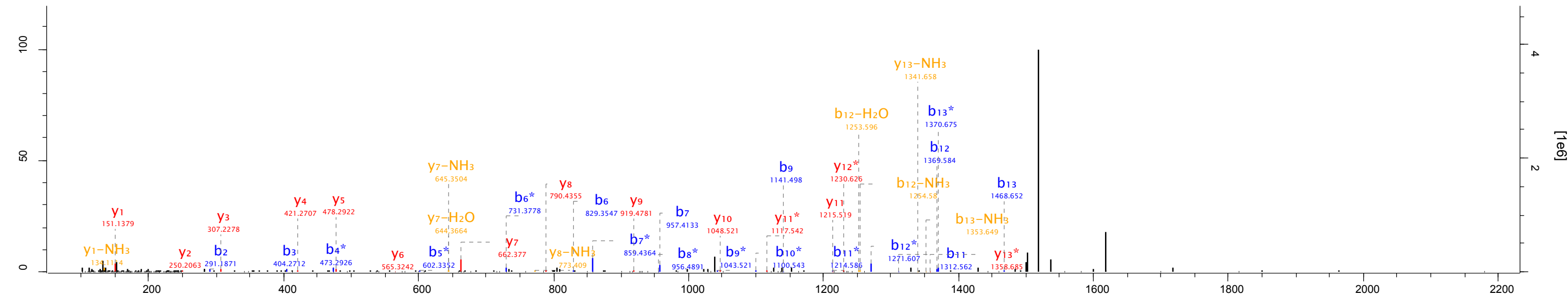


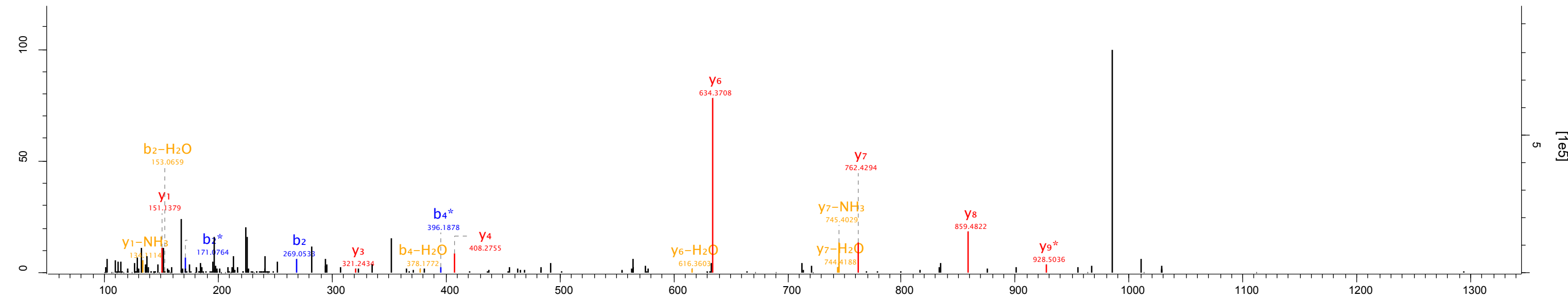
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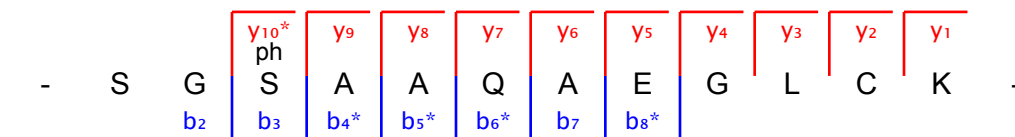
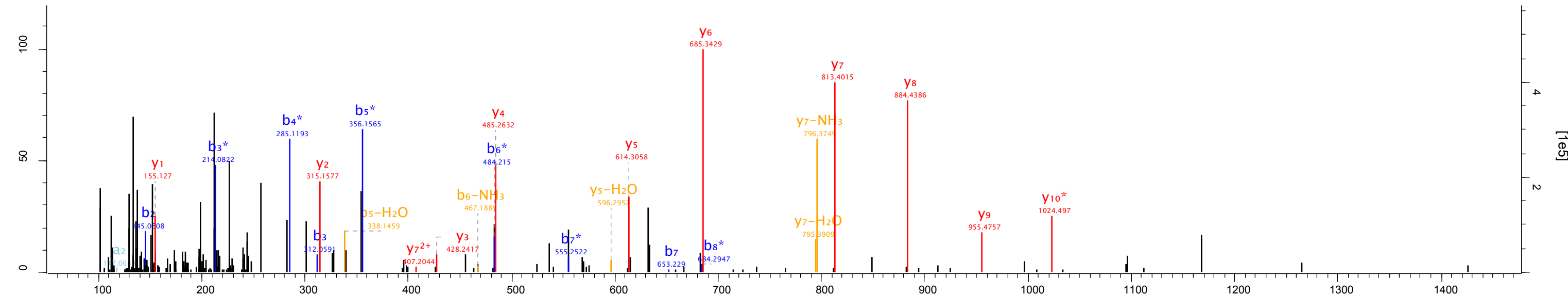


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 3360 Method FTMS; HCD Score 142.27 m/z 809.9 Gene names PCIF1

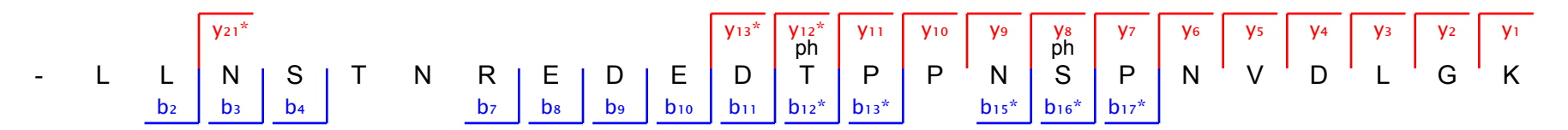
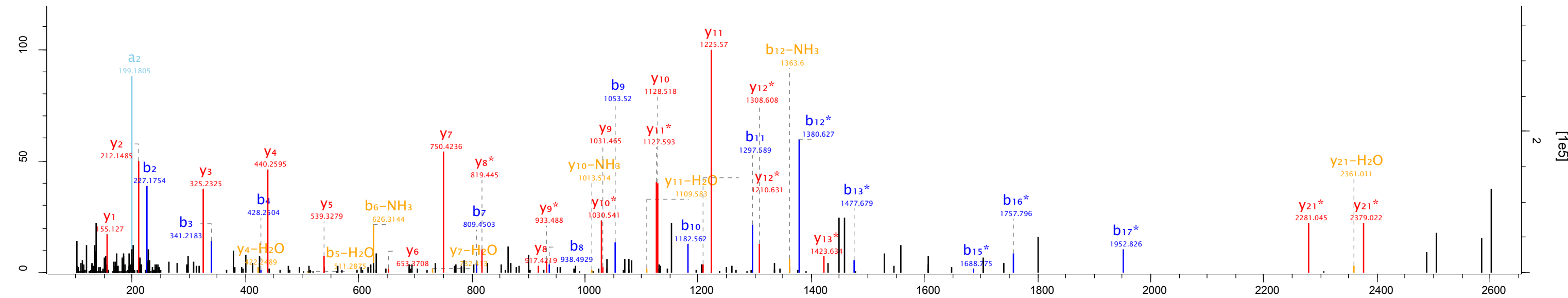




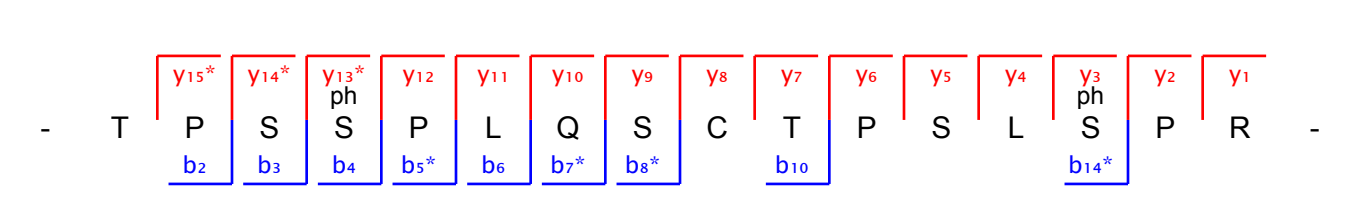
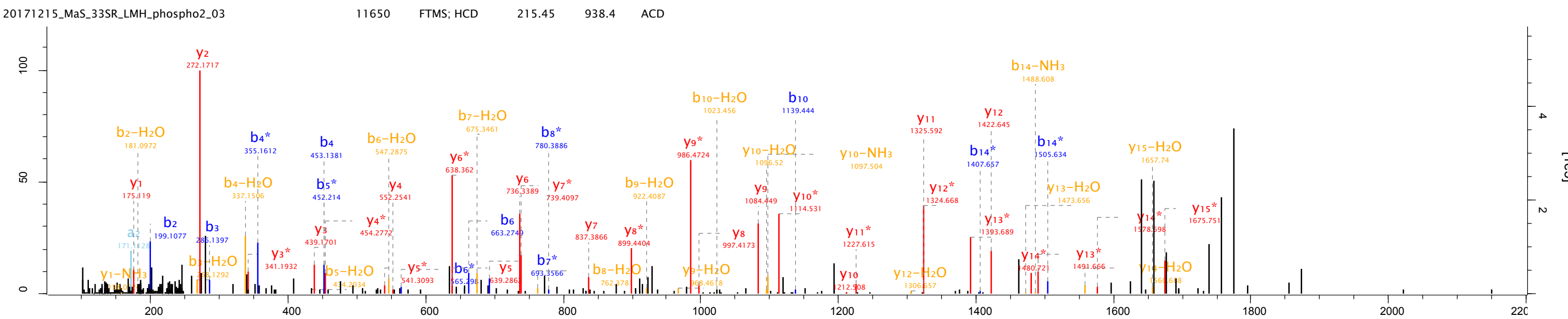
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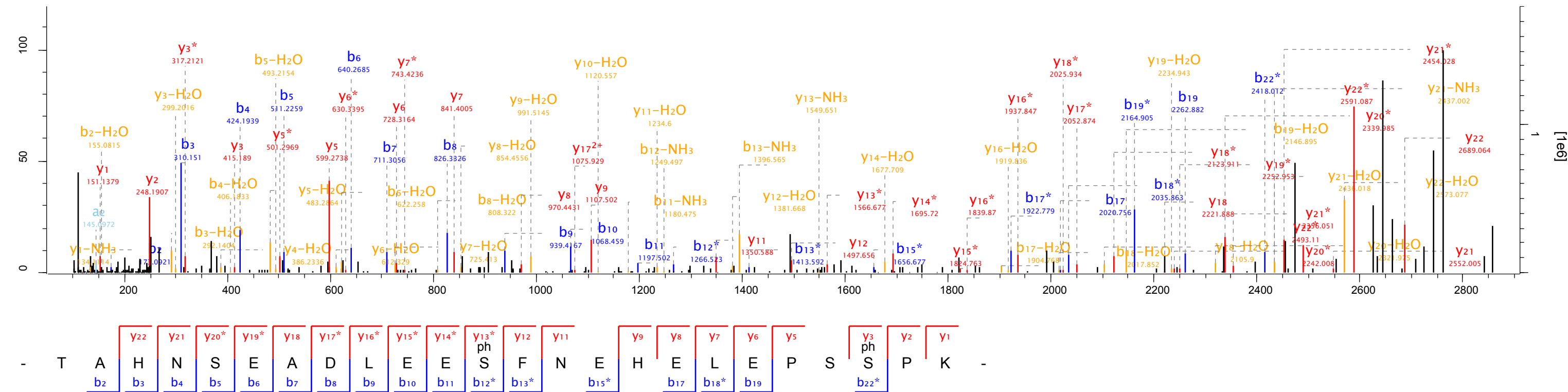
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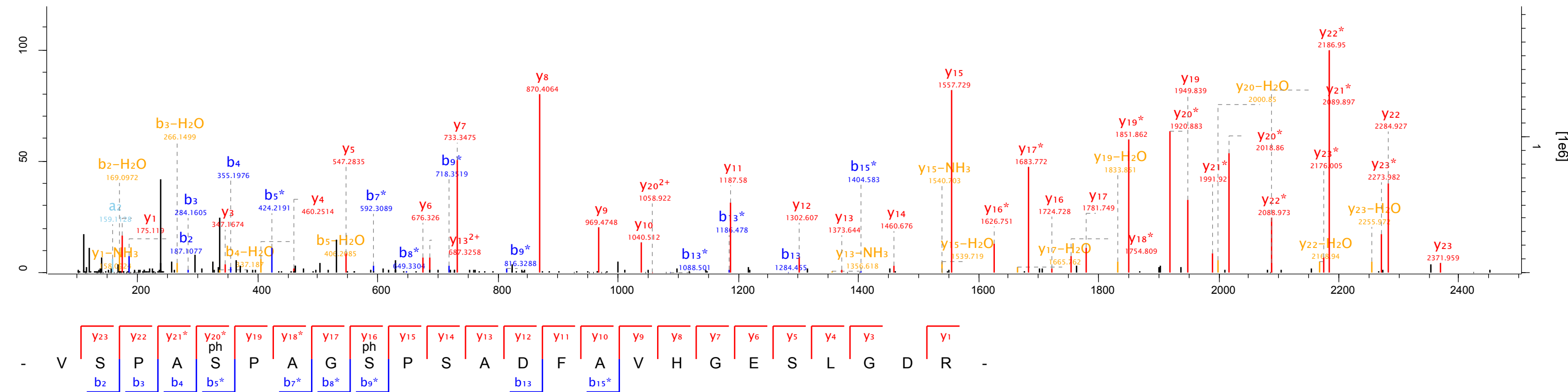
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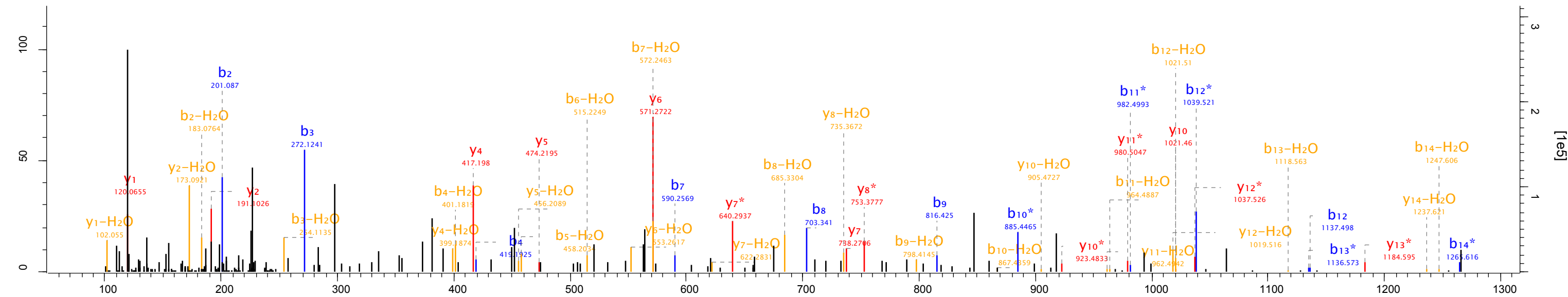
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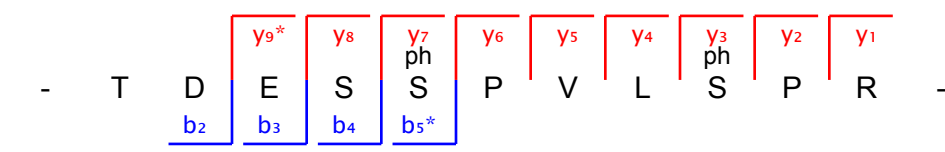
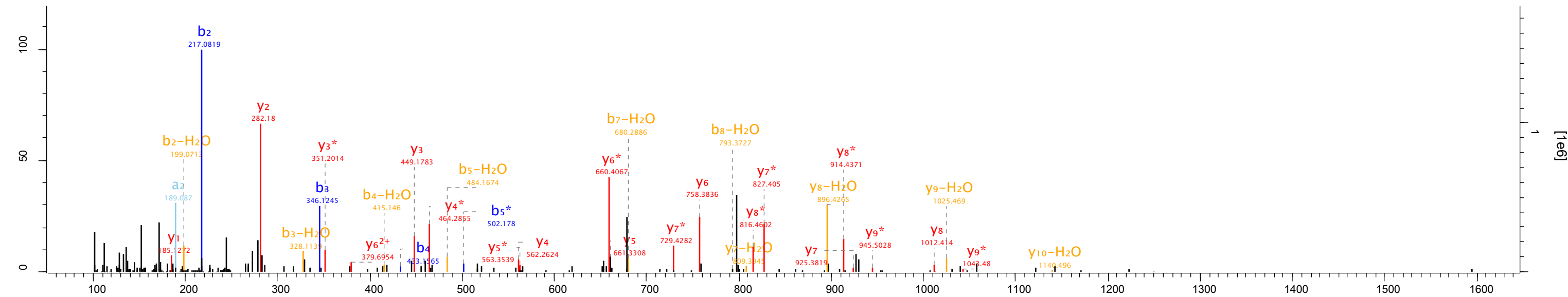


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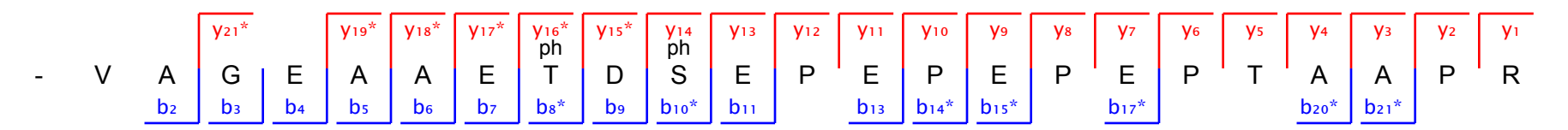
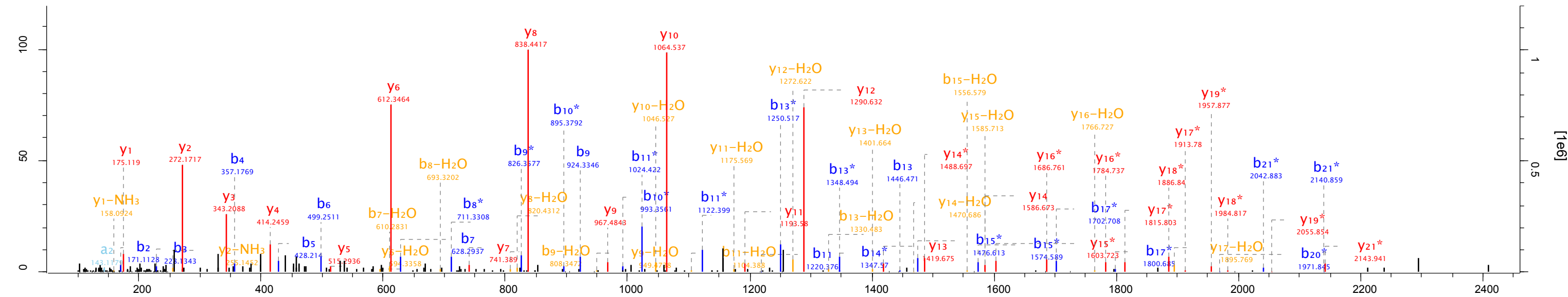
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20171215_MaS_33SR_LMH_phospho2_03

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

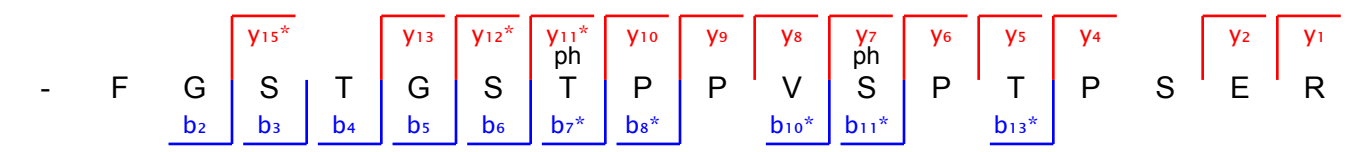
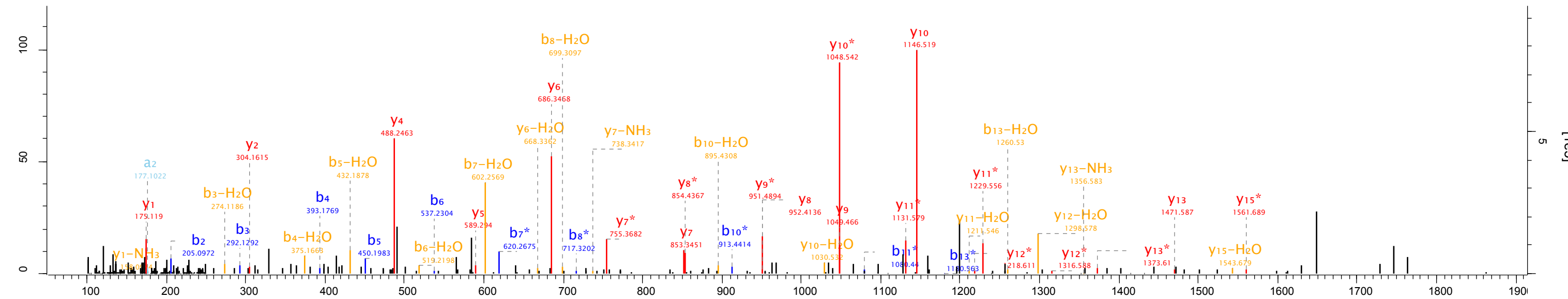


Raw file
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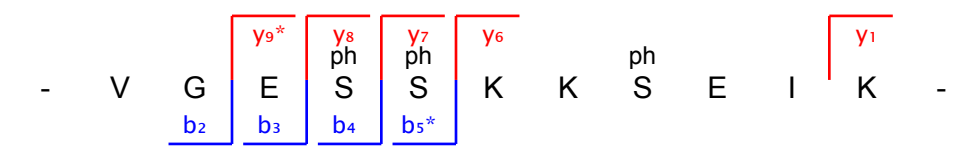
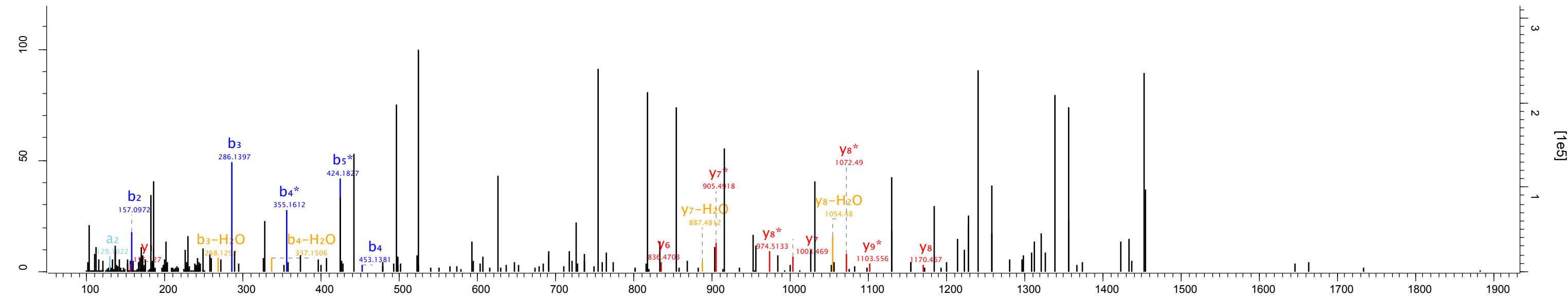
Scan Method Score m/z Gene names
8480 FTMS; HCD 257.77 1255.51 BLOC1S3

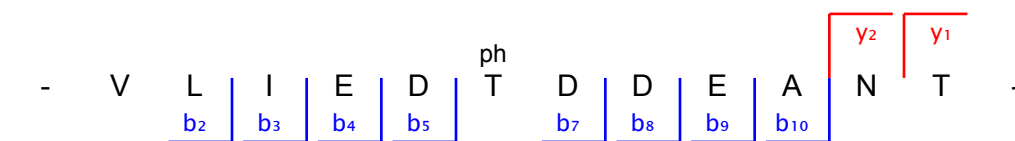
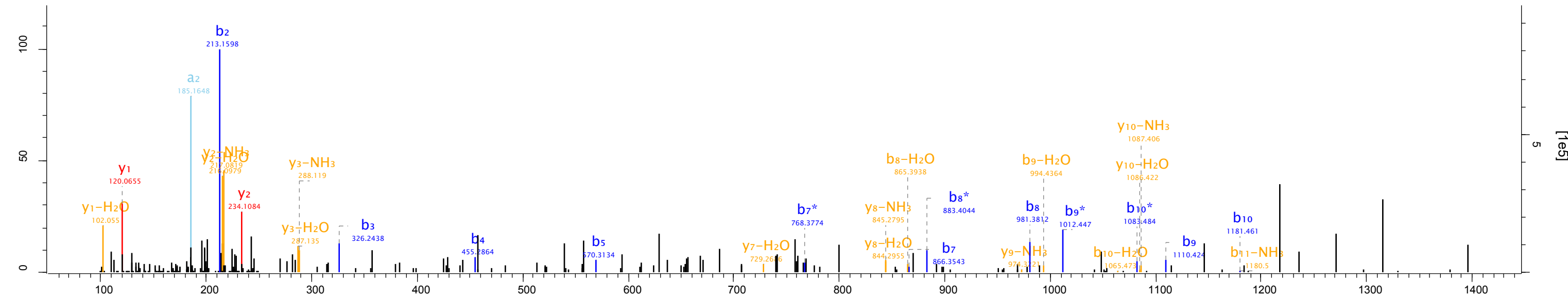


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 Scan: 8630 Method: FTMS; HCD Score: 149.93 m/z: 932.89 Gene names: MKL1; mkl1



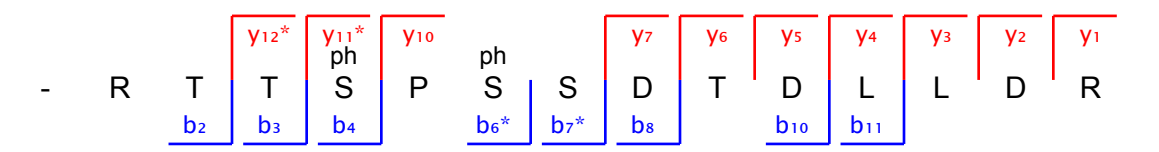
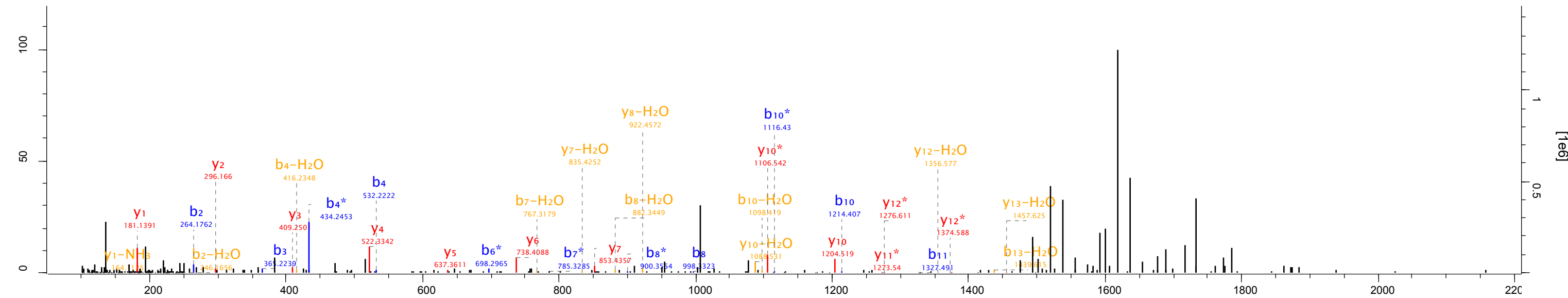
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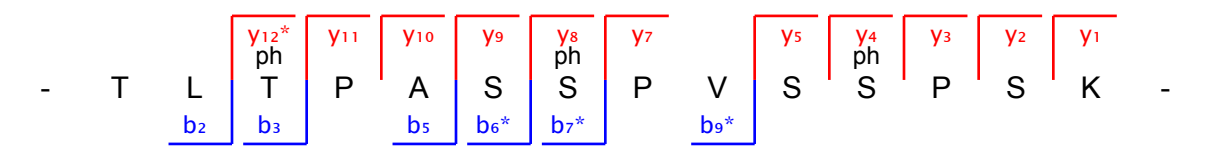
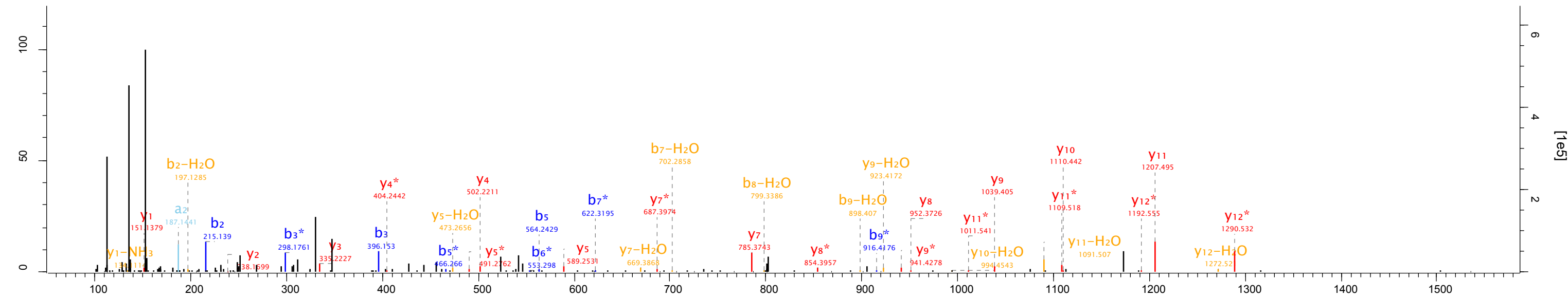


Raw file
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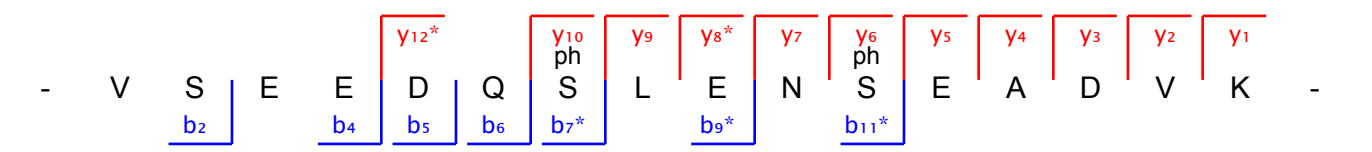
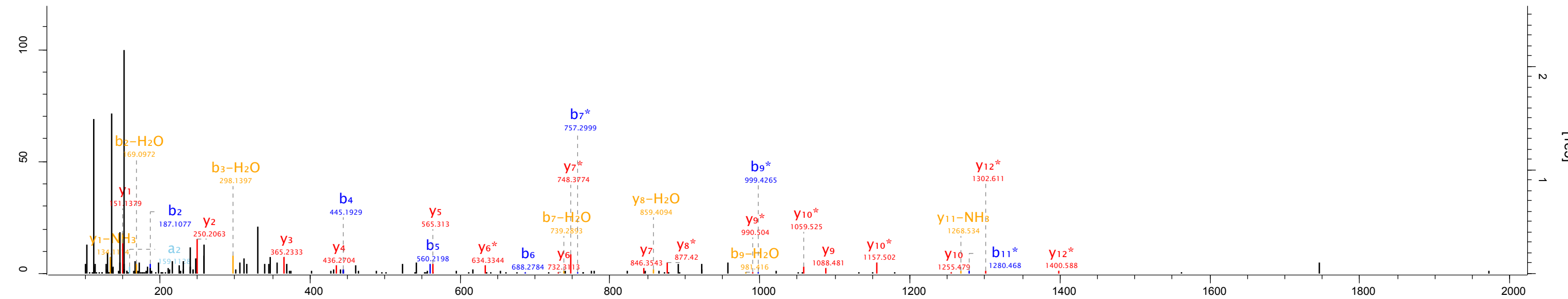
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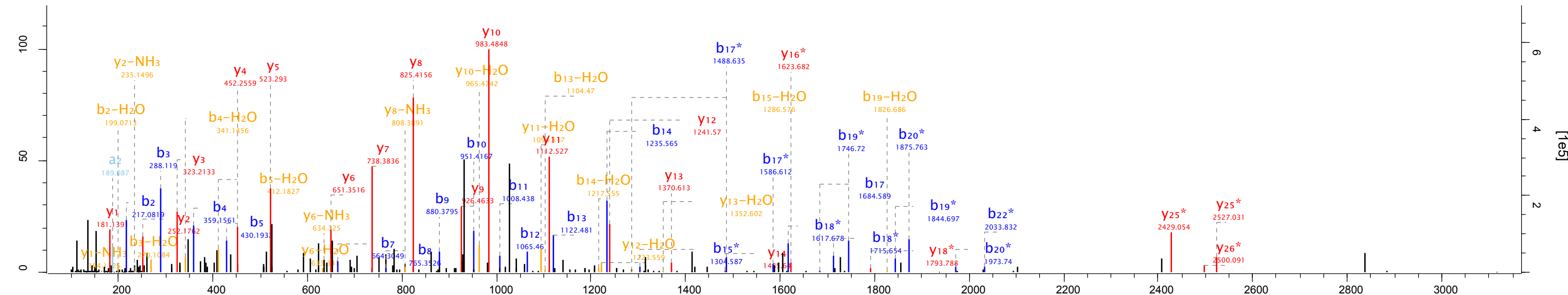


Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 5310 Method FTMS; HCD Score 82.22 m/z 801.82 Gene names FZR1



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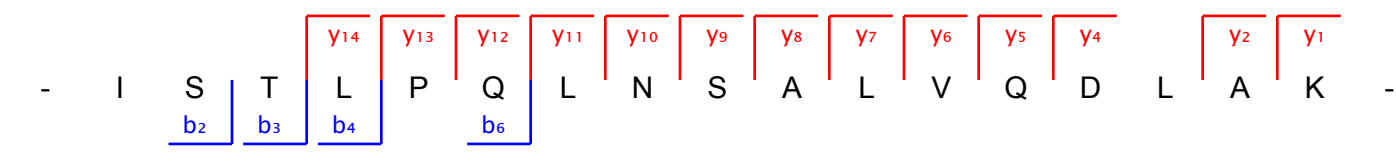
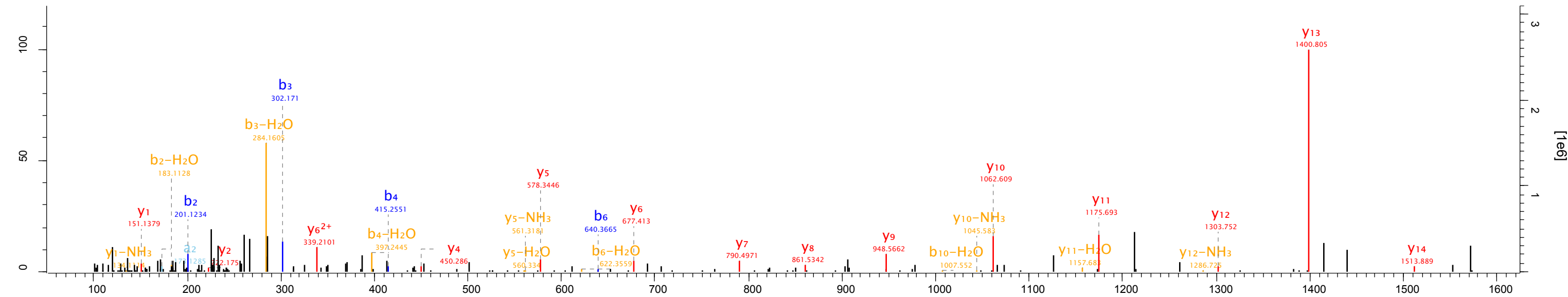




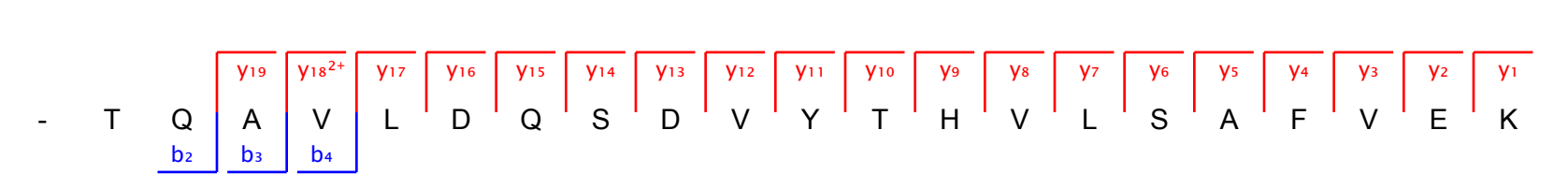
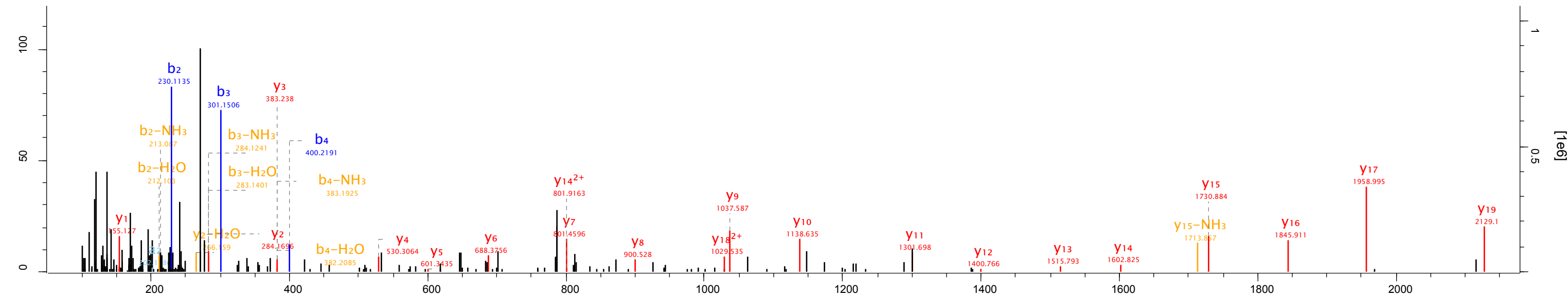
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b₈
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b₁₅*
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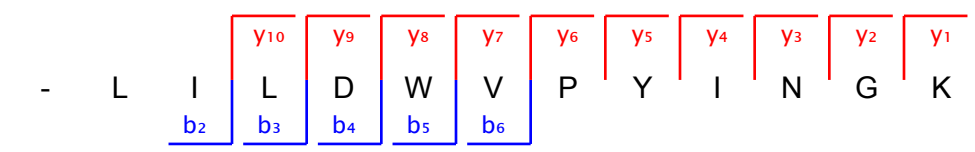
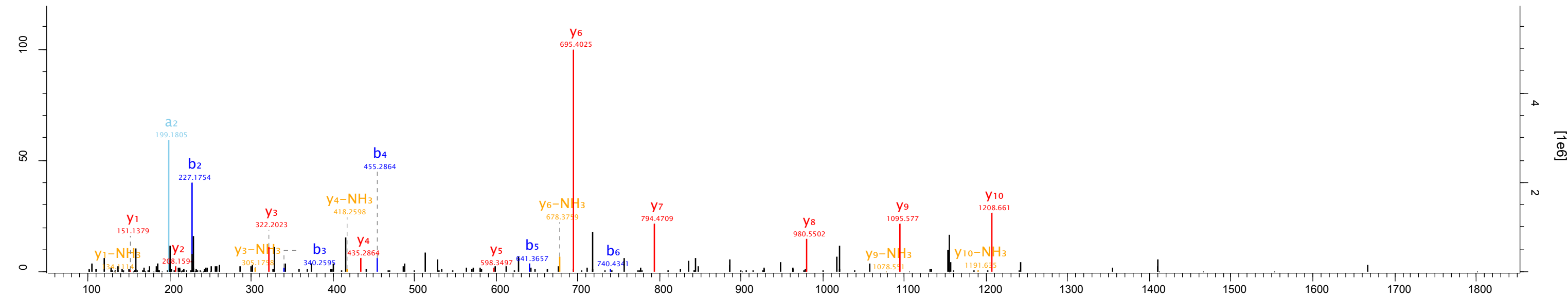
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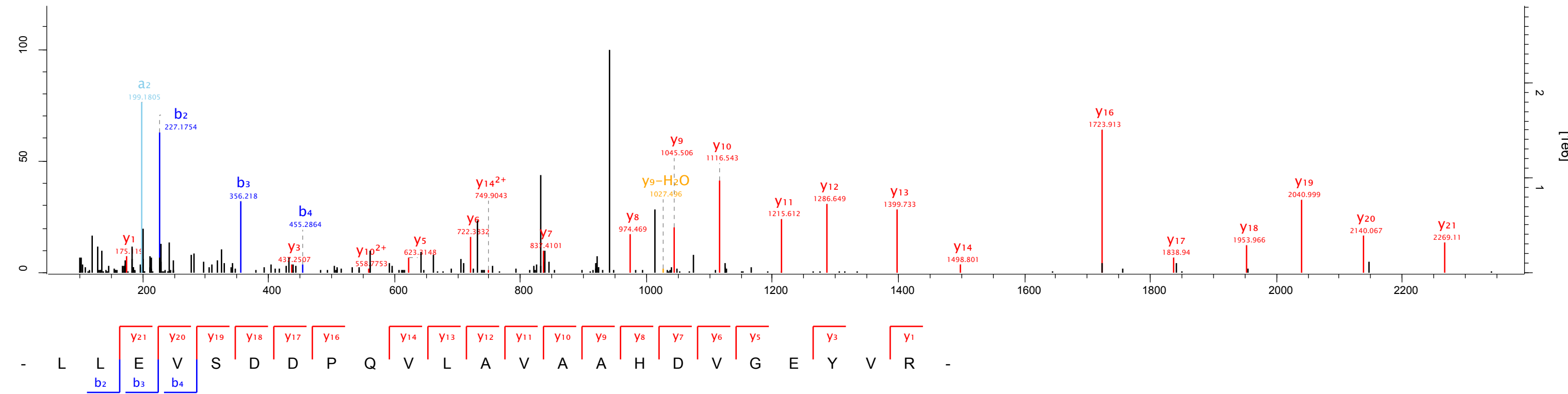


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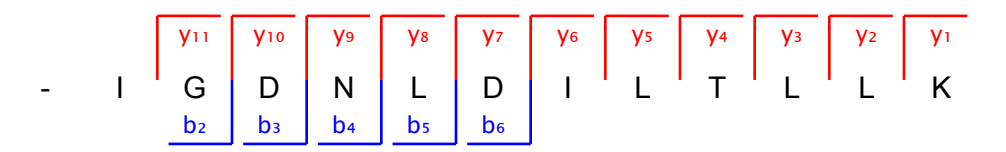
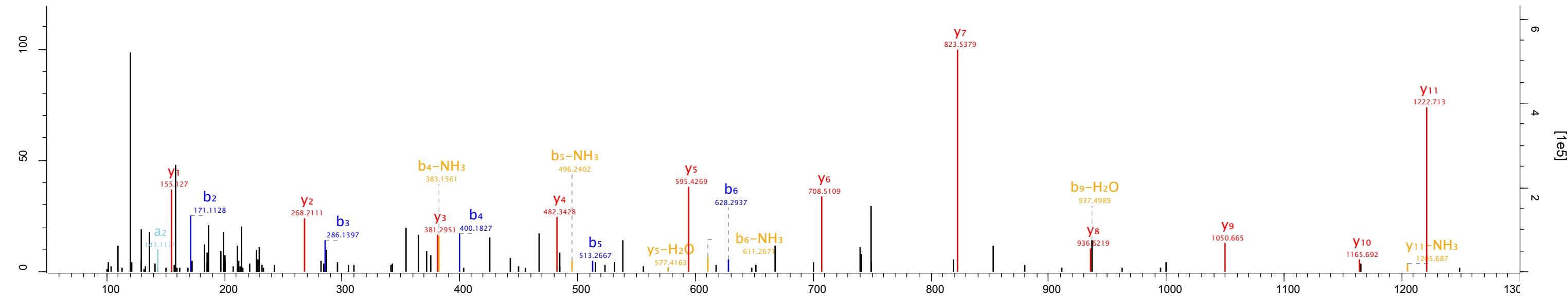


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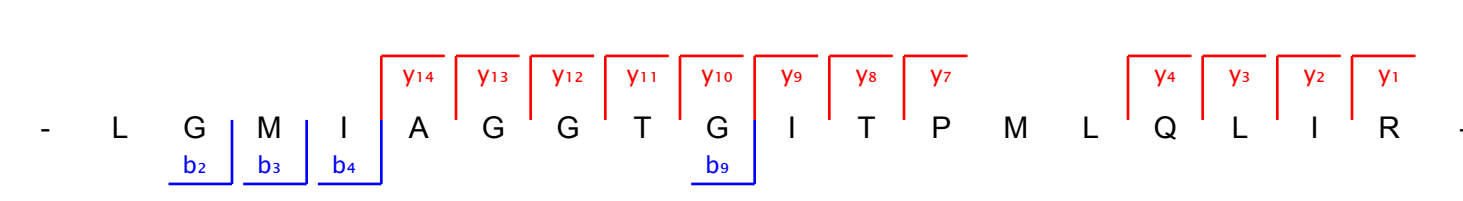
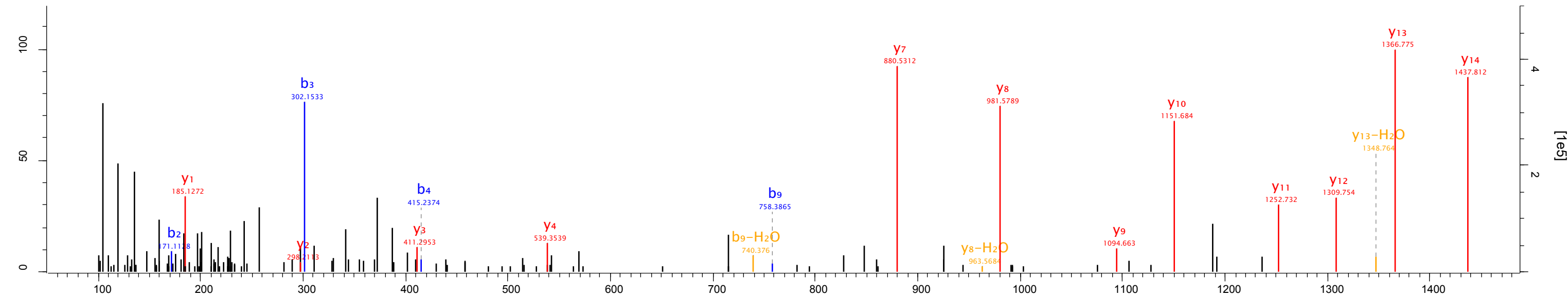




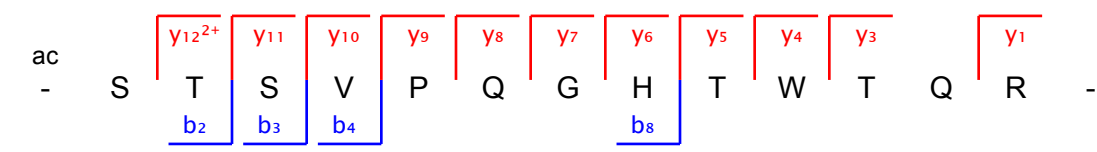
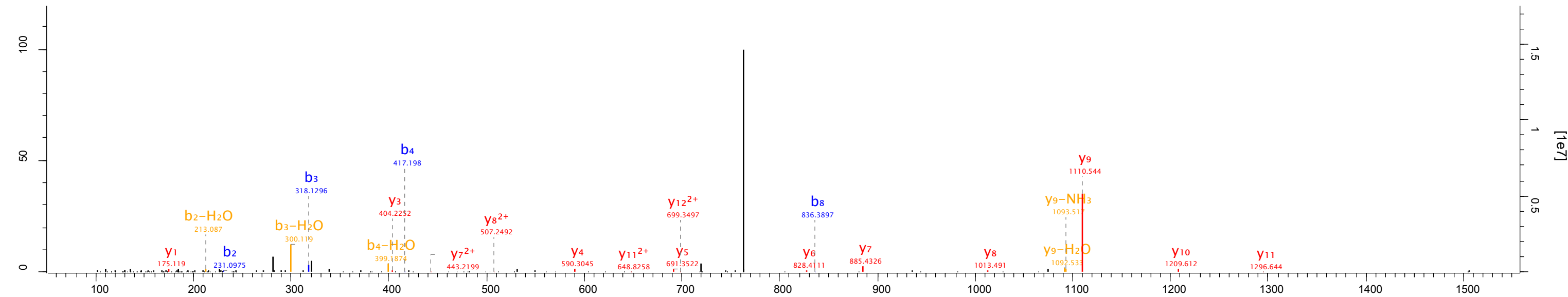
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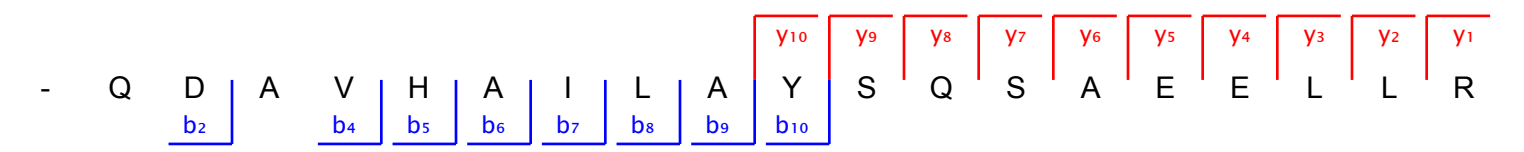
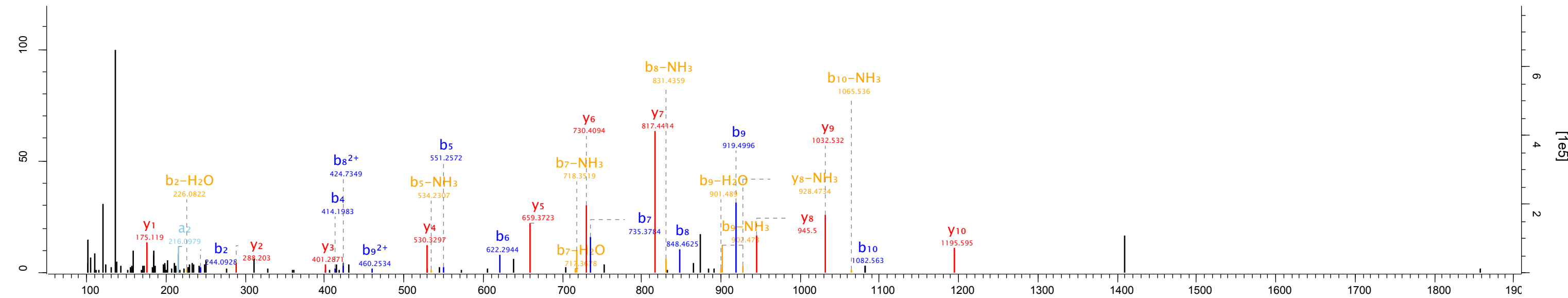
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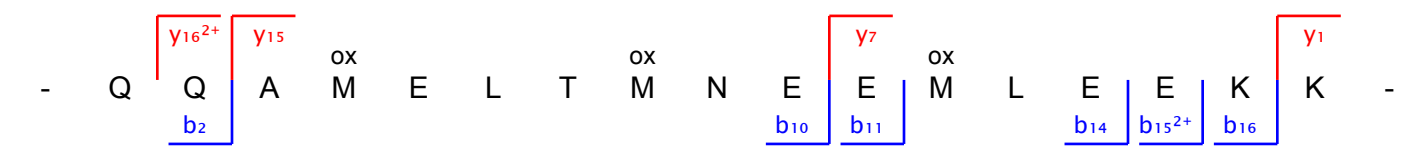
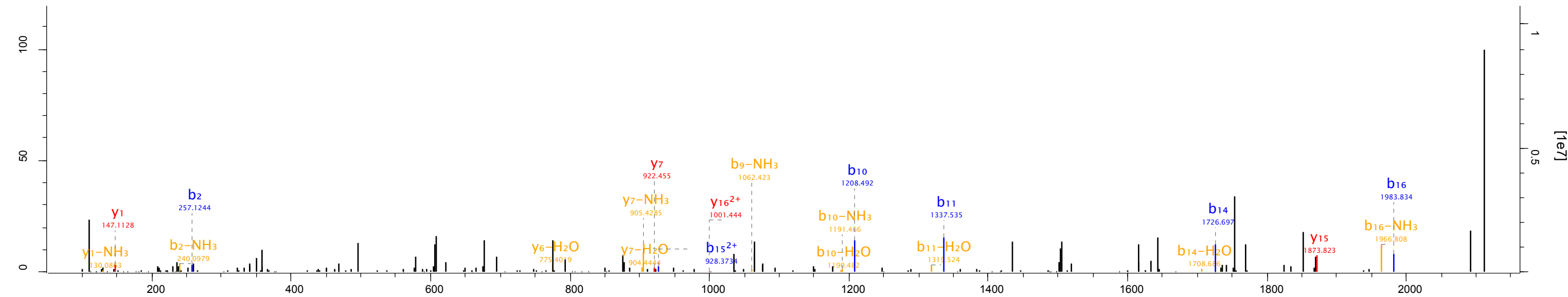
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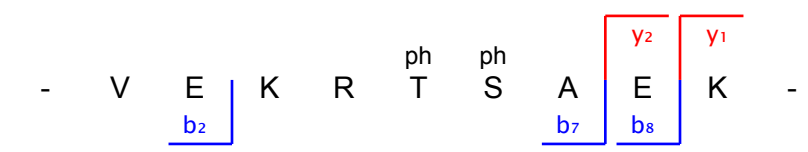
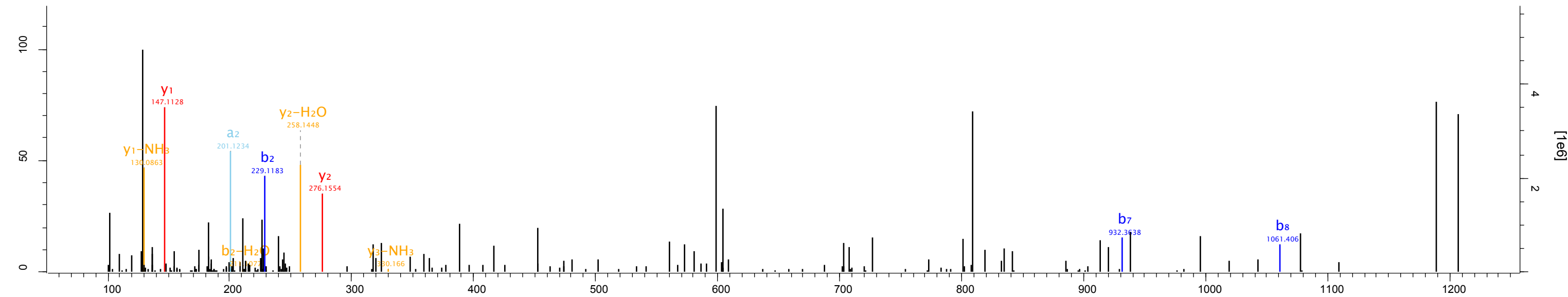


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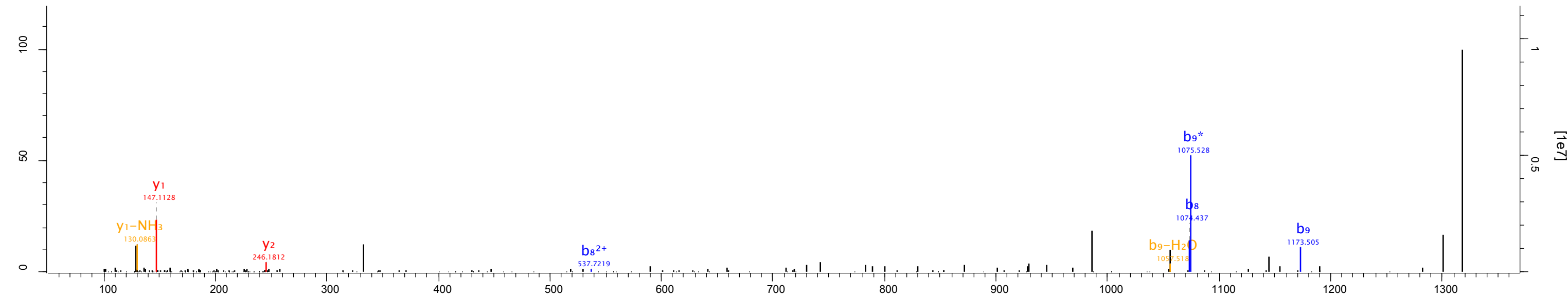


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20171215_MaS_33SR_LMH_proteome_01



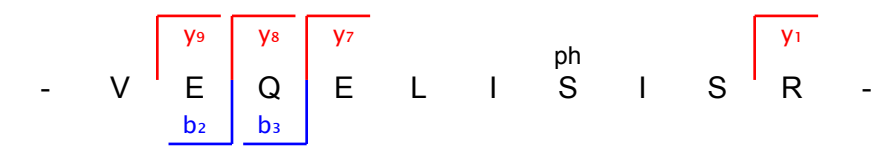
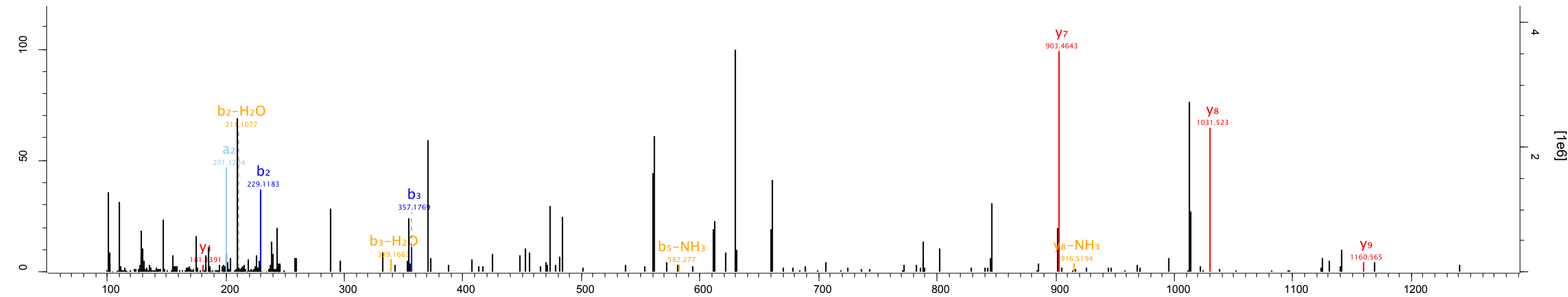
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b₈ y₂ y₁
b₉

Raw file
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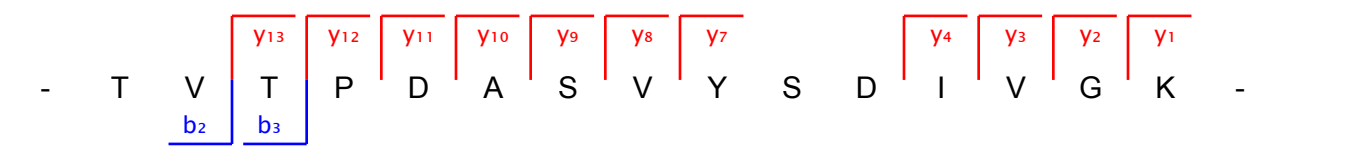
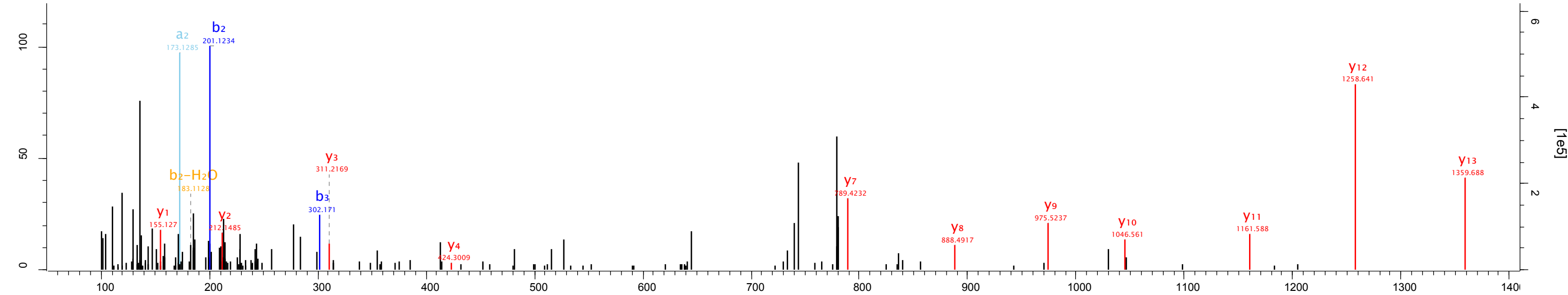
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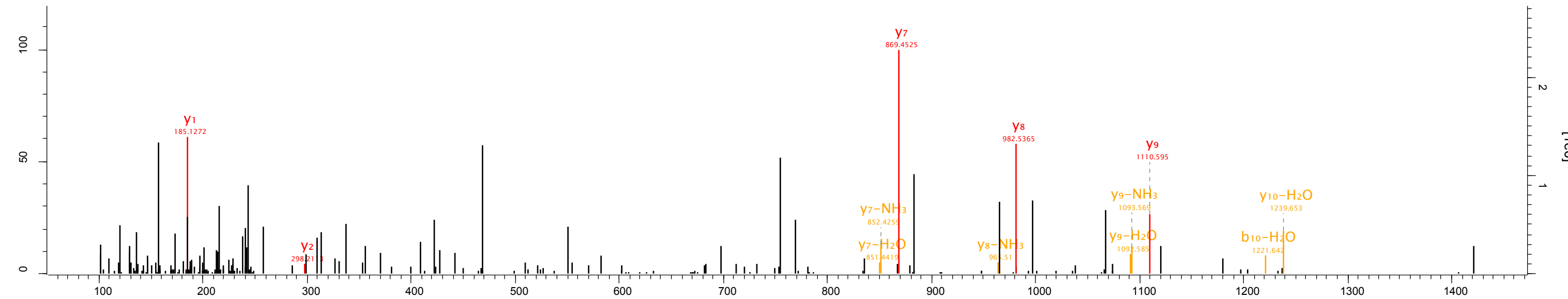
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20171215_MaS_33SR_LMH_proteome_01

Scan 58500 Method FTMS; HCD Score 49.59 m/z 780.41 Gene names TBC1D24



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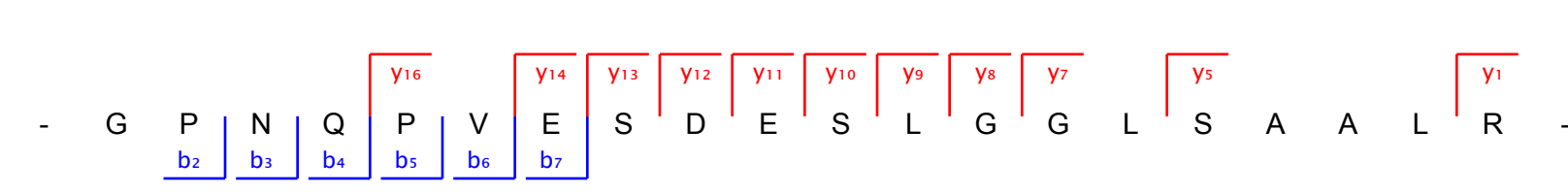
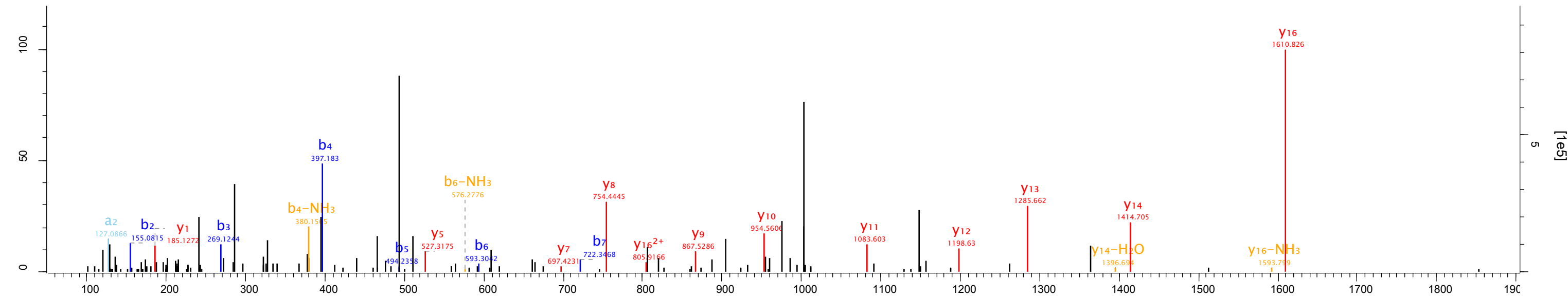


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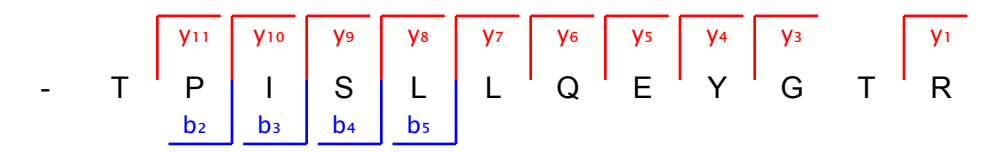
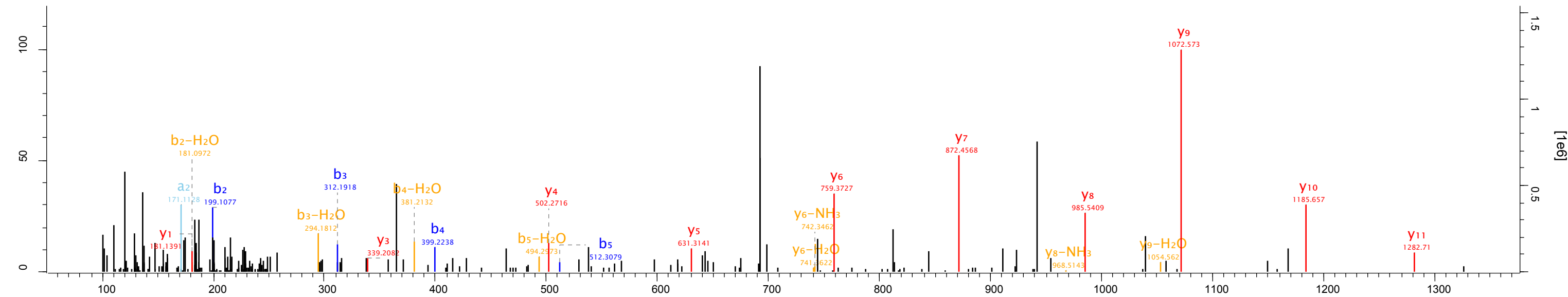
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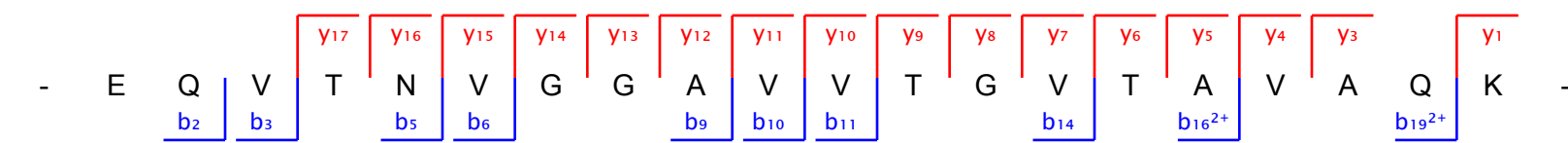
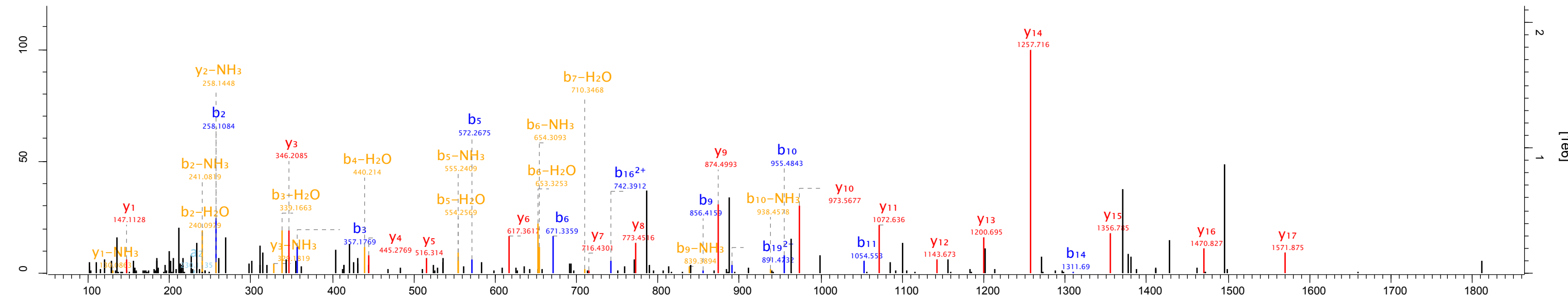
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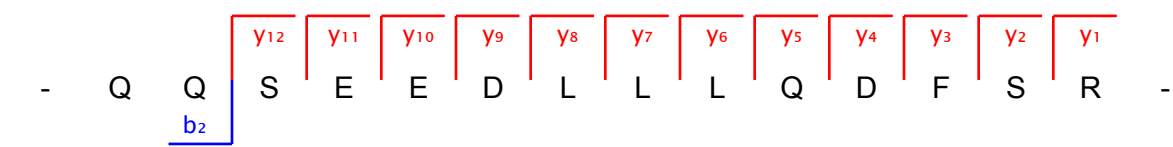
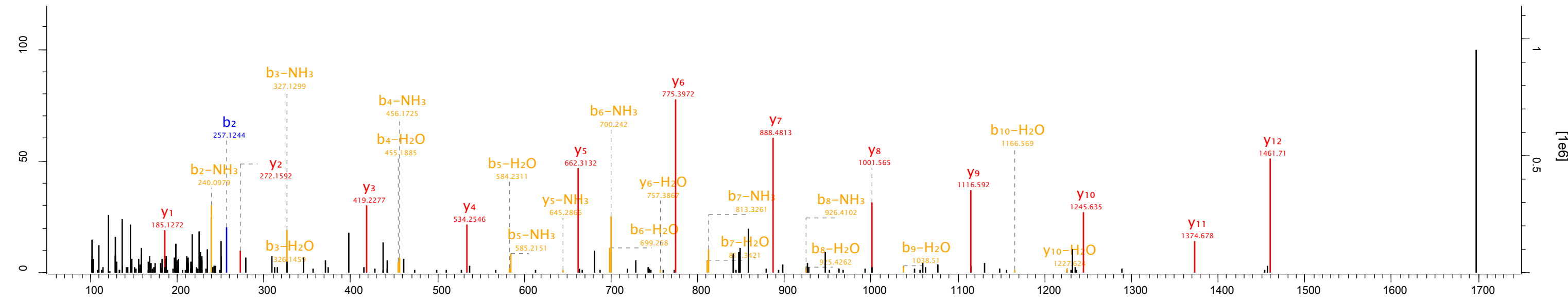


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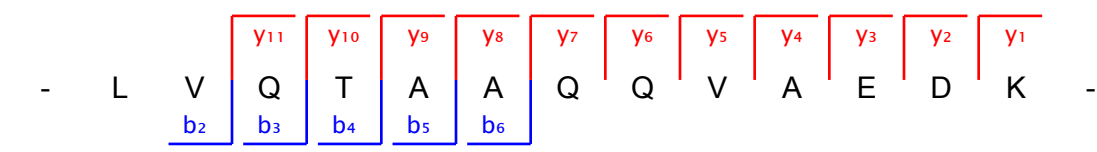
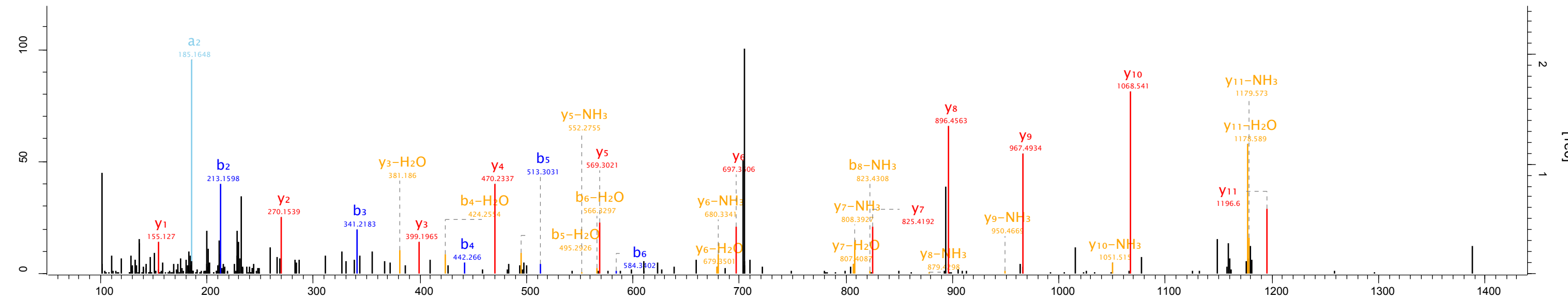


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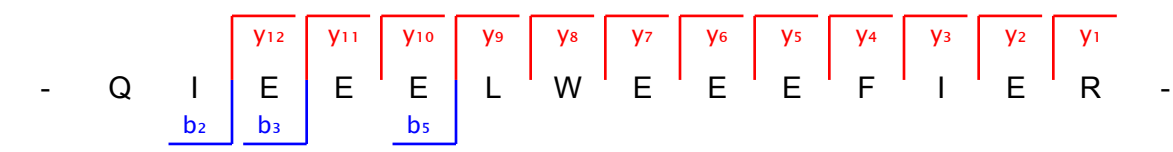
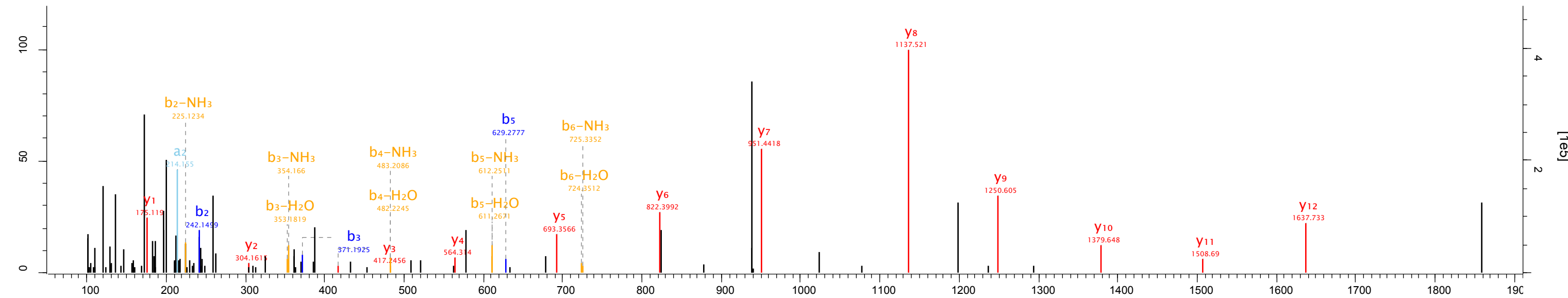




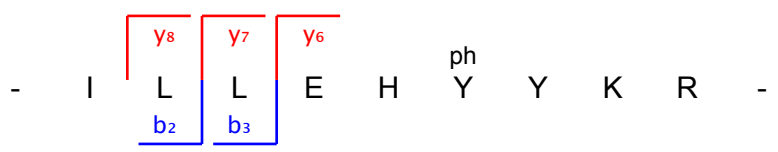
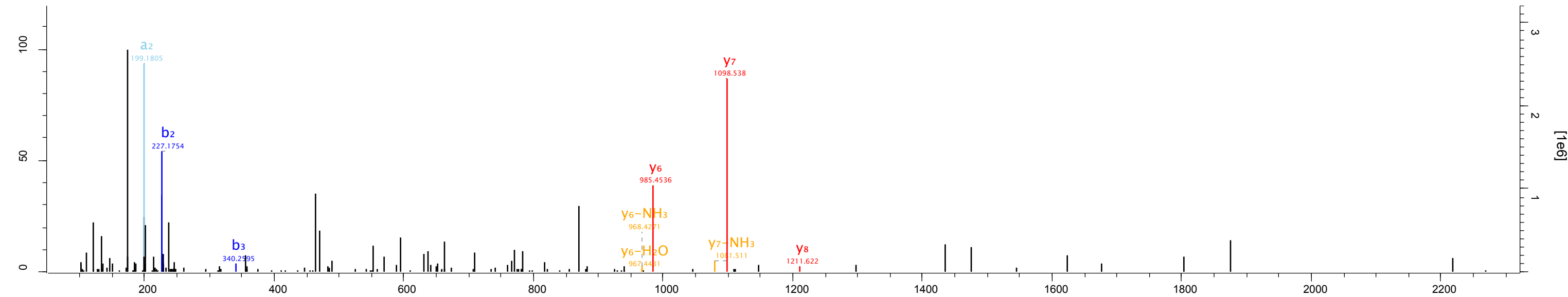
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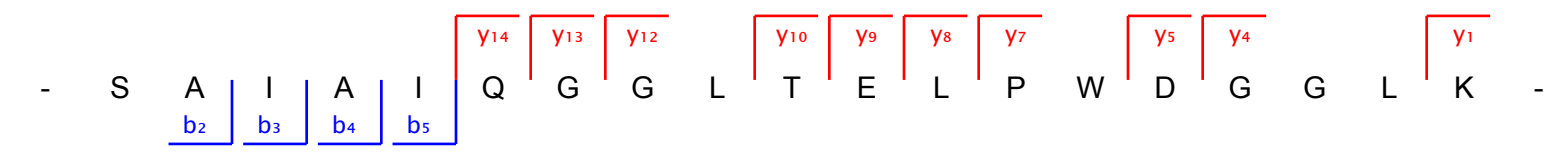
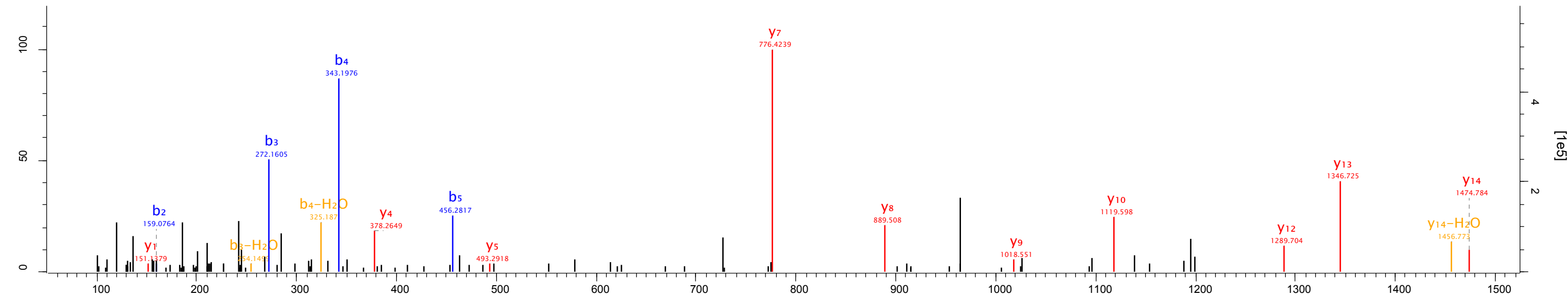
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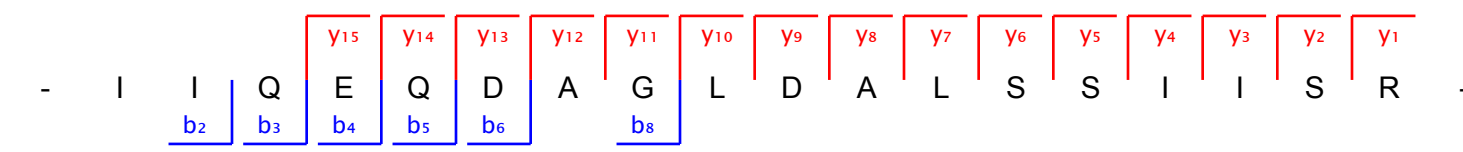
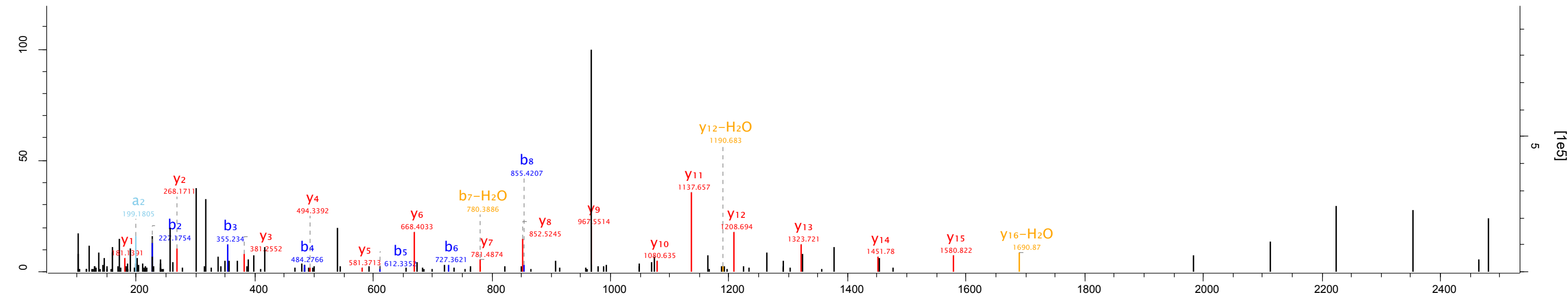
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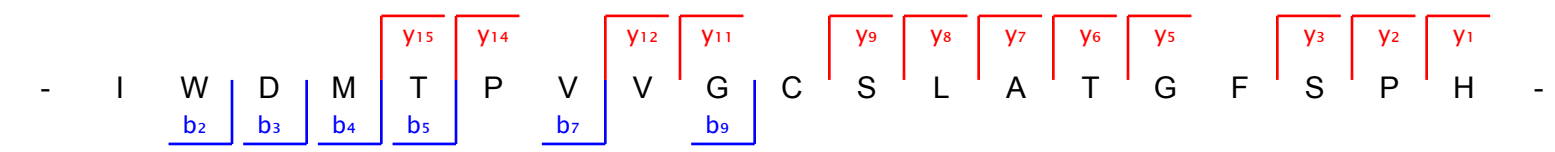
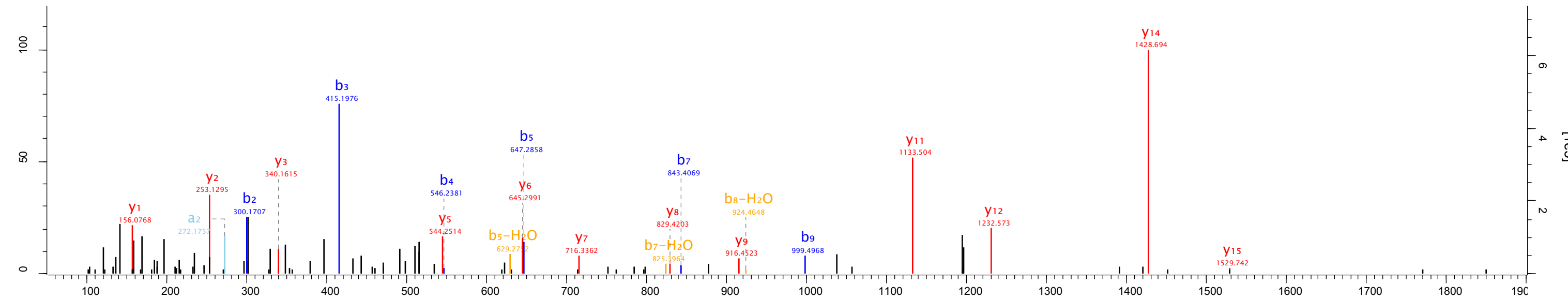
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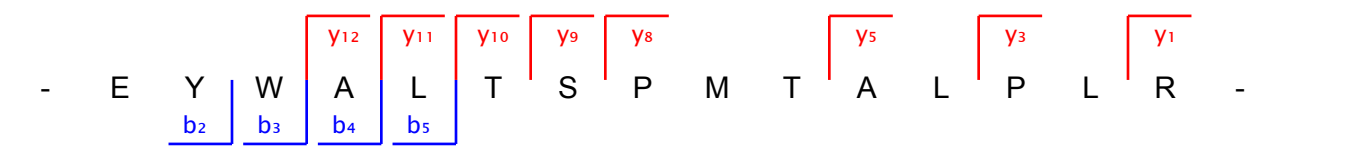
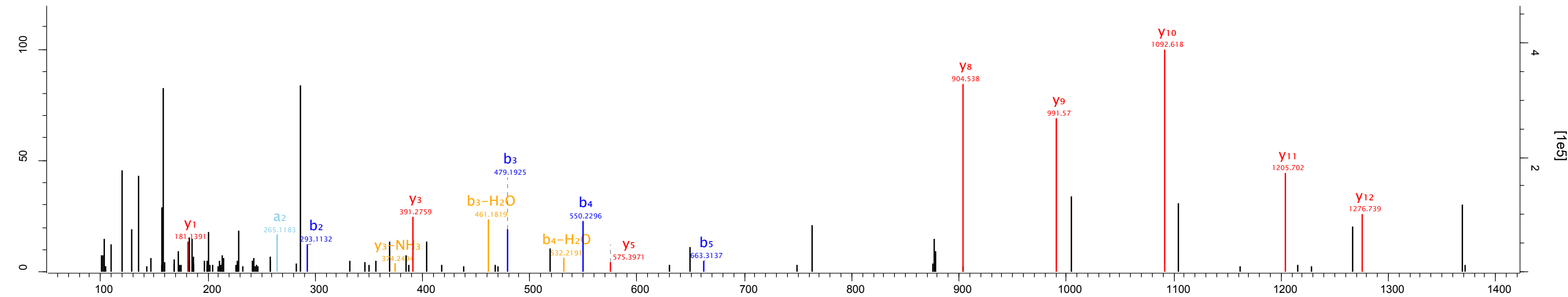
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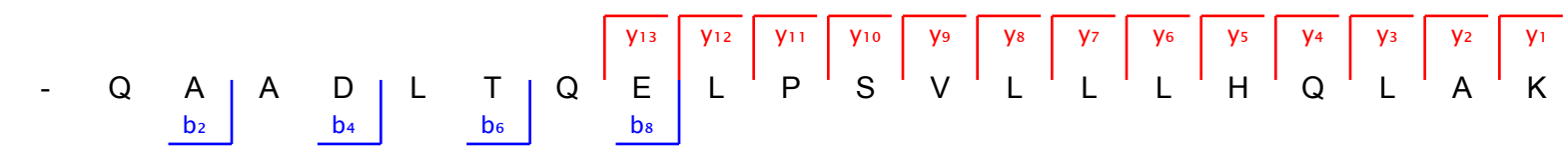
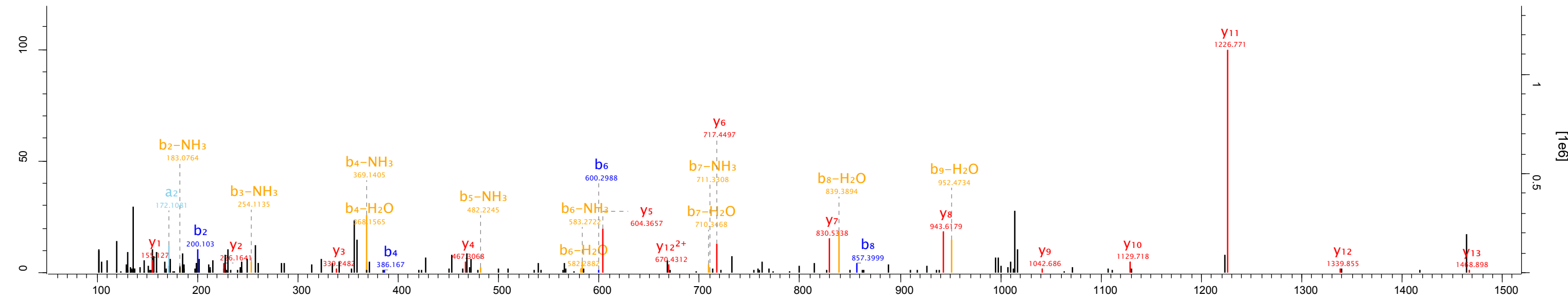


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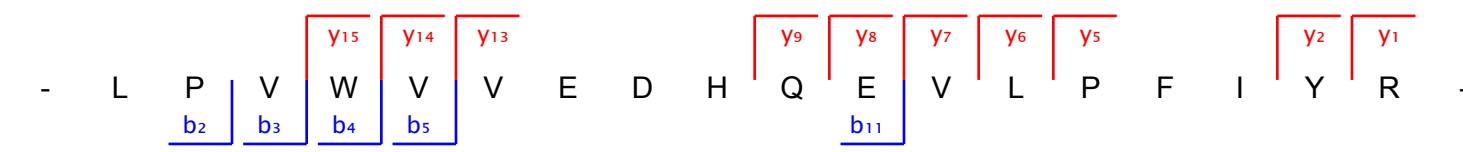
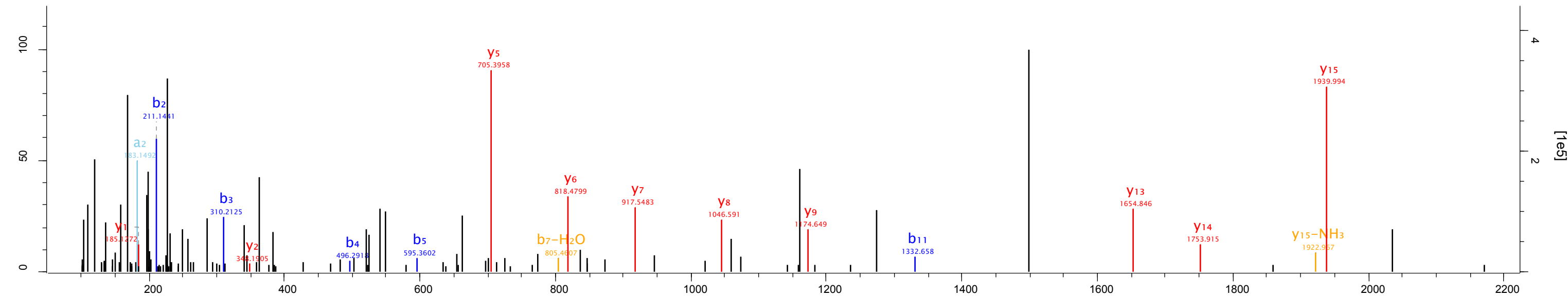


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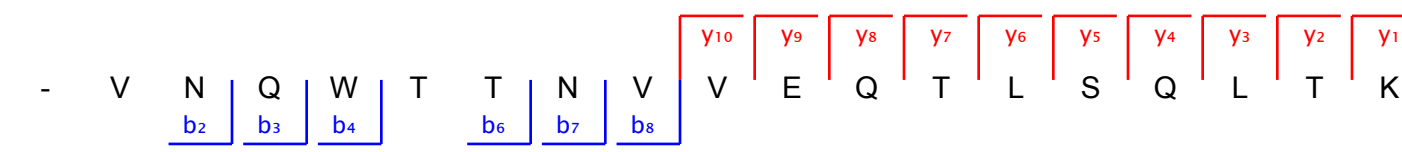
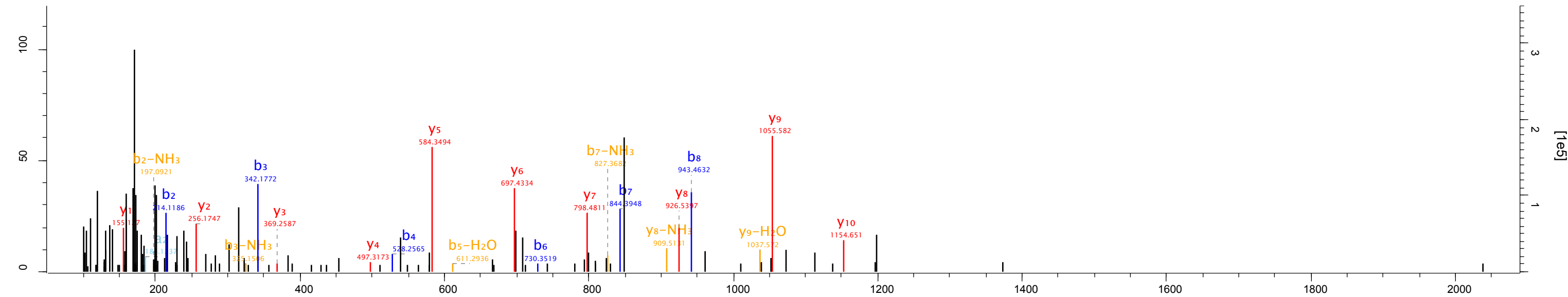
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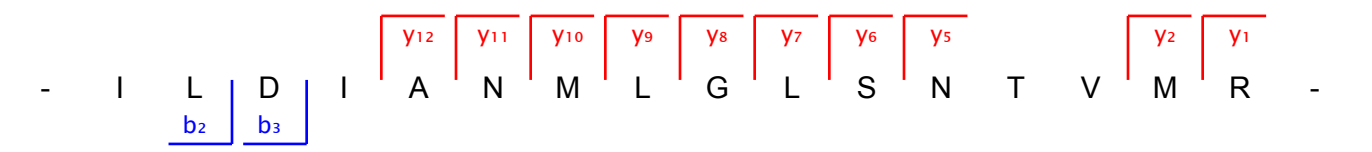
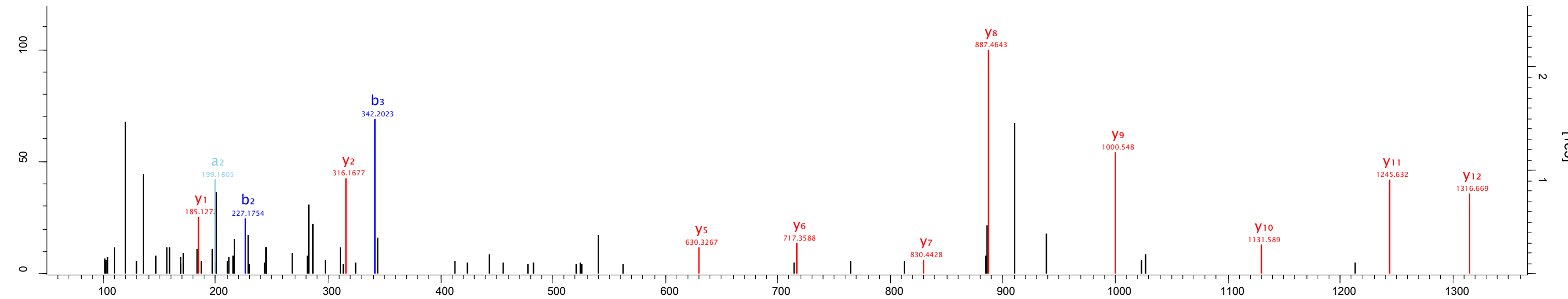
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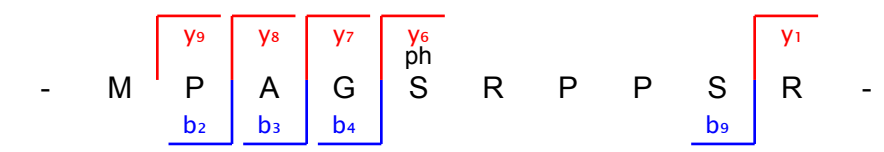
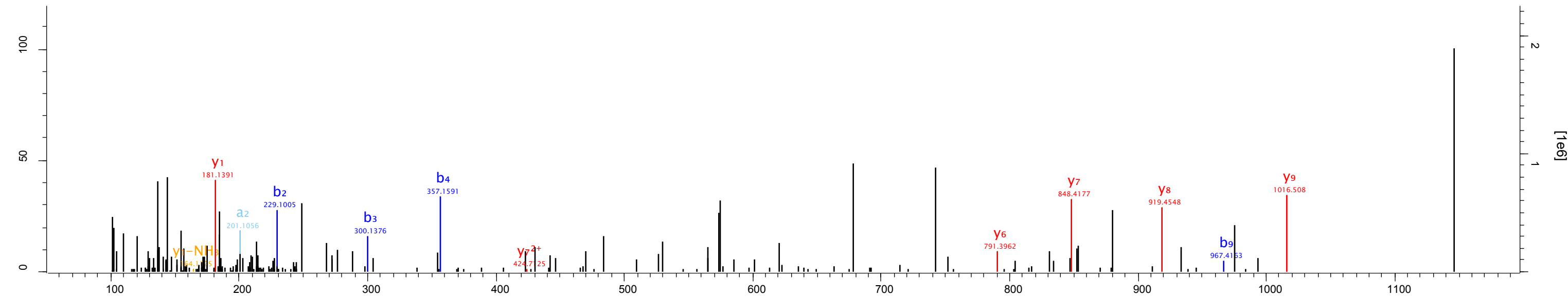
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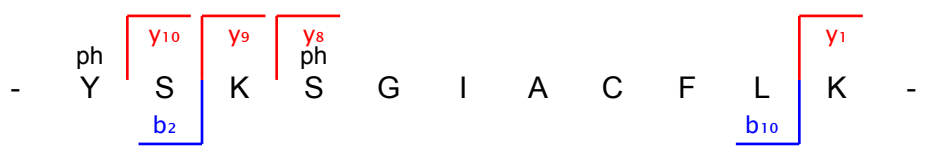
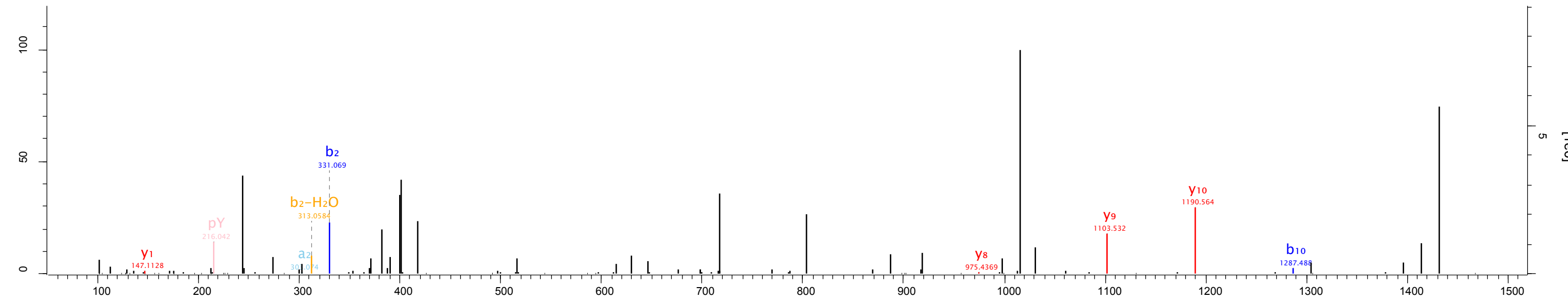
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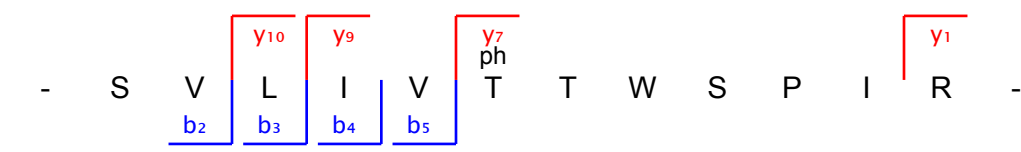
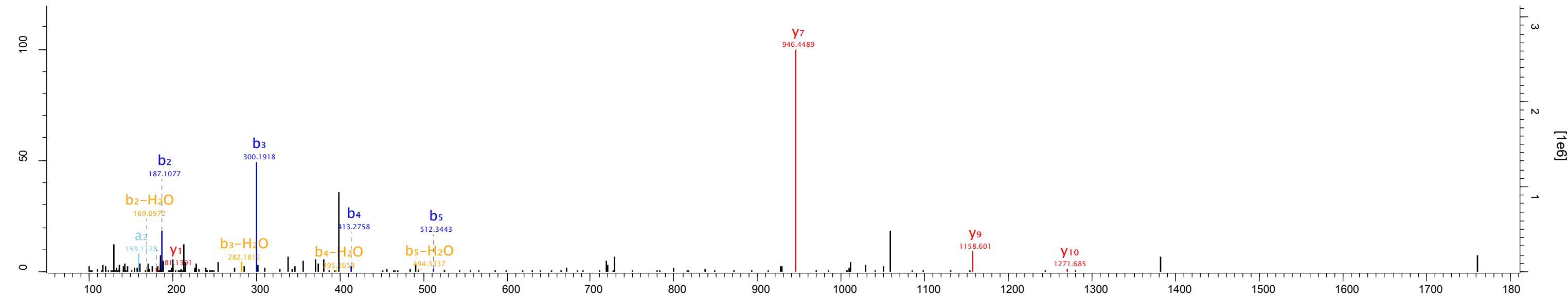
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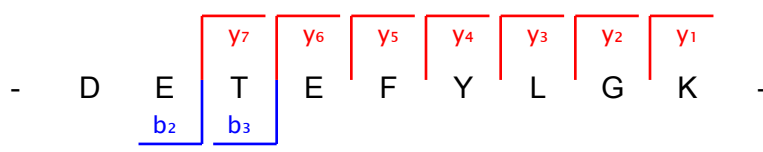
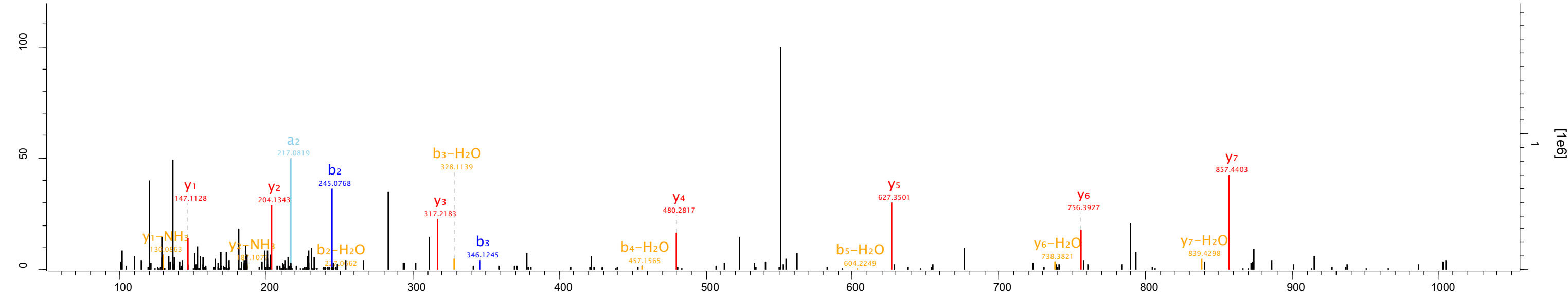
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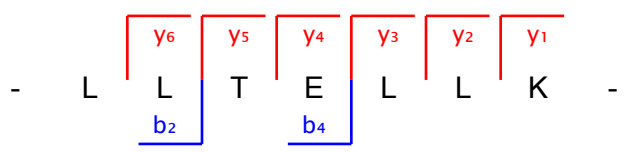
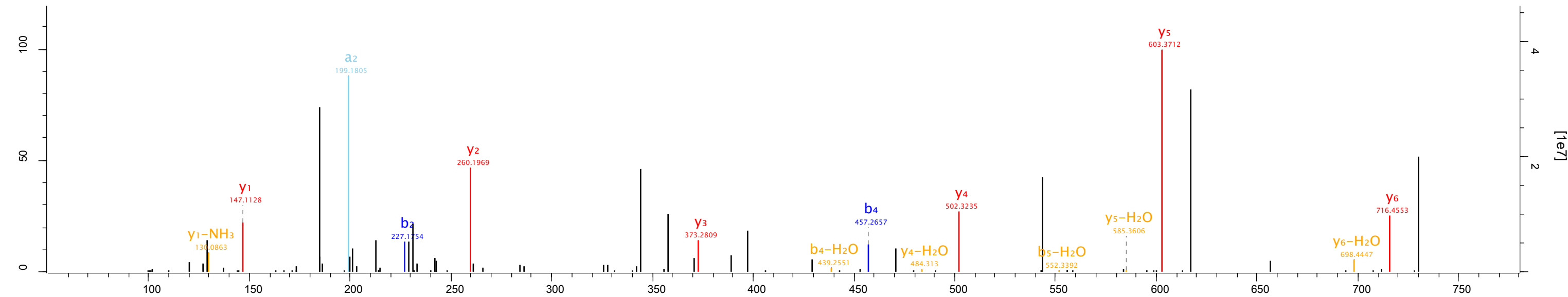
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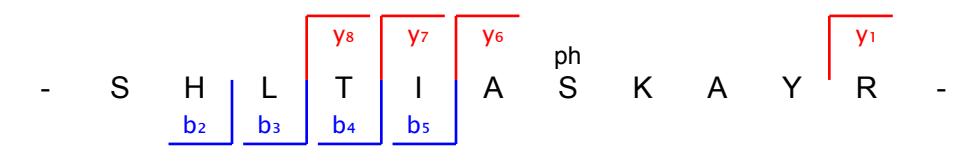
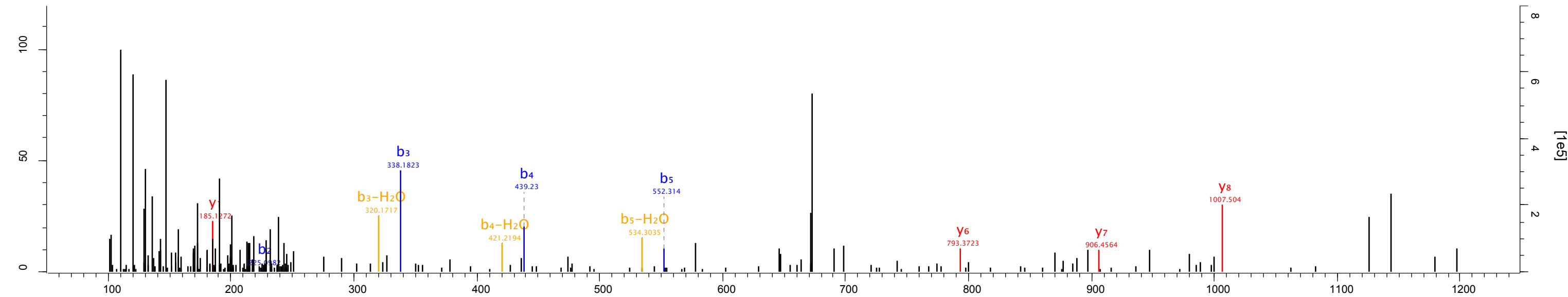
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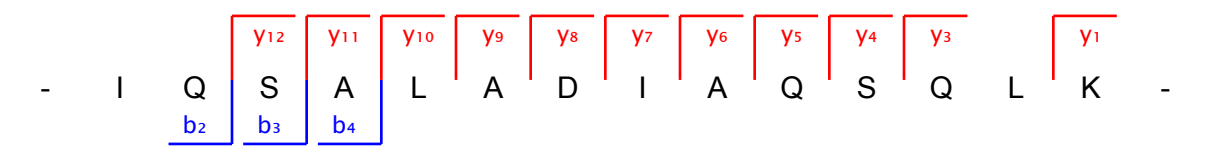
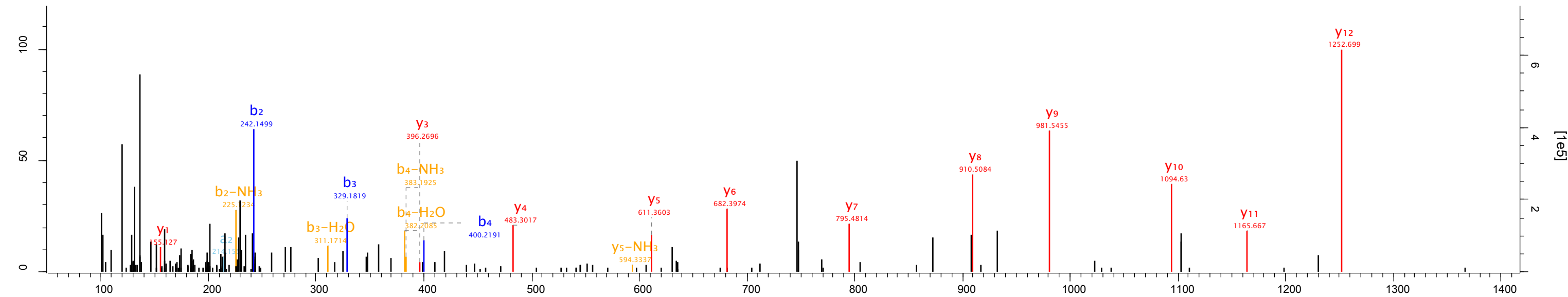
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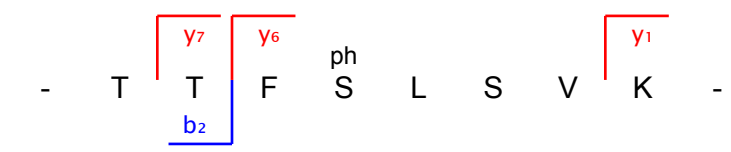
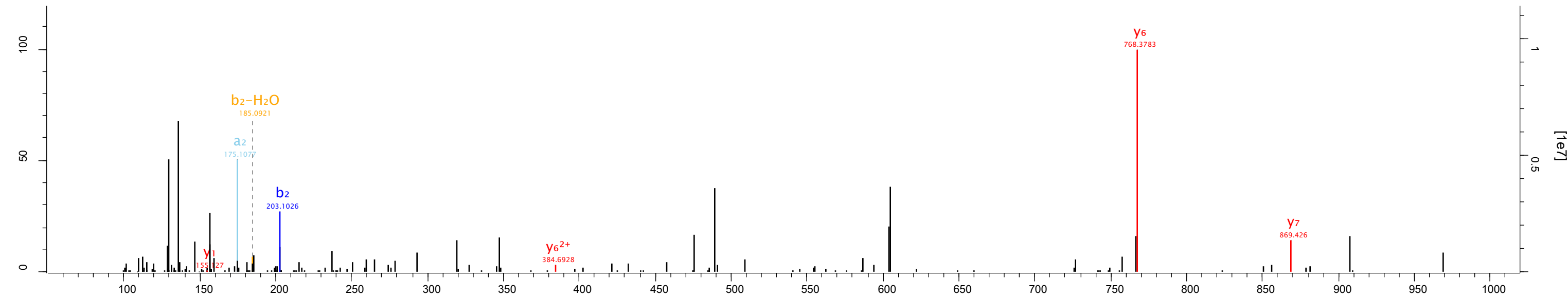
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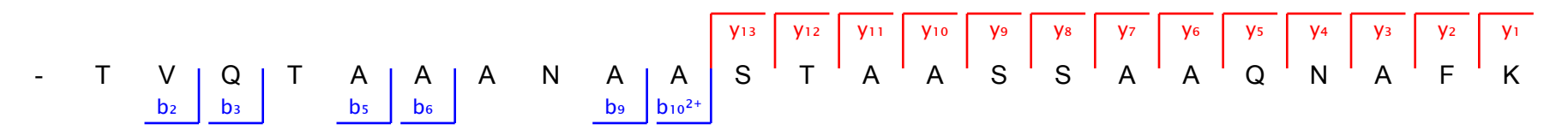
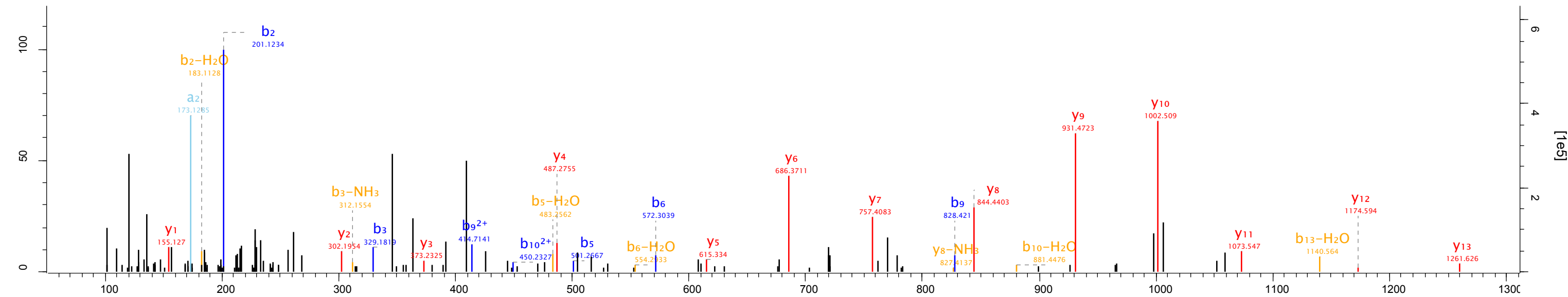
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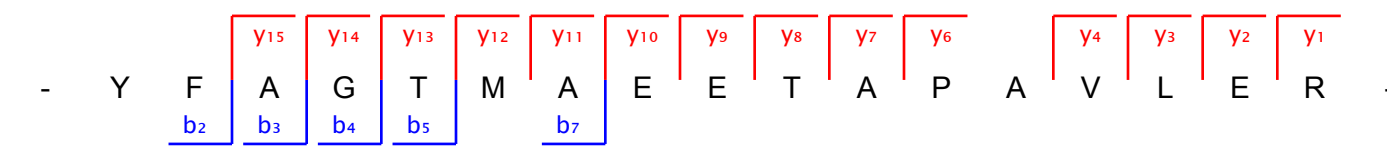
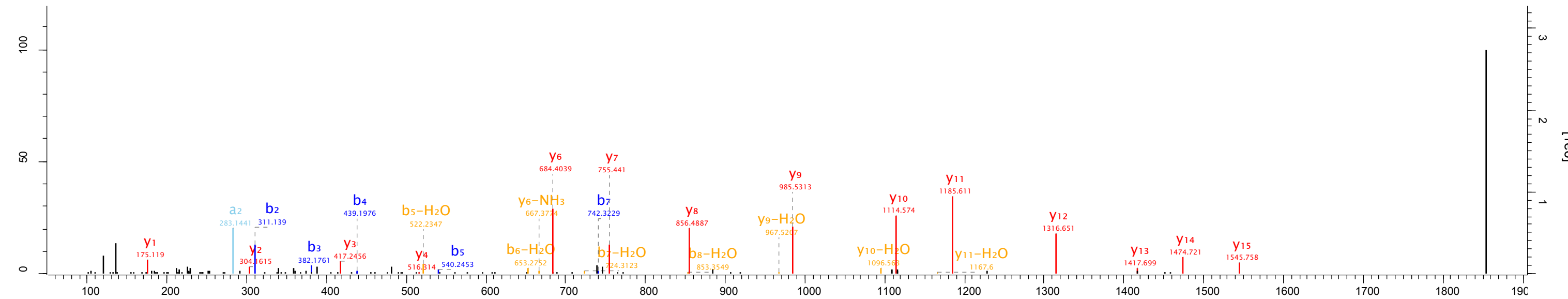
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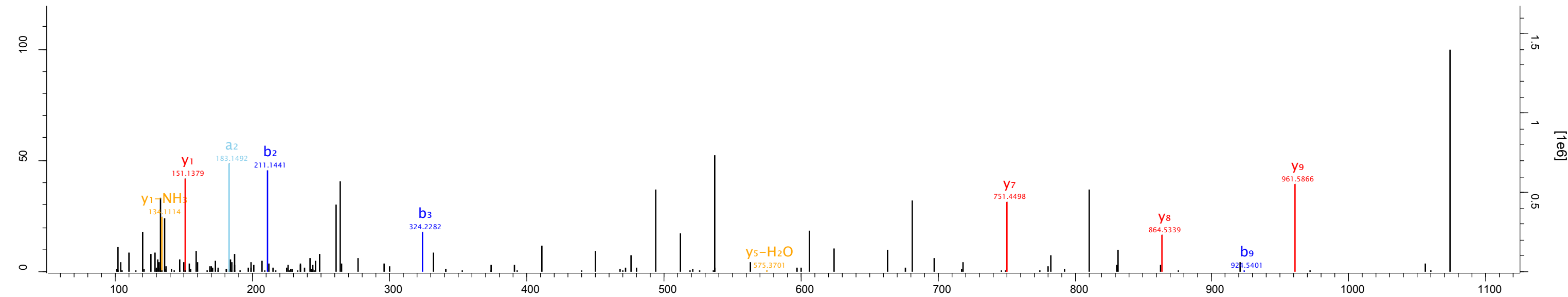
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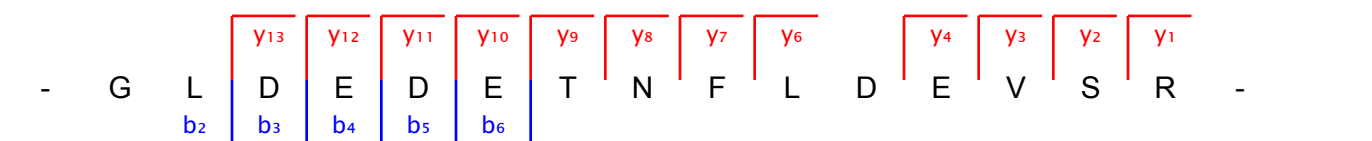
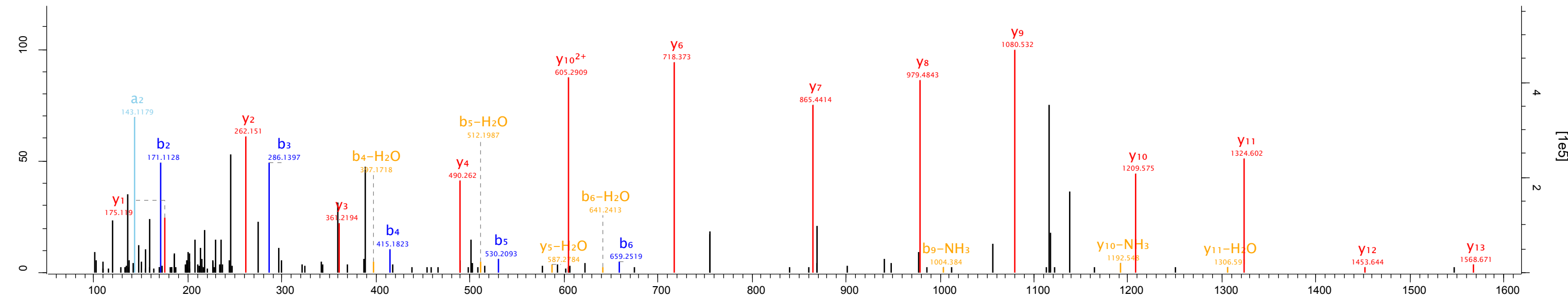
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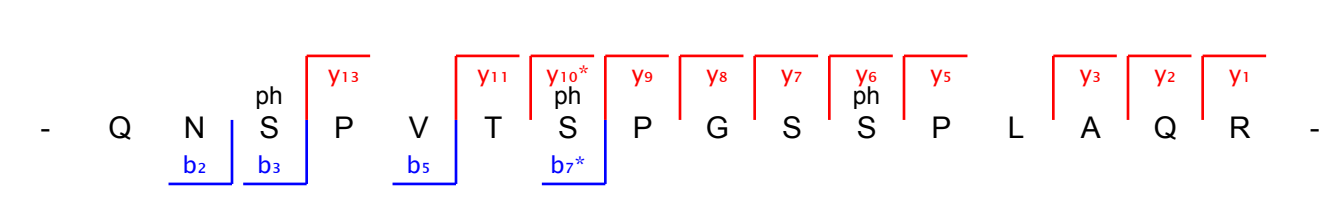
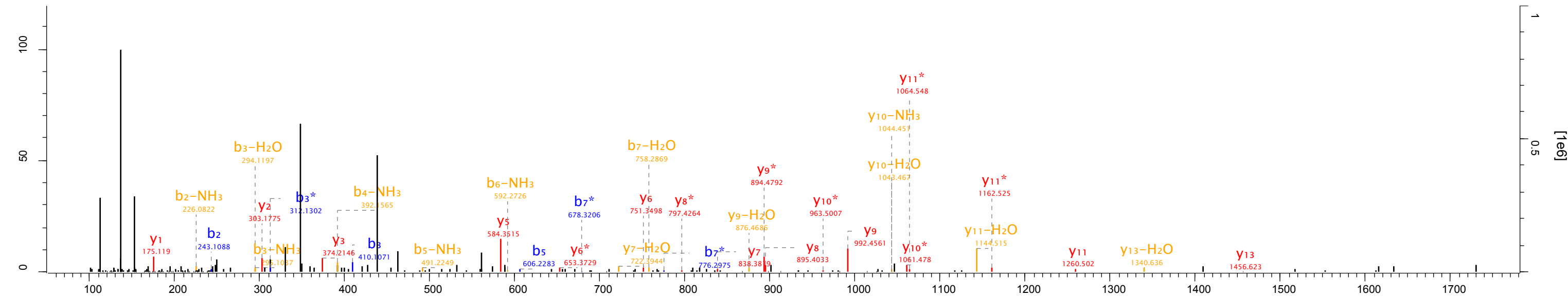
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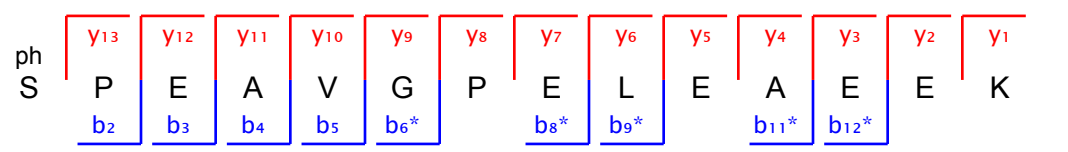
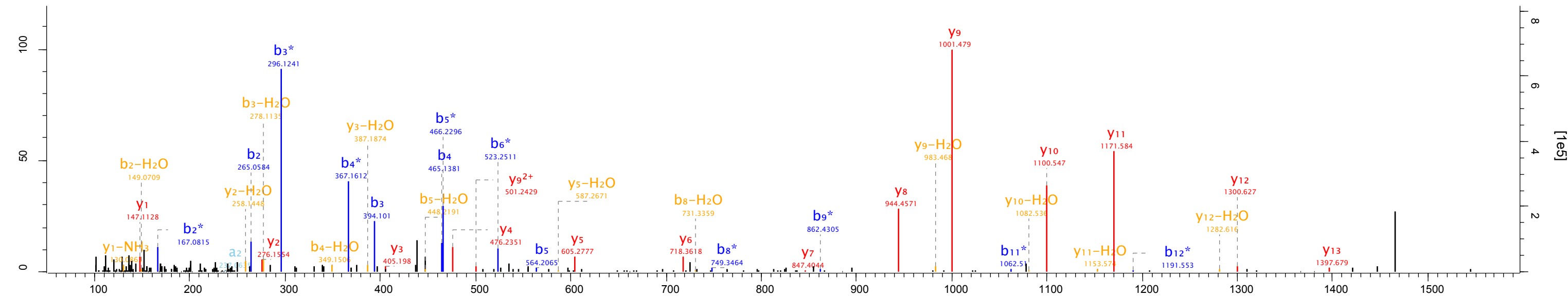
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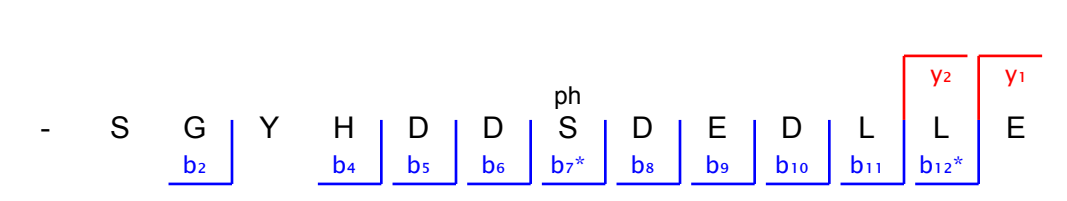
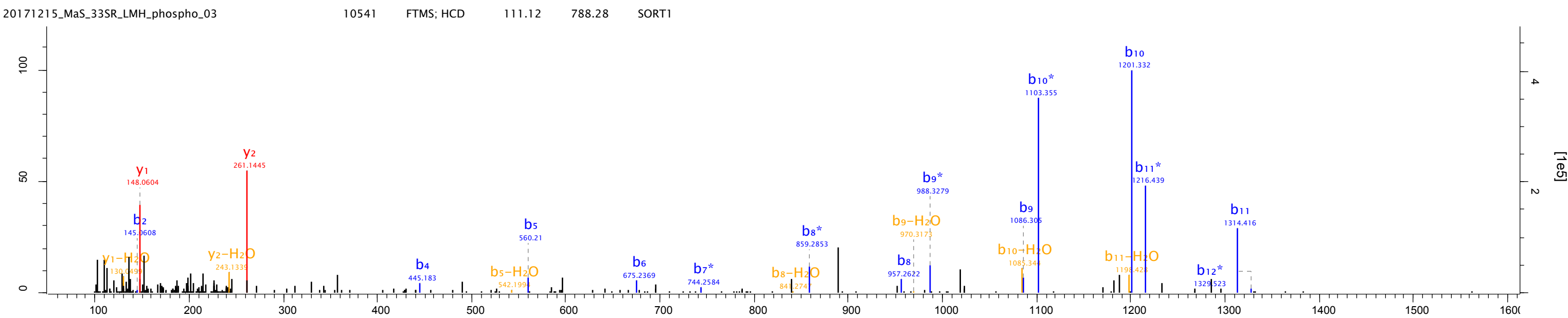
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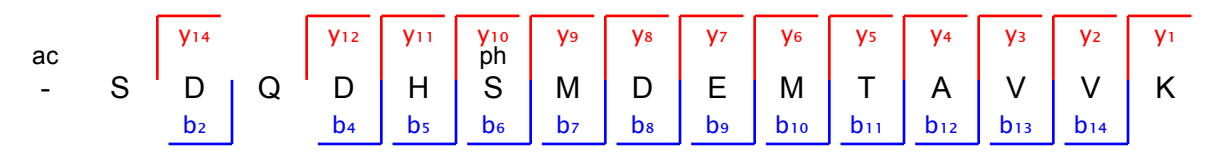
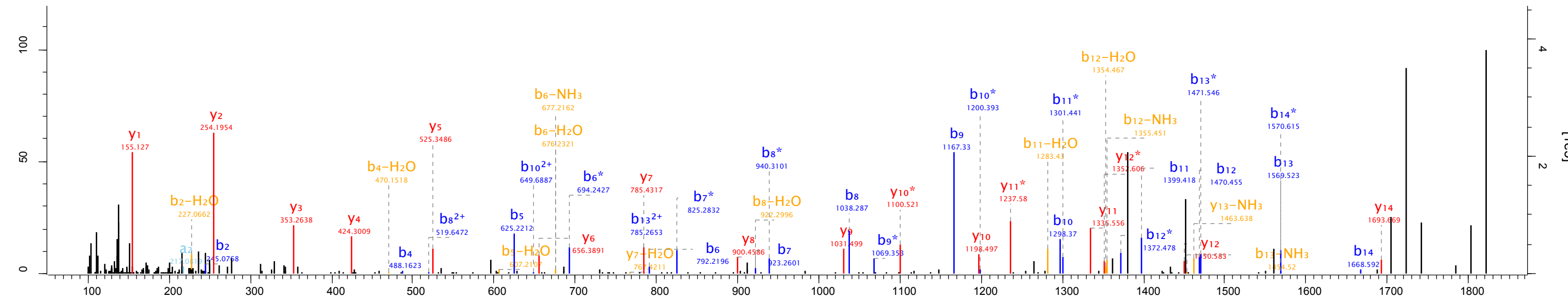
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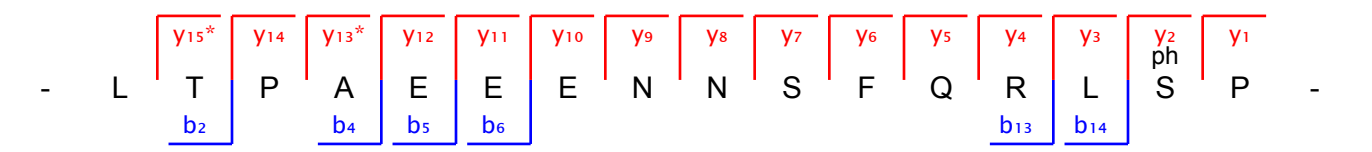
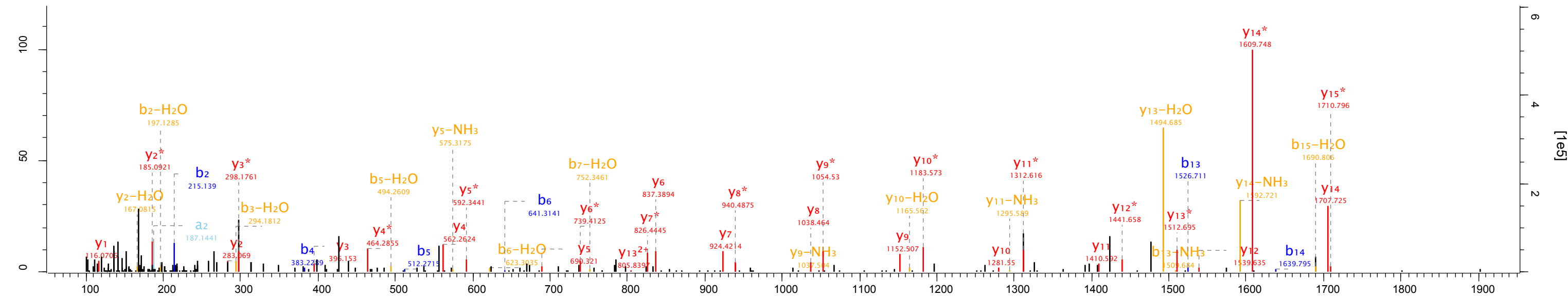
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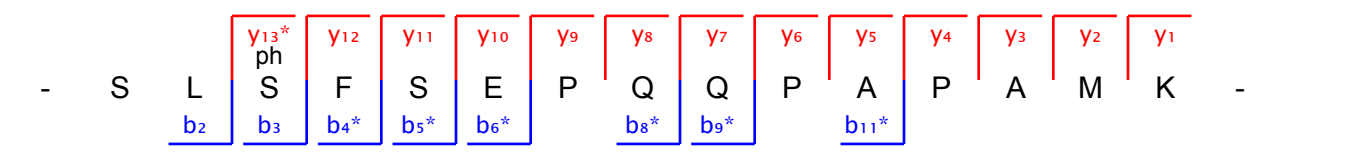
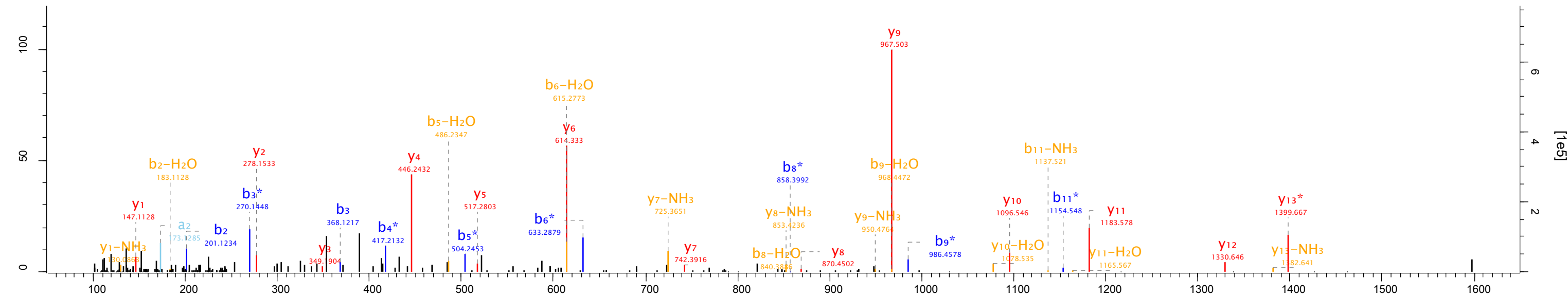
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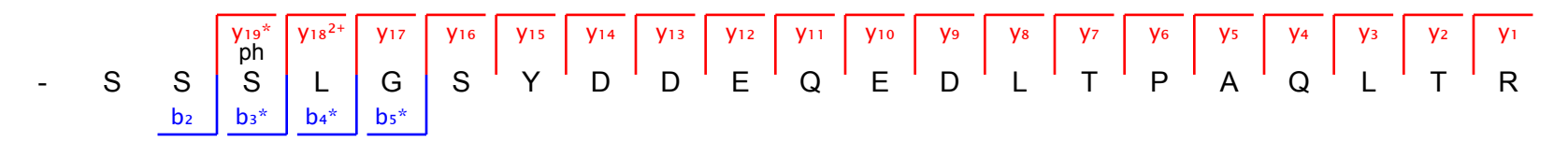
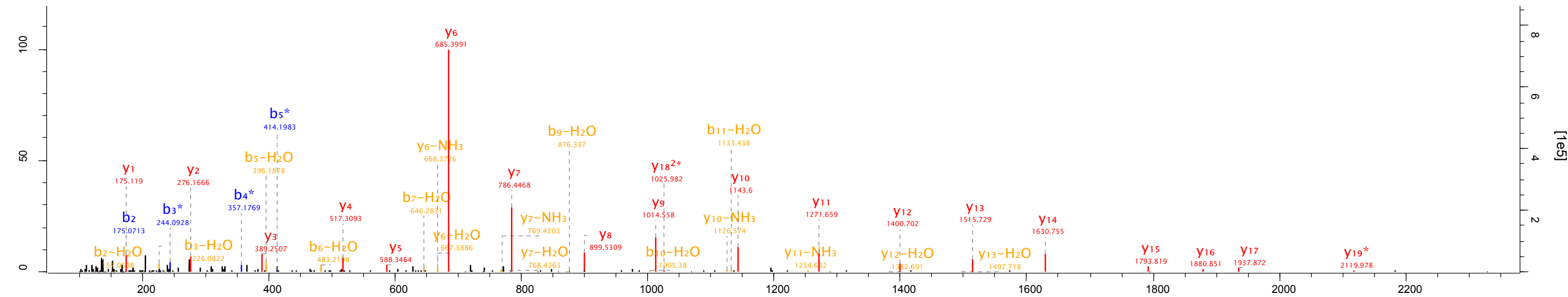
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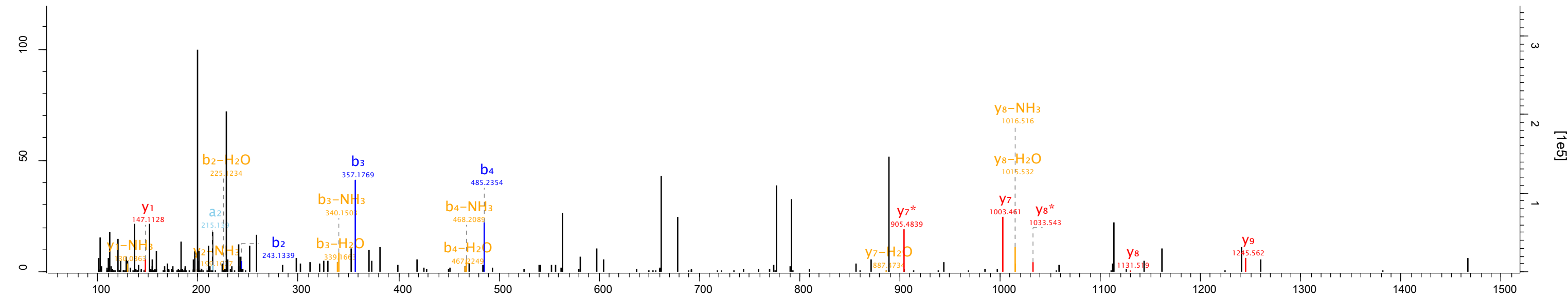
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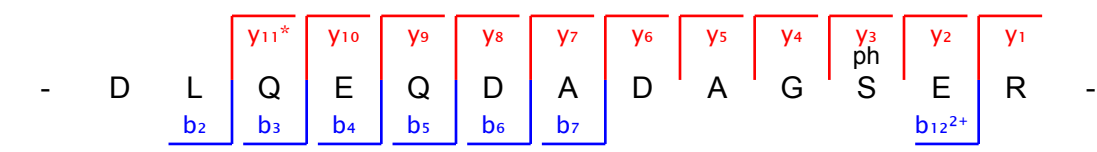
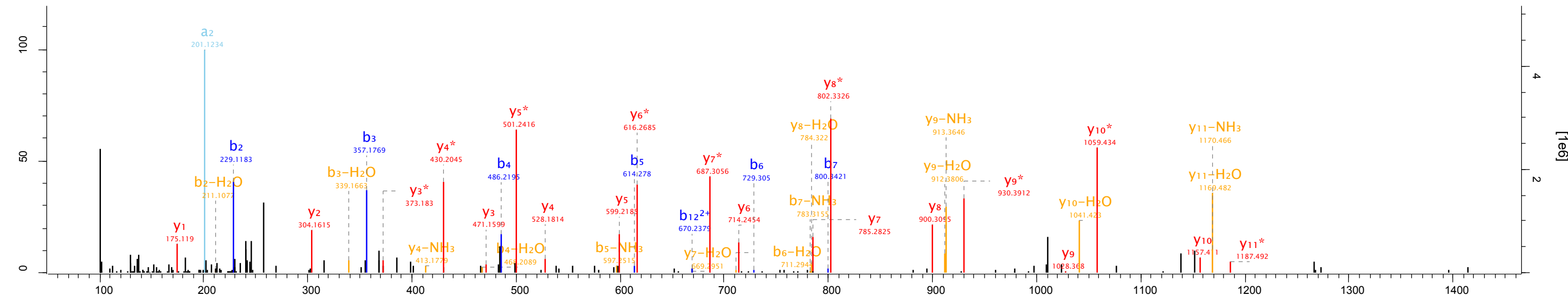


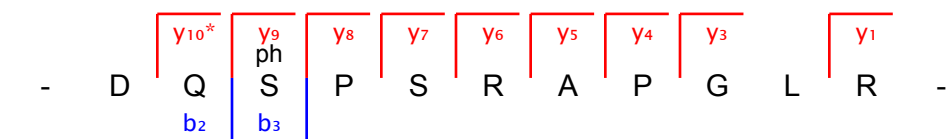
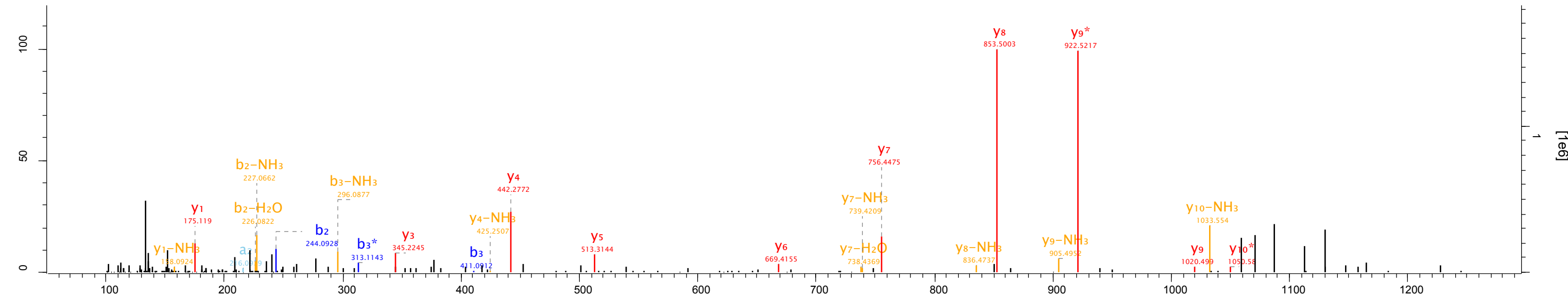
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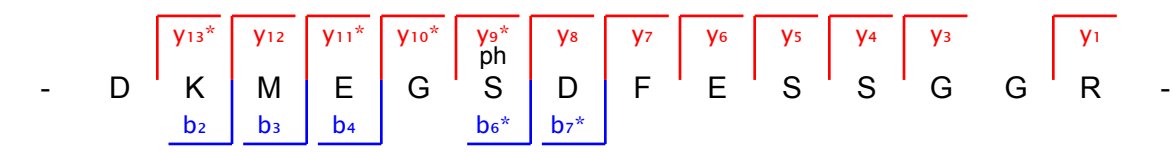
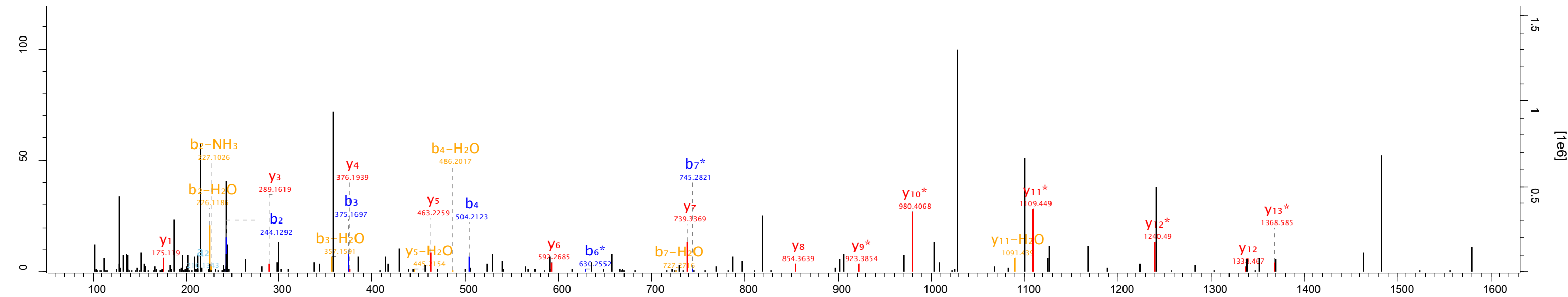
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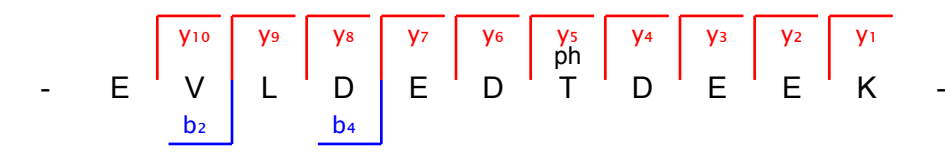
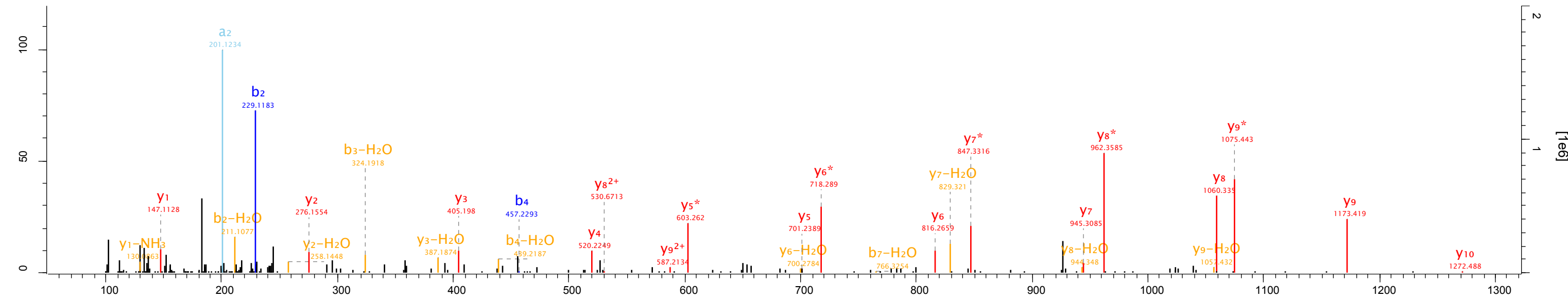




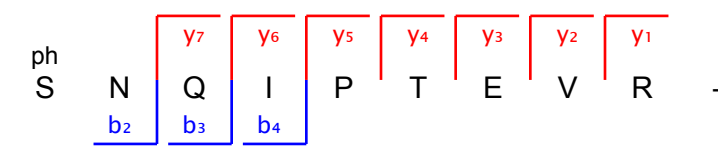
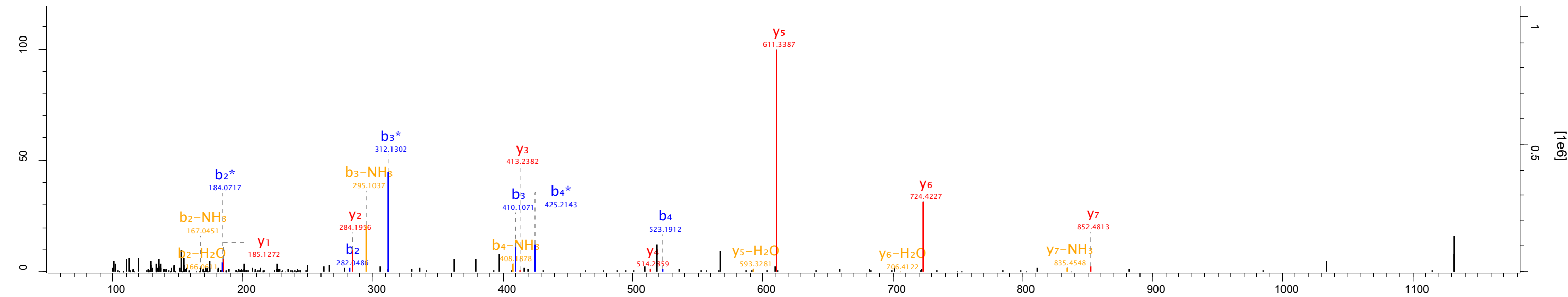
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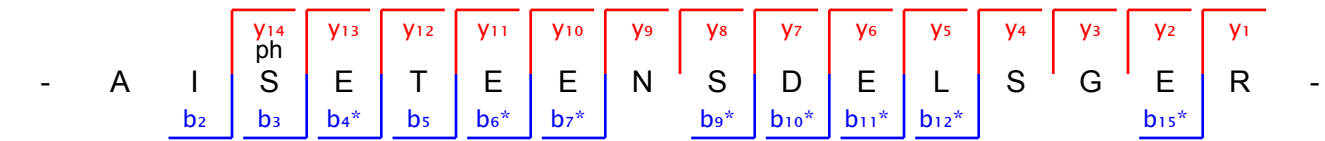
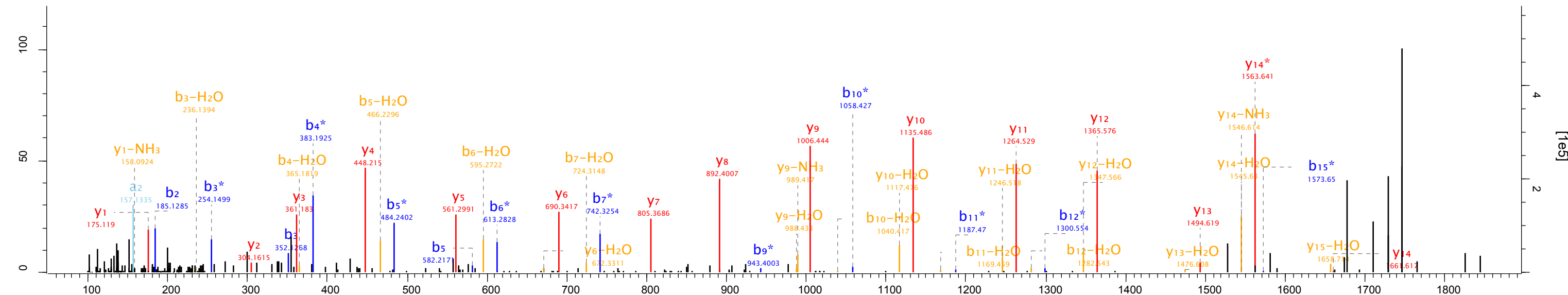
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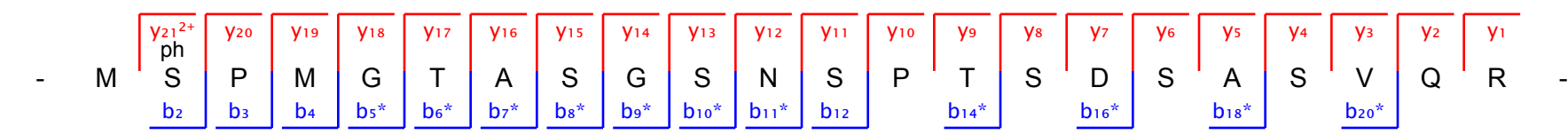
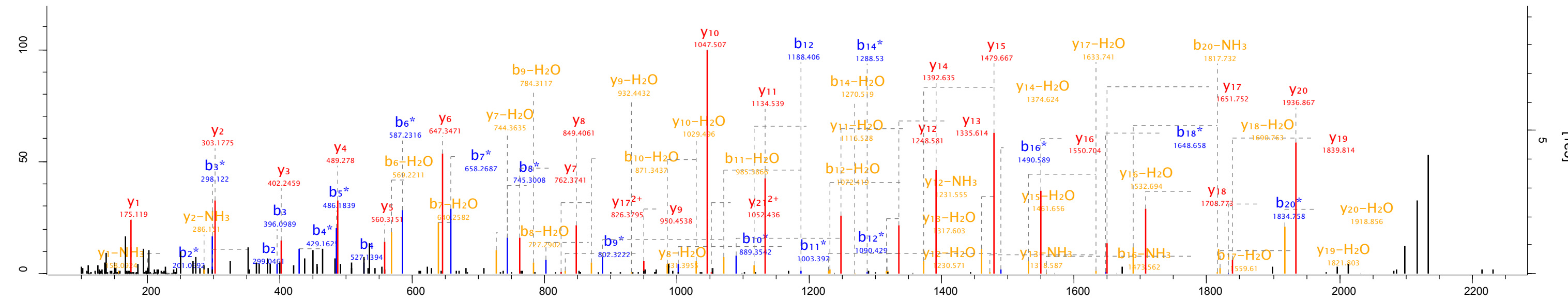
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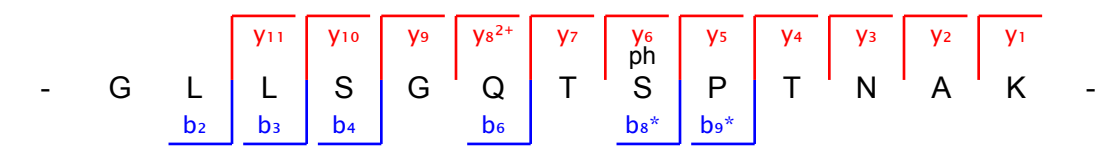
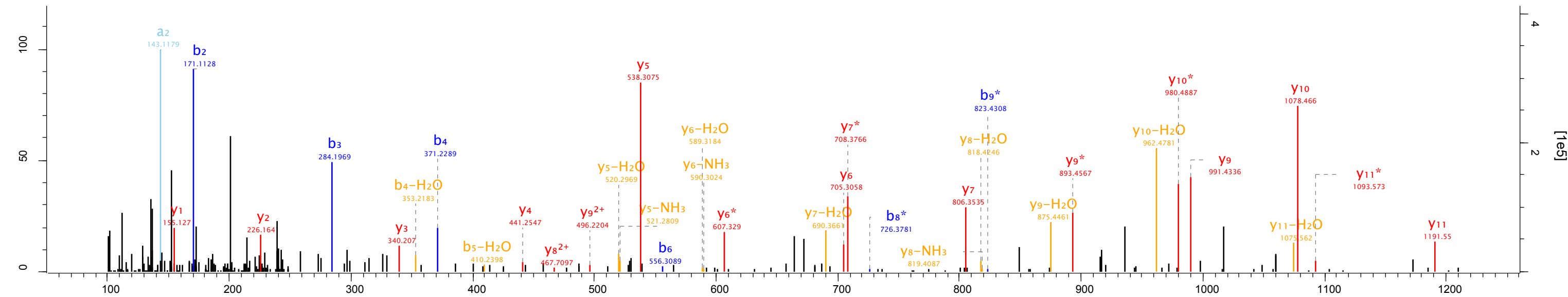
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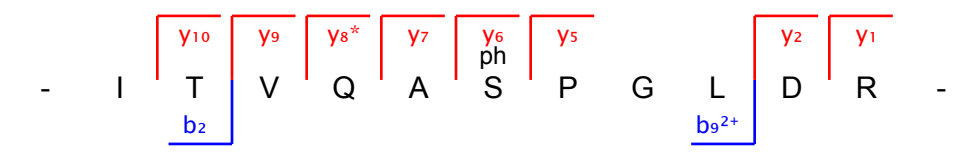
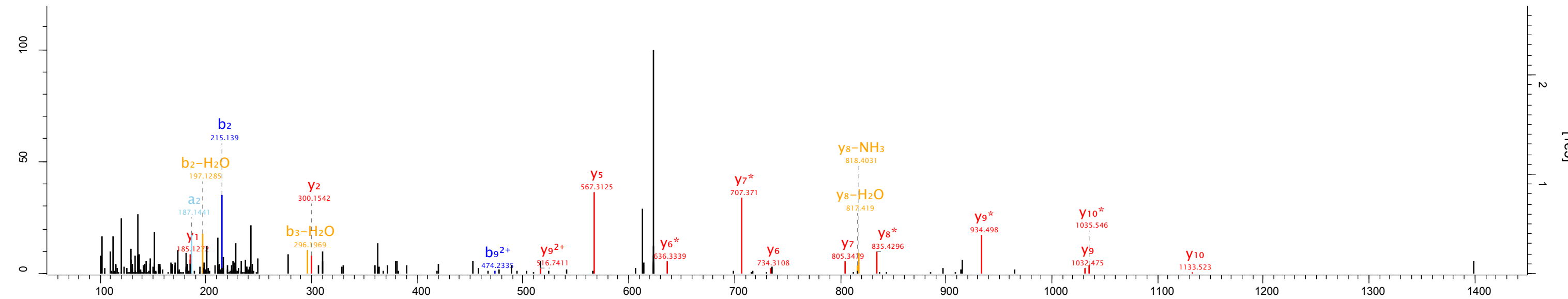
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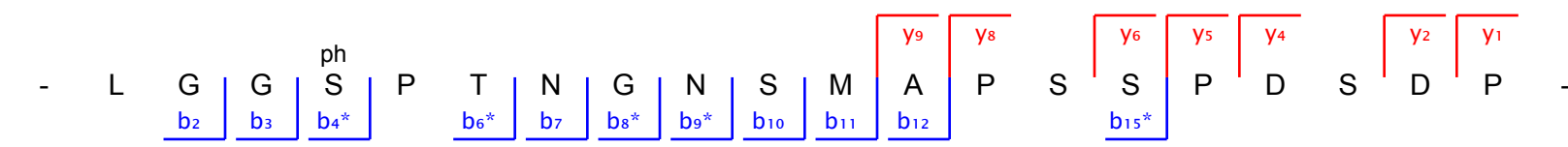
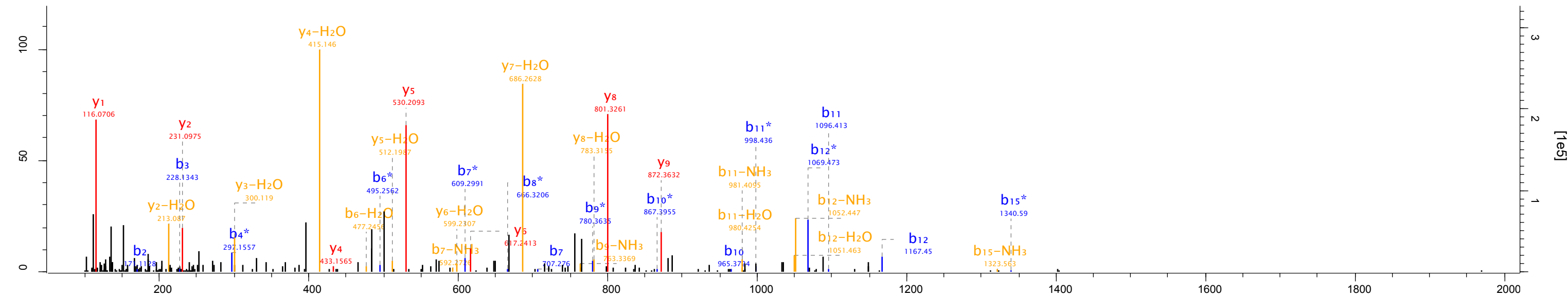


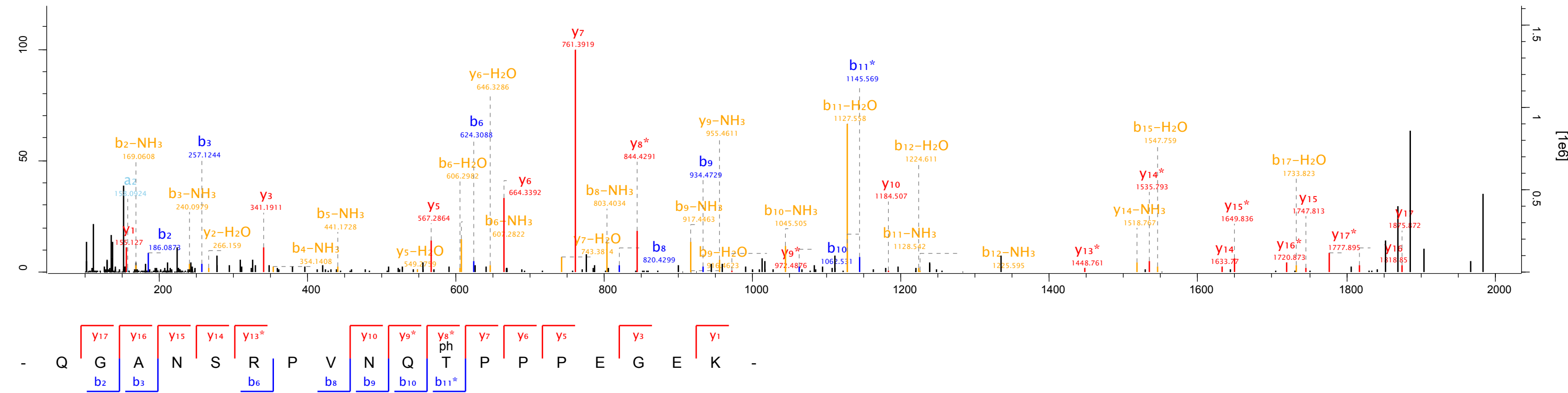
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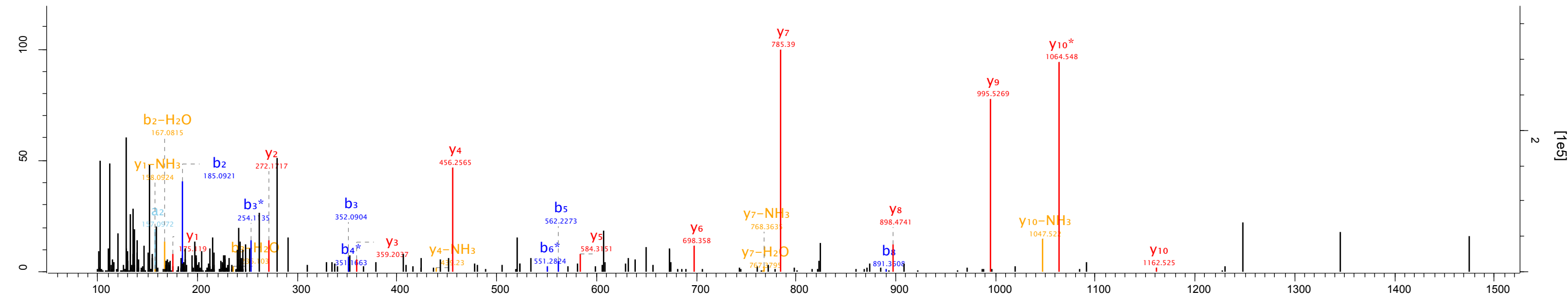




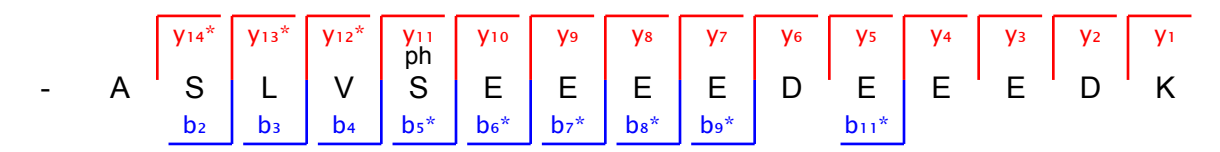
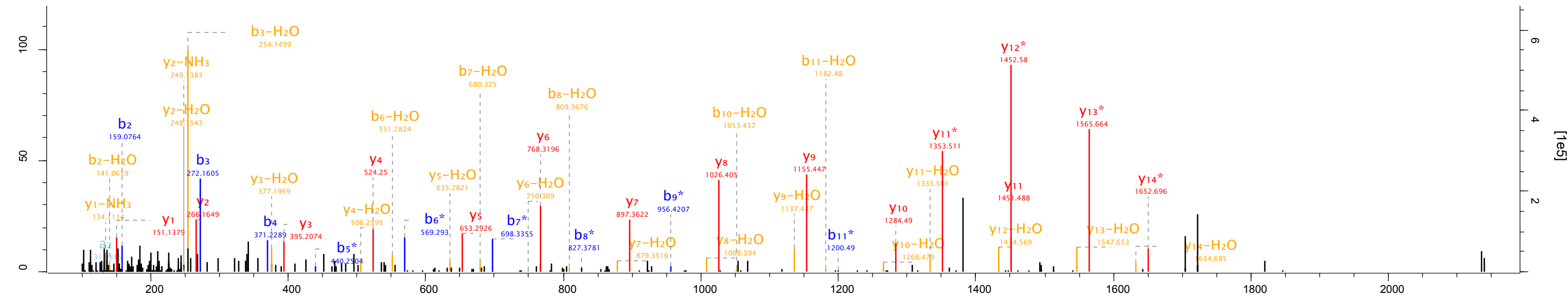


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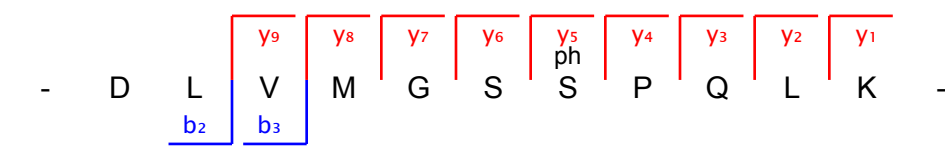
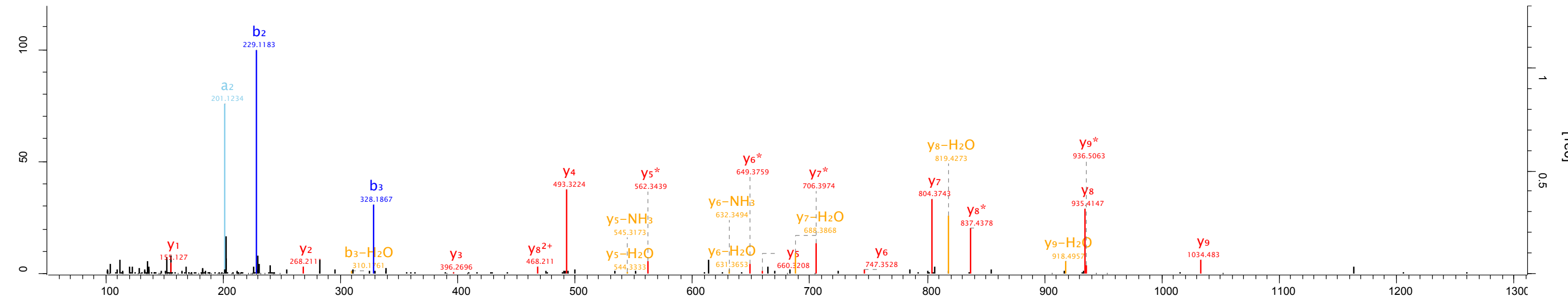
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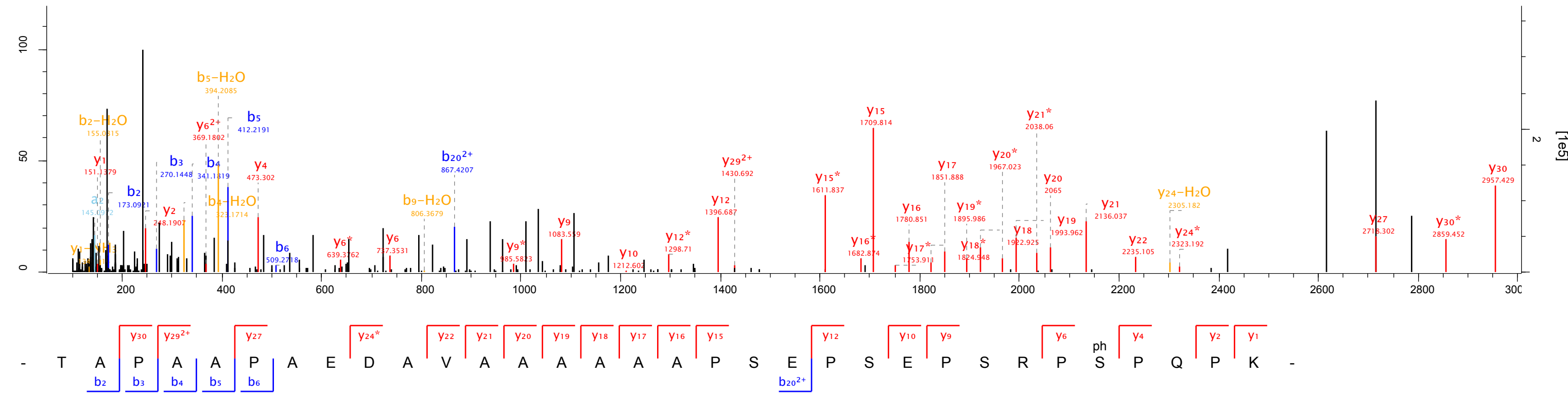
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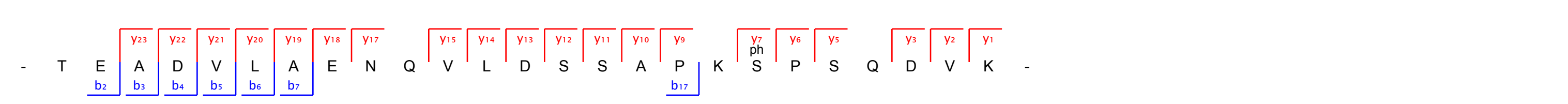
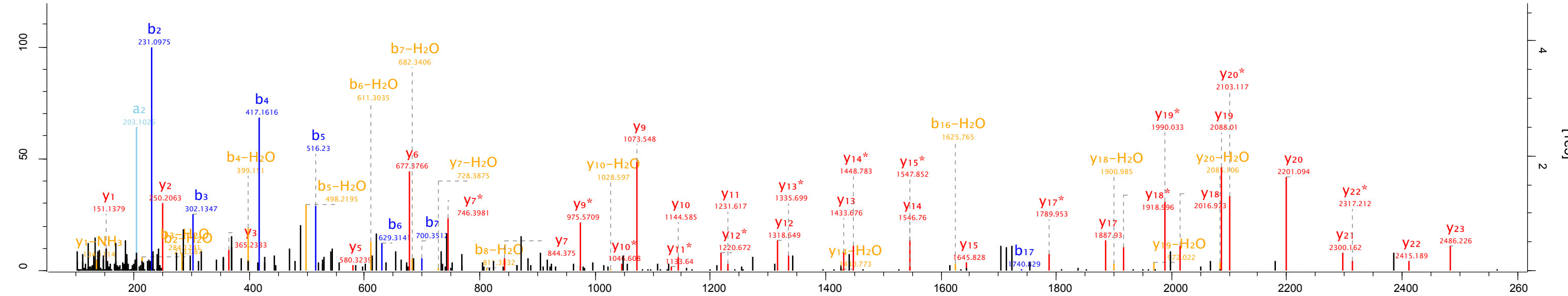
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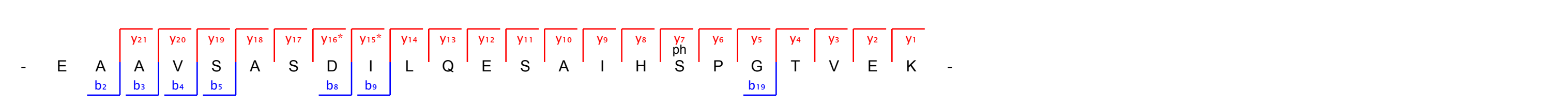
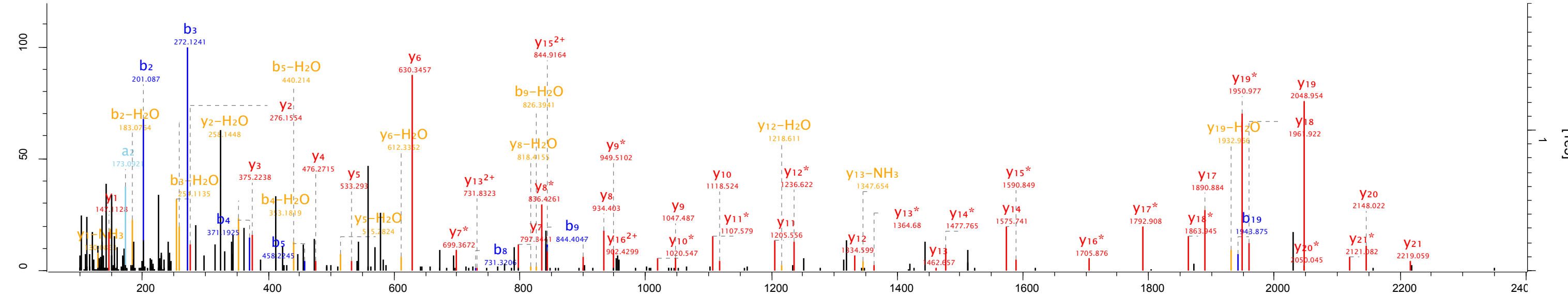


20171215_MaS_33SR_LMH_phospho_06 13231 FTMS; HCD 217.84 906.11 NUFIP1

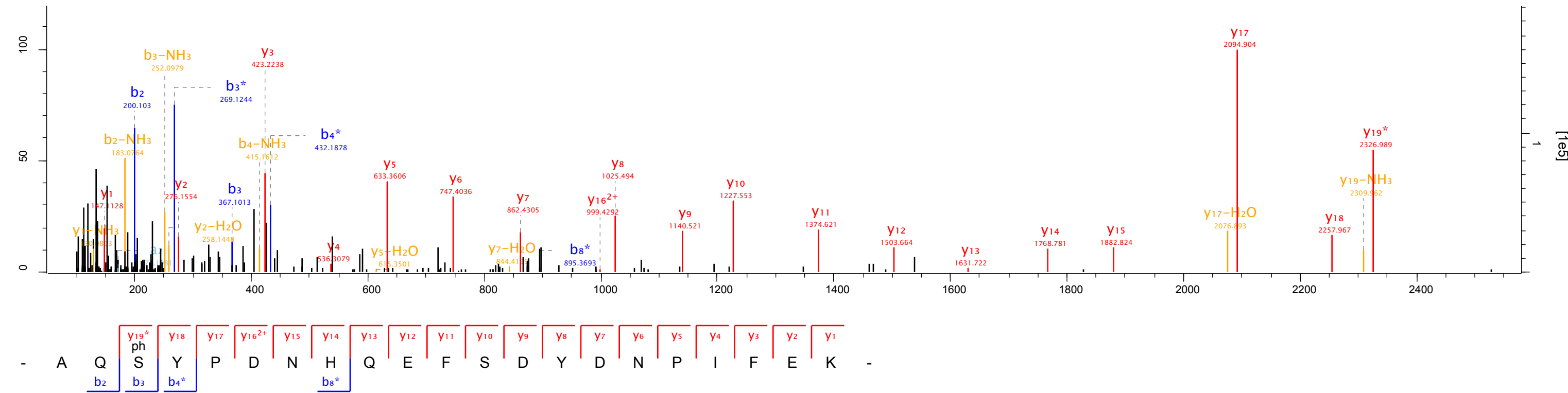


Raw file Scan Method Score m/z Gene names

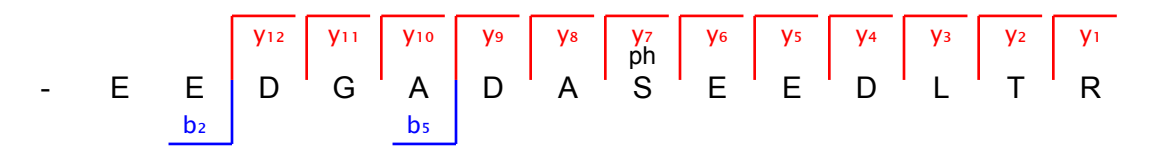
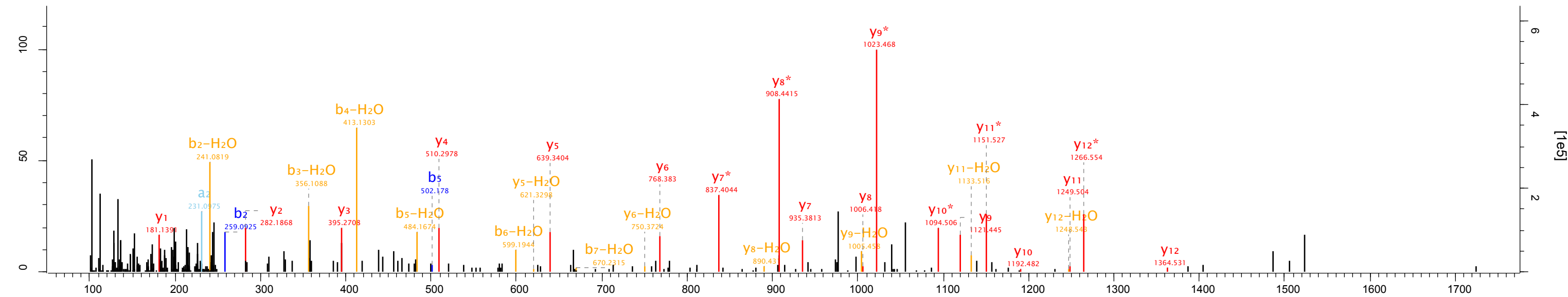
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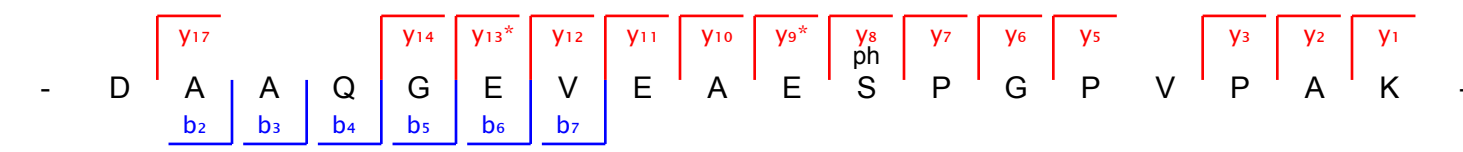
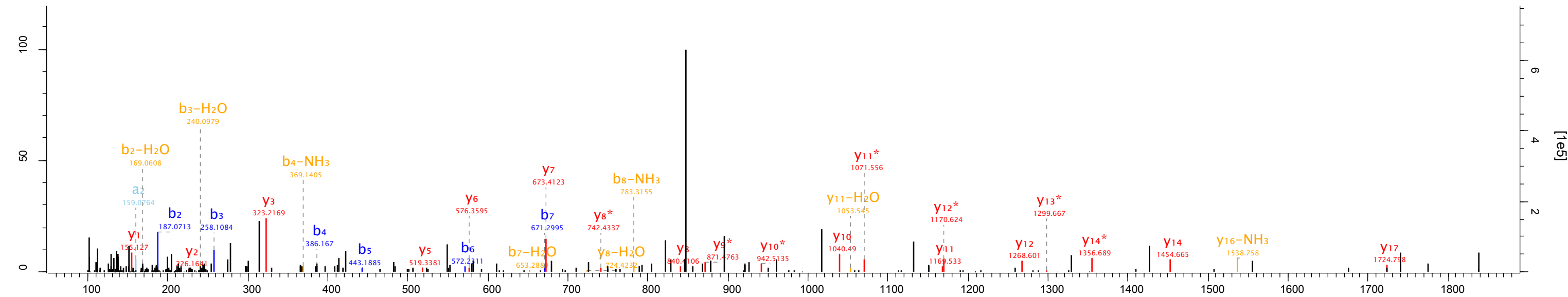
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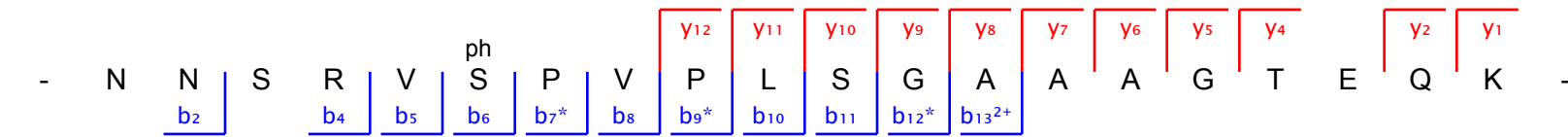
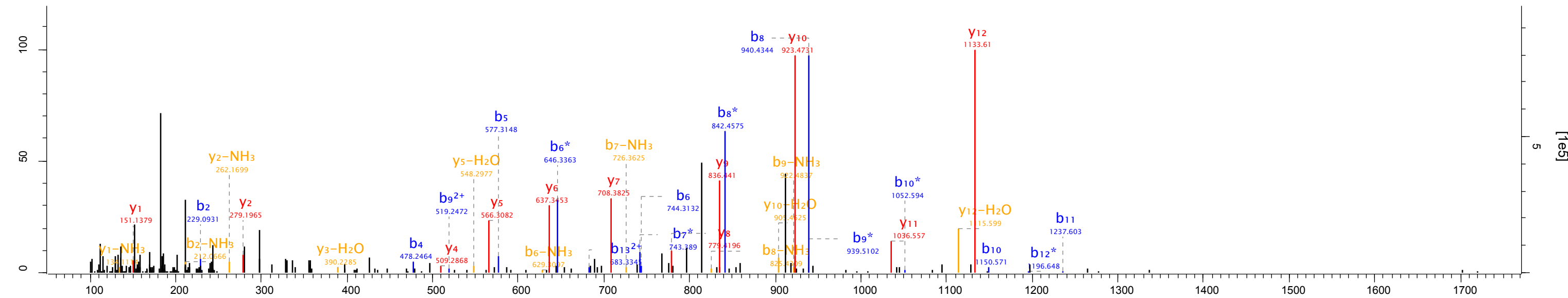


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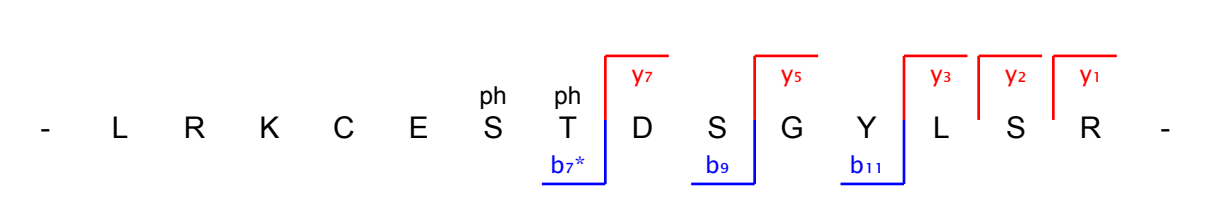
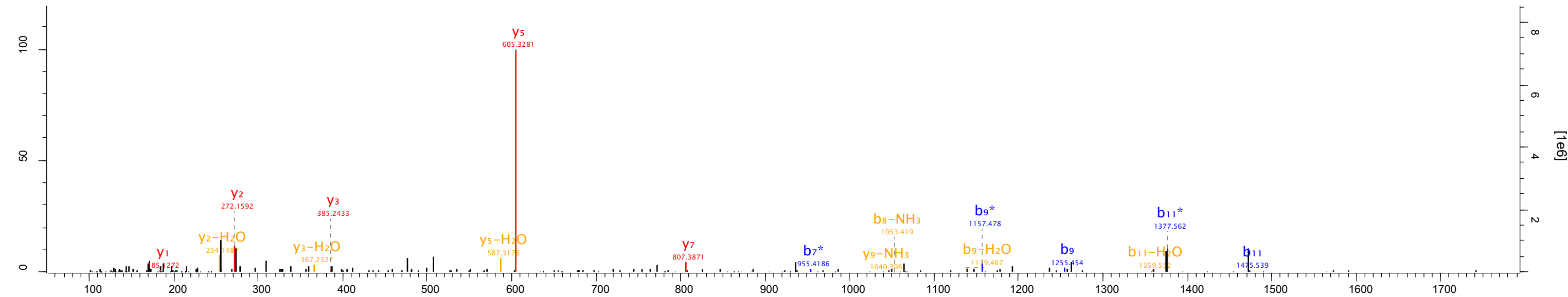


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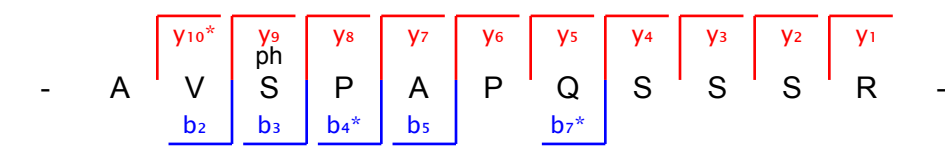
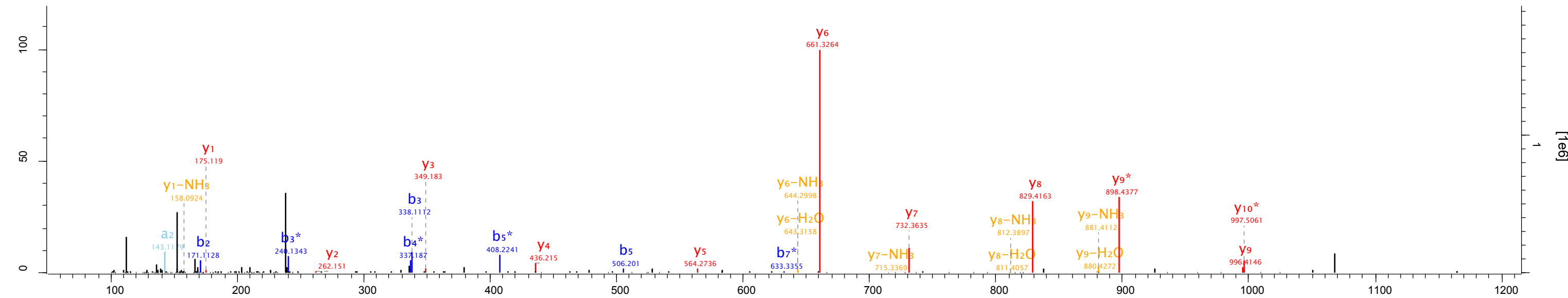




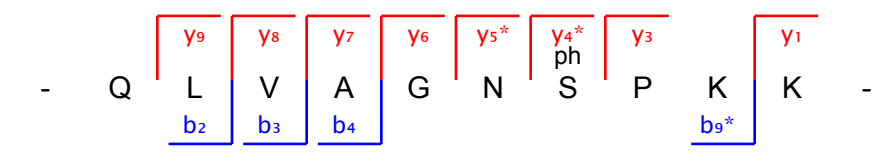
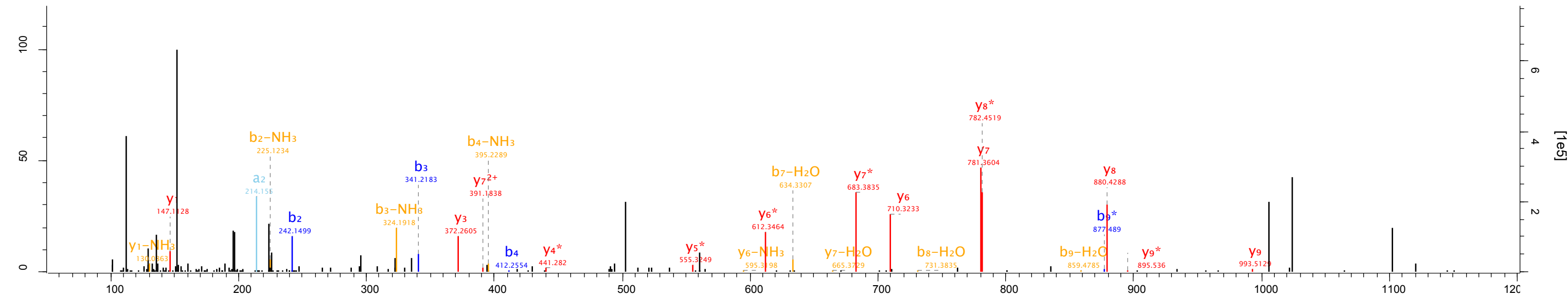
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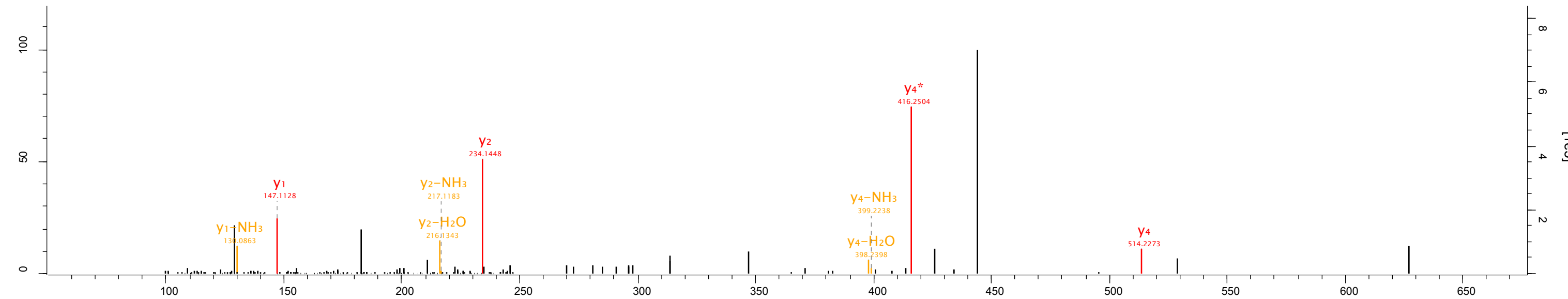
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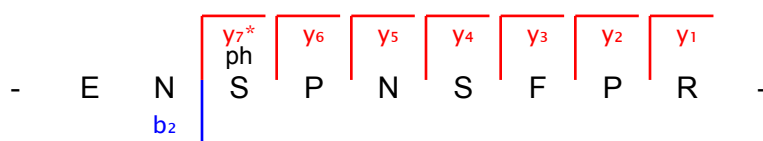
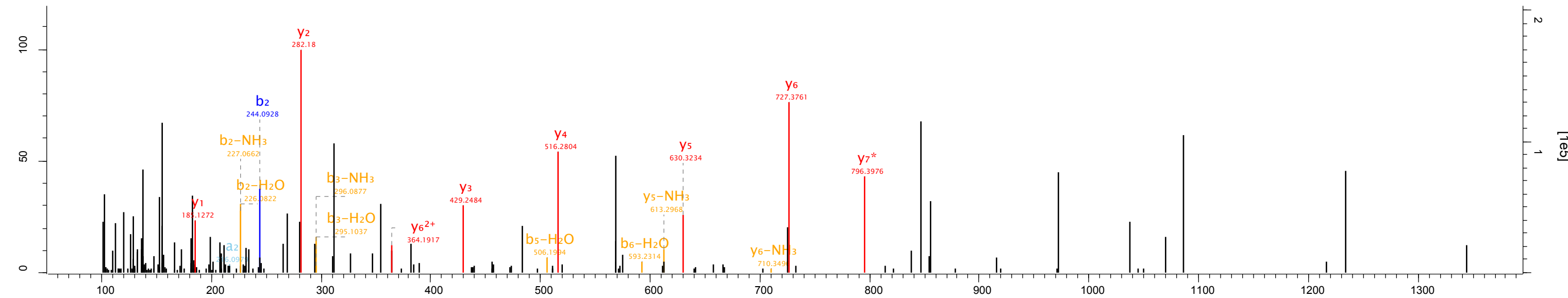
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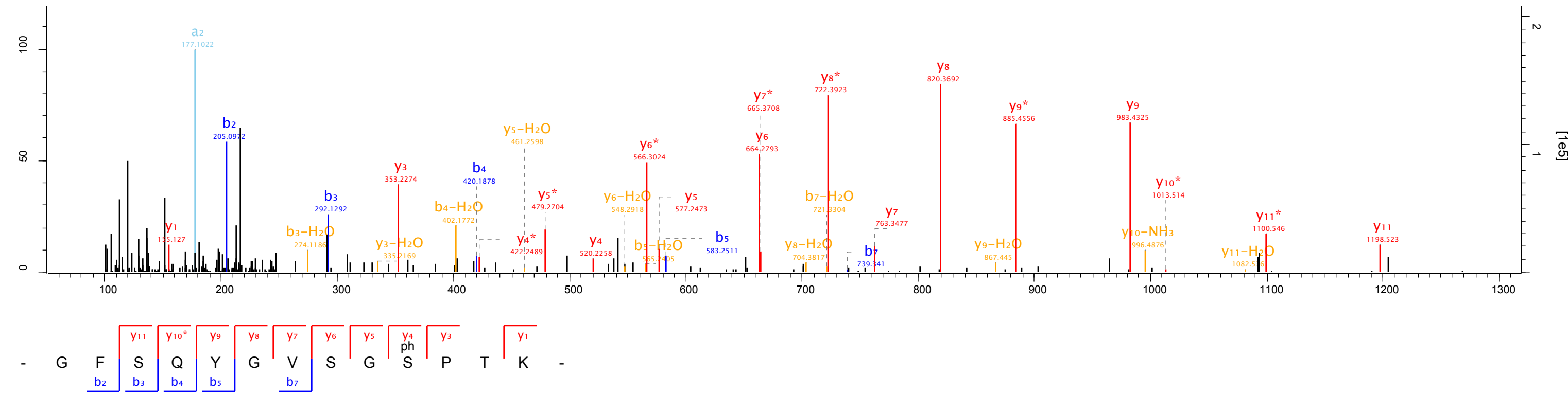


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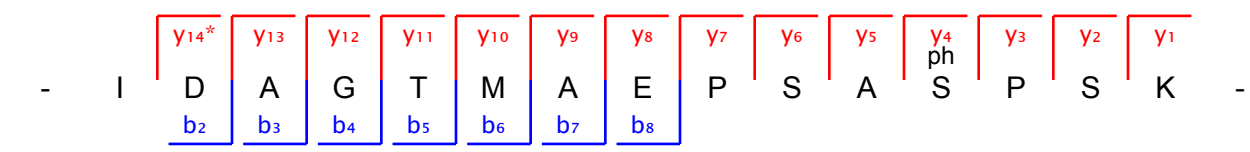
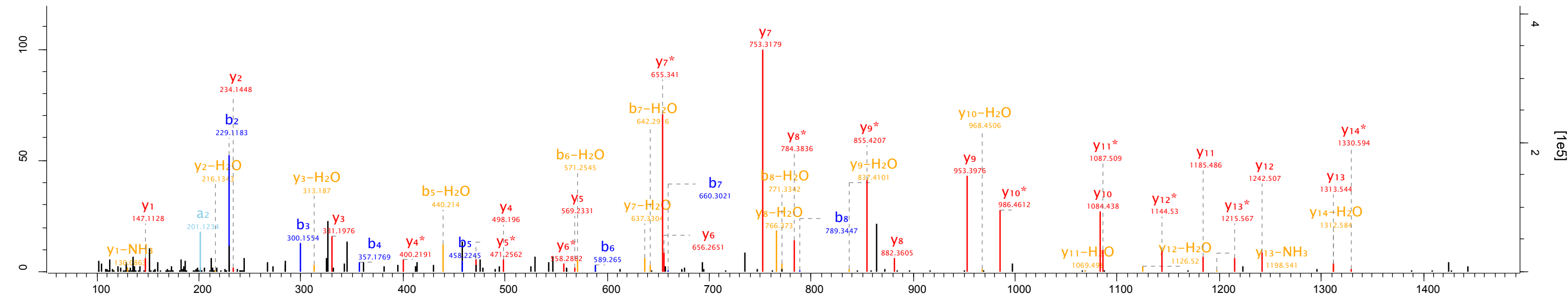
Fragmentation mapping: y4 covers I and S; y2 covers S; y1 covers K.

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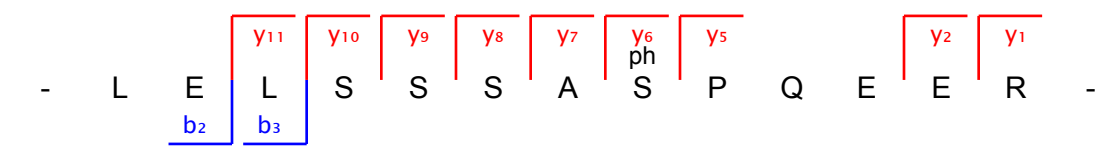
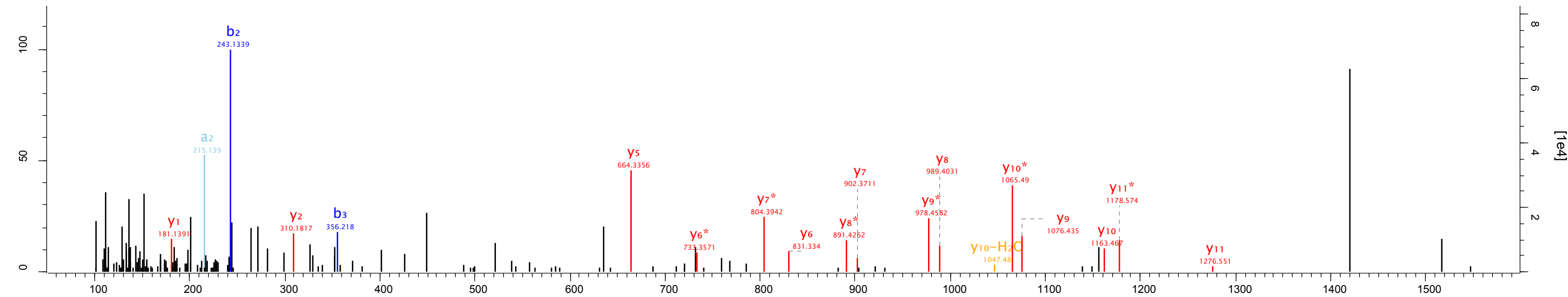




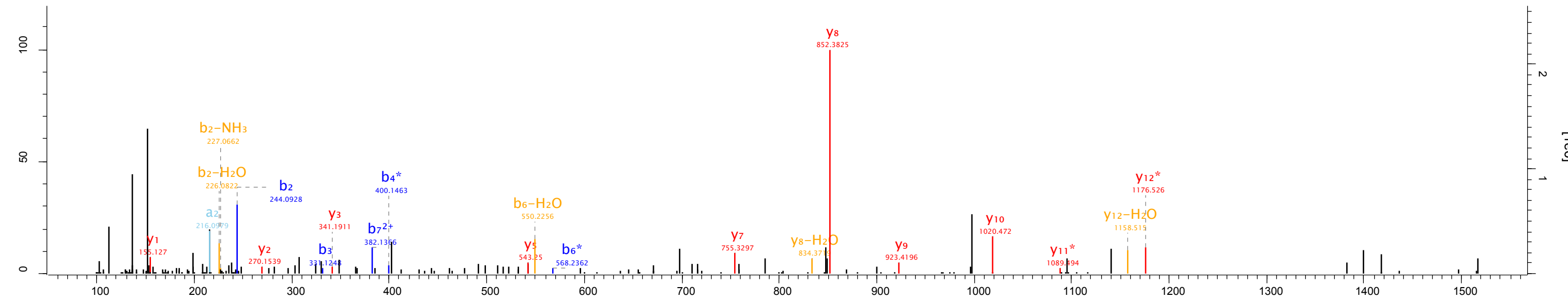
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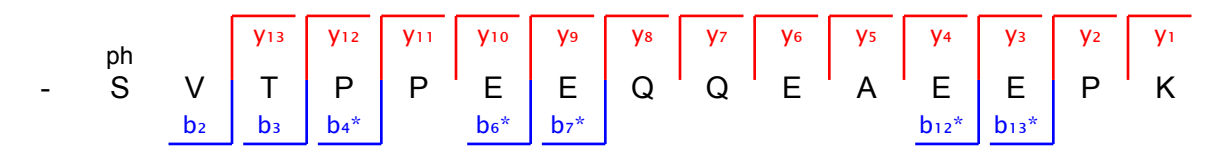
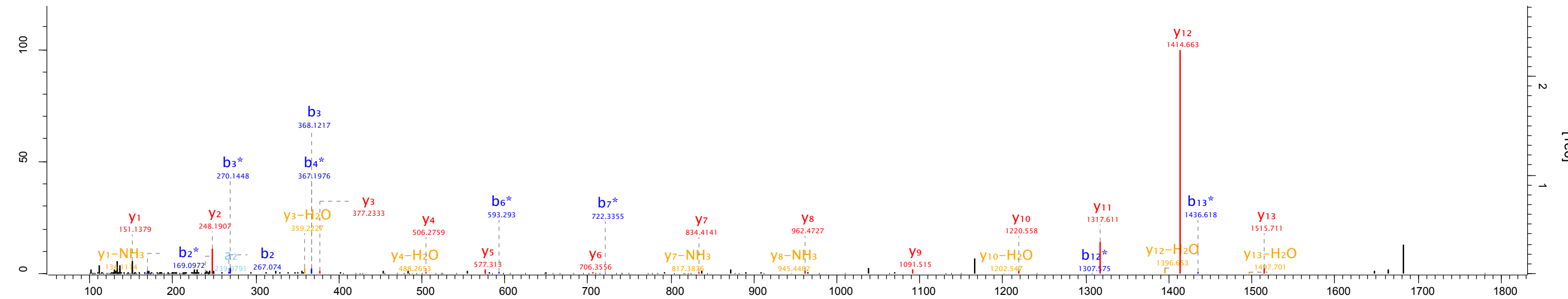
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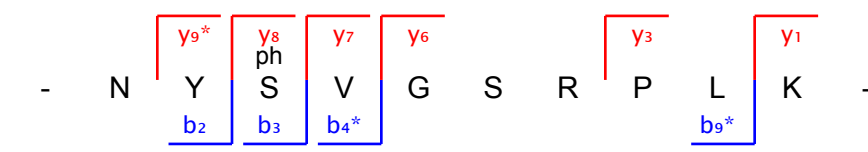
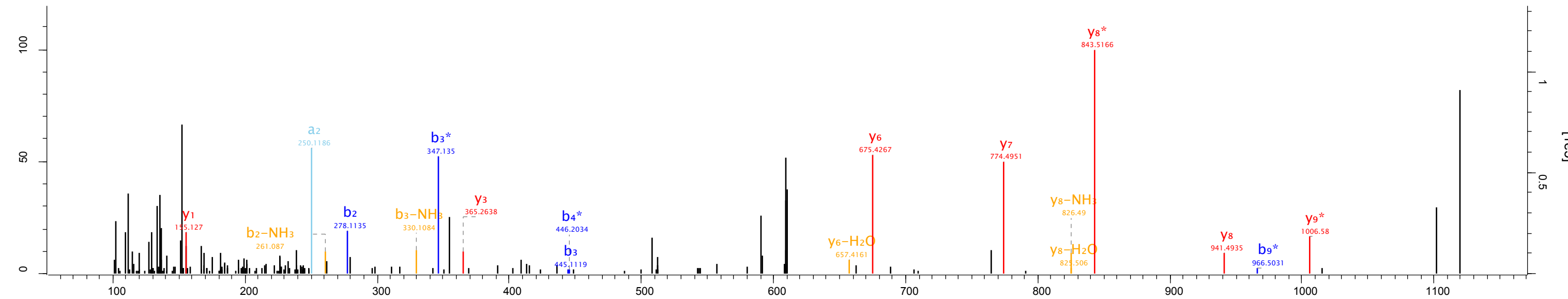
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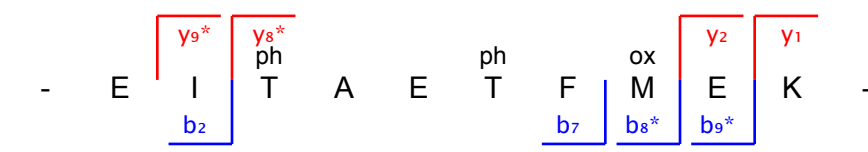
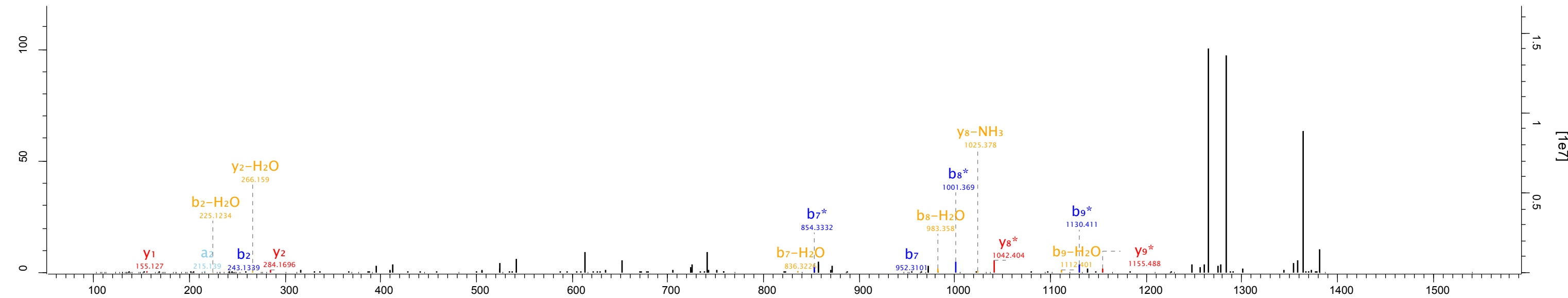


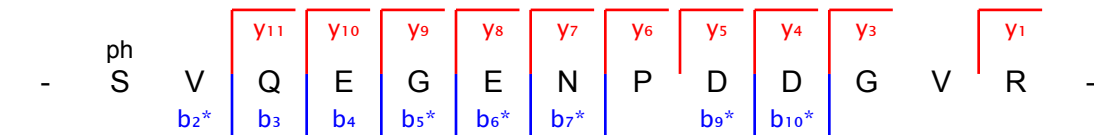
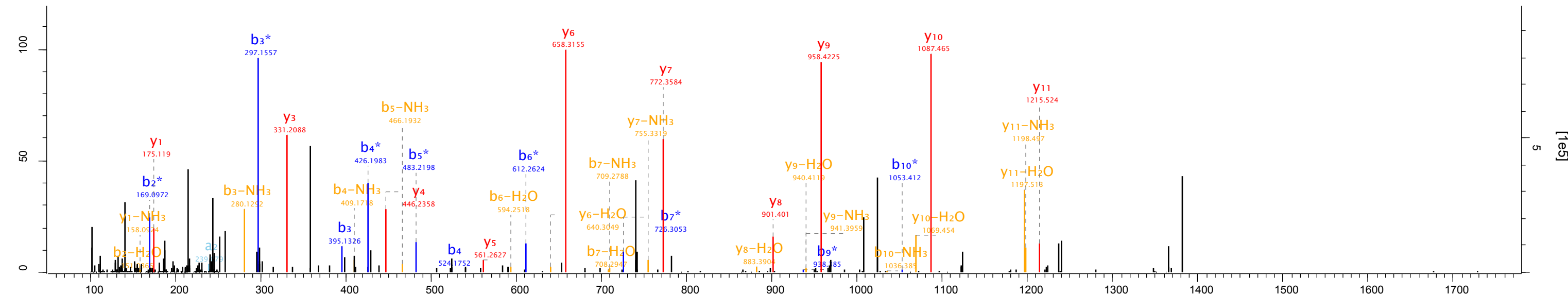
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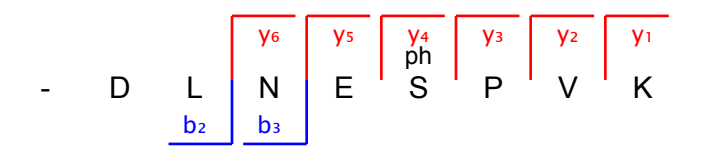
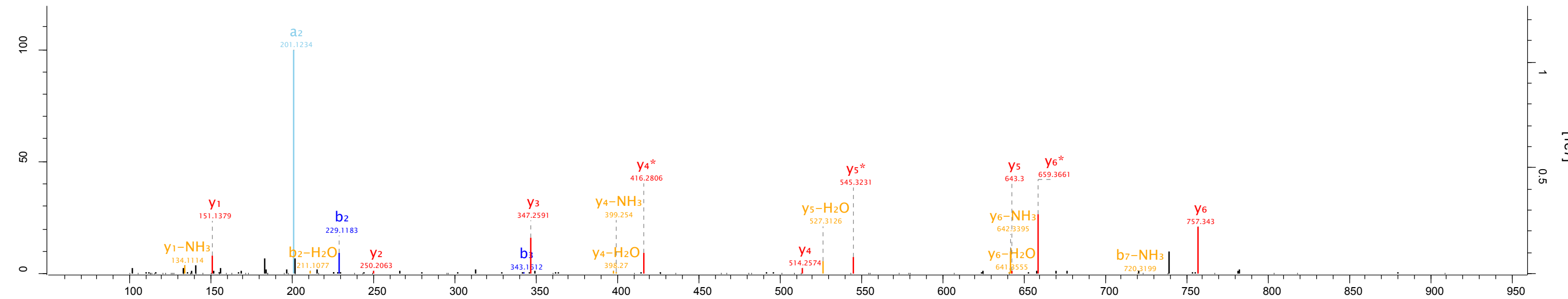
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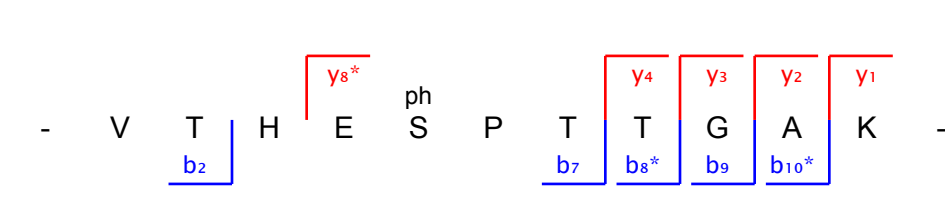
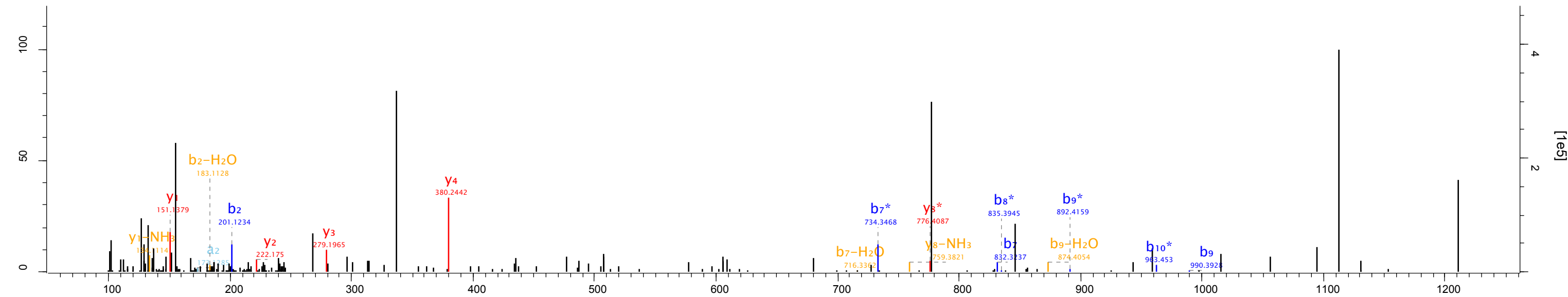




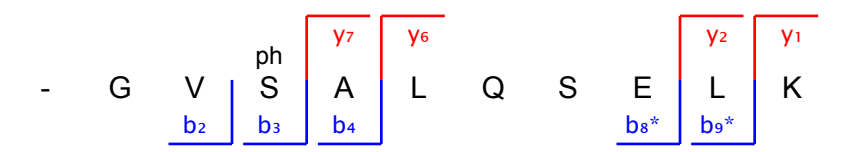
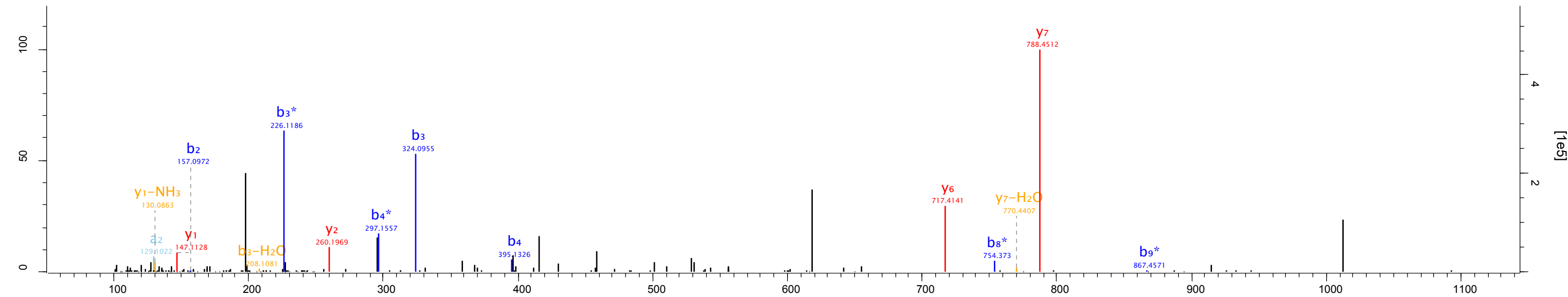
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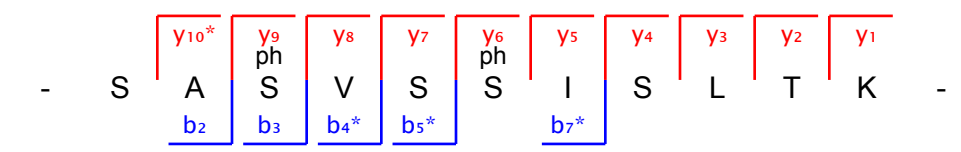
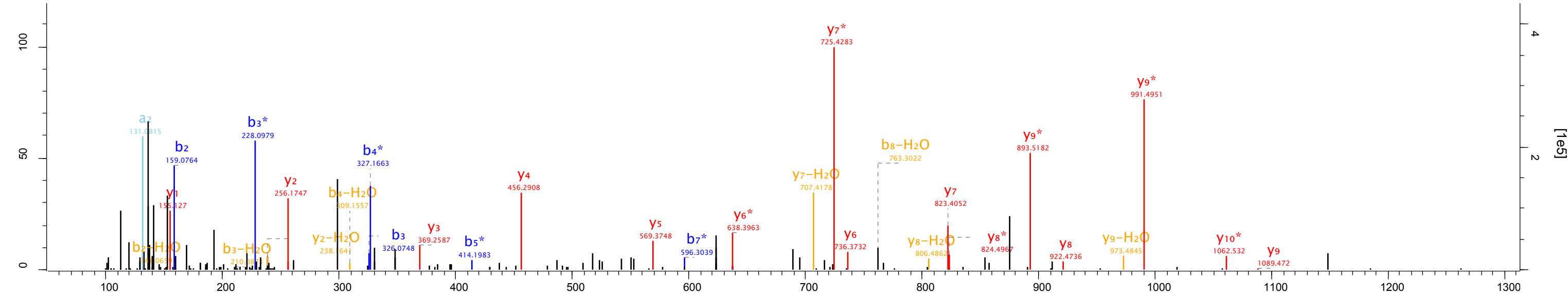


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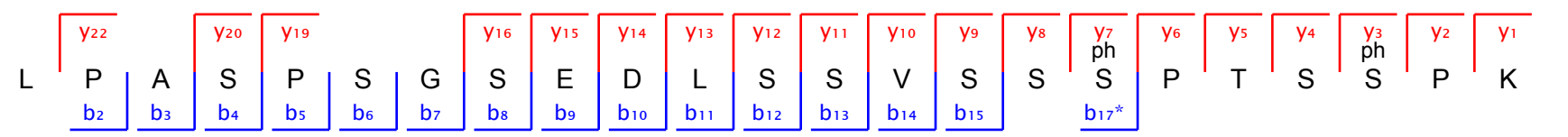
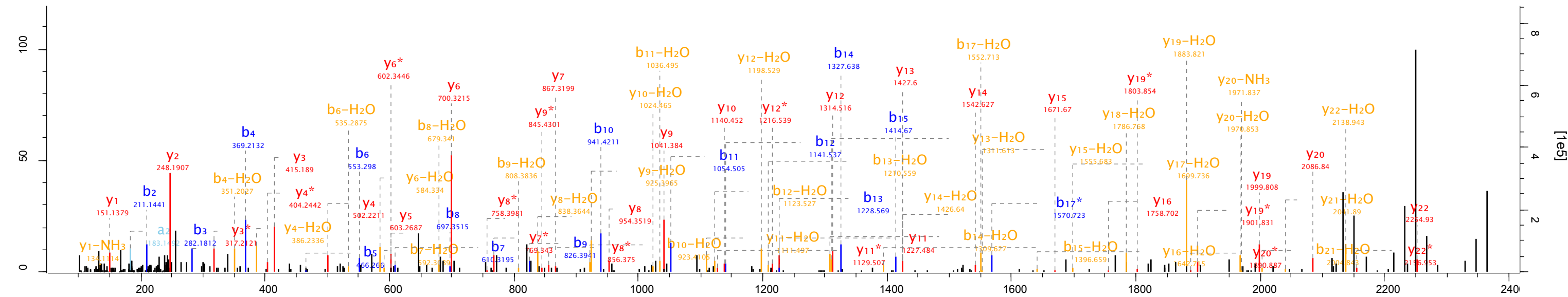


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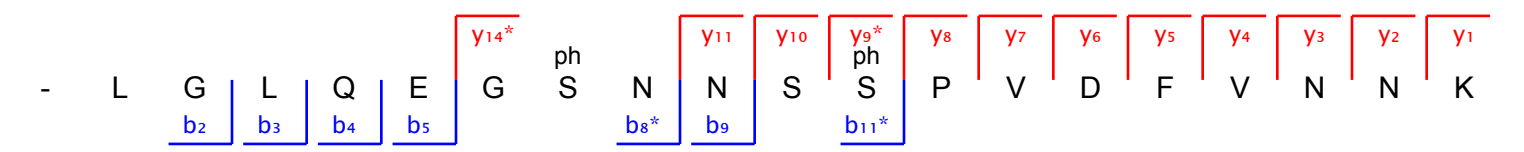
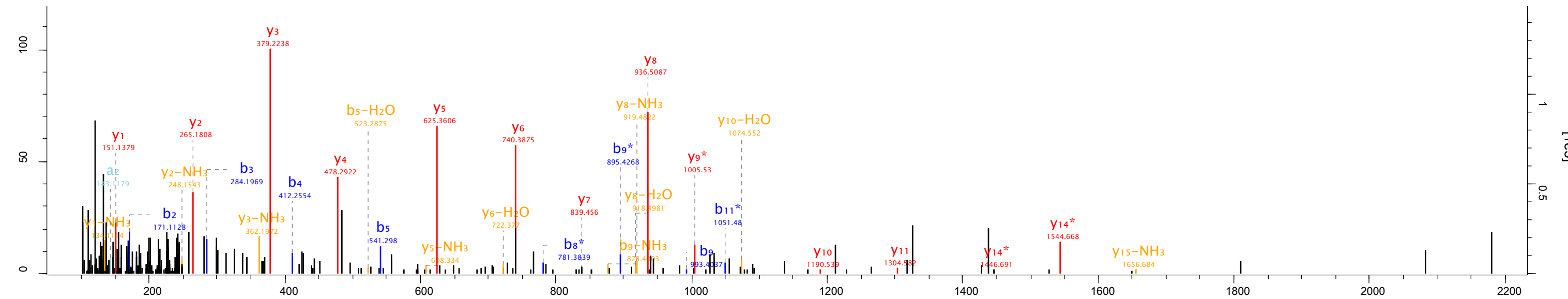




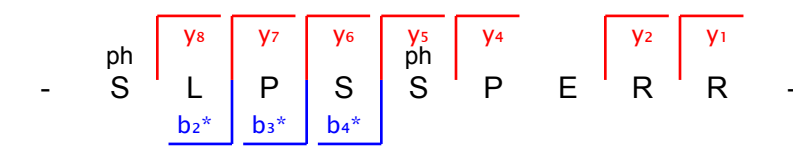
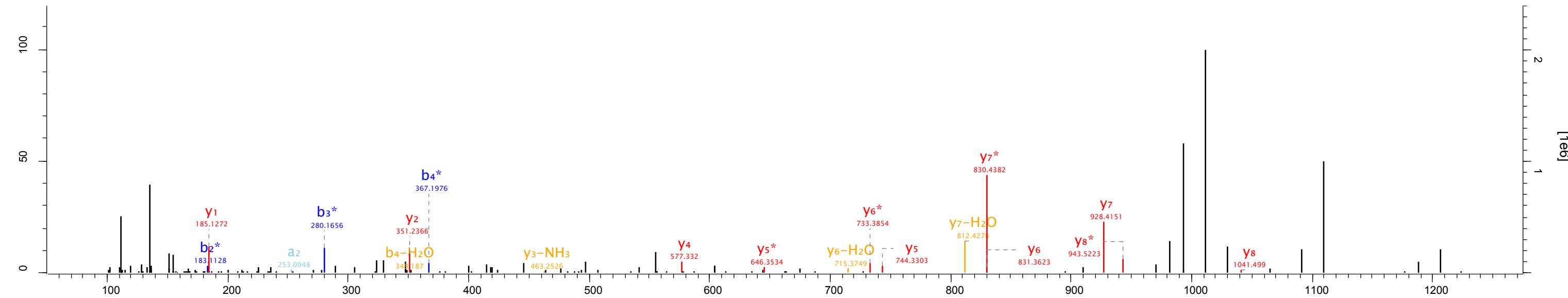
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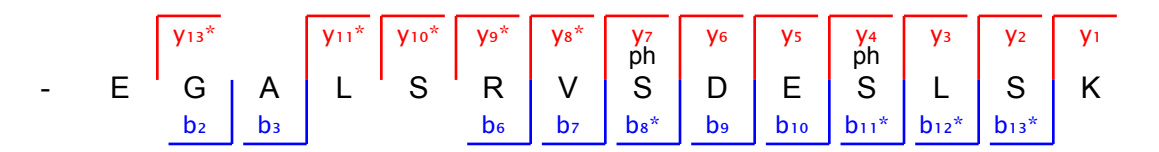
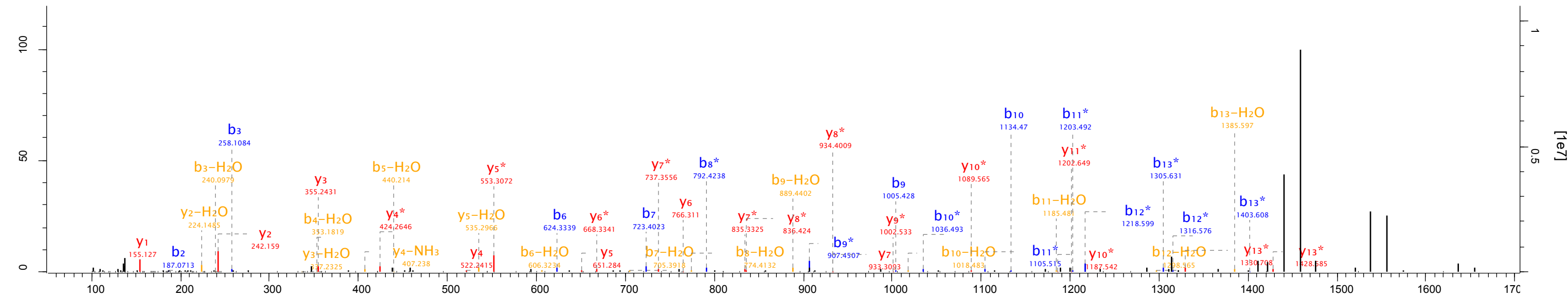
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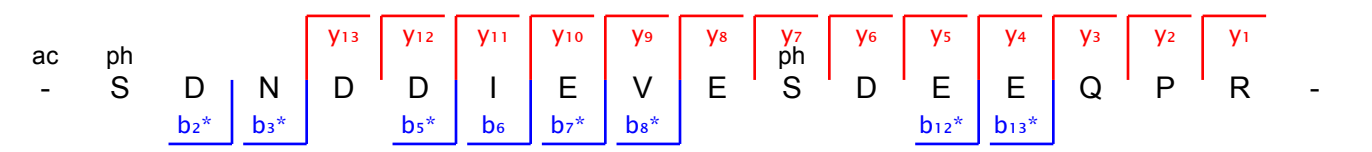
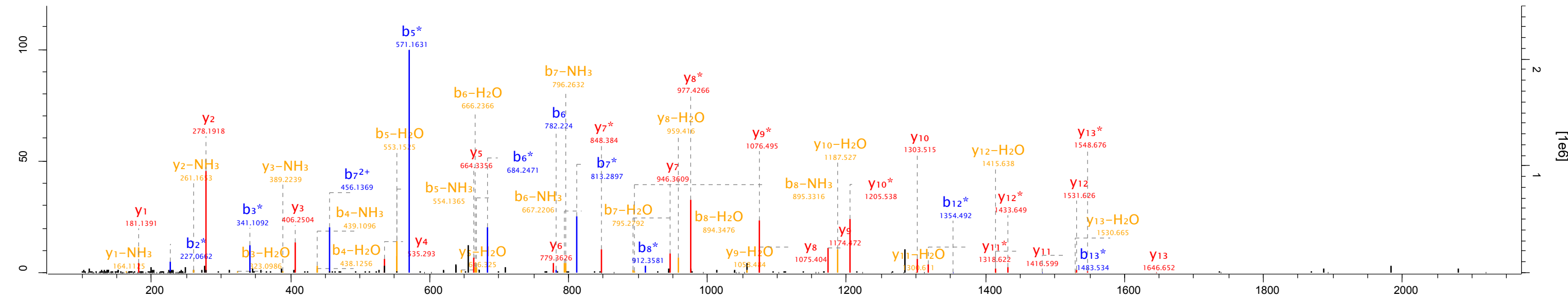
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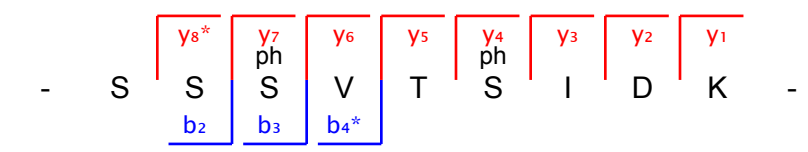
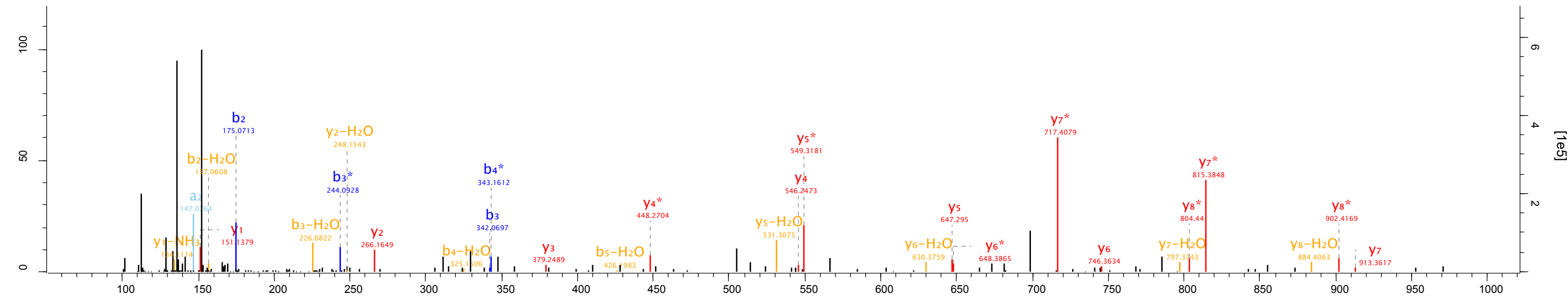
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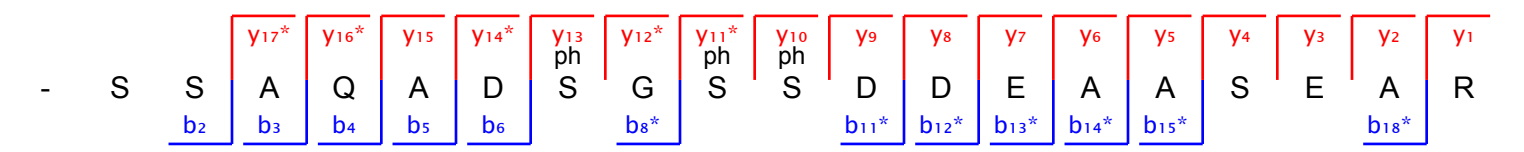
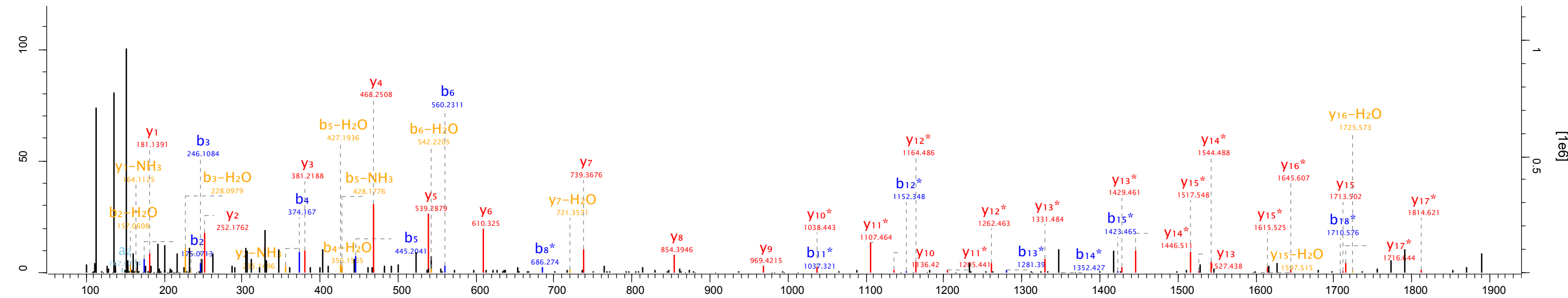
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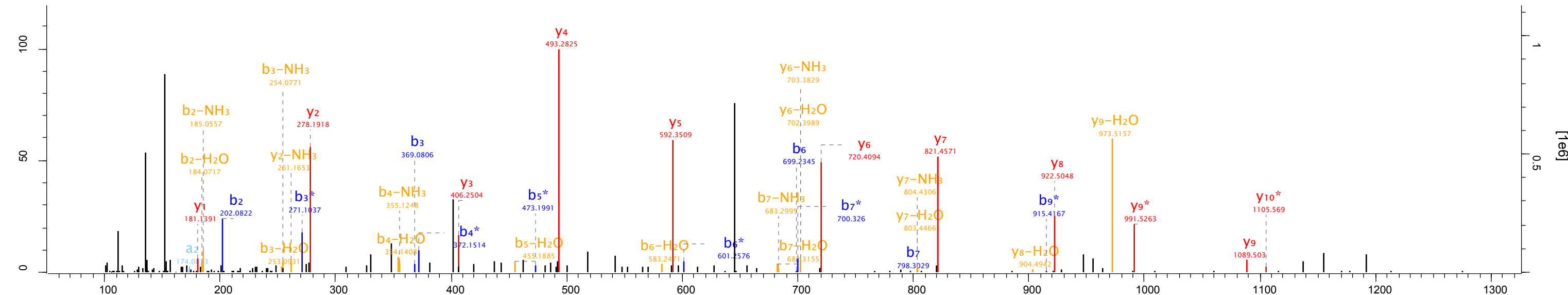


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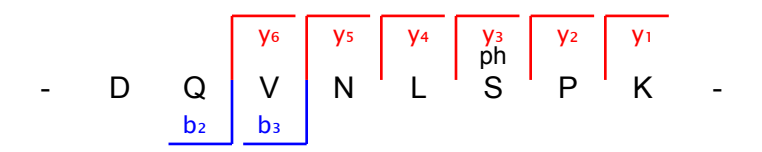
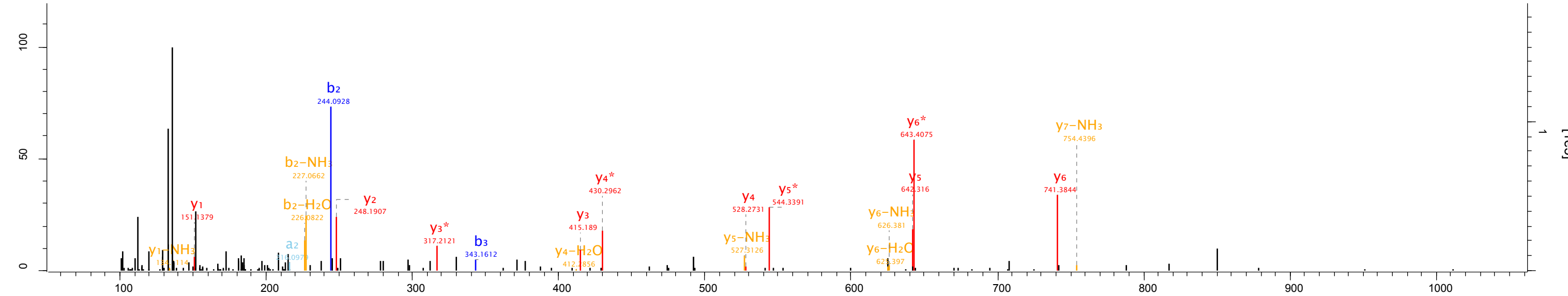


- S N S T T Q V S Q P R -

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y₁₀* y₉ ph y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

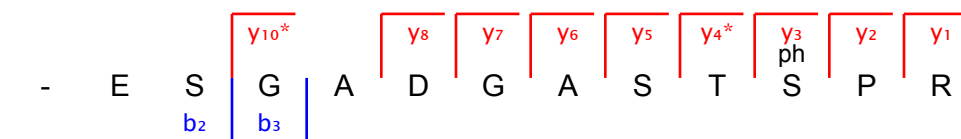
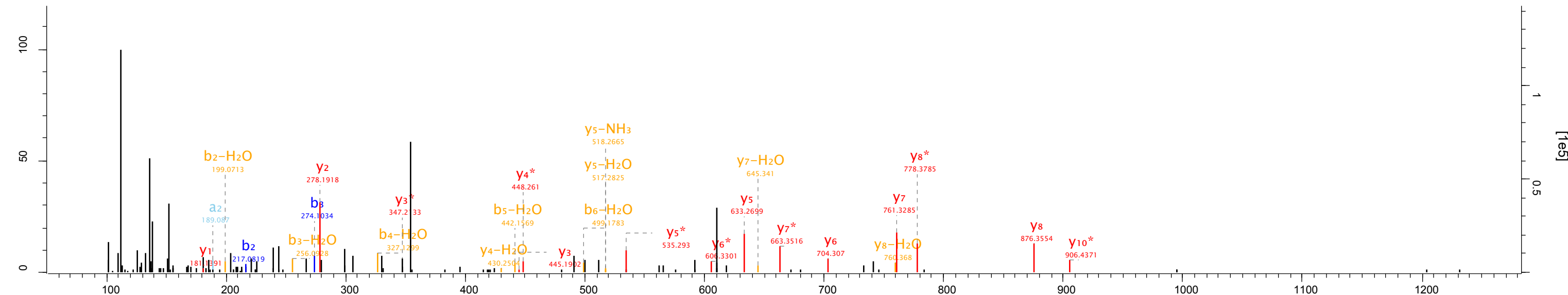
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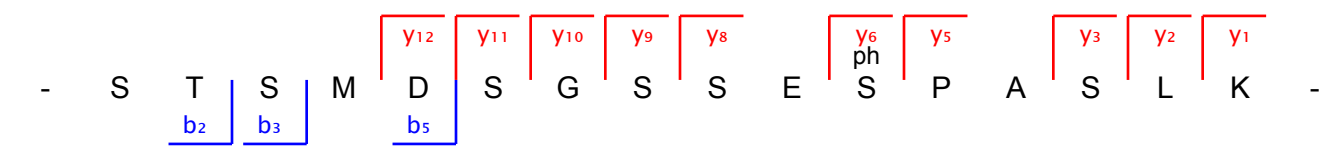
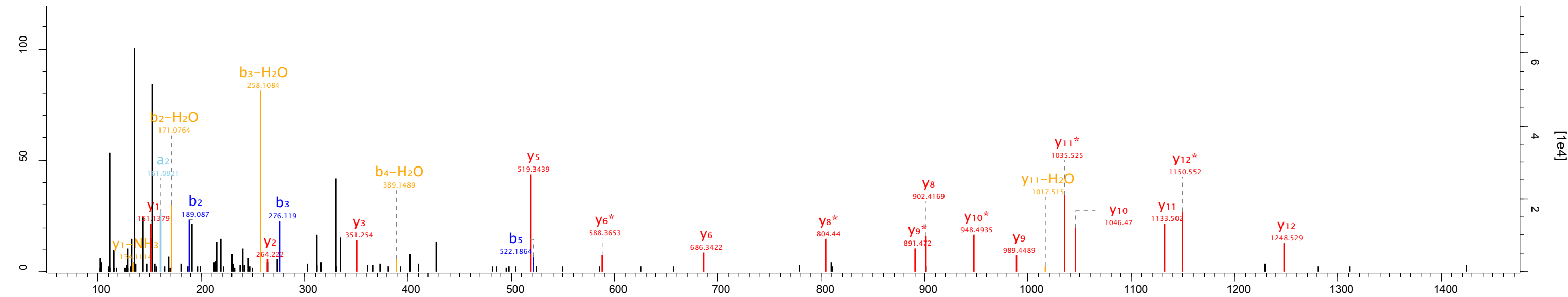
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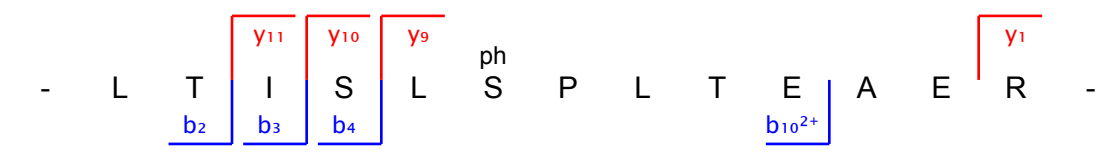
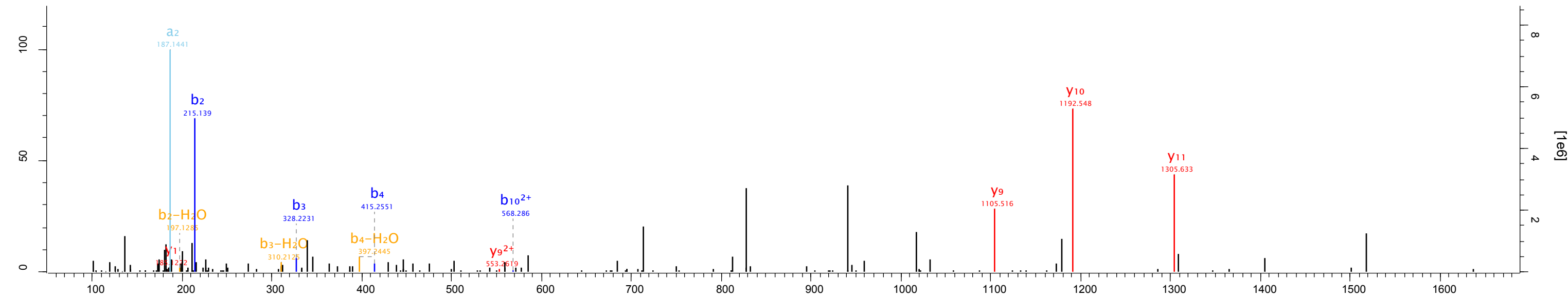
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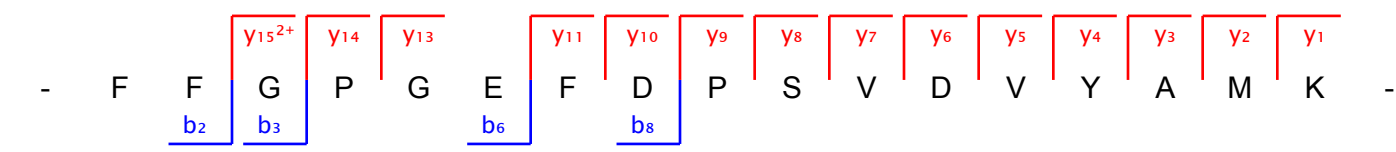
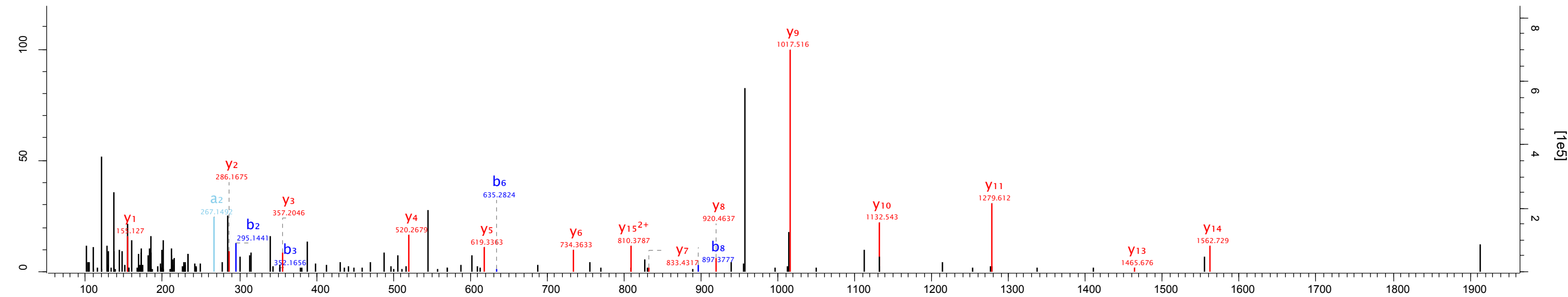
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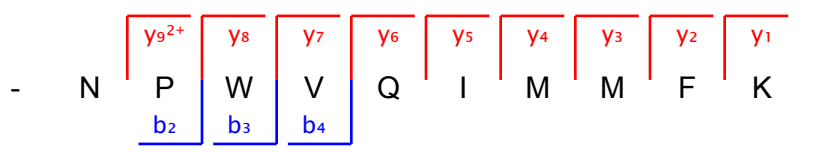
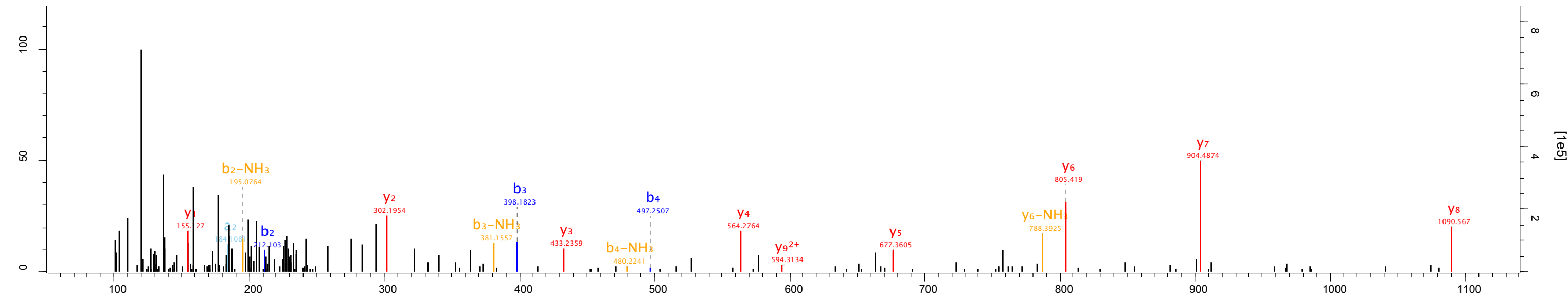
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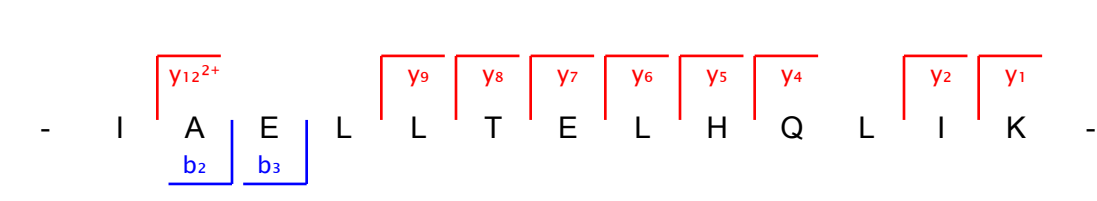
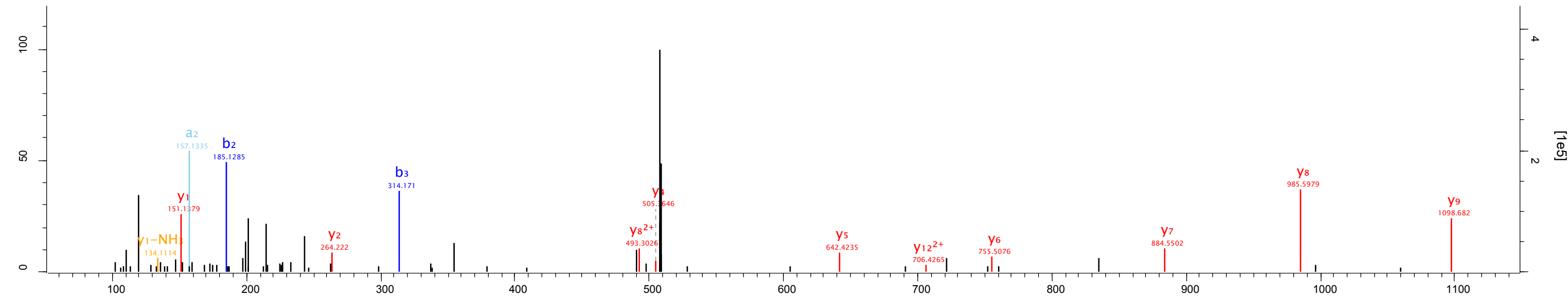
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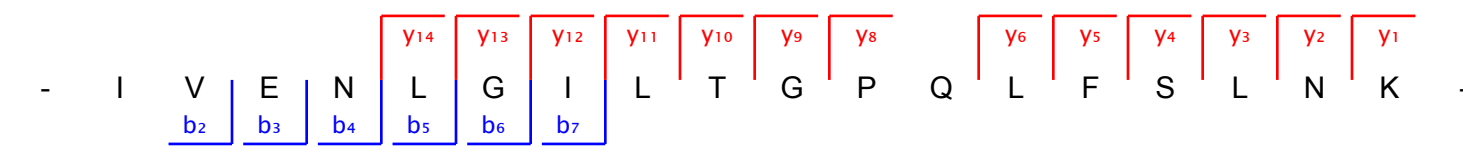
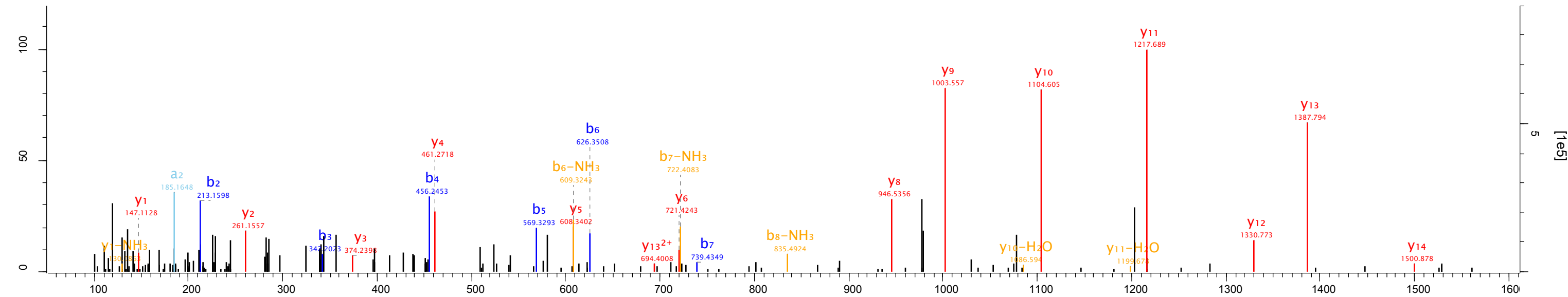
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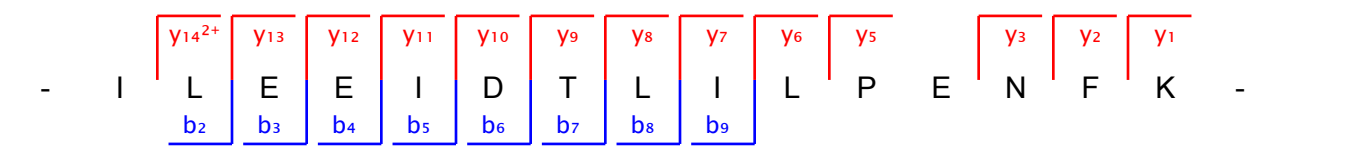
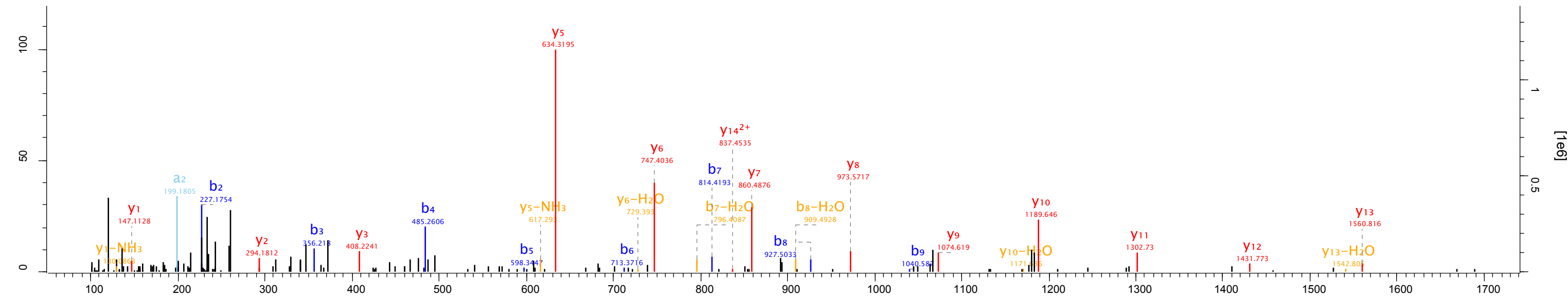
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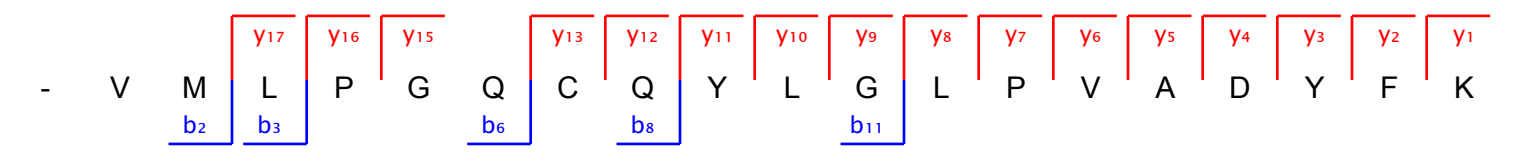
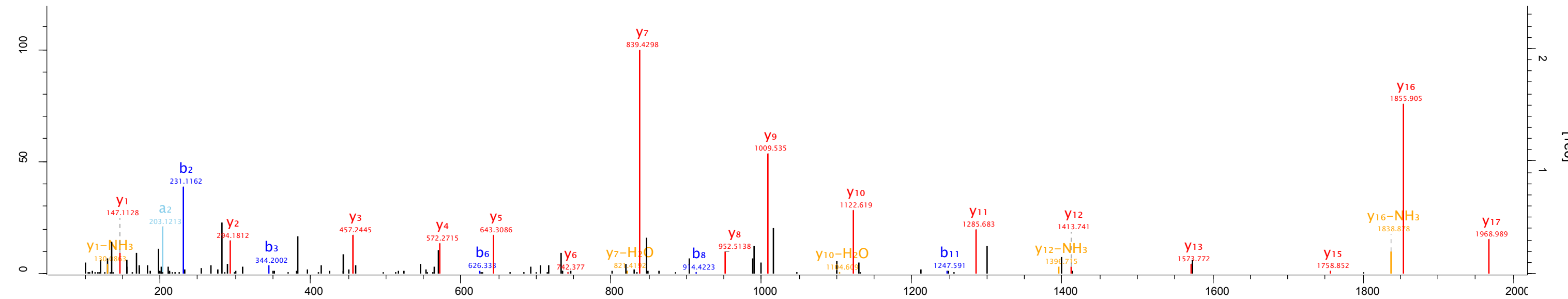
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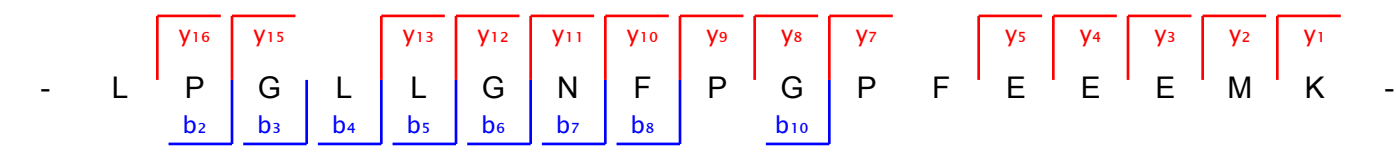
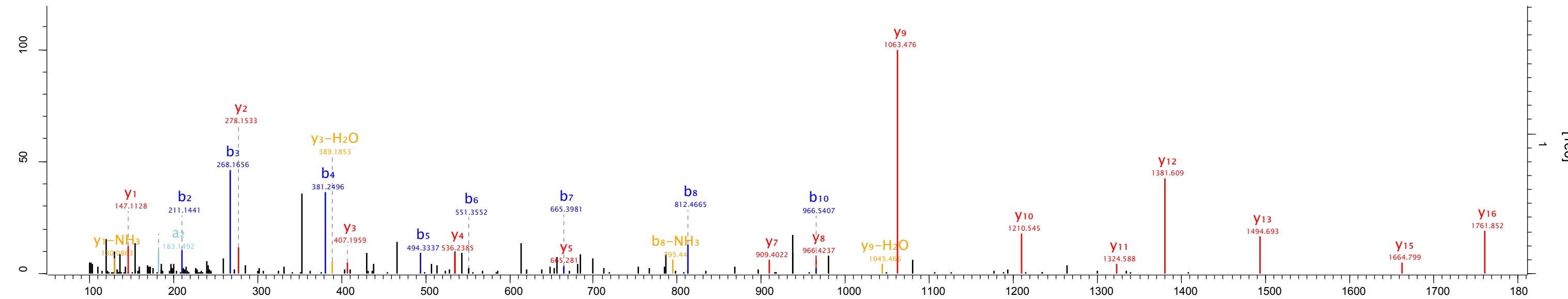
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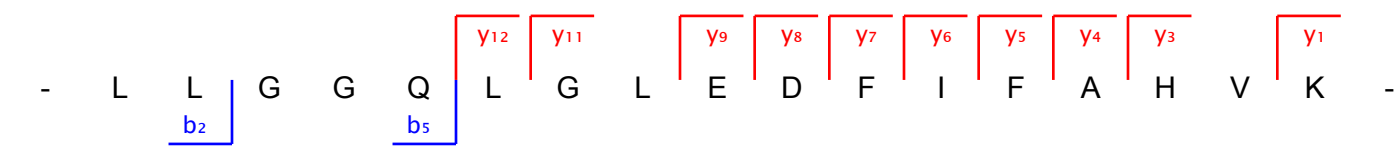
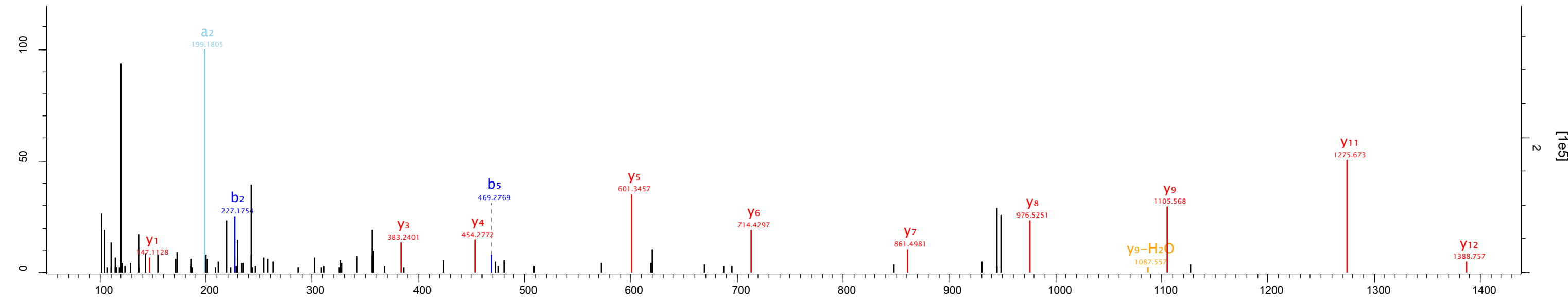
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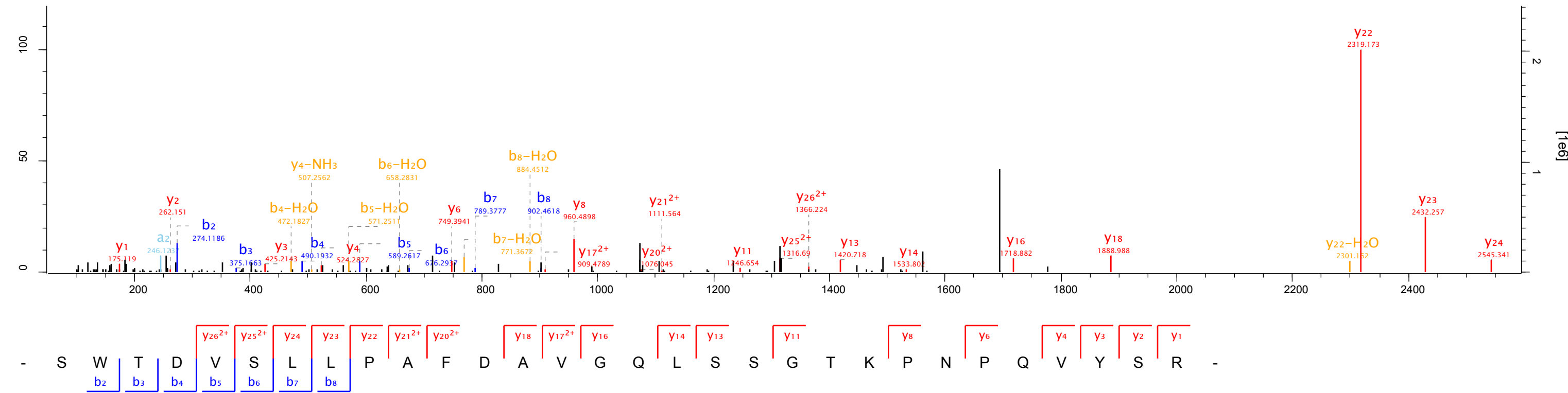
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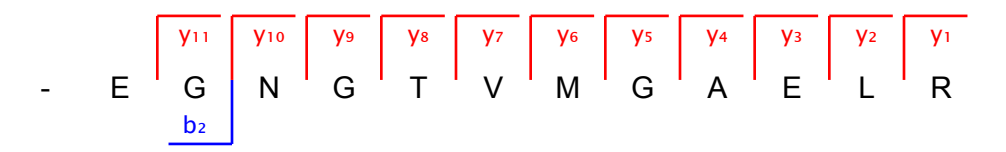
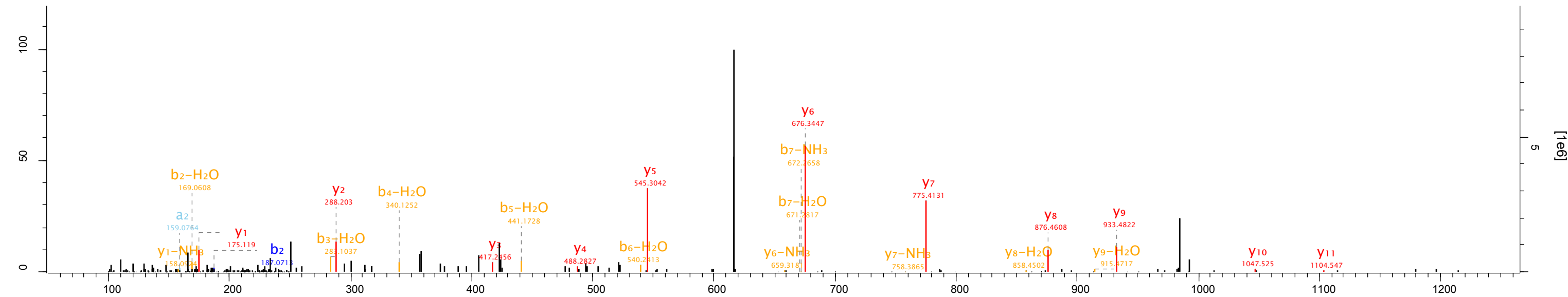
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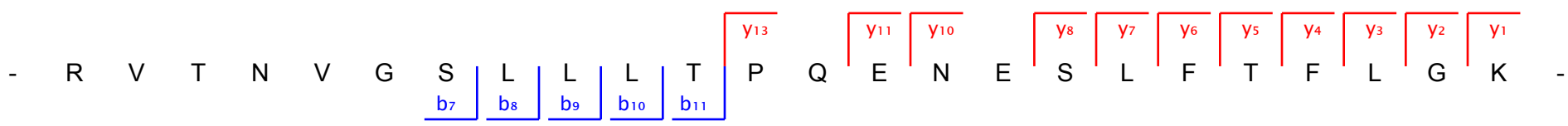
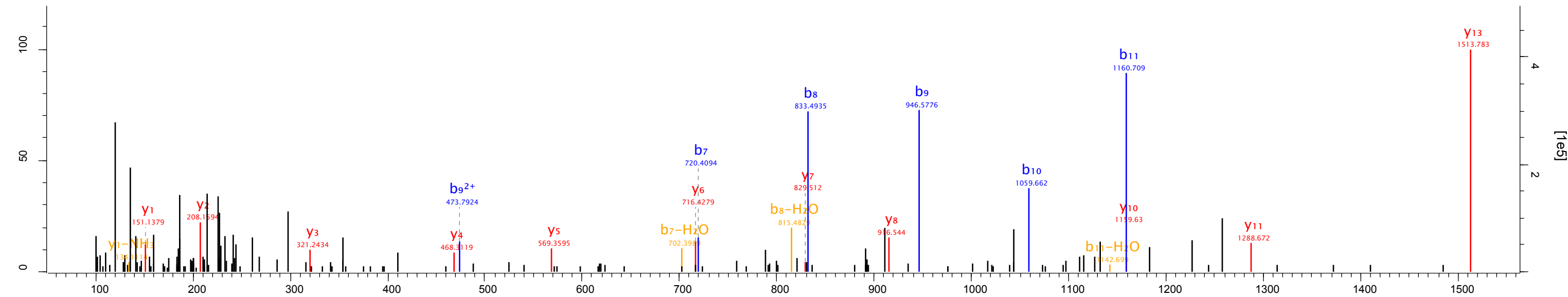
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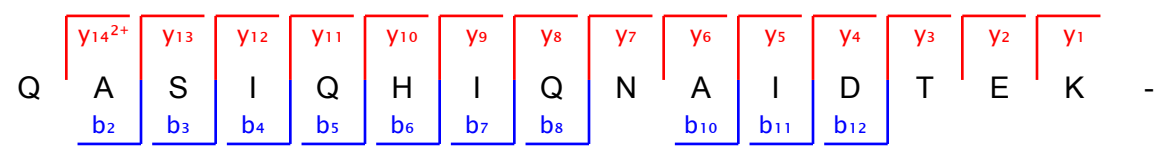
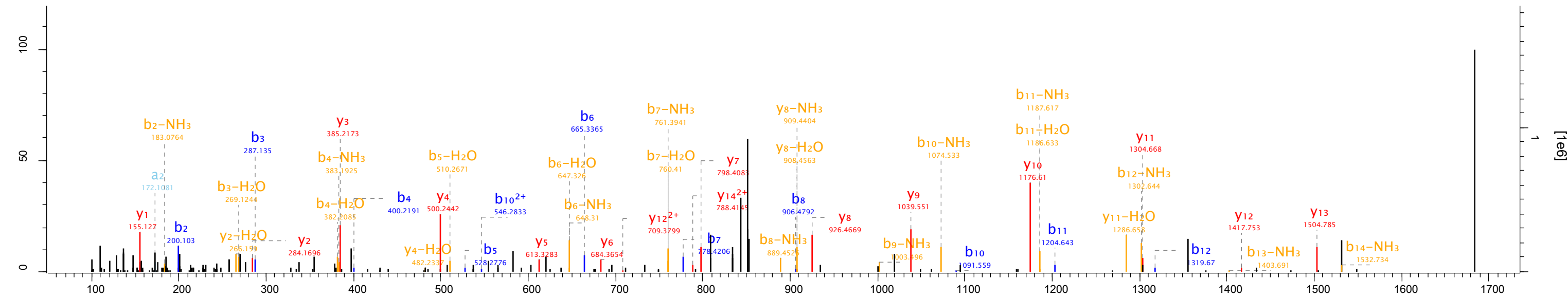
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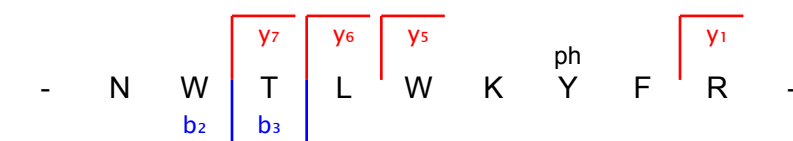
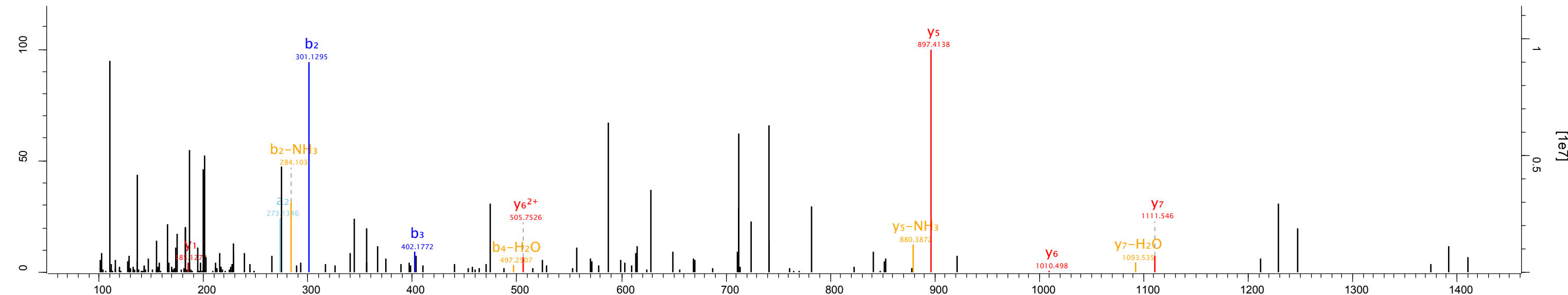
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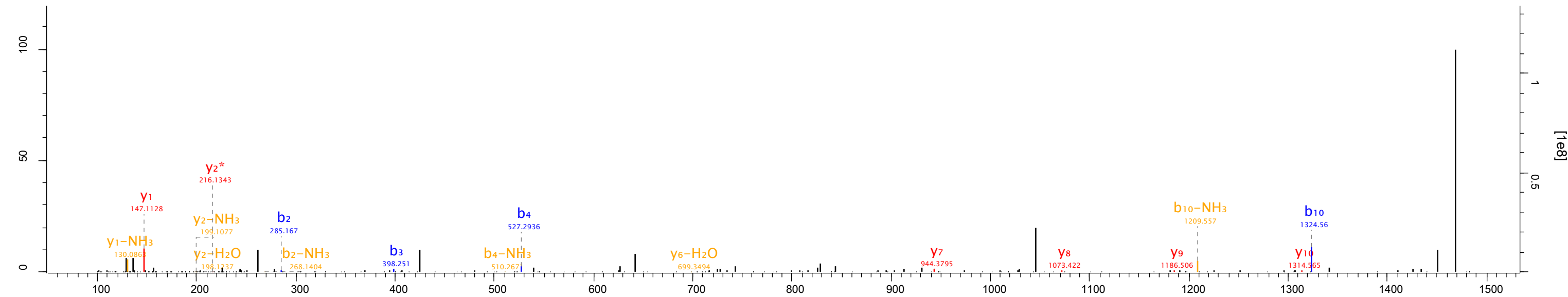
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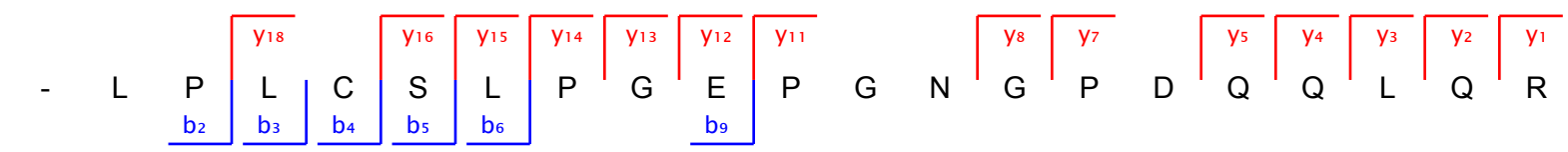
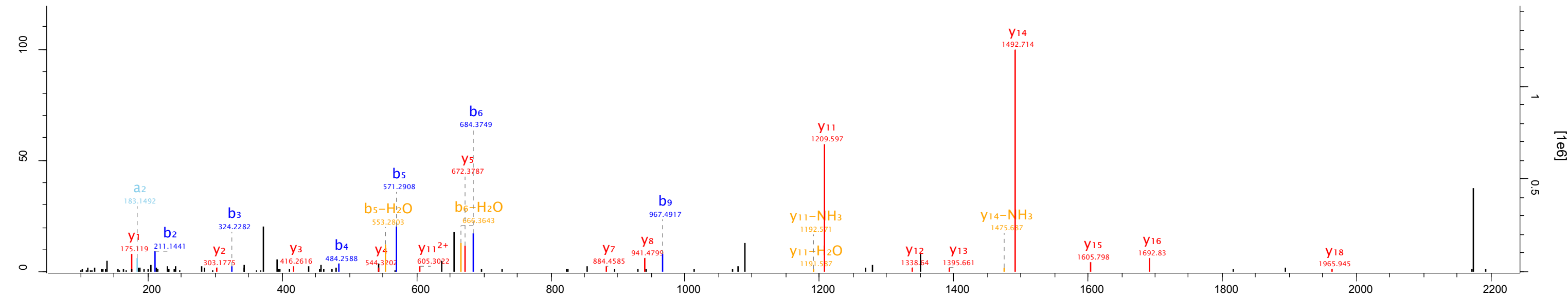


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Raw file
20171215_MaS_33SR_LMH_proteome_01

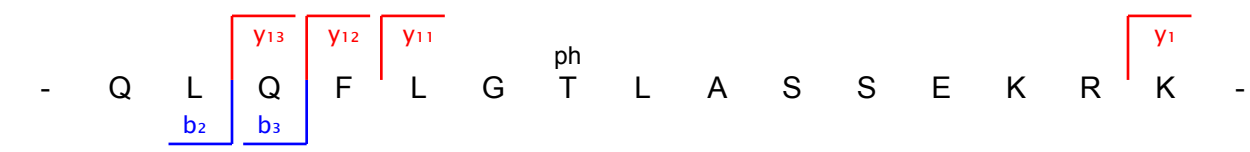
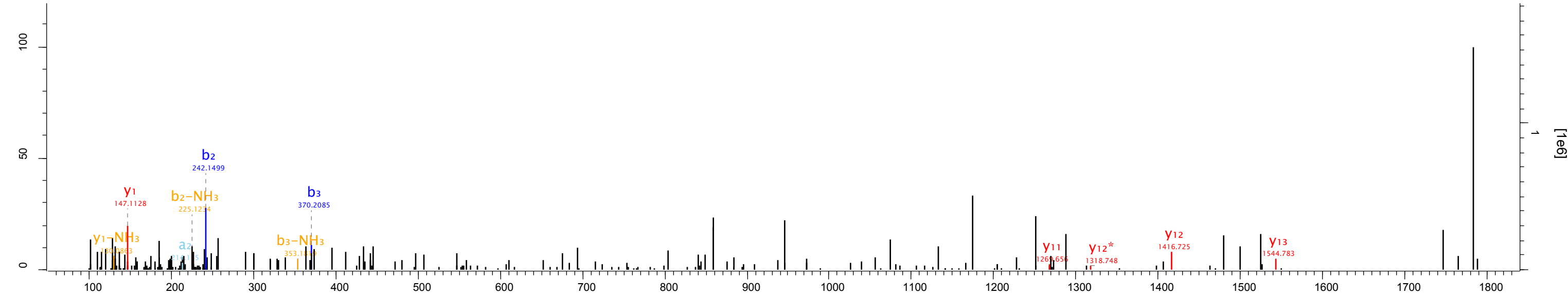
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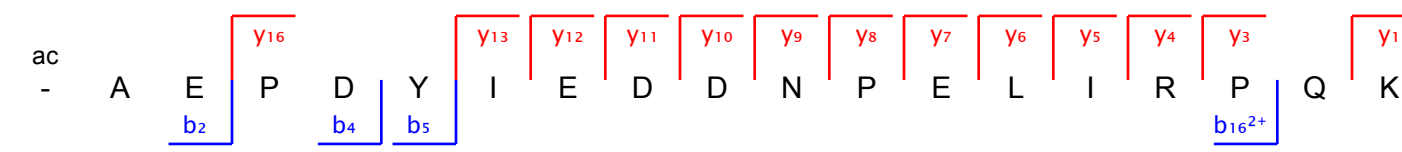
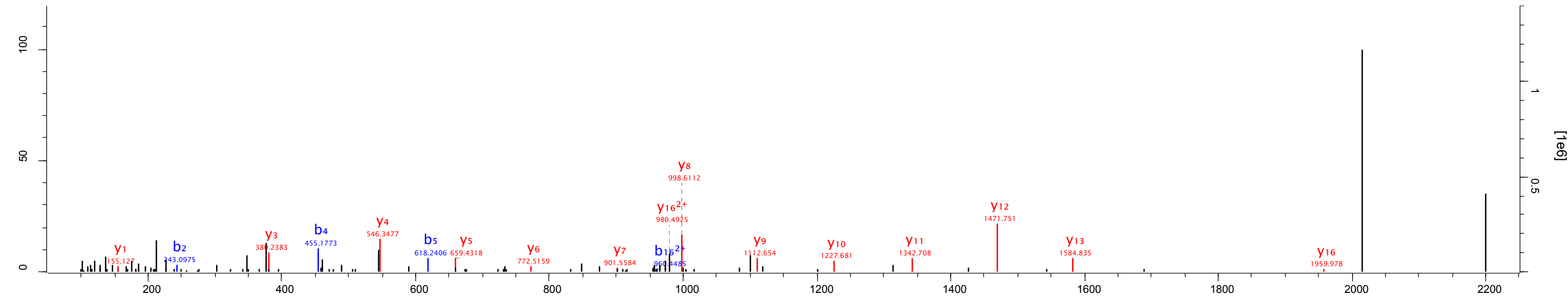
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20171215_MaS_33SR_LMH_proteome_01

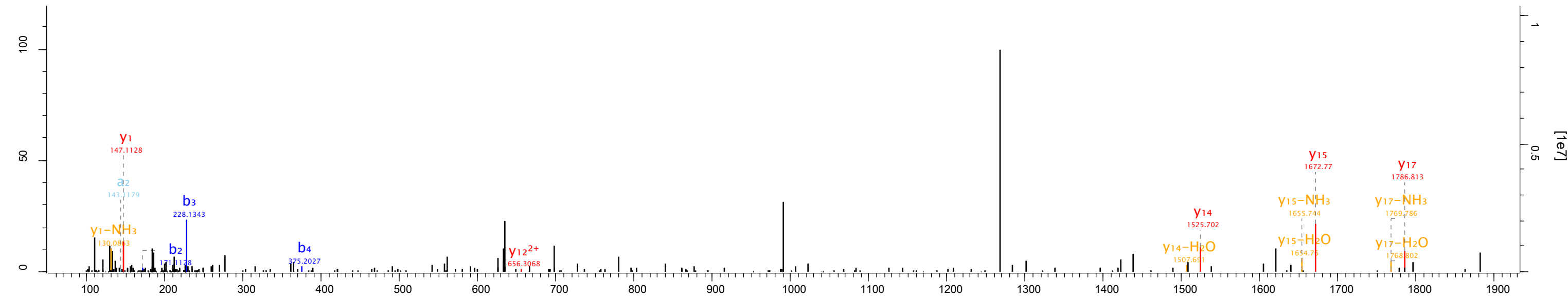
Scan	Method	Score	m/z	Gene names
62491	FTMS; HCD	48.47	893.47	FAM81B



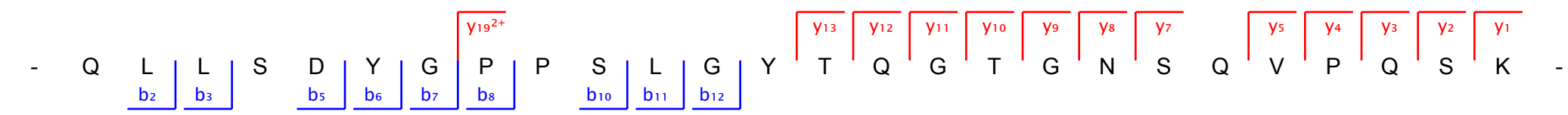
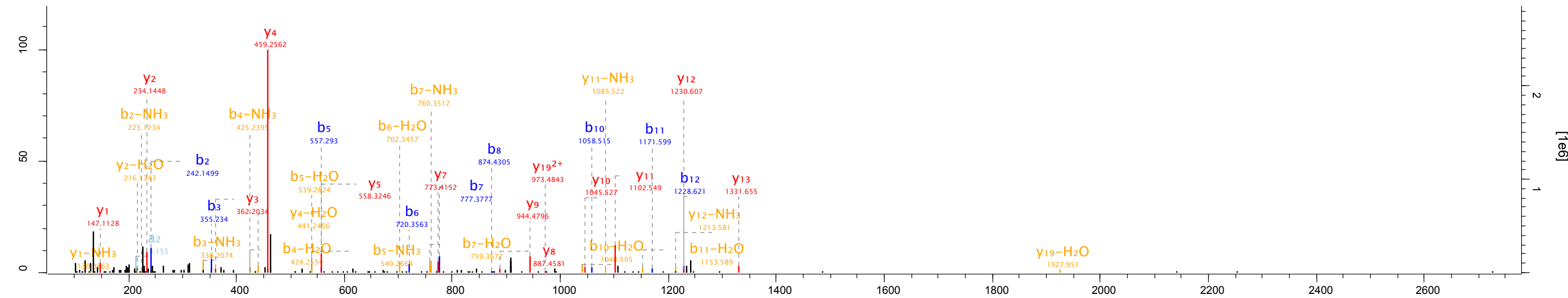
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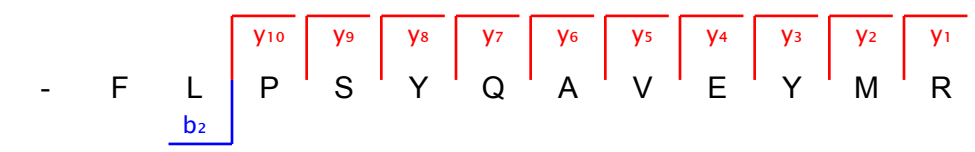
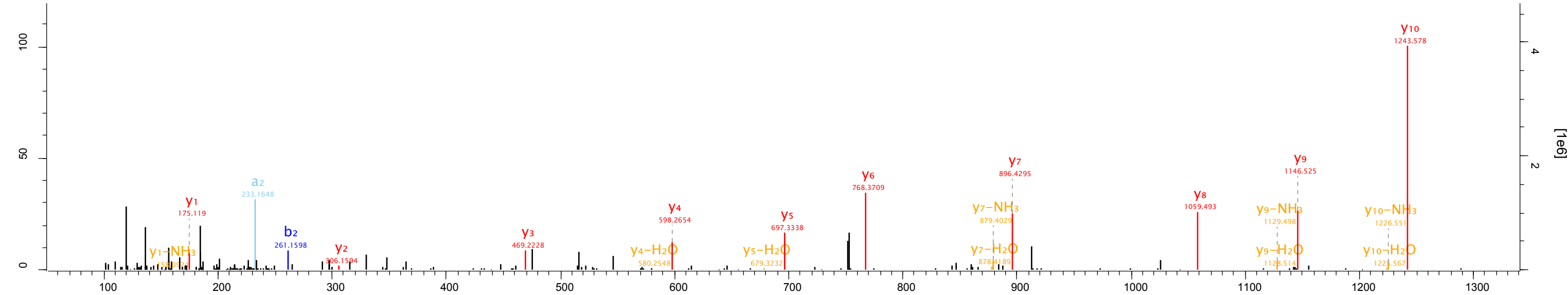
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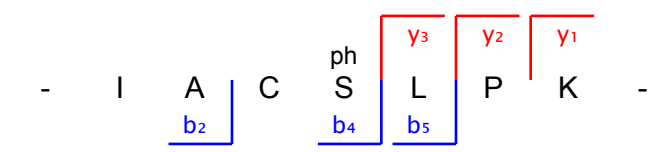
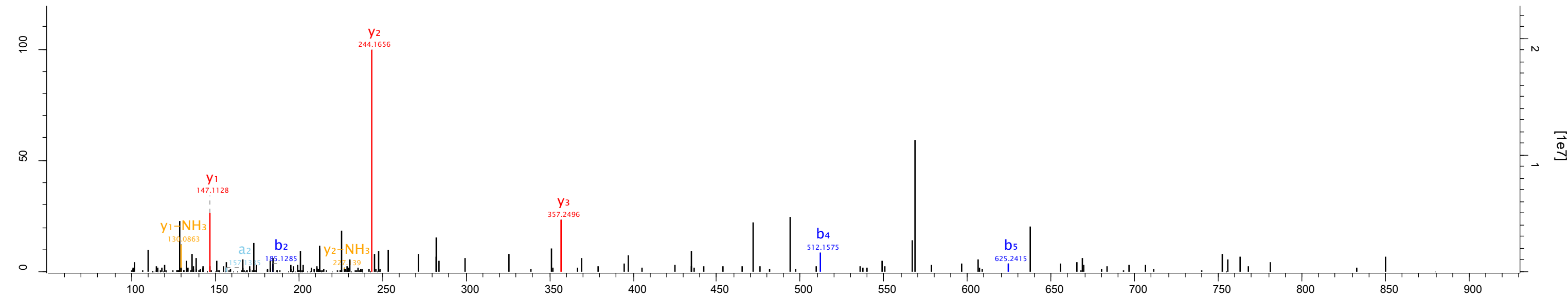
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 Scan: 71101 Method: FTMS; HCD Score: 113.23 m/z: 908.78 Gene names: CDK2AP1



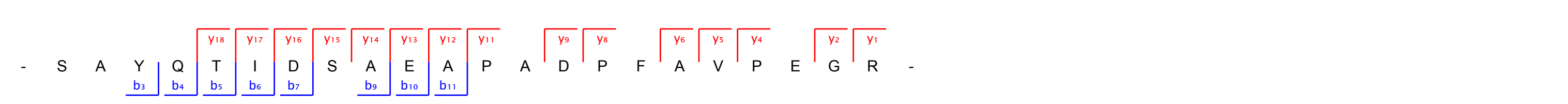
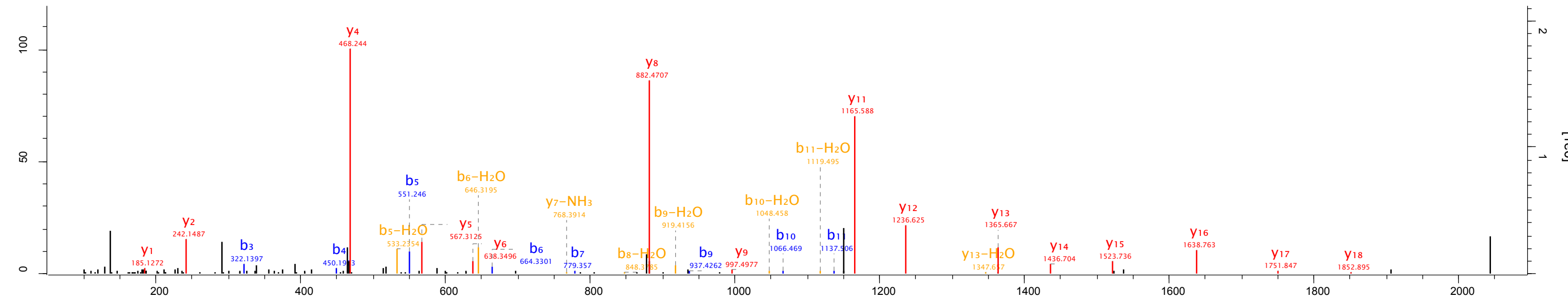
20171215_MaS_33SR_LMH_proteome_01 73121 FTMS; HCD 80.69 752.87 AGA



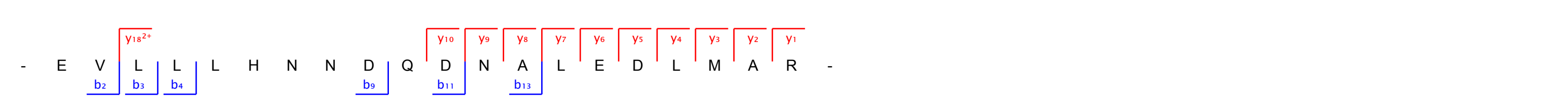
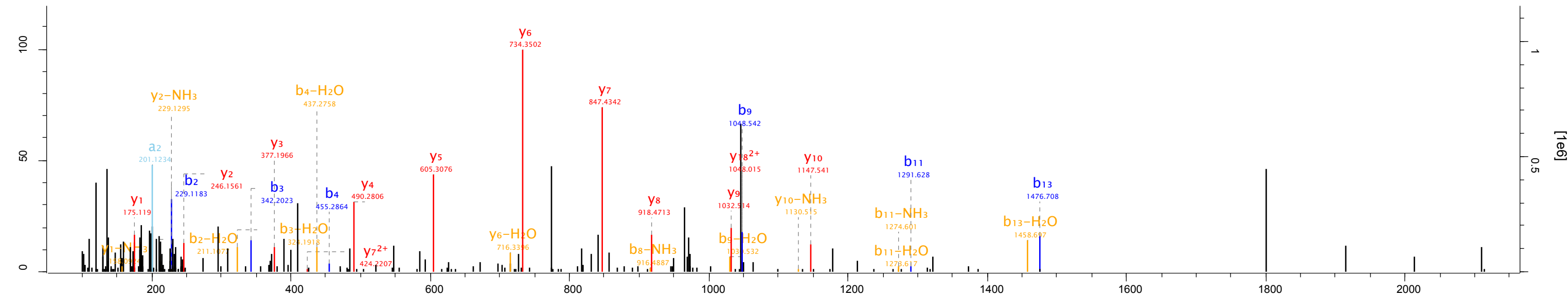
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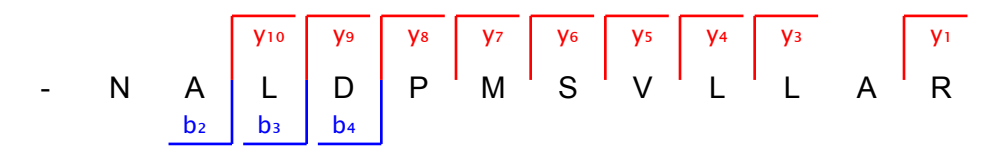
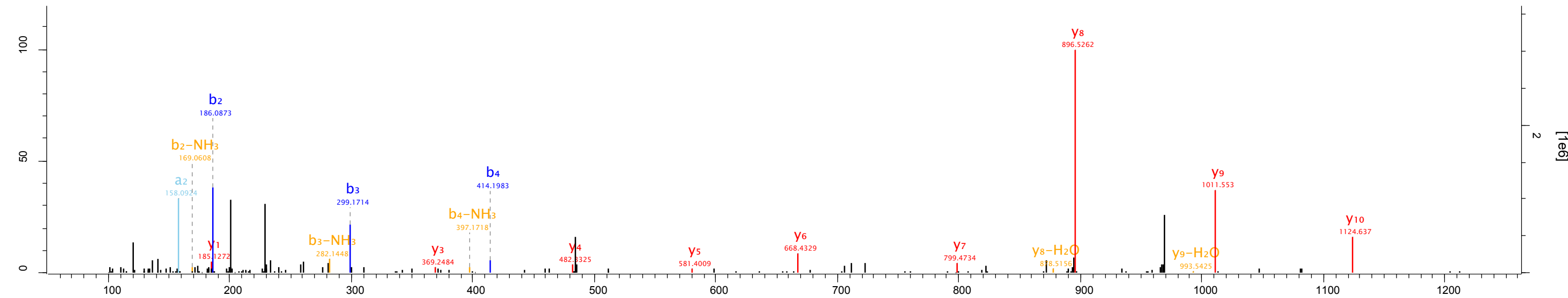
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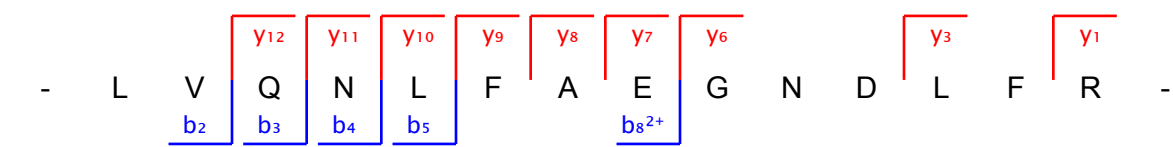
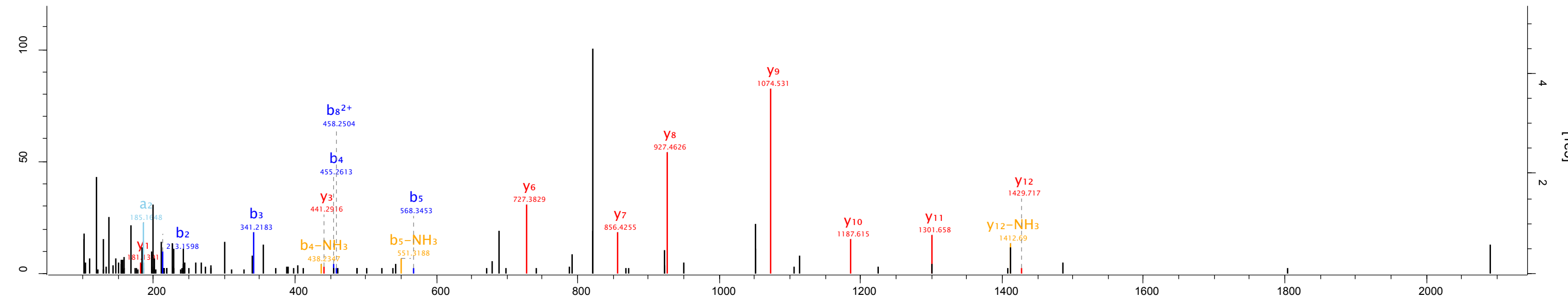
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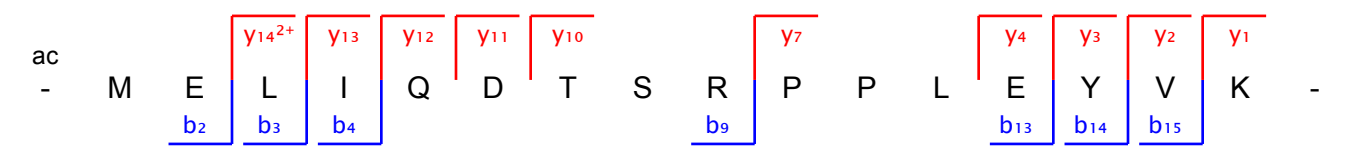
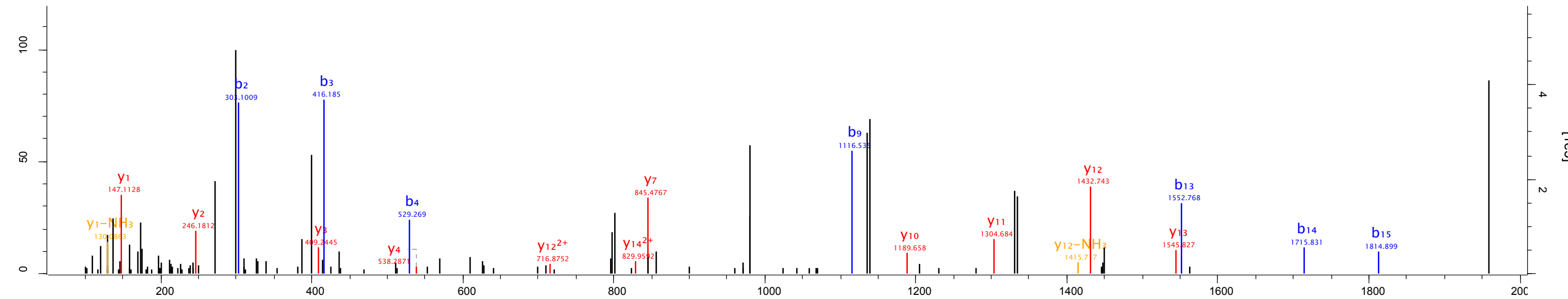
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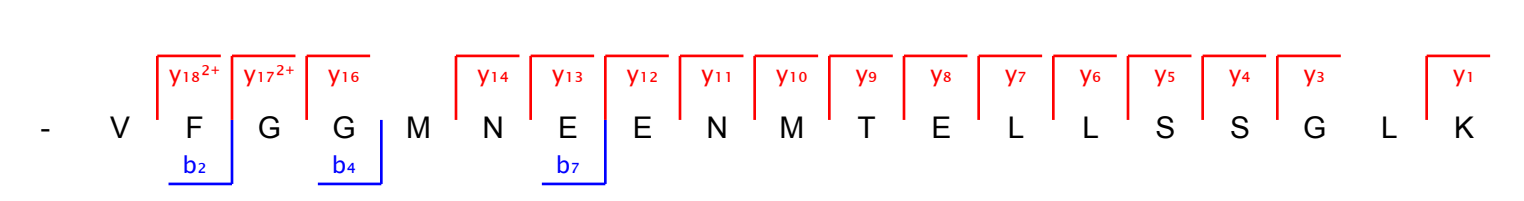
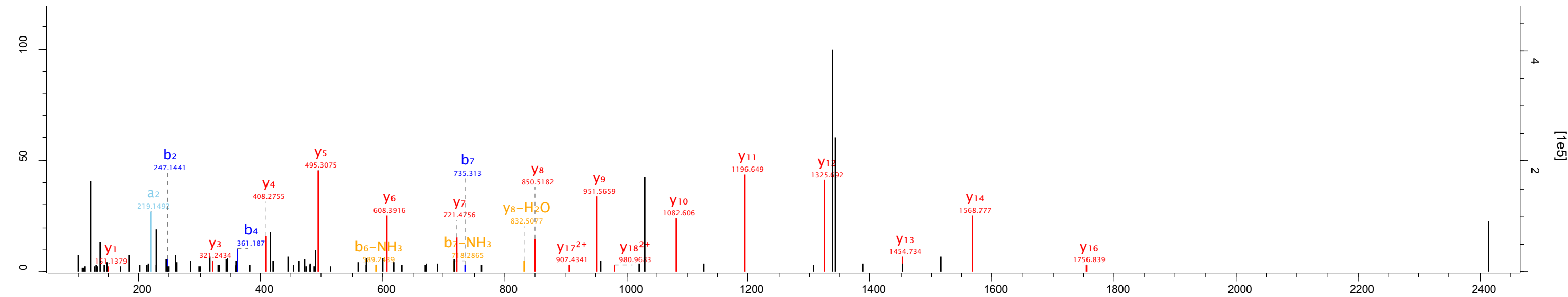
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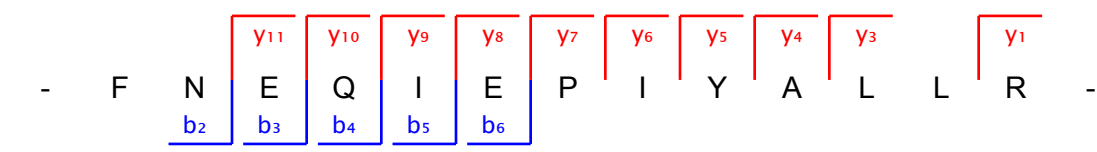
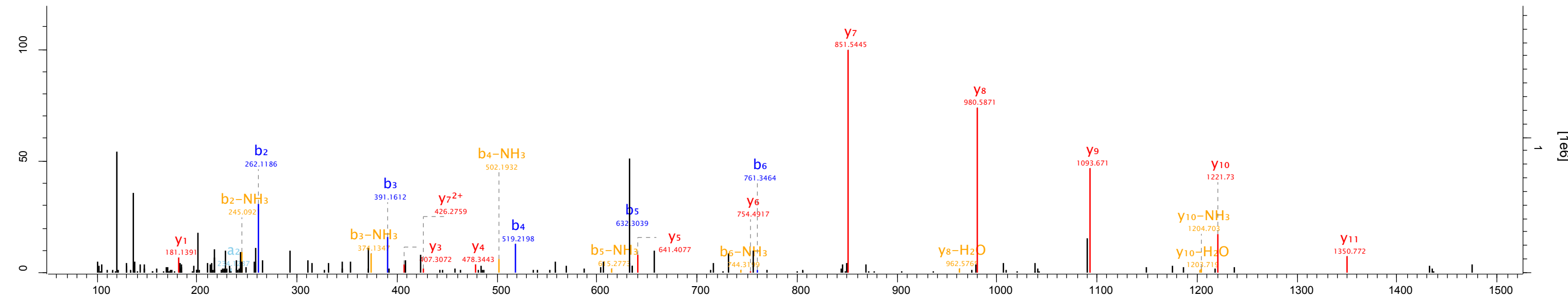
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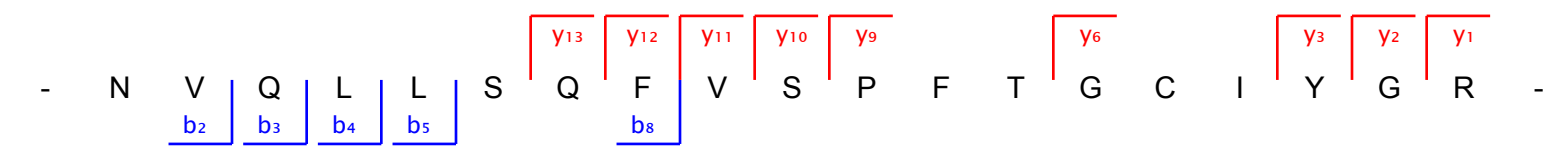
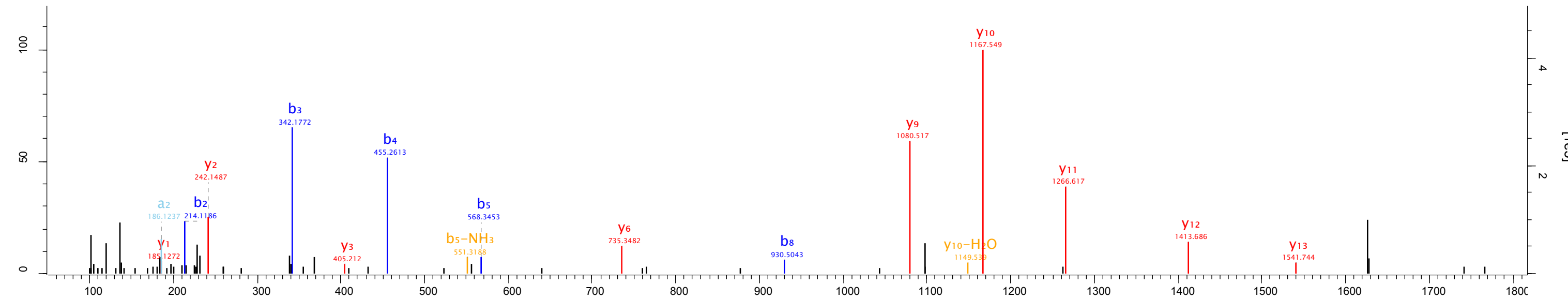
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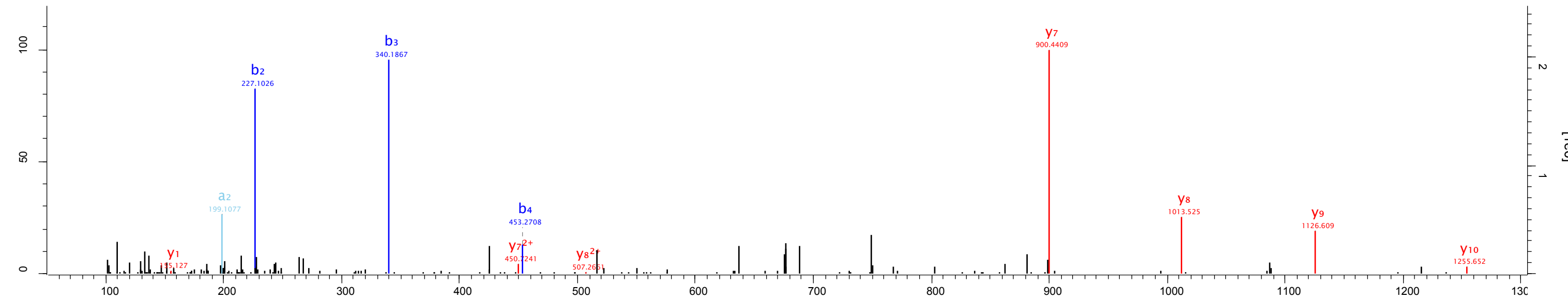
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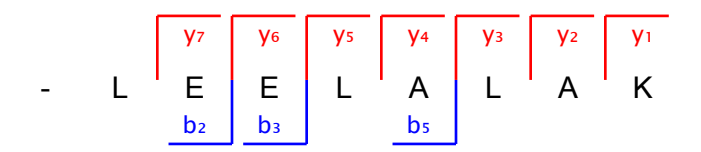
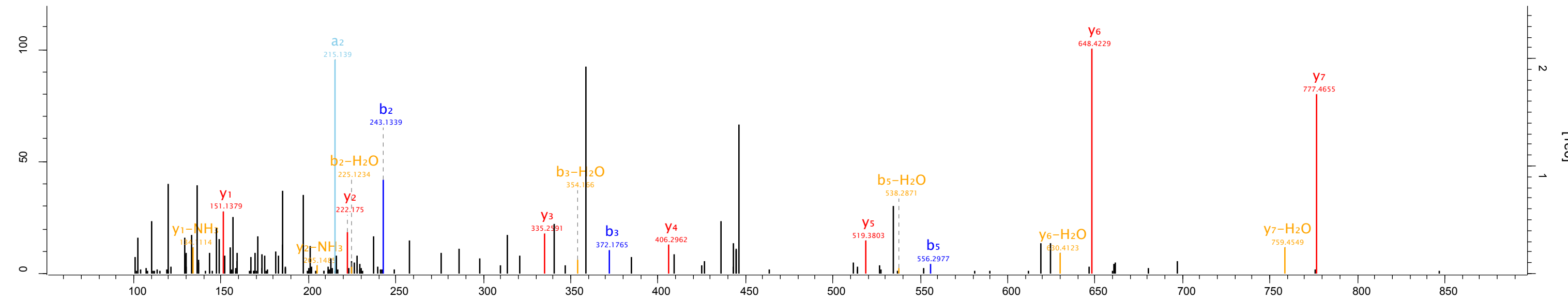
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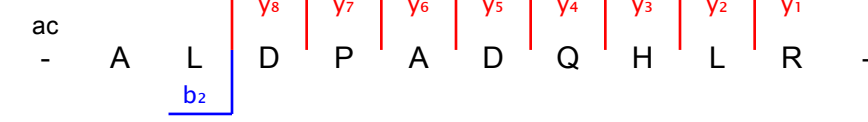
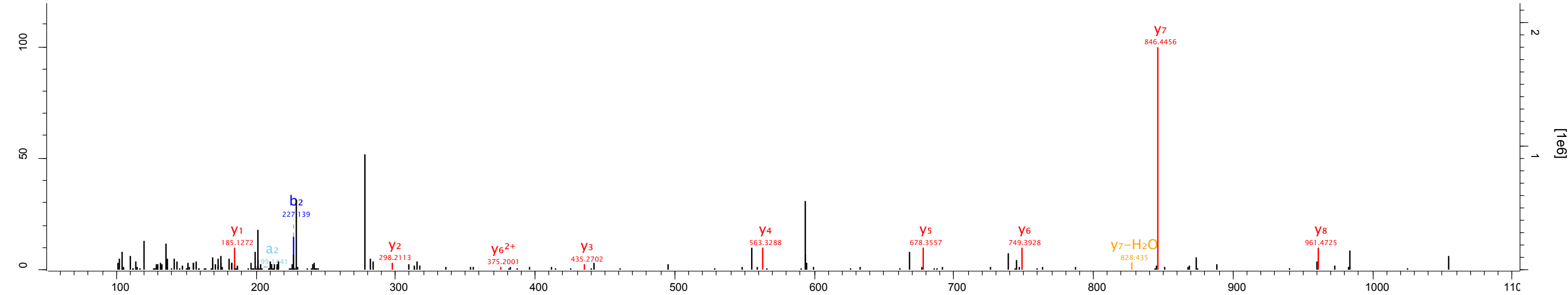
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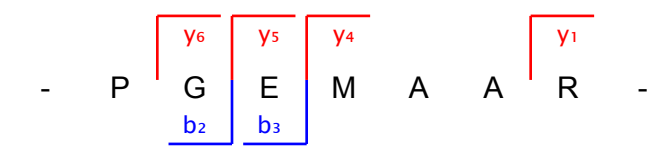
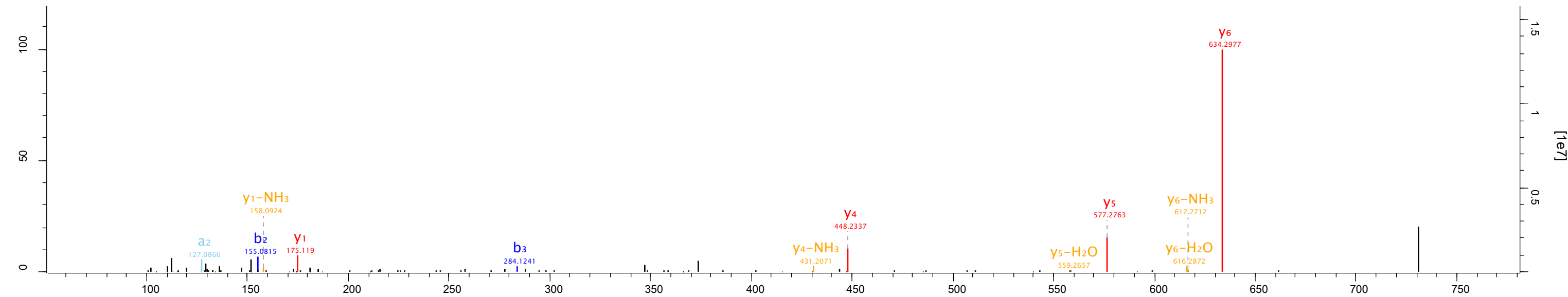
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20171215_MaS_33SR_LMH_proteome_02

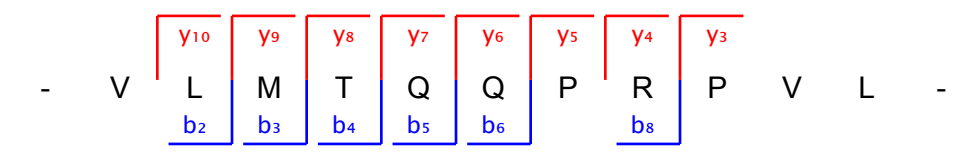
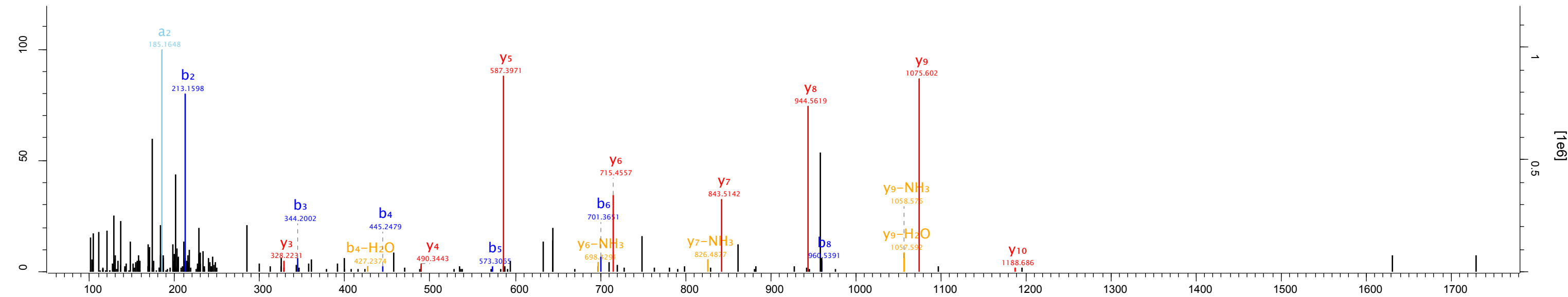
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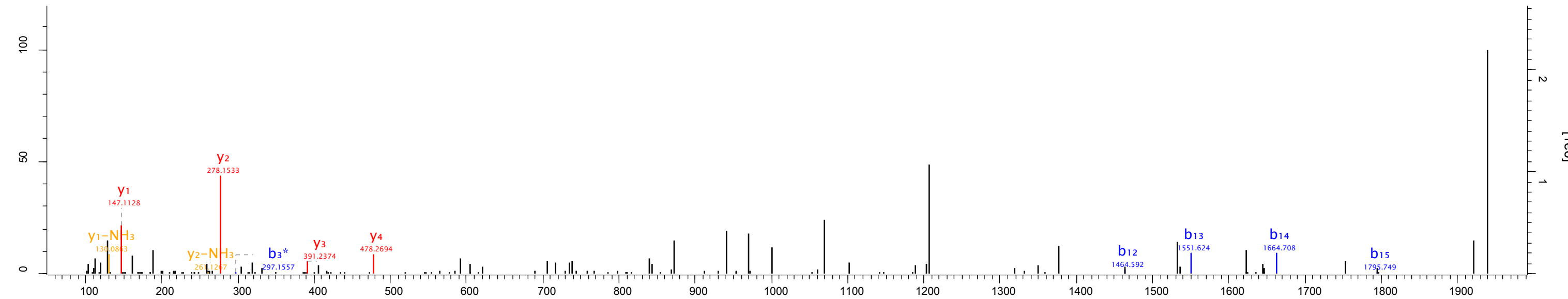
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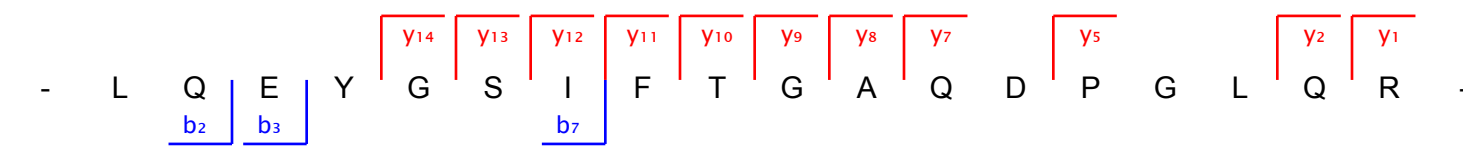
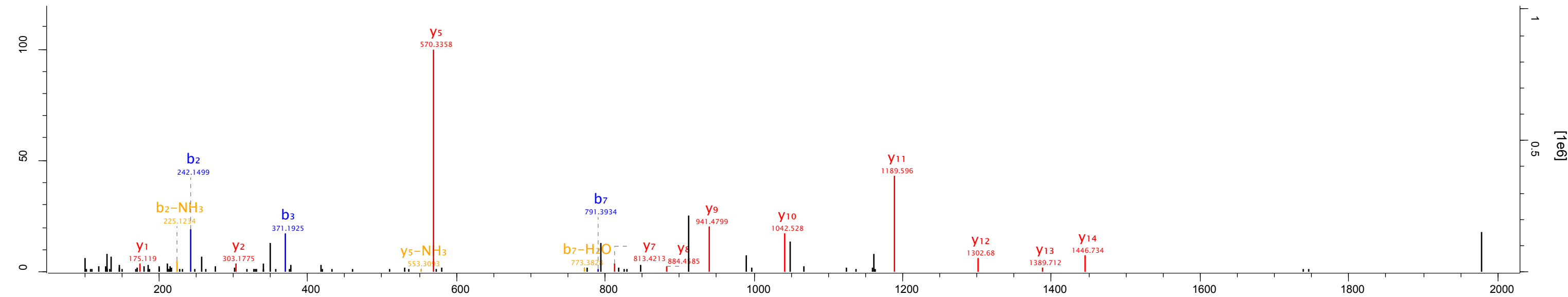
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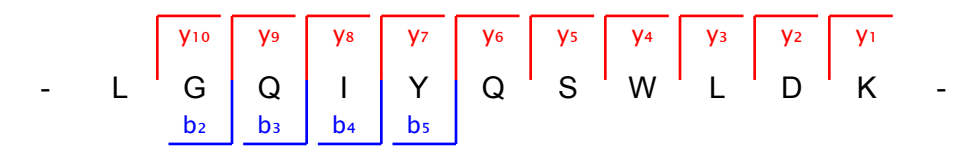
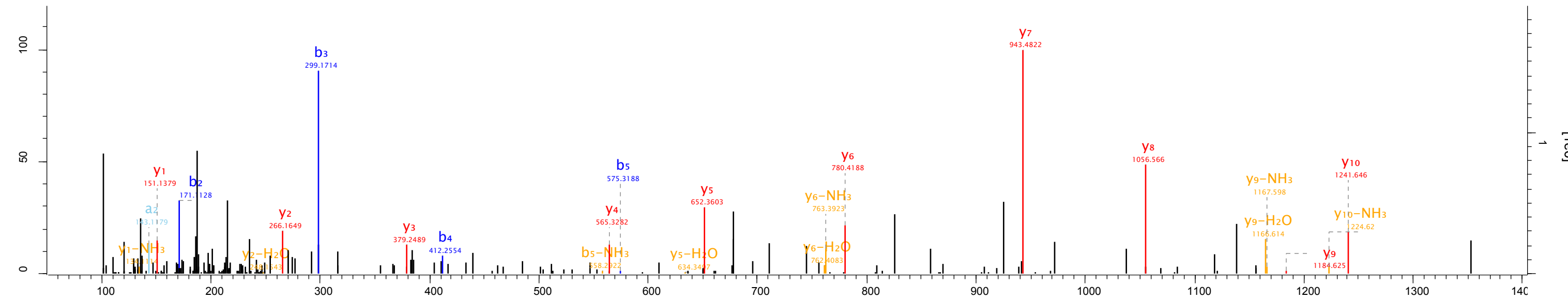
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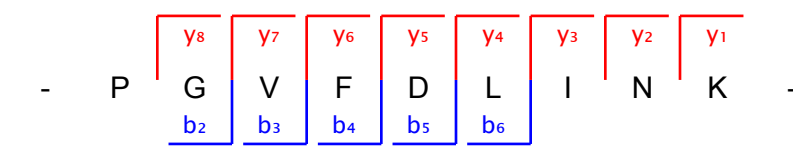
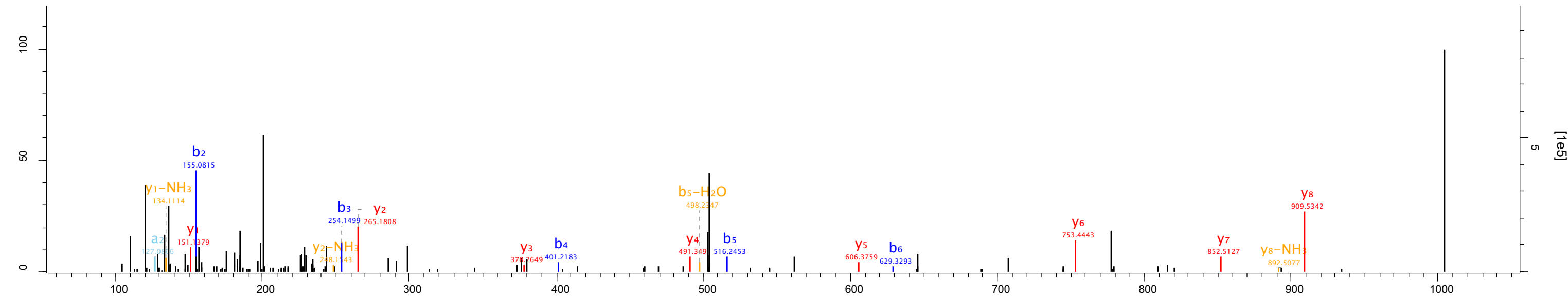
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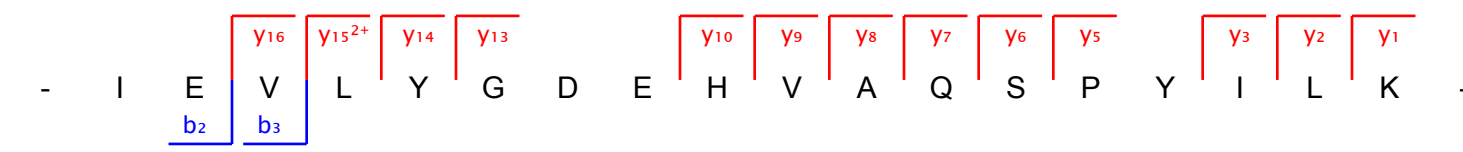
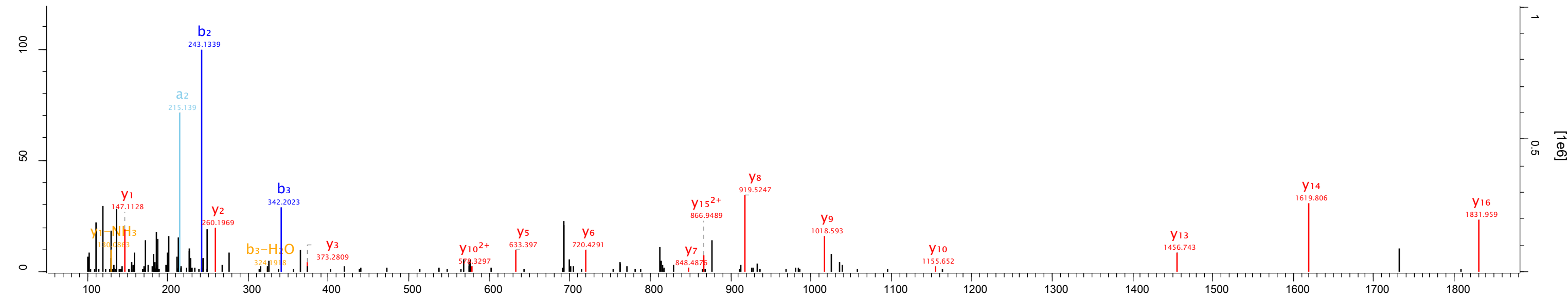
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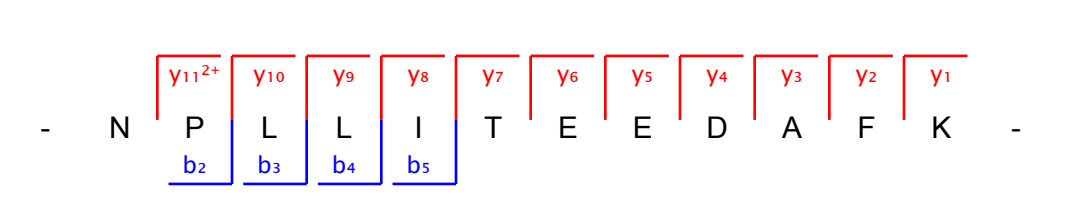
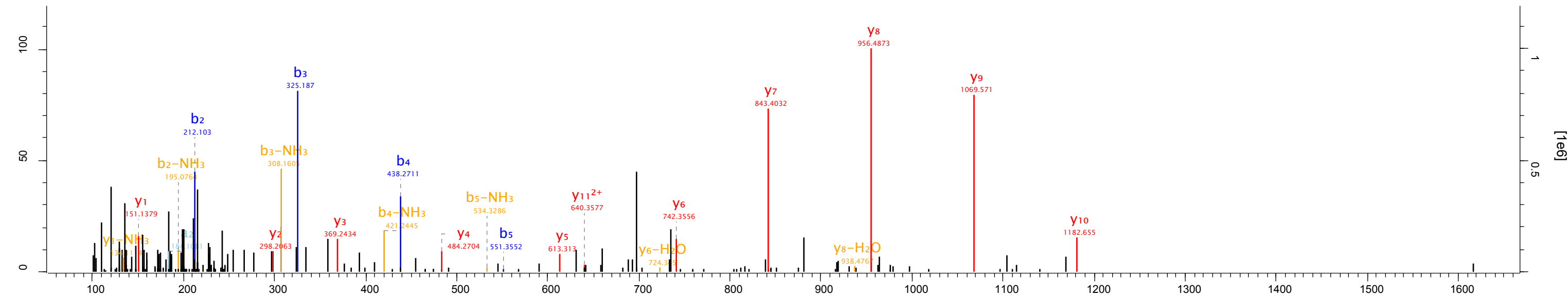
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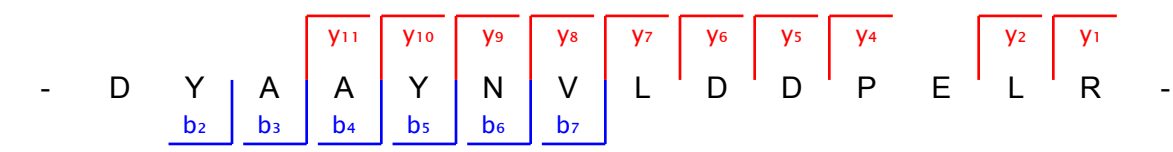
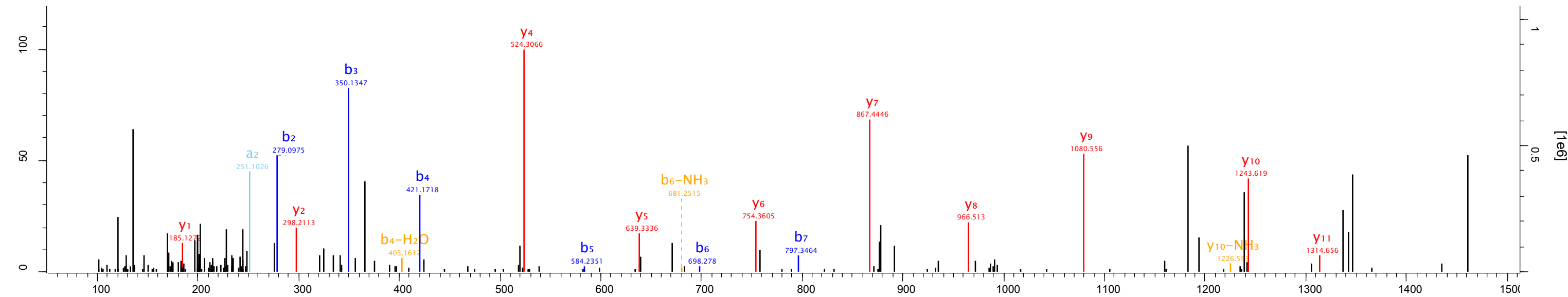
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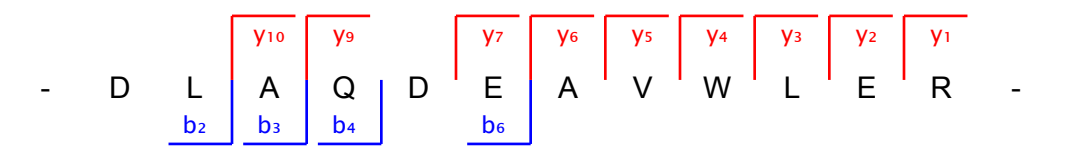
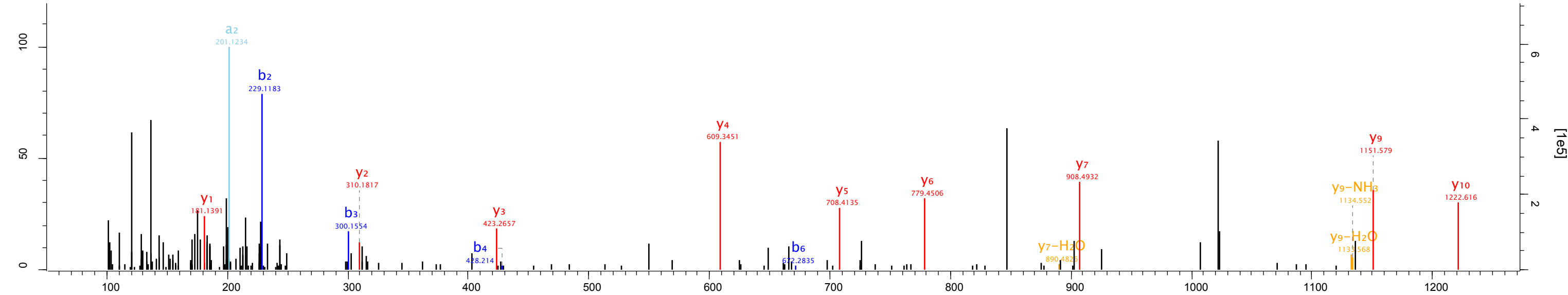
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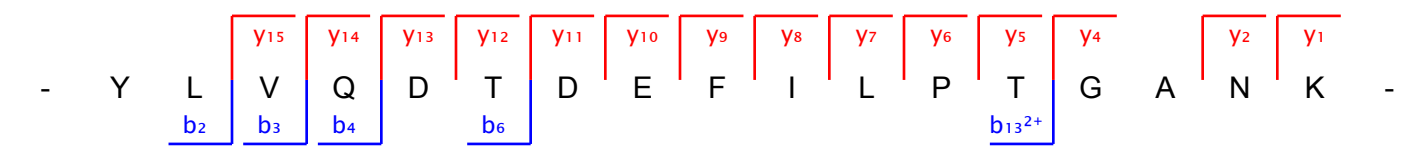
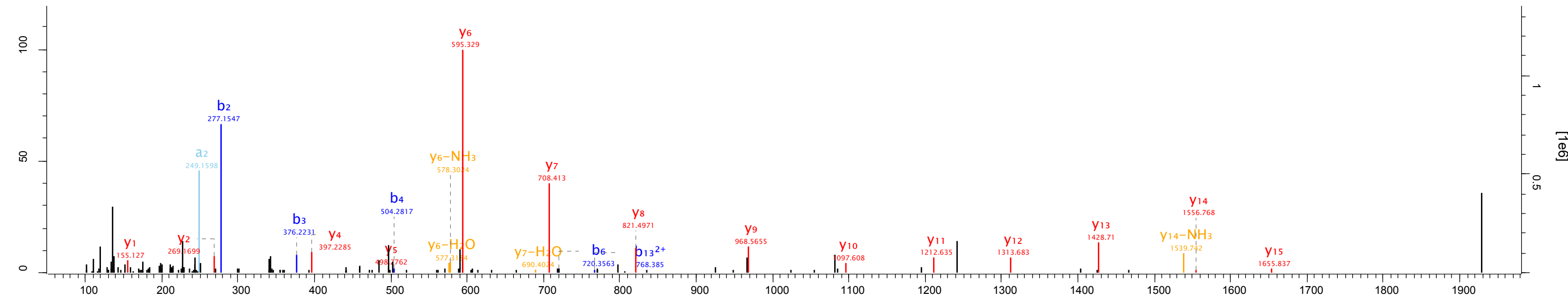
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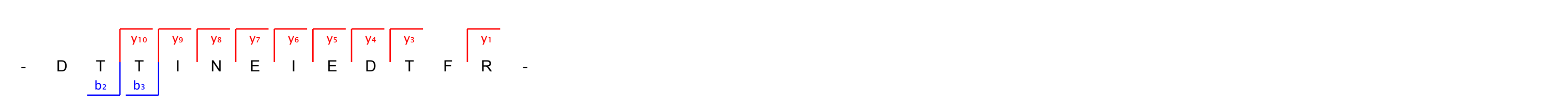
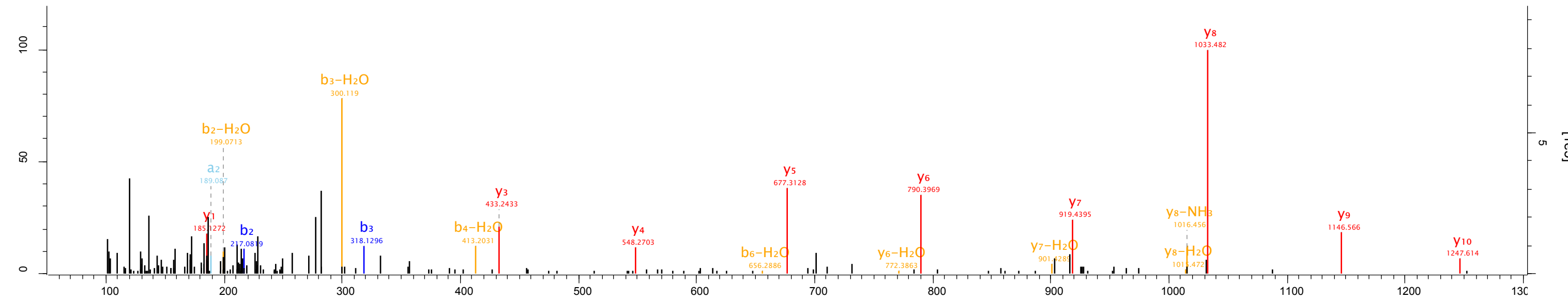
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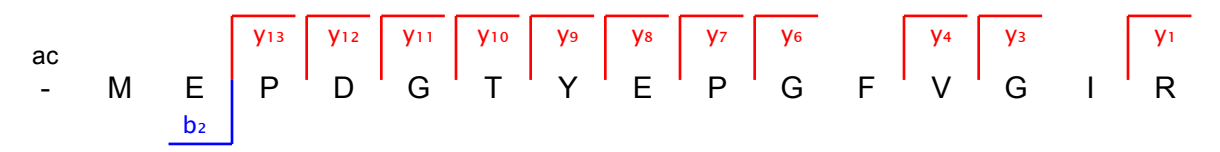
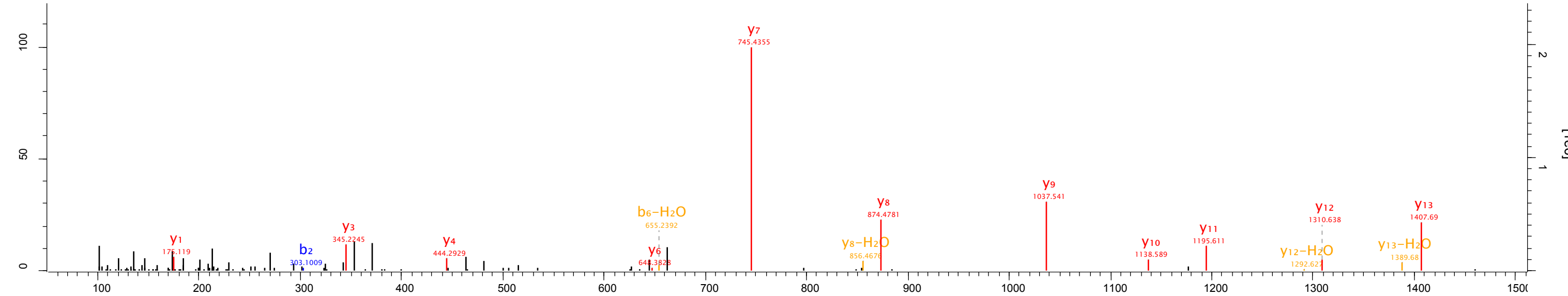
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Raw file

20171215_MaS_33SR_LMH_proteome_02

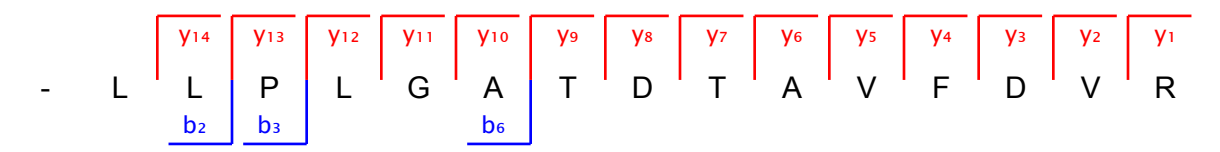
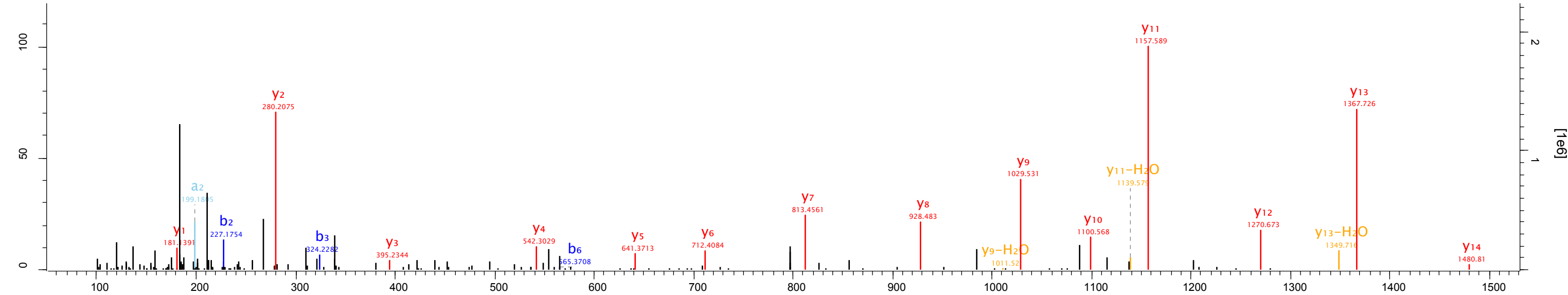
Scan 92841 Method FTMS; HCD Score 58.89 m/z 855.89 Gene names POLR21



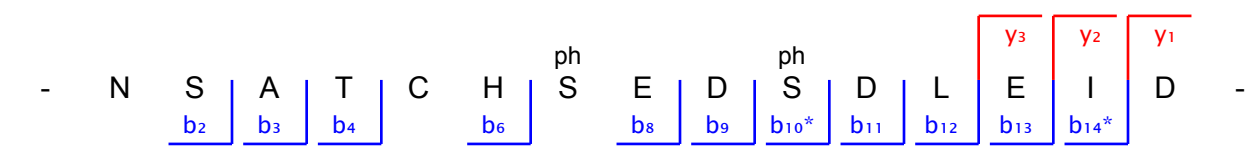
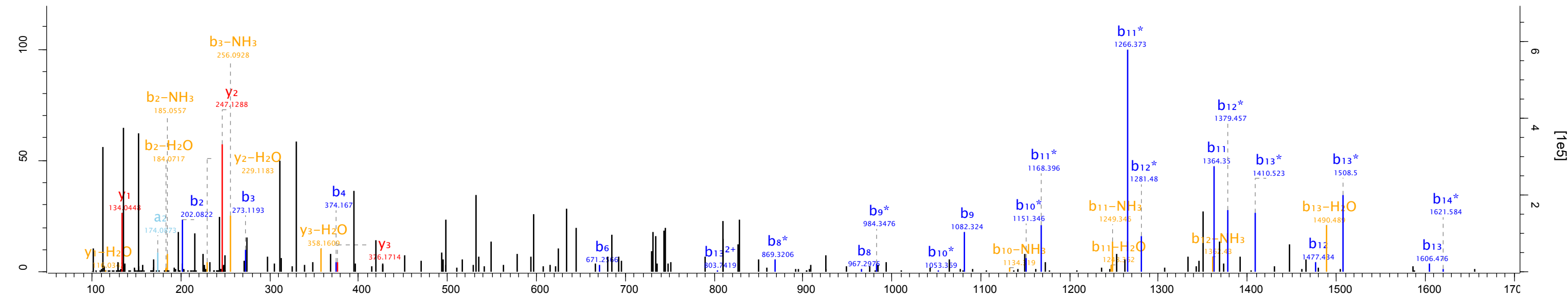
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20171215_MaS_33SR_LMH_proteome_02

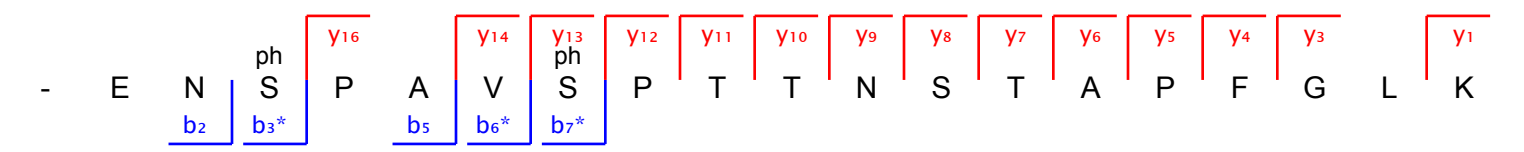
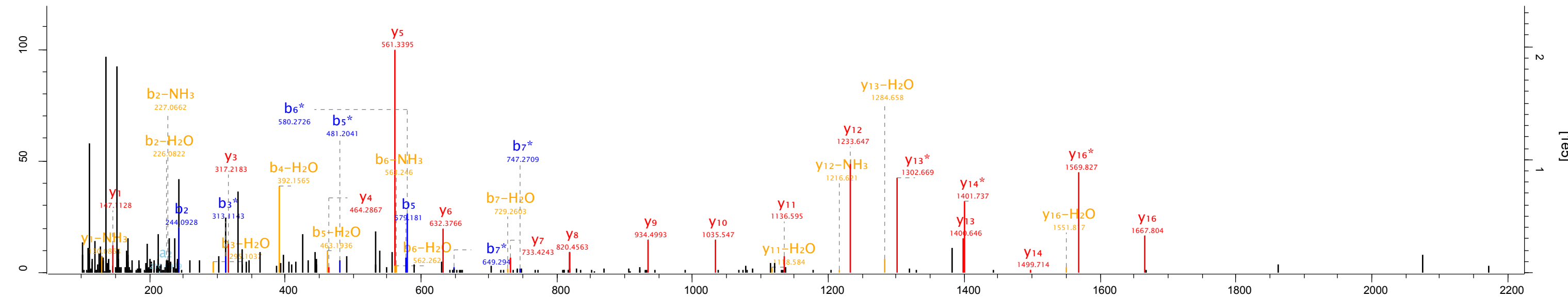
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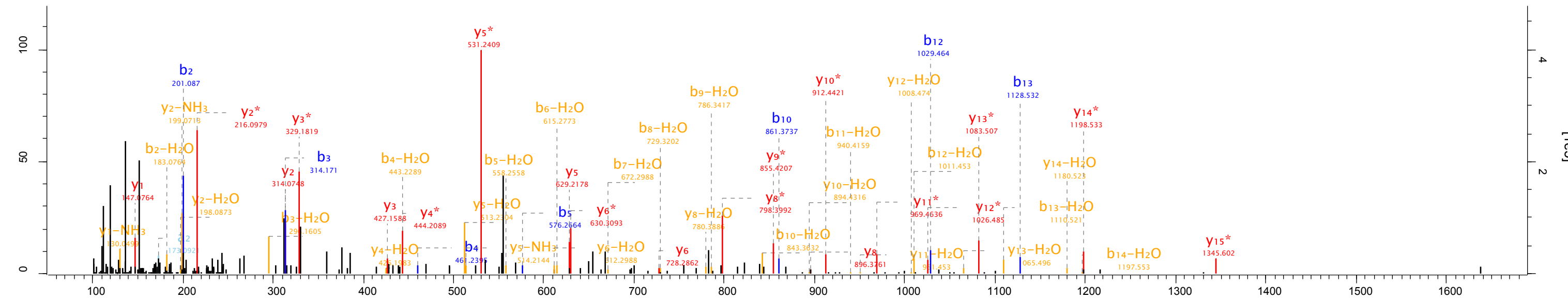
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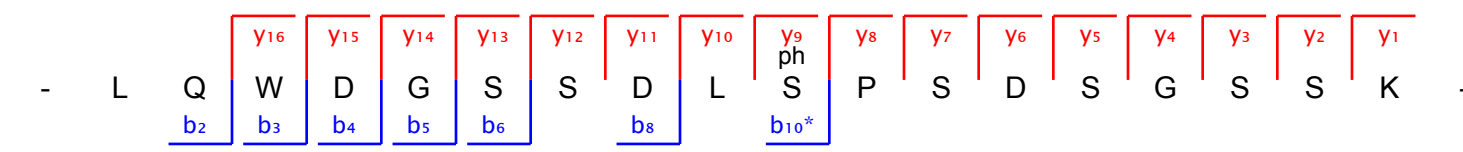
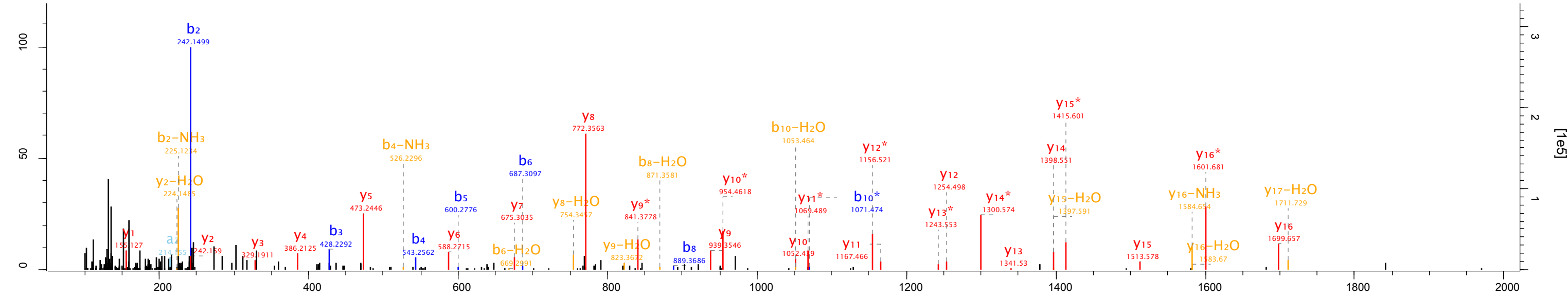
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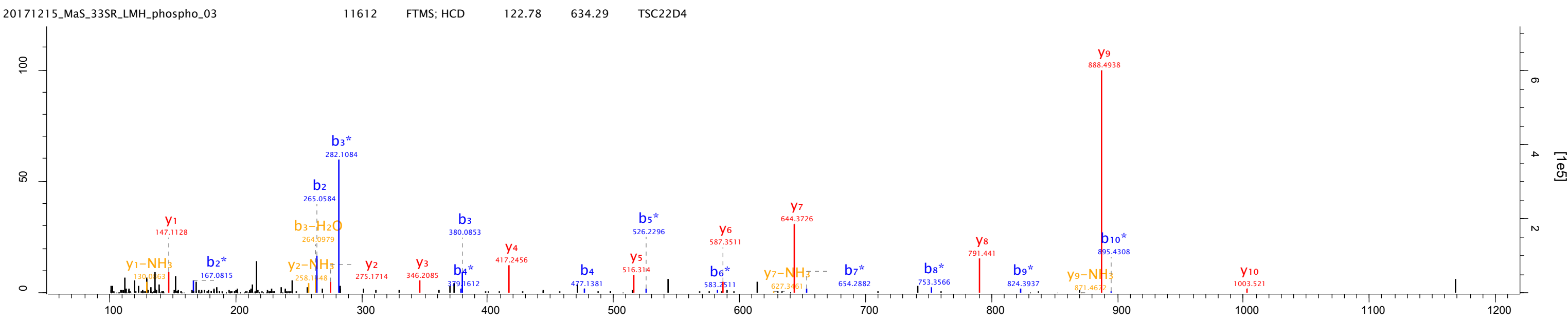
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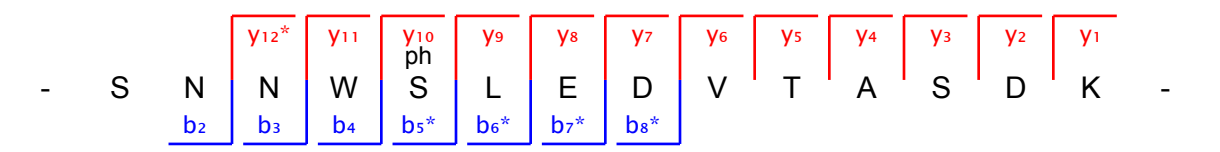
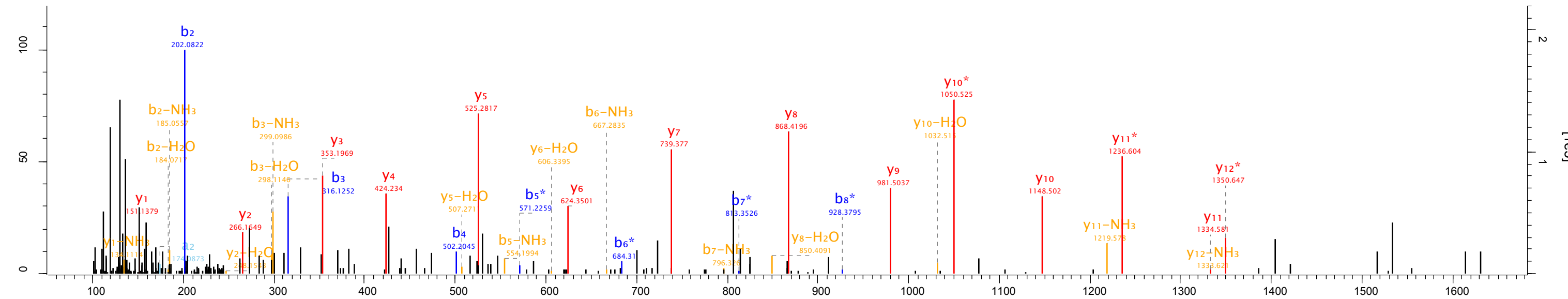


20171215_MaS_33SR_LMH_phospho_03 11252 FTMS; HCD 173.01 970.9 ATXN7L3

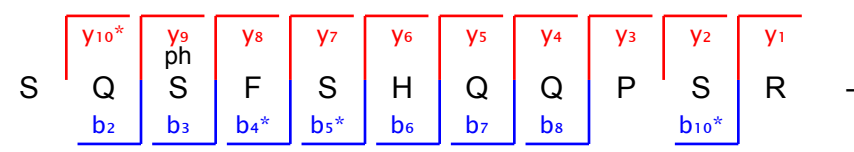
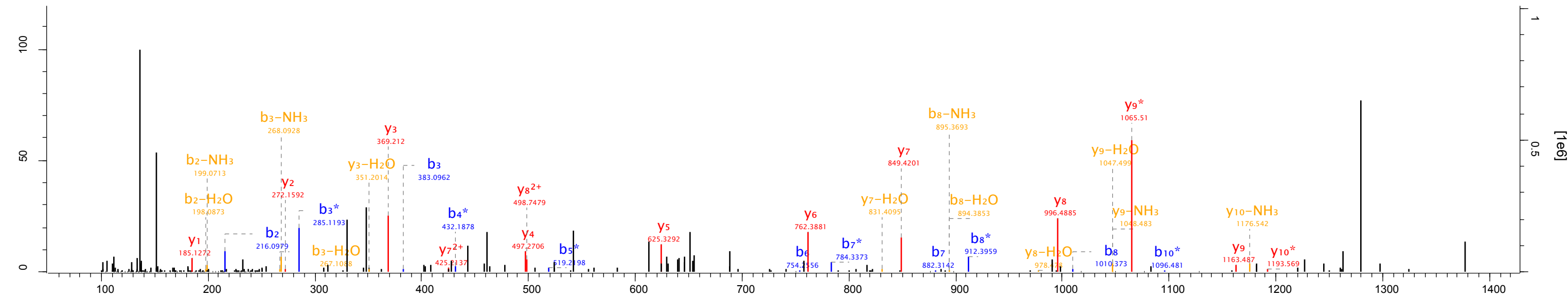


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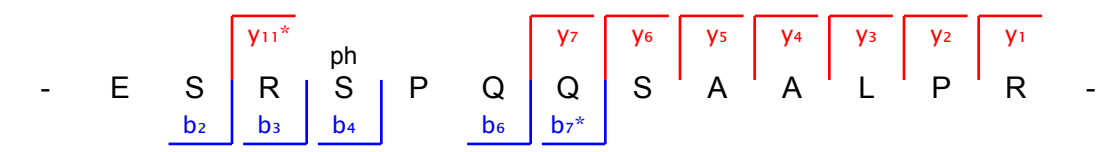
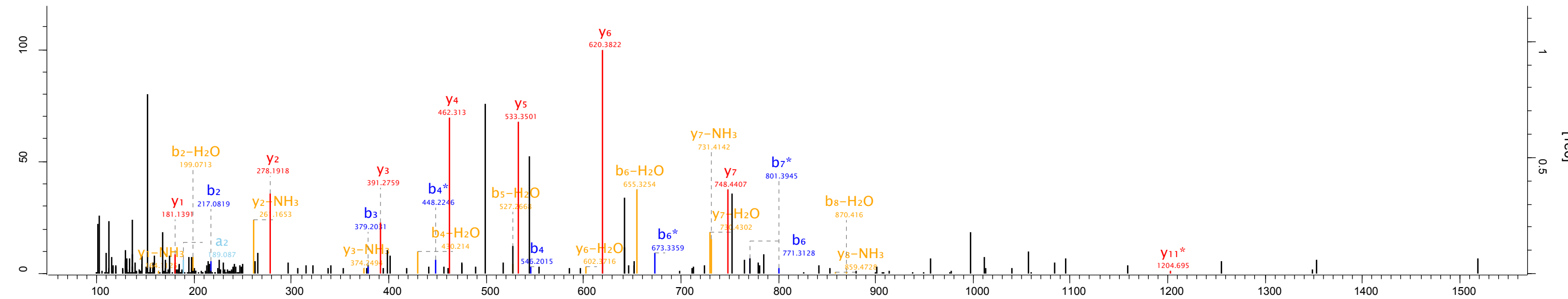




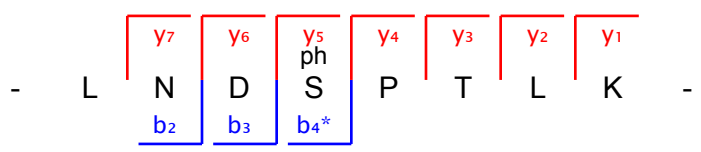
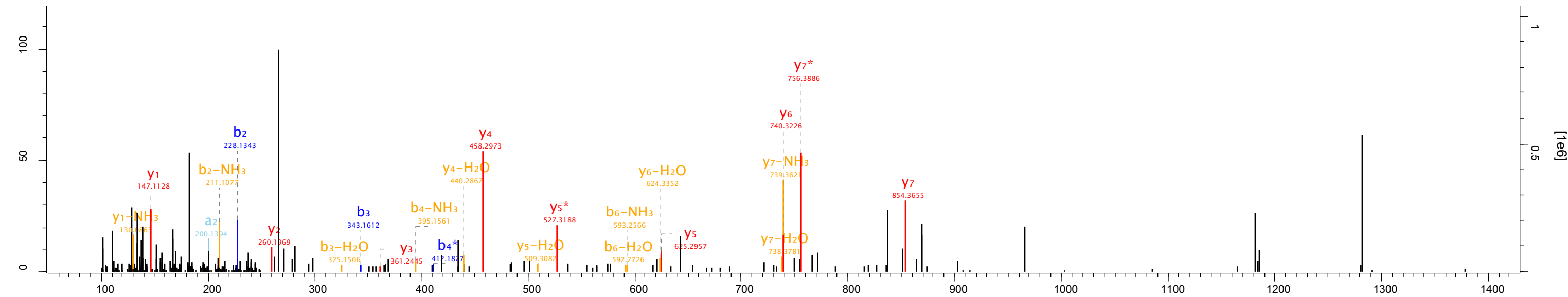
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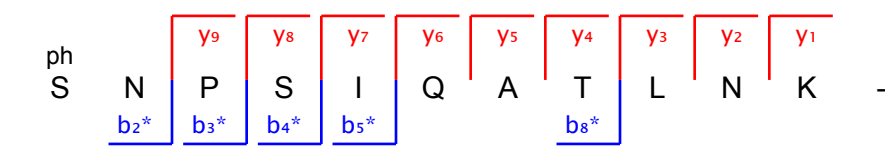
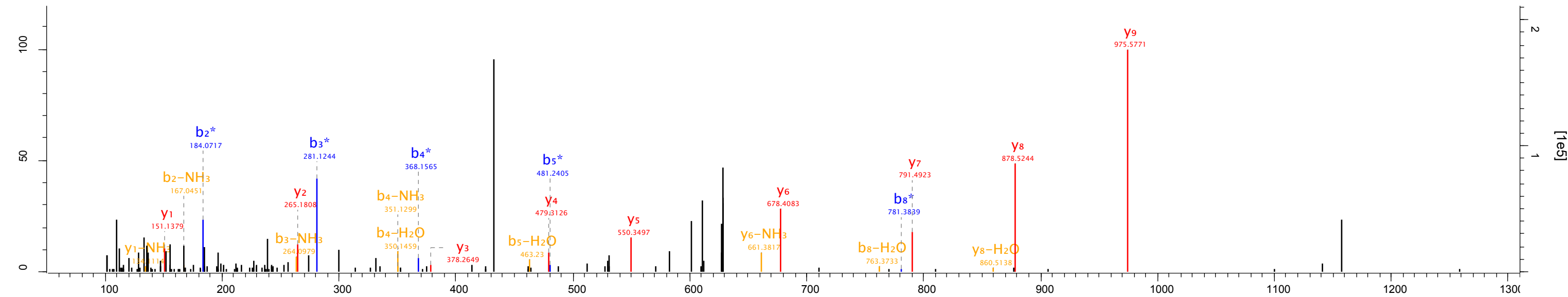
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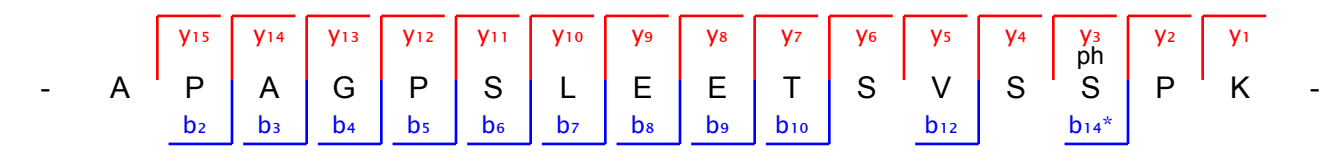
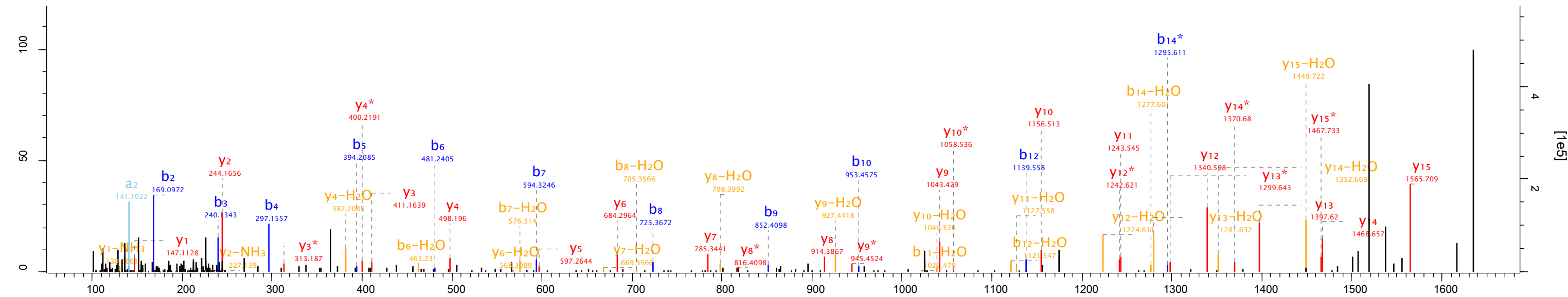
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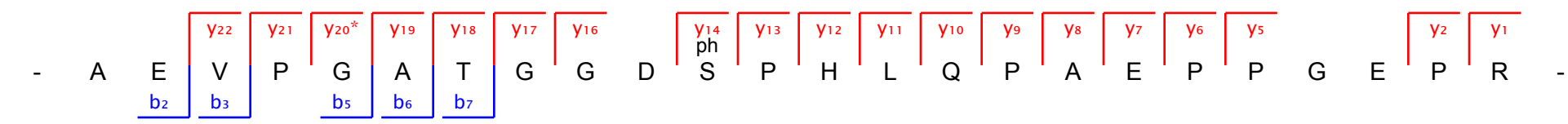
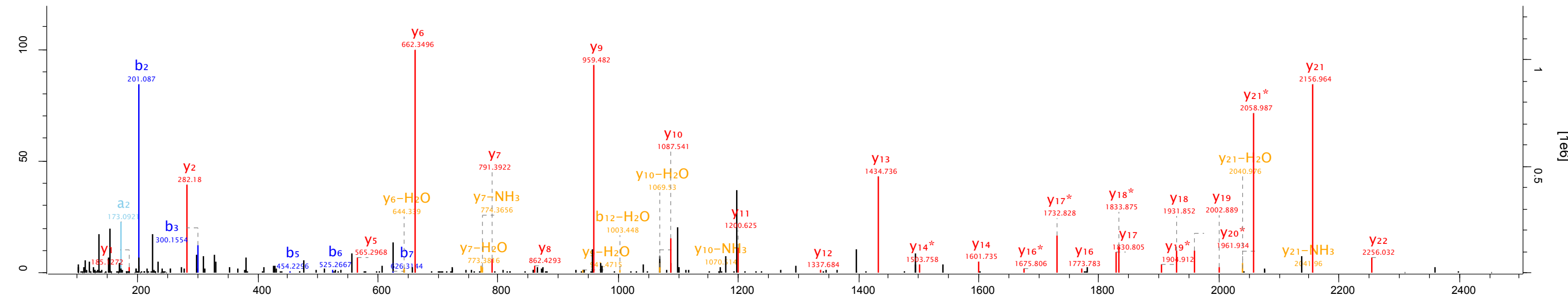
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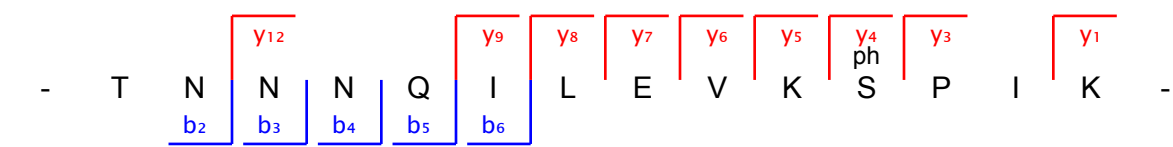
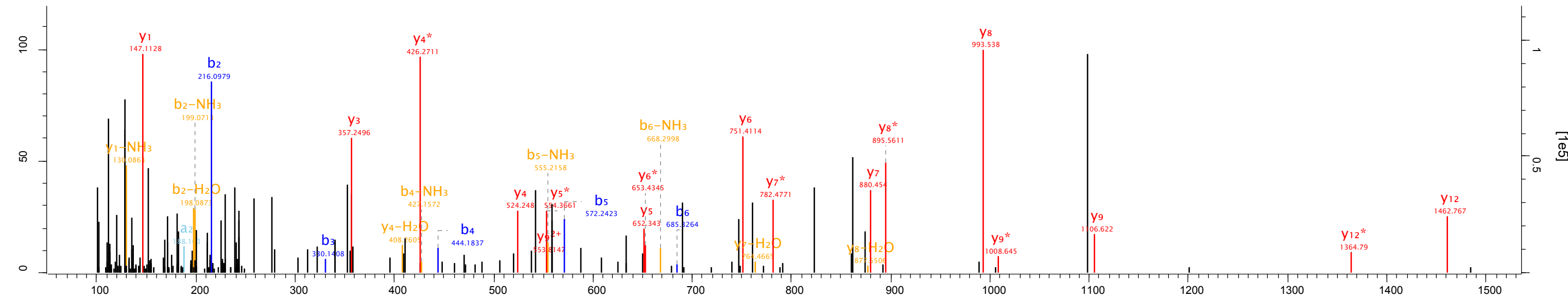
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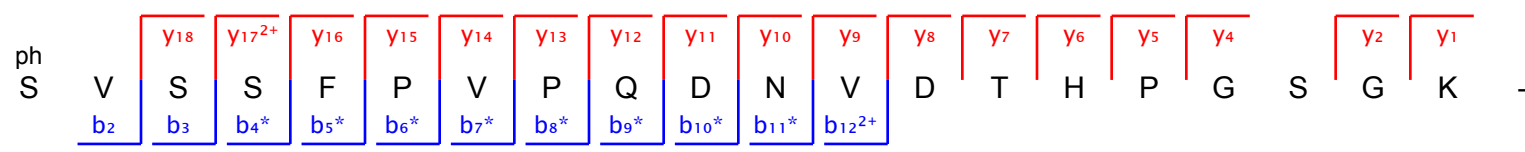
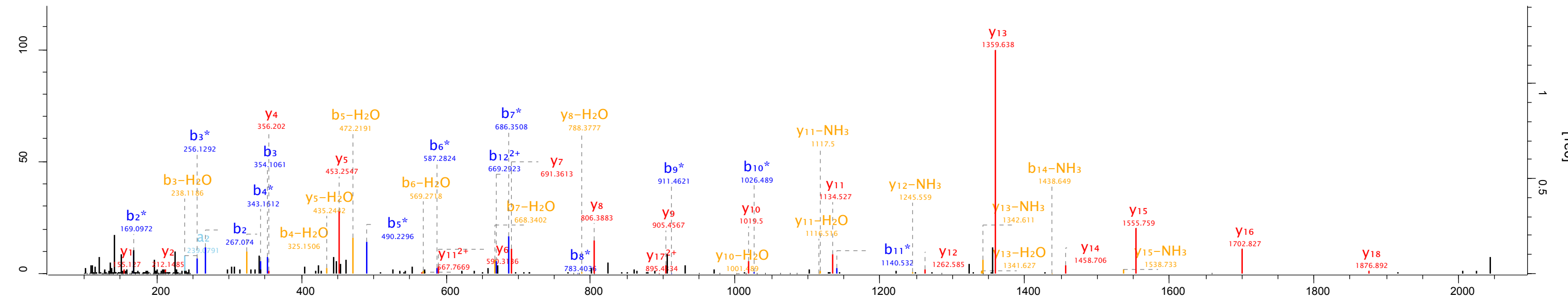
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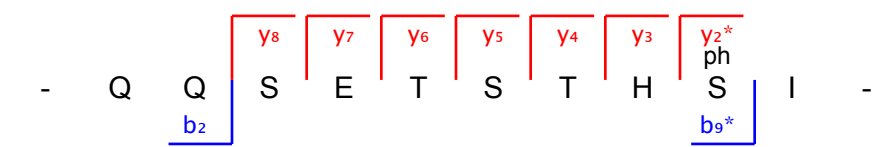
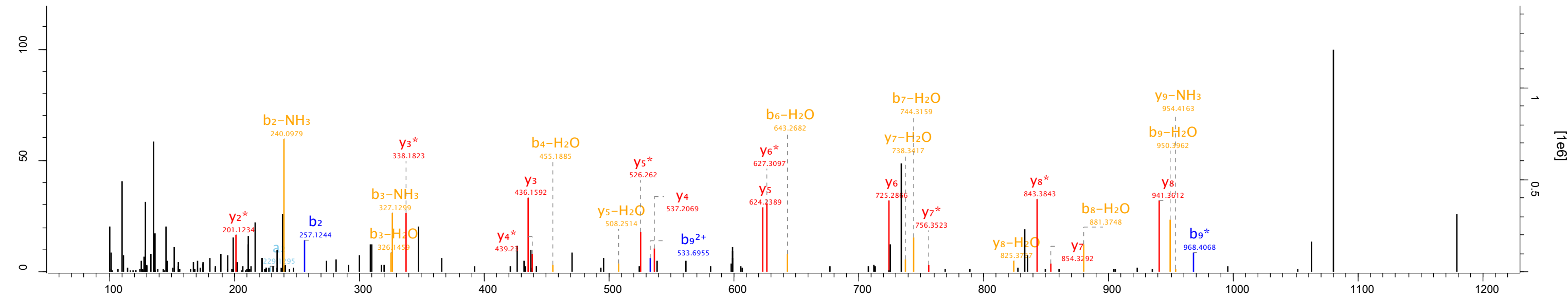


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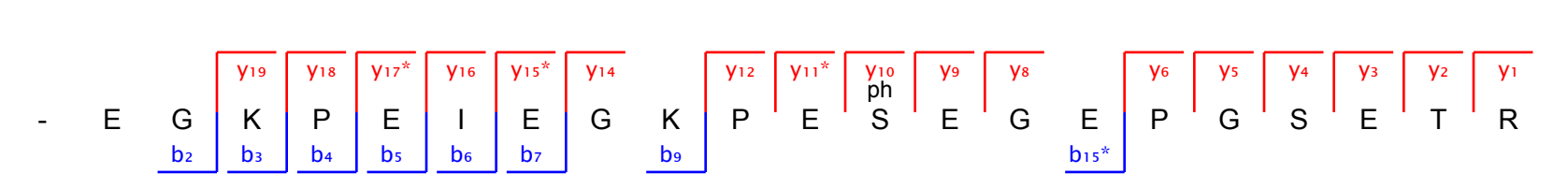
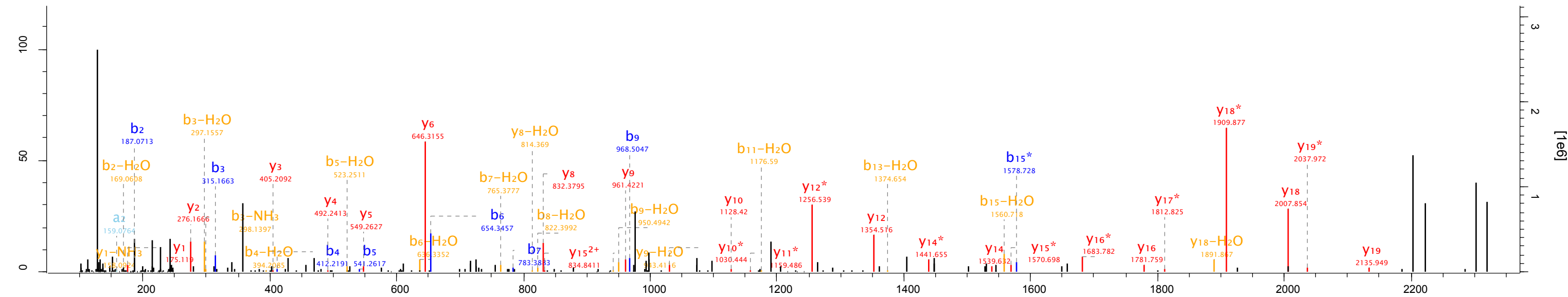


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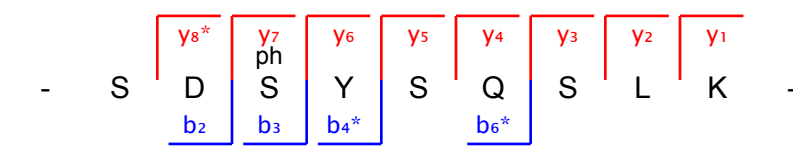
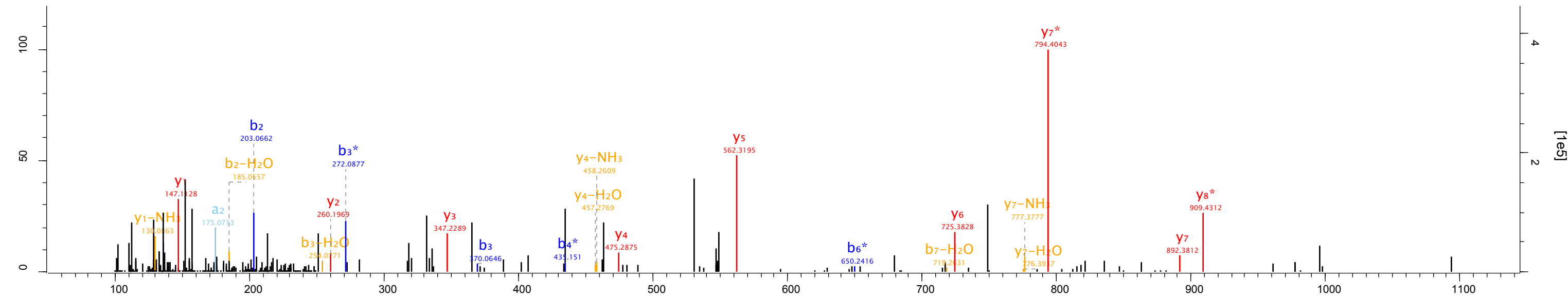




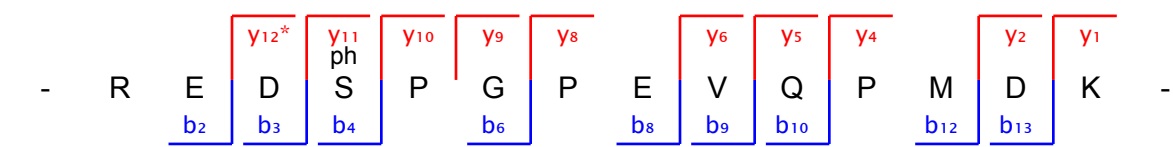
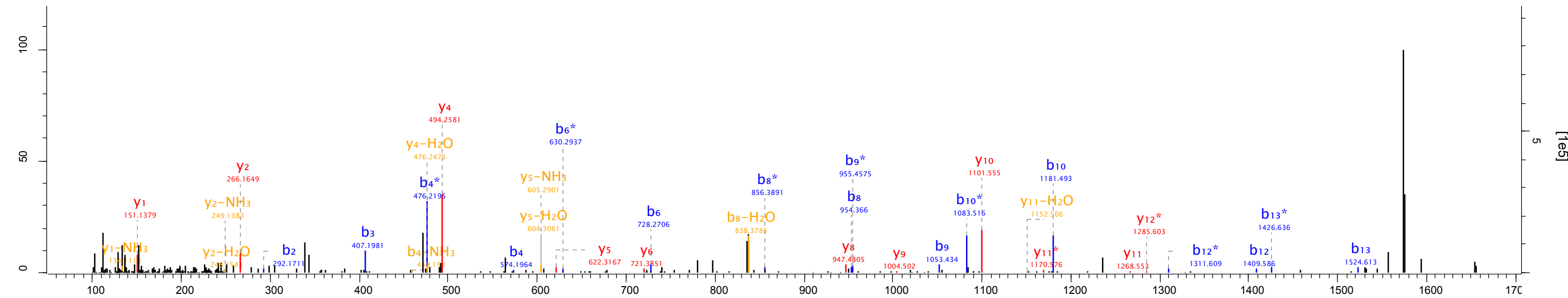
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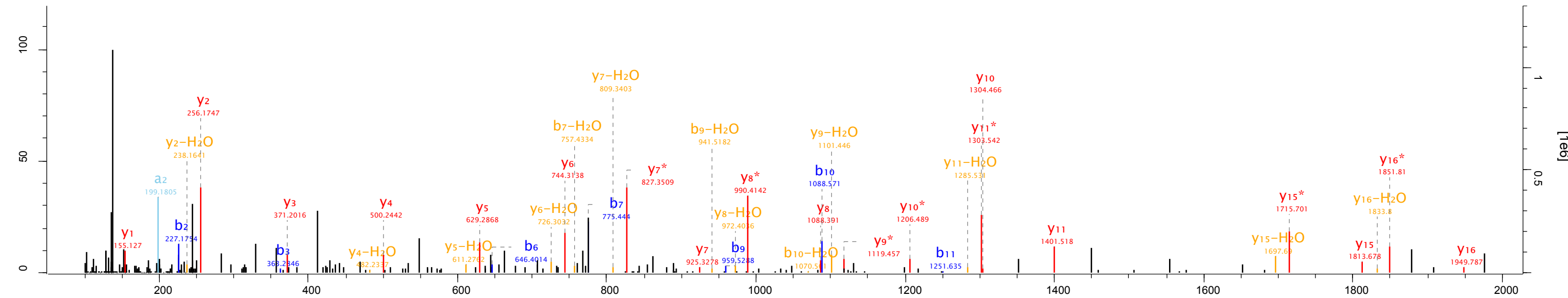
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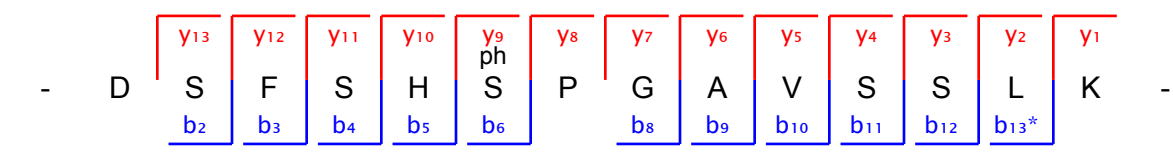
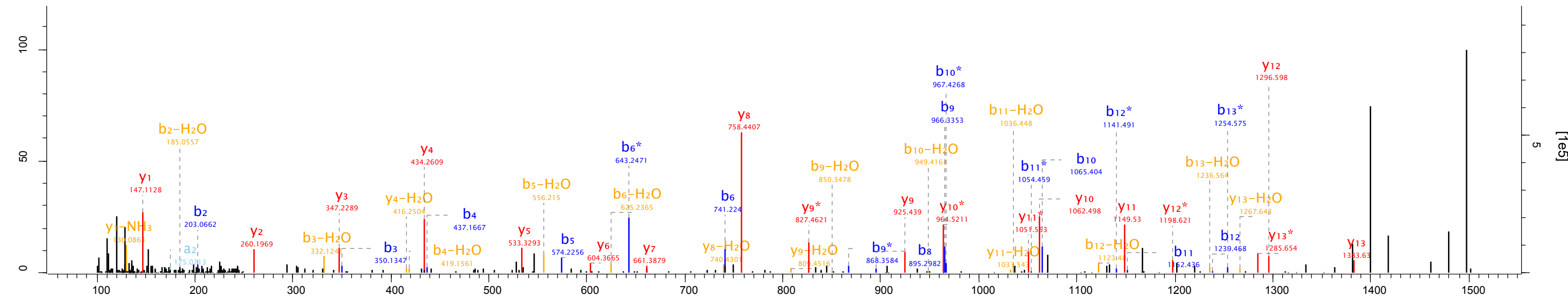
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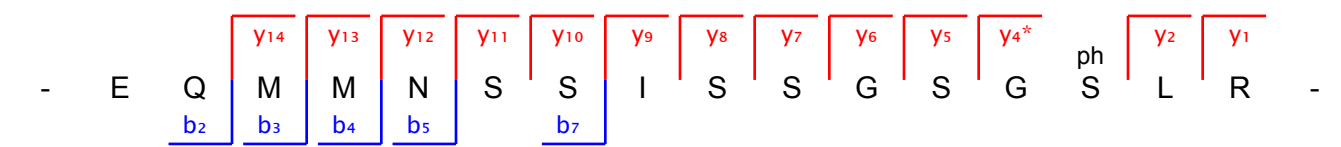
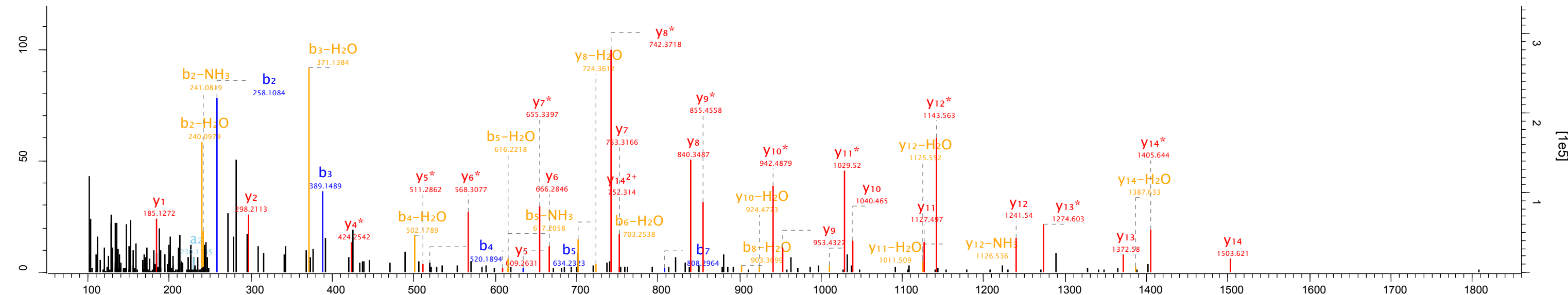
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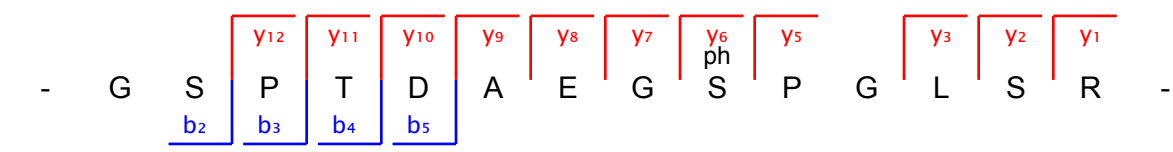
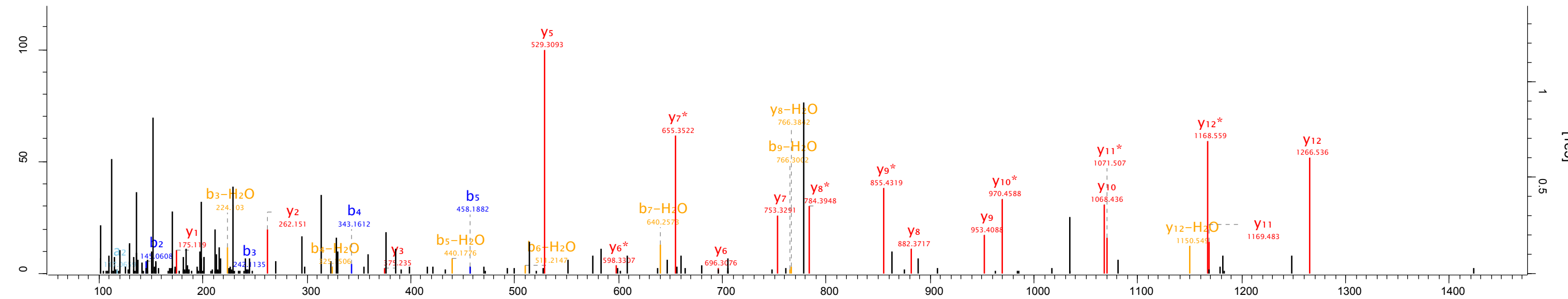
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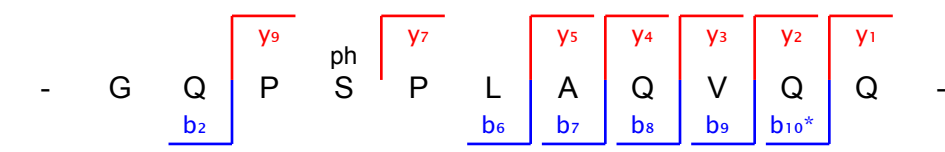
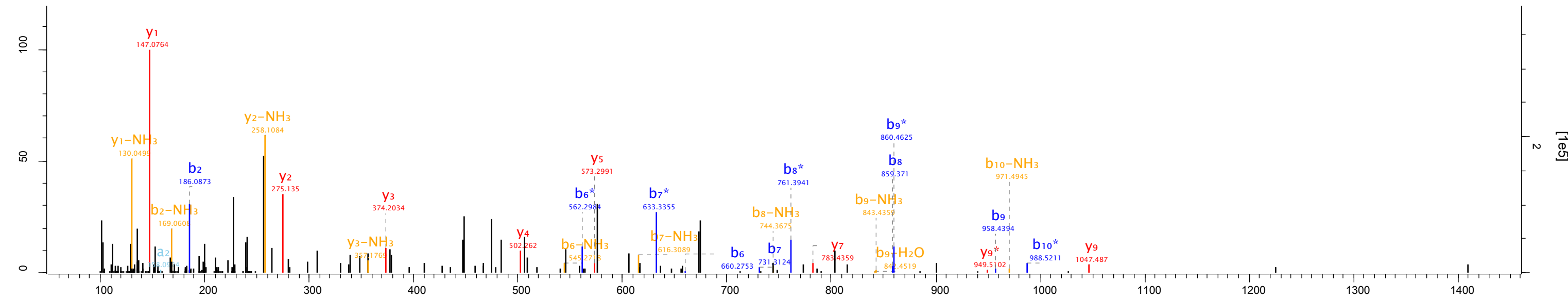
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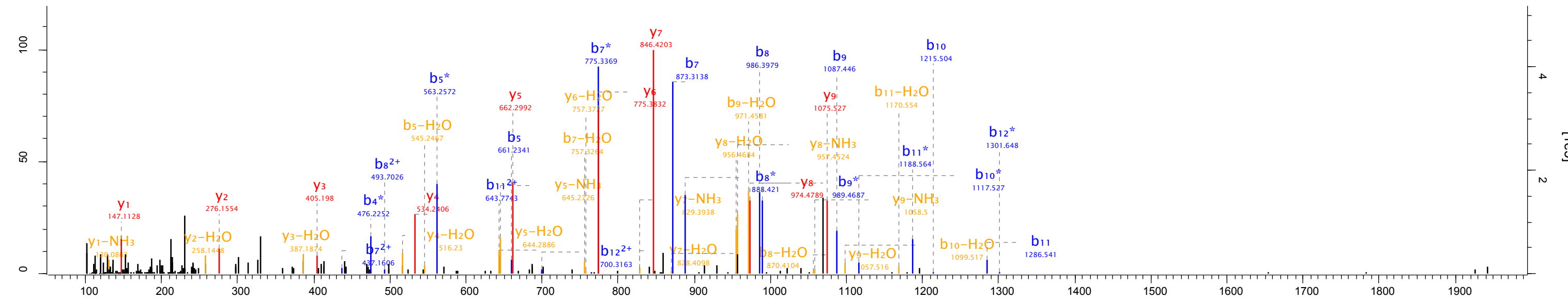
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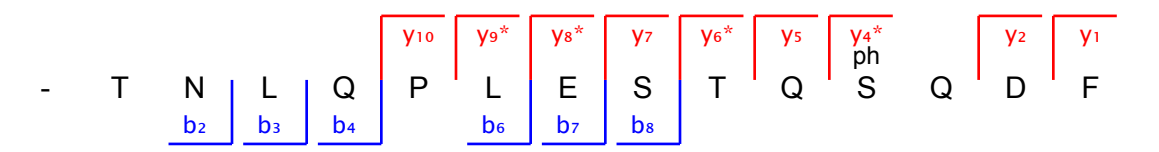
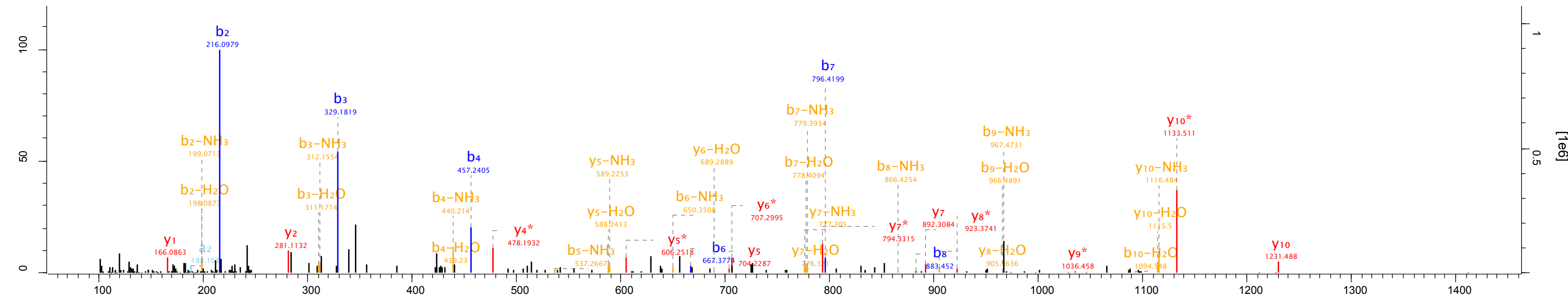
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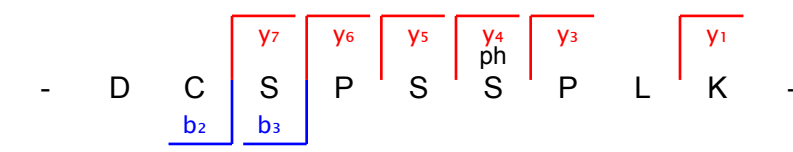
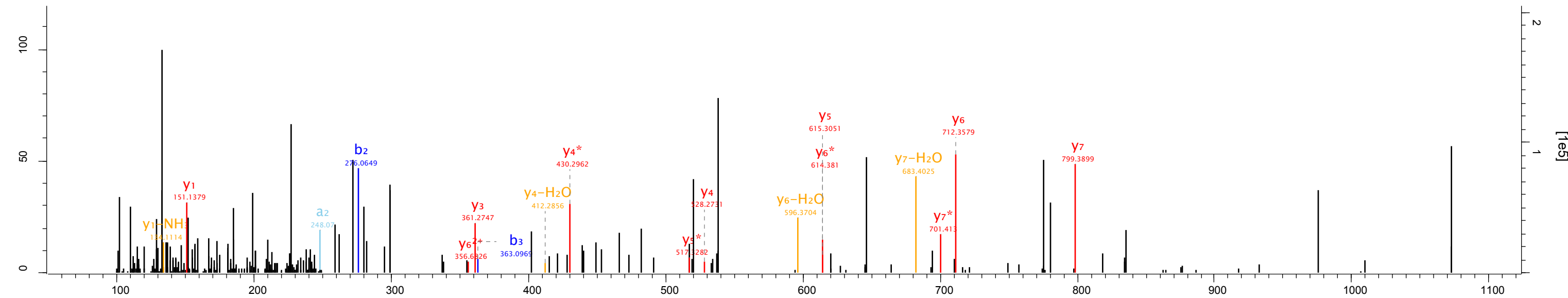
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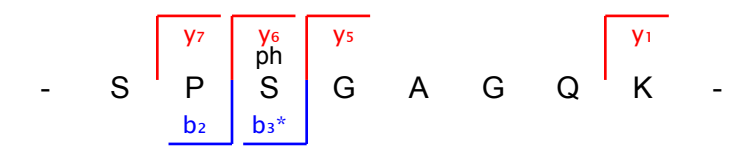
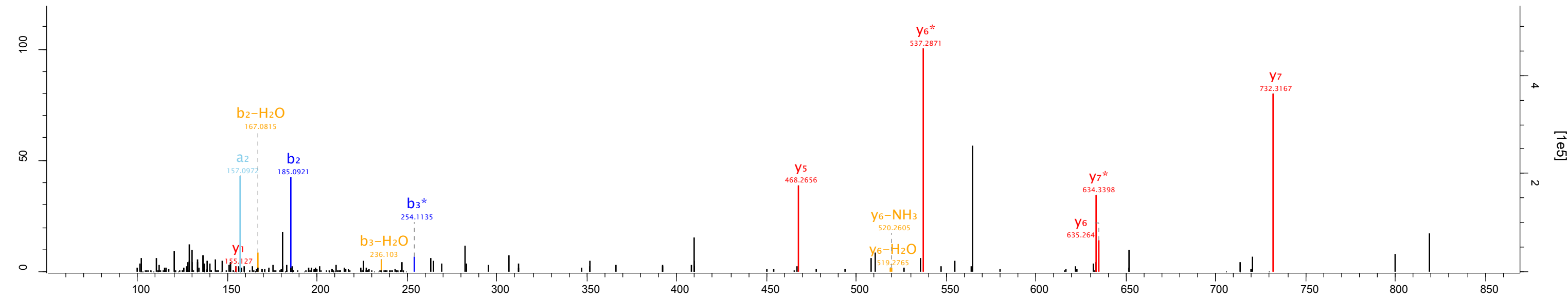
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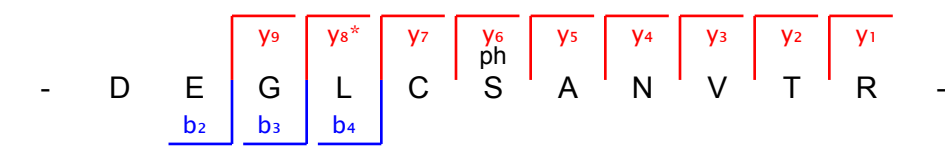
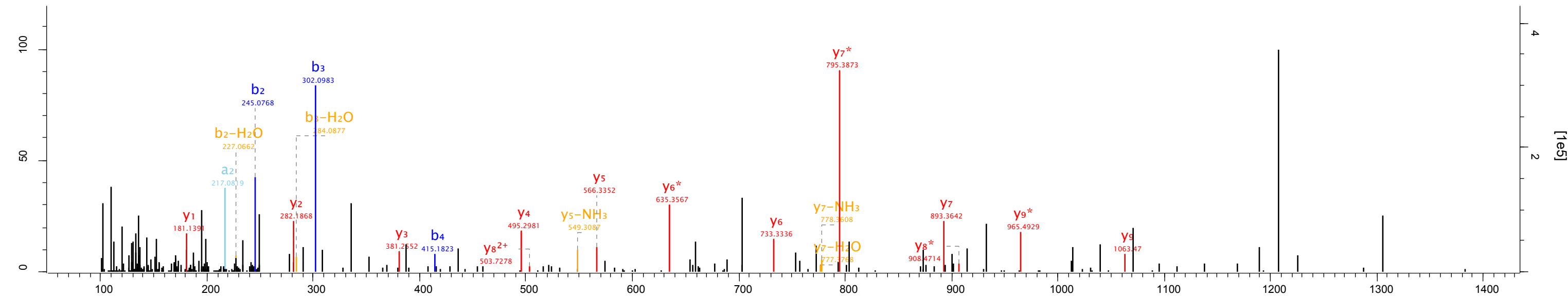
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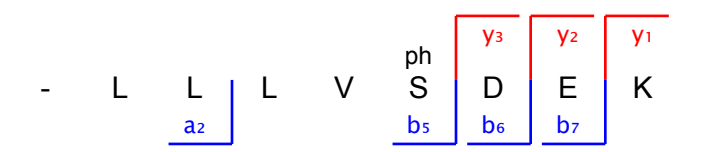
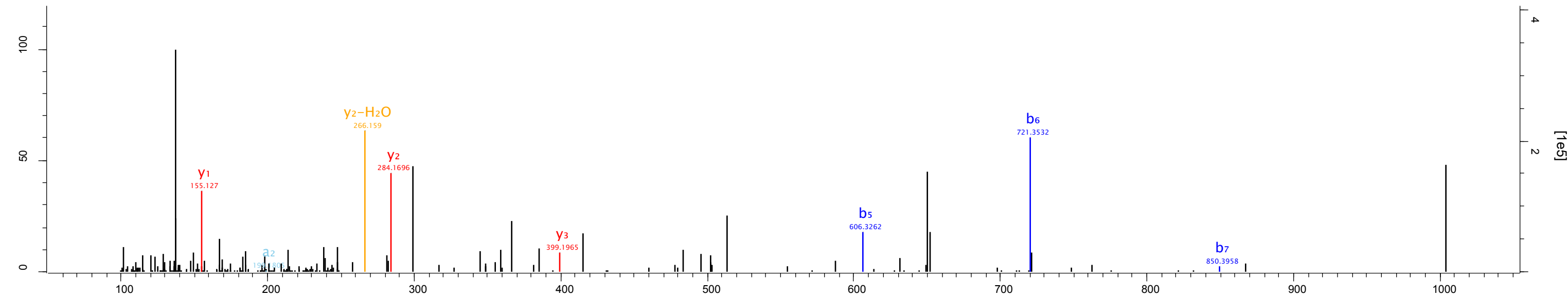
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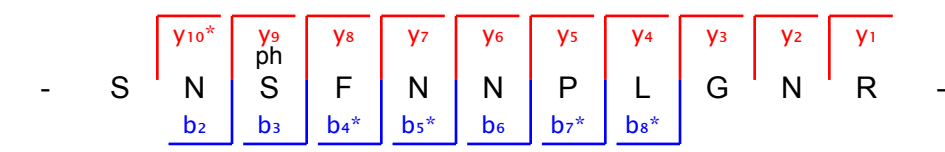
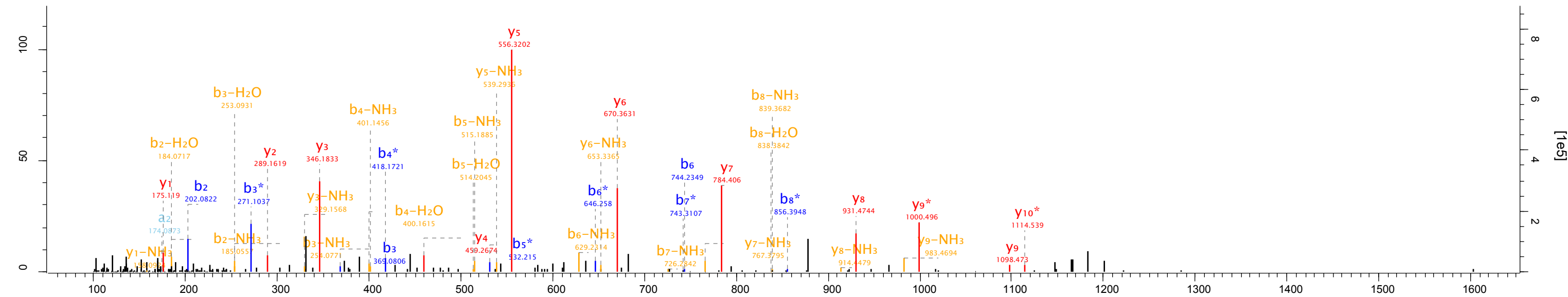
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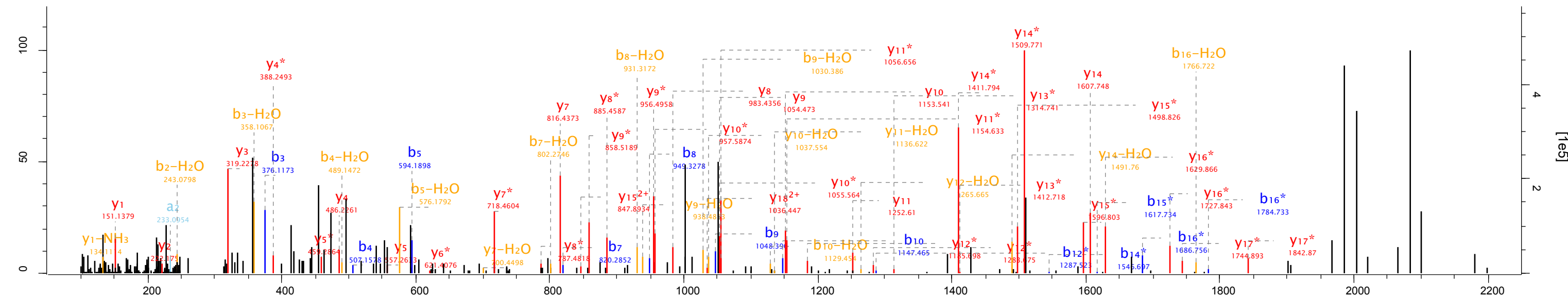
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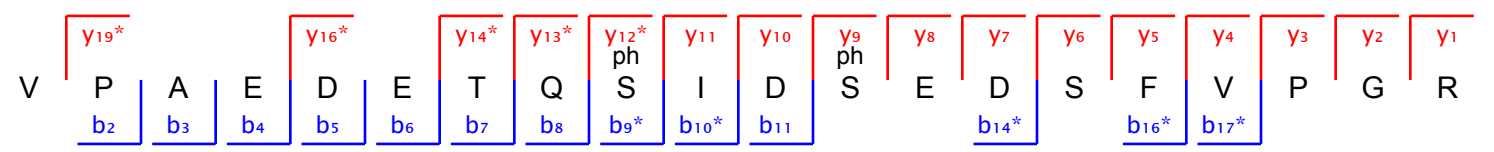
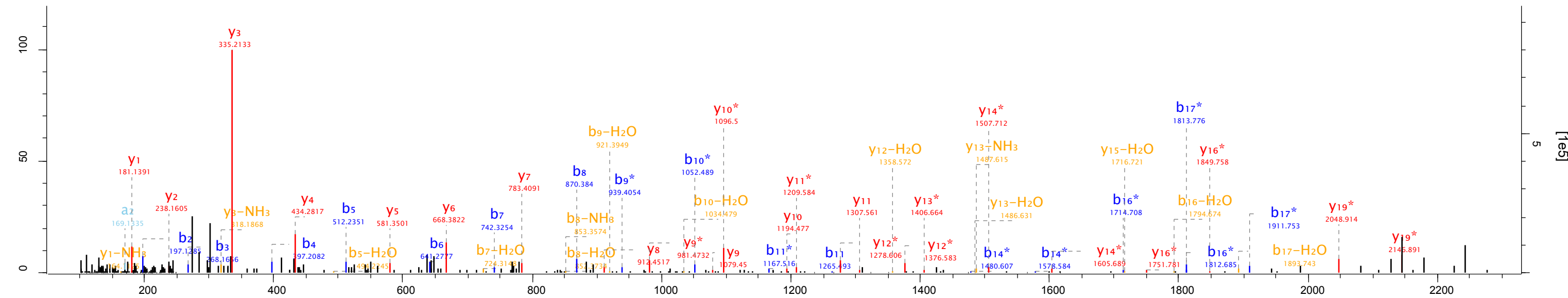


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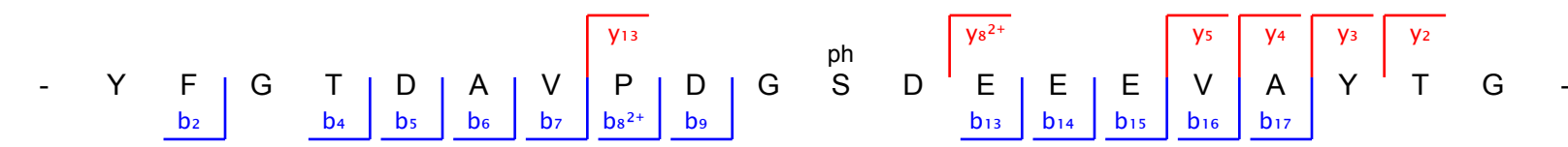
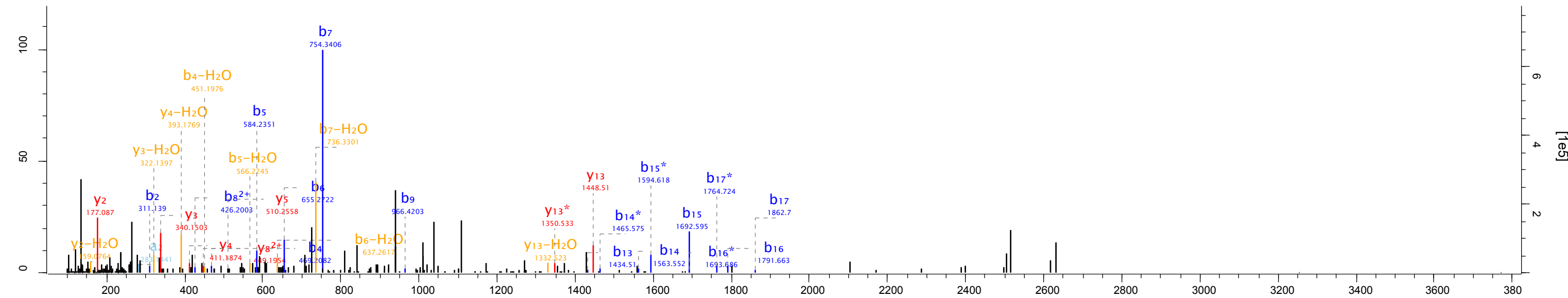
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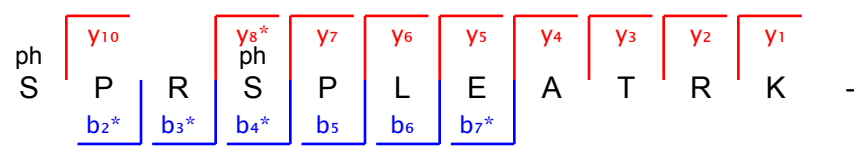
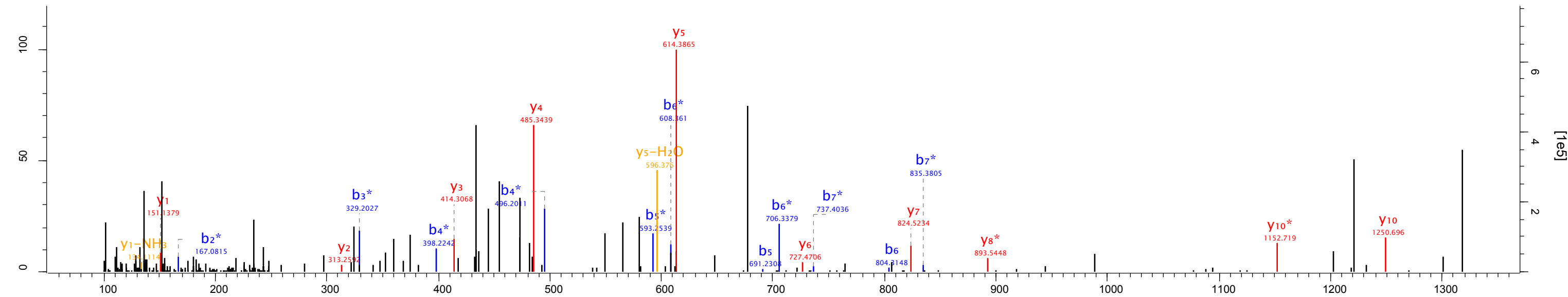
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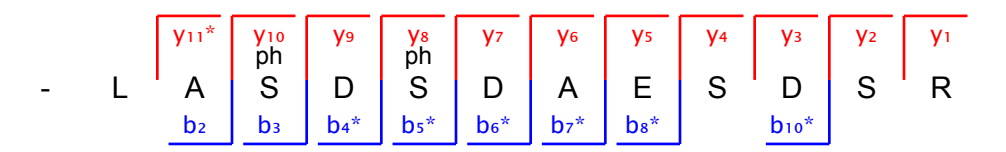
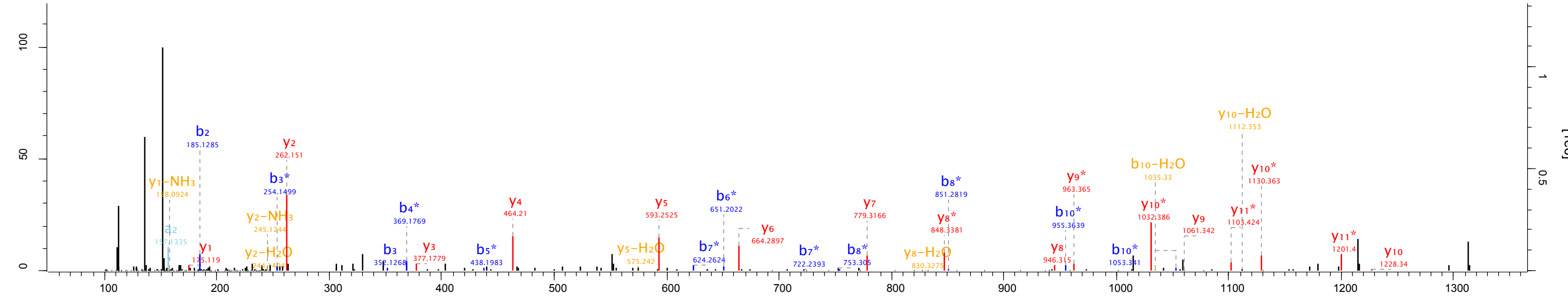
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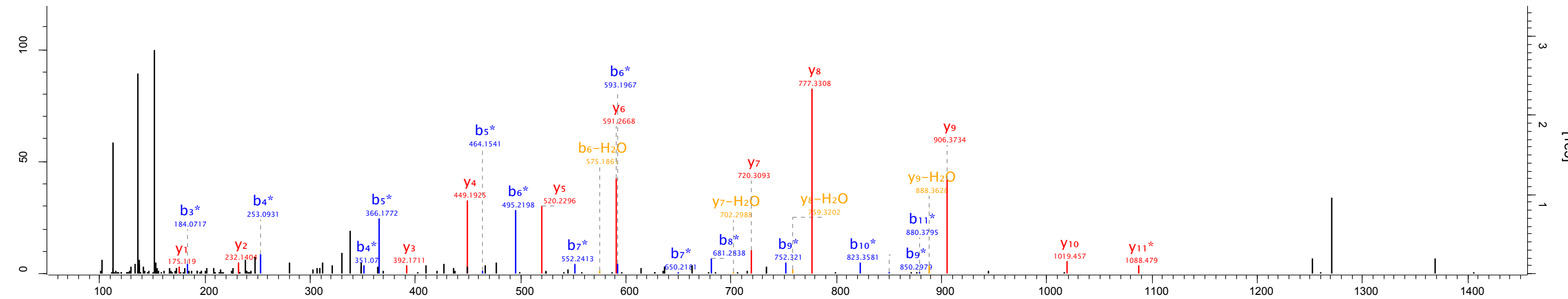
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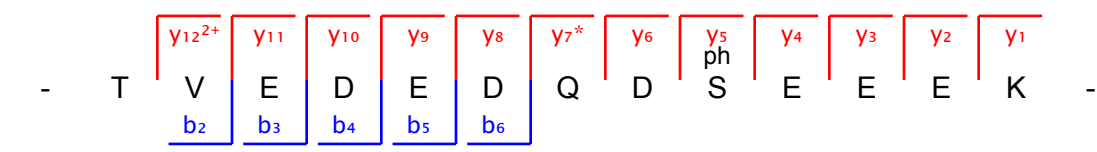
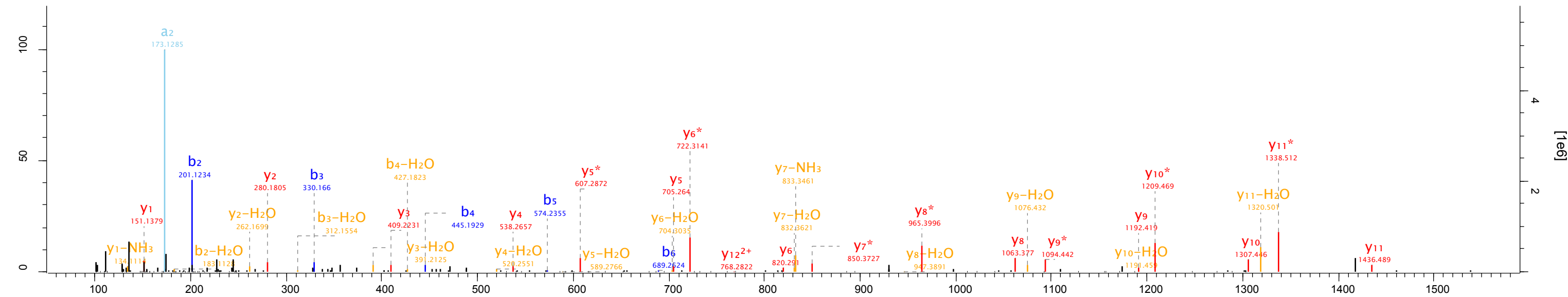


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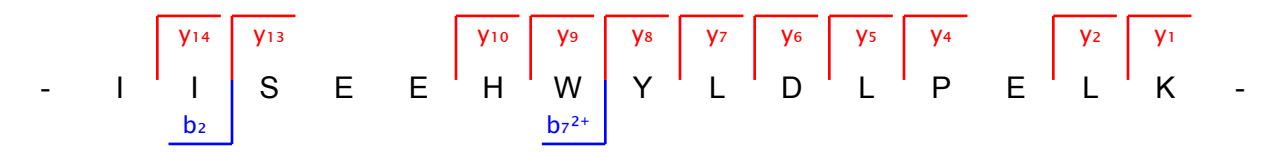
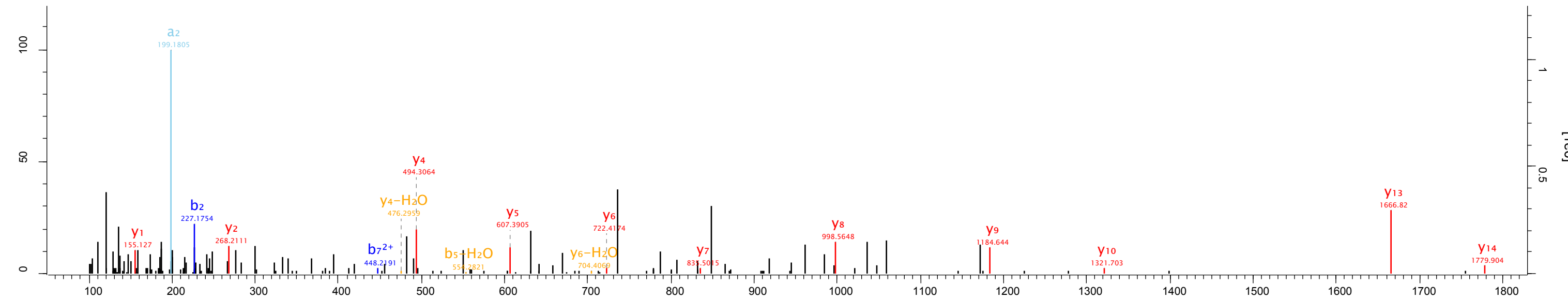


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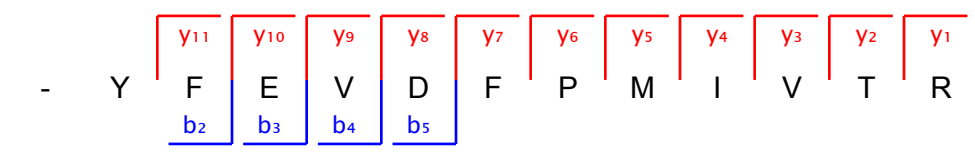
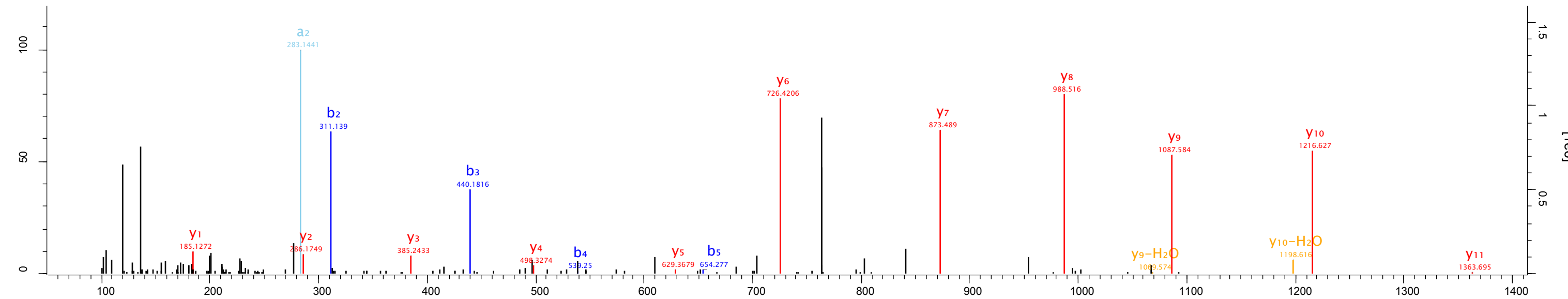
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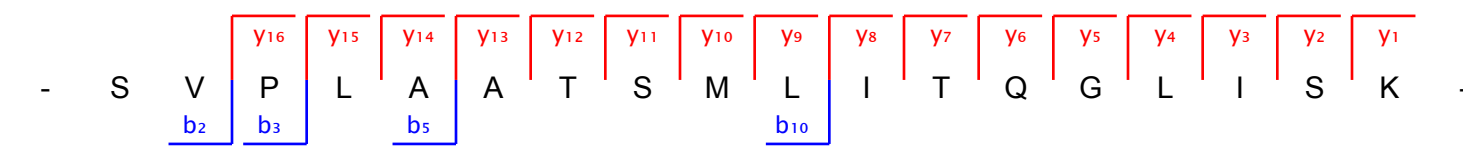
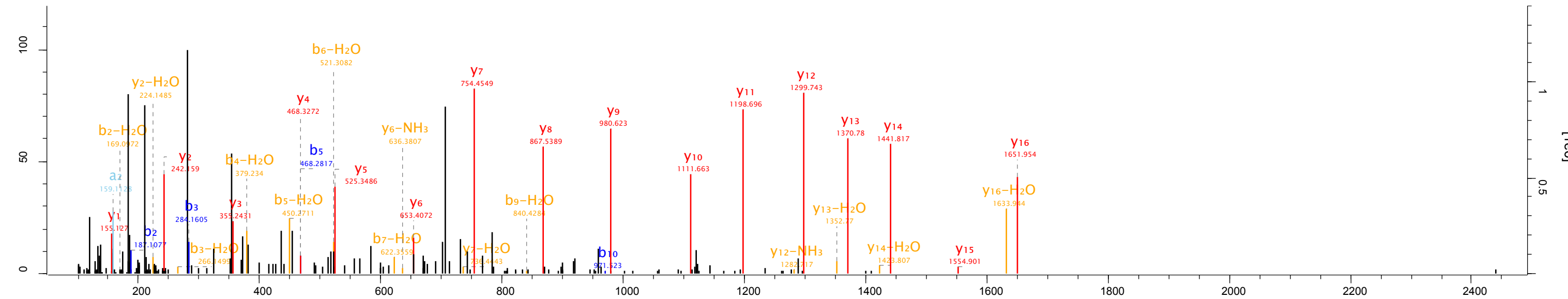
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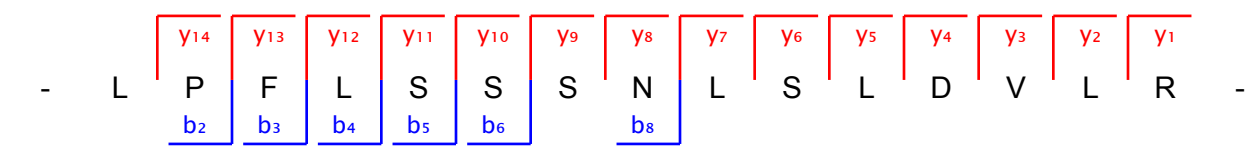
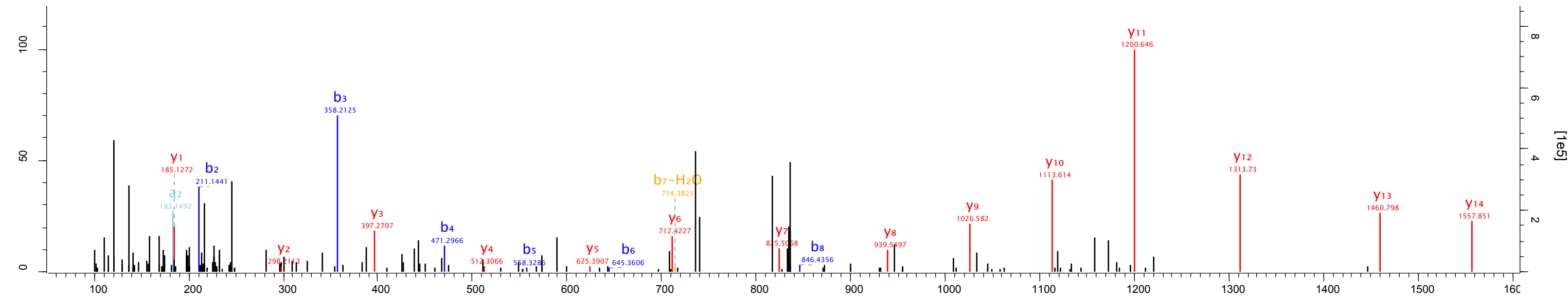
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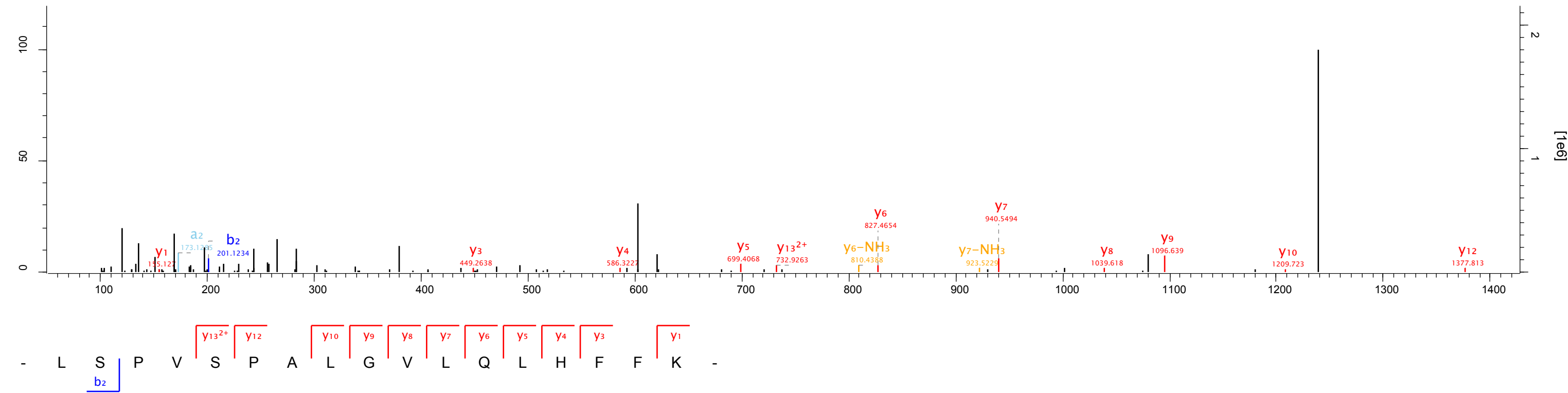
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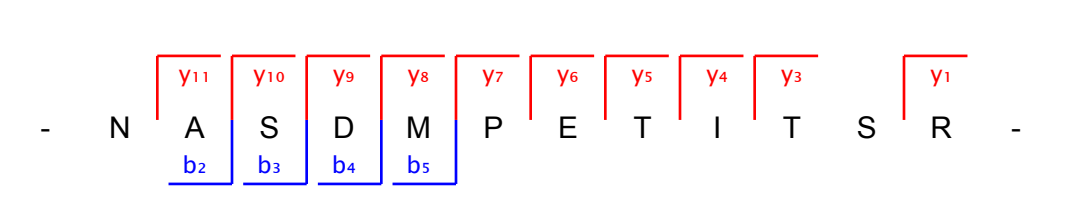
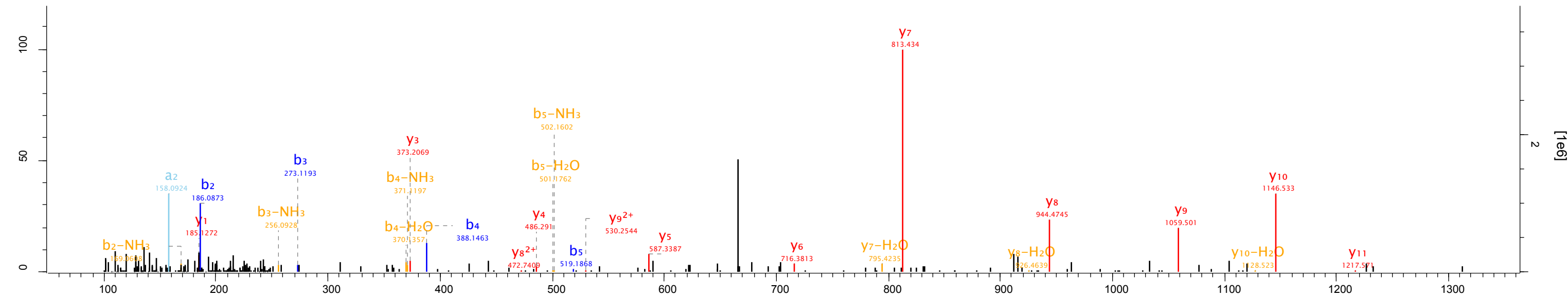


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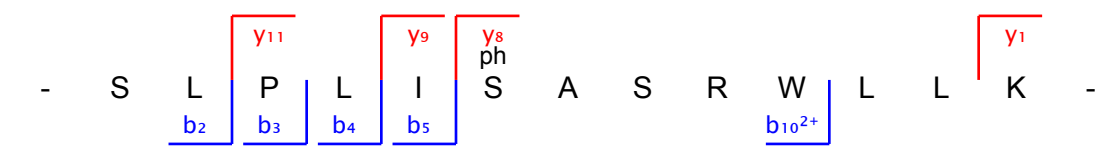
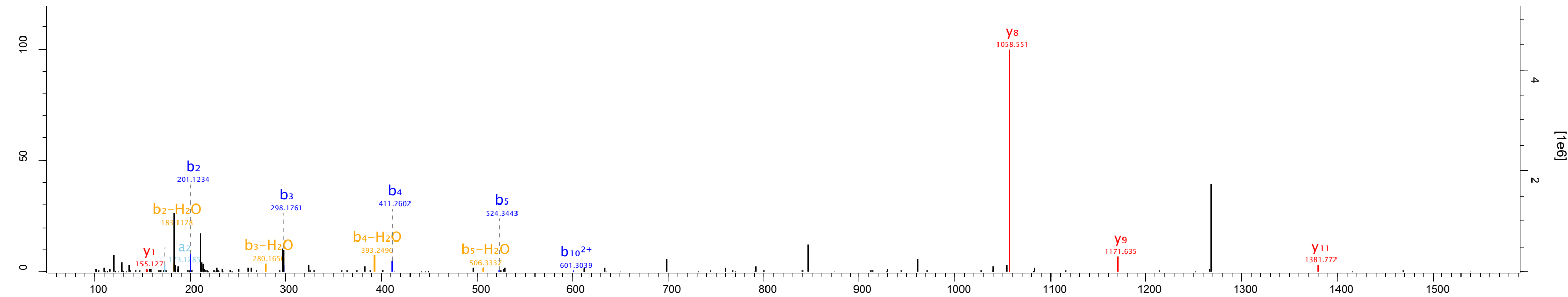


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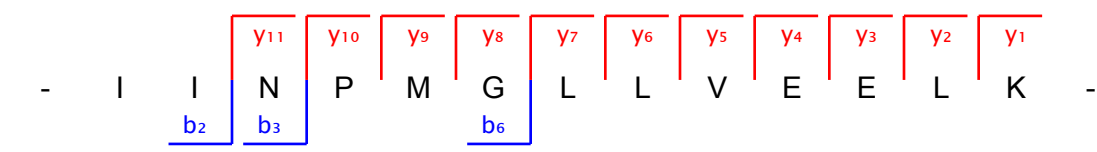
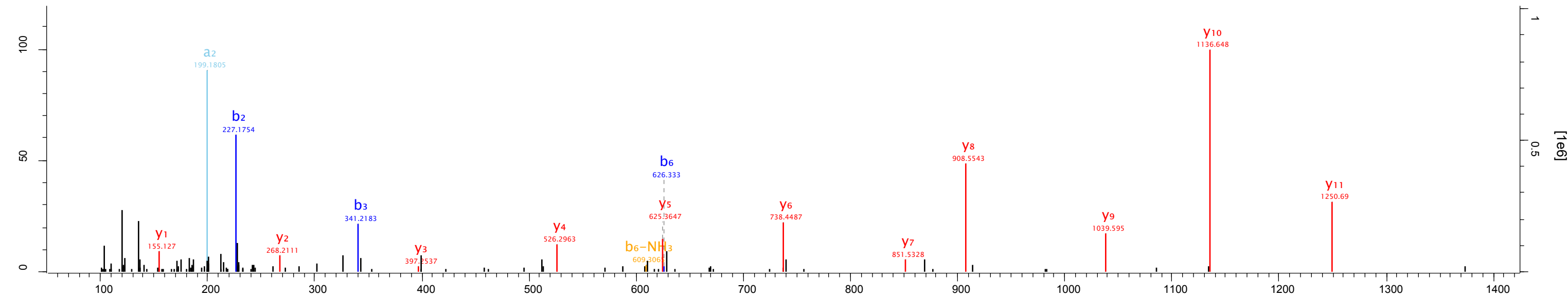
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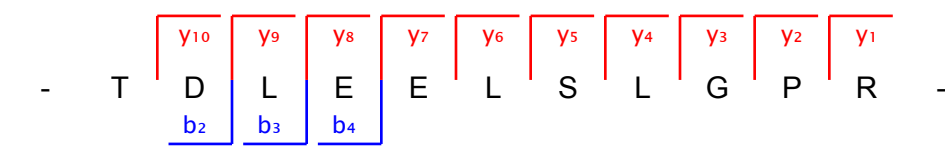
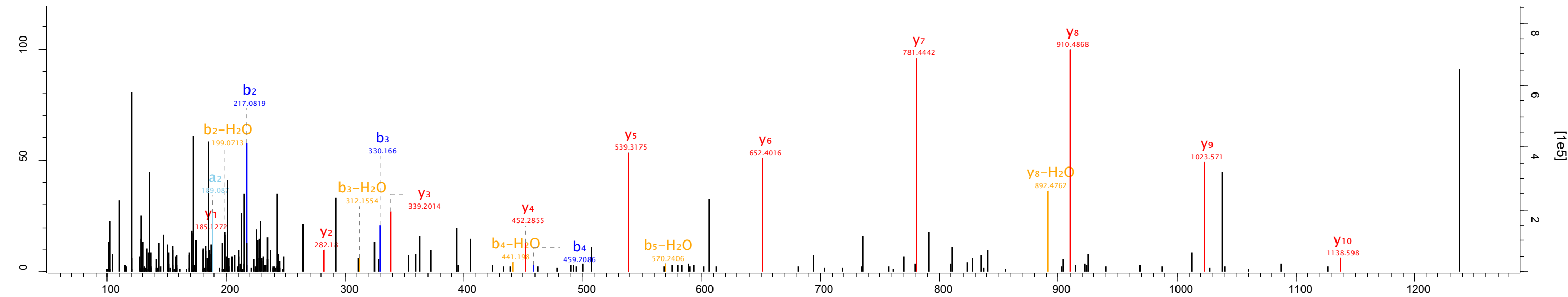
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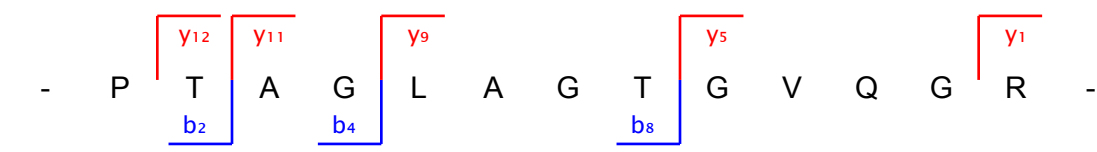
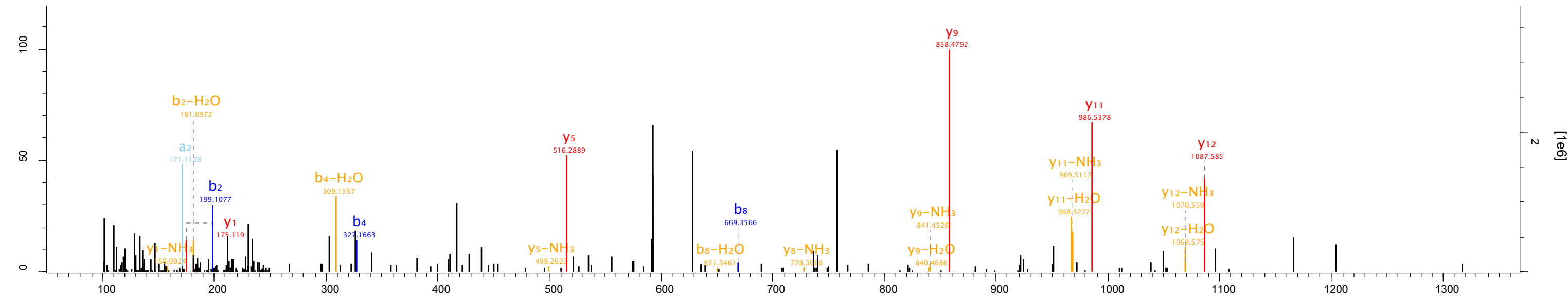
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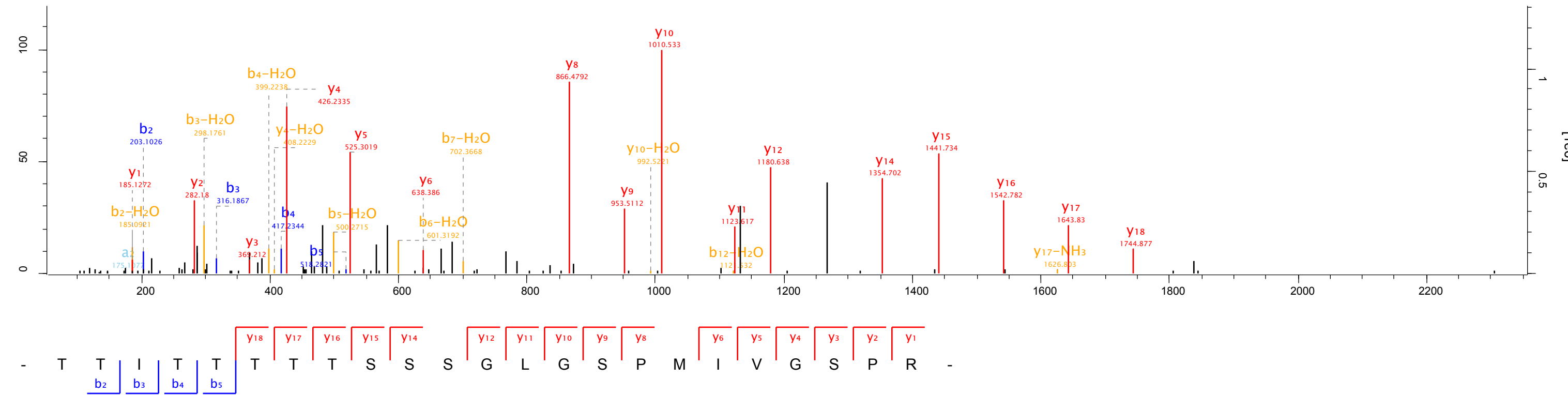
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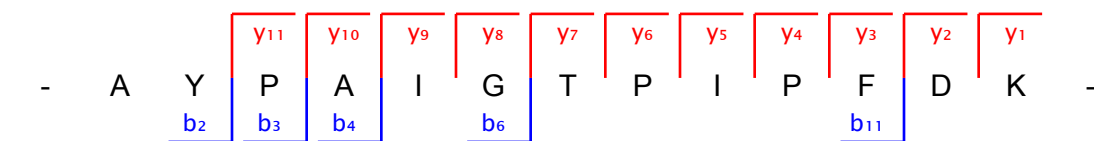
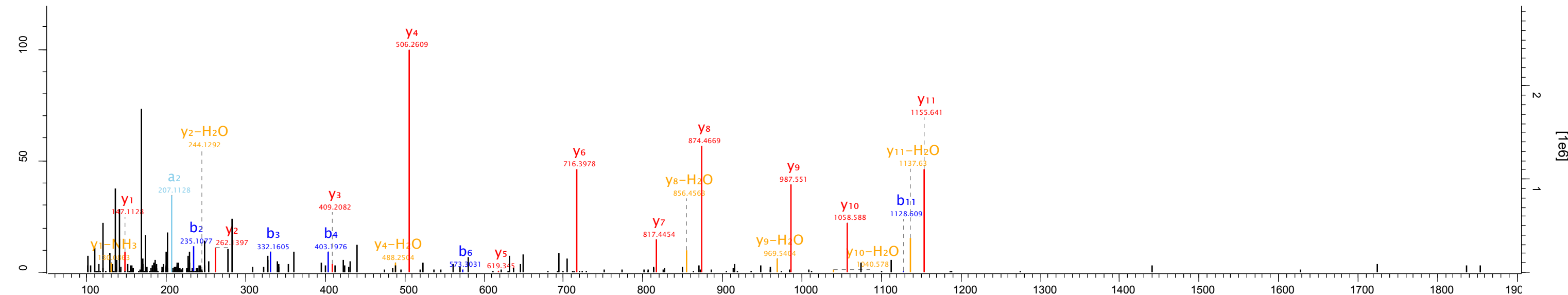


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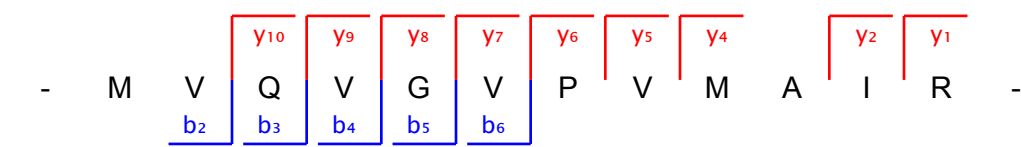
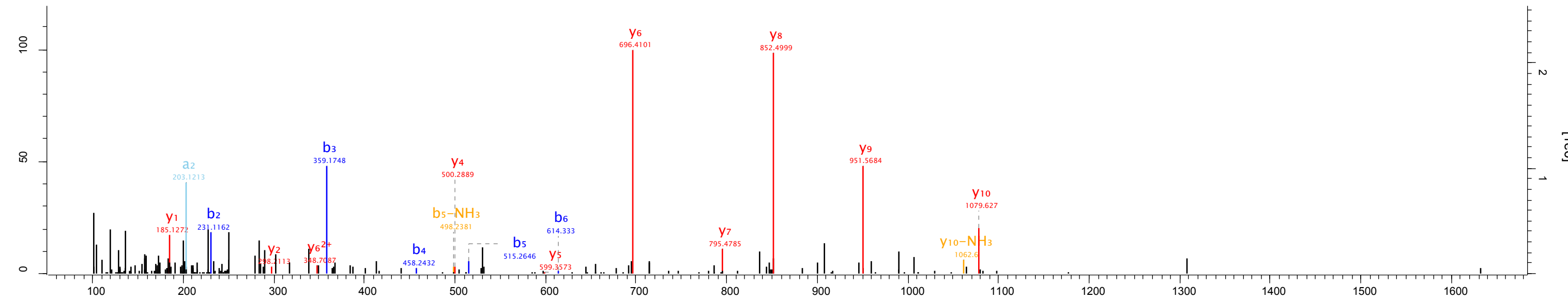




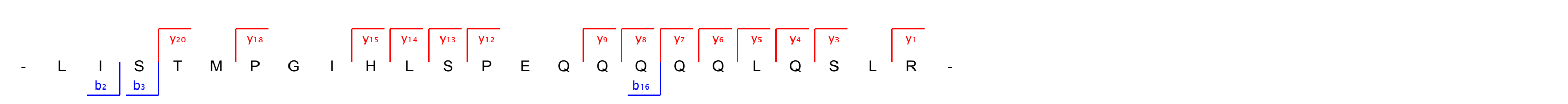
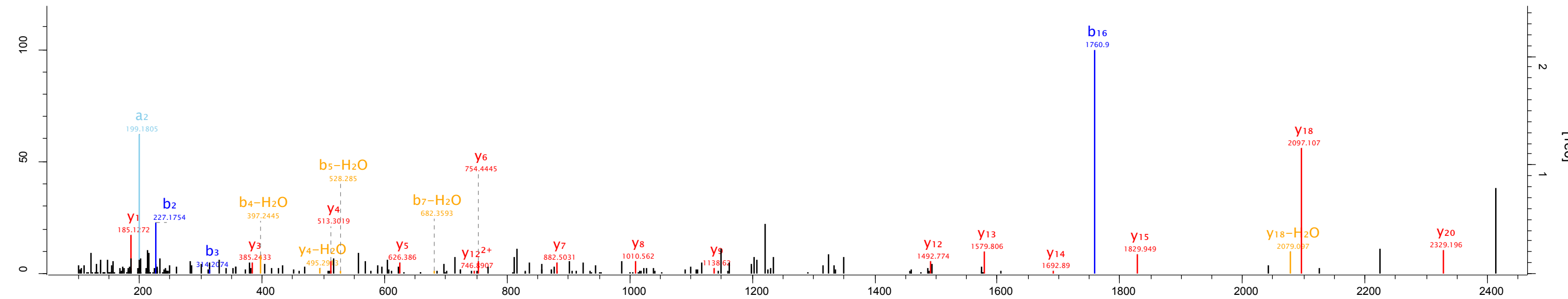
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20171215_MaS_33SR_LMH_proteome_01

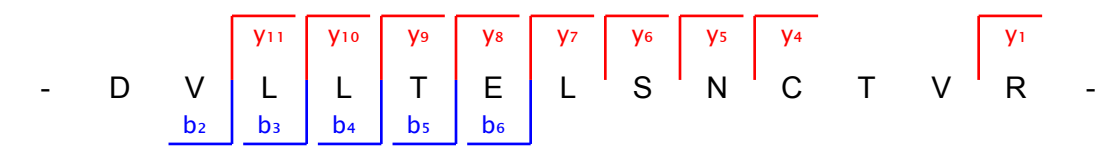
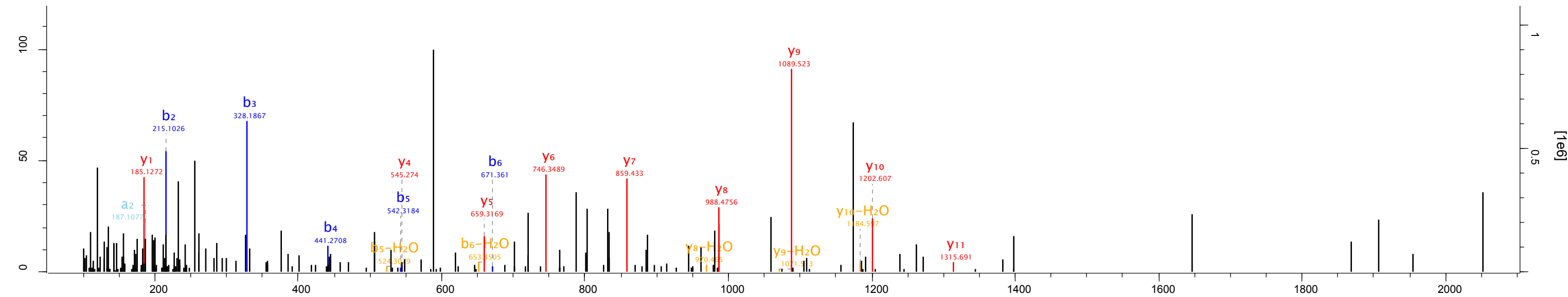
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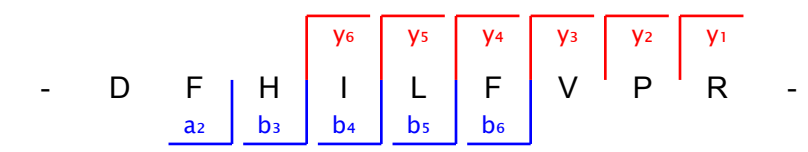
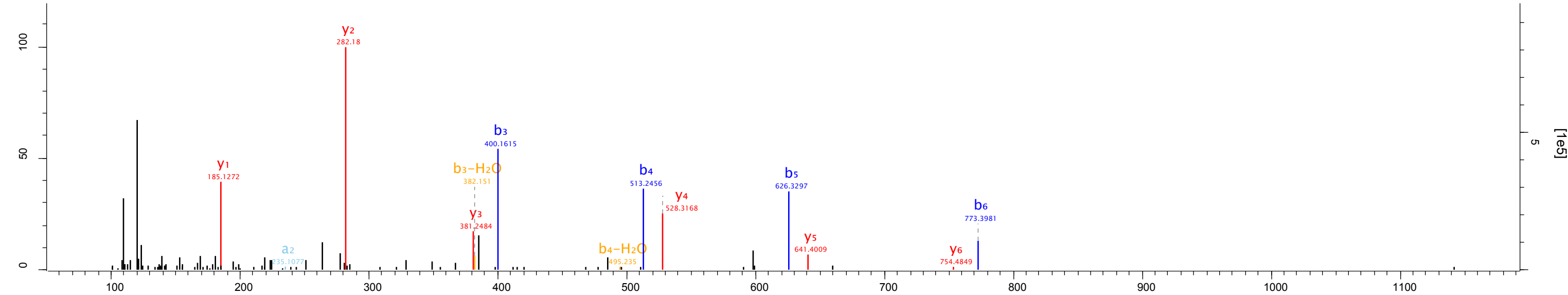
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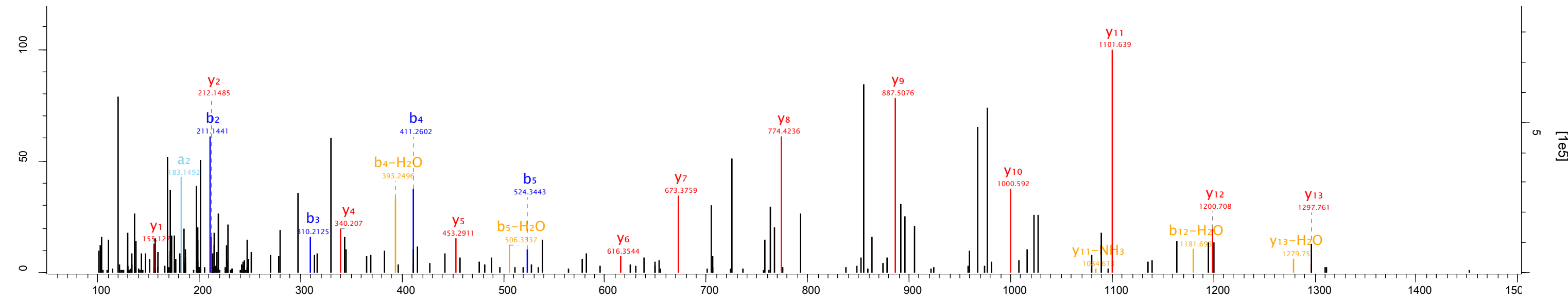


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20171215_MaS_33SR_LMH_proteome_01

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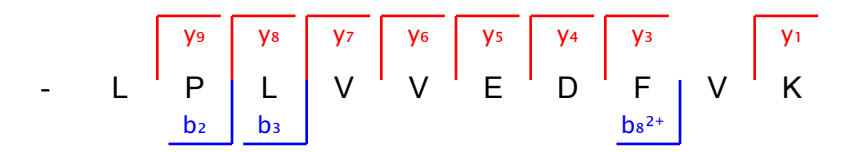
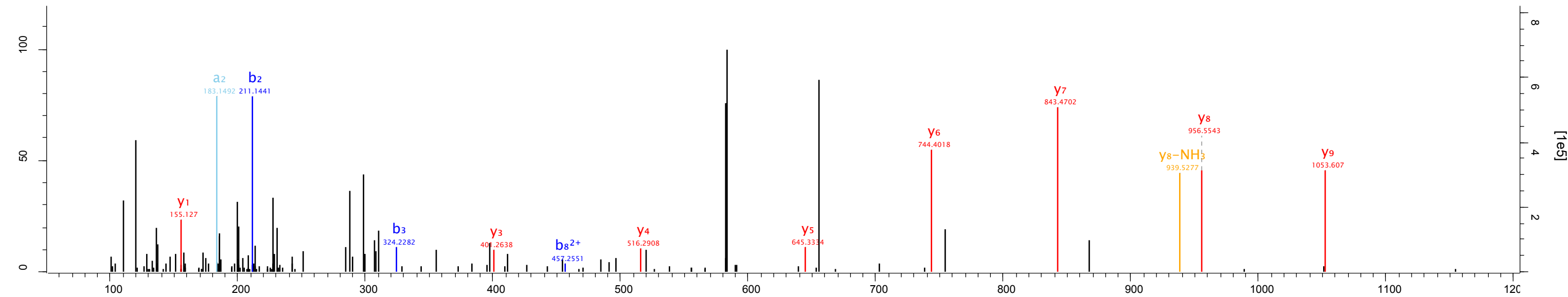
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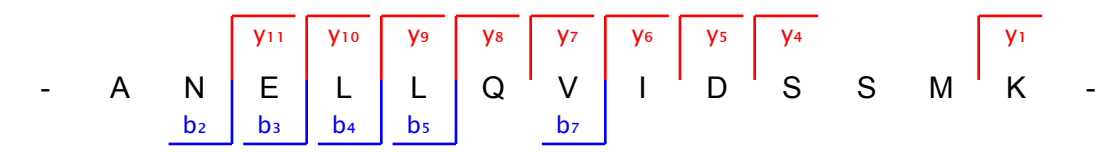
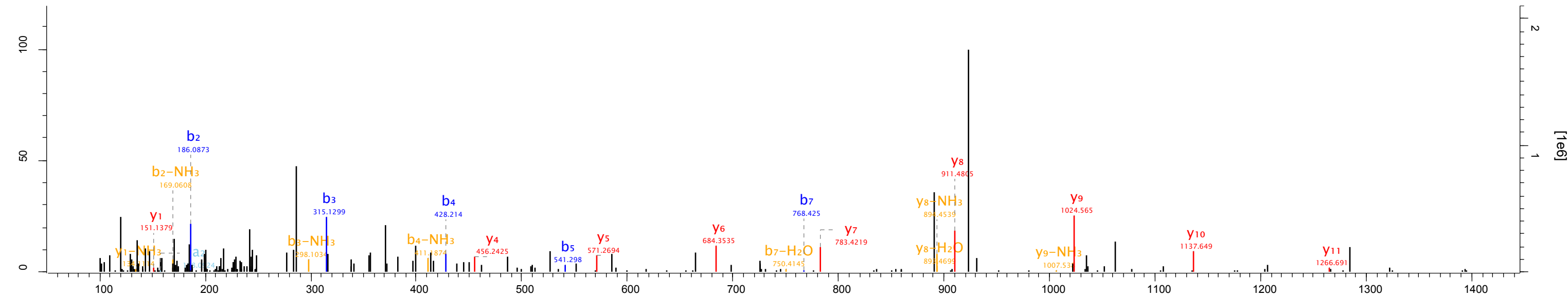
- Red boxes: y13 (I), y12 (V), y11 (T), y10 (I), y9 (I), y8 (T), y7 (G), y6 (Y), y5 (L), y4 (G), y2 (G), y1 (K)
- Blue boxes: b2 (P), b3 (V), b4 (T), b5 (I)

Raw file
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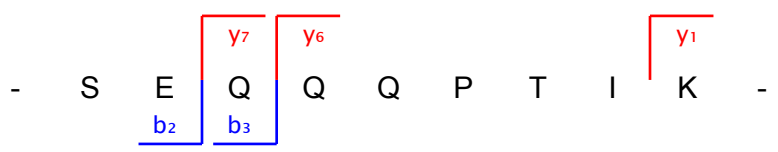
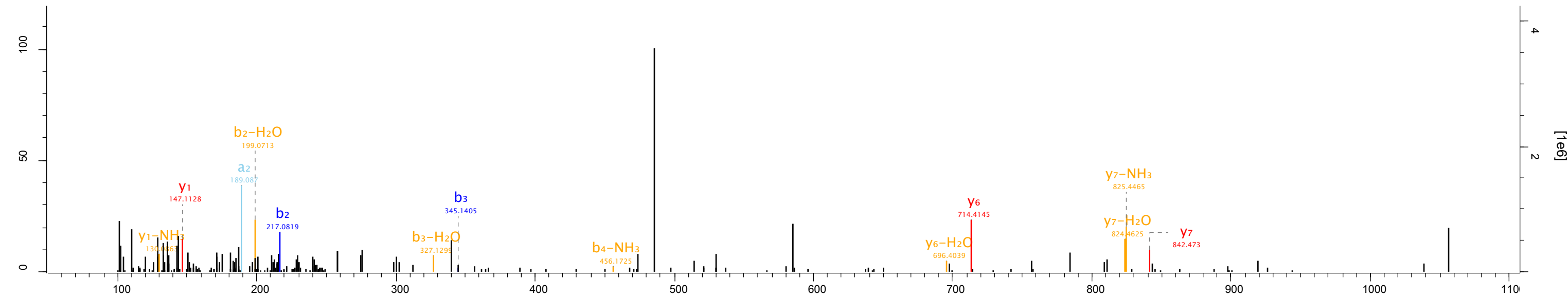
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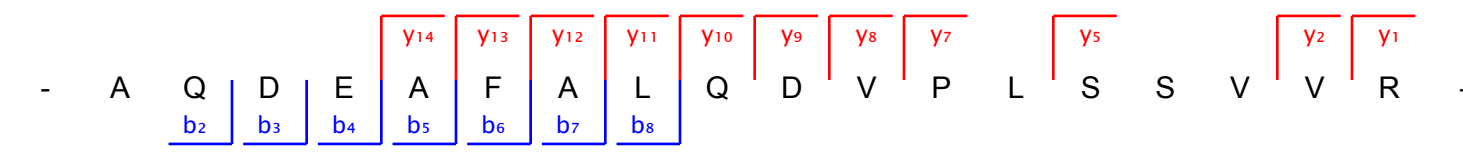
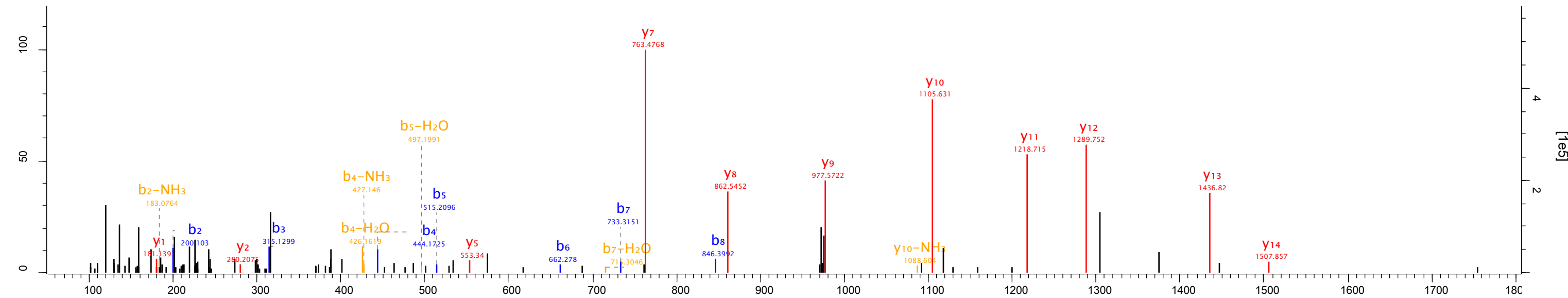


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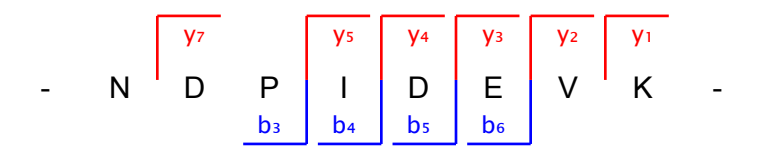
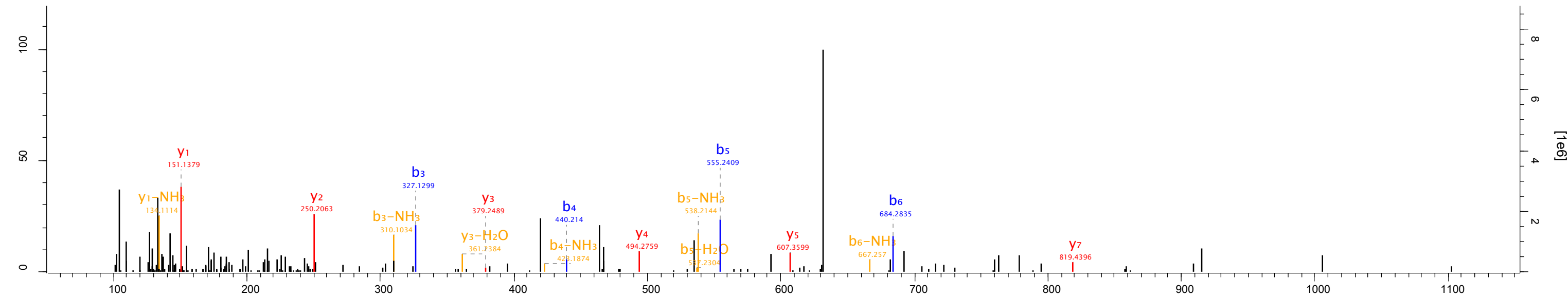


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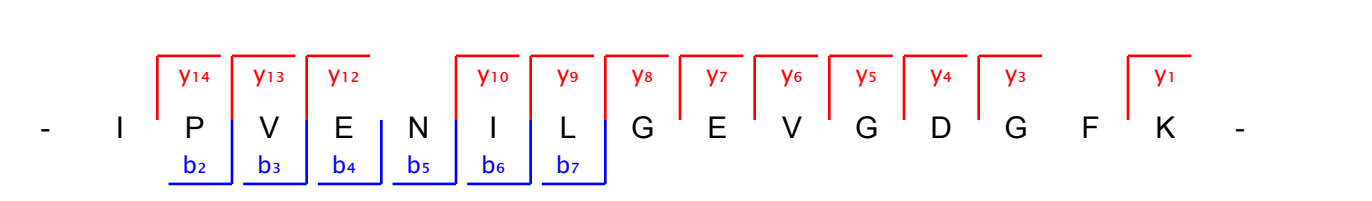
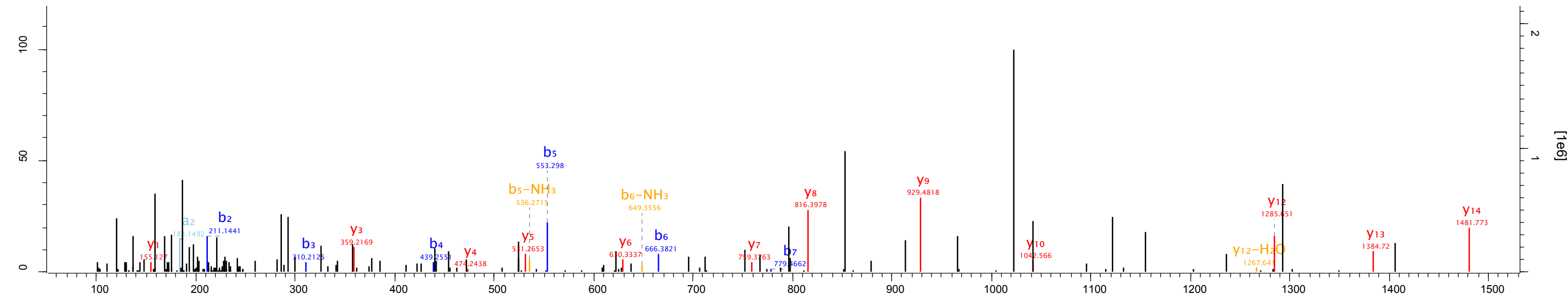
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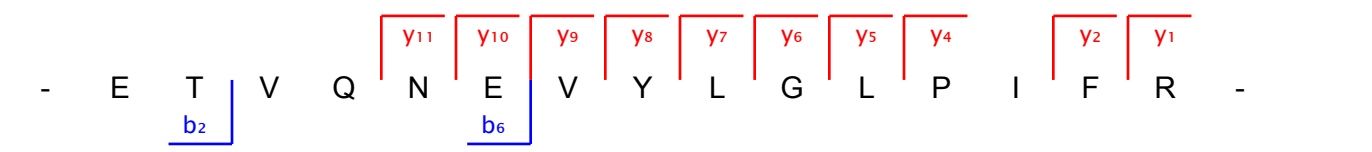
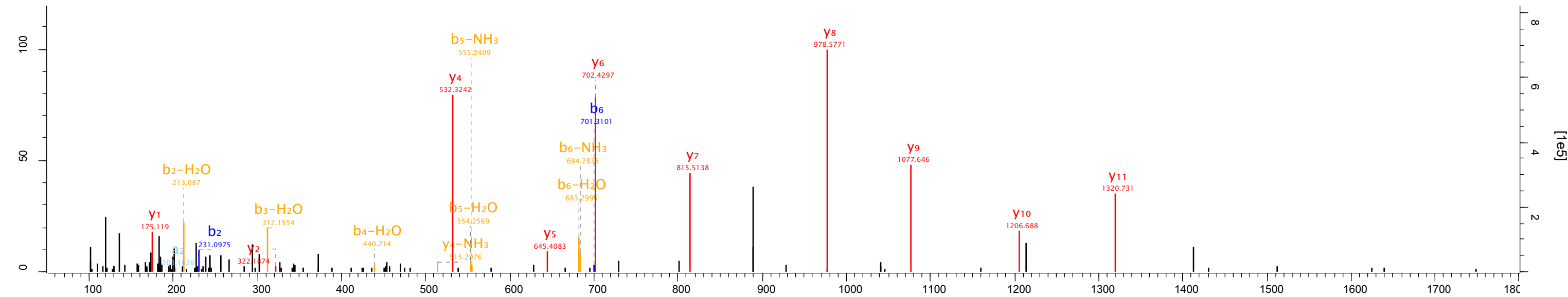
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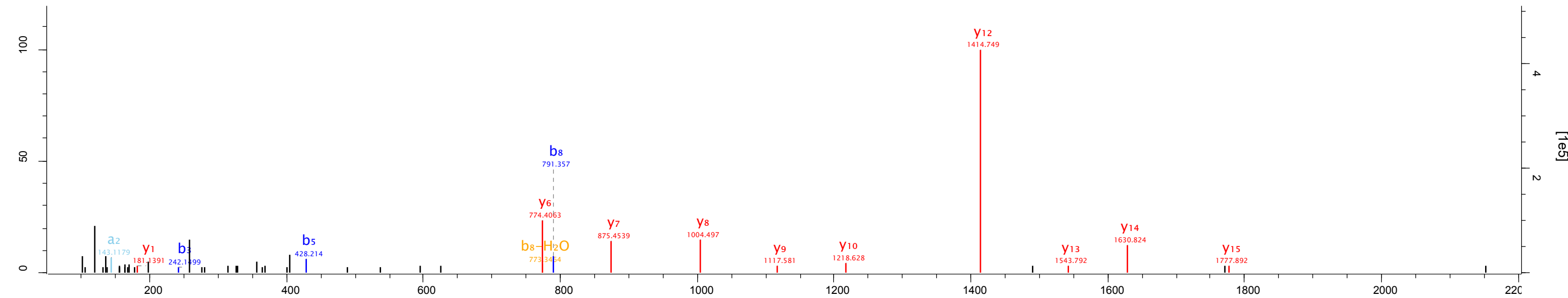
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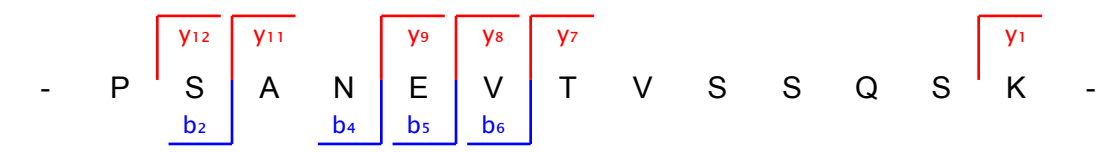
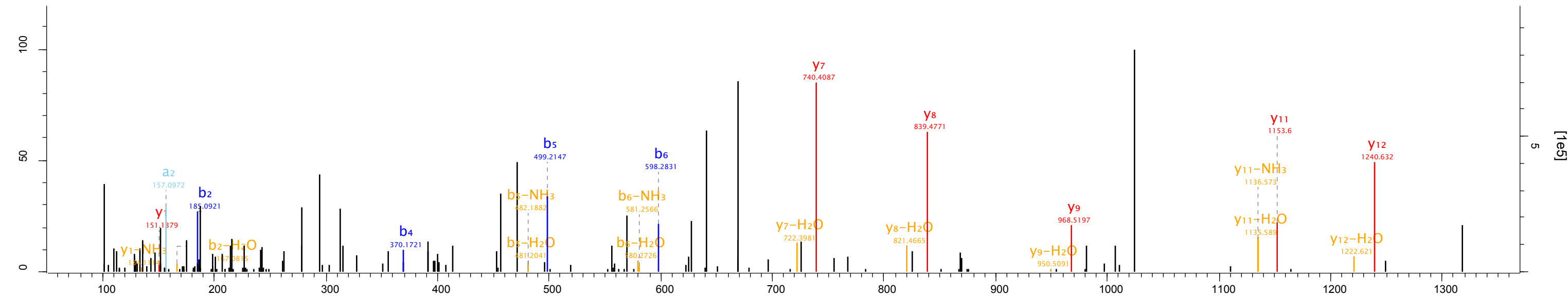
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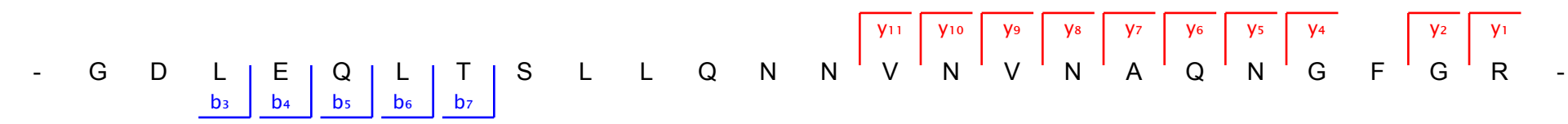
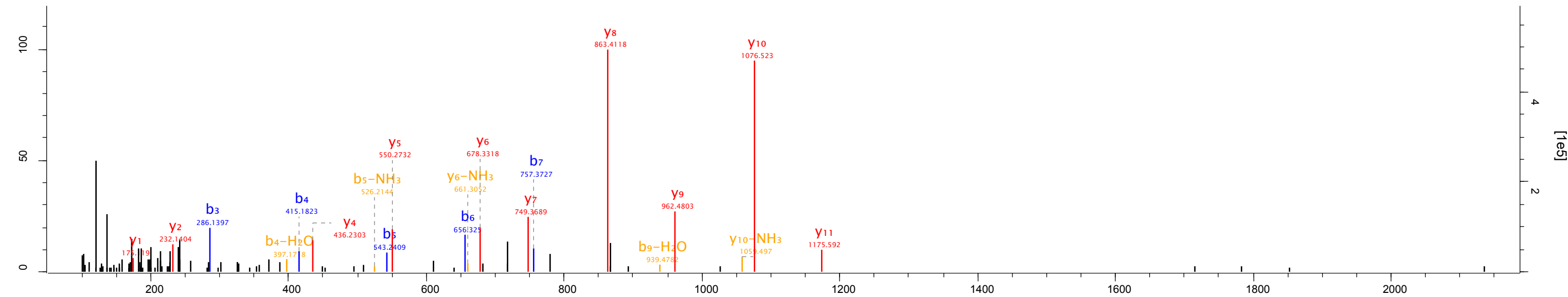
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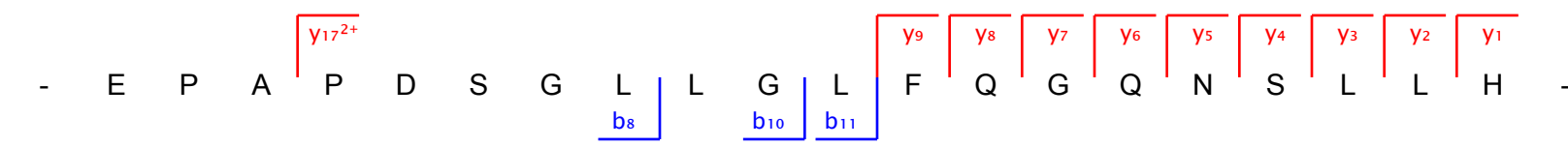
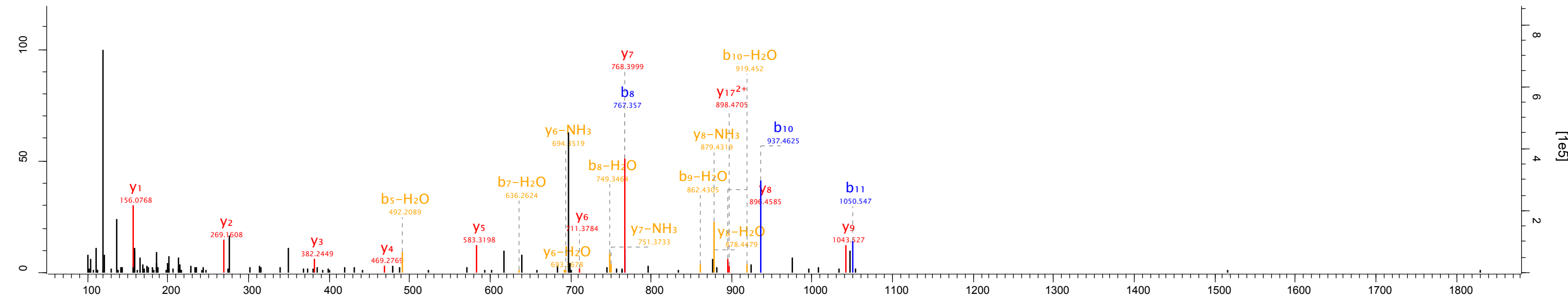


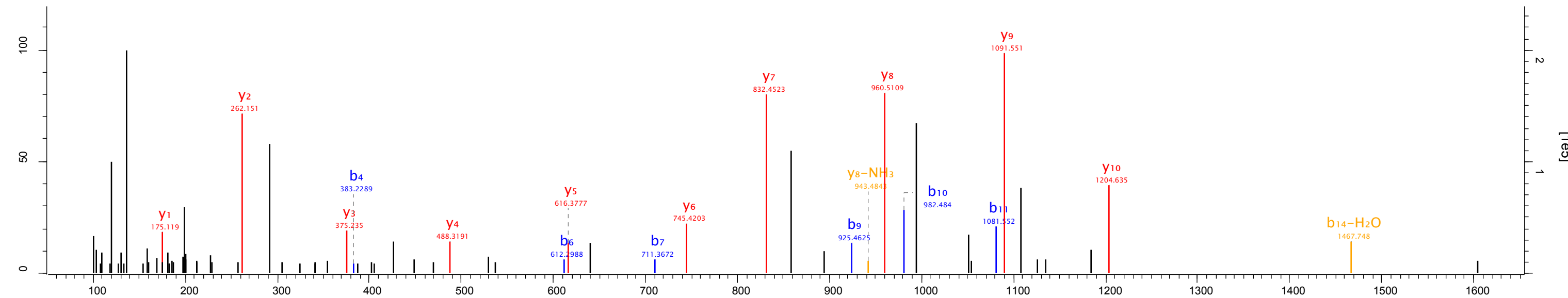
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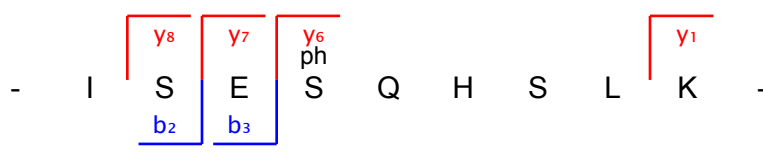
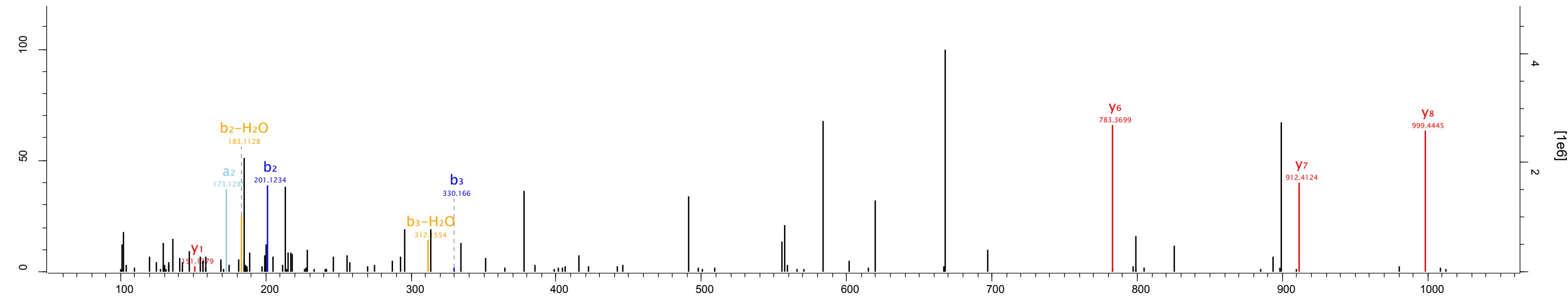




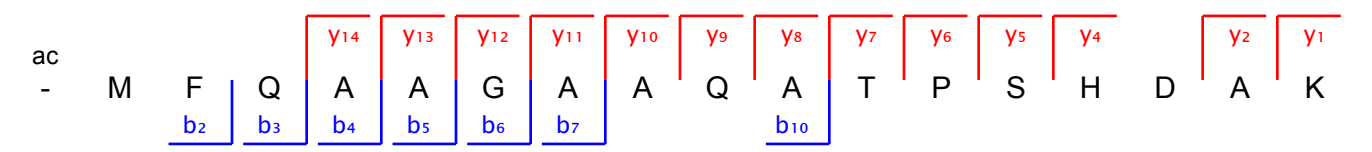
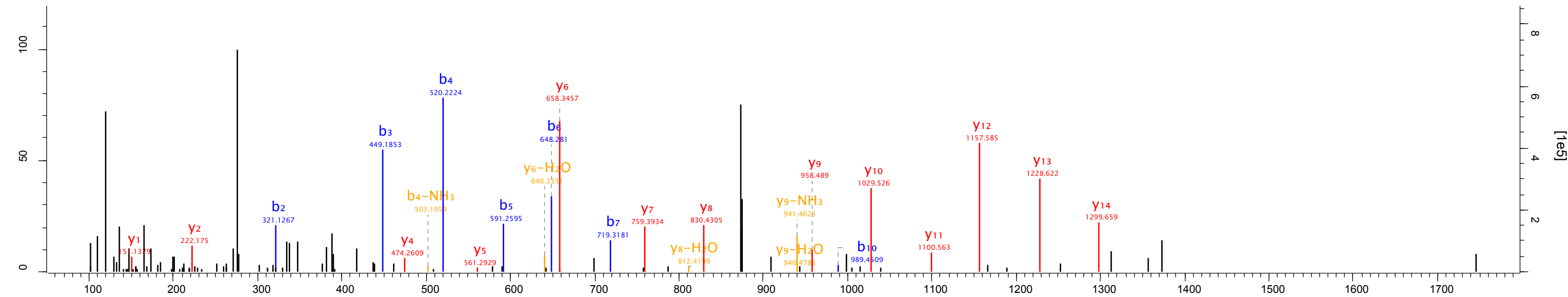
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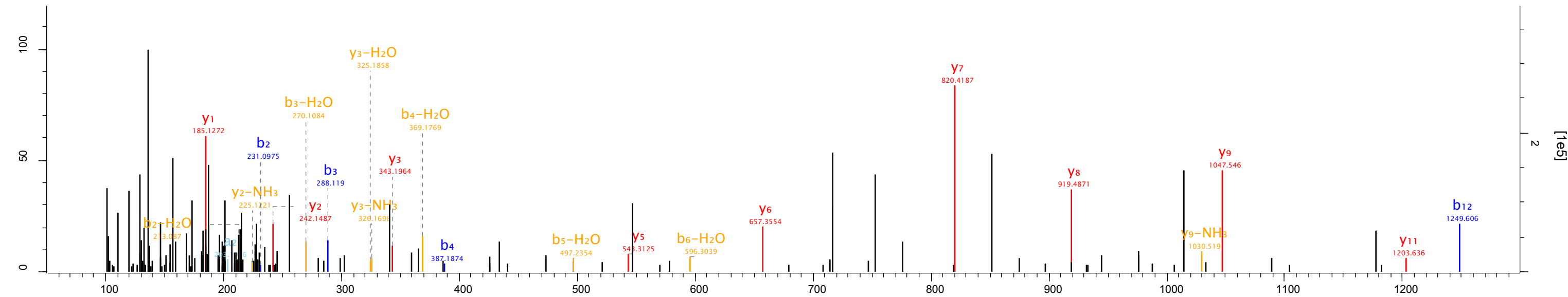
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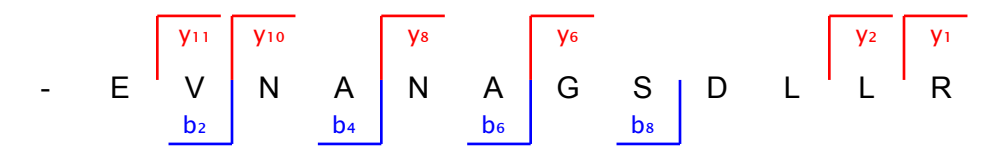
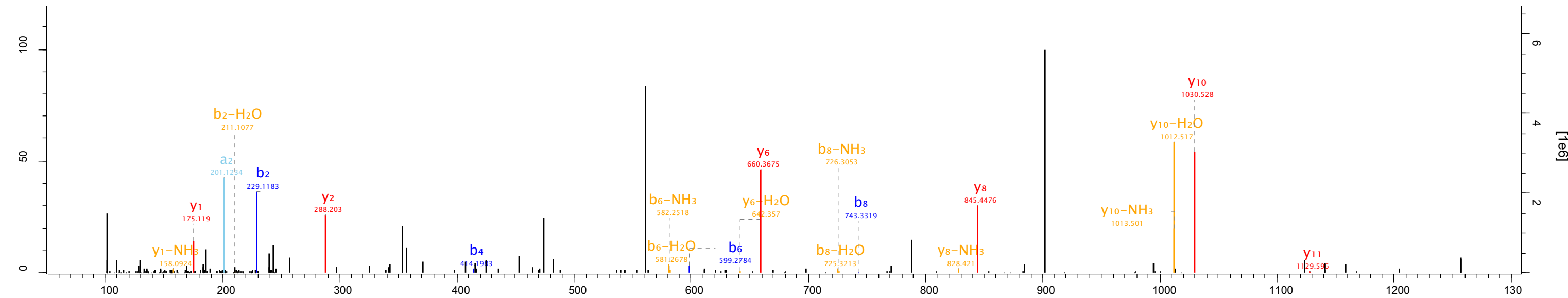
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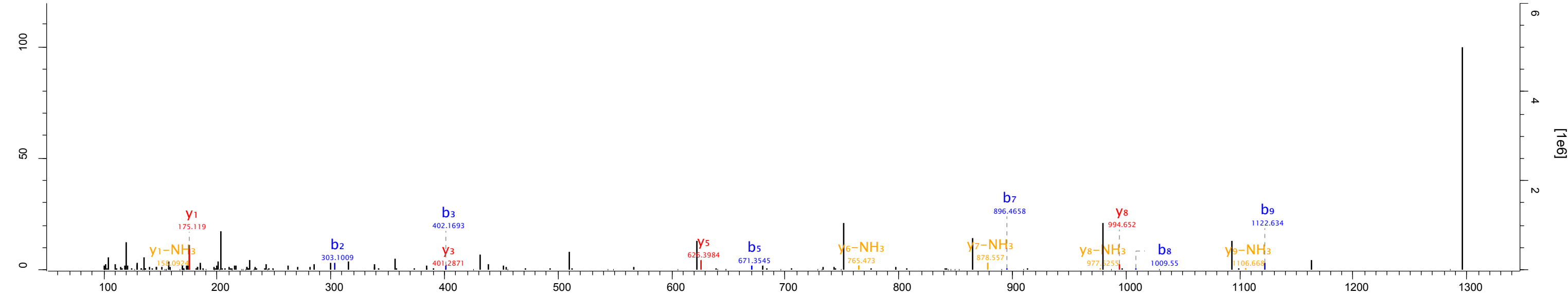
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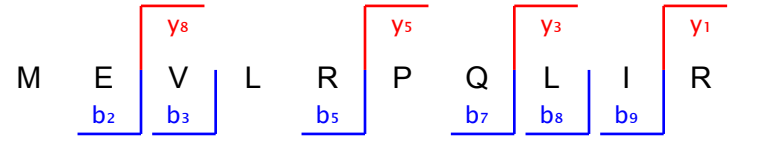
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20171215_MaS_33SR_LMH_proteome_02

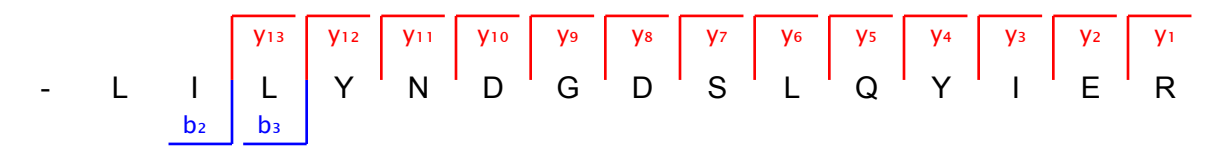
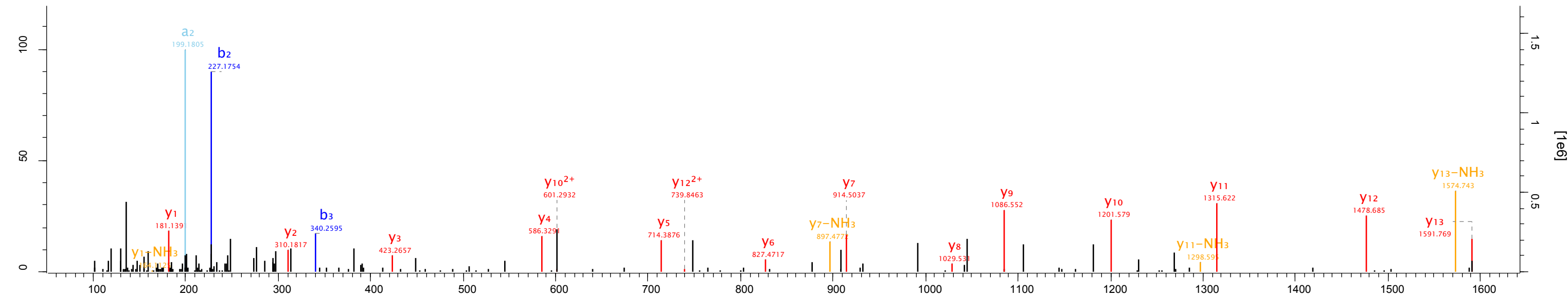
Scan	Method	Score	m/z	Gene names
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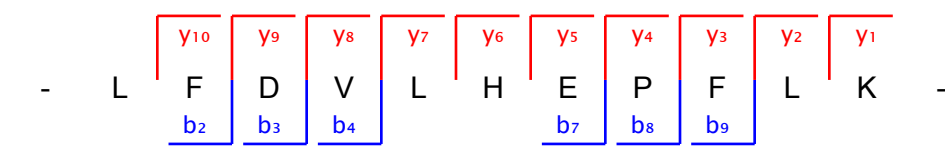
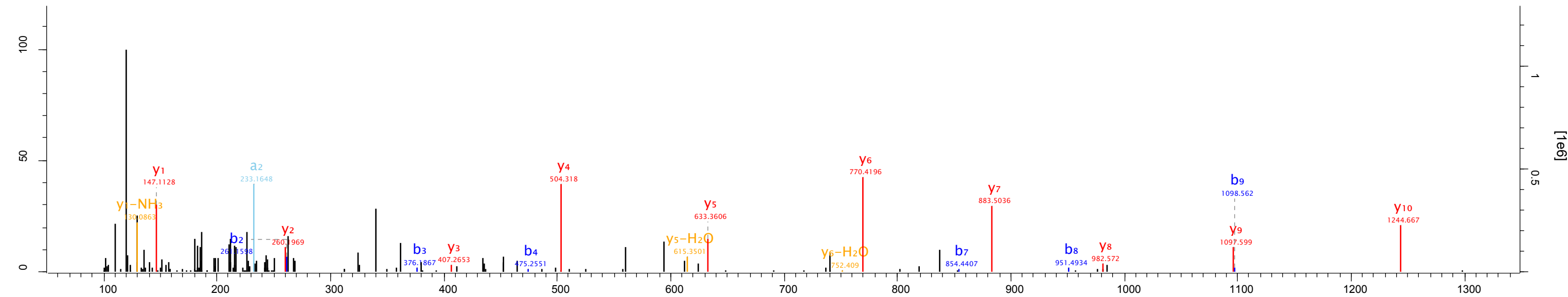
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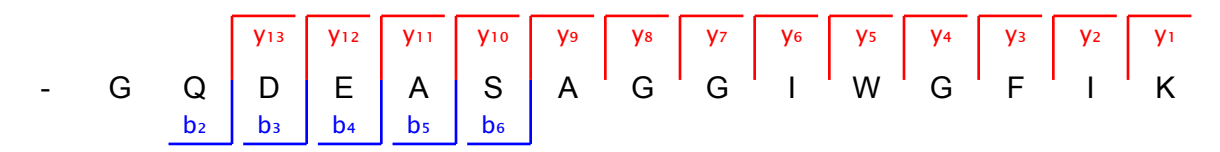
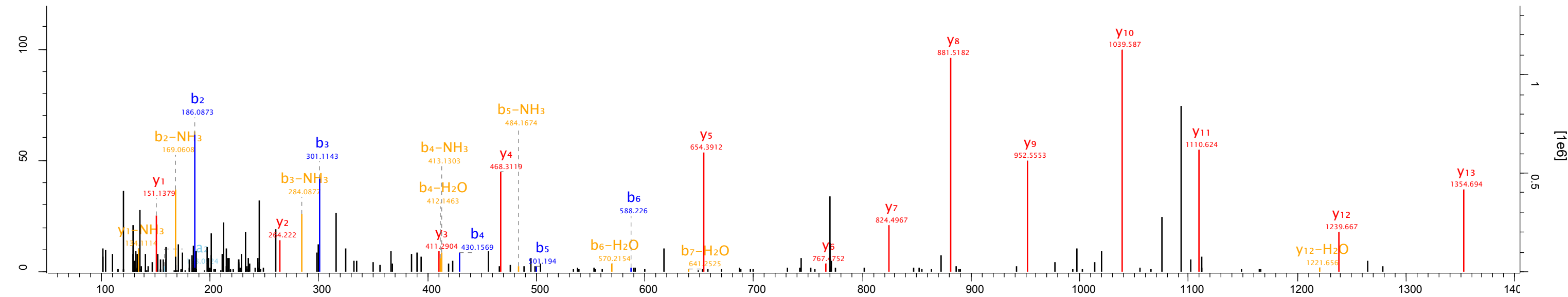
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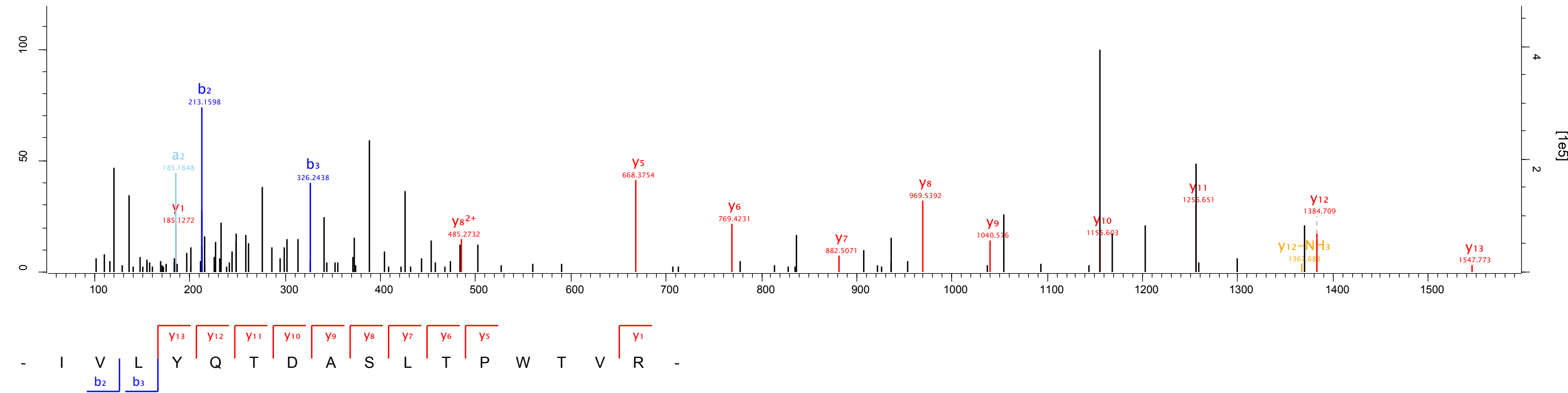


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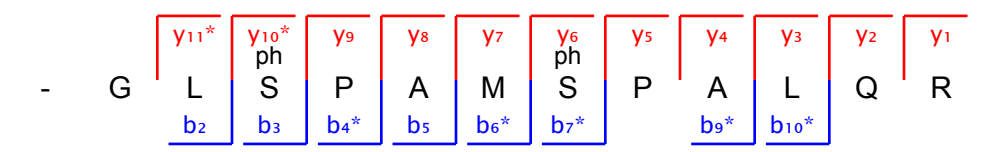
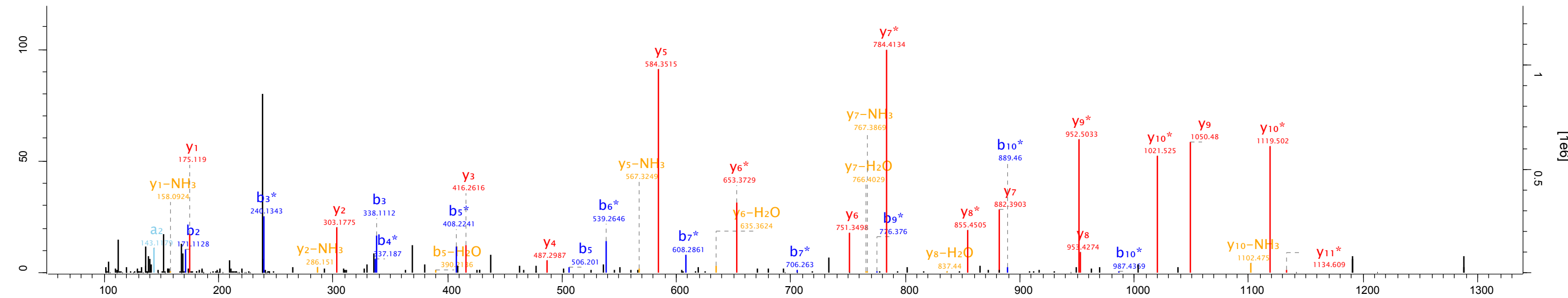


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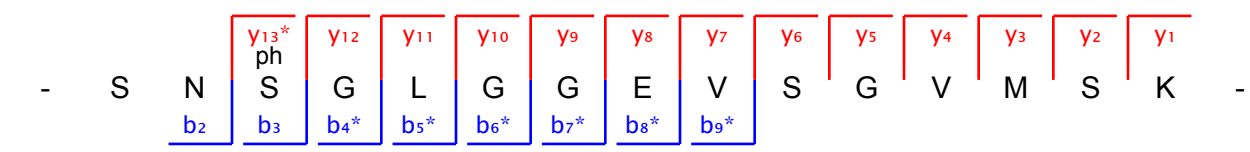
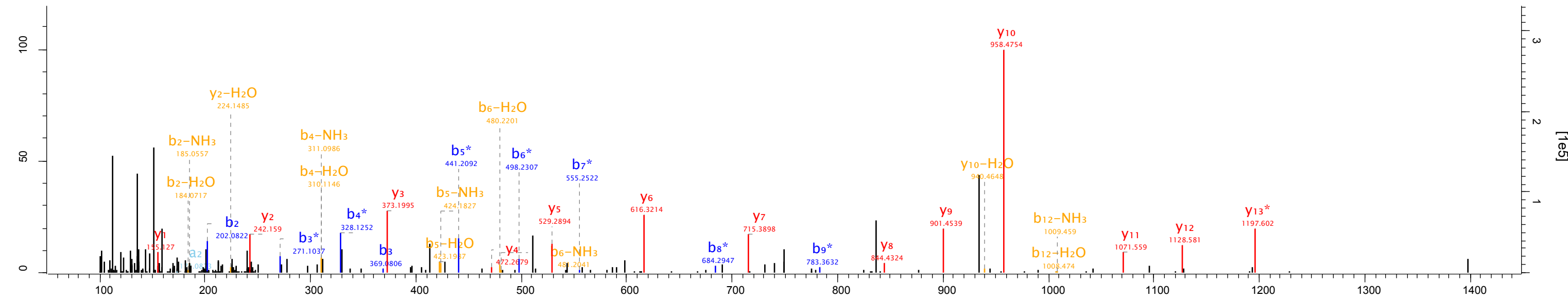




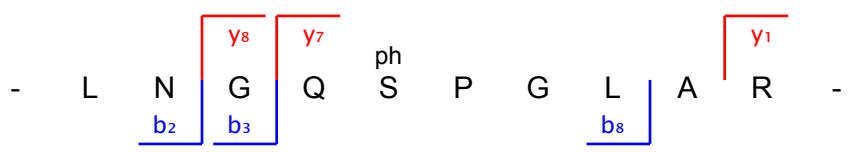
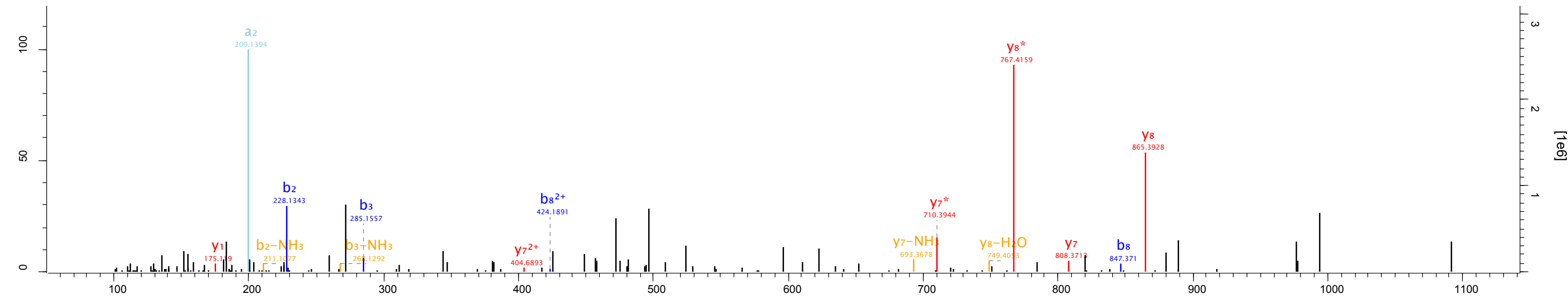
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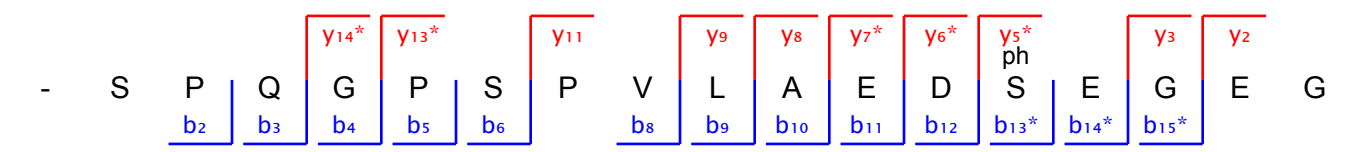
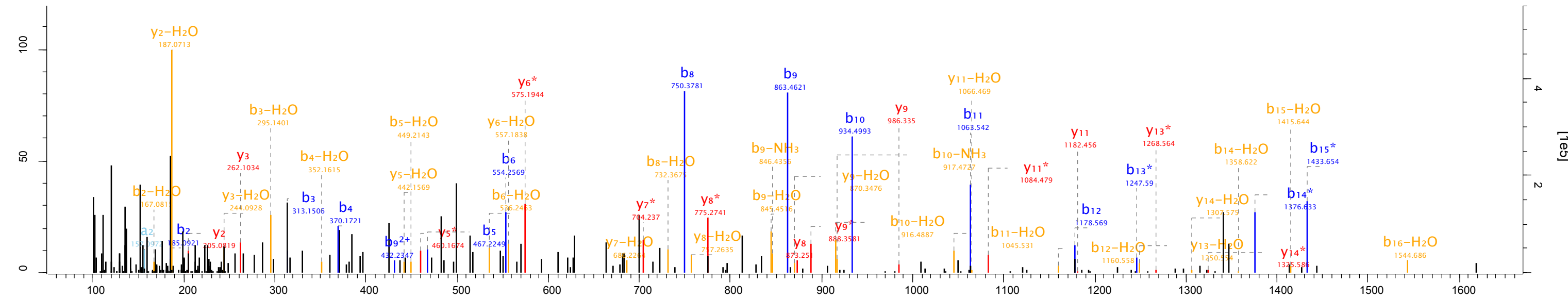
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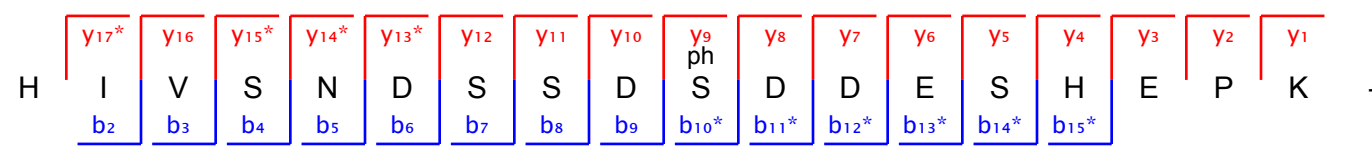
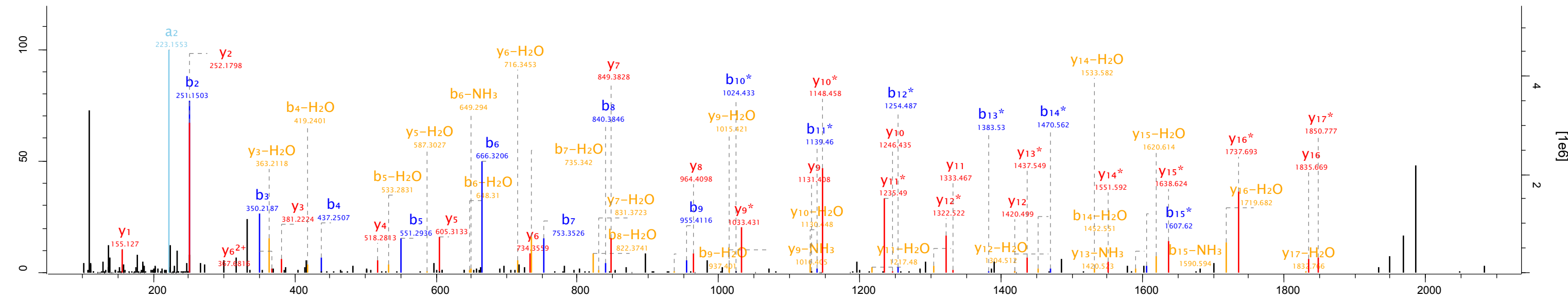
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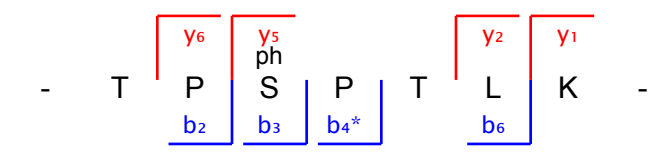
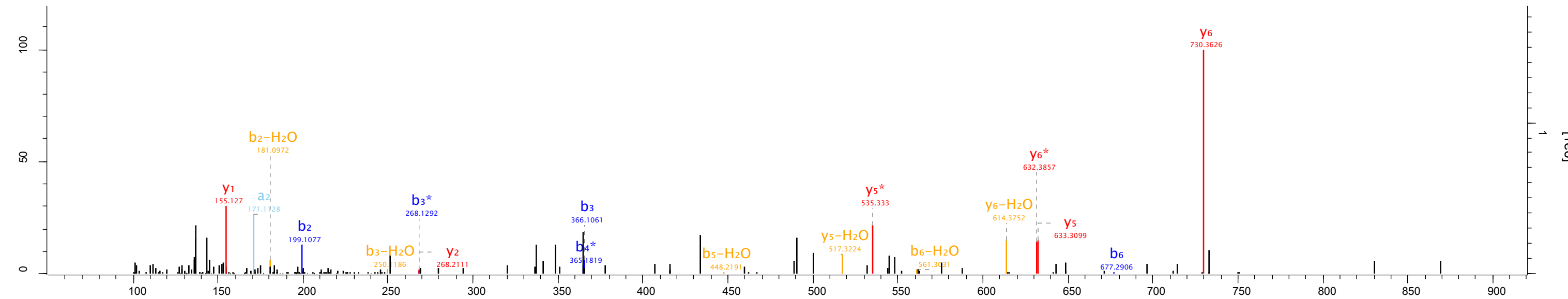
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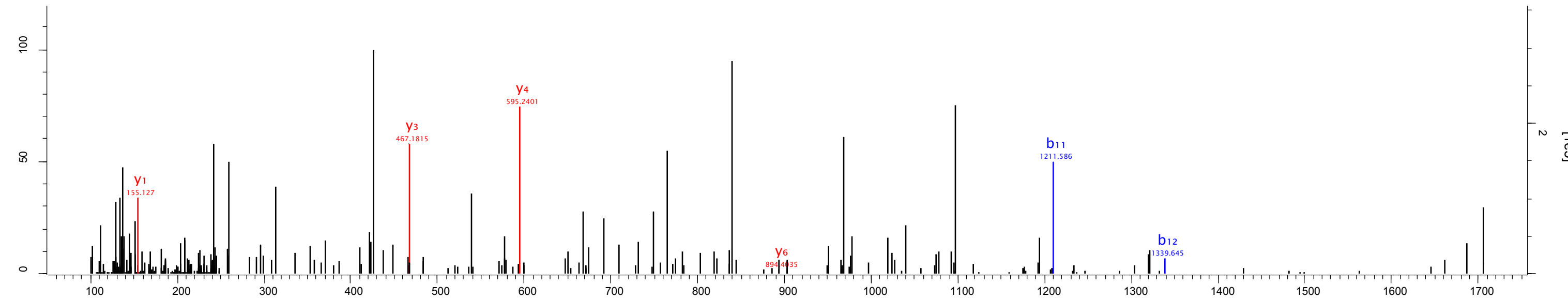
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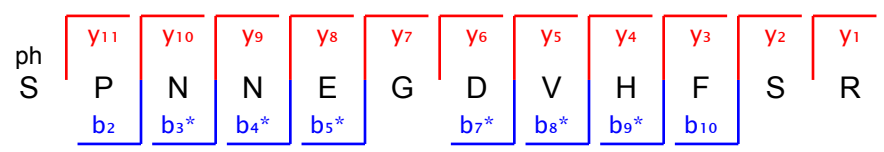
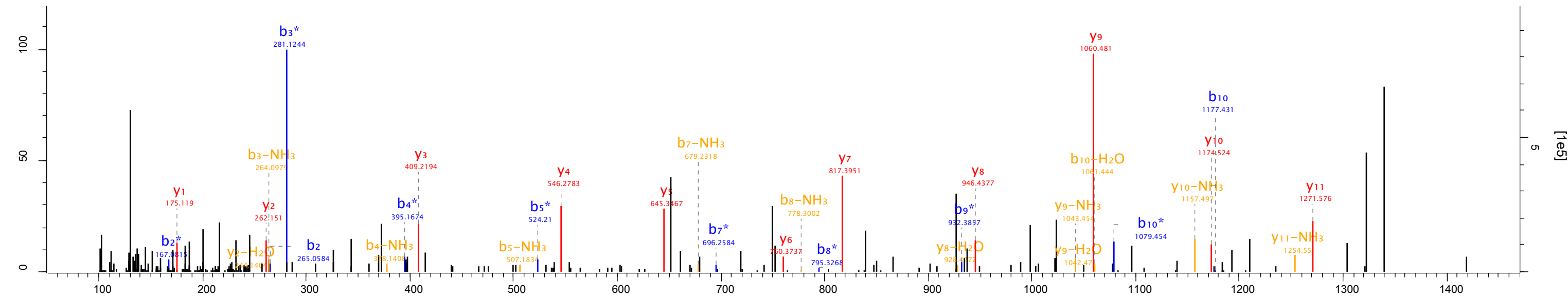
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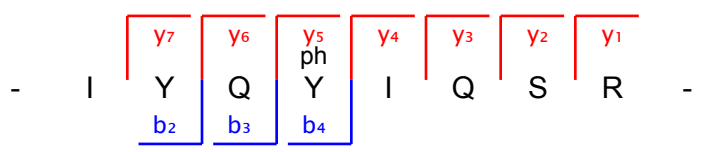
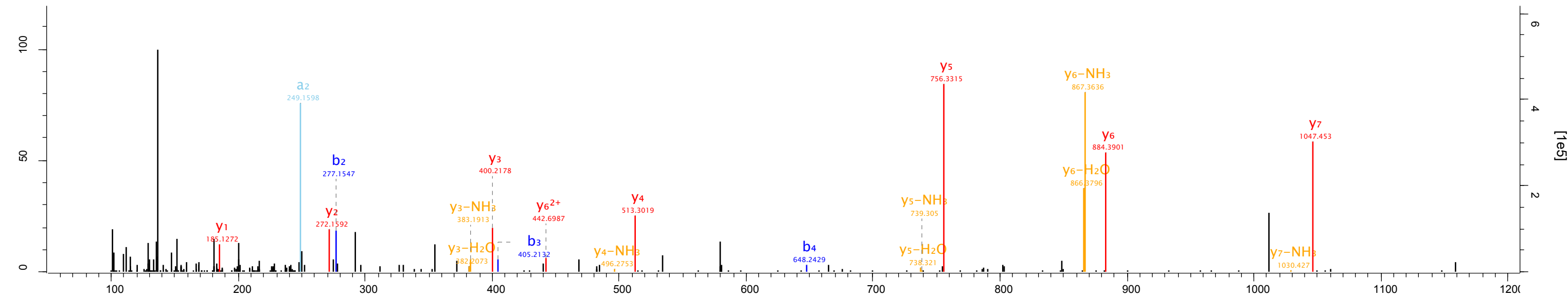
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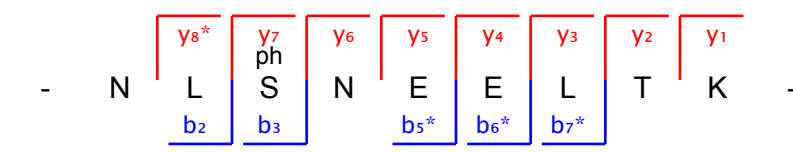
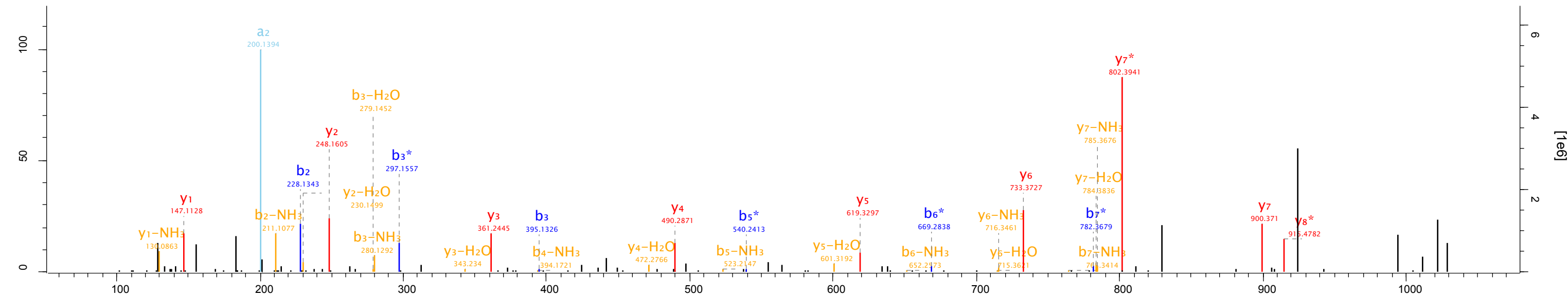
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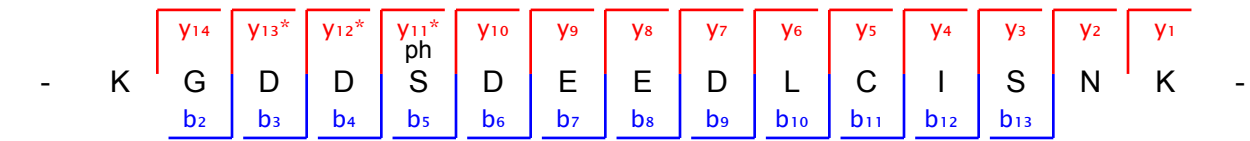
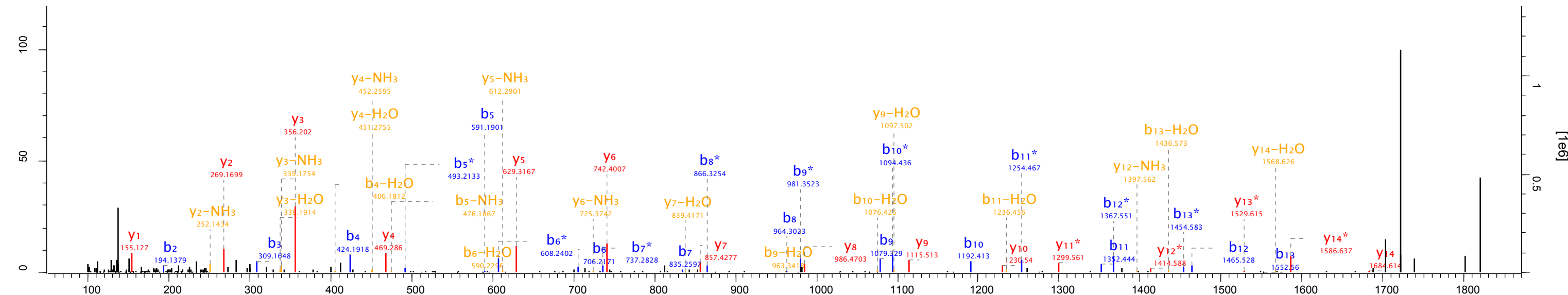
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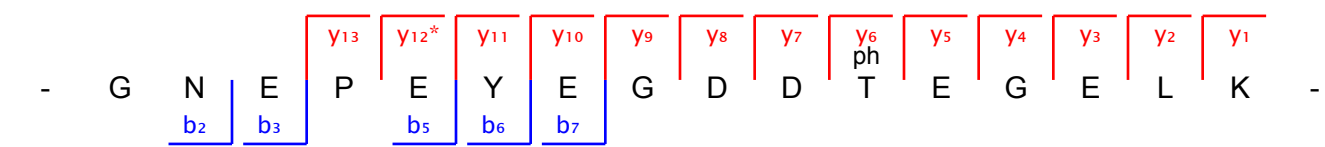
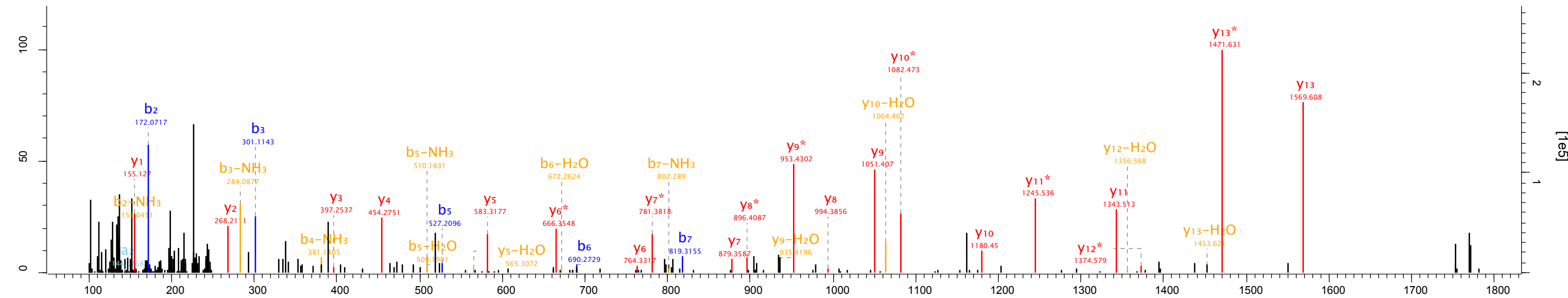
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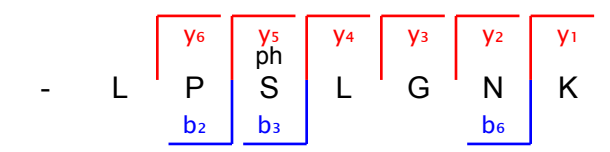
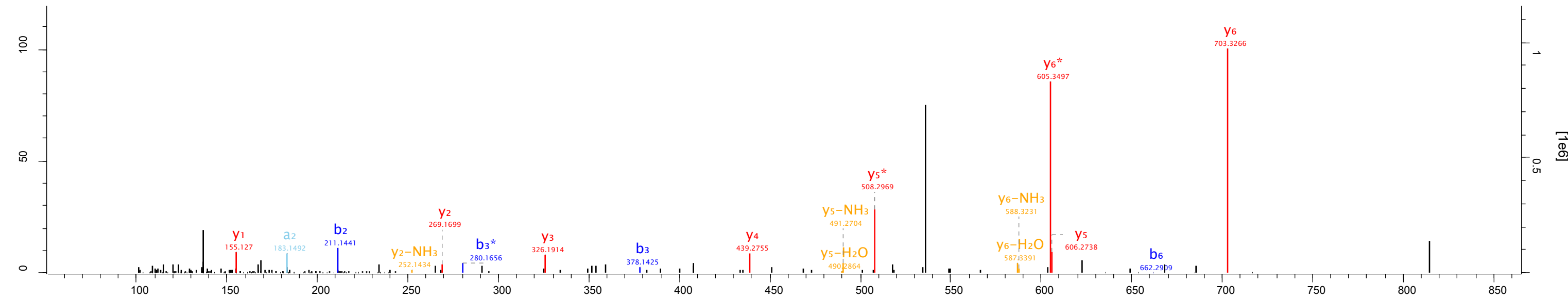
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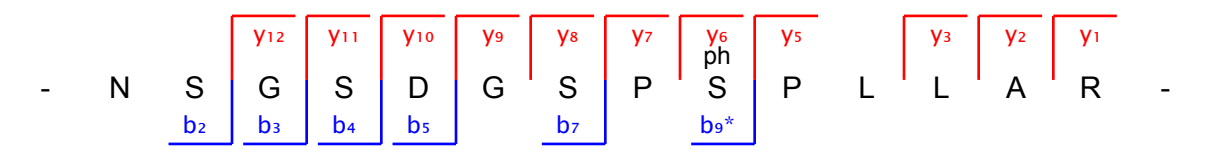
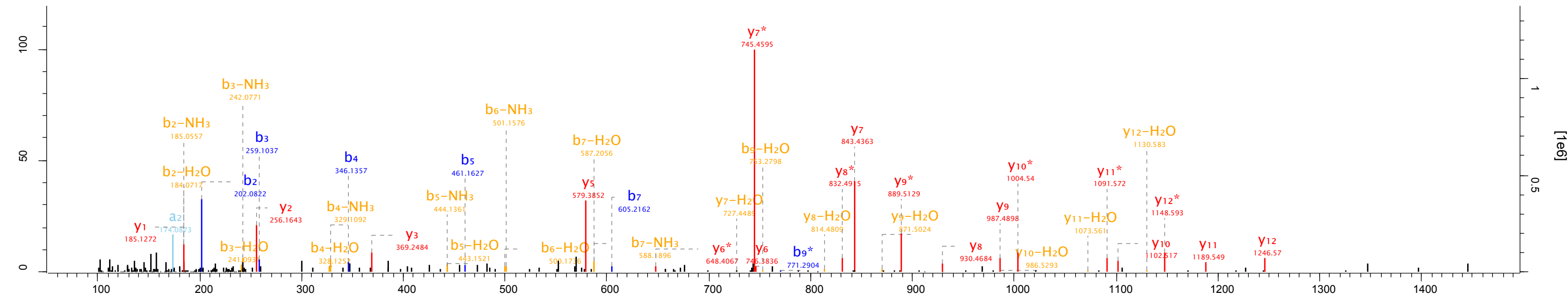
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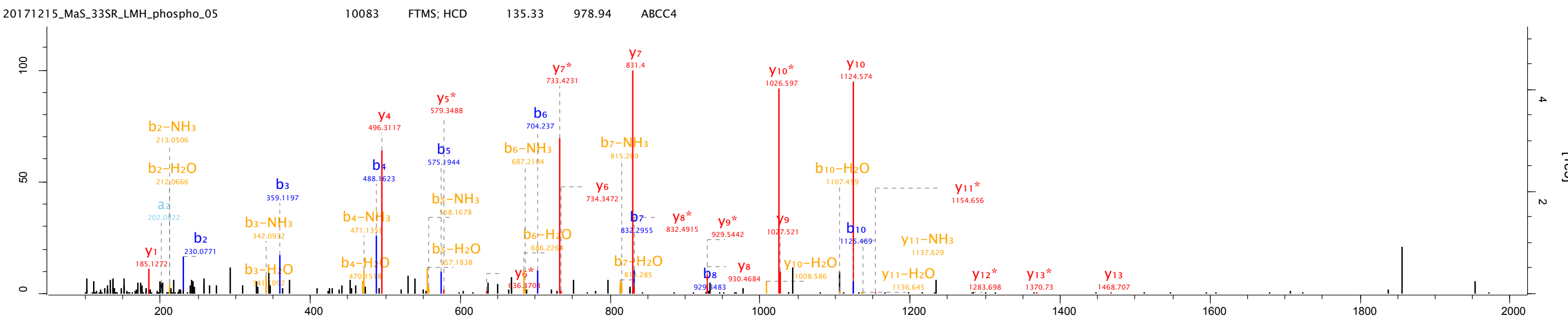
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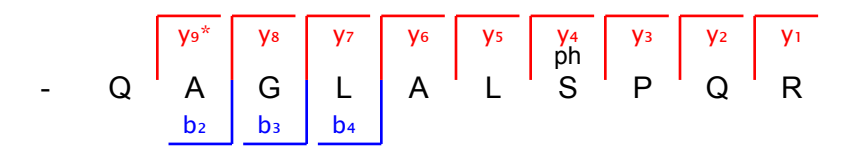
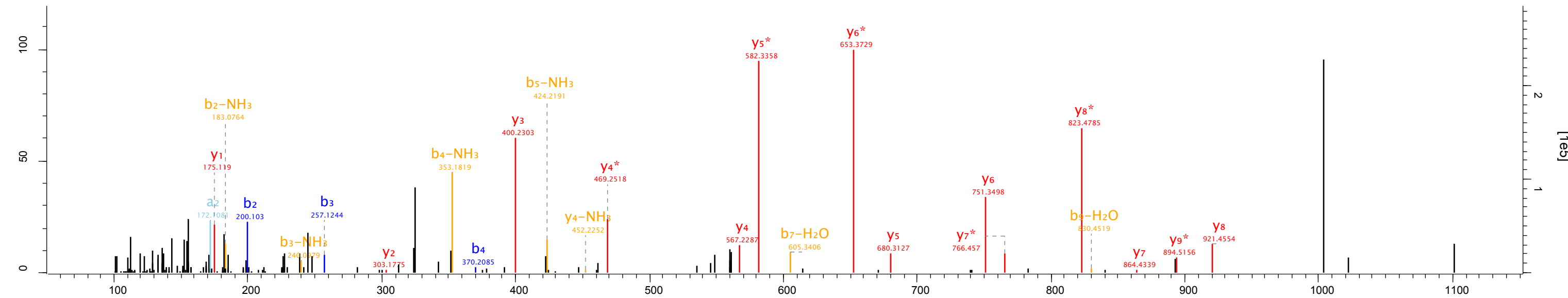
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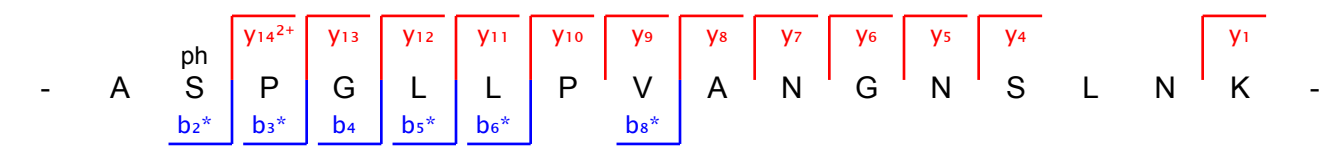
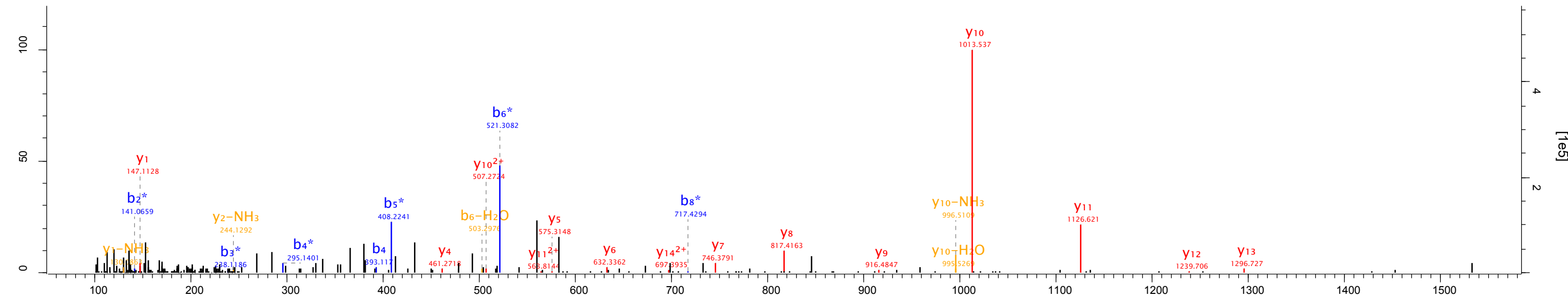
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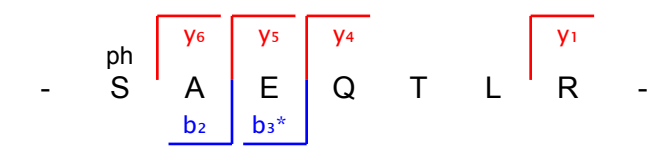
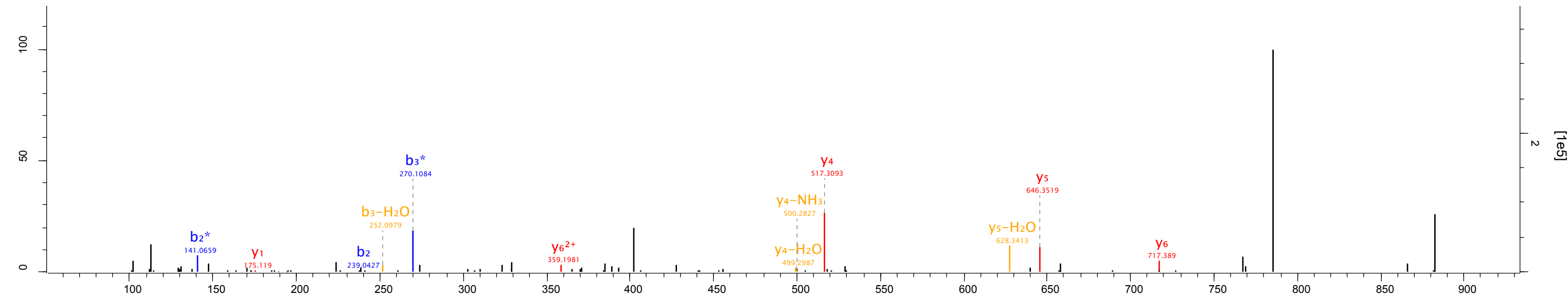
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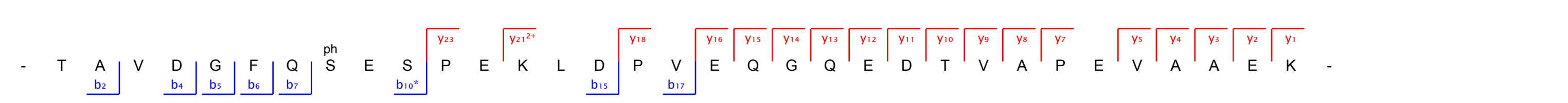
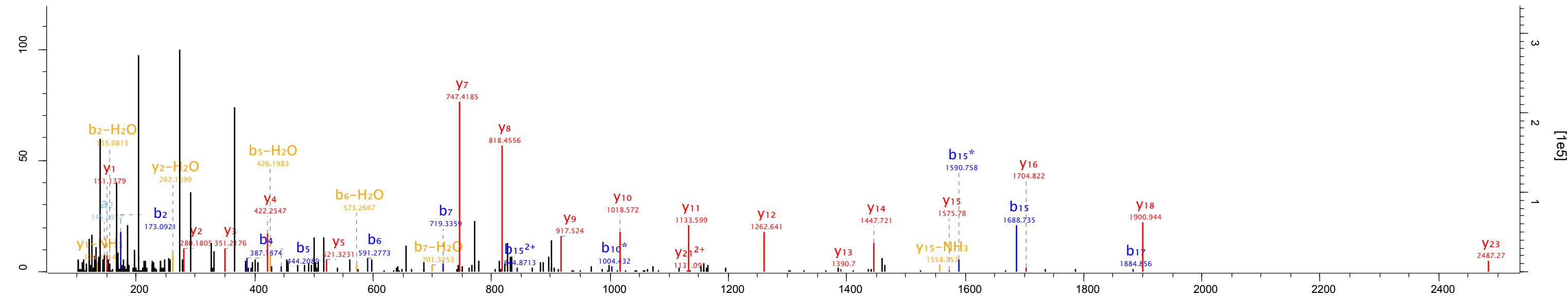
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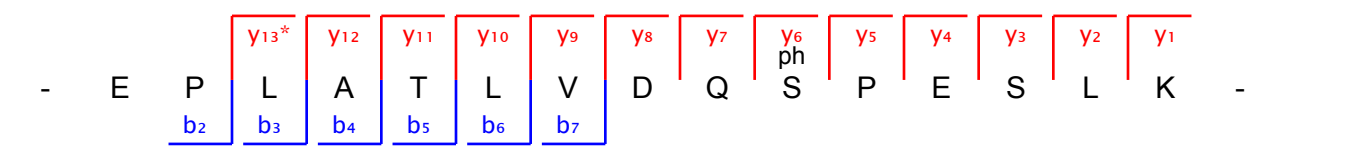
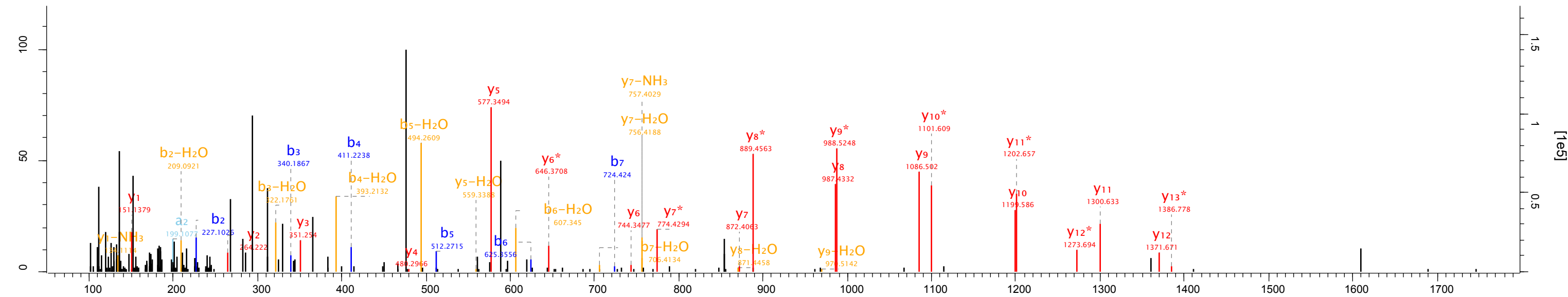
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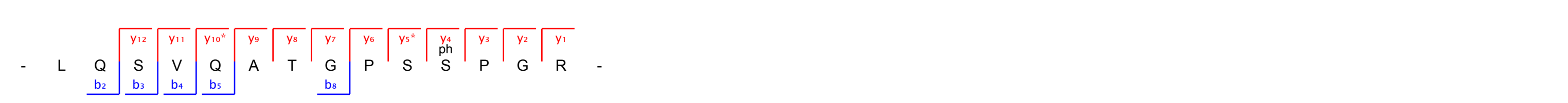
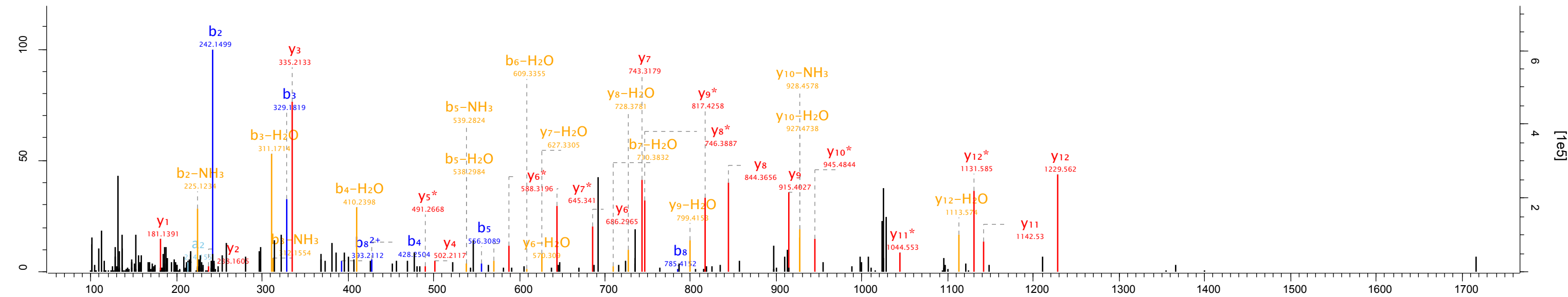
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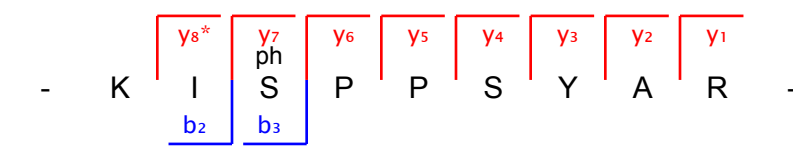
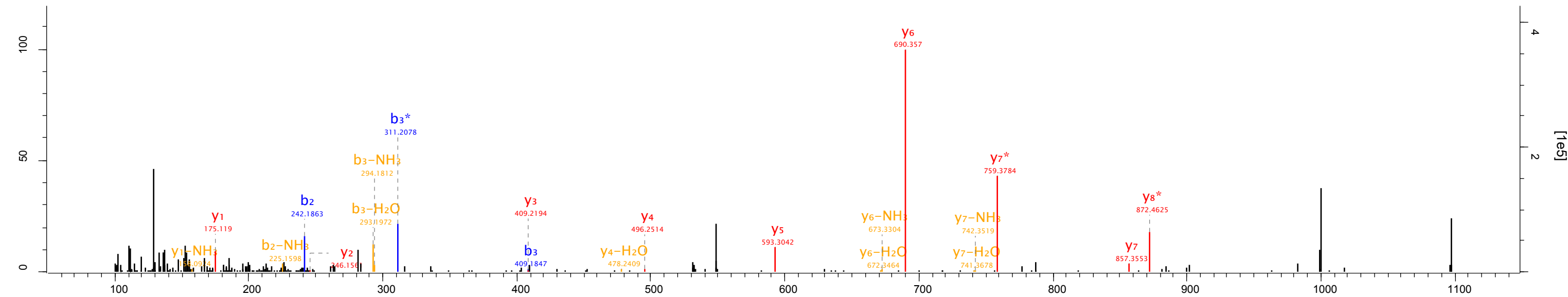
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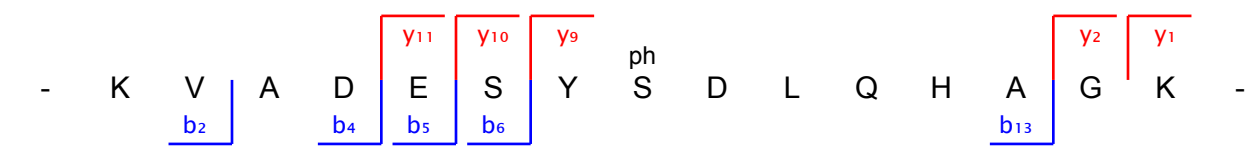
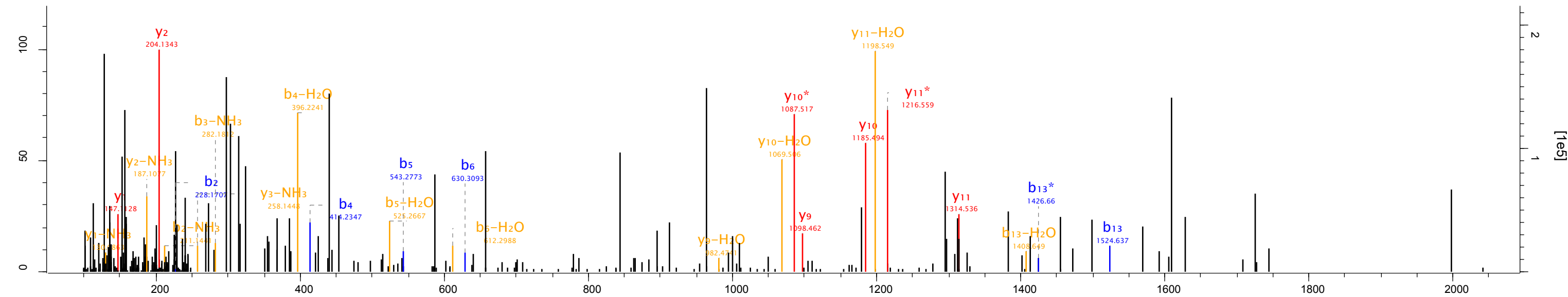
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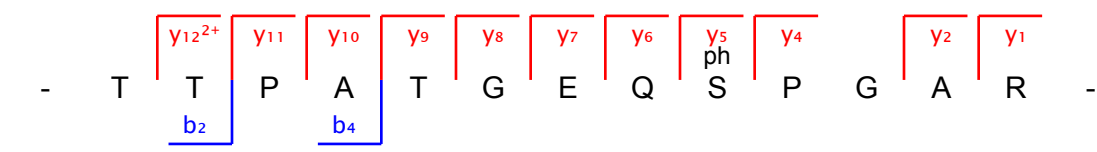
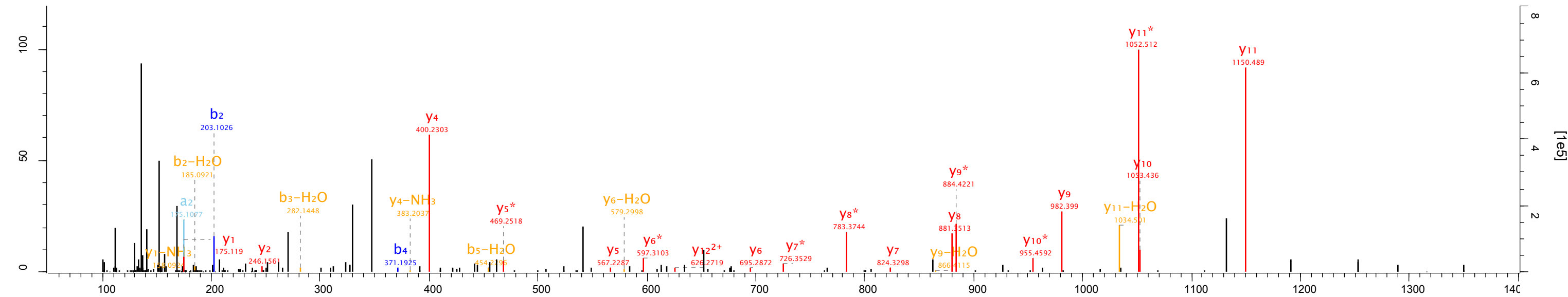
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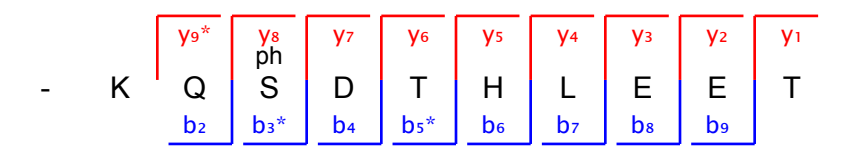
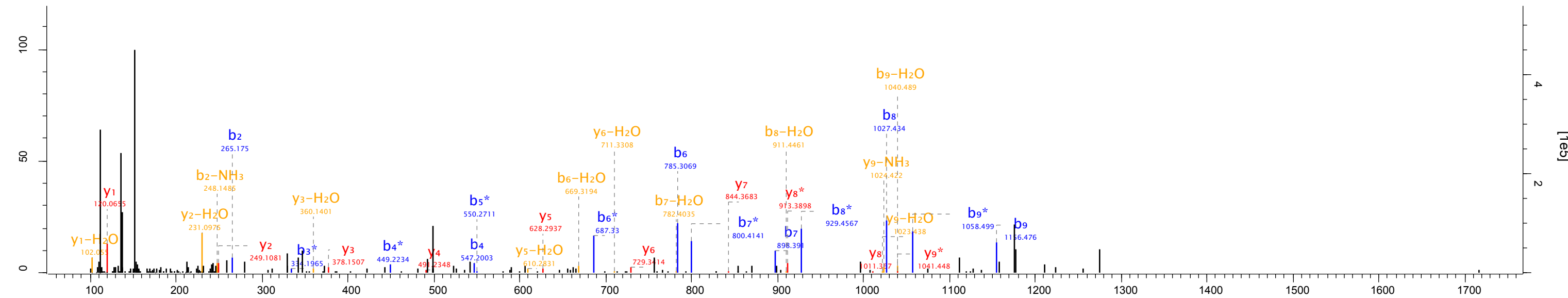
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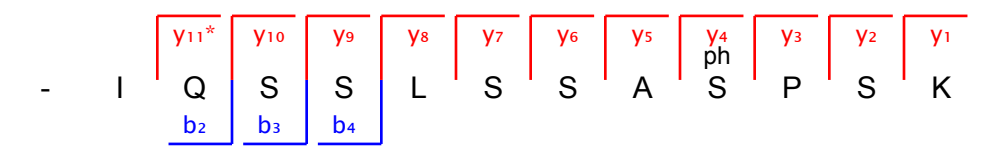
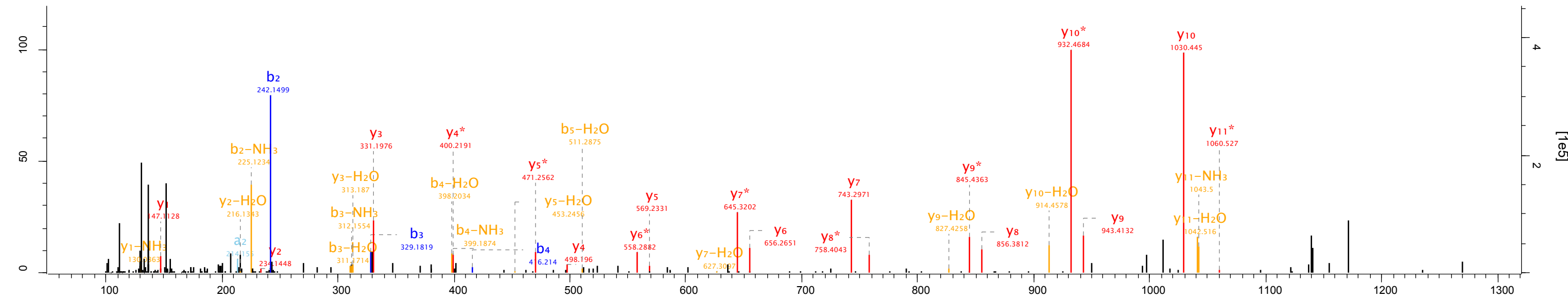
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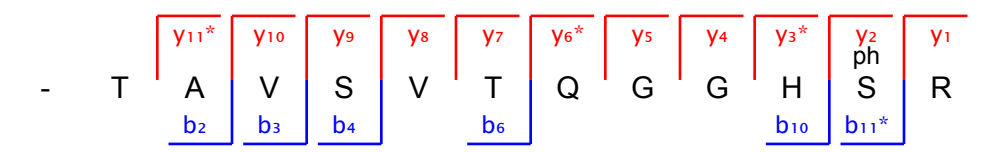
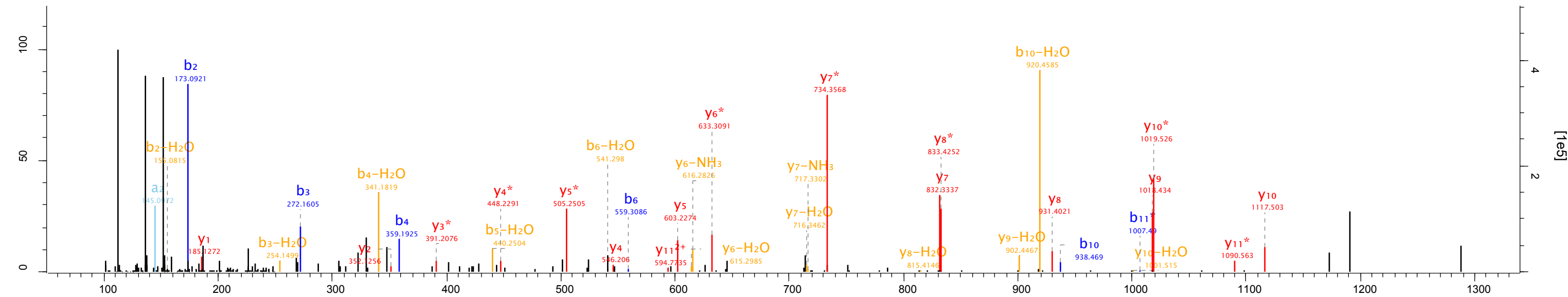
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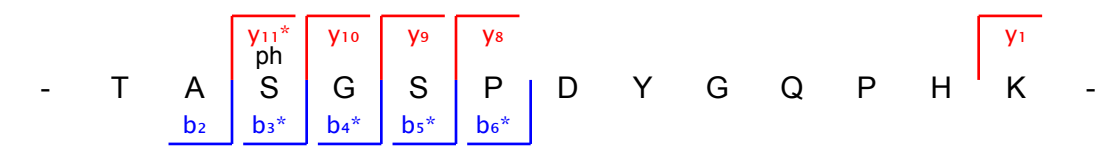
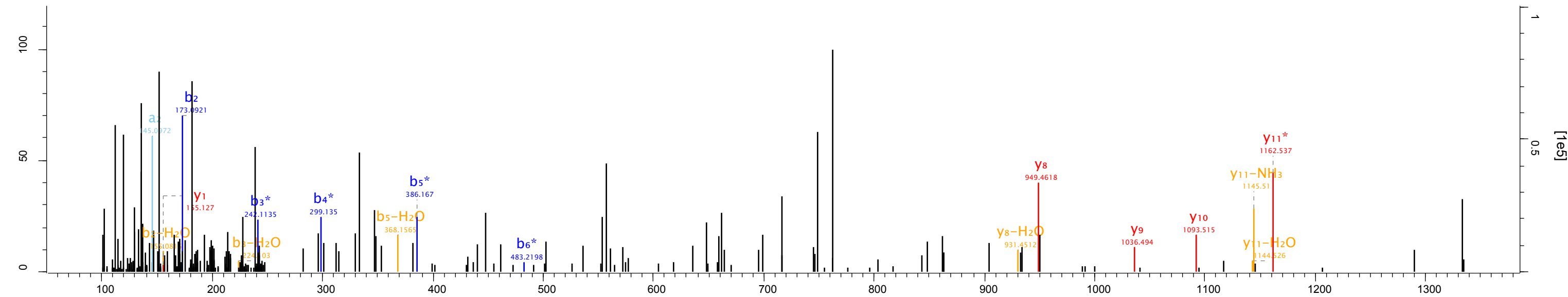
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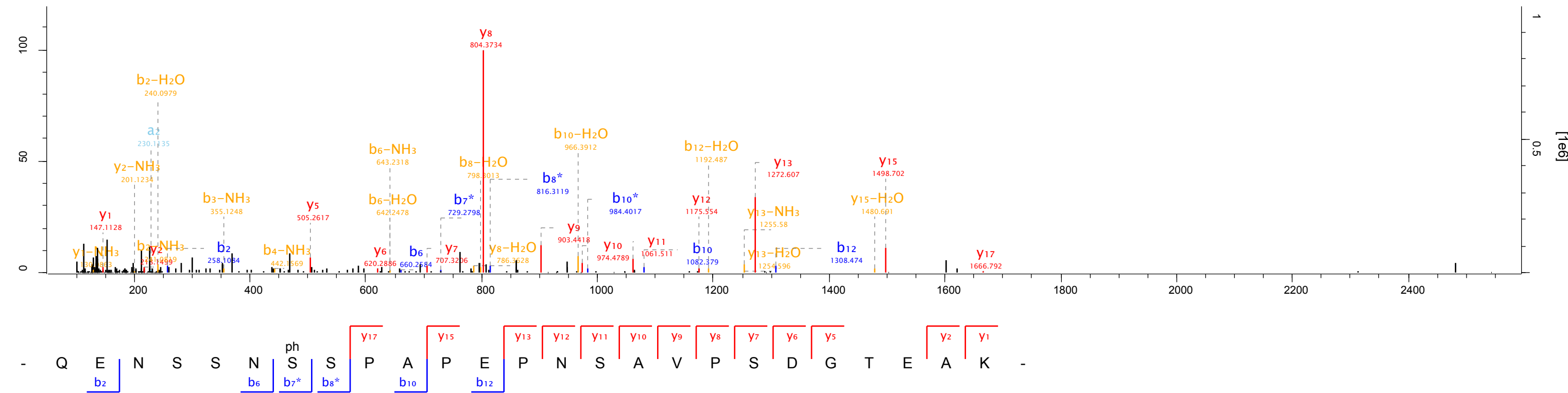


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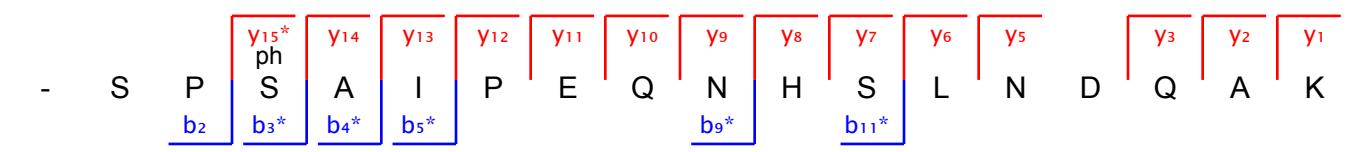
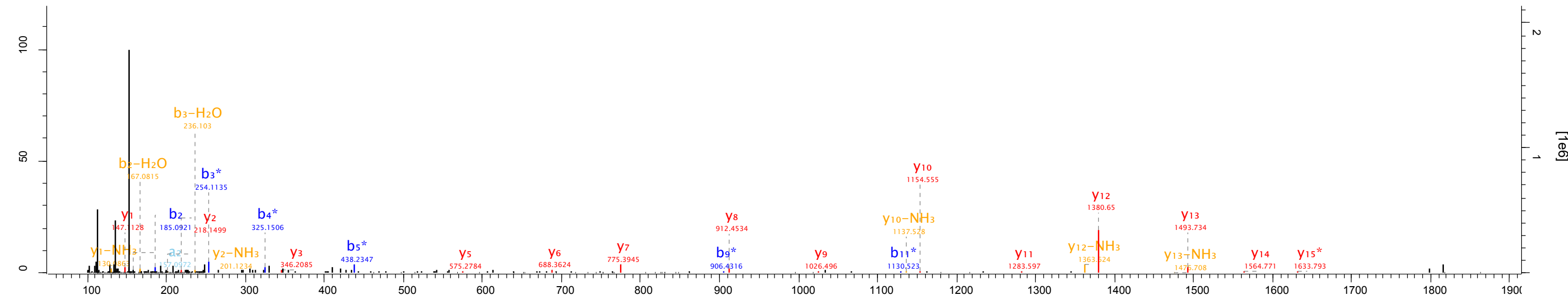


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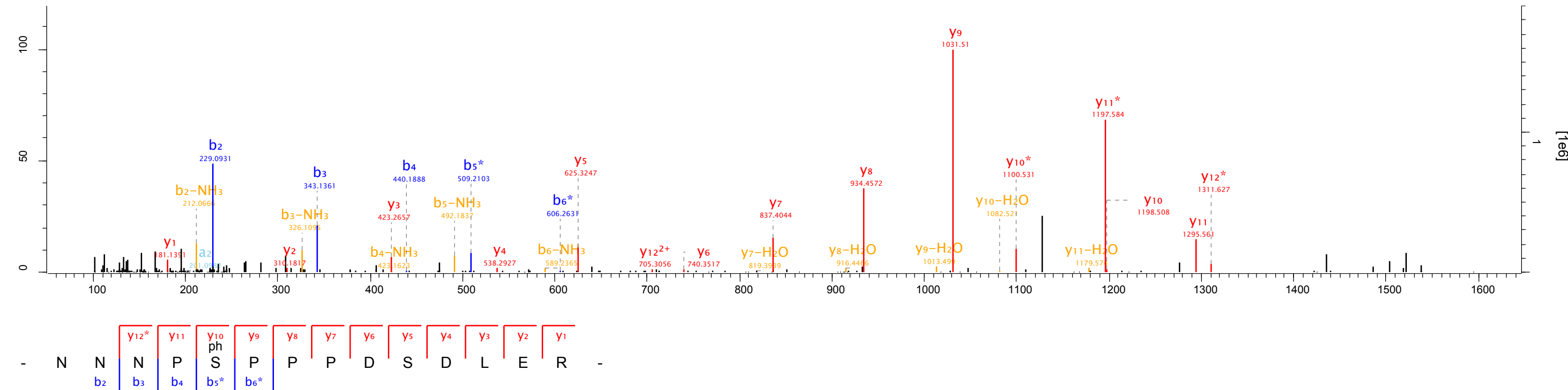
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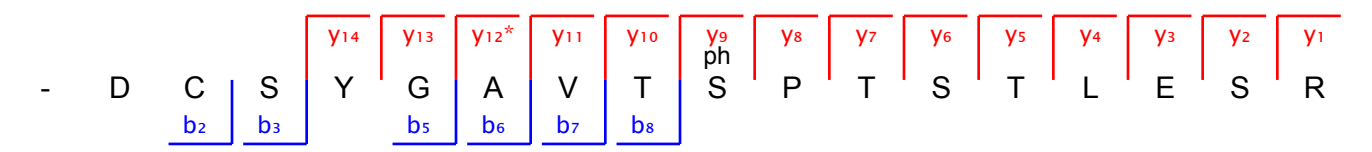
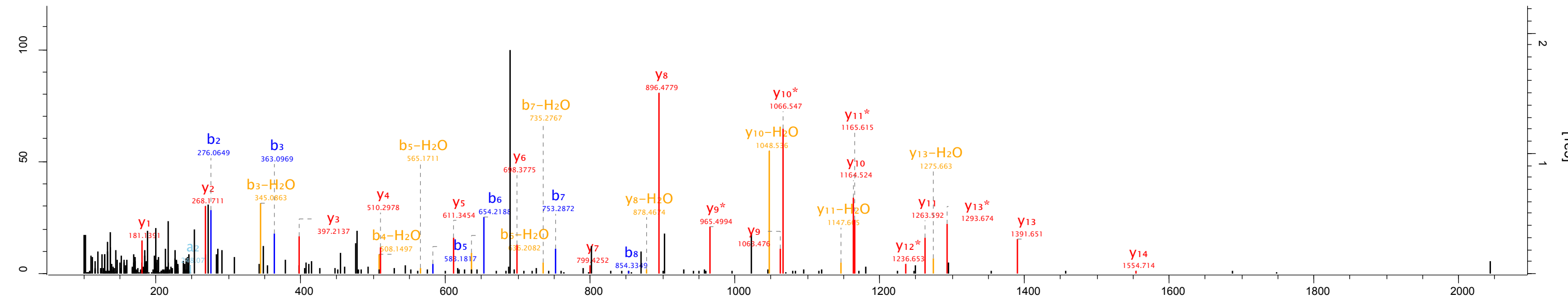
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20171215_MaS_33SR_LMH_phospho2_01

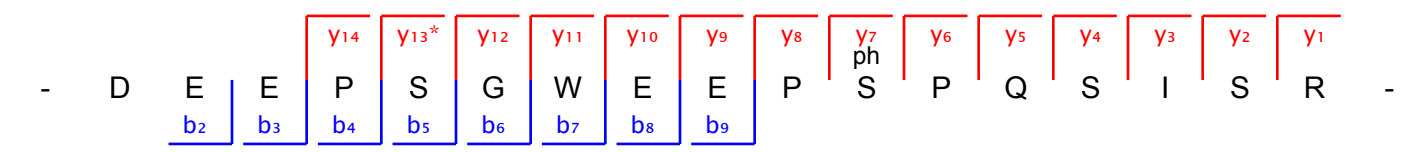
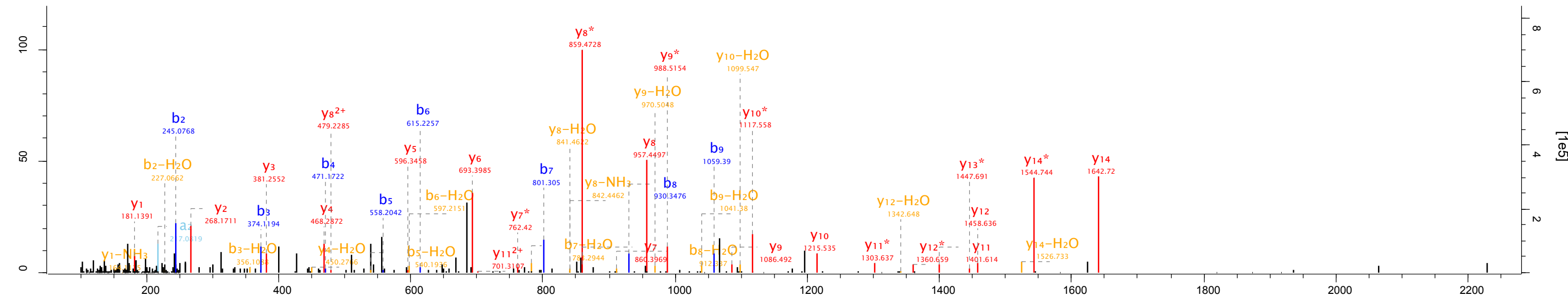
Scan	Method	Score	m/z	Gene names
6243	FTMS; HCD	127.61	819.35	EYA1

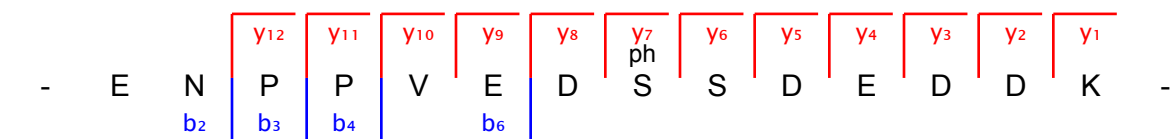
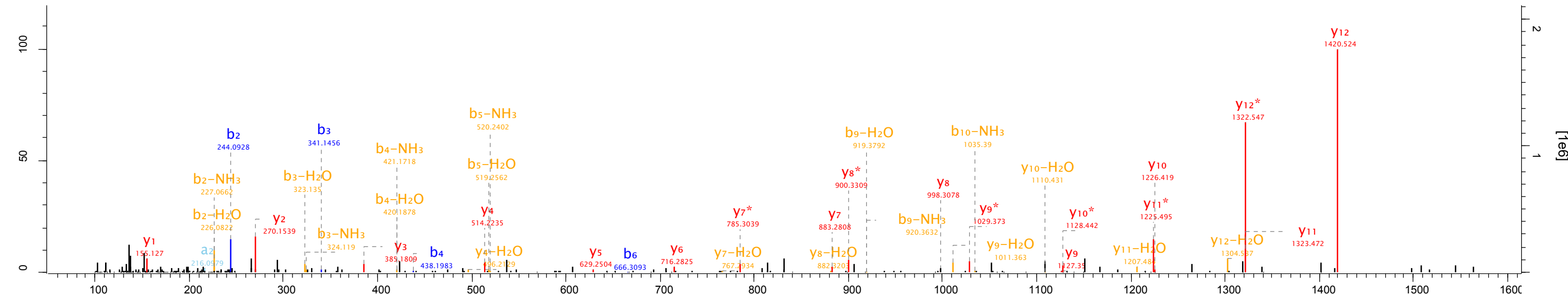


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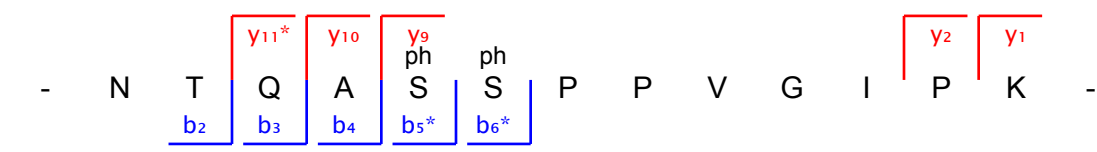
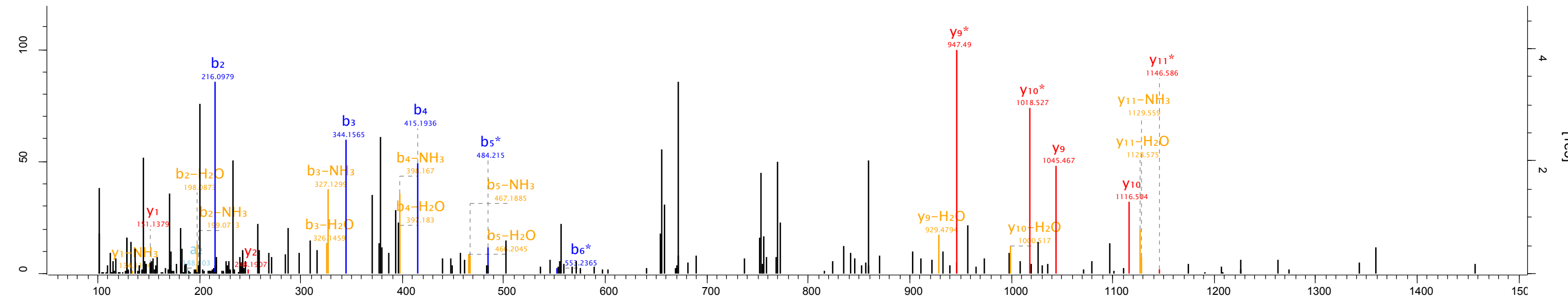


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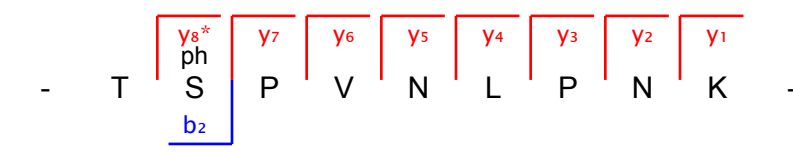
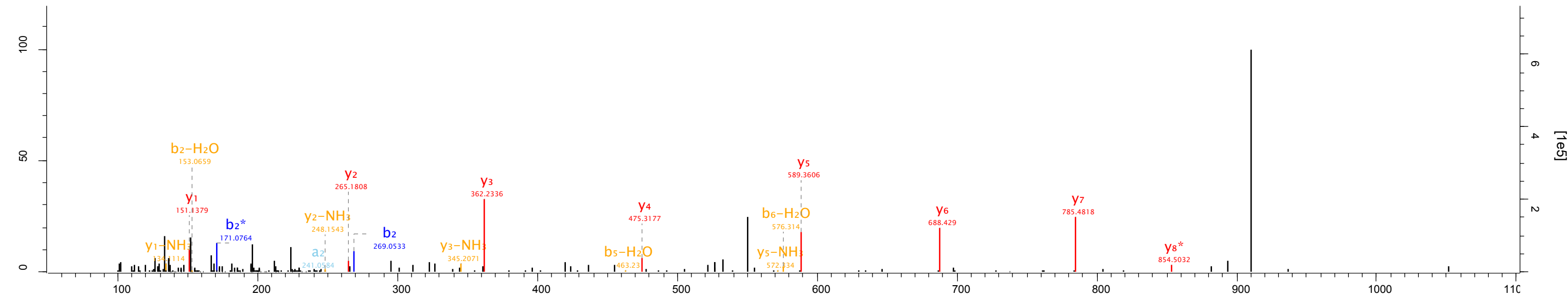


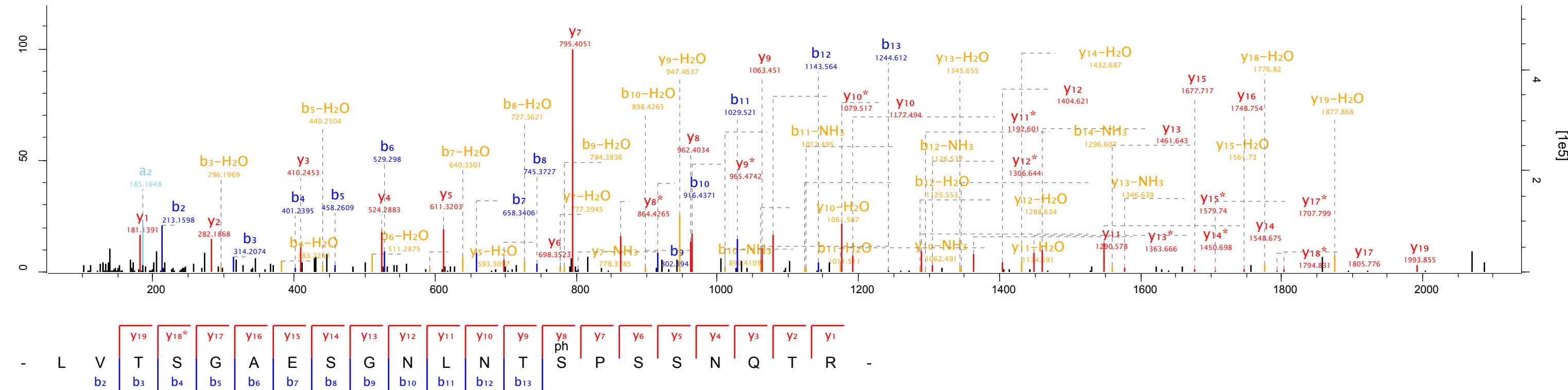


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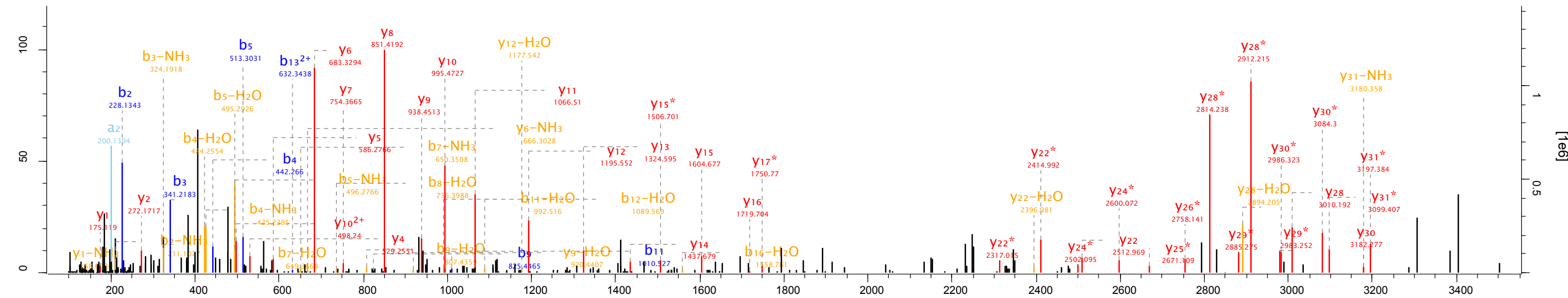


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 6073 Method FTMS; HCD Score 54.2 m/z 527.27 Gene names SOX6





Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 12093 Method FTMS; HCD Score 133.81 m/z 1175.5 Gene names KLHDC4

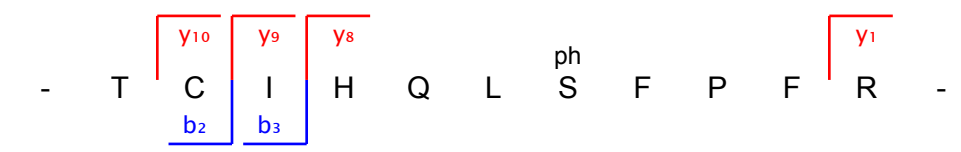
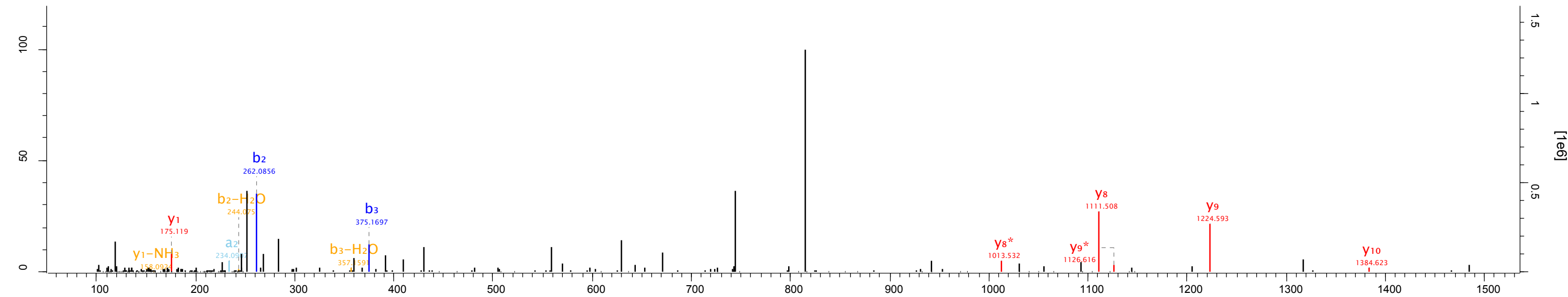


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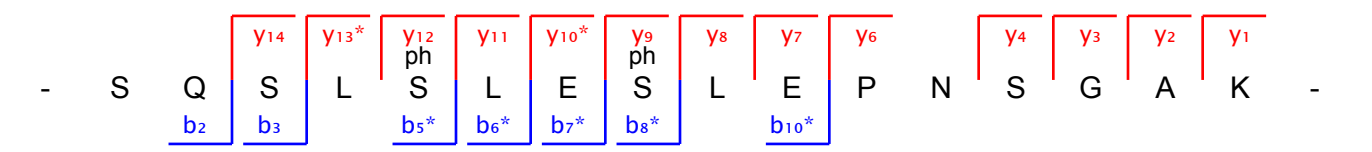
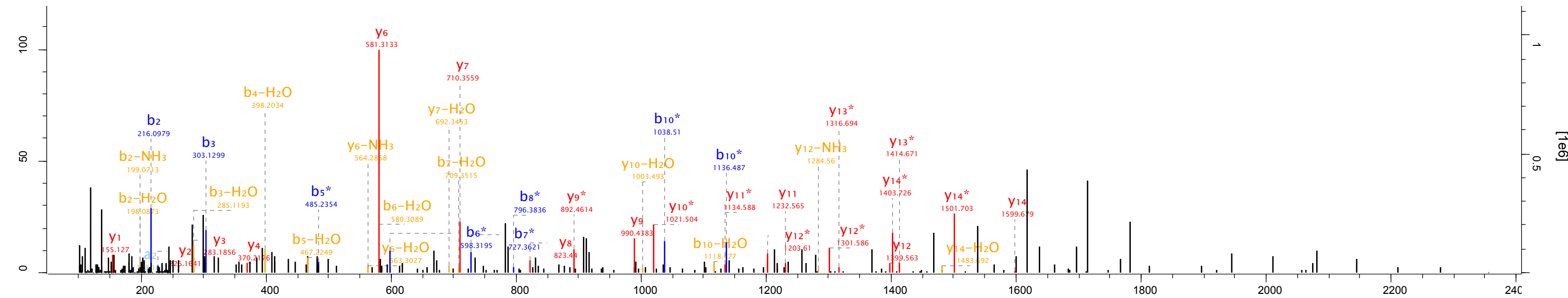
Fragmentation mapping (b and y ions) is shown below the sequence:

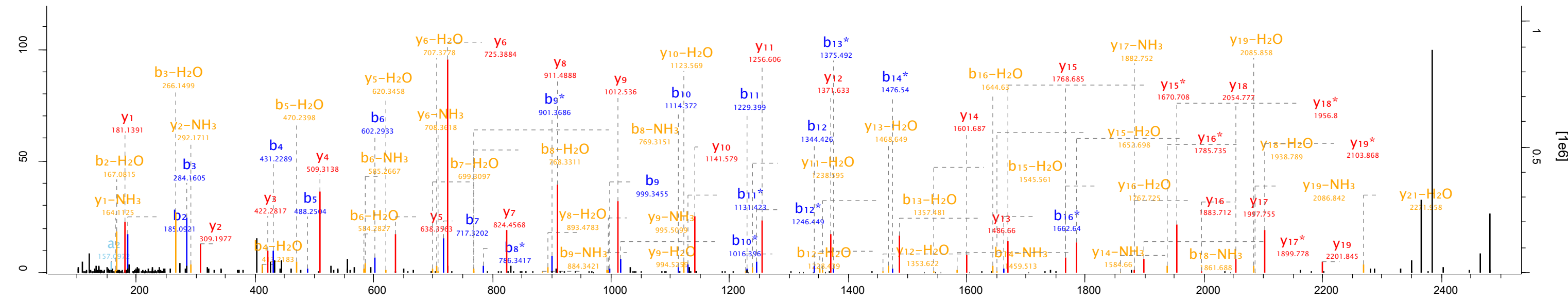
- b ions (blue boxes):** b₂ (V), b₃ (L), b₄ (T), b₅ (A), b₉ (A), b₁₁ (Q), b₁₃²⁺ (P)
- y ions (red boxes):** y₁ (R), y₂ (C), y₄ (P), y₅ (G), y₆ (A), y₇ (S), y₈ (P), y₉ (A), y₁₀ (G), y₁₁ (A), y₁₂ (E), y₁₃ (E), y₁₄ (L), y₁₅ (S), y₁₆ (D), y₁₇ (E), y₂₂ (P), y₂₄ (G), y₂₅ (A), y₂₆ (S), y₂₈ (P), y₂₉ (A), y₃₀ (P), y₃₁ (L)

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



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 14593 Method FTMS; HCD Score 92.54 m/z 908.39 Gene names GPR39



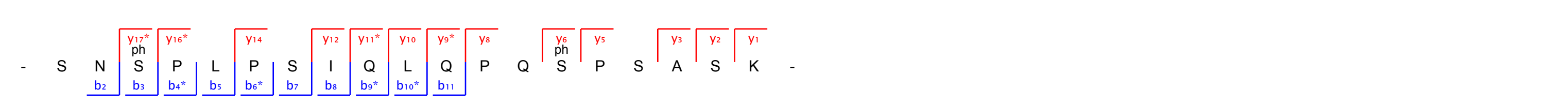
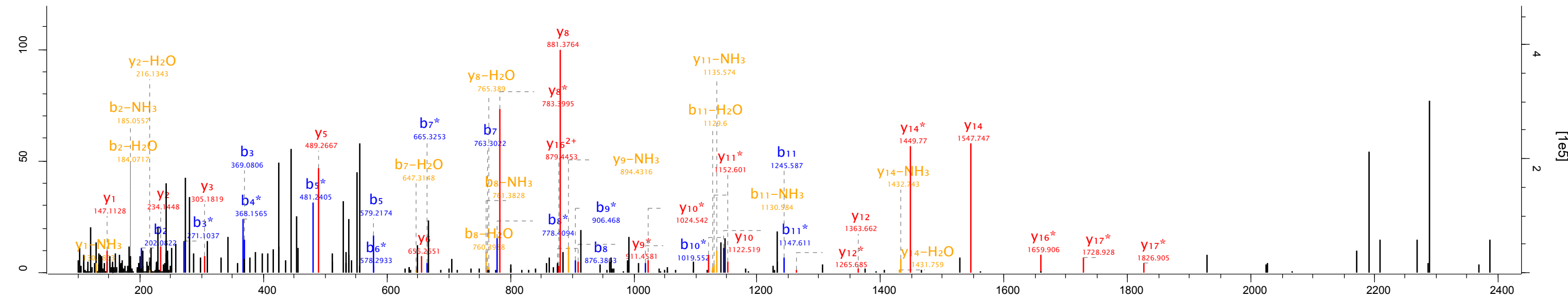


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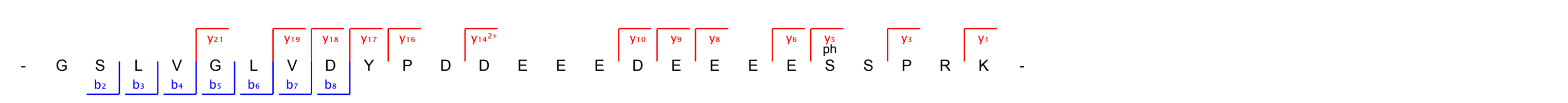
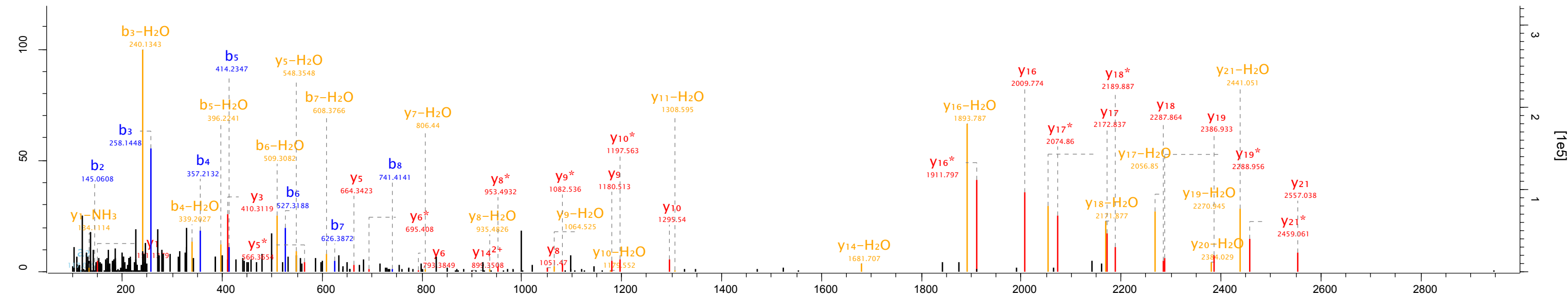
b₂ b₃ b₄ b₅ b₆ b₇ b₈^{*} b₉ b₁₀ b₁₁ b₁₂ b₁₃^{*} b₁₄^{*} b₁₆^{*}

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

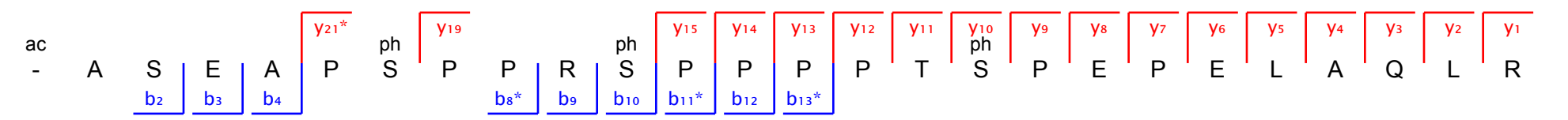
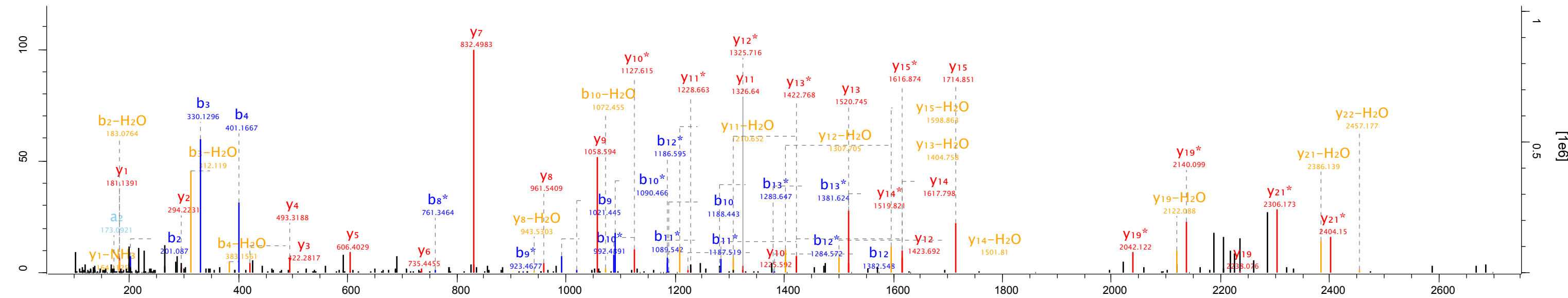
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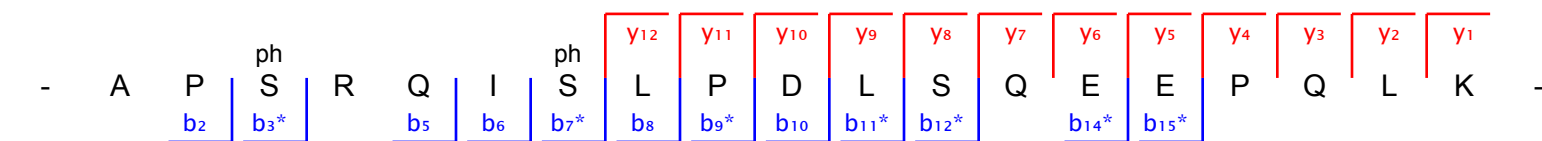
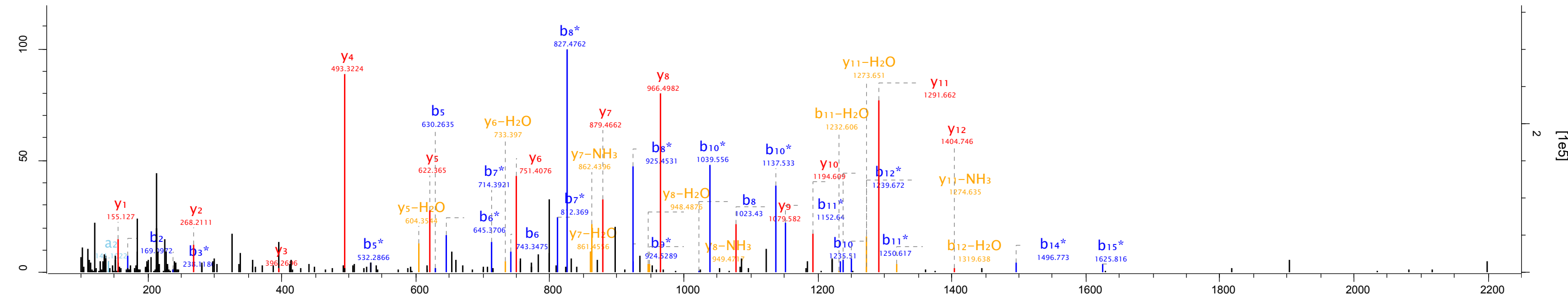


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 Scan: 15783 Method: FTMS; HCD Score: 129.35 m/z: 972.42 Gene names: SMEK2

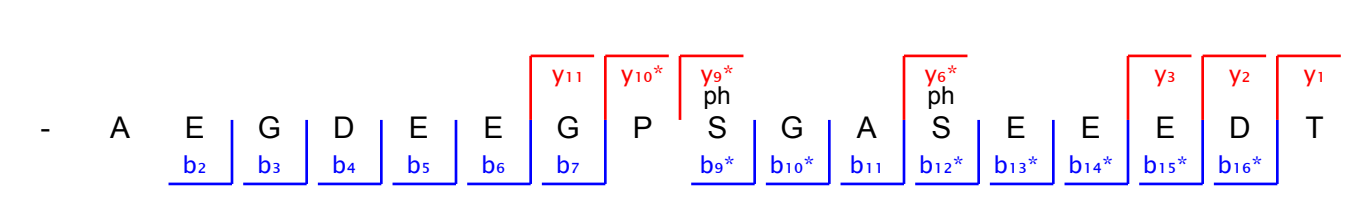
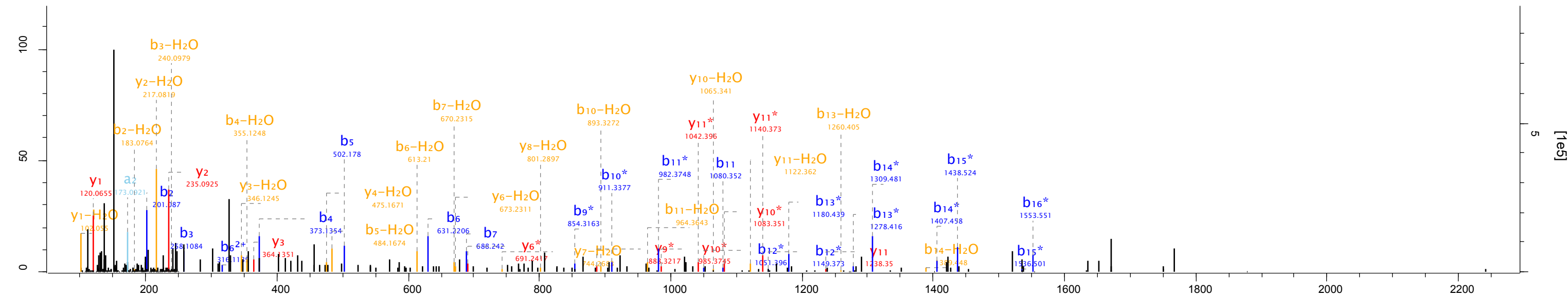


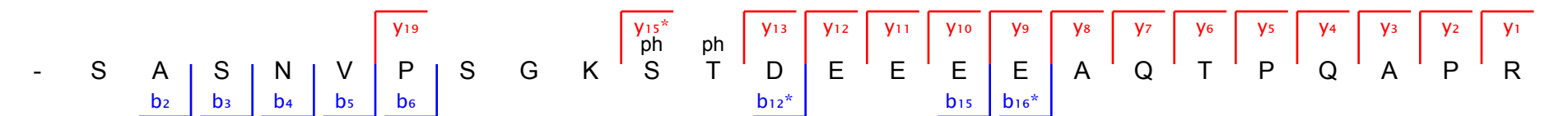
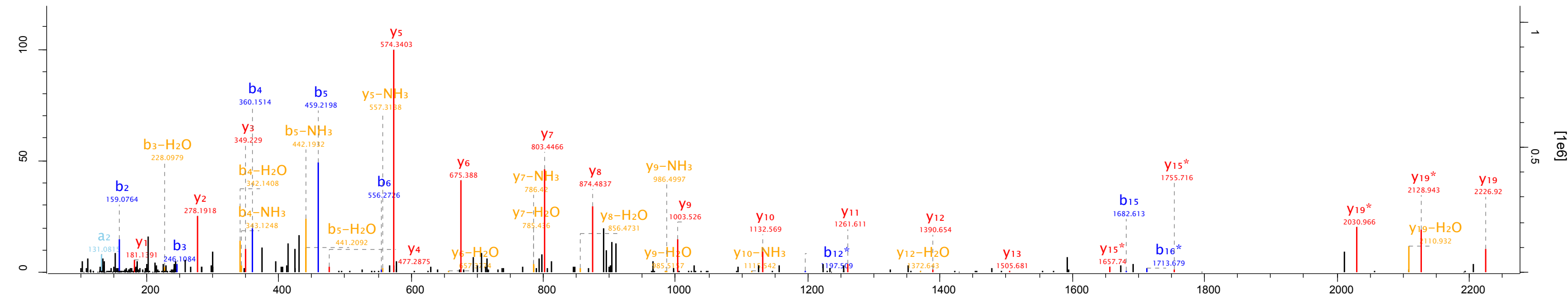
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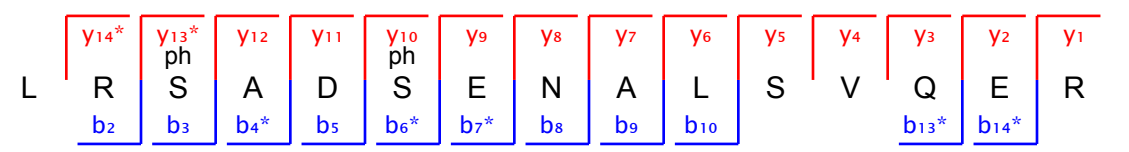
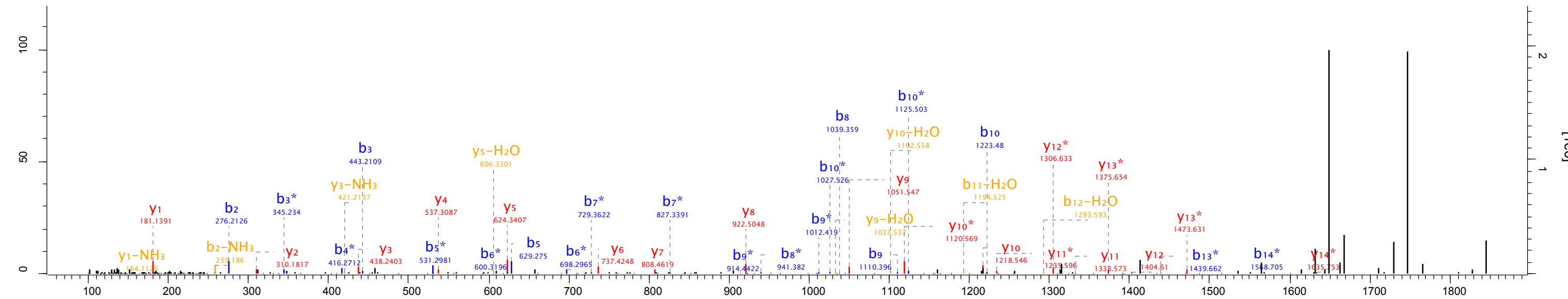


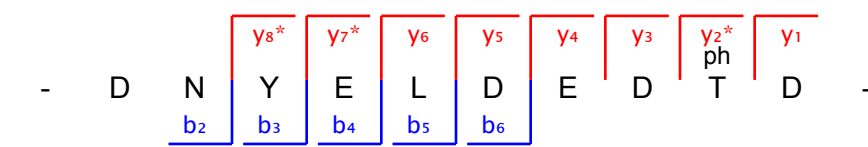
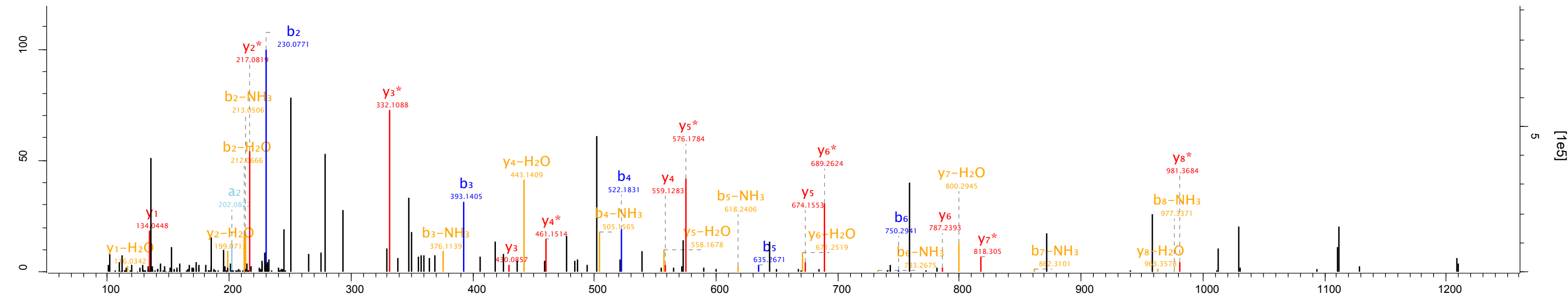
Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 4113 Method FTMS; HCD Score 156.48 m/z 934.79 Gene names TRIM44

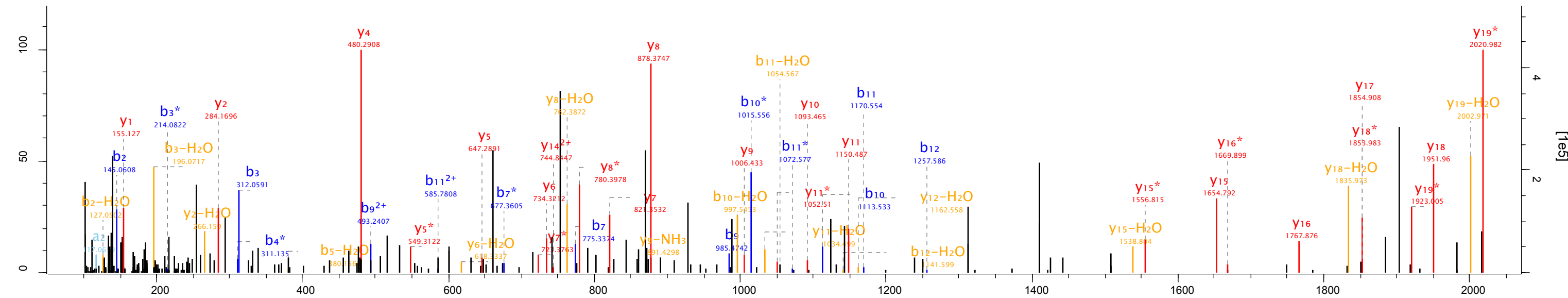




Raw file: 20171215_MaS_33SR_LMH_phospho2_03
 Scan: 7893 Method: FTMS; HCD Score: 142.45 m/z: 923.91 Gene names: MAP3K3



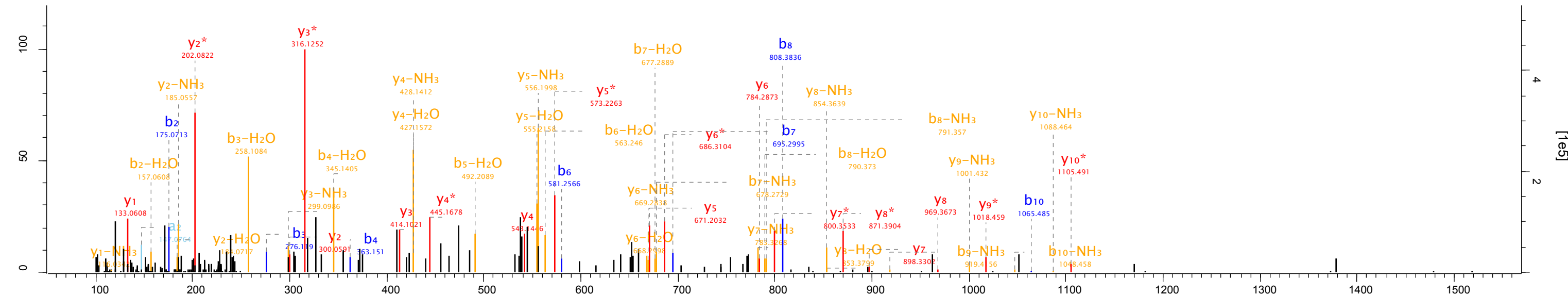




- G S S P S I R P I Q G S Q G S S ph S P V E K -

Fragmentation sites are indicated by brackets below the sequence:

- Red brackets (y-series): y₁₉^{*} (S), y₁₈ (P), y₁₇ (S), y₁₆ (I), y₁₅ (R), y₁₄²⁺ (P)
- Blue brackets (b-series): b₂ (S), b₃ (S), b₄^{*} (P), b₇ (R), b₉ (I), b₁₀ (Q), b₁₁ (G), b₁₂ (S)

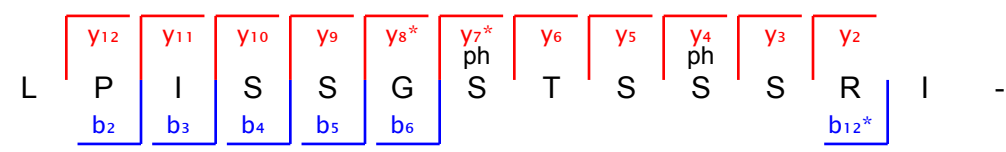
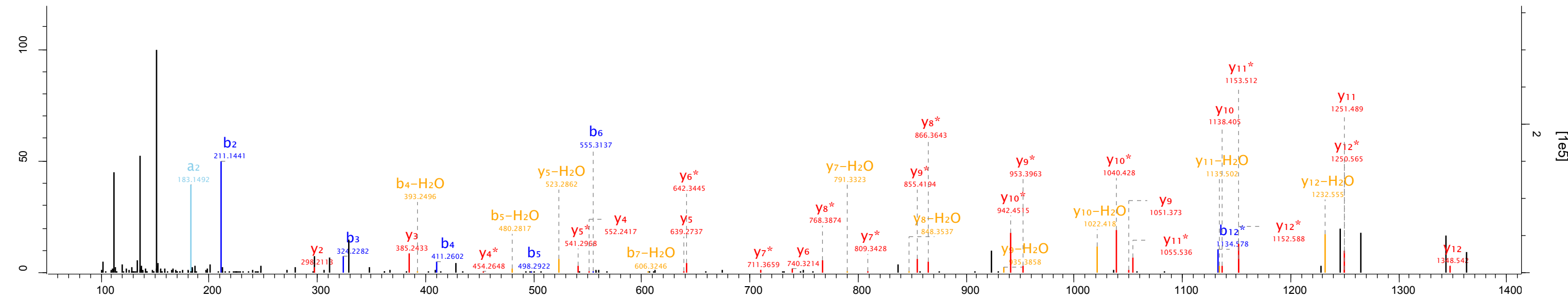


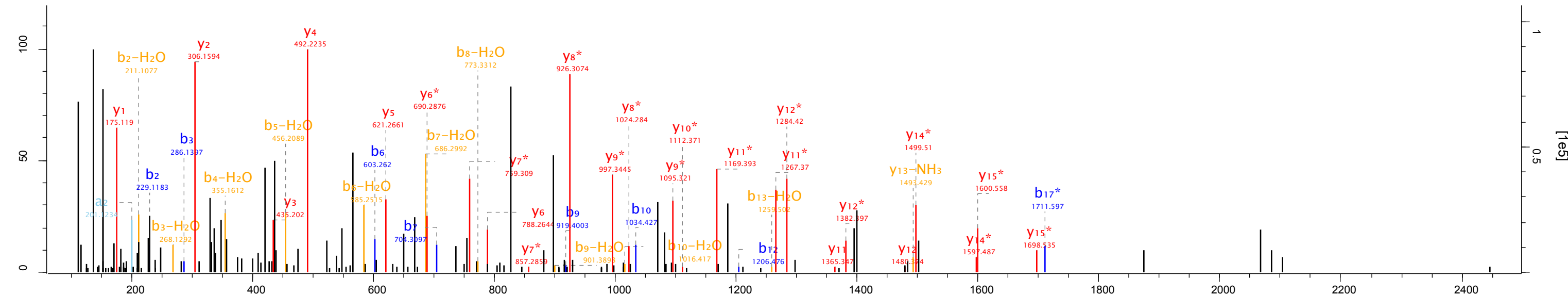
- S S T S F A N I Q E N S N -

b₂ b₃ b₄ b₆ b₇ b₈ b₁₀ y₁₀* y₉* y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

ph S N

Raw file 20171215_MaS_33SR_LMH_phospho2_04 Scan 10003 Method FTMS; HCD Score 176.85 m/z 731.32 Gene names GPR56



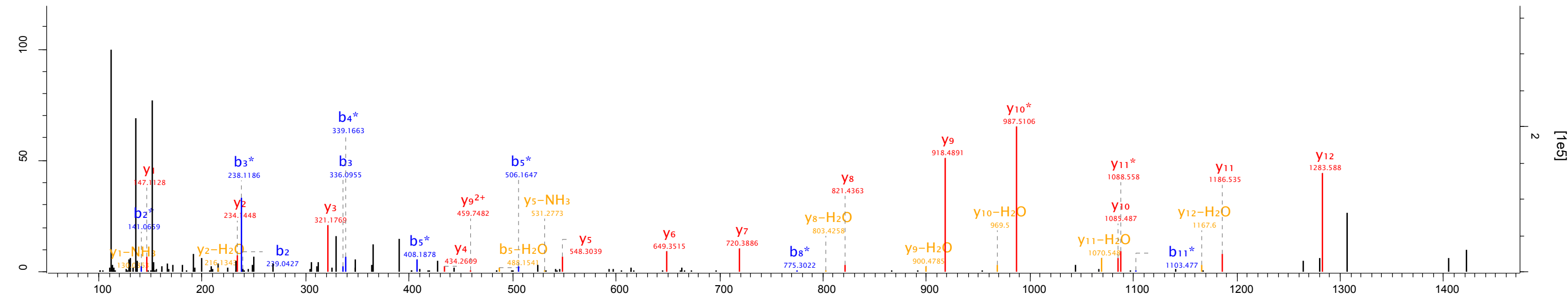


- E V G S T E T S Q D G D A S S S E G E M R -

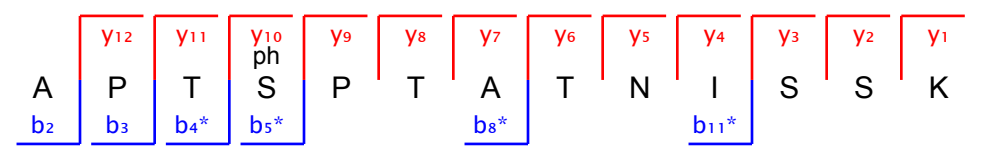
b2 b3 b6 b7 b9 b10 b12 b17*

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

Raw file 20171215_MaS_33SR_LMH_phospho2_05 Scan 4963 Method FTMS; HCD Score 112.74 m/z 761.32 Gene names PEAK1

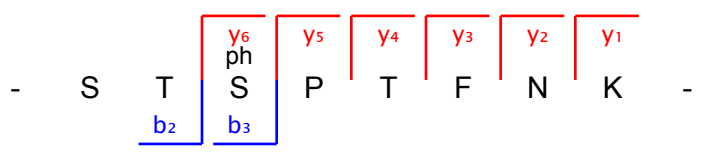
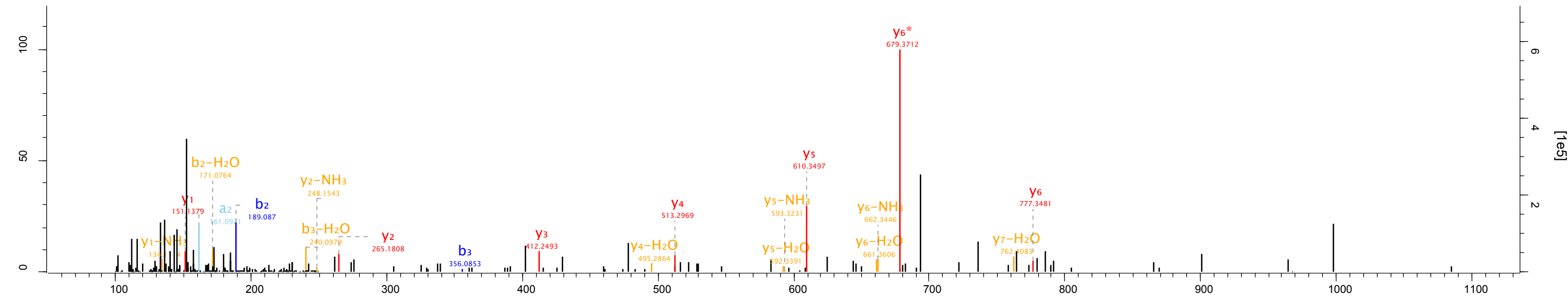


ph
S



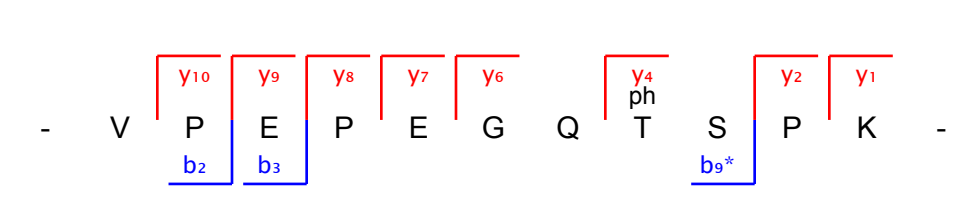
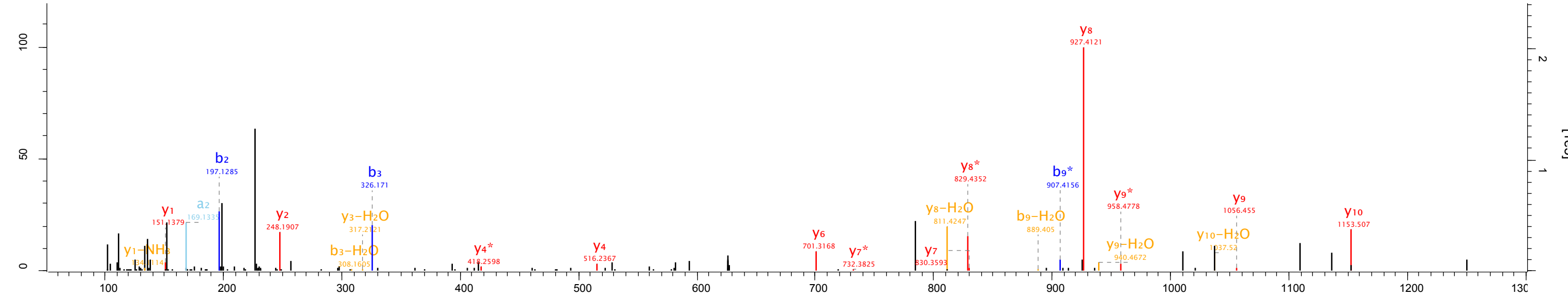
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20171215_MaS_33SR_LMH_phospho2_06

Scan 3443 Method FTMS; HCD Score 67.7 m/z 483.22 Gene names BRIP1

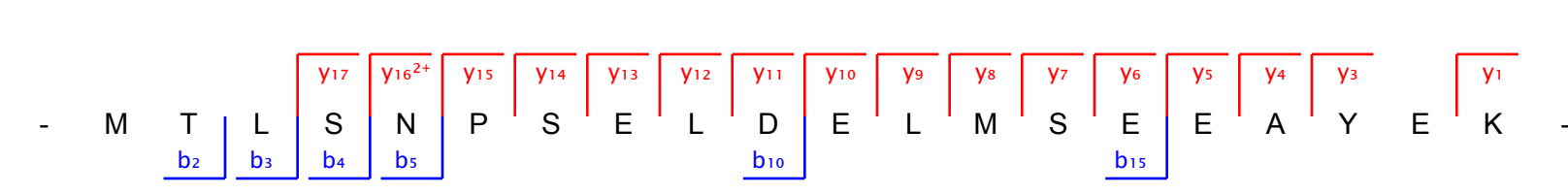
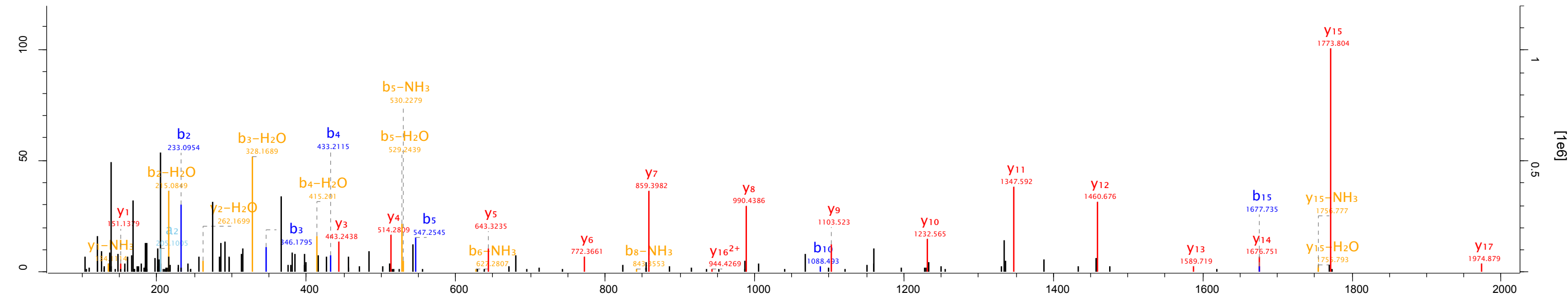


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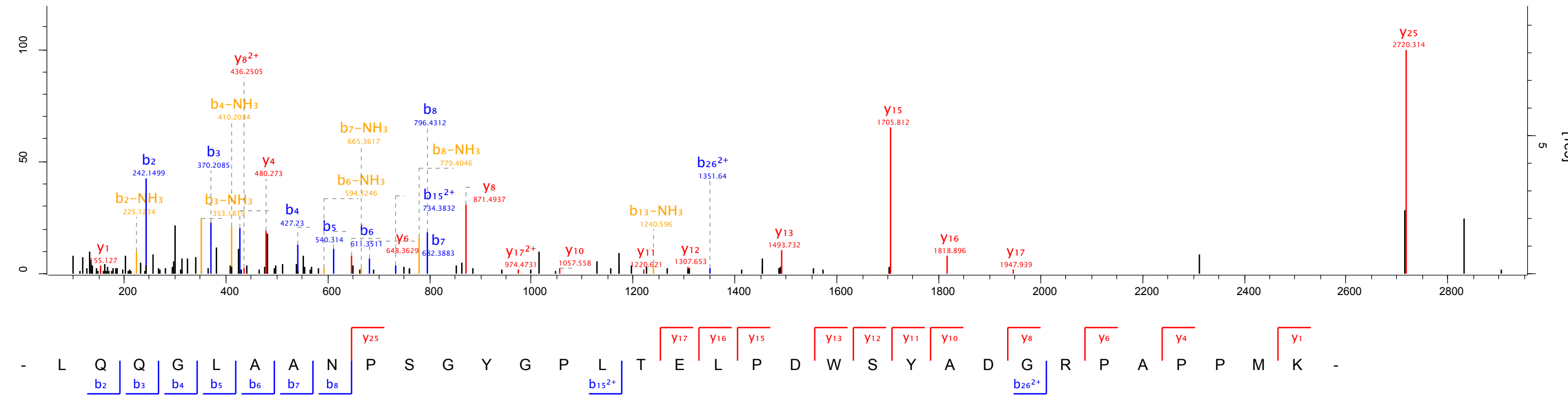
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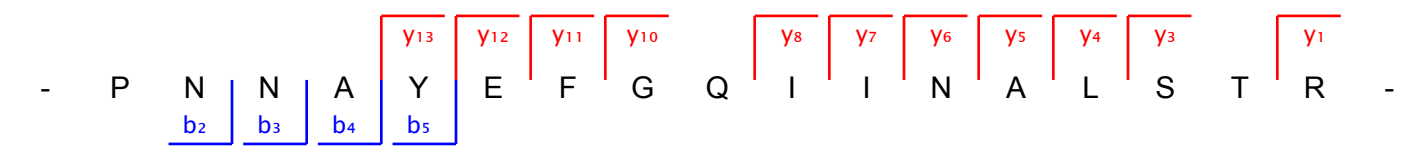
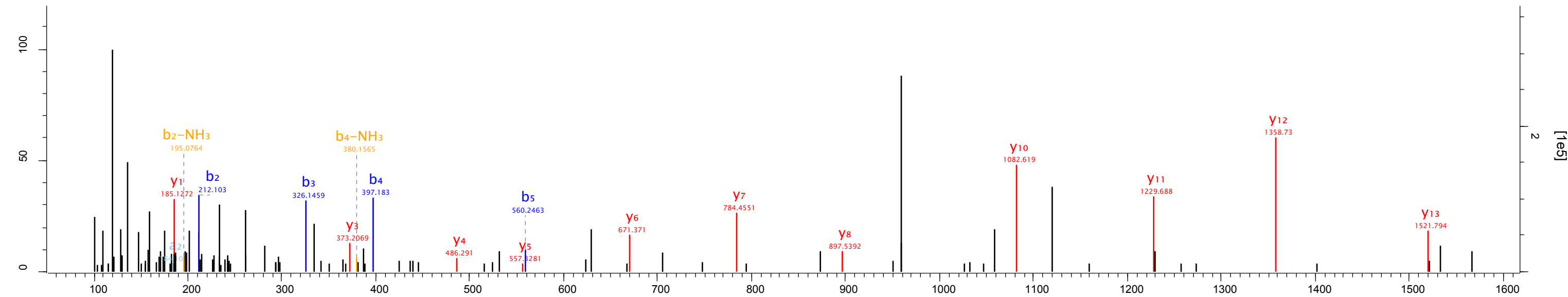
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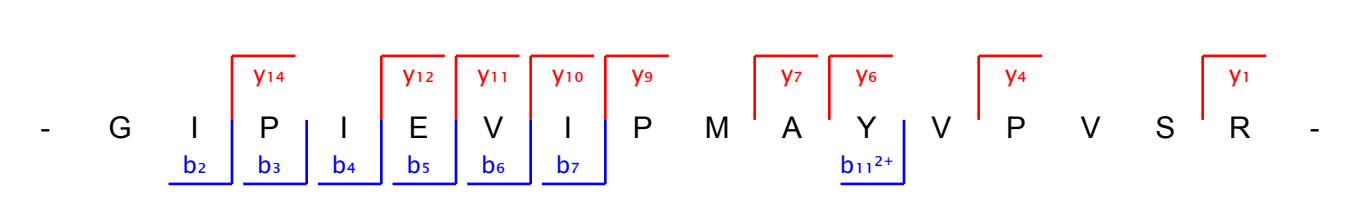
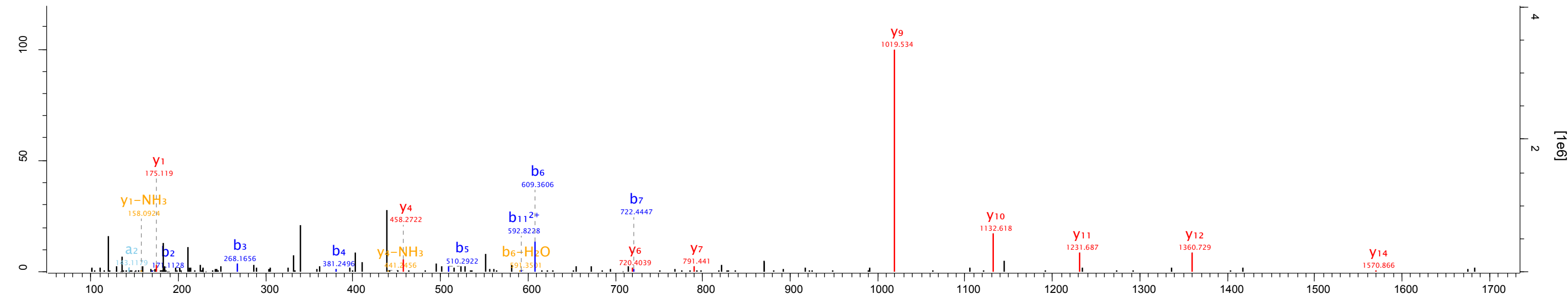
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 Scan: 107033 Method: FTMS; HCD Score: 83.94 m/z: 1172.58 Gene names: MRPL52



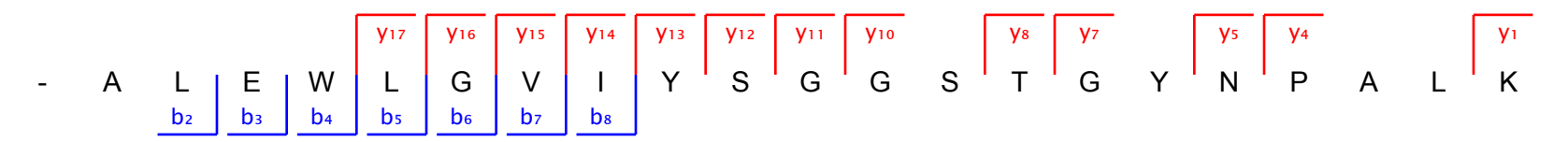
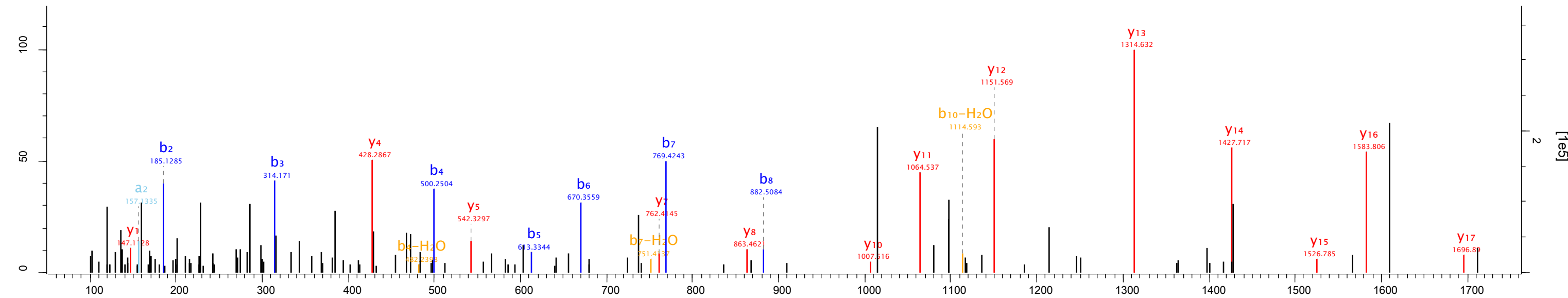
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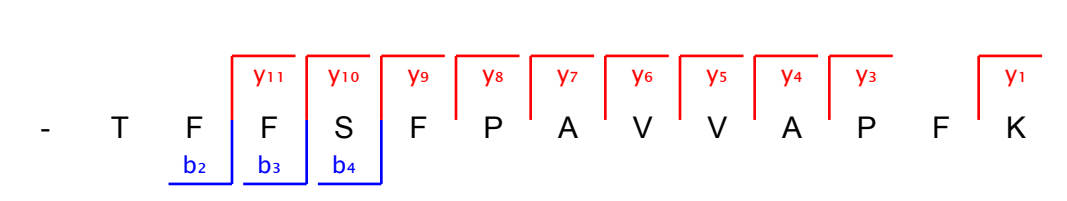
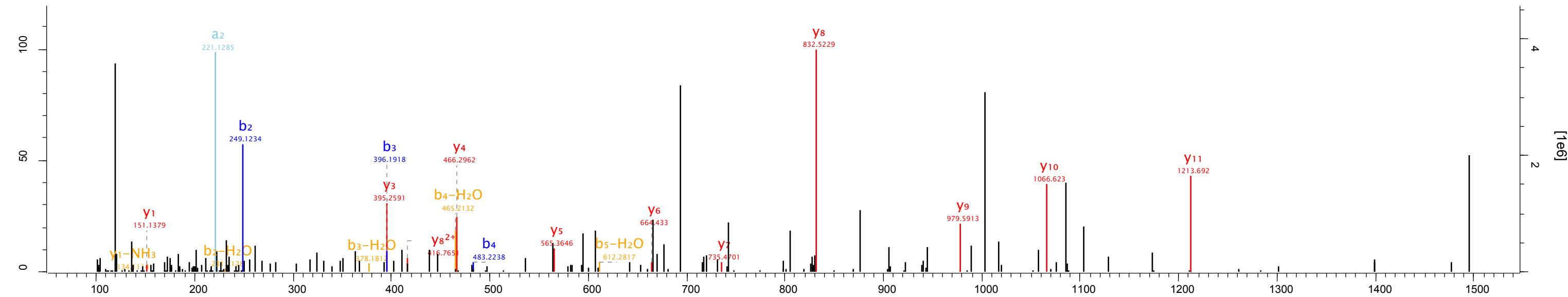
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 Scan: 122573 Method: FTMS; HCD Score: 46.89 m/z: 870.99 Gene names: RPIA



Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 123223 Method FTMS; HCD Score 71.85 m/z 1098.57

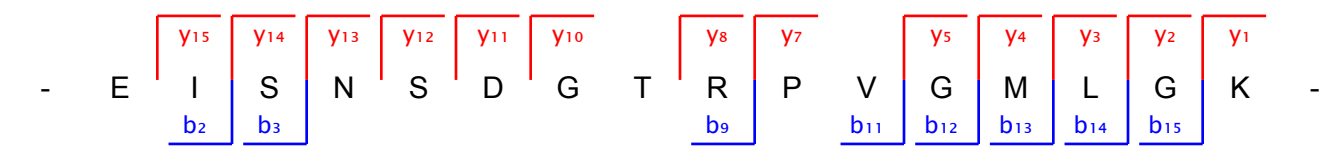
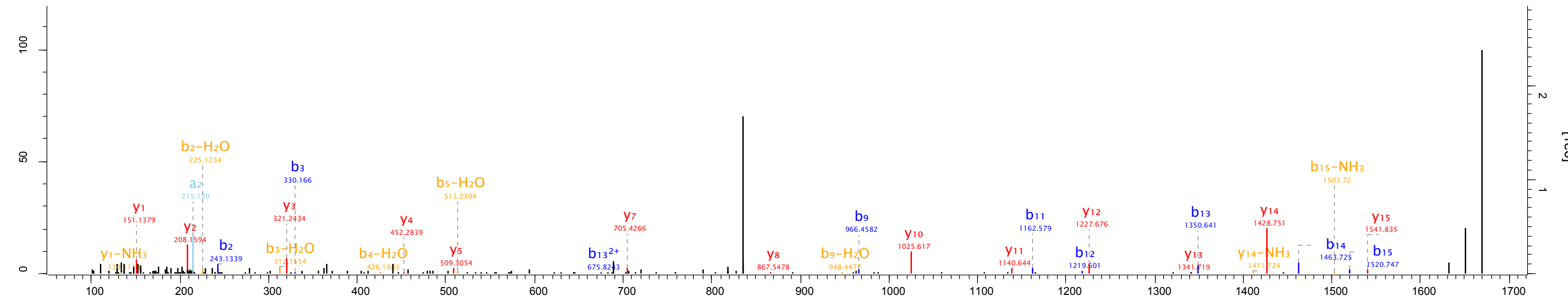


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 Scan: 132153 Method: FTMS; HCD Score: 43.76 m/z: 731.41 Gene names: GARS

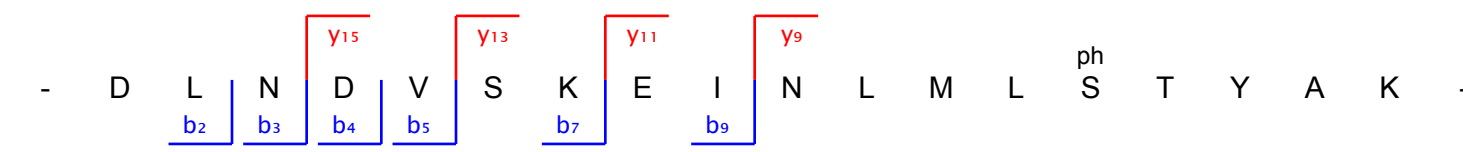
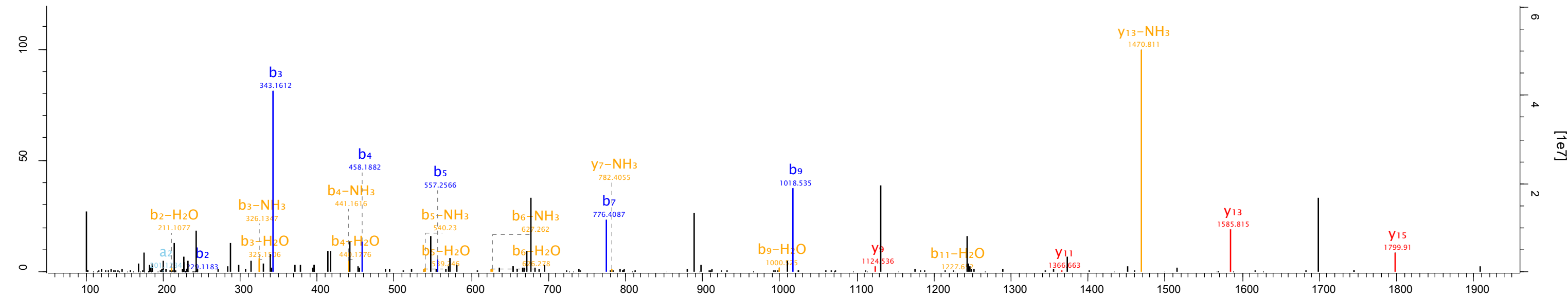


Raw file
20171215_MaS_33SR_LMH_proteome_01

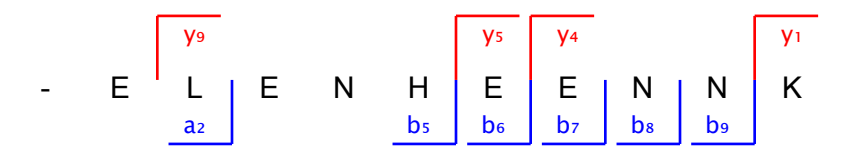
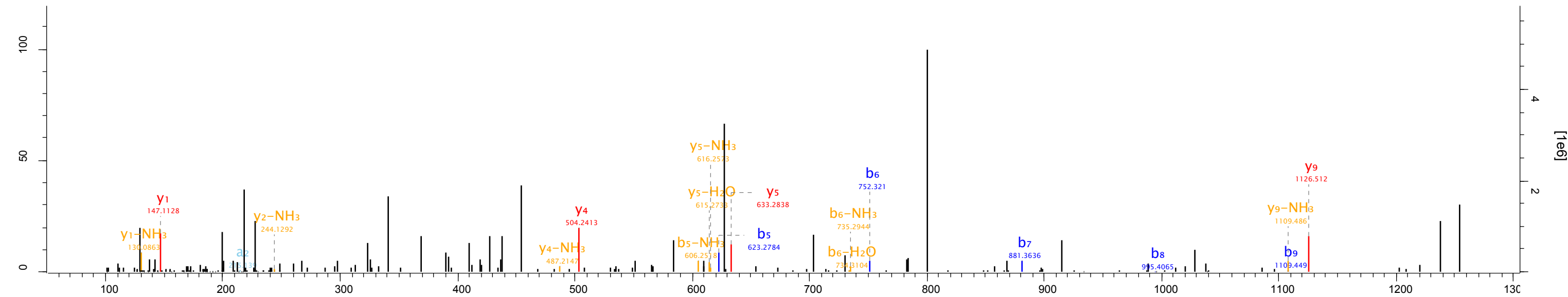
Scan 13613 Method FTMS; HCD Score 110.12 m/z 835.94 Gene names RBM22



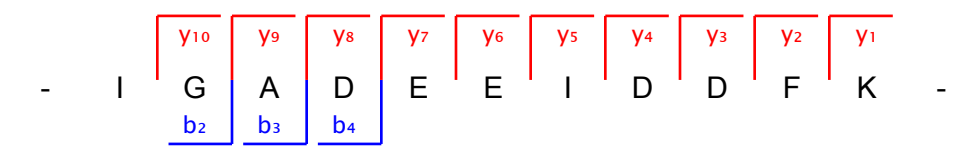
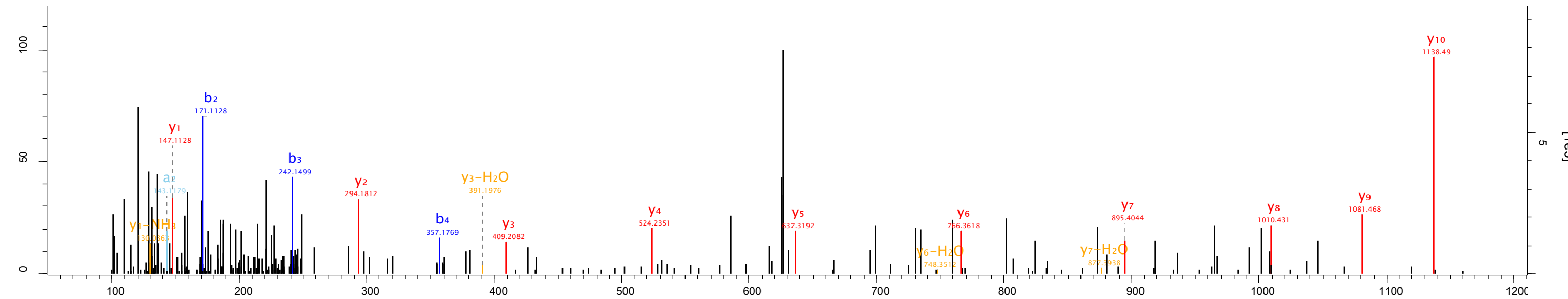
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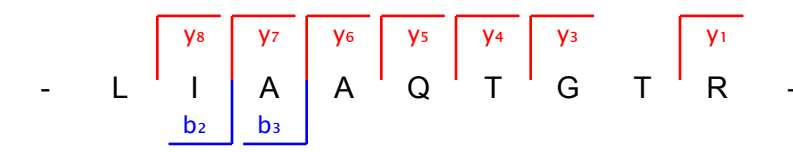
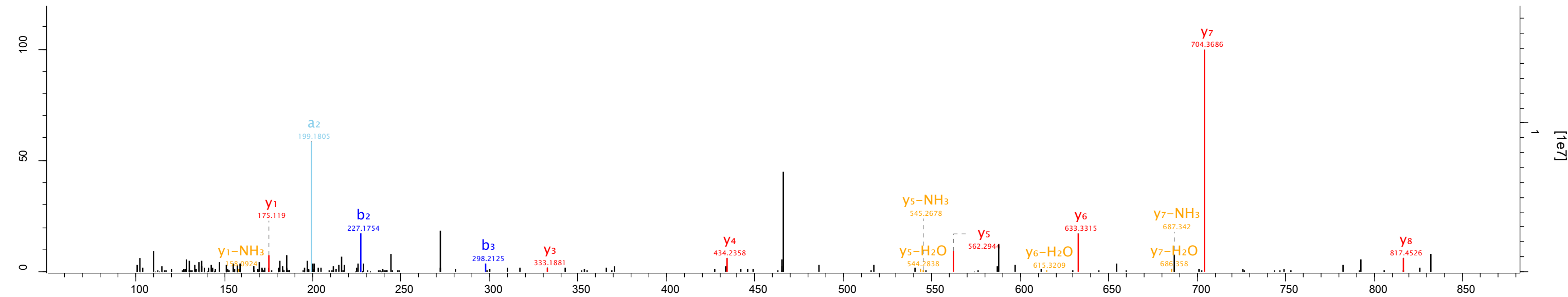
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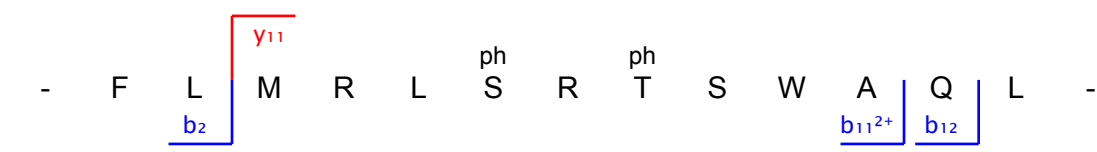
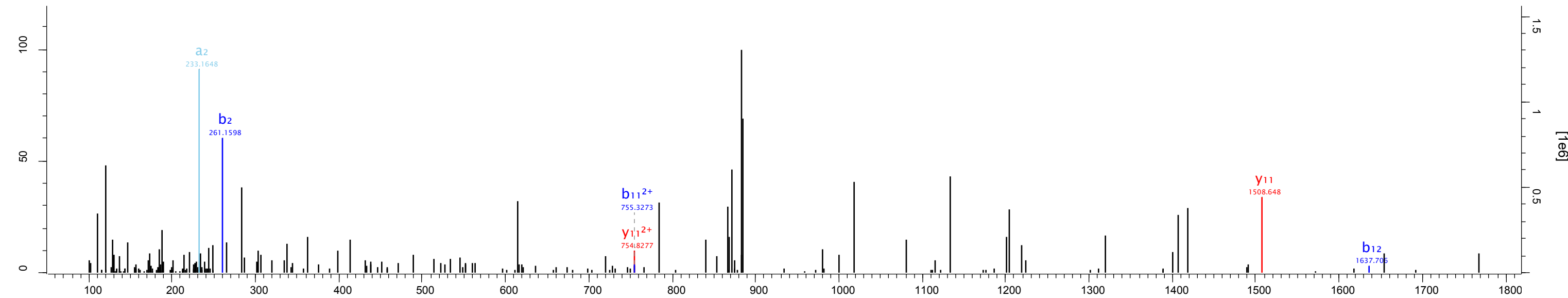
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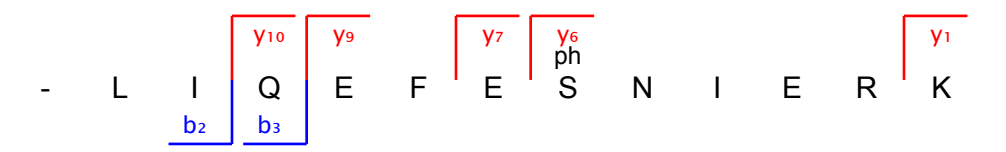
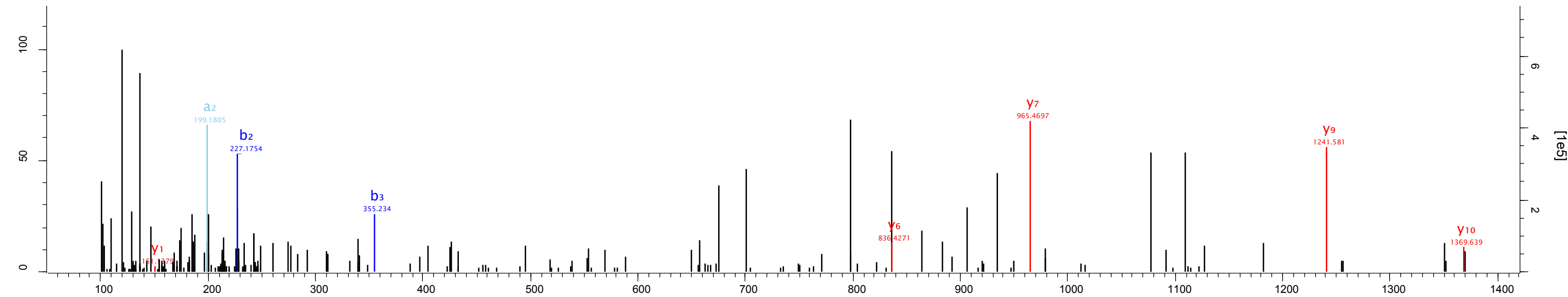
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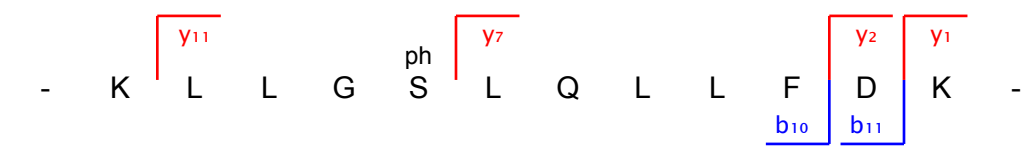
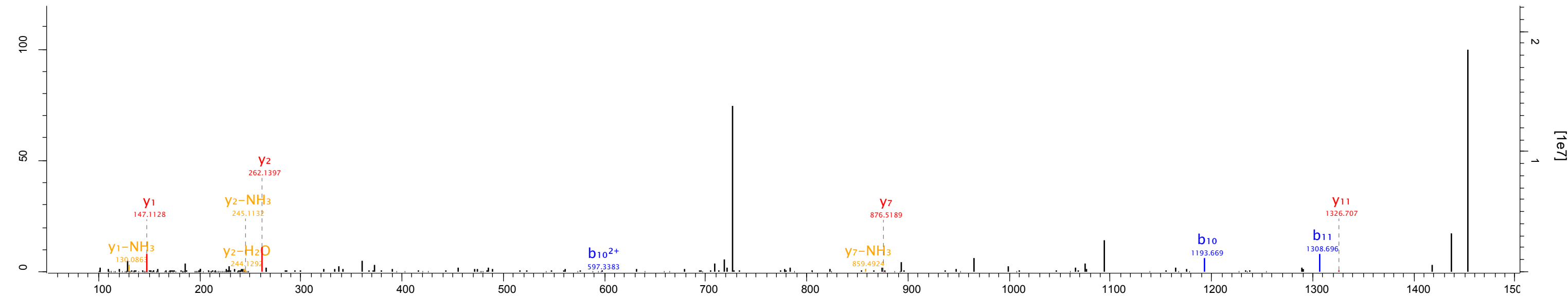
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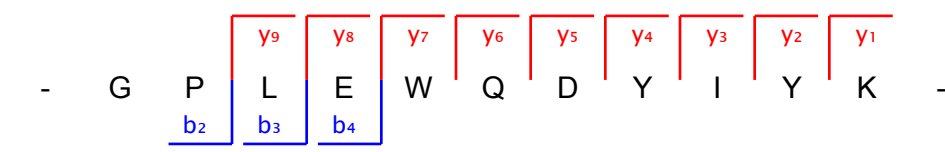
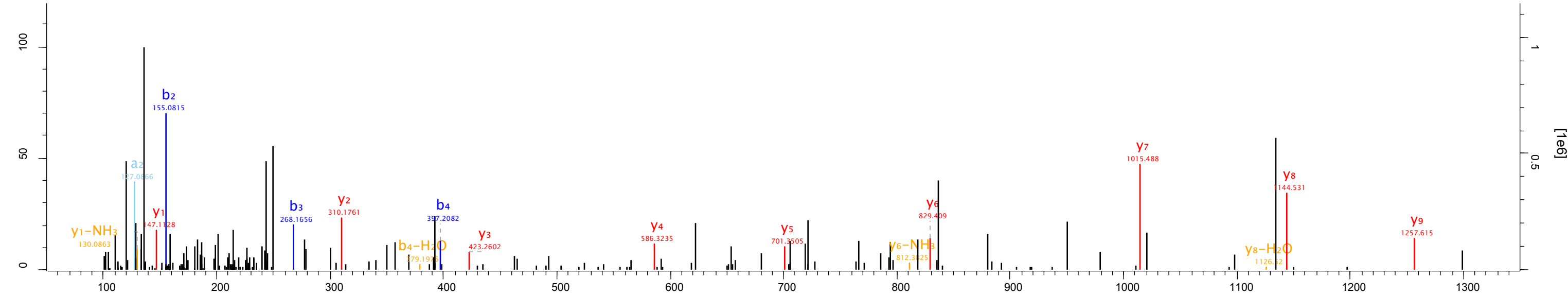
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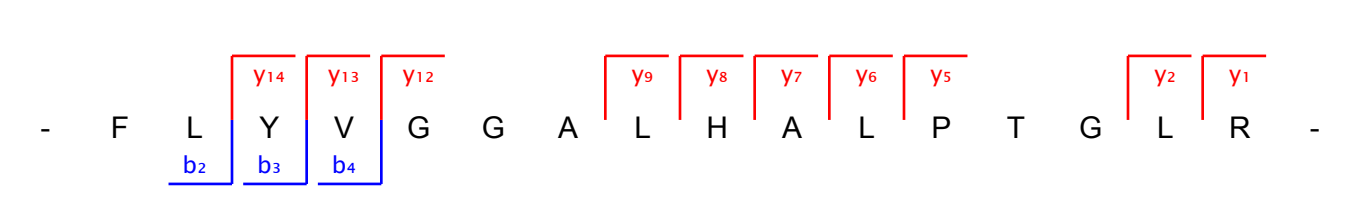
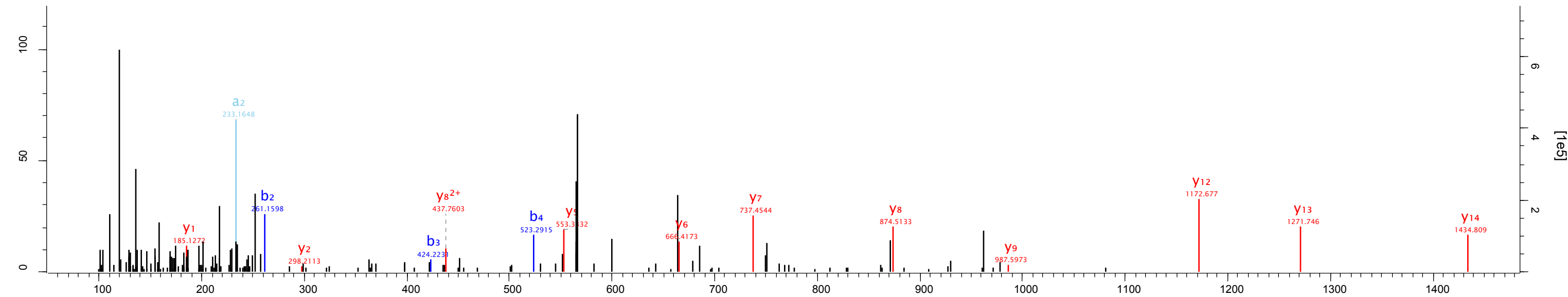
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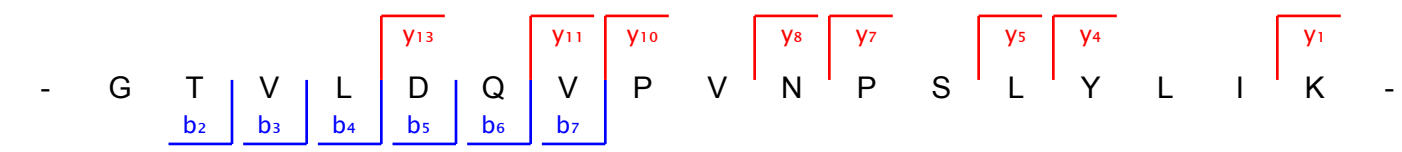
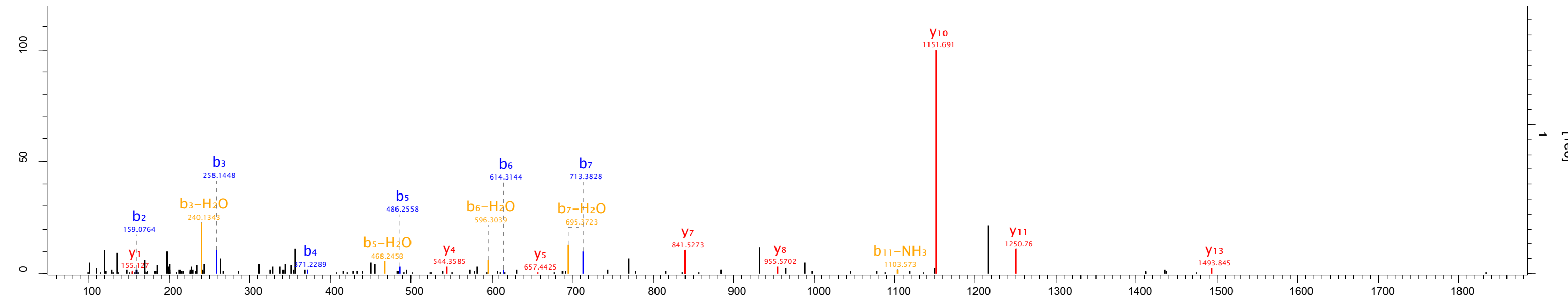
20171215_MaS_33SR_LMH_proteome_01 87533 FTMS; HCD 68.54 706.35 GEMIN6



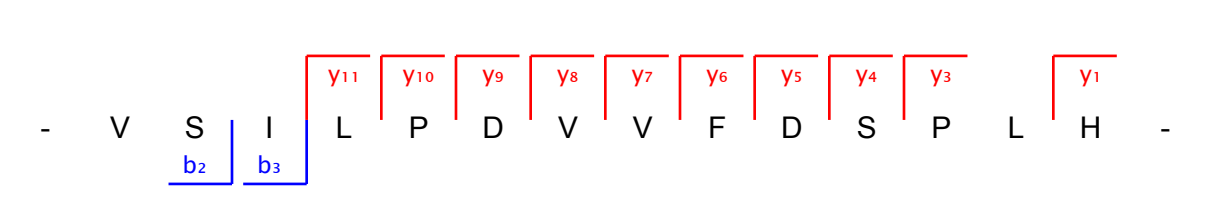
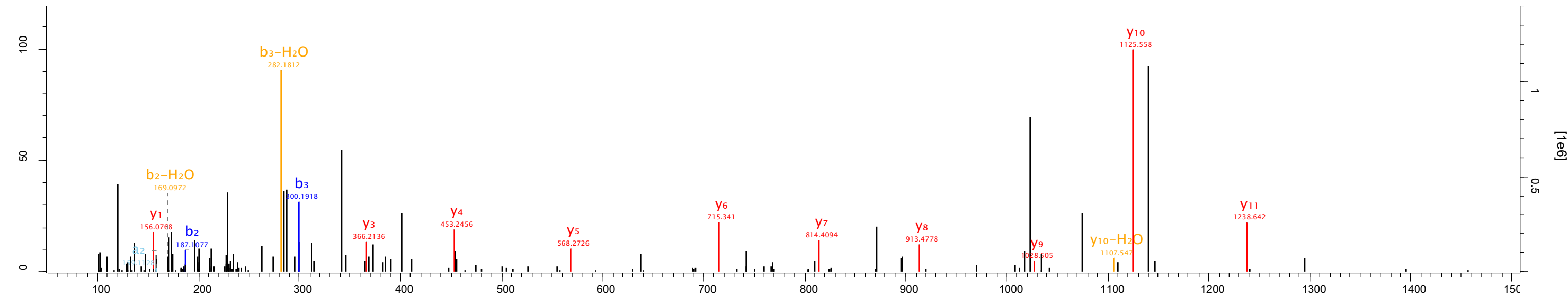
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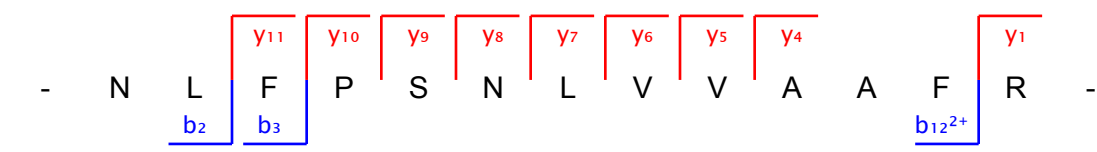
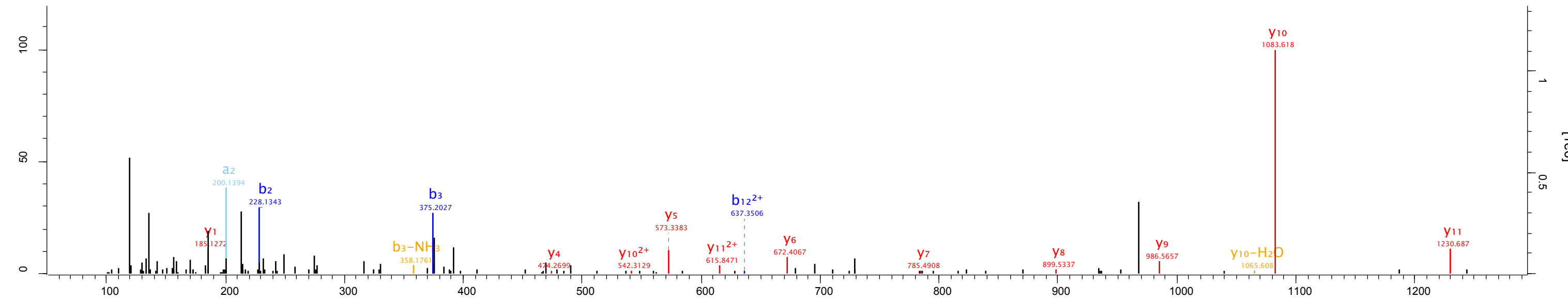
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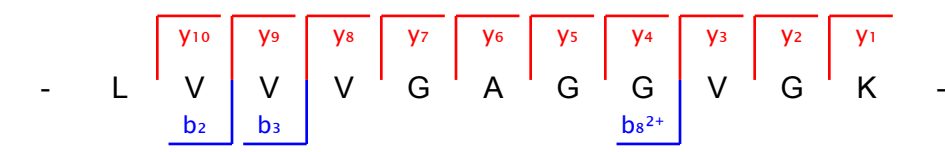
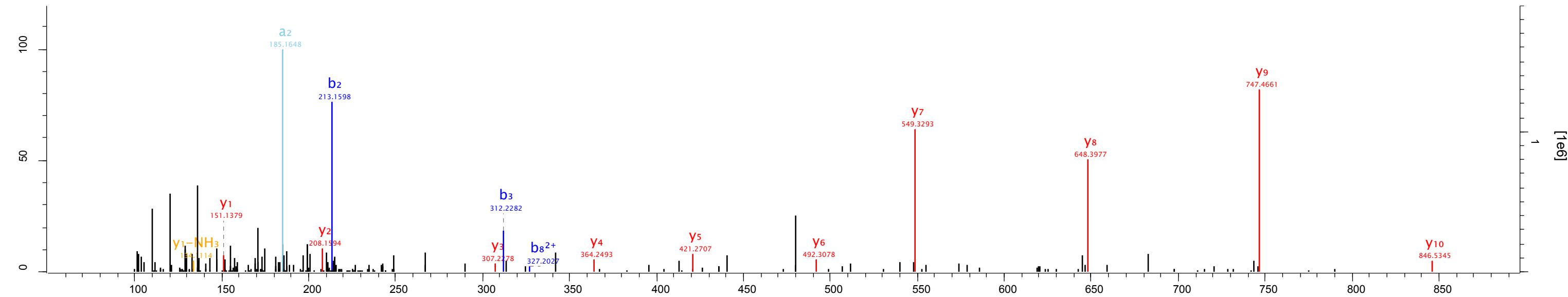
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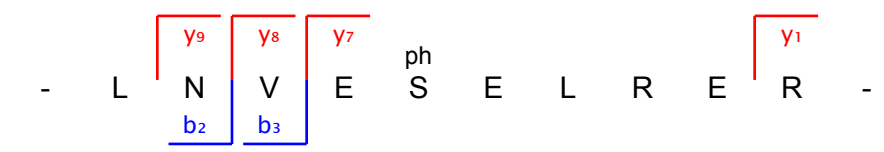
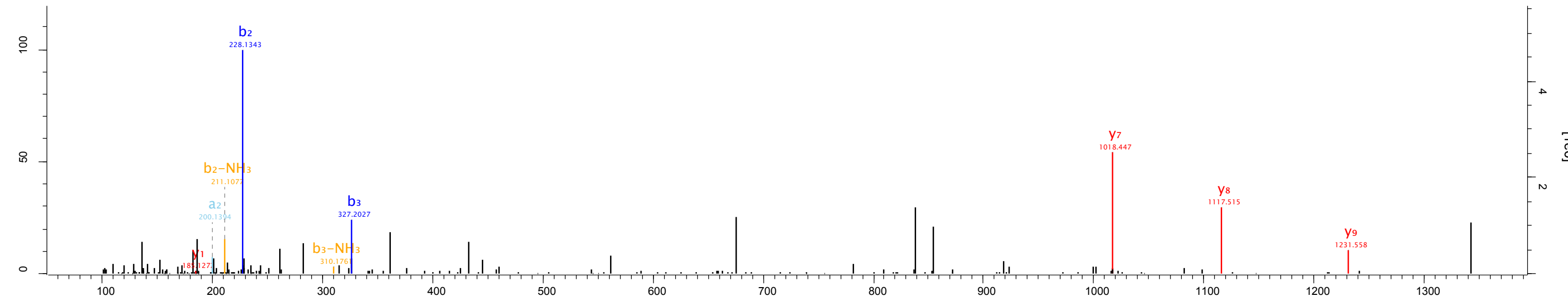
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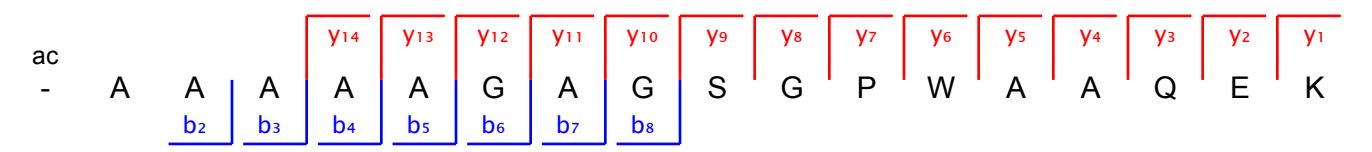
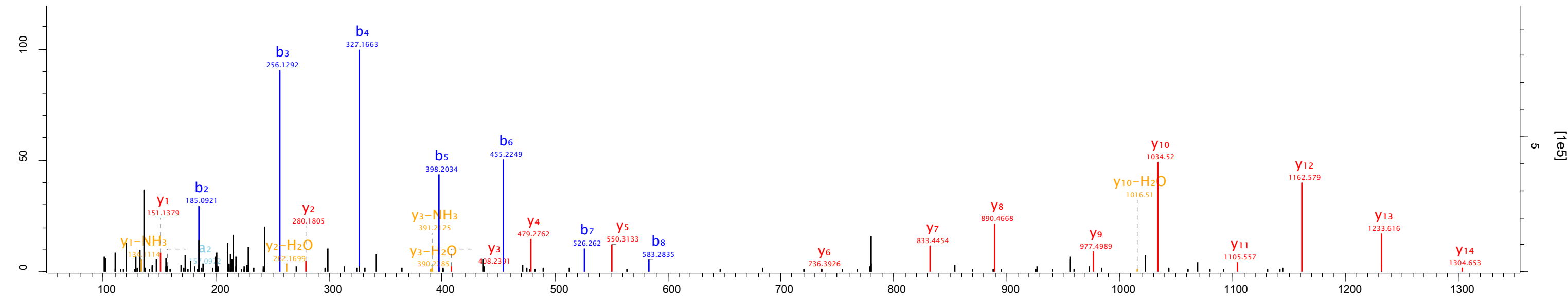
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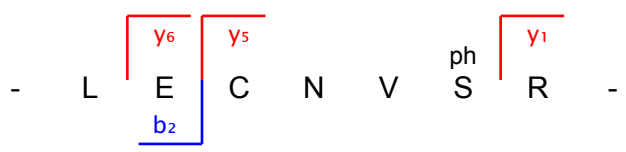
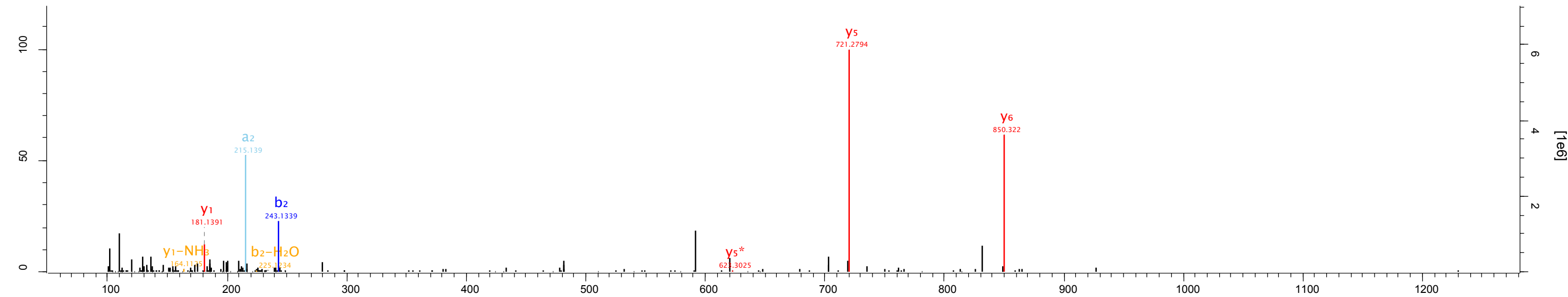
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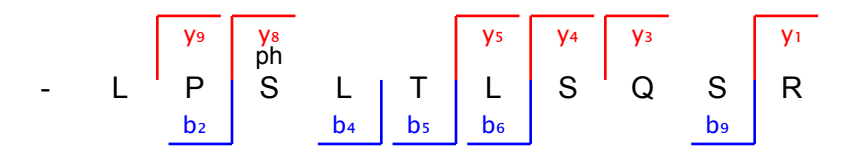
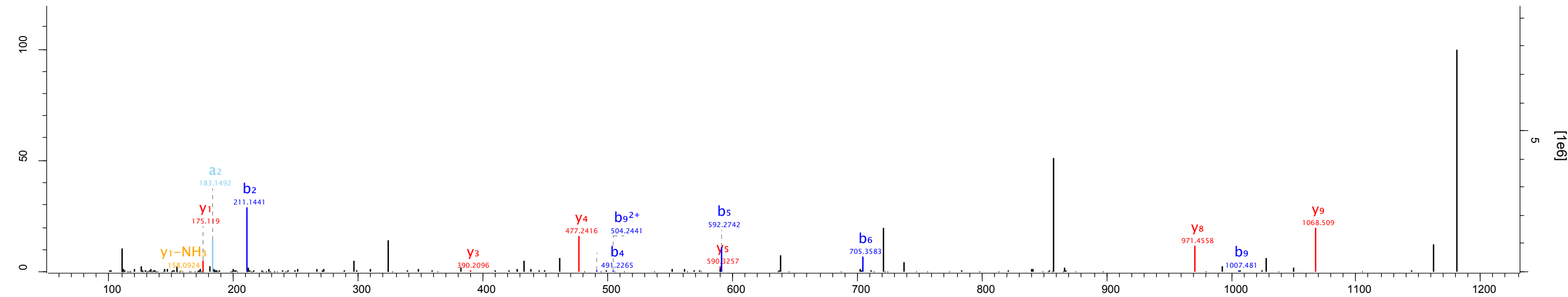
Raw file: 20171215_MaS_33SR_LMH_proteome_02
 Scan: 42563 Method: FTMS; HCD Score: 77.22 m/z: 780.39 Gene names: CCZ1B;CCZ1



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 6253 Method FTMS; HCD Score 62.71 m/z 482.2

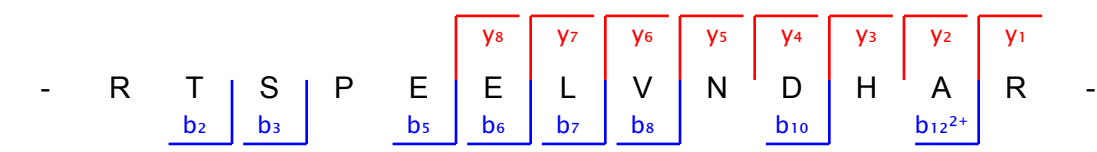
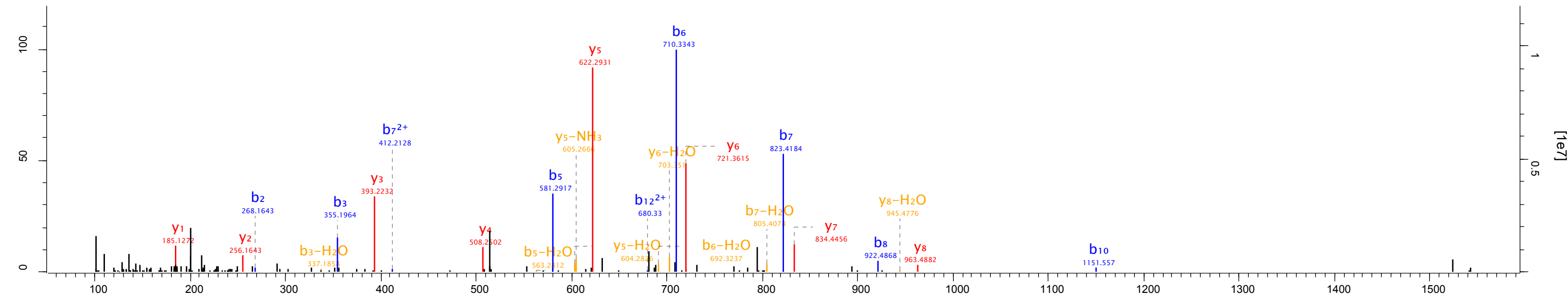


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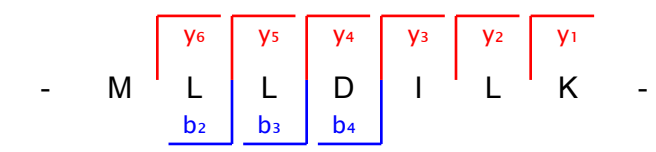
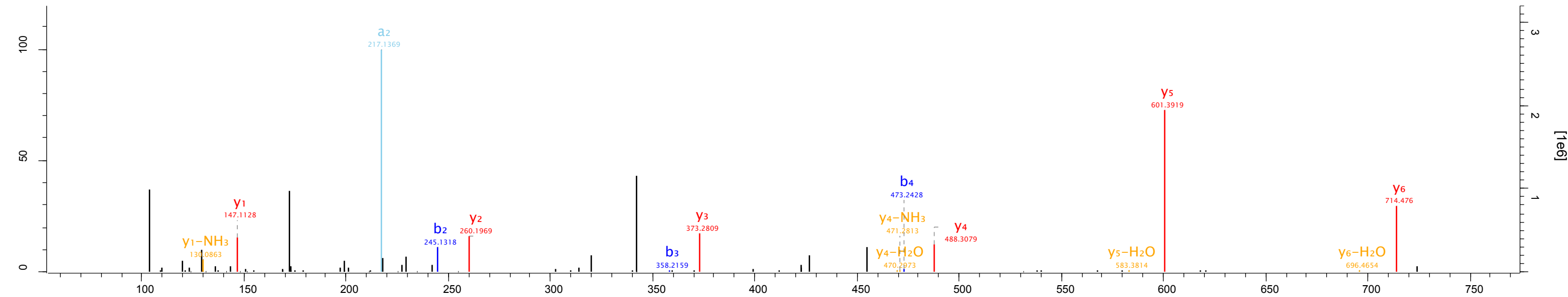


Raw file
20171215_MaS_33SR_LMH_proteome_02

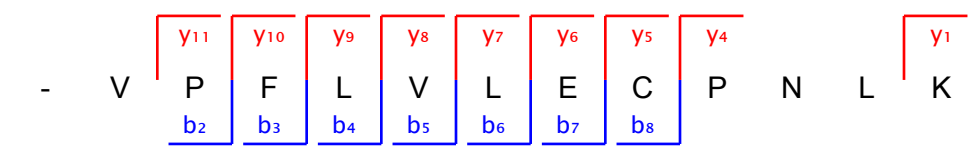
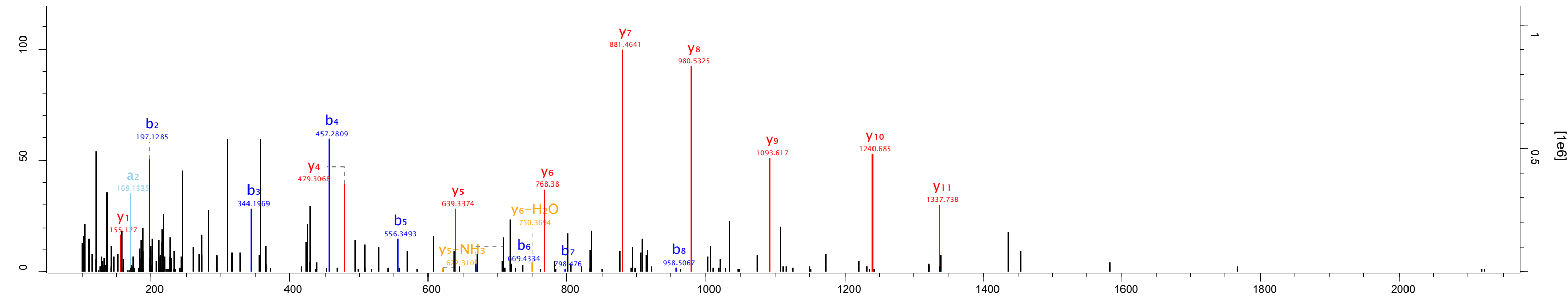
Scan 7813 Method FTMS; HCD Score 95.98 m/z 515.6 Gene names SPANXC;SPANXD



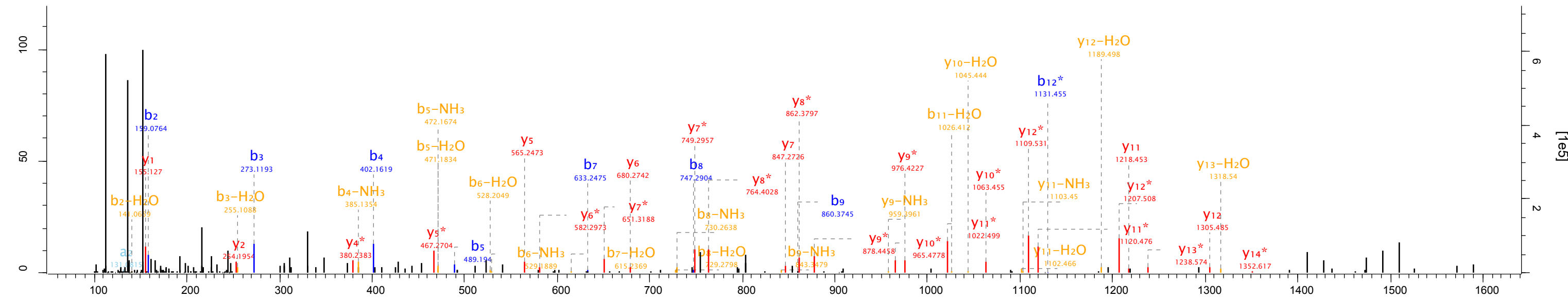
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 Scan: 83823 Method: FTMS; HCD Score: 99.14 m/z: 423.26 Gene names: TRPC4;TRPC5



Raw file: 20171215_MaS_33SR_LMH_proteome_02
 Scan: 96273 Method: FTMS; HCD Score: 71.18 m/z: 719.41 Gene names: OSTC



Raw file 20171215_MaS_33SR_LMH_phospho_01 Scan 3384 Method FTMS; HCD Score 140.2 m/z 853.82 Gene names CLIP2



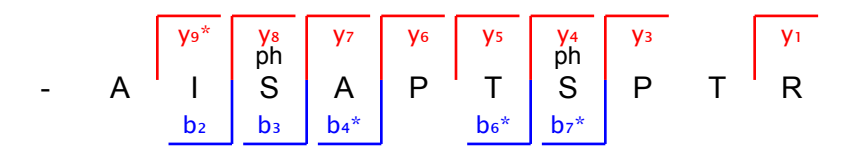
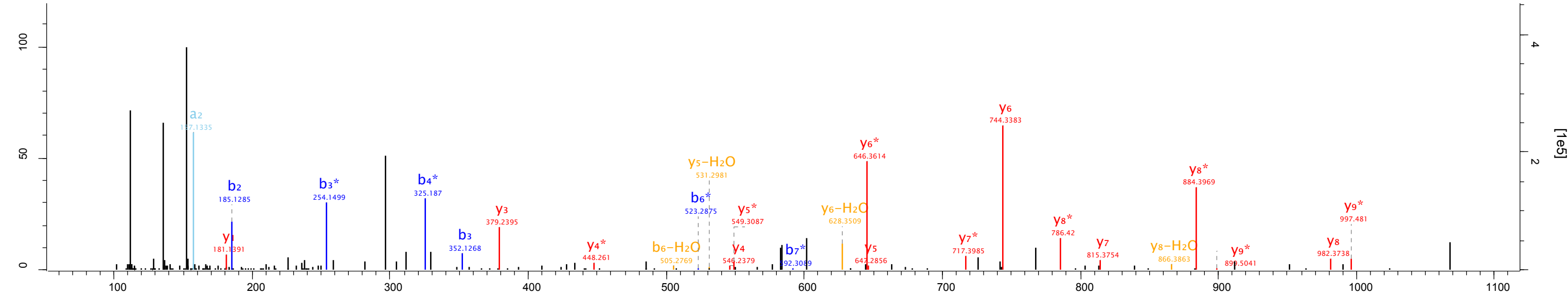
- T G N E S G S N L S G ph S V K -

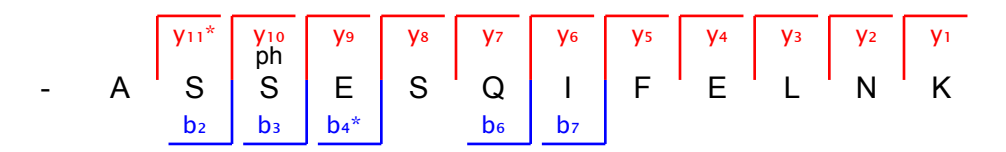
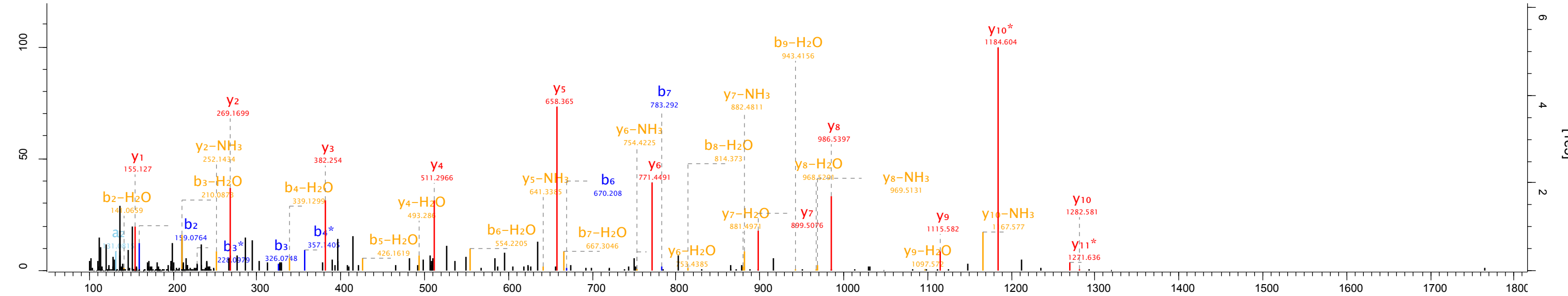
Fragmentation mapping (b and y ions):

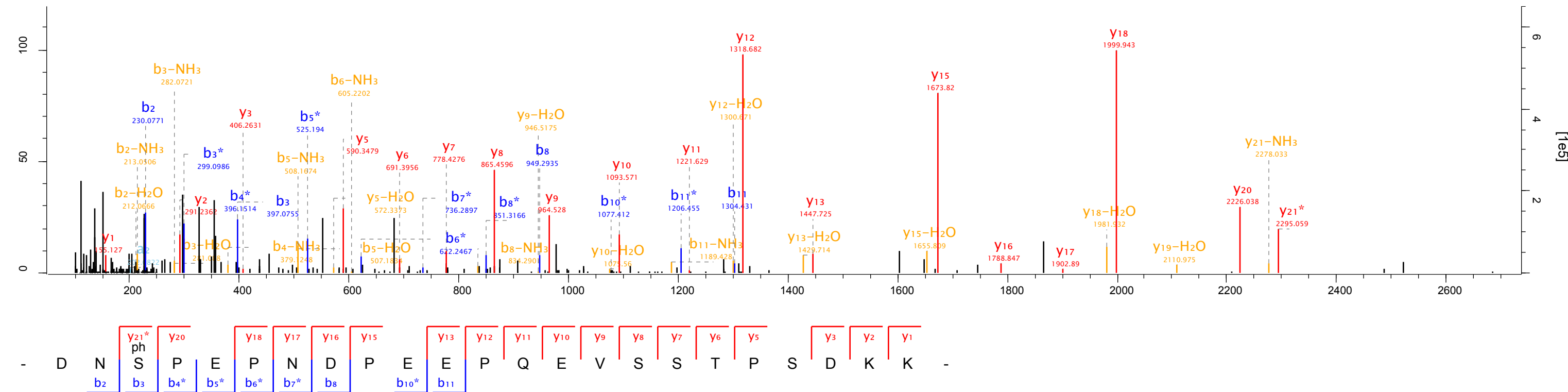
- b2: G
- b3: N
- b4: E
- b5: S
- b7: S
- b8: N
- b9: L
- b12*: S
- y1: K
- y2: V
- y4*: G
- y5: S
- y6: D
- y7: ph
- y8*: L
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- y10*: S
- y11: G
- y12: S
- y13*: E
- y14*: N

Raw file Scan Method Score m/z Gene names

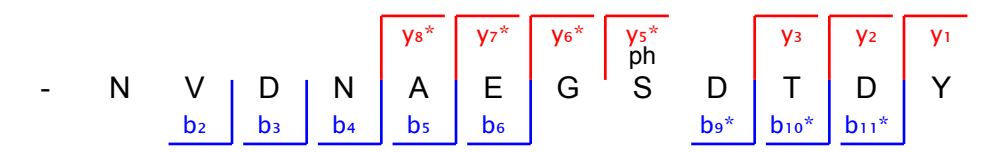
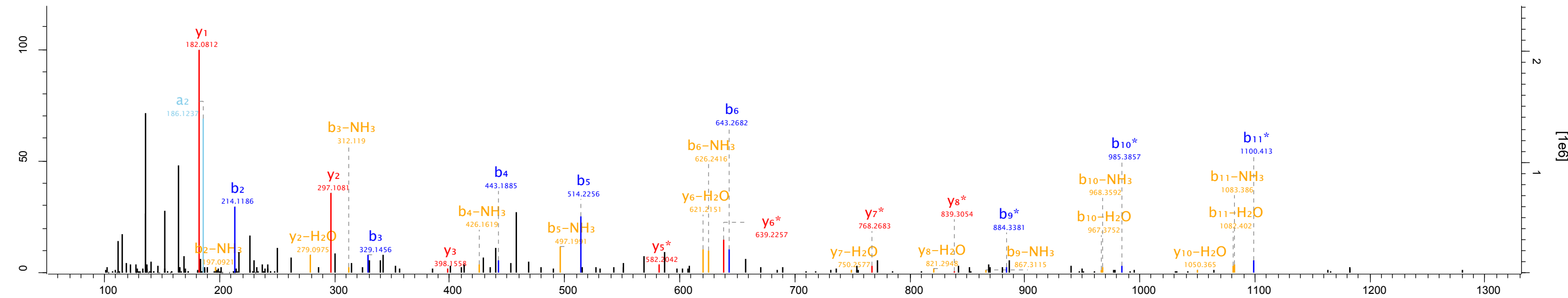
20171215_MaS_33SR_LMH_phospho_01 4934 FTMS; HCD 115.1 583.75 MIEF1



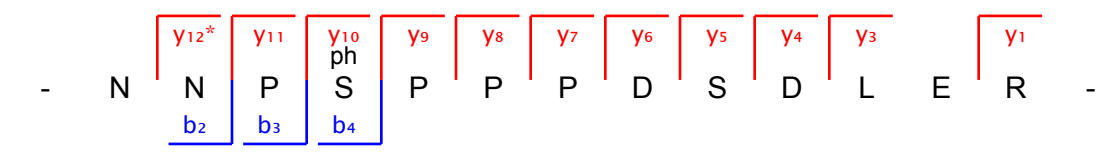
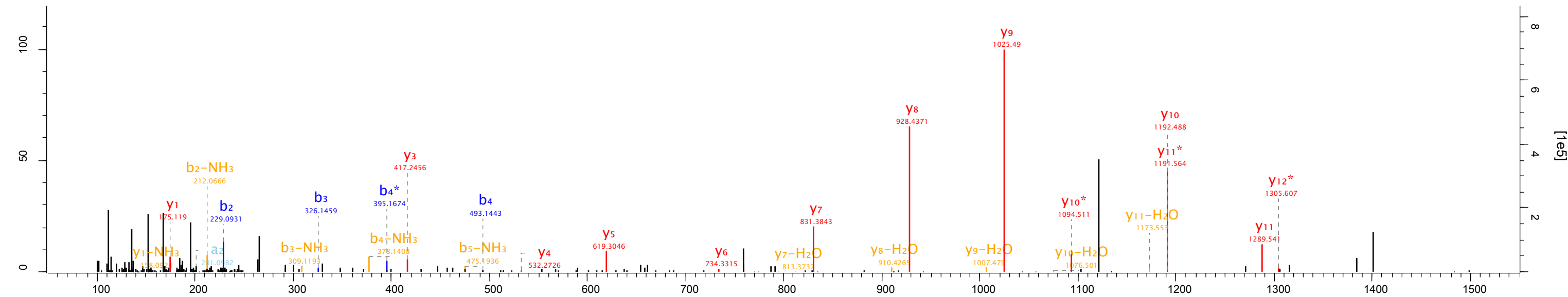




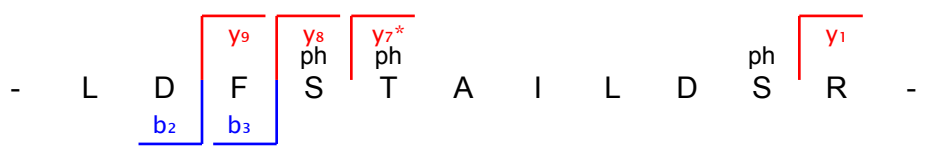
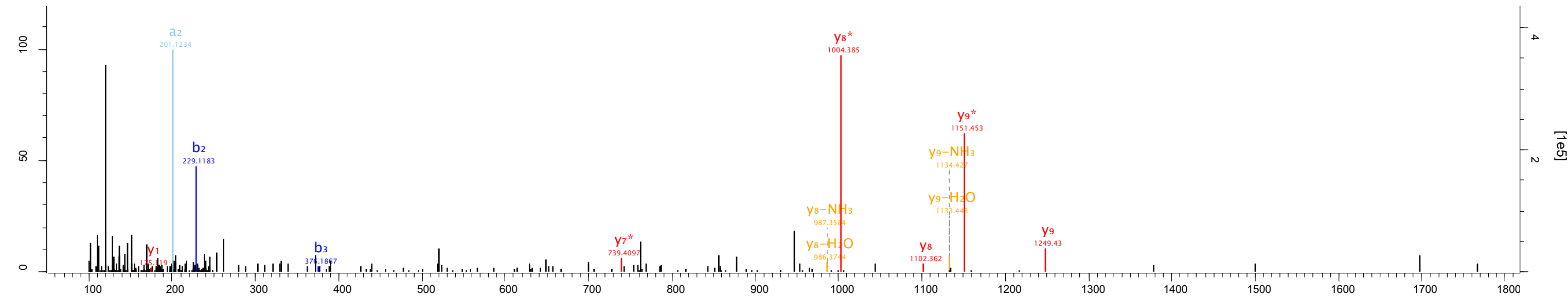
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 Scan: 5634 Method: FTMS; HCD Score: 108.23 m/z: 690.23 Gene names: HERC1



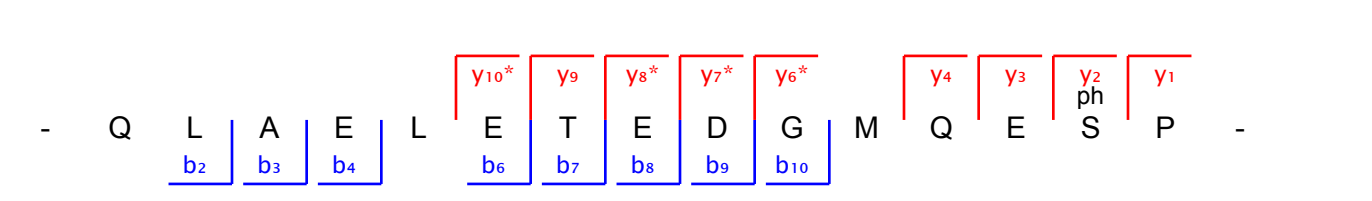
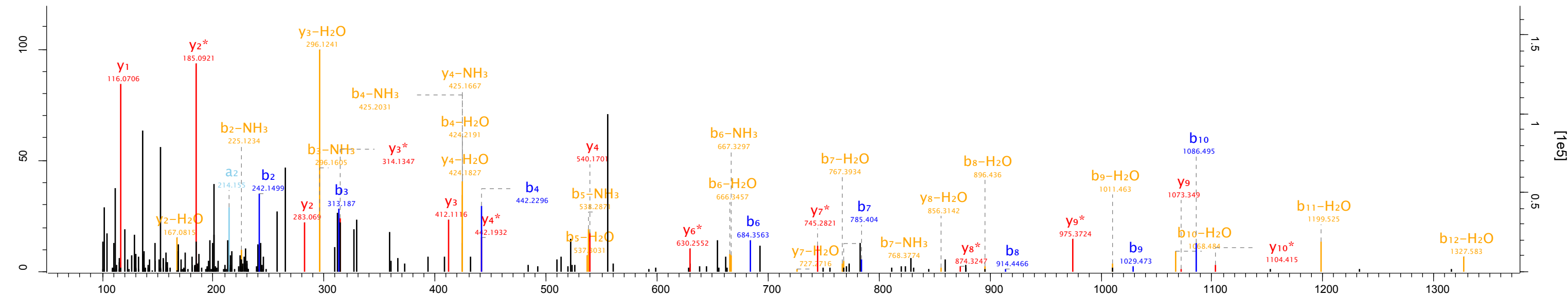
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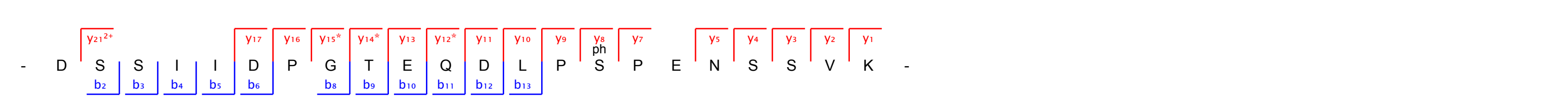
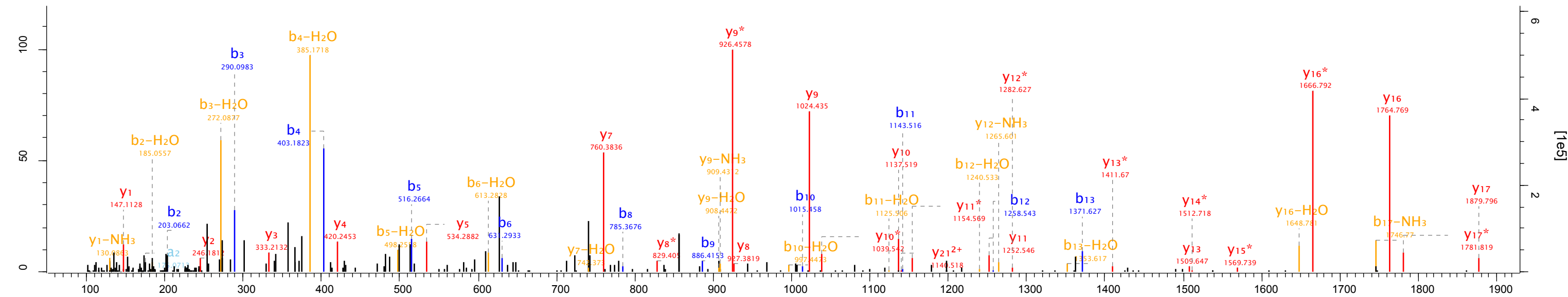
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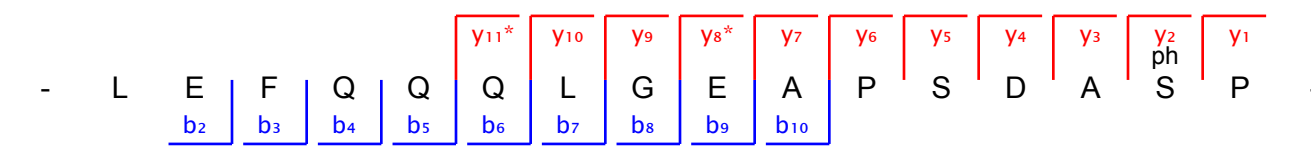
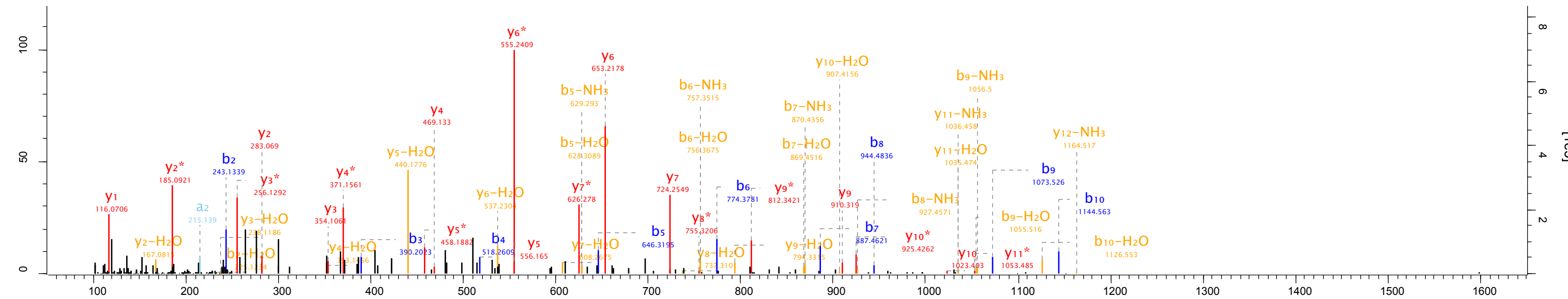
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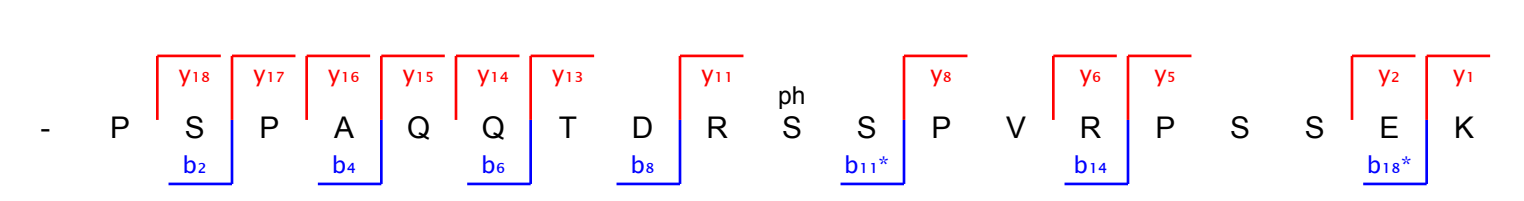
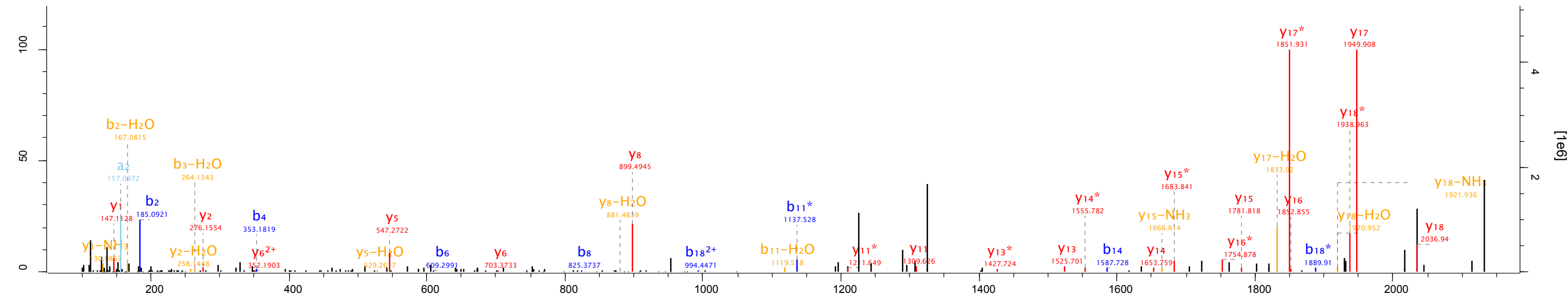
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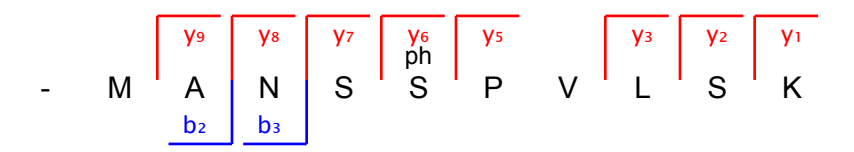
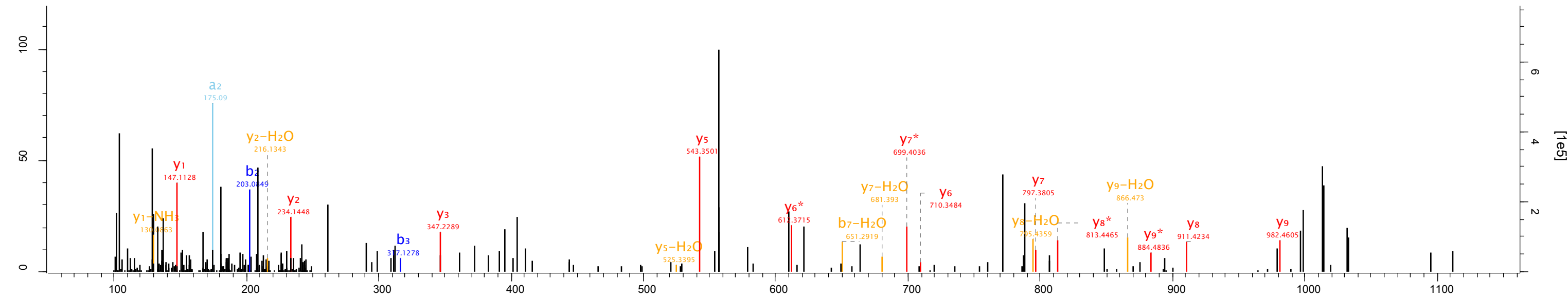
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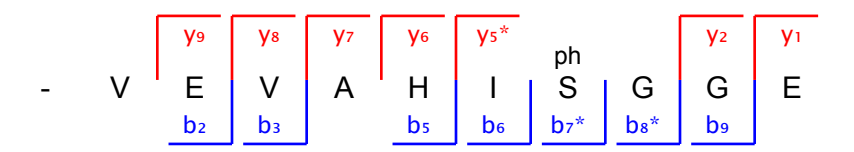
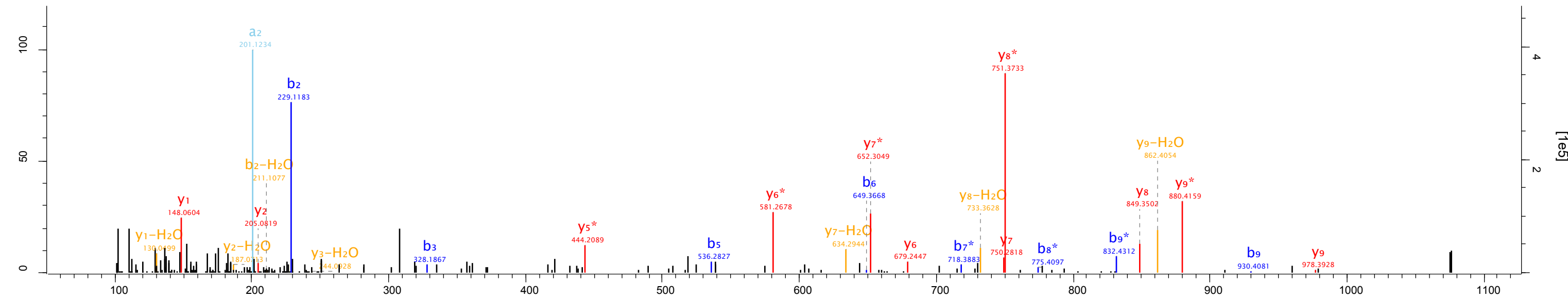
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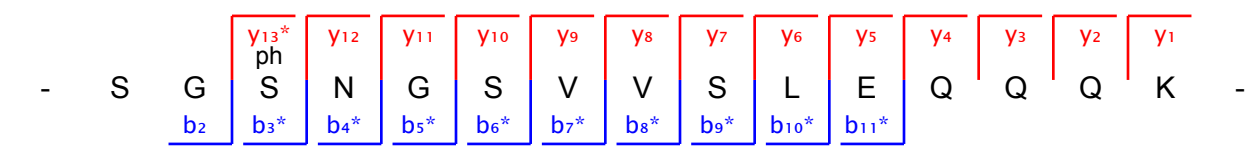
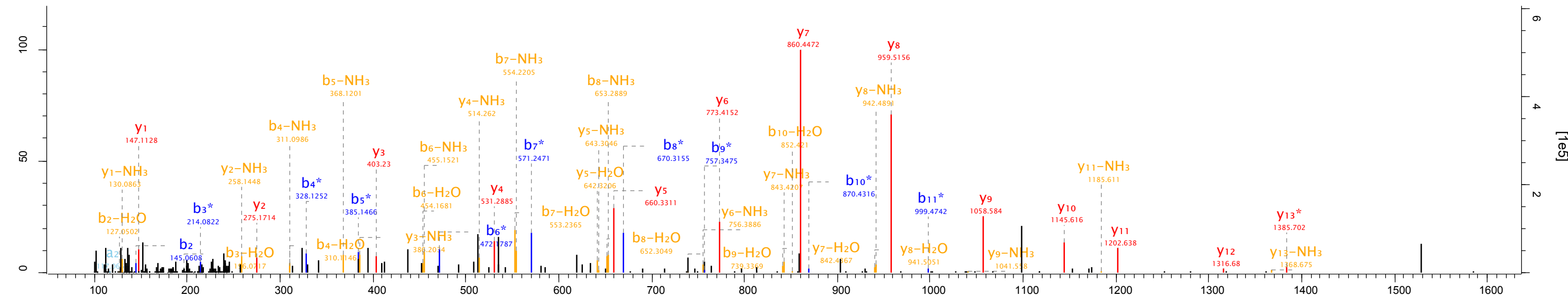
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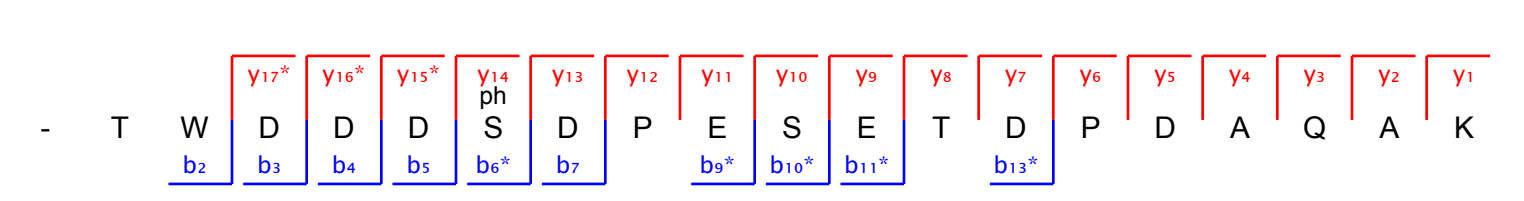
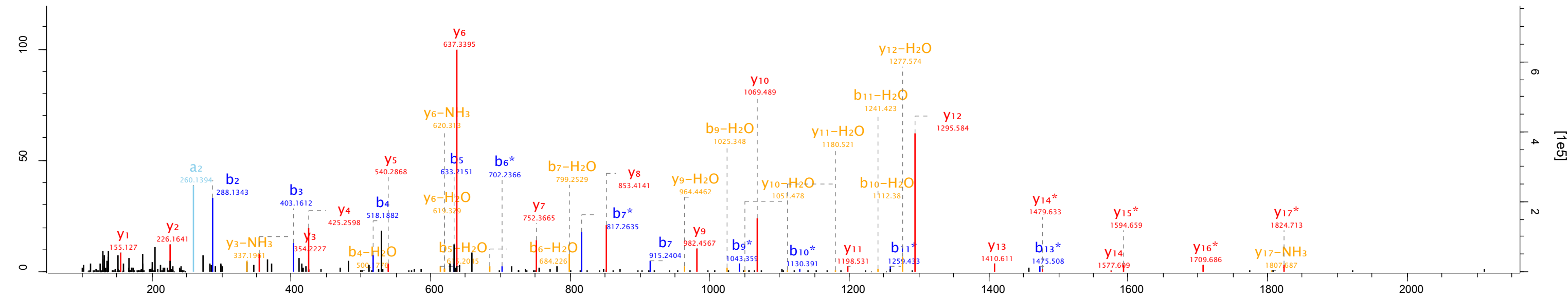
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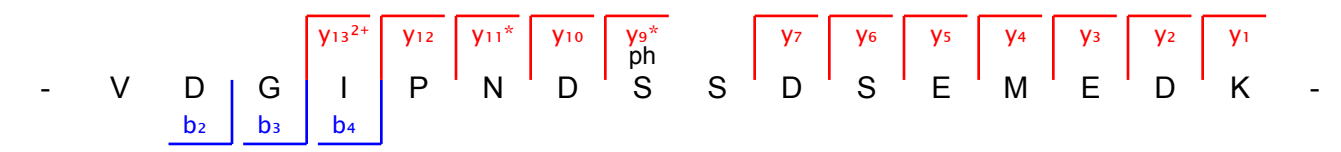
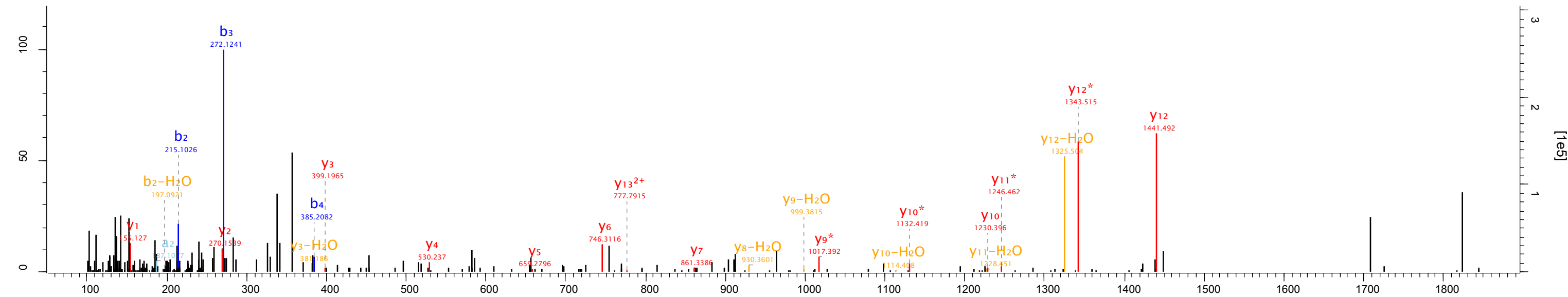
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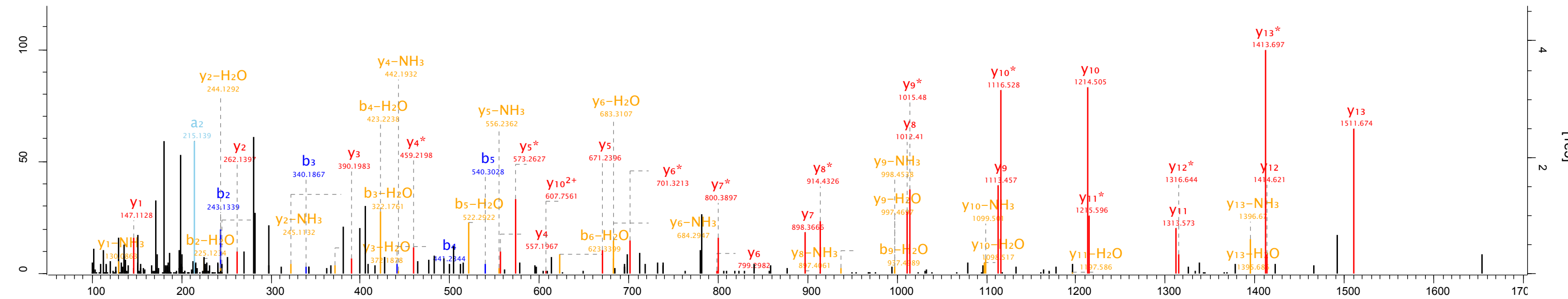
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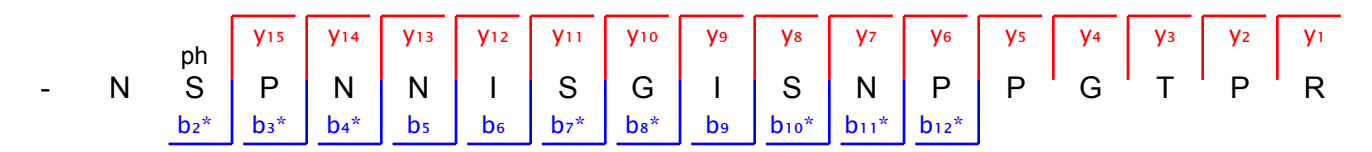
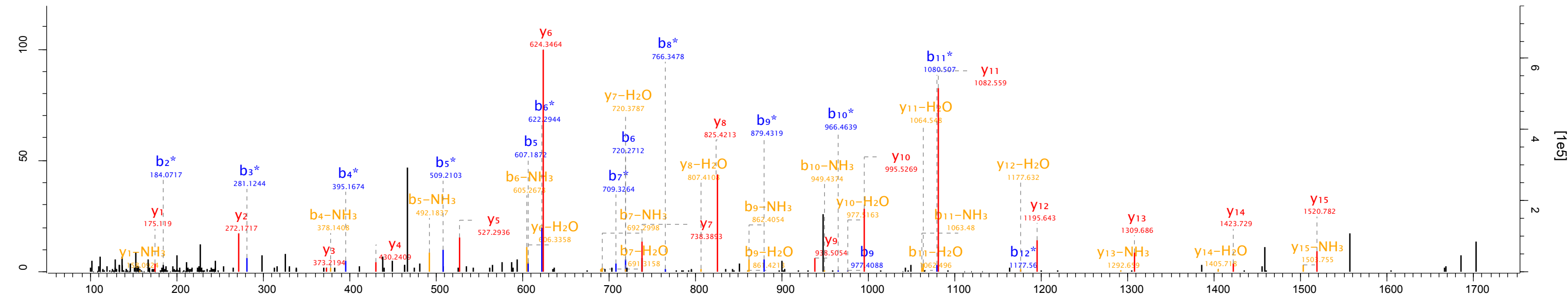
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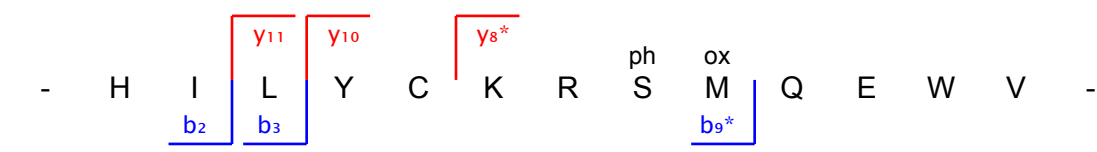
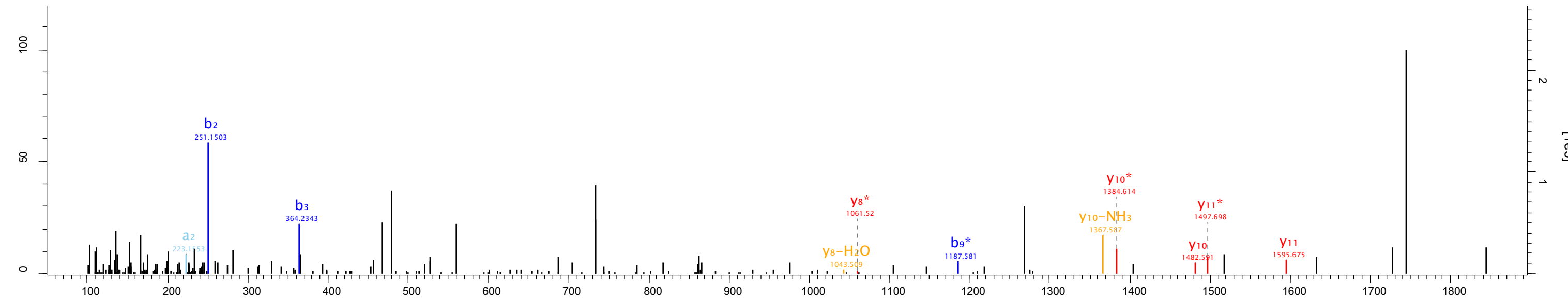
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Fragmentation labels: b2, b3, b4, b5 (under L, P, T, V); y13, y12, y11, y10, y9, y8, y7, y6, y5, y4-ph, y3, y2, y1 (above P, T, V, T, T, N, V, Q, N, S, Q, D, K).

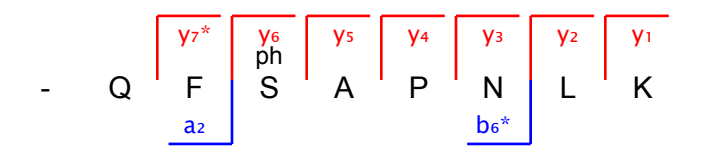
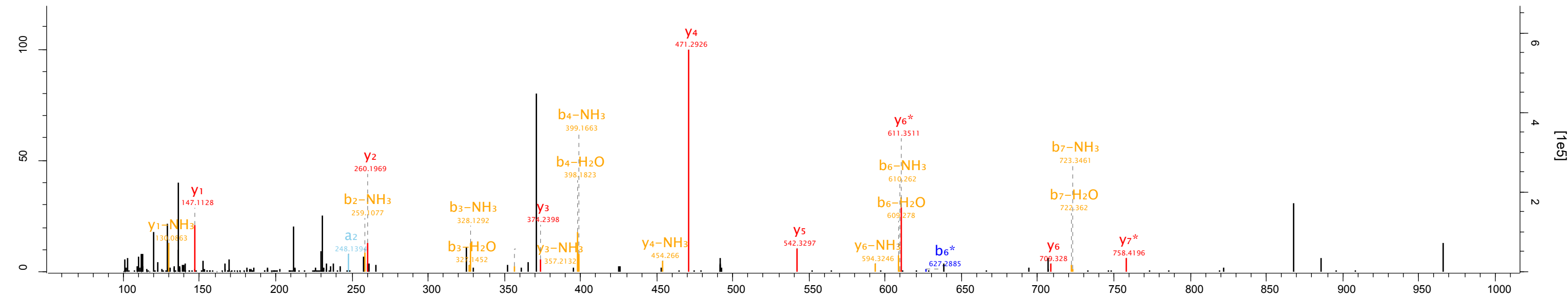
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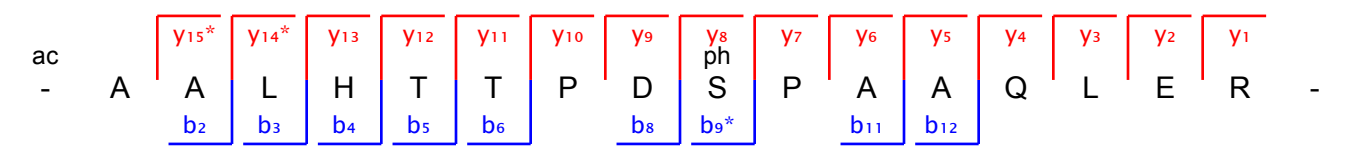
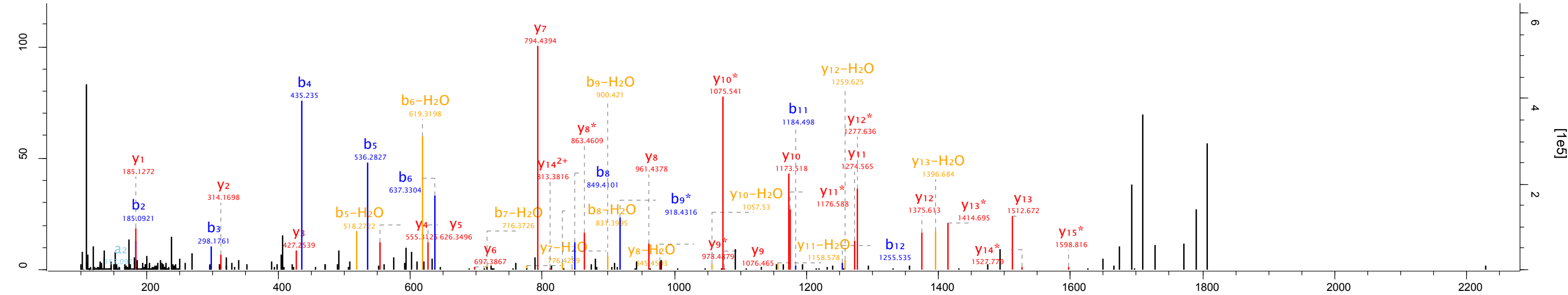


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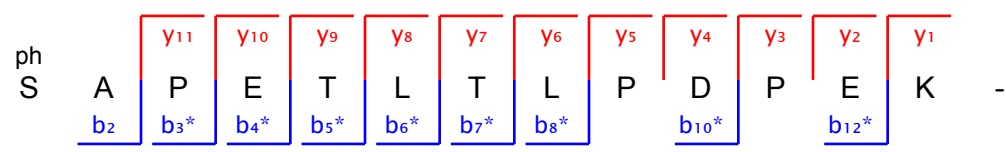
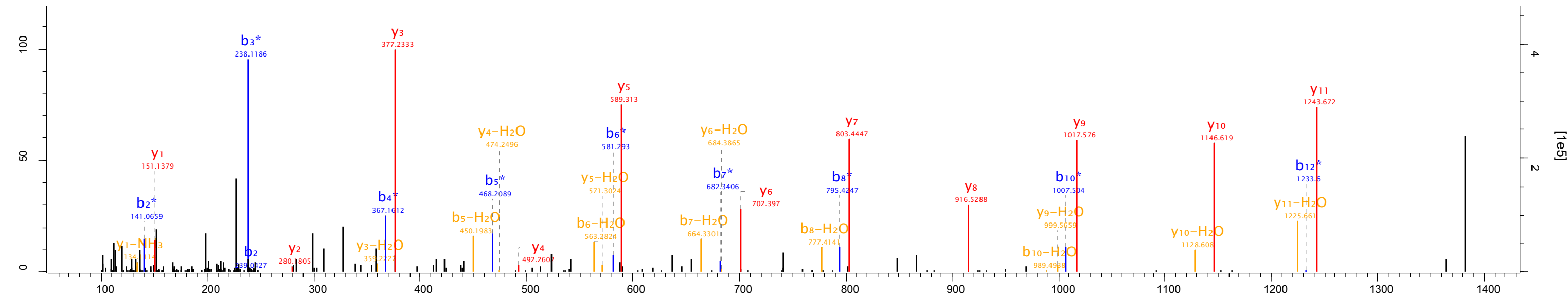


Raw file Scan Method Score m/z Gene names

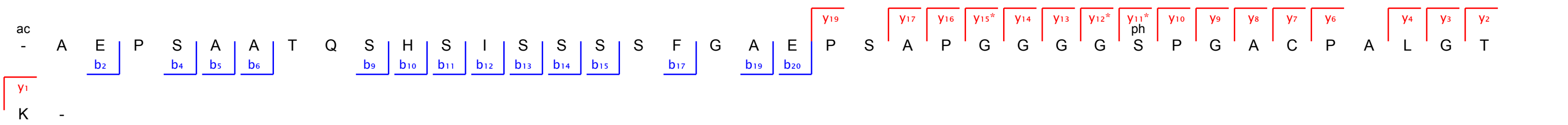
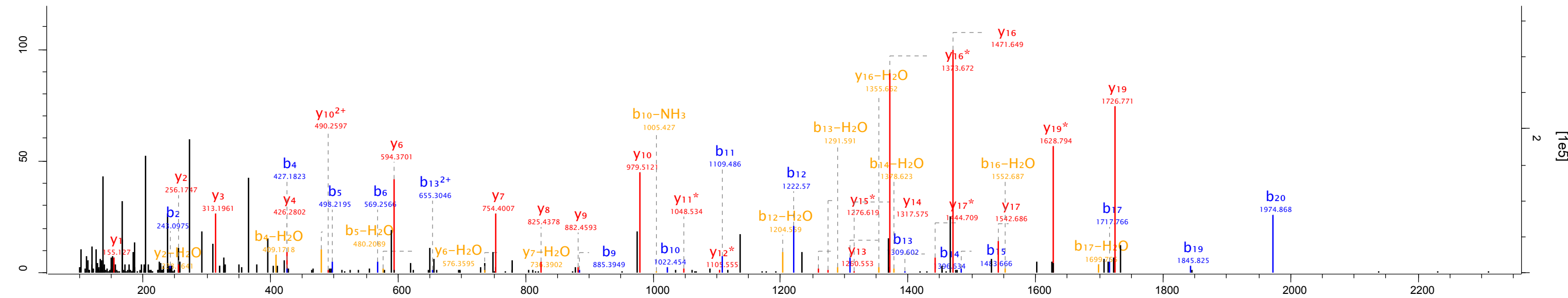
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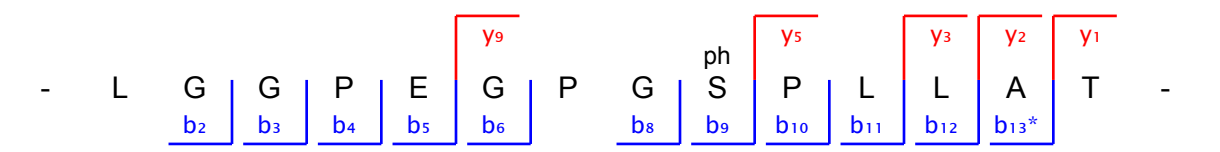
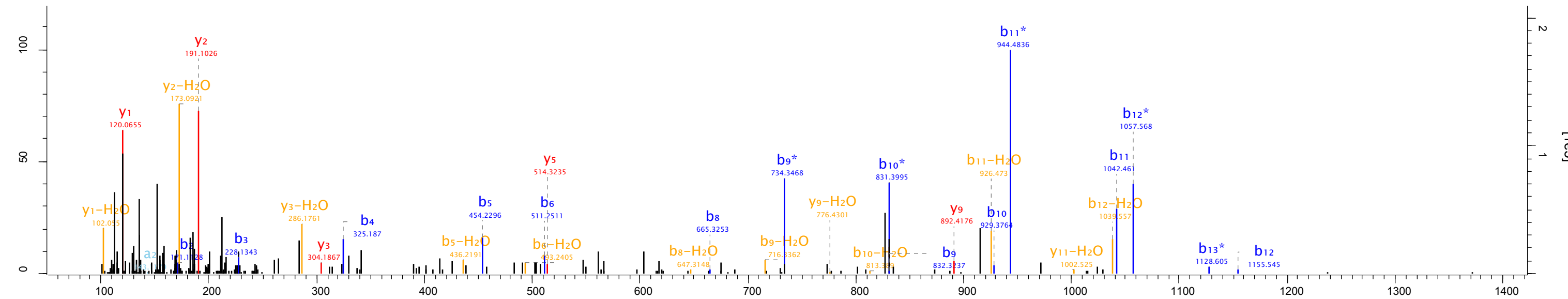
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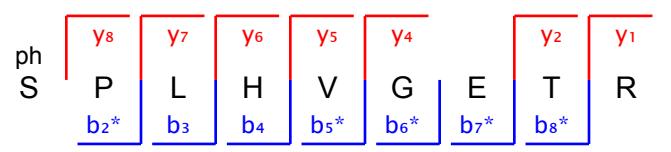
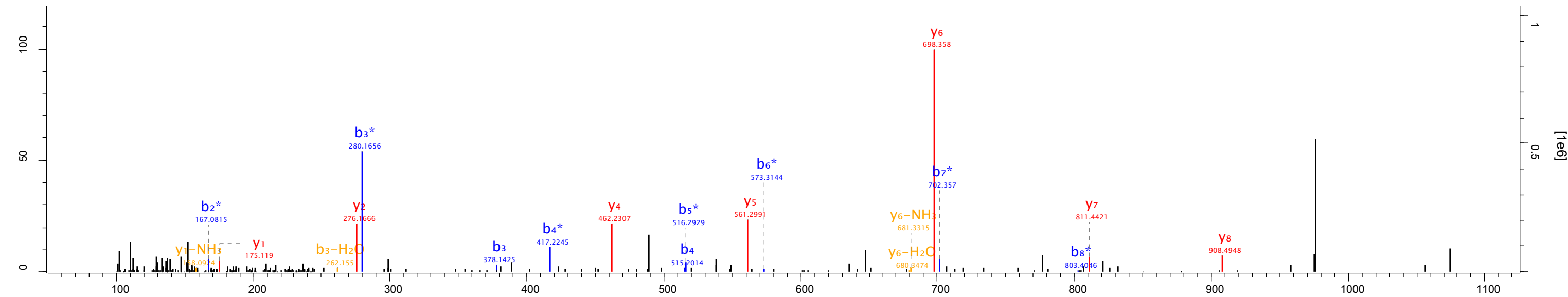
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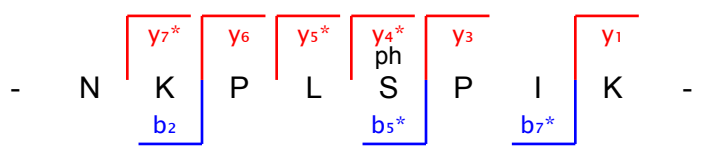
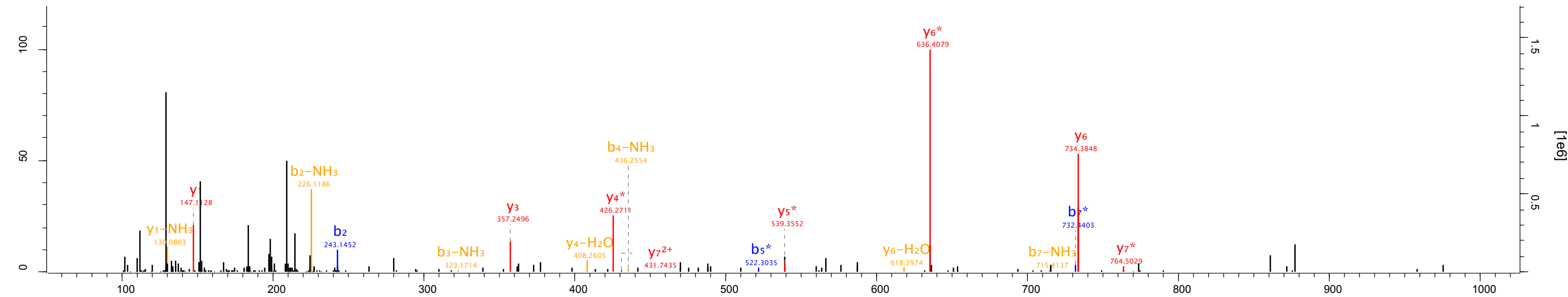
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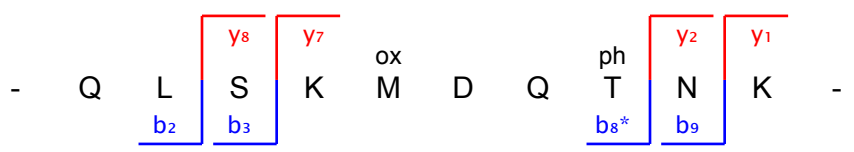
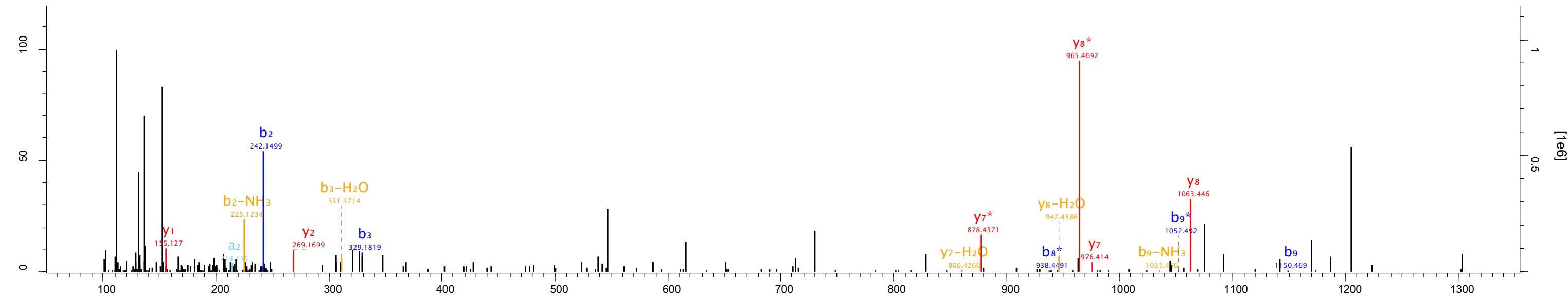
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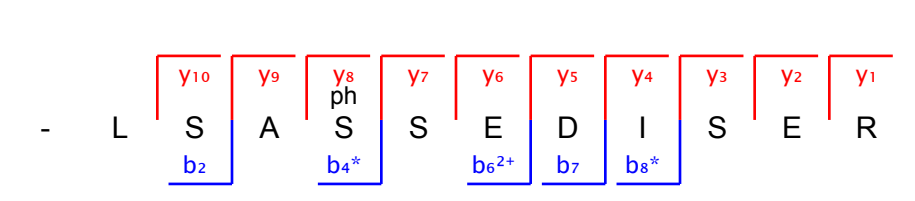
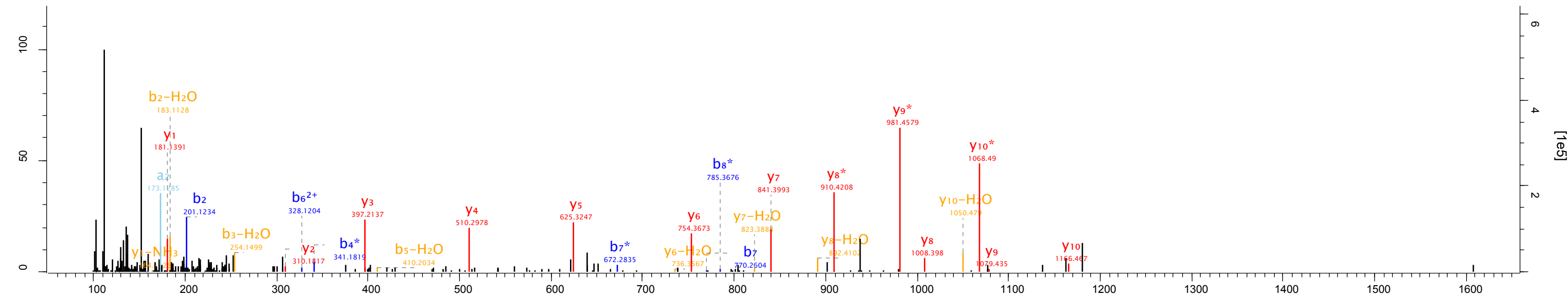
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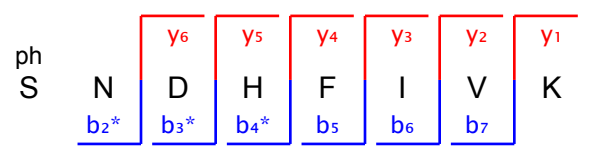
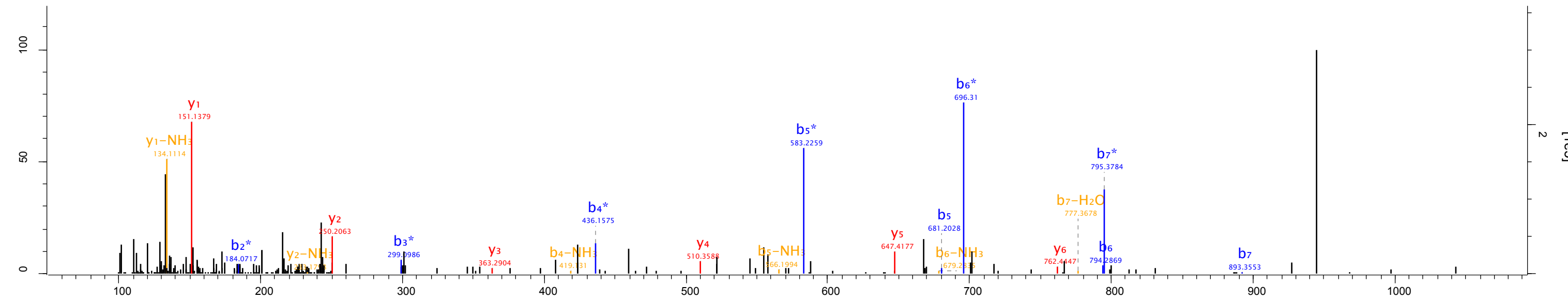
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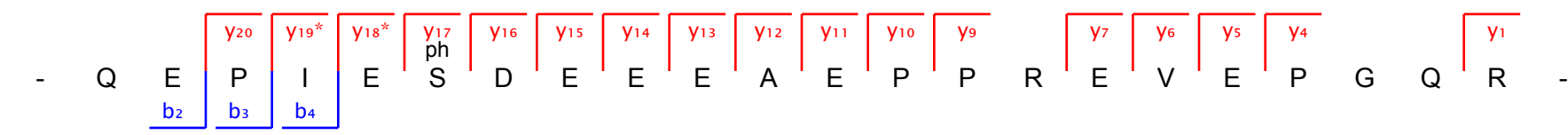
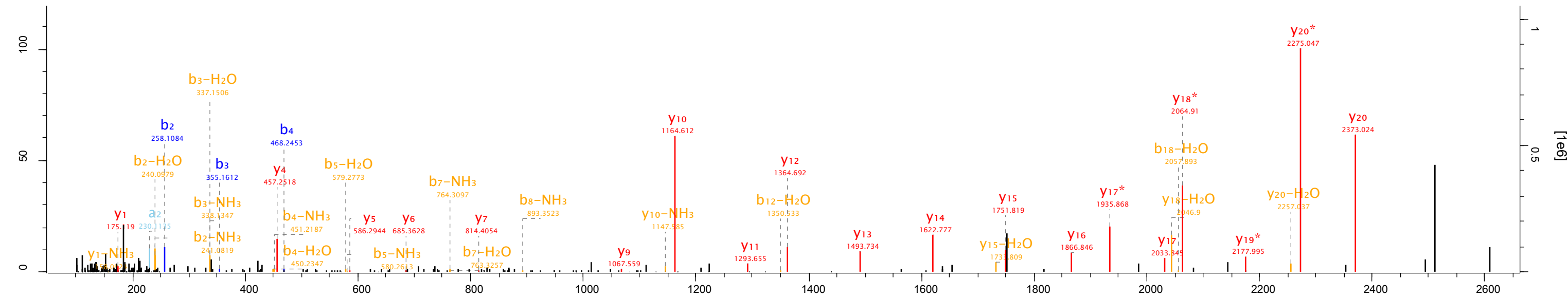
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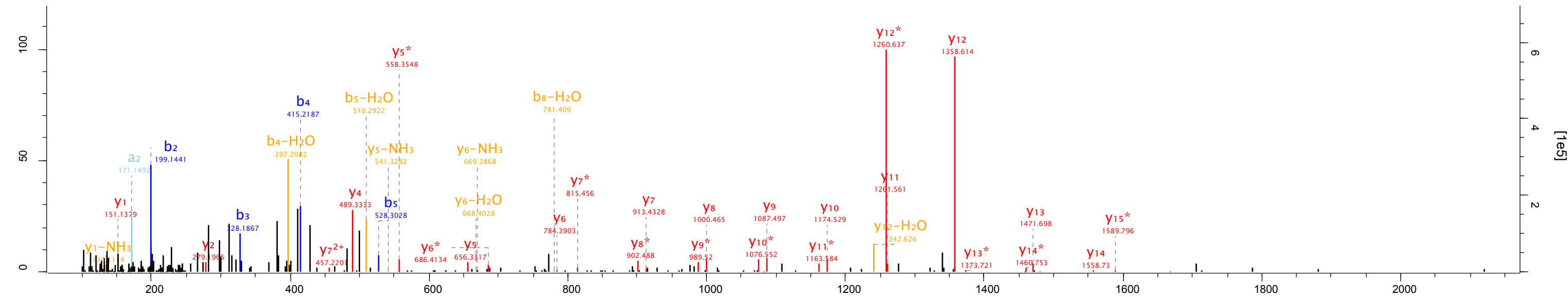


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Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 9344 Method FTMS; HCD Score 111.55 m/z 877.72 Gene names HDAC4





- V V E S L P S S S S E Q S P L Q K -

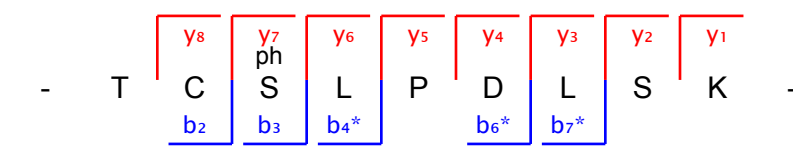
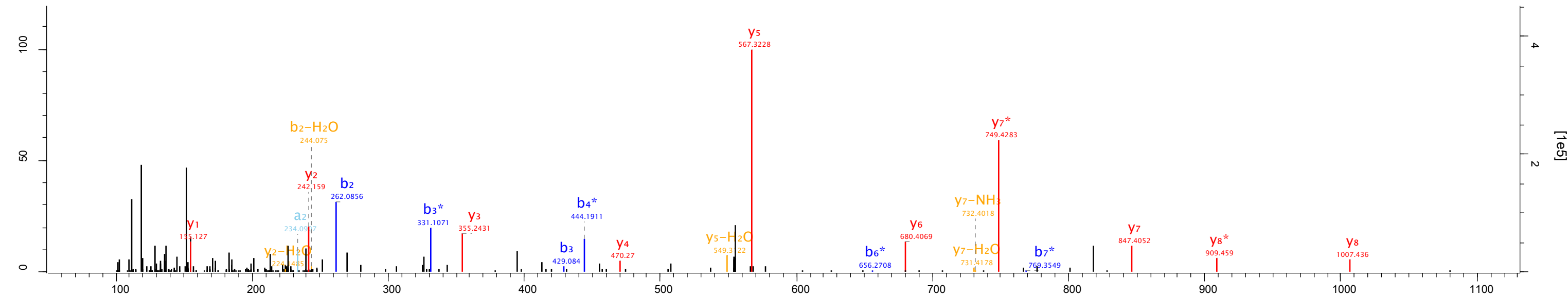
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- Blue boxes: b₂ (V), b₃ (E), b₄ (S), b₅ (L)
- Red boxes: y₁₅* (E), y₁₄ (S), y₁₃ (L), y₁₂ (P), y₁₁ (S), y₁₀ (S), y₉ (S), y₈ (S), y₇ (E), y₆ (Q), y₅ (S), y₄ (P), y₂ (Q), y₁ (K)

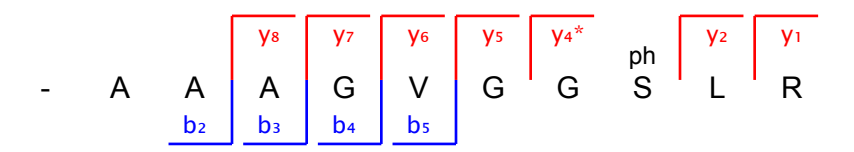
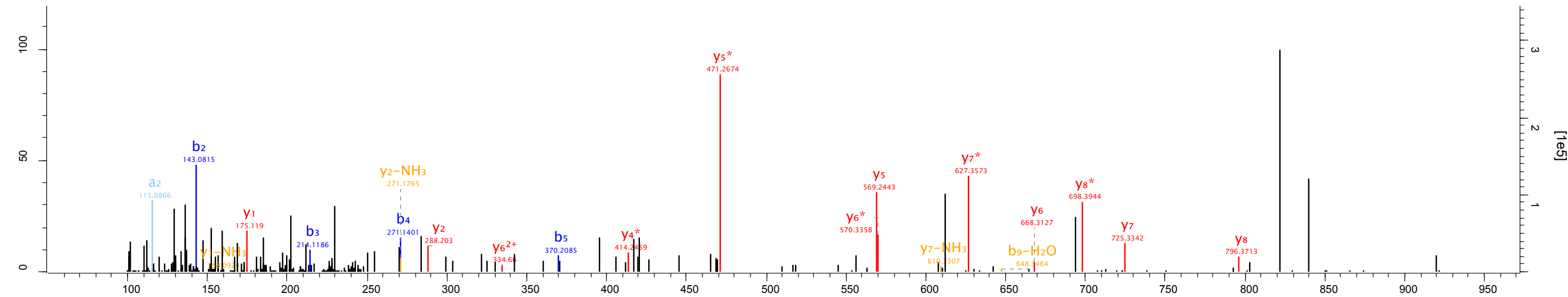
Raw file

20171215_MaS_33SR_LMH_phospho_06

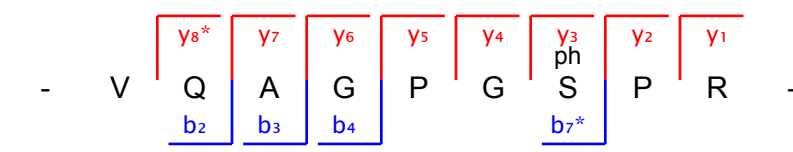
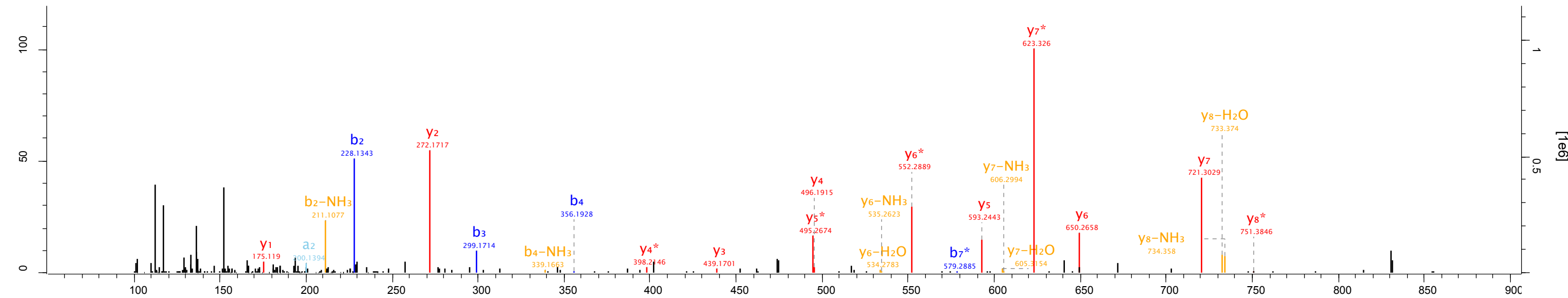
Scan 9914 Method FTMS; HCD Score 87.72 m/z 554.75 Gene names NEK1



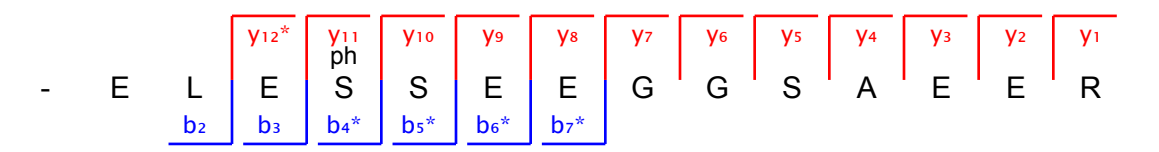
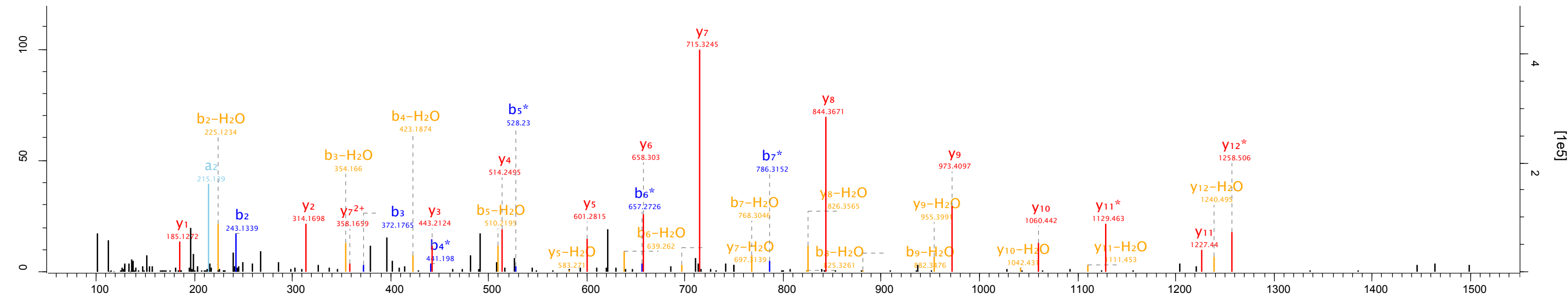
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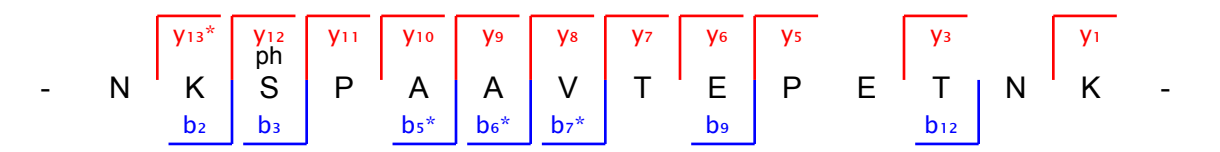
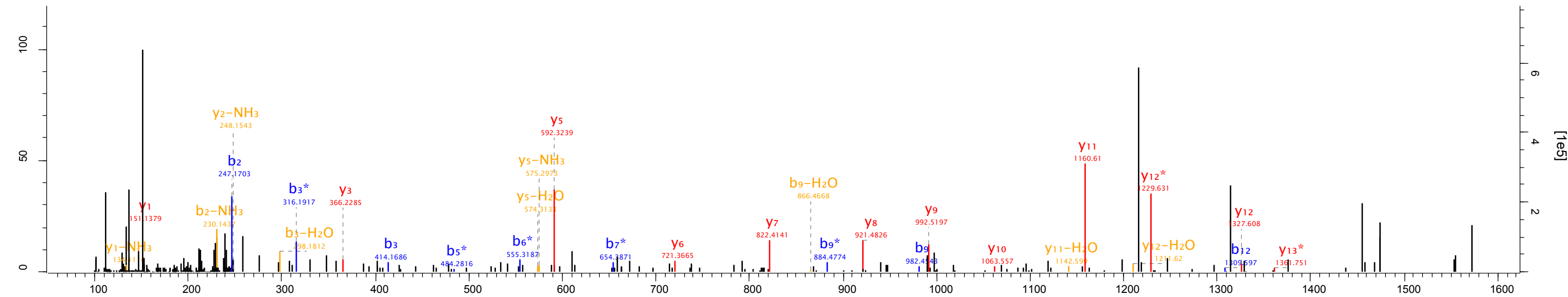
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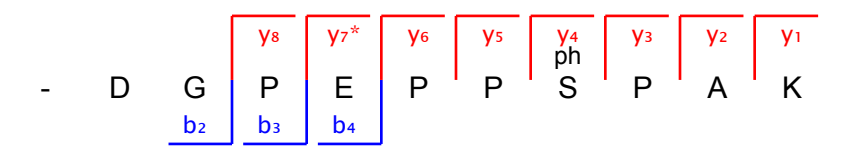
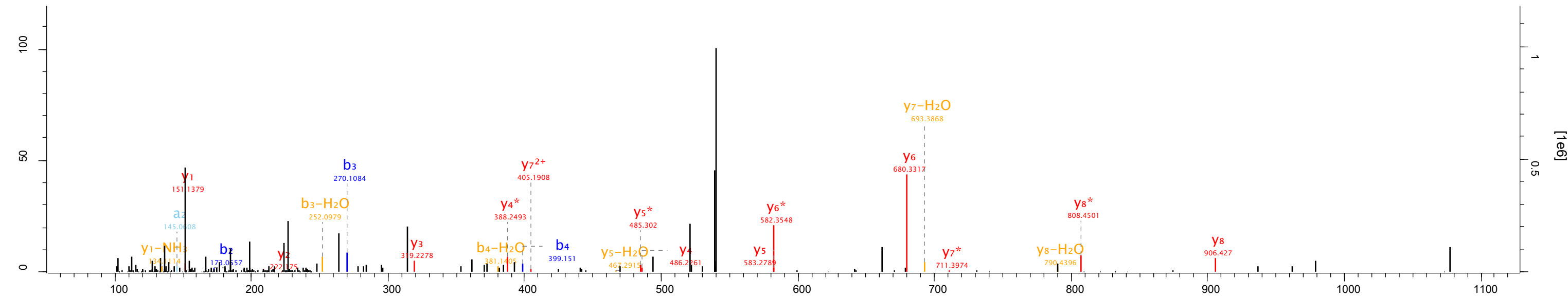
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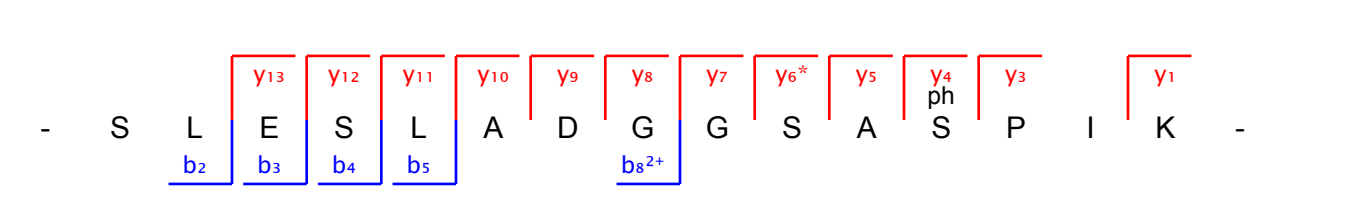
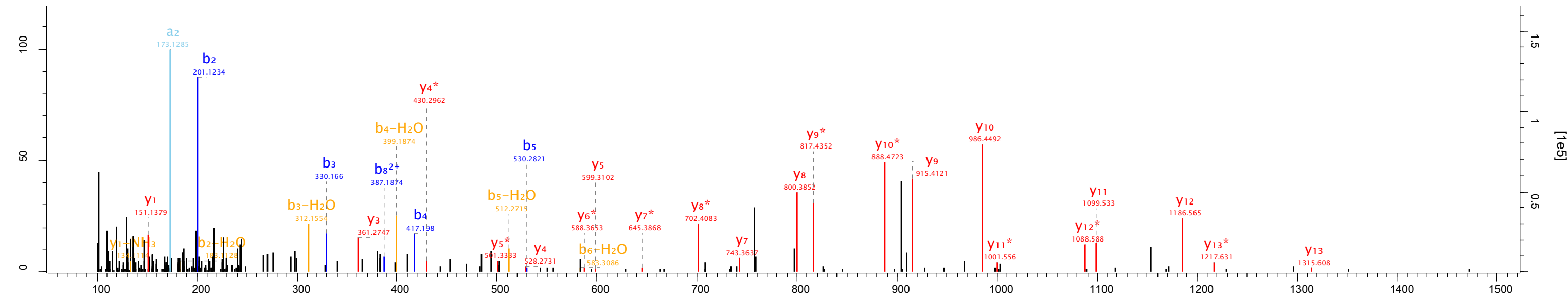
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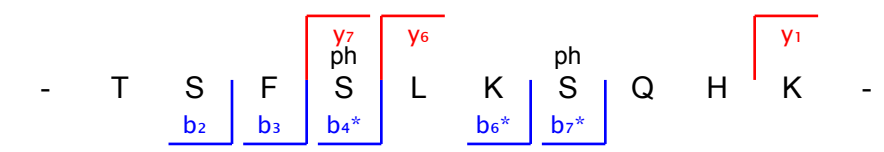
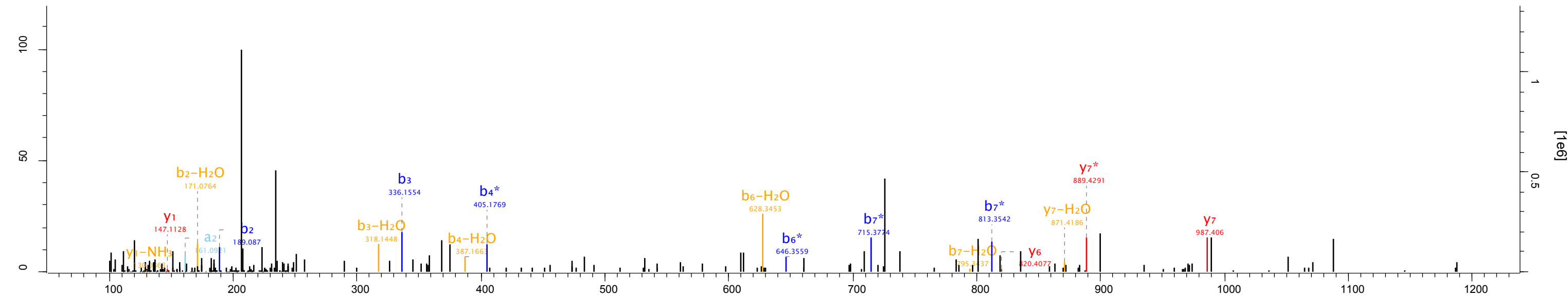
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Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 11864 Method FTMS; HCD Score 108.25 m/z 758.36 Gene names FANCE

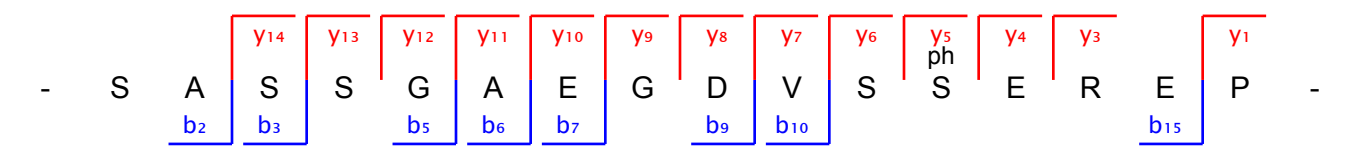
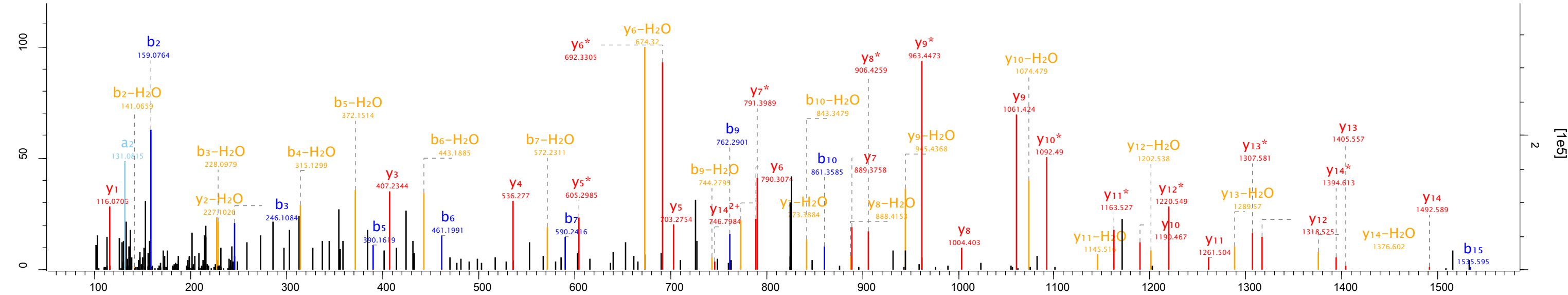


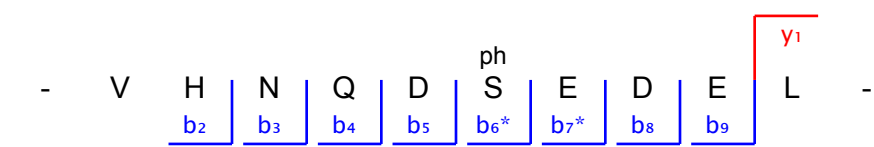
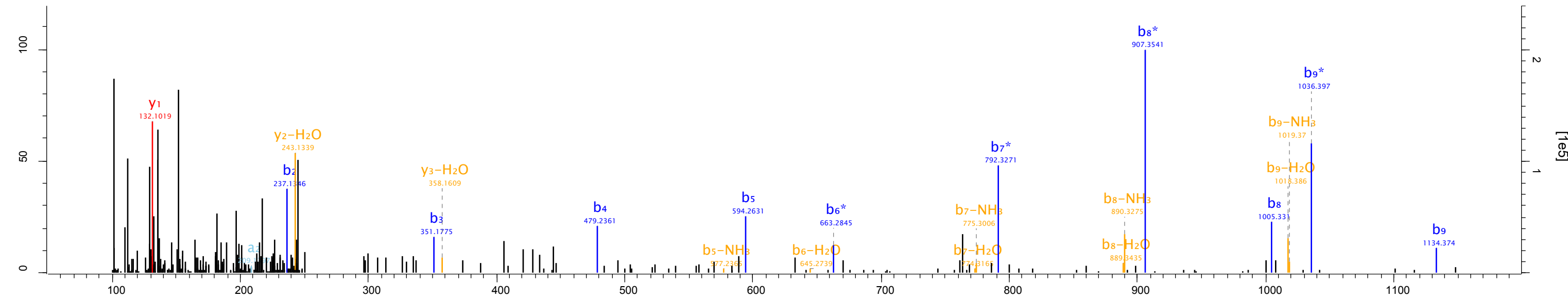
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 Scan 4084 Method FTMS; HCD Score 55.72 m/z 661.78



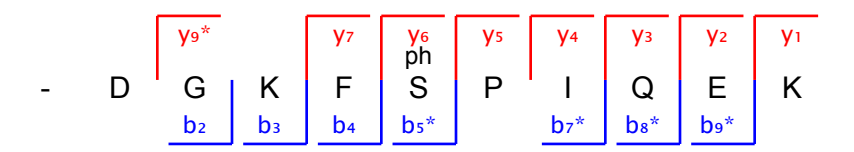
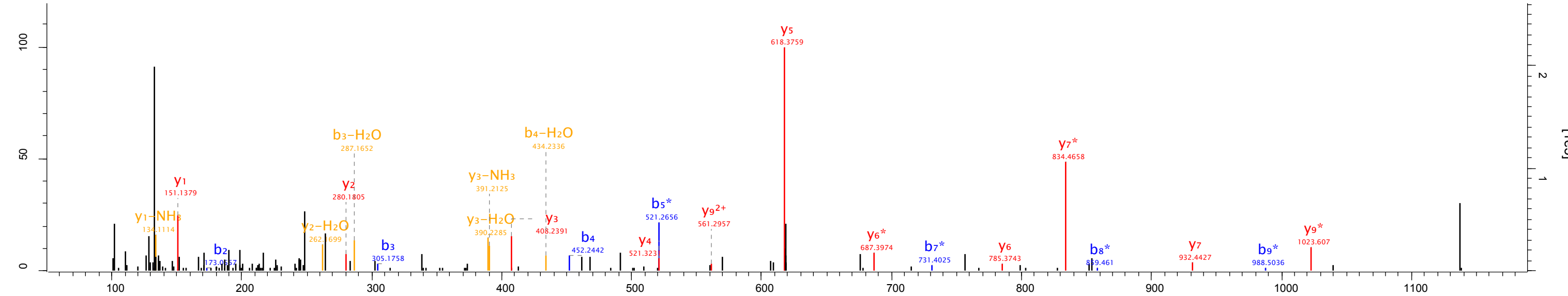
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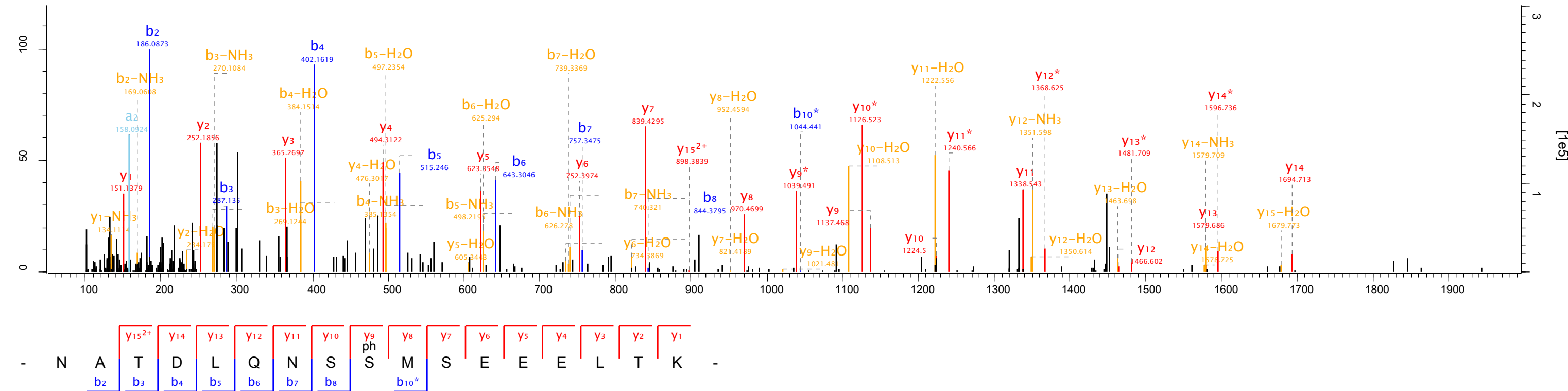
4144 FTMS; HCD 250.79 825.83 DTD1



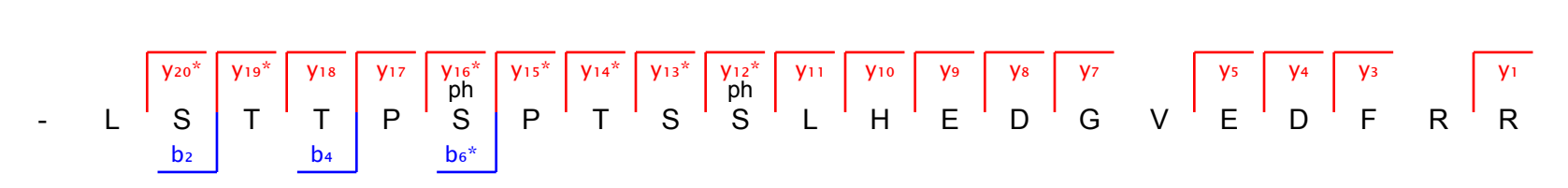
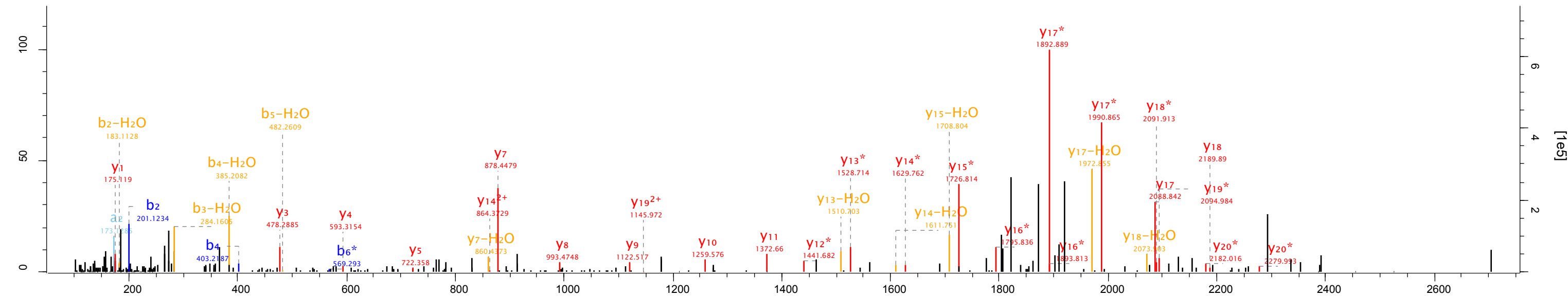


20171215_MaS_33SR_LMH_phospho2_02 6114 FTMS; HCD 105.99 618.81 BUB1

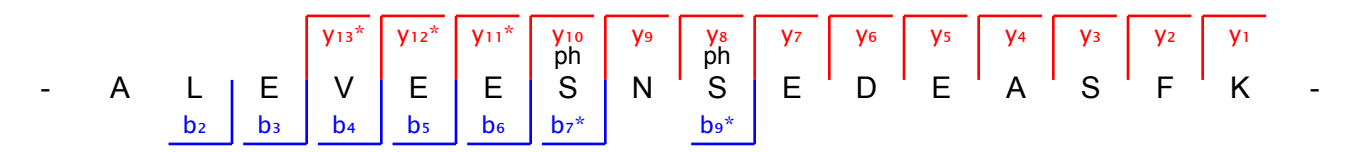
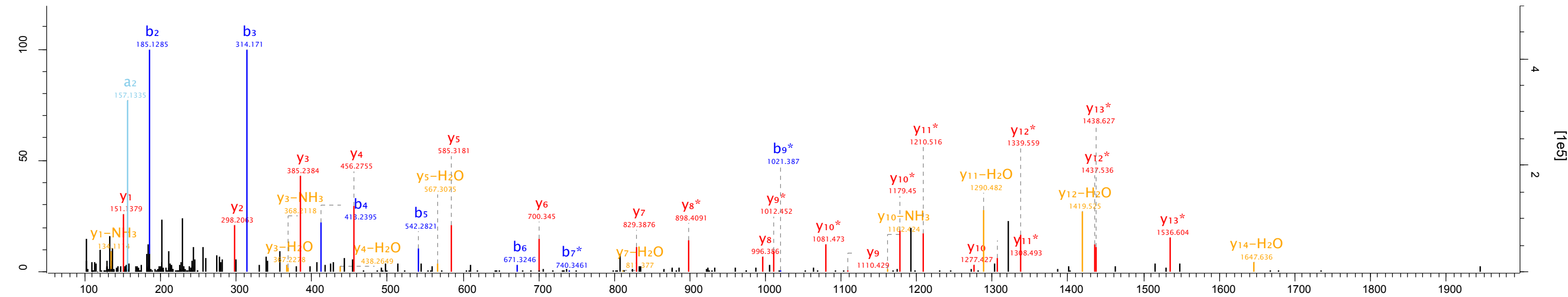




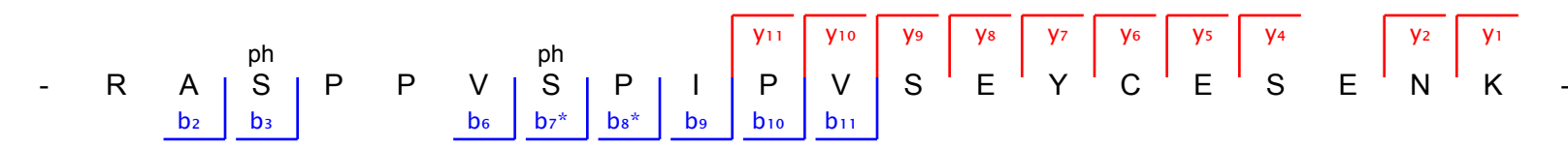
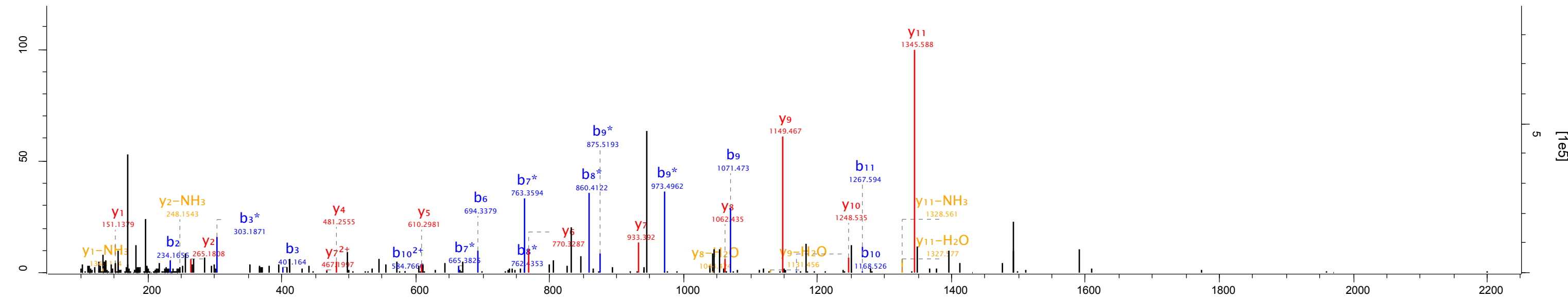
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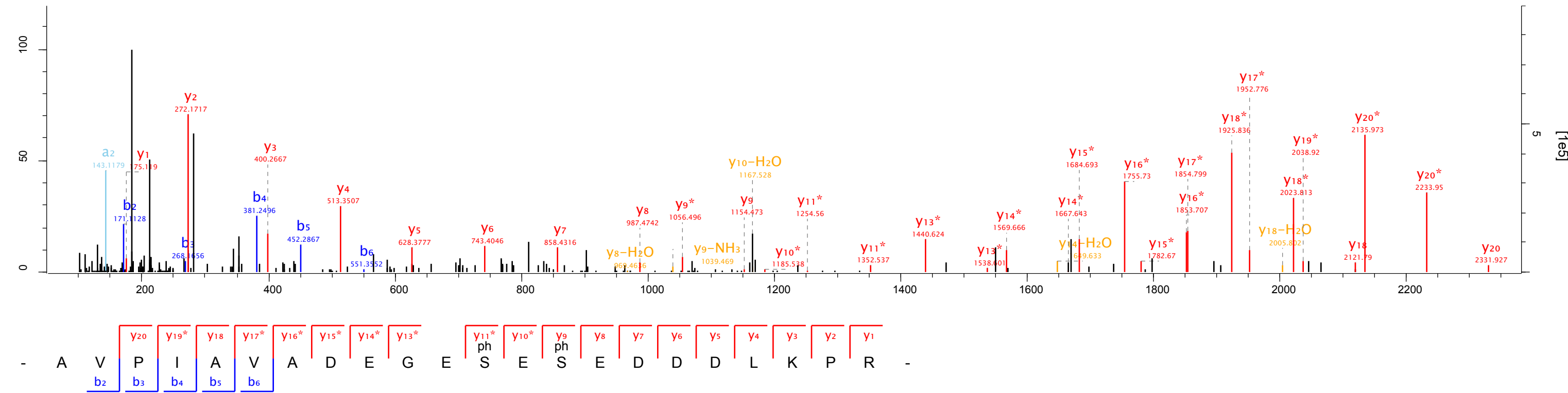
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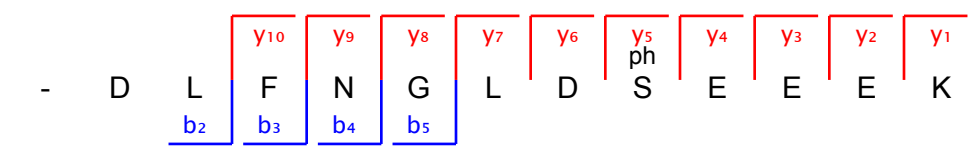
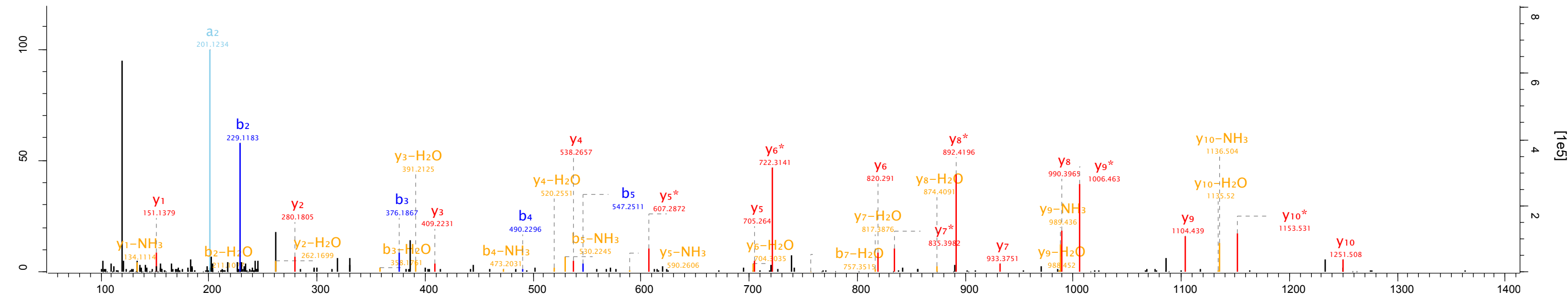
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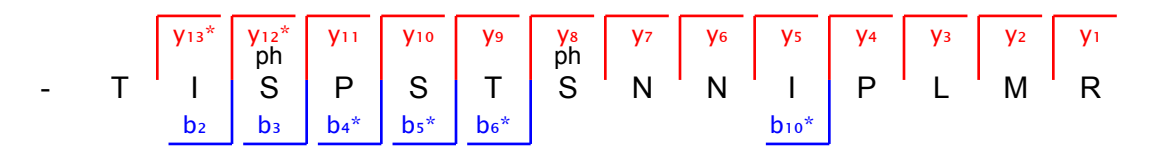
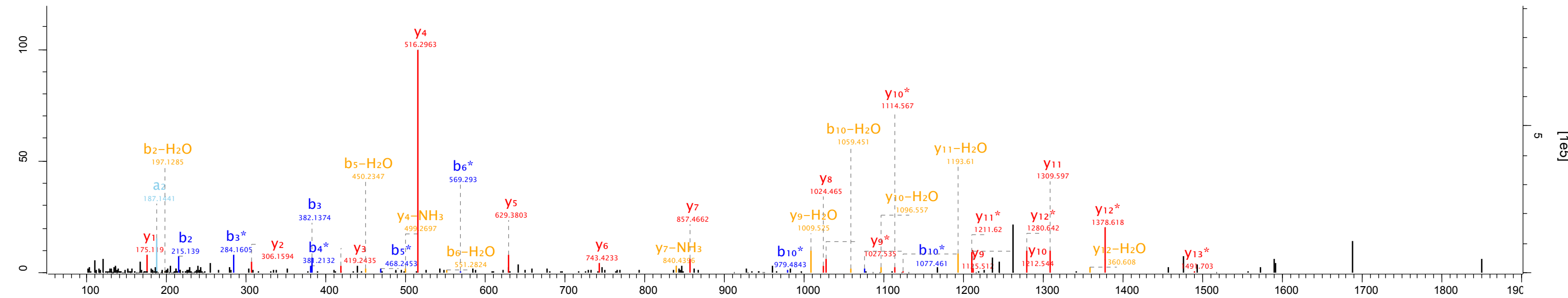
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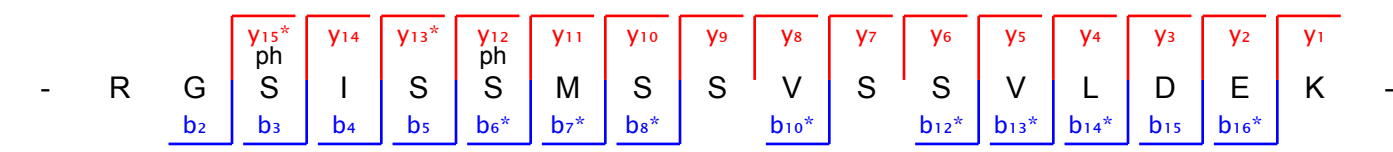
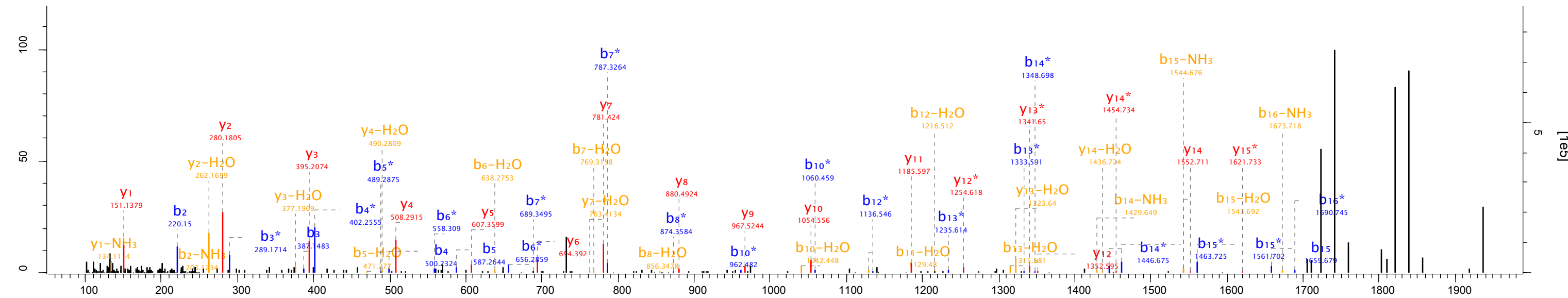
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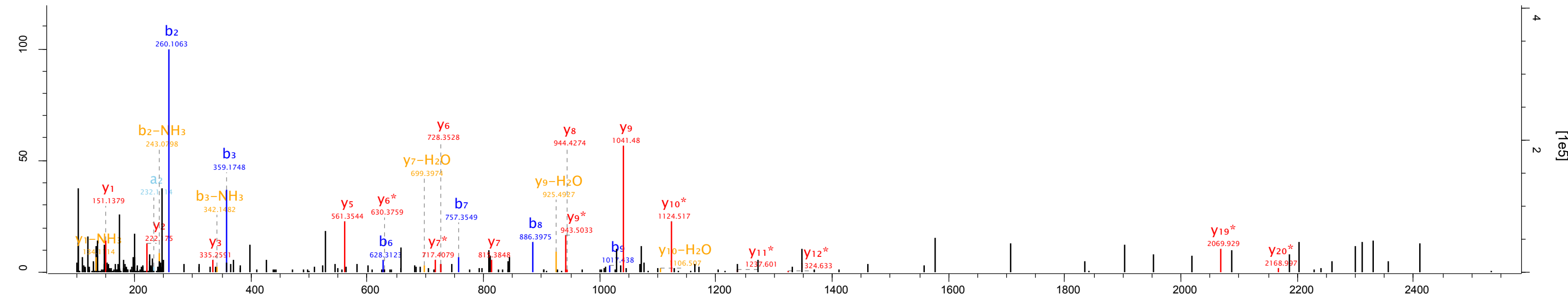


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20171215_MaS_33SR_LMH_phospho2_03

16544 FTMS; HCD 49.52 843.37 BRSK1

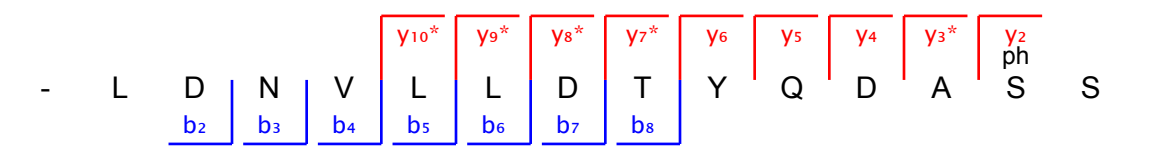
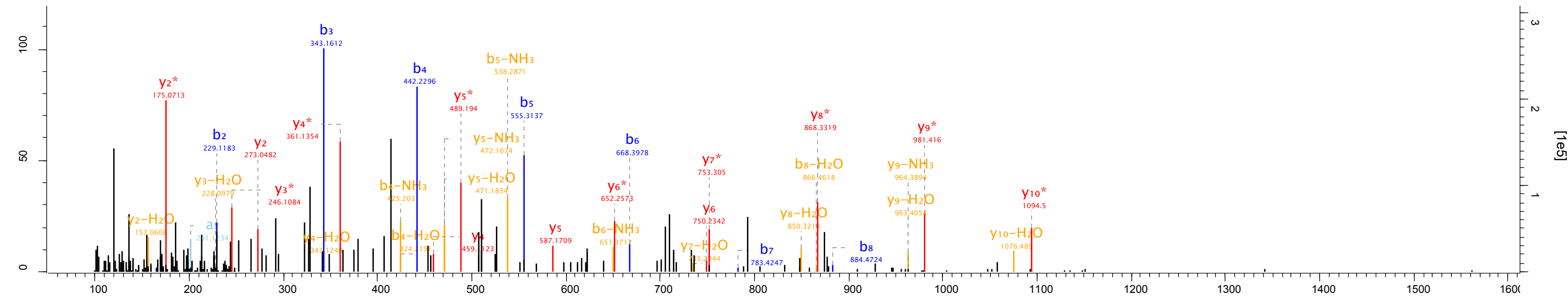


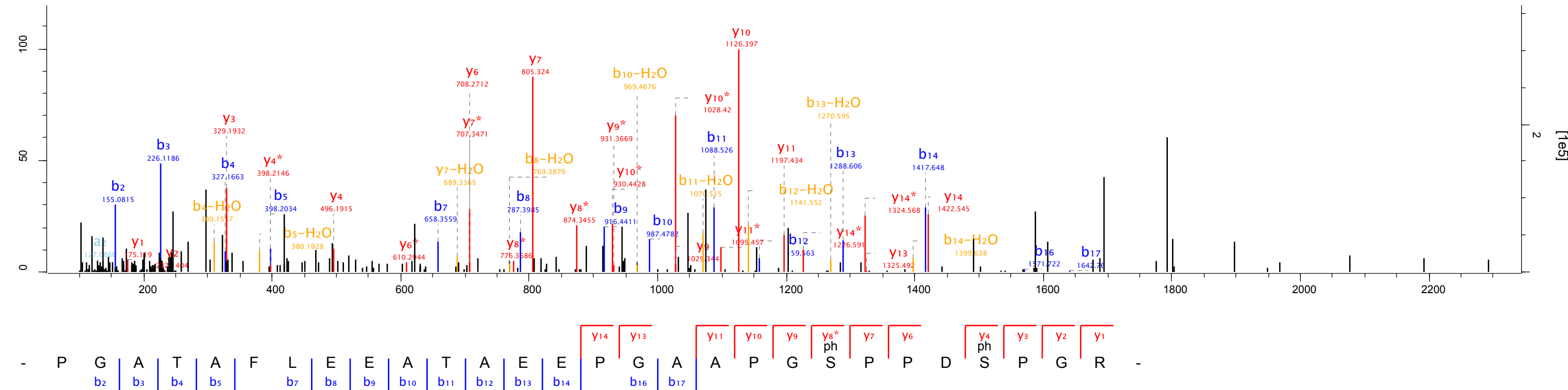
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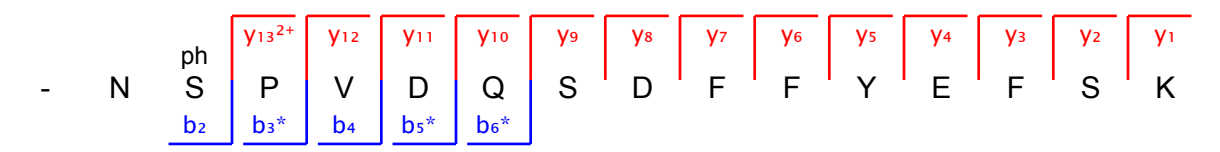
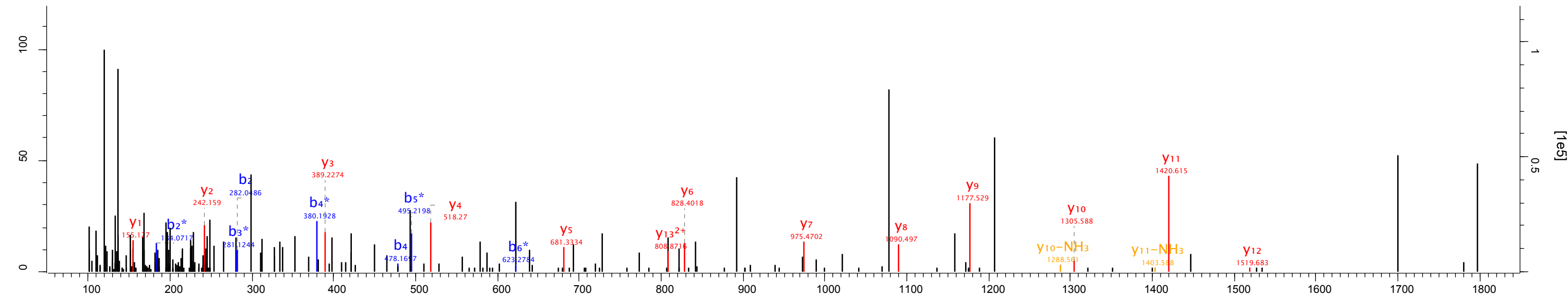
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- Red brackets (y-ions): V-P, P-T, T-S, S-L, L-T, T-P, P-E, E-S, S-S, S-P, P-E, E-L, L-A, A-K.

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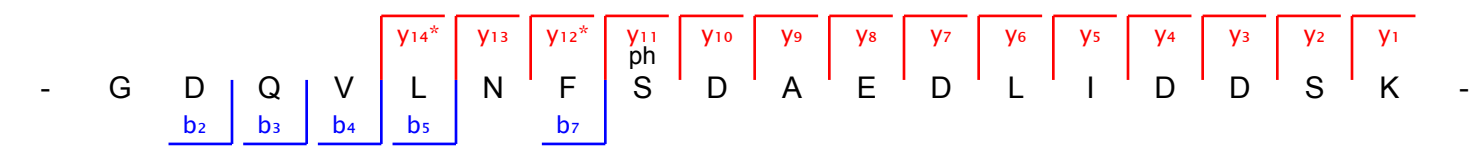
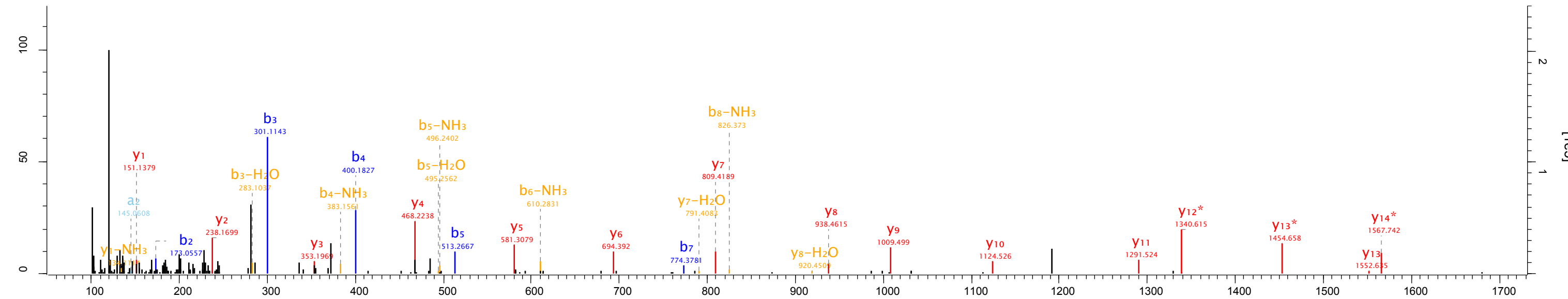


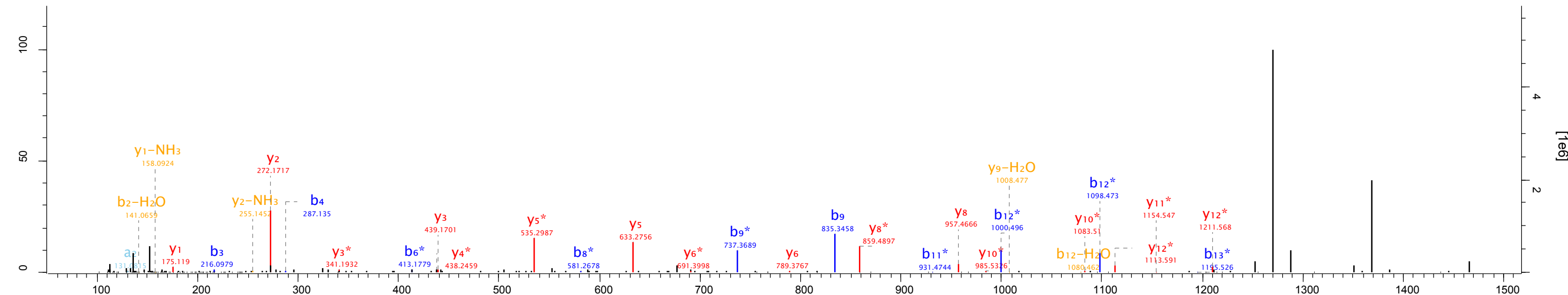


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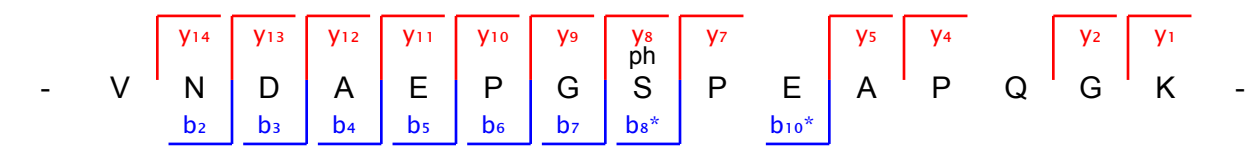
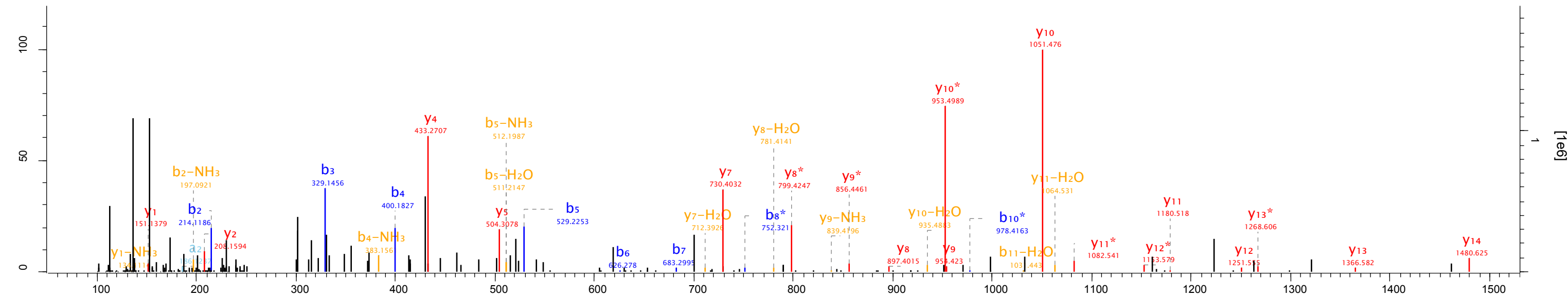
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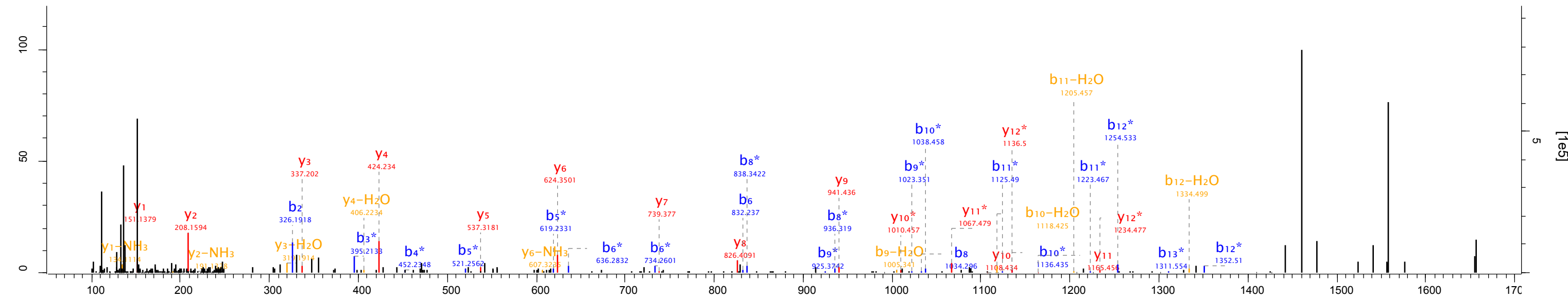




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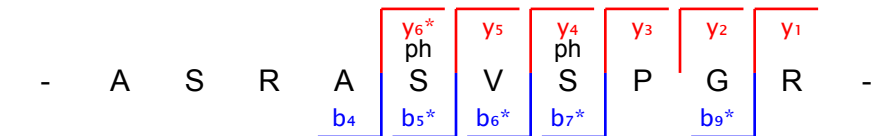
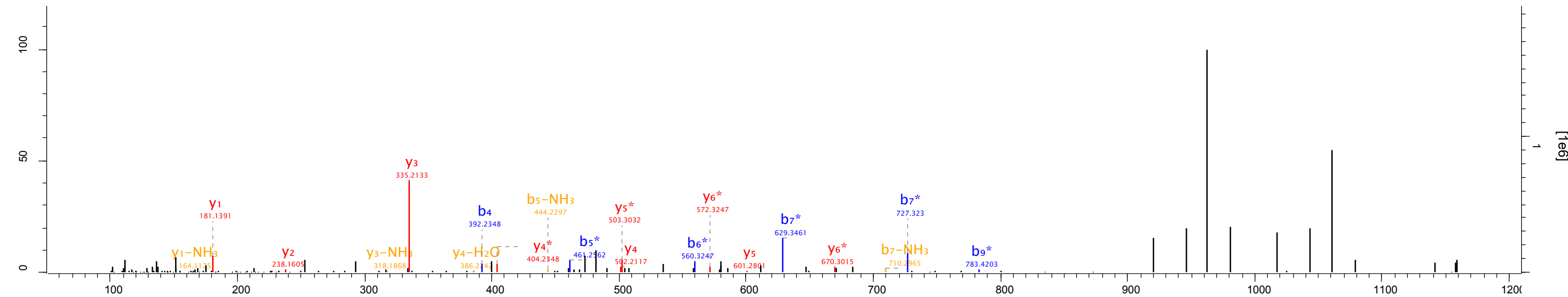
a₂
b₃
b₄
b₆*
b₈*
b₉
b₁₁*
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y₄*
y₃ph
y₂
y₁



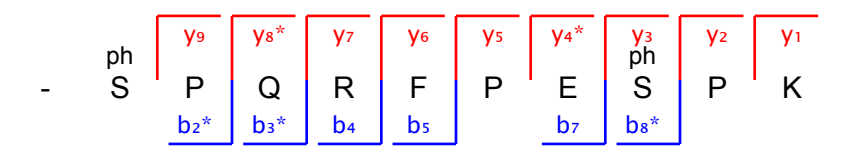
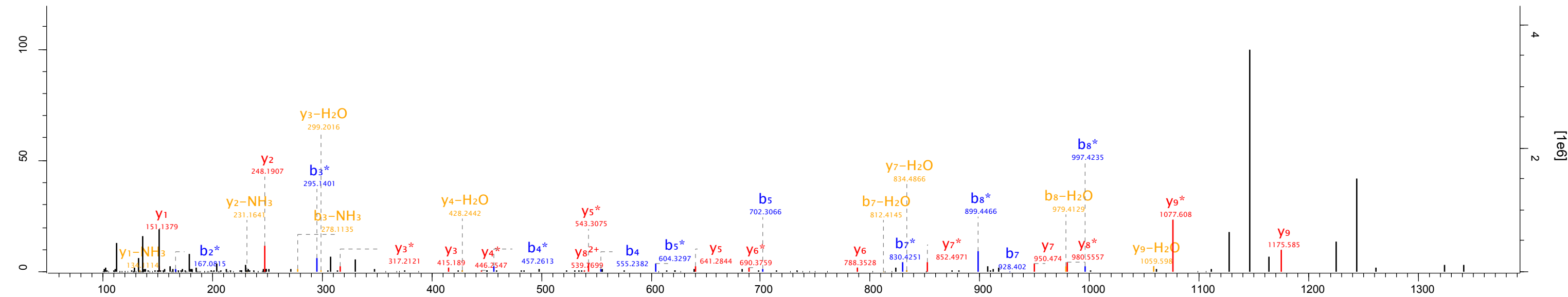


- R Y Y₁₂^{*}
ph
S Y₁₁
G Y₁₀
ph
S Y₉
D S Y₈
D Y₇
D Y₆
S Y₅
I Y₄
S Y₃
E Y₂
G Y₁
K -

b₂ b₃^{*} b₄^{*} b₅^{*} b₆
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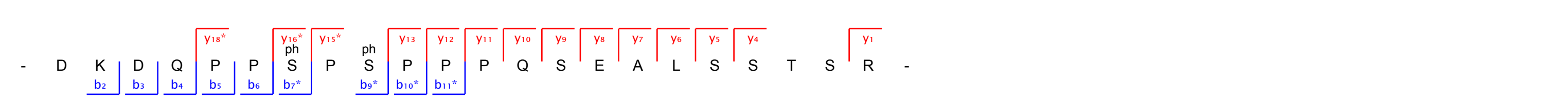
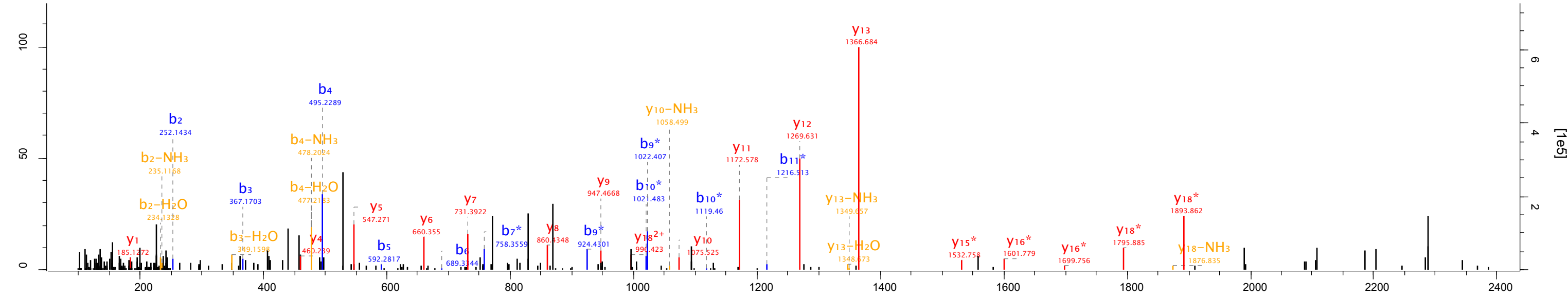


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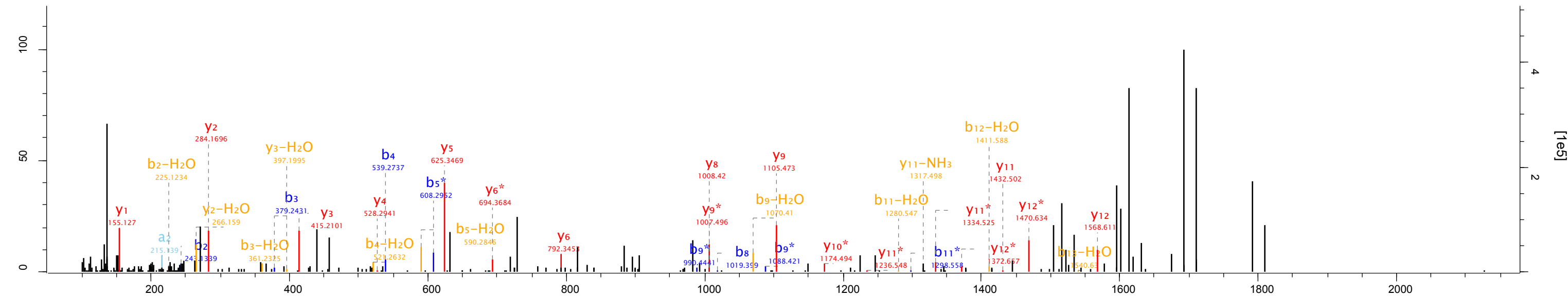


Raw file Scan Method Score m/z Gene names

20171215_MaS_33SR_LMH_phospho2_03 8394 FTMS; HCD 81.28 829.69 MON1B

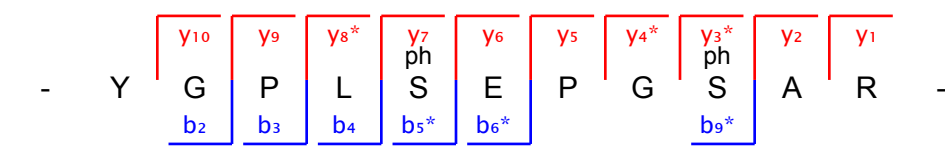
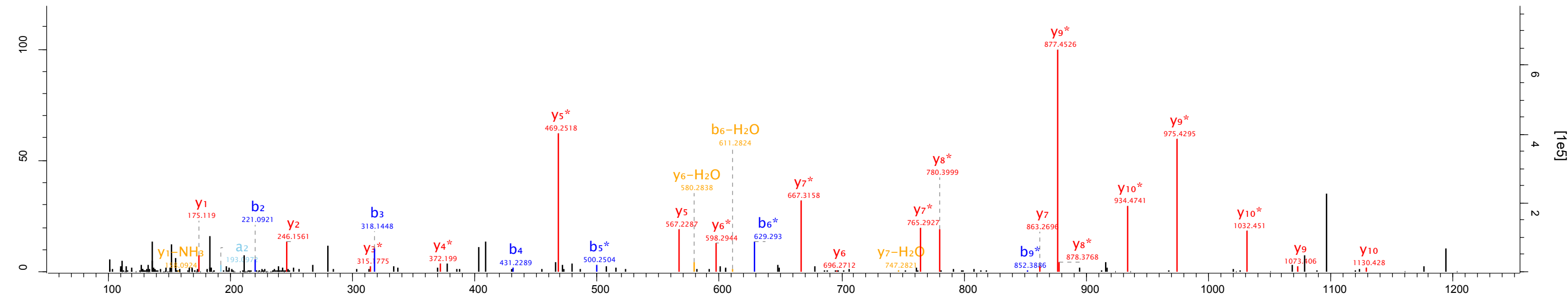


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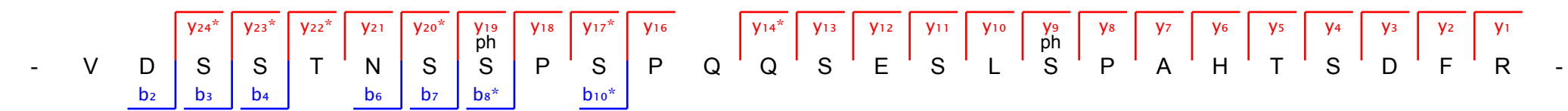
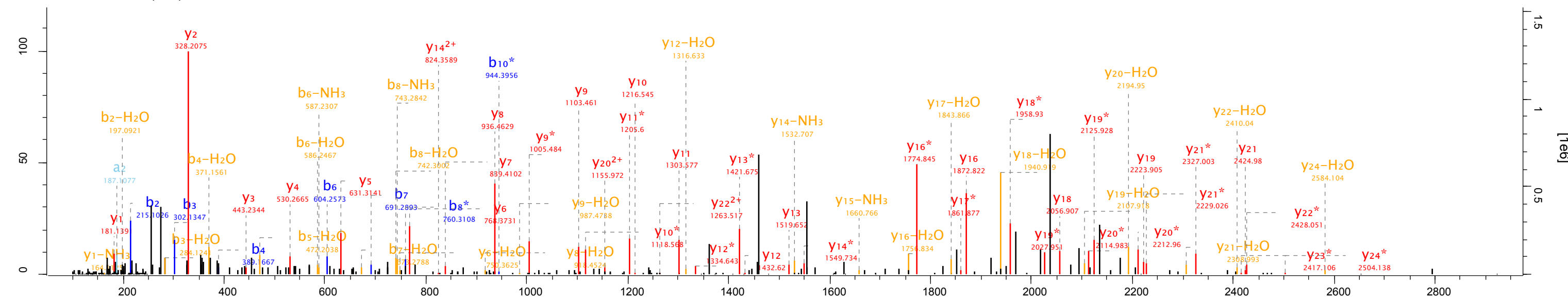
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20171215_MaS_33SR_LMH_phospho2_03

Scan 9534 Method FTMS; HCD Score 104.21 m/z 647.75 Gene names WDR13

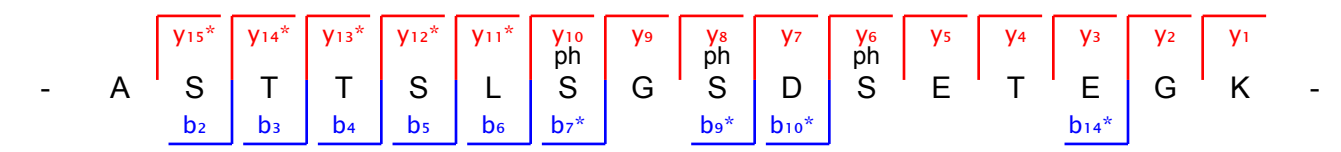
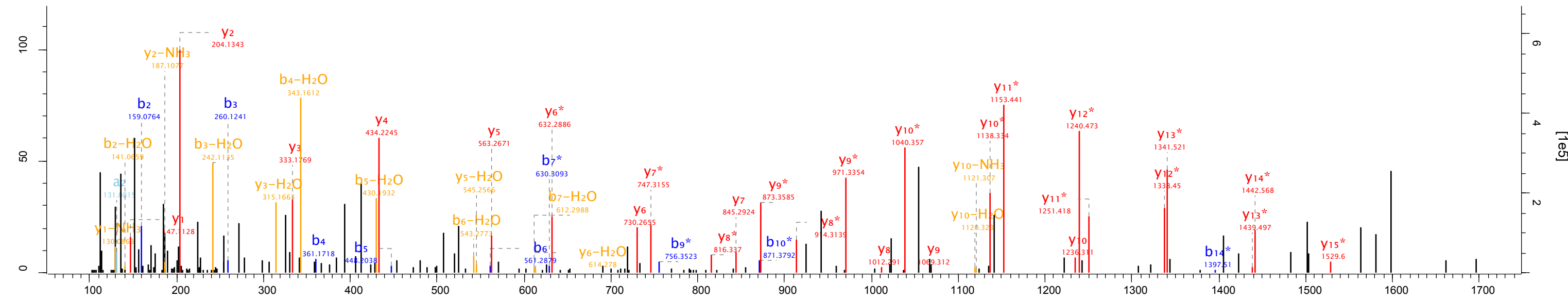


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20171215_MaS_33SR_LMH_phospho2_03

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



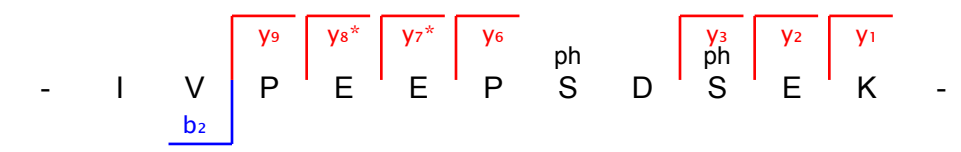
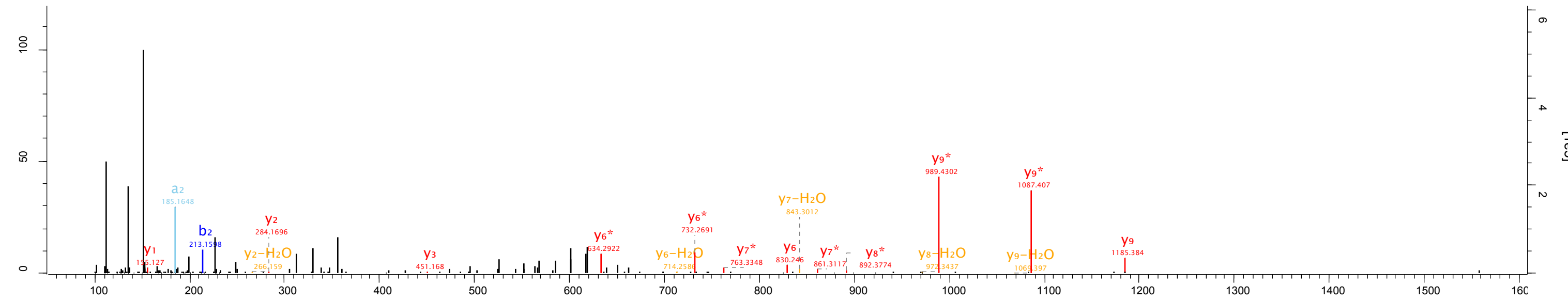
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Raw file

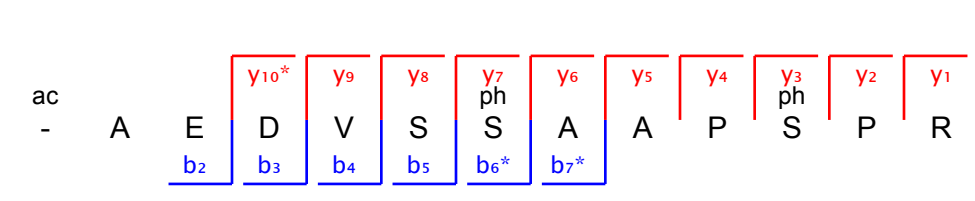
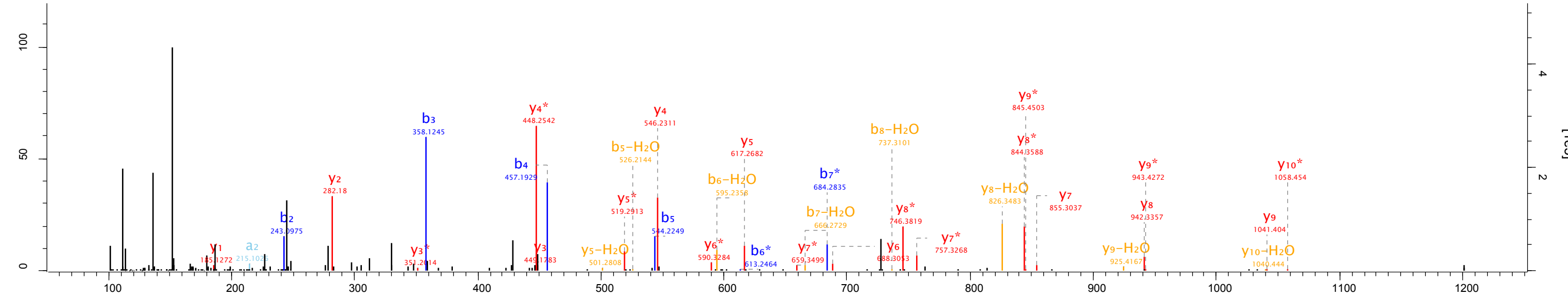
20171215_MaS_33SR_LMH_phospho2_04

Scan	Method	Score	m/z	Gene names
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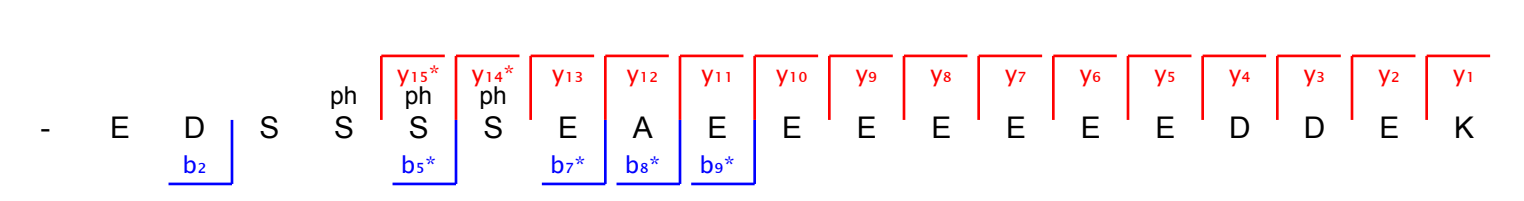
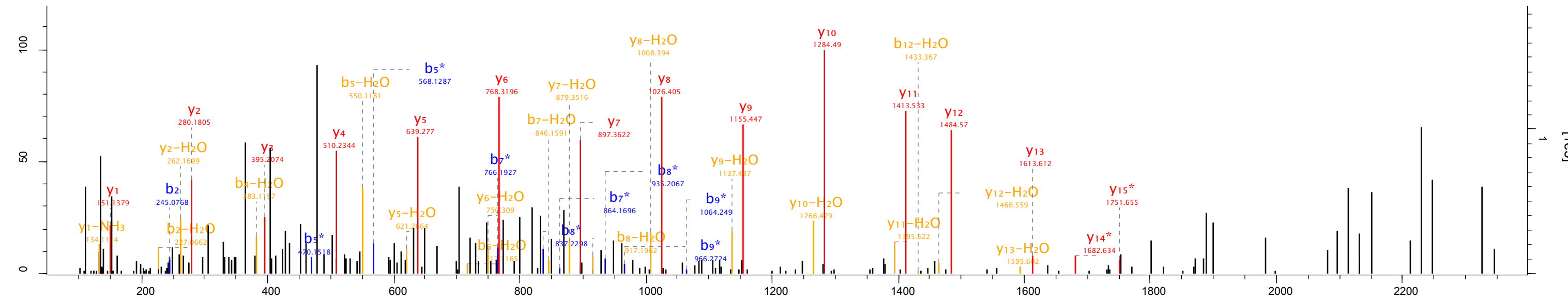


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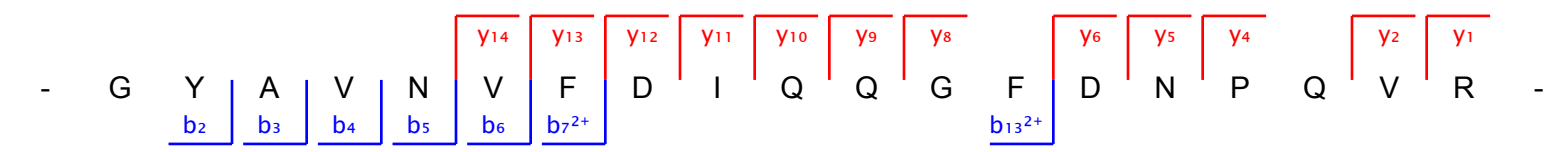
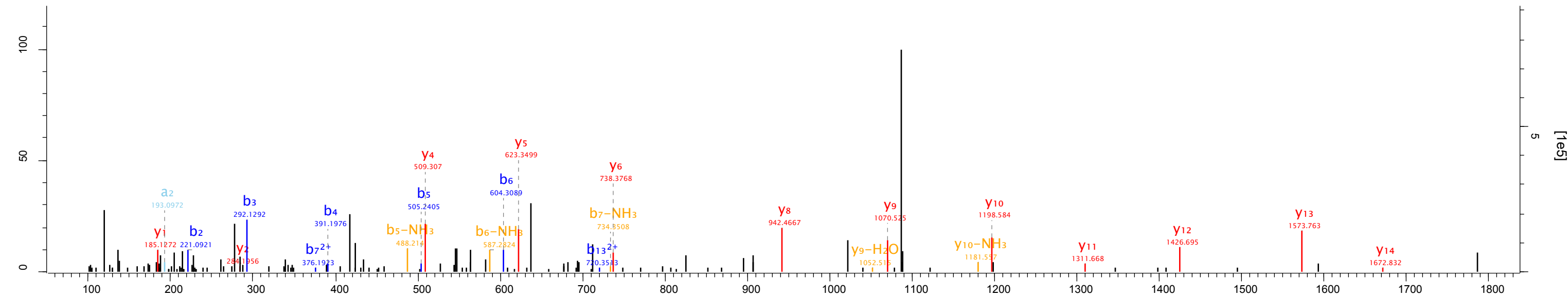
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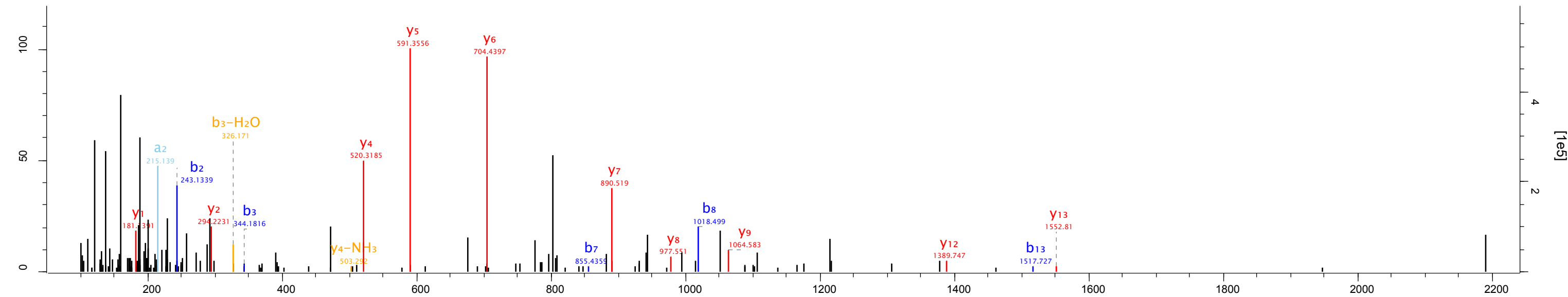
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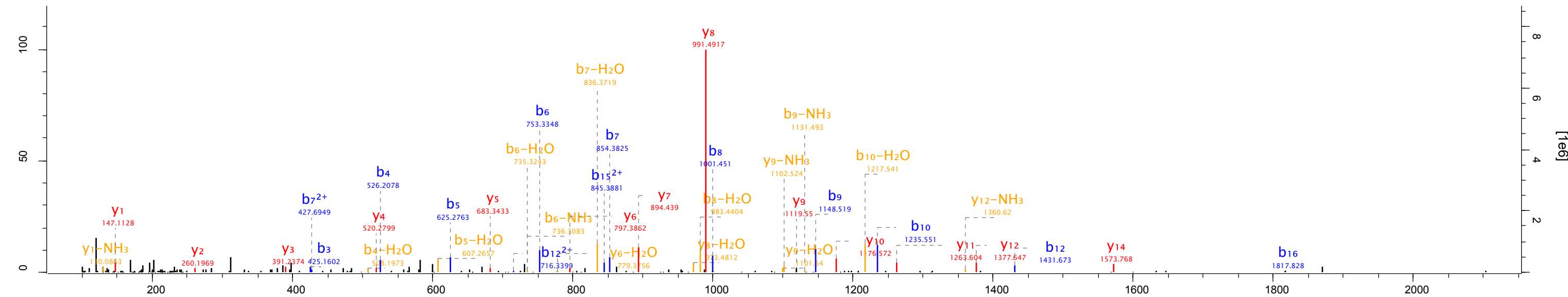


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 Scan: 101544 Method: FTMS; HCD Score: 68.24 m/z: 1089.04 Gene names: NSDHL



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 Scan: 111004 Method: FTMS; HCD Score: 47.5 m/z: 803.42 Gene names: DHX30





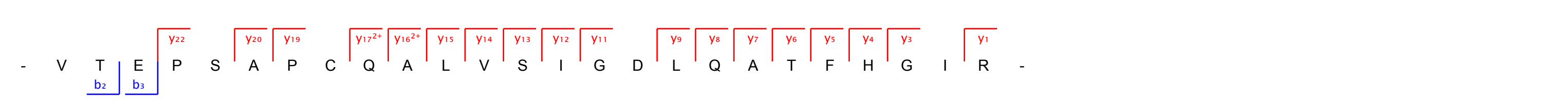
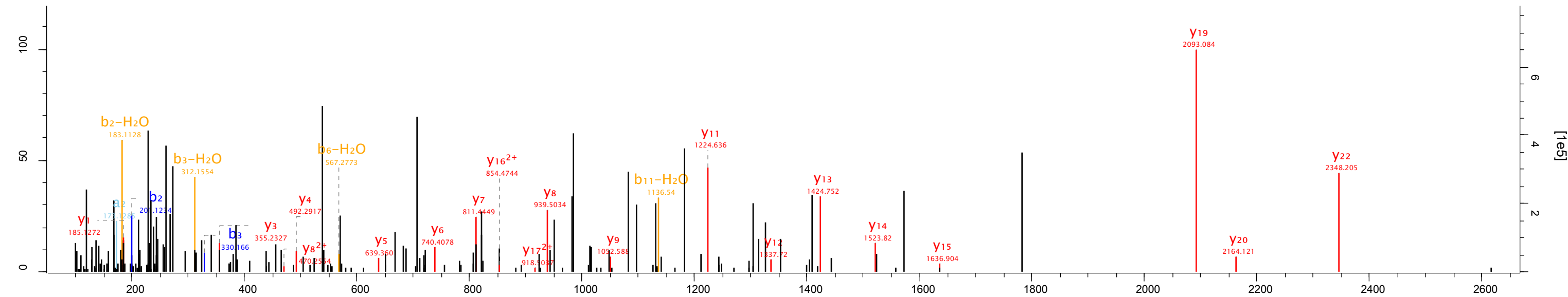
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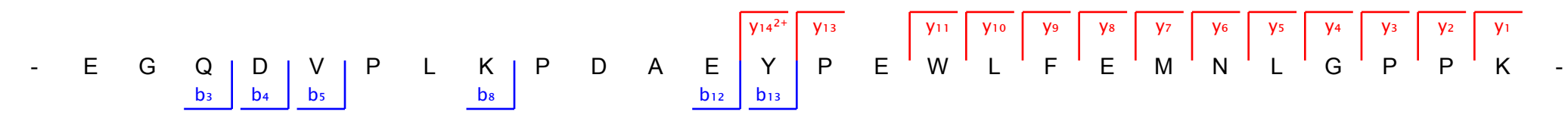
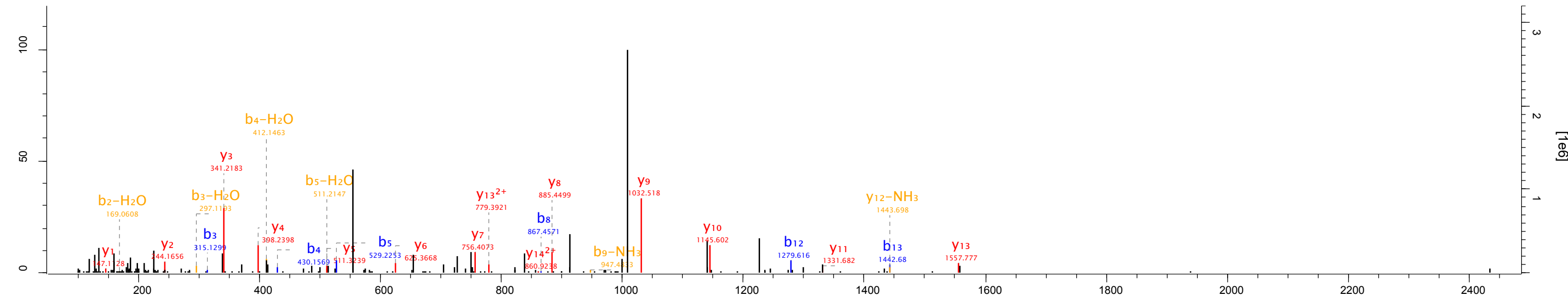
Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets (b₃ to b₁₀) are located under H, T, V, Q, T, F, F, S.
- Blue brackets (b₁₂, b₁₅²⁺, b₁₆) are located under P, G, Q.
- Red brackets (y₁ to y₁₄) are located under P, V, N, S, G, Q, P, P, N, Y, E, M, L, K.

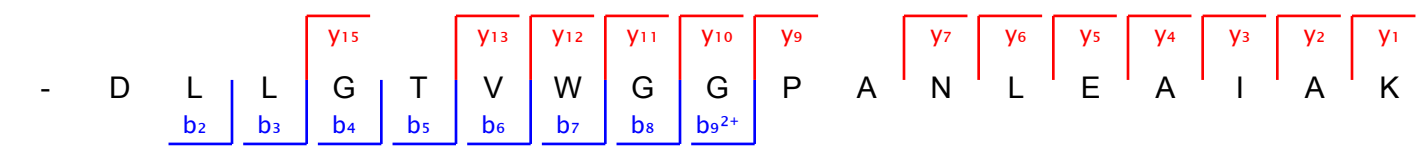
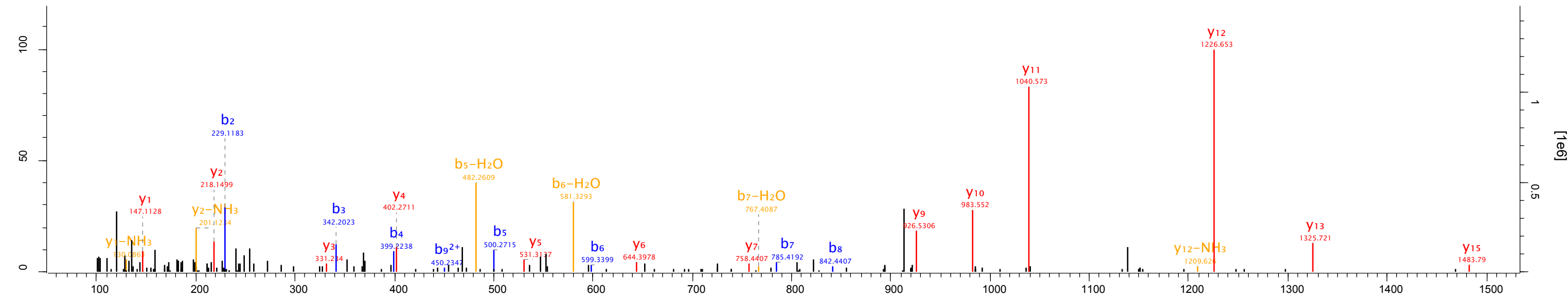
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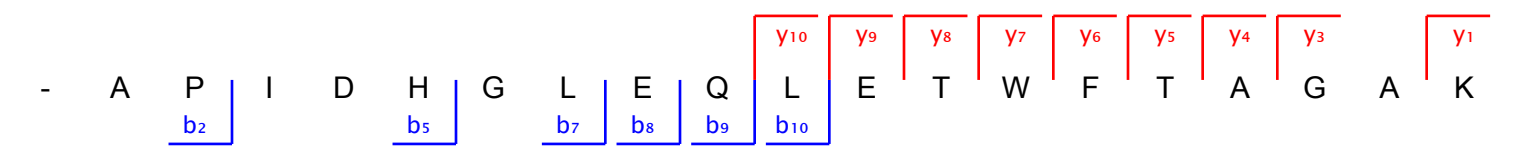
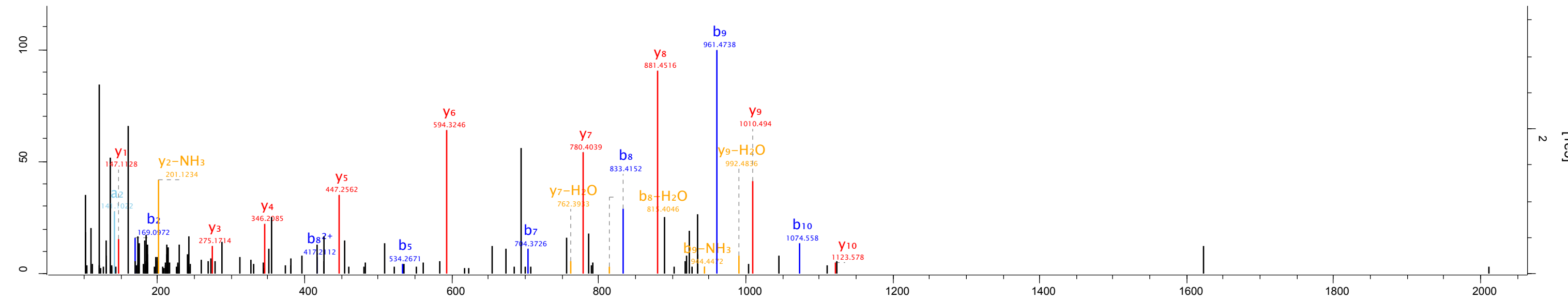
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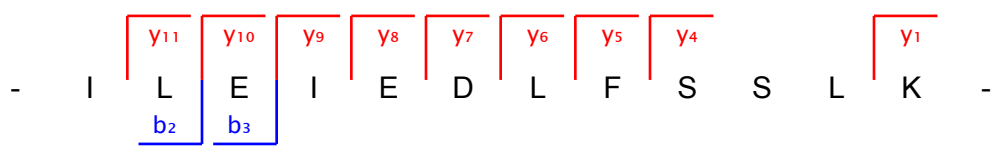
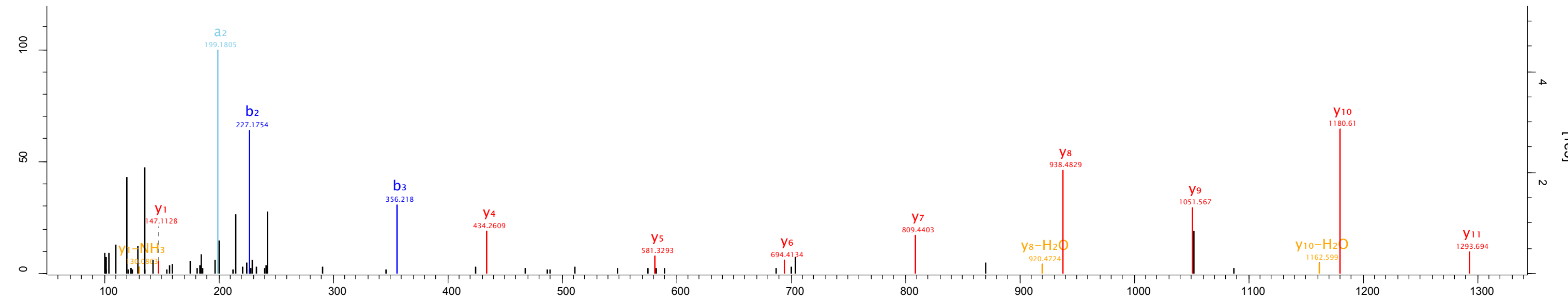
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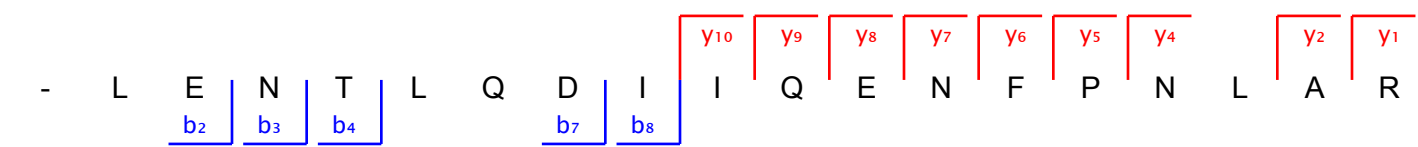
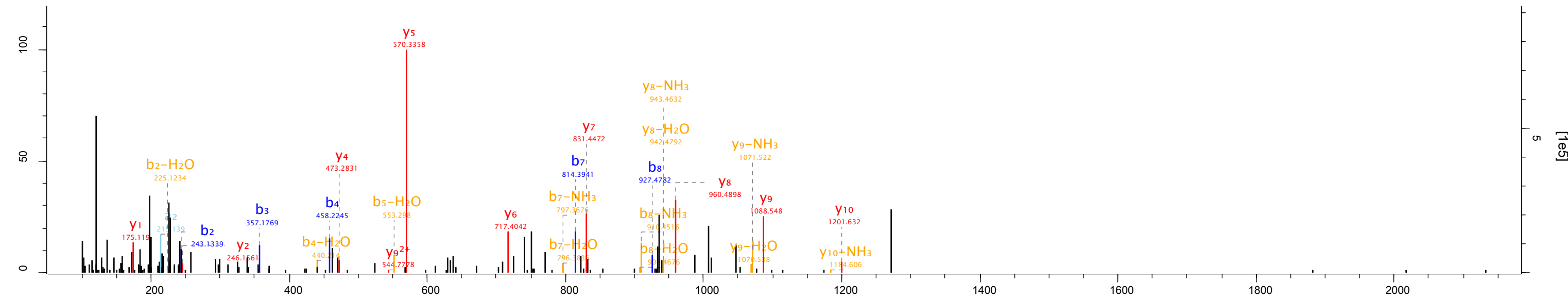


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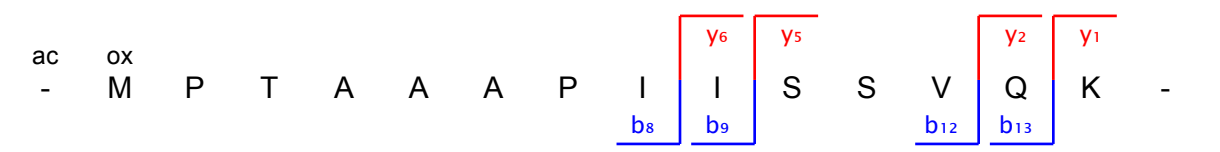
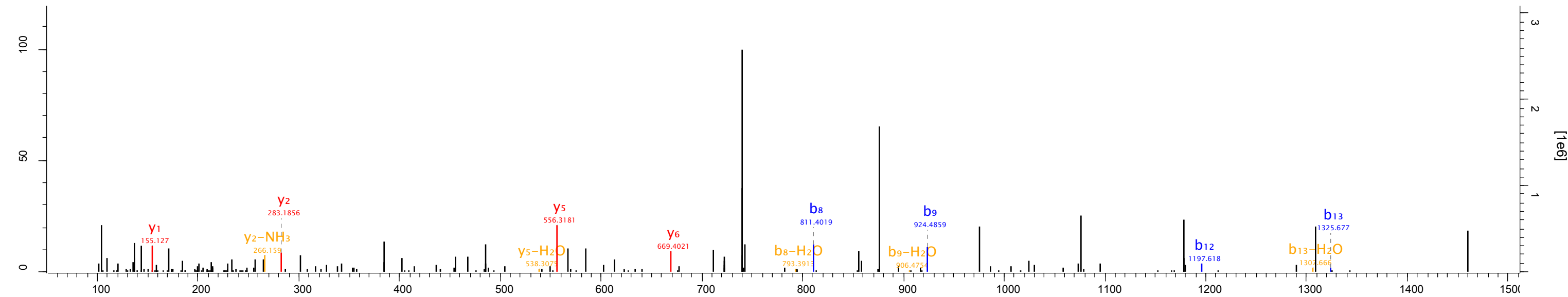


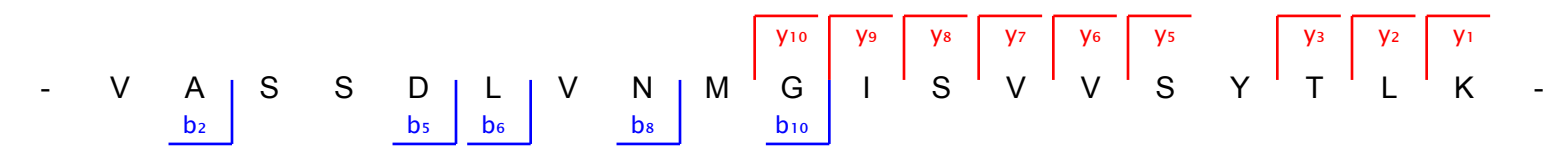
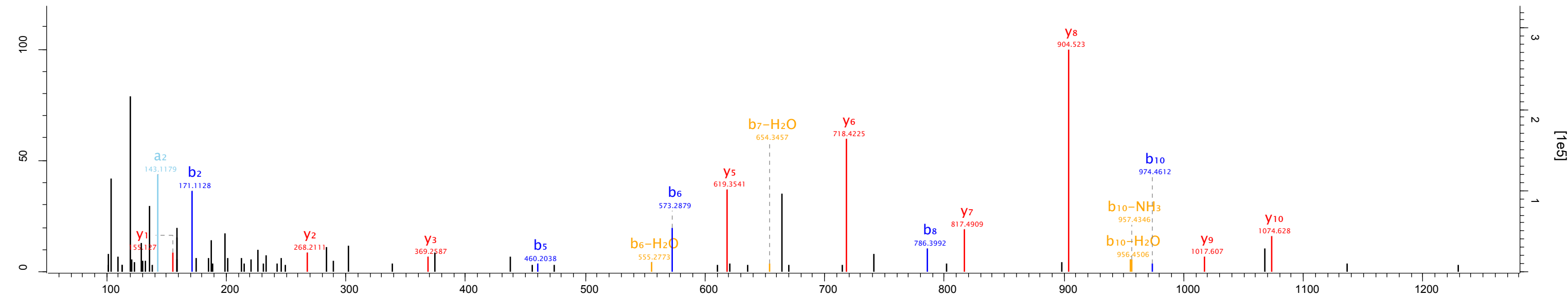
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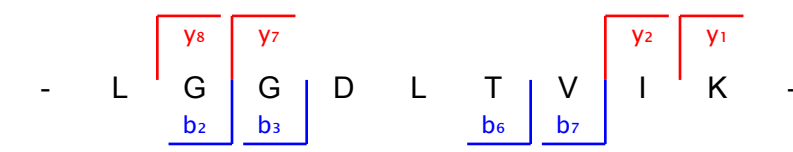
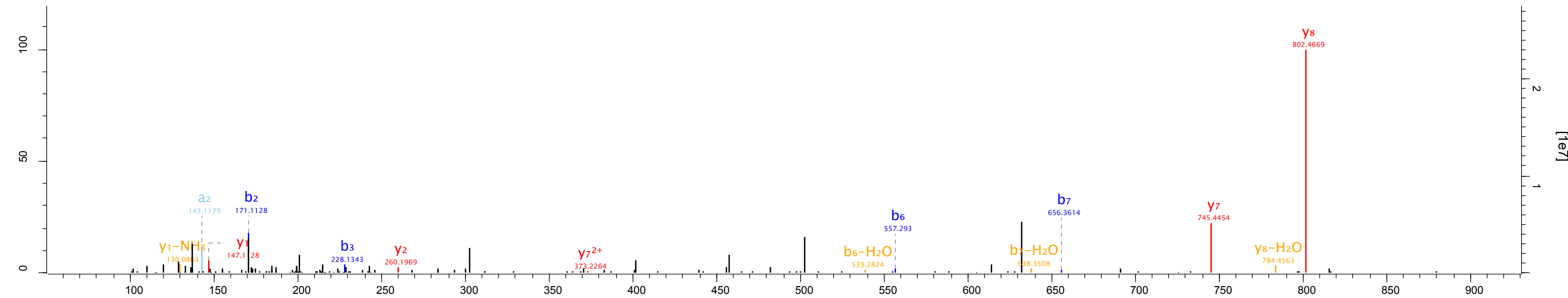


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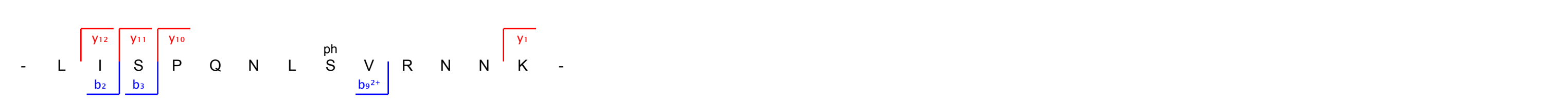
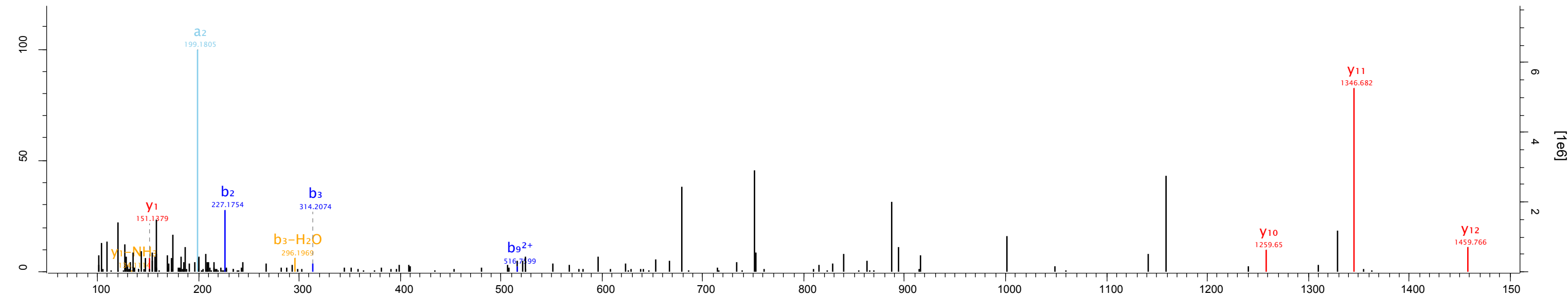




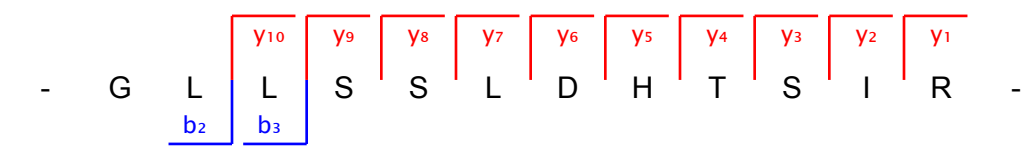
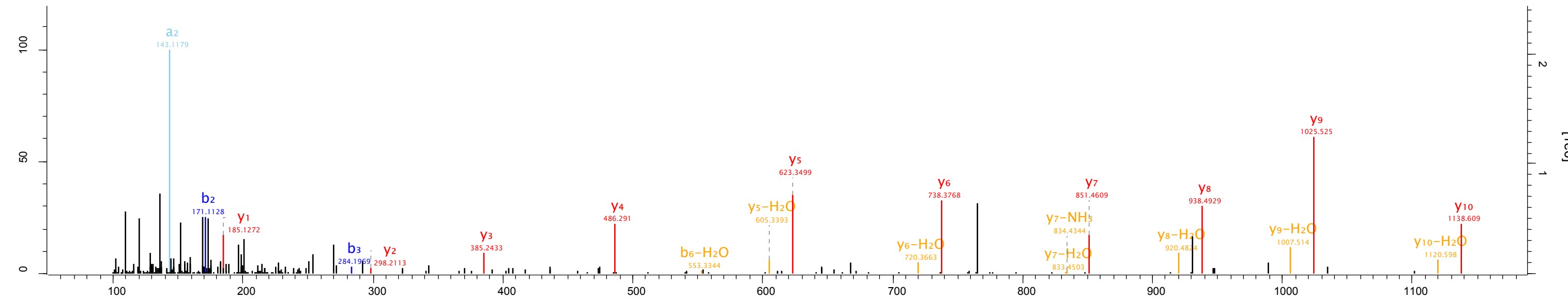
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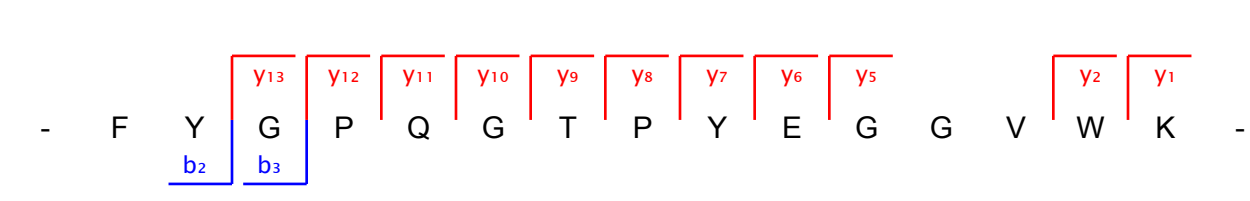
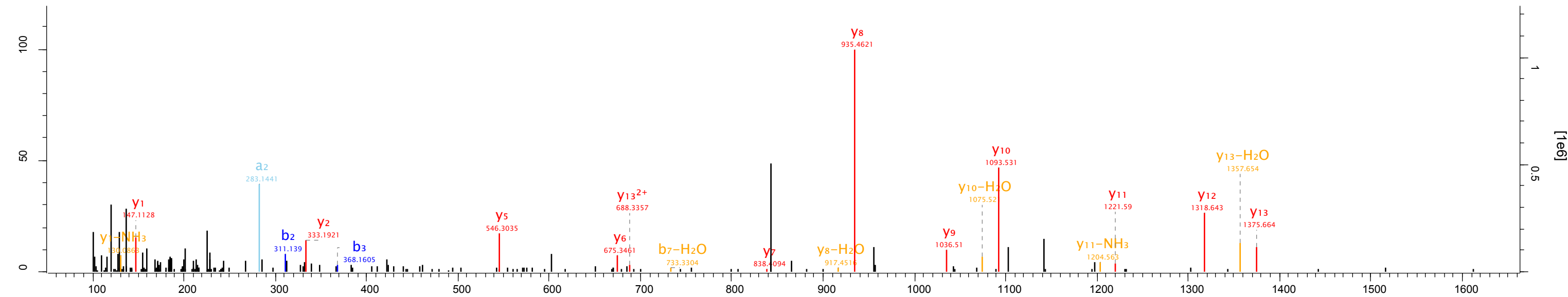
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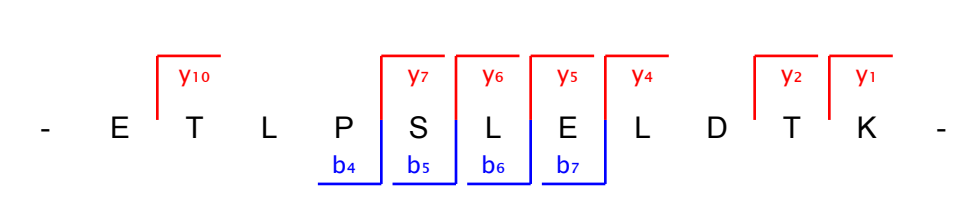
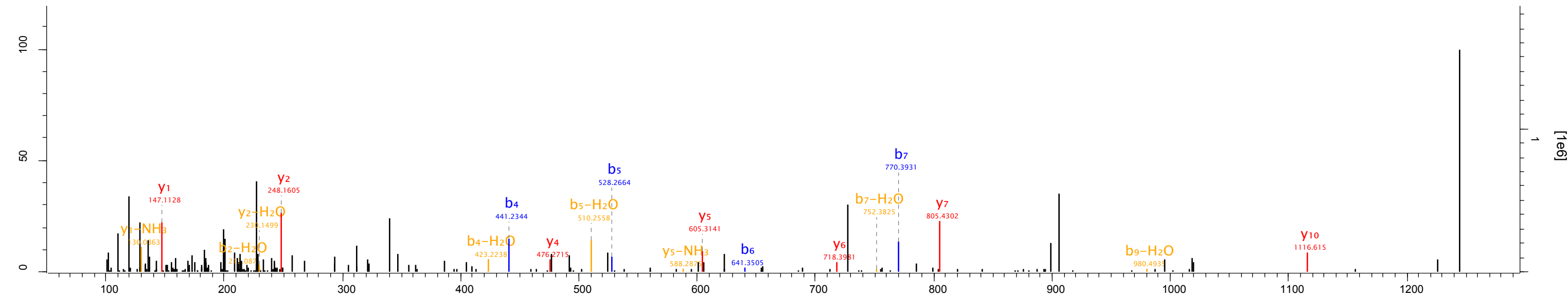
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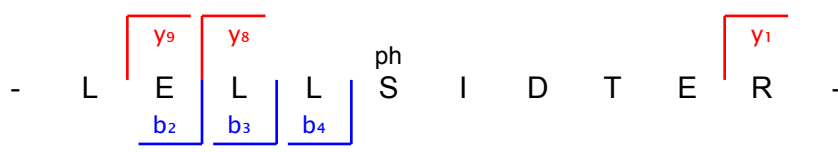
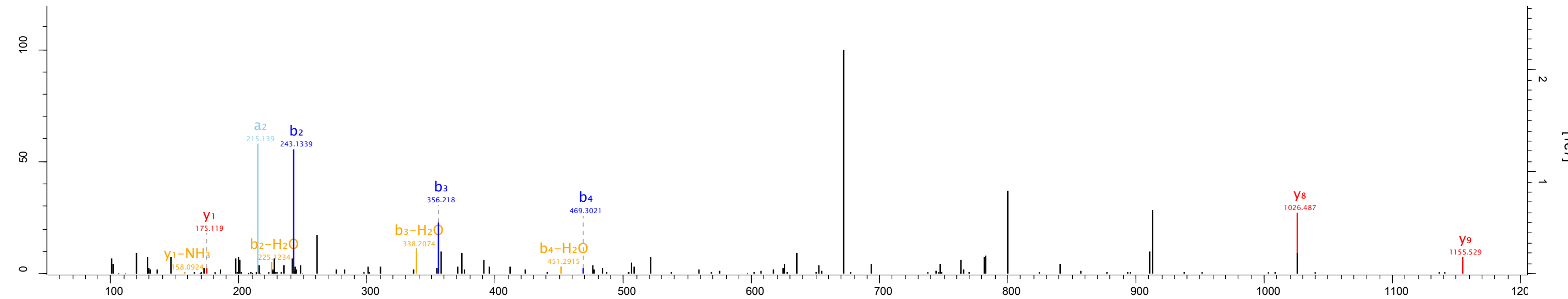
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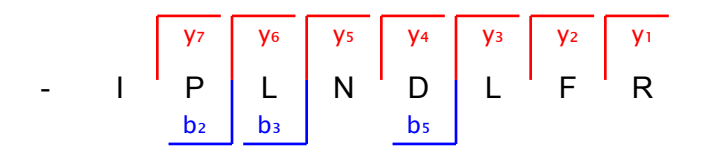
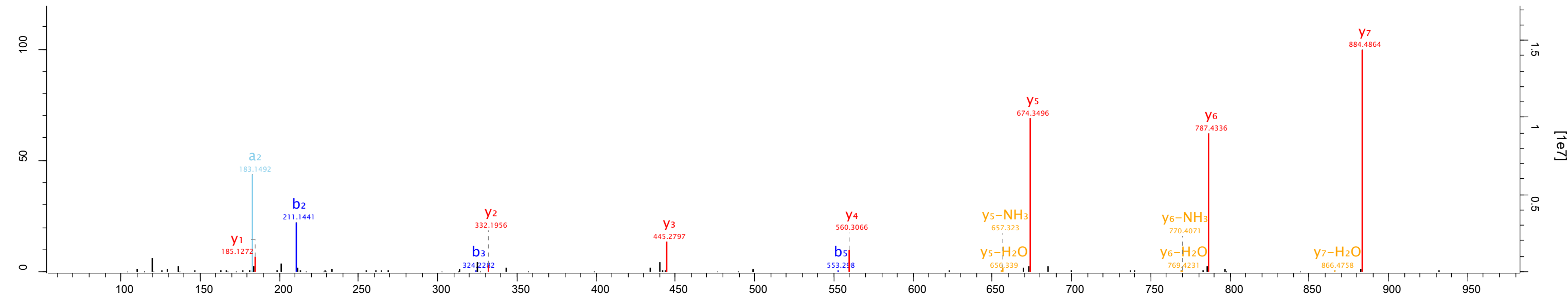
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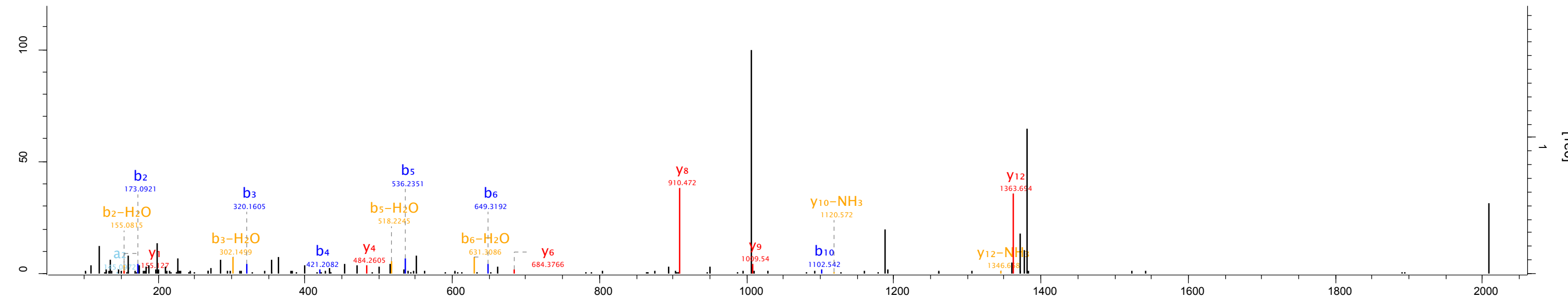
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 Scan: 68144 Method: FTMS; HCD Score: 55.46 m/z: 634.81 Gene names: CEP135



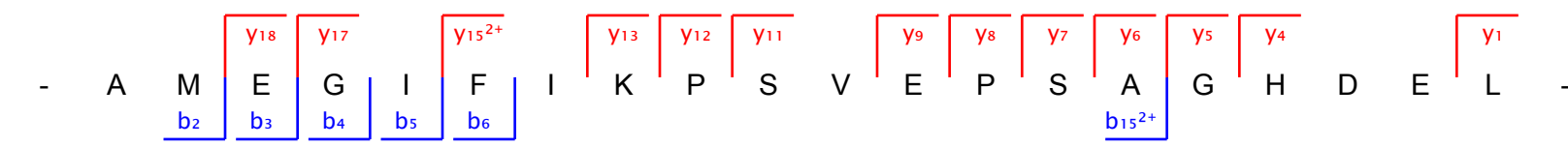
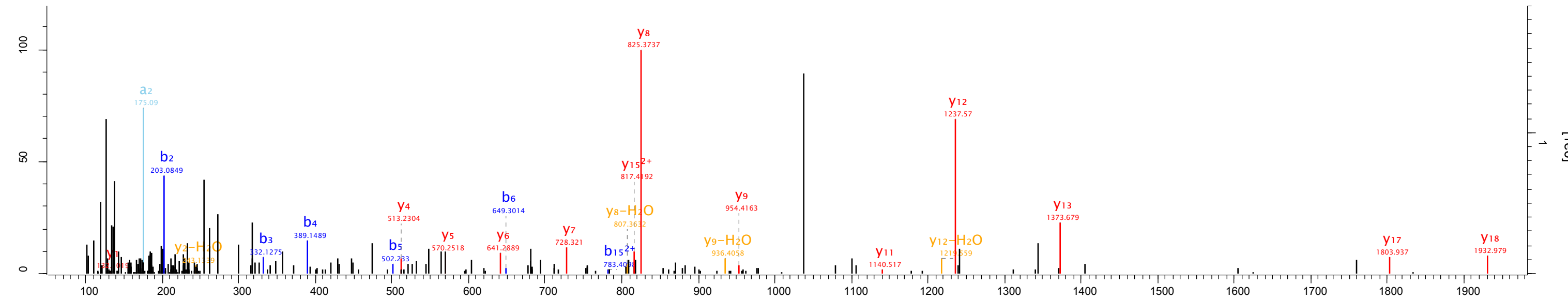
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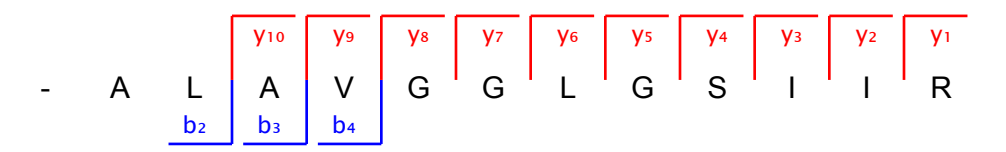
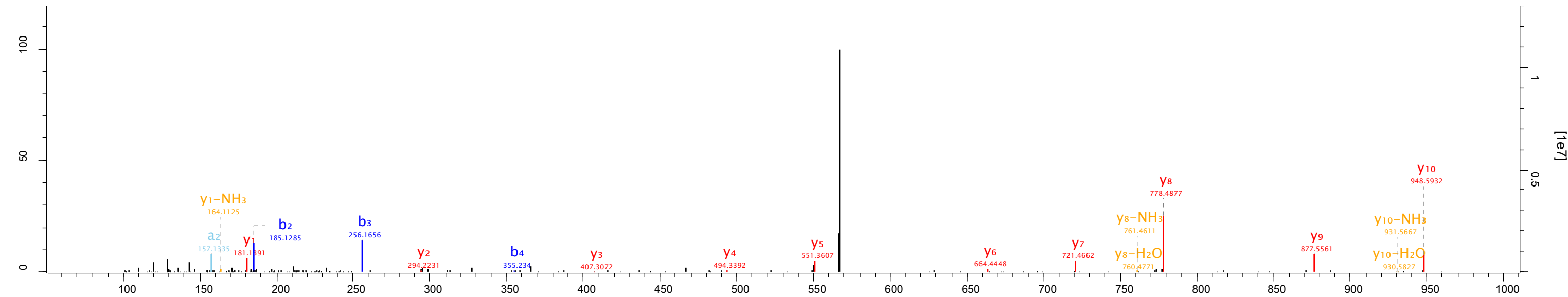
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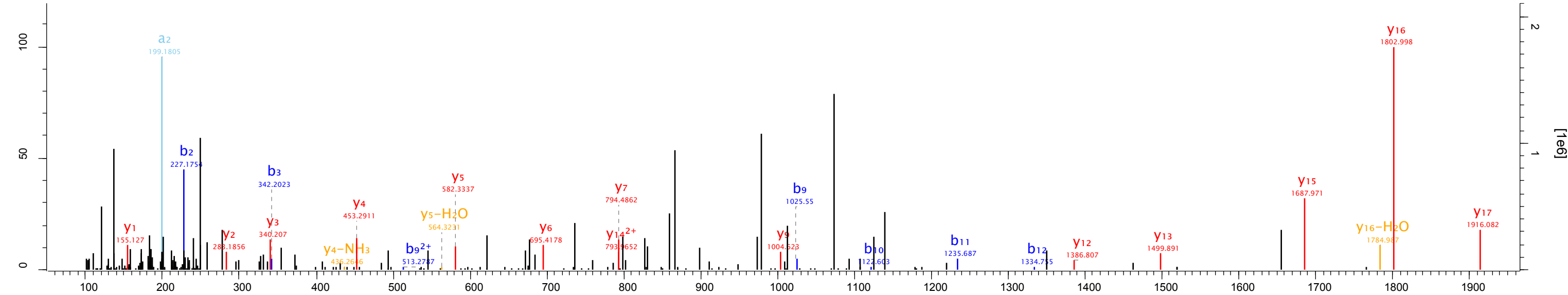


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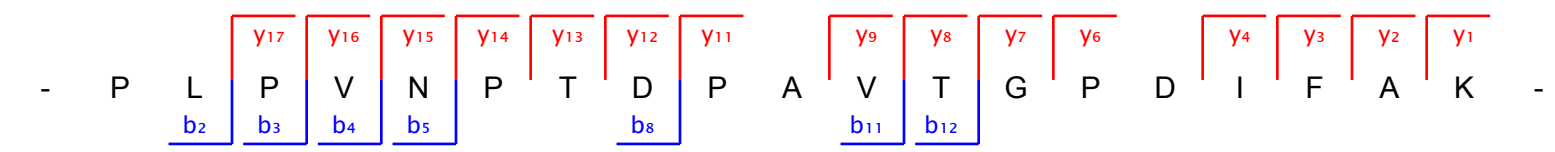
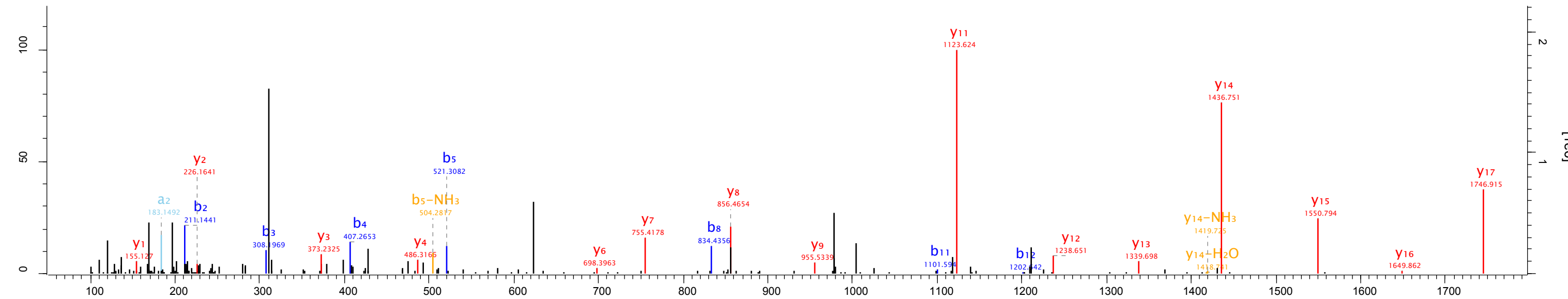


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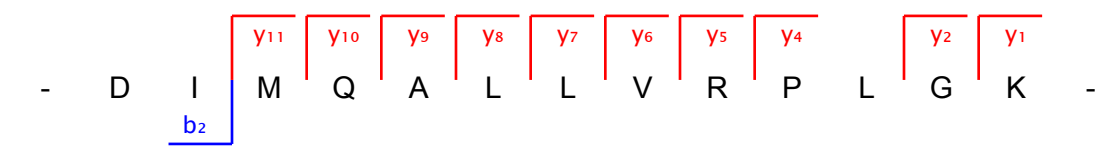
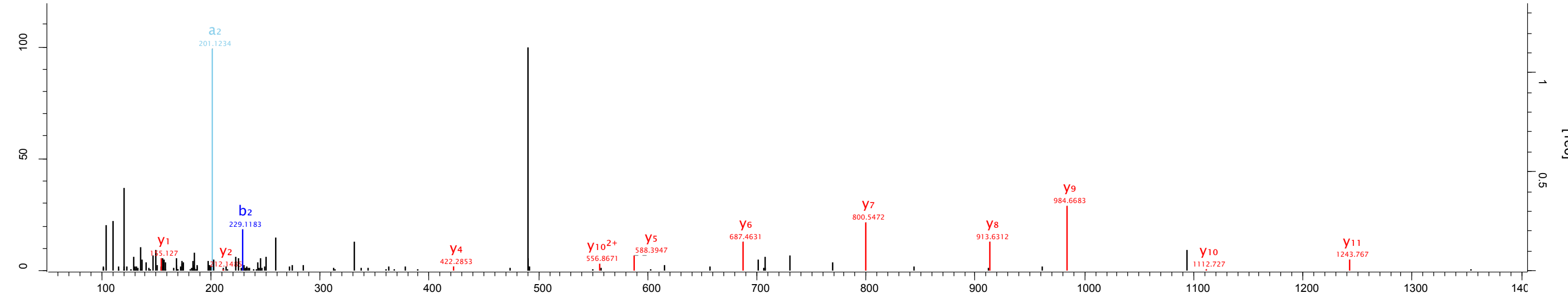
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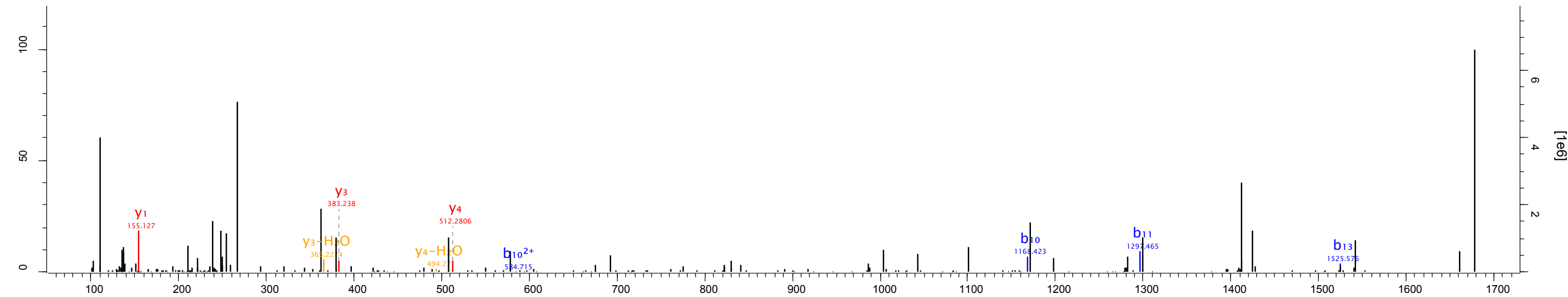
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20171215_MaS_33SR_LMH_proteome_01

Scan	Method	Score	m/z	Gene names
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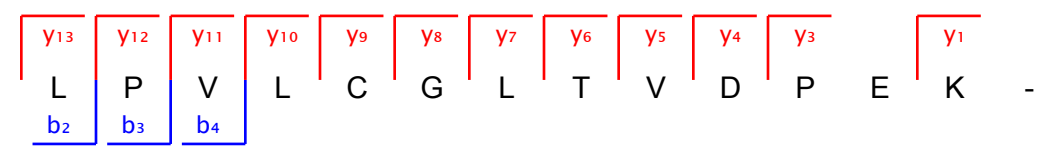
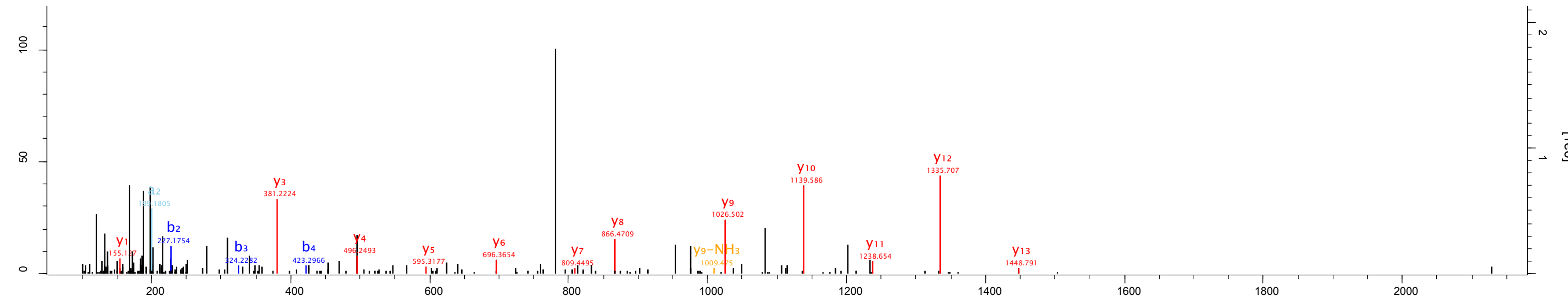
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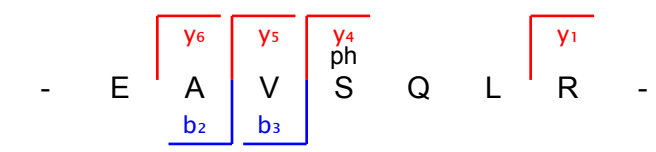
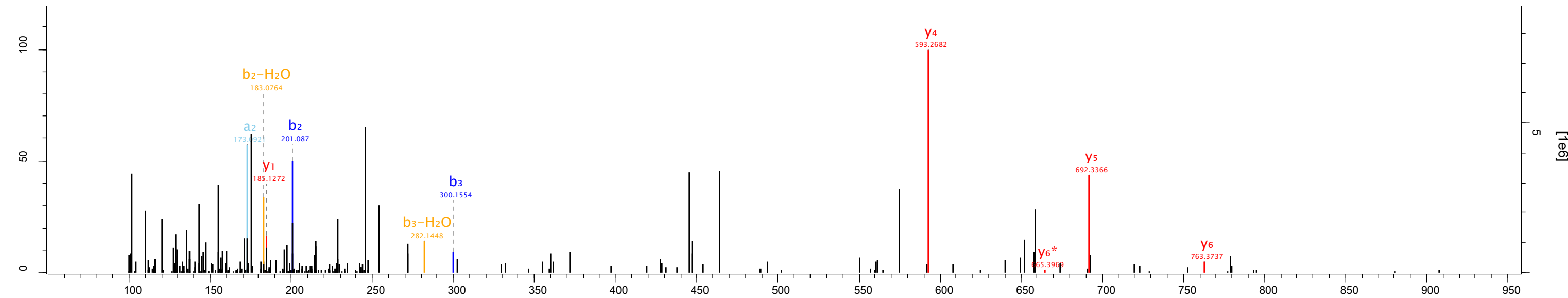
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20171215_MaS_33SR_LMH_proteome_01

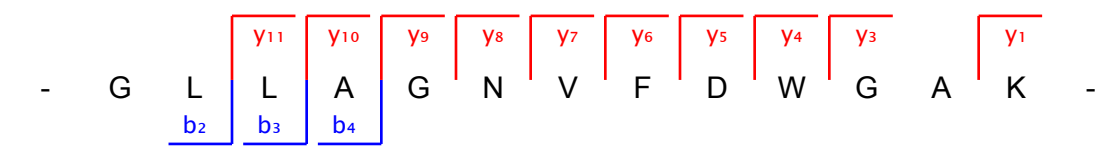
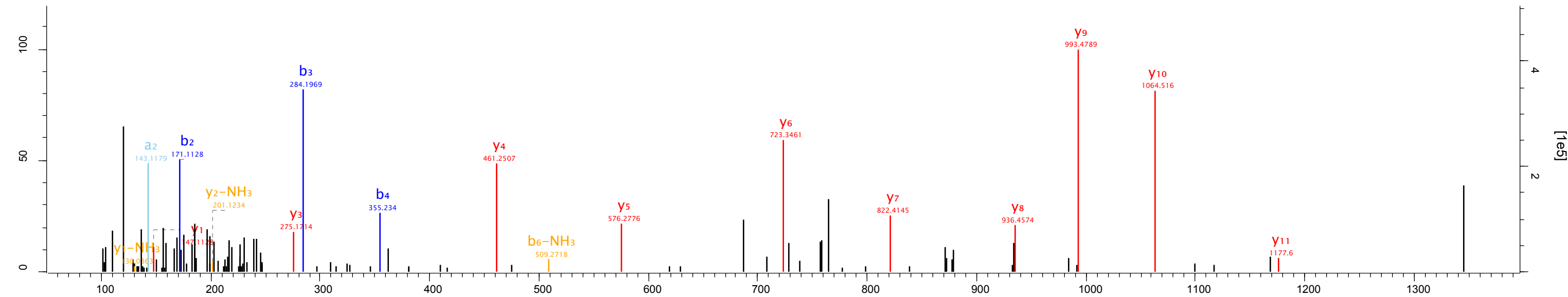
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97864	FTMS; HCD	62.36	781.44	SCYL1



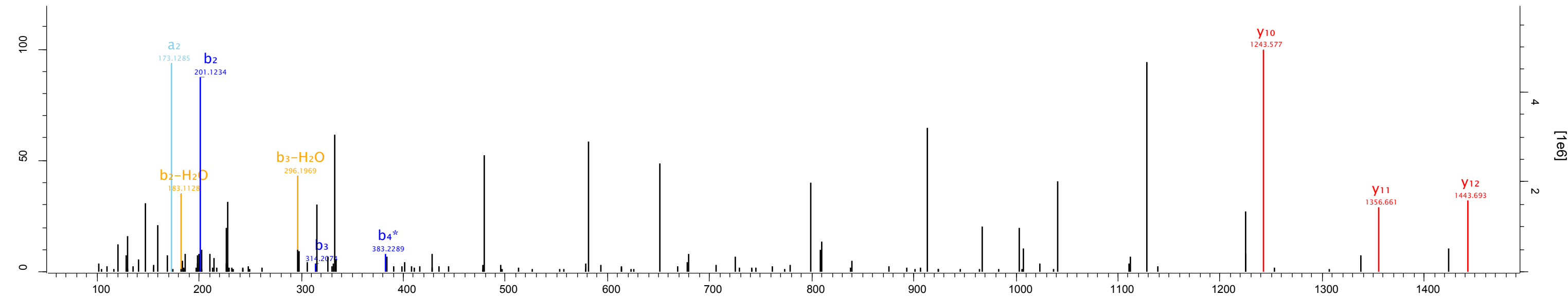
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 Scan: 9824 Method: FTMS; HCD Score: 50.13 m/z: 446.71 Gene names: ZNF24



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 101334 Method FTMS; HCD Score 66.99 m/z 674.36 Gene names PANK4



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 103724 Method FTMS; HCD Score 58.17 m/z 778.89 Gene names PROM1

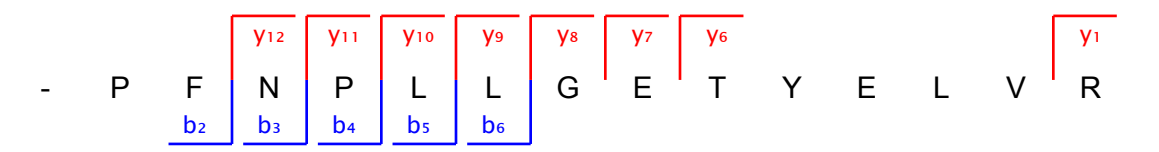
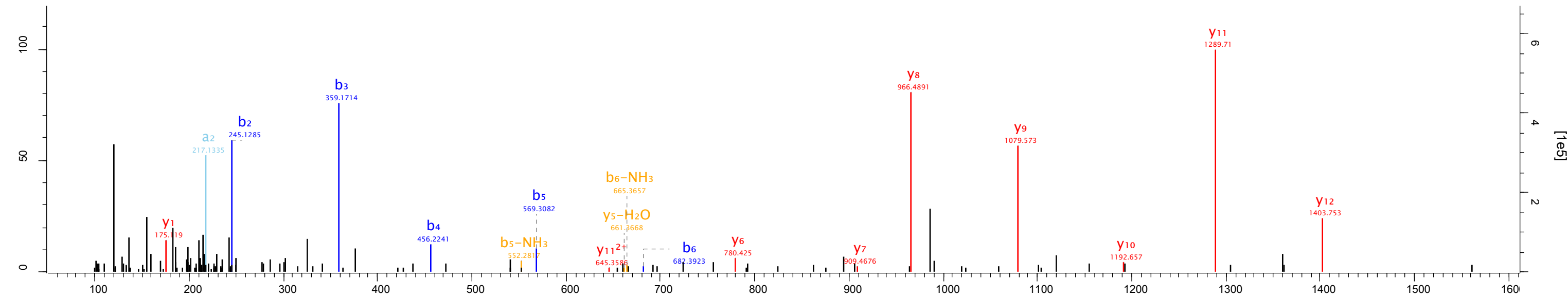


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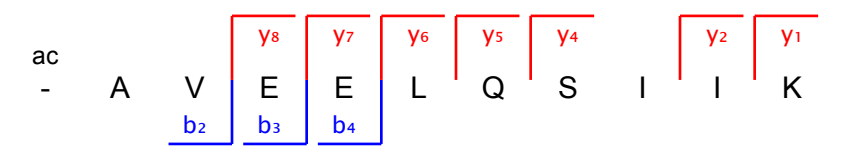
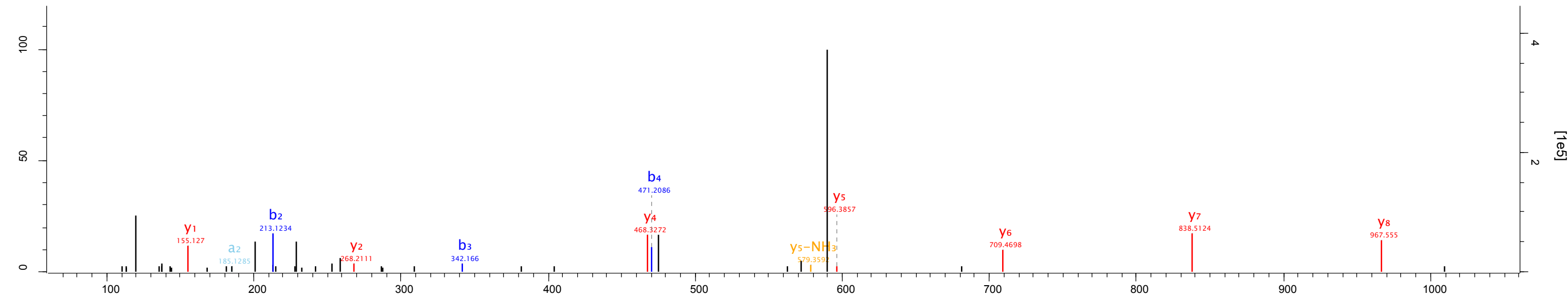
b₂
b₃
b₄*

y₁₂
y₁₁
y₁₀
ph

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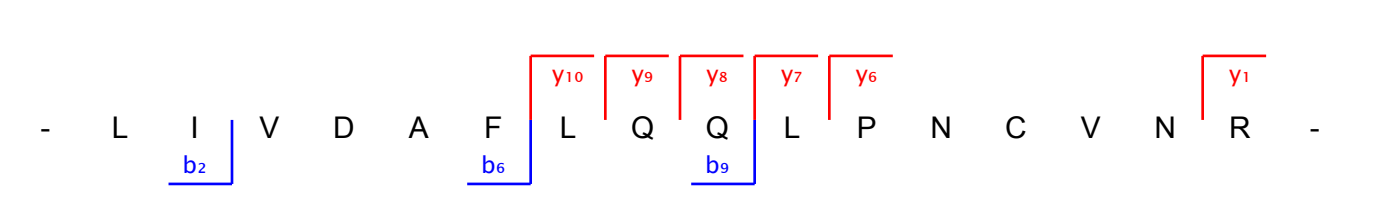
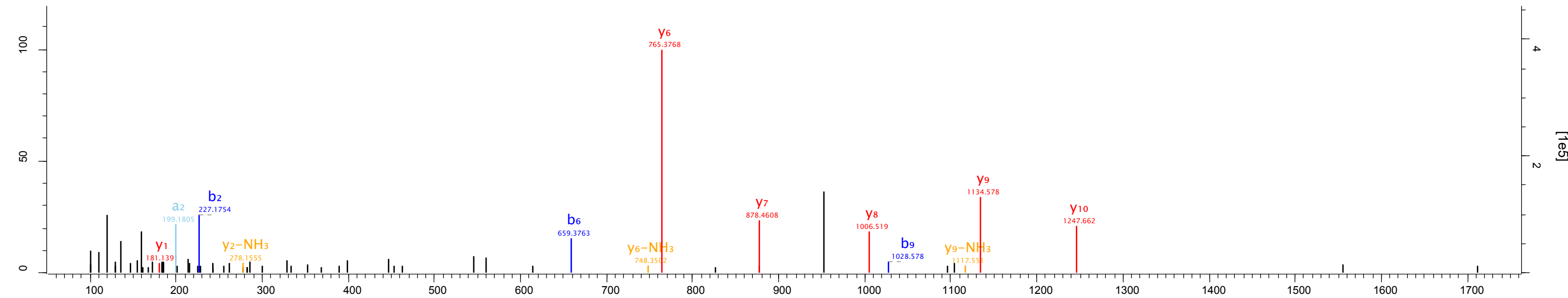


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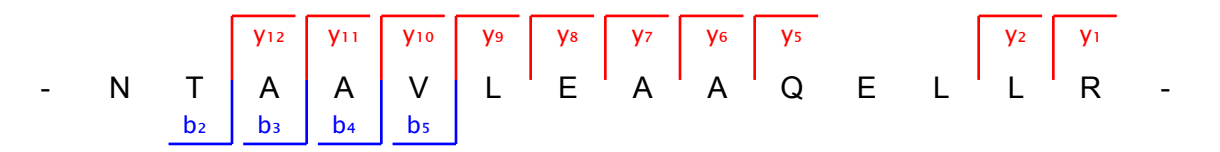
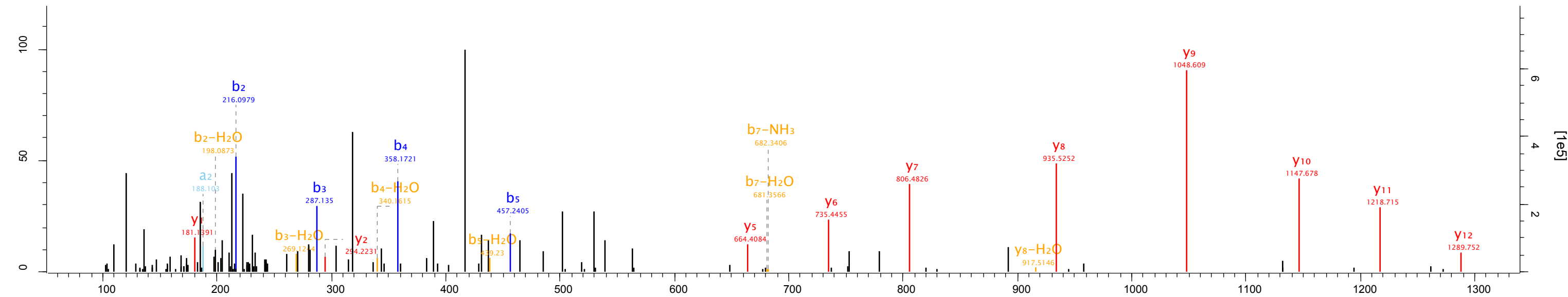


Raw file
20171215_MaS_33SR_LMH_proteome_02

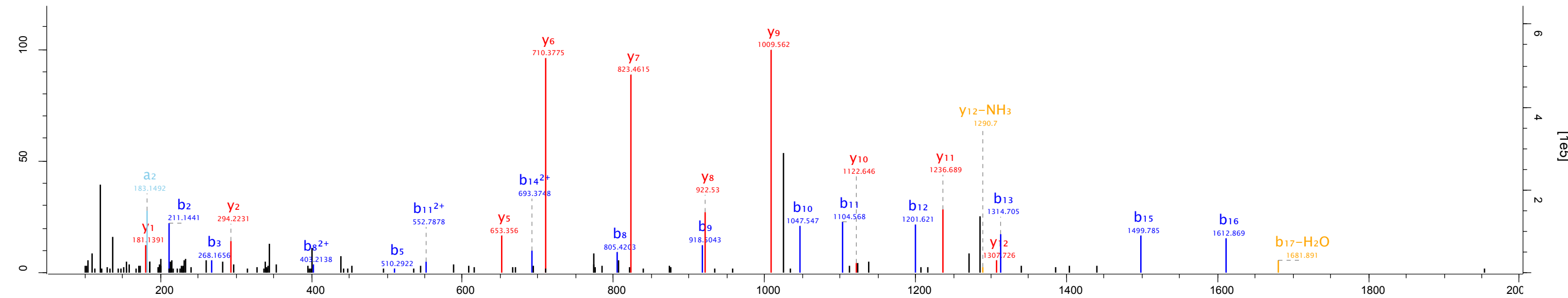
Scan	Method	Score	m/z	Gene names
119824	FTMS; HCD	47.04	953.52	UPF2



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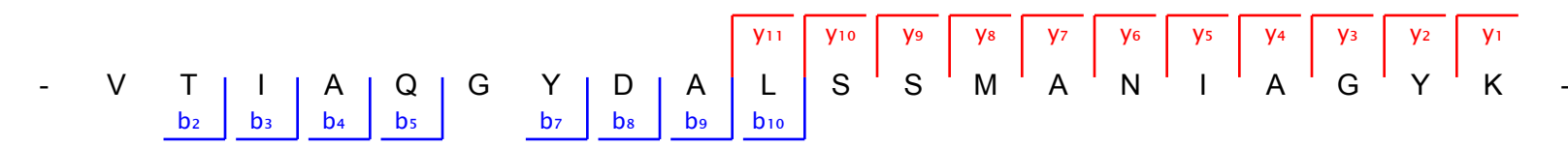
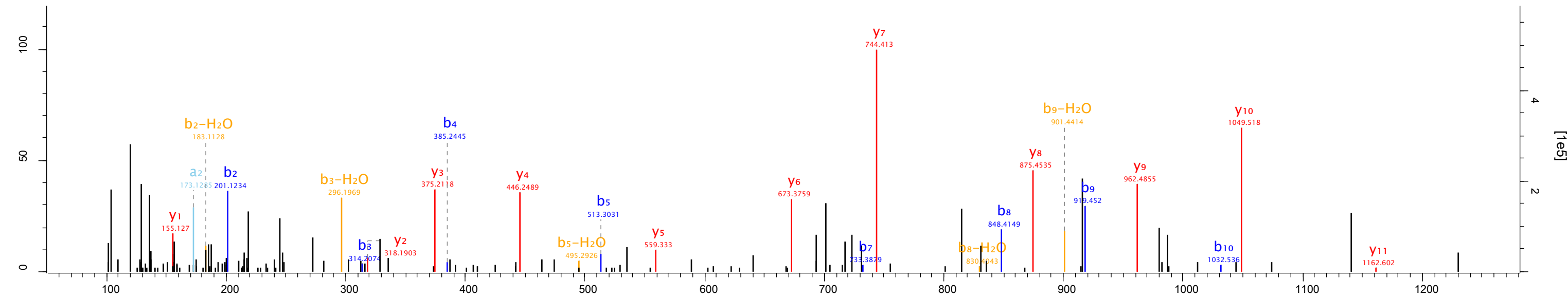
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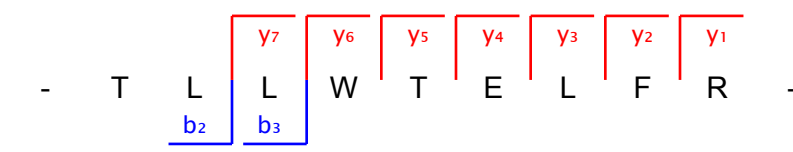
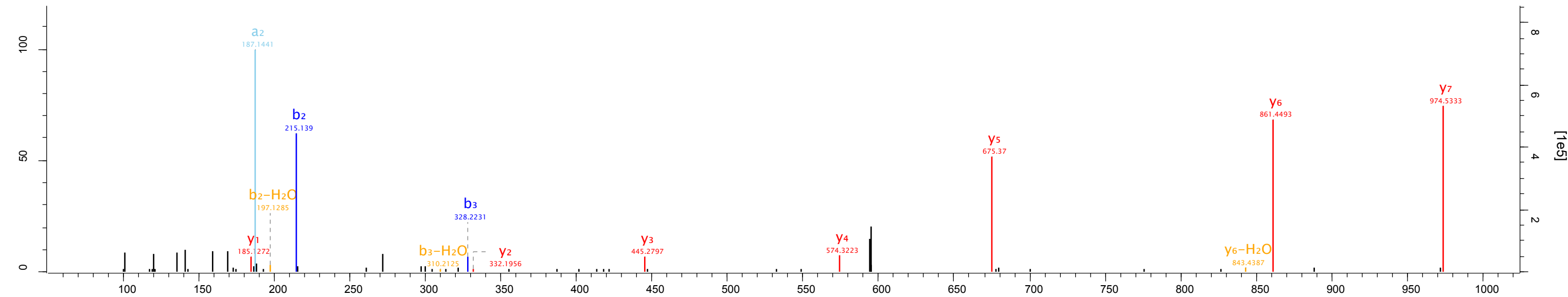
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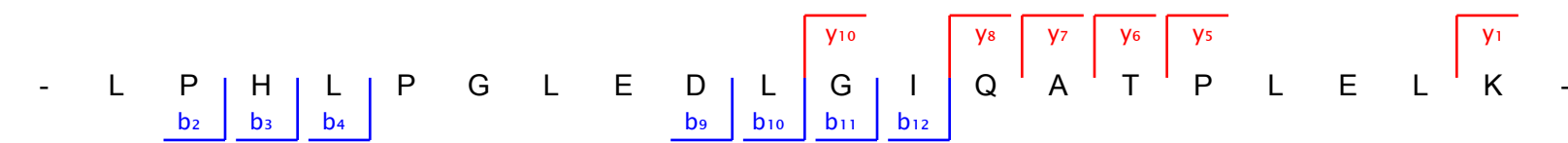
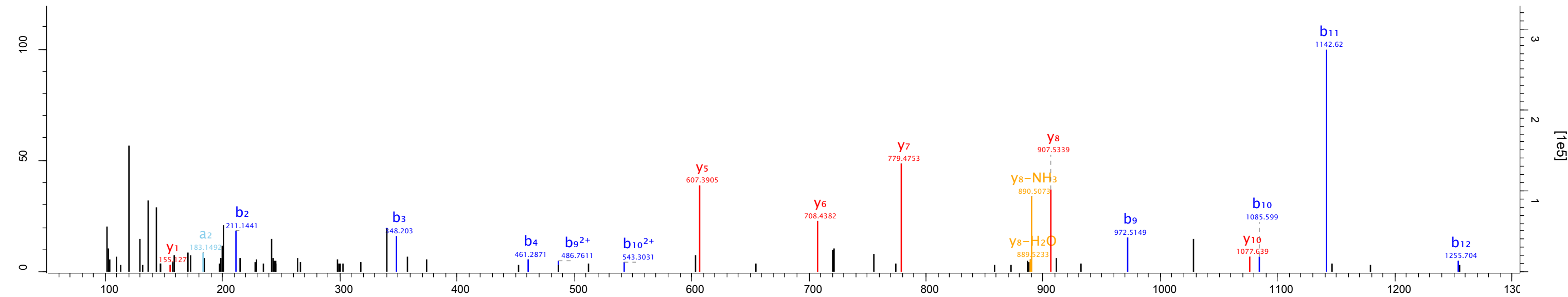
Fragmentation labels below the sequence:

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- b8 (under S), b9 (under I), b10 (under E), b11 (under G), b12 (under P), b13 (under I), b14²⁺ (under A), b15 (under N), b16 (under L)
- y12 (under A), y11 (under N), y10 (under L), y9 (under S), y8 (under V), y7 (under L), y6 (under G), y5 (under T)
- y2 (under L), y1 (under R)

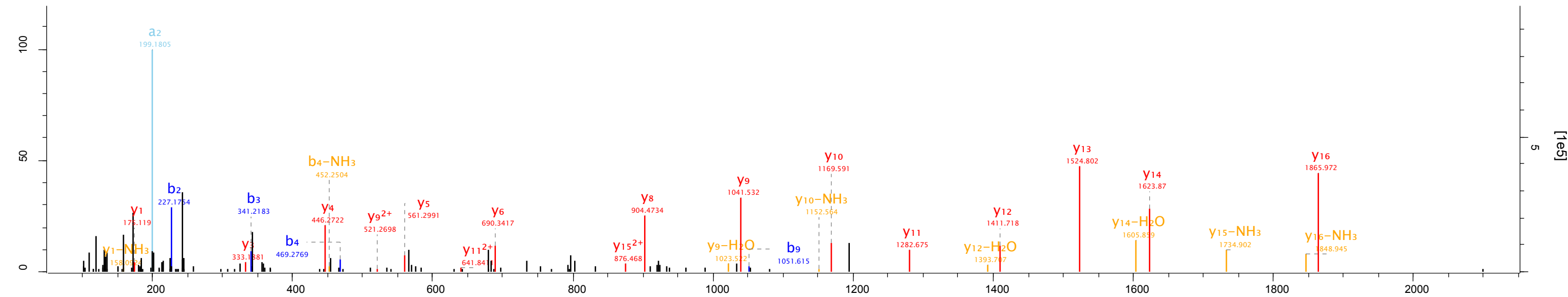


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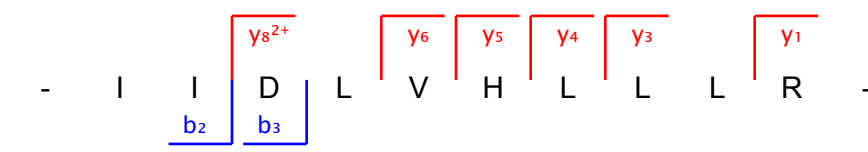
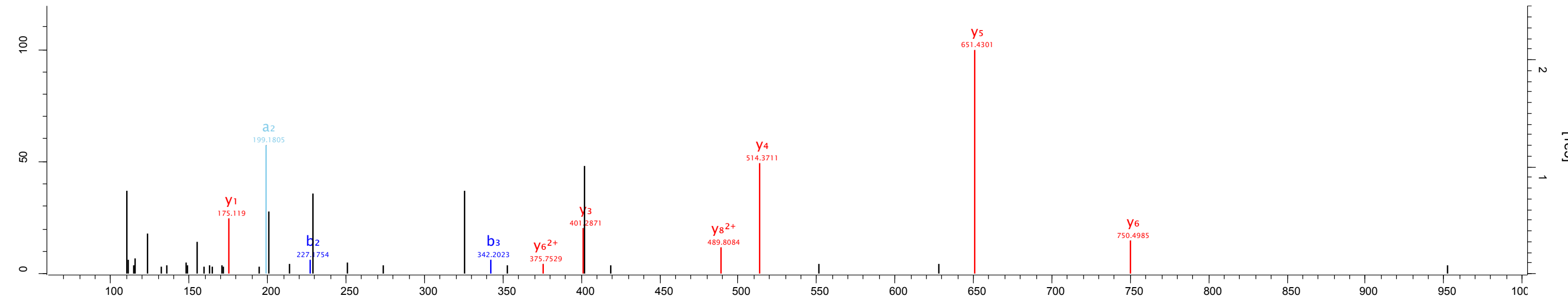




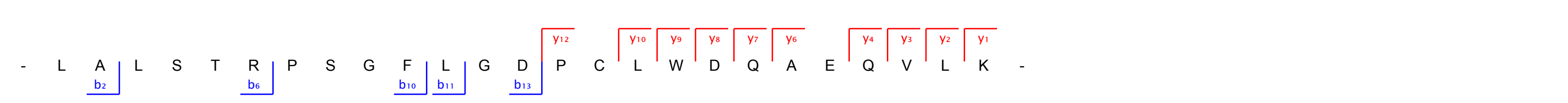
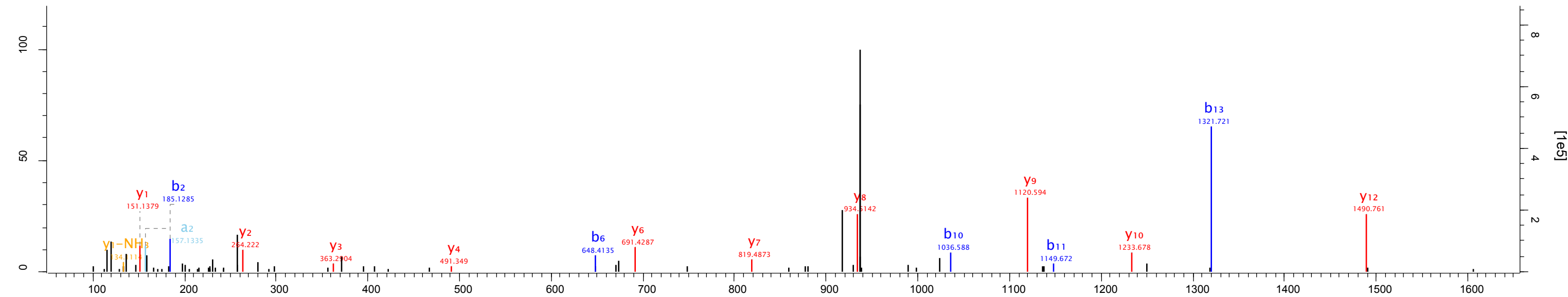
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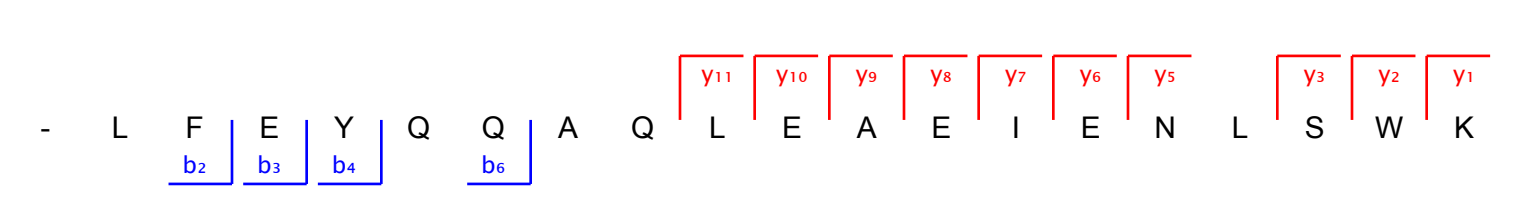
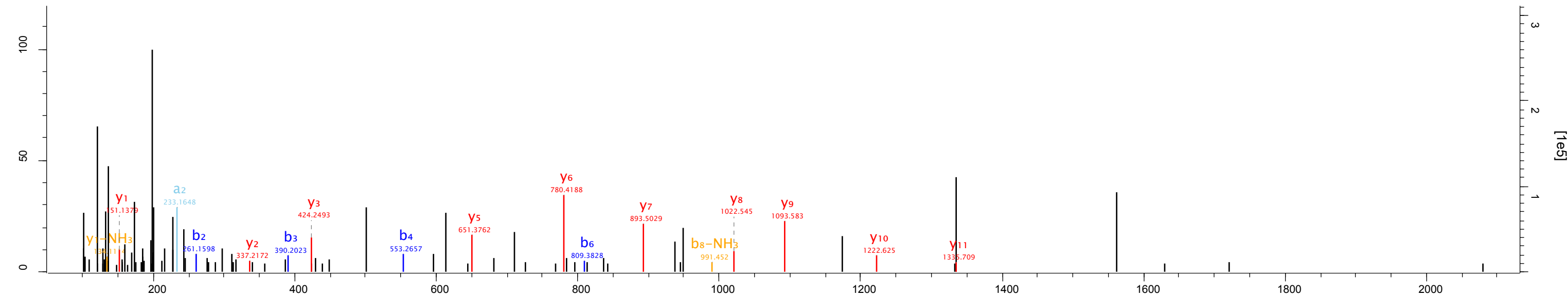
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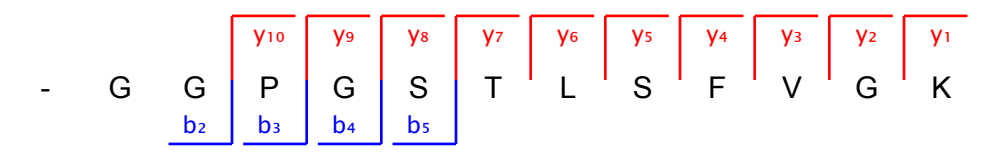
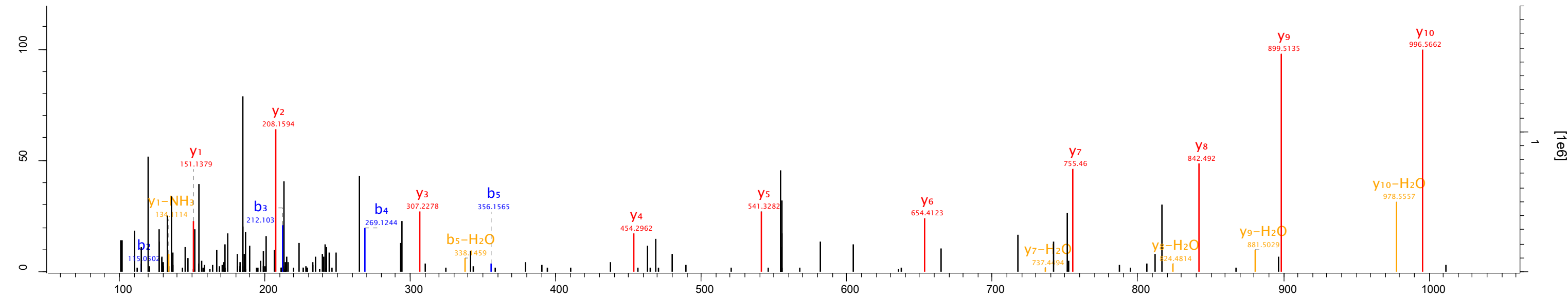
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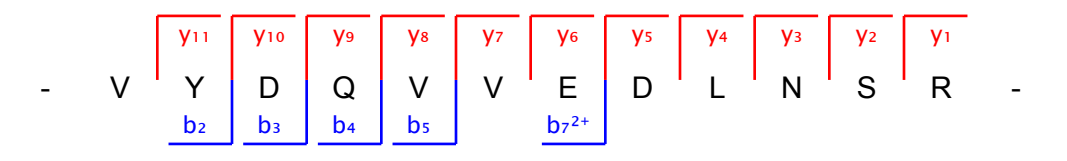
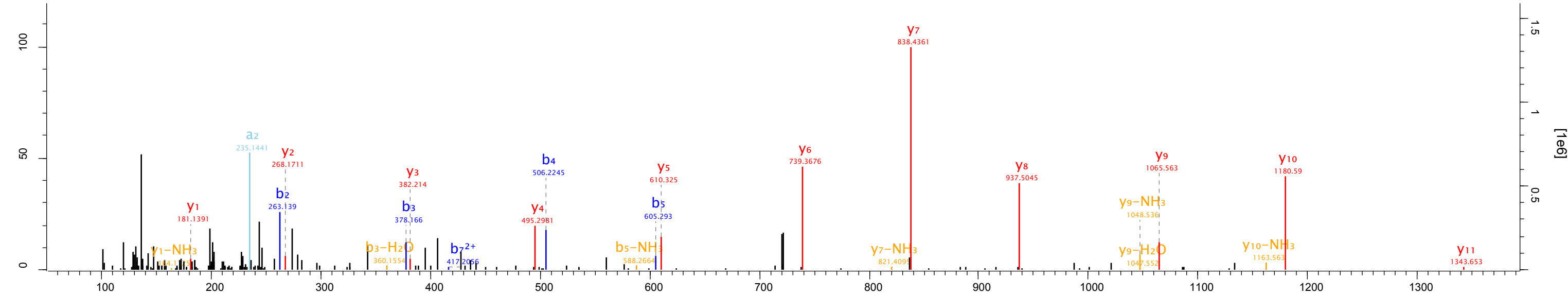
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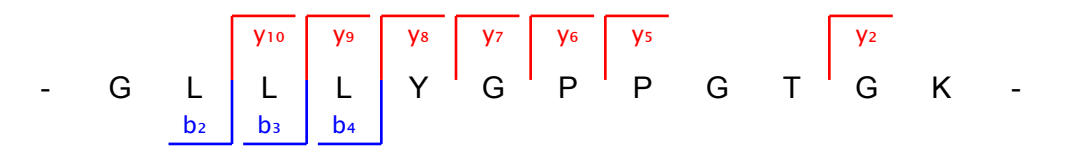
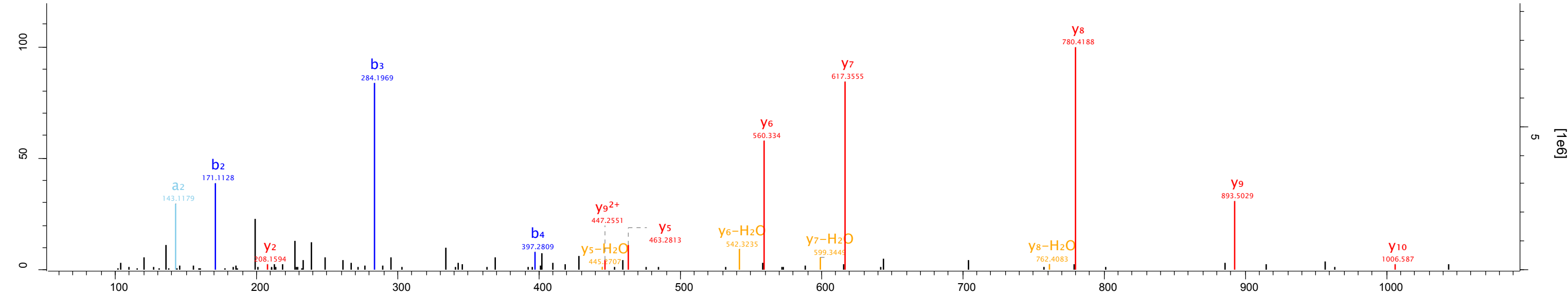
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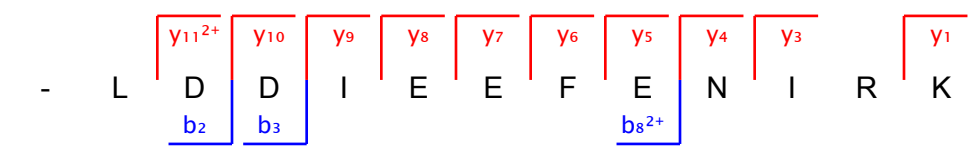
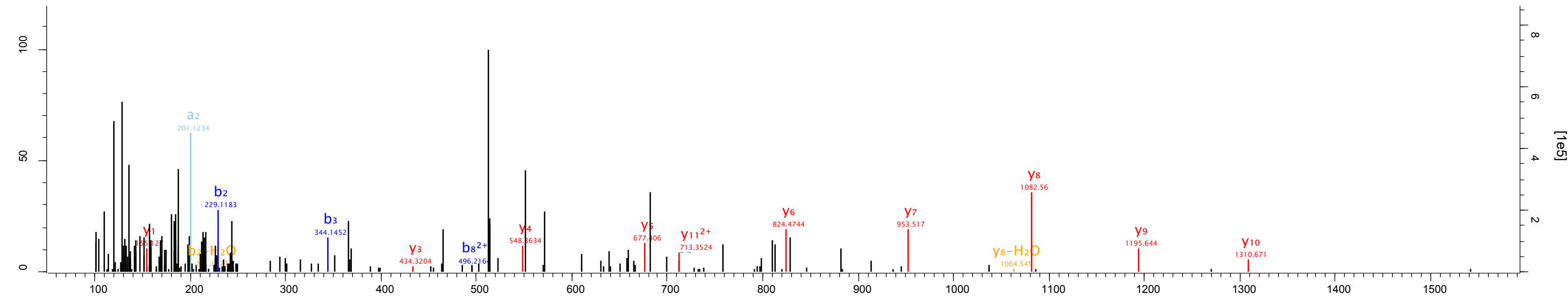
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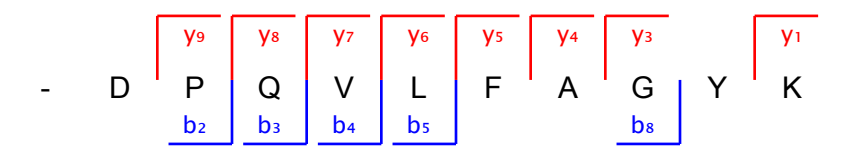
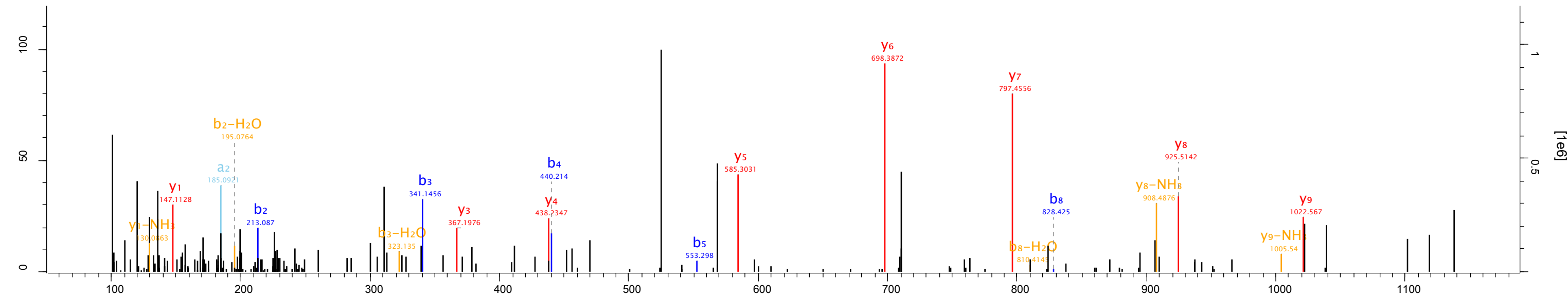
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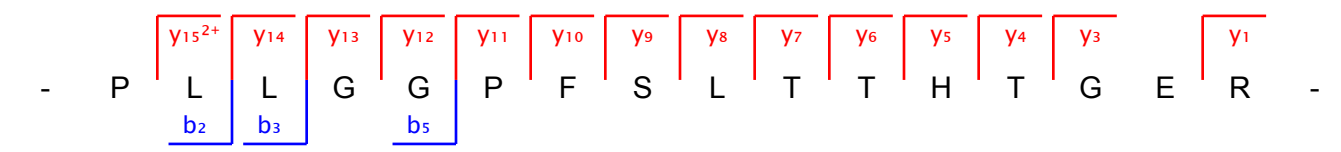
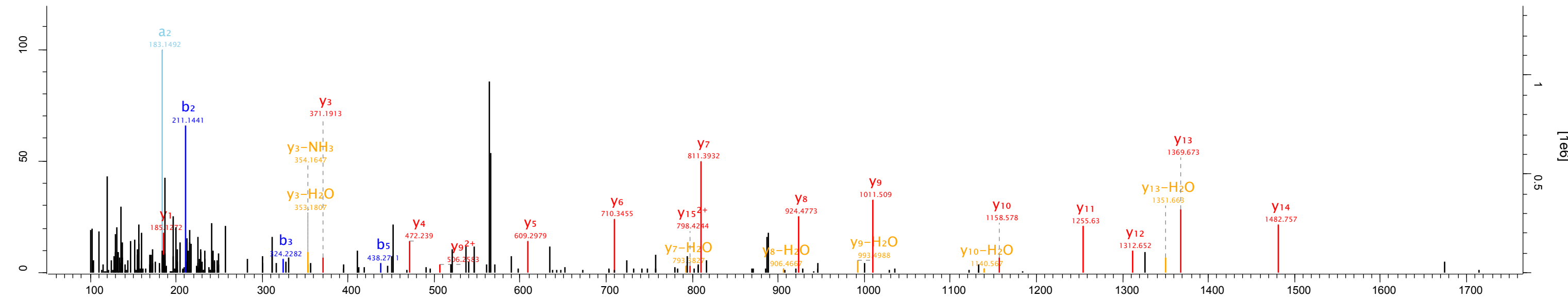
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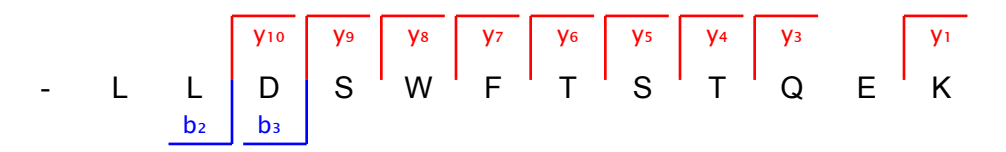
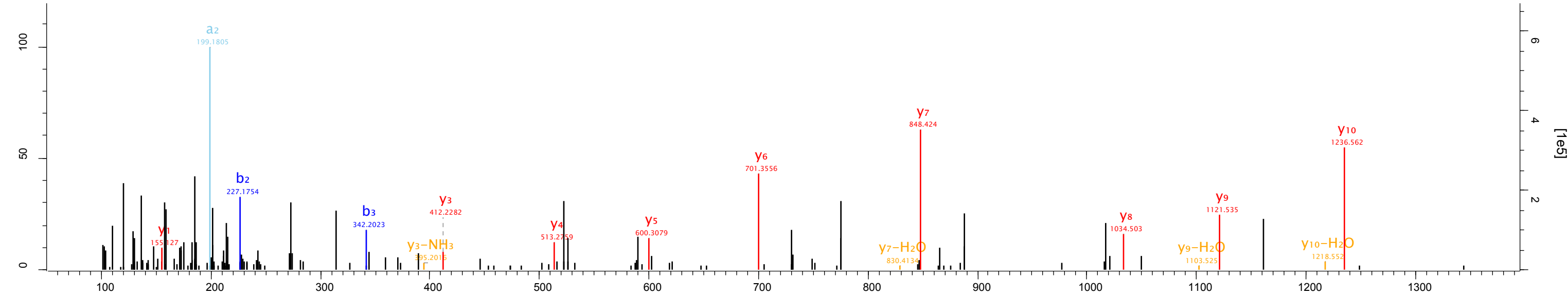
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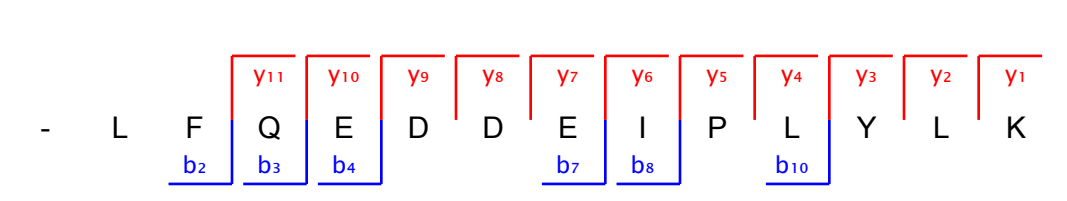
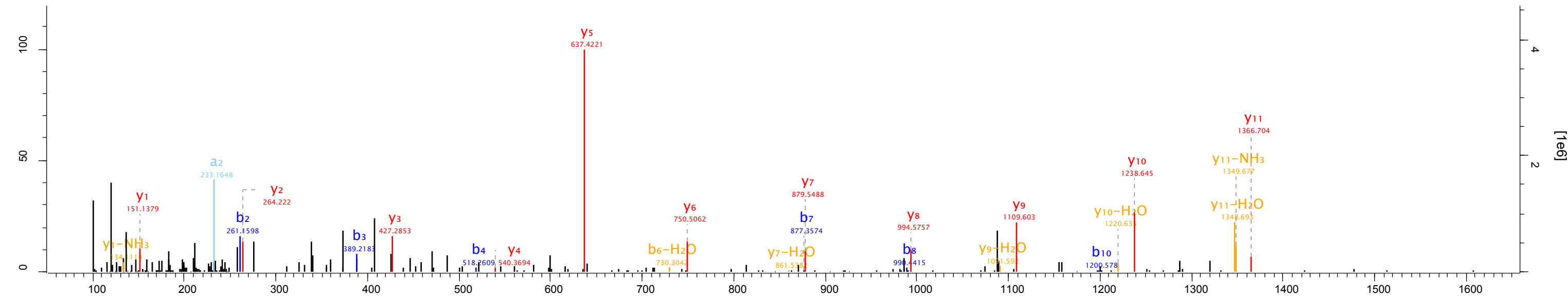
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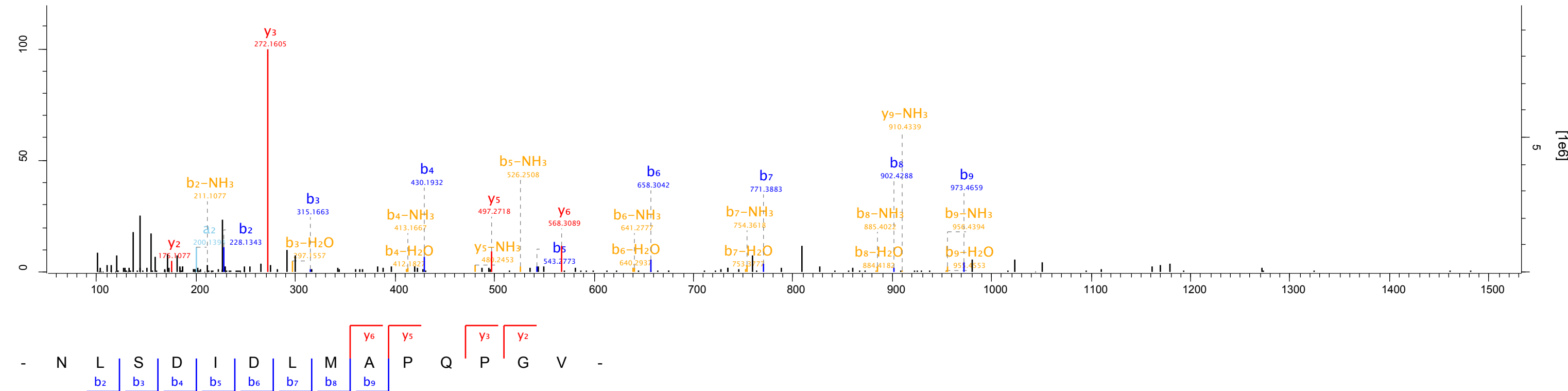
20171215_MaS_33SR_LMH_proteome_02

Scan	Method	Score	m/z	Gene names
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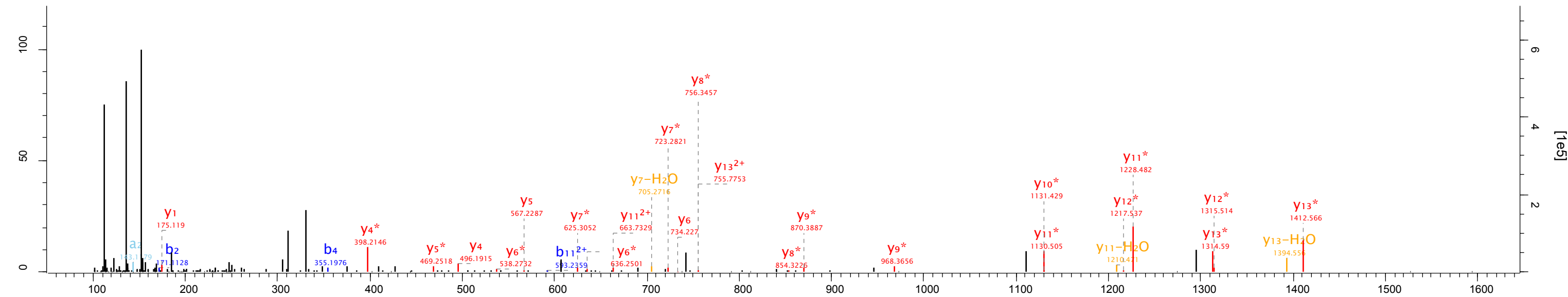


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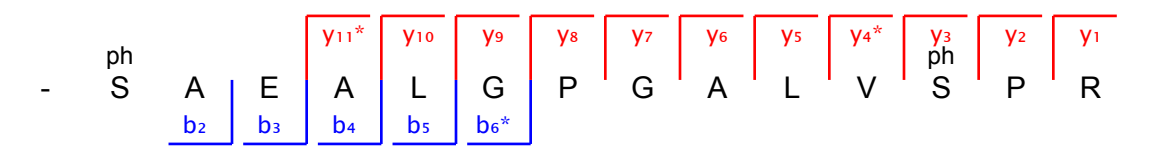
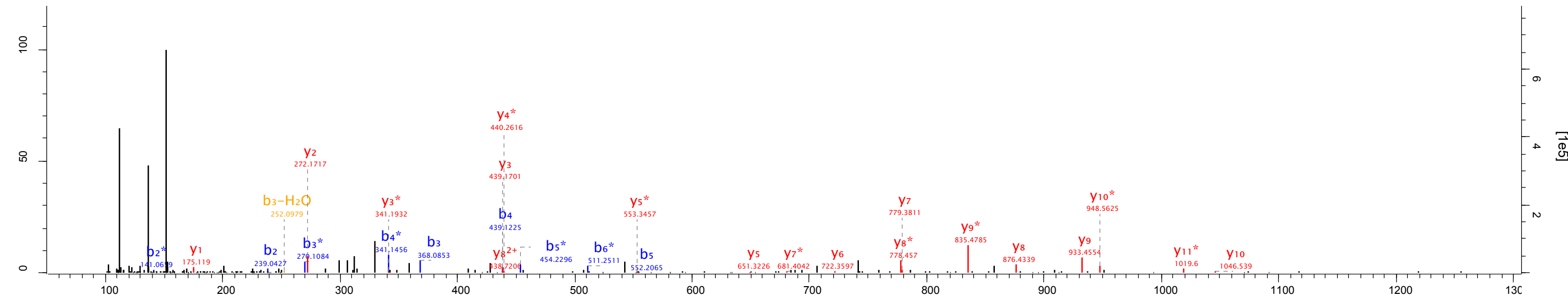




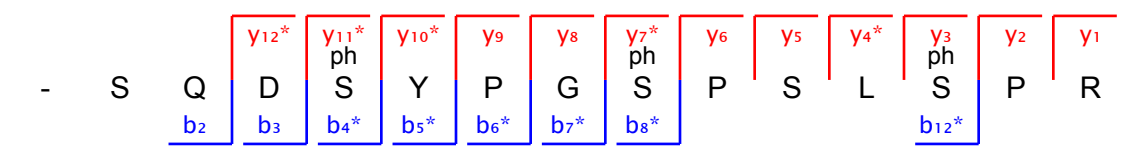
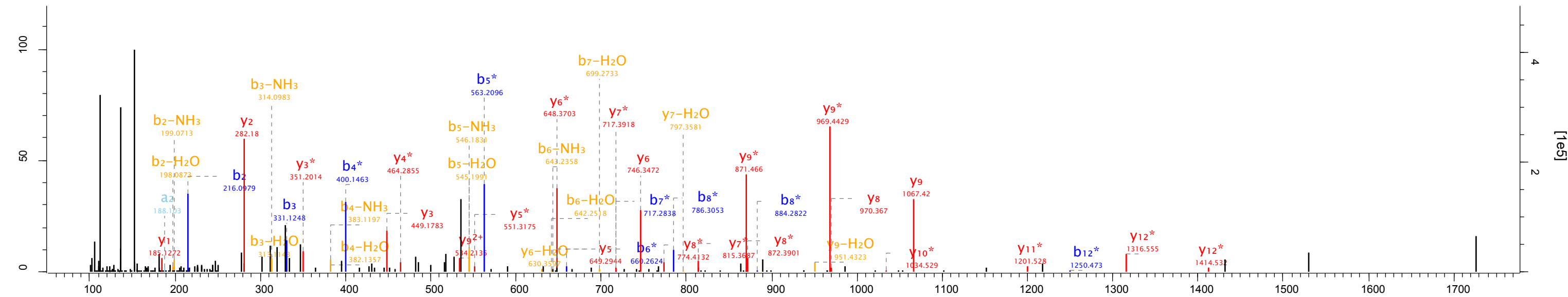
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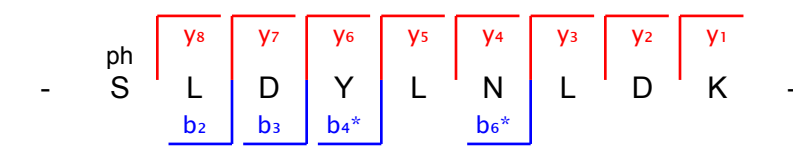
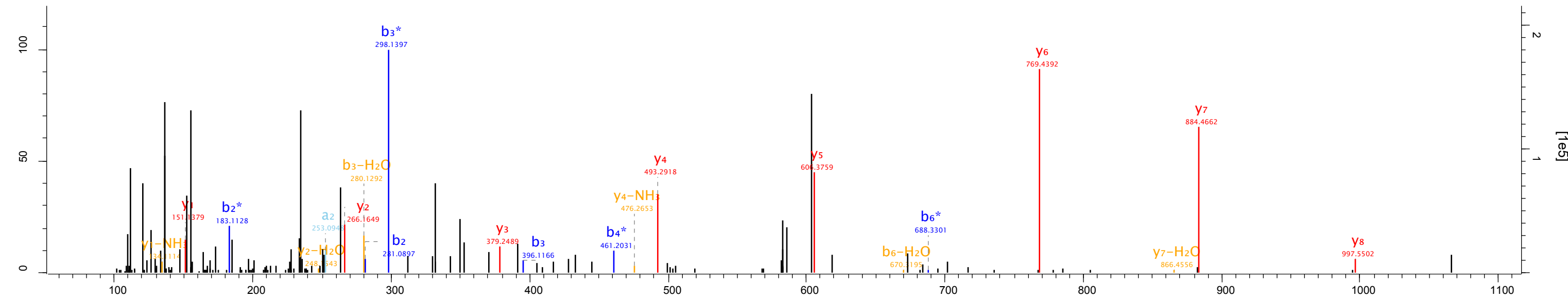
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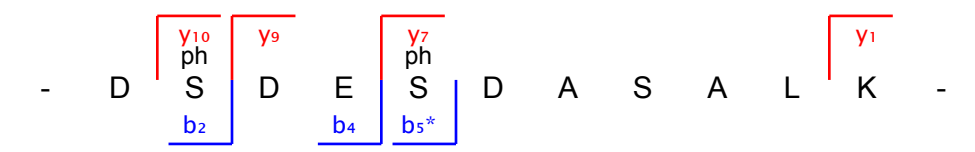
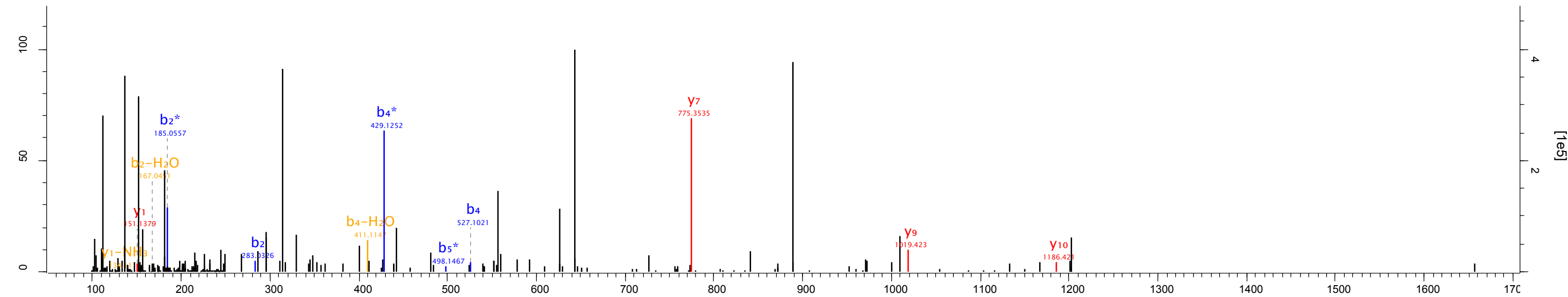


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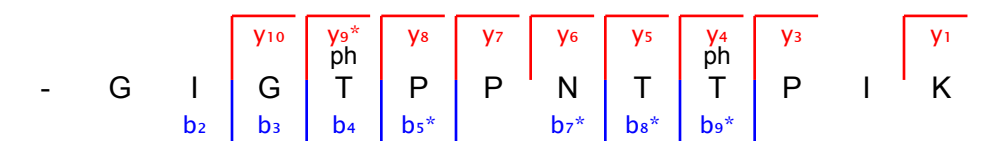
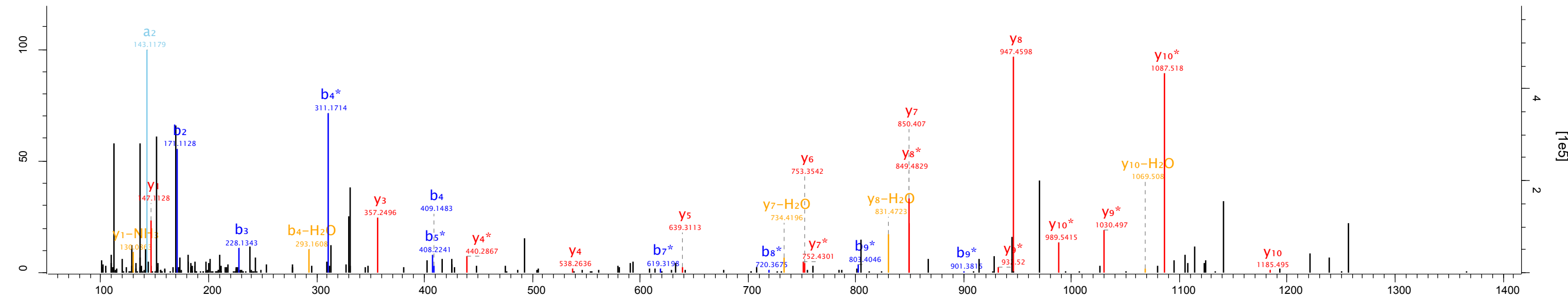


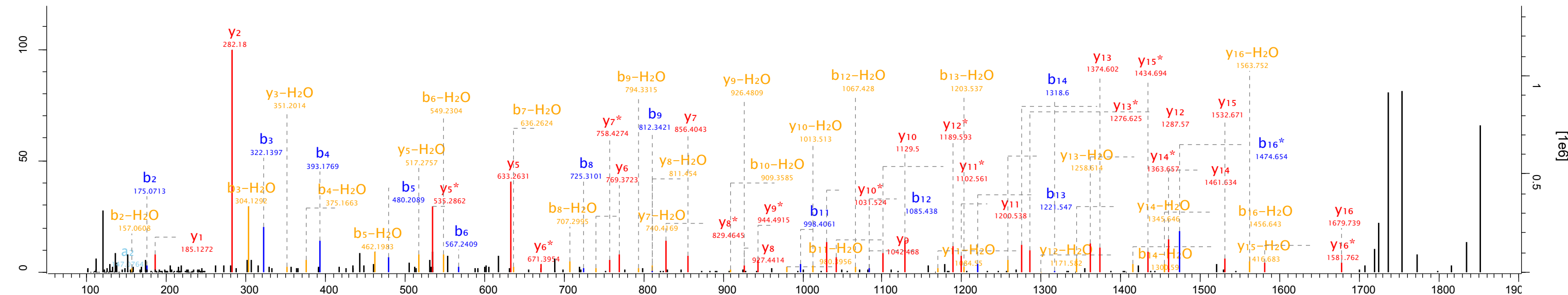
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20171215_MaS_33SR_LMH_phospho_02

Scan 7445 Method FTMS; HCD Score 42 m/z 651.23 Gene names DOCK11



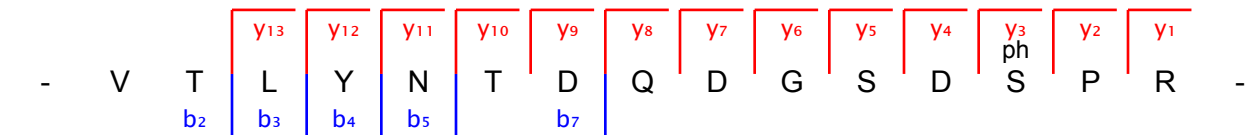
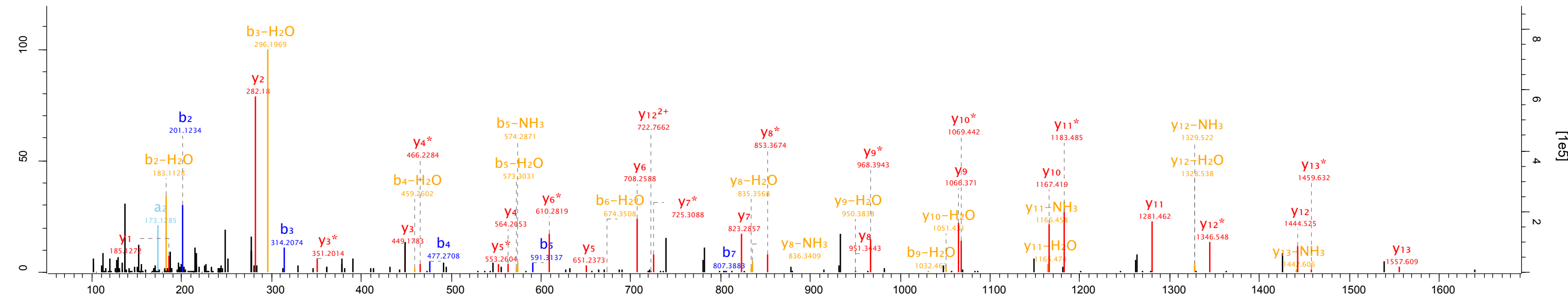
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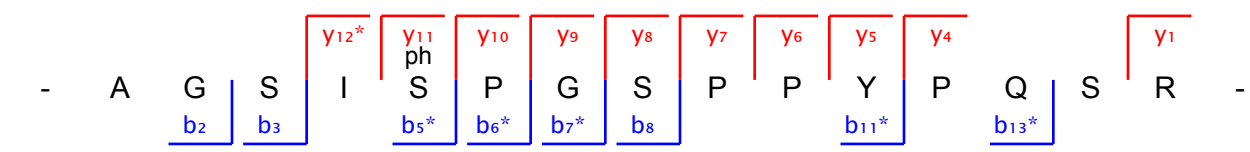
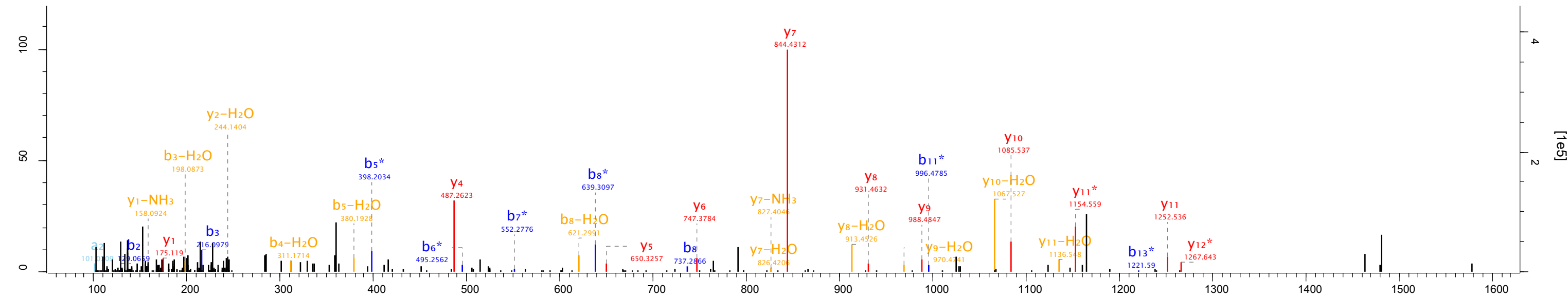


- S S F A S S S A S D A S K P ph S S P R -

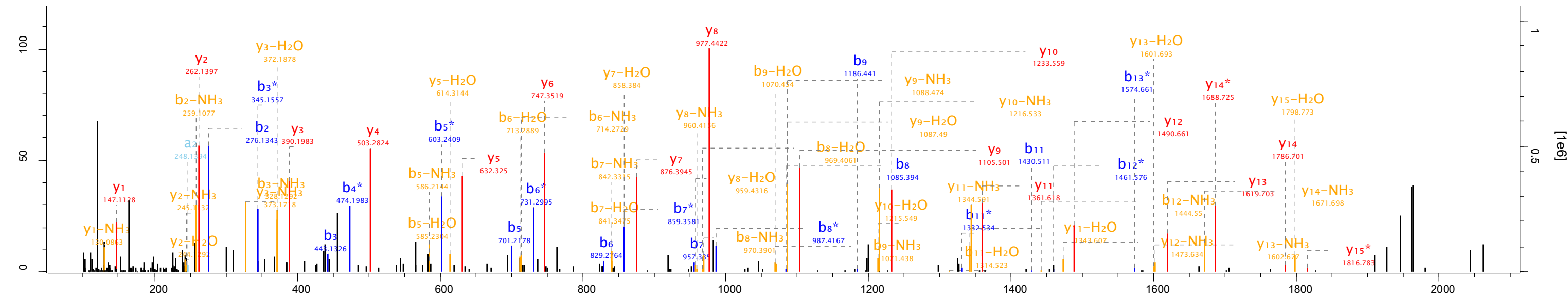
Fragmentation scheme diagram showing amino acid residues (S, F, A, S, S, S, A, S, D, A, S, K, P) and their corresponding b and y ion fragments. The residues are grouped into boxes labeled b₂ through b₁₆* and y₁ through y₁₆. The 'ph' label is positioned between the 'S' and 'S' residues.



Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 8605 Method FTMS; HCD Score 118.48 m/z 790.86 Gene names TENC1



Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 8705 Method FTMS; HCD Score 334.14 m/z 1031.92

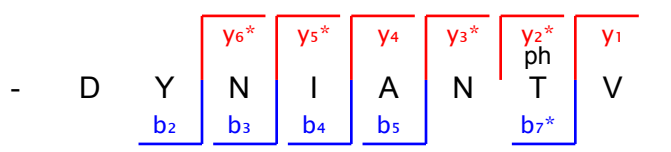
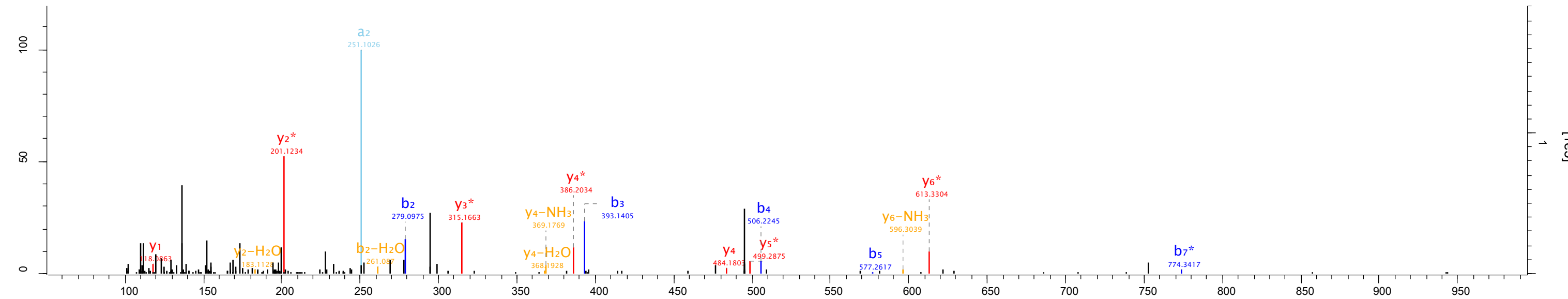


- F Q S E E Q Q Q T E D E L Q D K -

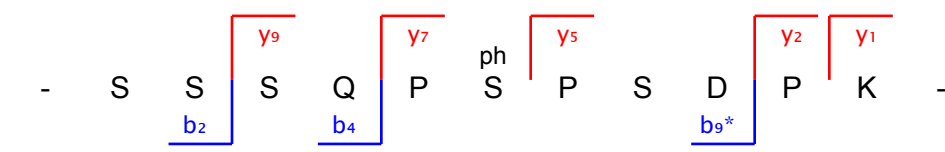
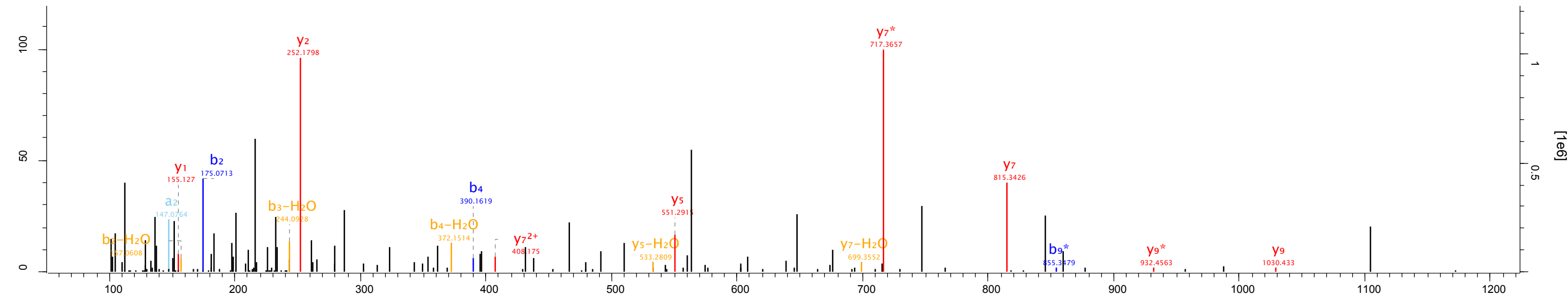
y15*
y14
y13
y12
y11
y10
y9
y8
y7
y6
y5
y4
y3
y2
y1

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

Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 9885 Method FTMS; HCD Score 68.54 m/z 495.2 Gene names RNF13



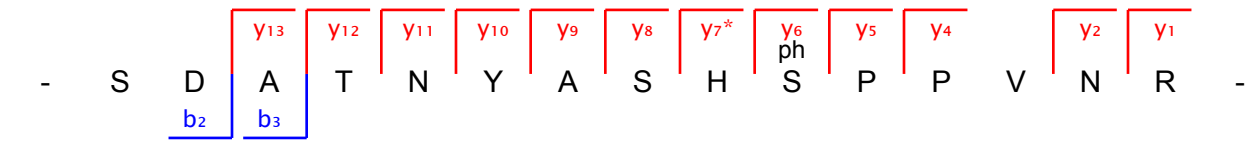
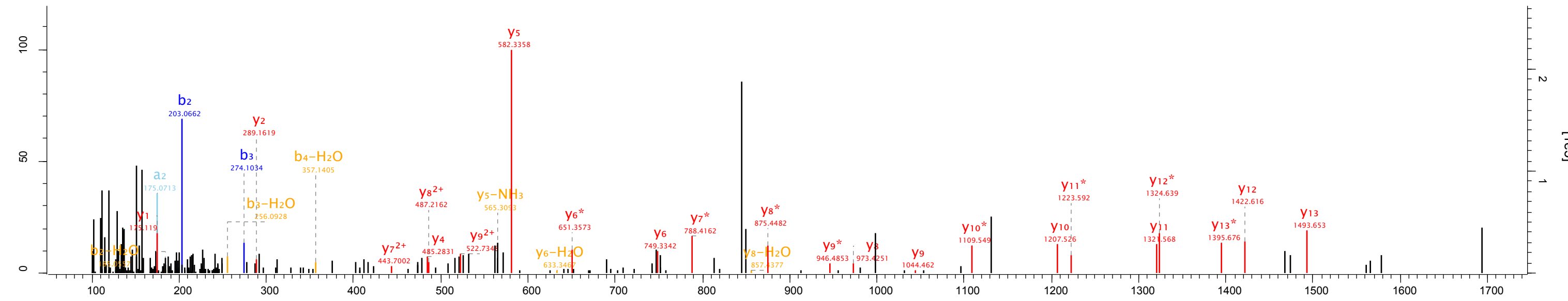
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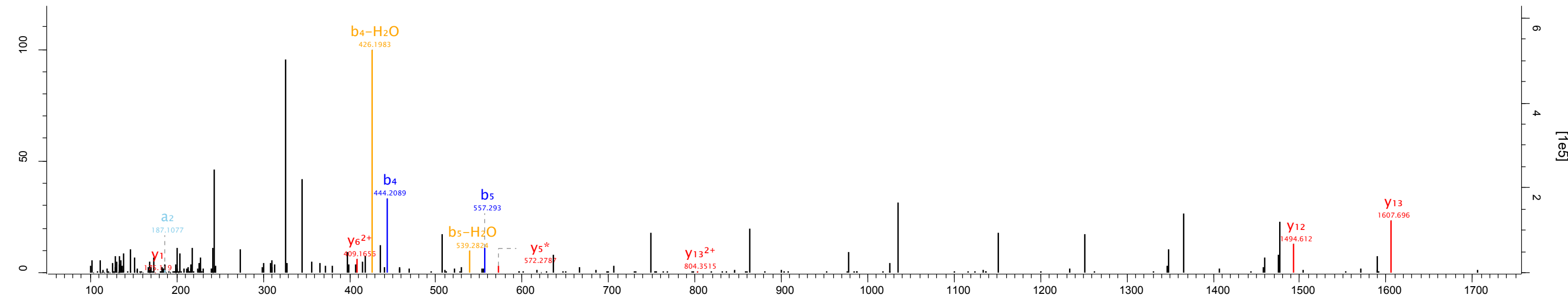


Raw file

20171215_MaS_33SR_LMH_phospho_05

Scan	Method	Score	m/z	Gene names
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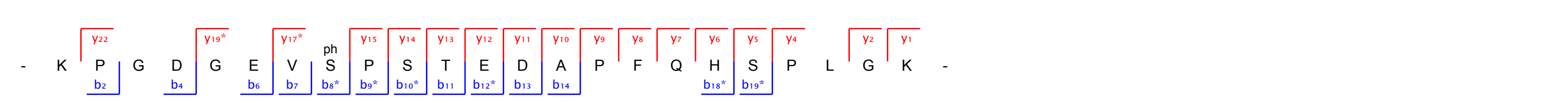
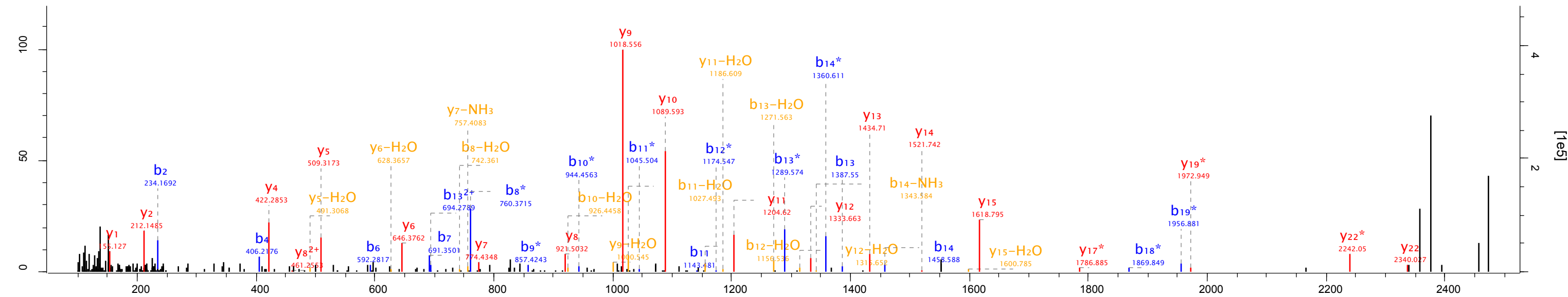




- D V Q T L A ox M L C S V F E A Q S R -

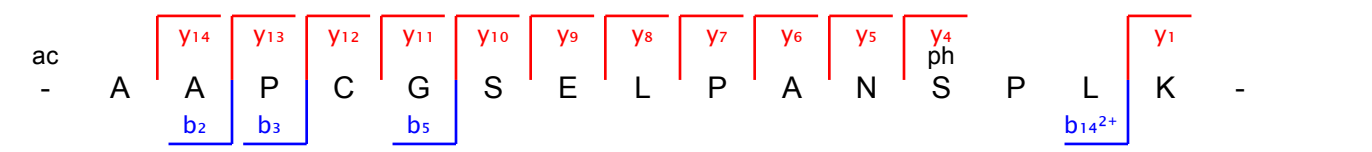
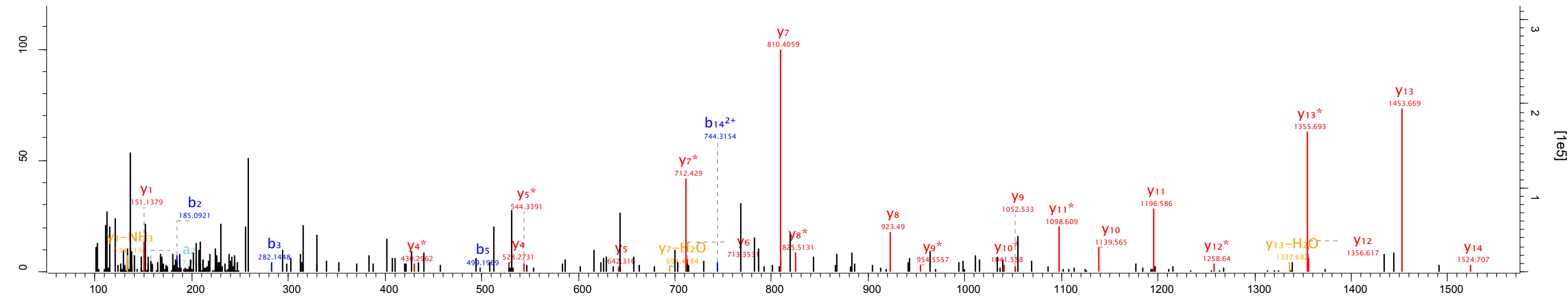
Fragmentation labels (a2, b4, b5, y13, y12, y6^2+, y5*, y1) are shown above the corresponding amino acids in the sequence.

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 Scan: 11525 Method: FTMS; HCD Score: 171.02 m/z: 826.05 Gene names: MCM3AP

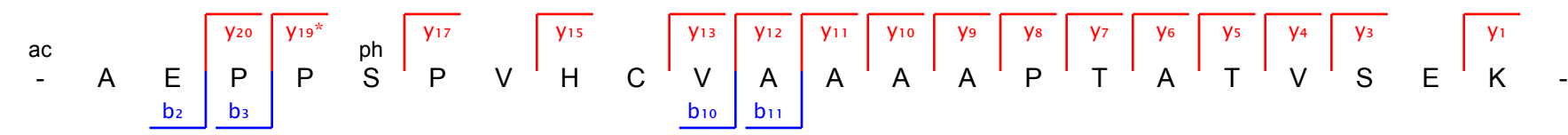
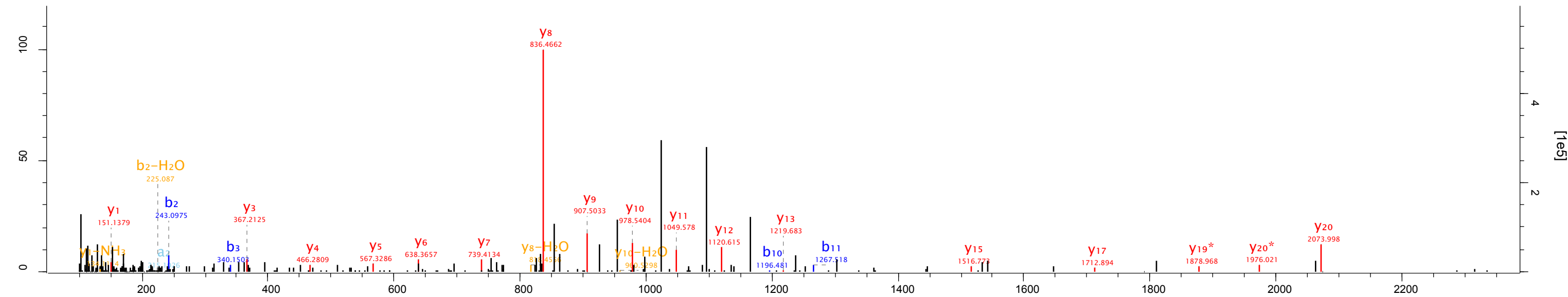


Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12345 Method FTMS; HCD Score 67.19 m/z 819.38 Gene names MSANTD2

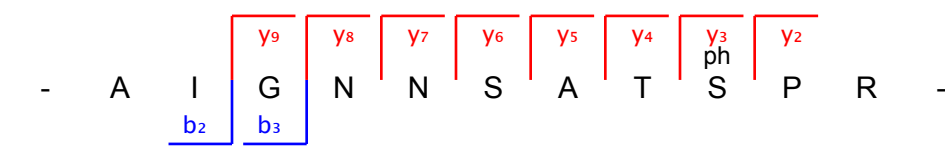
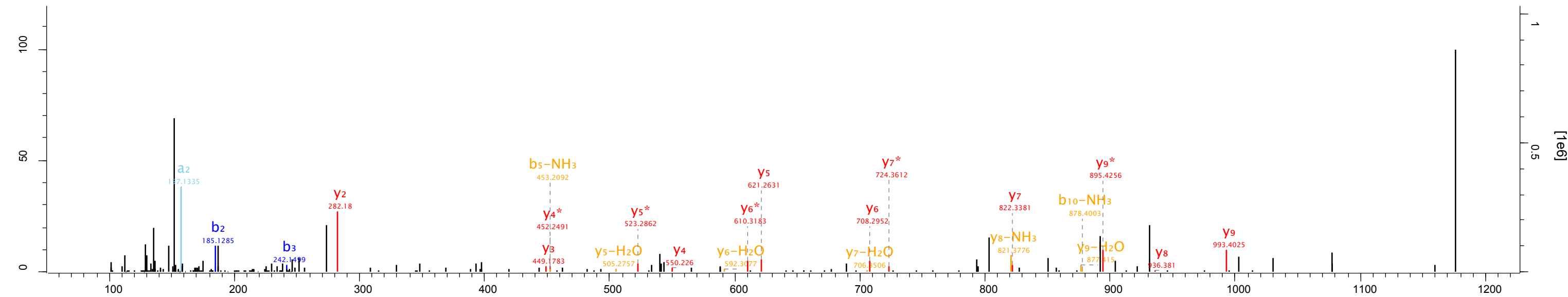
20171215_MaS_33SR_LMH_phospho_06



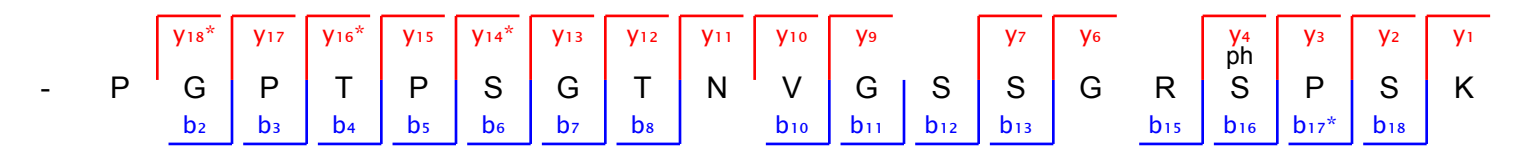
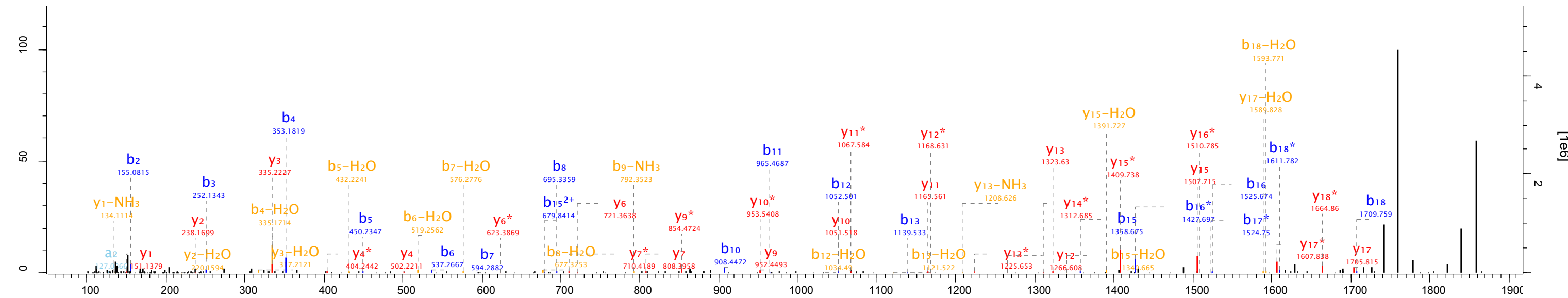
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 20171215_MaS_33SR_LMH_phospho_06
 Scan 13755 Method FTMS; HCD Score 46.41 m/z 773.03 Gene names RSBN1L



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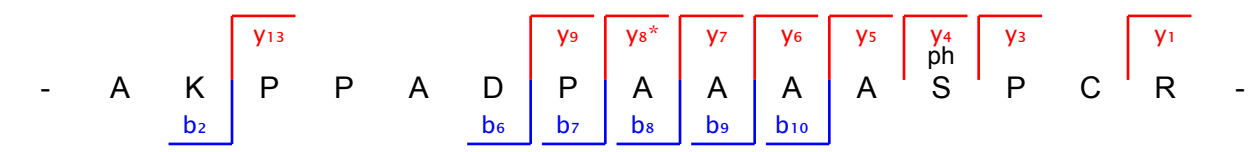
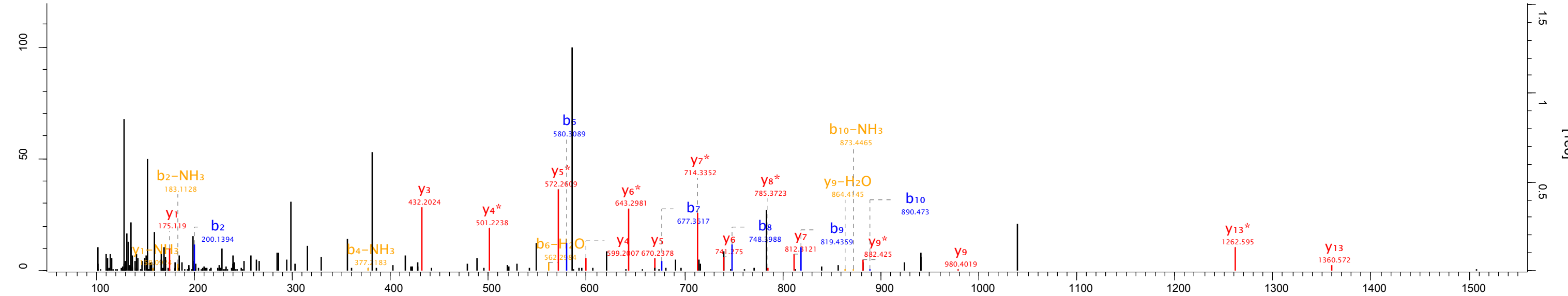


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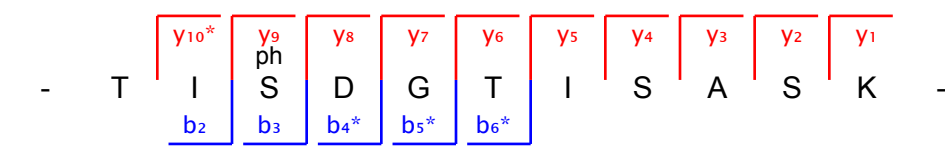
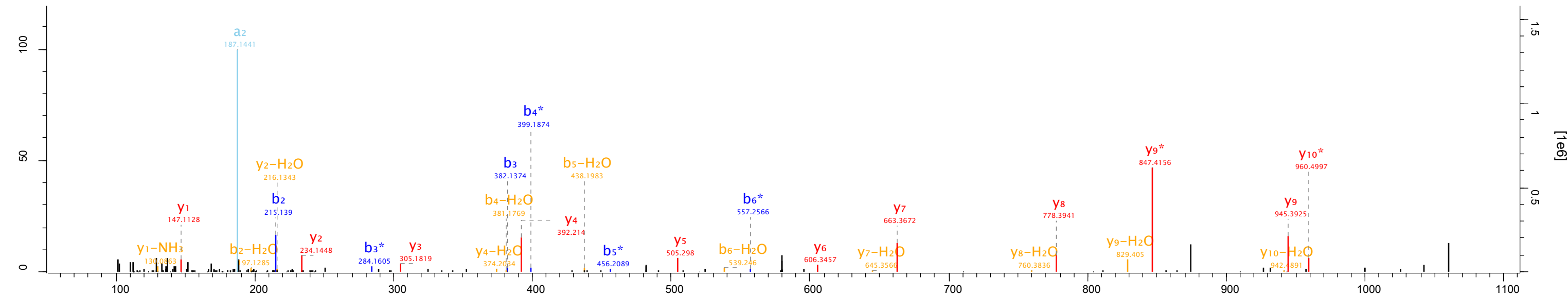


Raw file Scan Method Score m/z Gene names

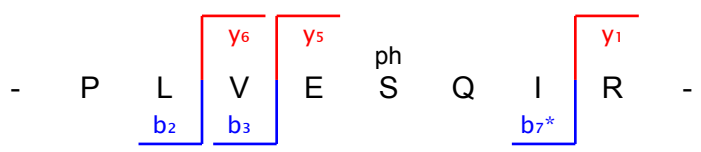
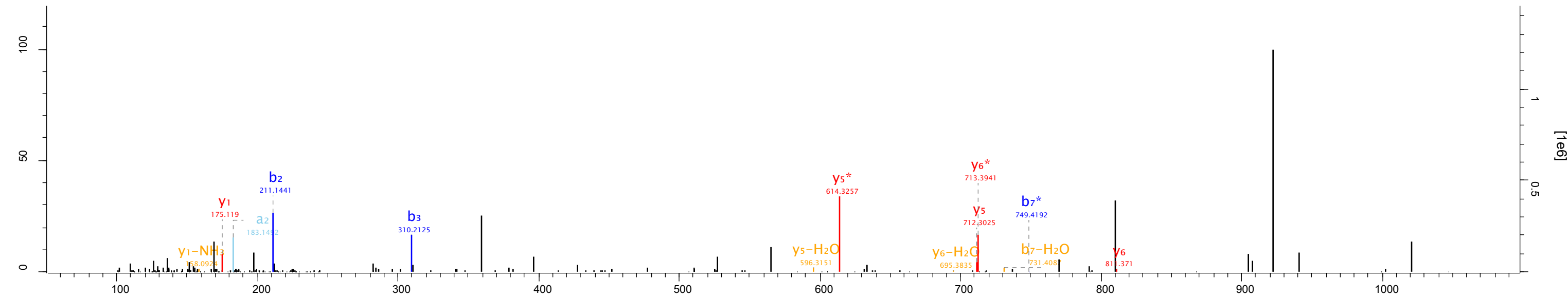
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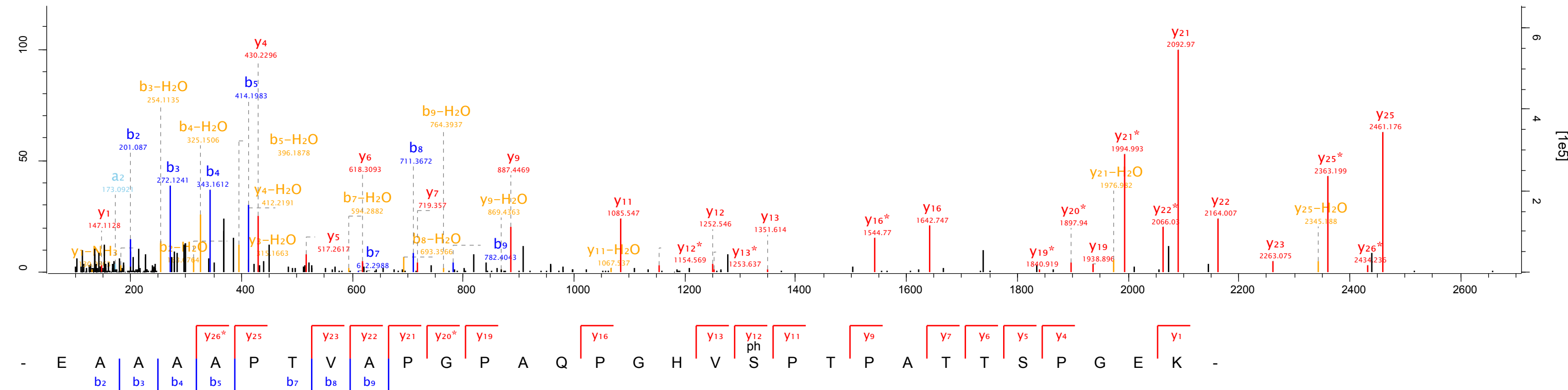


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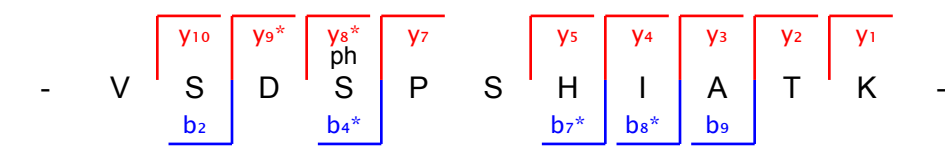
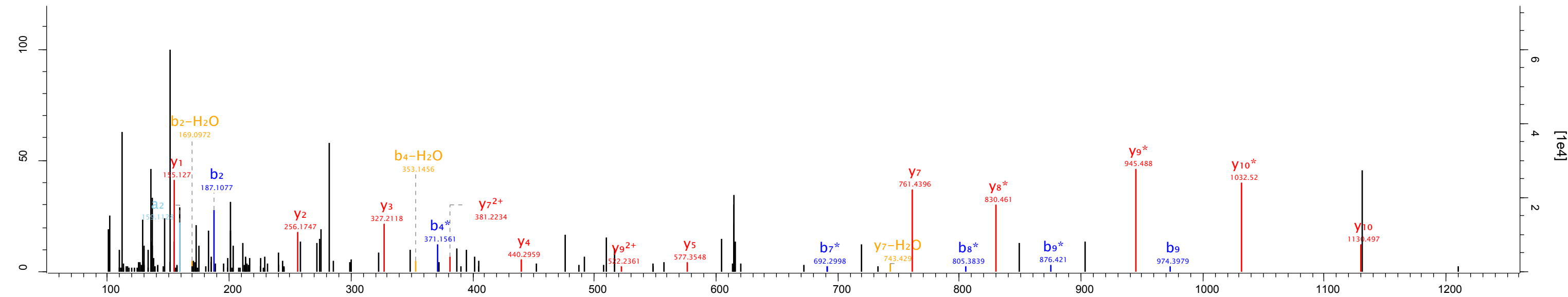


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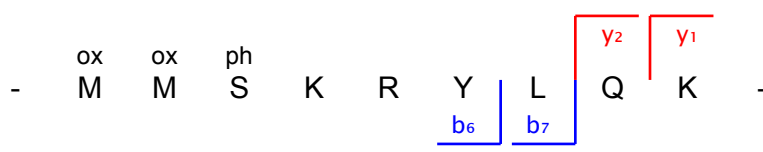
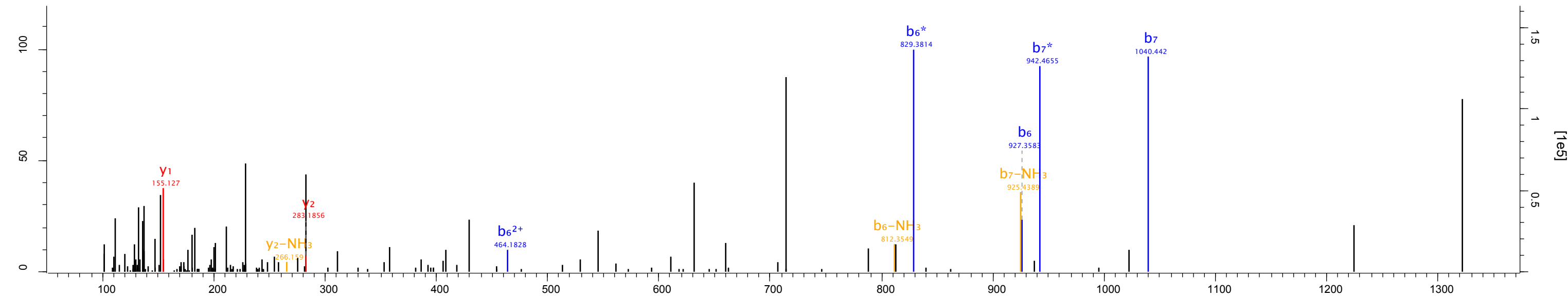




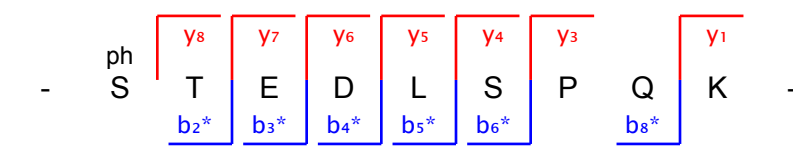
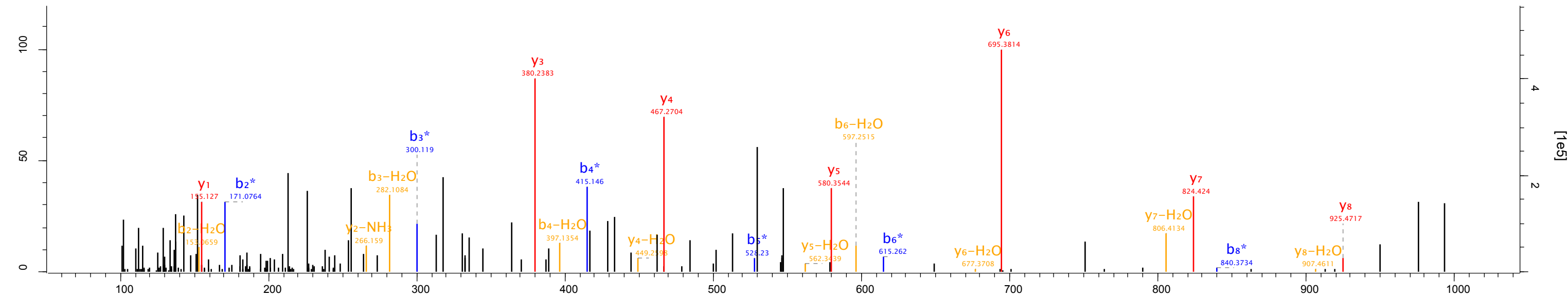
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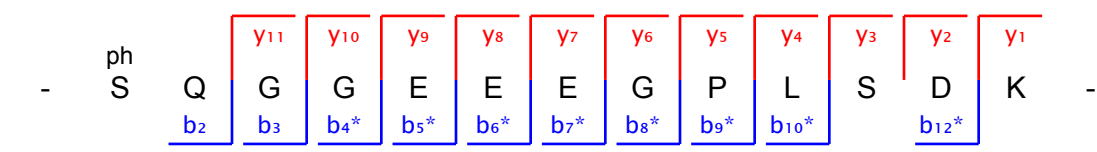
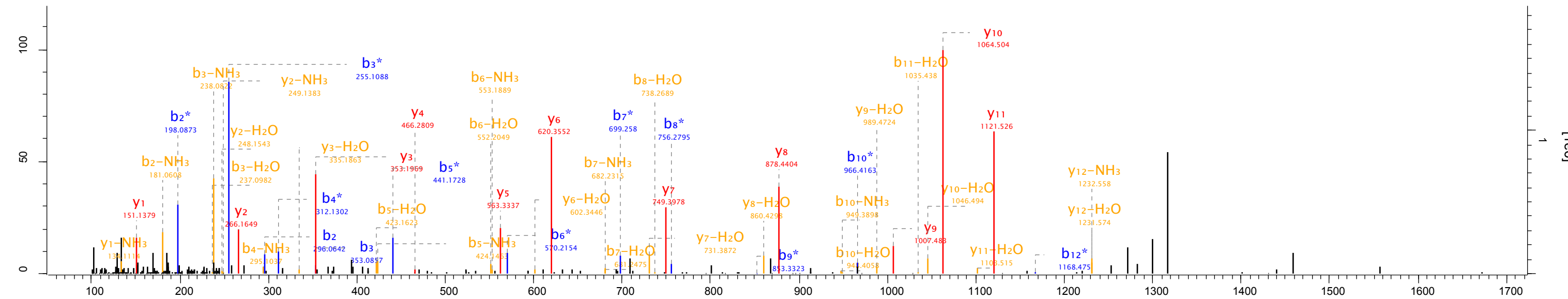
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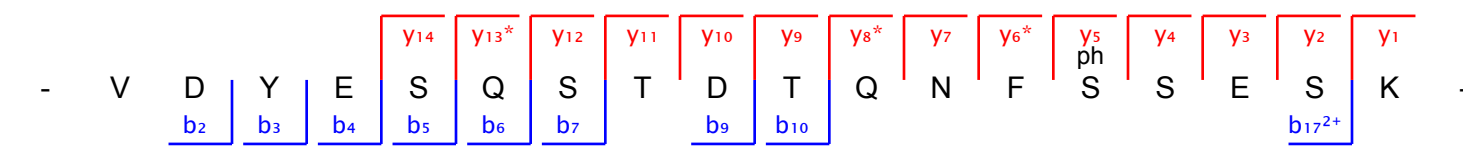
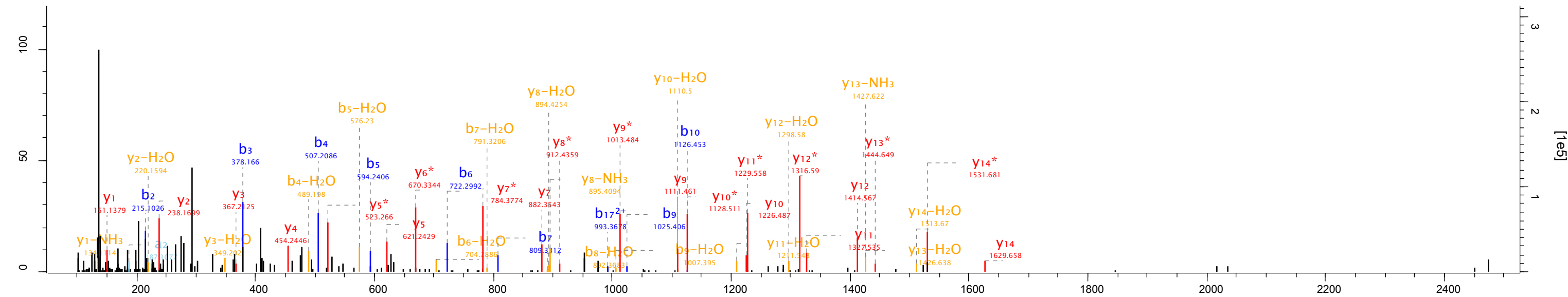
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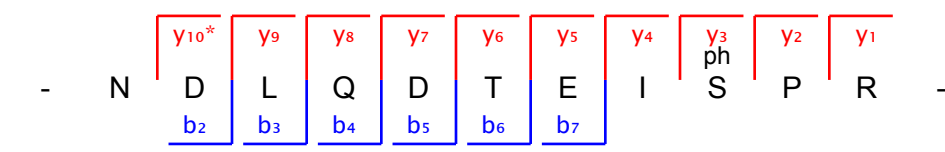
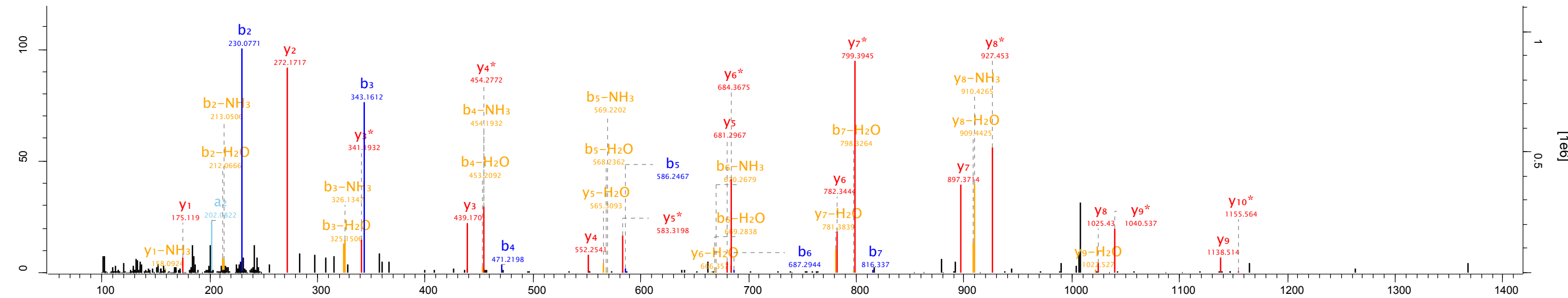
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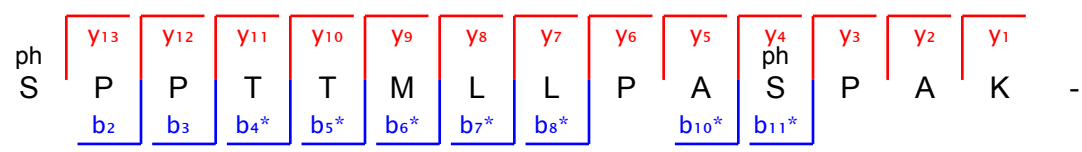
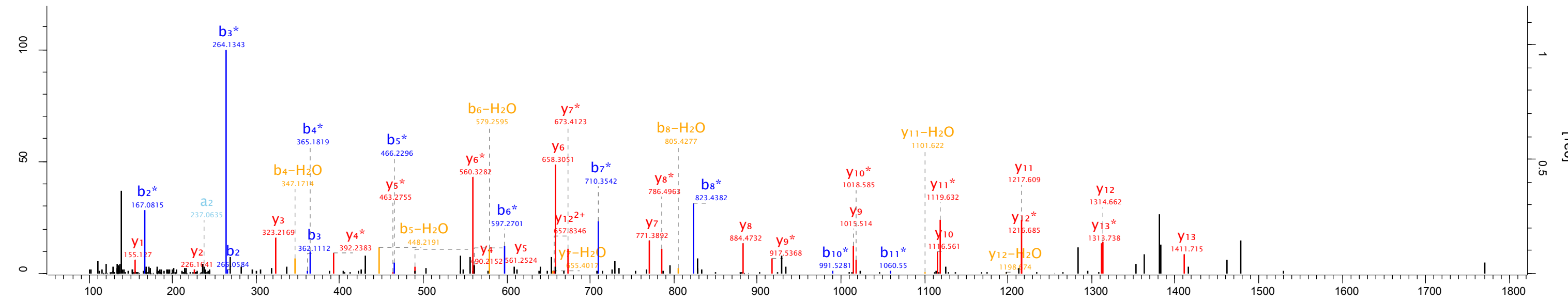
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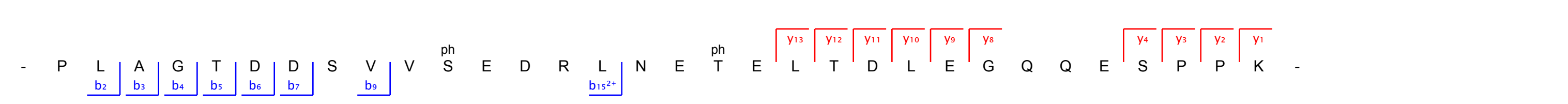
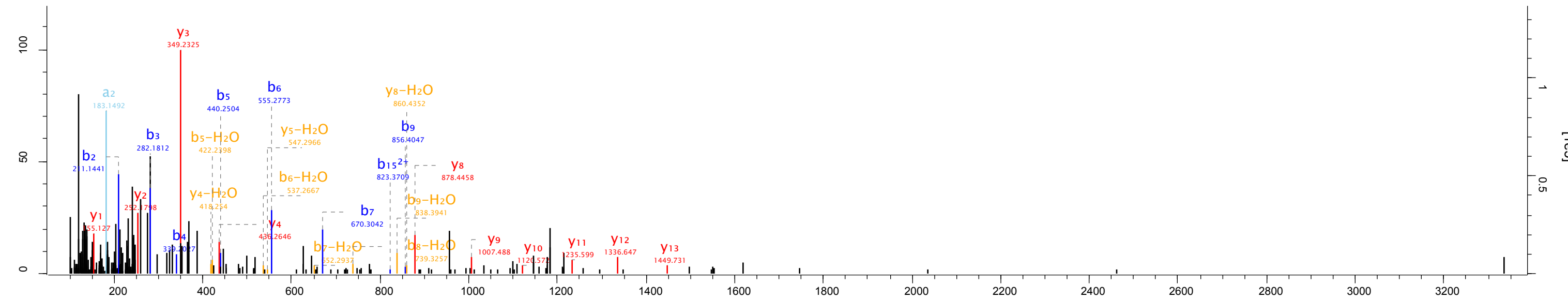
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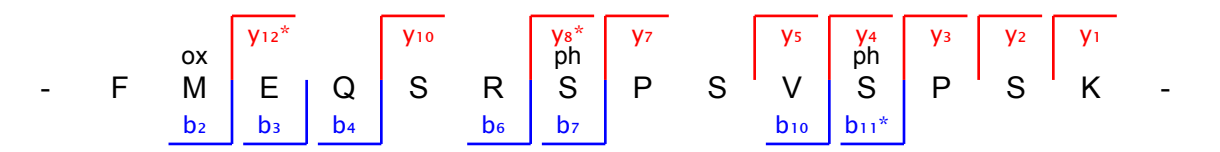
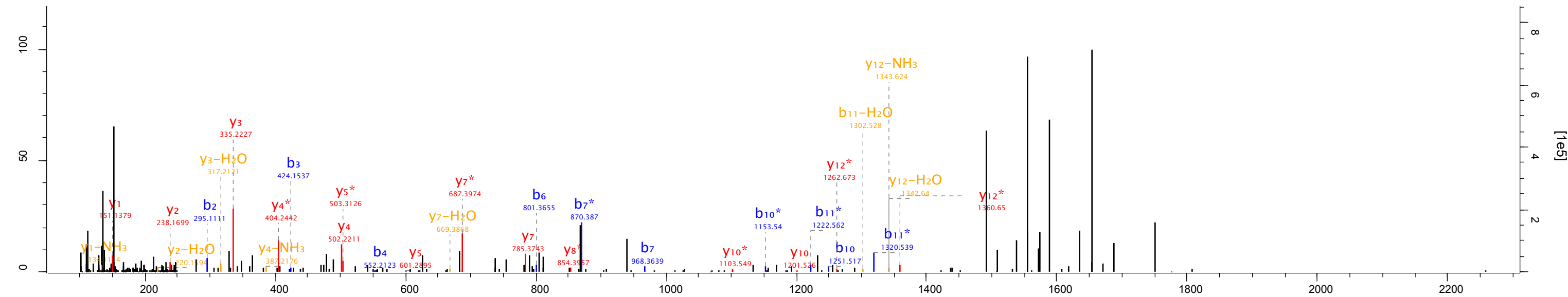
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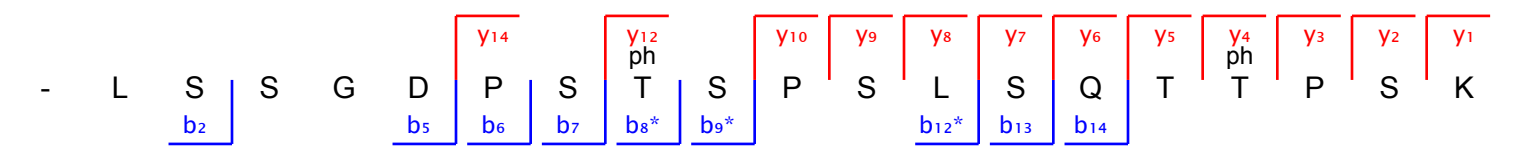
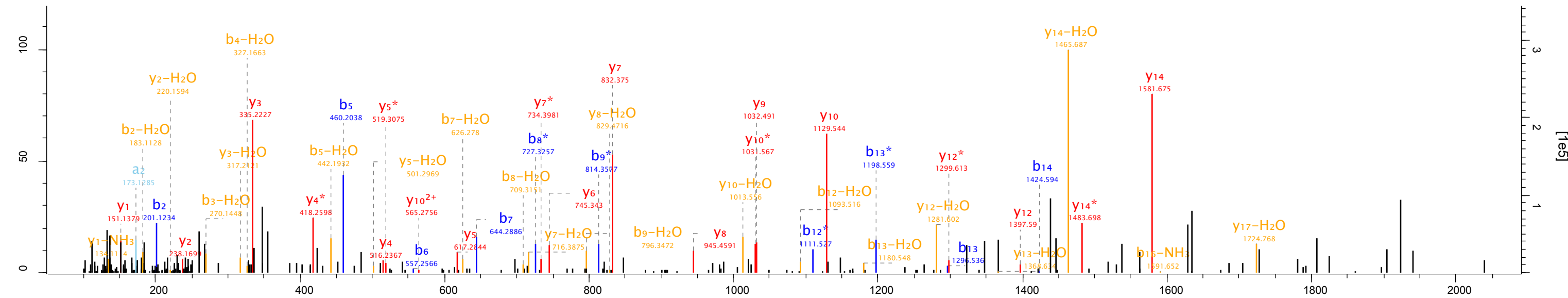
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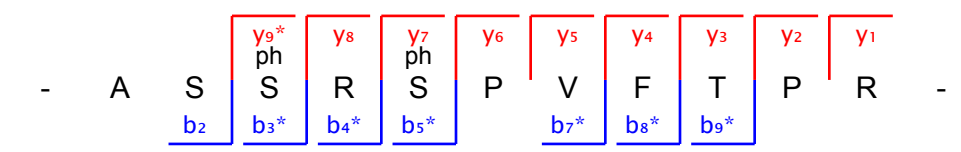
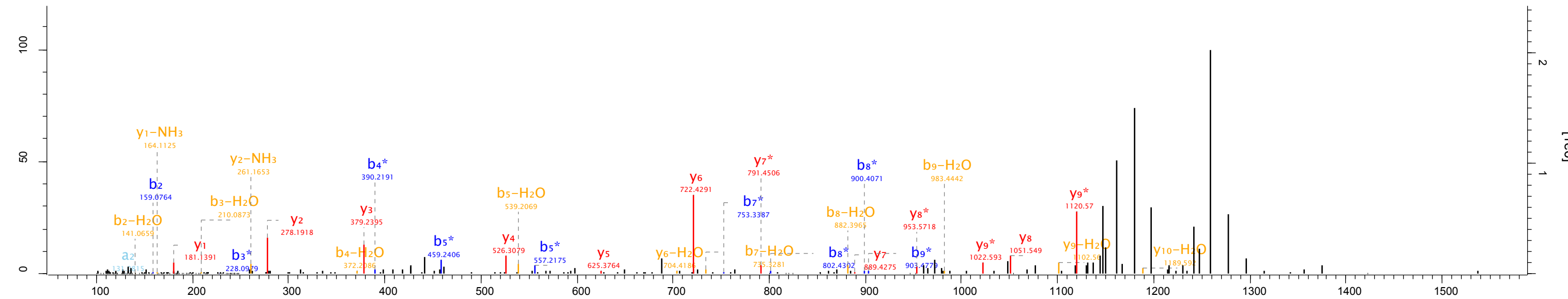
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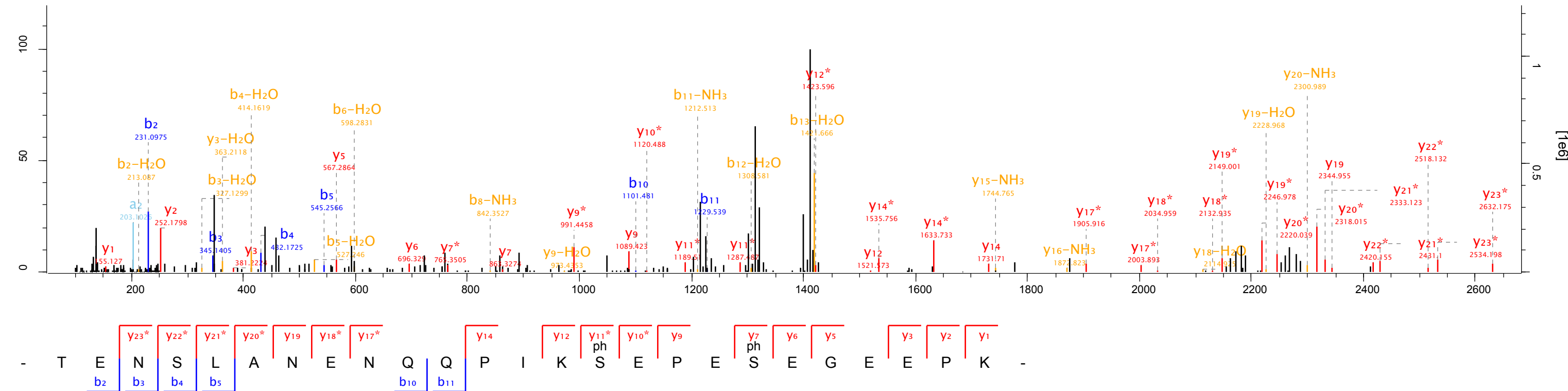


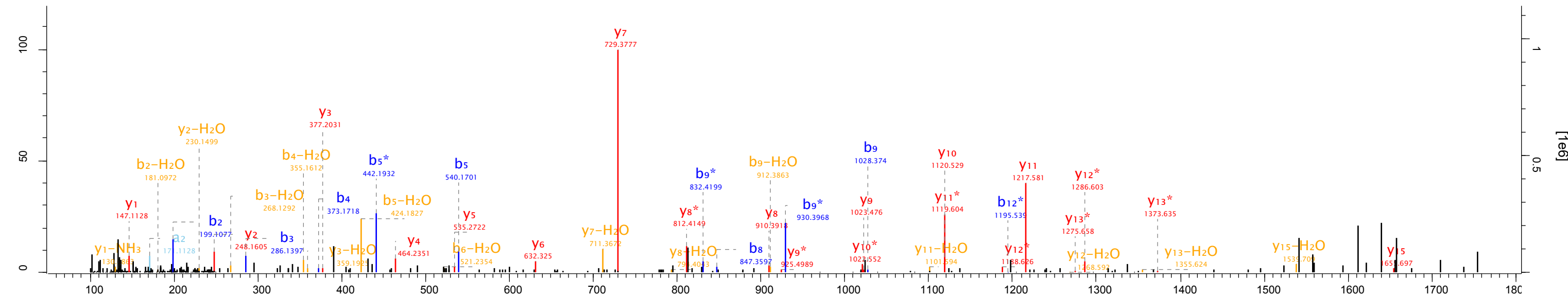
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- T P S S P P I T P P A S E T K -

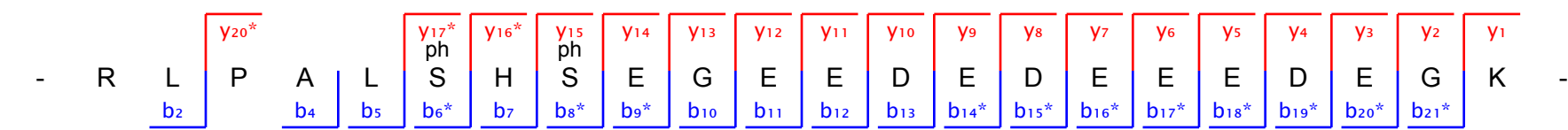
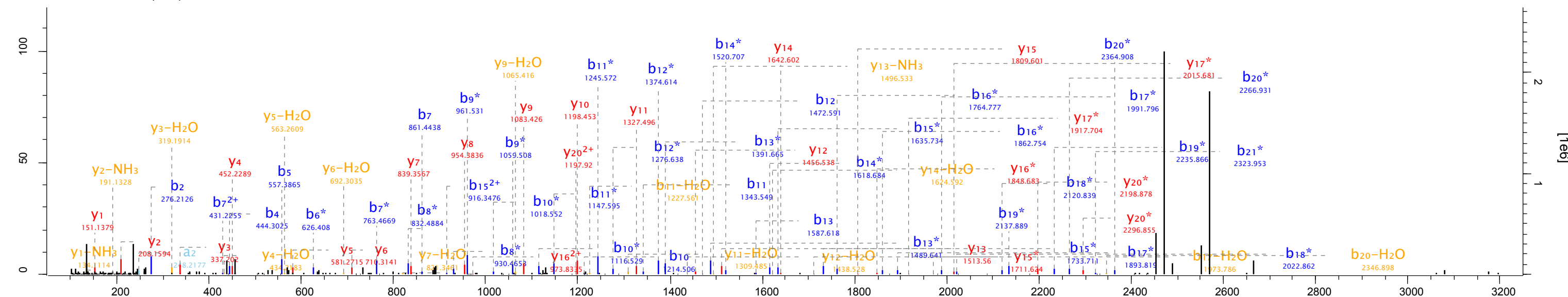
b₂ b₃ b₄ b₅ b₈ b₉ b₁₂*

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

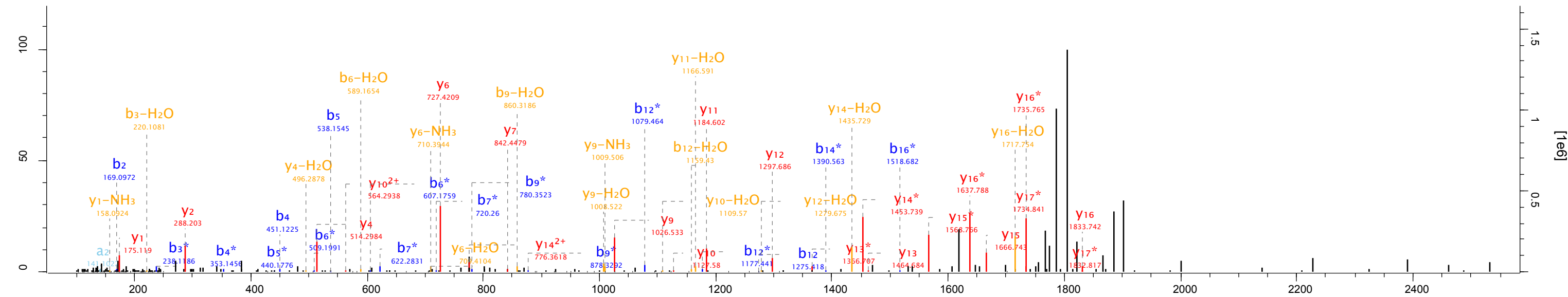
ph

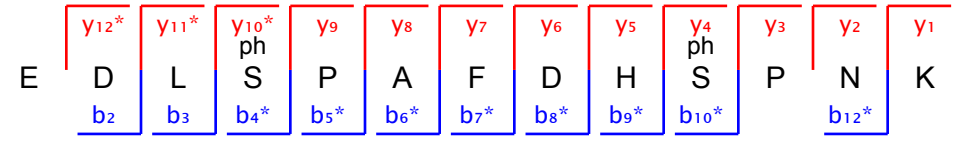
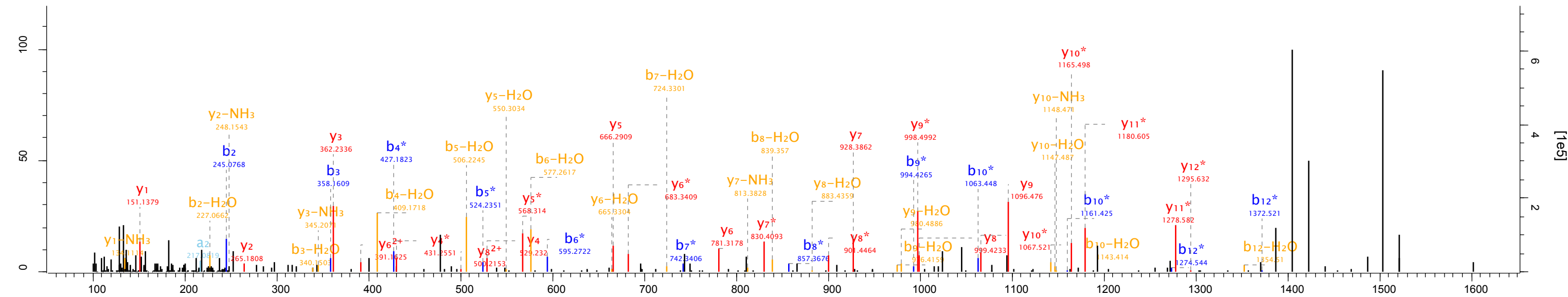
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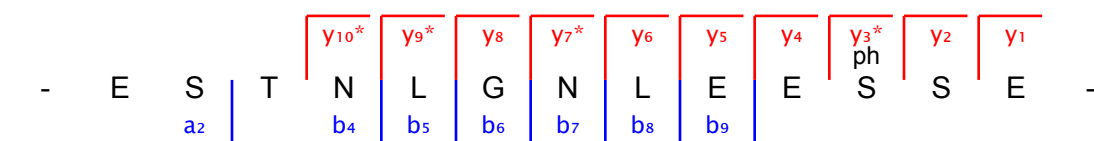
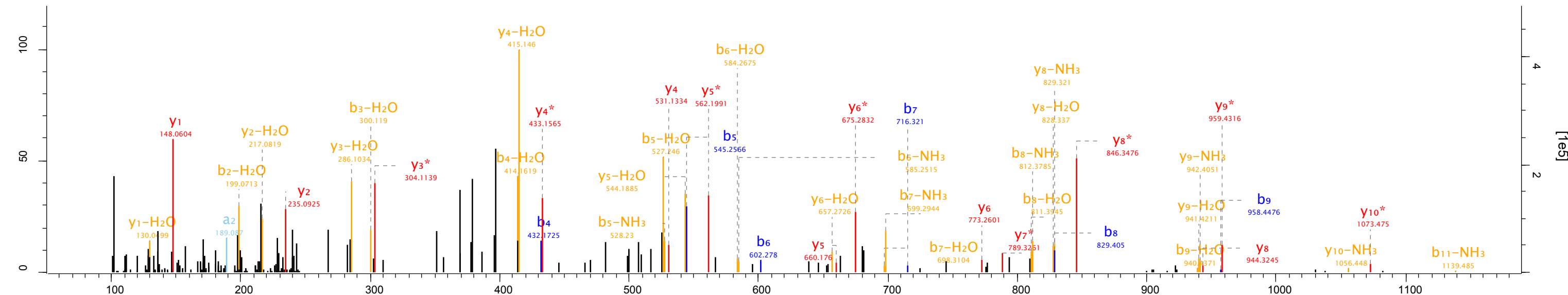
Scan 8255 Method FTMS; HCD Score 291.68 m/z 890.68 Gene names BRPF1



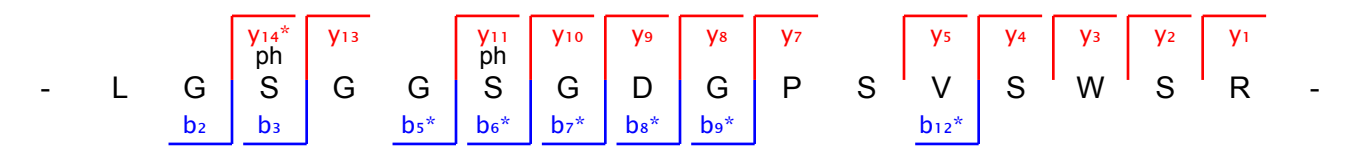
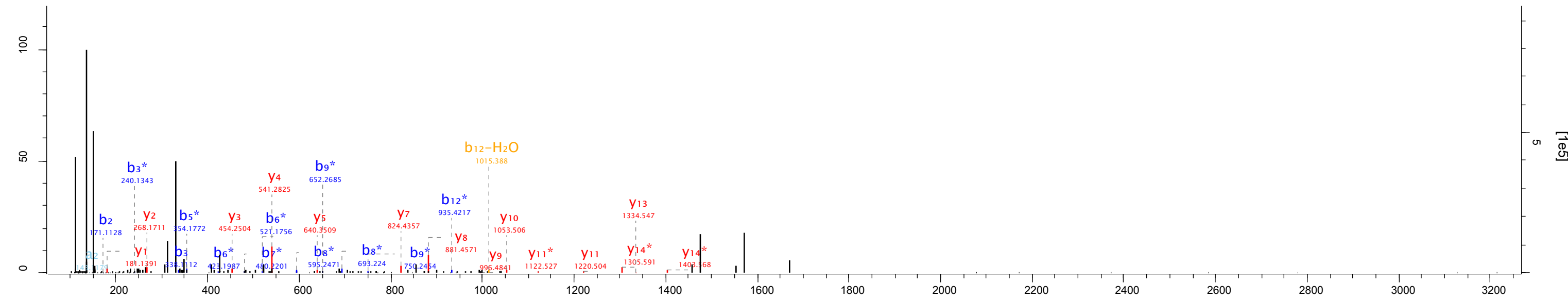
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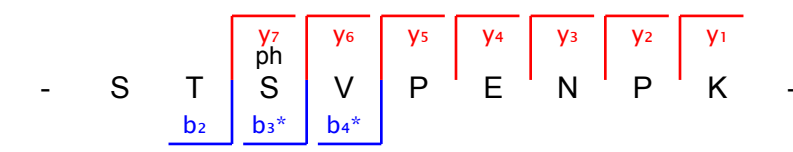
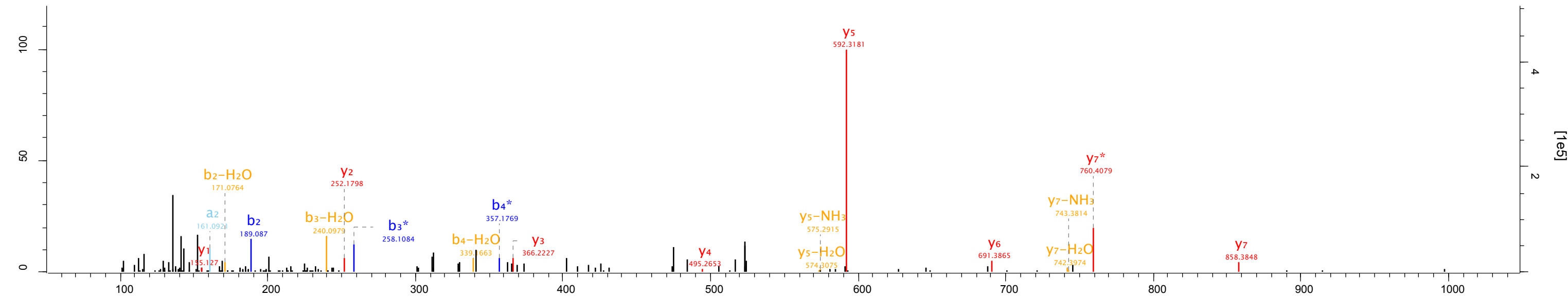




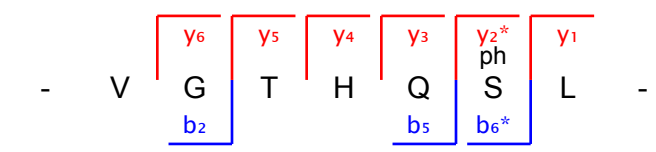
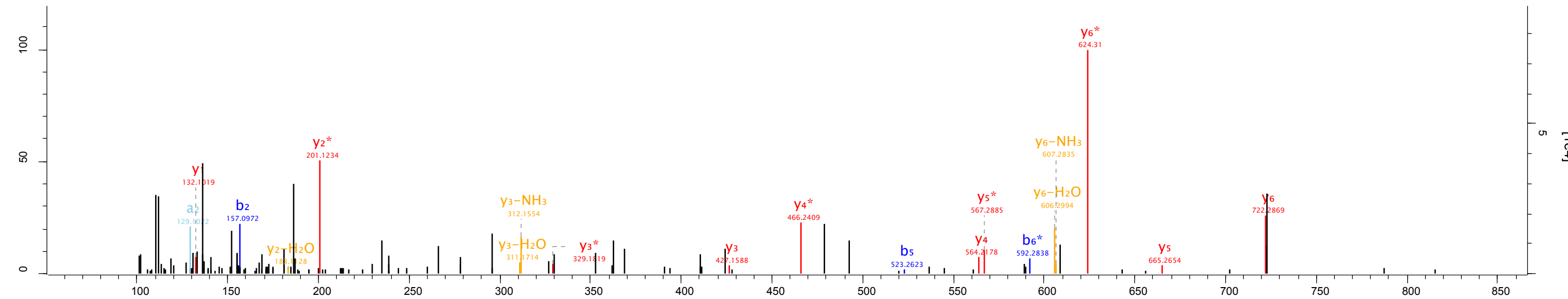
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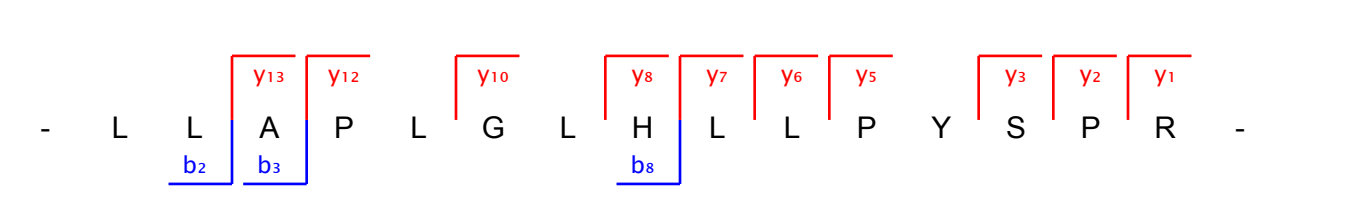
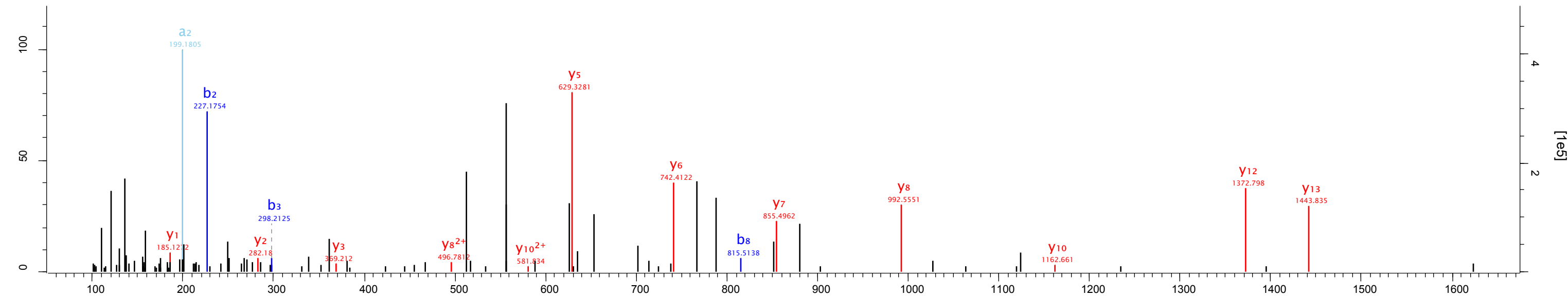


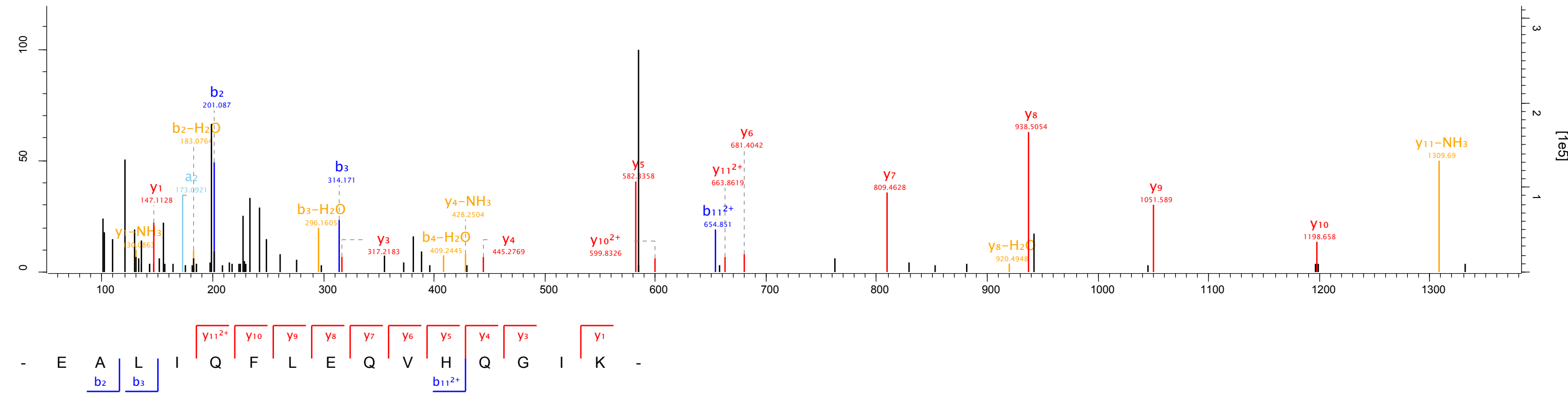
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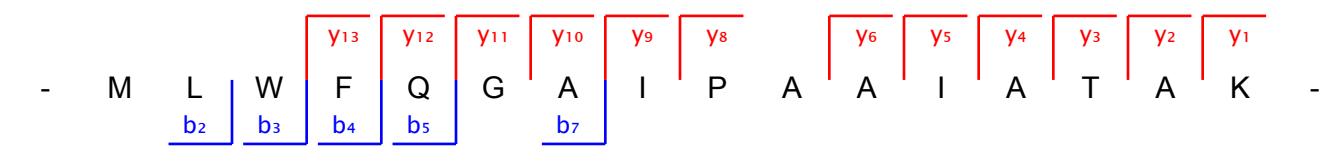
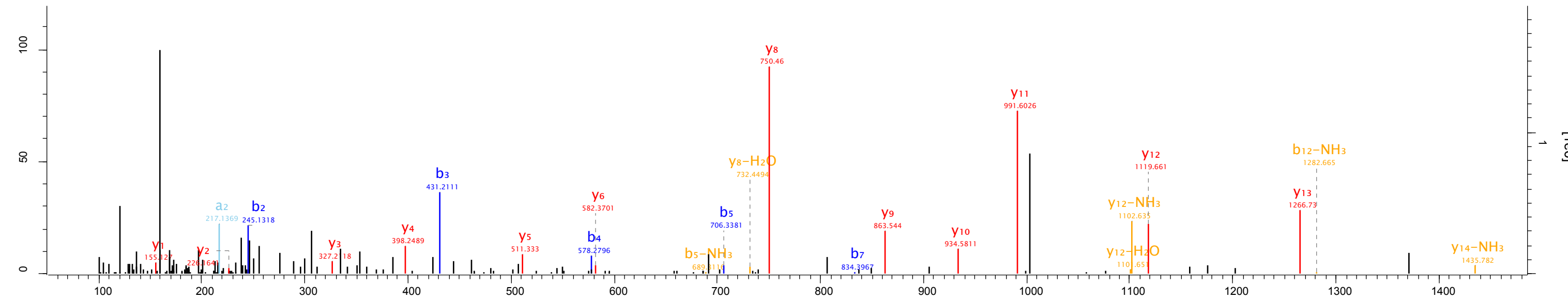
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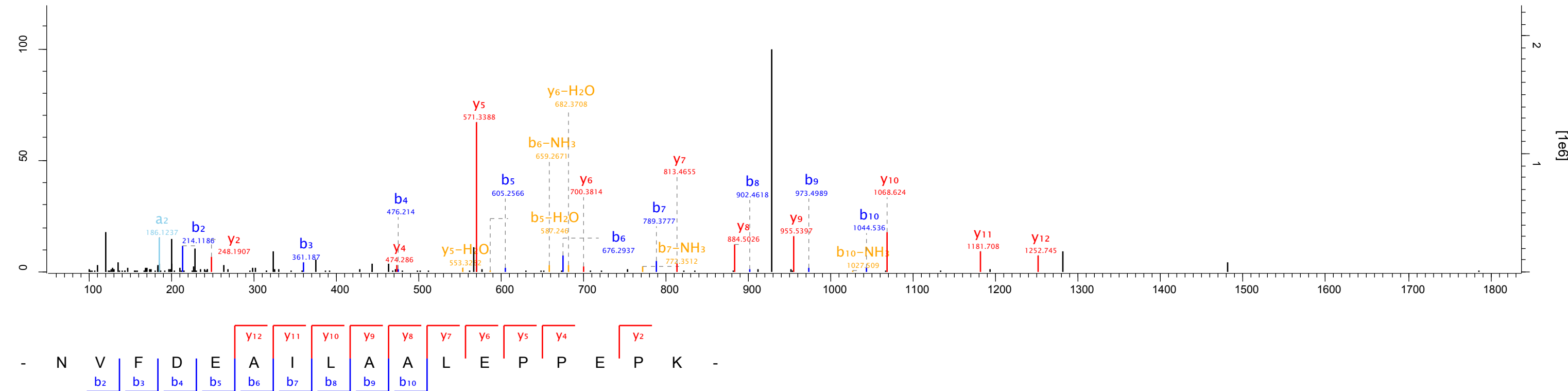
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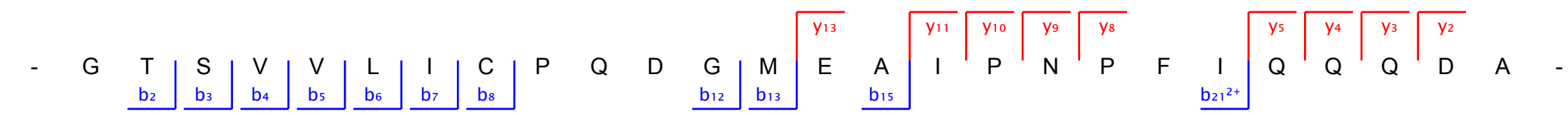
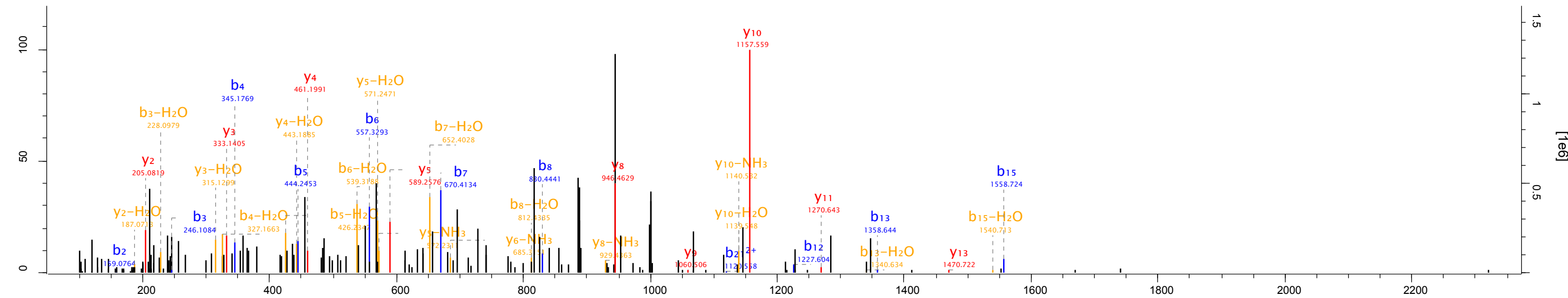


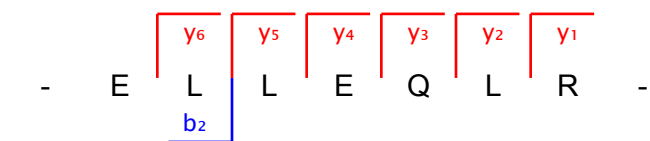
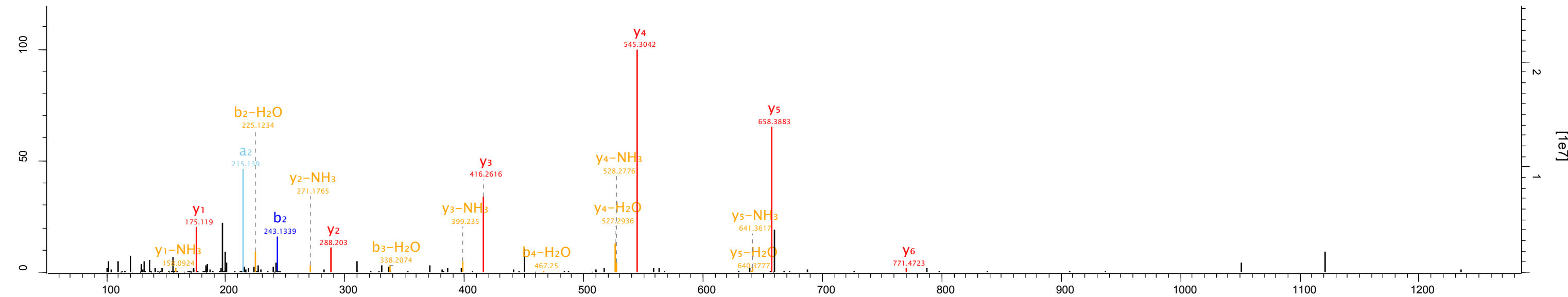
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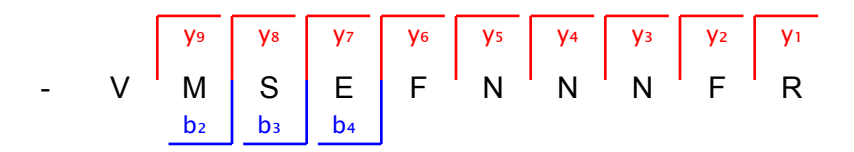
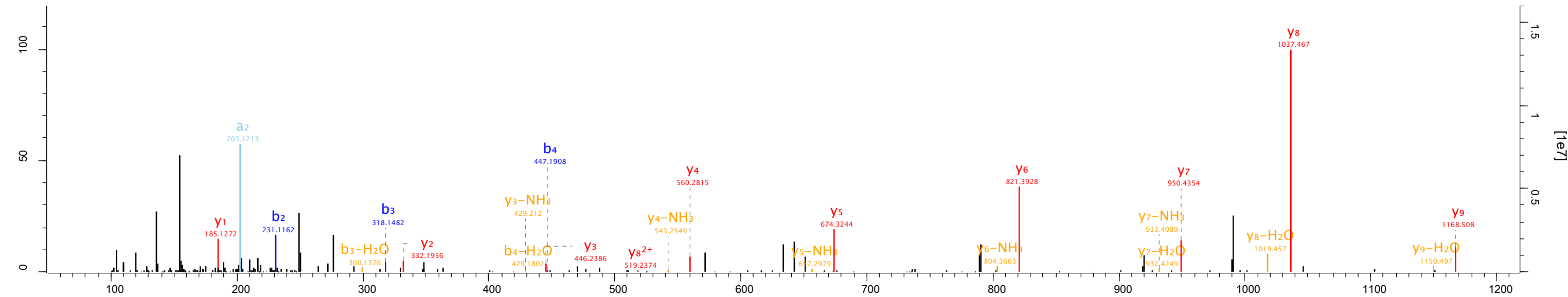


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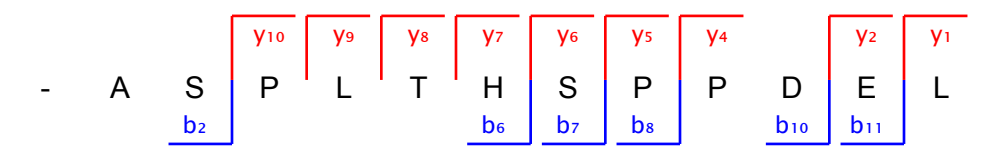
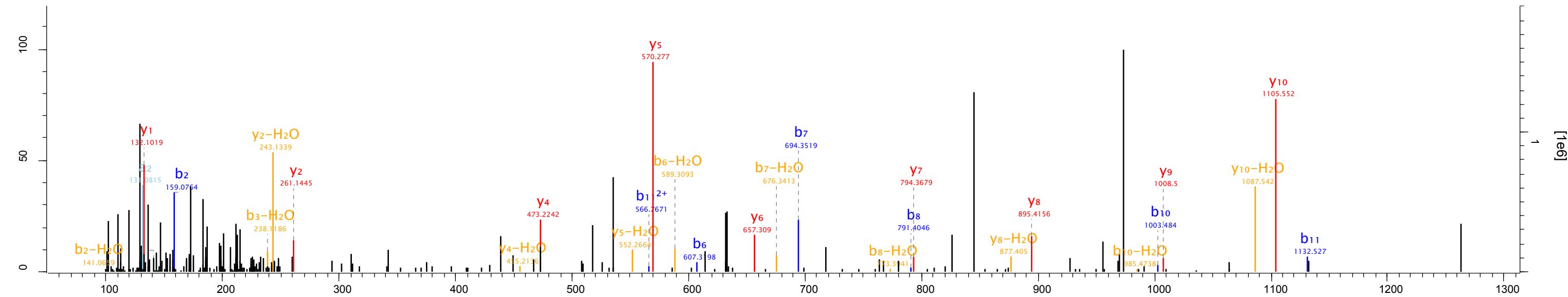




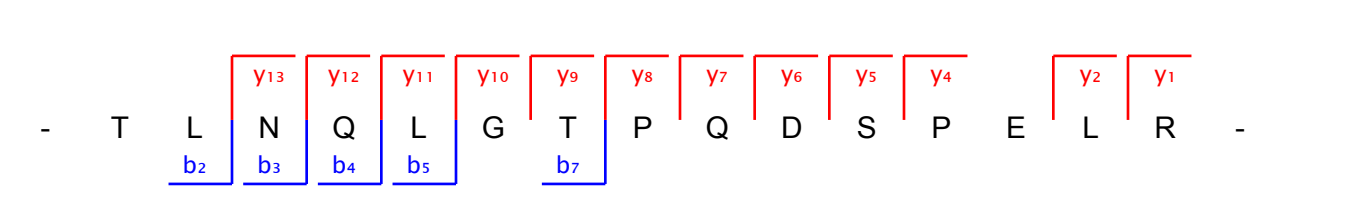
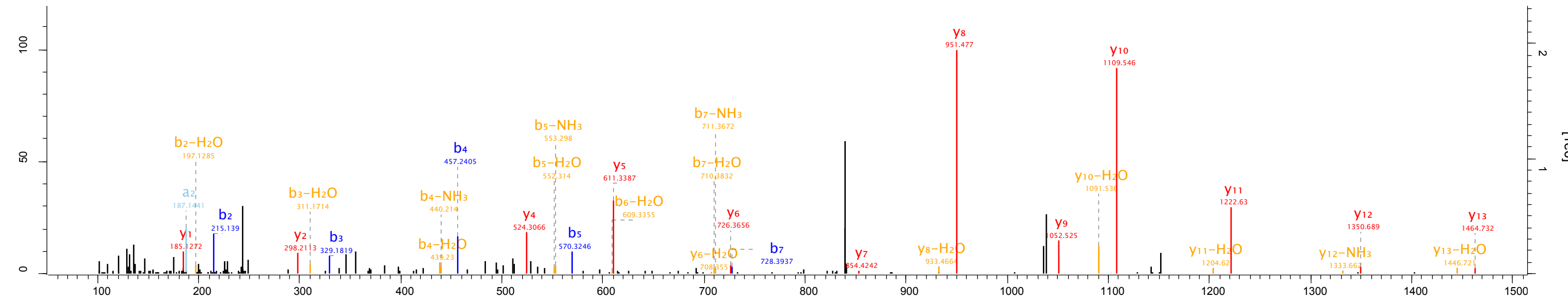
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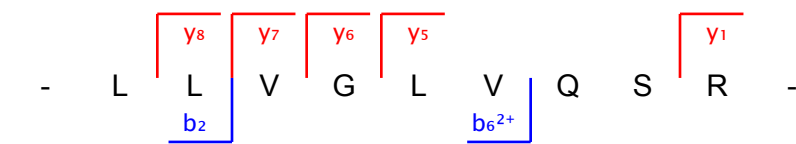
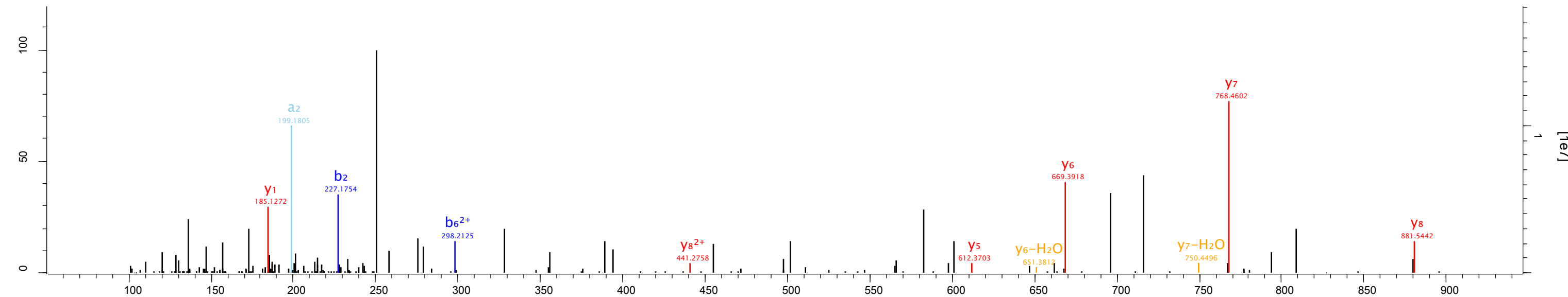
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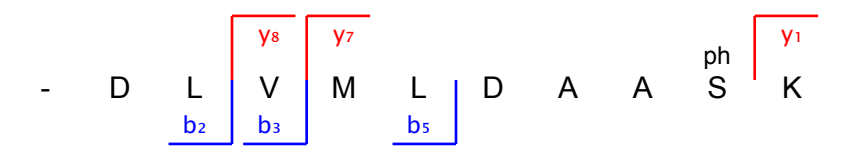
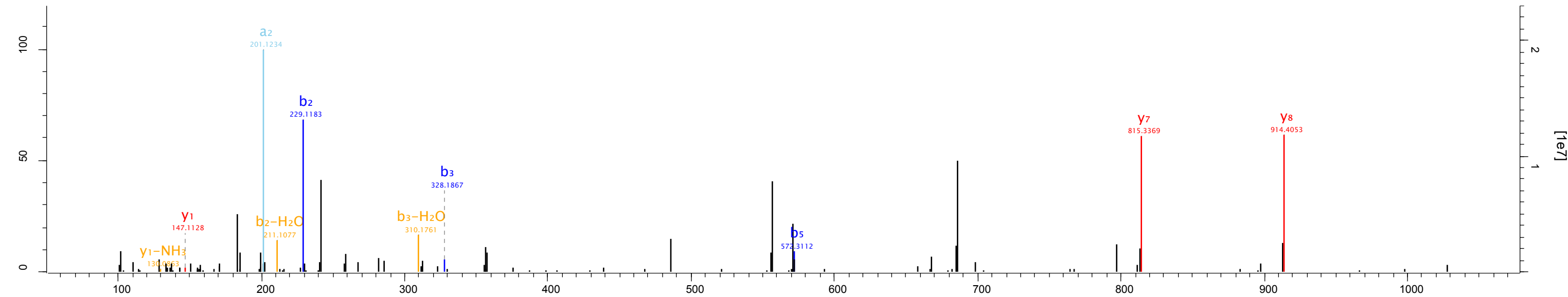
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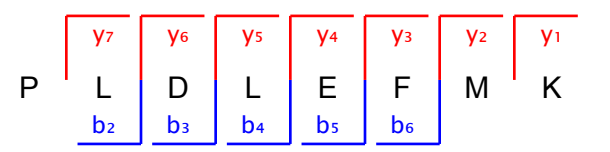
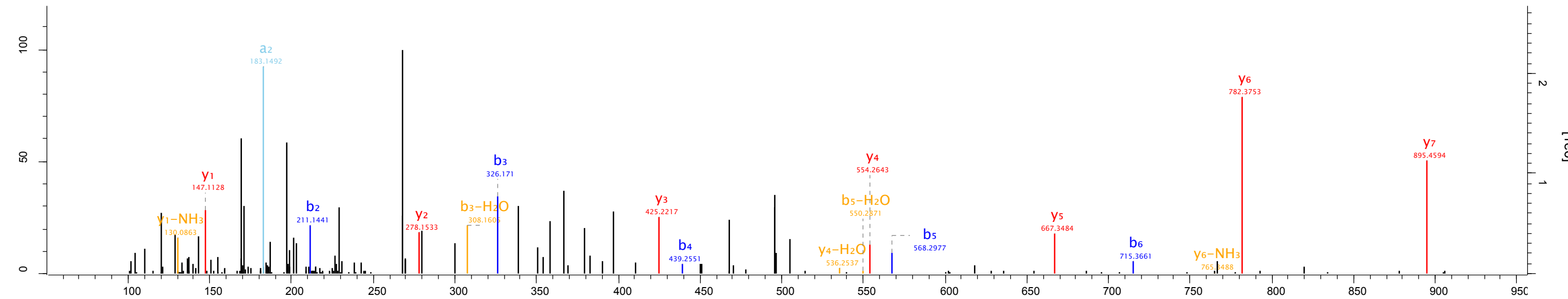
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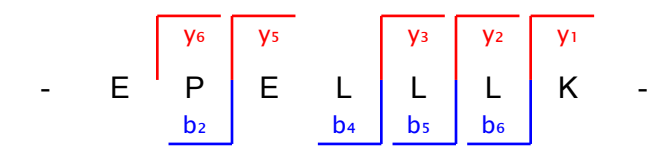
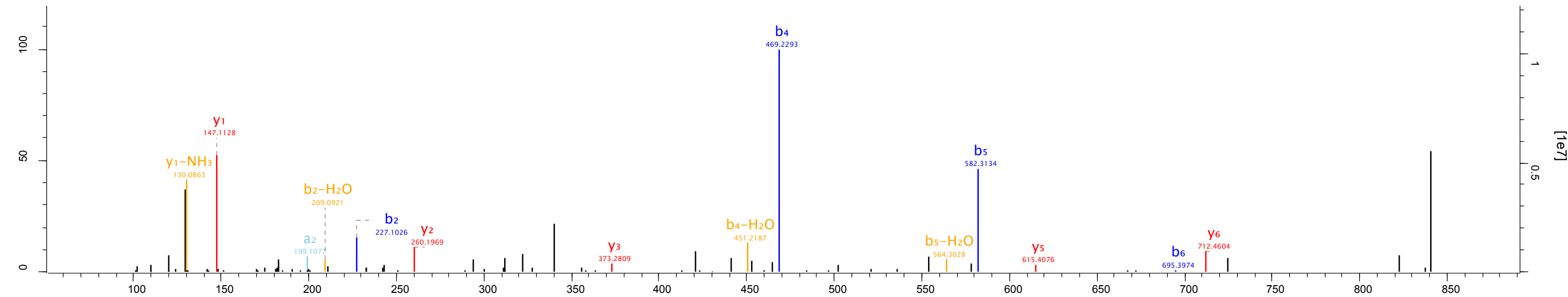
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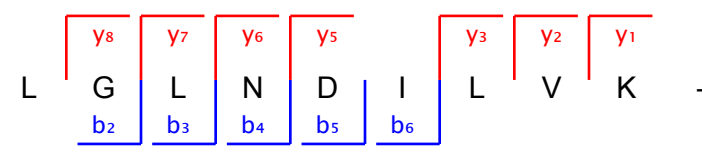
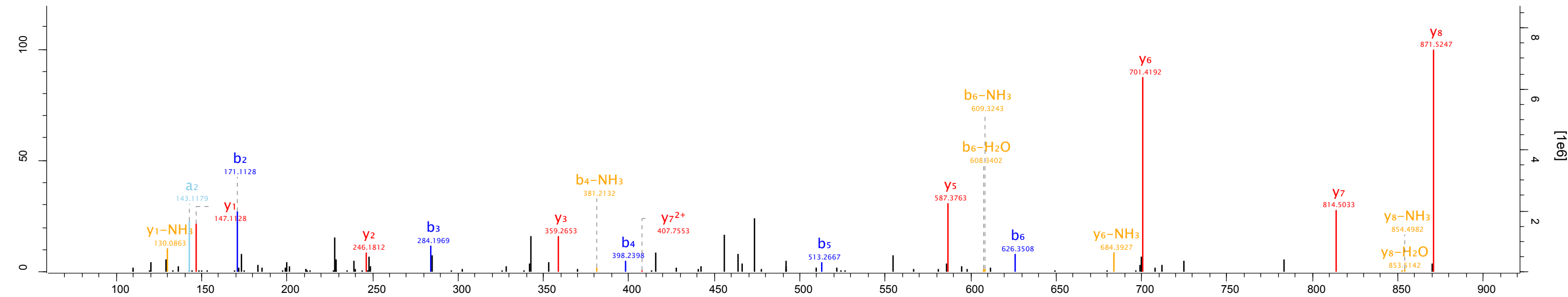
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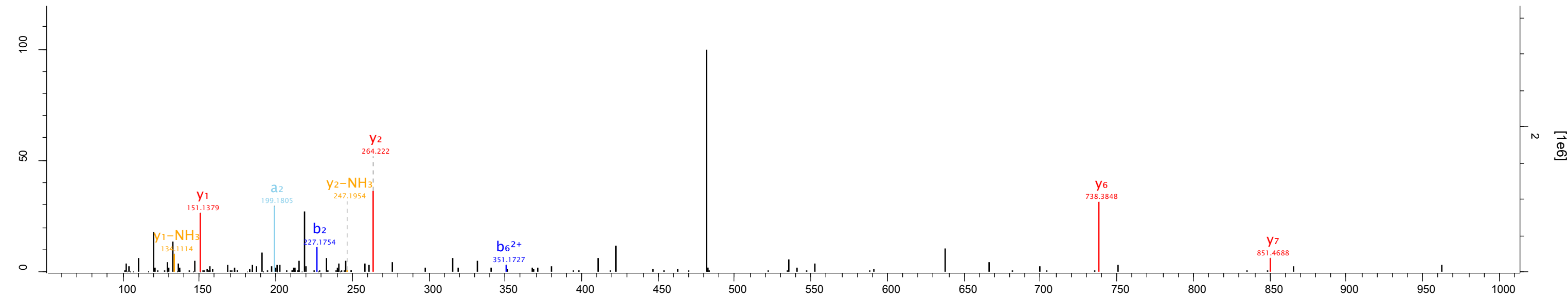
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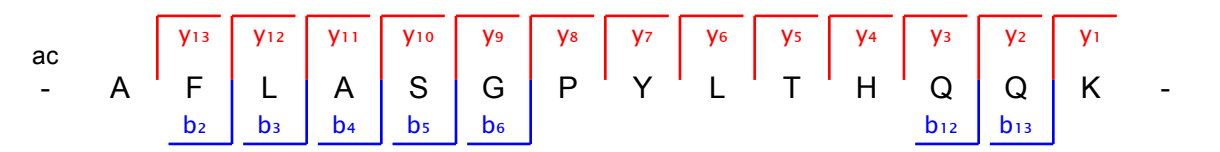
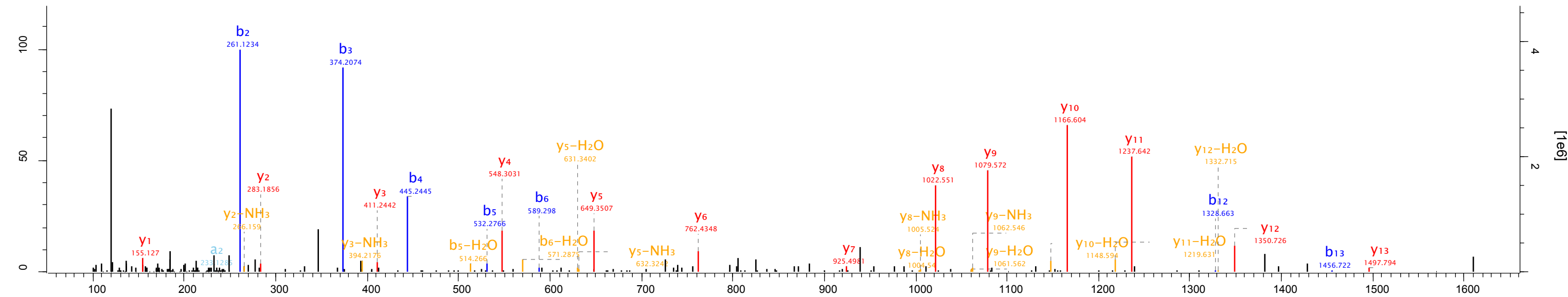
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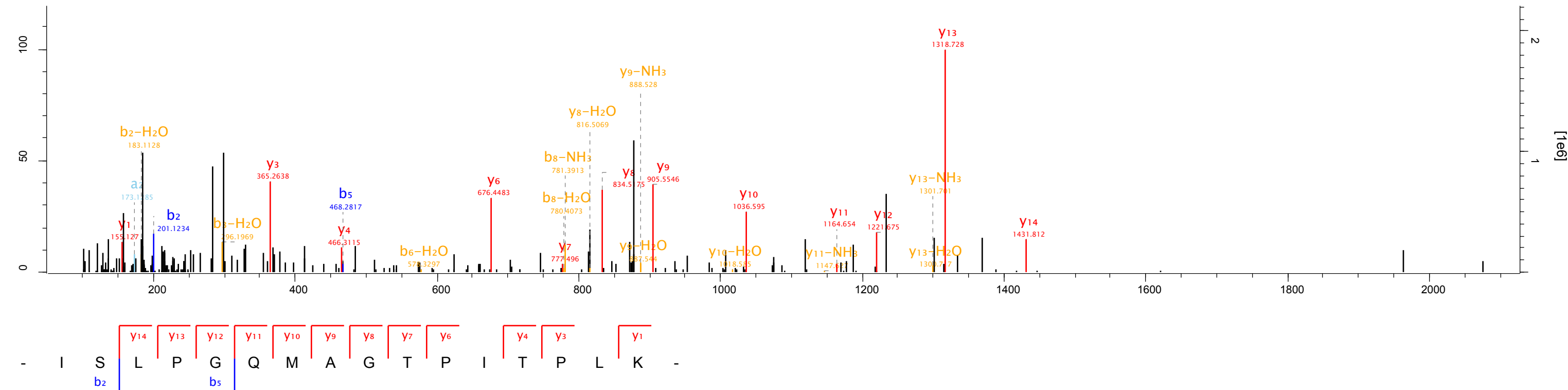
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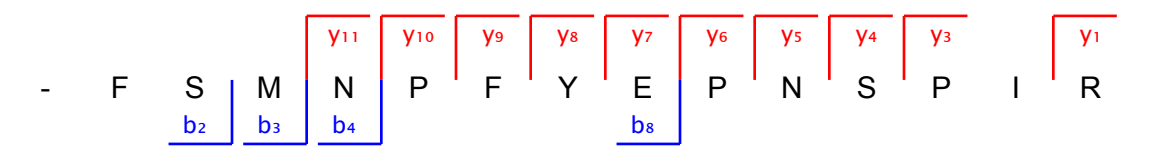
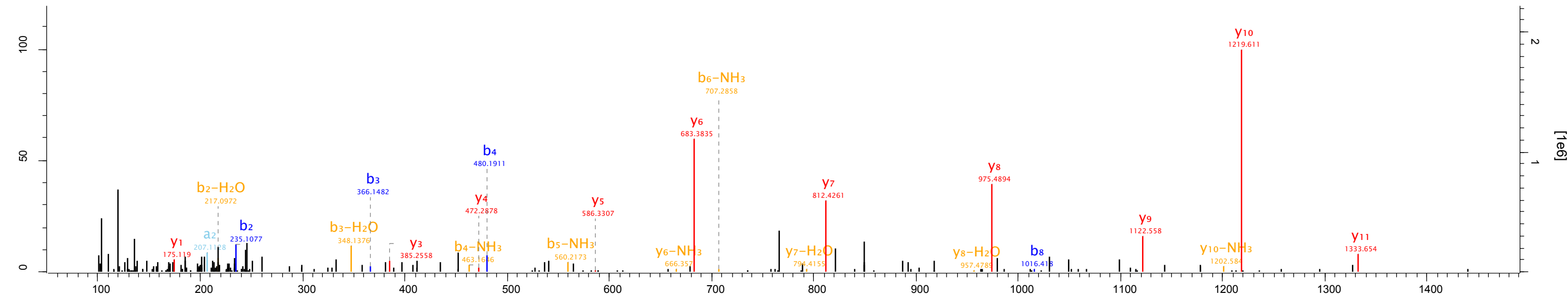
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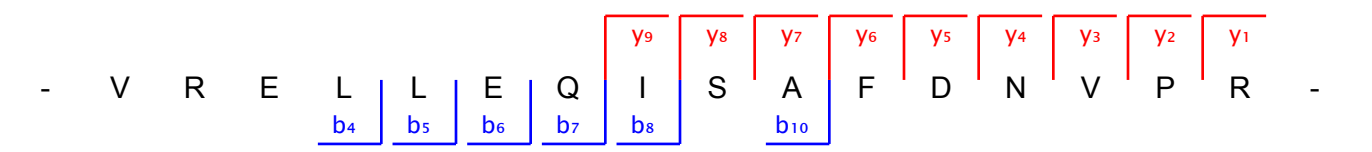
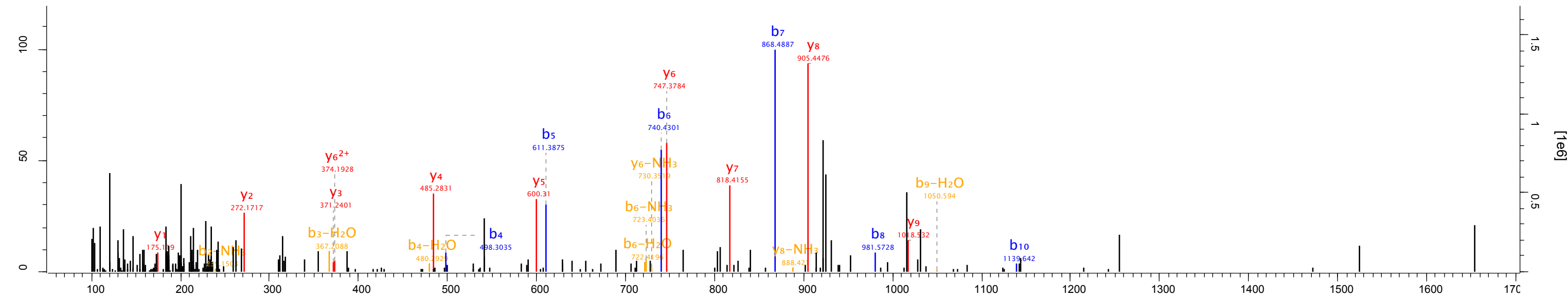
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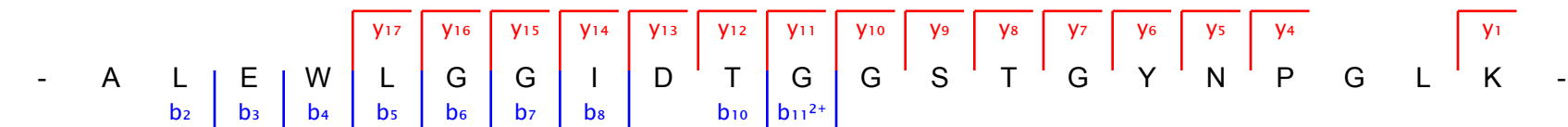
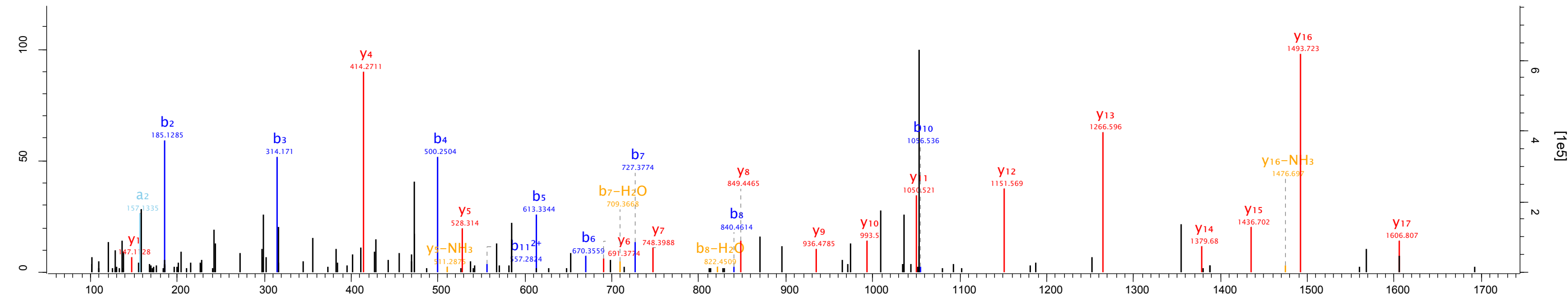


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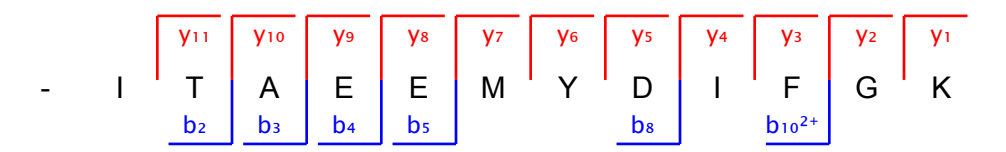
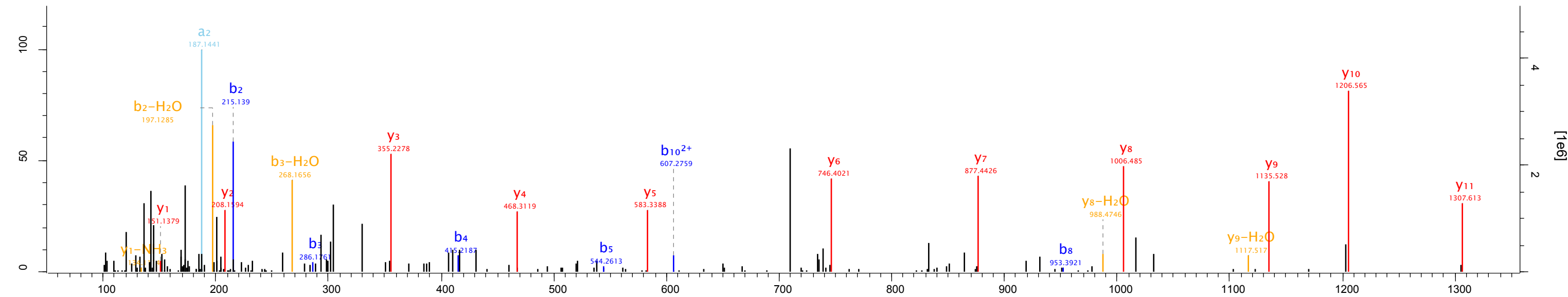


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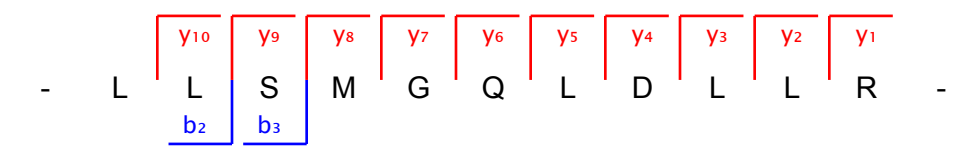
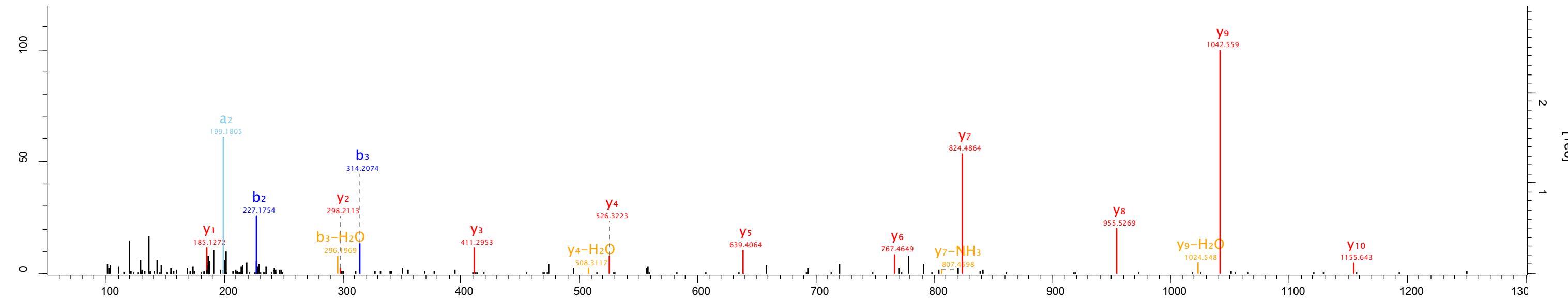




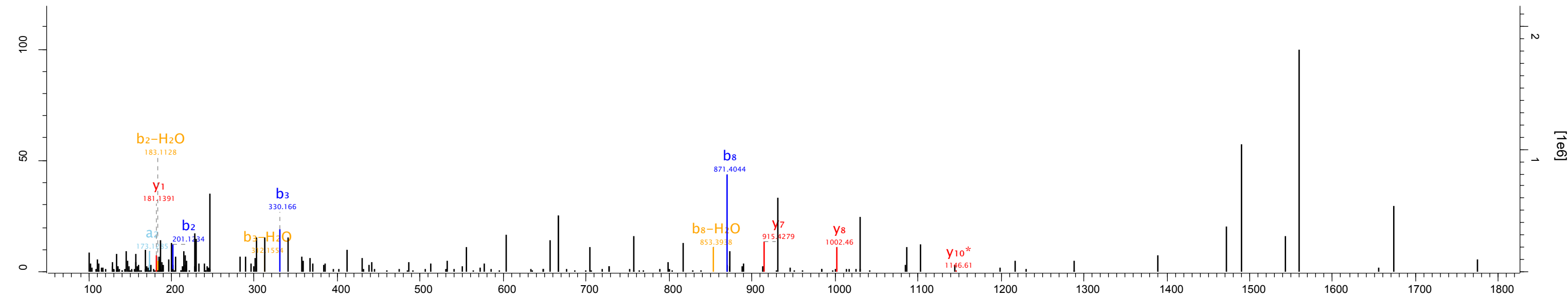
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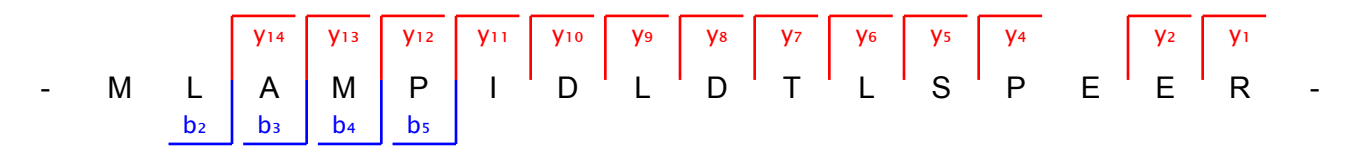
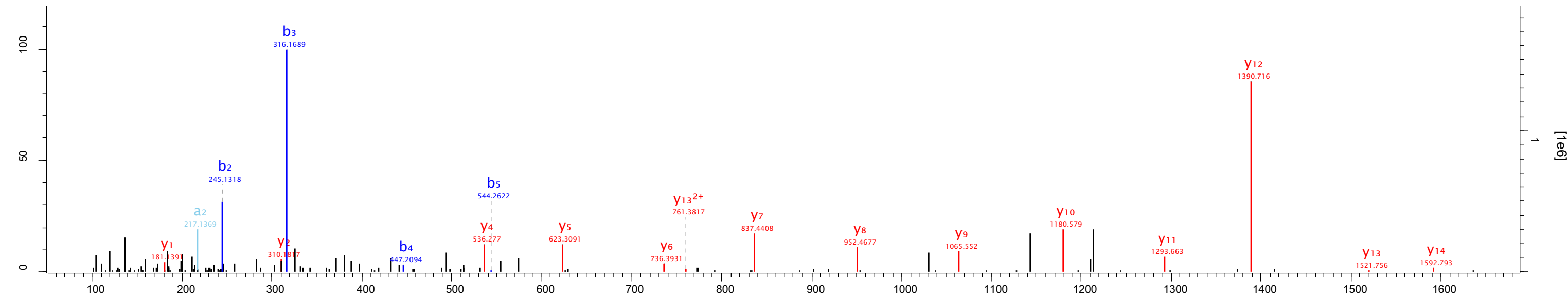
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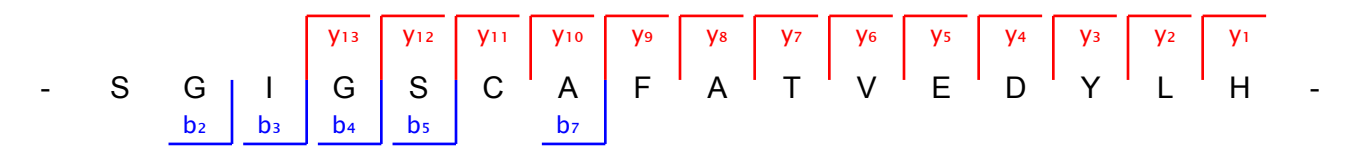
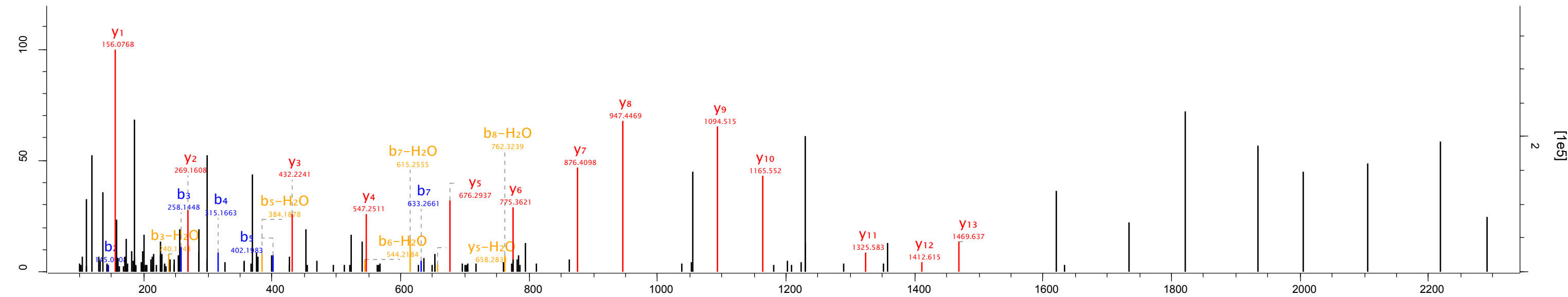
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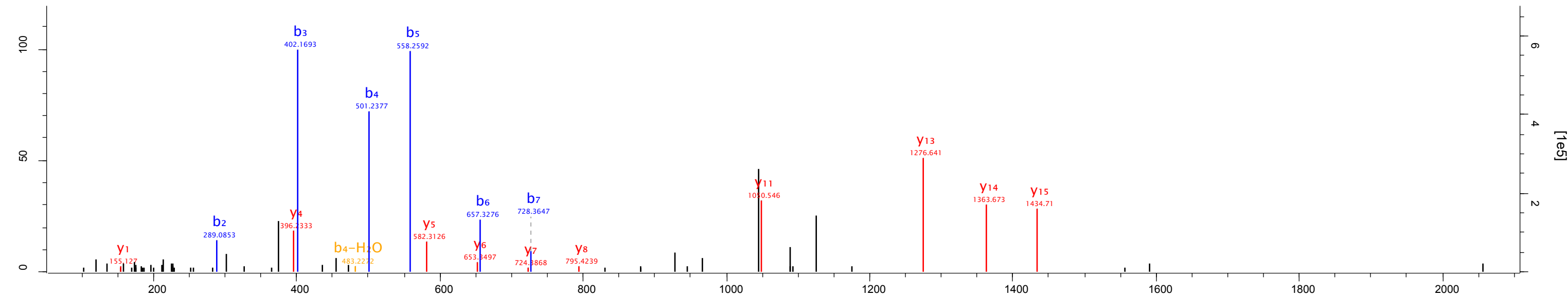
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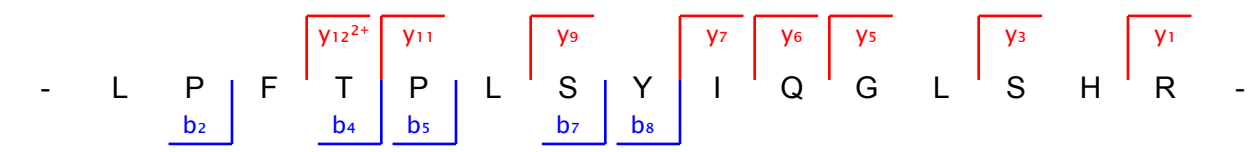
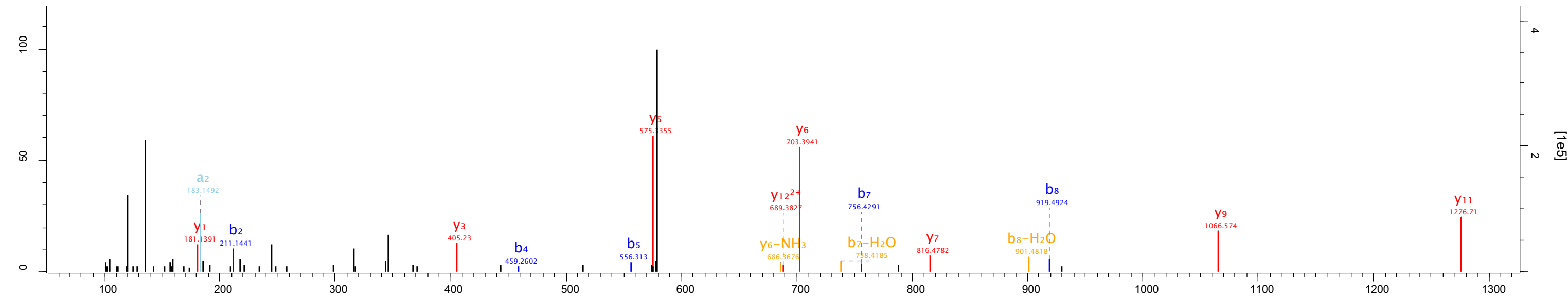
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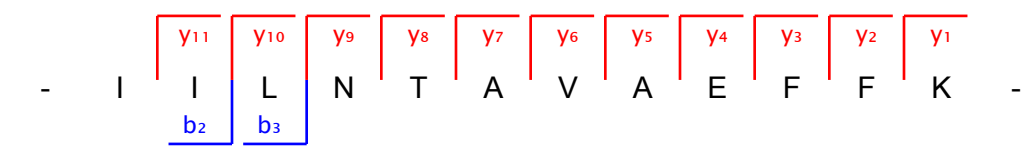
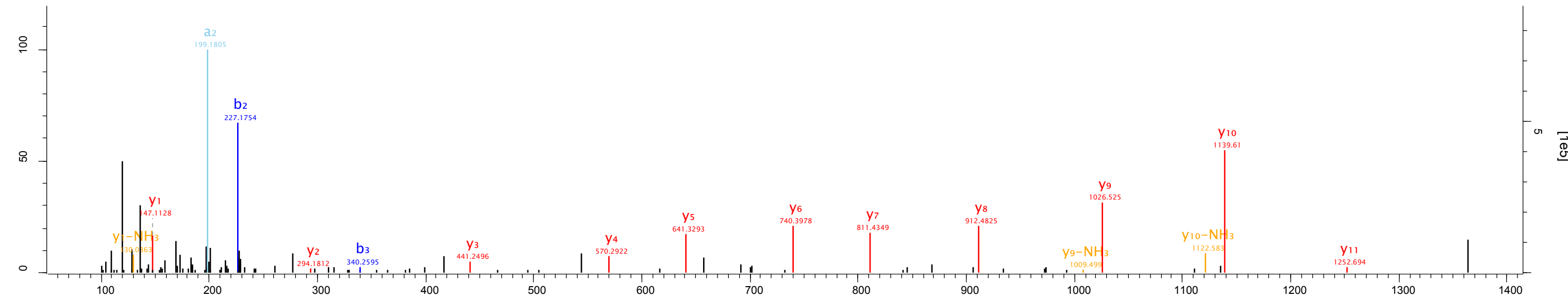
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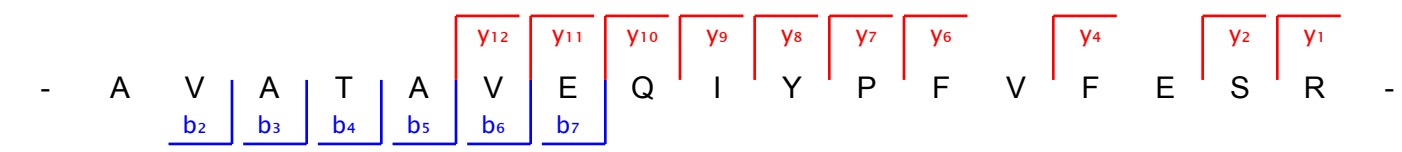
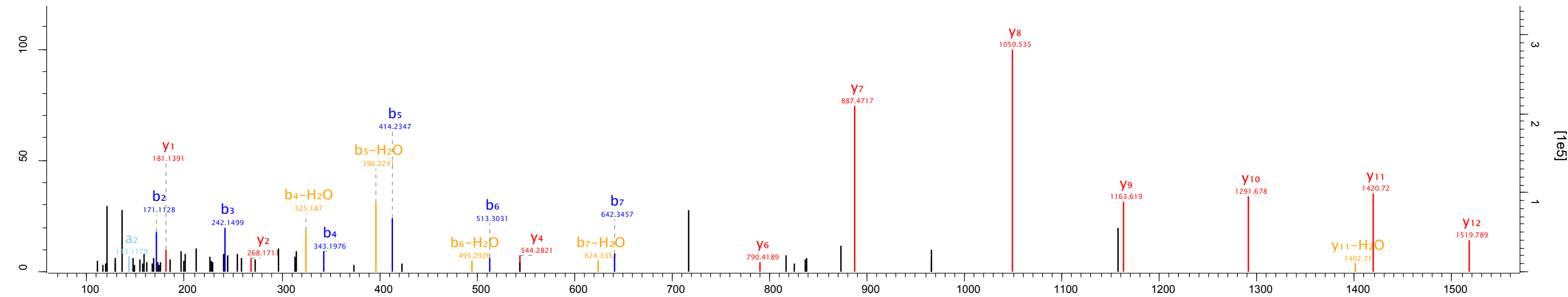
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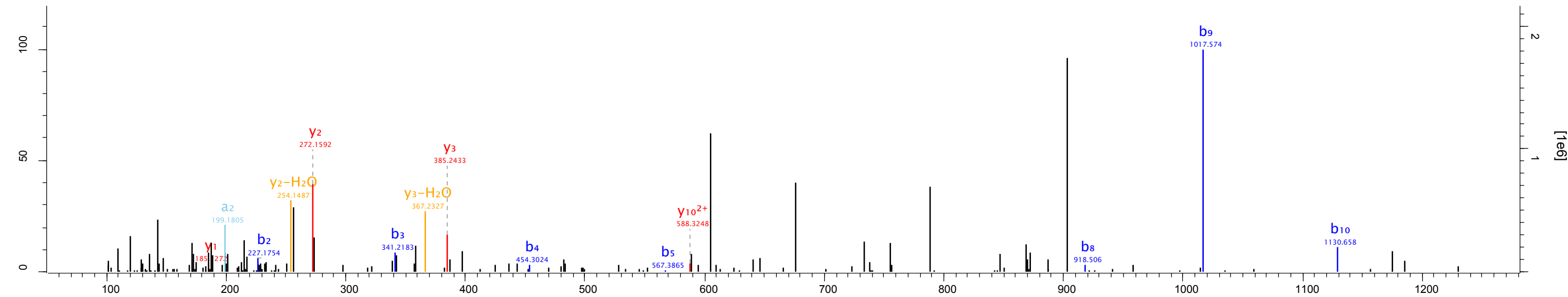
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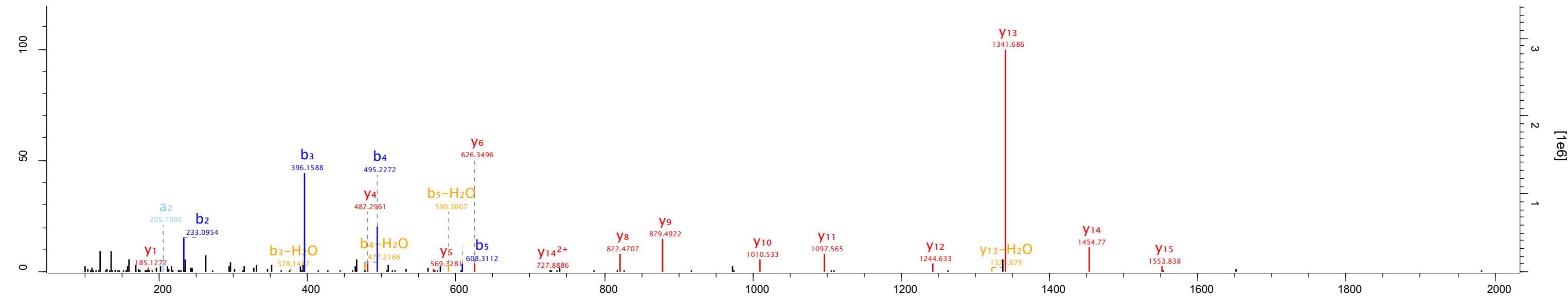
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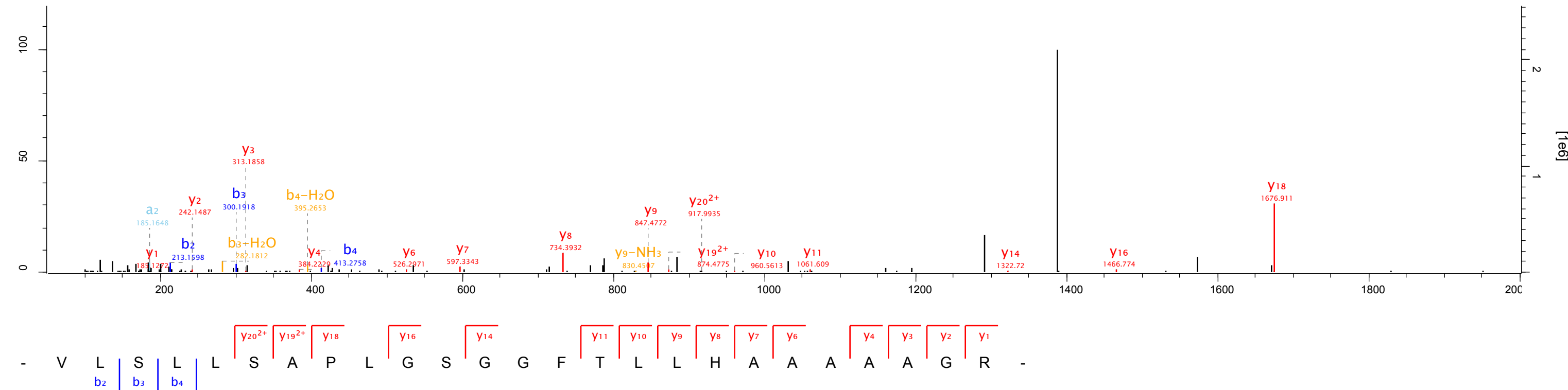
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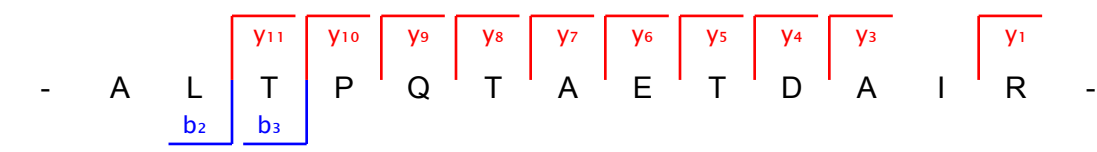
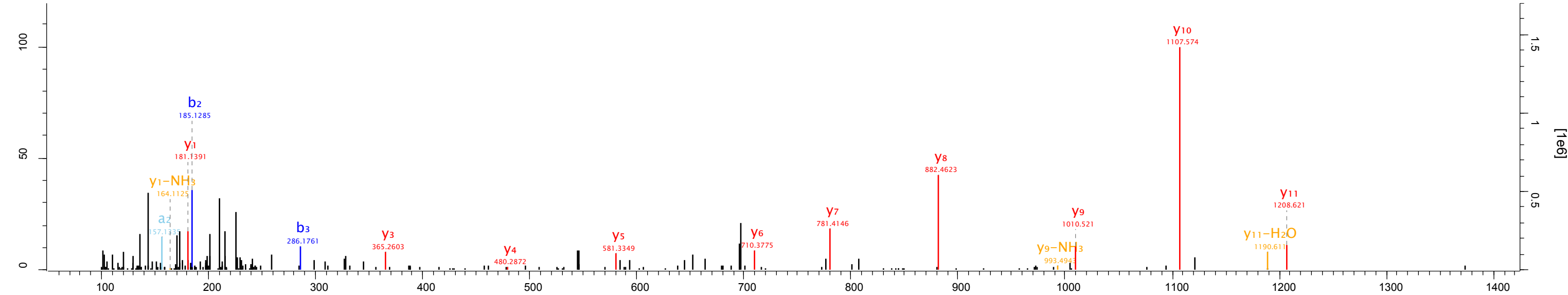
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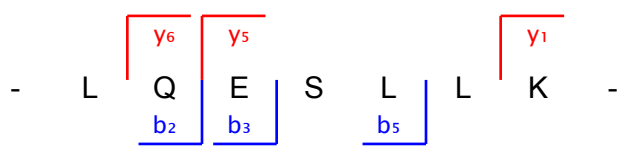
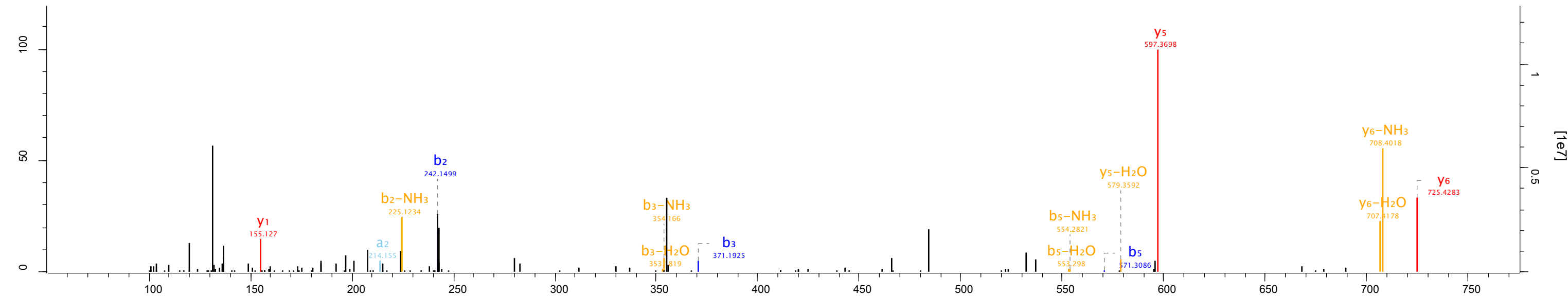
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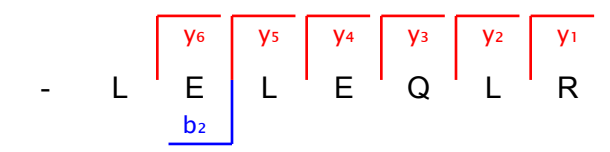
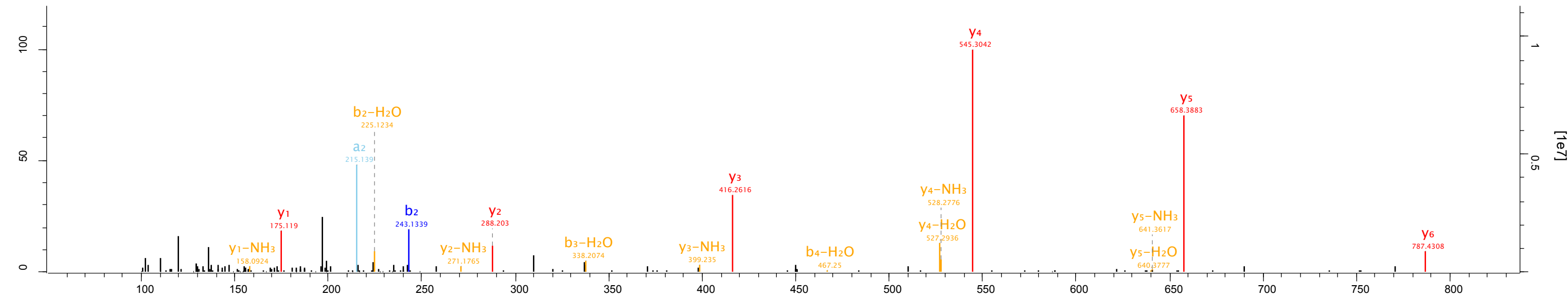
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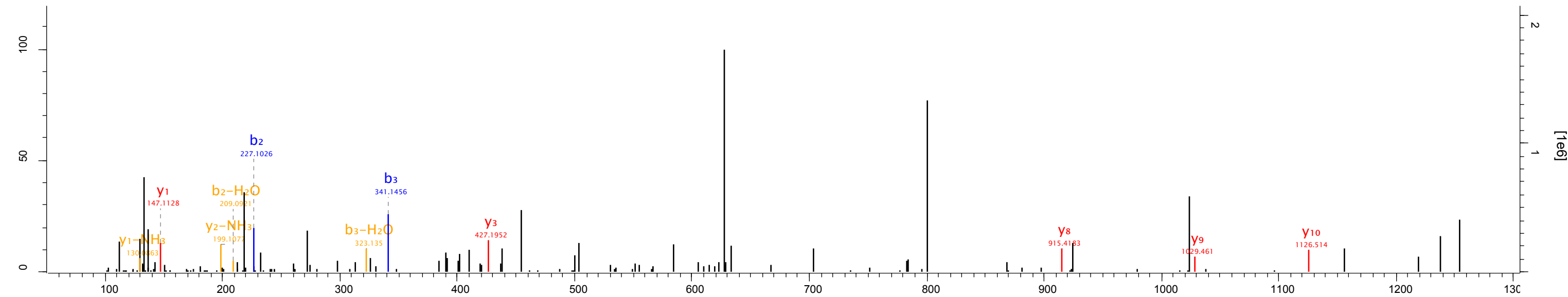
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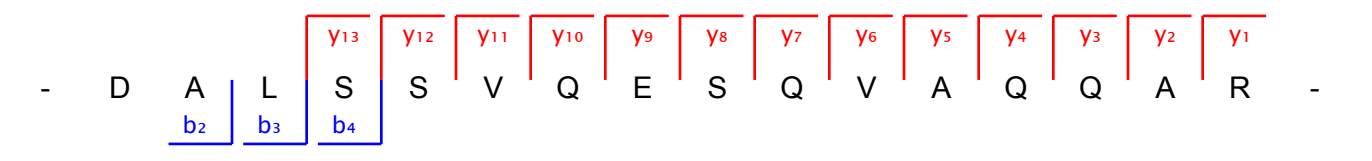
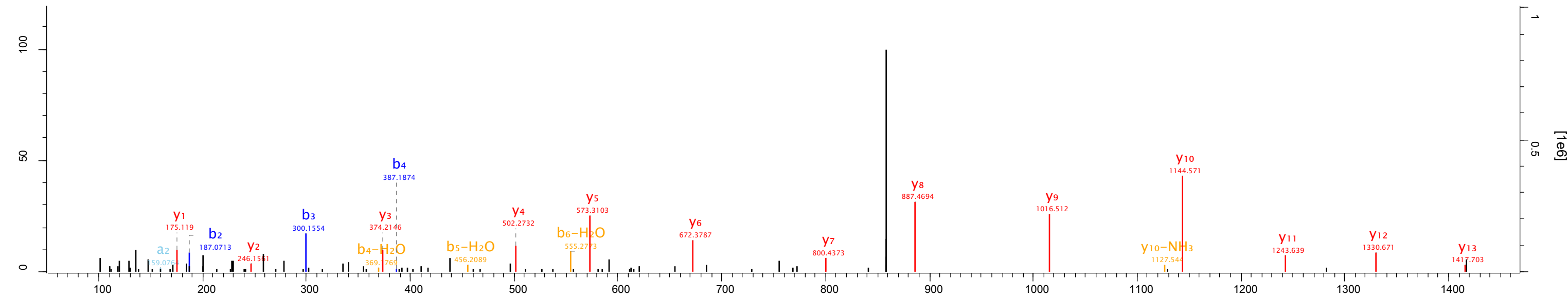
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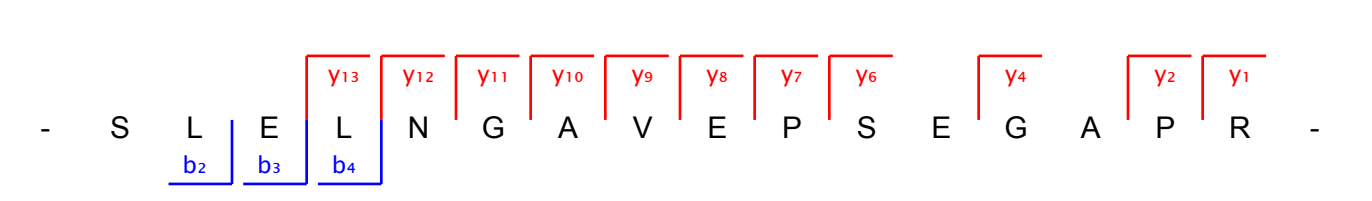
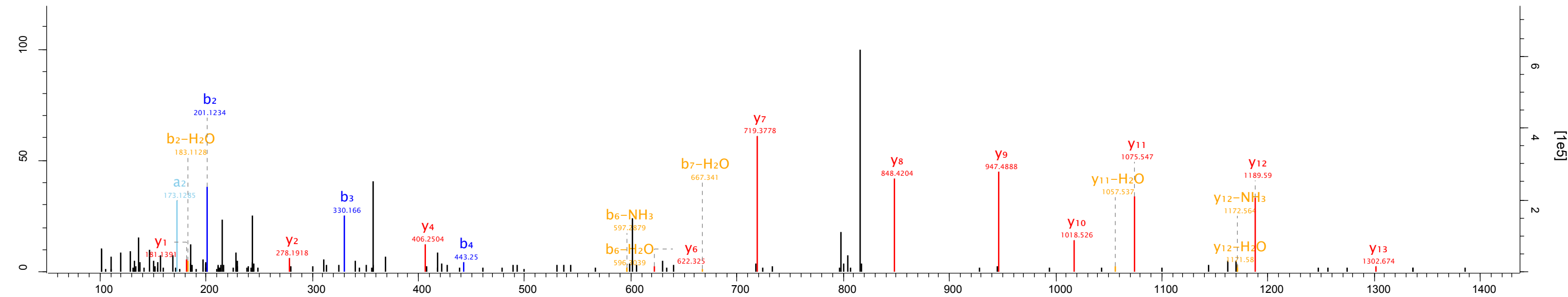
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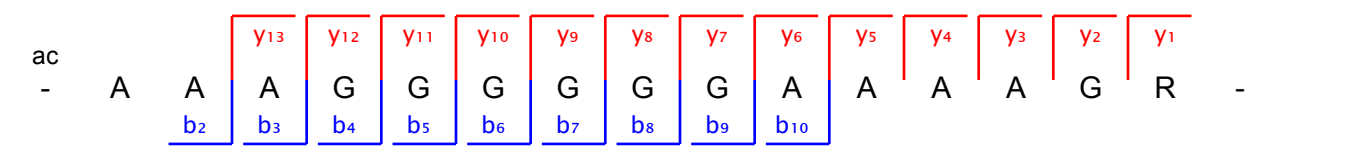
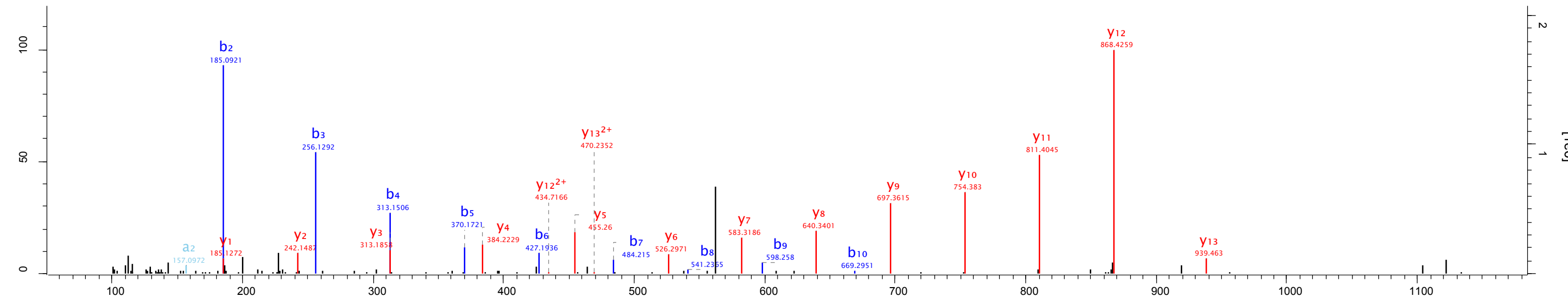
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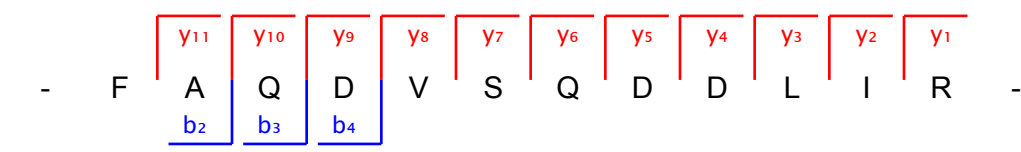
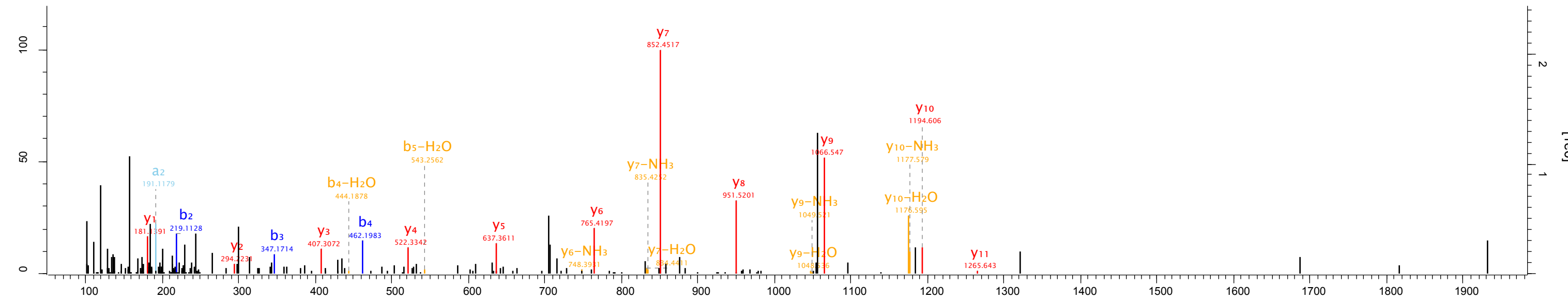
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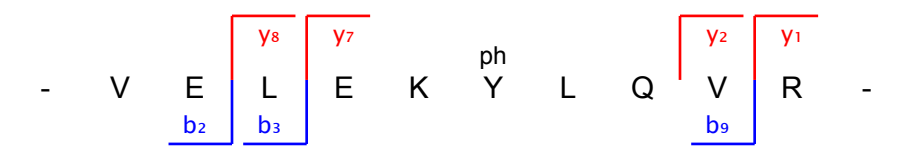
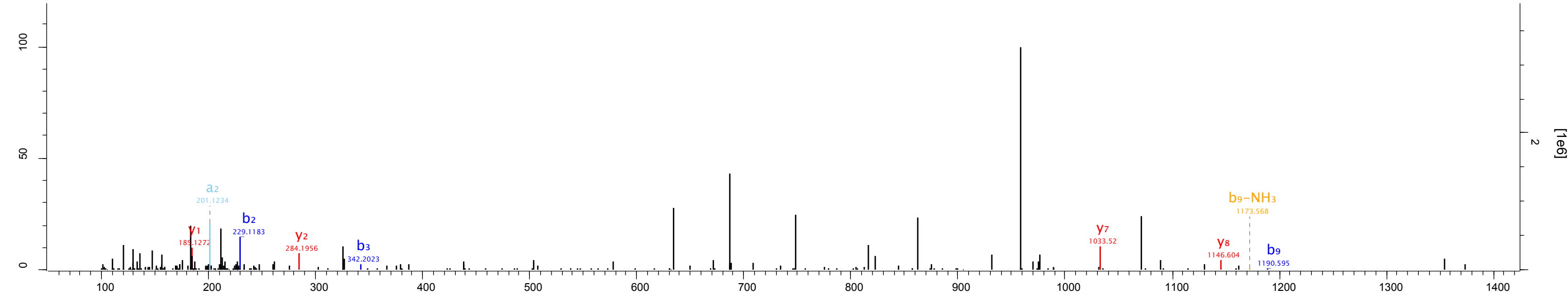
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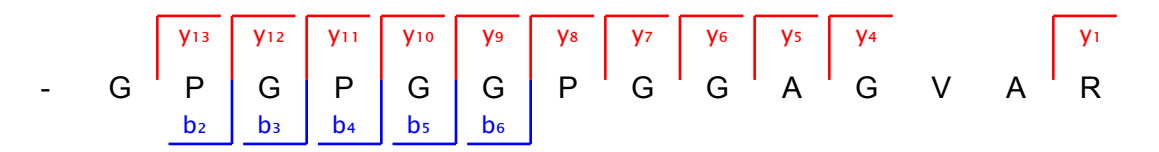
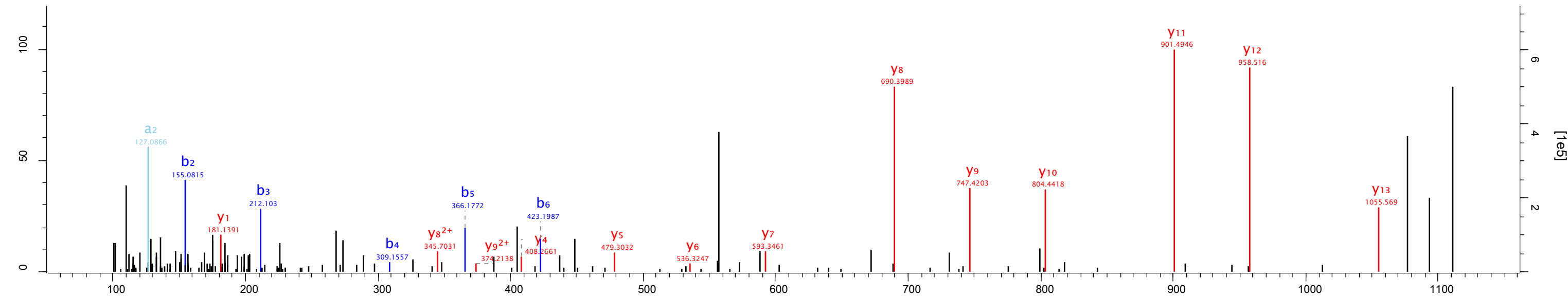
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20171215_MaS_33SR_LMH_proteome_02

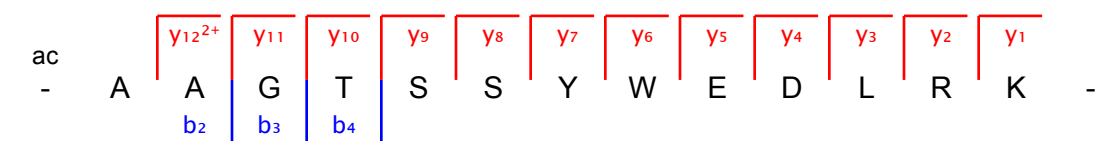
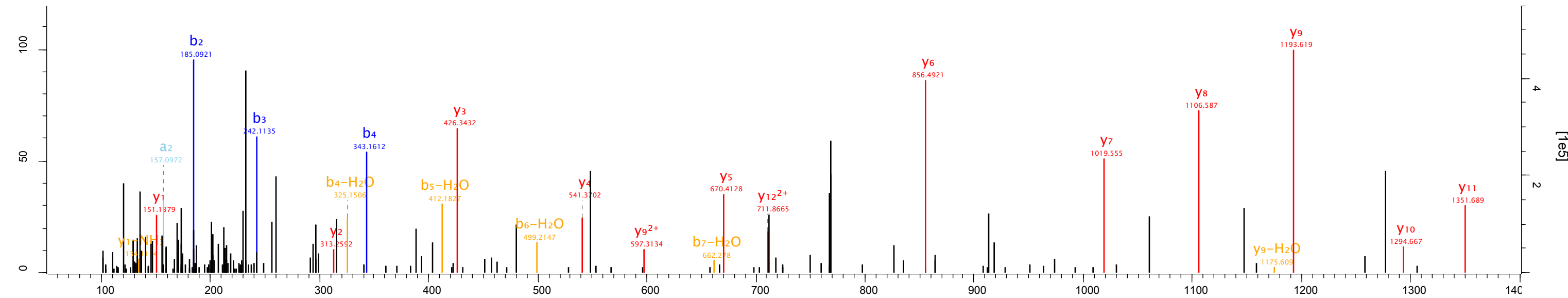
Scan	Method	Score	m/z	Gene names
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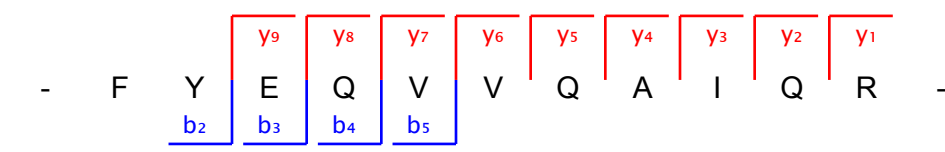
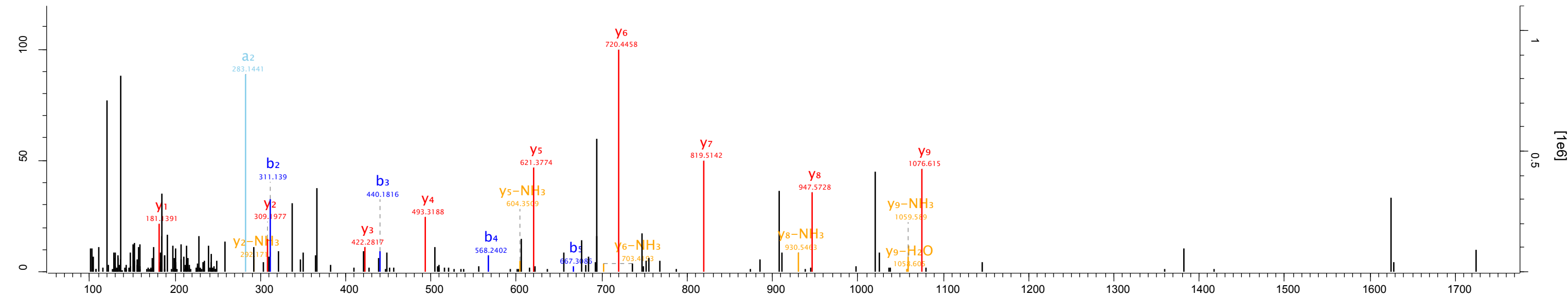
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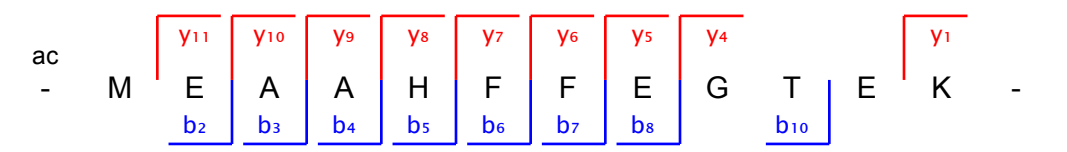
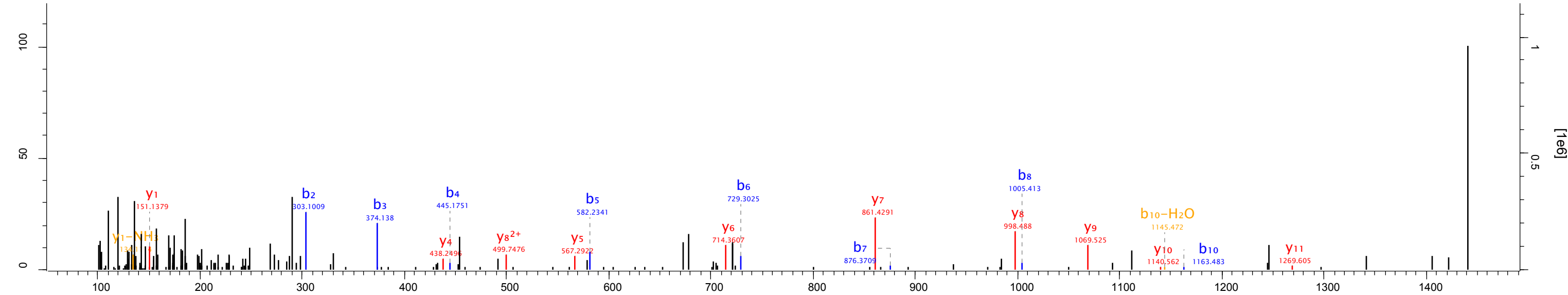


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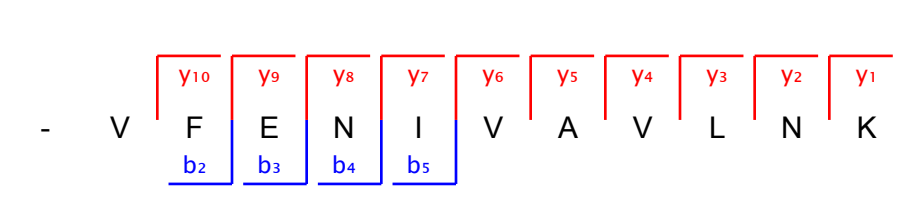
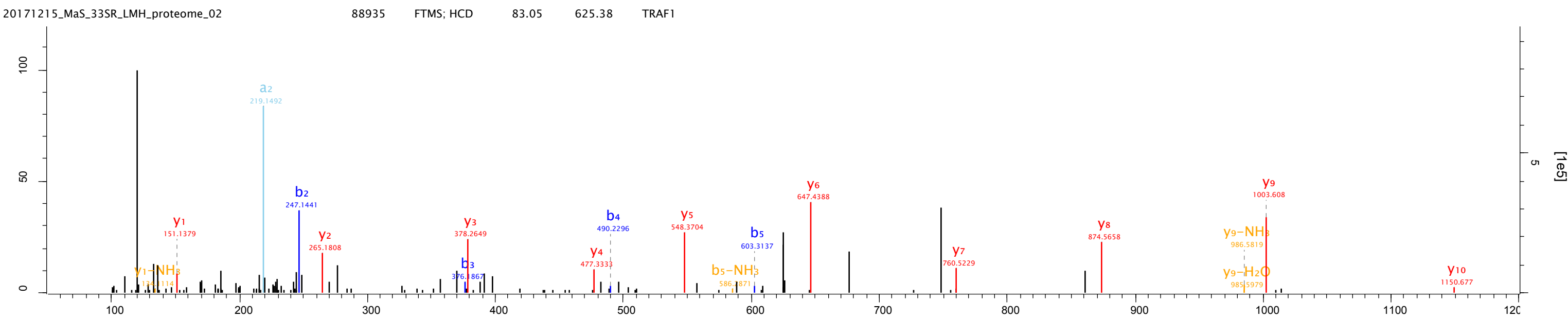


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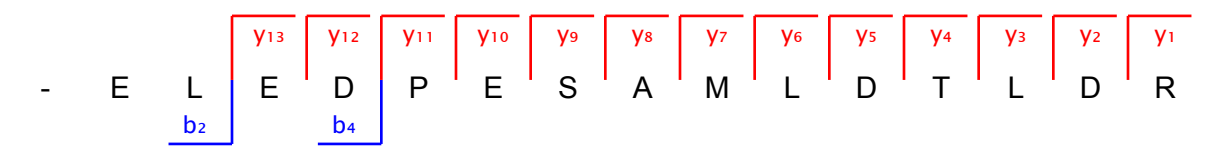
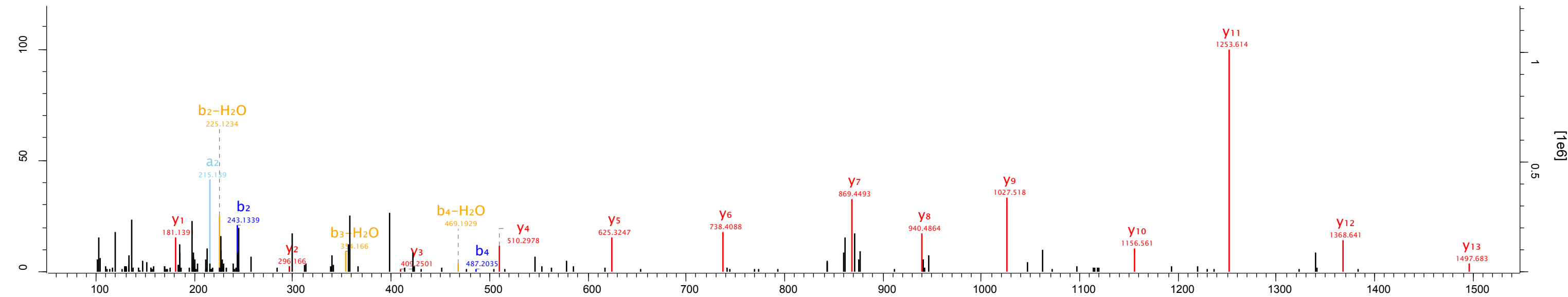




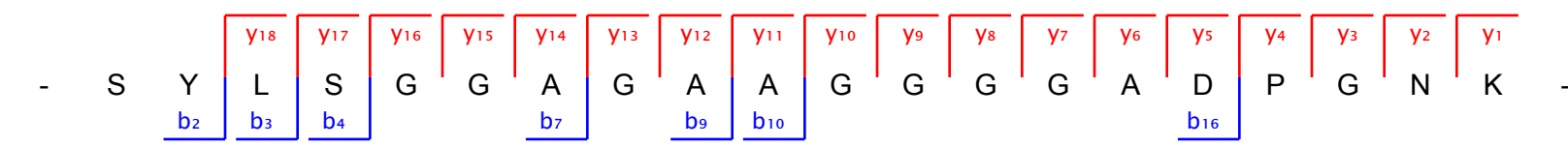
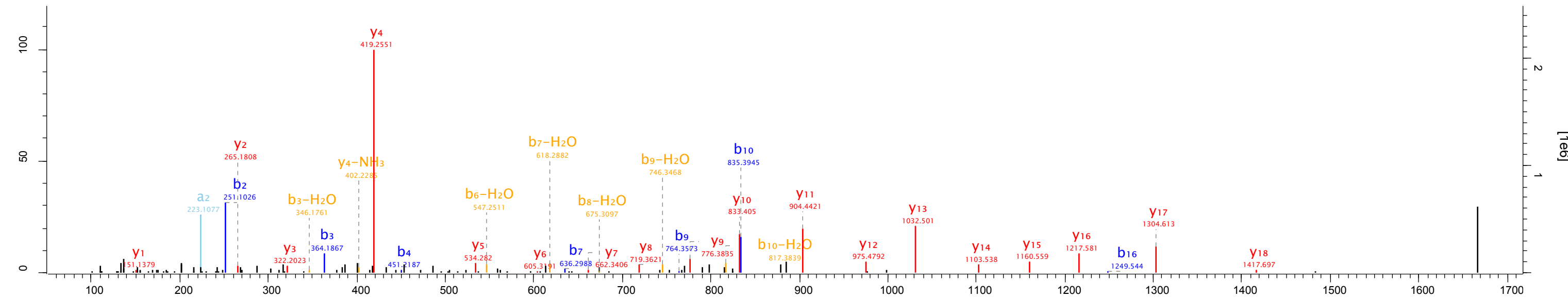
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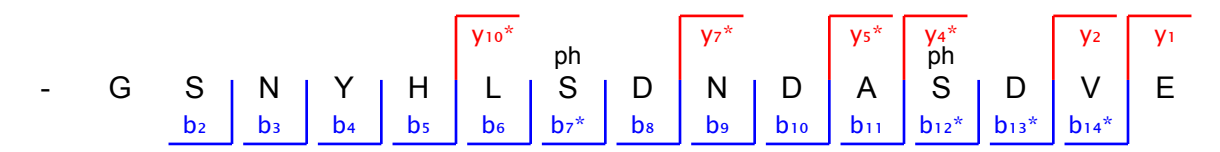
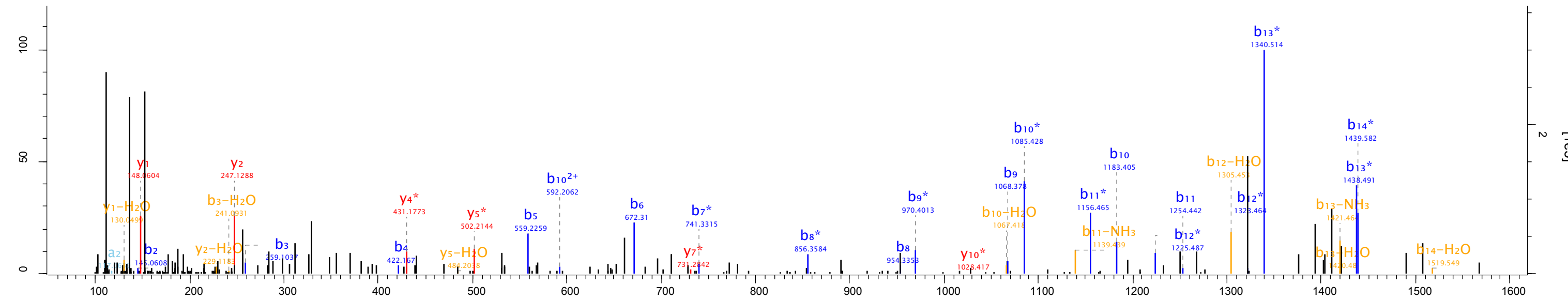
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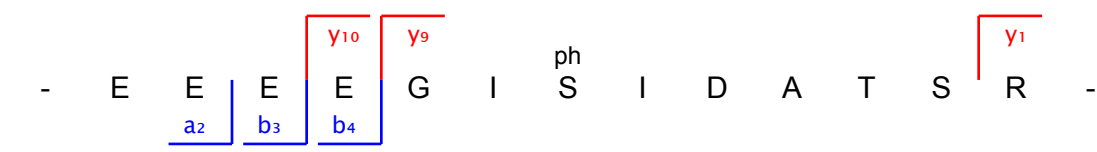
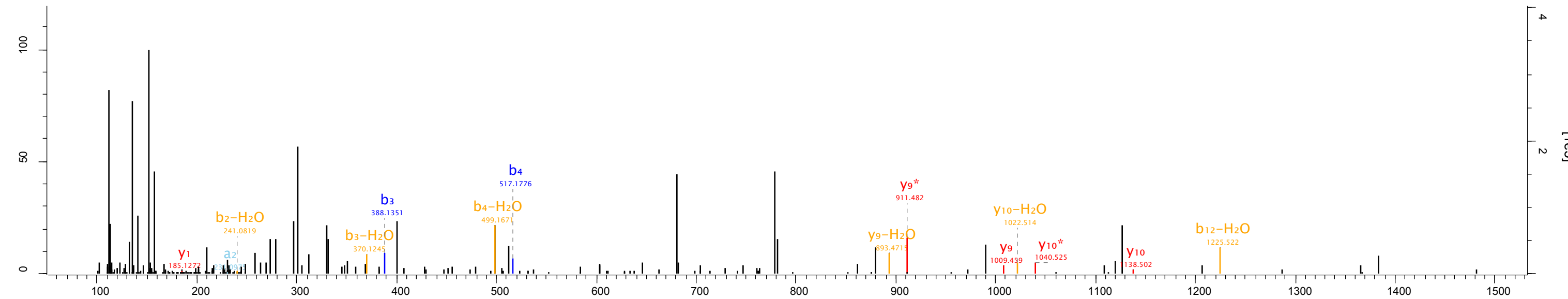
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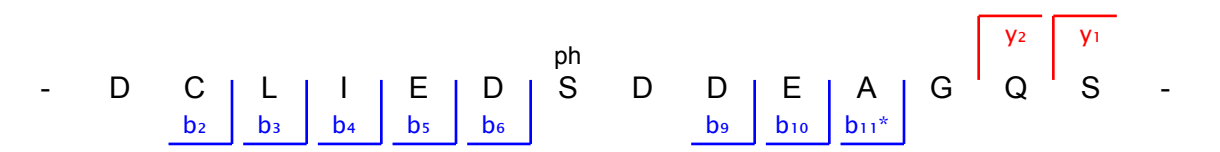
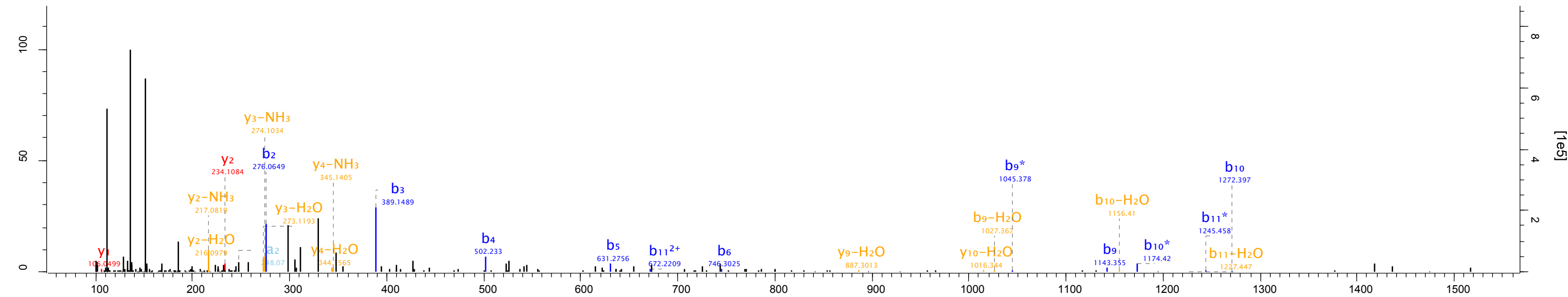
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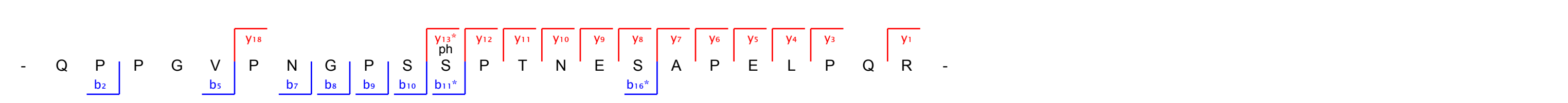
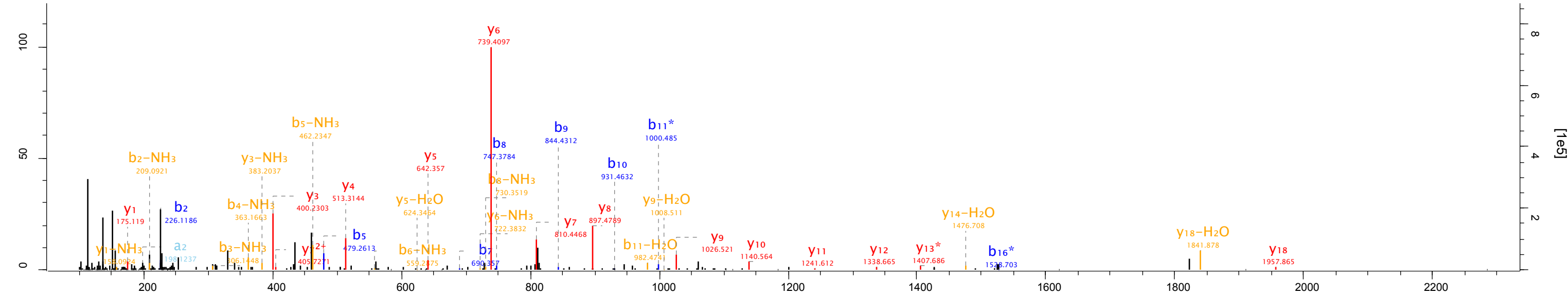
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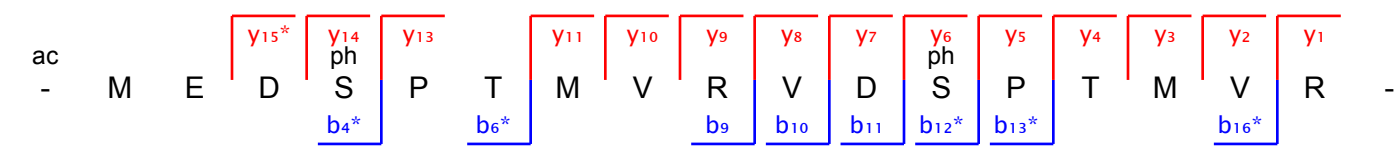
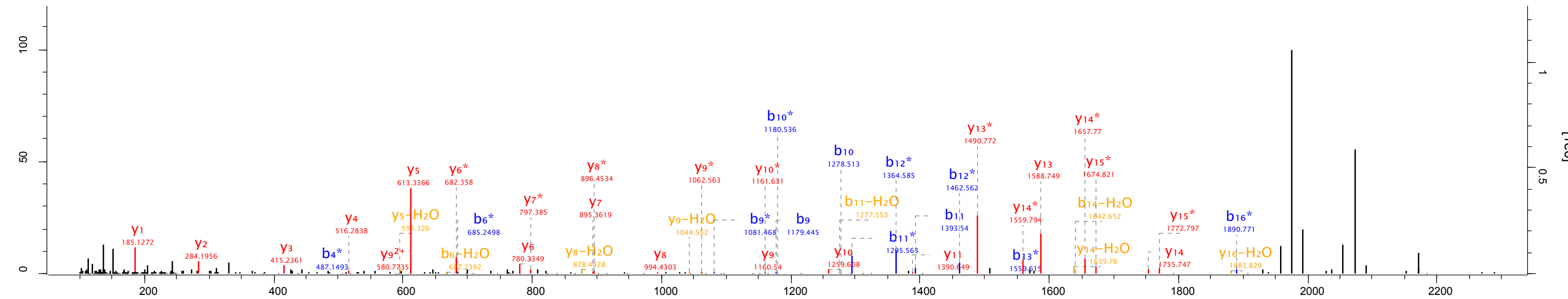
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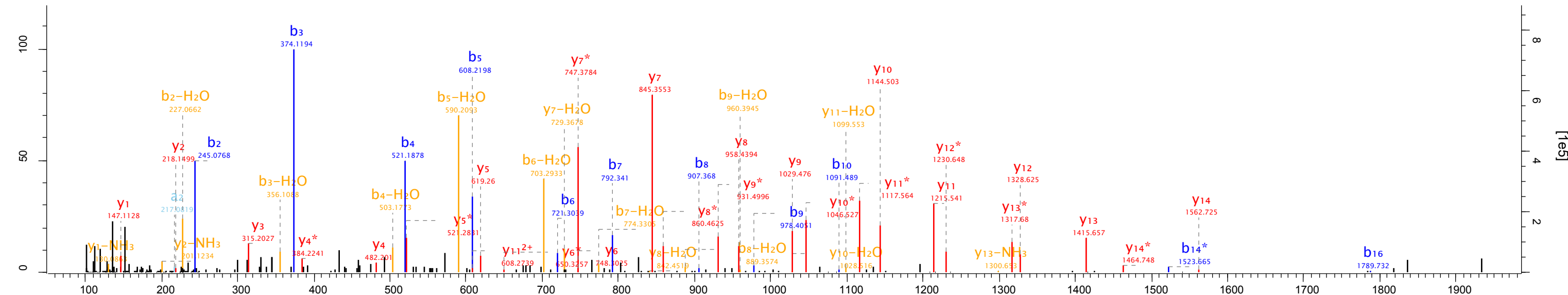
20171215_MaS_33SR_LMH_phospho_02

Scan	Method	Score	m/z	Gene names
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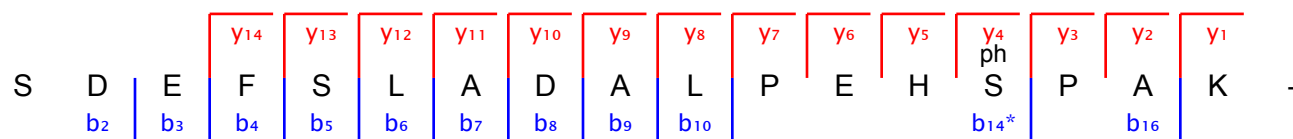
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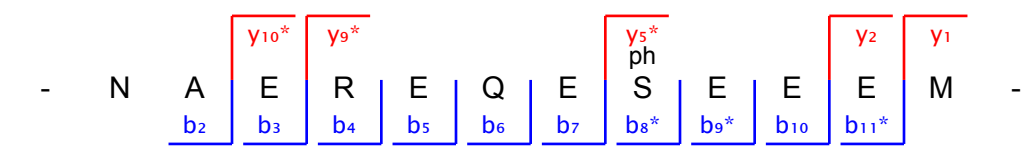
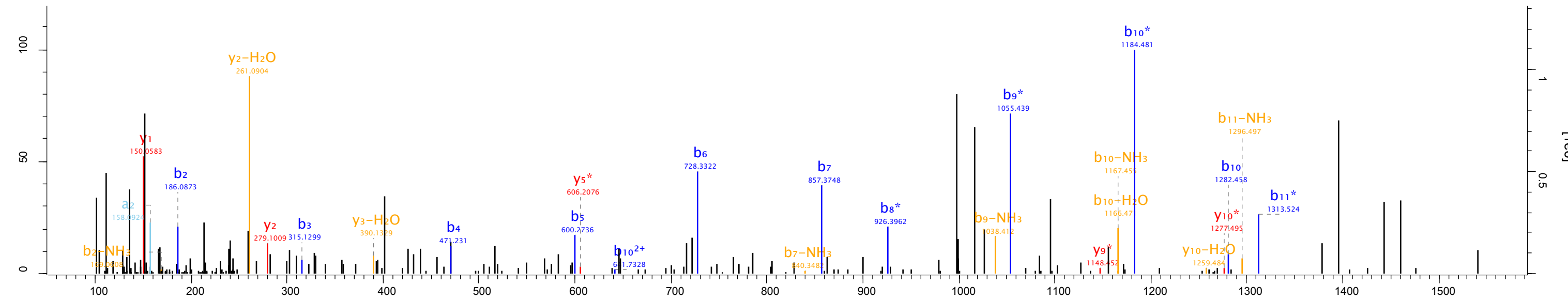


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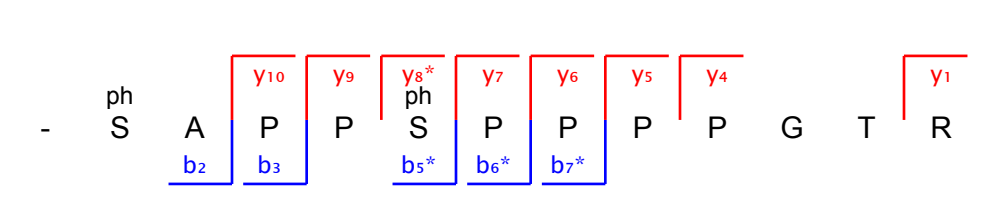
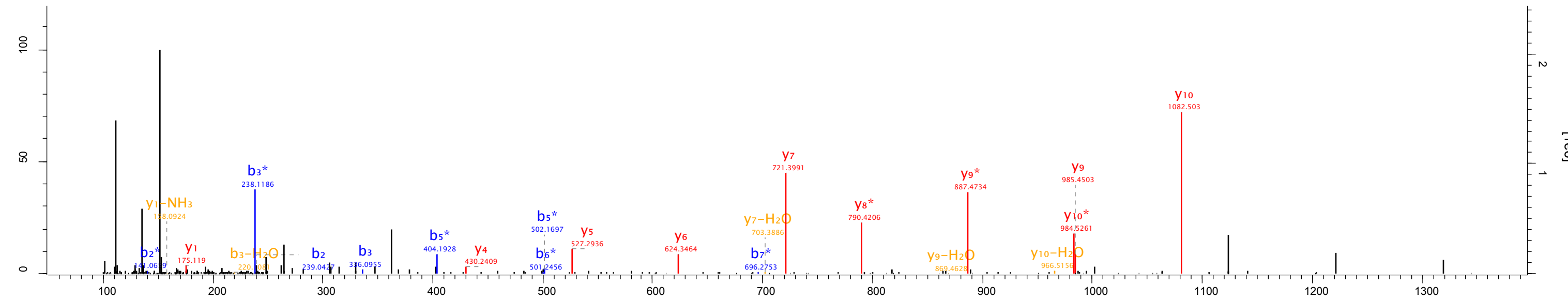
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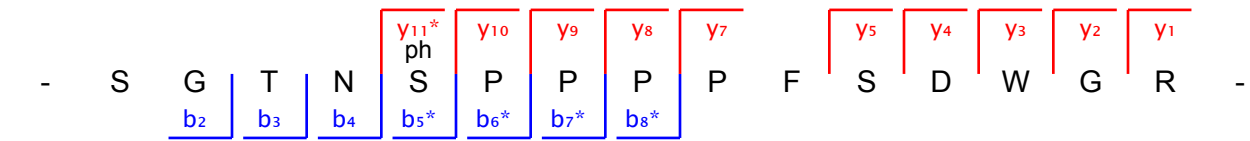
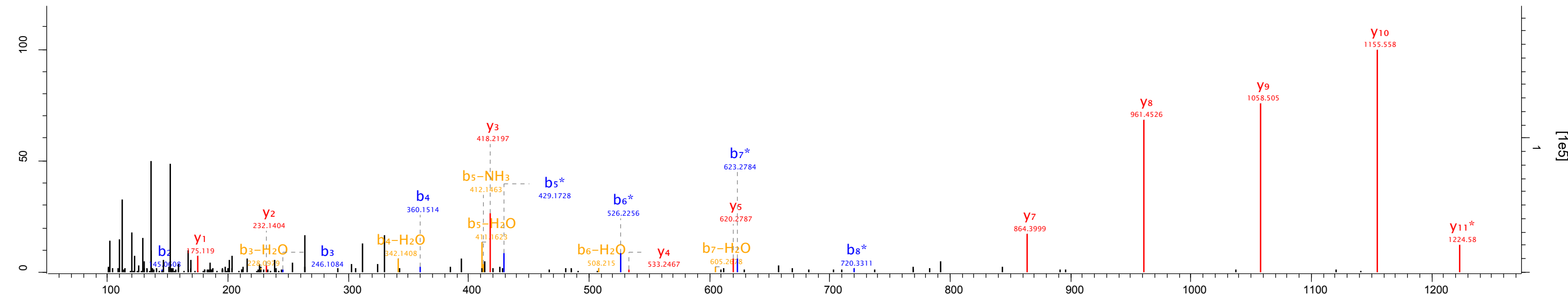
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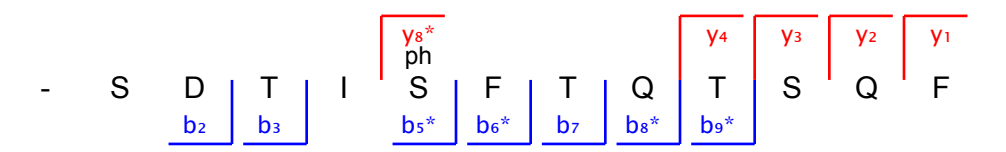
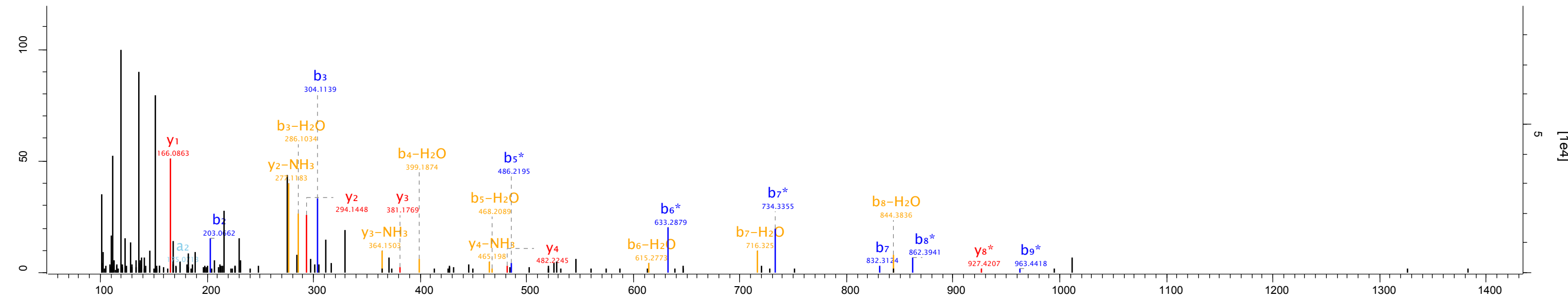
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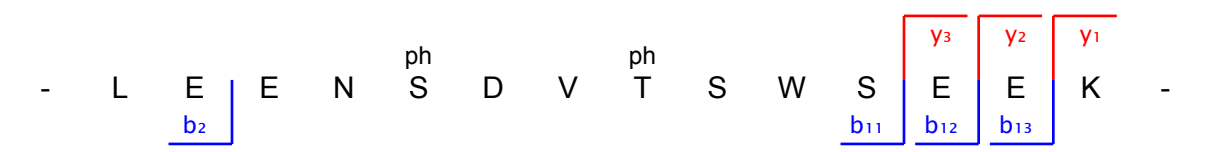
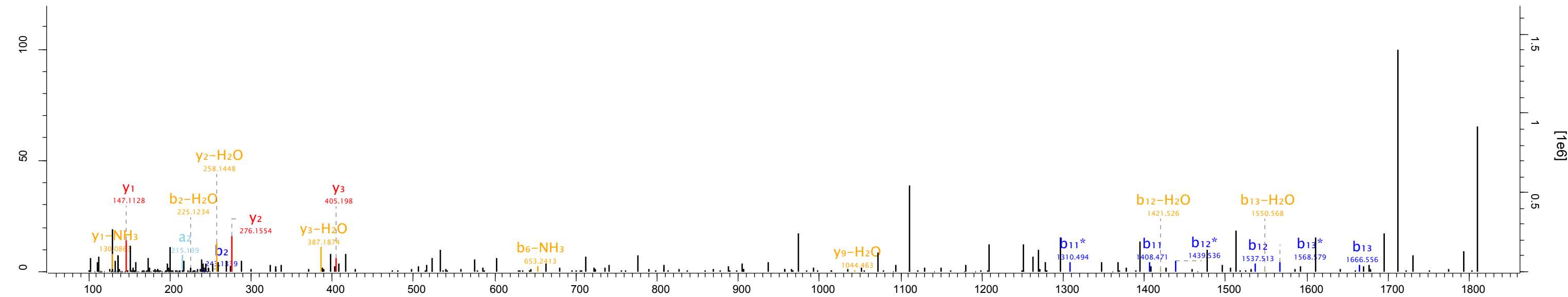
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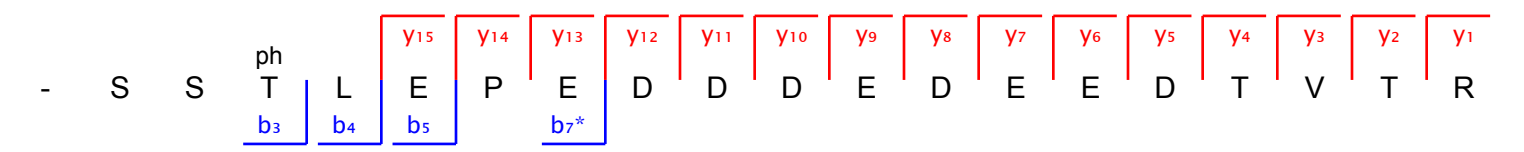
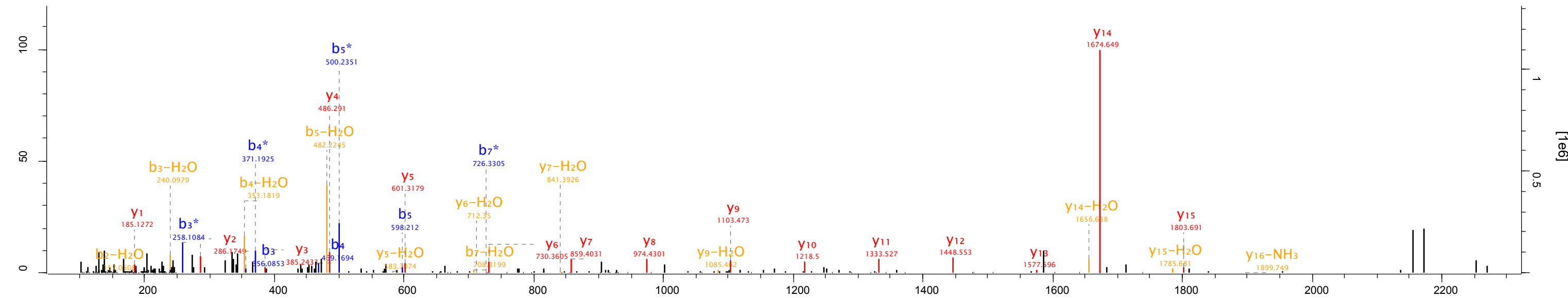
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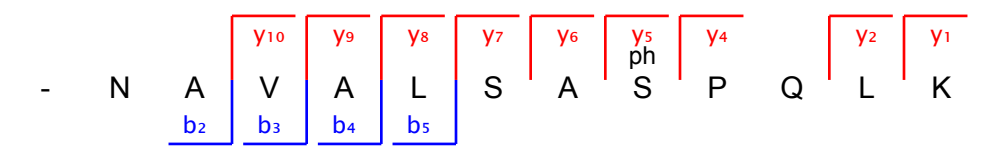
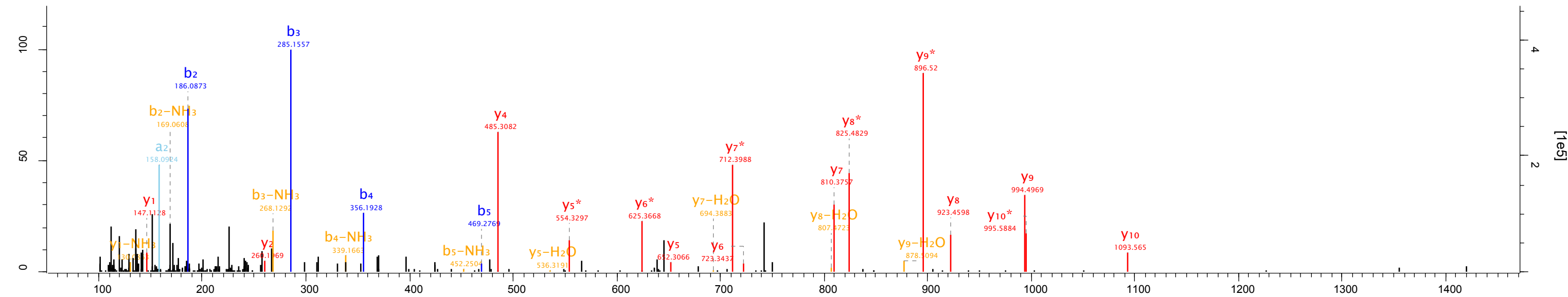
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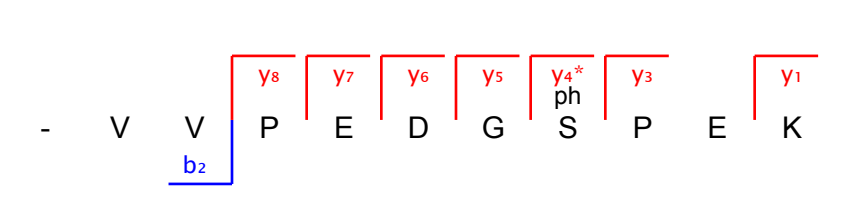
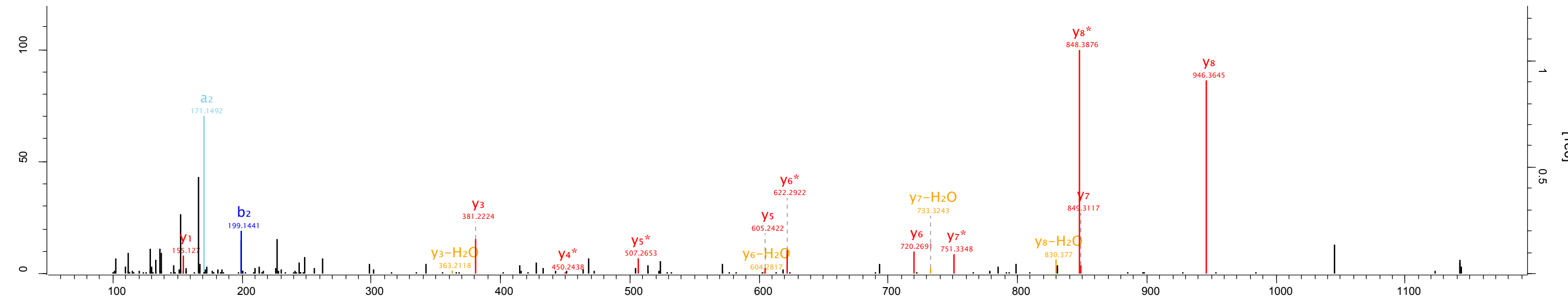
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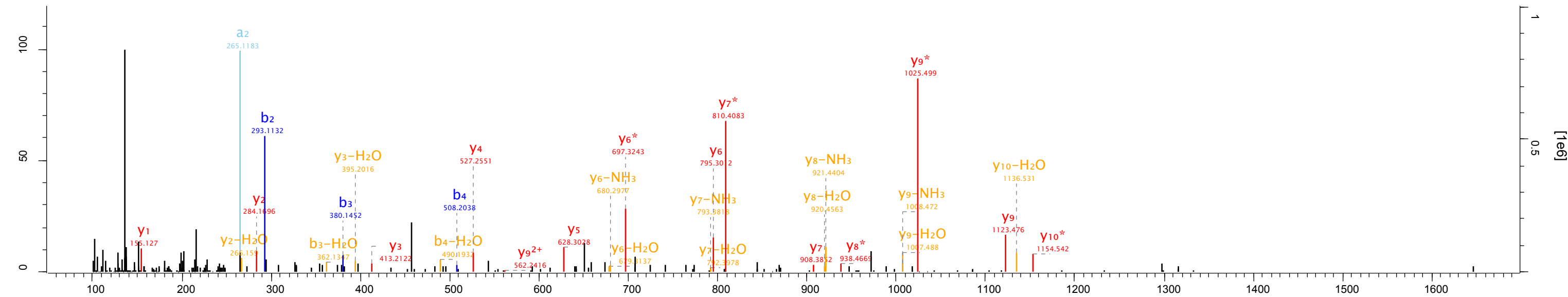
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- Y E S Q L S T N E E K -

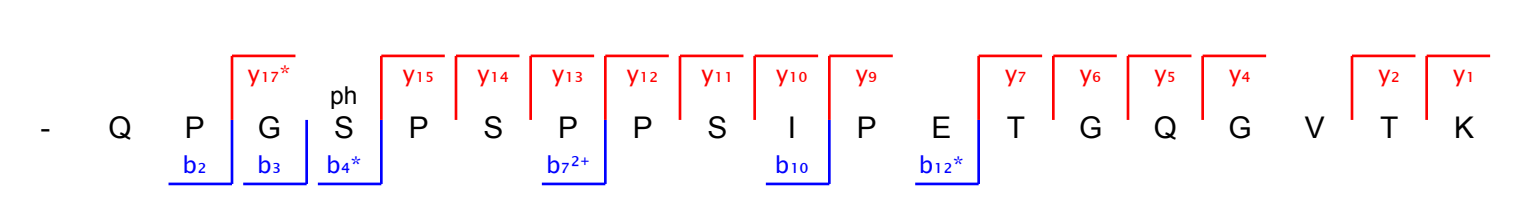
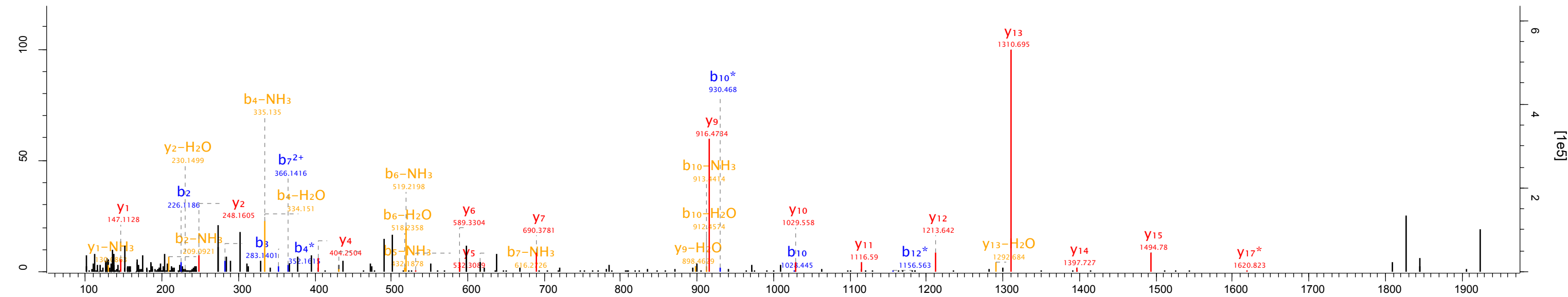
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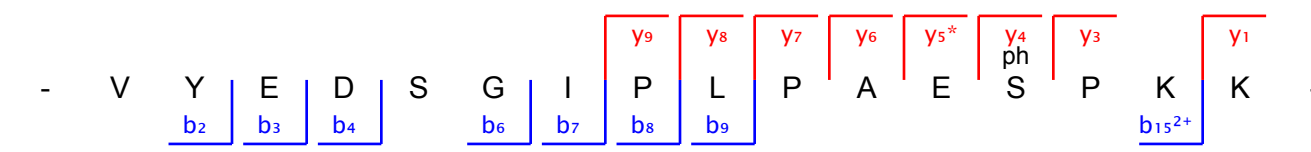
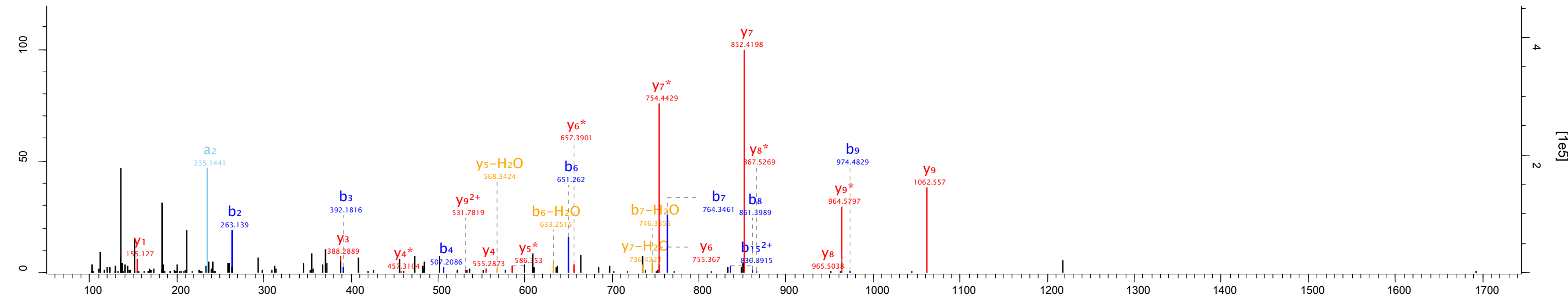
- y10* (E)
- y9 (S)
- y8* (Q)
- y7 (L)
- y6 ph (S)
- y5 (T)
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- y3 (E)
- y2 (E)
- y1 (K)

Fragmentation mapping (blue boxes):

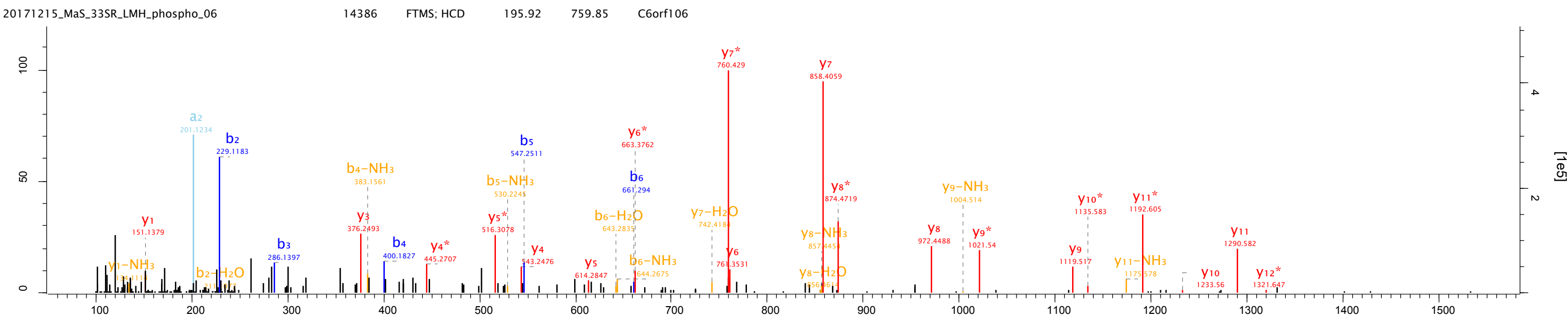
- b2 (E)
- b3 (S)
- b4 (Q)

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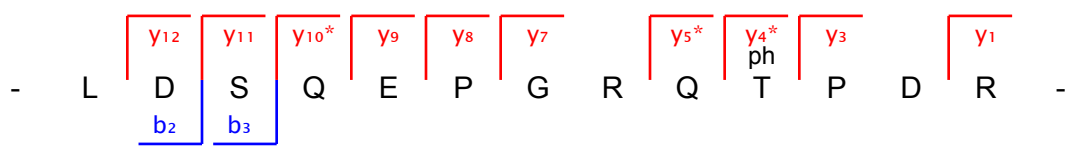
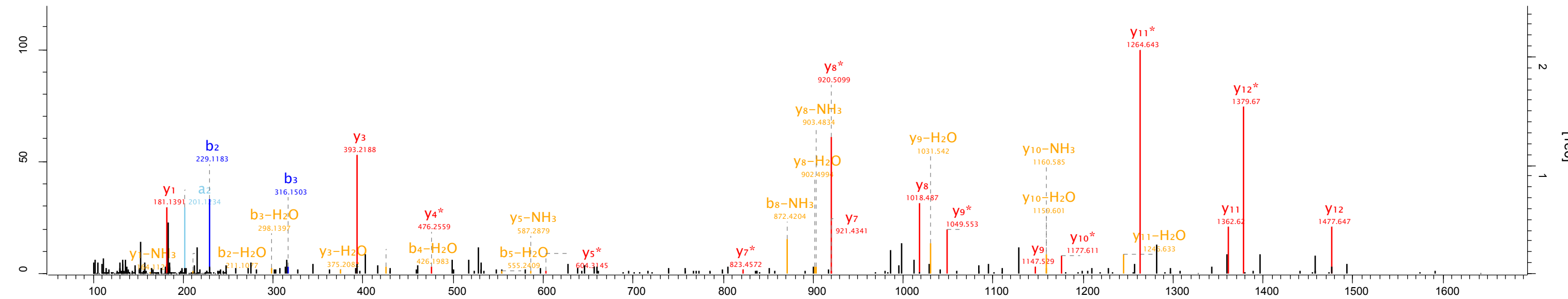




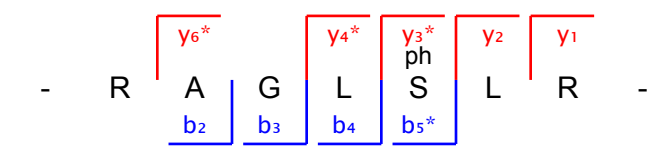
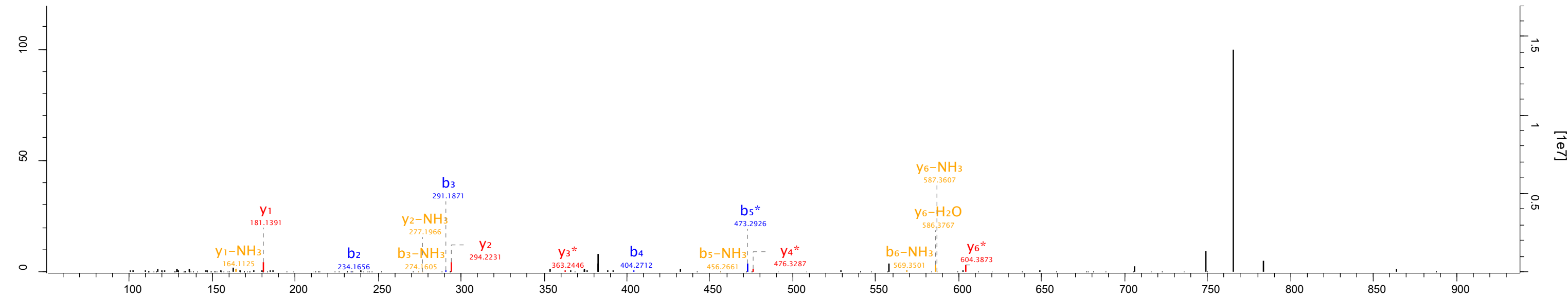
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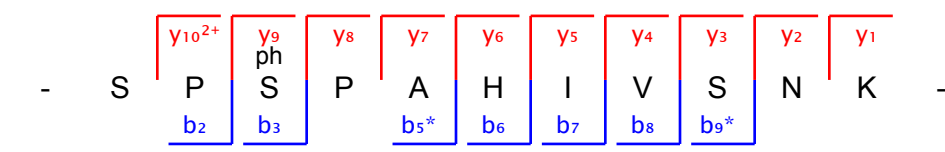
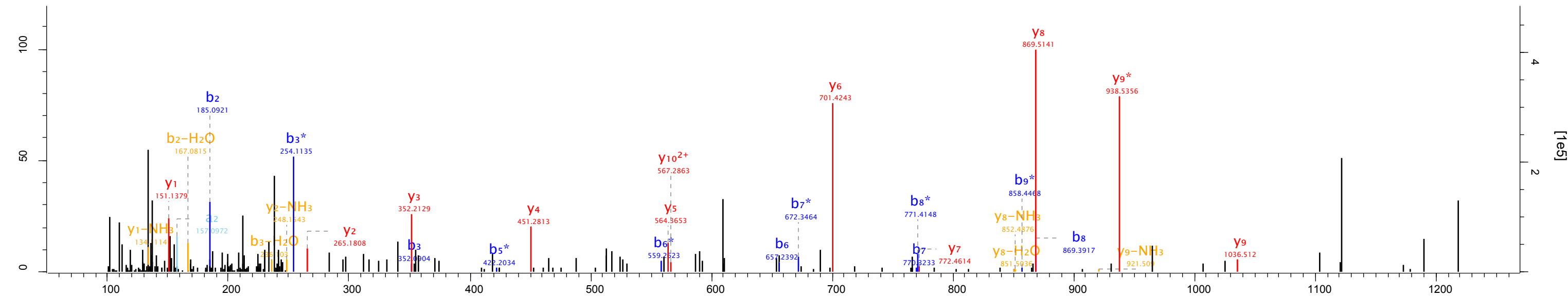
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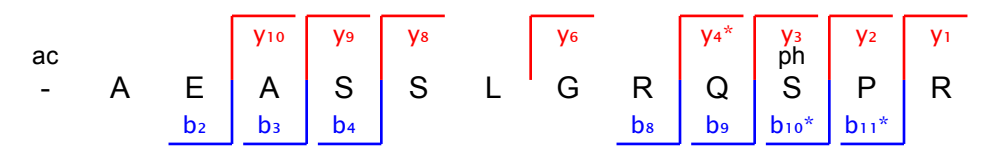
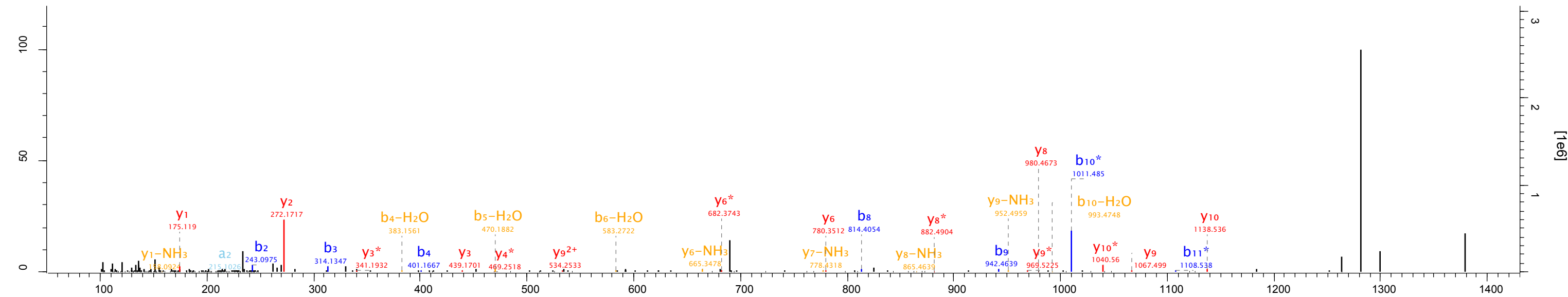
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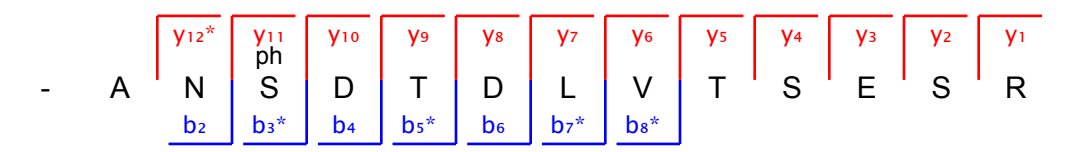
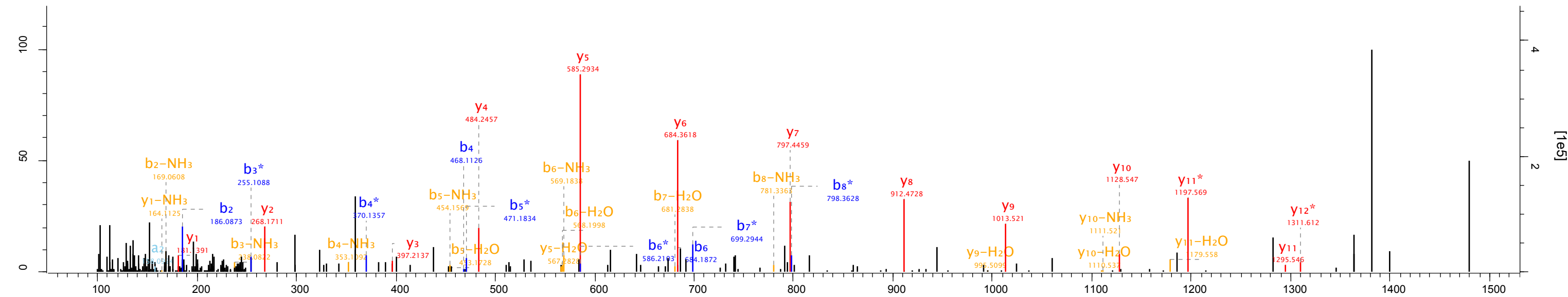
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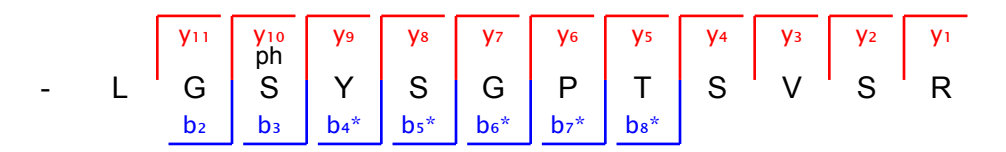
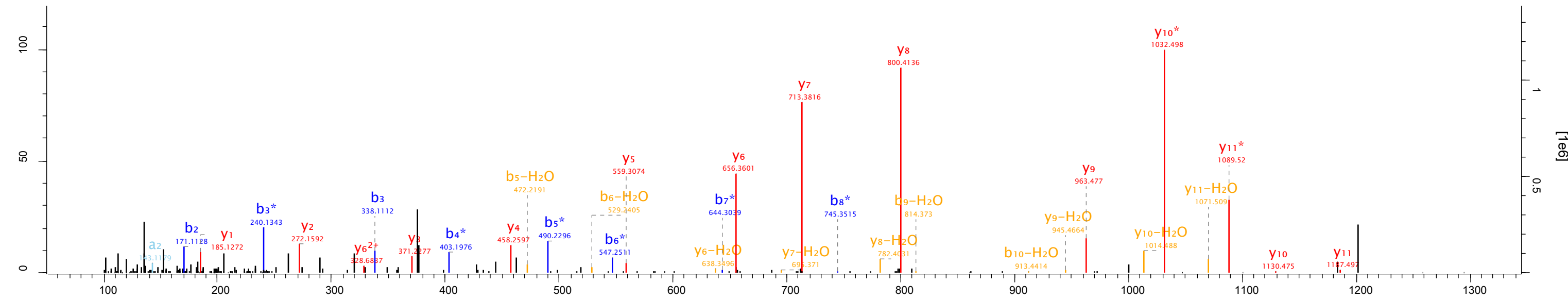
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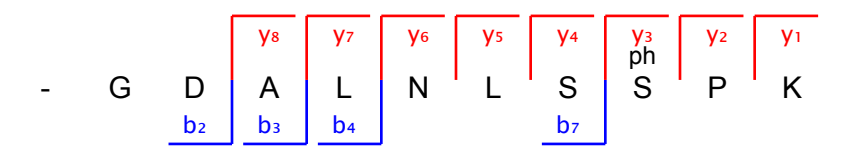
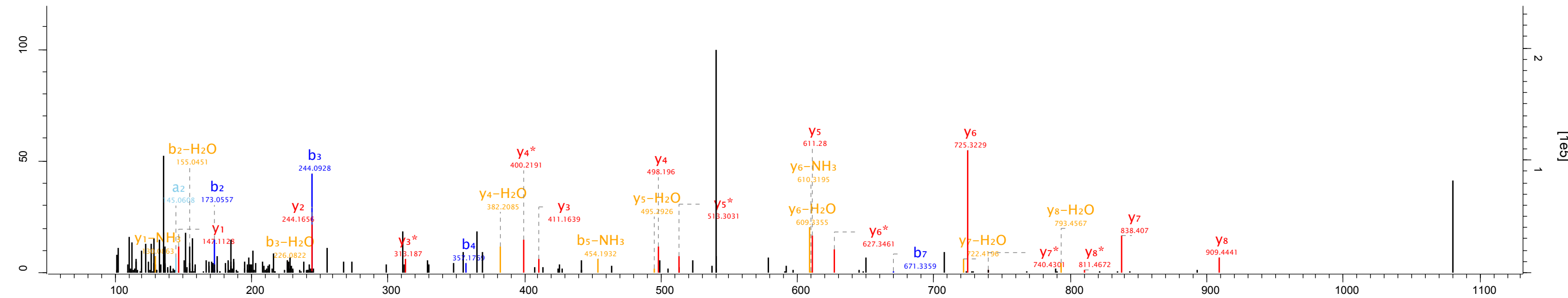
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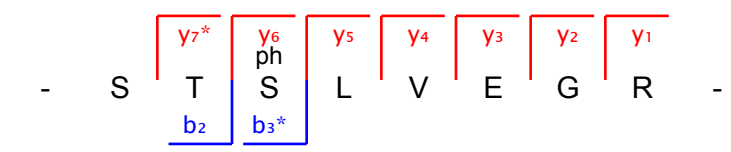
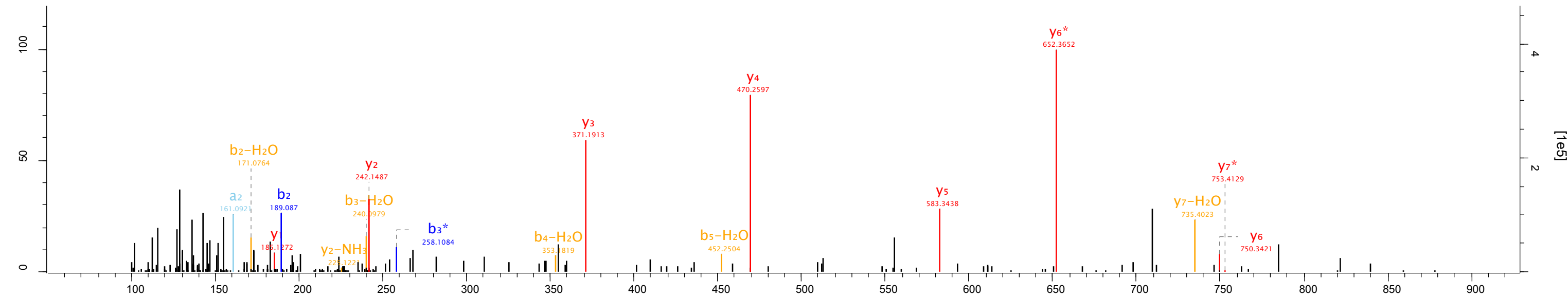
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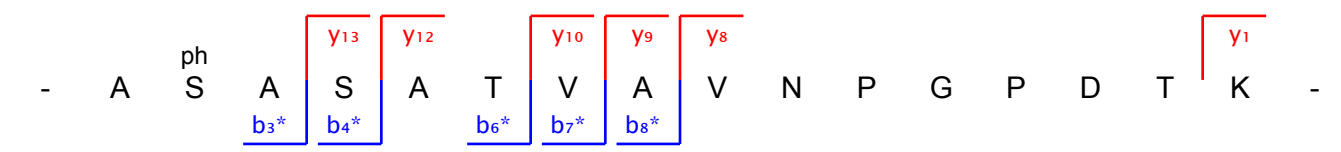
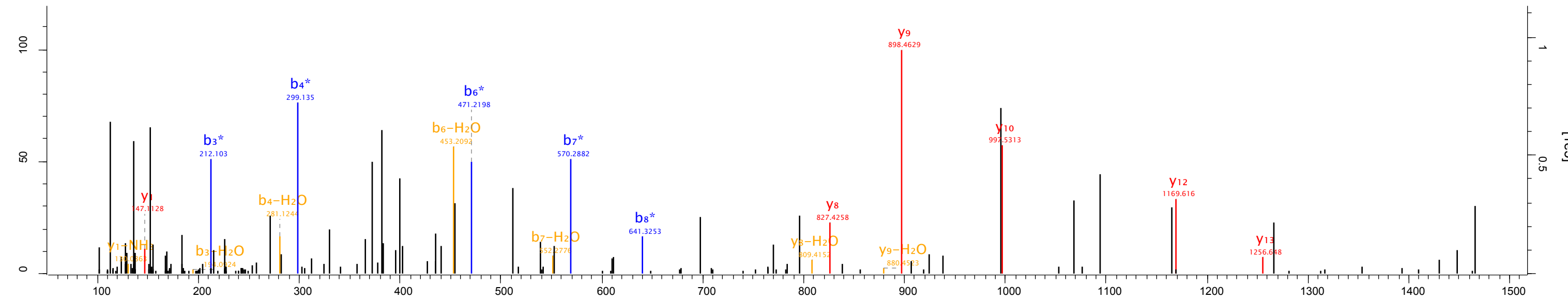
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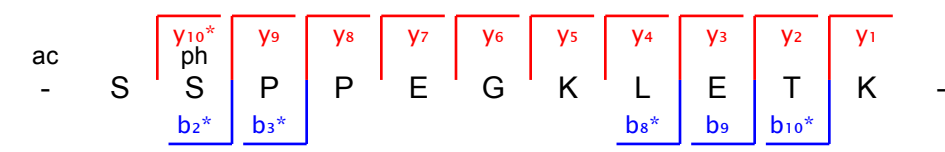
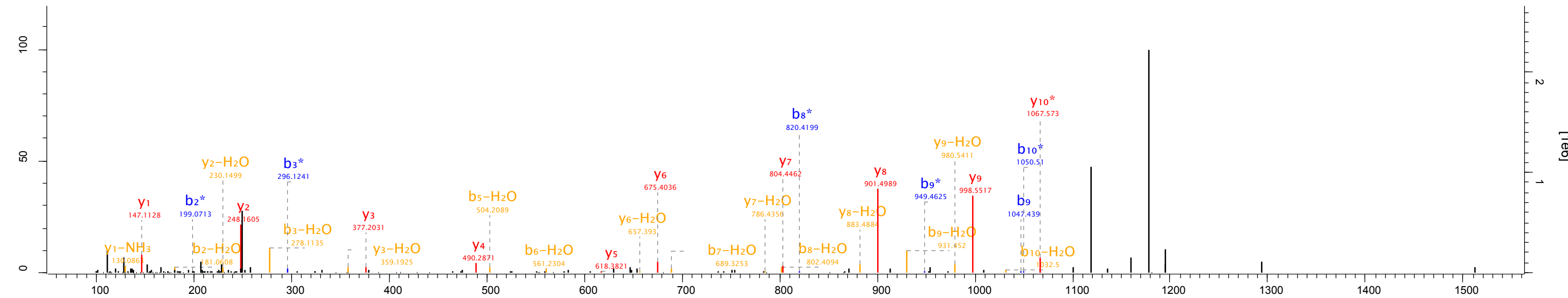
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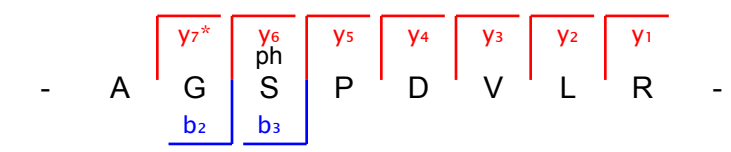
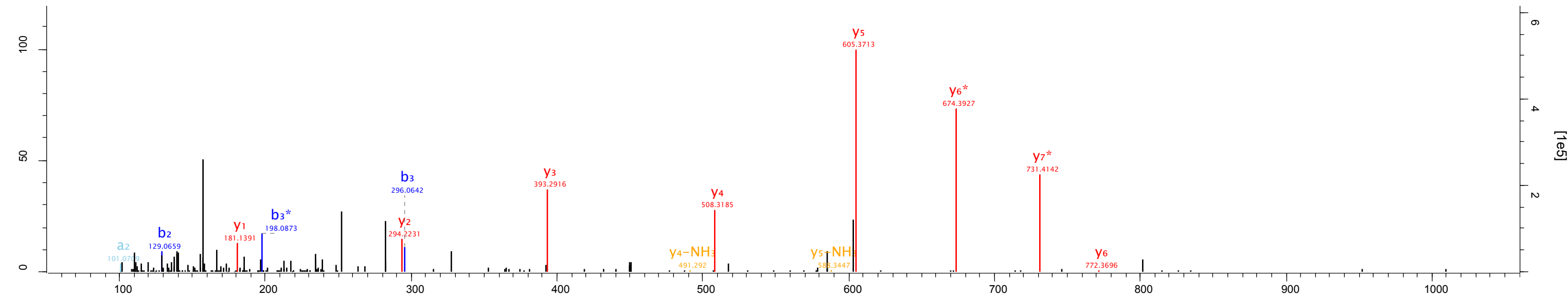
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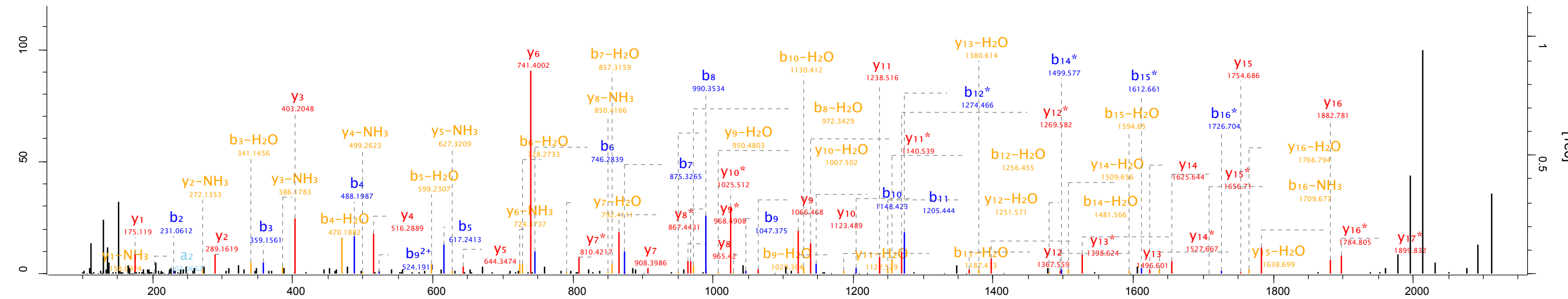
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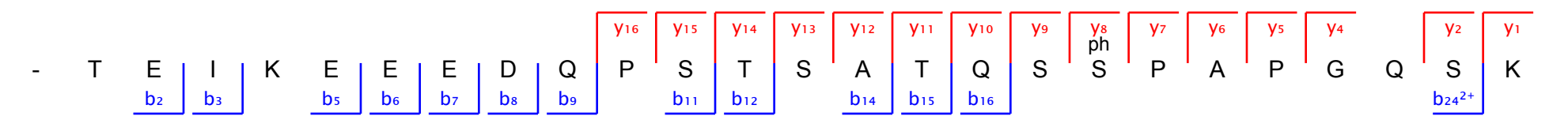
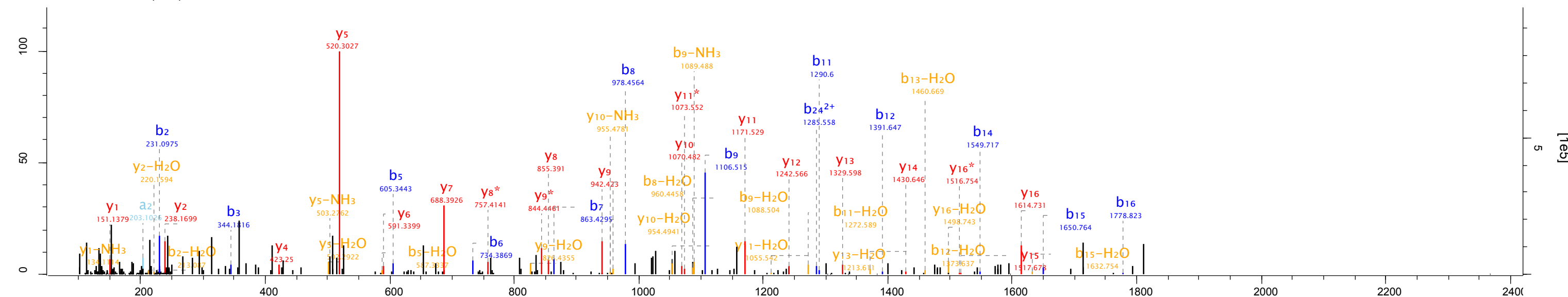


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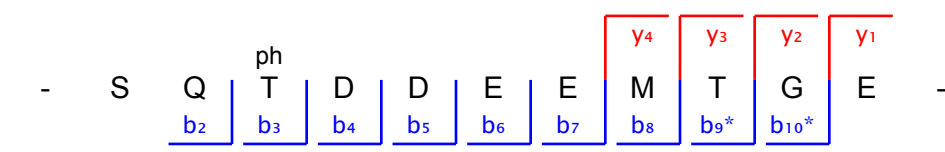
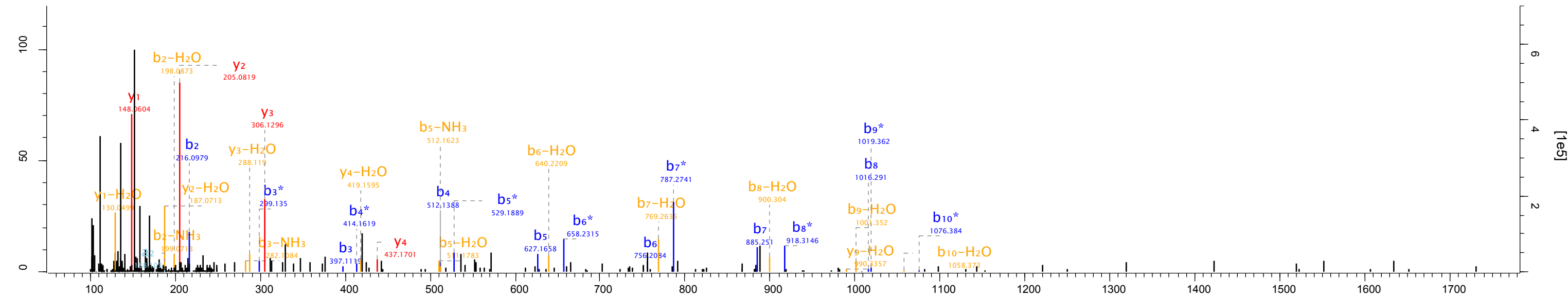


Raw file
20171215_MaS_33SR_LMH_phospho2_01

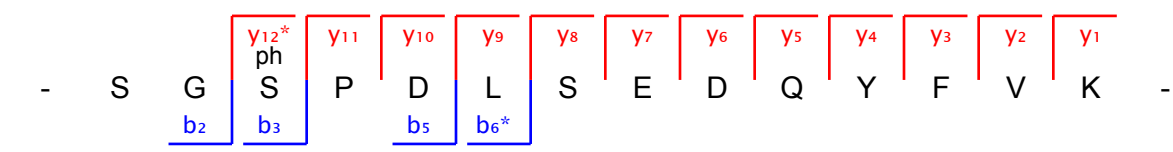
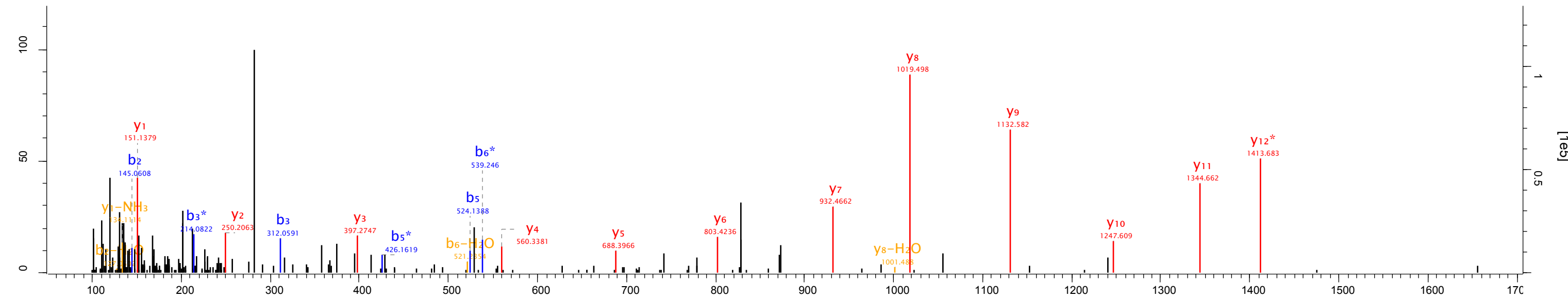
Scan 4186 Method FTMS; HCD Score 112.09 m/z 907.42 Gene names EP300



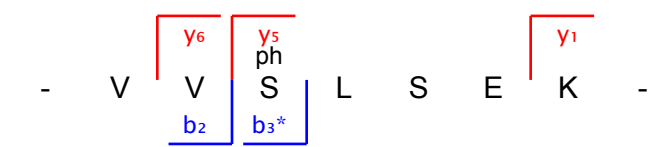
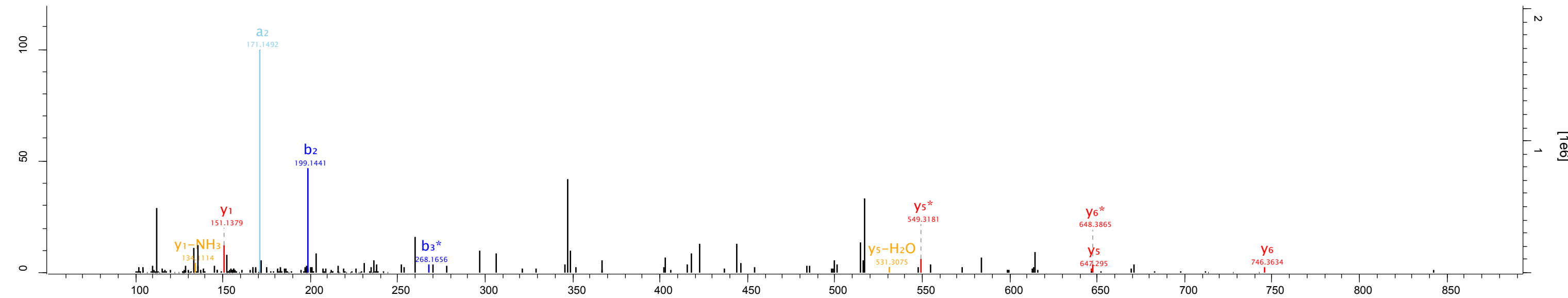
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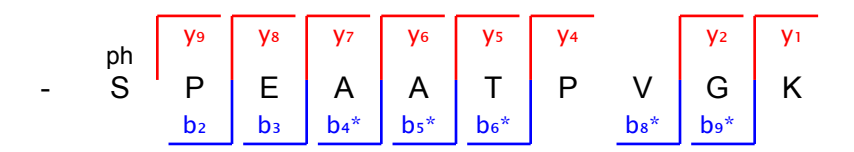
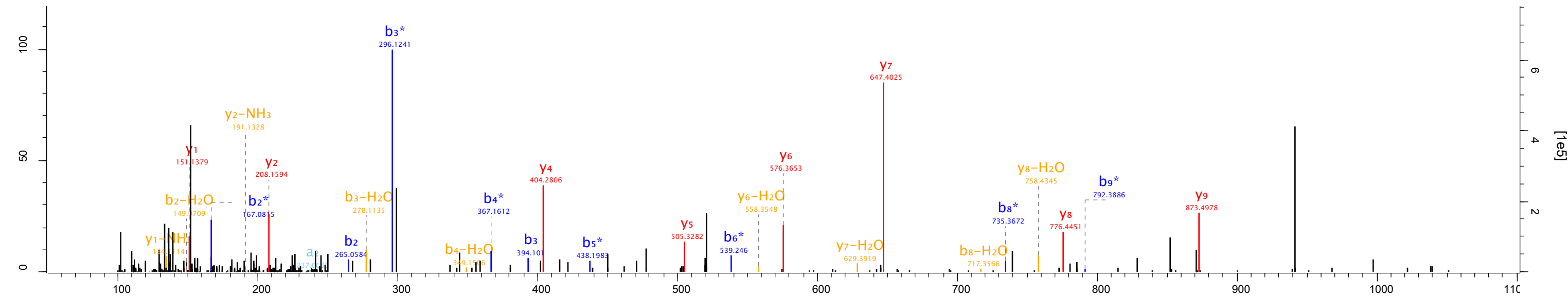
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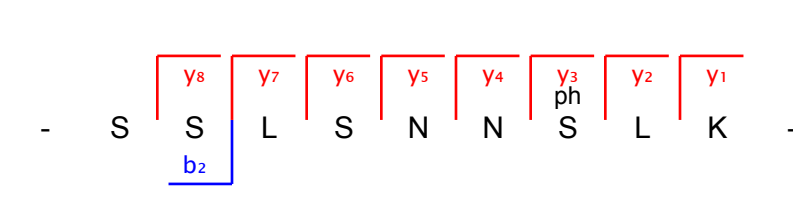
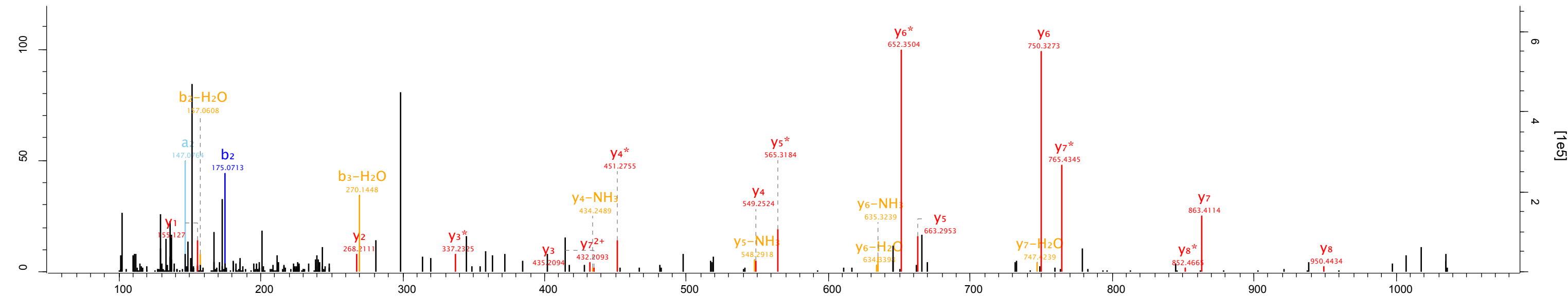
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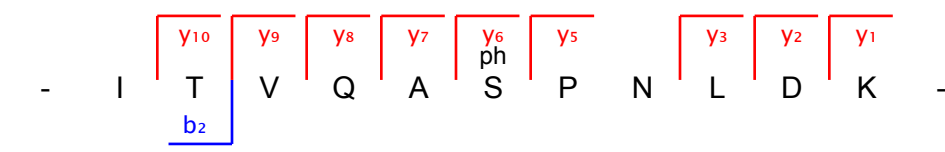
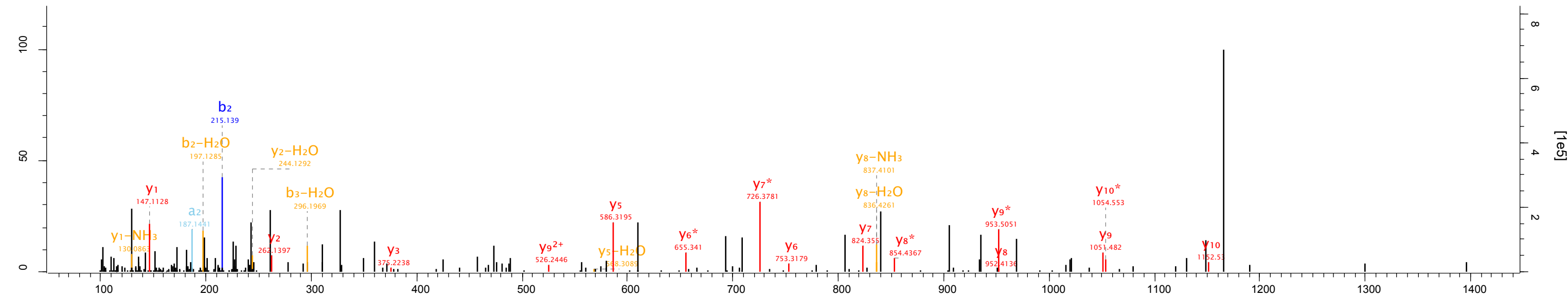
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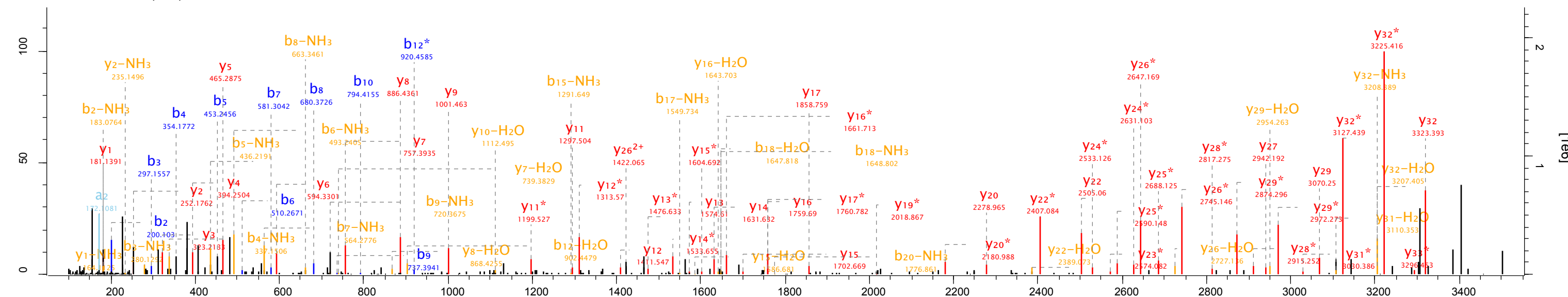


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20171215_MaS_33SR_LMH_phospho2_03

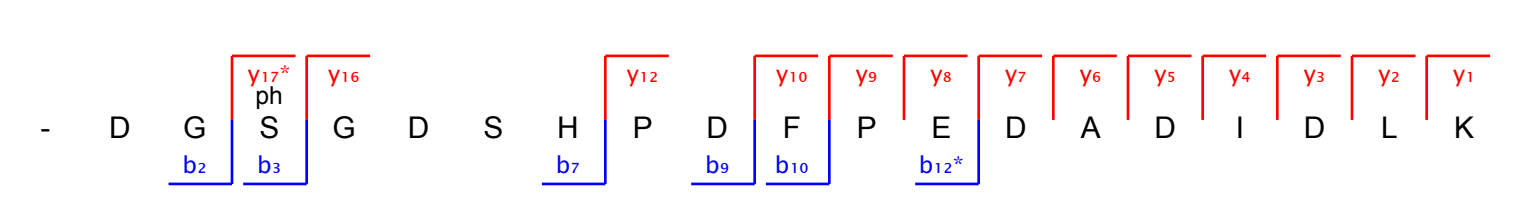
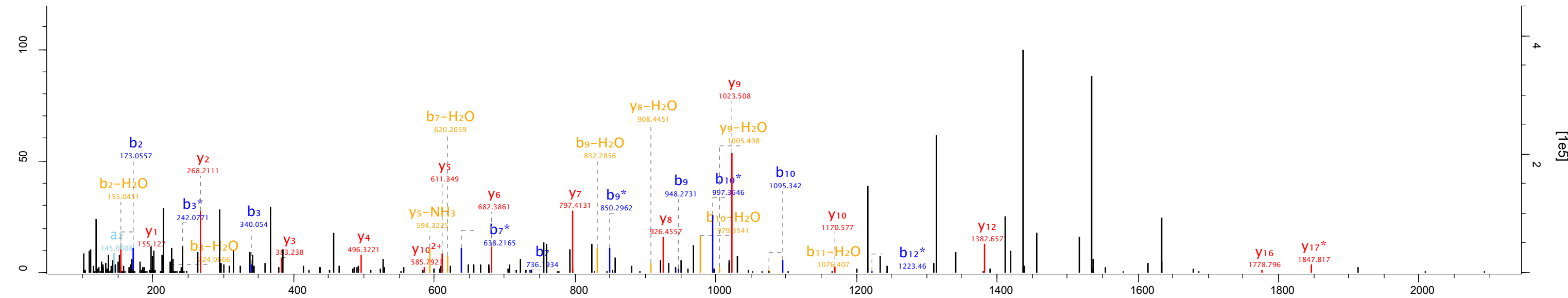
Scan 12676 Method FTMS; HCD Score 223.49 m/z 1175.51 Gene names OTUD5



- Q A P G V G A V G G S P E R E E V G A G Y N S E D E Y E A A A A R -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀
b₁₂^{*}
y₂₃^{*} ph

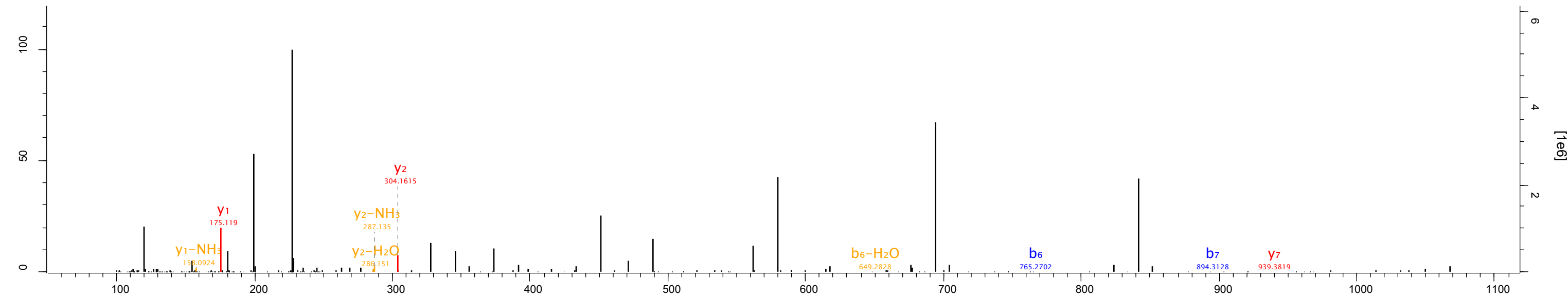
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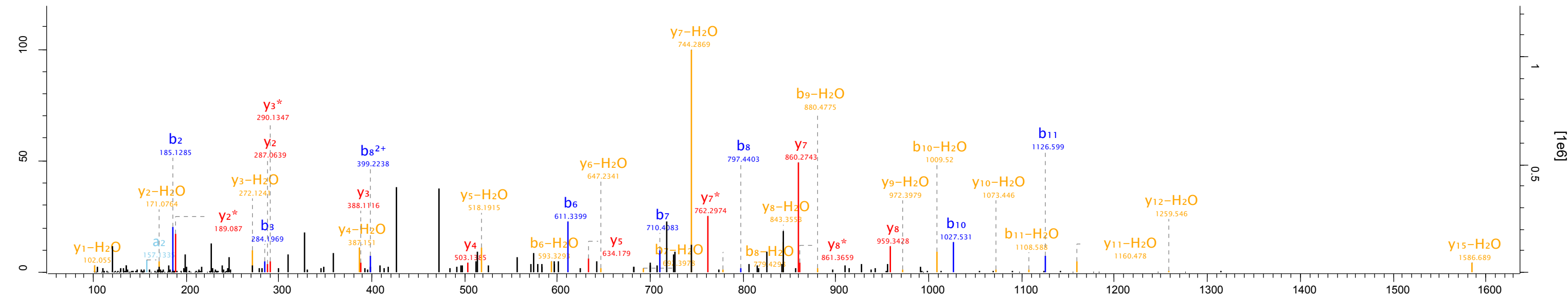


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20171215_MaS_33SR_LMH_phospho2_03

Scan	Method	Score	m/z	Gene names
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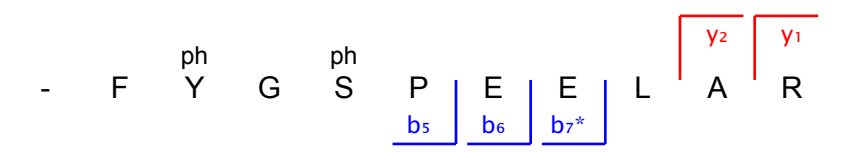
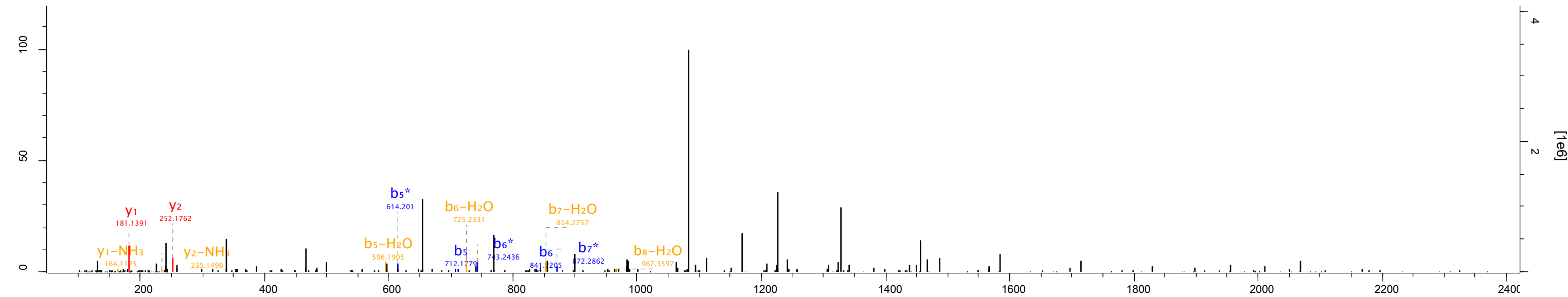
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Fragmentation mapping (b and y ions):

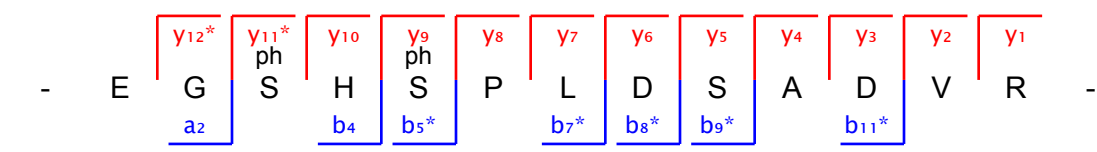
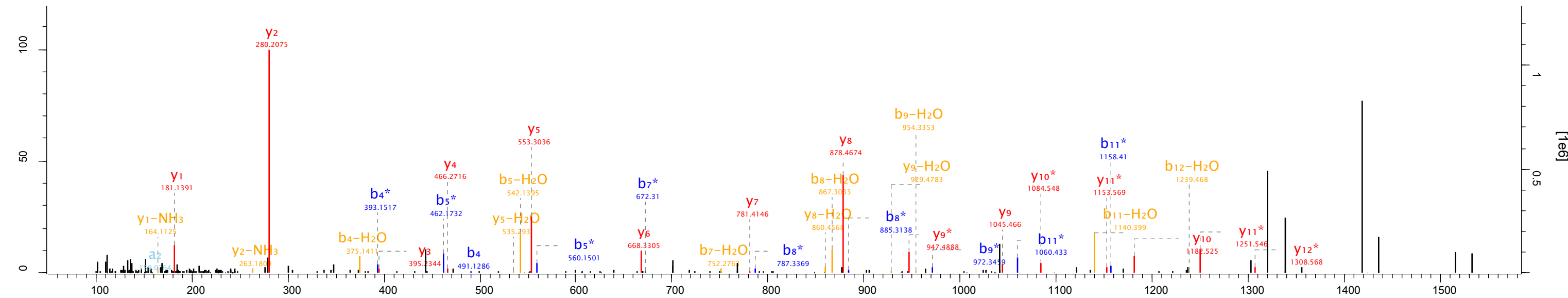
- Blue boxes (b ions): A-V, V-P, E-V, V-S, S-T, E-V, V-P, E-M, M-D, D-T, T-S.
- Red boxes (y ions): V-P, E-M, M-D, D-T, T-S.

Raw file
20171215_MaS_33SR_LMH_phospho2_03

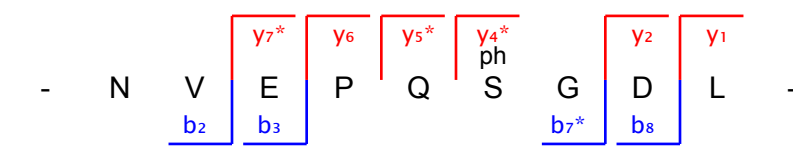
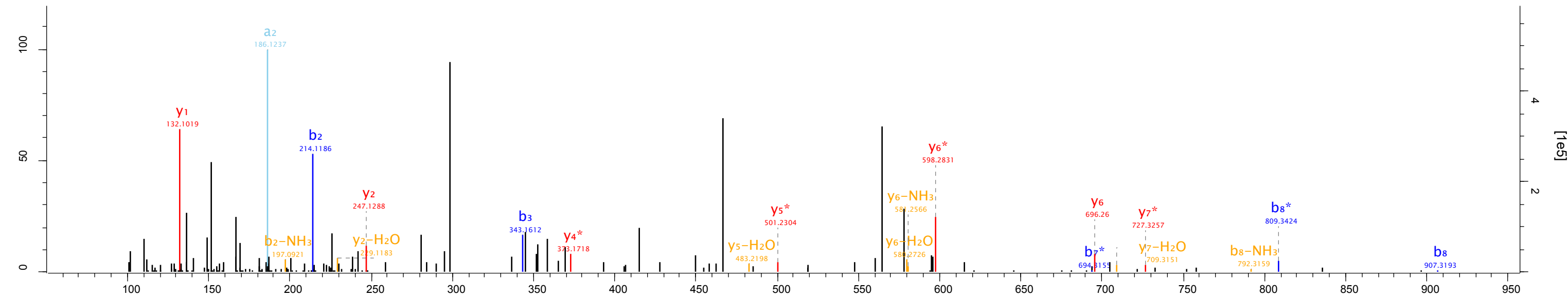
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Method: FTMS; HCD
Score: 43.77
m/z: 1334.52
Gene names: AOC1



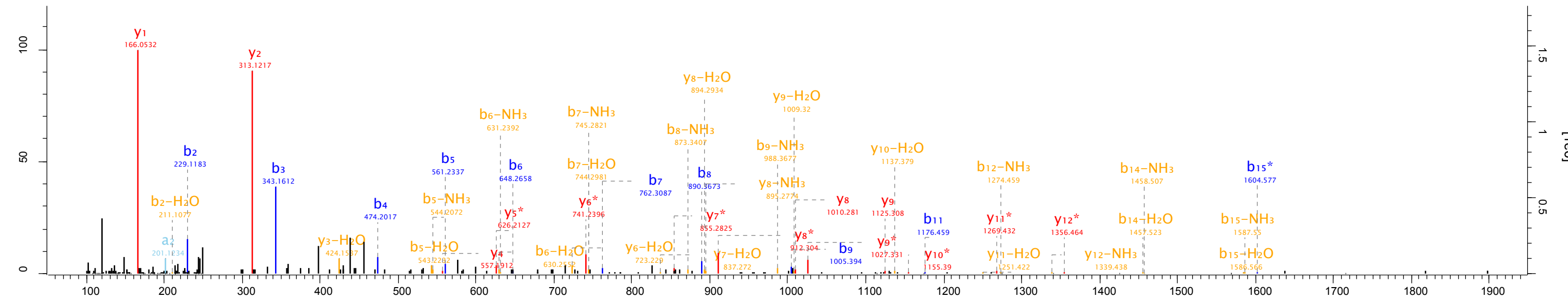
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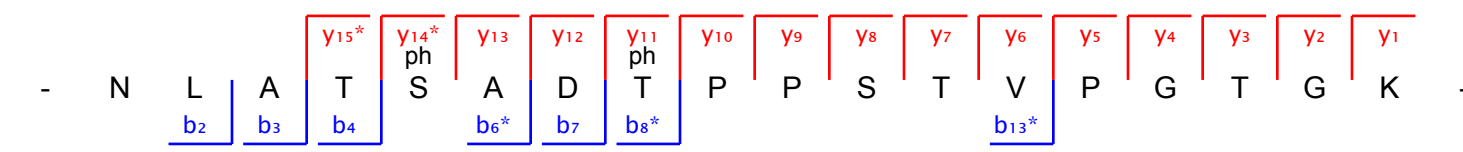
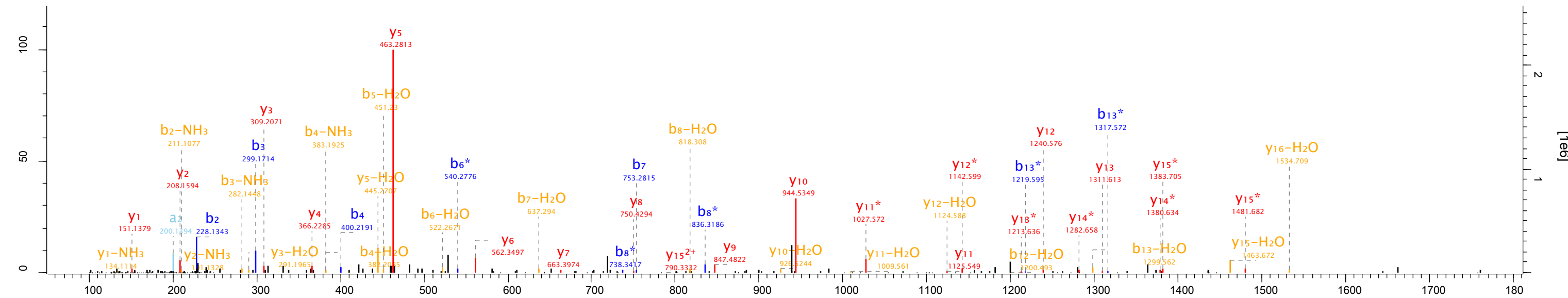


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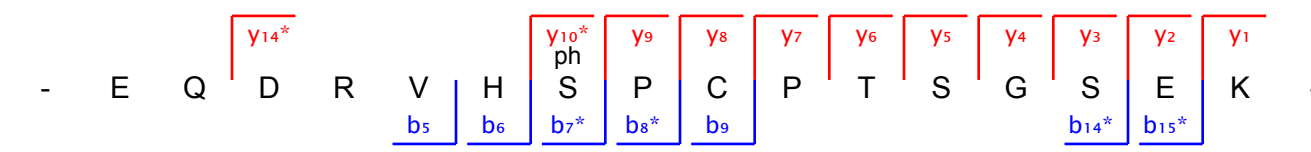
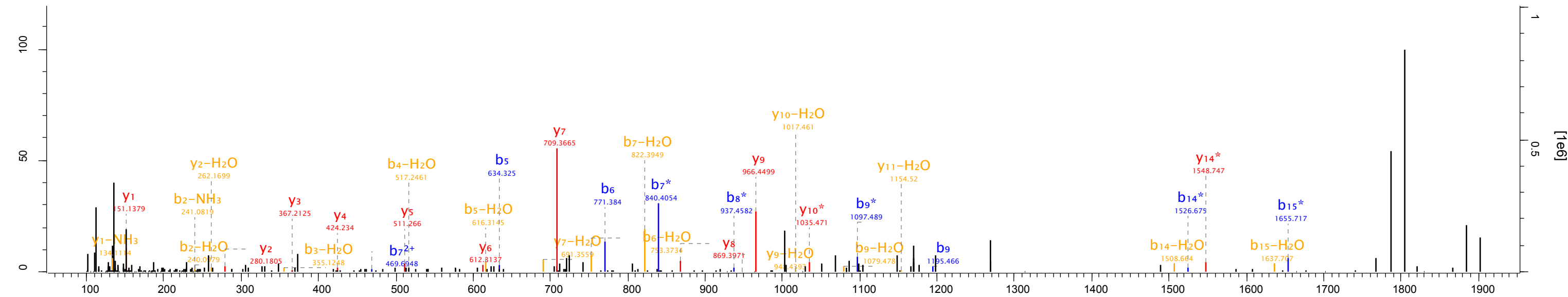
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20171215_MaS_33SR_LMH_phospho2_03

Scan 9696 Method FTMS; HCD Score 123.71 m/z 939.92 Gene names SMG1

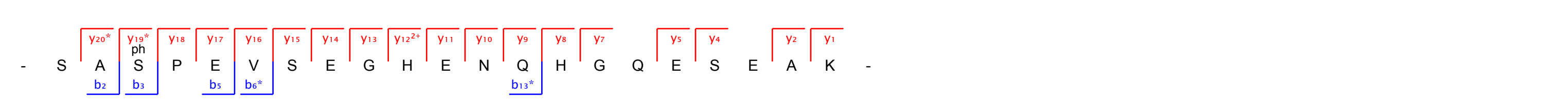
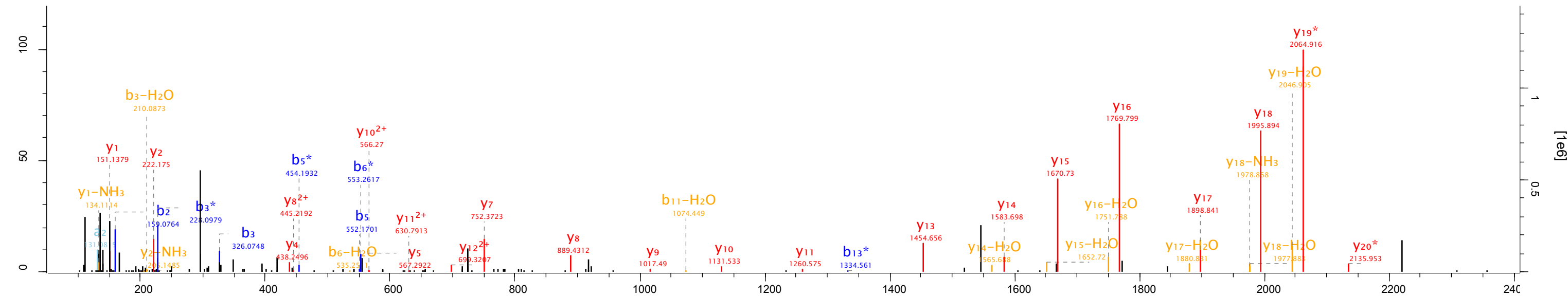


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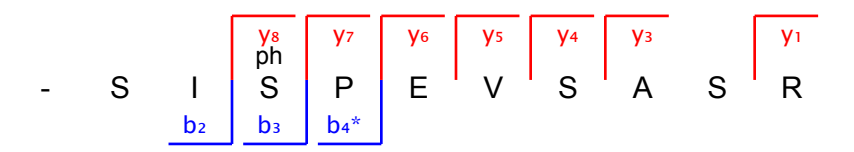
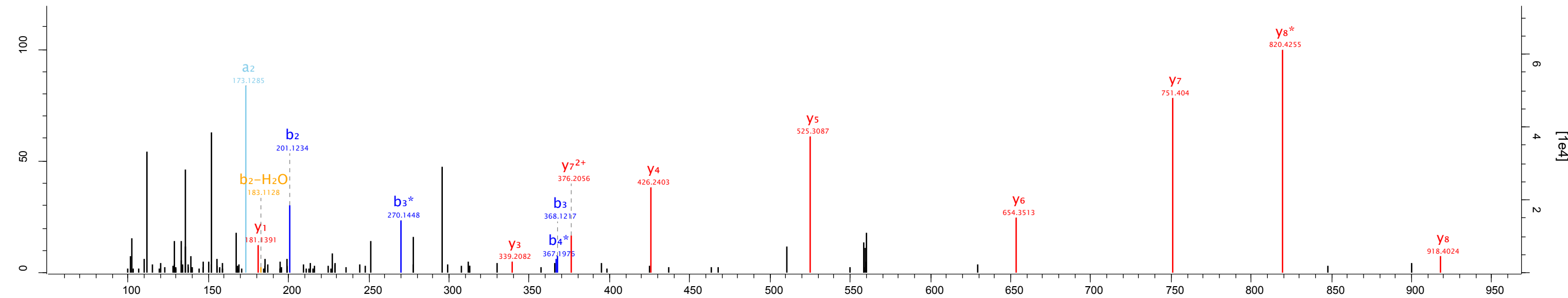
Scan Method Score m/z Gene names
2076 FTMS; HCD 89.83 635.61 RNPC3



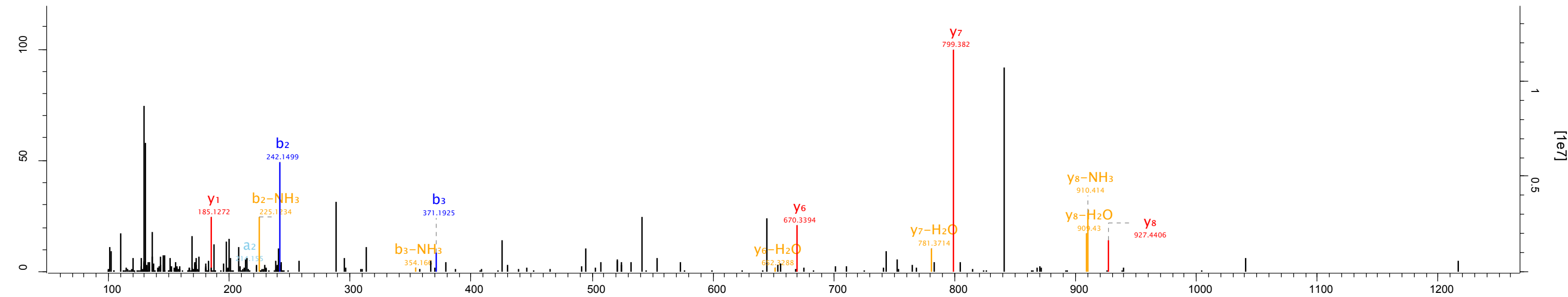
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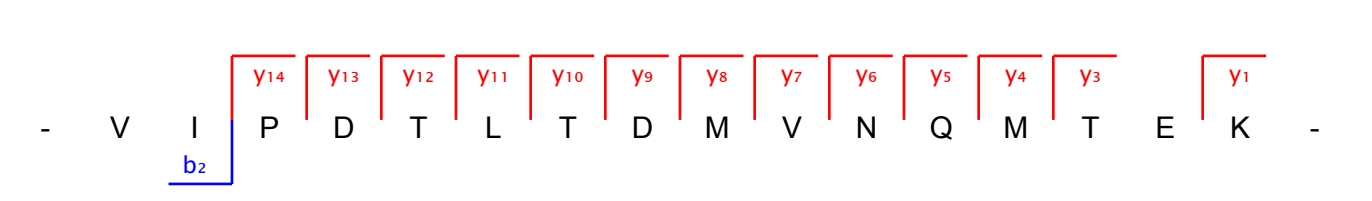
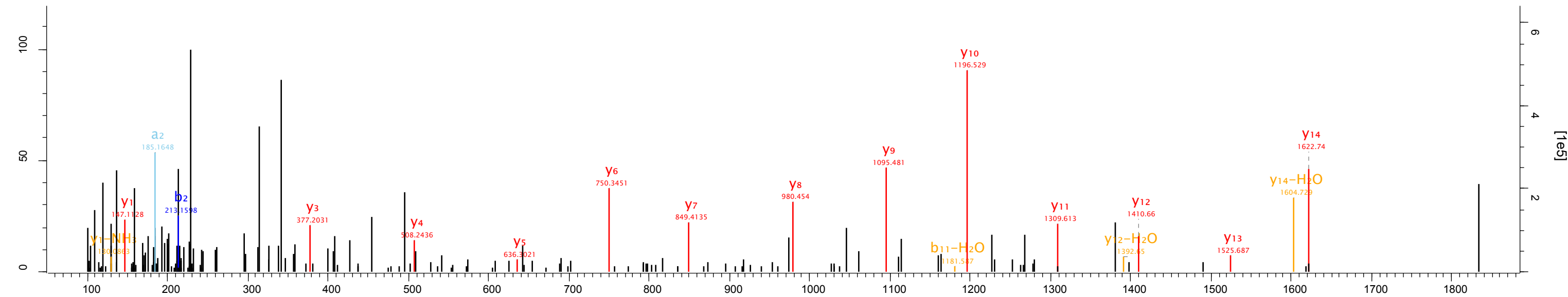
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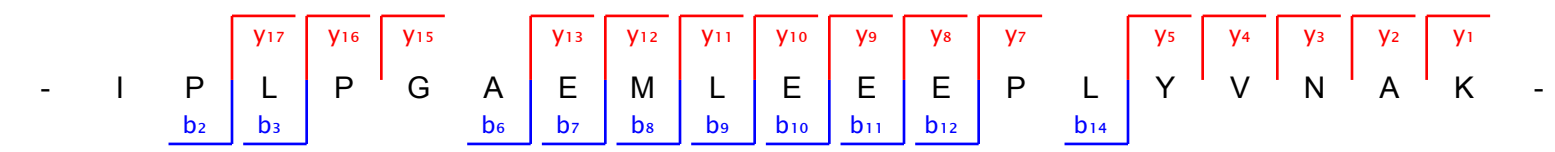
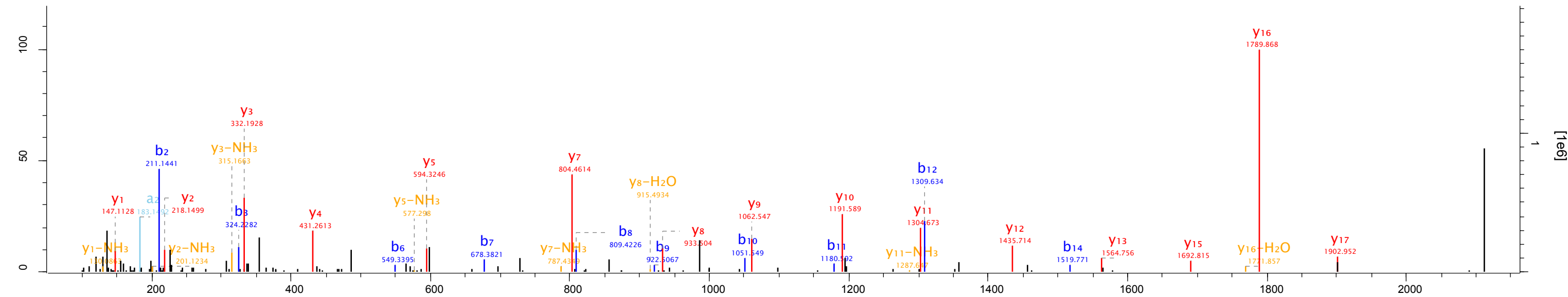
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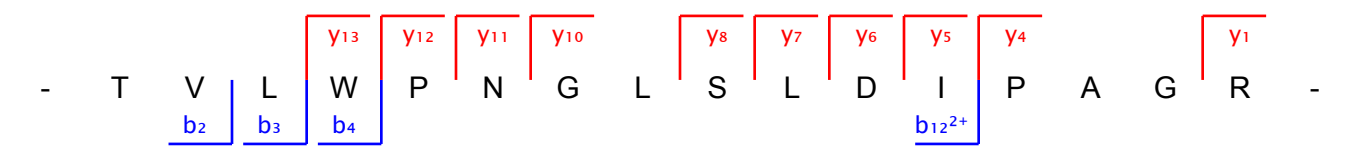
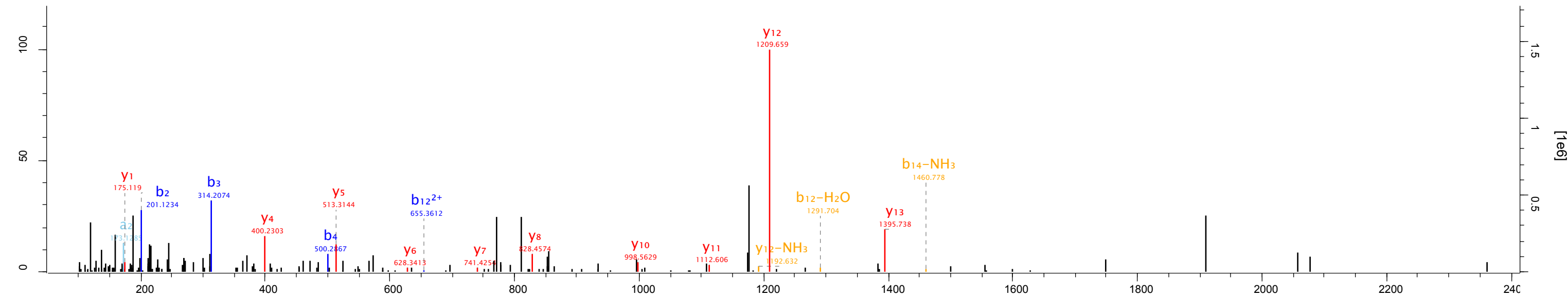
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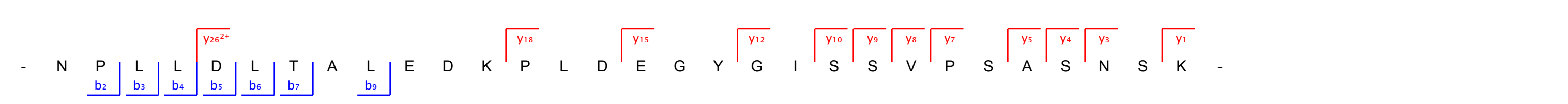
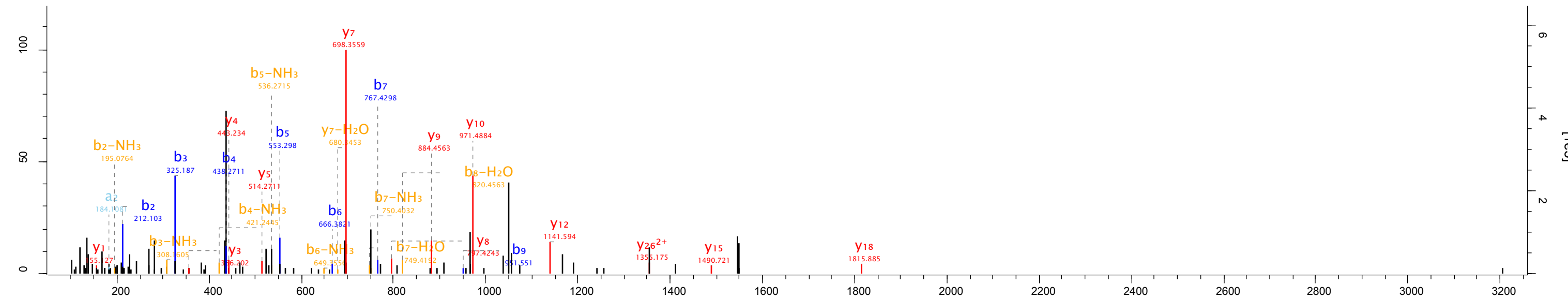
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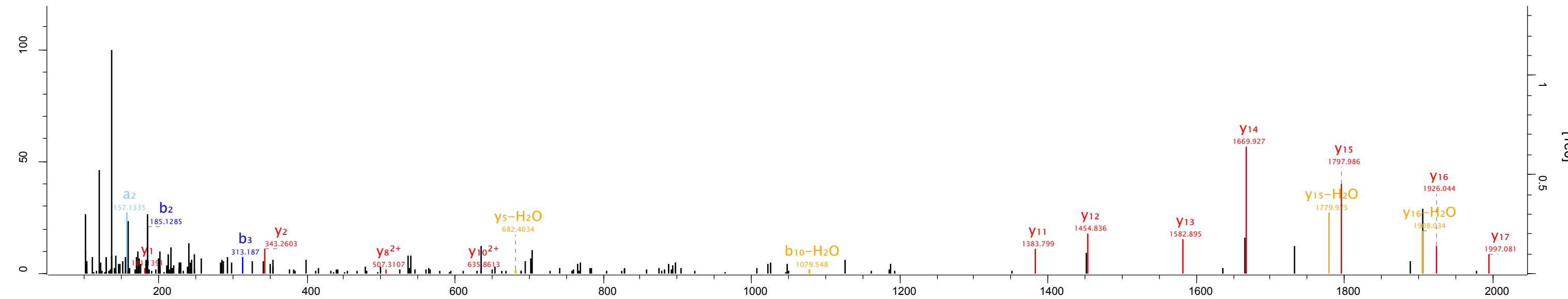
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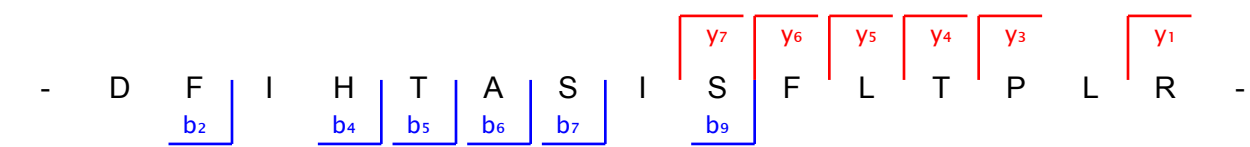
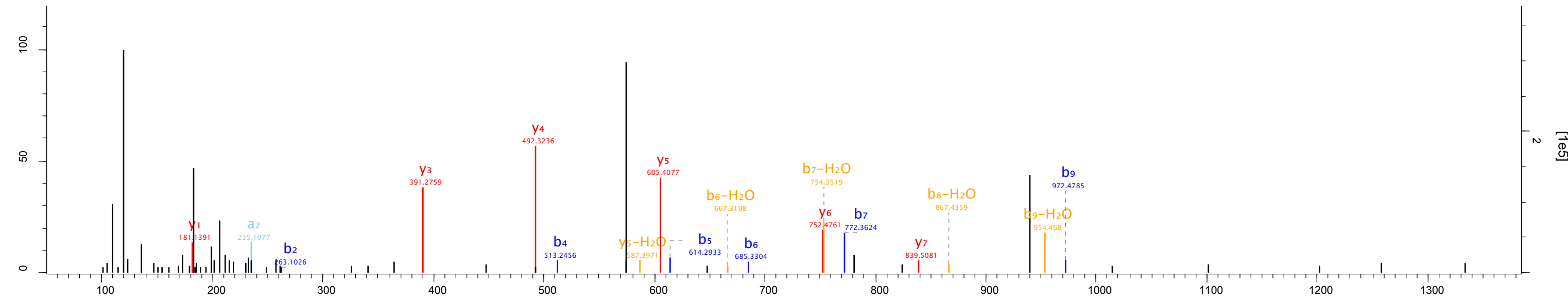


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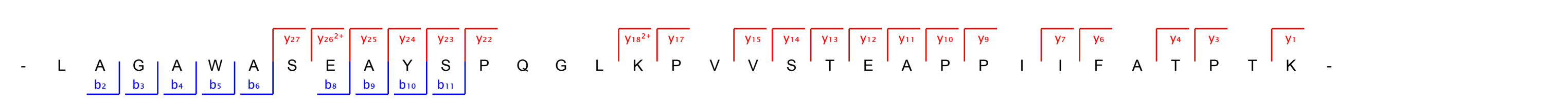
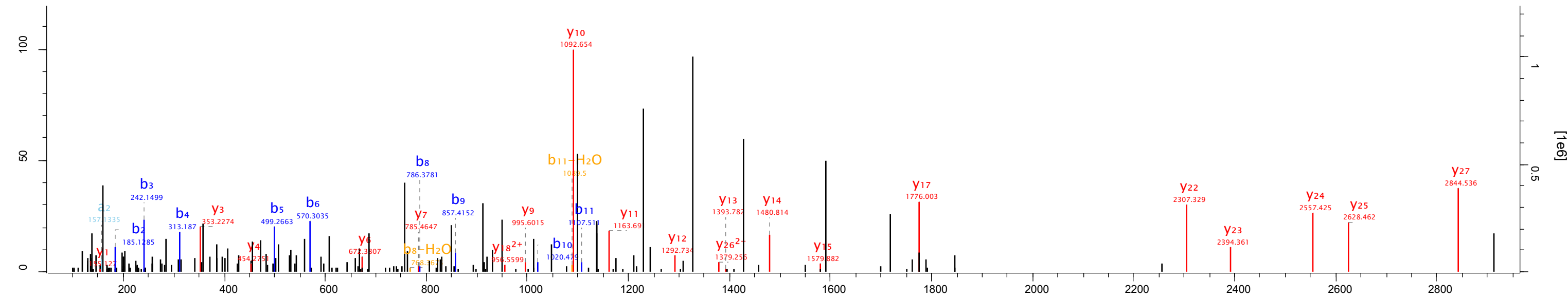


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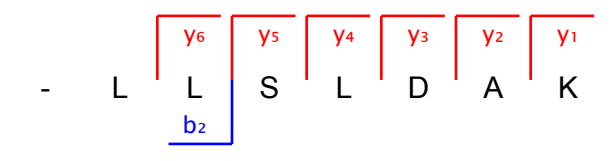
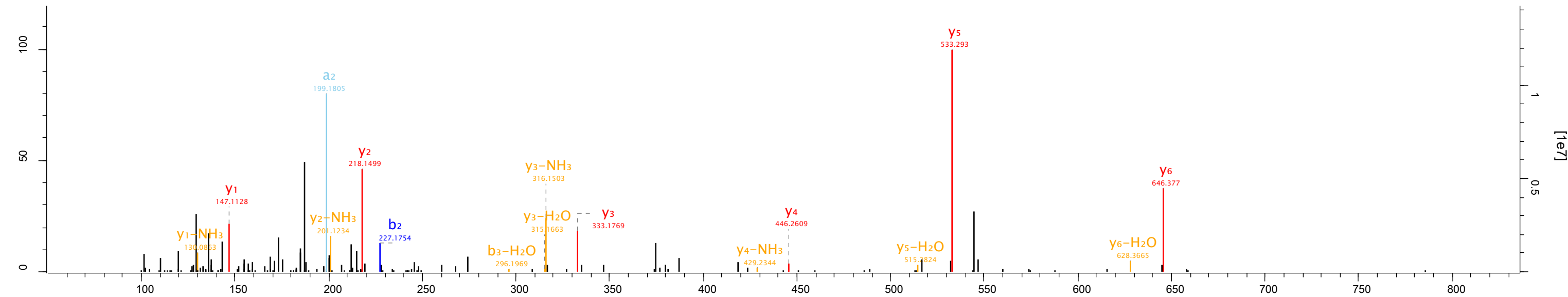




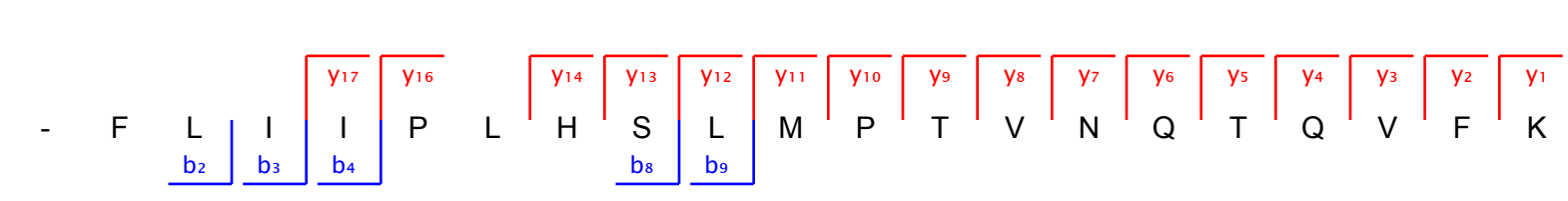
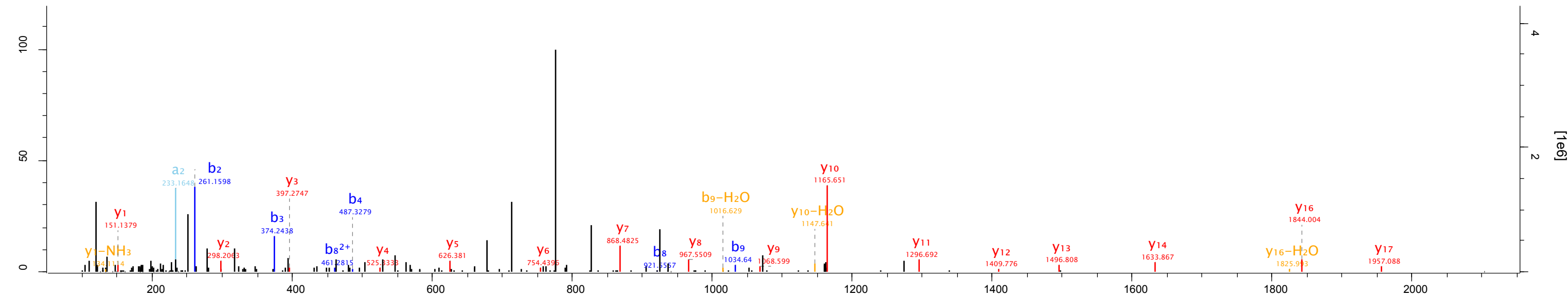
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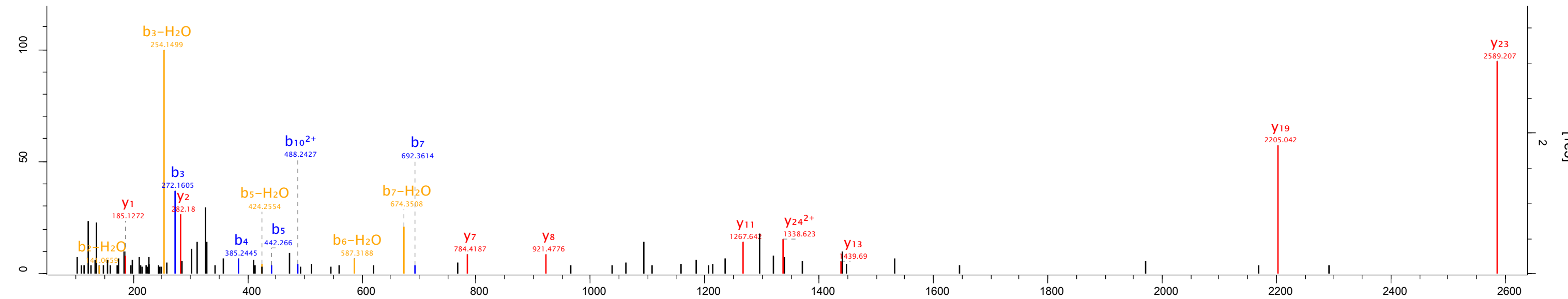
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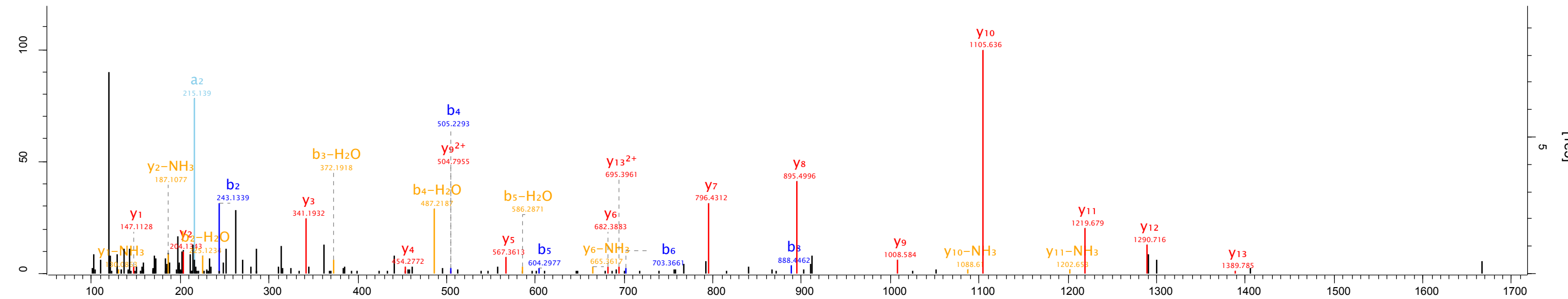


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[1e5]

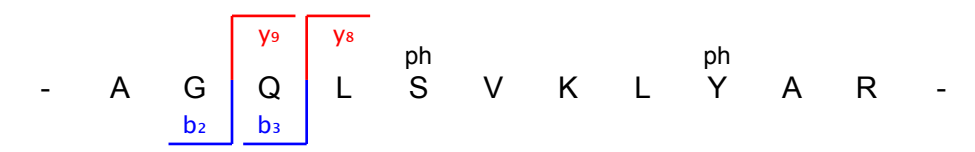
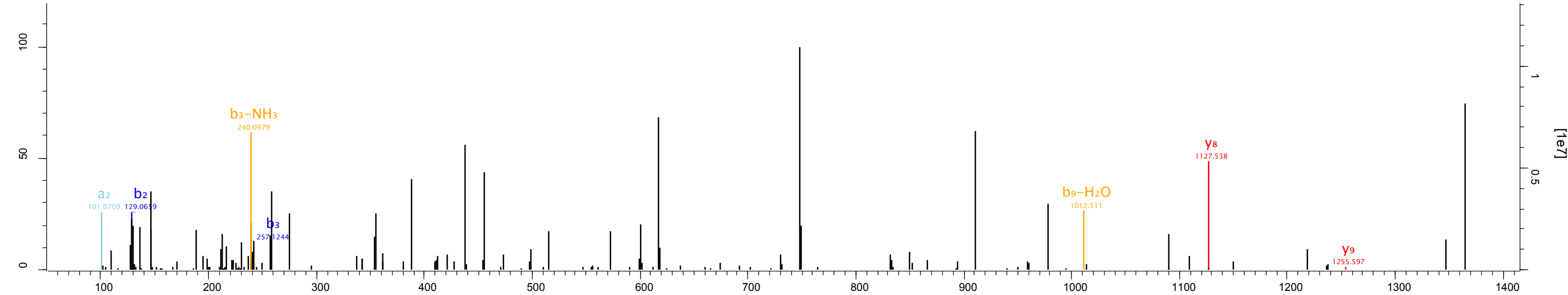
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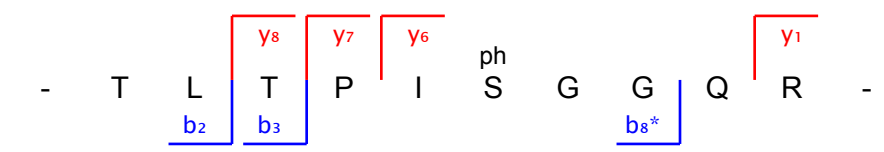
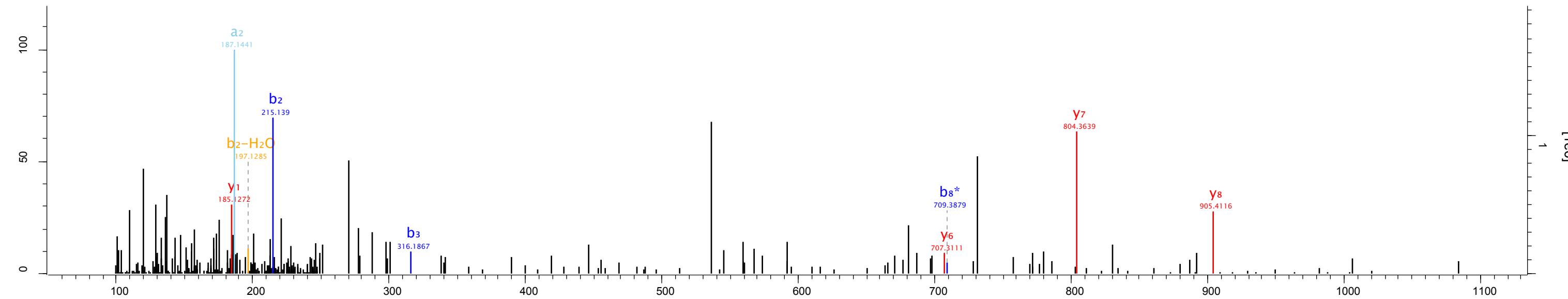
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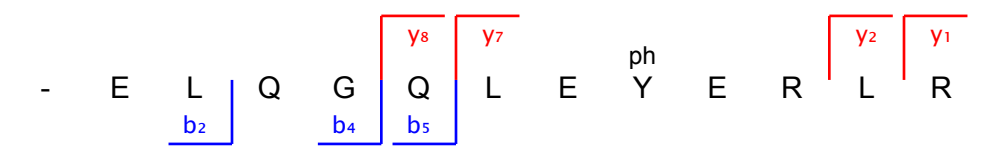
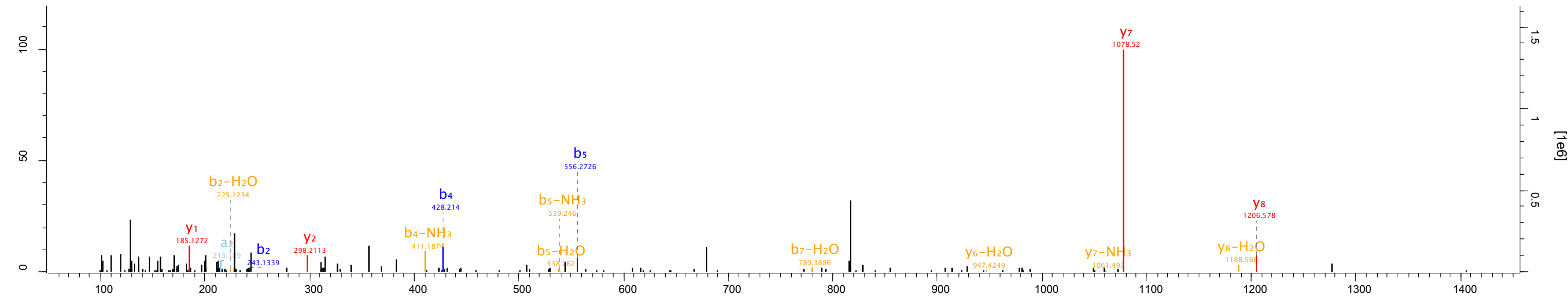
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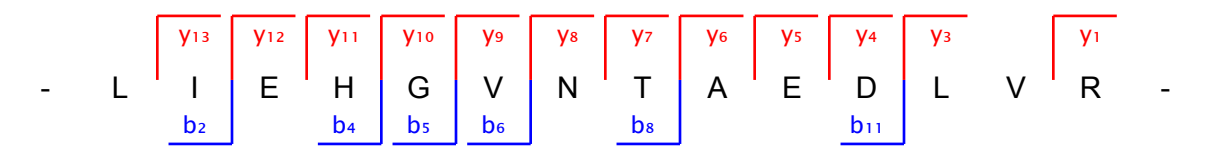
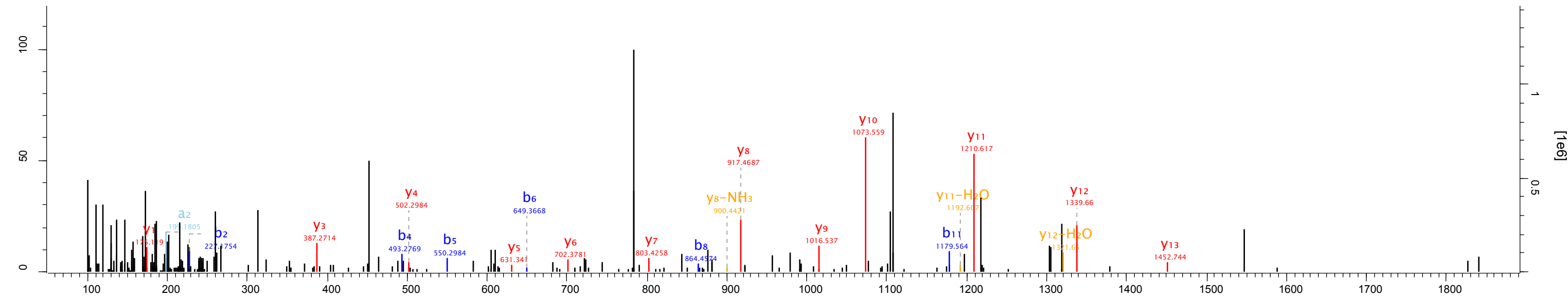
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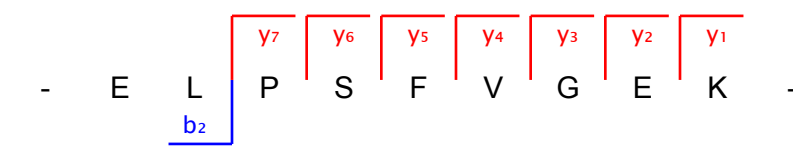
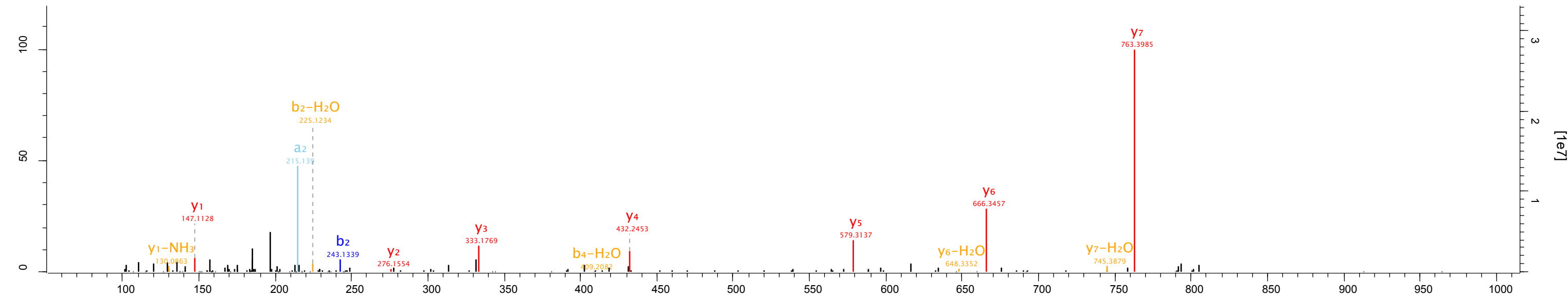
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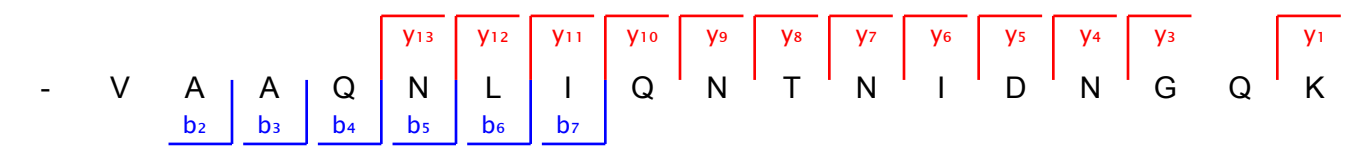
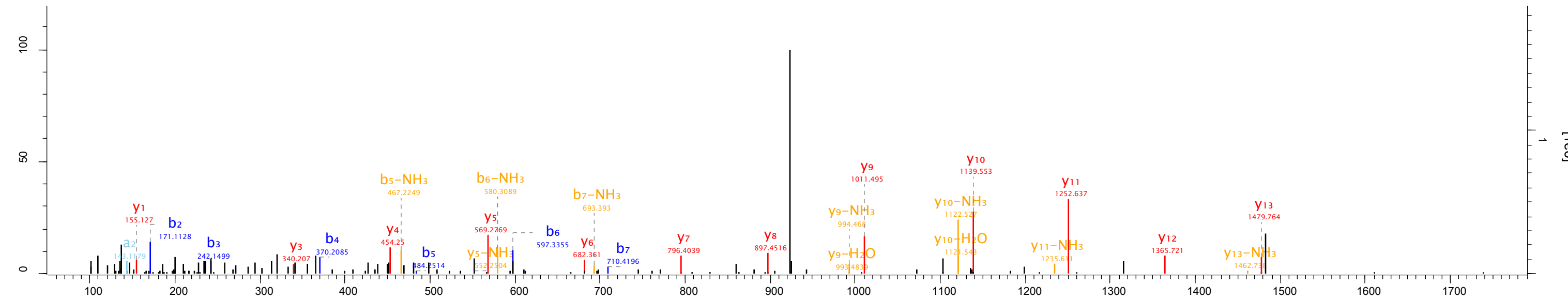
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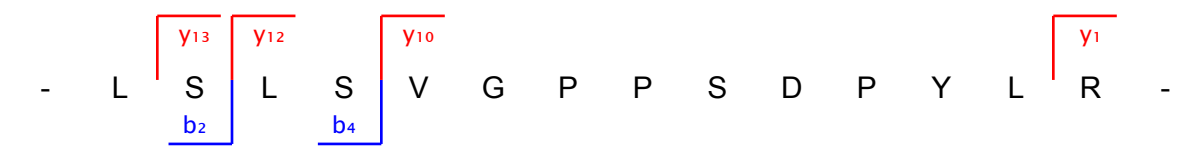
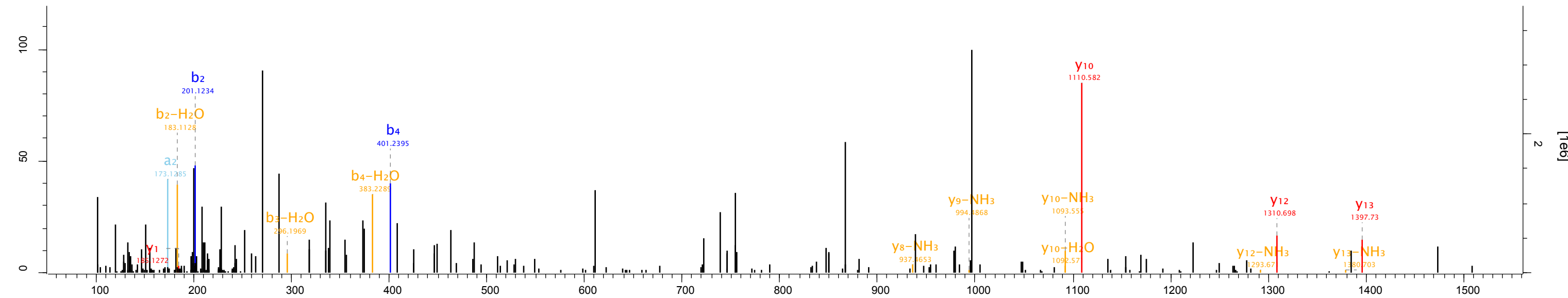
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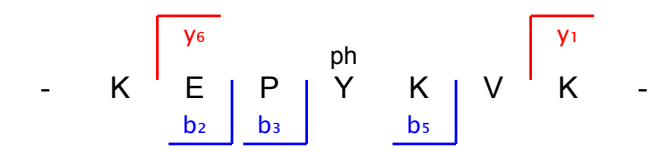
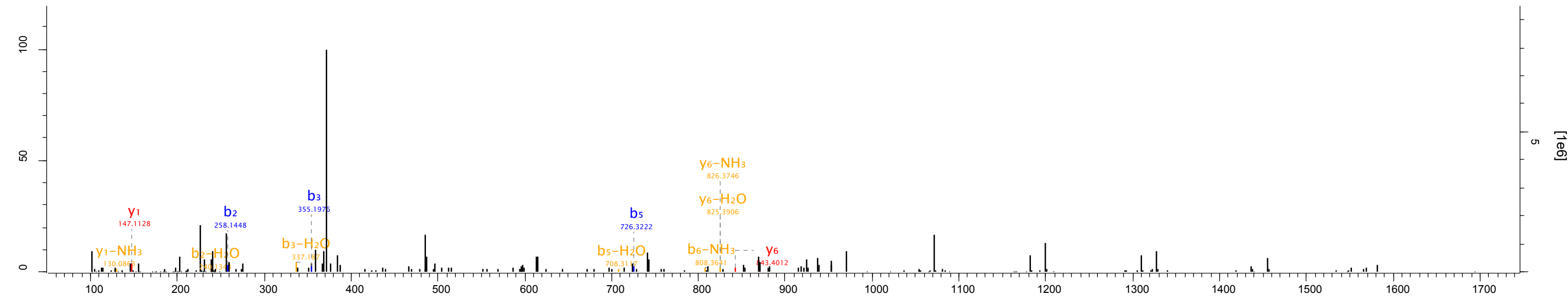
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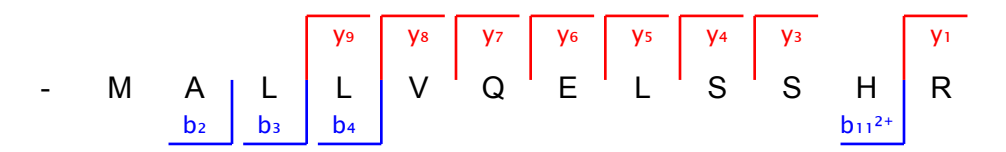
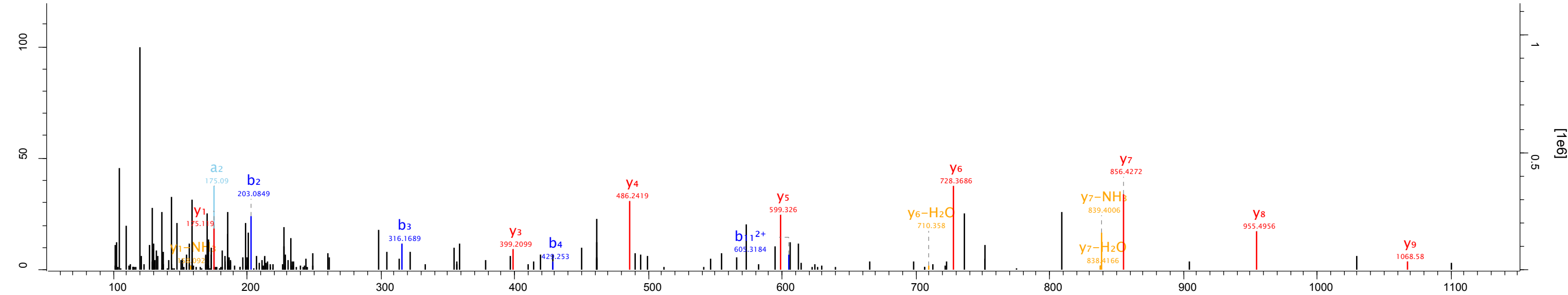
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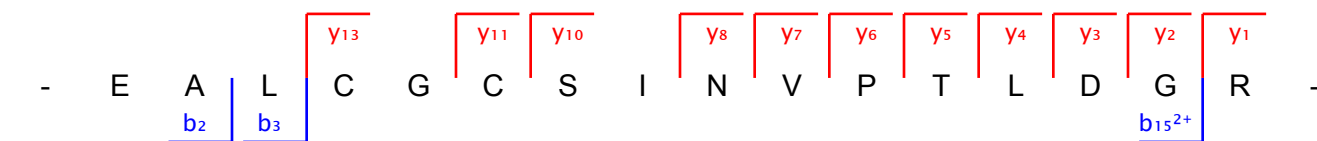
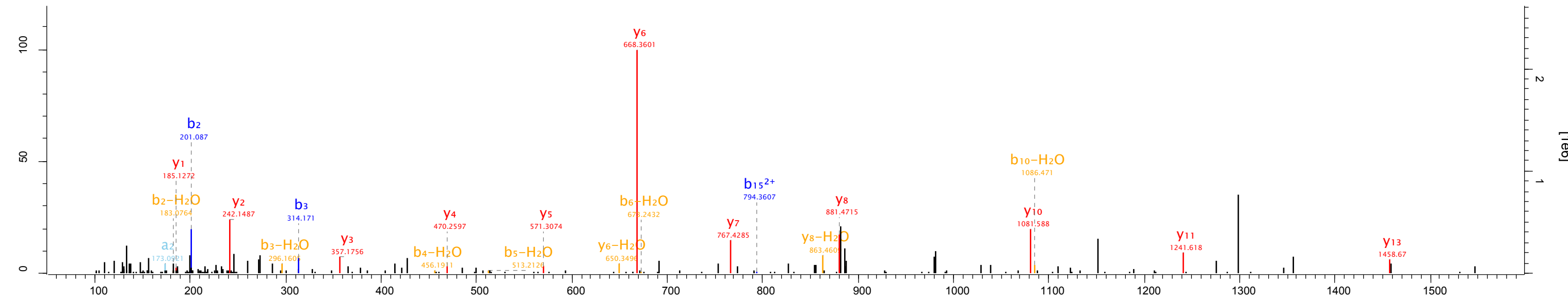


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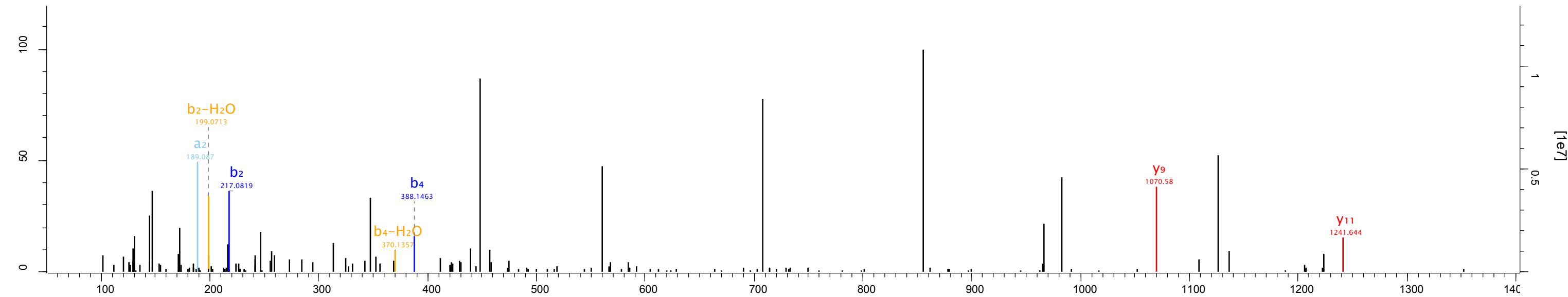
20171215_MaS_33SR_LMH_proteome_01

Scan	Method	Score	m/z	Gene names
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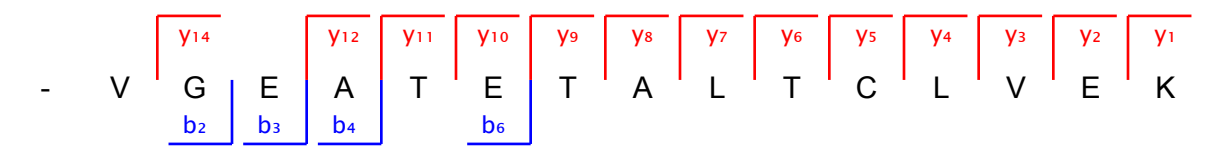
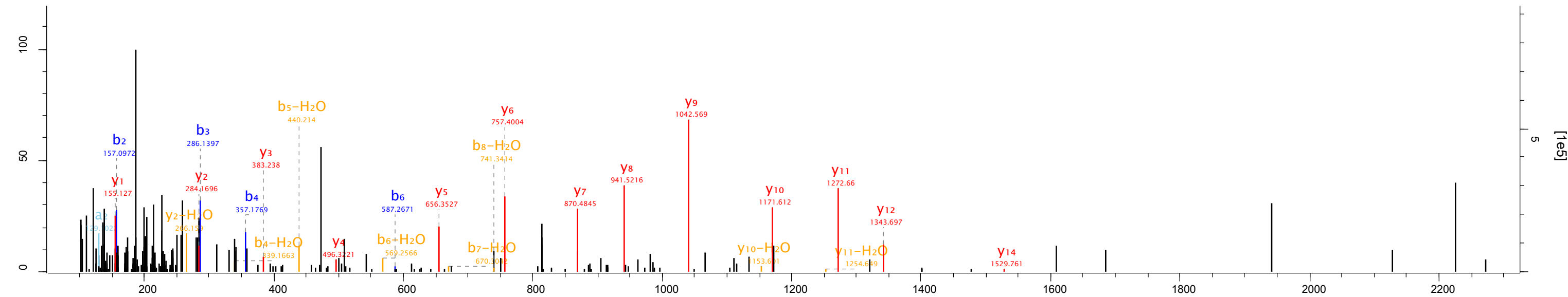




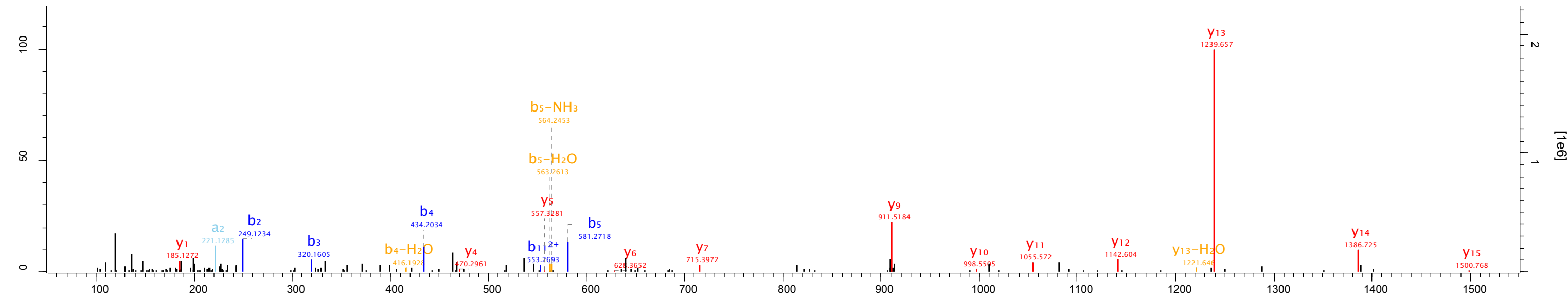
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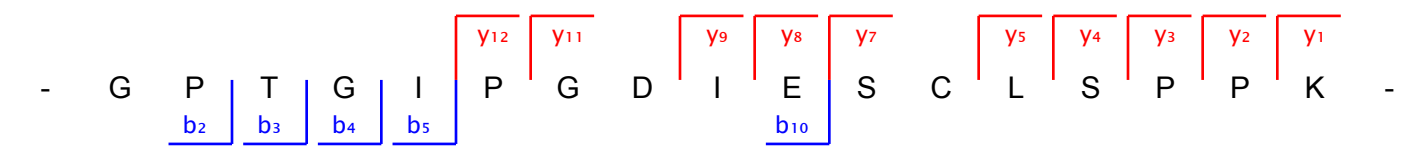
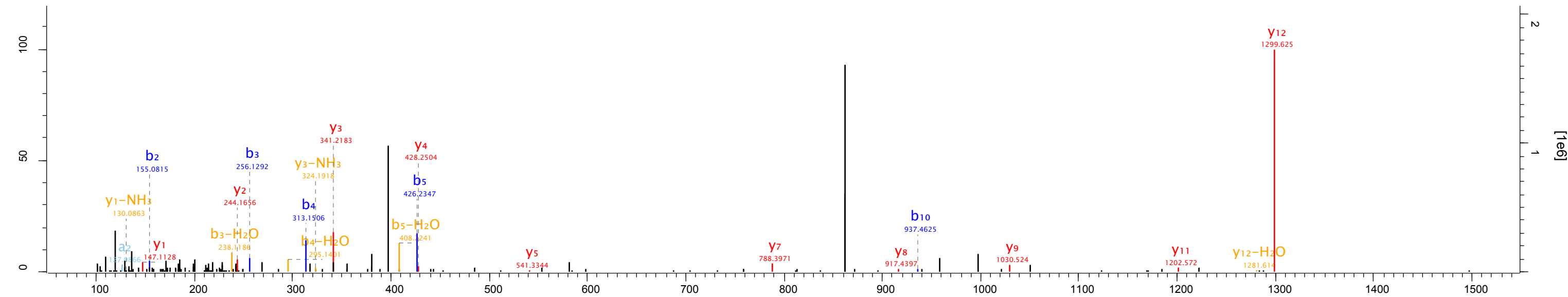
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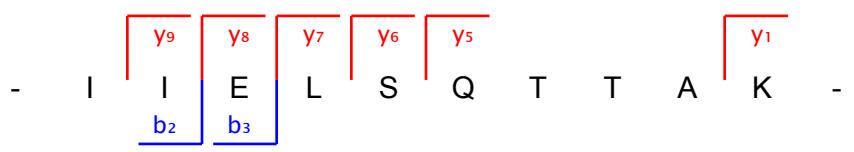
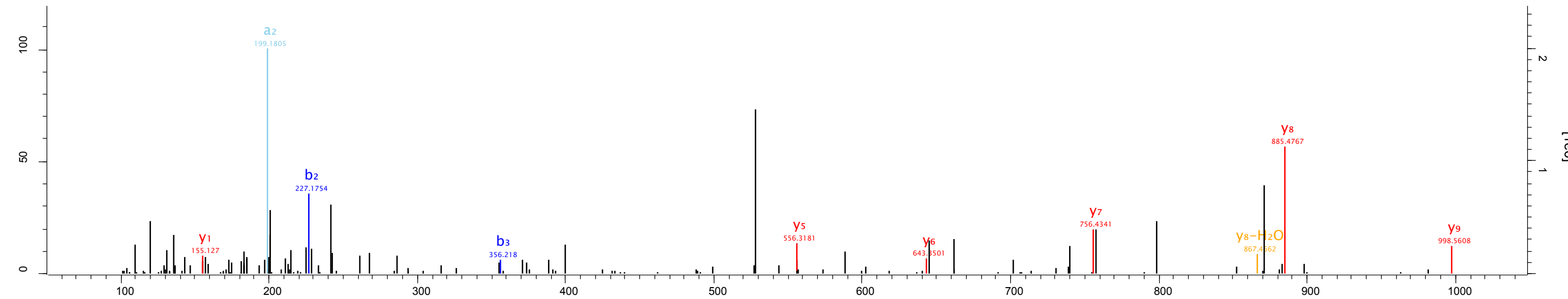
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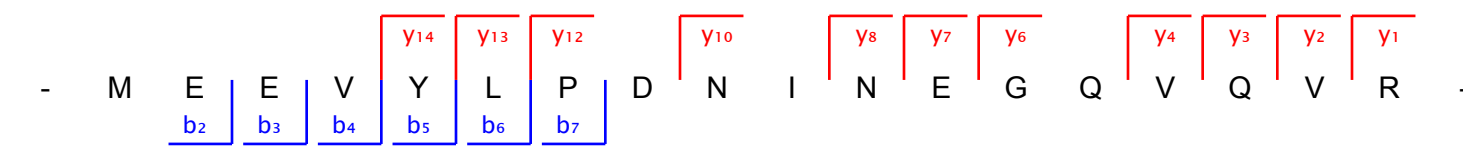
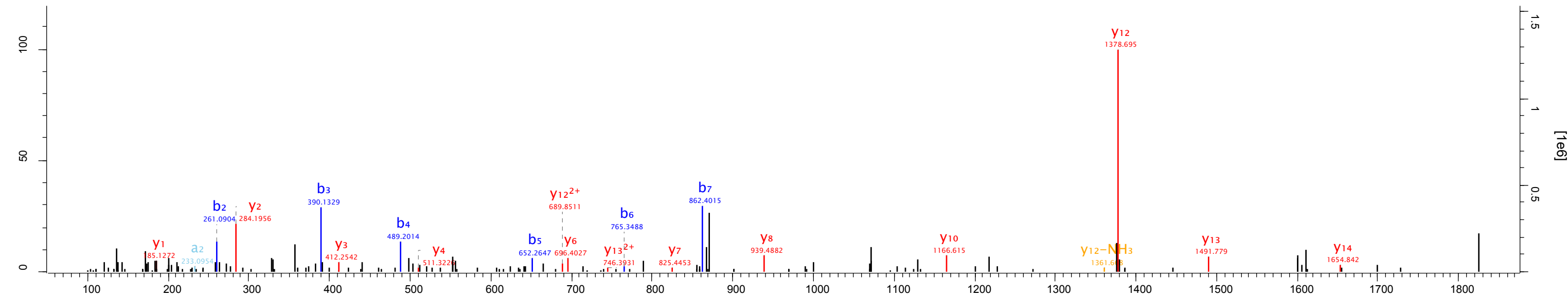
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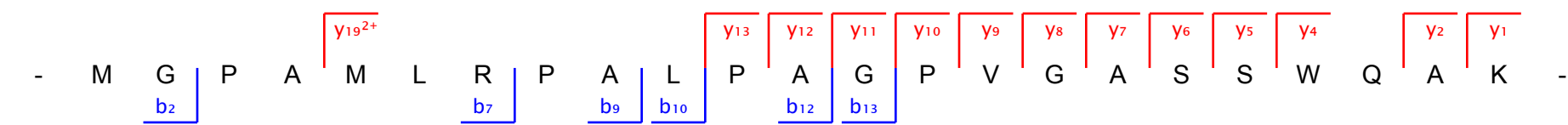
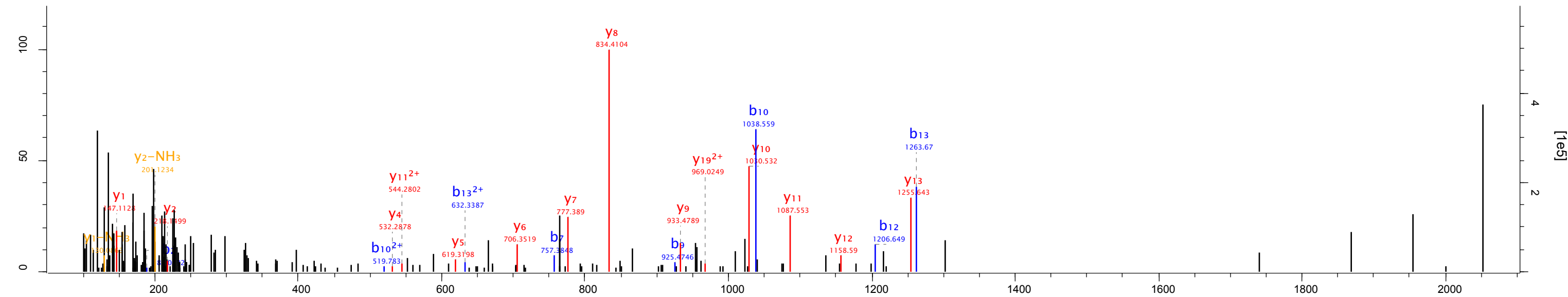


Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 71646 Method FTMS; HCD Score 48.28 m/z 556.33 Gene names NCAM2



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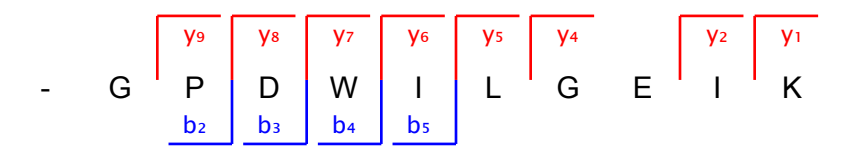
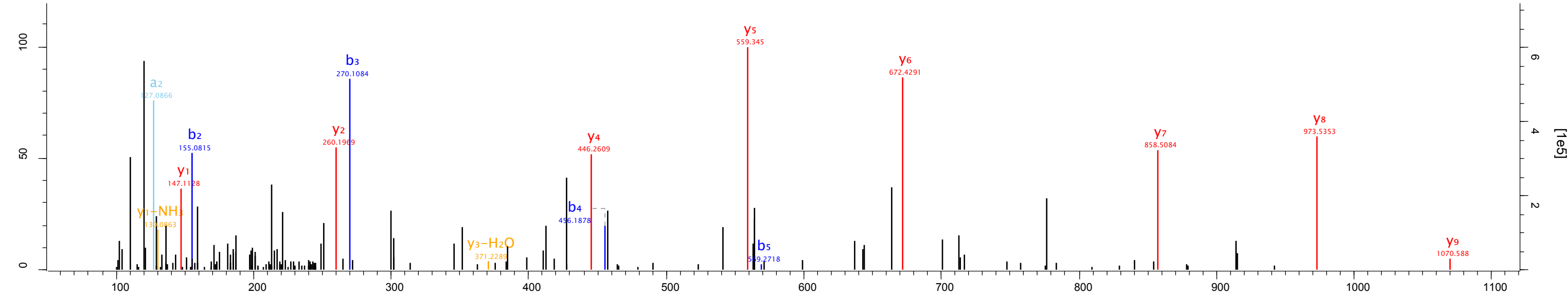




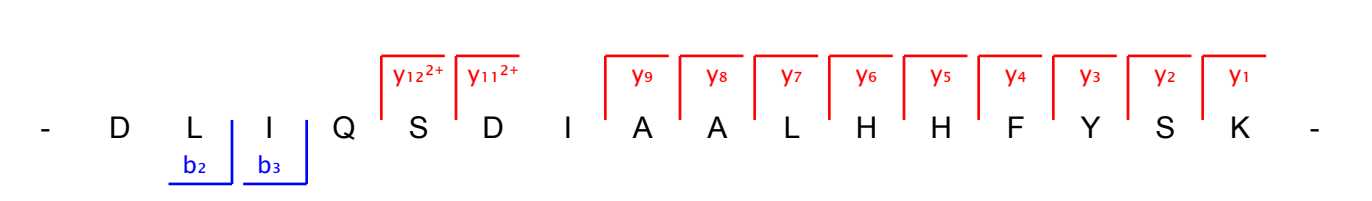
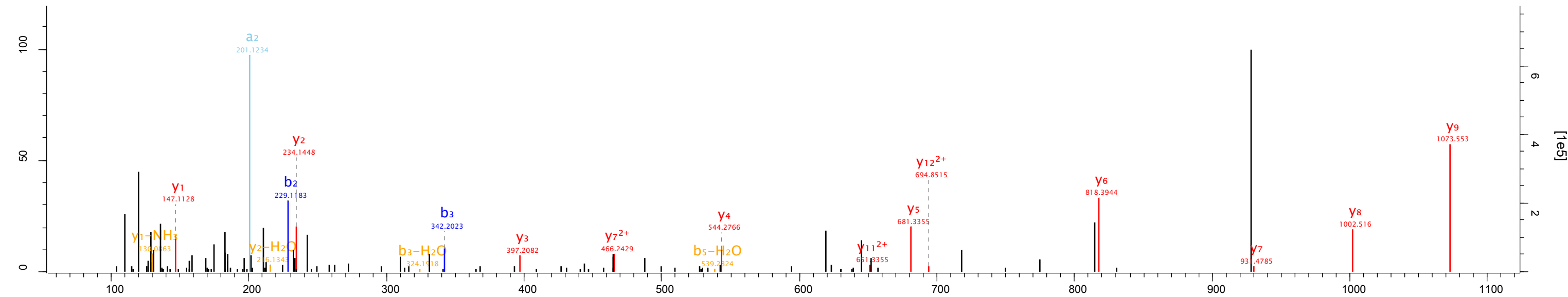
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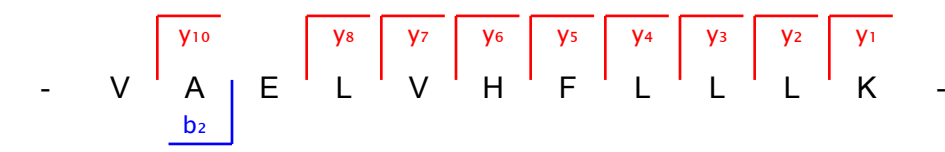
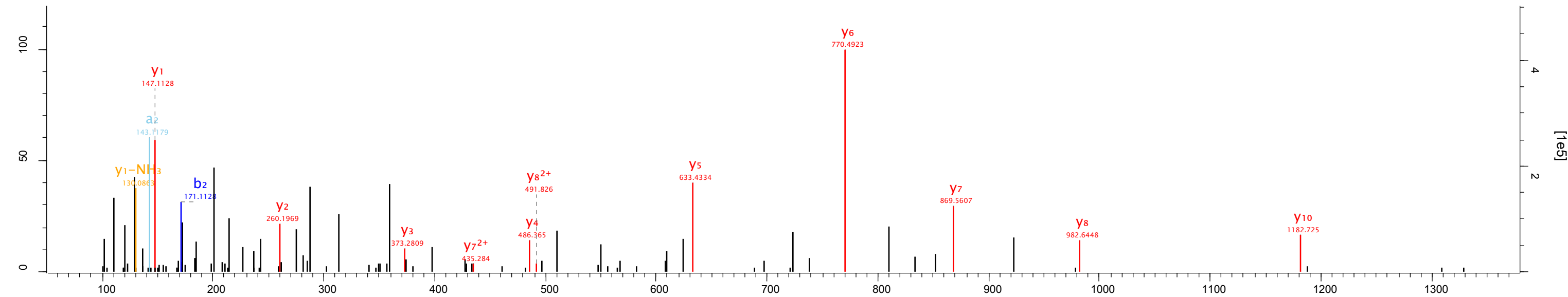
Scan 85506 Method FTMS; HCD Score 61.34 m/z 564.31 Gene names NDUFV1



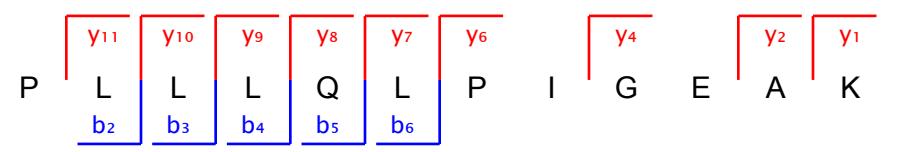
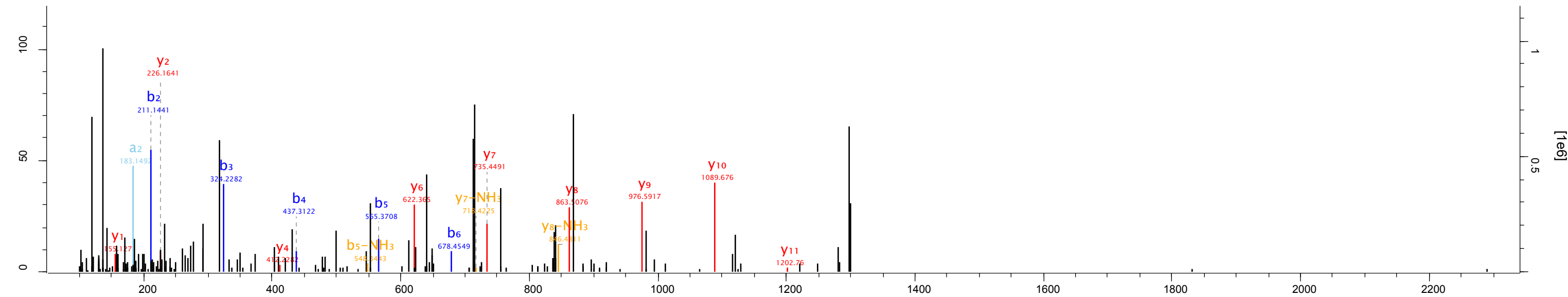
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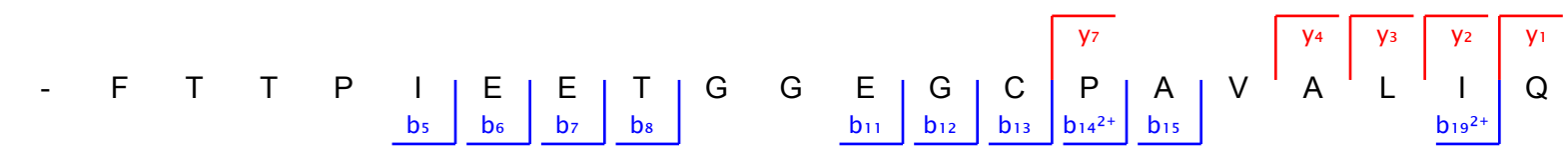
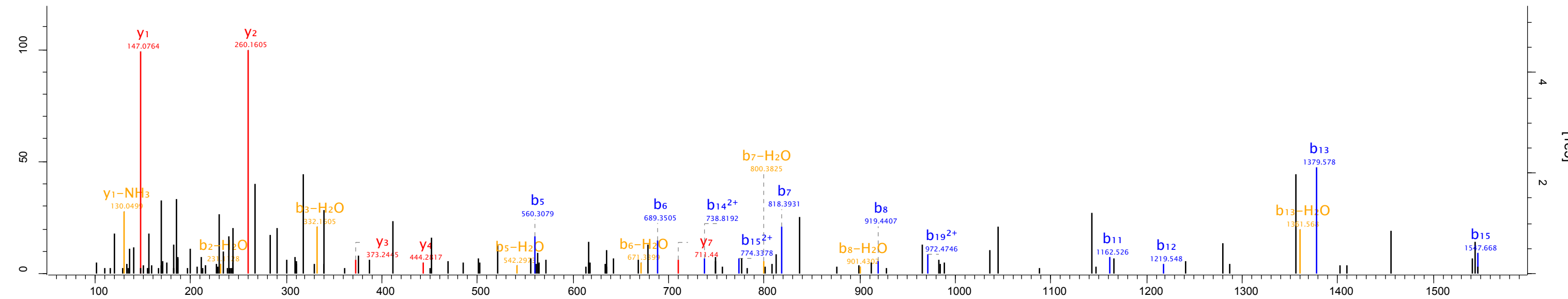
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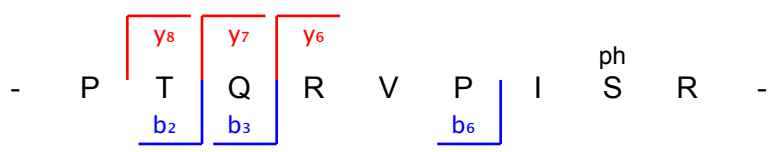
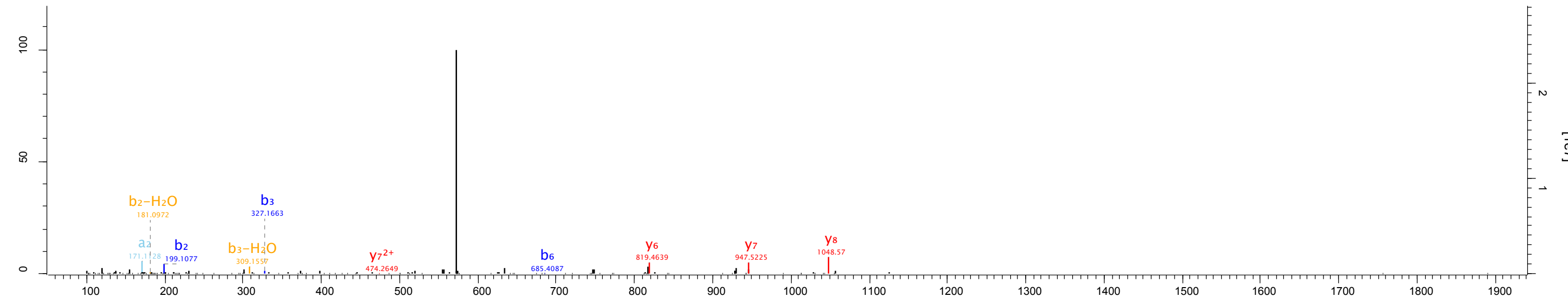
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20171215_MaS_33SR_LMH_proteome_02

Scan	Method	Score	m/z	Gene names
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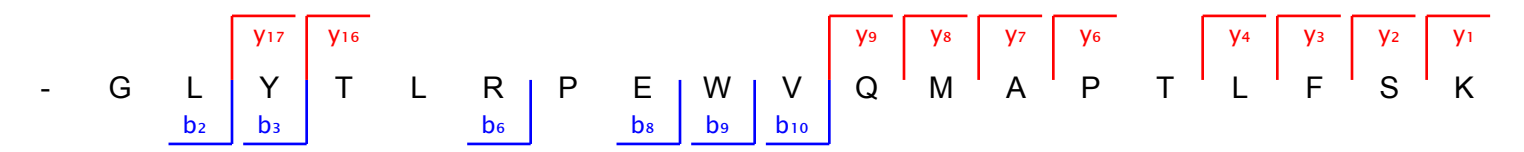
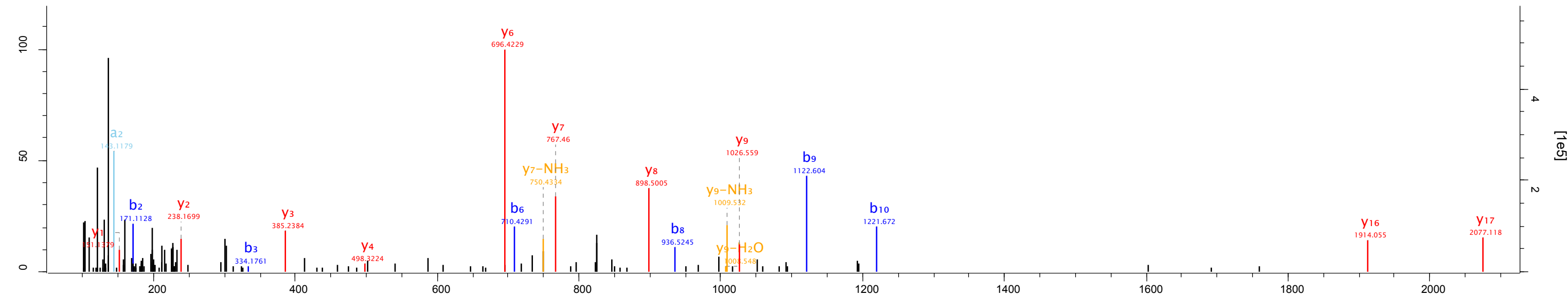


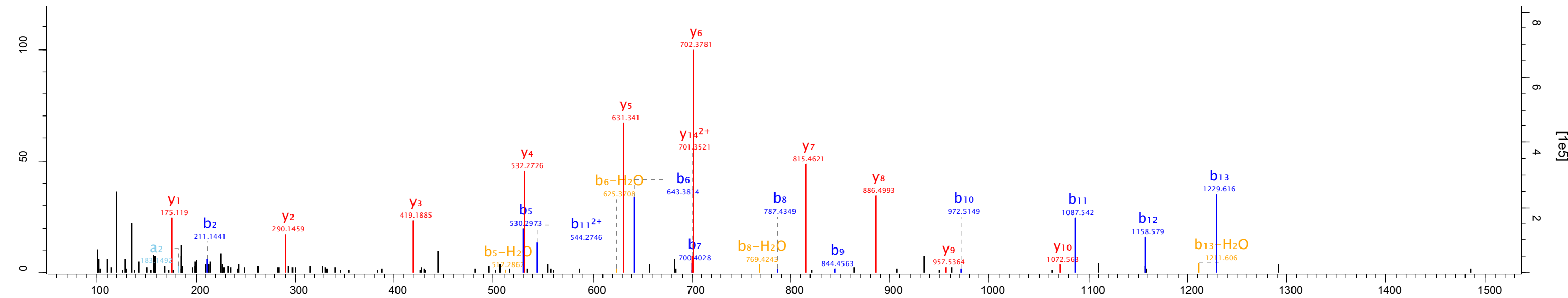
Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 105476 Method FTMS; HCD Score 68.37 m/z 573.57



Raw file
20171215_MaS_33SR_LMH_proteome_02

Scan 121846 Method FTMS; HCD Score 70.84 m/z 750.41 Gene names CACUL1



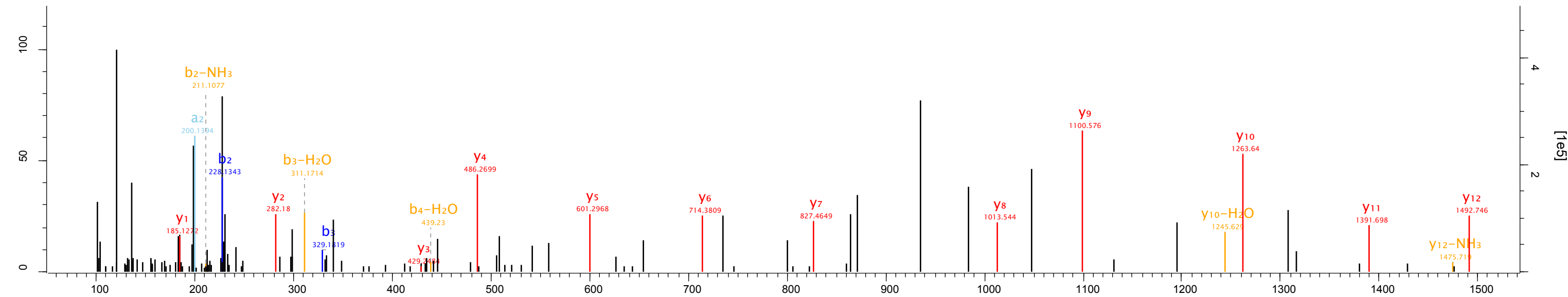


- L P F T A L G S G Q D A A L A V L E D R -

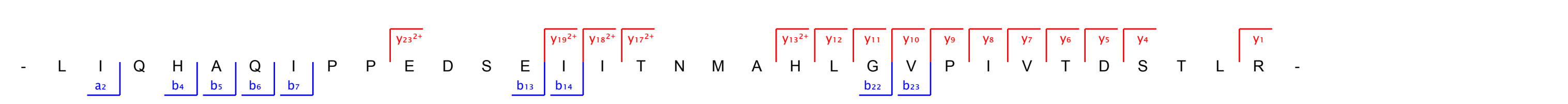
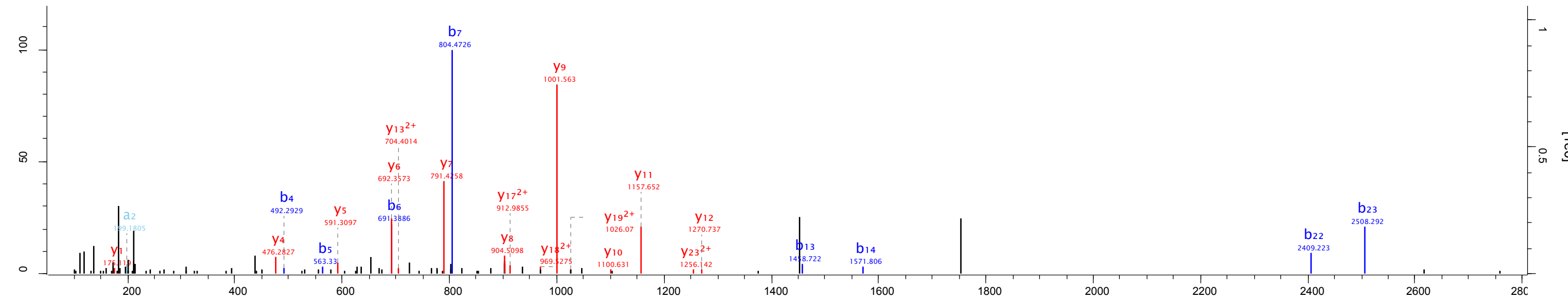
Fragmentation sites are indicated by brackets below the sequence:

- b2: [P]
- b5: [A]
- b6: [L]
- b7: [G]
- b8: [S]
- b9: [G]
- b10: [Q]
- b11: [D]
- b12: [A]
- b13: [A]
- y1: [R]
- y2: [D]
- y3: [E]
- y4: [L]
- y5: [V]
- y6: [A]
- y7: [L]
- y8: [A]
- y9: [D]
- y10: [Q]
- y14²⁺: [G]

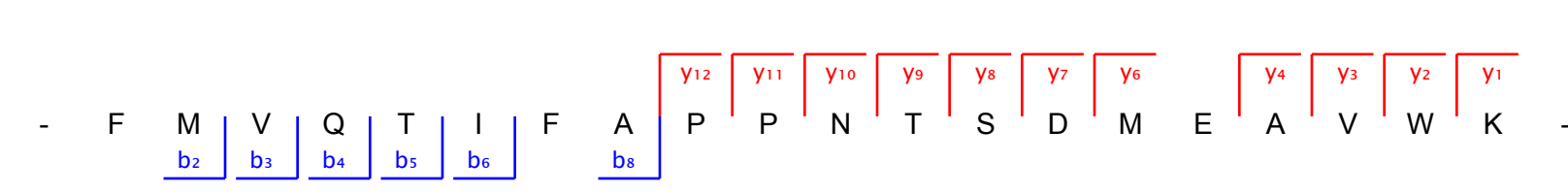
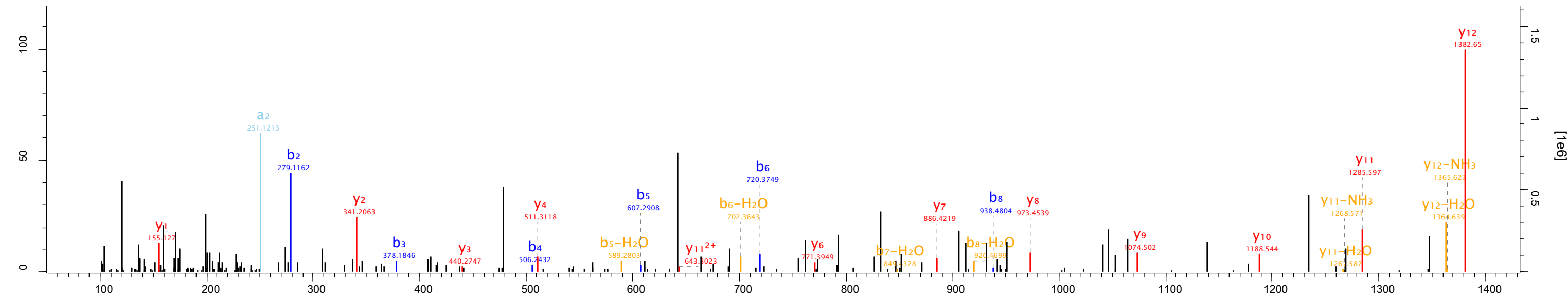
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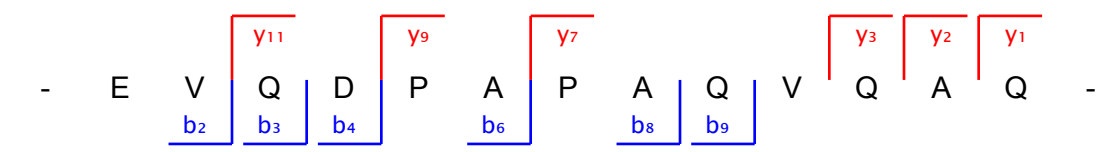
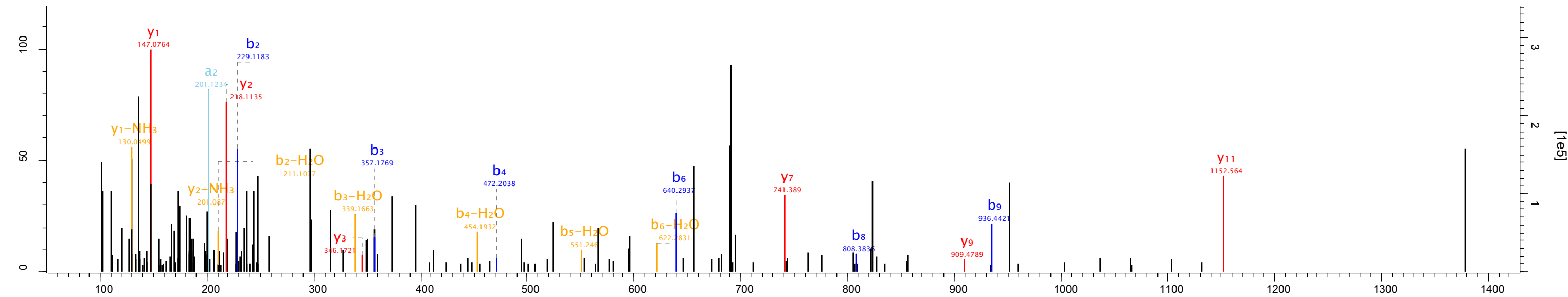
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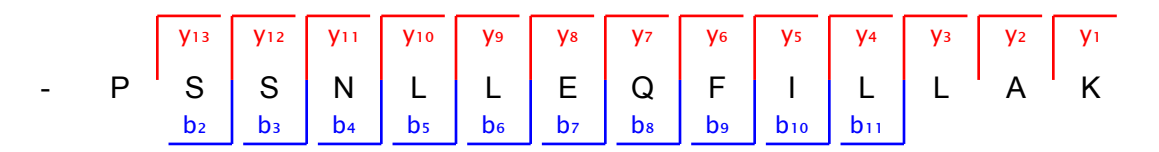
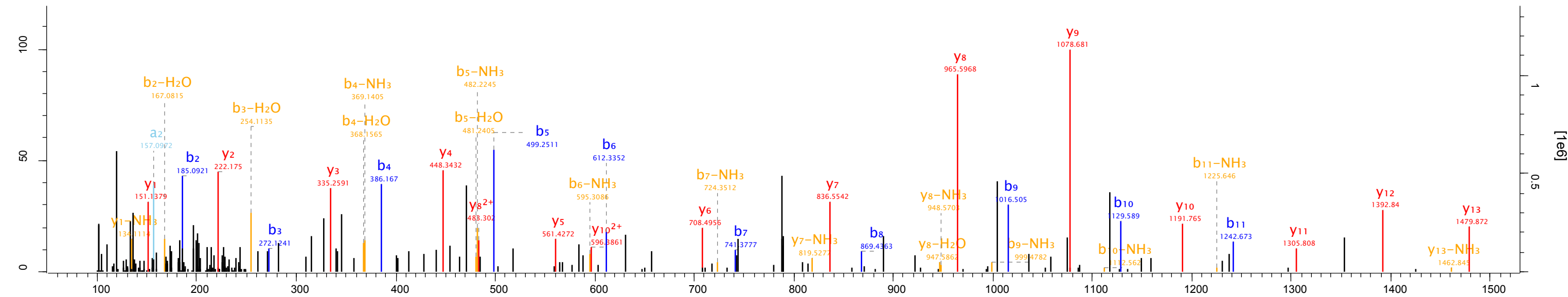
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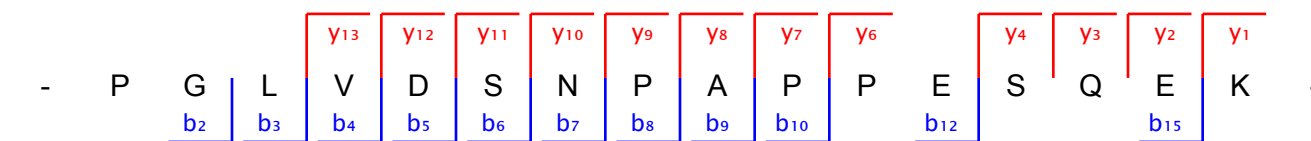
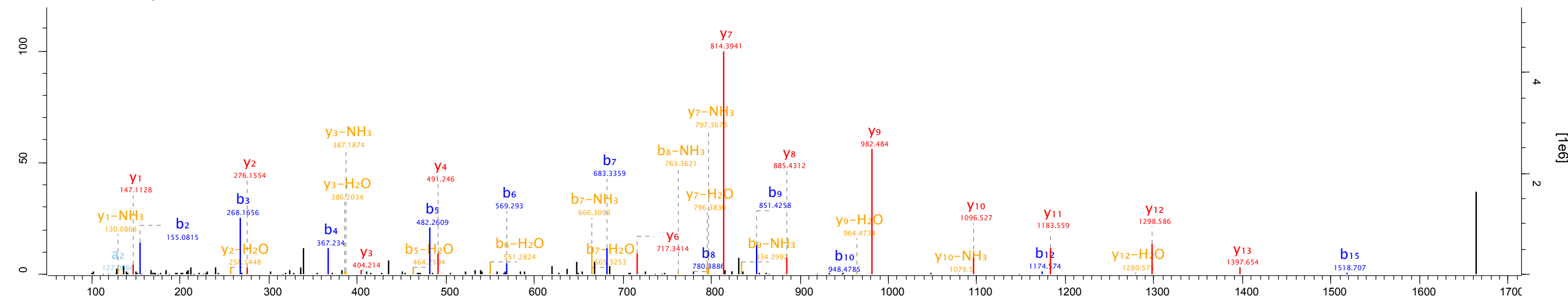


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Raw file
20171215_MaS_33SR_LMH_proteome_02

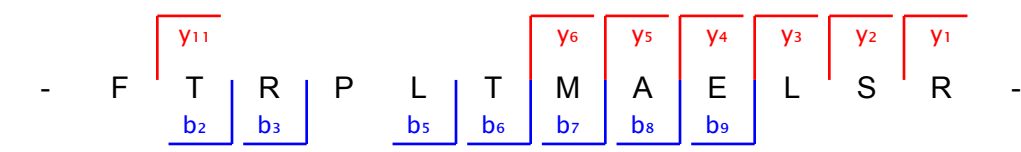
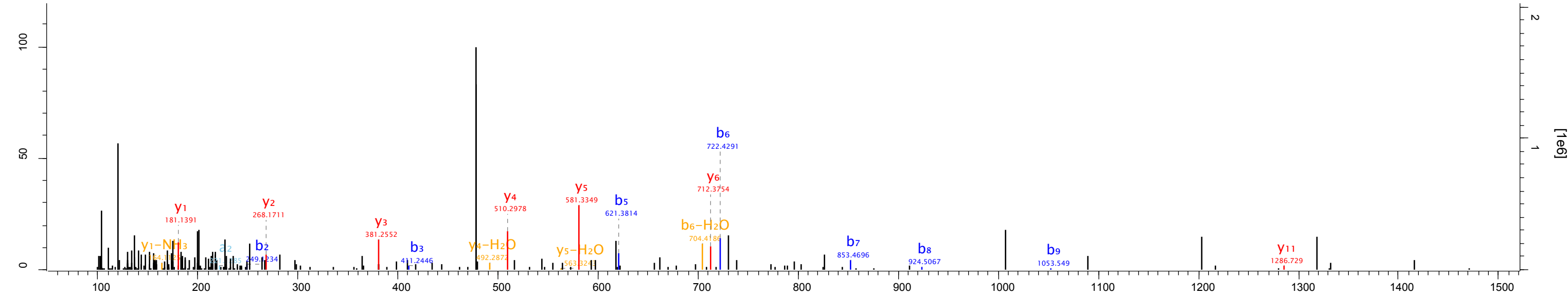
Scan 16086 Method FTMS; HCD Score 177.04 m/z 832.91 Gene names COX17



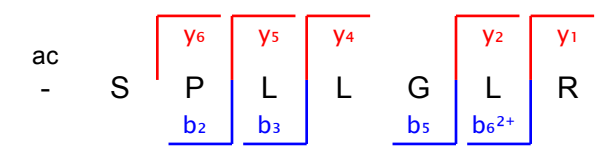
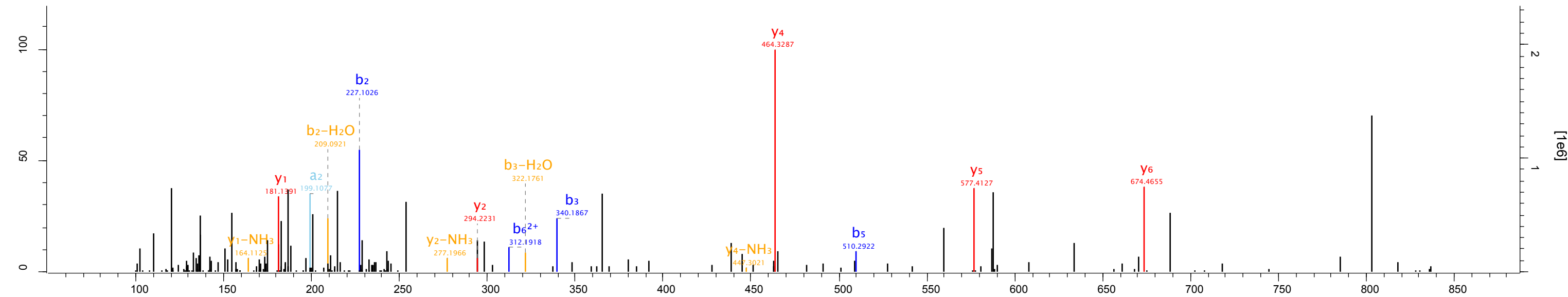
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20171215_MaS_33SR_LMH_proteome_02

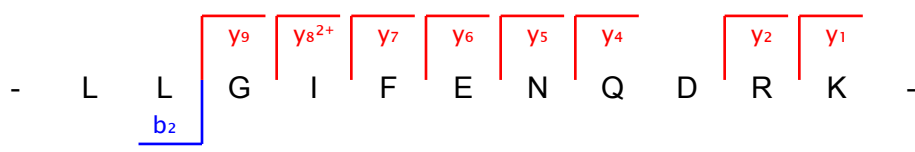
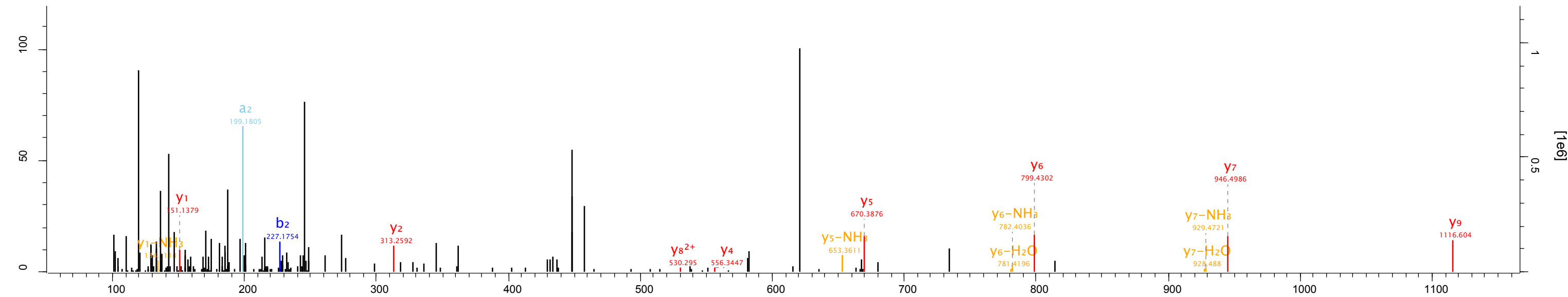
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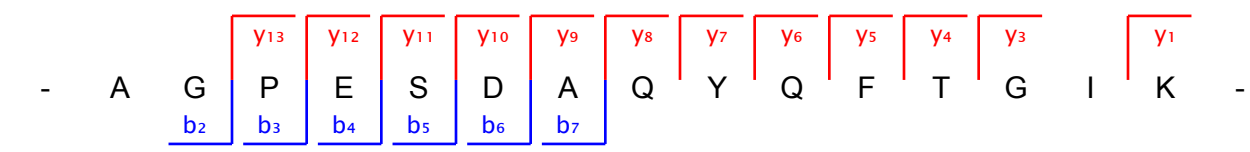
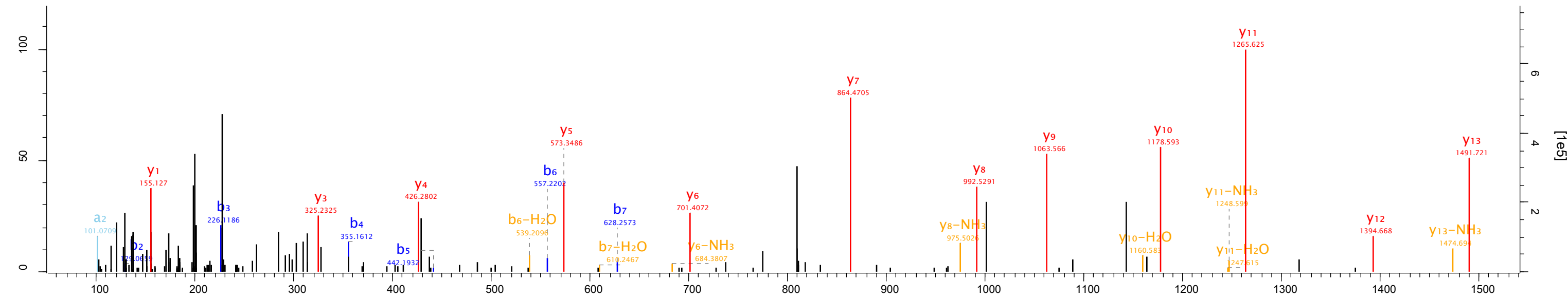
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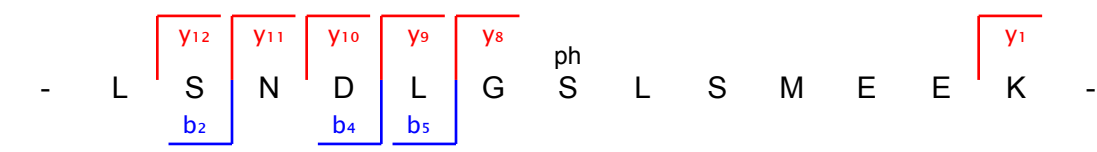
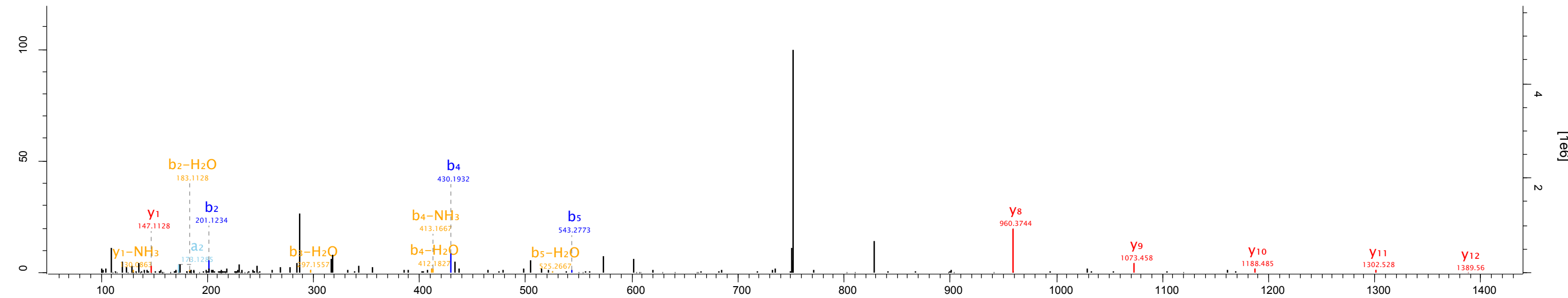
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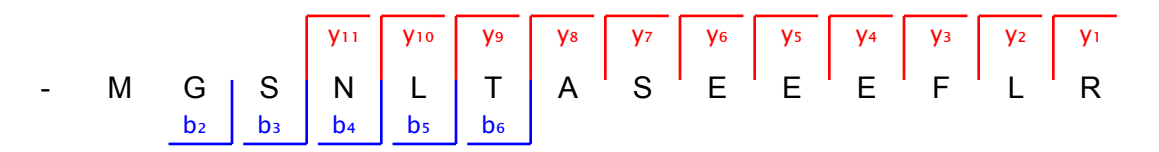
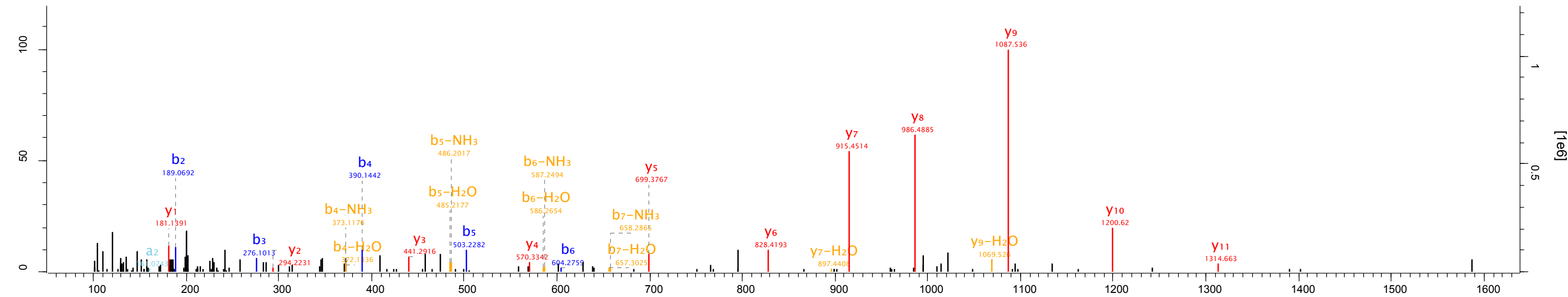
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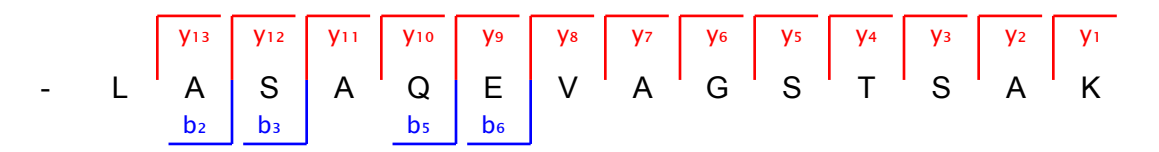
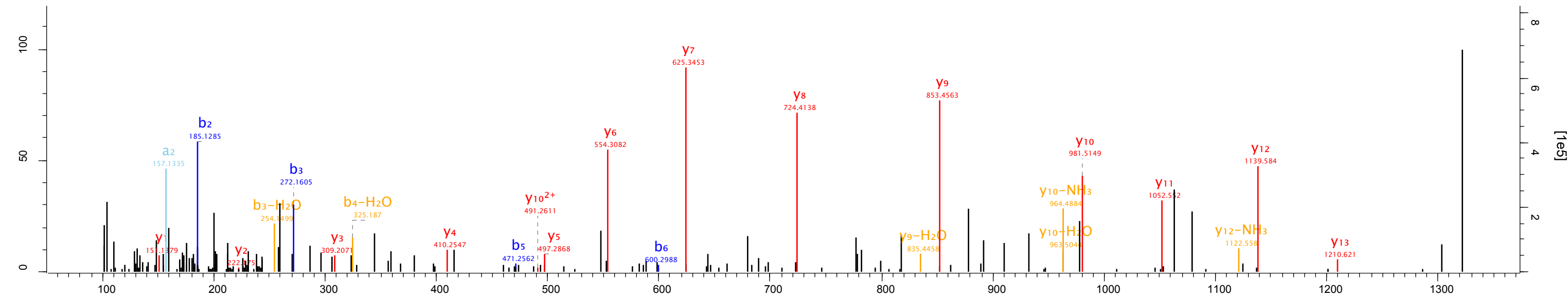
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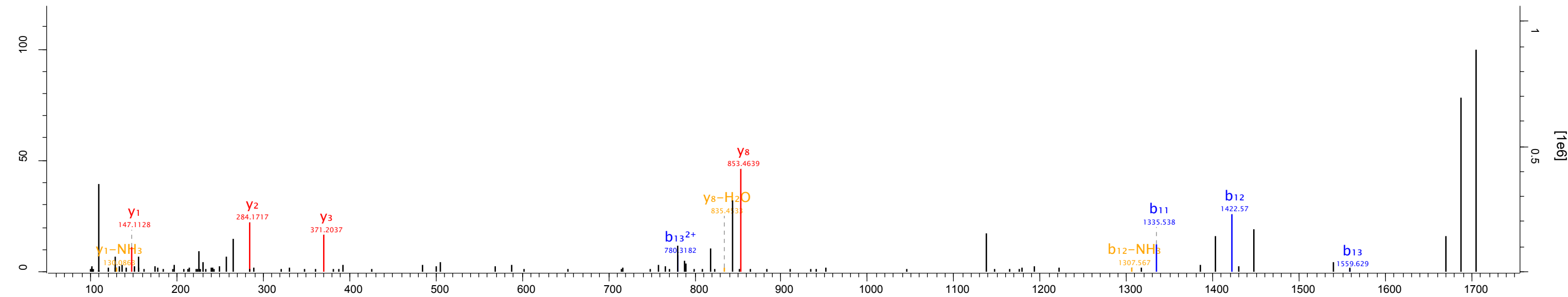
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Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 6806 Method FTMS; HCD Score 80.39 m/z 662.36 Gene names C1orf174



Raw file
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 Scan 7166 Method FTMS; HCD Score 42 m/z 853.37



- L S S E Y L A S R A P S H K -

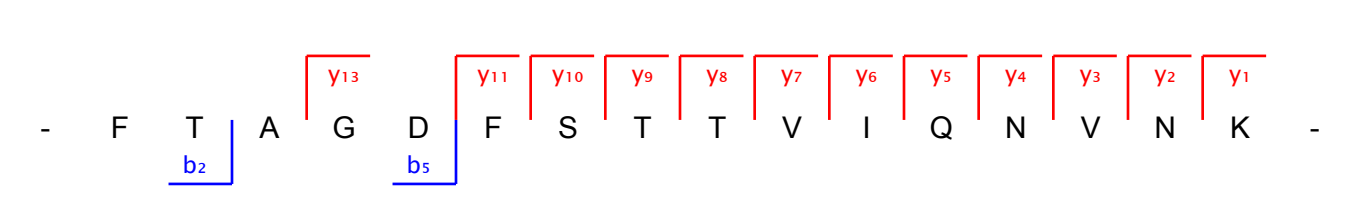
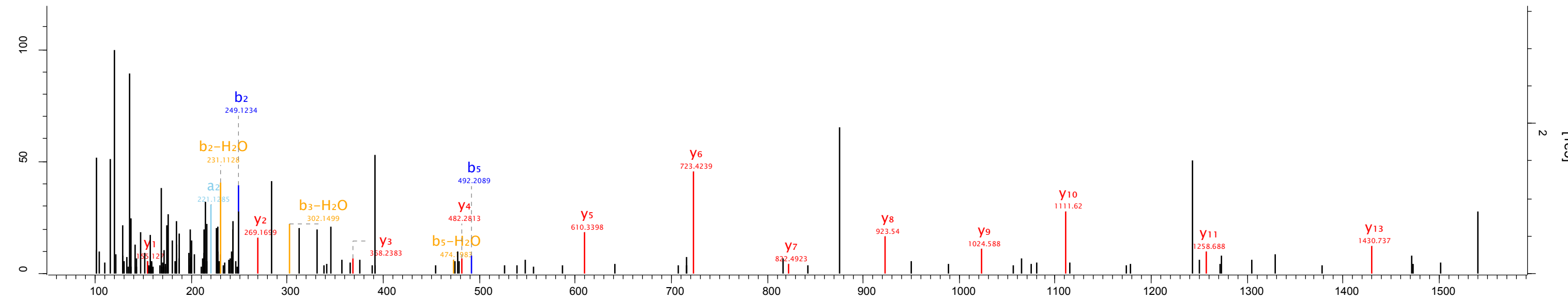
Fragmentation labels above the sequence:

- y_8 above A
- y_3 above S
- y_2 above H
- y_1 above K

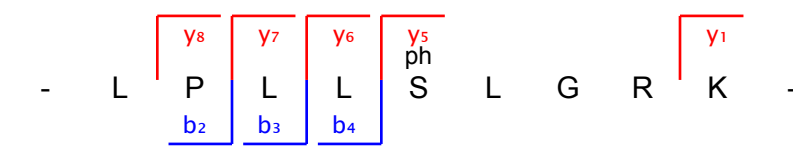
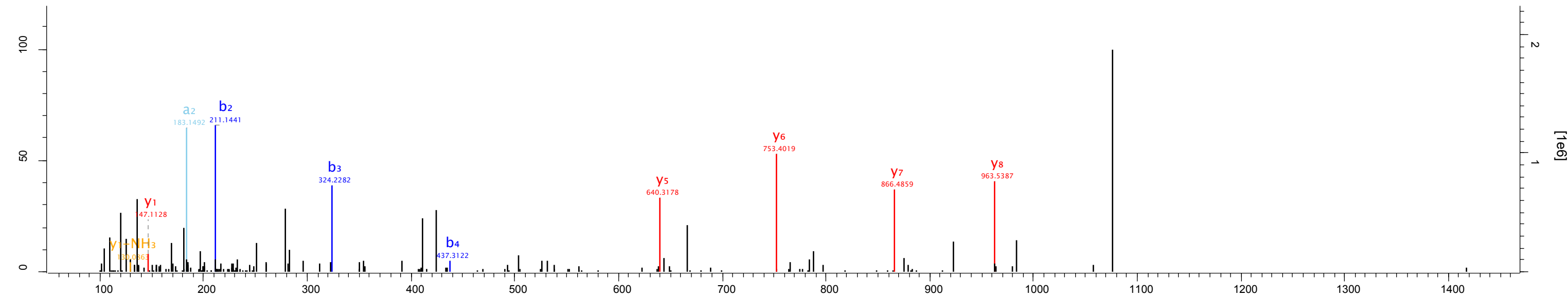
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- b_{11} below P
- b_{12} below S
- b_{13} below H

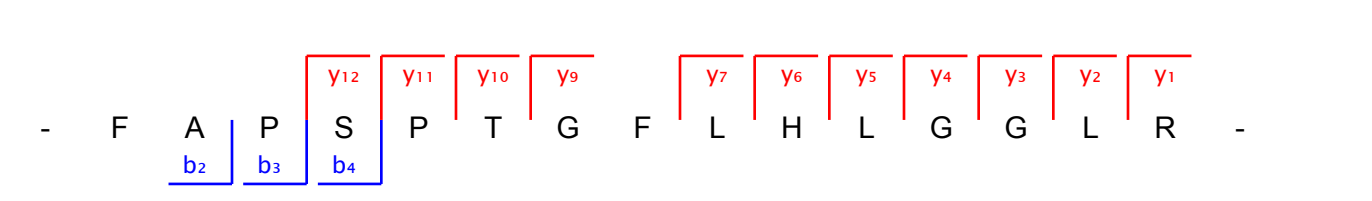
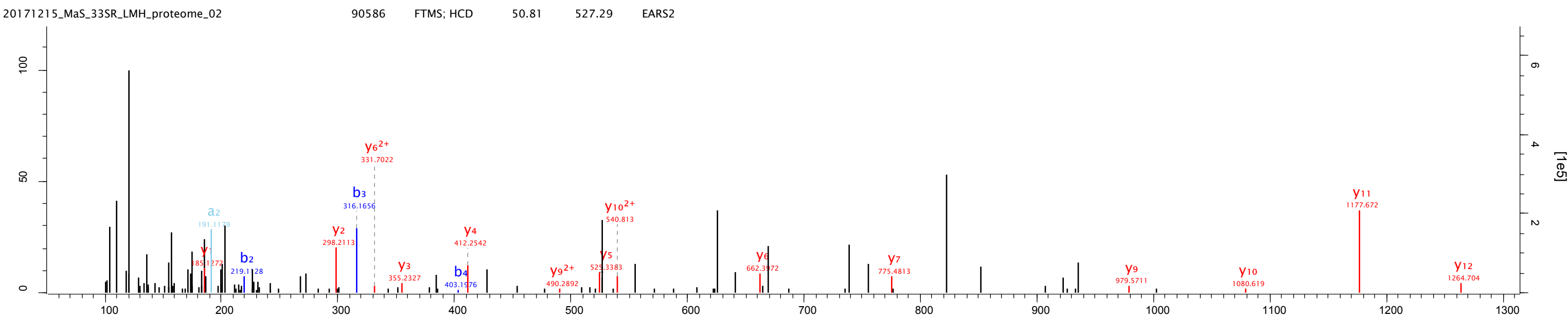
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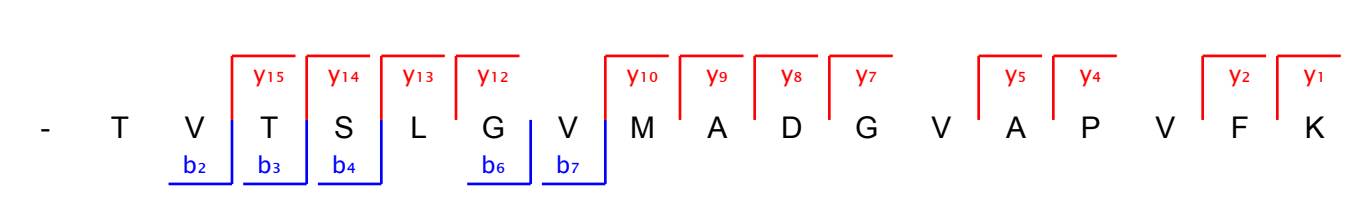
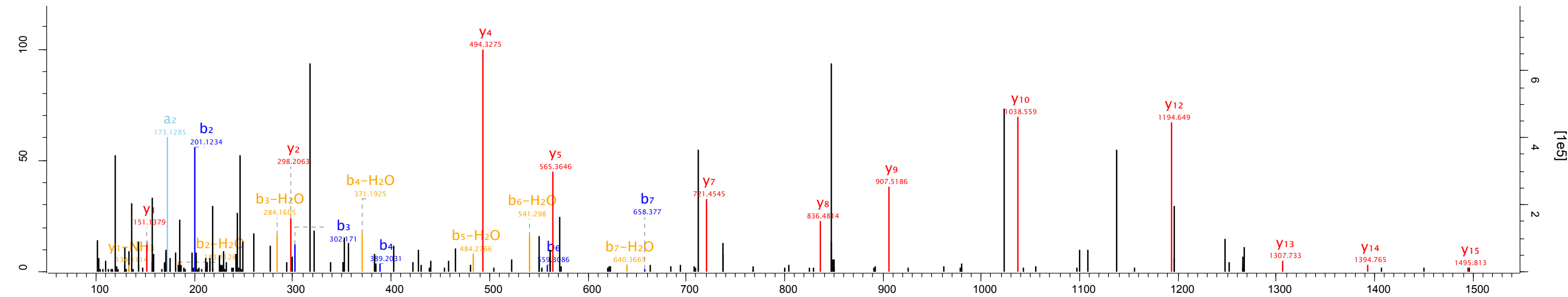
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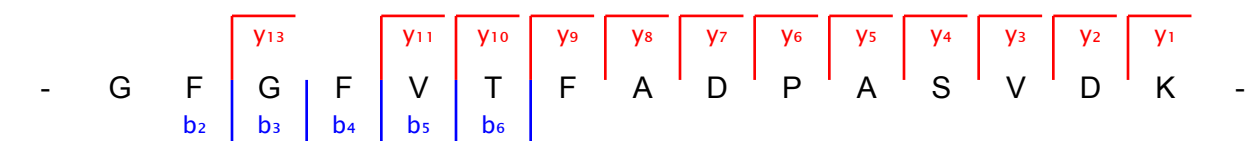
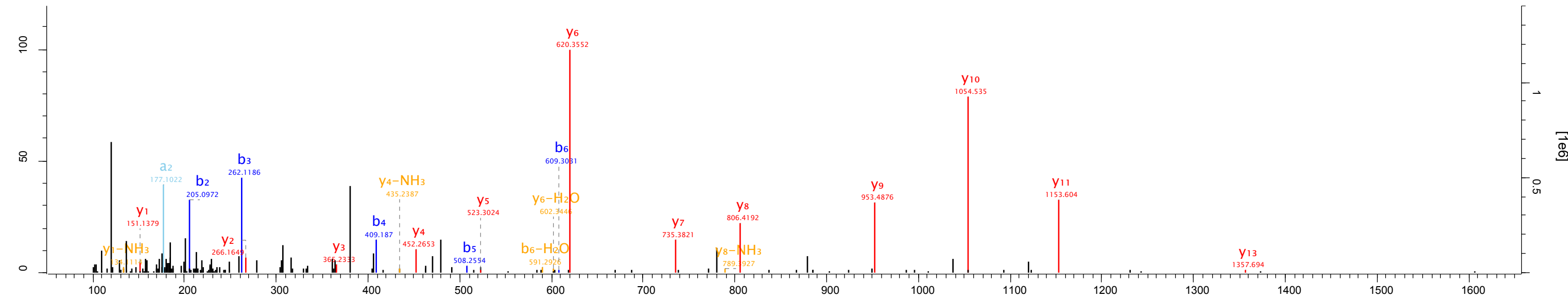
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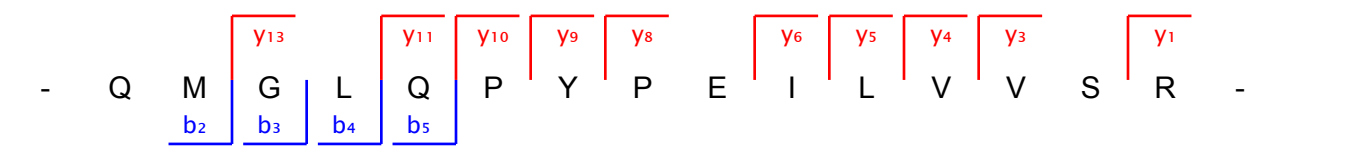
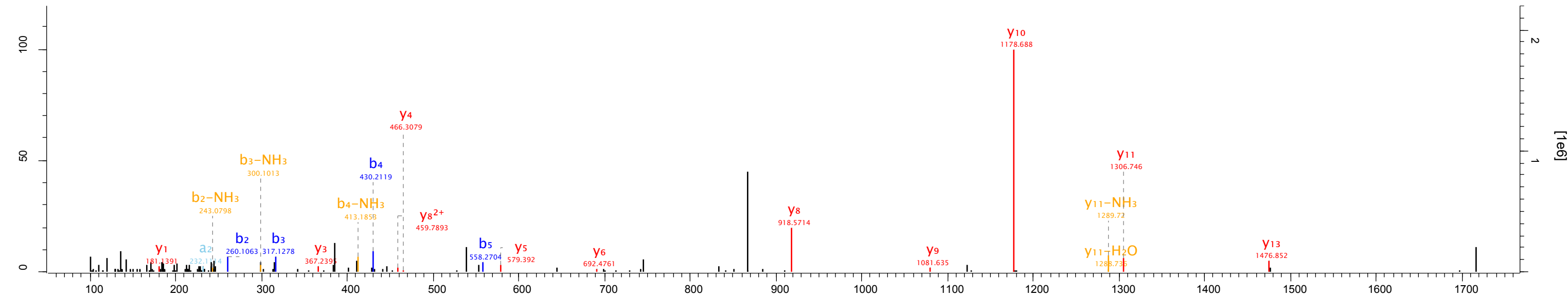
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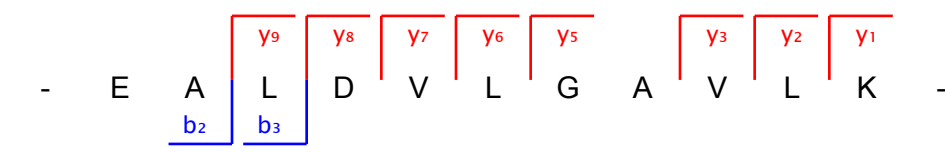
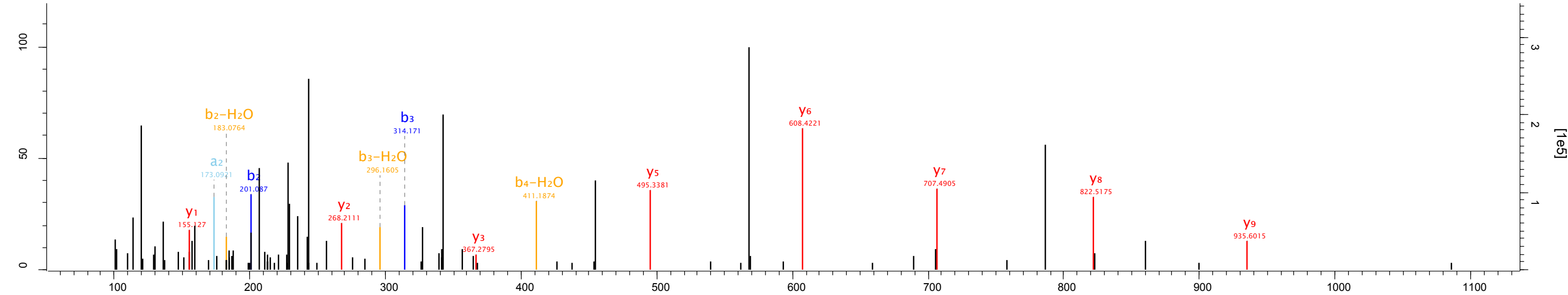
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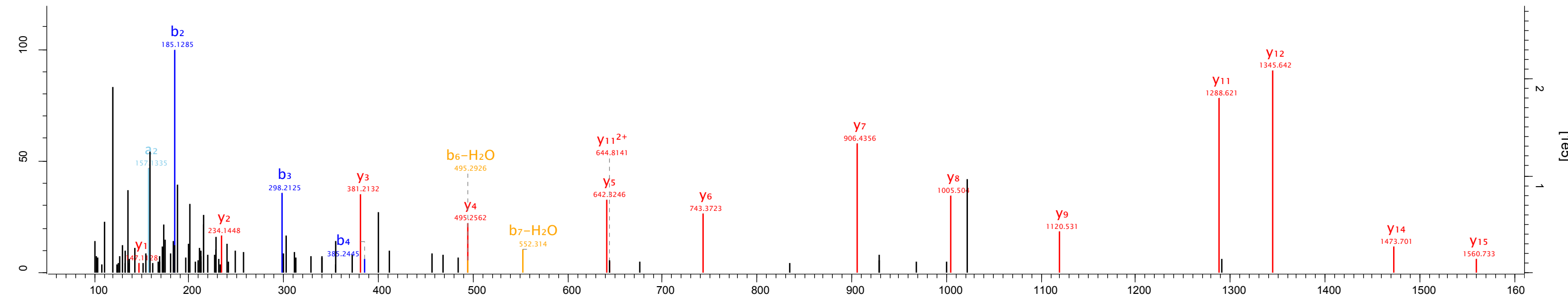


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 Scan: 96536 Method: FTMS; HCD Score: 62.86 m/z: 868.48 Gene names: RIPK2



20171215_MaS_33SR_LMH_proteome_02 98696 FTMS; HCD 48.19 568.34 MRPS27



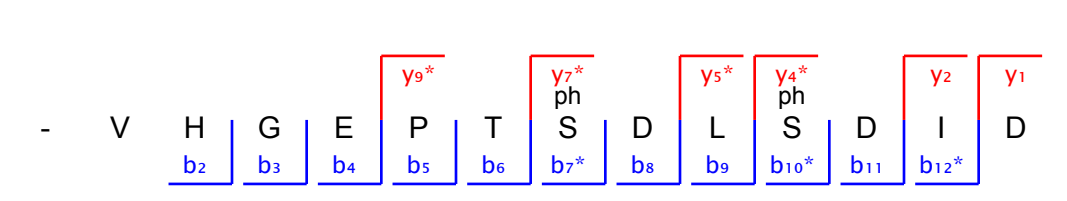
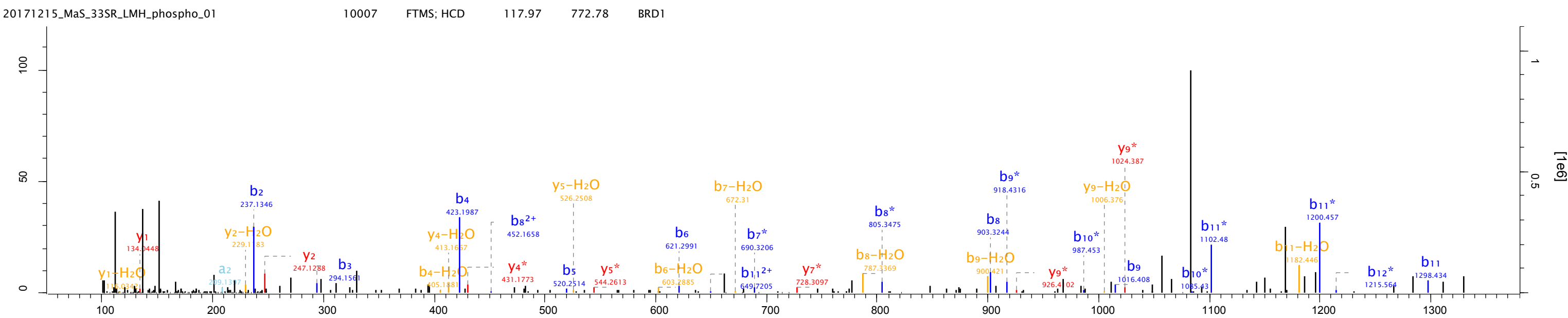


- A L L S G A G P A D V Y T F N F S K -

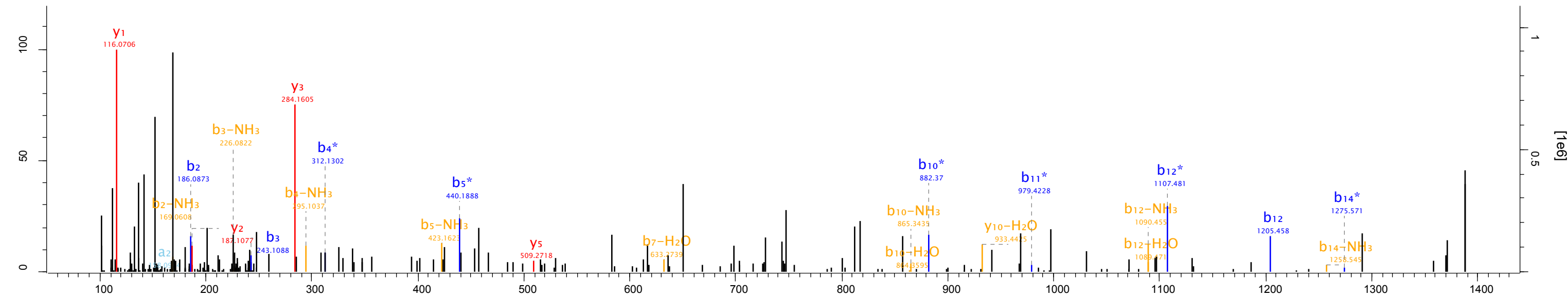
Fragmentation sites are indicated by brackets below the sequence:

- b₂ (L)
- b₃ (L)
- b₄ (S)
- y₁₅ (S)
- y₁₄ (G)
- y₁₂ (G)
- y₁₁ (P)
- y₉ (D)
- y₈ (V)
- y₇ (Y)
- y₆ (T)
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- y₄ (N)
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- y₂ (S)
- y₁ (K)

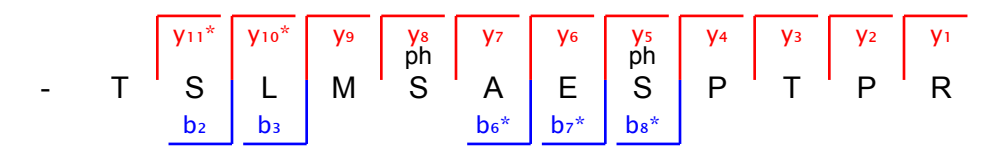
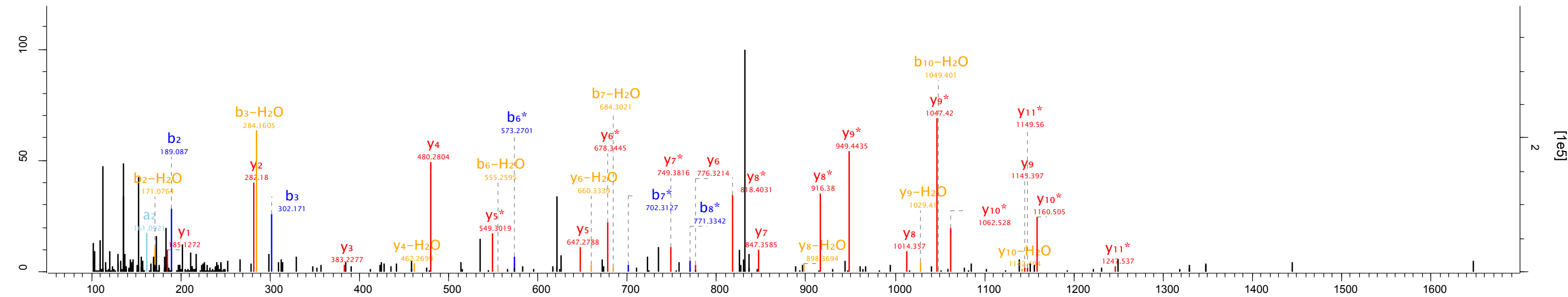
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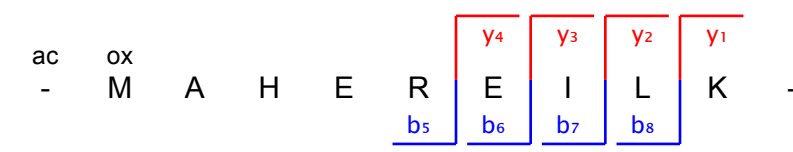
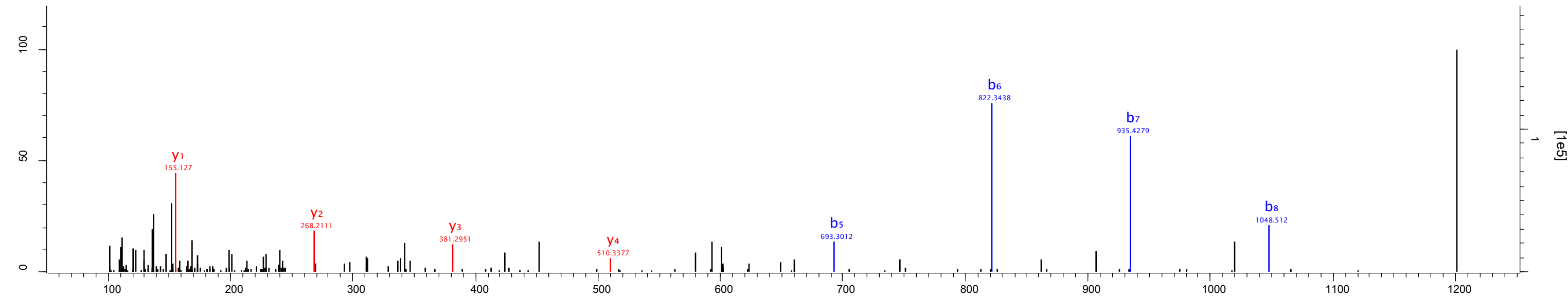
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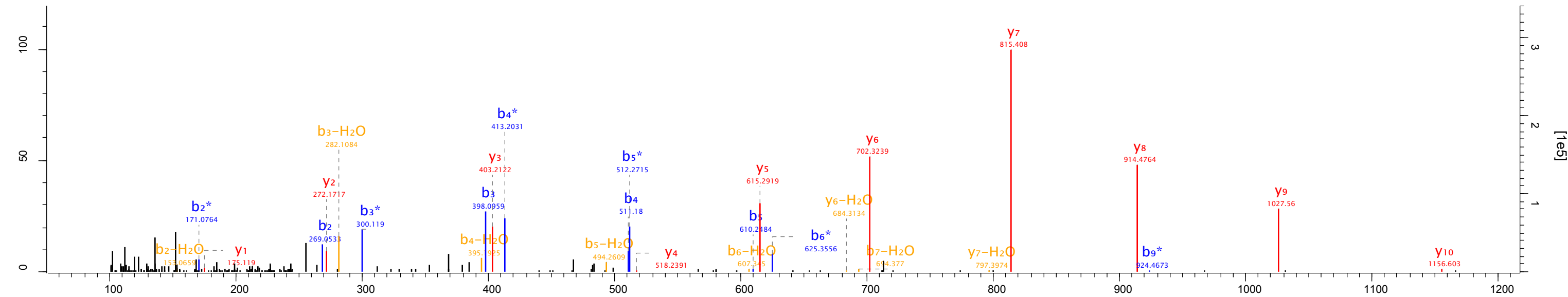
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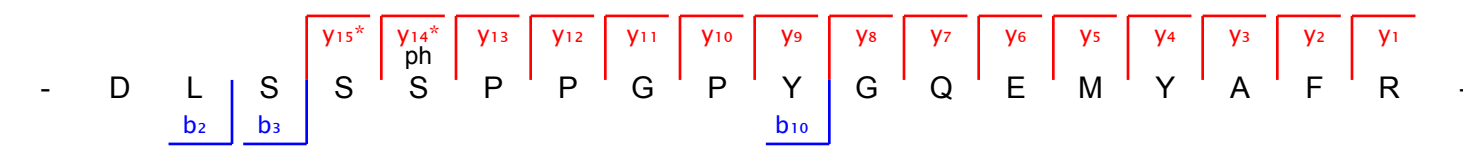
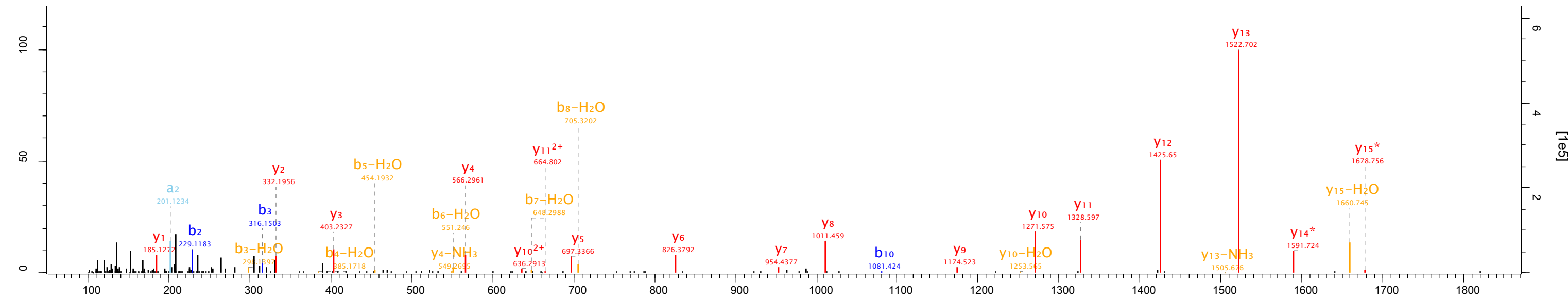
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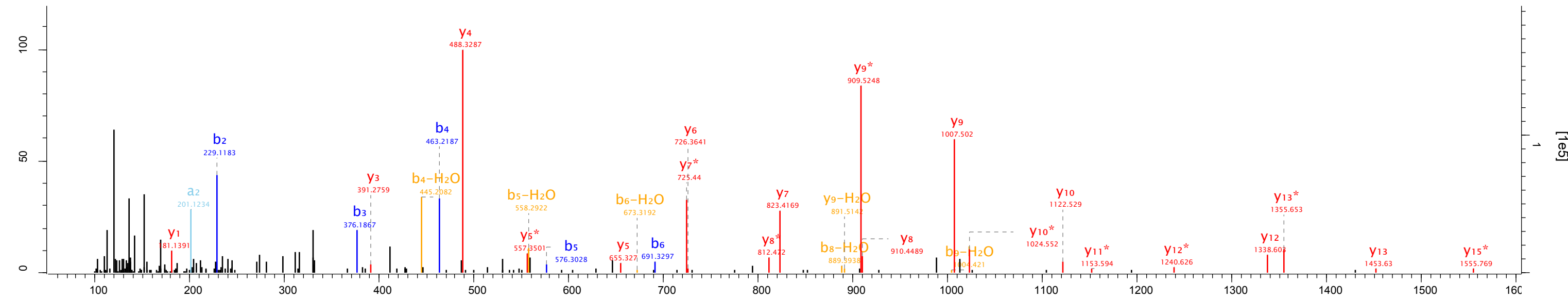
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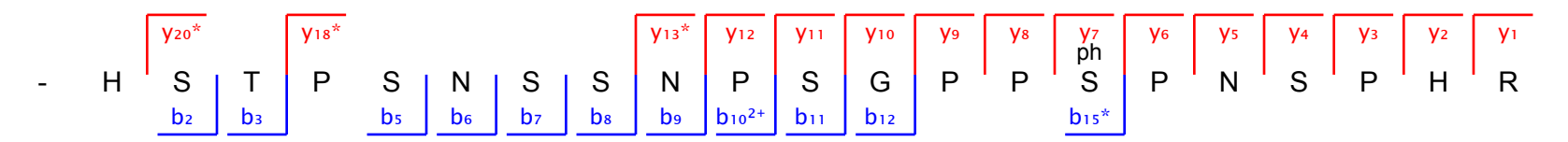
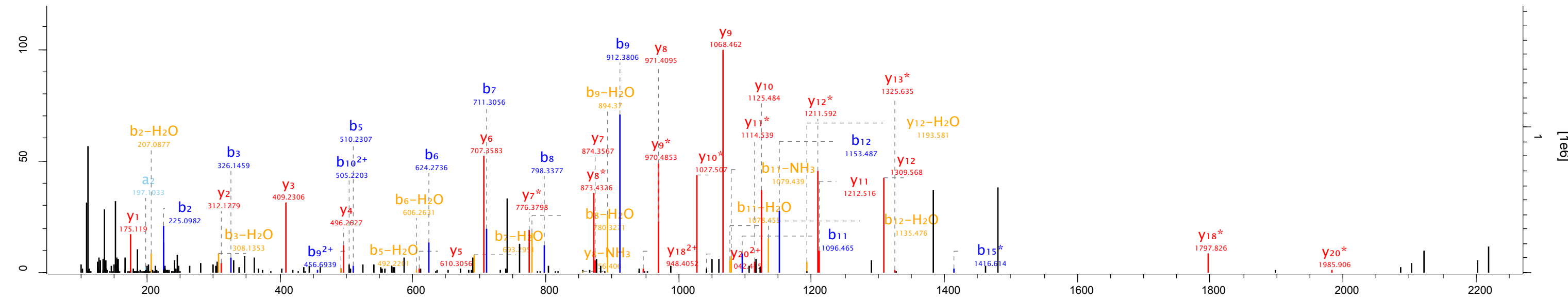


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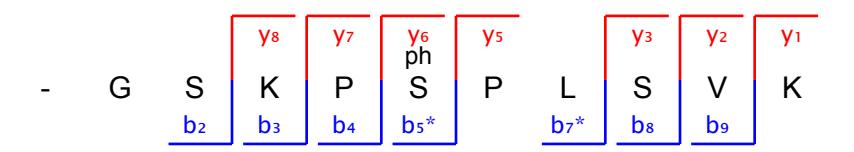
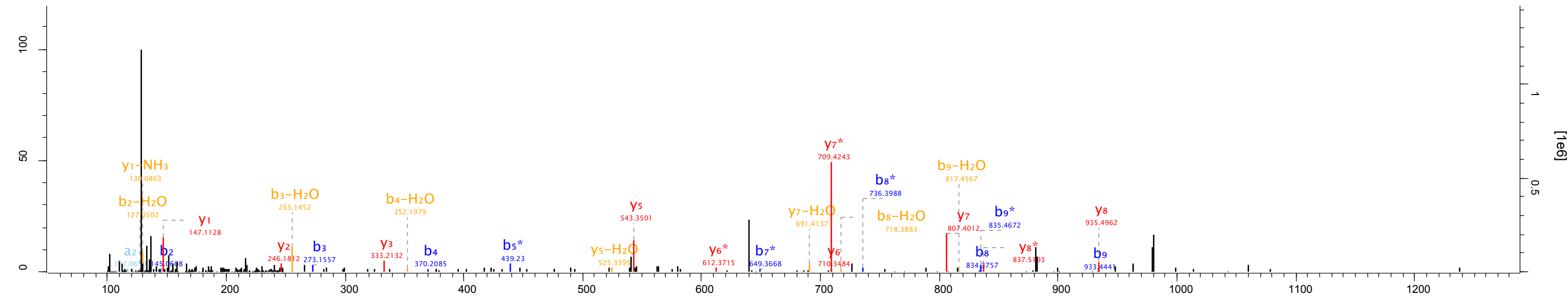
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- b2: L
- b3: F
- b4: S
- b5: L
- b6: D
- y1: R
- y3: P
- y4: S
- y5: A
- y6: P
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- y10: E
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- y13: F
- y15: D

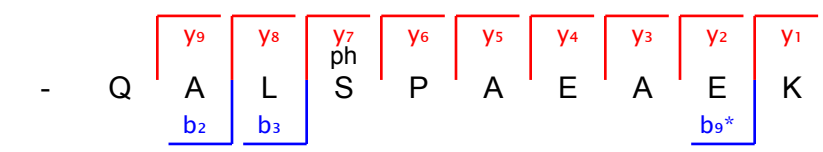
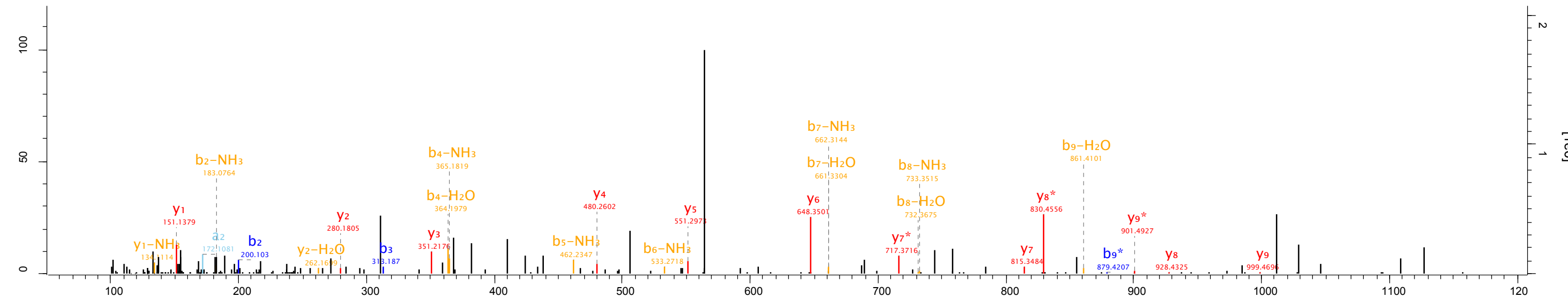
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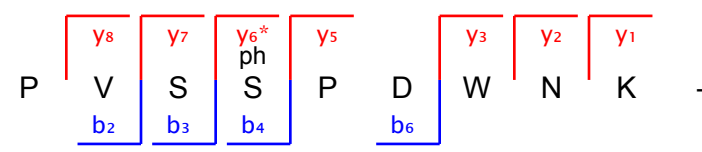
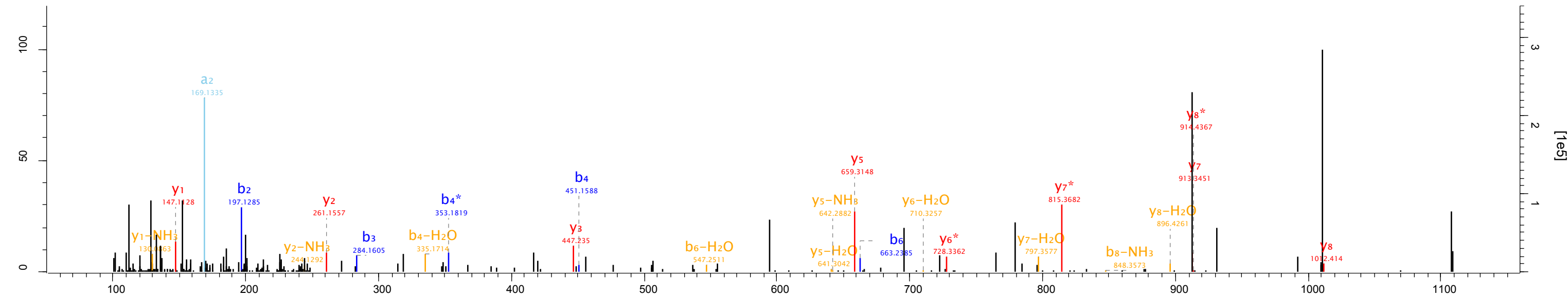
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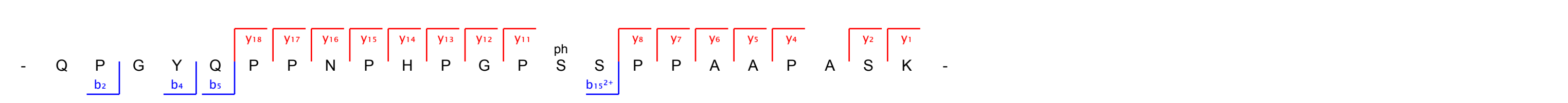
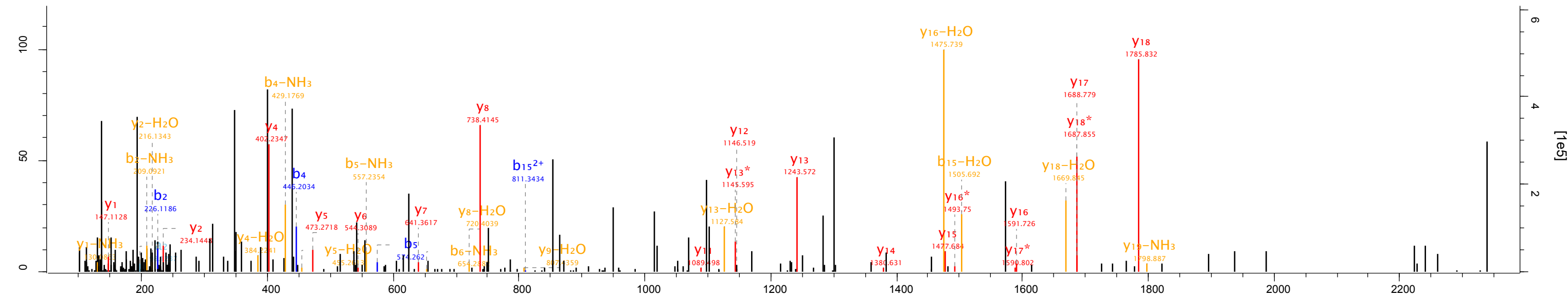
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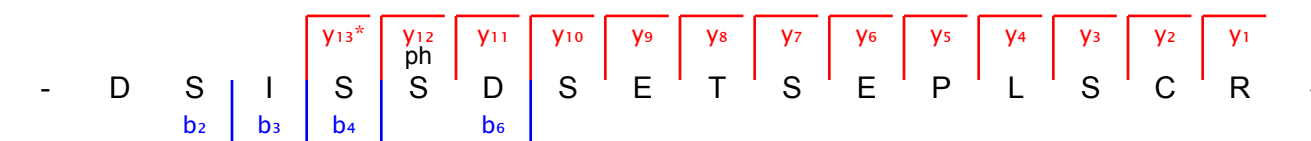
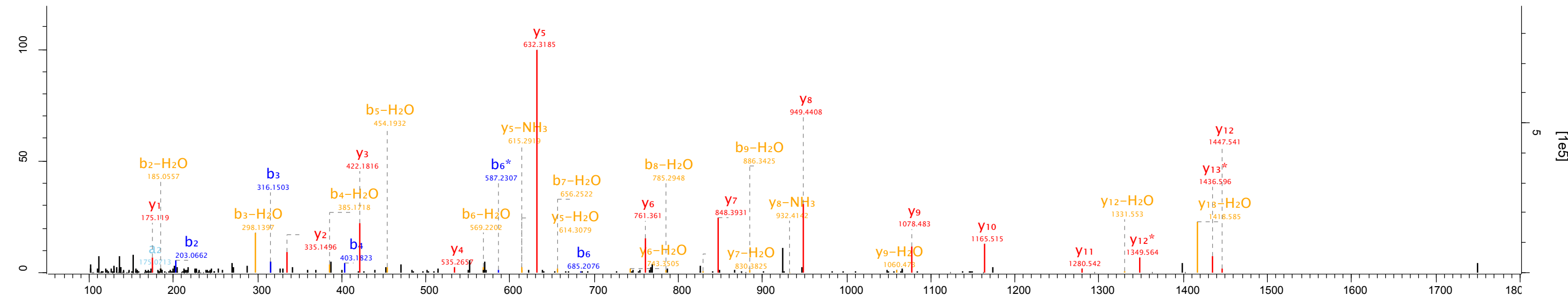
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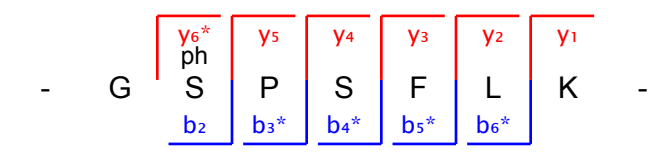
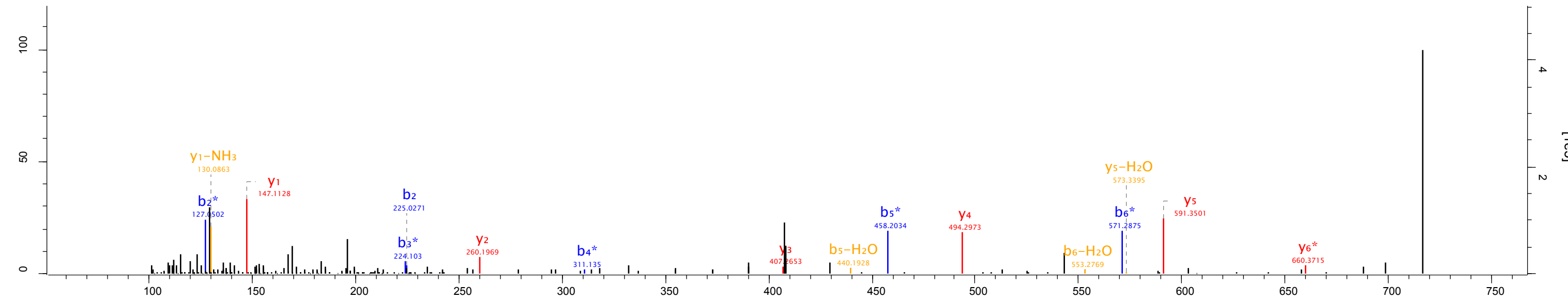
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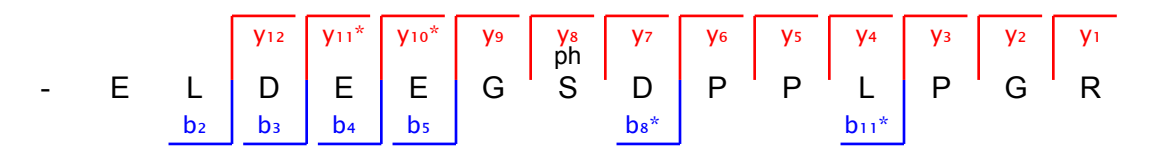
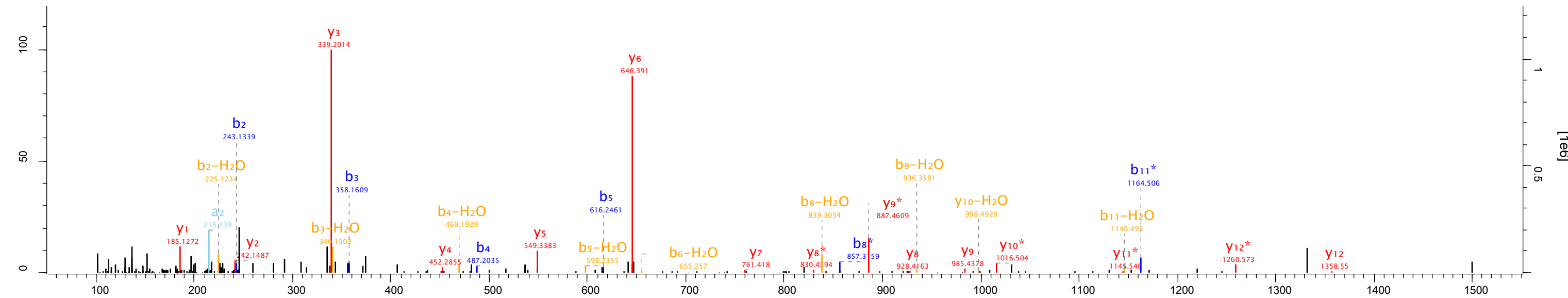
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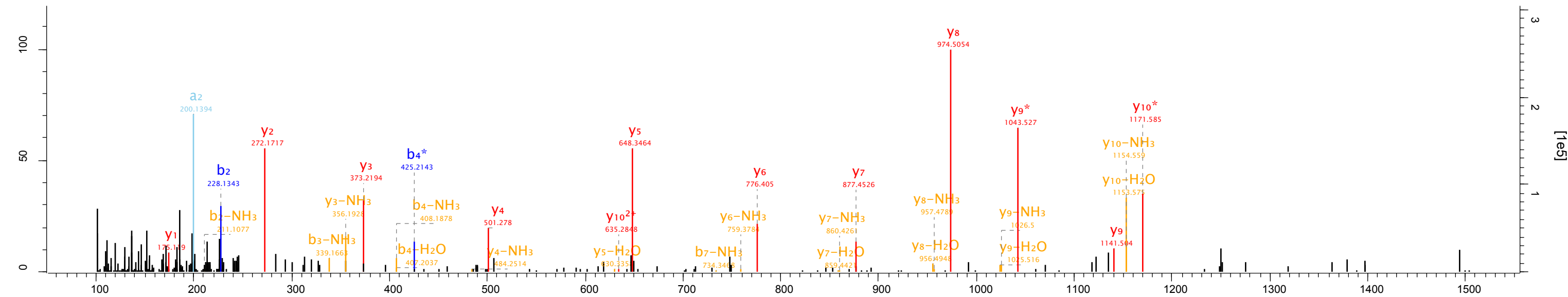
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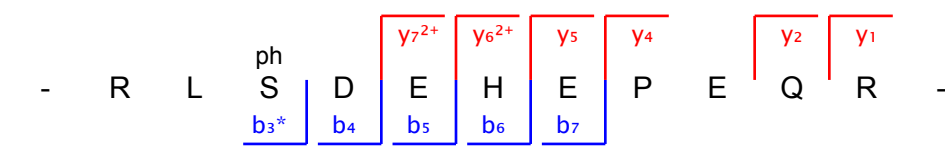
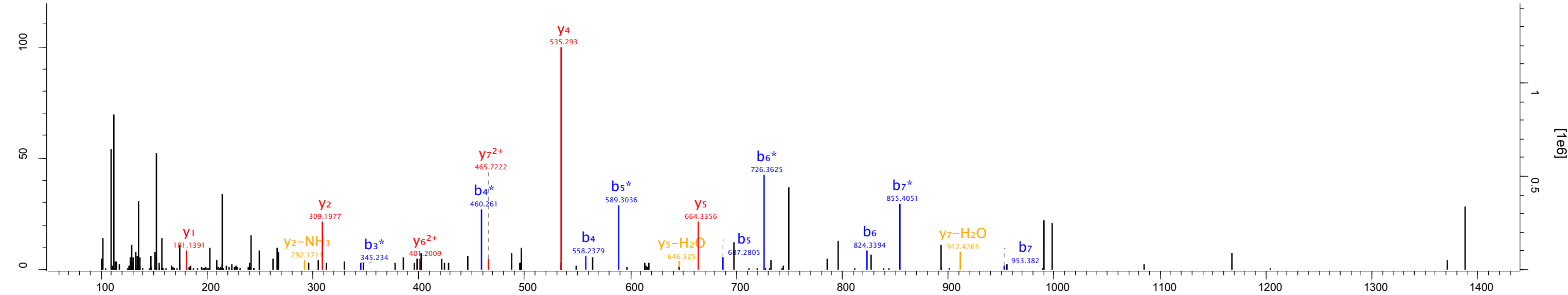


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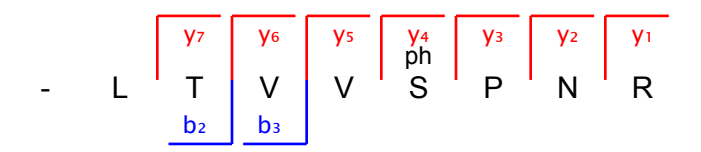
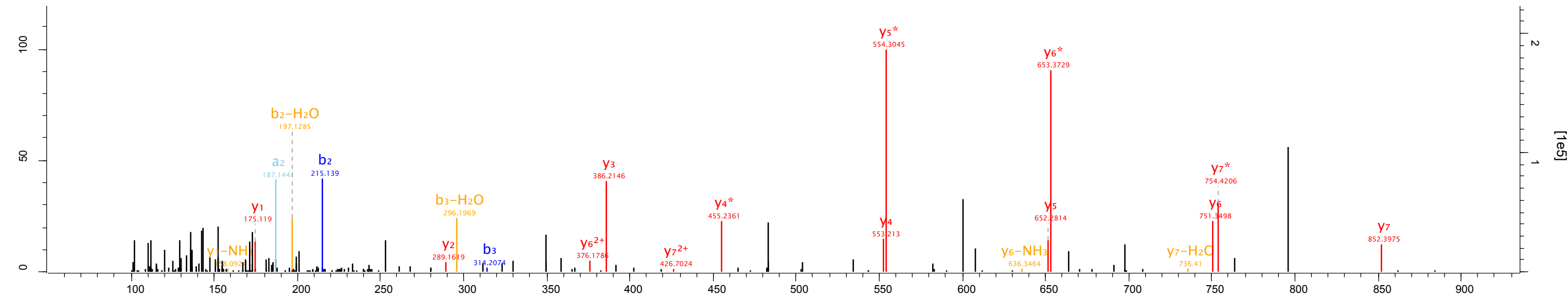


Raw file Scan Method Score m/z Gene names

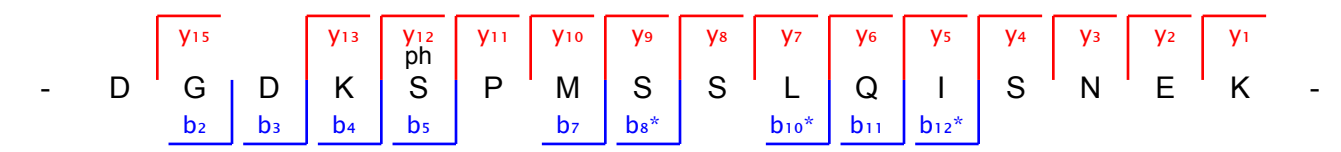
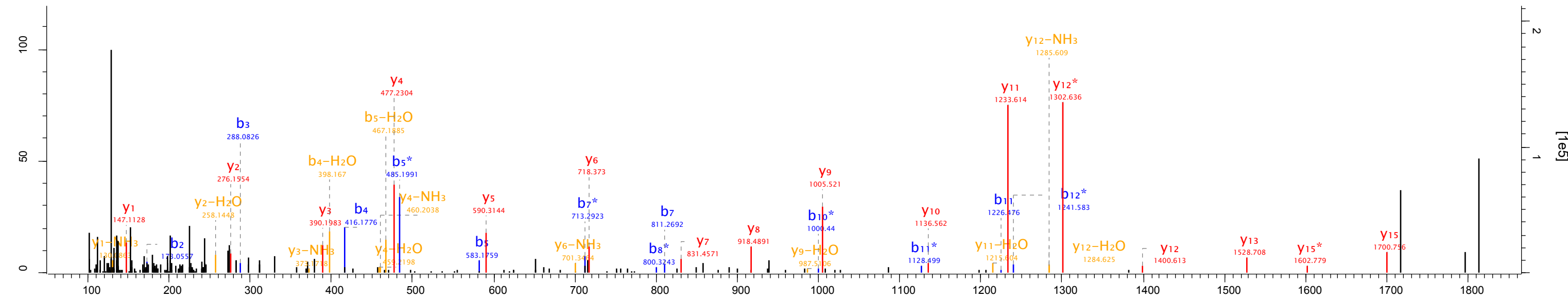
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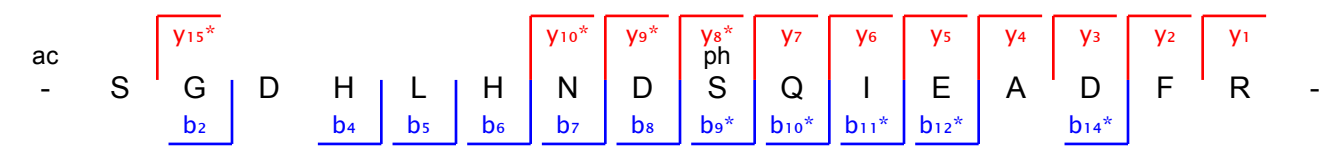
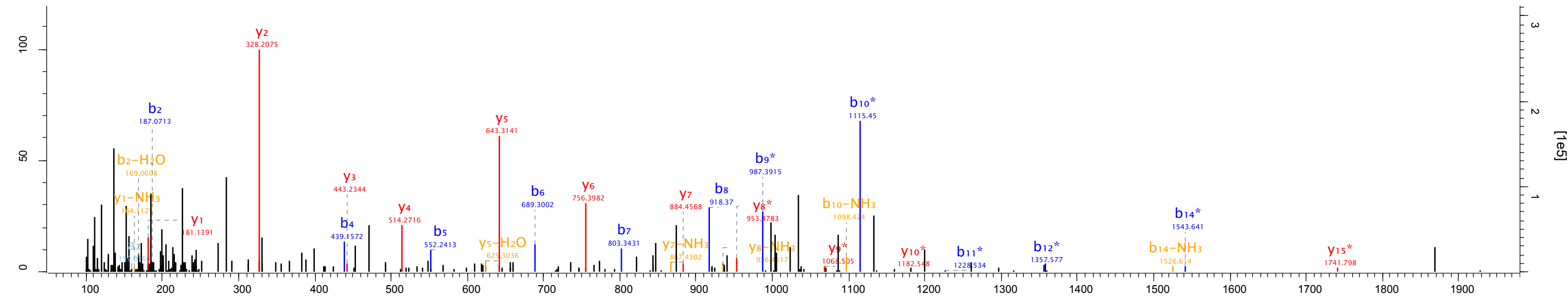
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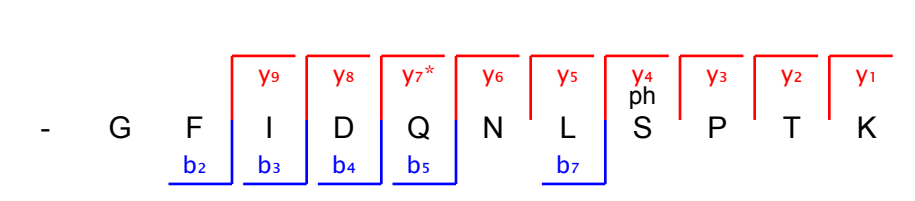
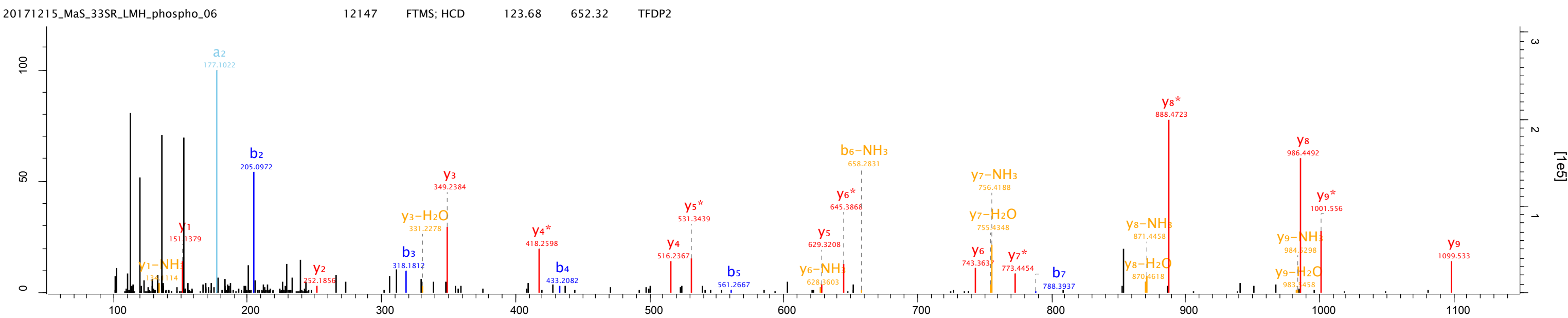
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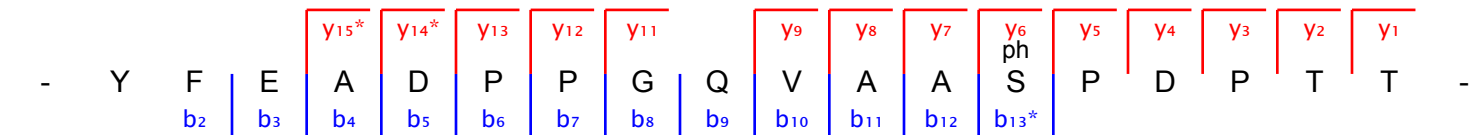
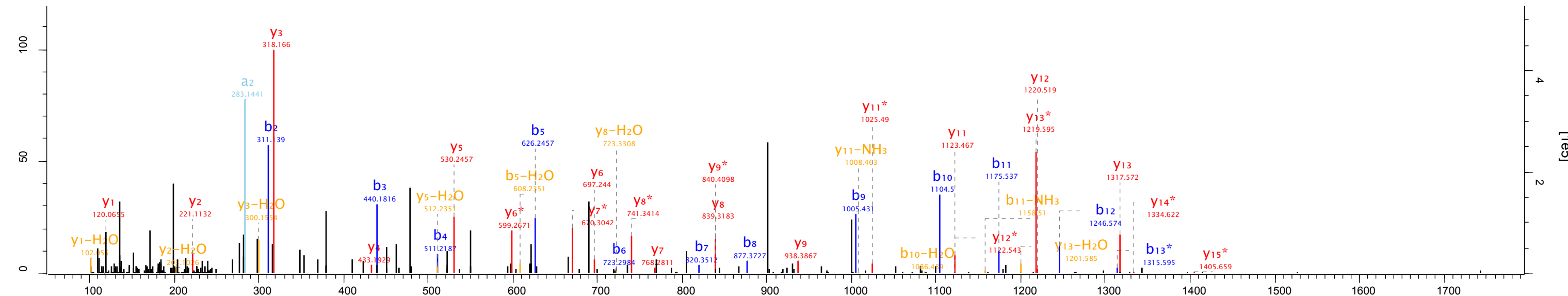


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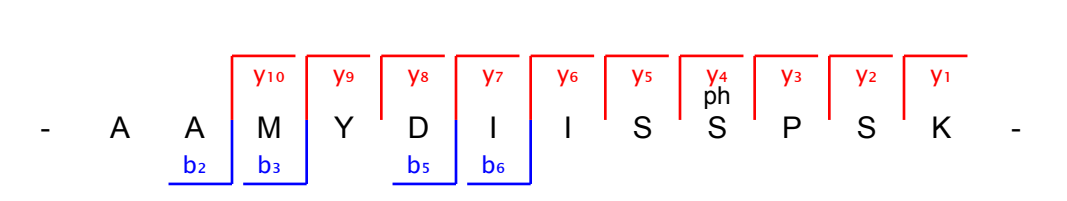
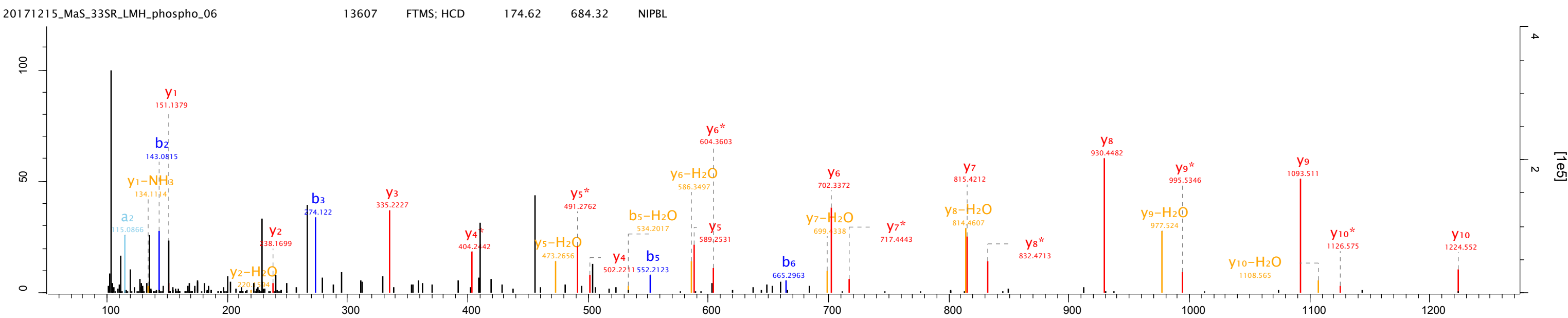


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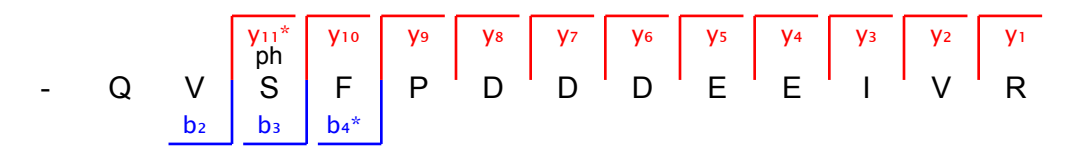
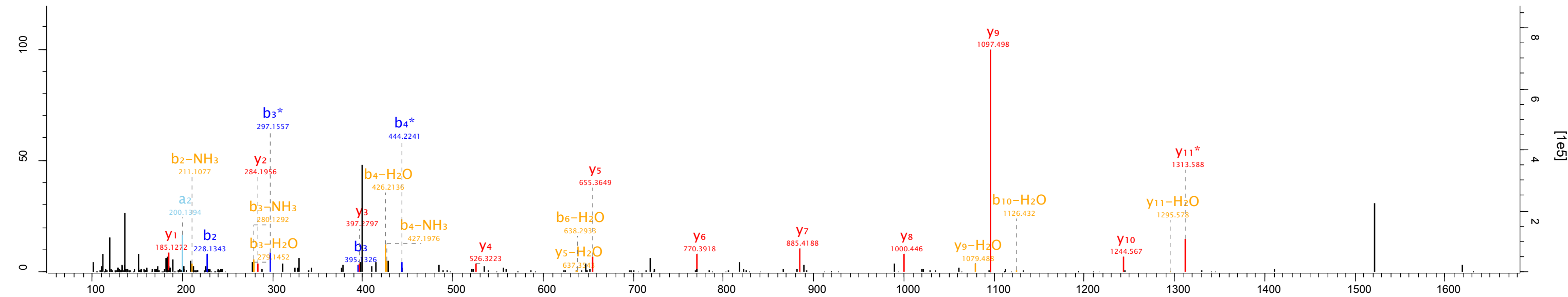




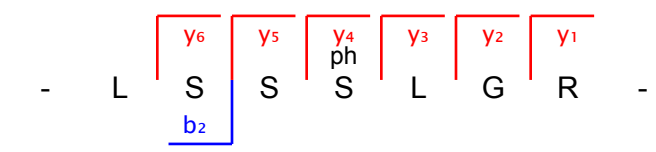
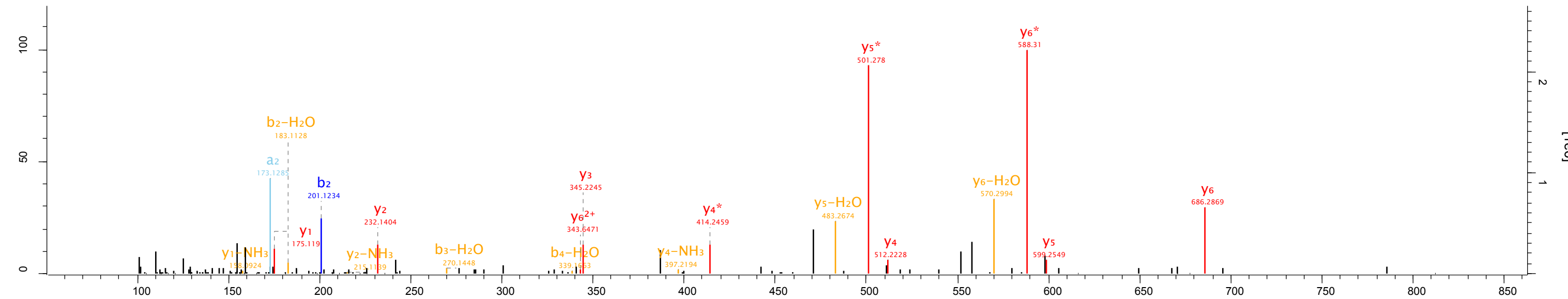
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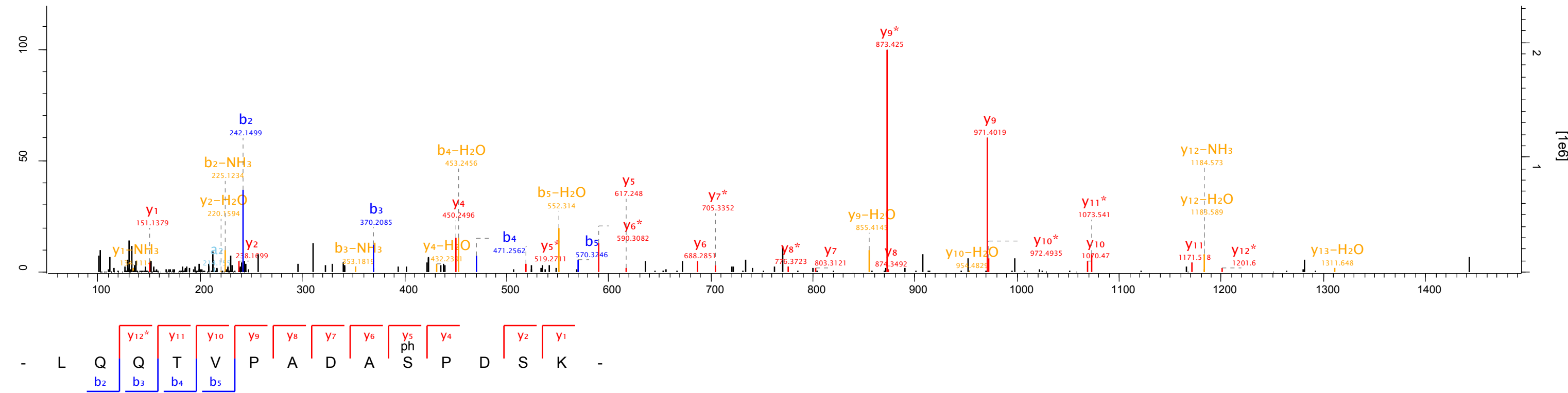


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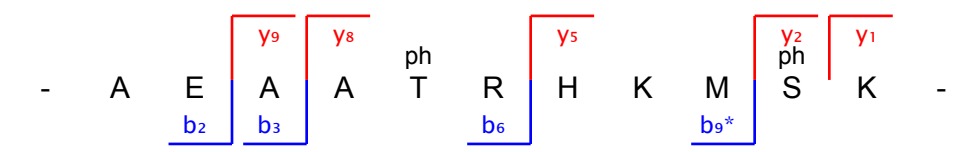
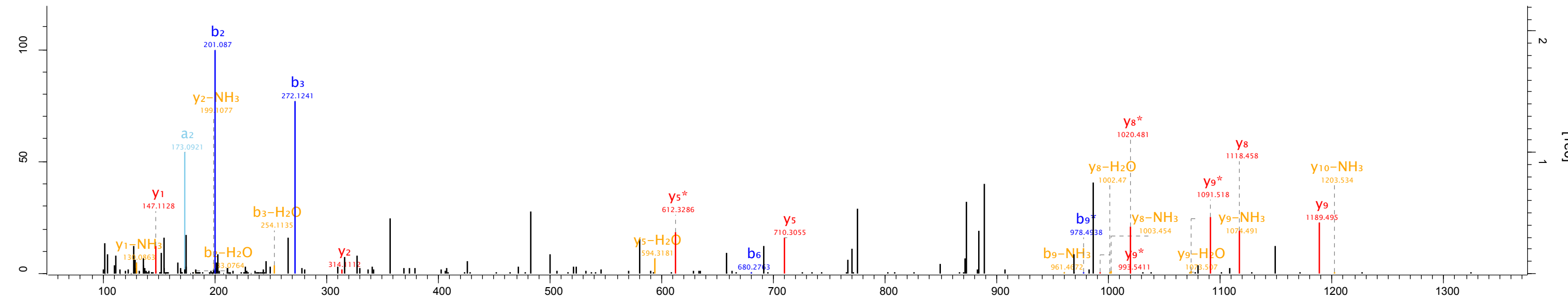


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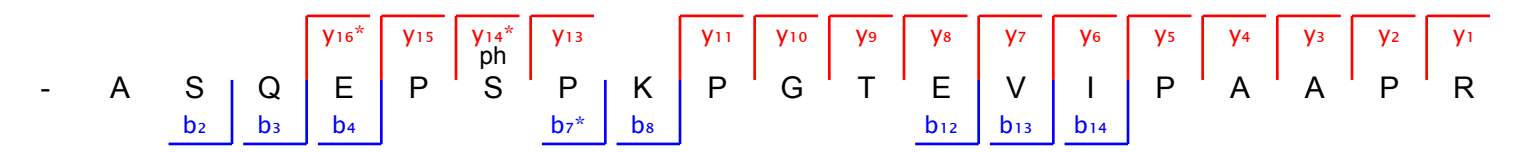
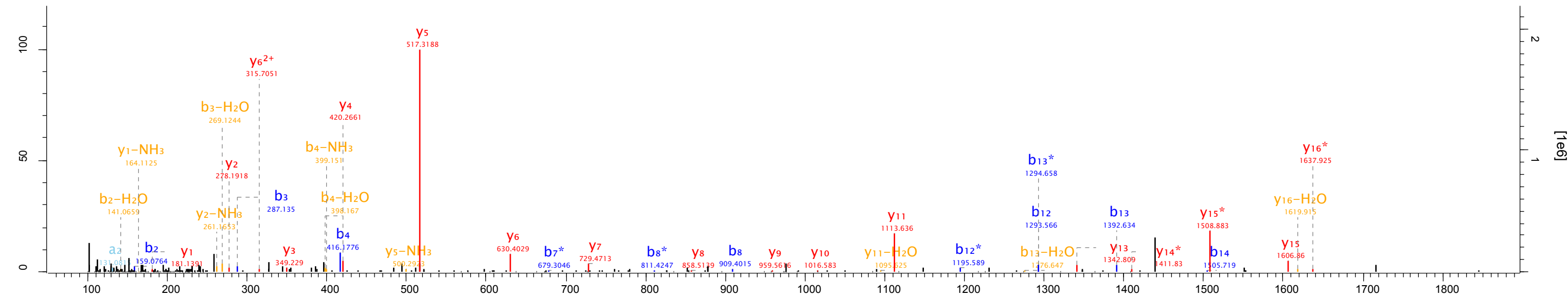




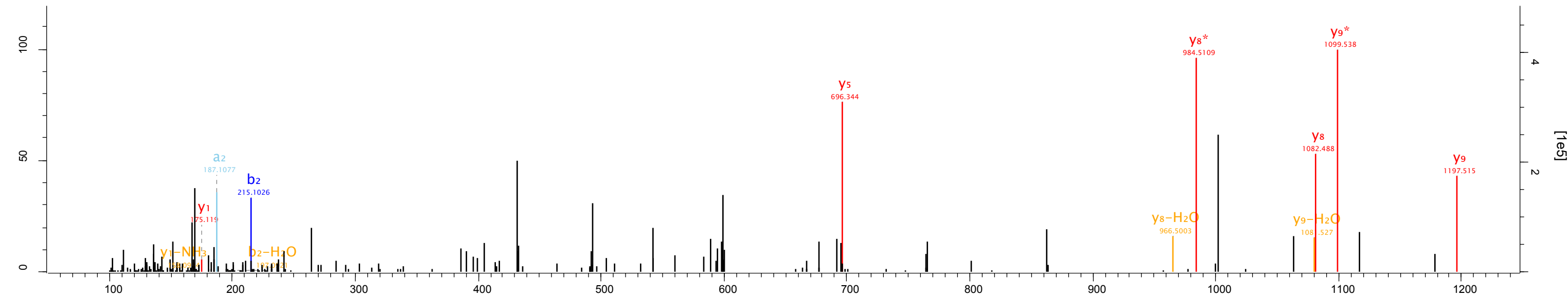
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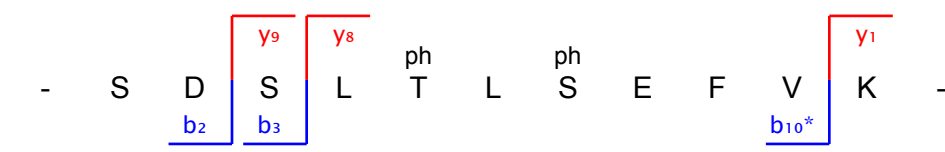
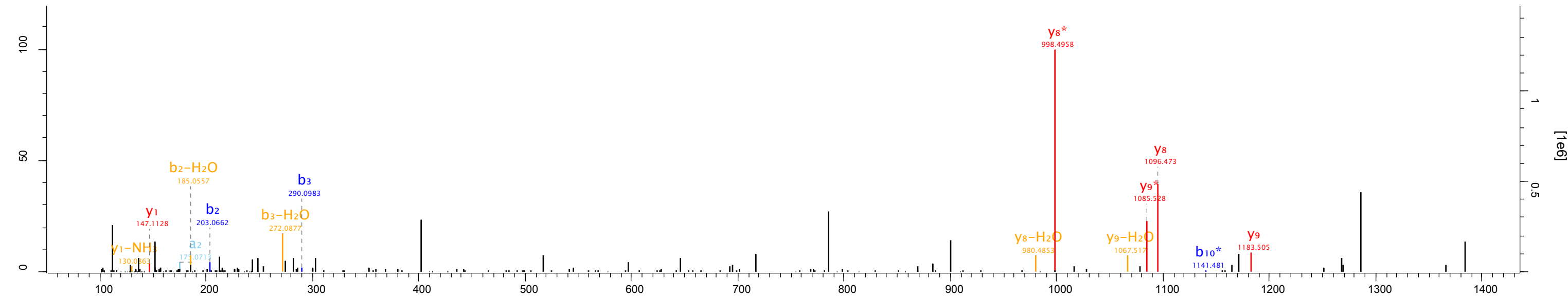
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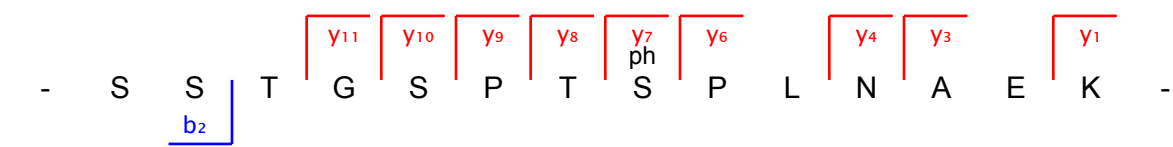
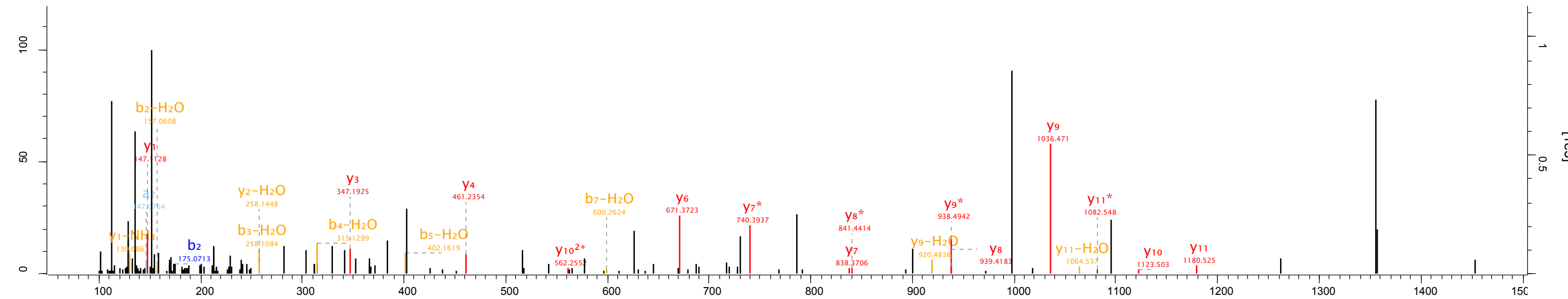
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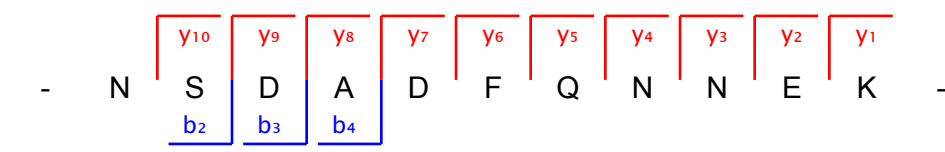
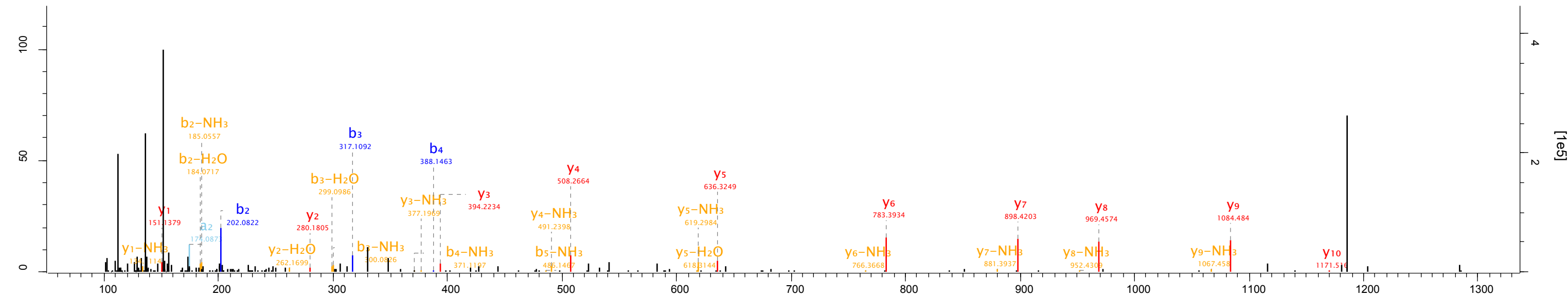
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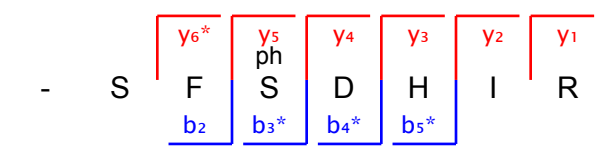
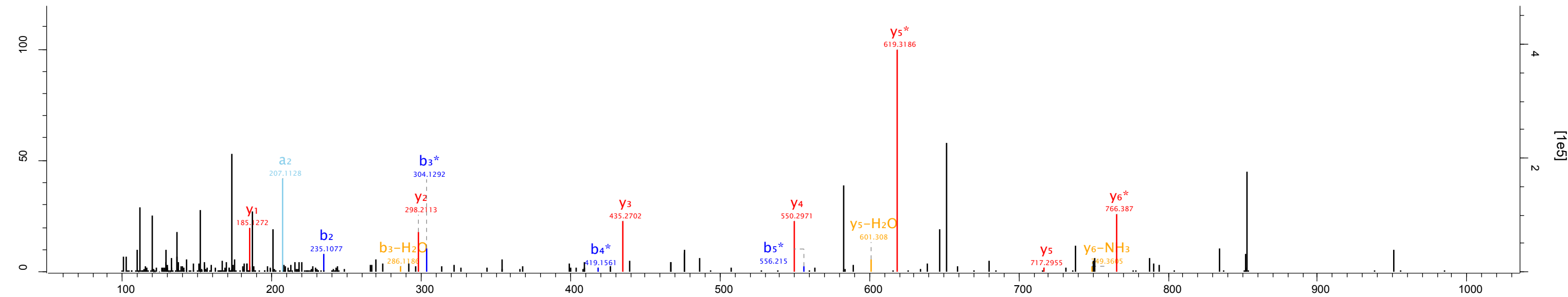
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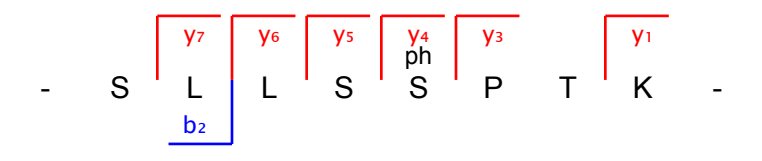
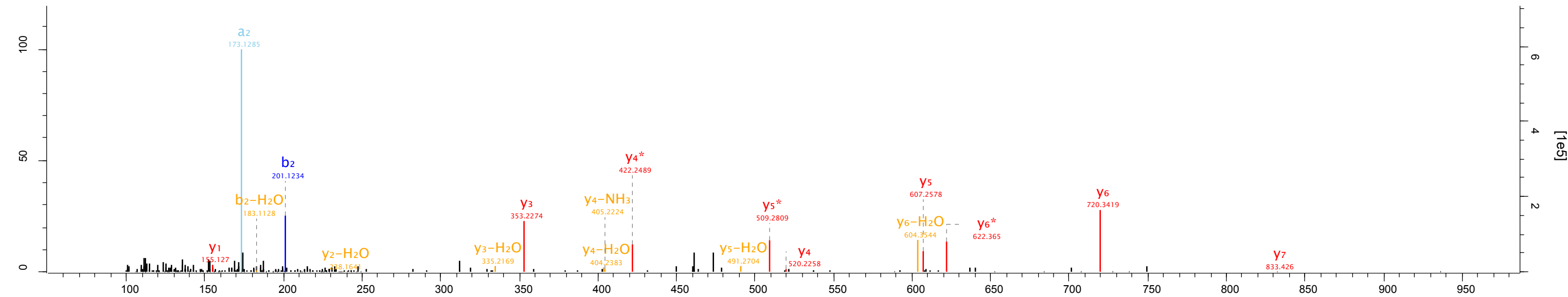
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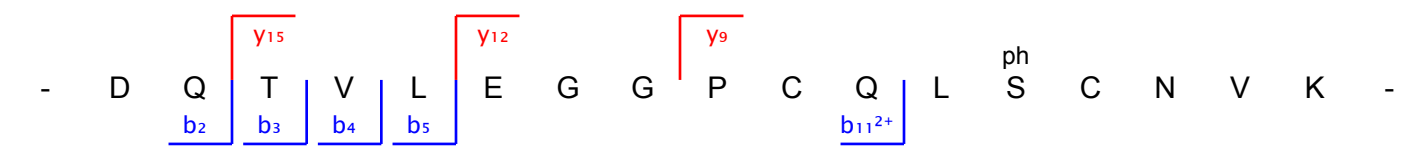
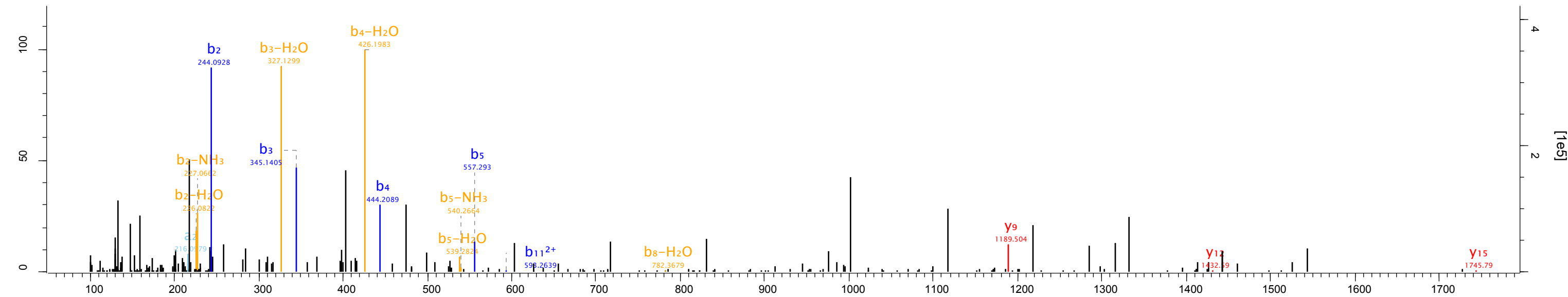
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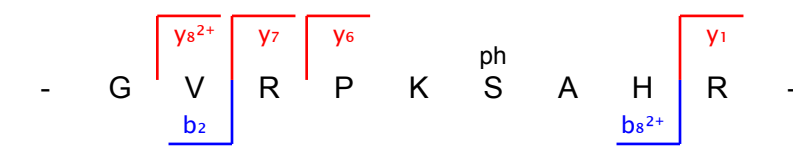
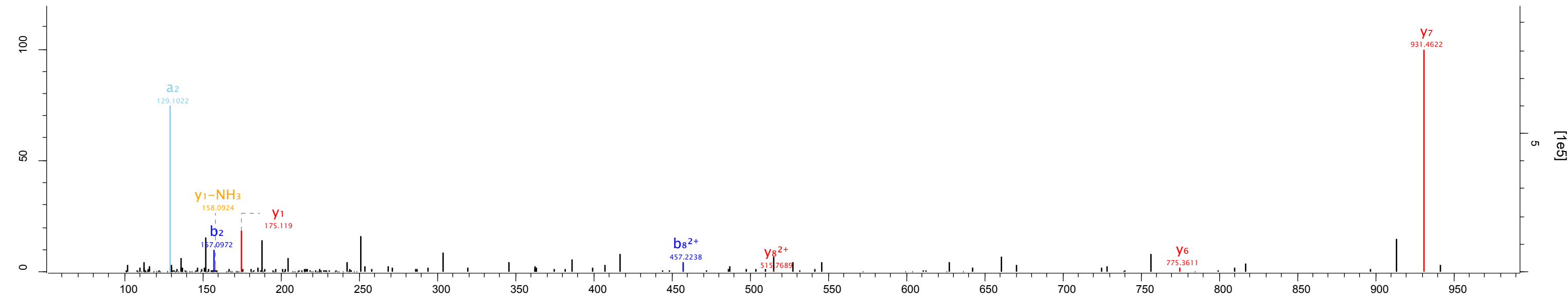
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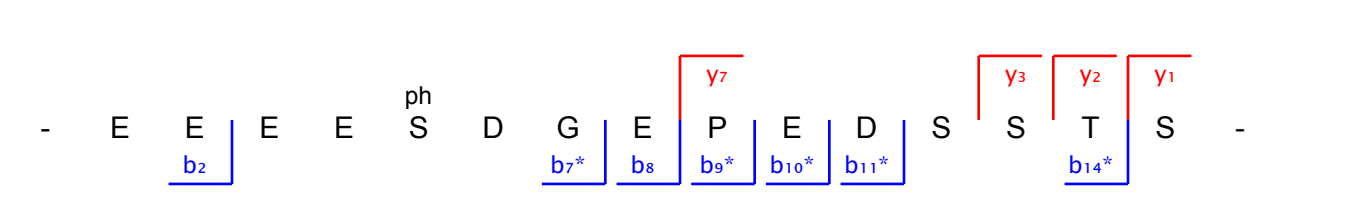
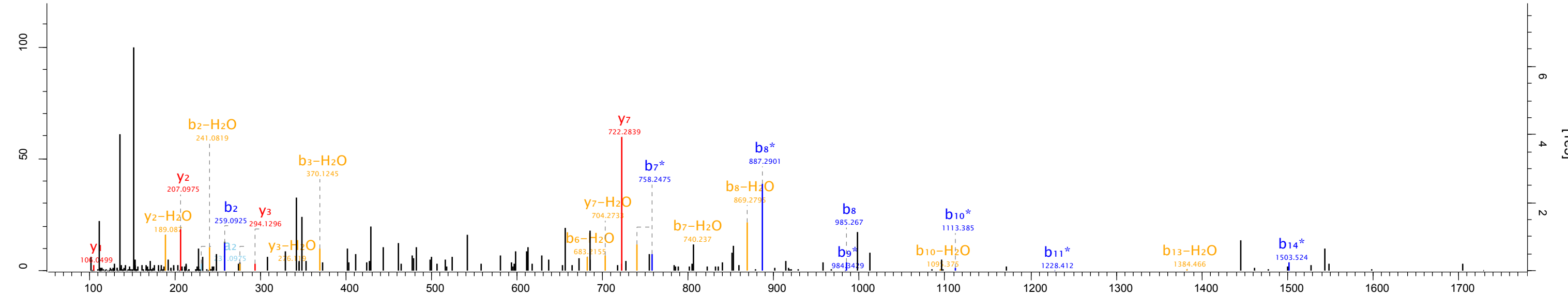
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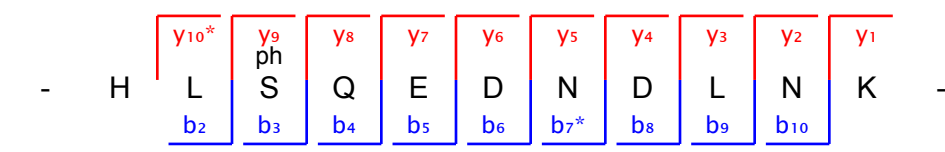
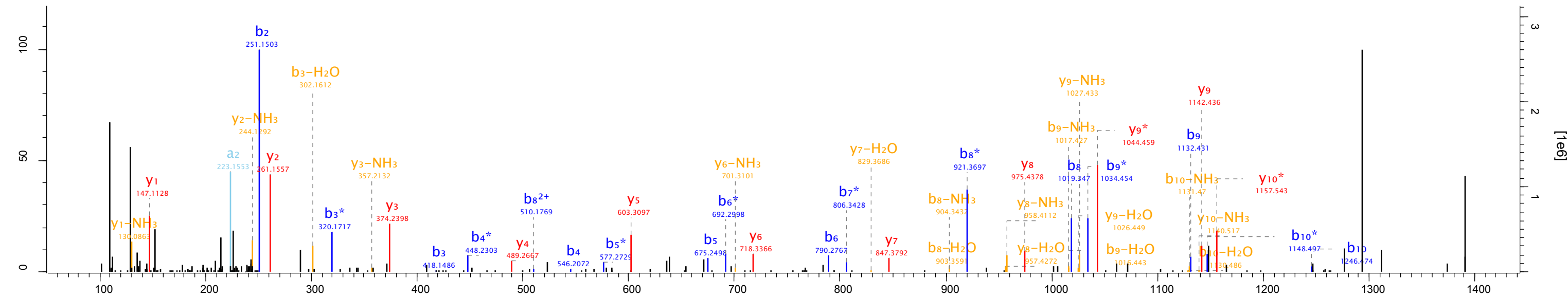
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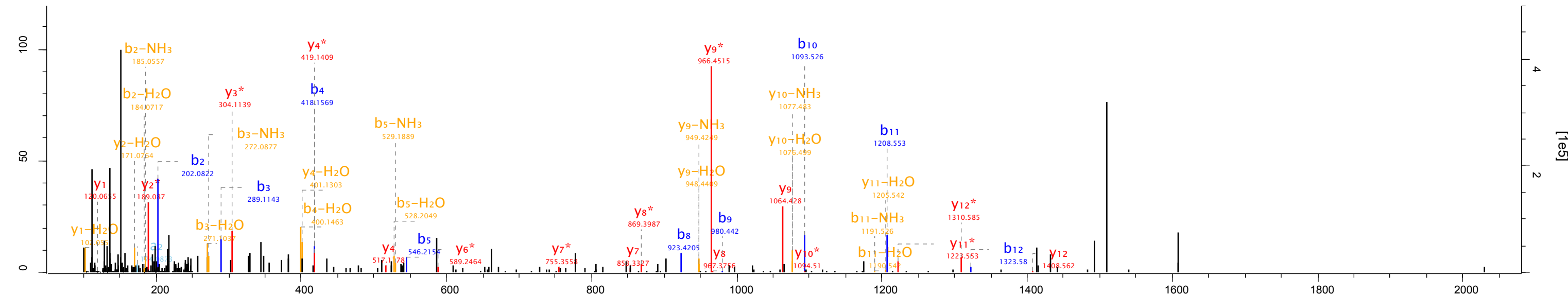


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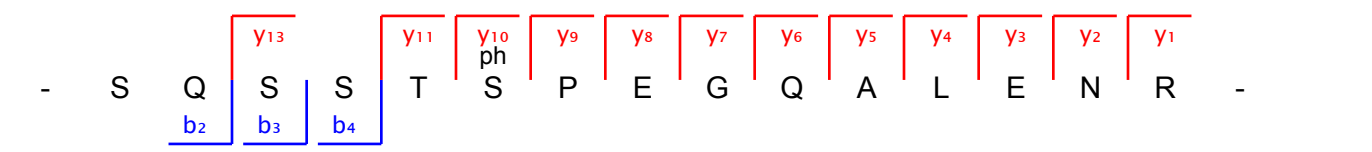
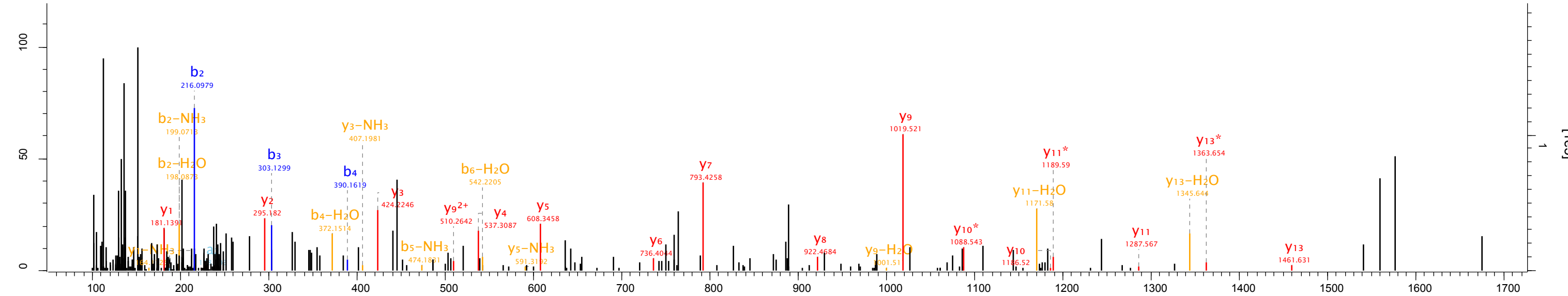


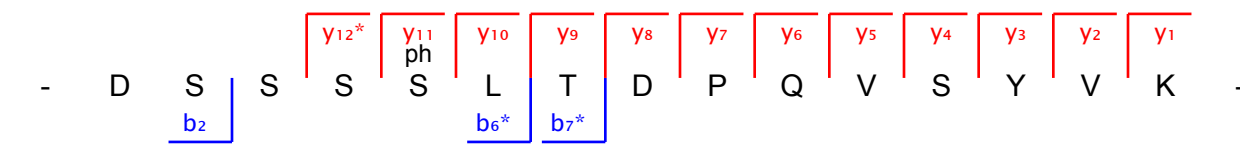
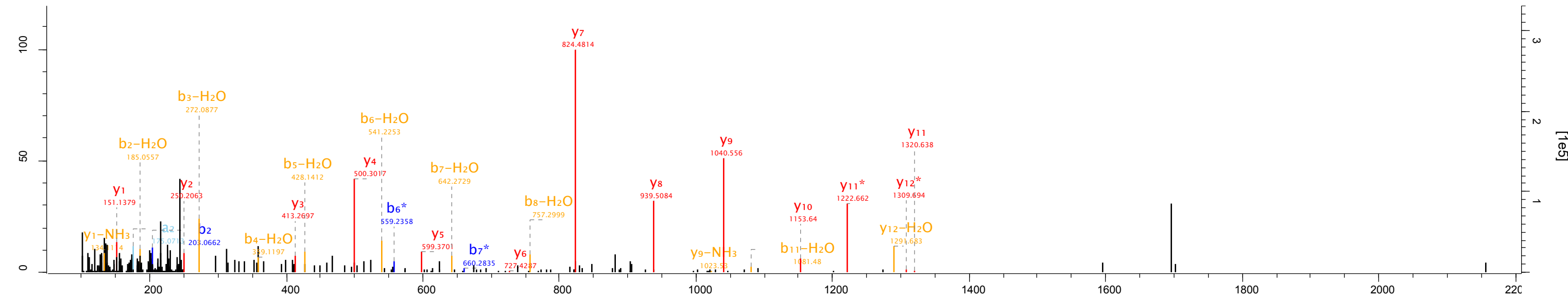
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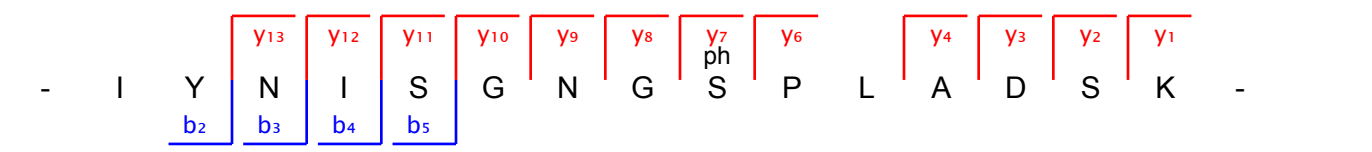
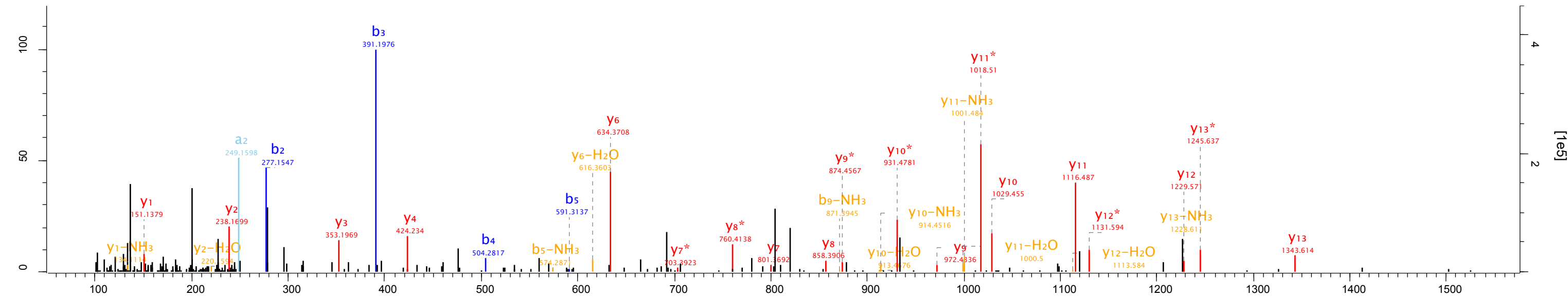
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20171215_MaS_33SR_LMH_phospho2_01 5197 FTMS; HCD 59.98 838.86 SH3BP5



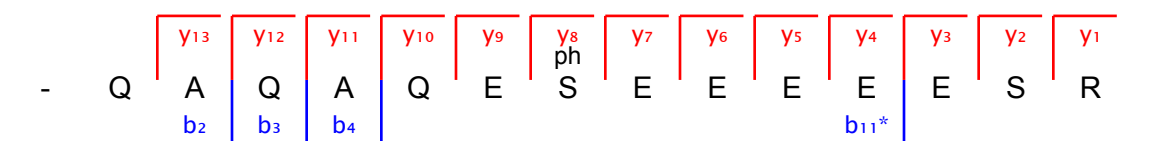
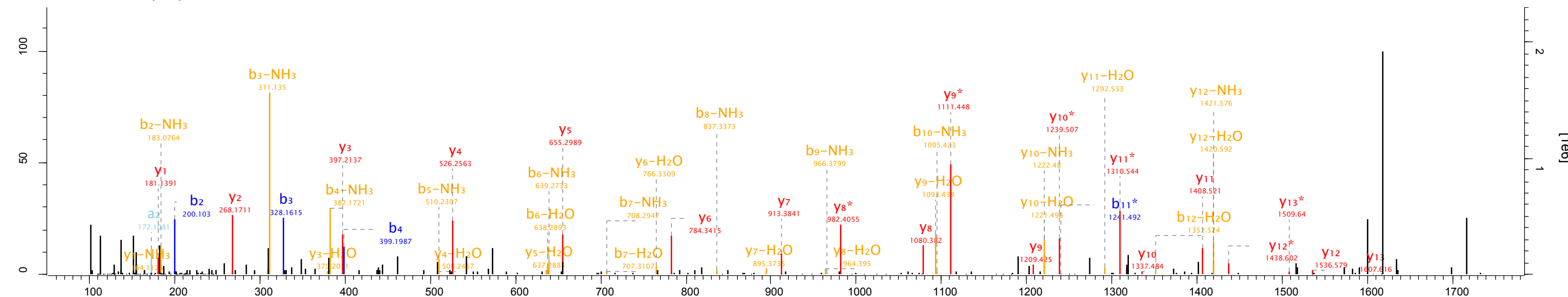


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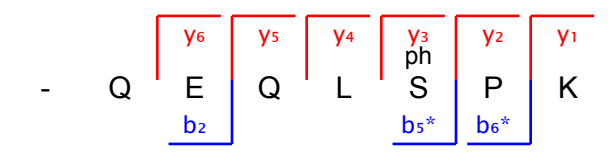
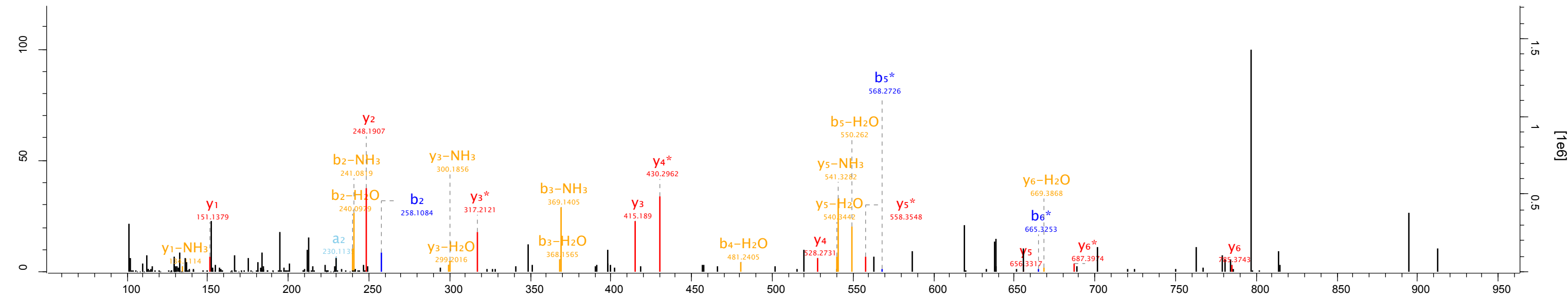


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Scan 2357 Method FTMS; HCD Score 184.21 m/z 868.34 Gene names DNAJC17

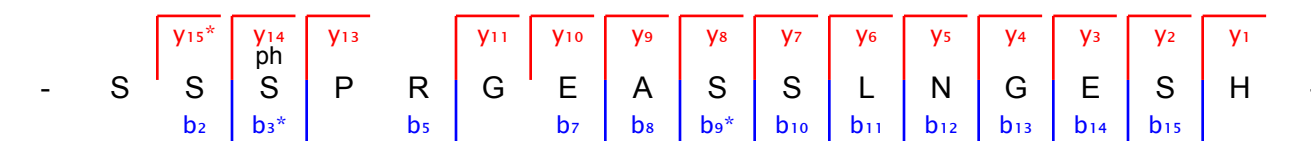
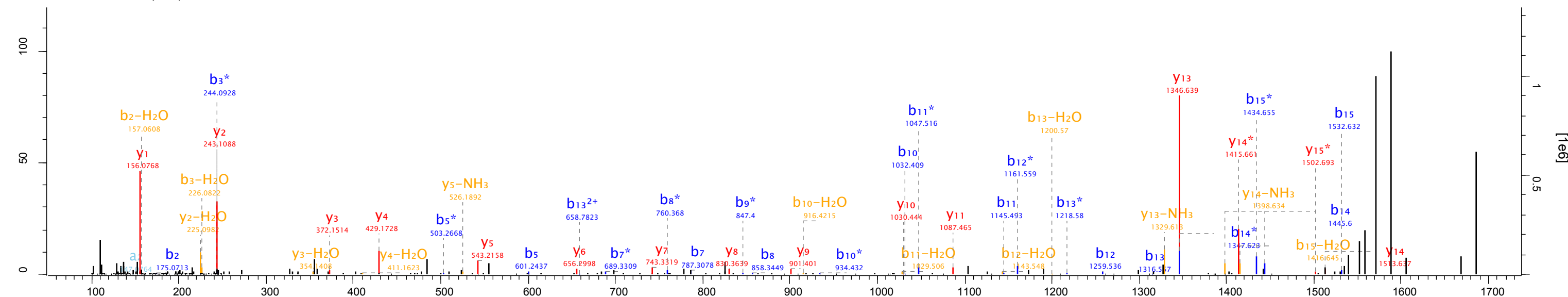


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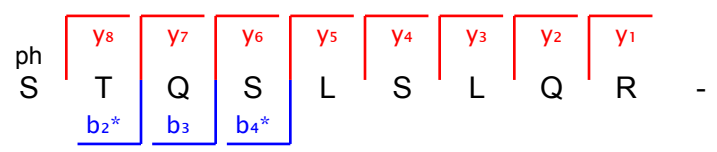
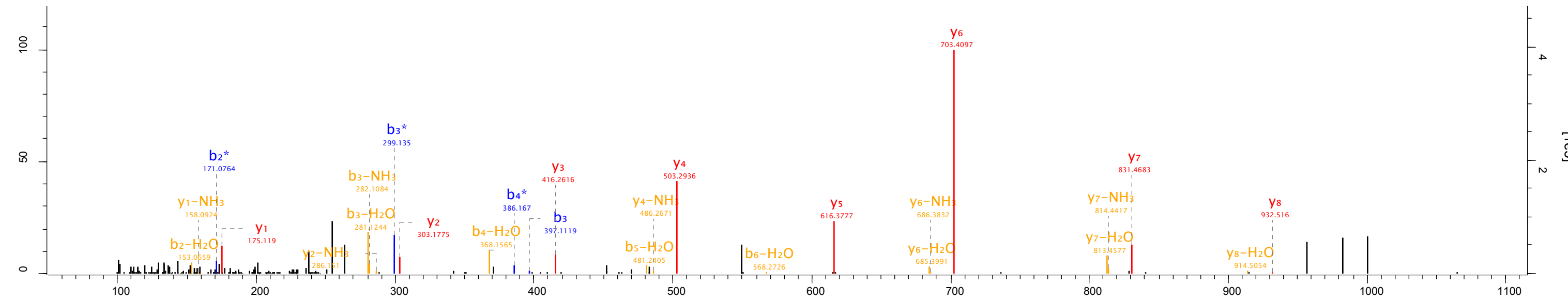


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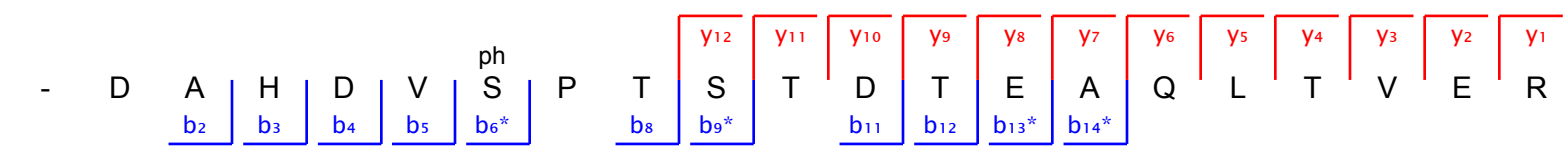
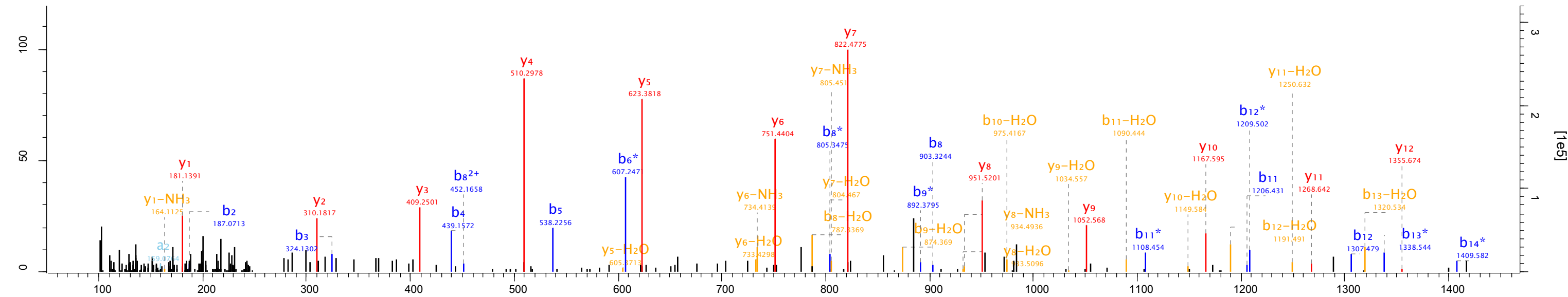
Scan 4017 Method FTMS; HCD Score 160.12 m/z 844.36 Gene names YAF2



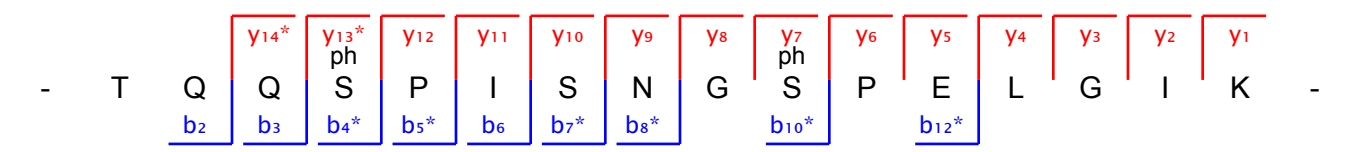
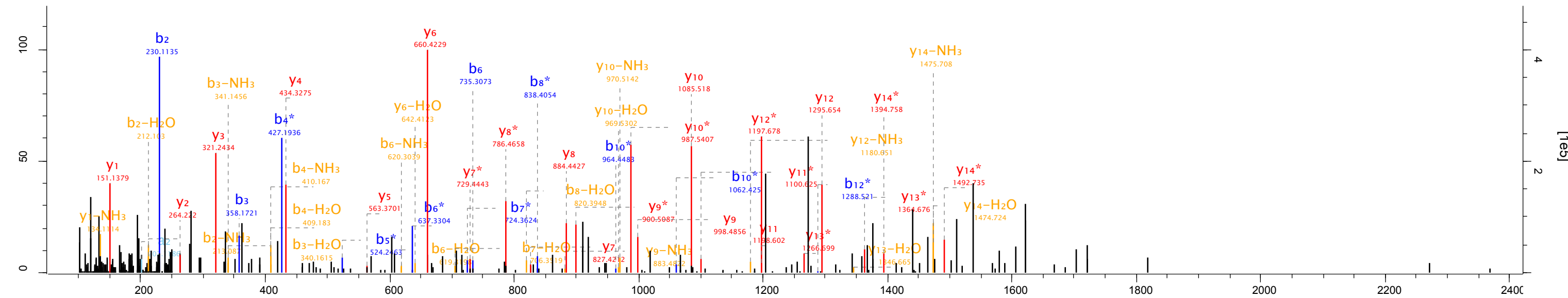
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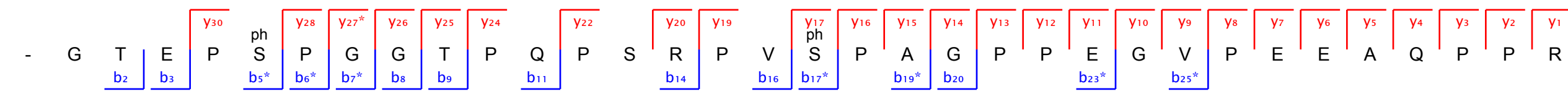
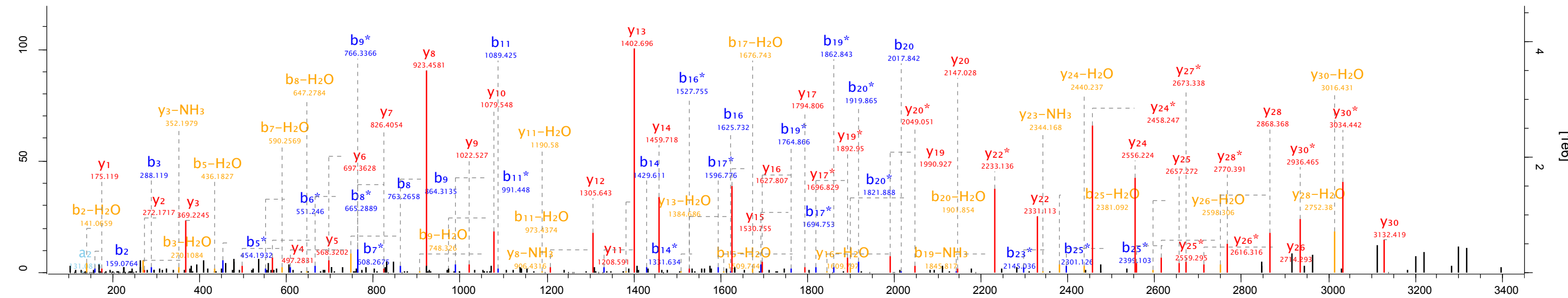
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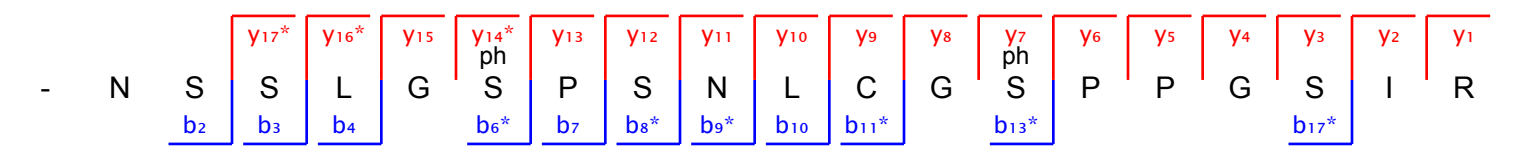
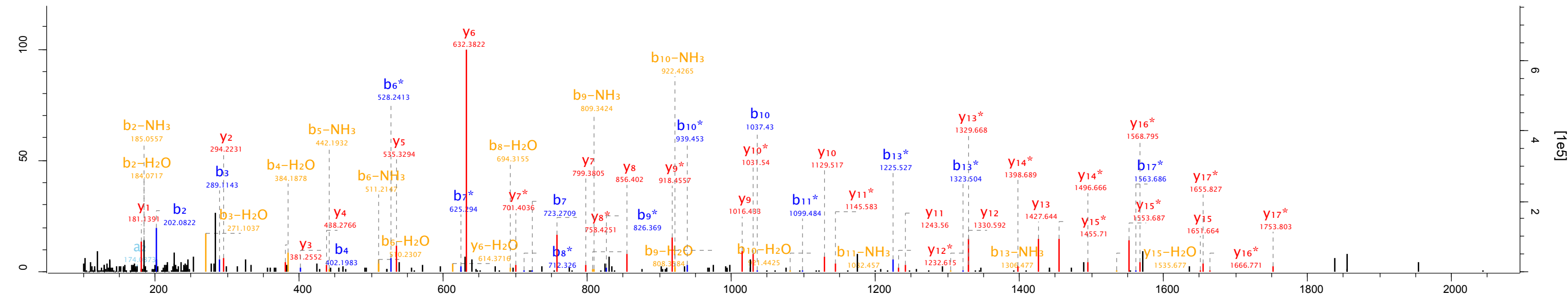
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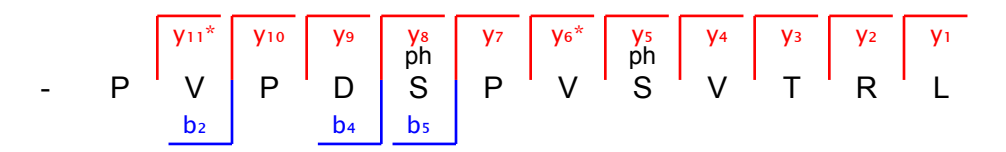
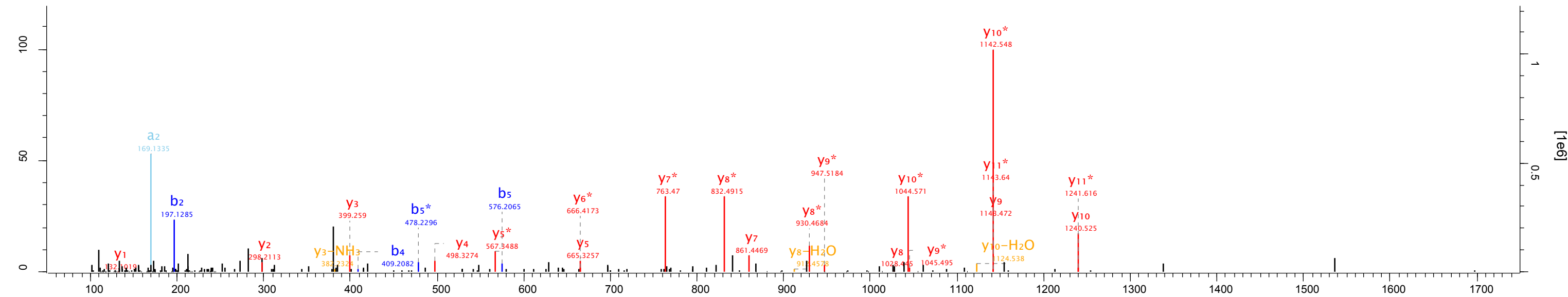
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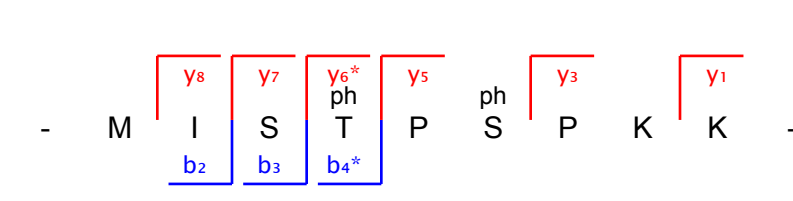
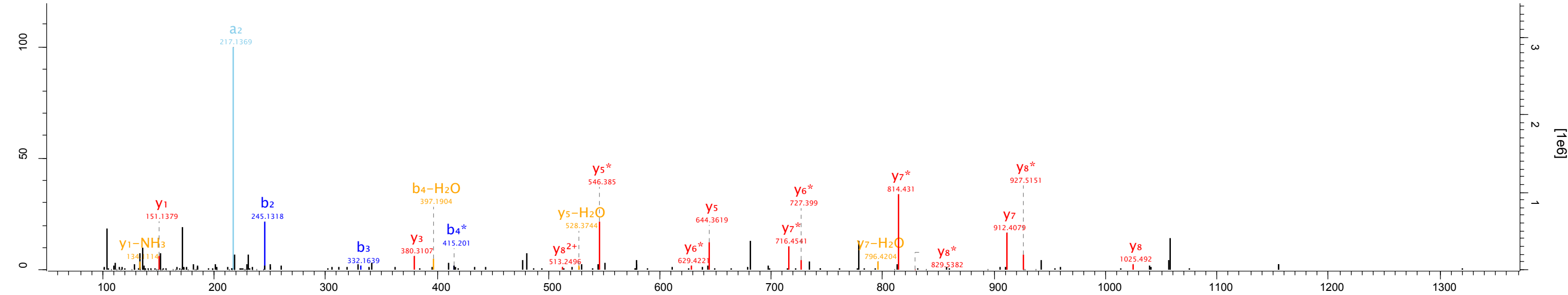
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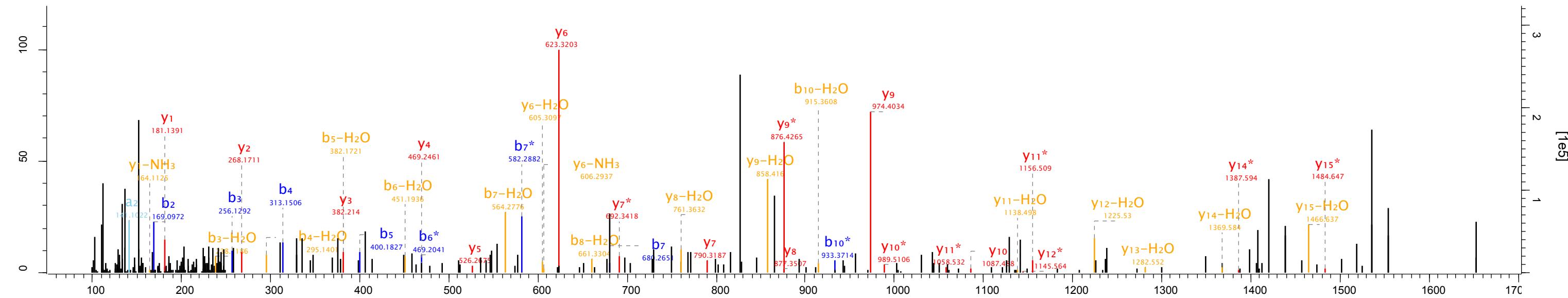


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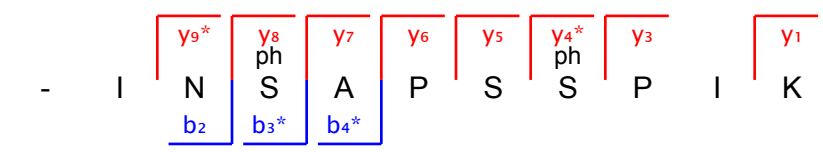
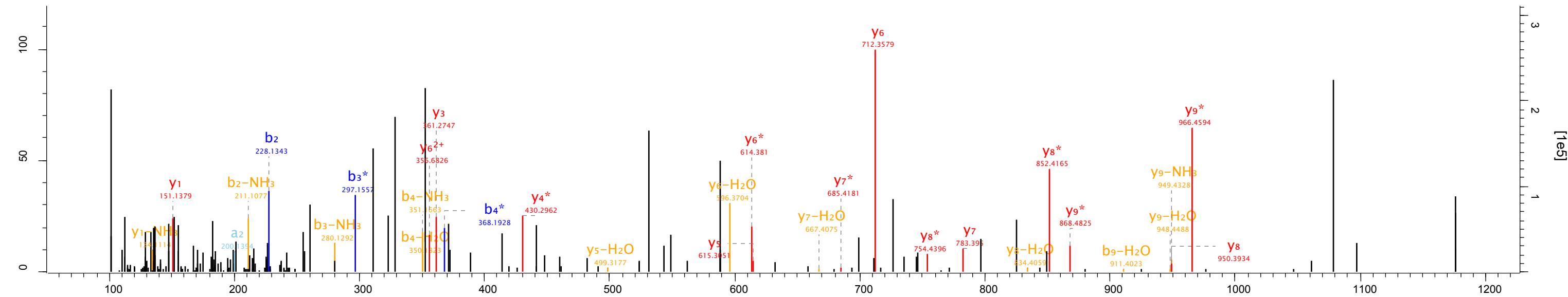


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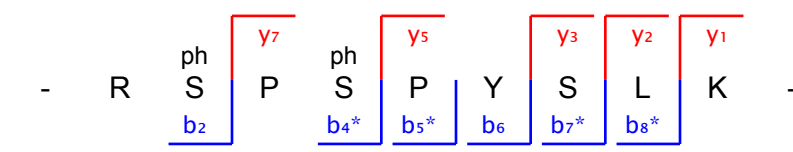
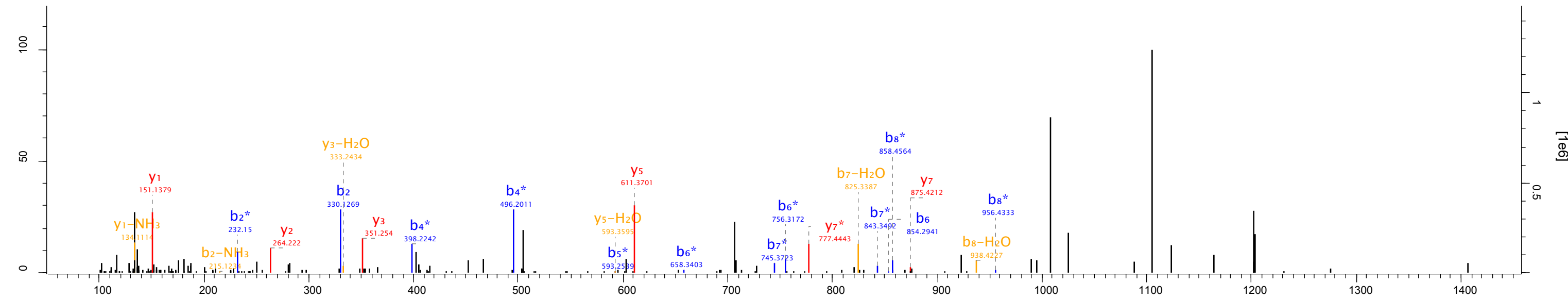
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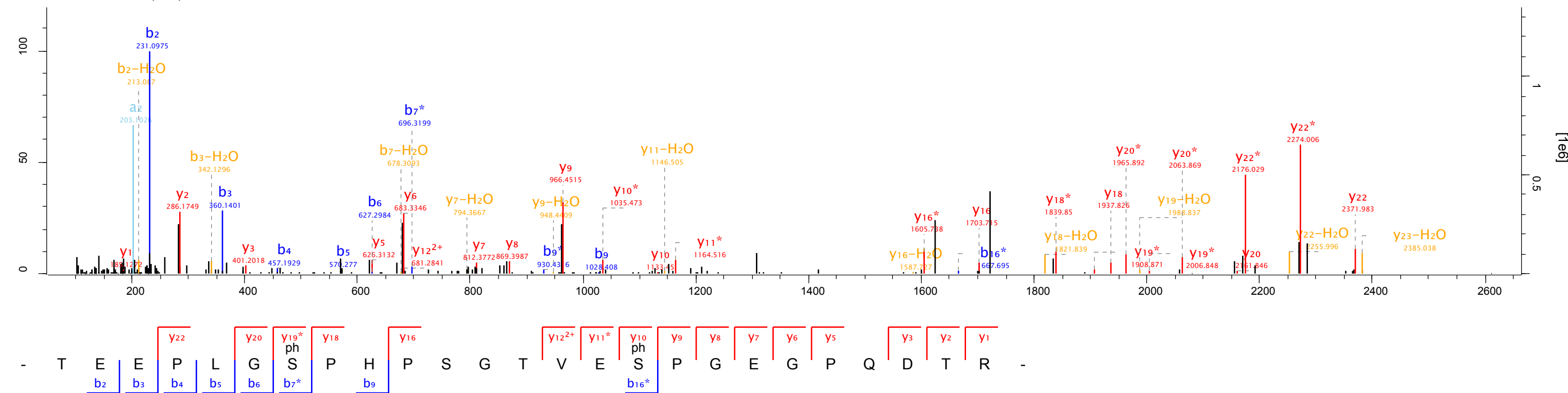


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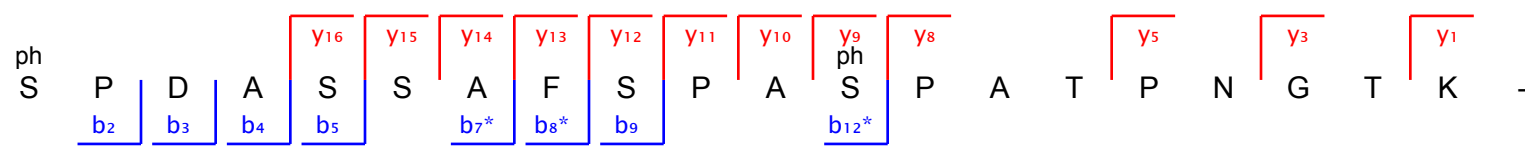
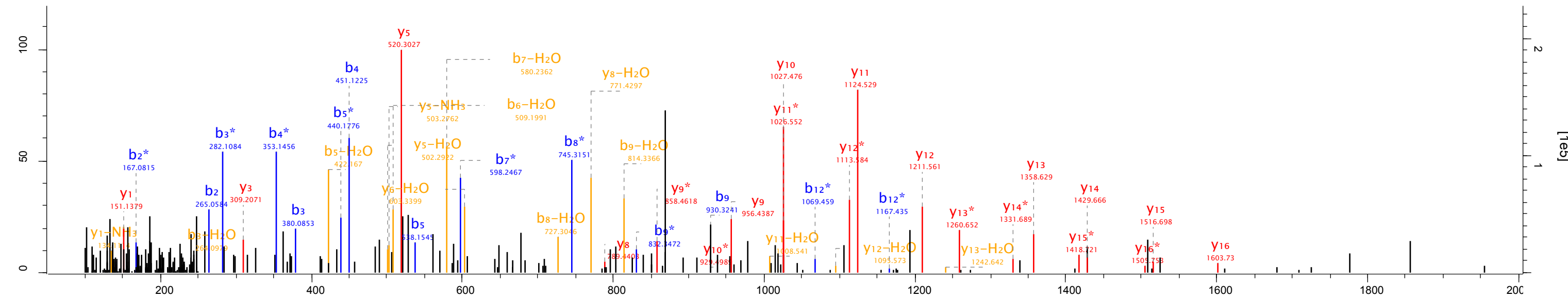


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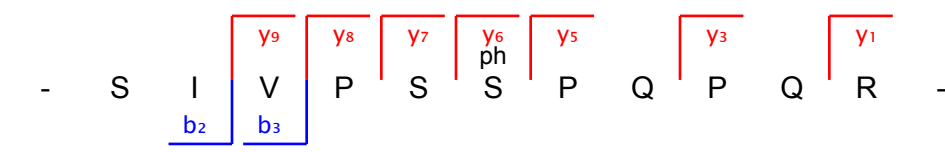
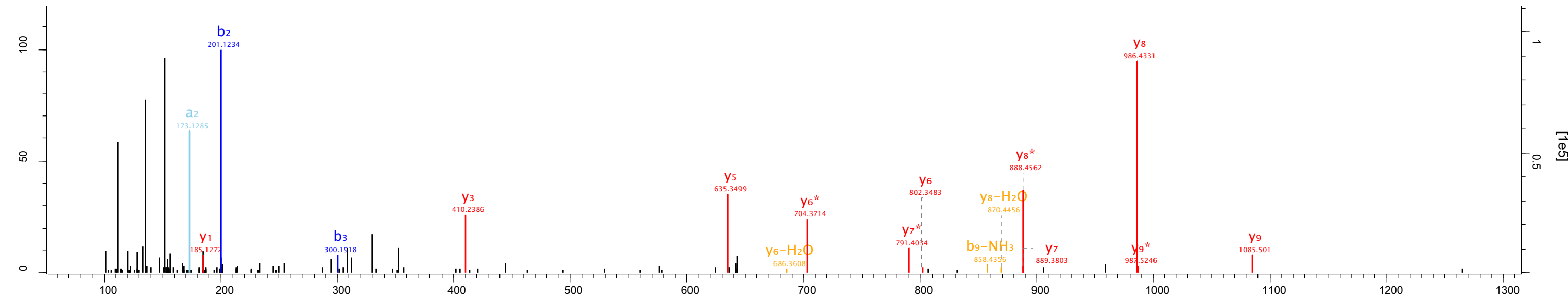
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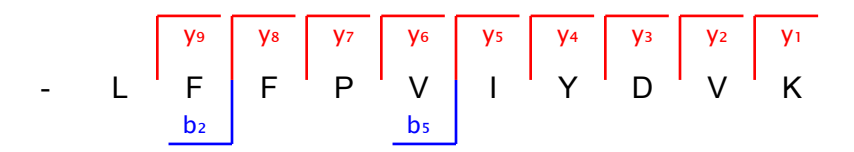
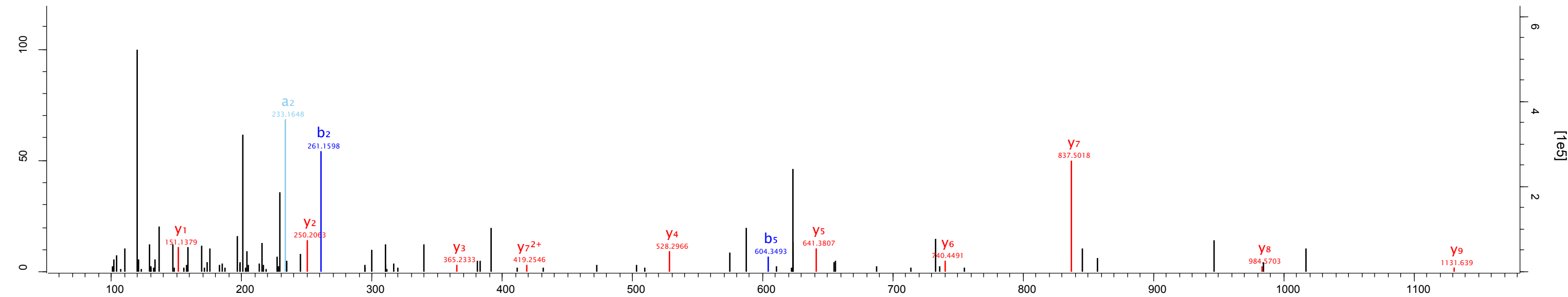
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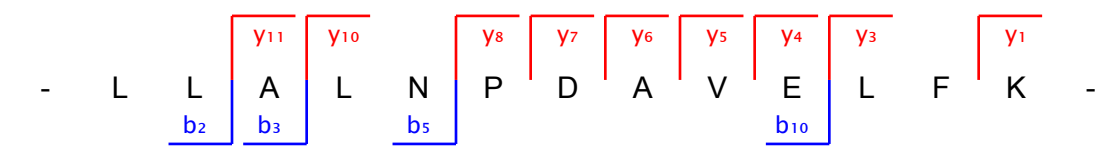
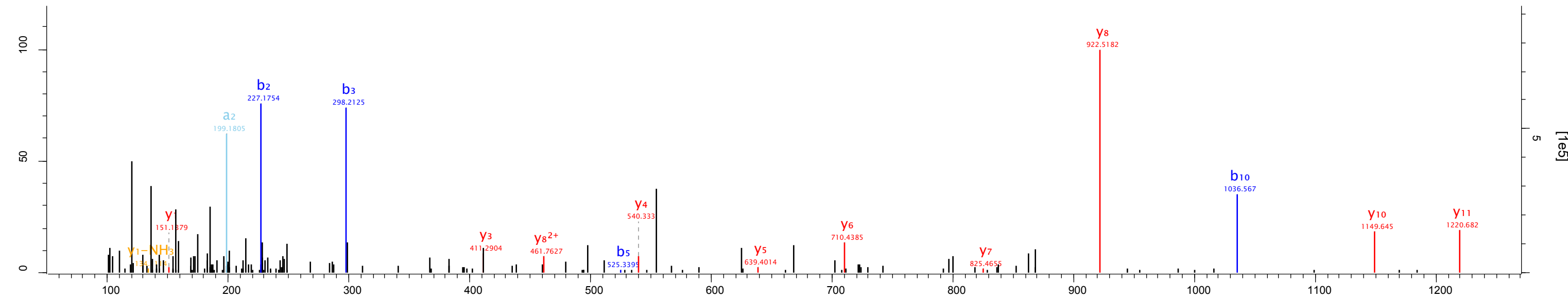
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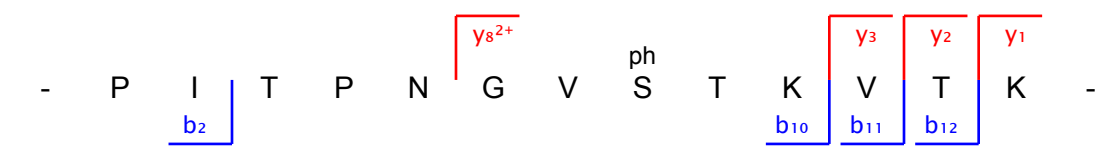
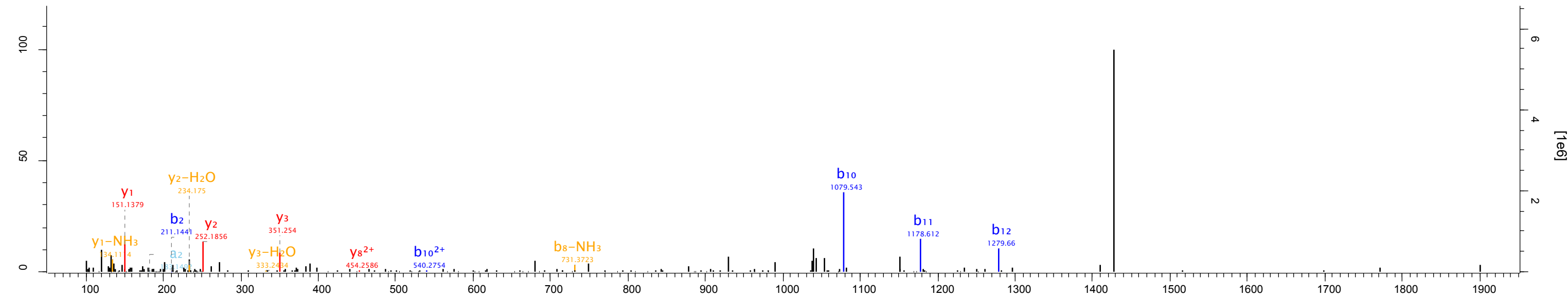
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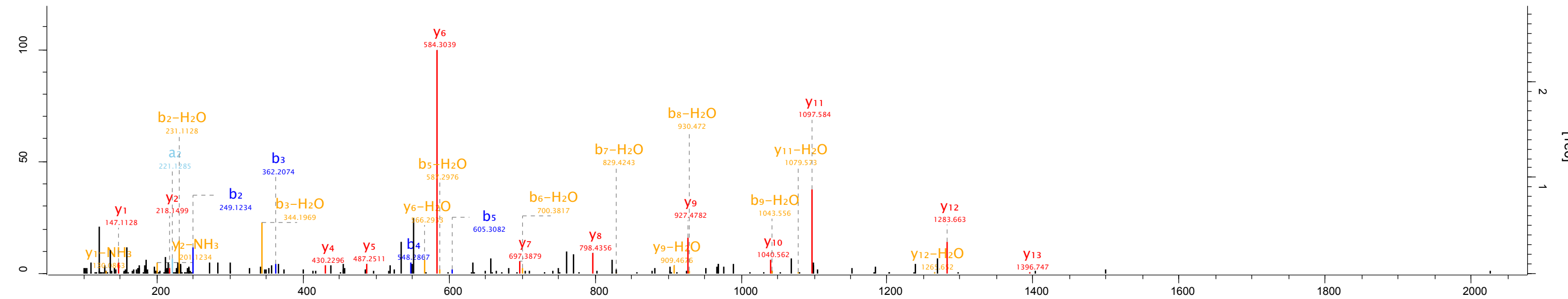
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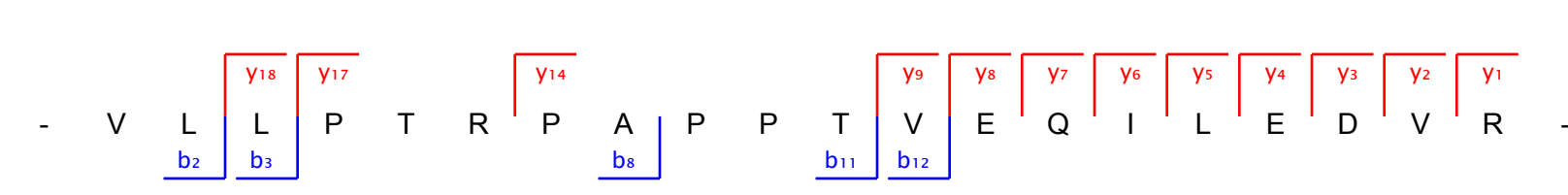
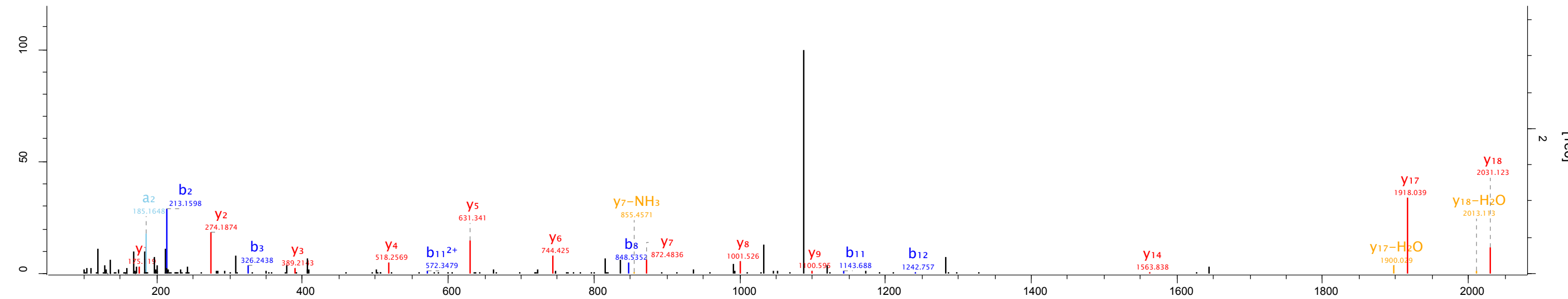
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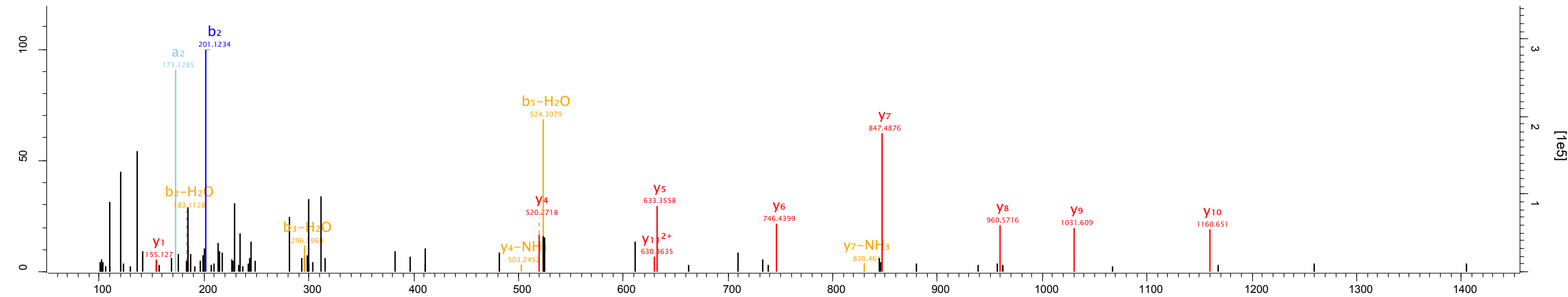
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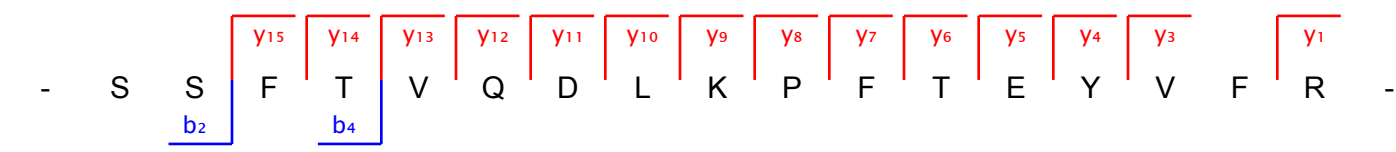
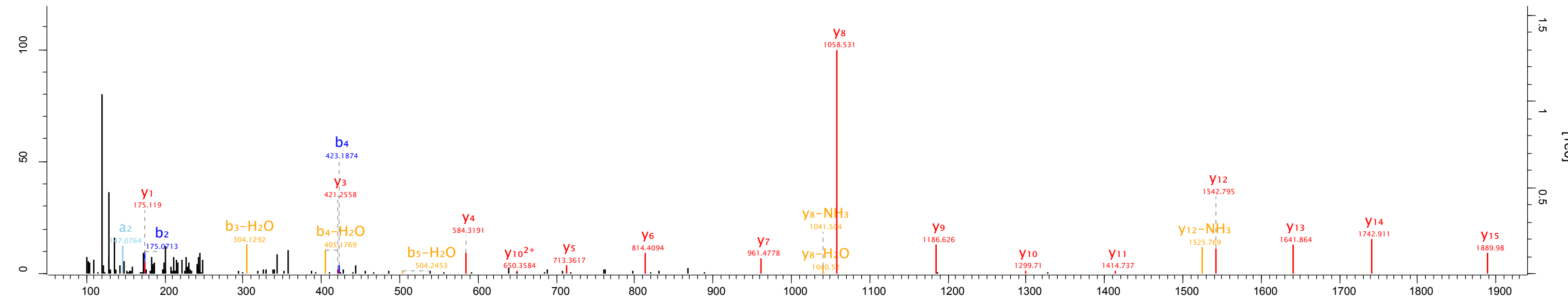
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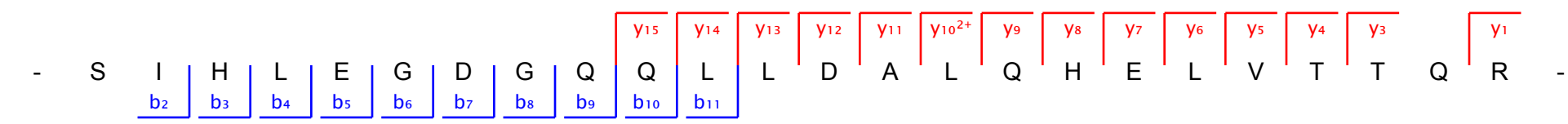
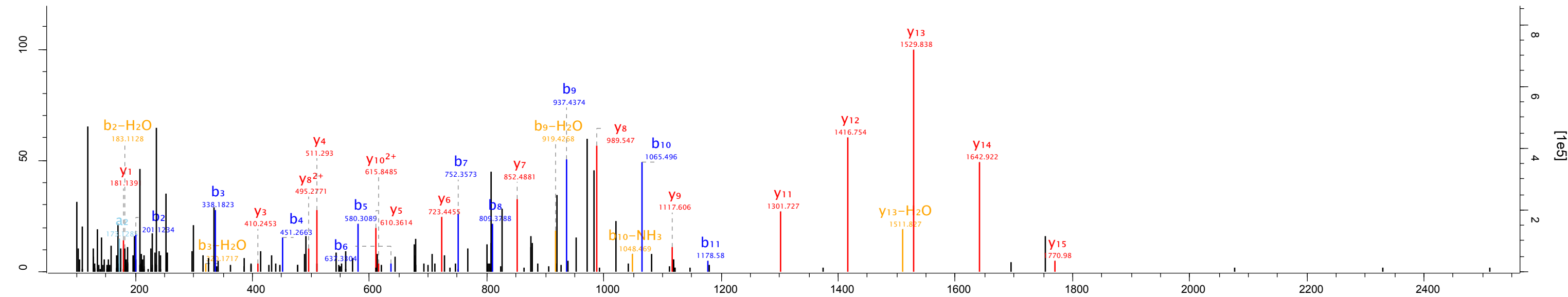
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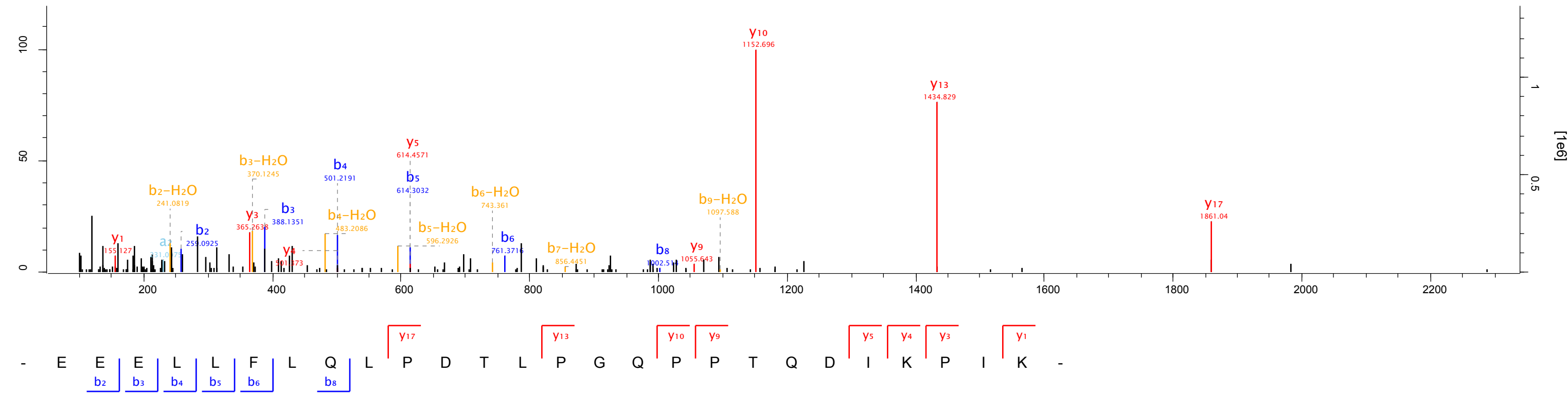
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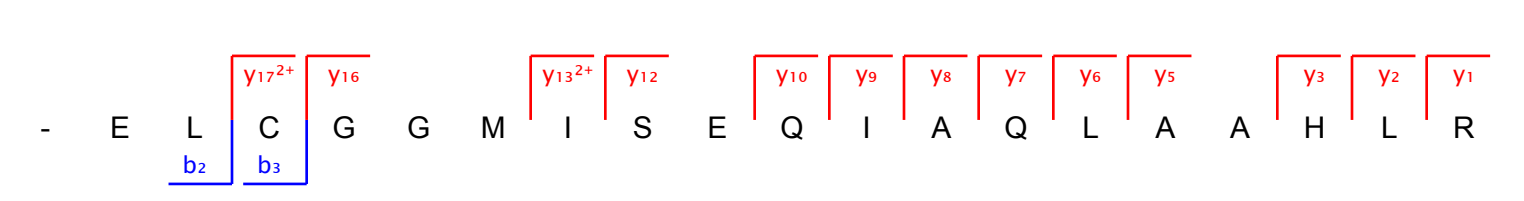
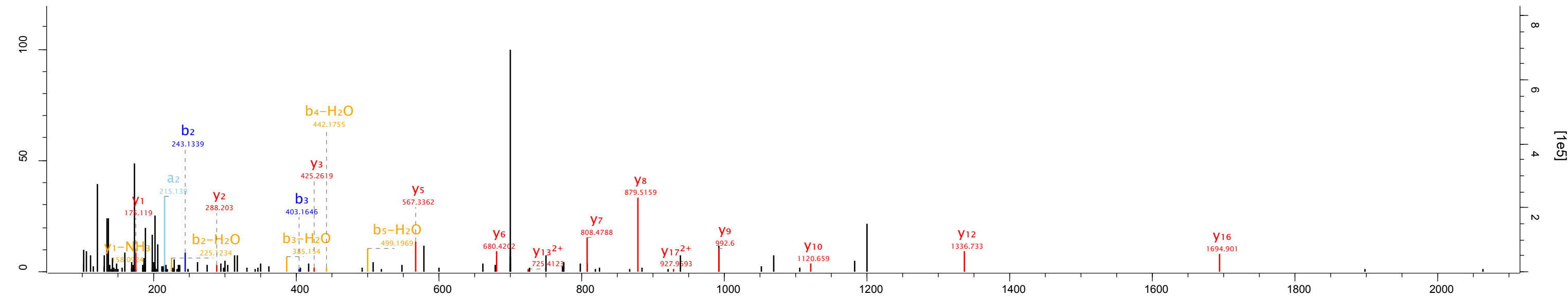
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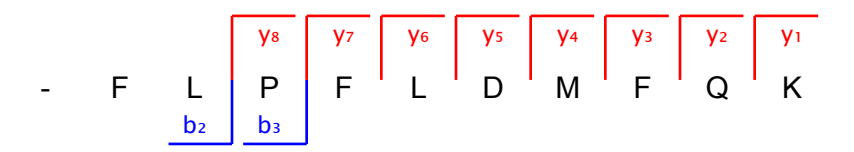
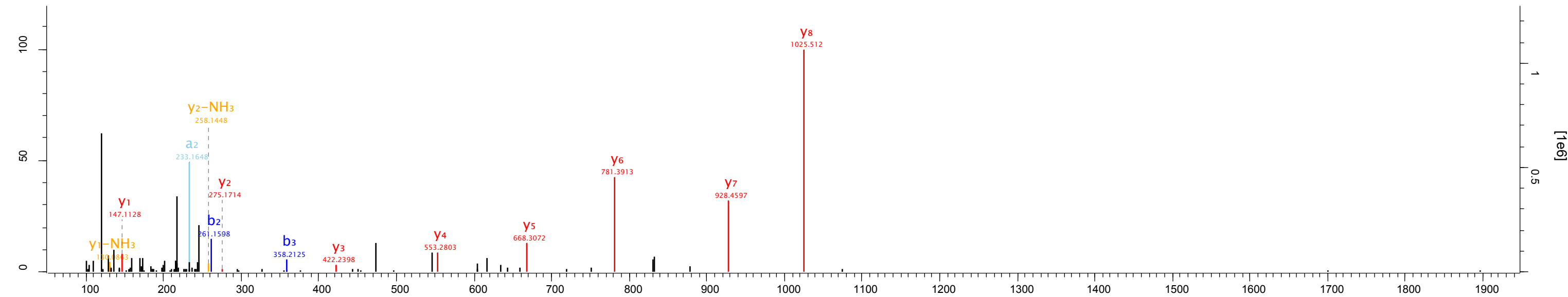
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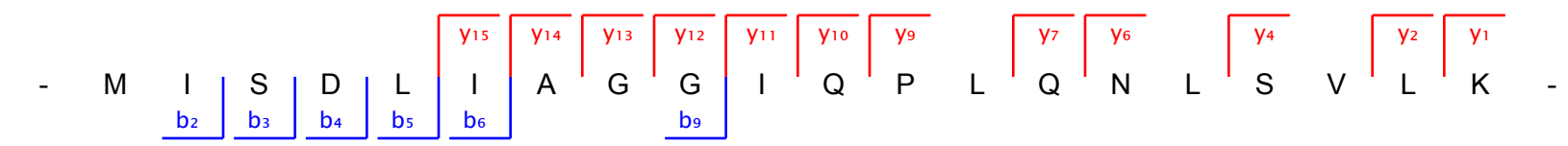
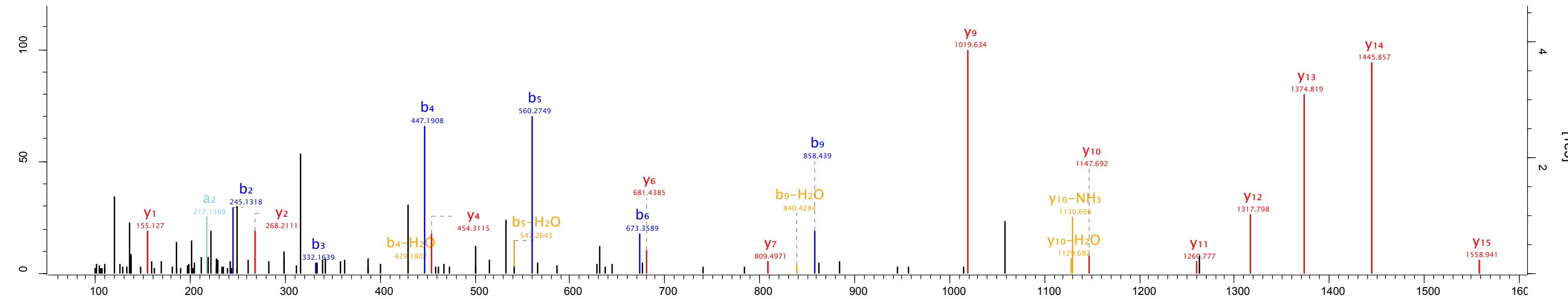
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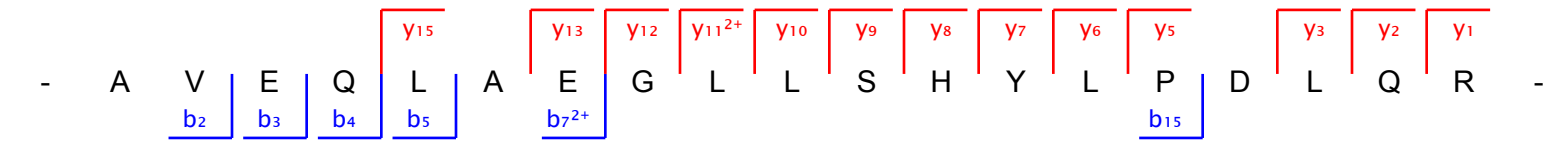
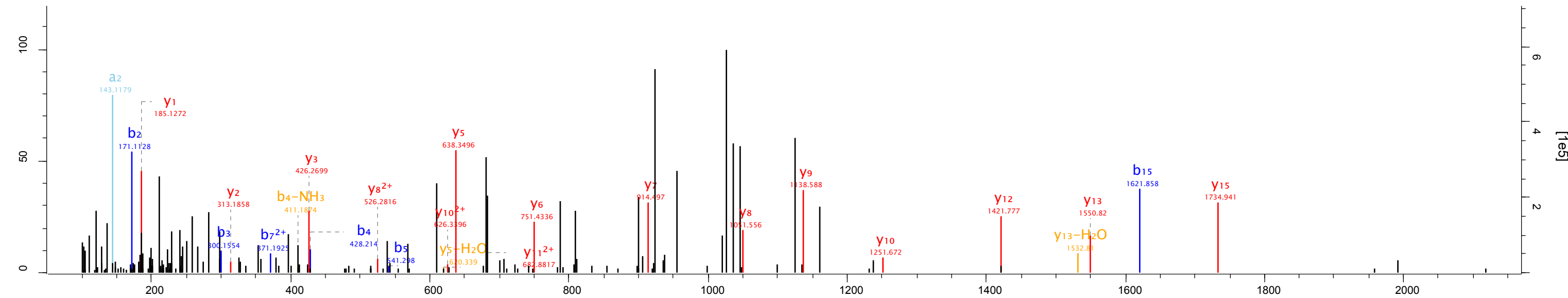


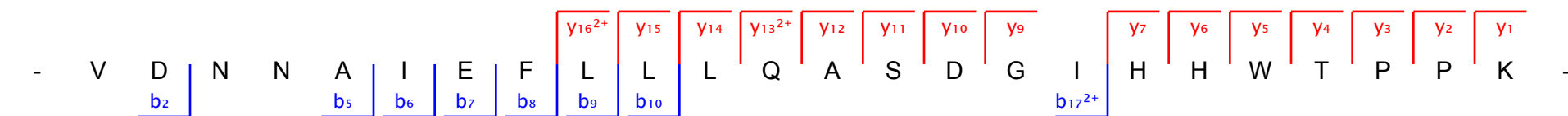
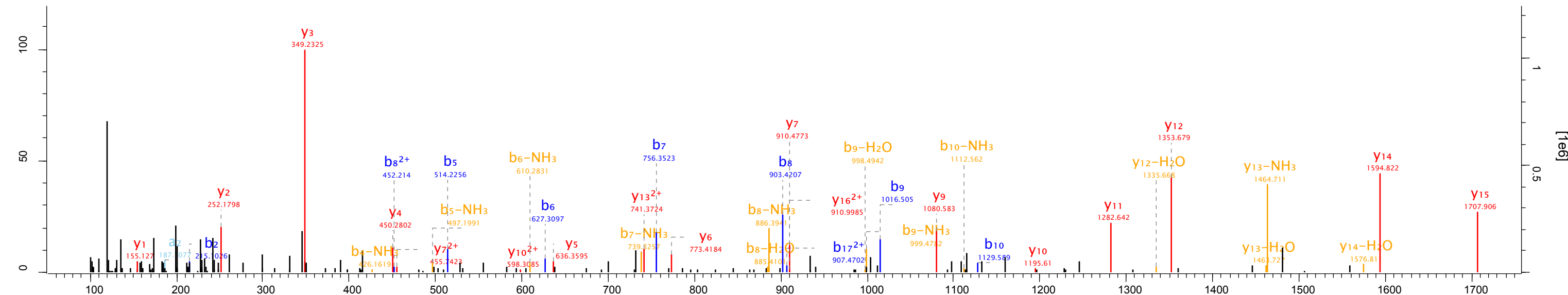
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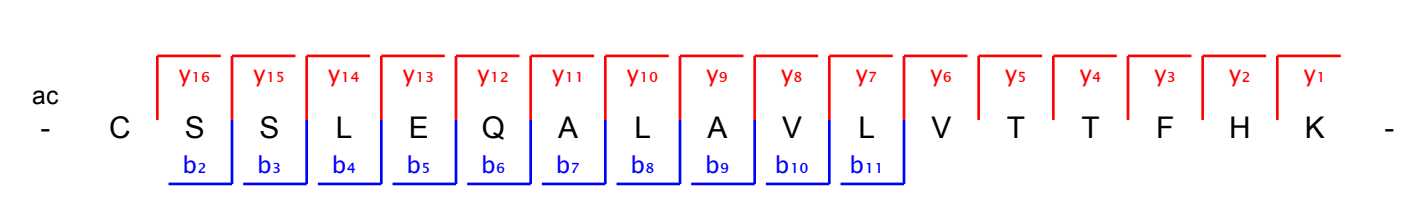
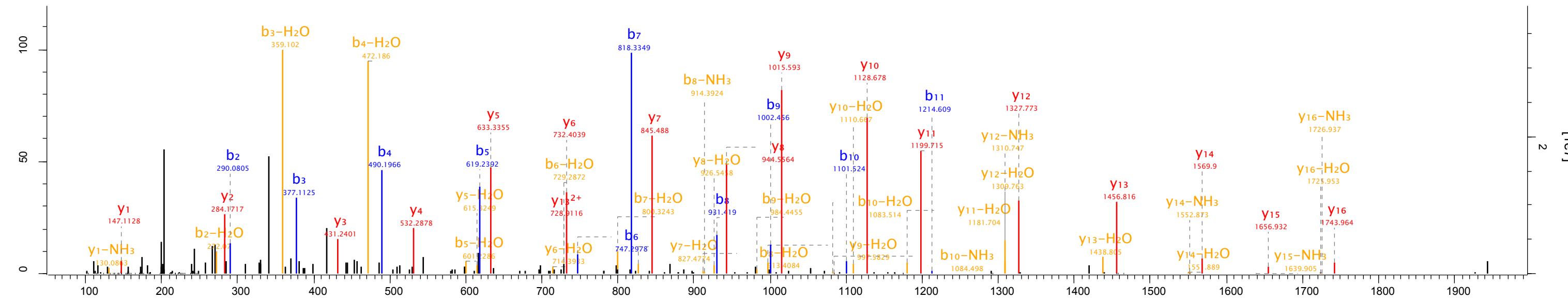
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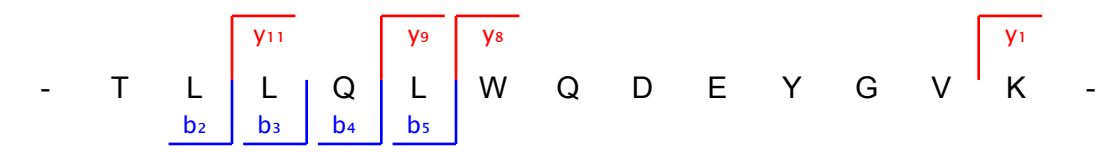
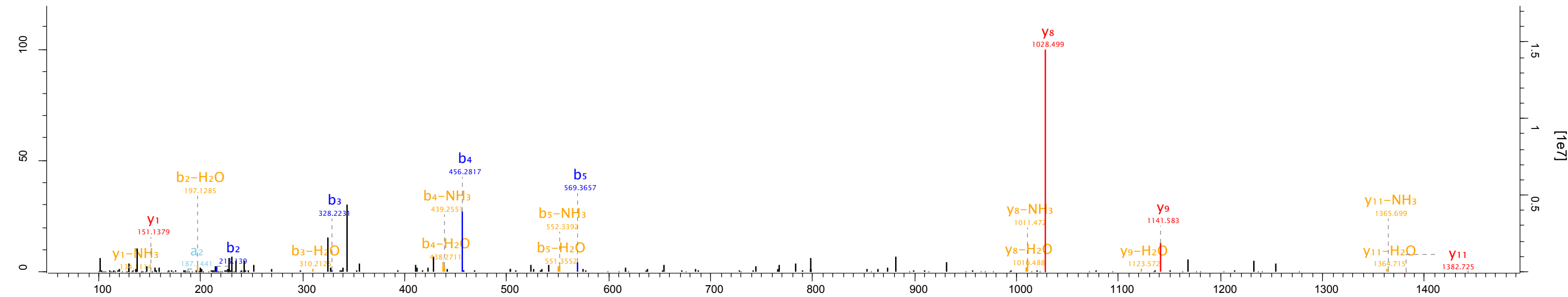




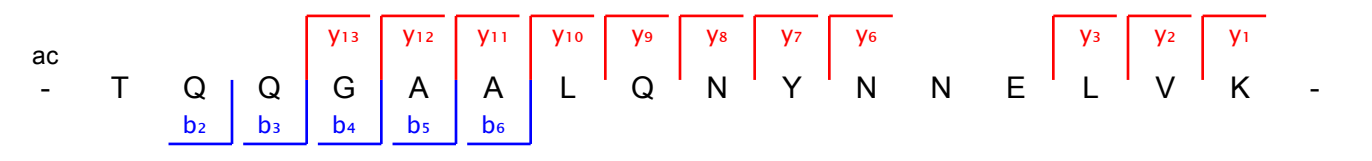
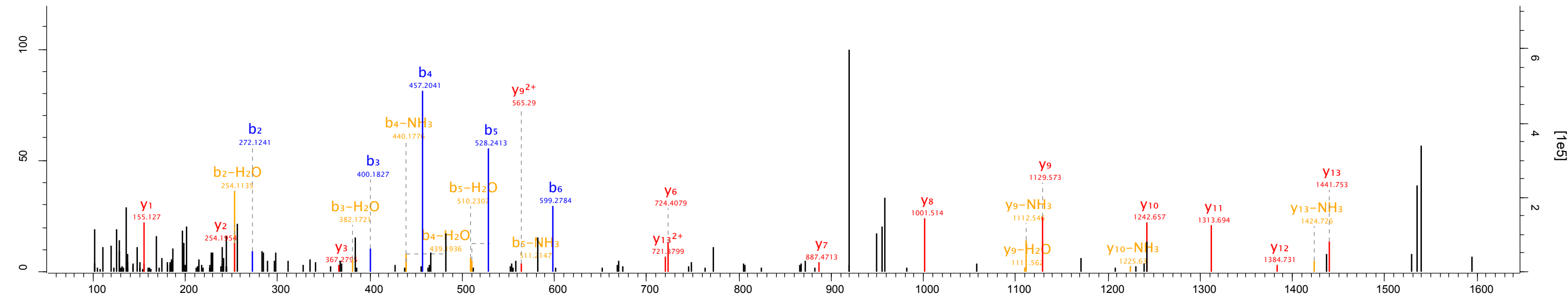
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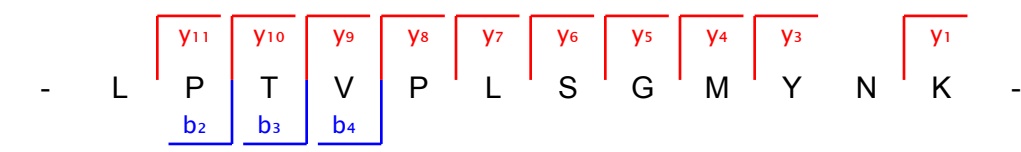
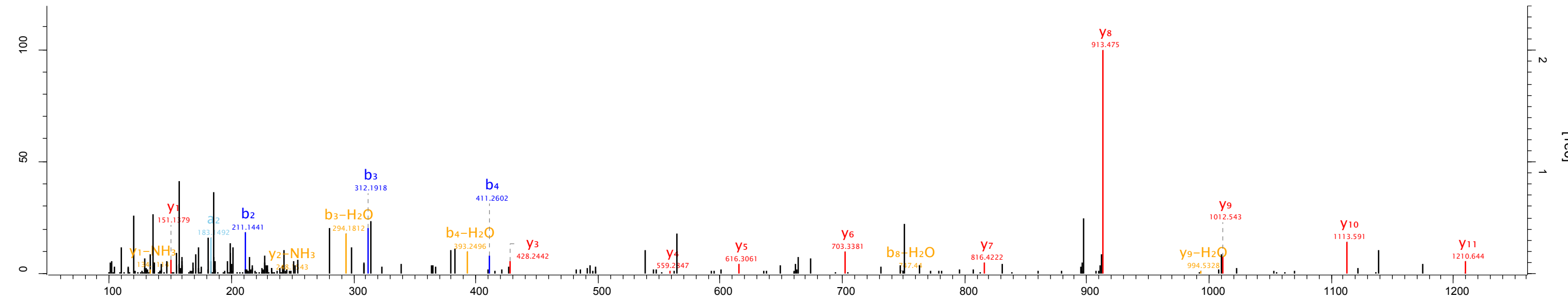
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Raw file

20171215_MaS_33SR_LMH_proteome_01

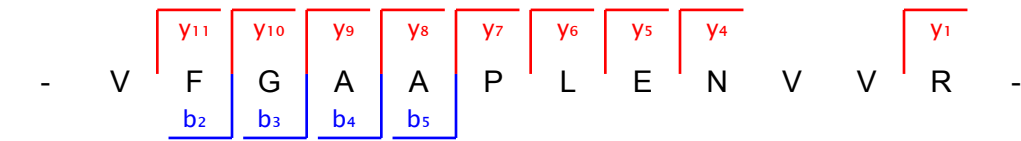
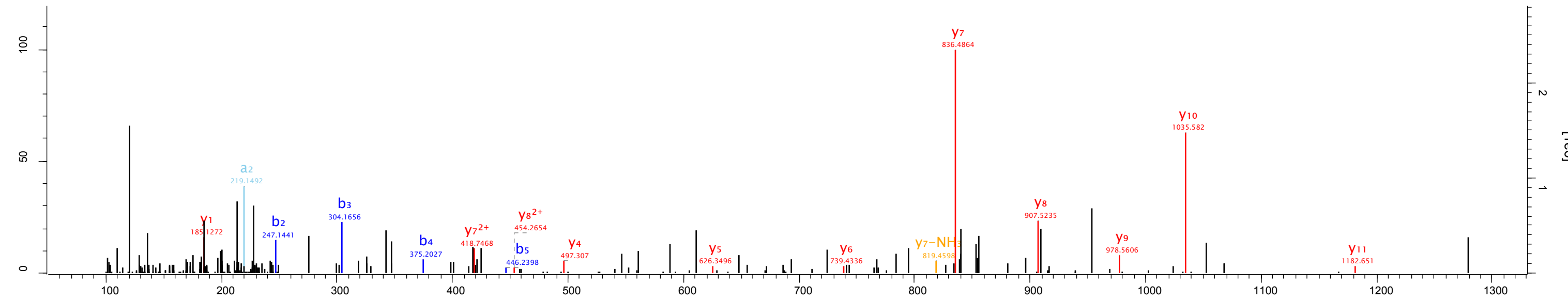
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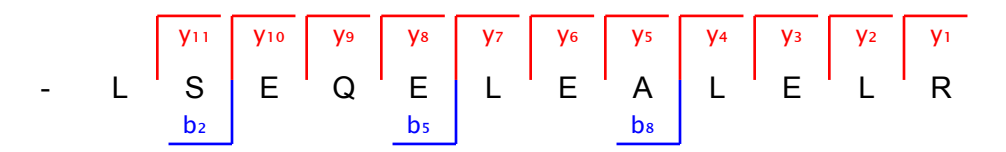
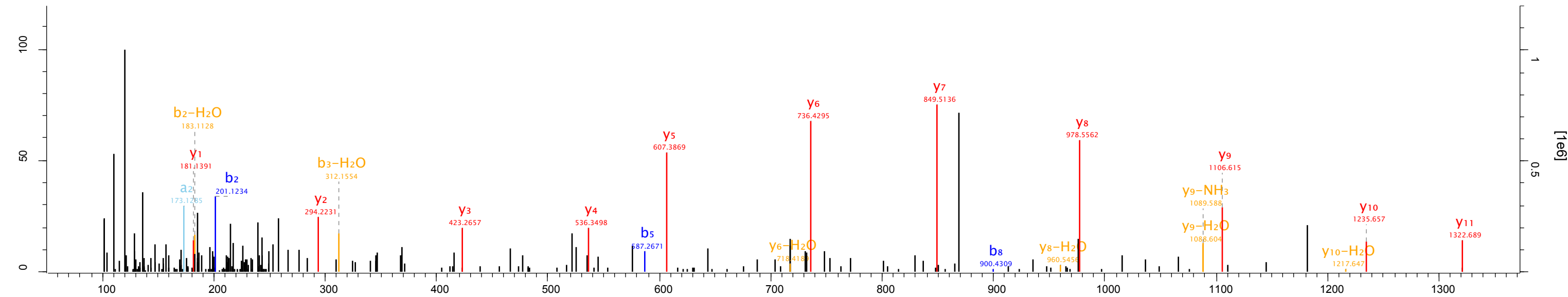
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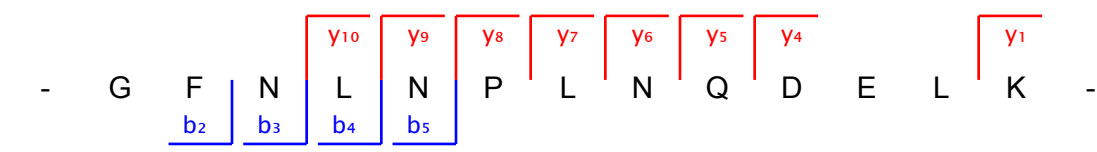
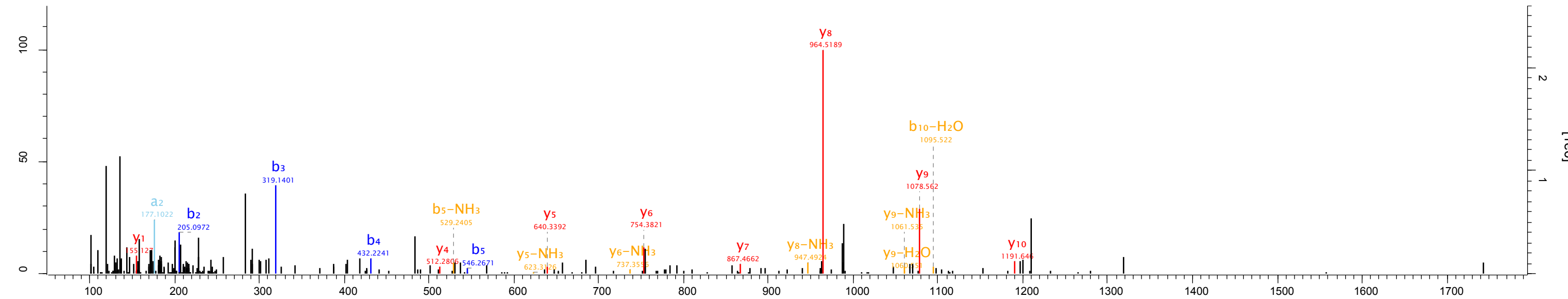
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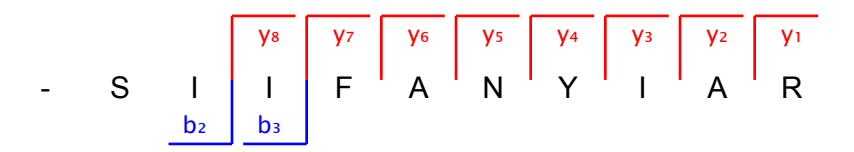
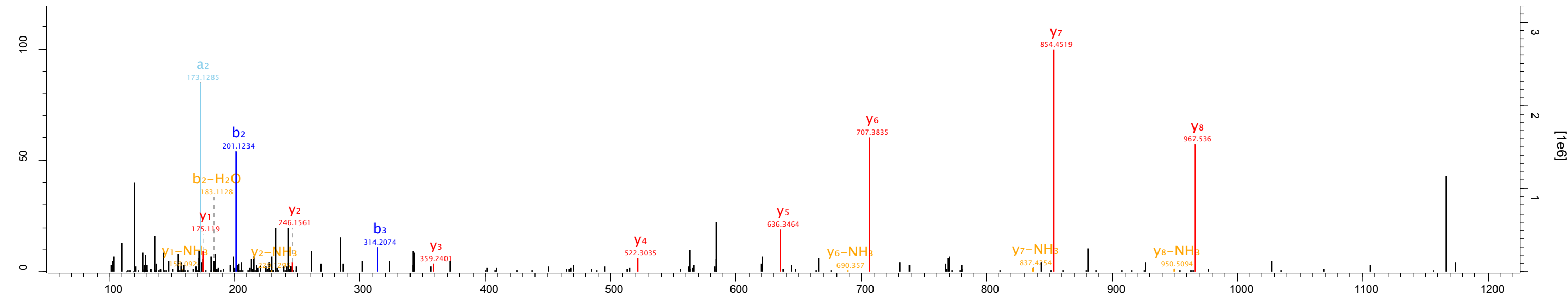
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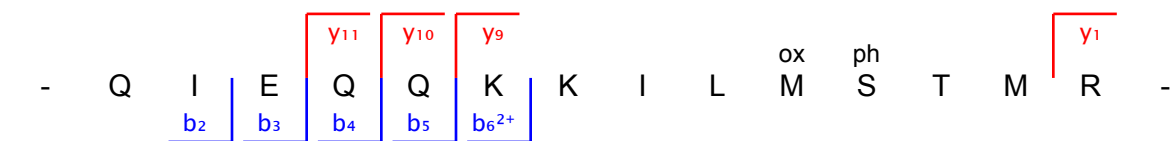
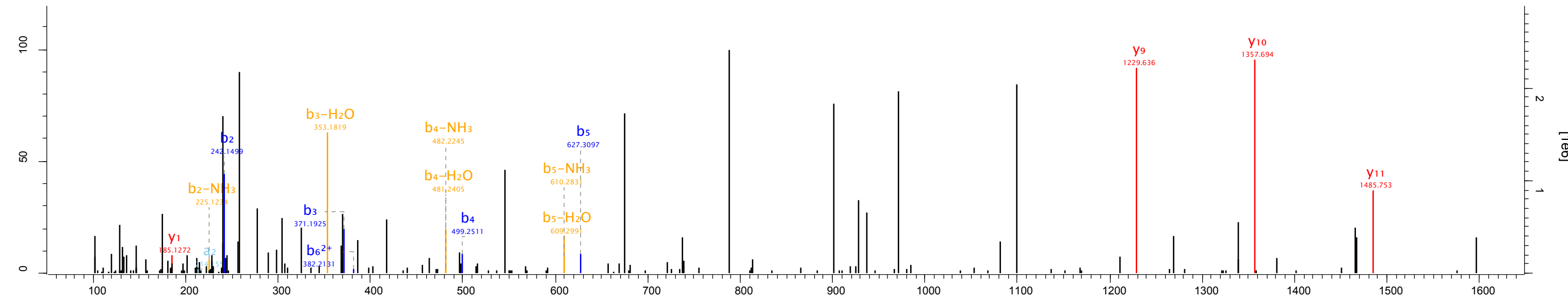


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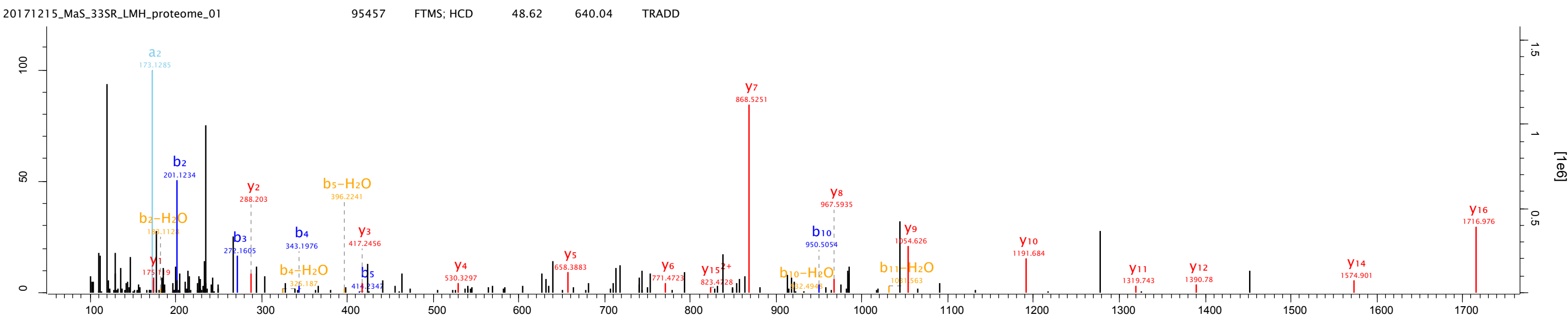
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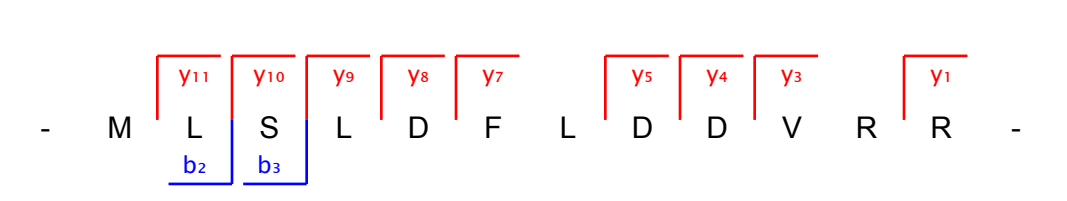
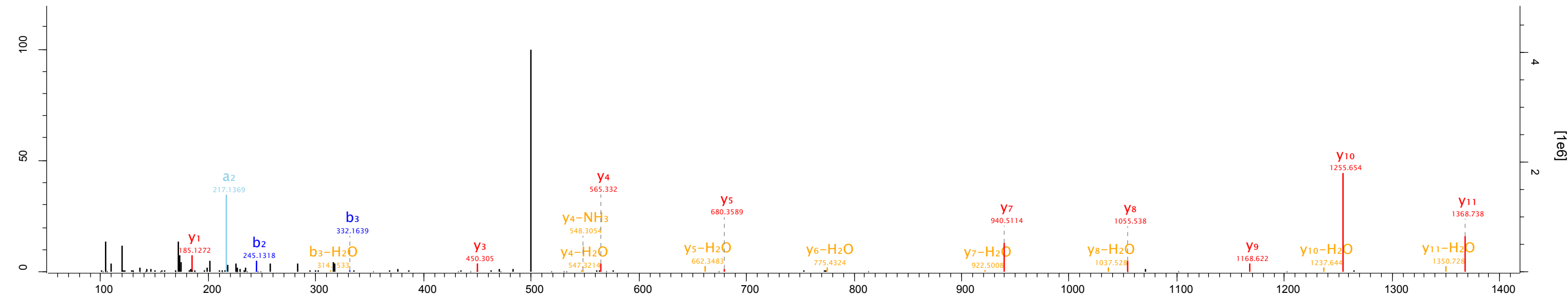


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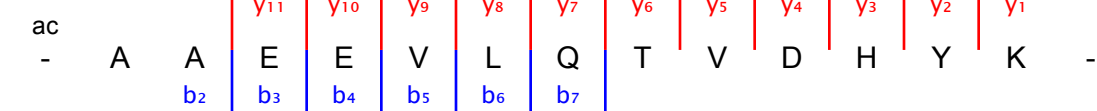
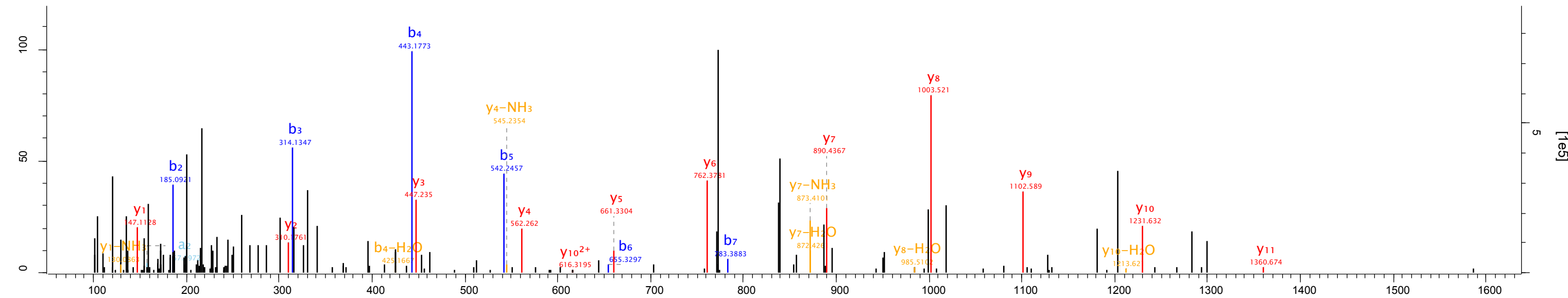
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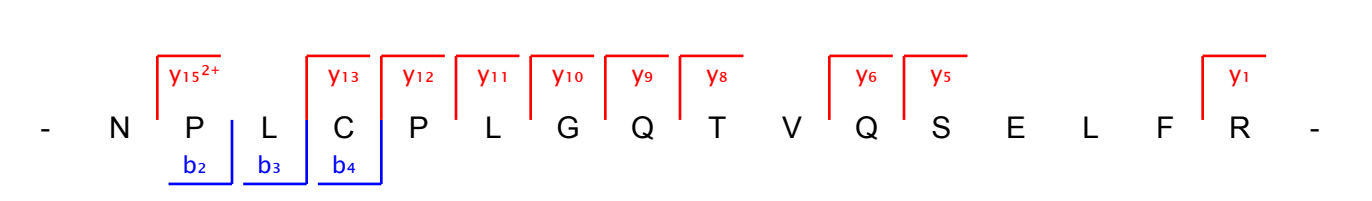
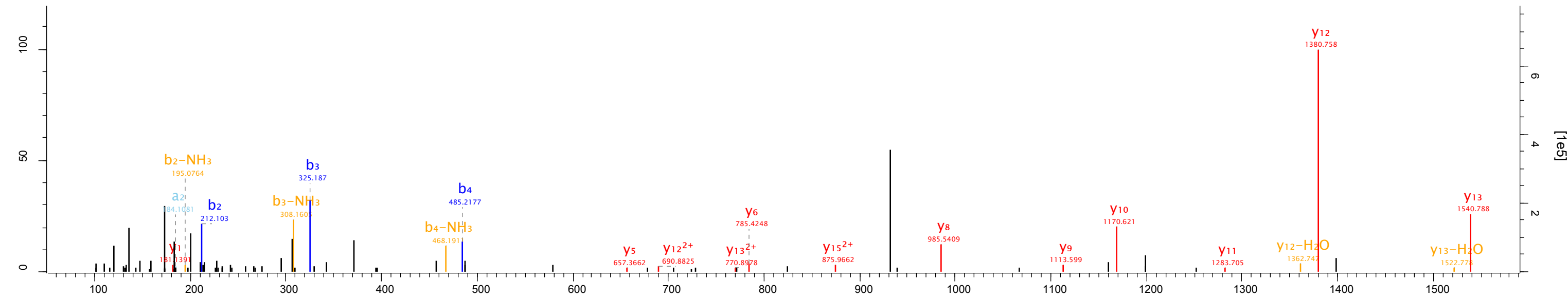
Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 97727 Method FTMS; HCD Score 106.67 m/z 500.6 Gene names SEC11A



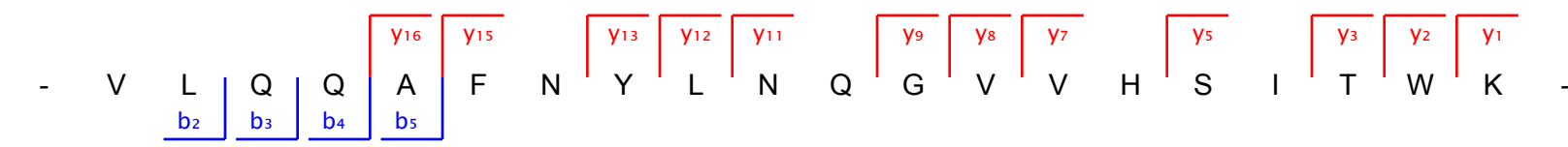
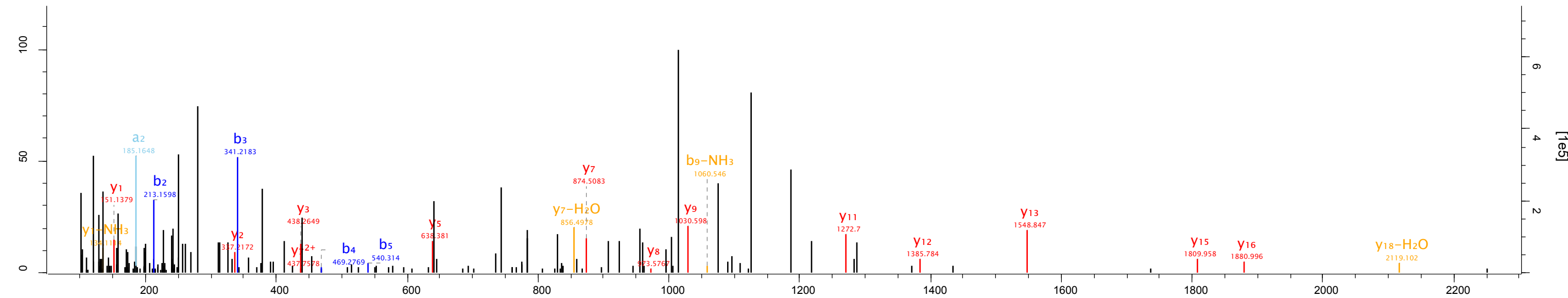
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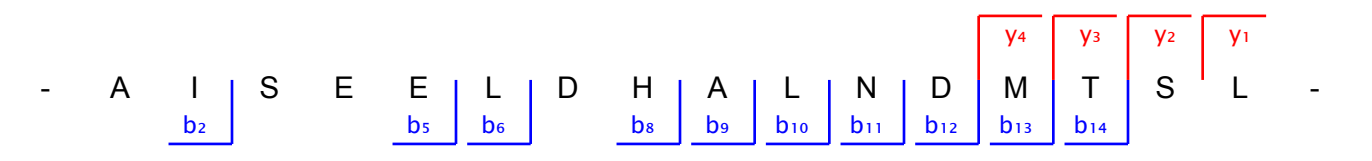
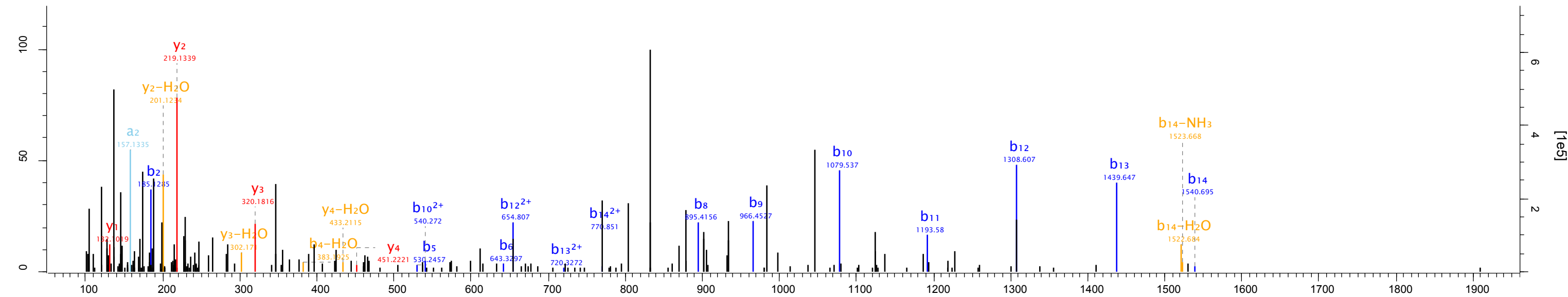
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 Scan: 102187 Method: FTMS; HCD Score: 96.67 m/z: 932.99 Gene names: TRAPPC1

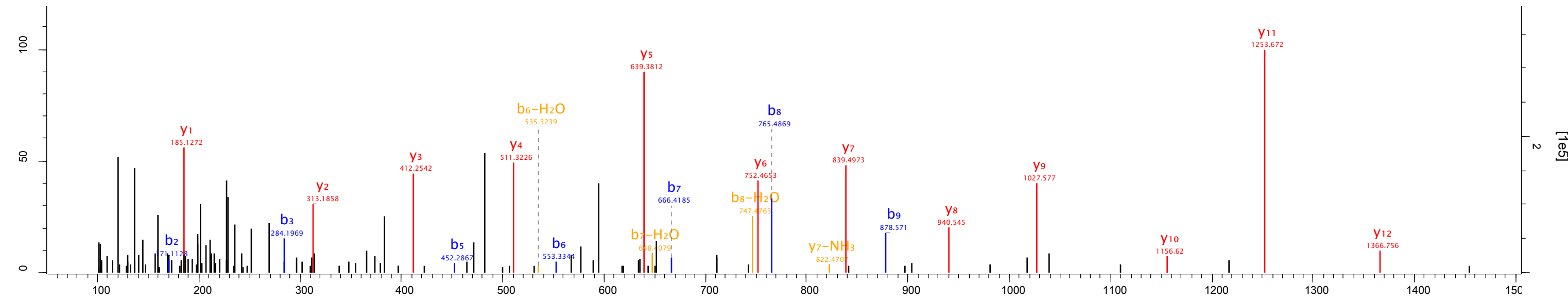


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 Scan: 110697
 Method: FTMS; HCD
 Score: 48.05
 m/z: 784.09
 Gene names: IPO8



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 112177 Method FTMS; HCD Score 73.83 m/z 879.92 Gene names TPM4





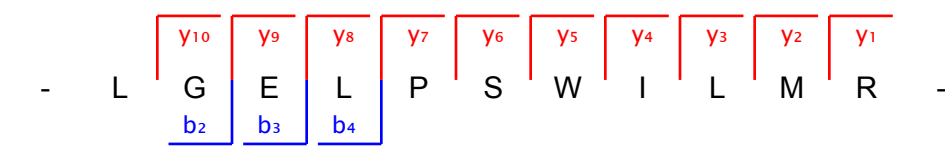
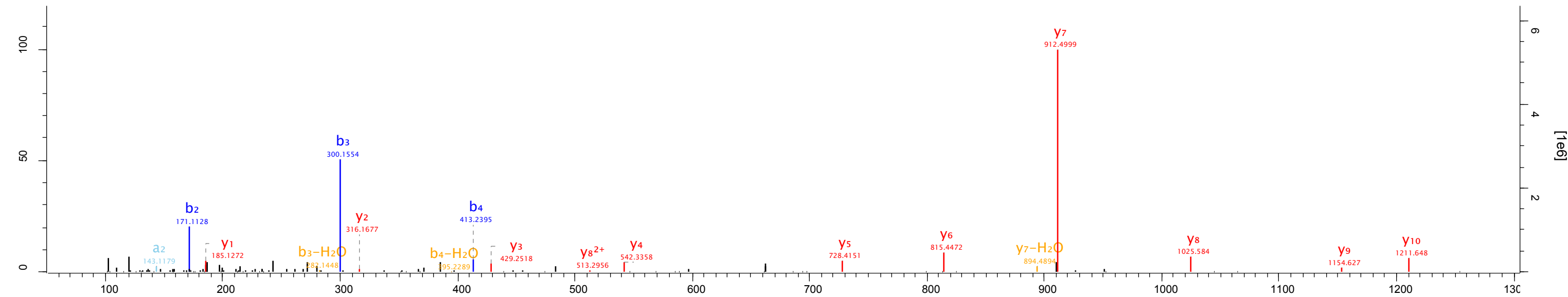
- L G I P A T I V L P E S T S L Q V V Q R -

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

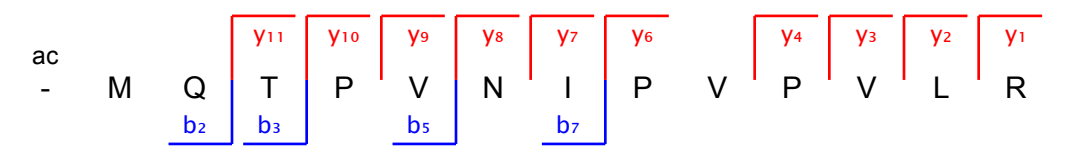
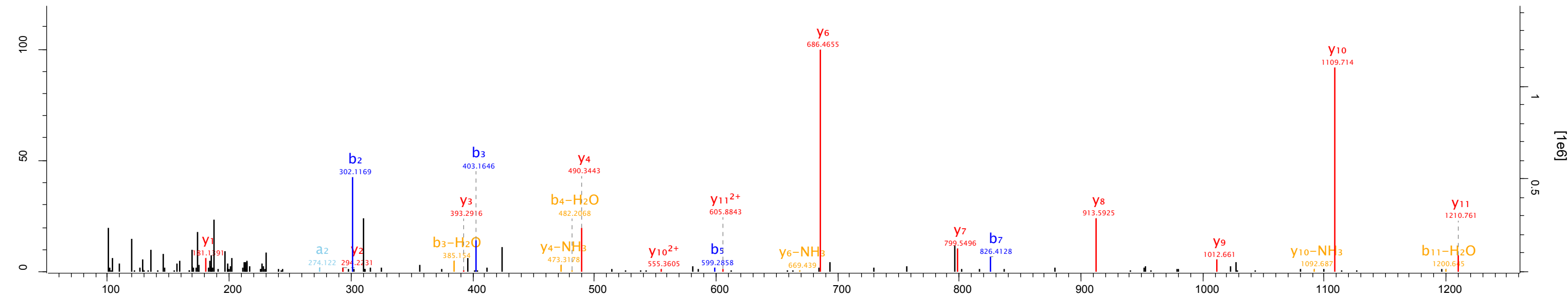
- b2: G-I
- b3: I-P
- b5: A-T
- b6: T-I
- b7: I-V
- b8: V-L
- b9: L-P

Y-series fragments are labeled above the sequence from L to R.

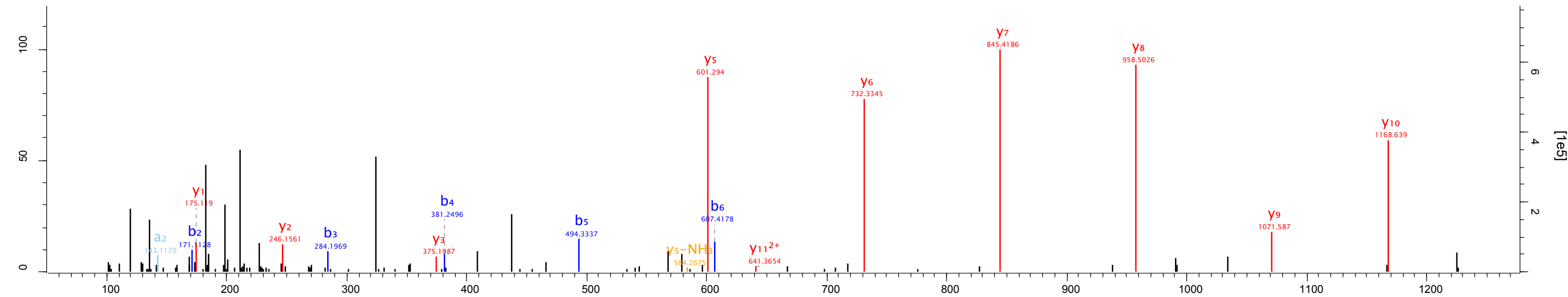
Raw file: 20171215_MaS_33SR_LMH_proteome_02
 Scan: 115827 Method: FTMS; HCD Score: 85.81 m/z: 662.87 Gene names: ATP5J2-PTCD1;ATP5J2



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 123927 Method FTMS; HCD Score 84.36 m/z 756.94 Gene names GEMIN7



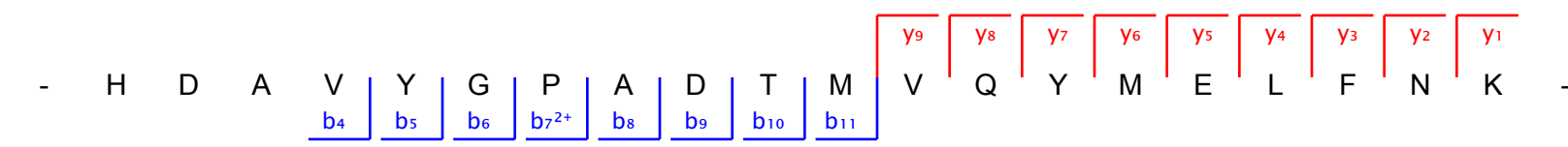
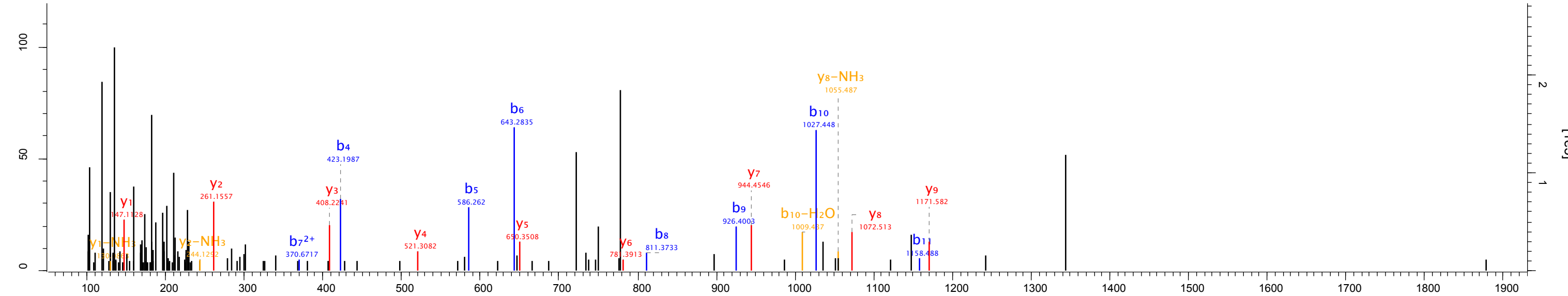
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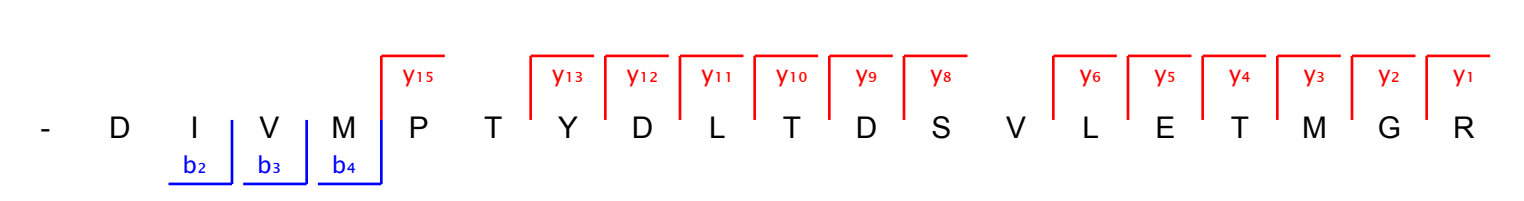
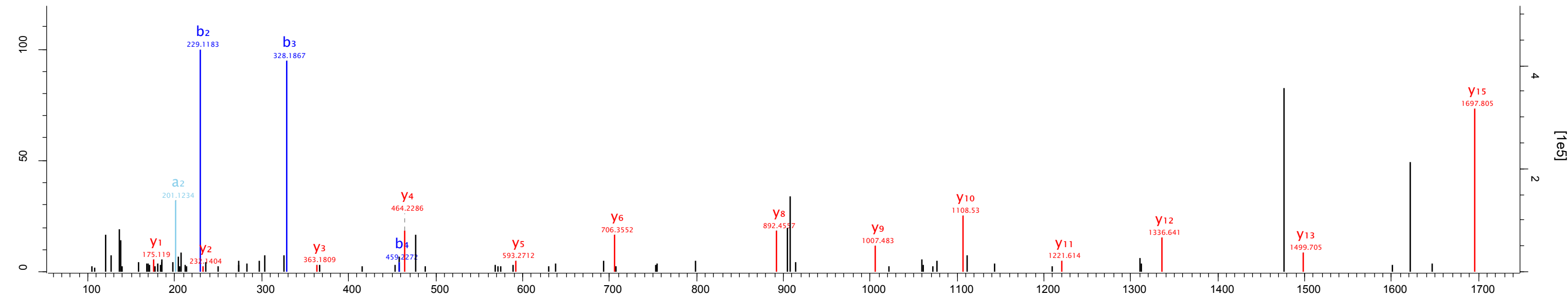
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20171215_MaS_33SR_LMH_proteome_02

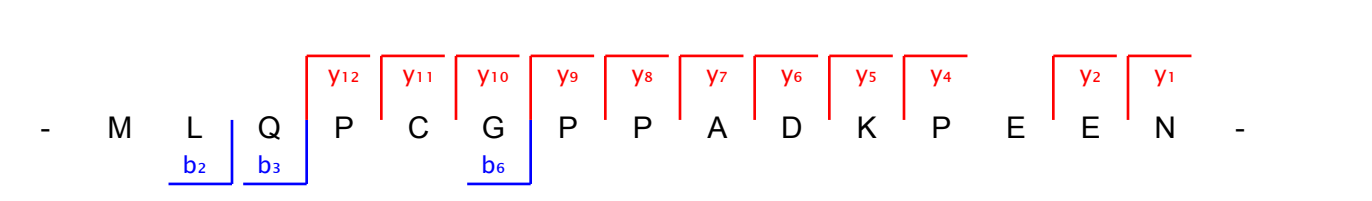
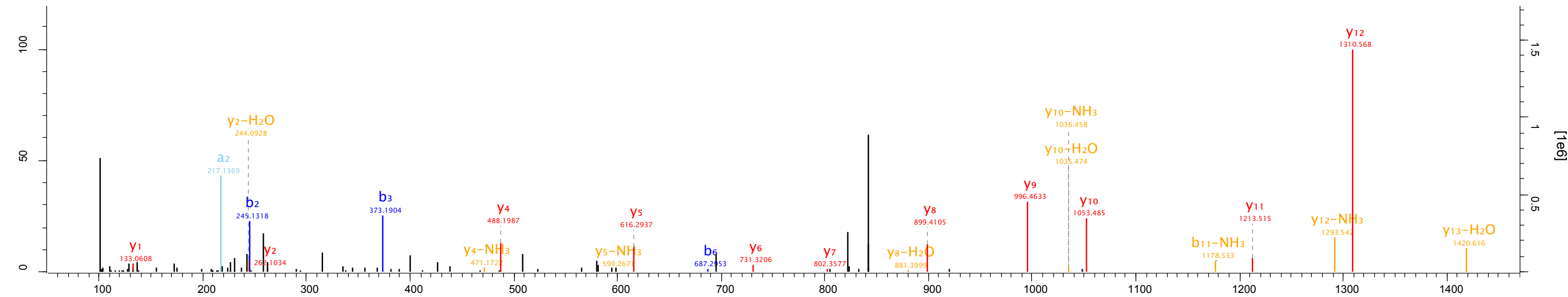
Scan 128967 Method FTMS; HCD Score 64.7 m/z 777.7 Gene names MED20



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 Scan: 141007 Method: FTMS; HCD Score: 56.72 m/z: 1078.52 Gene names: KDELC1



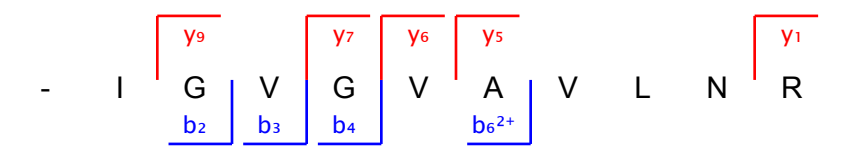
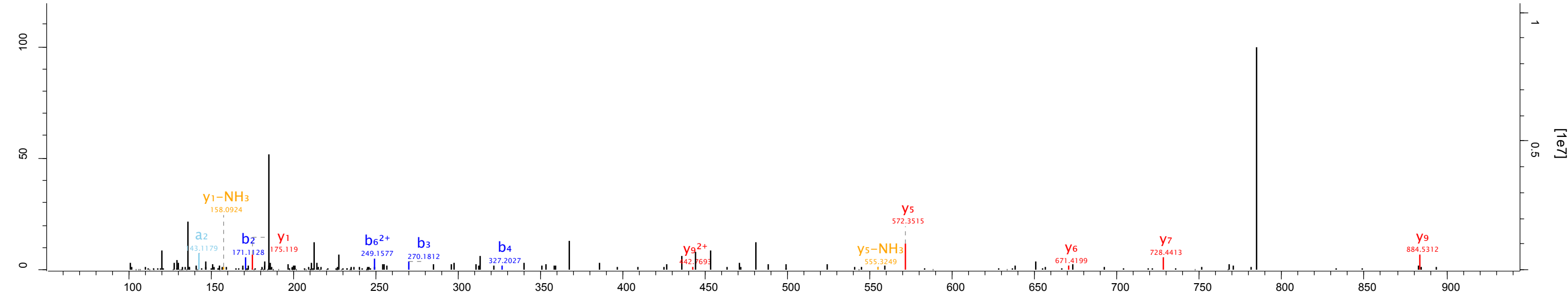
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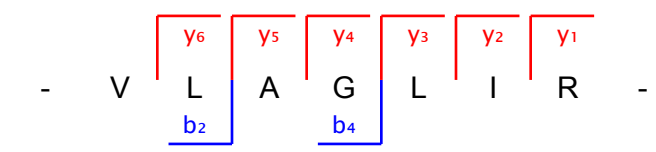
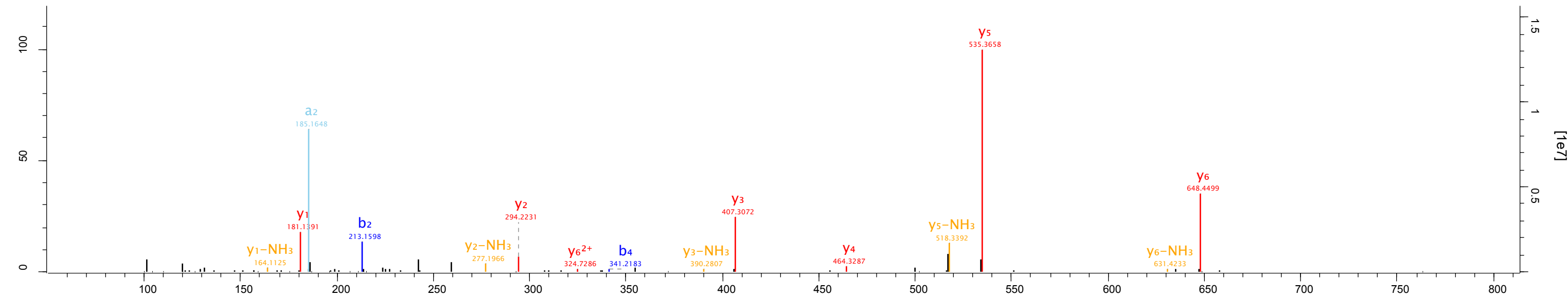
Raw file

20171215_MaS_33SR_LMH_proteome_02

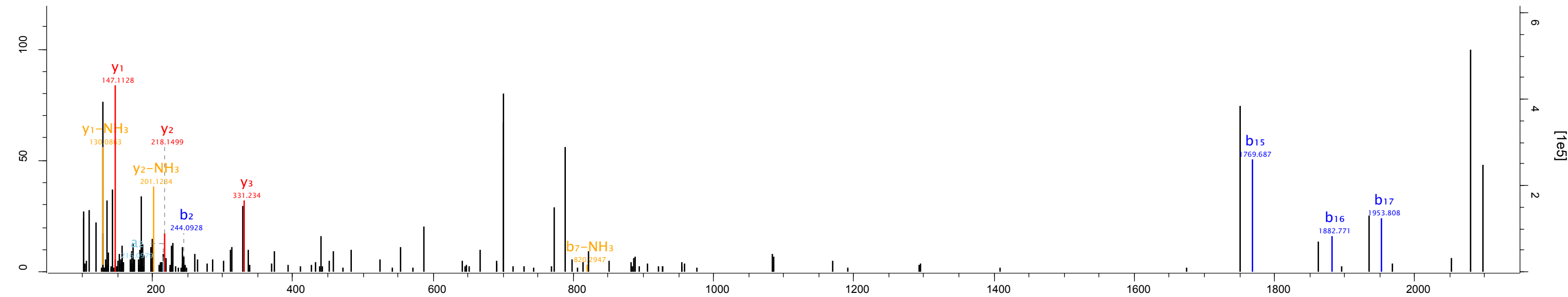
Scan	Method	Score	m/z	Gene names
27647	FTMS; HCD	53.49	499.31	KEAP1



Raw file: 20171215_MaS_33SR_LMH_proteome_02
 Scan: 31257 Method: FTMS; HCD Score: 132.8 m/z: 374.26 Gene names: RTTN



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 Scan: 35747 Method: FTMS; HCD Score: 40.49 m/z: 700.64 Gene names: RALGAPB

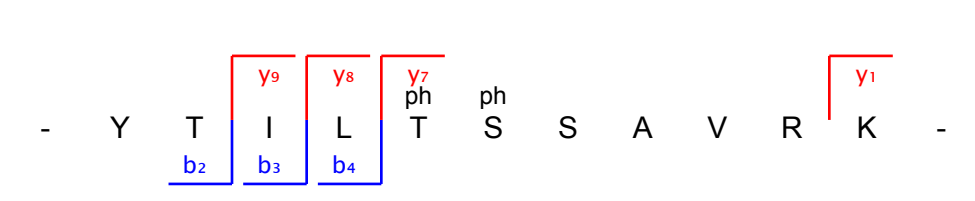
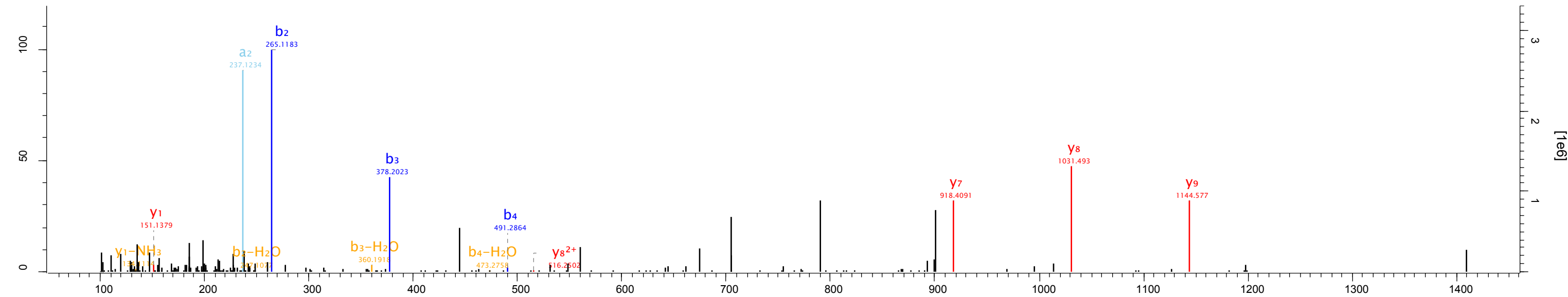


- Q D M ph S I ph S L A A L E L L S G L A K -

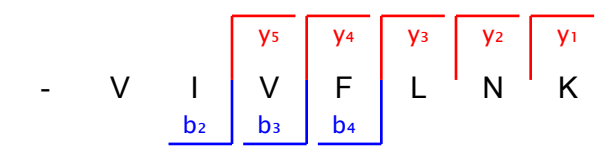
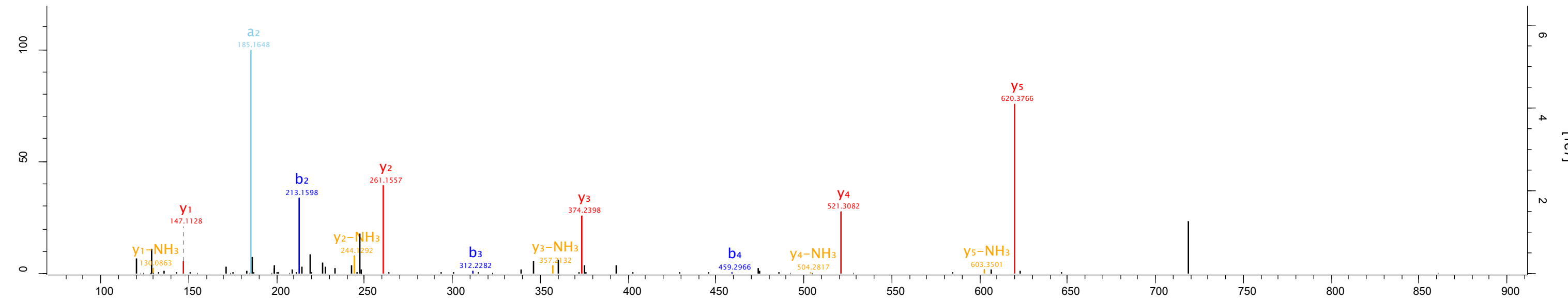
Annotations below the sequence:

- b₂ is underlined under 'D'.
- b₁₅ is underlined under 'G'.
- b₁₆ is underlined under 'L'.
- b₁₇ is underlined under 'A'.
- y₃ is above 'L'.
- y₂ is above 'A'.
- y₁ is above 'K'.

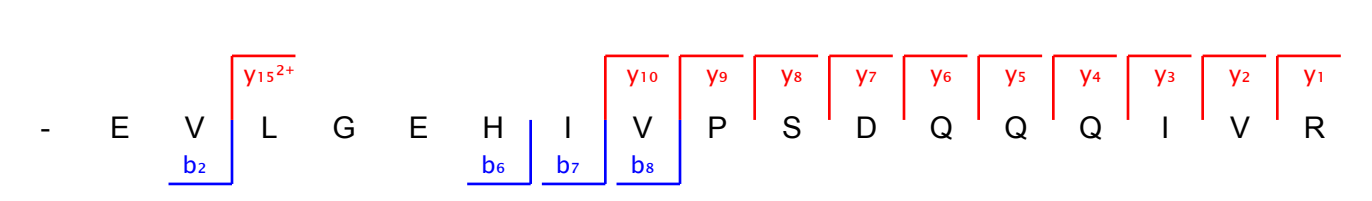
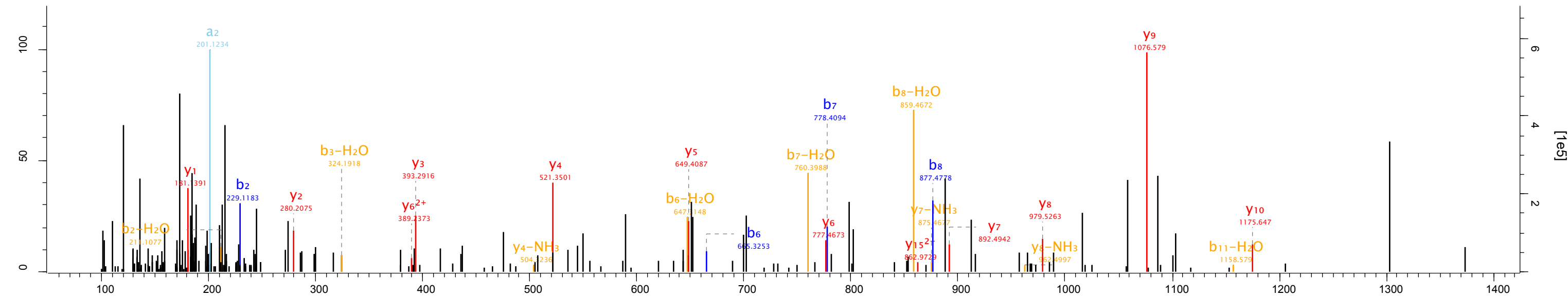
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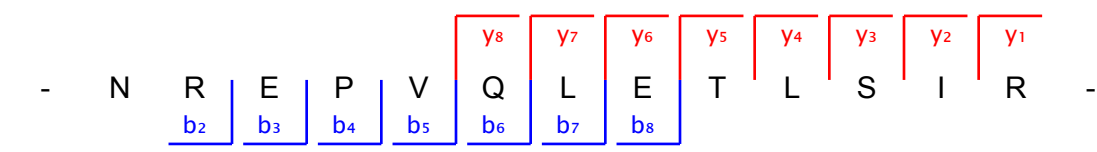
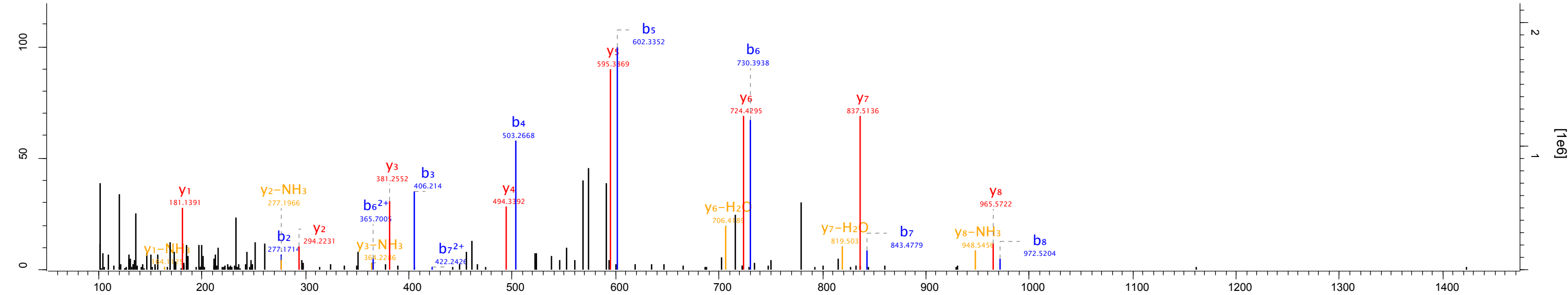
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 Scan: 36777 Method: FTMS; HCD Score: 93.59 m/z: 416.77 Gene names: VN1R5



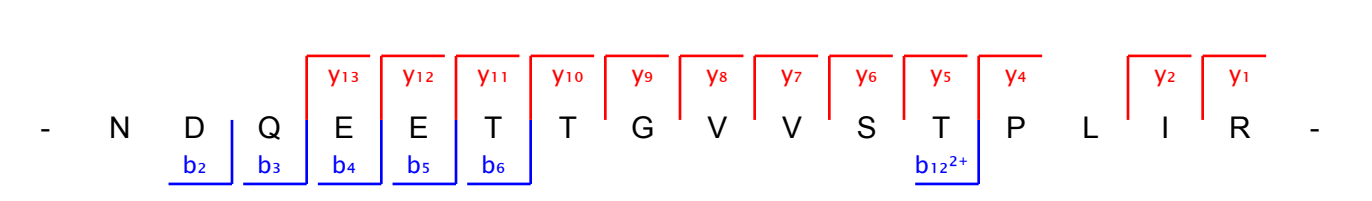
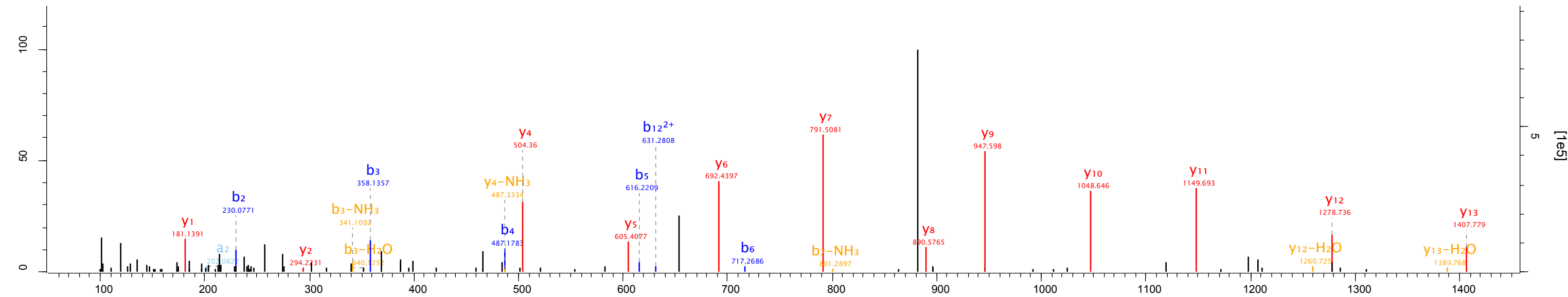
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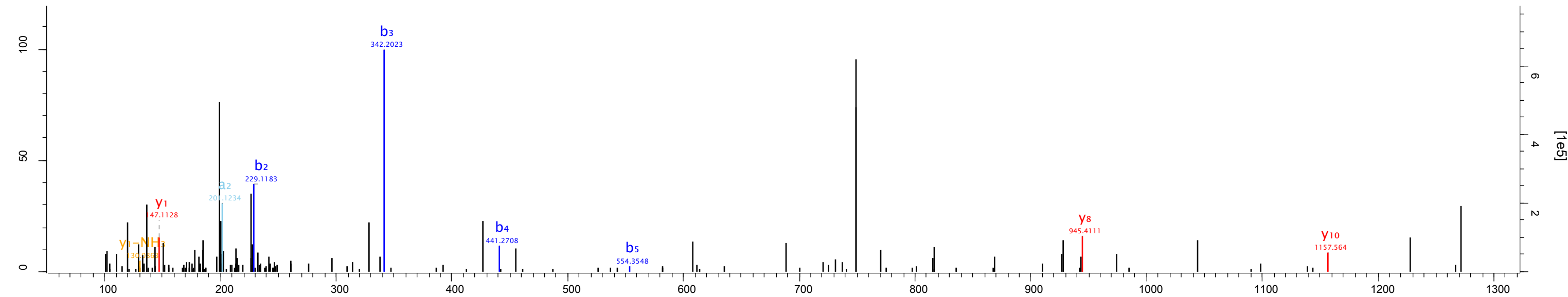
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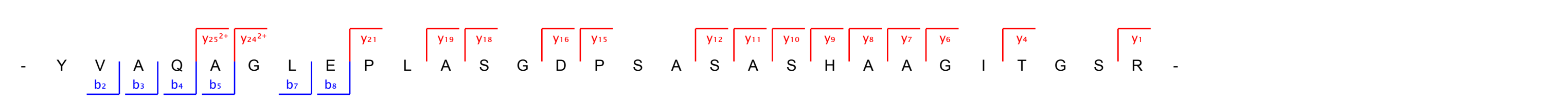
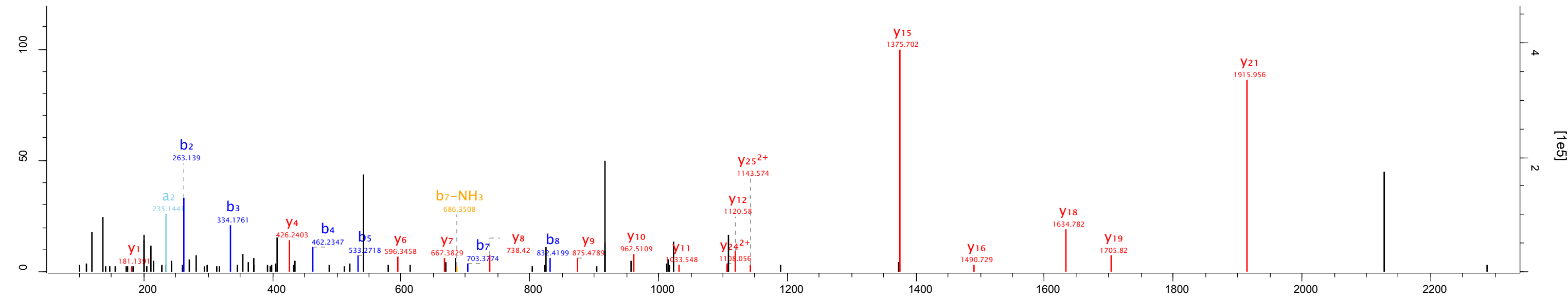
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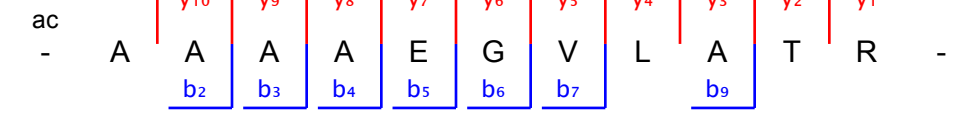
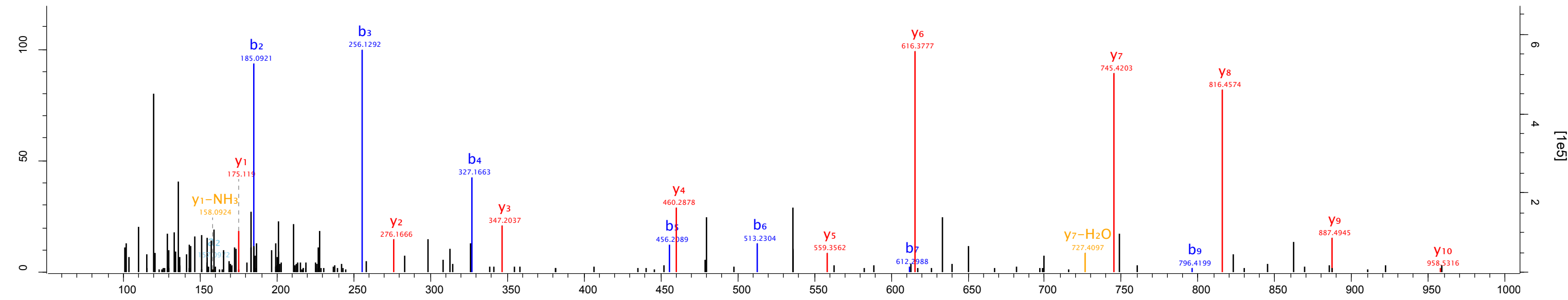
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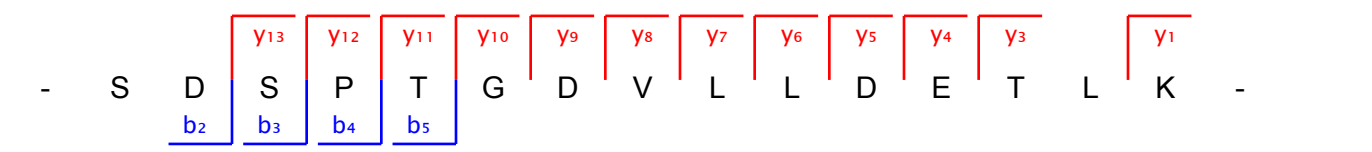
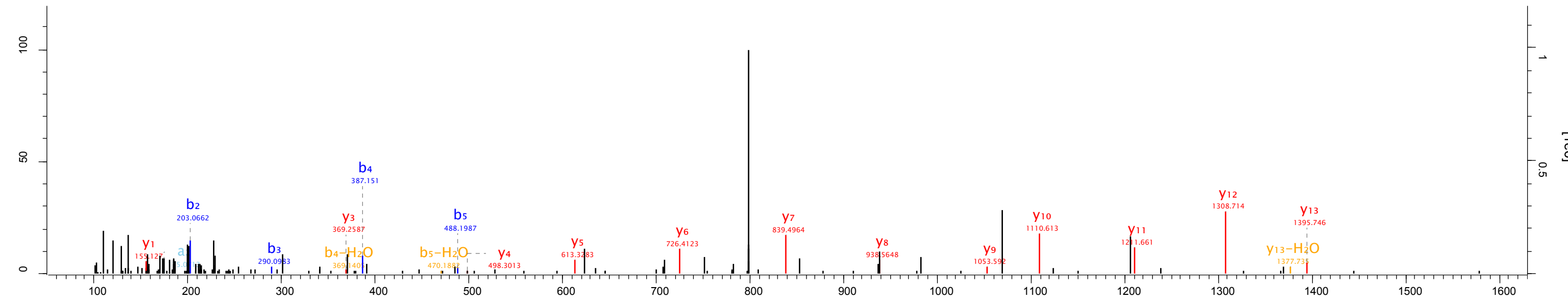
Raw file

20171215_MaS_33SR_LMH_proteome_02

Scan 56707 Method FTMS; HCD Score 71.27 m/z 536.29 Gene names BLOC1S2

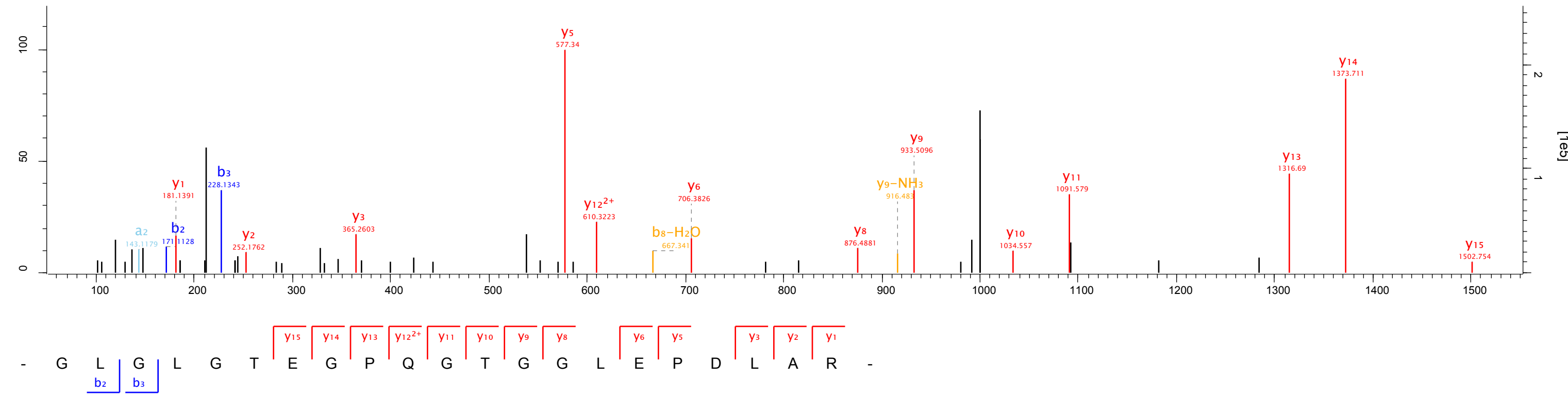


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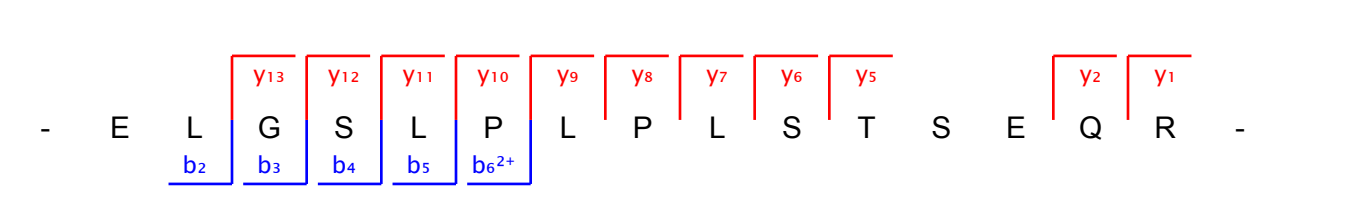
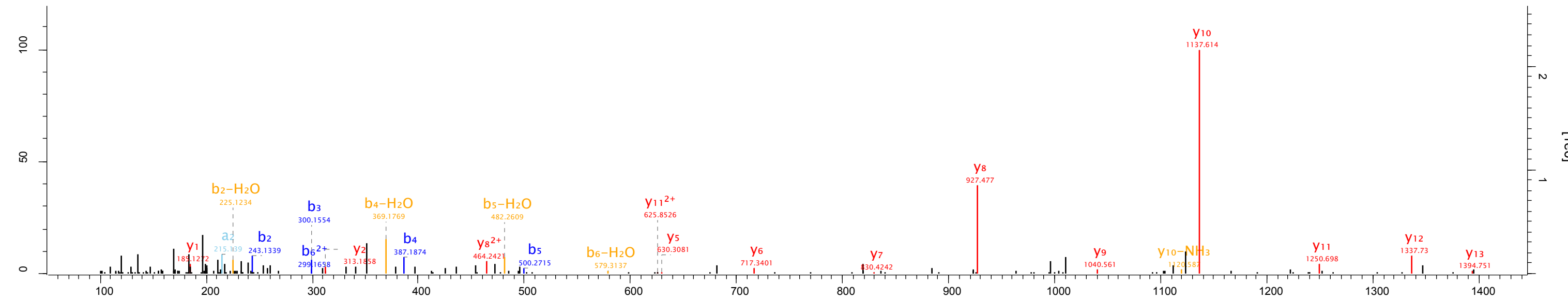


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20171215_MaS_33SR_LMH_proteome_02

Scan 70267 Method FTMS; HCD Score 54.83 m/z 1001.02 Gene names RNF31



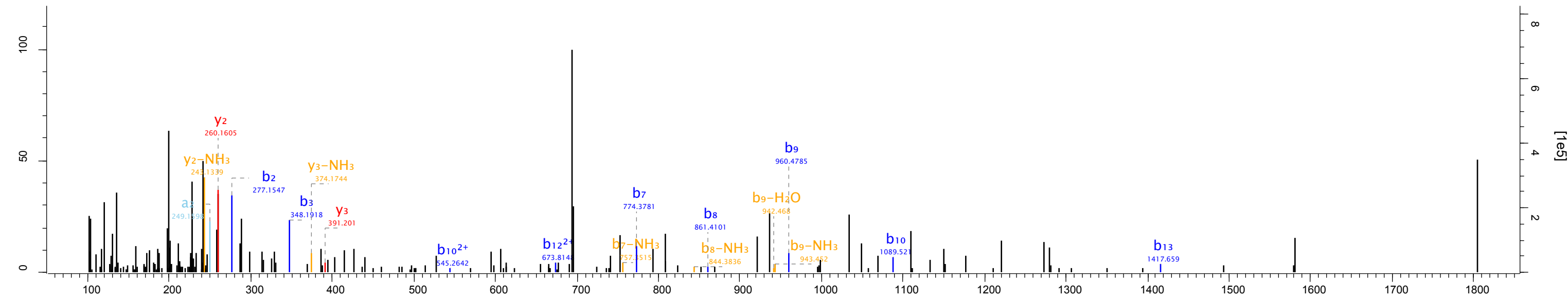
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Raw file

20171215_MaS_33SR_LMH_proteome_02

Scan	Method	Score	m/z	Gene names
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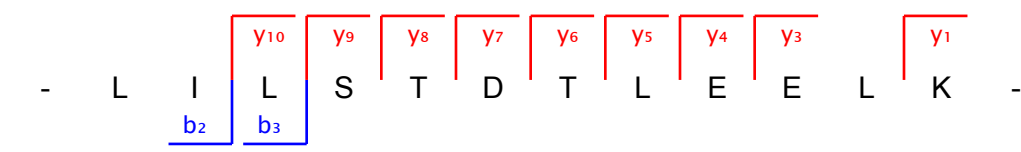
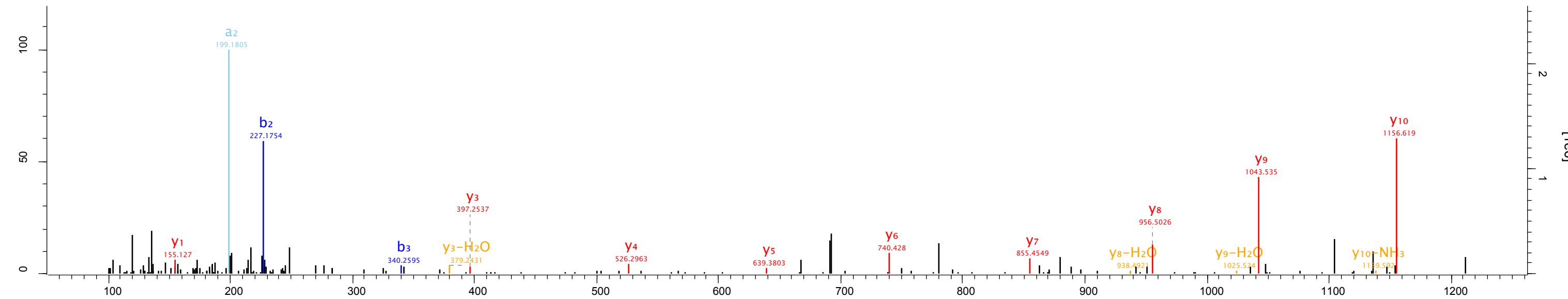


- Y L A P S N Q S V E Q E A M Q L -

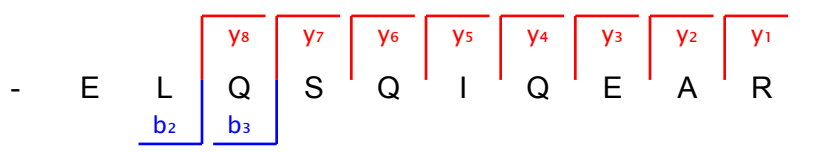
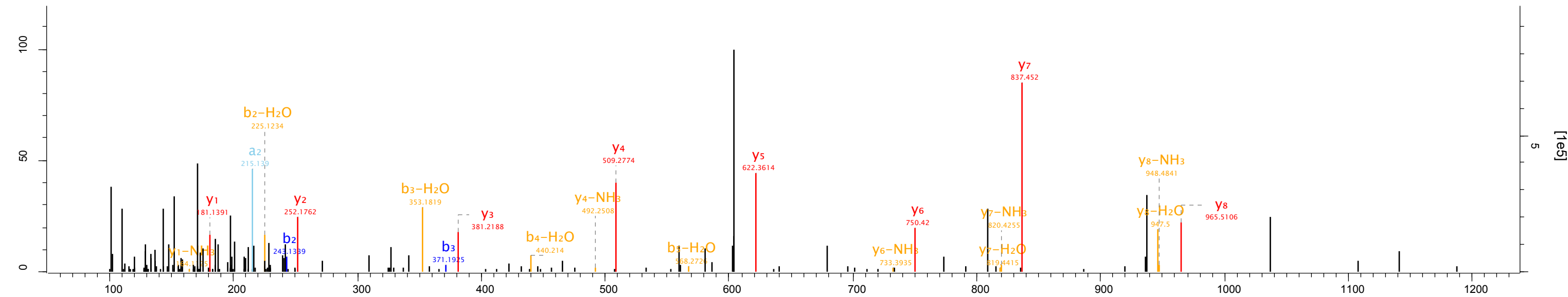
Fragmentation sites are indicated by brackets below the sequence:

- b₂ (L, A)
- b₃ (A)
- b₇ (Q, S)
- b₈ (S, V)
- b₉ (V, E)
- b₁₀ (E, Q)
- b₁₂²⁺ (E, A)
- b₁₃ (A, M)
- y₃ (M)
- y₂ (Q)

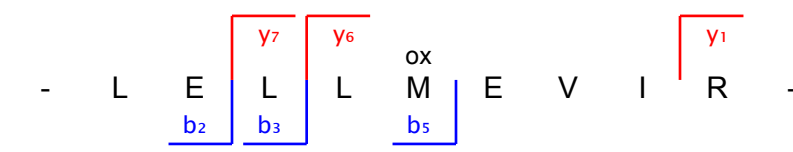
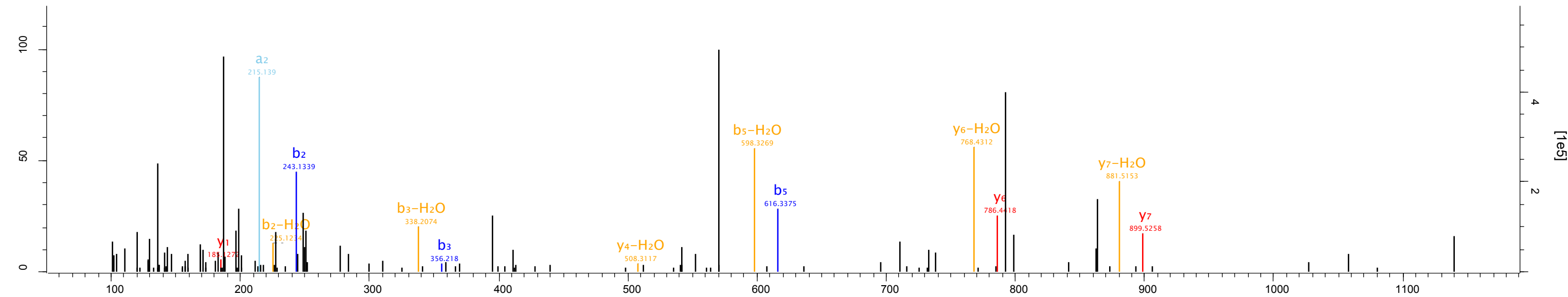
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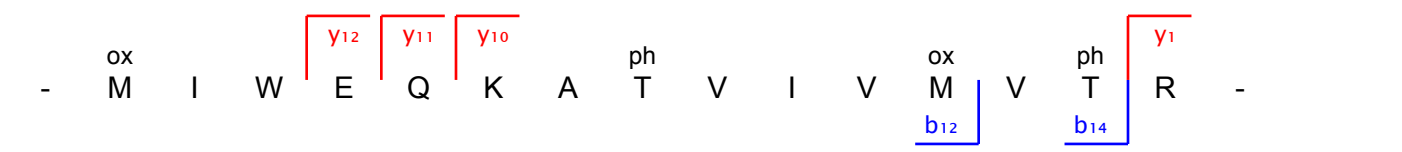
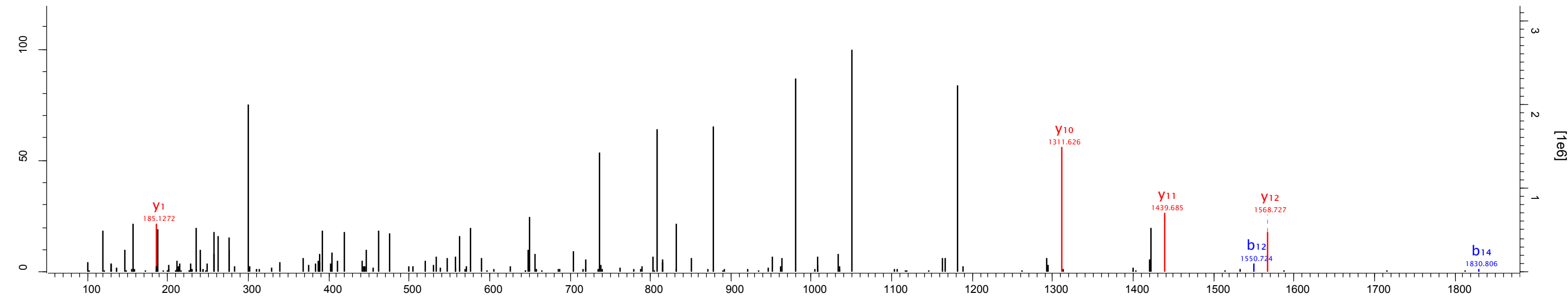
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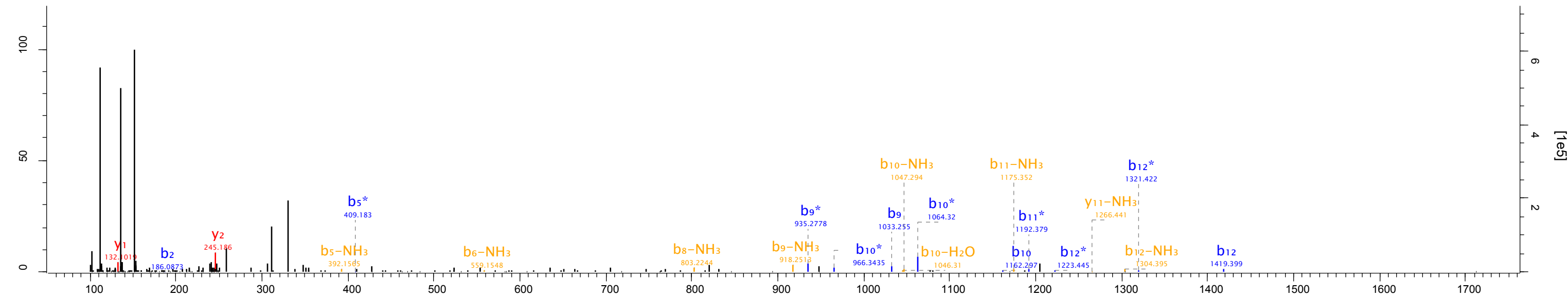
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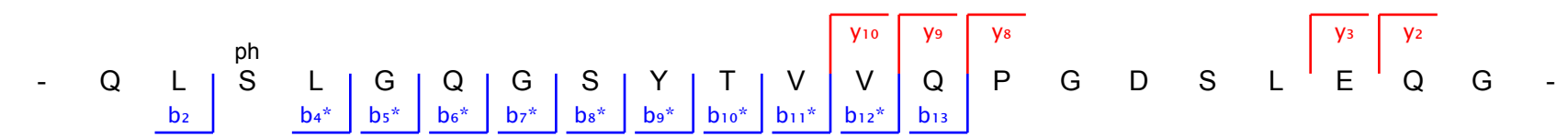
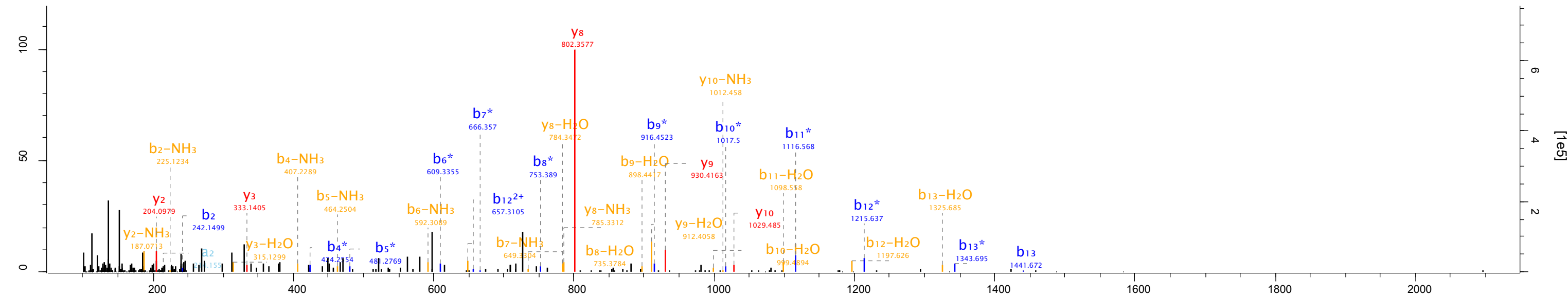
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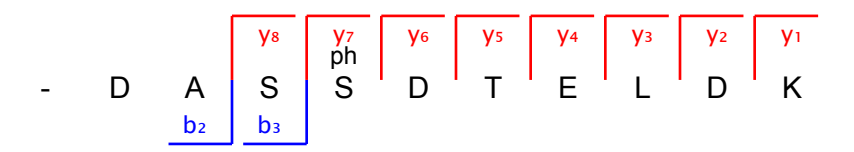
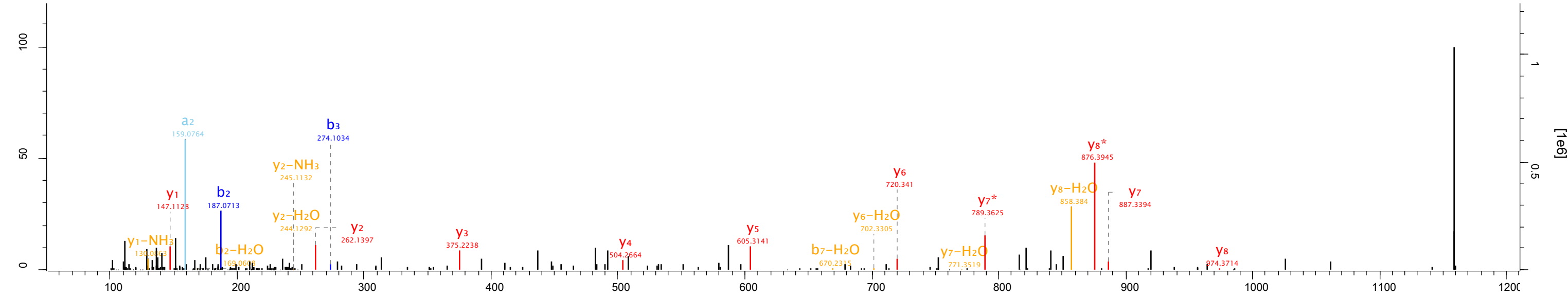


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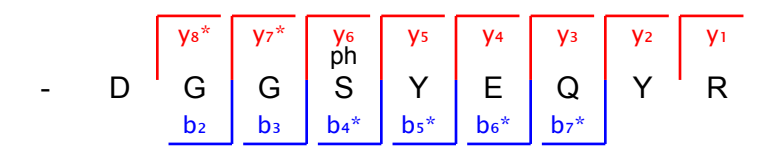
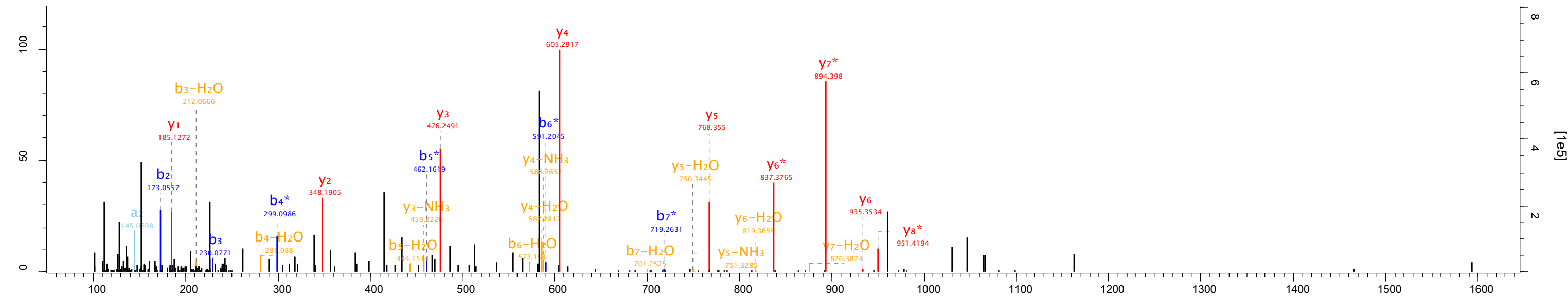


20171215_MaS_33SR_LMH_phospho_02

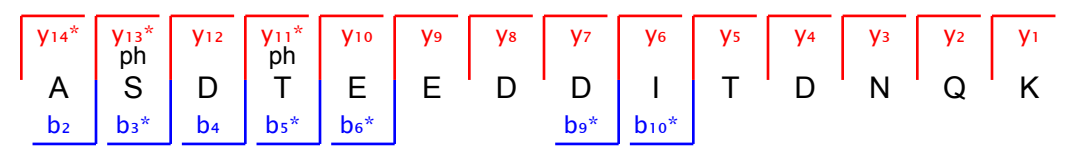
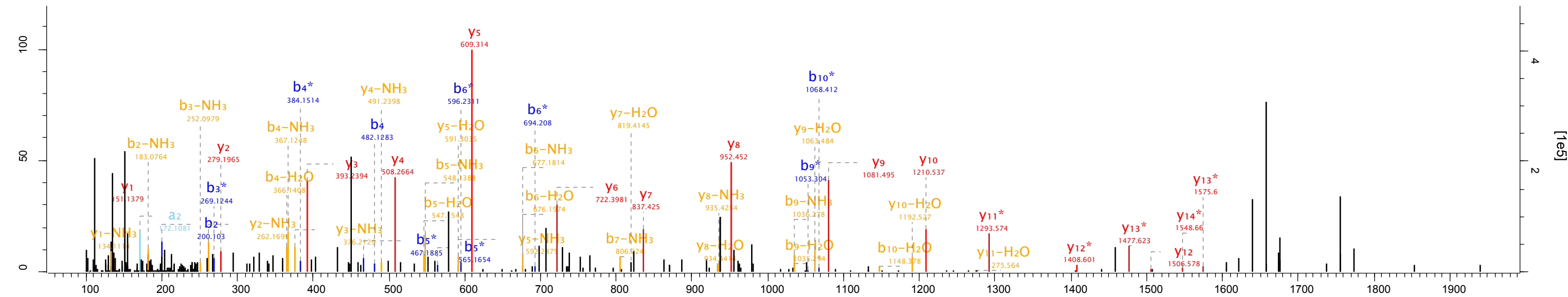
3638 FTMS; HCD 47.62 580.72 ZFPM2

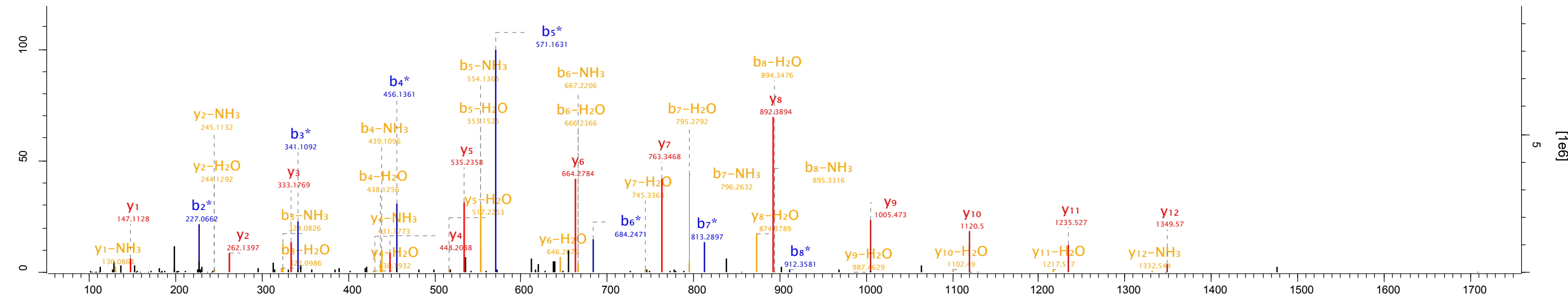


Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 4958 Method FTMS; HCD Score 144.27 m/z 582.71 Gene names SULF2



Raw file 20171215_MaS_33SR_LMH_phospho_02 Scan 5158 Method FTMS; HCD Score 155.7 m/z 937.34 Gene names UBN2



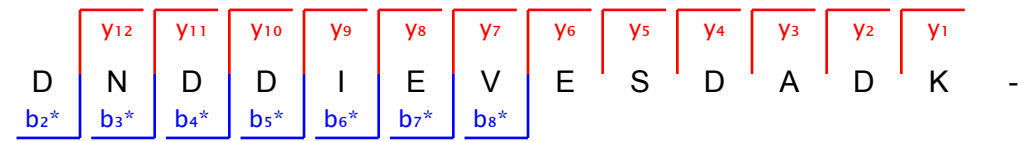


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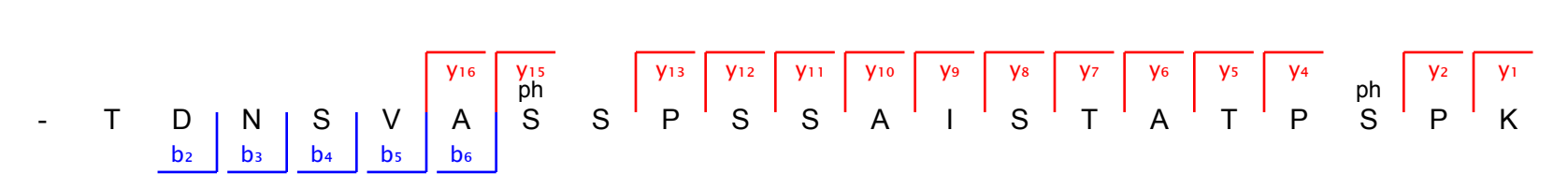
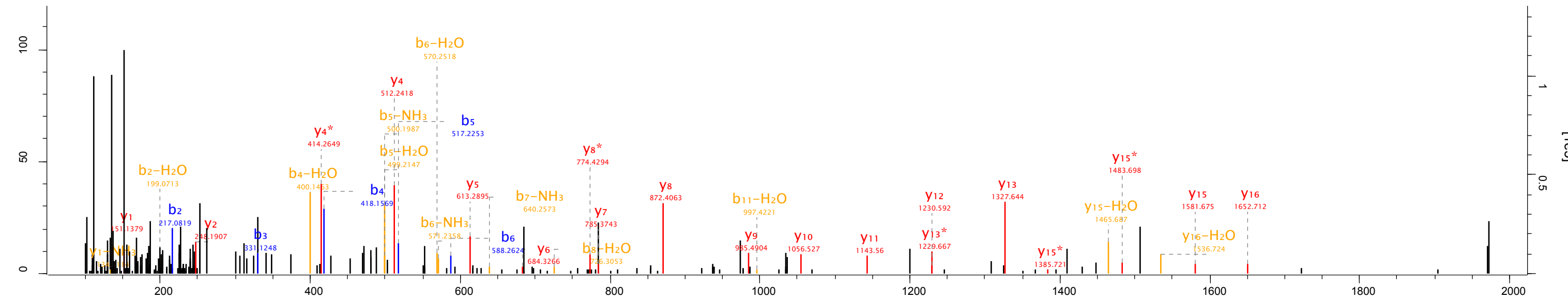
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ph

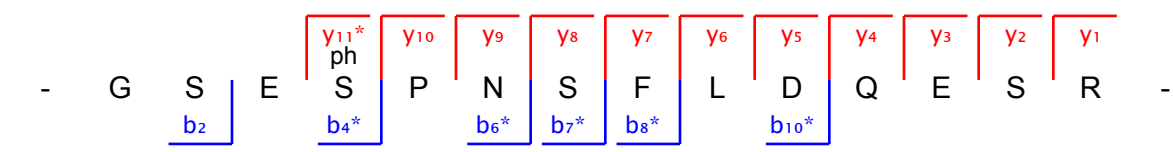
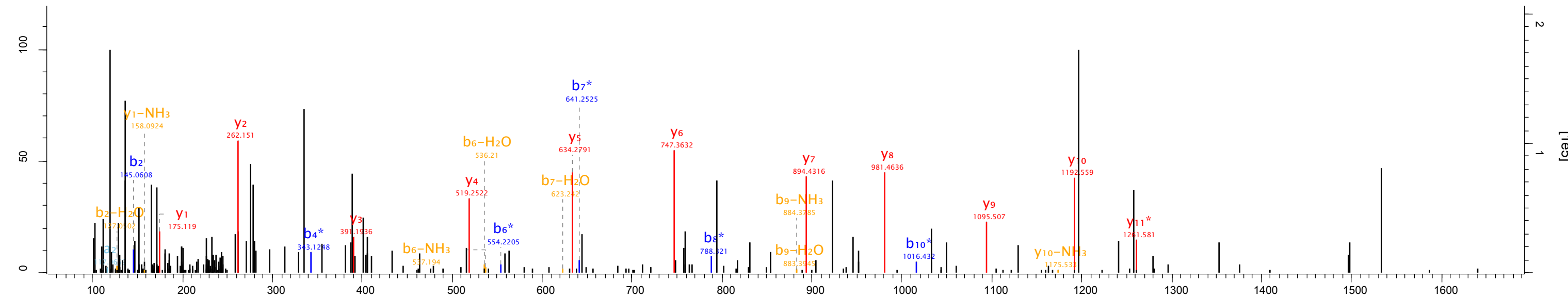
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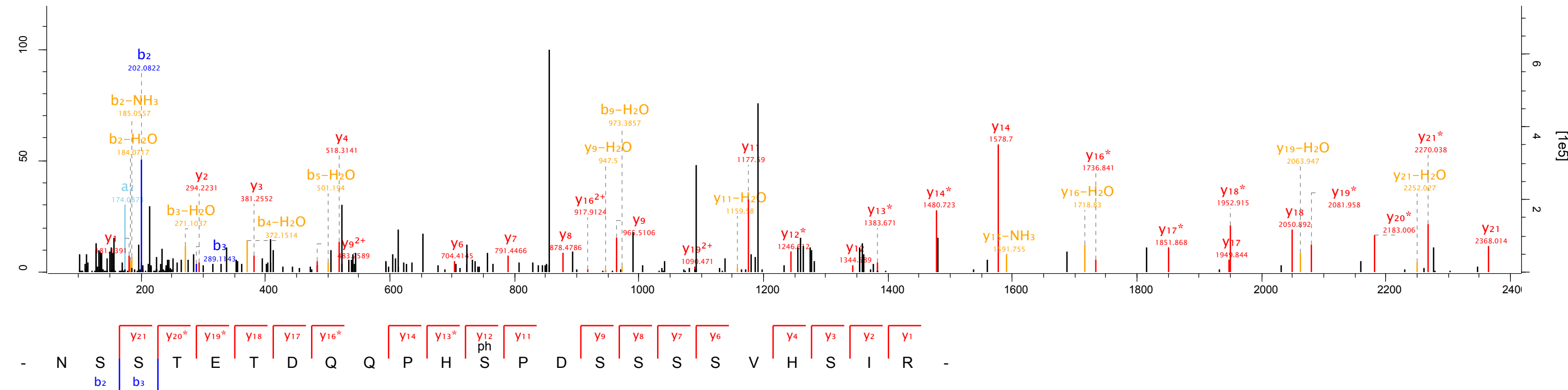
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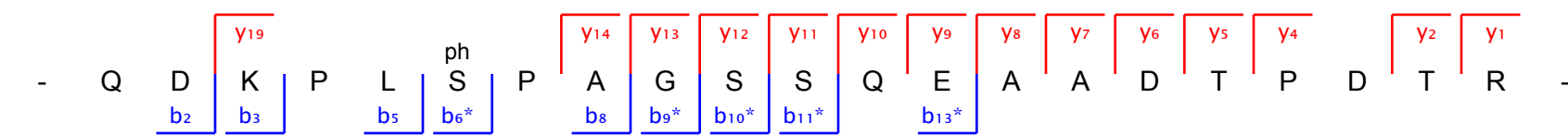
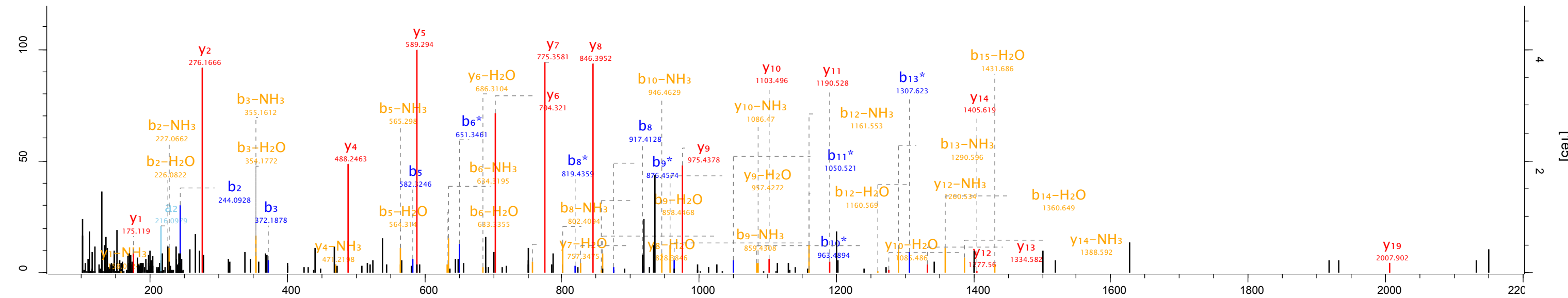


Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 11458 Method FTMS; HCD Score 40.38 m/z 816.83 Gene names CNKSR3

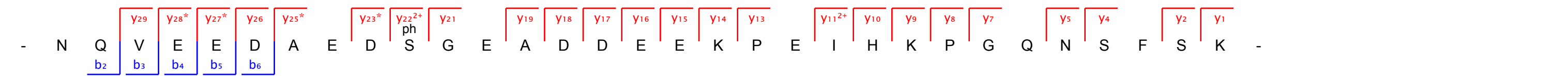
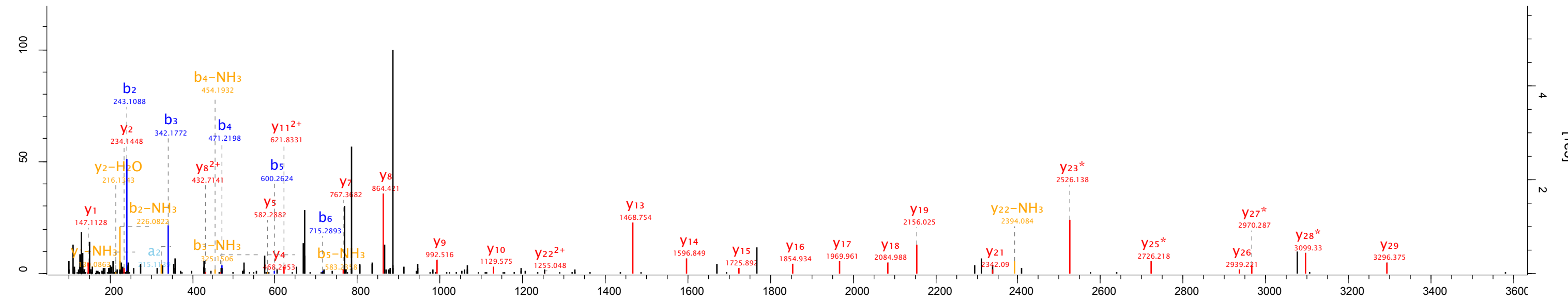


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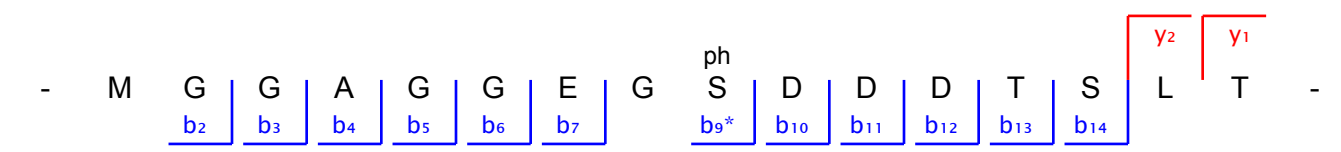
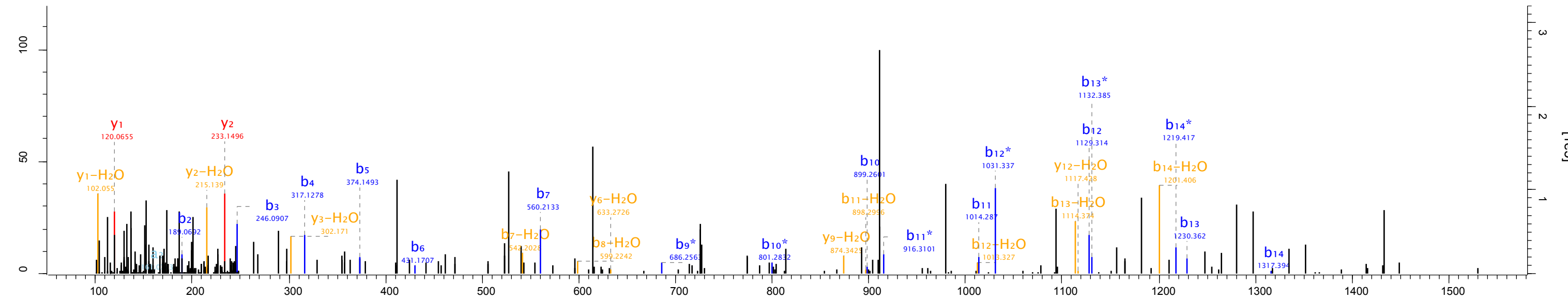




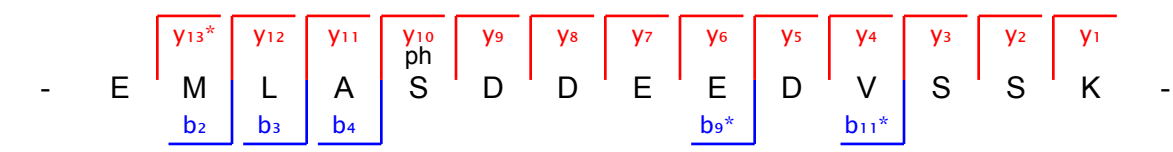
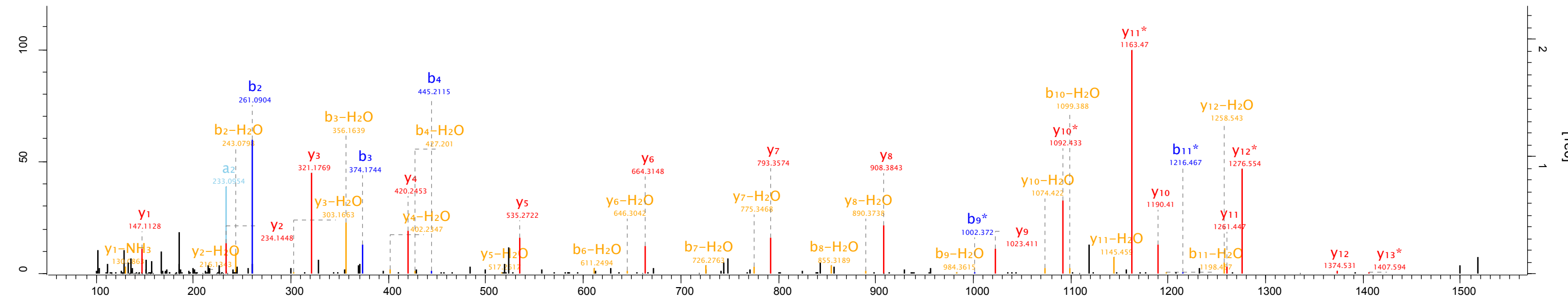
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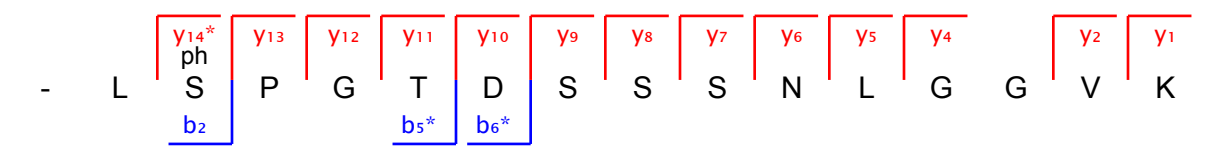
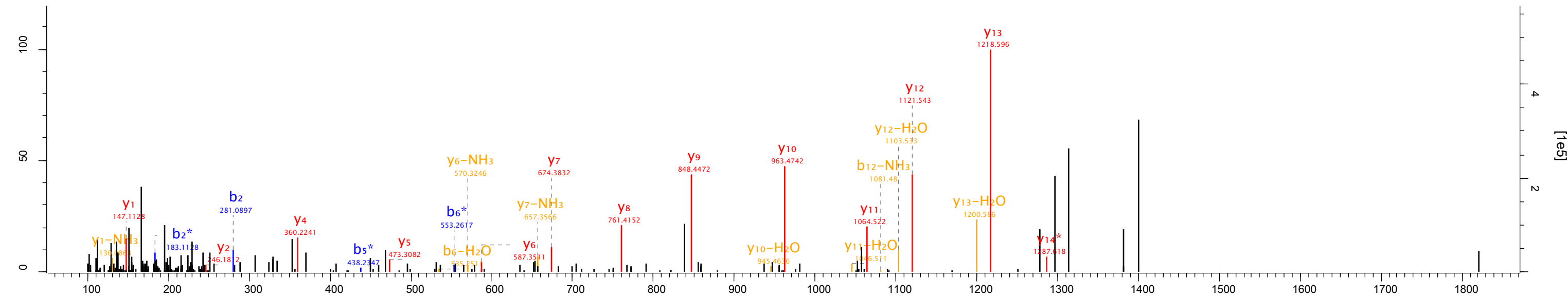
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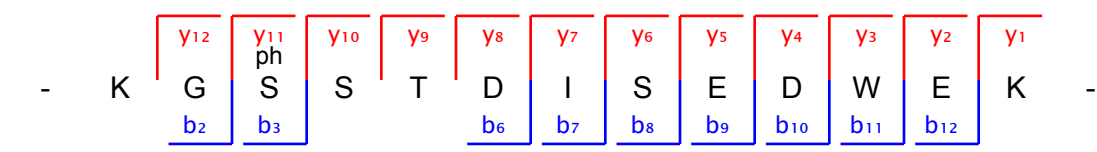
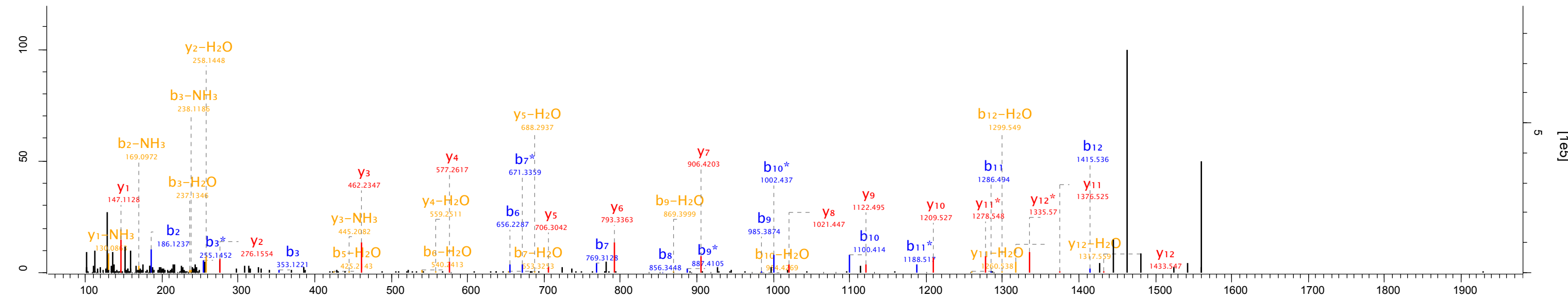
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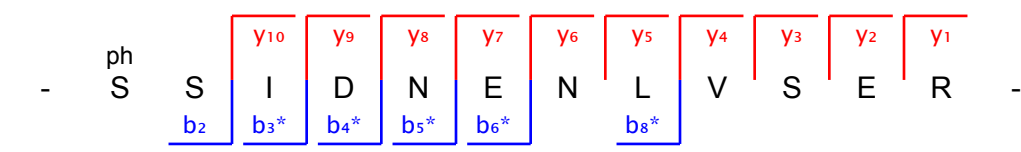
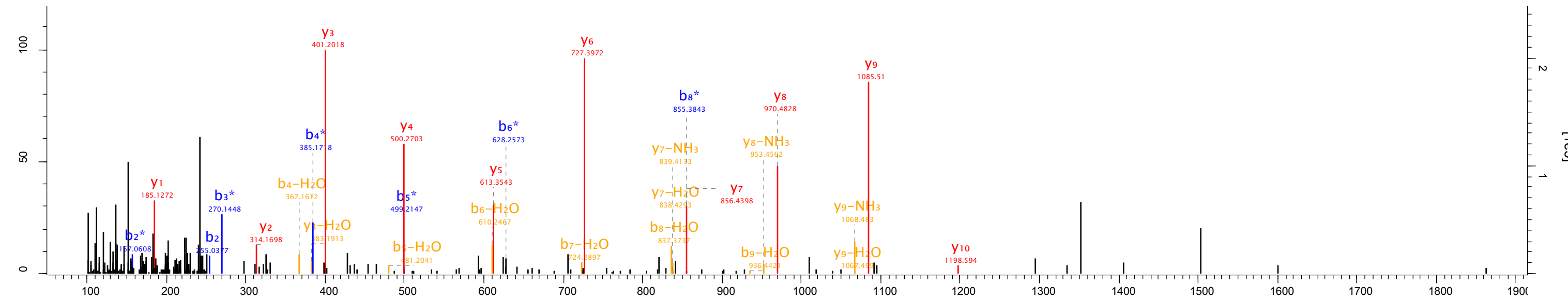
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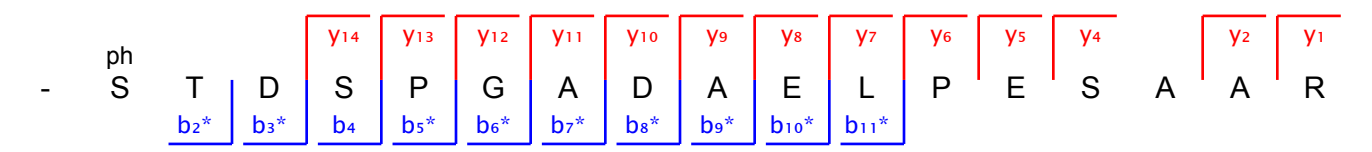
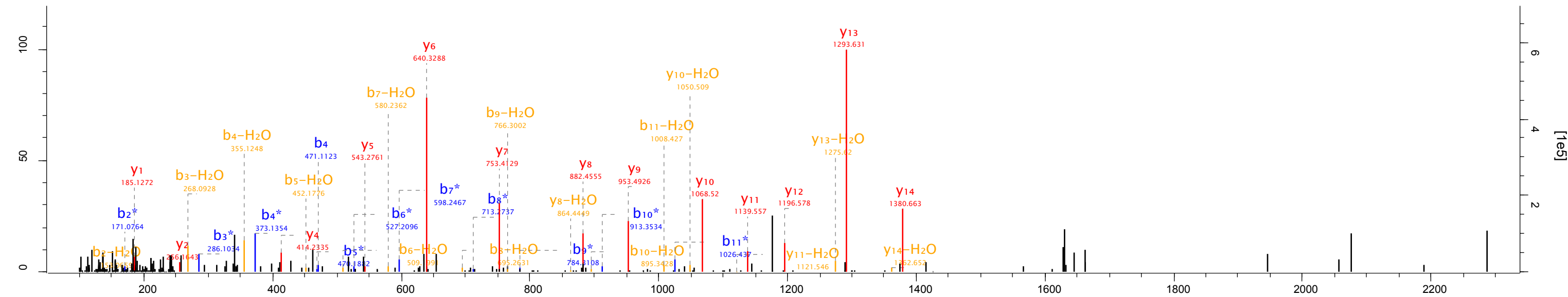
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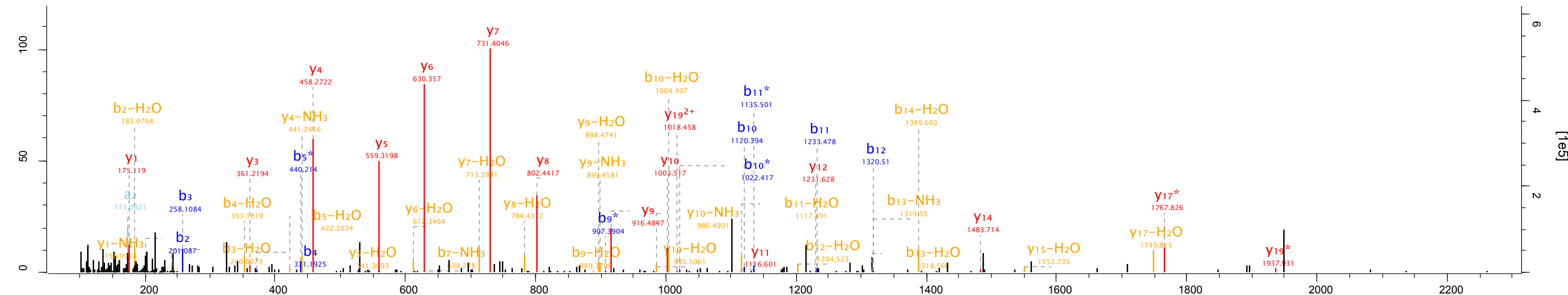


Raw file 20171215_MaS_33SR_LMH_phospho_03 Scan 8538 Method FTMS; HCD Score 84.05 m/z 726.82 Gene names AKAP9



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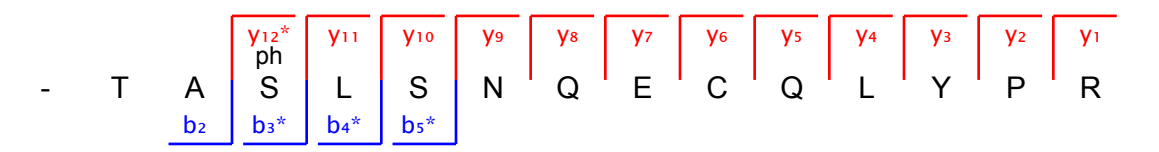
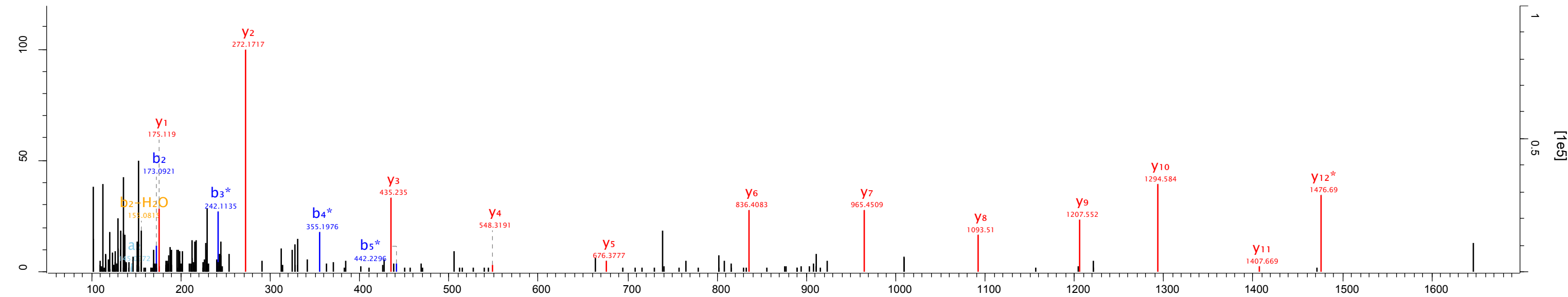




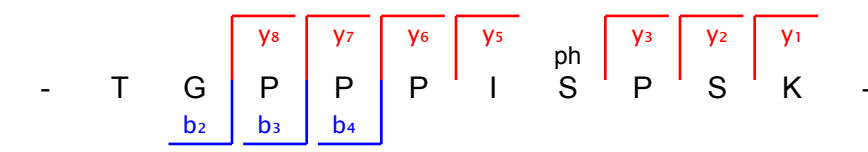
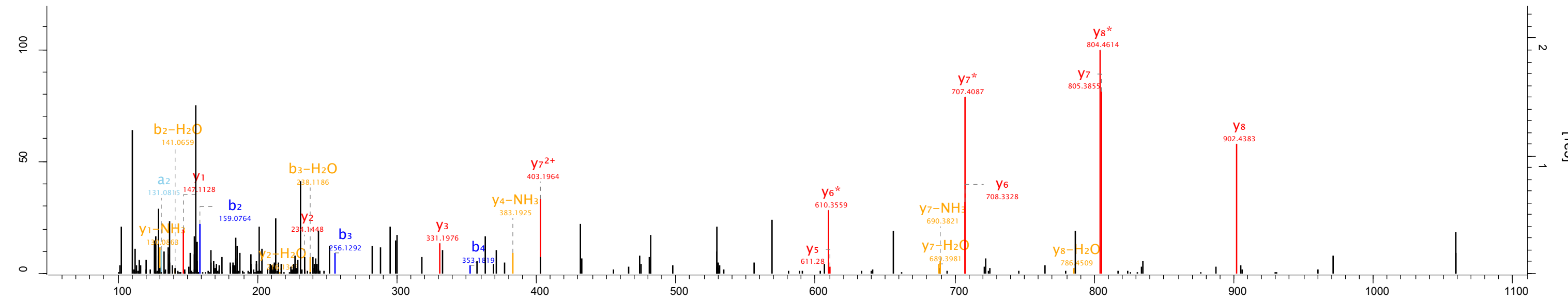
- E A G L S Q S H D D L S N A T A T P S V R -

b₂ b₃ b₄ b₅^{*}
y₁₉^{*} y₁₇^{ph}
y₁₄ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁

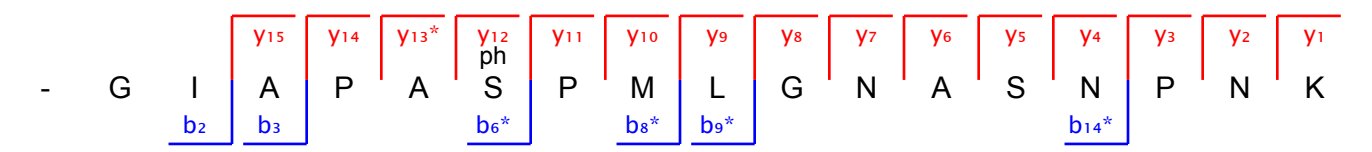
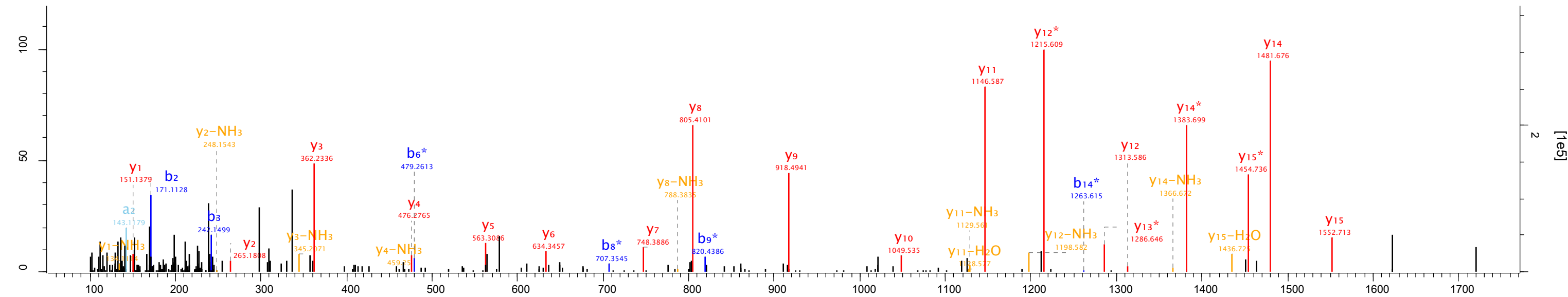
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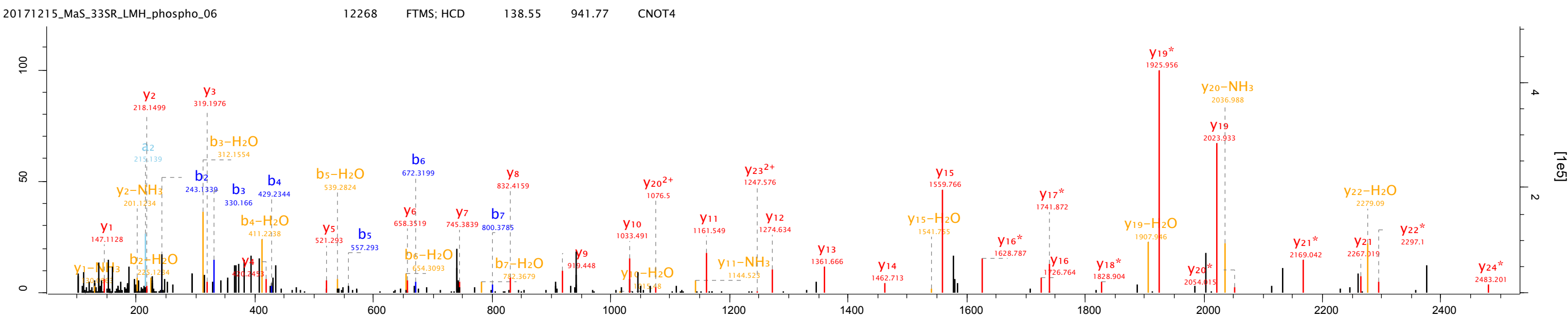
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Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 11318 Method FTMS; HCD Score 121.21 m/z 861.91 Gene names MARK3



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12268 Method FTMS; HCD Score 138.55 m/z 941.77 Gene names CNOT4

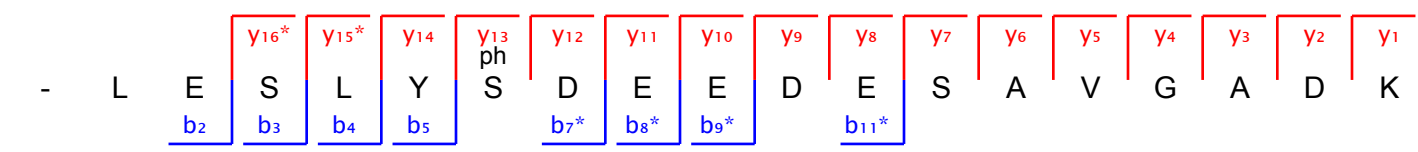
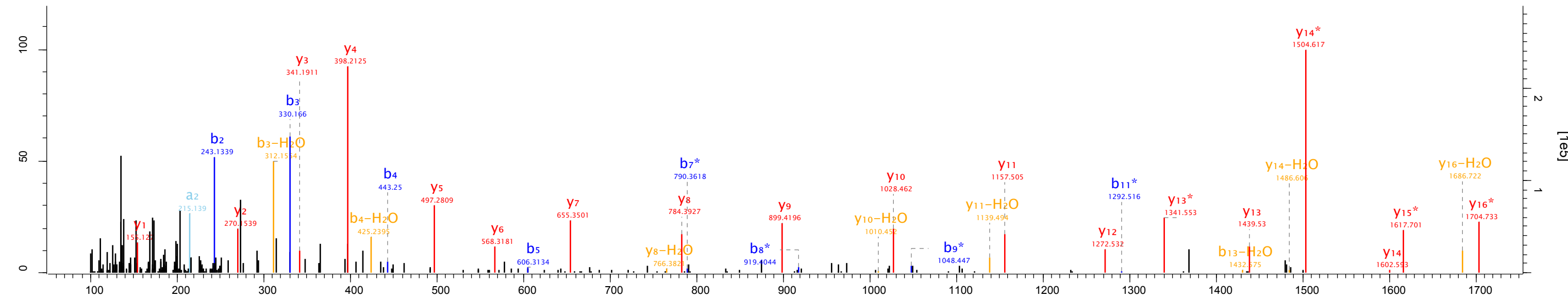


- E L S V Q D Q P S L S P T S L Q N S S S H T T T A K -

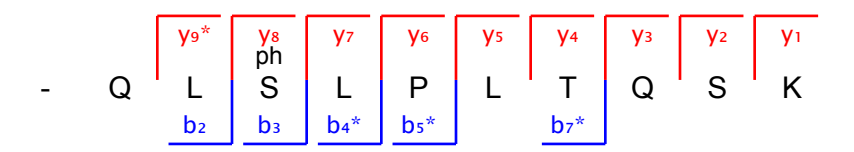
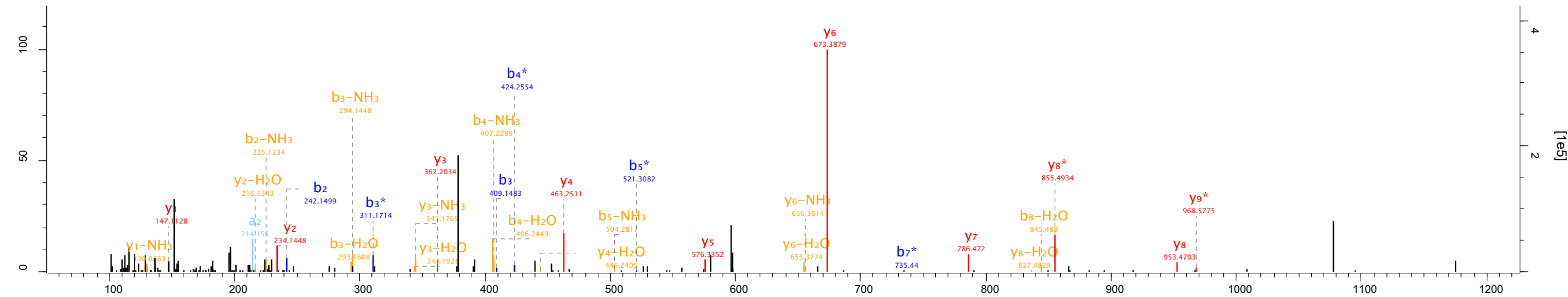
Fragmentation sites are indicated by boxes below the sequence:

- Red boxes: y24*, y23²⁺, y22*, y21, y20*, y19, y18*, y17*, y16, y15, y14, y13, y12, y11, y10, y9, y8, y7, y6, y5, y4, y3, y2, y1
- Blue boxes: b2, b3, b4, b5, b6, b7

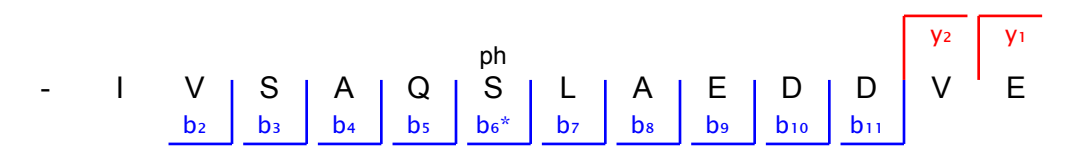
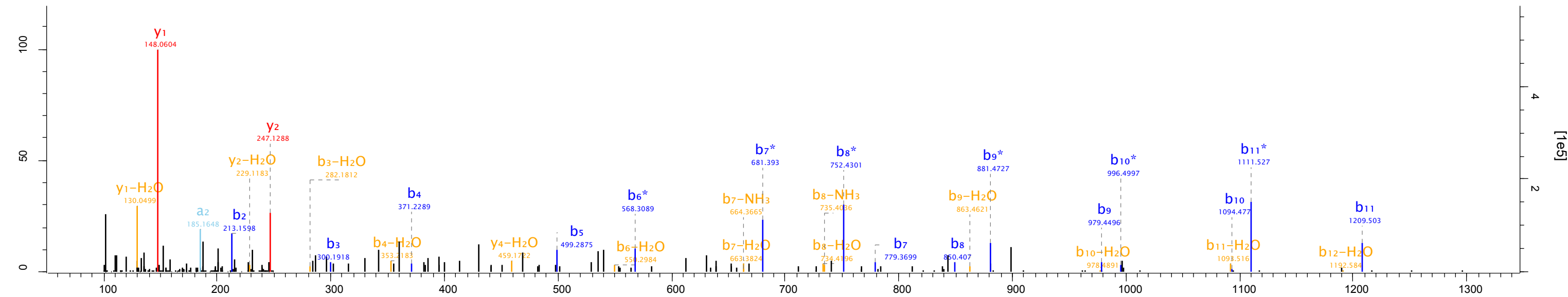
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 12308 Method FTMS; HCD Score 113.42 m/z 1022.93 Gene names SLC12A4



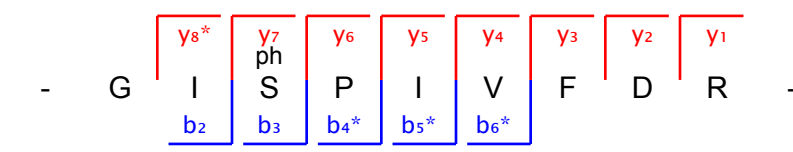
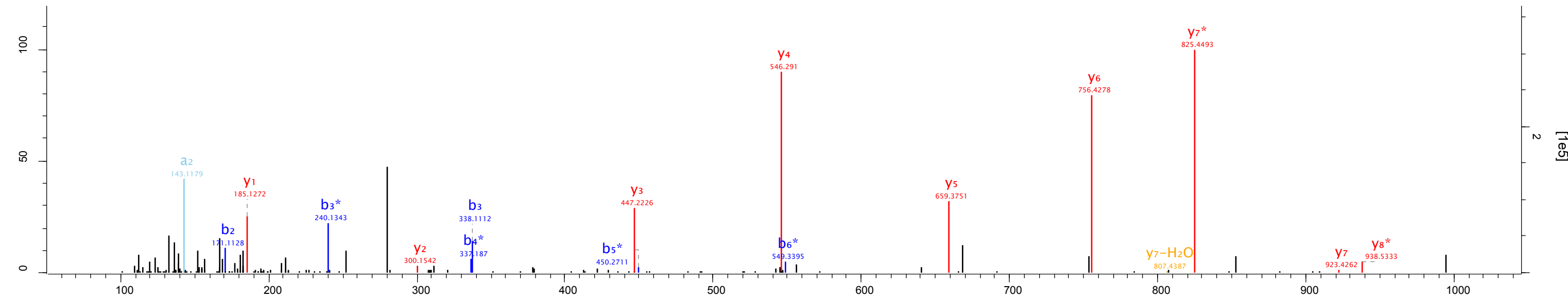
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 Scan: 14008 Method: FTMS; HCD Score: 115.69 m/z: 597.81 Gene names: MTMR12



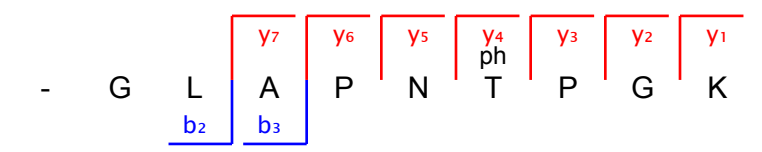
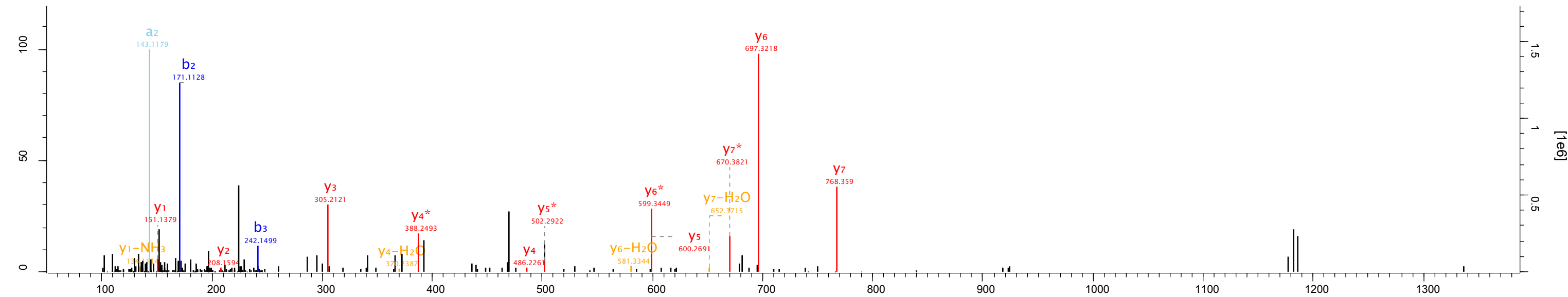
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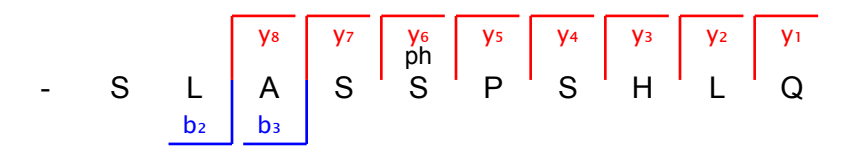
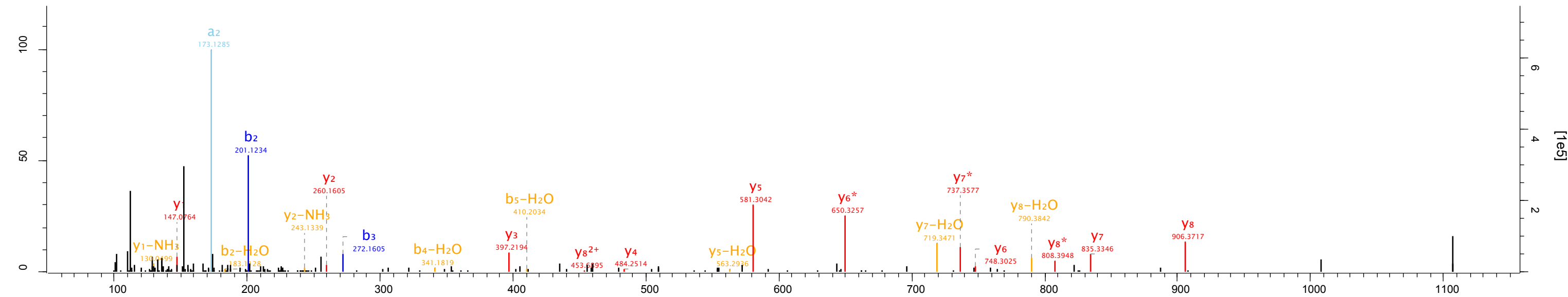
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 15658 Method FTMS; HCD Score 92.25 m/z 547.27 Gene names YTHDC1



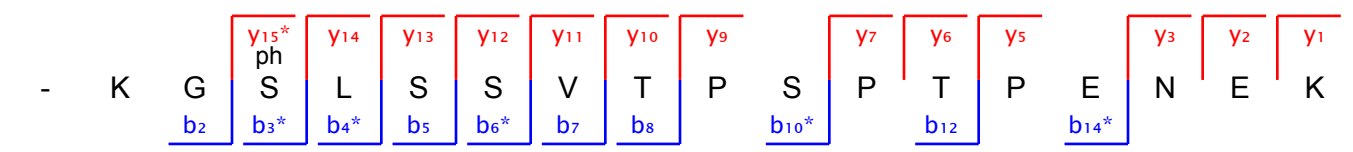
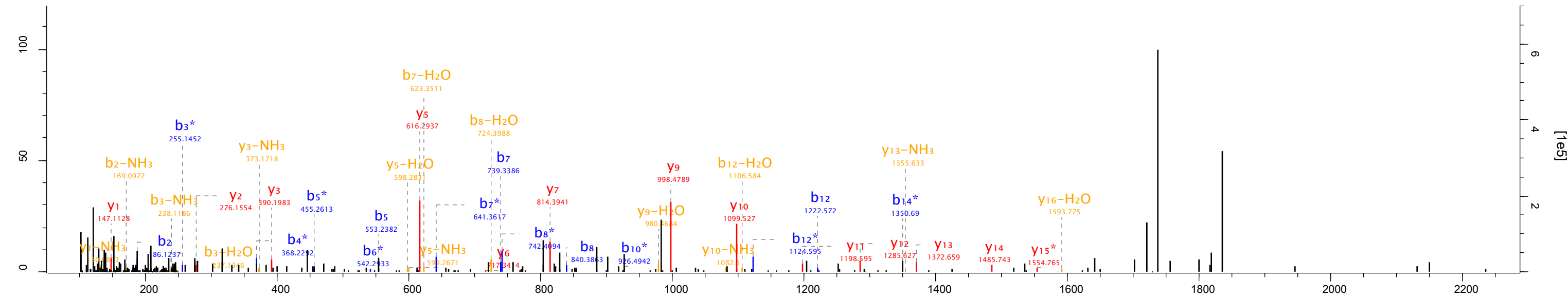
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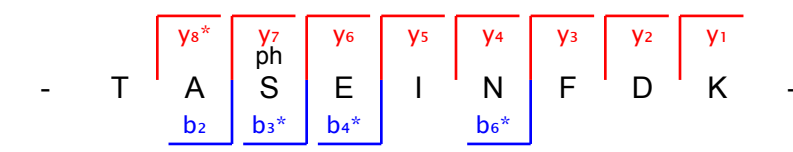
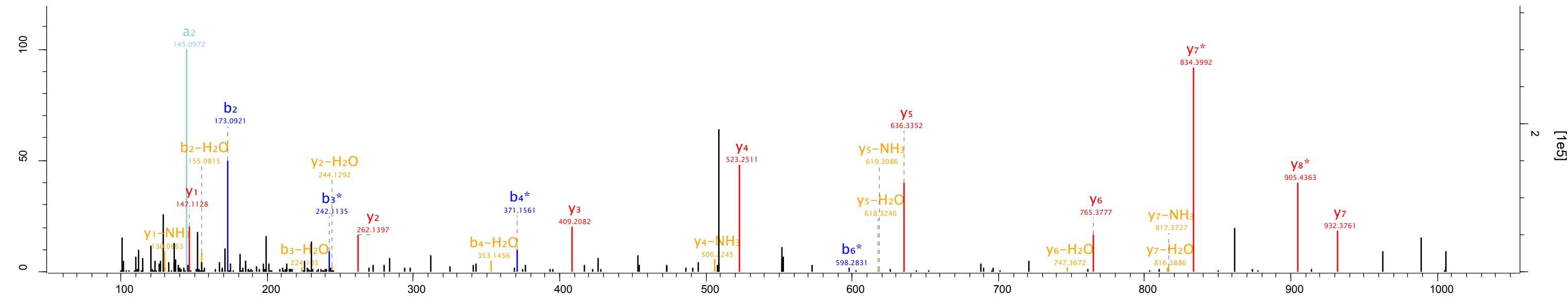
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 Scan: 6228 Method: FTMS; HCD Score: 67.95 m/z: 554.25 Gene names: BNC1



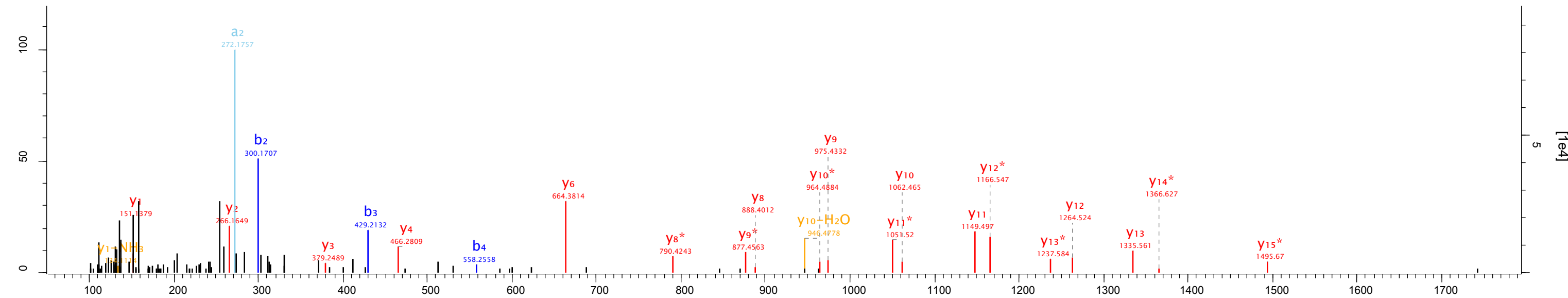
Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 6698 Method FTMS; HCD Score 107.88 m/z 919.93 Gene names APBB2



Raw file 20171215_MaS_33SR_LMH_phospho_06 Scan 9018 Method FTMS; HCD Score 111.52 m/z 552.73 Gene names MAP4K5



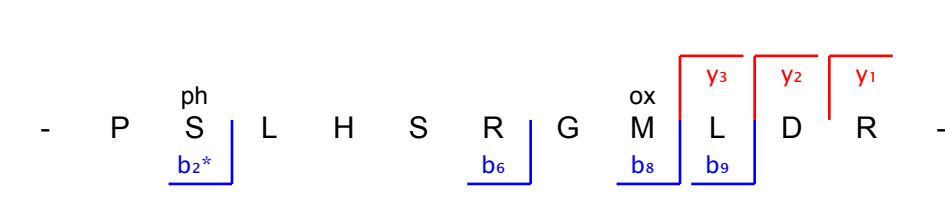
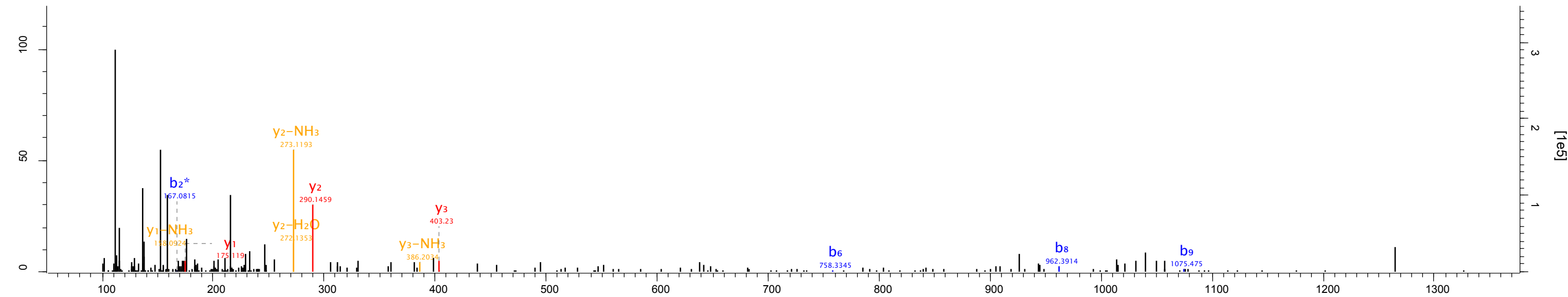
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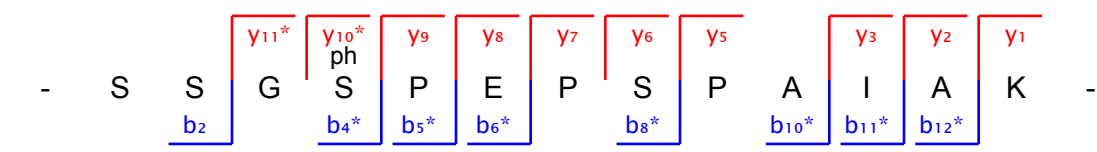
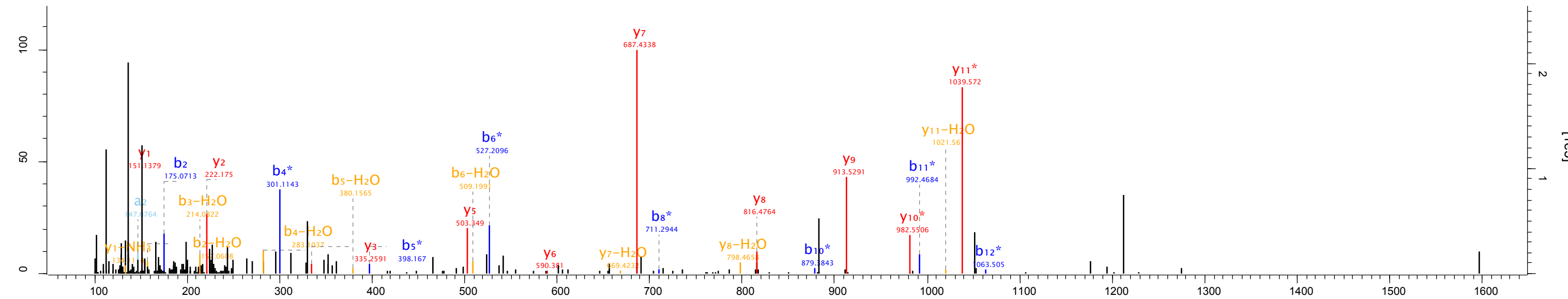
- W L E E A D S S S G S P T S I D K -

Fragmentation mapping: b2 (L), b3 (E), b4 (E), y15* (E), y14* (E), y13 (A), y12 (D), y11 (S), y10 (S), y9 (S), y8 (G), y6 (P), y4 (S), y3 (I), y2 (D), y1 (K).

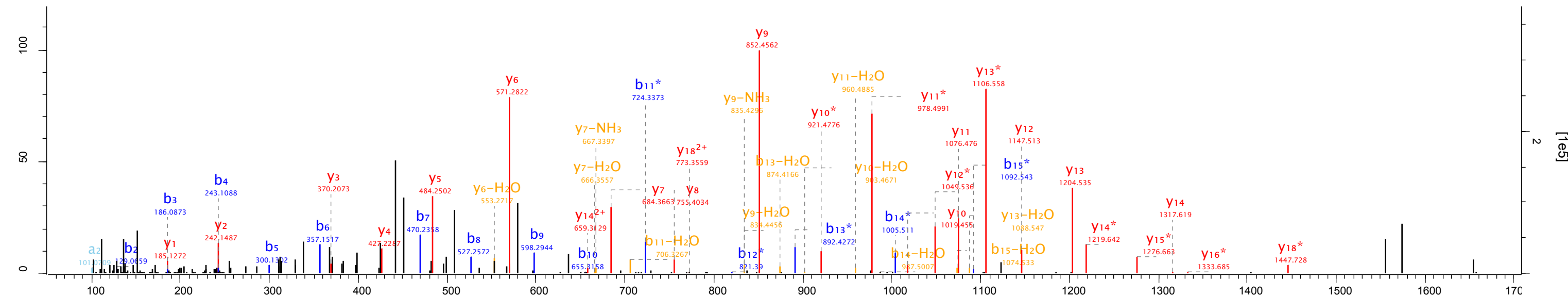
Raw file 20171215_MaS_33SR_LMH_phospho_08 Scan 2628 Method FTMS; HCD Score 45.43 m/z 682.81 Gene names SREBF1



Raw file: 20171215_MaS_33SR_LMH_phospho_08
 Scan: 4958 Method: FTMS; HCD Score: 71.24 m/z: 656.31 Gene names: DCAF15



Raw file
 20171215_MaS_33SR_LMH_phospho_08
 Scan 6498 Method FTMS; HCD Score 161.46 m/z 837.39 Gene names RAB12



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

Peptide sequence: A G G G G G L G A G S P A L S G G Q G R

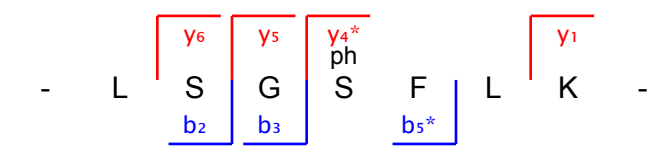
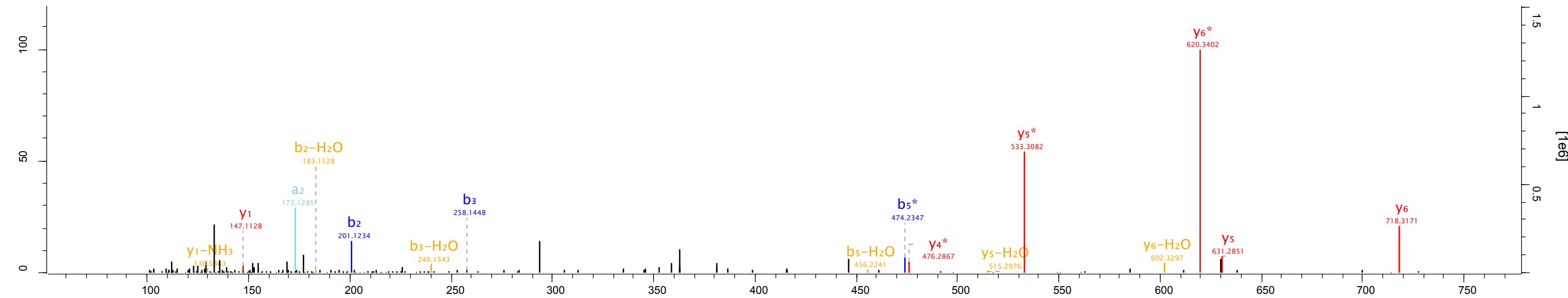
Fragmentation sites (b and y ions):

- b₂ (under G)
- b₃ (under G)
- b₄ (under G)
- b₅ (under G)
- b₆ (under G)
- b₇ (under L)
- b₈ (under G)
- b₉ (under A)
- b₁₀ (under G)
- b₁₁* (under S)
- b₁₂* (under P)
- b₁₃* (under A)
- b₁₄* (under L)
- b₁₅* (under S)

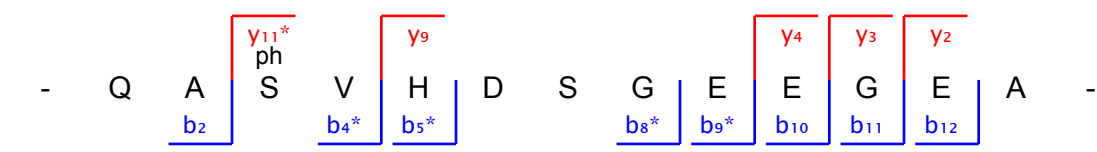
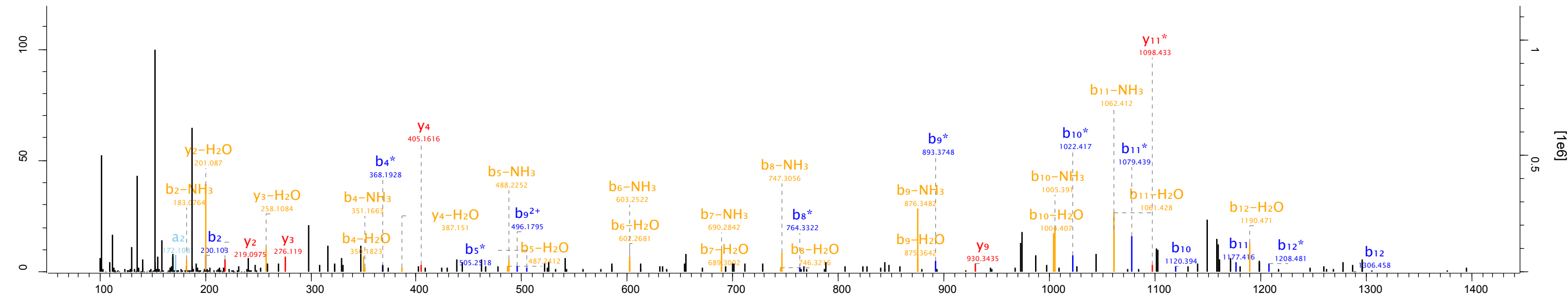
Fragmentation sites (b and y ions):

- y₁ (under R)
- y₂ (under G)
- y₃ (under Q)
- y₄ (under G)
- y₅ (under S)
- y₆ (under L)
- y₇ (under A)
- y₈ (under P)
- y₉ (under S)
- y₁₀ (under G)
- y₁₁ (under A)
- y₁₂ (under L)
- y₁₃ (under S)
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- y₁₅* (under R)
- y₁₆* (under -)
- y₁₈* (under -)

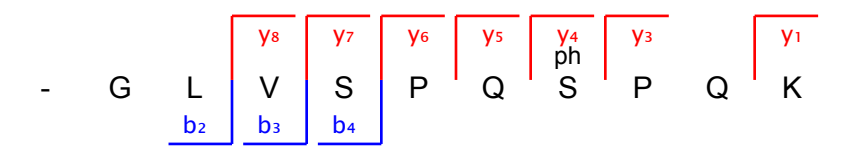
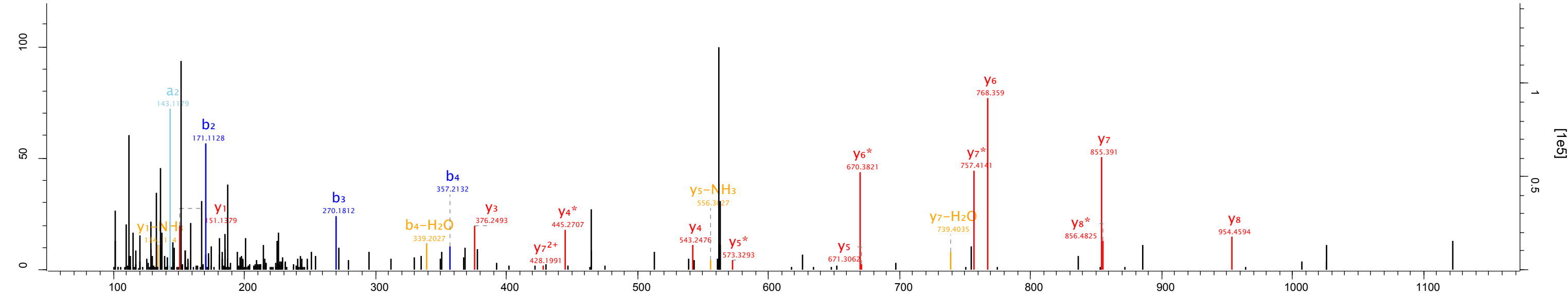
Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 11618 Method FTMS; HCD Score 83.78 m/z 416.2 Gene names PDYN



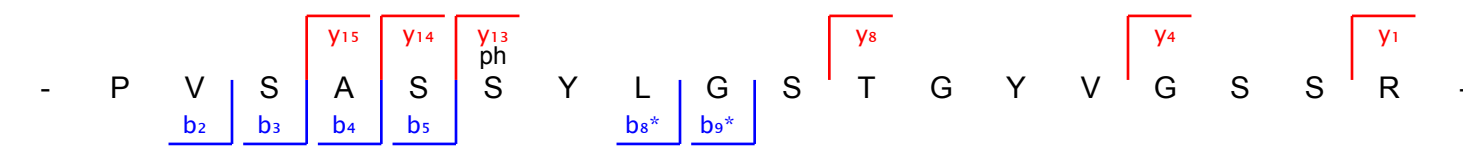
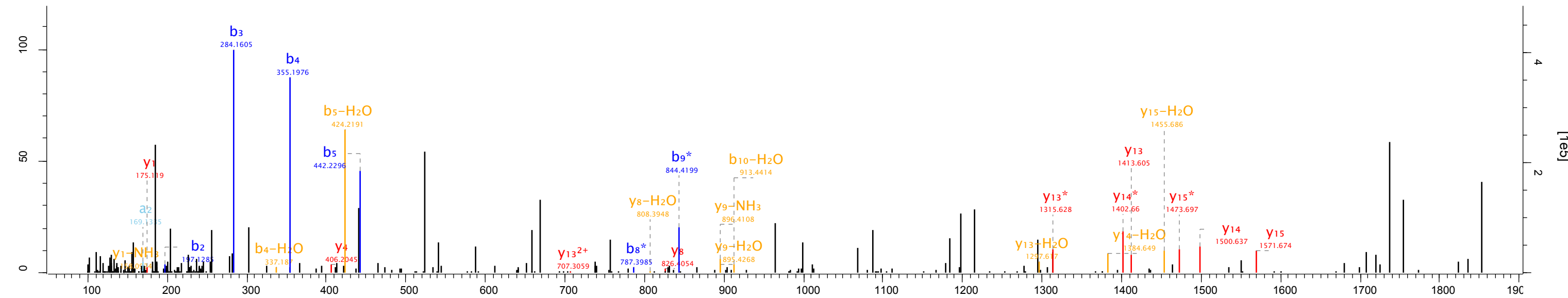
Raw file 20171215_MaS_33SR_LMH_phospho2_01 Scan 2638 Method FTMS; HCD Score 135.08 m/z 698.26 Gene names SSH3

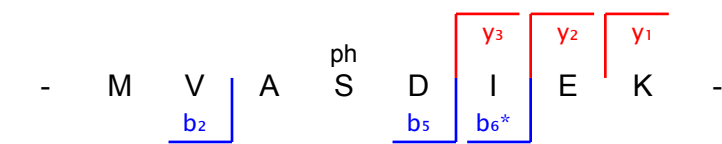
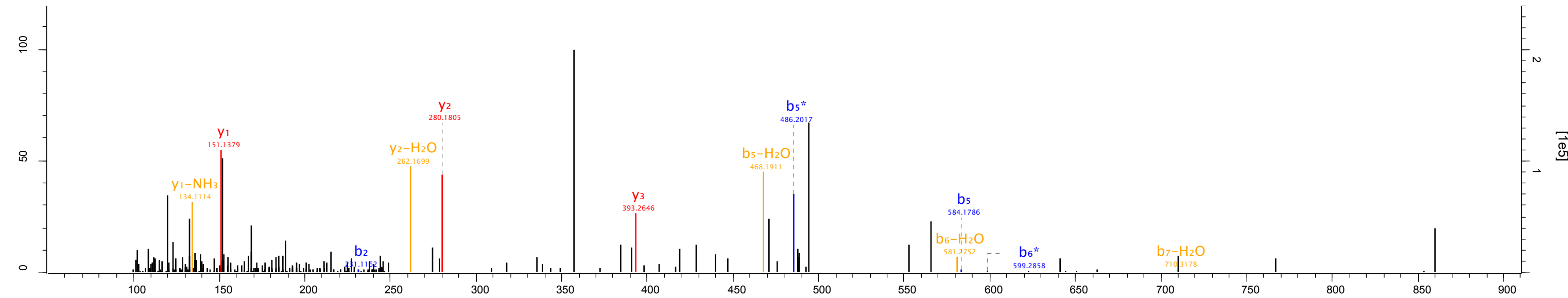


20171215_MaS_33SR_LMH_phospho2_01 5058 FTMS; HCD 82.07 562.79 BCL6

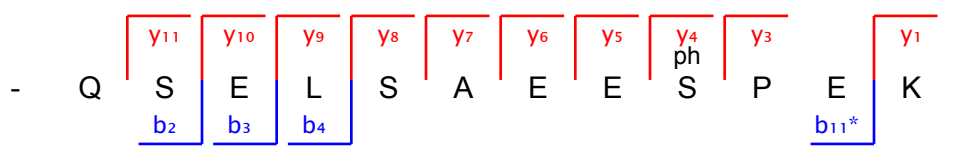
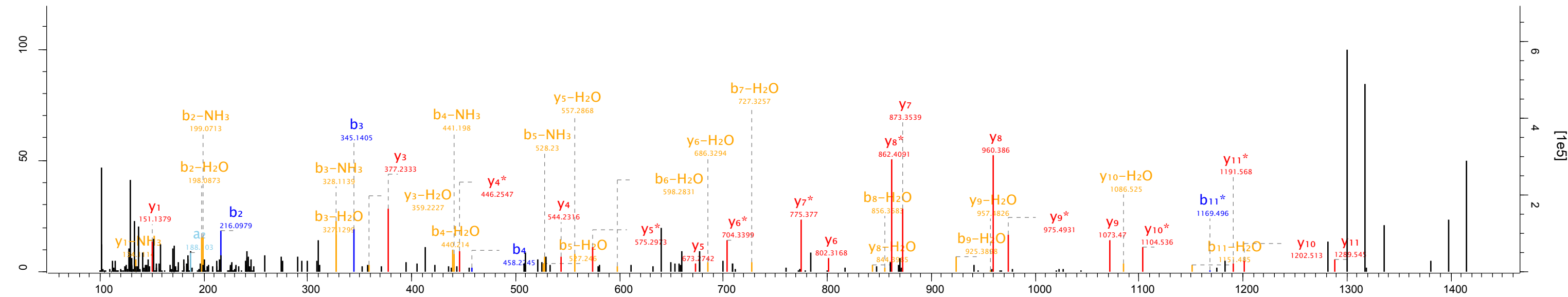


Raw file: 20171215_MaS_33SR_LMH_phospho2_02
 Scan: 10648 Method: FTMS; HCD Score: 64.38 m/z: 928.42 Gene names: CCDC114

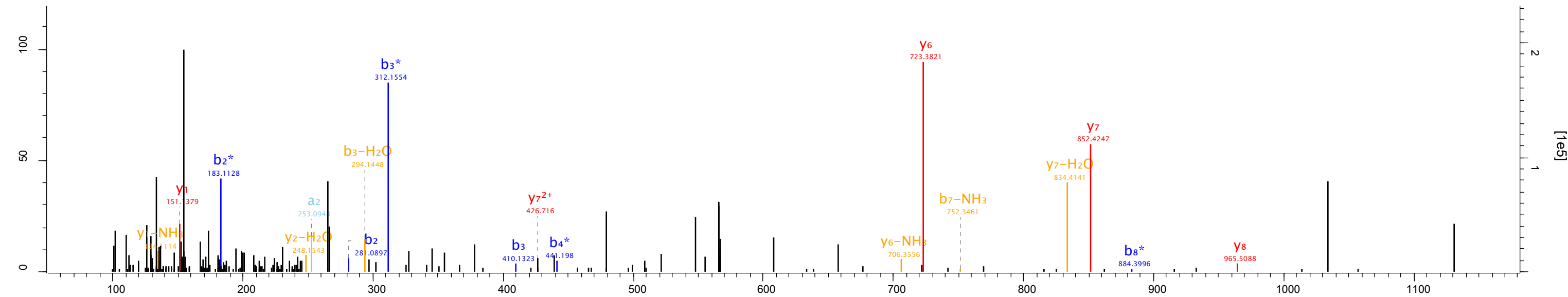


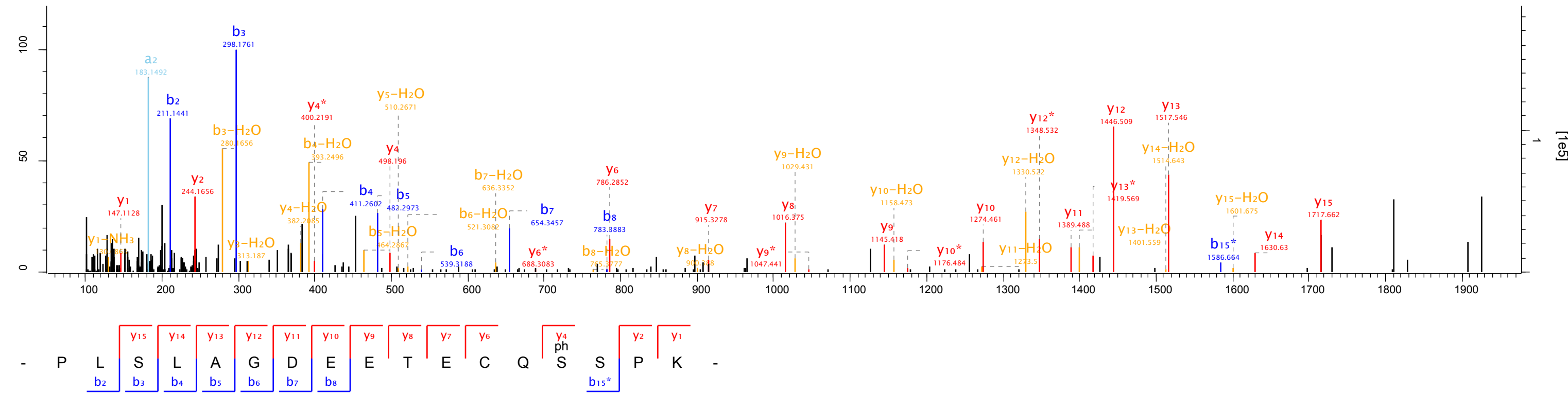


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 4558 Method FTMS; HCD Score 158.17 m/z 709.3 Gene names CCDC93

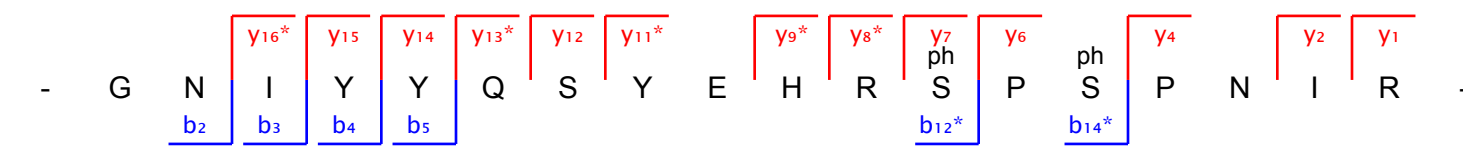
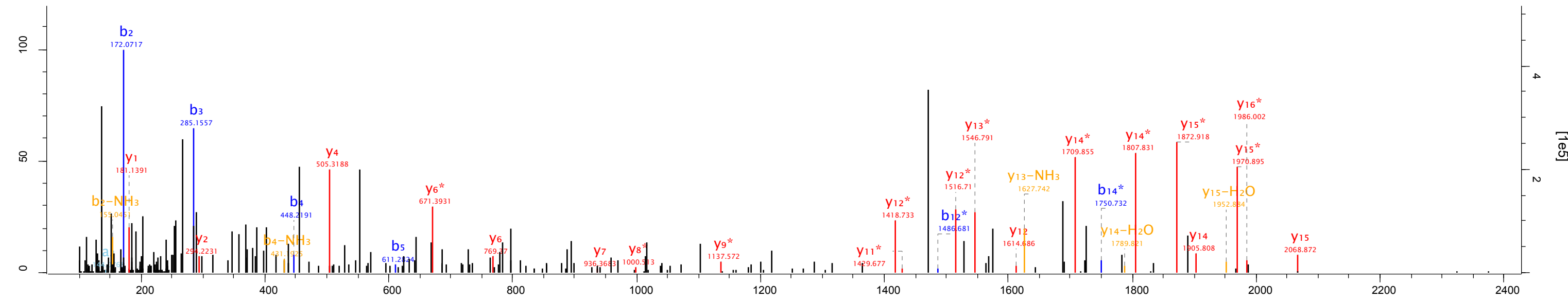


Raw file 20171215_MaS_33SR_LMH_phospho2_02 Scan 5178 Method FTMS; HCD Score 59.42 m/z 566.76

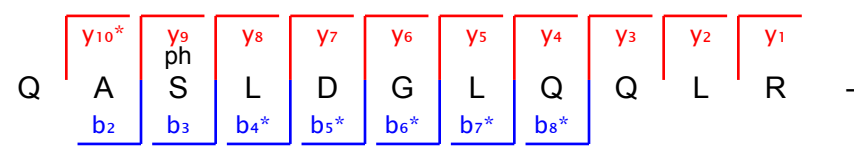
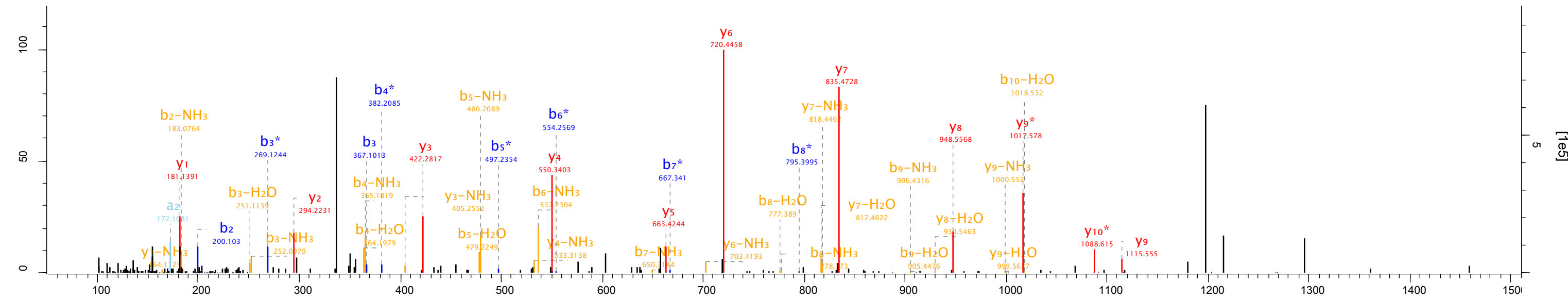


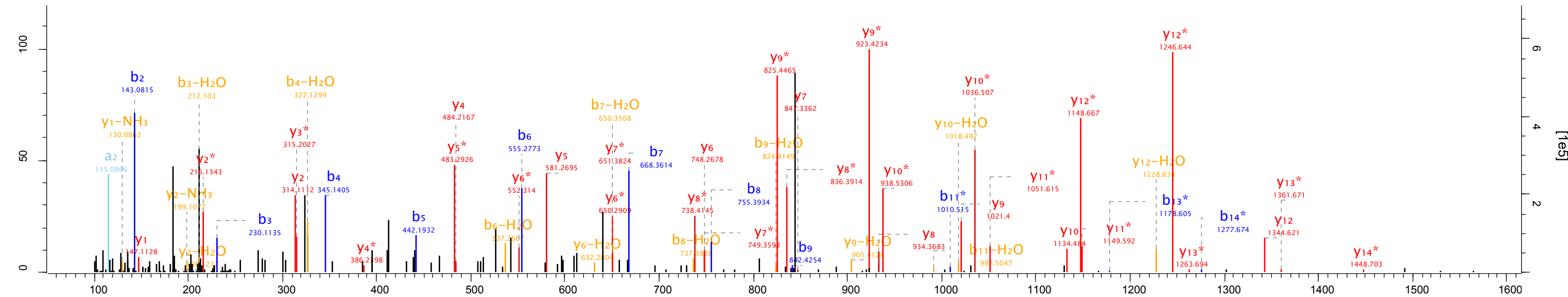


Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 10008 Method FTMS; HCD Score 54.66 m/z 785.34 Gene names CXorf23



Raw file 20171215_MaS_33SR_LMH_phospho2_03 Scan 13548 Method FTMS; HCD Score 202.24 m/z 657.83 Gene names TBC1D25



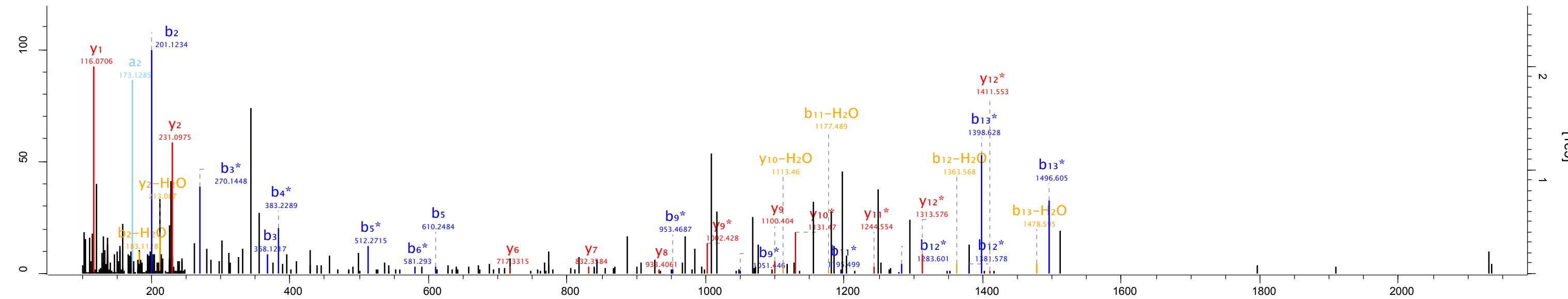


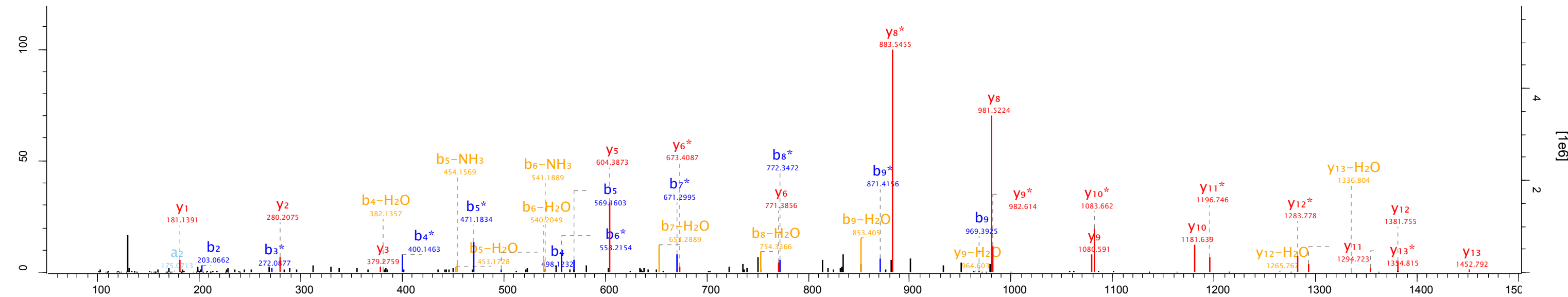
- A A S D P L L S S V S P A V S K -

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 16358 Method FTMS; HCD Score 78.42 m/z 855.33 Gene names CDC42BPA



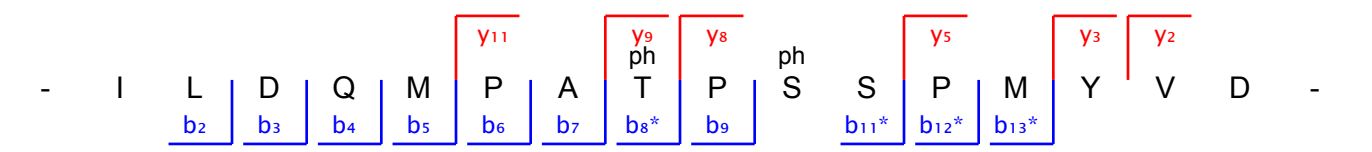
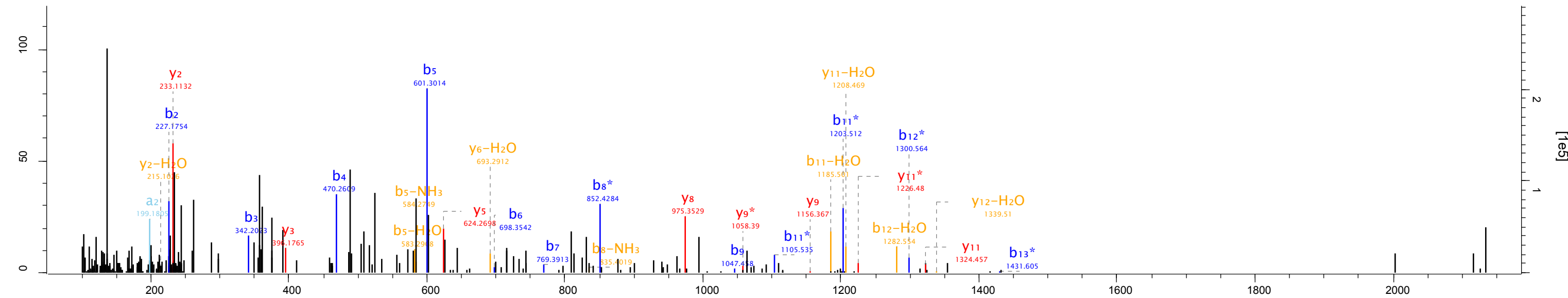


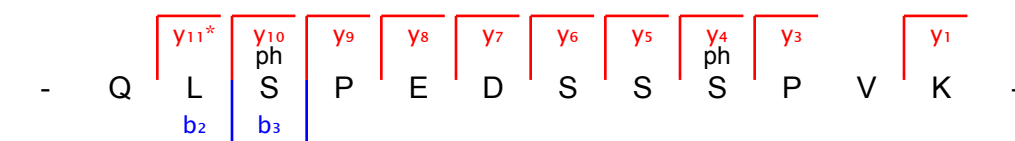
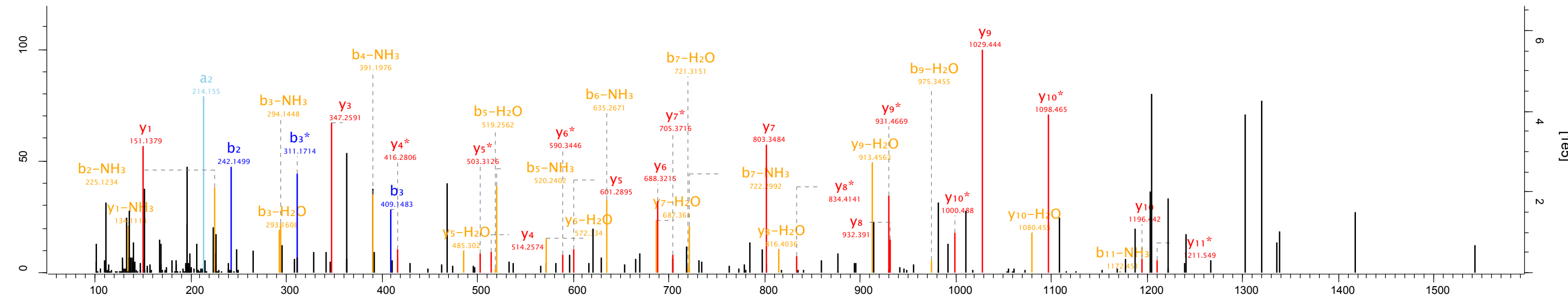
- S D S ph Q A S L T V P L S ph P Q V V R -

Fragmentation mapping (b and y ions):

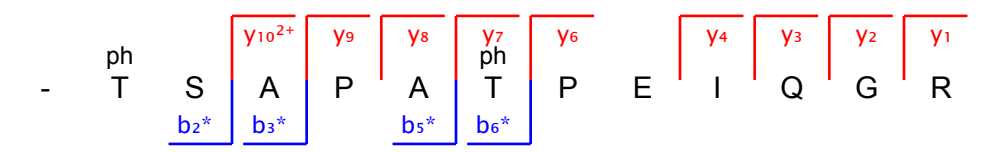
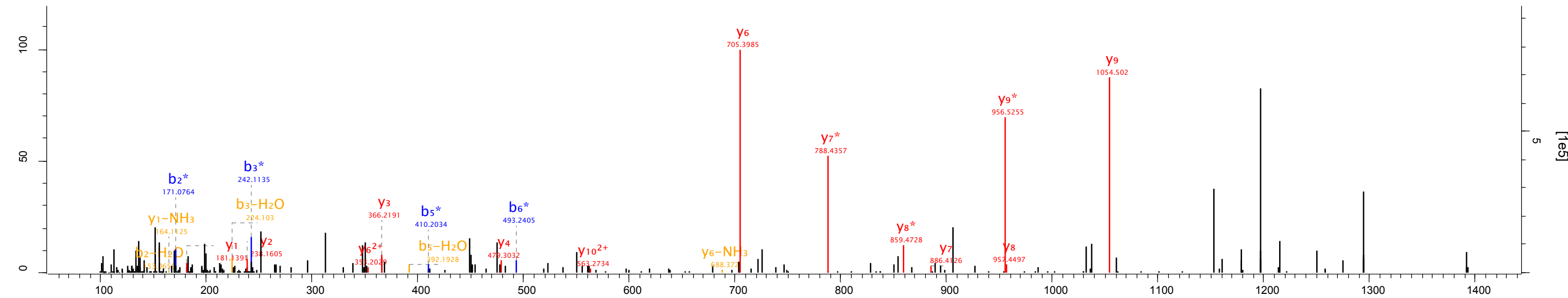
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- b3*: S
- b4: Q
- b5: A
- b6*: S
- b7*: L
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- y2: V
- y1: R

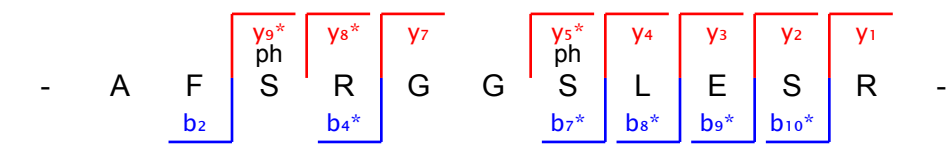
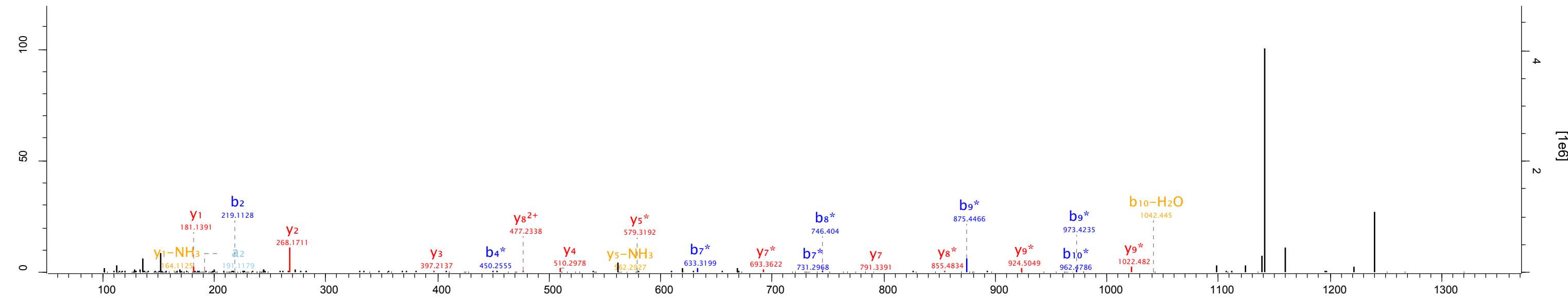
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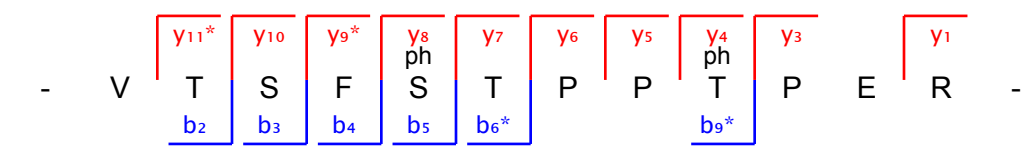
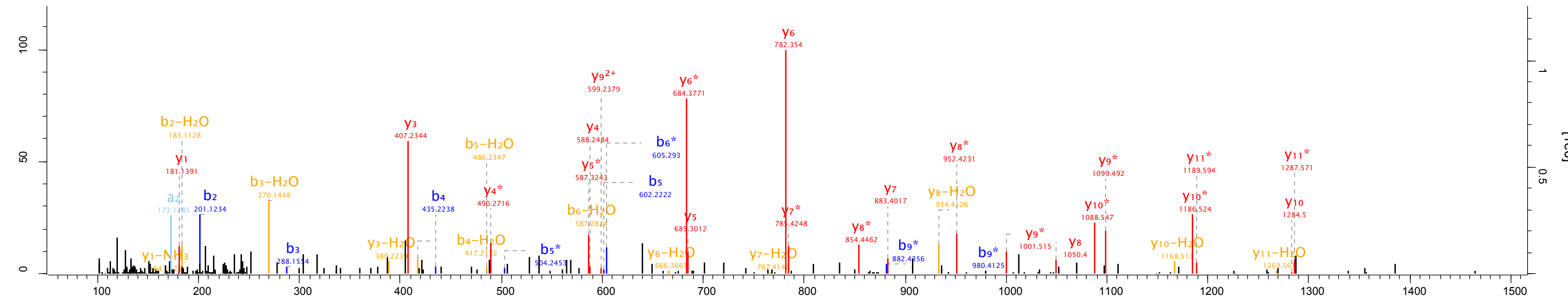
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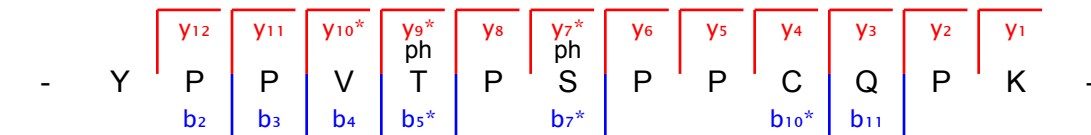
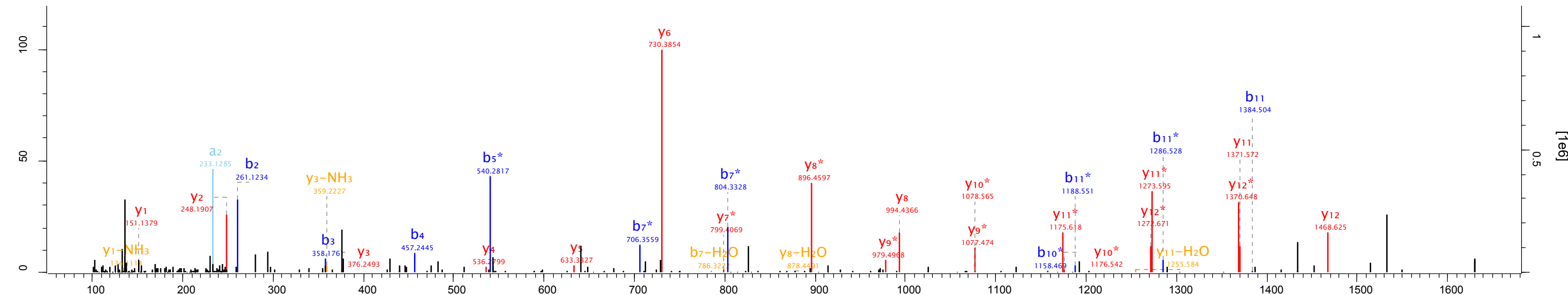




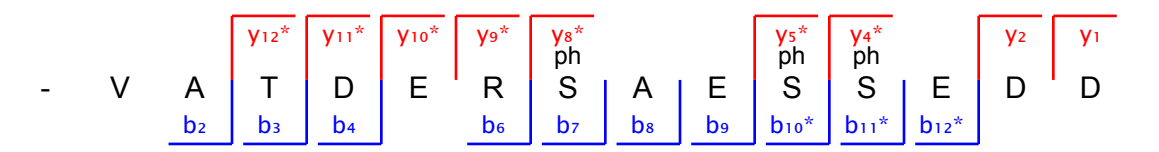
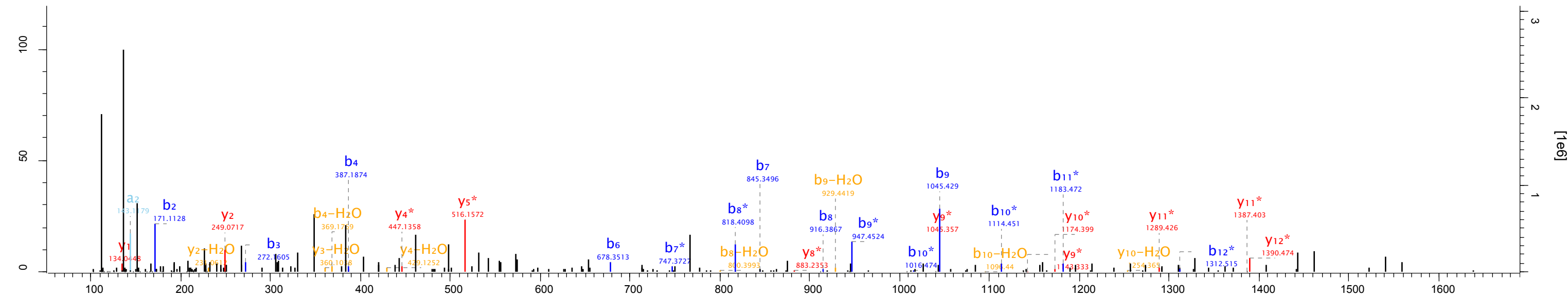
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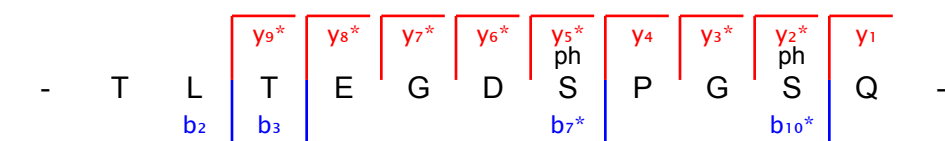
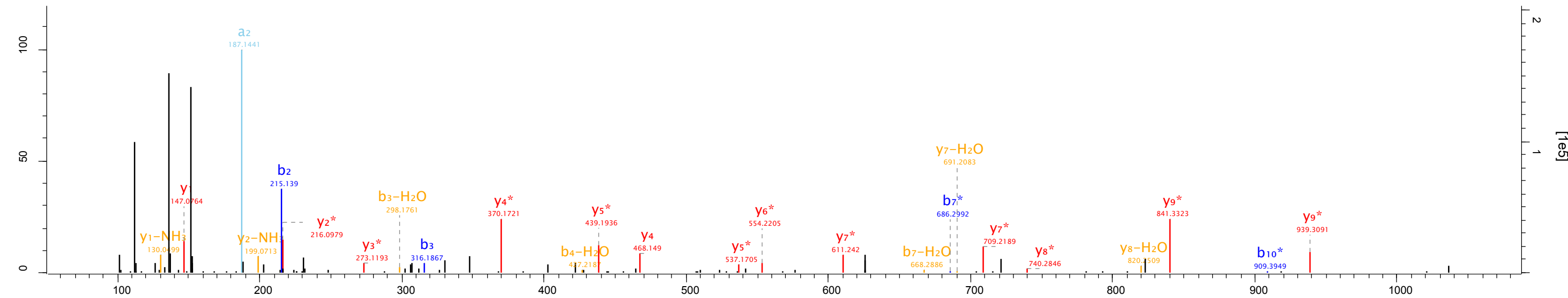
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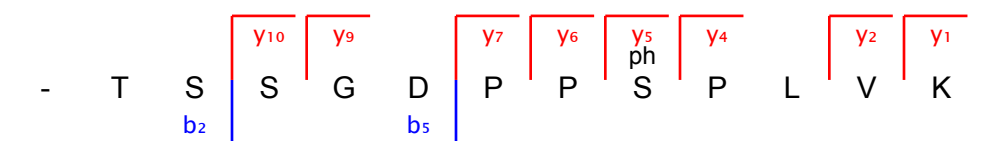
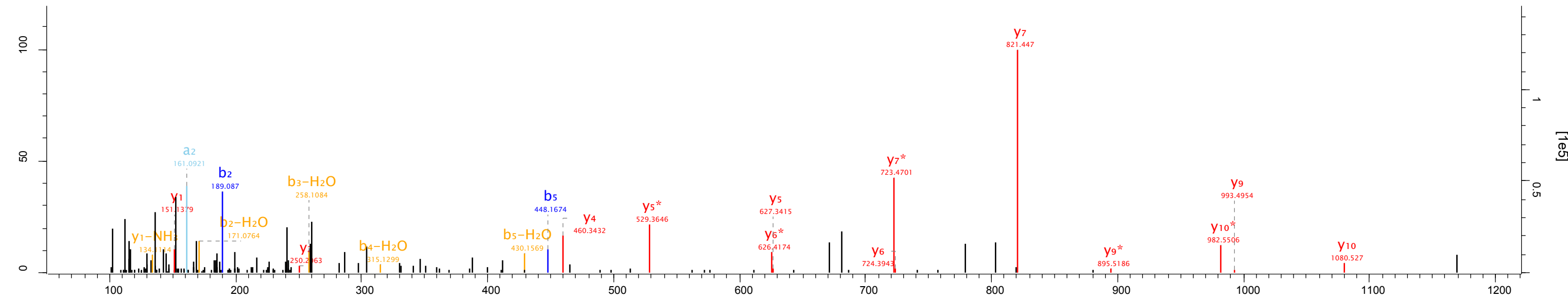




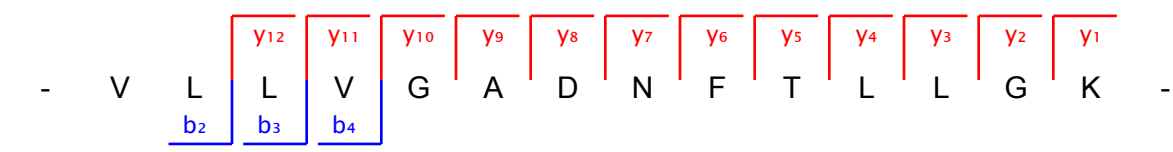
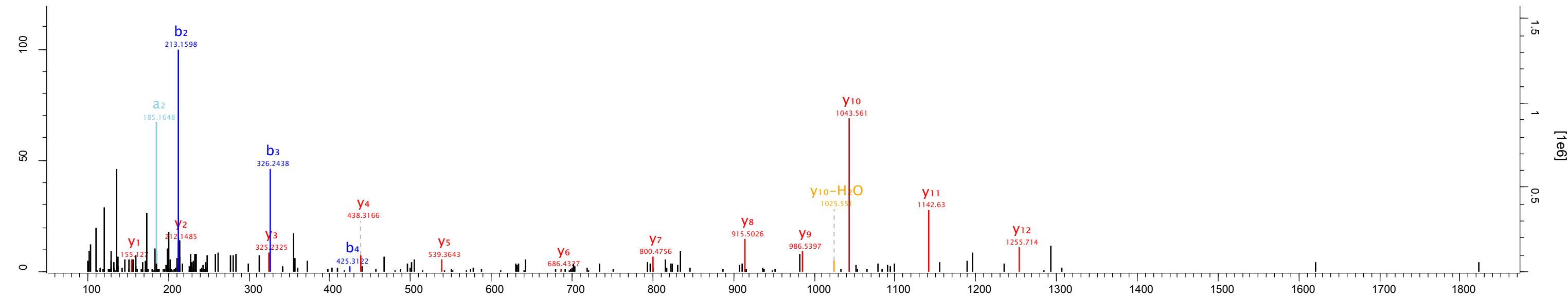
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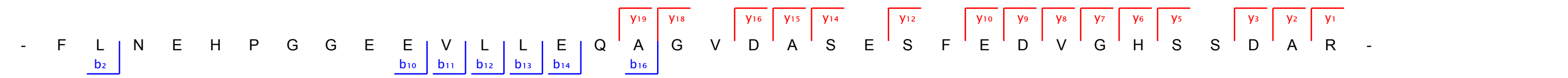
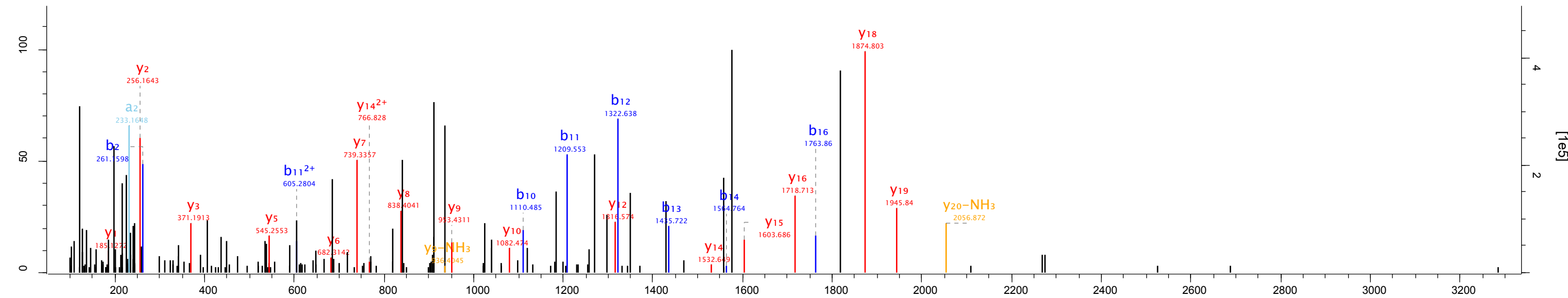




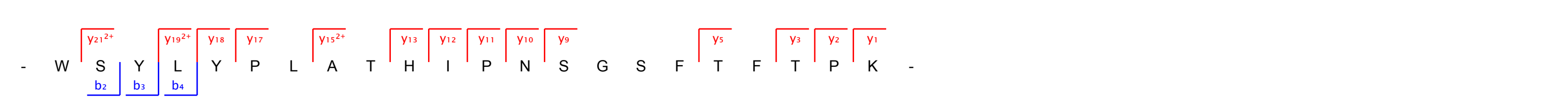
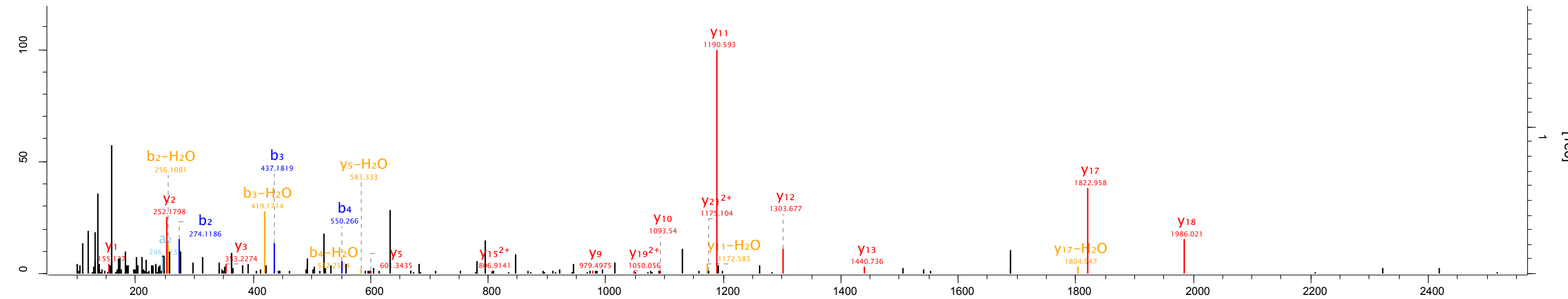
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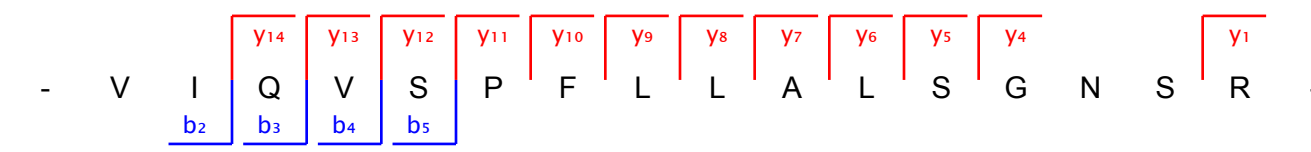
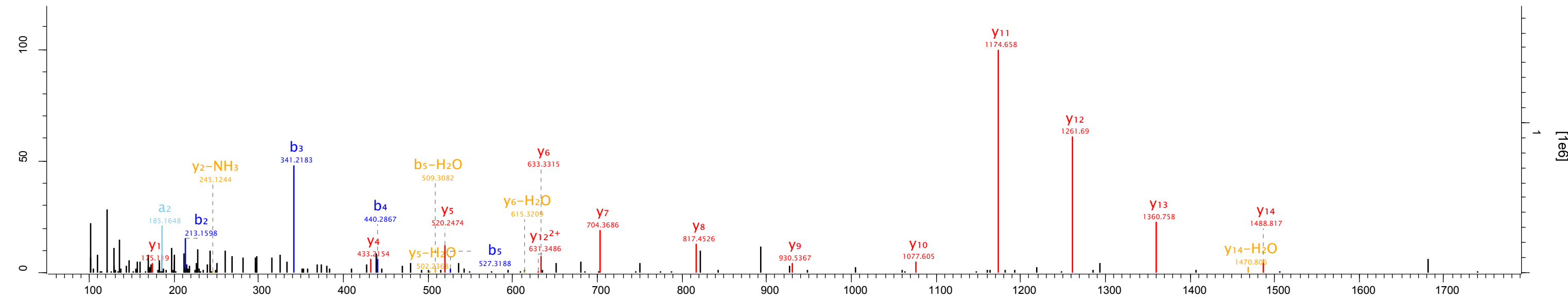
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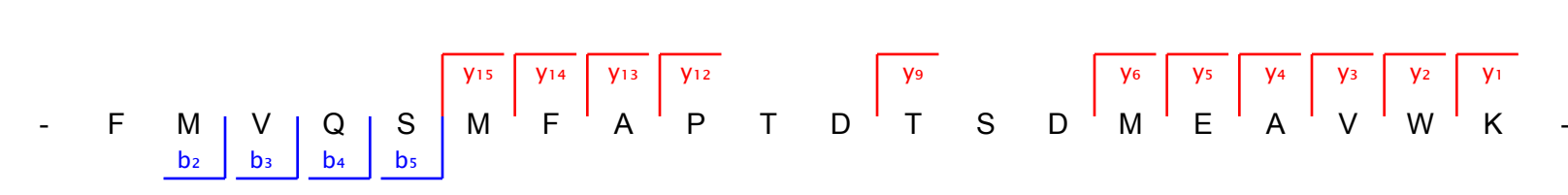
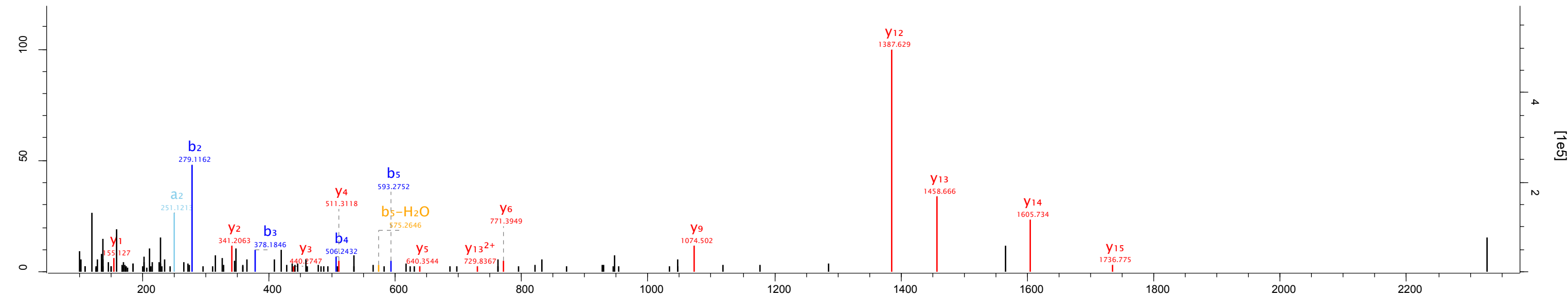
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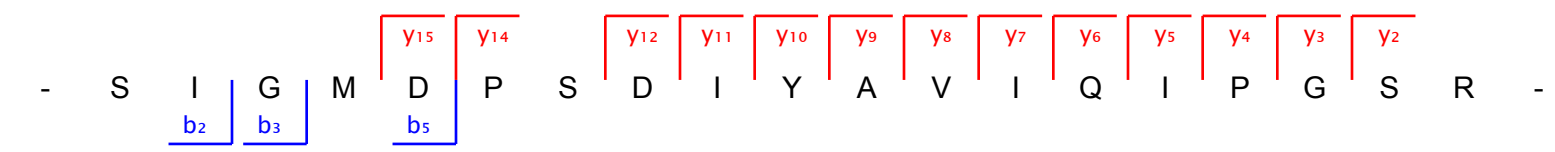
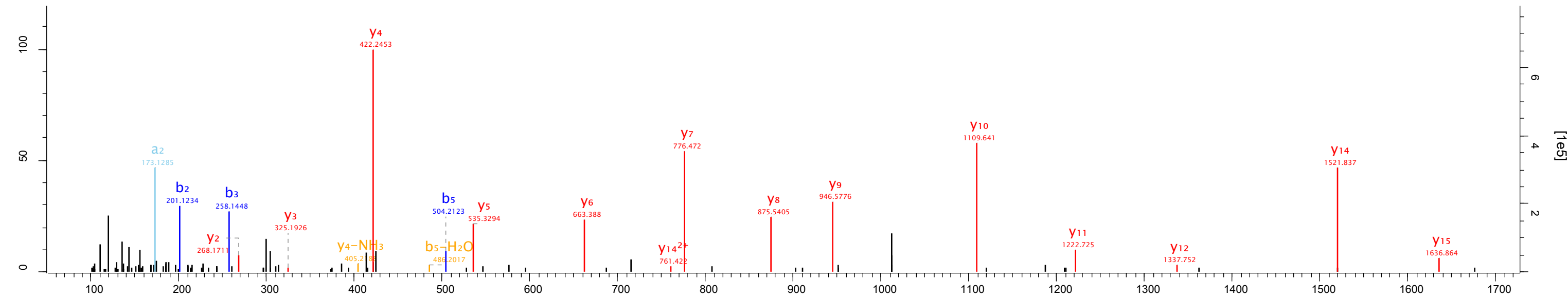
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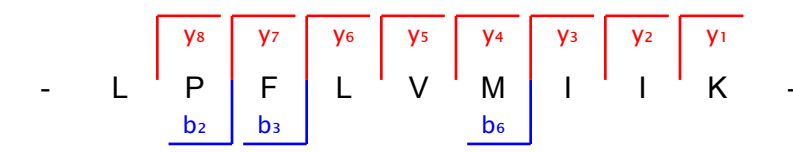
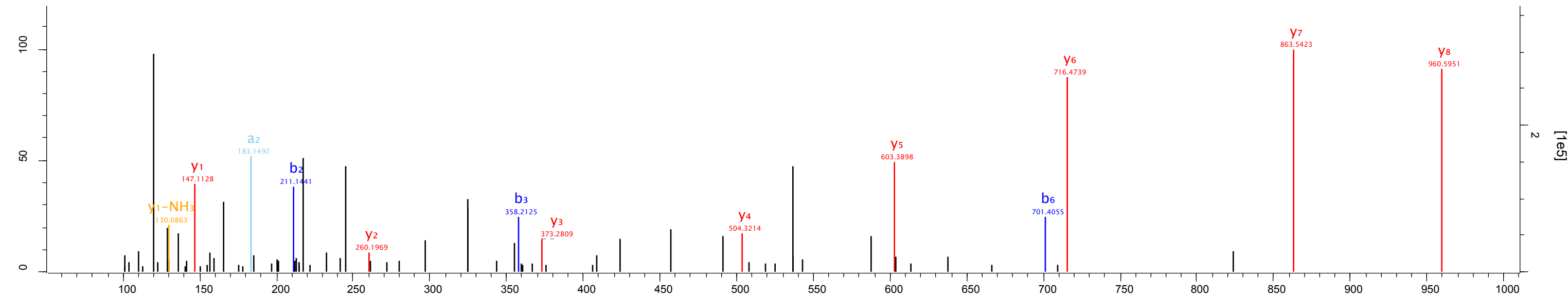
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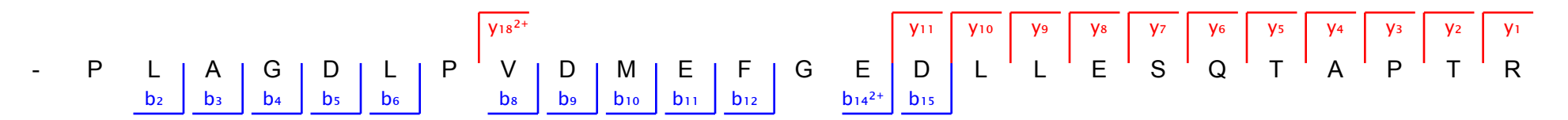
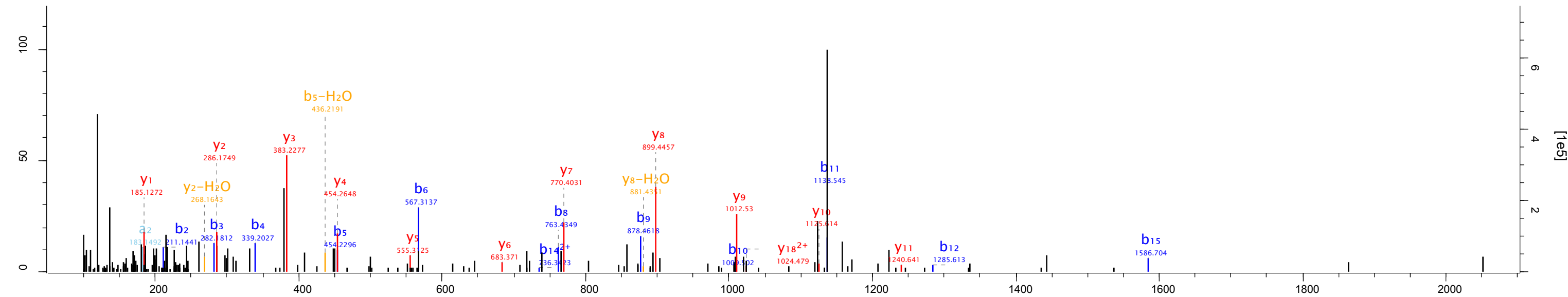
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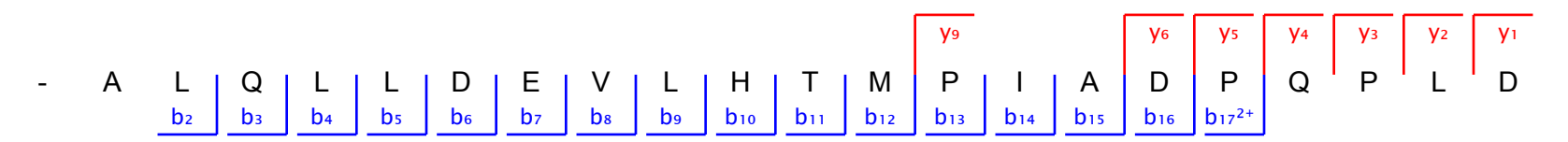
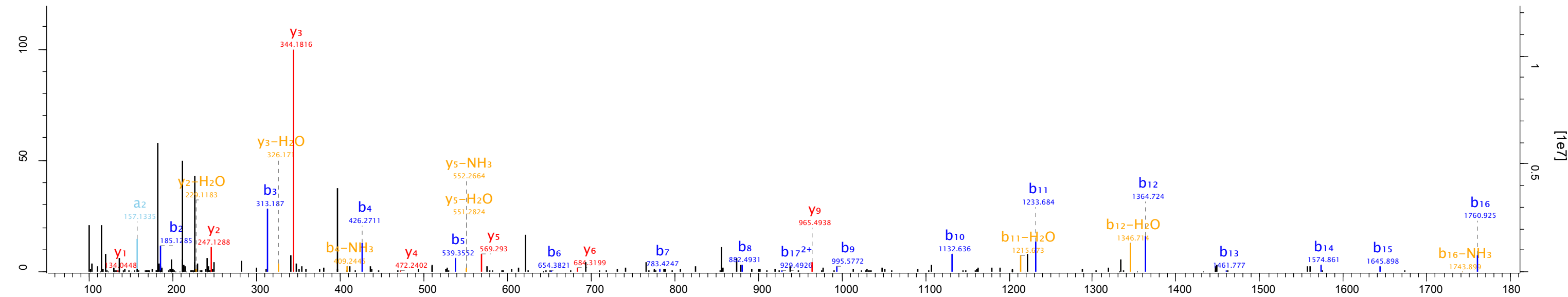
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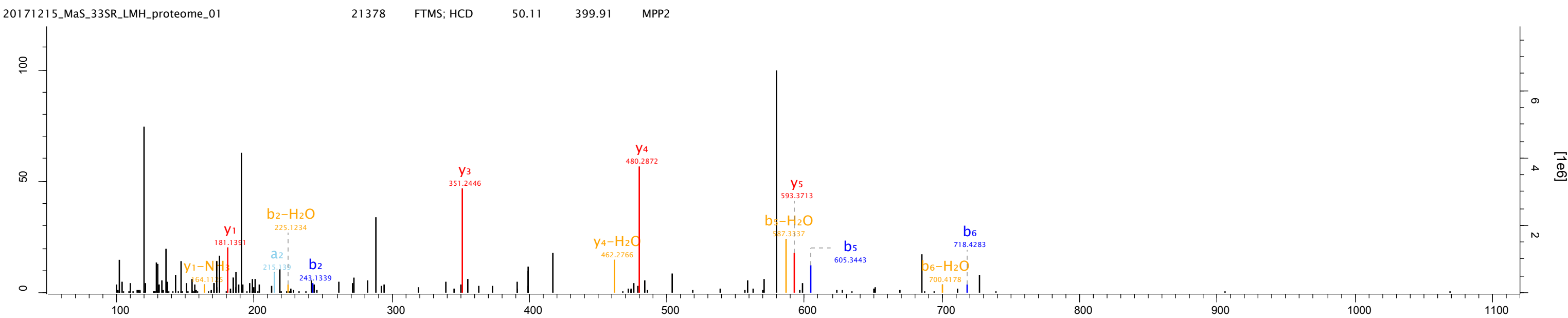


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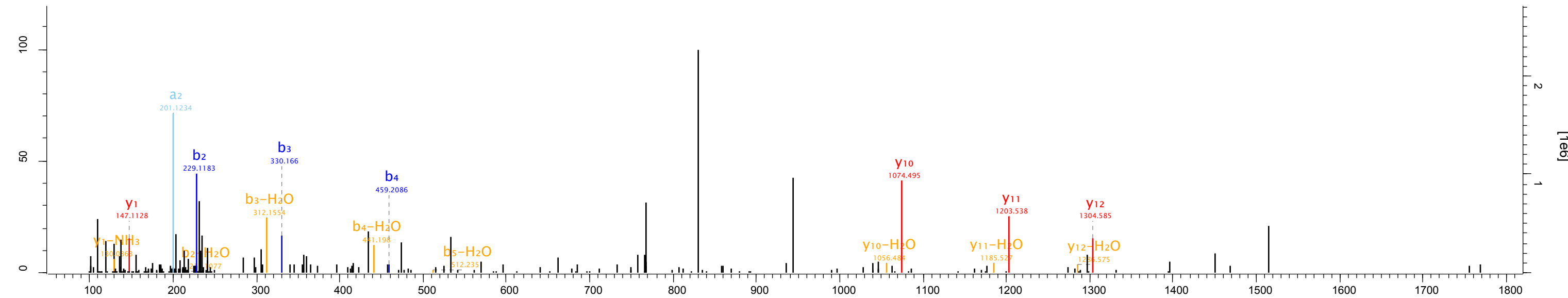
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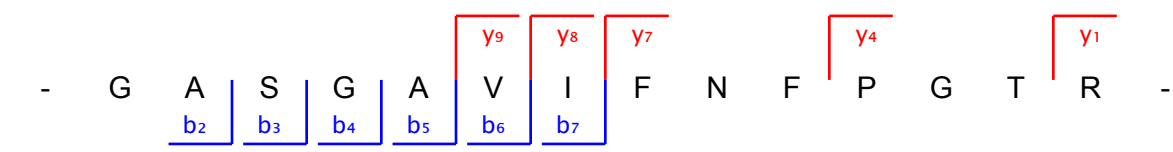
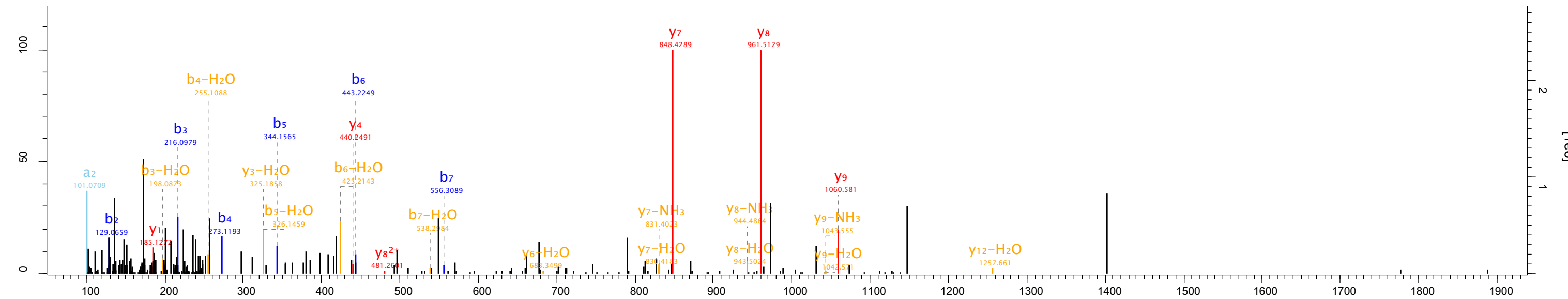


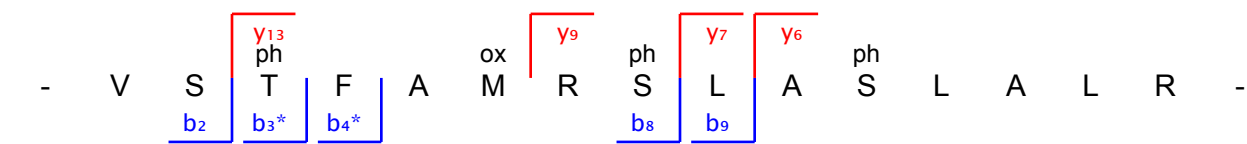
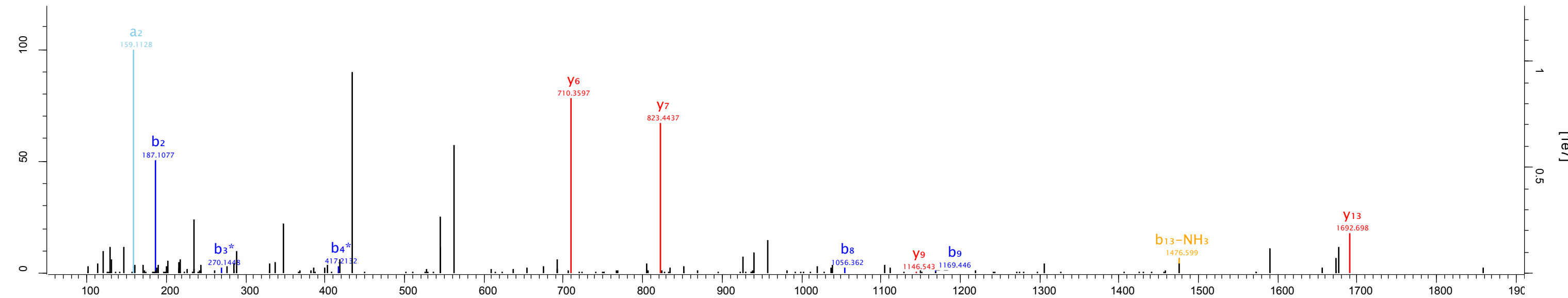
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Scan Method Score m/z Gene names
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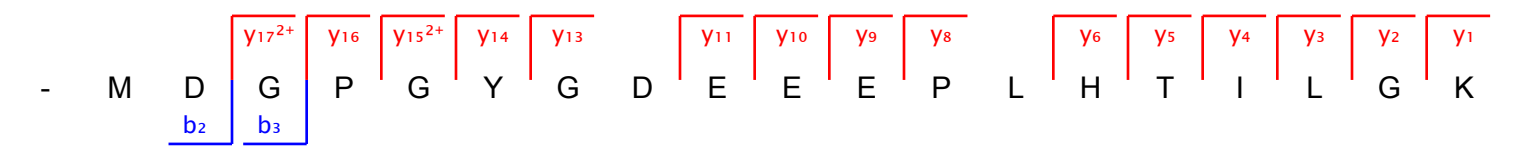
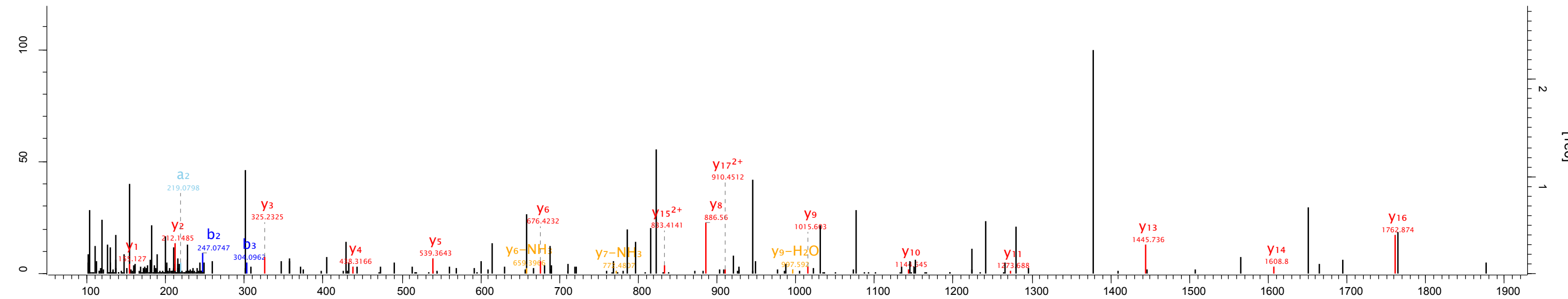


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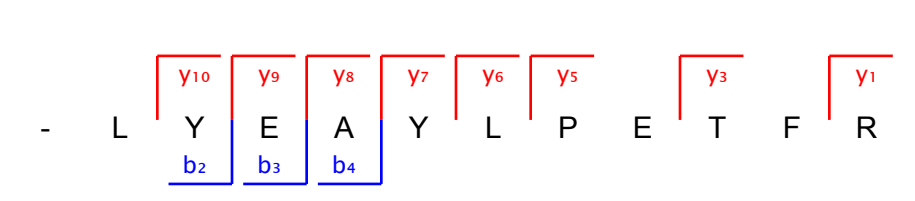
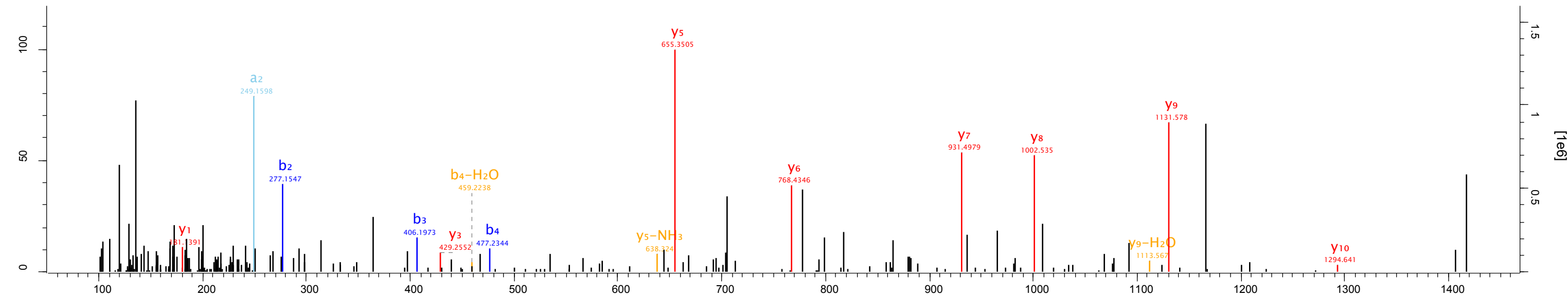




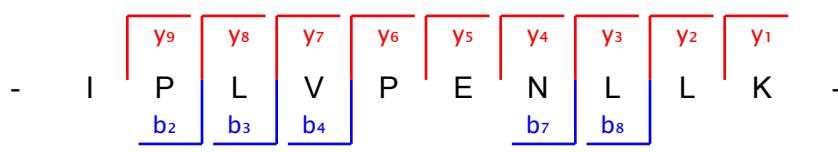
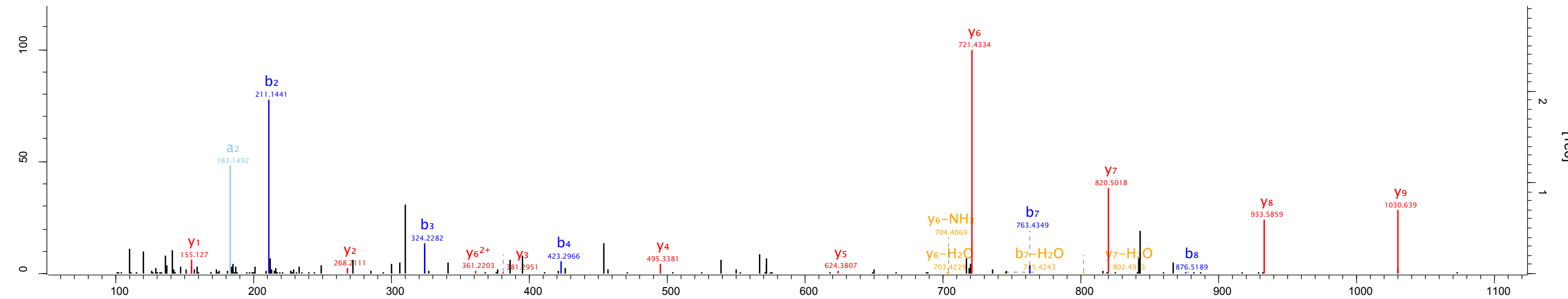
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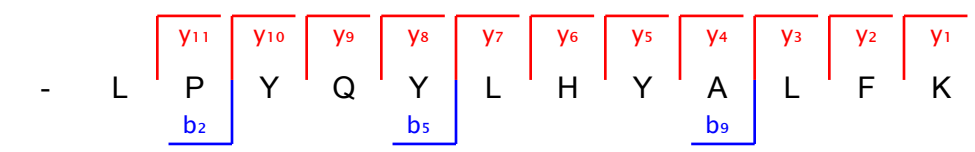
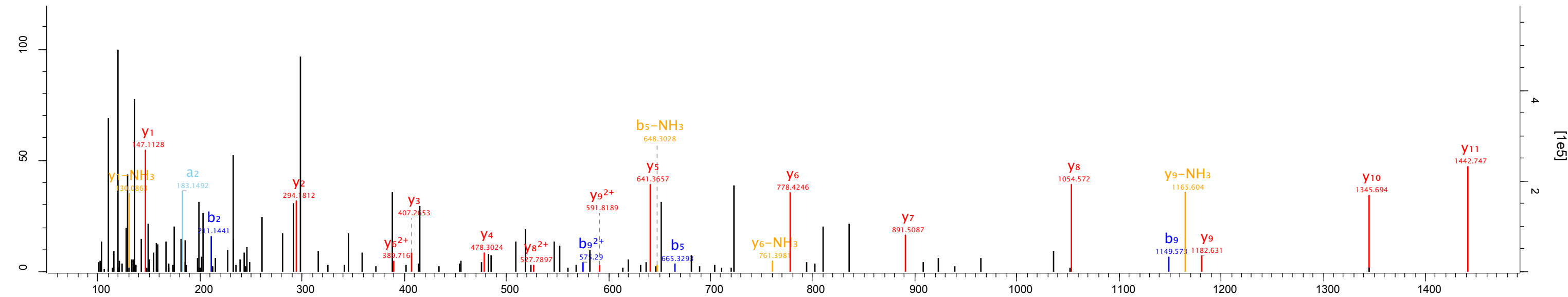
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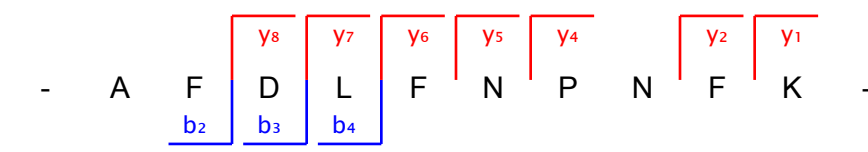
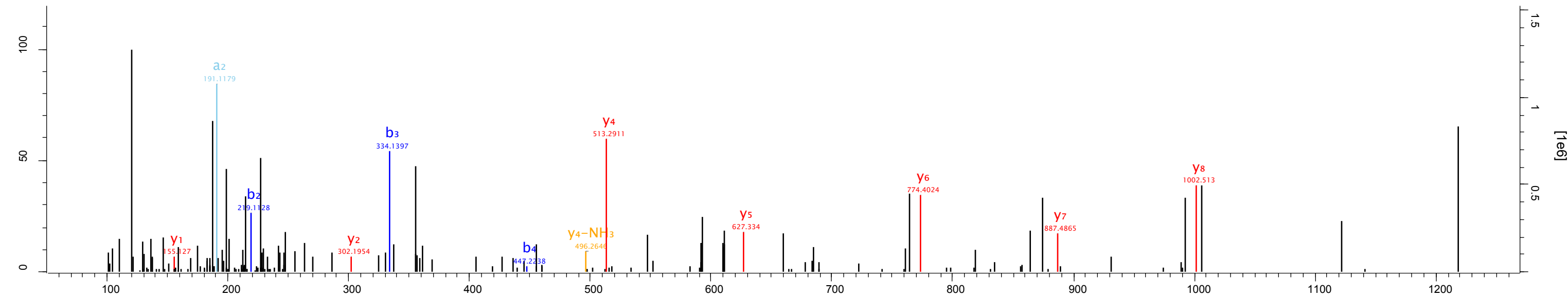
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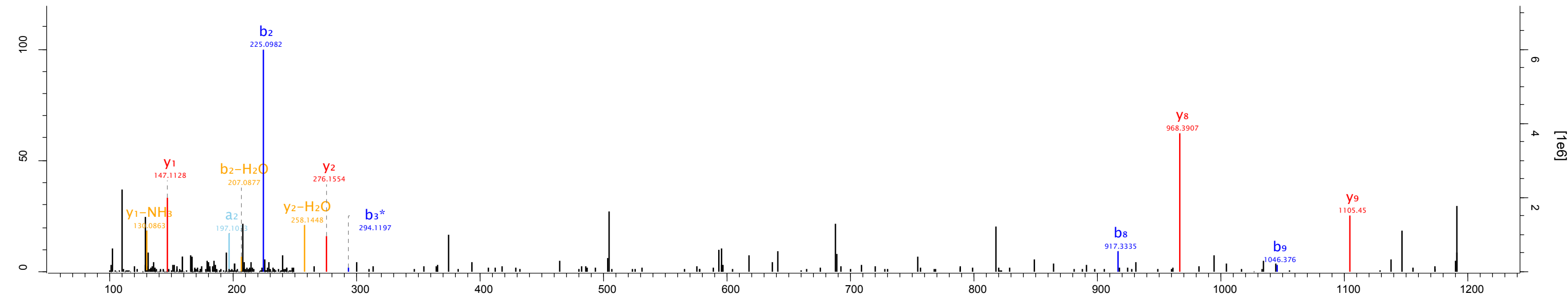
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20171215_MaS_33SR_LMH_proteome_01

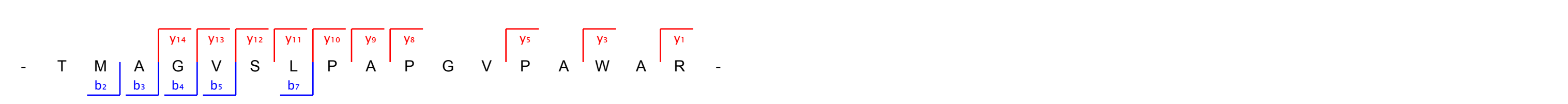
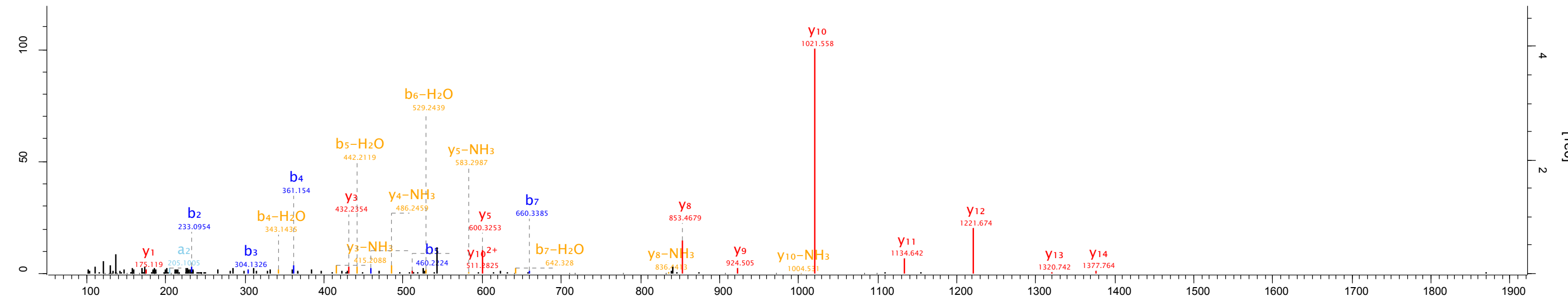
Scan	Method	Score	m/z	Gene names
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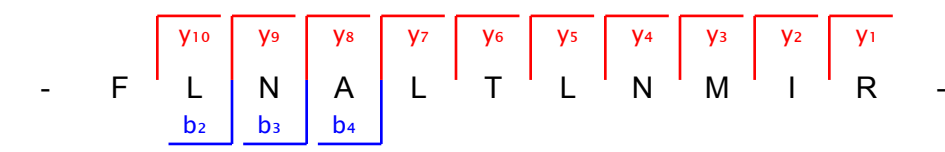
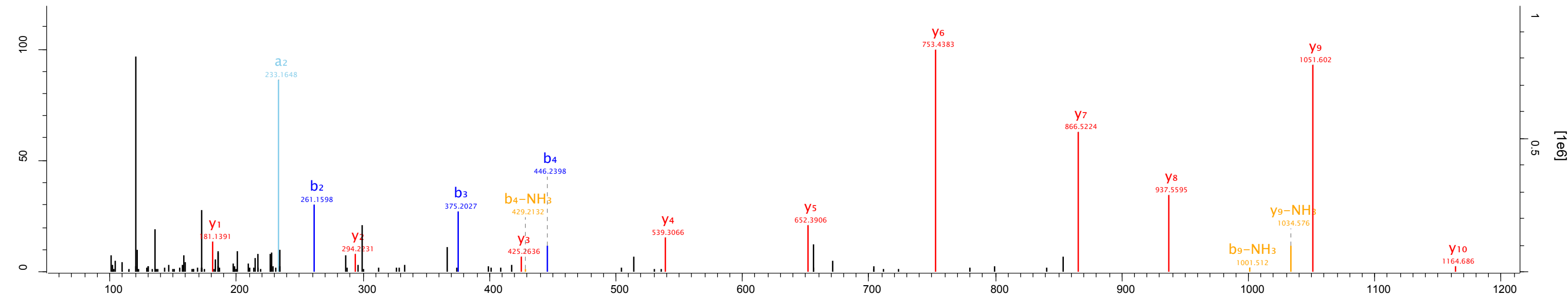
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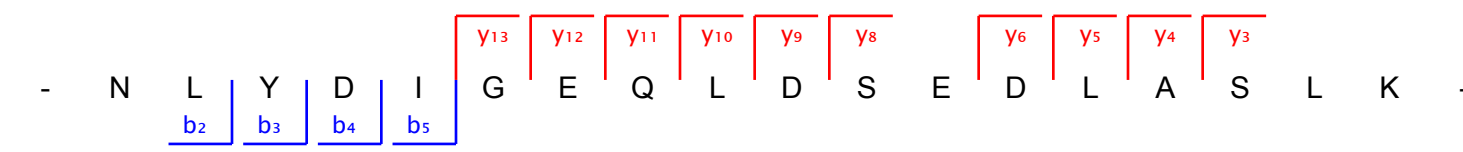
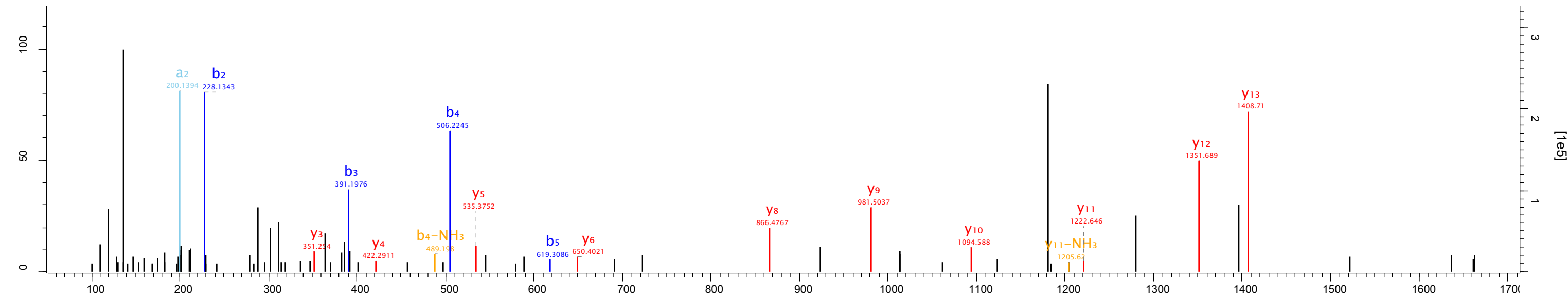
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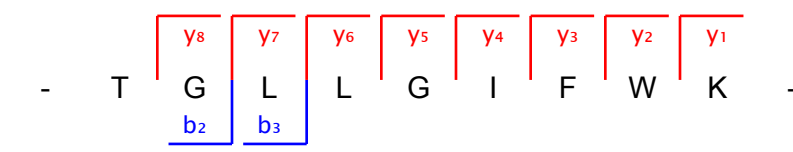
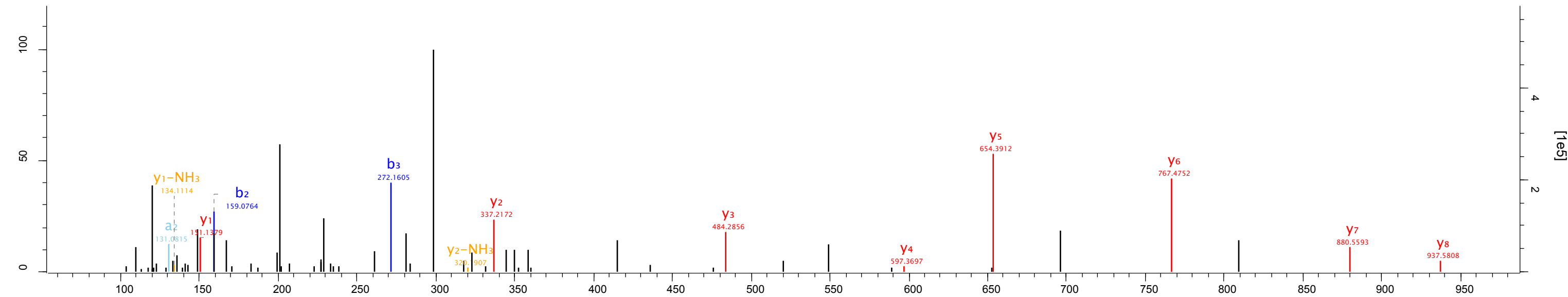
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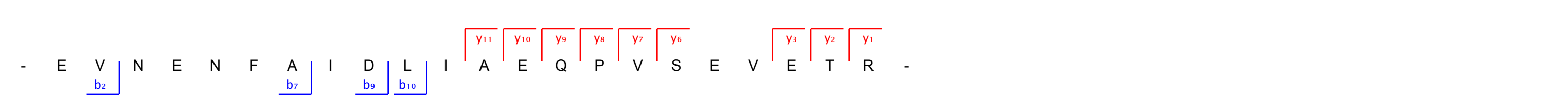
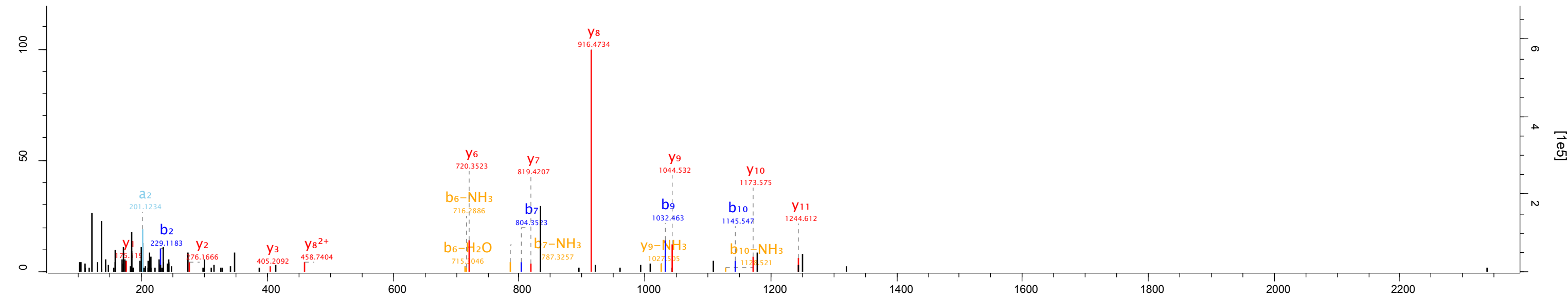
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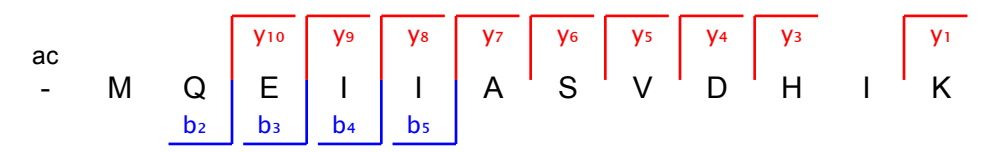
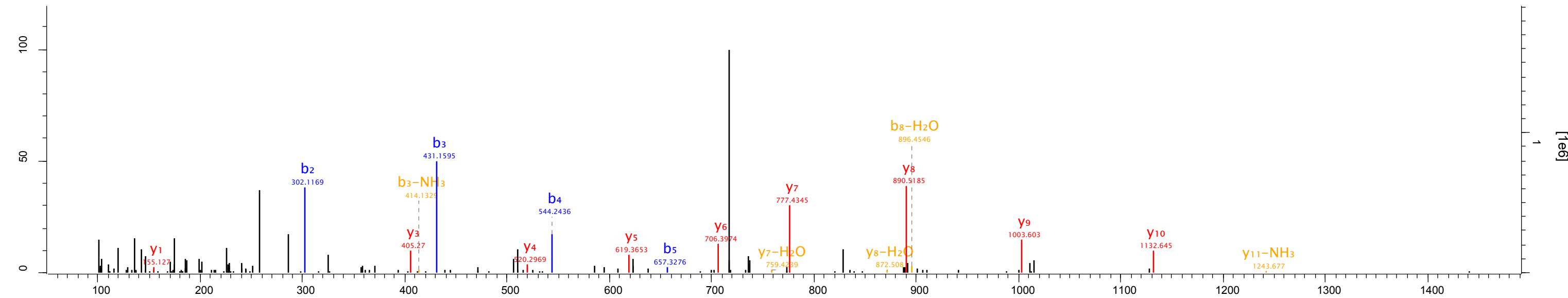
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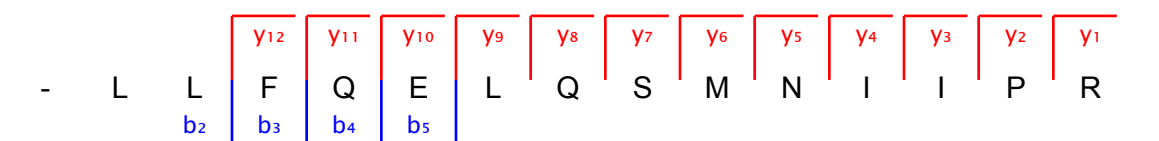
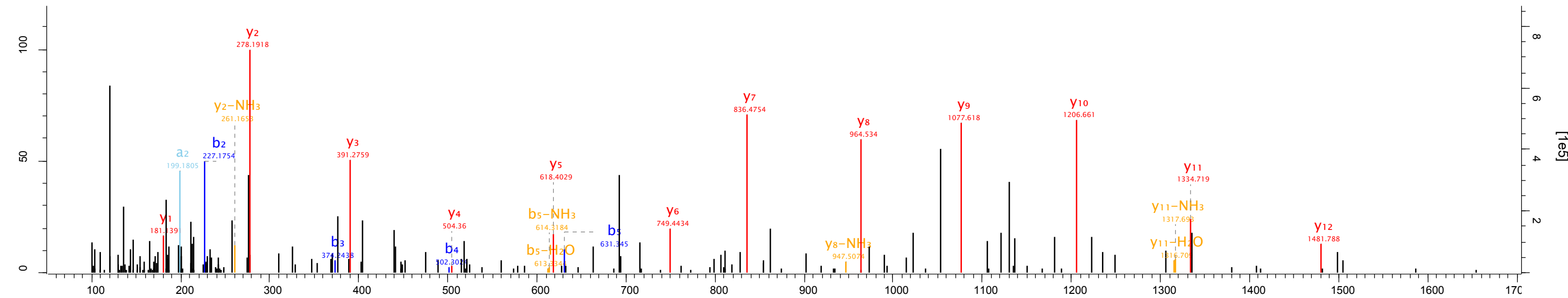
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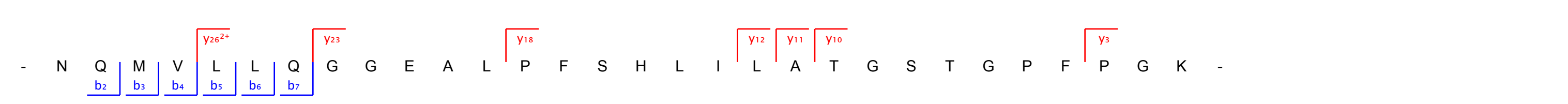
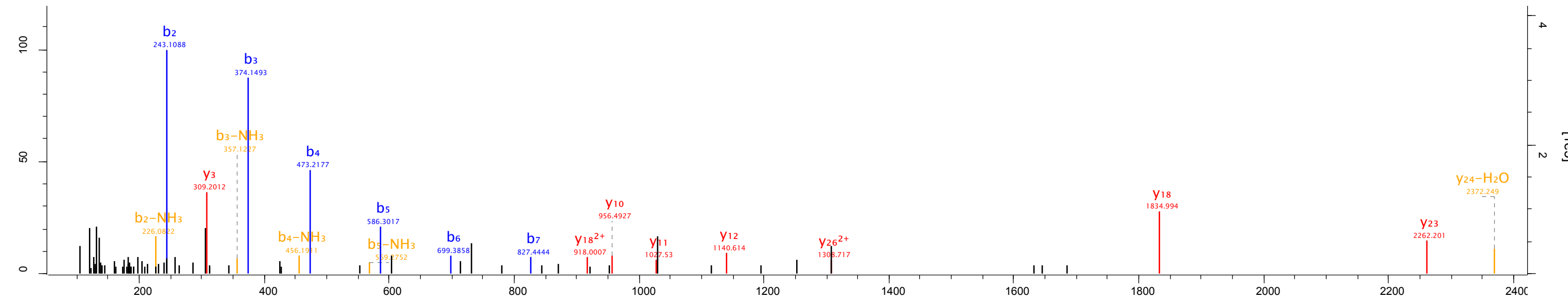
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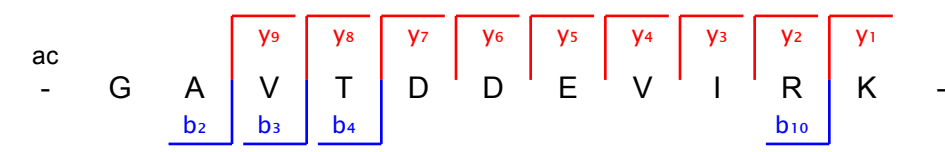
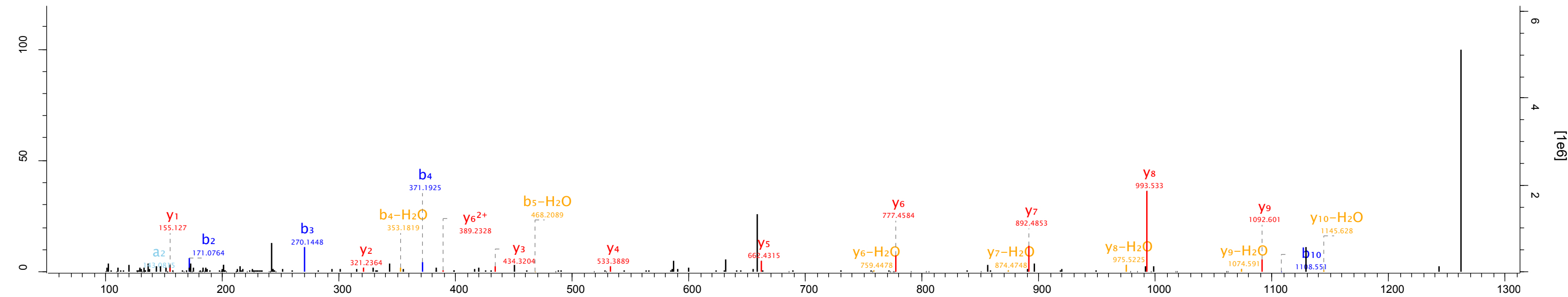
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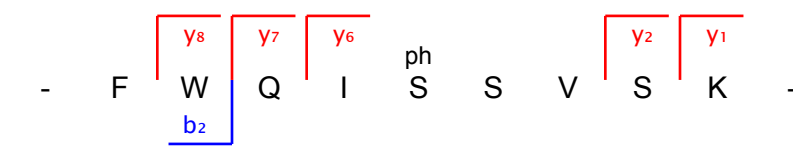
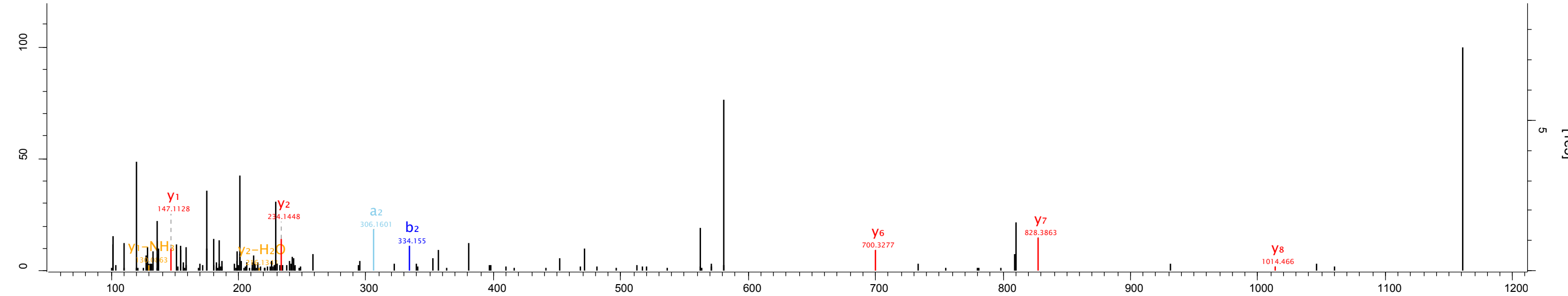
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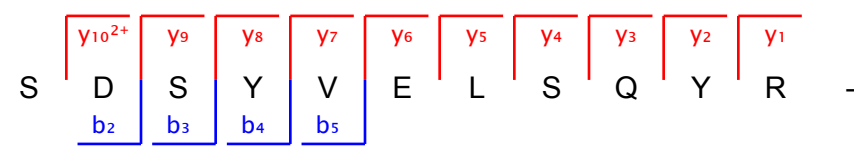
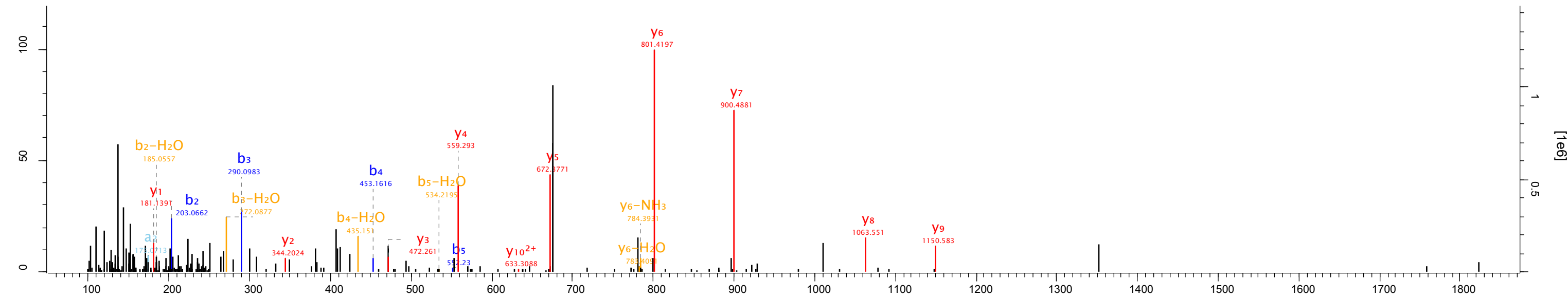
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20171215_MaS_33SR_LMH_proteome_02

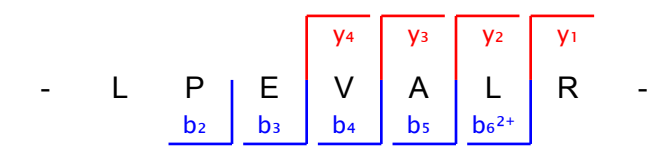
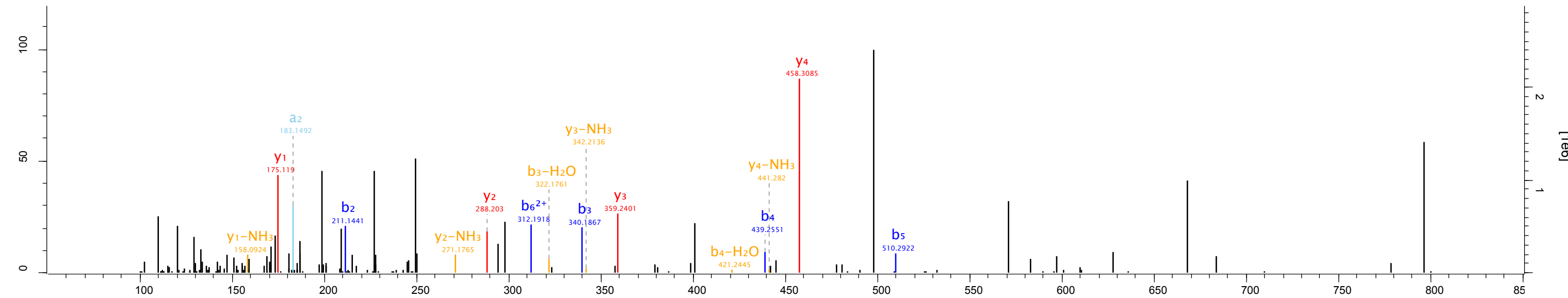
Scan	Method	Score	m/z	Gene names
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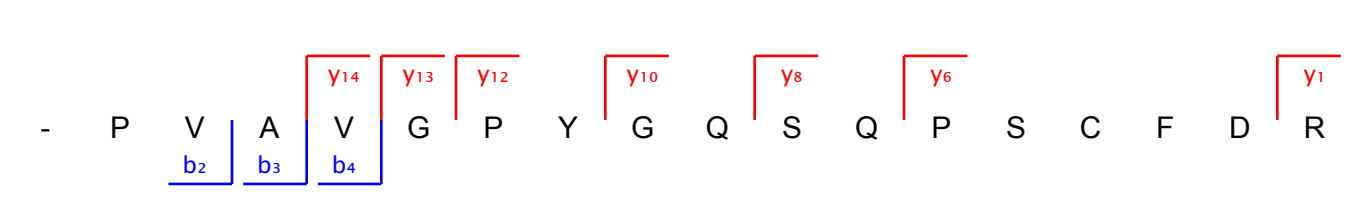
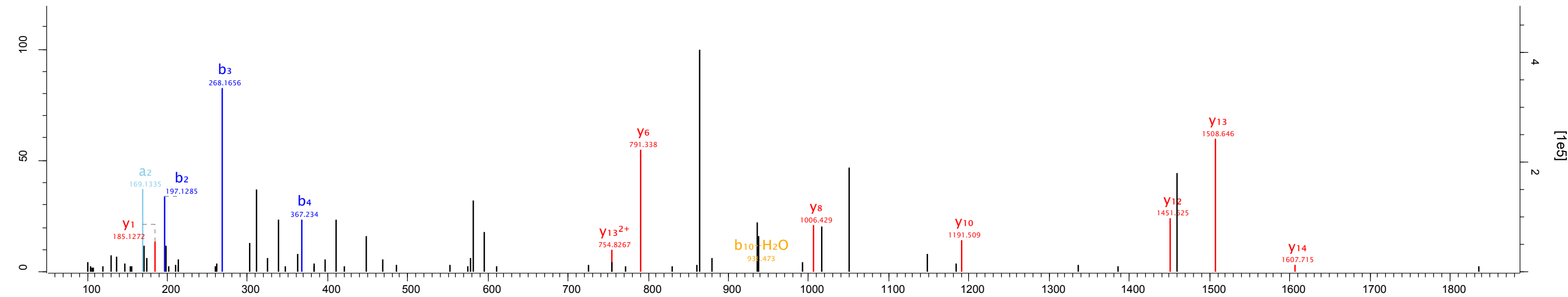
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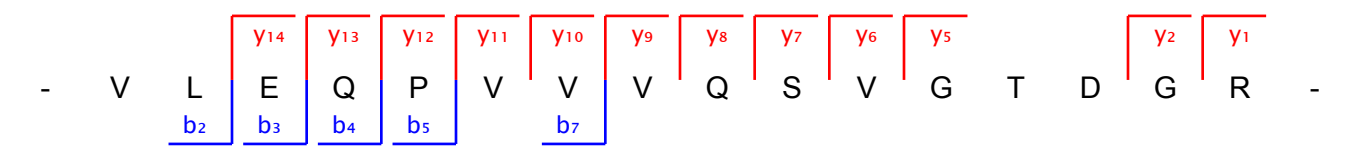
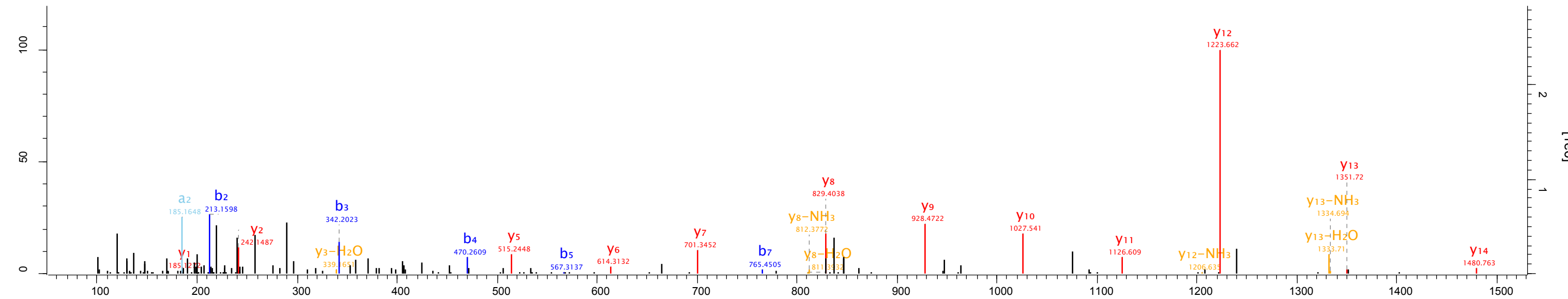
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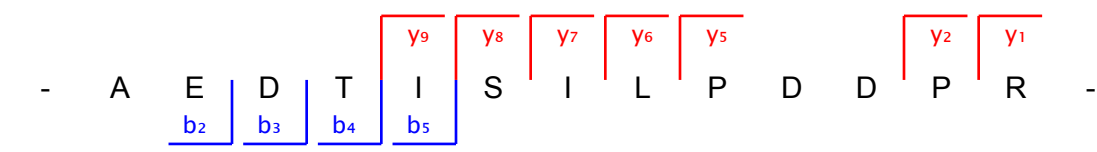
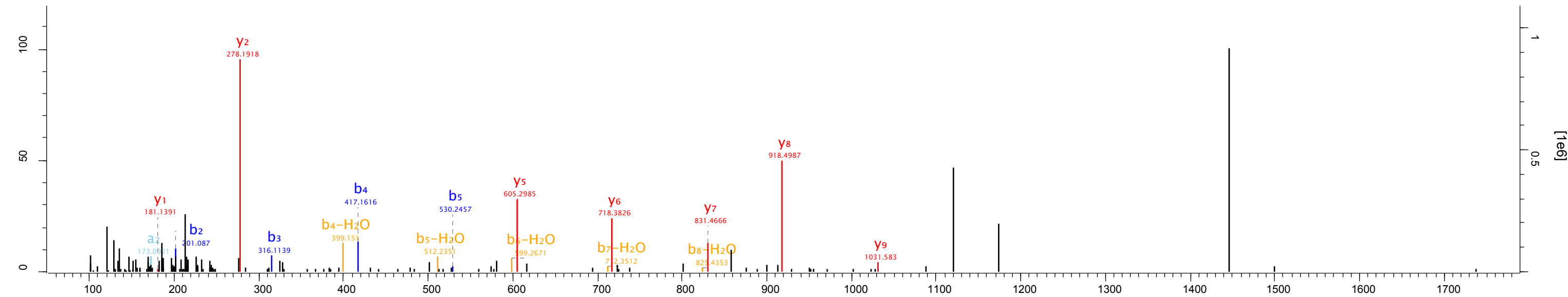
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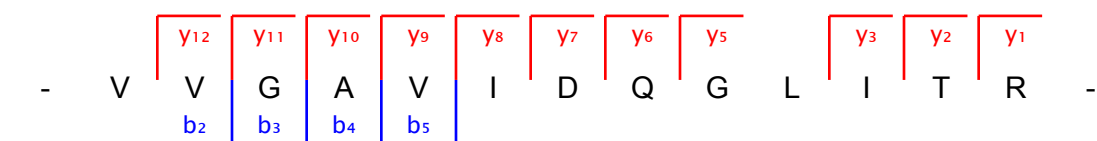
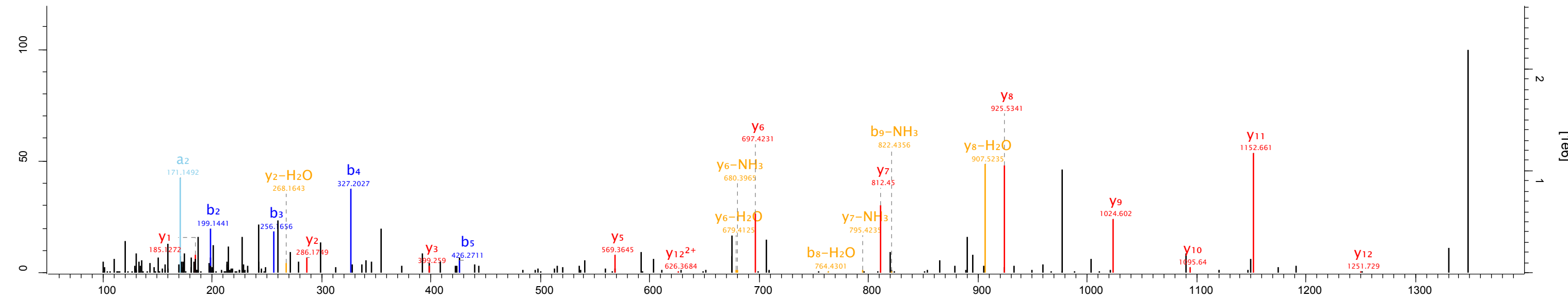
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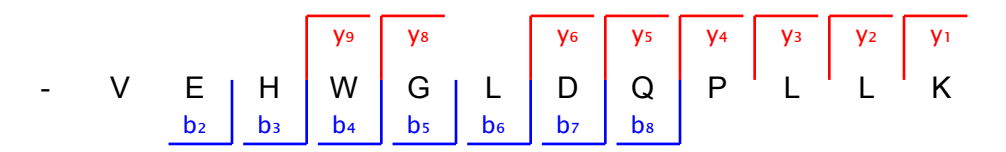
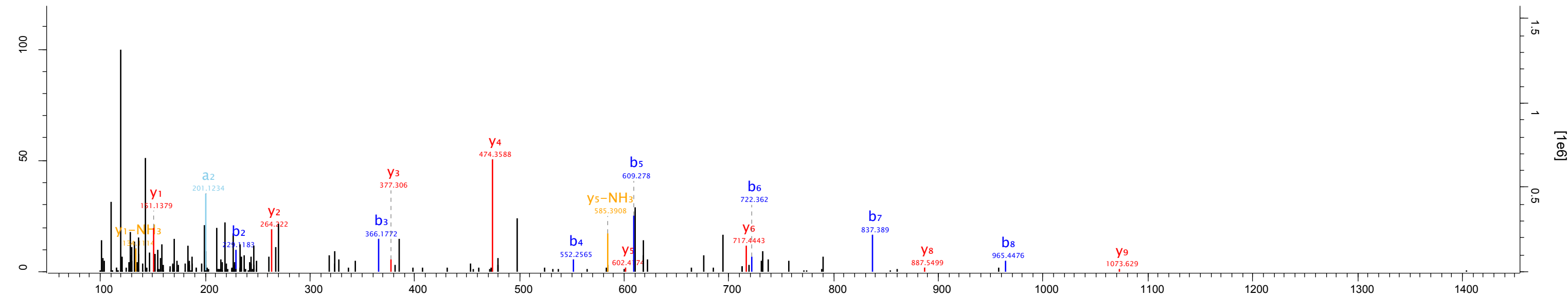
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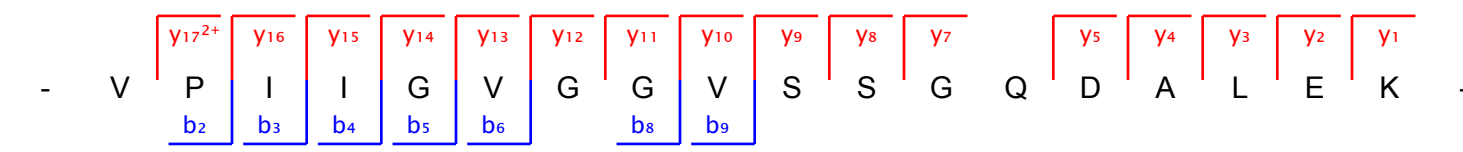
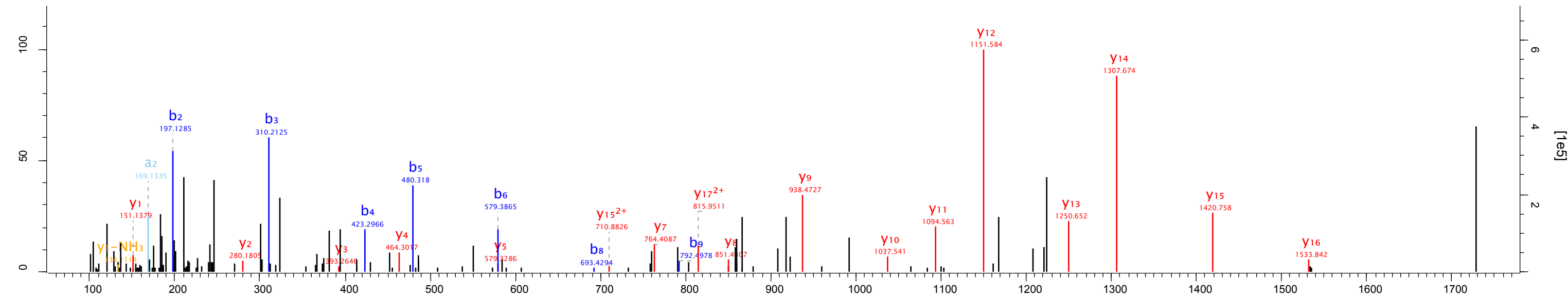
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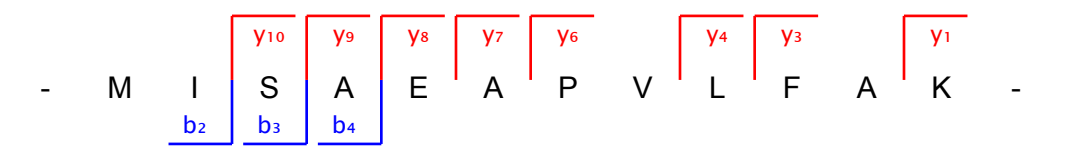
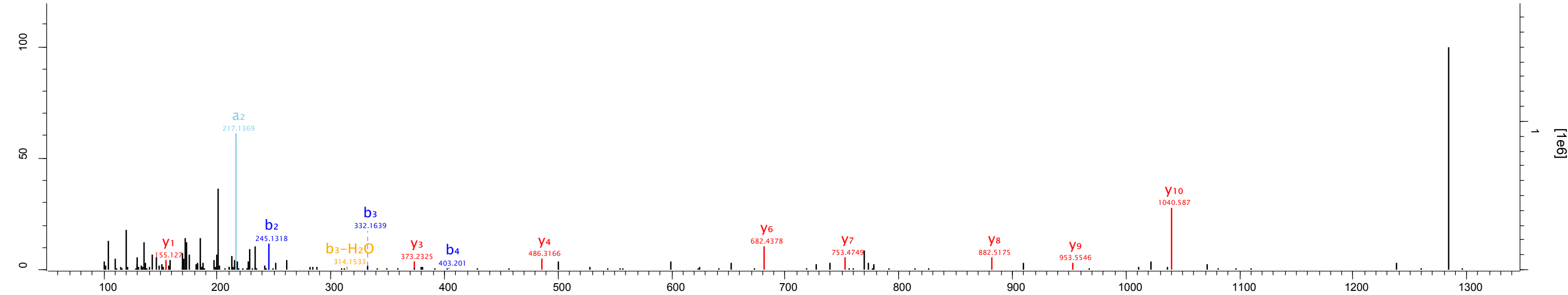
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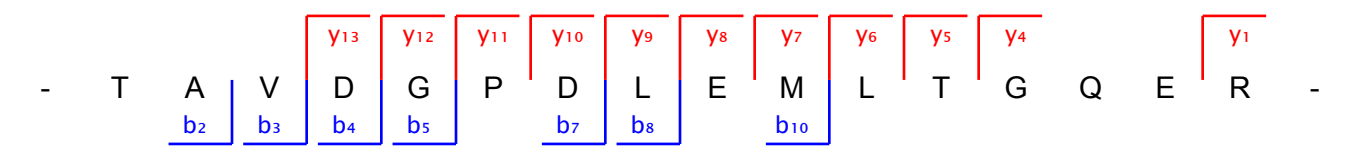
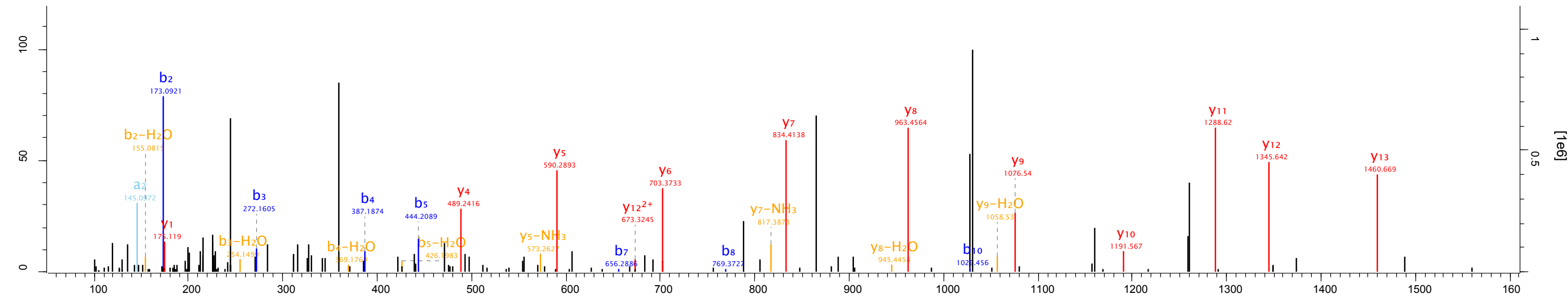
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20171215_MaS_33SR_LMH_proteome_02

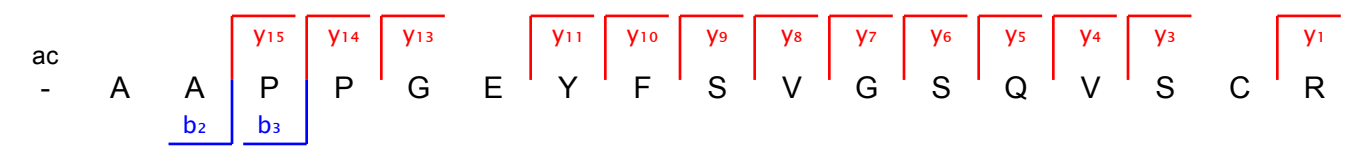
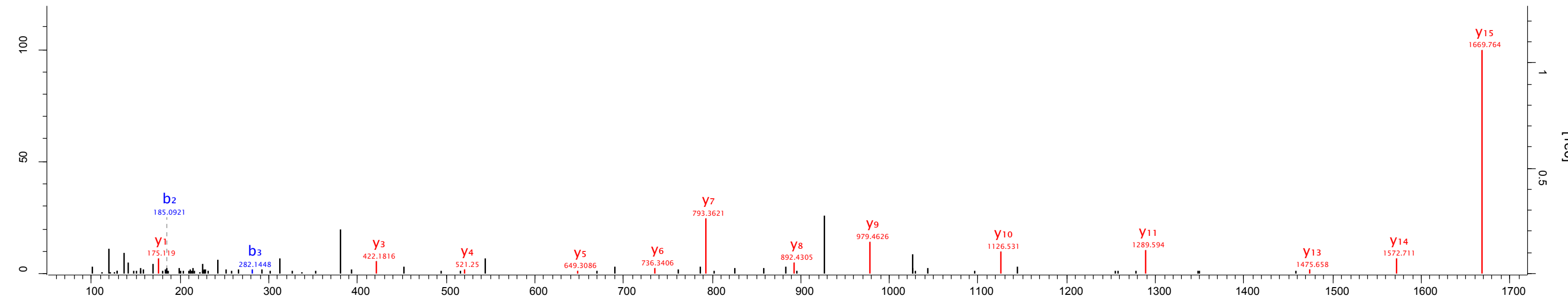
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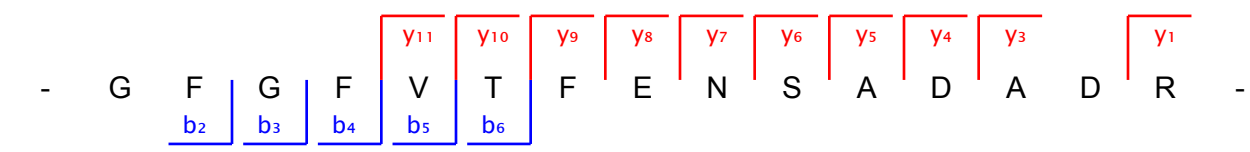
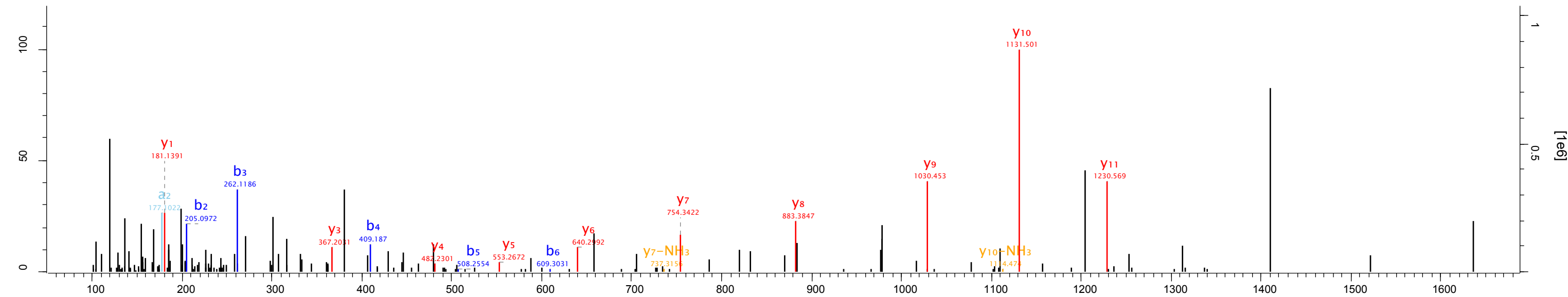
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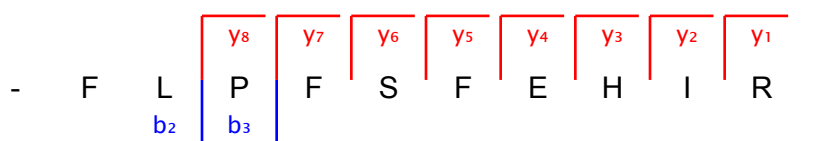
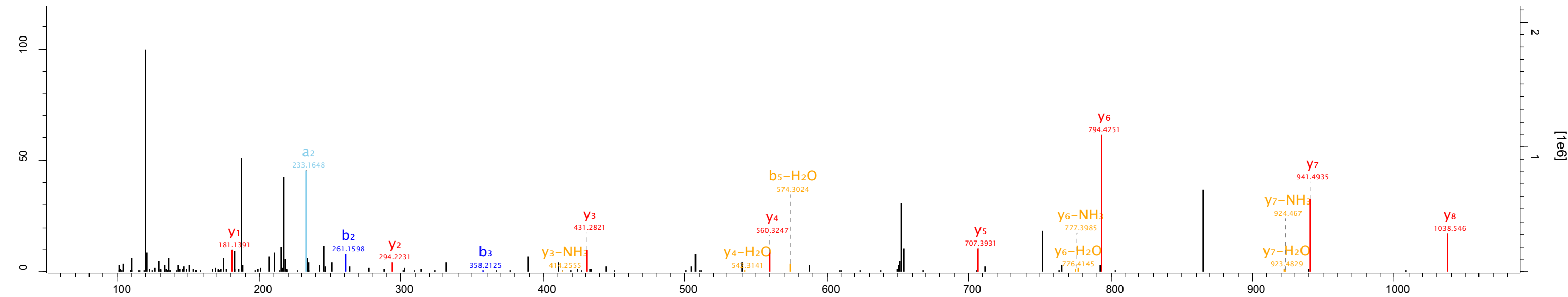
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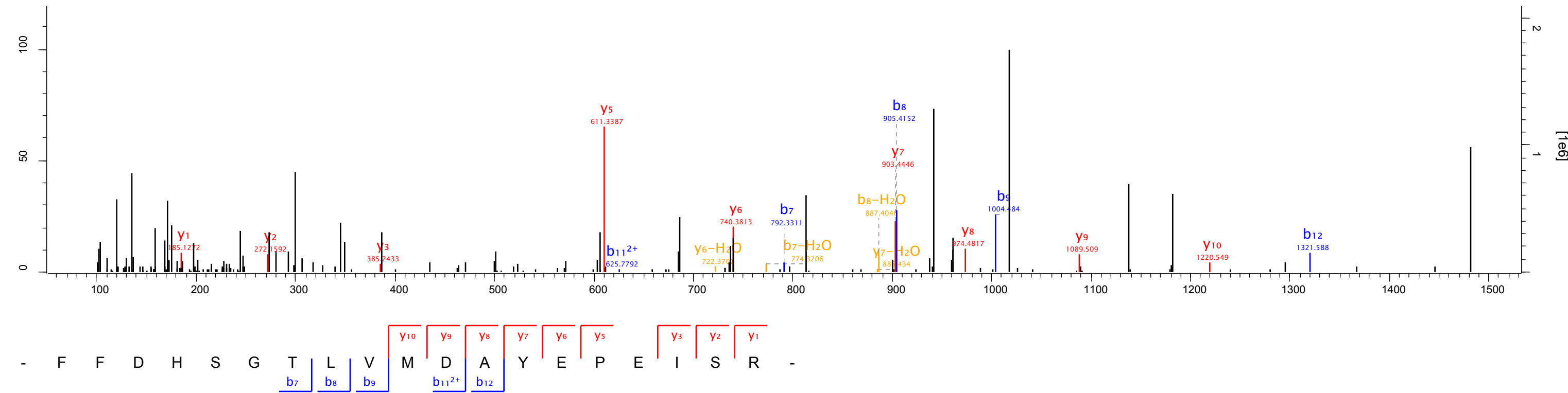


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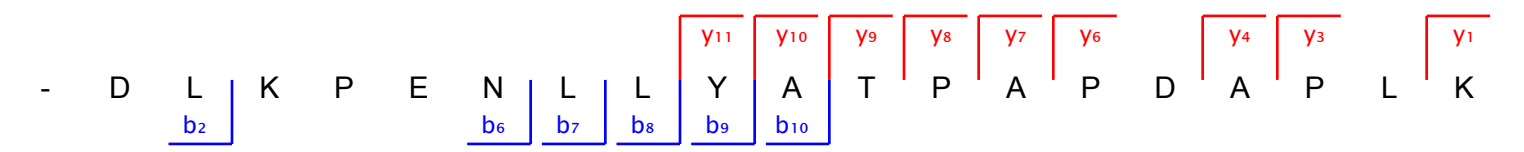
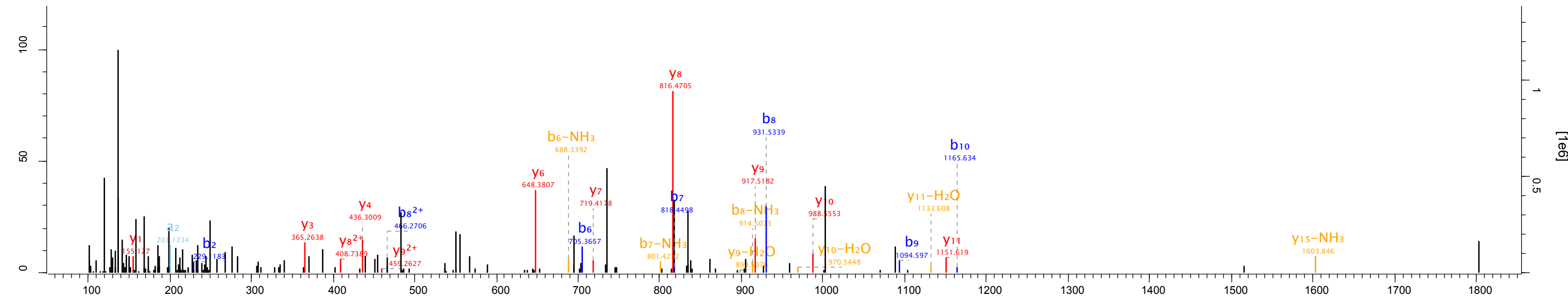
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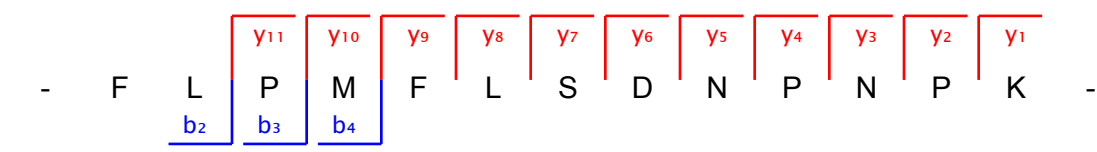
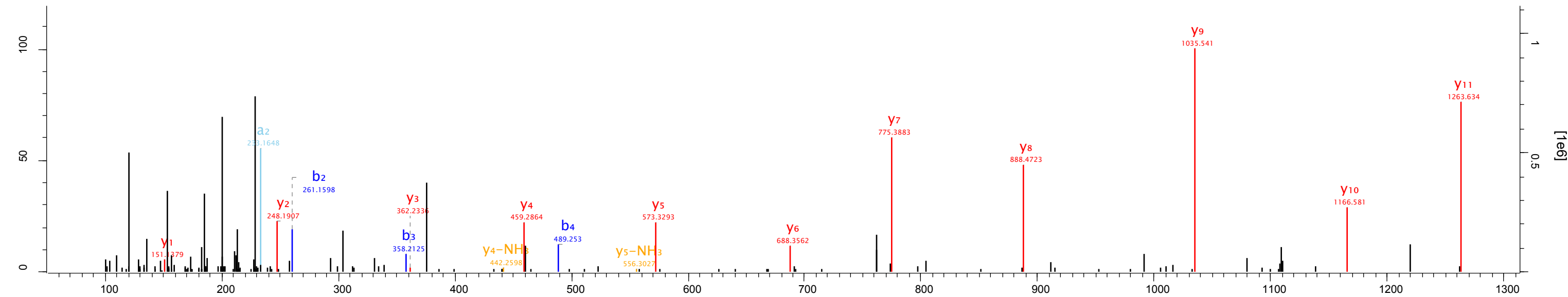


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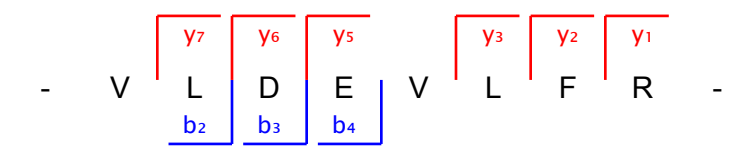
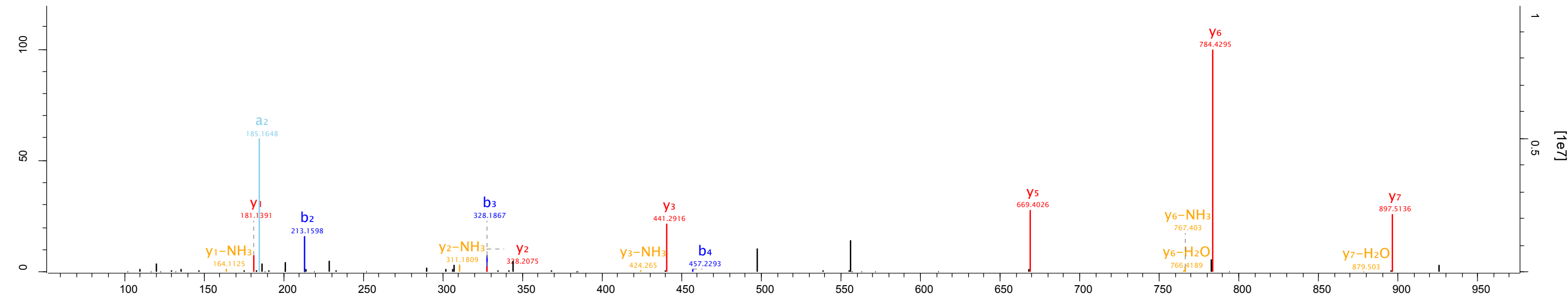
Scan Method Score m/z Gene names
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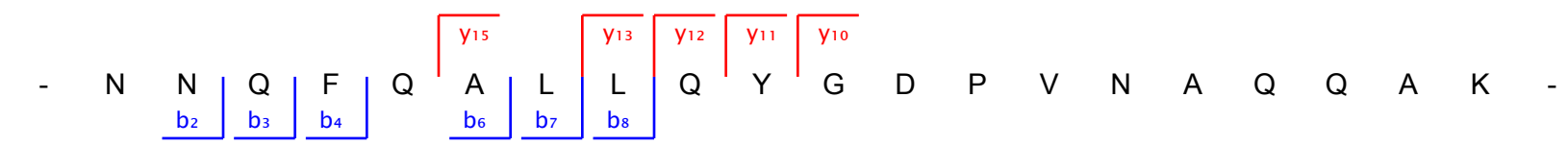
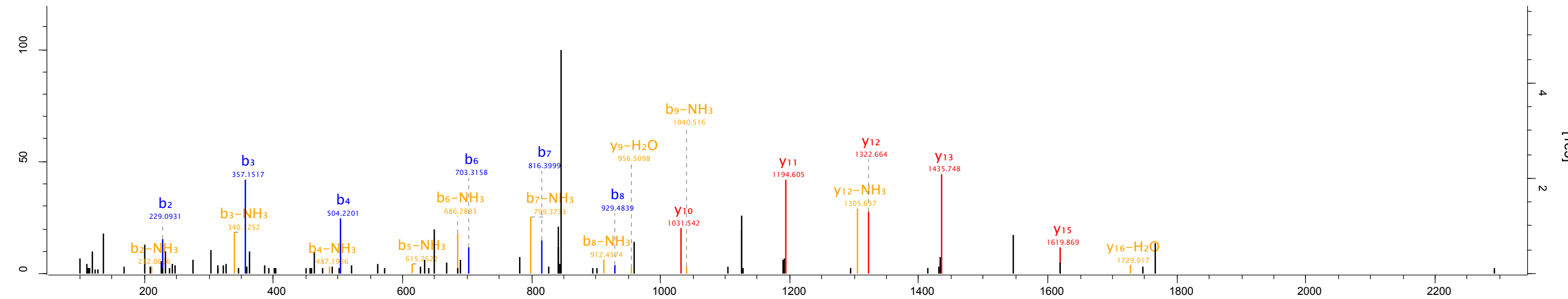
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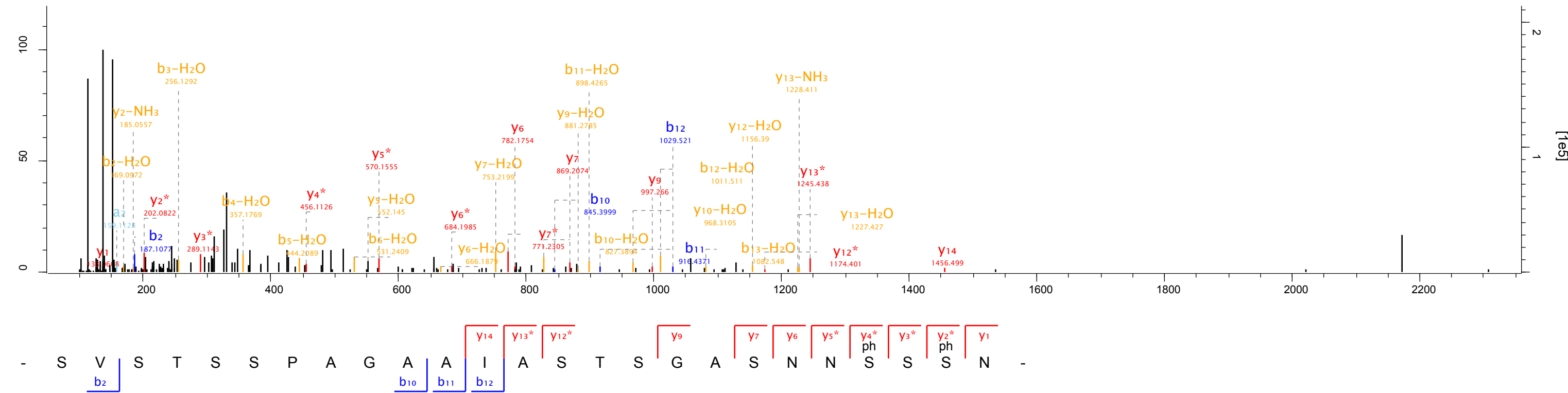
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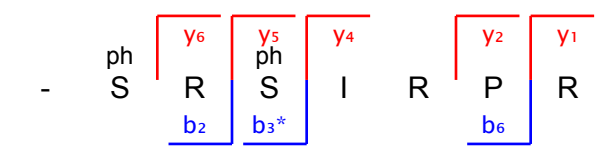
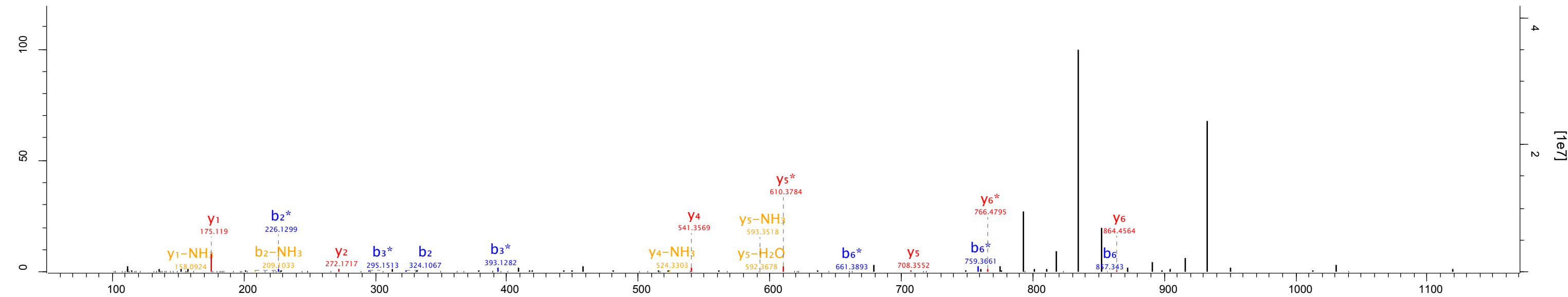
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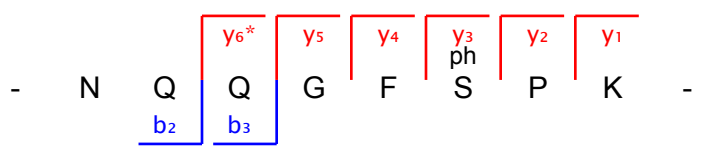
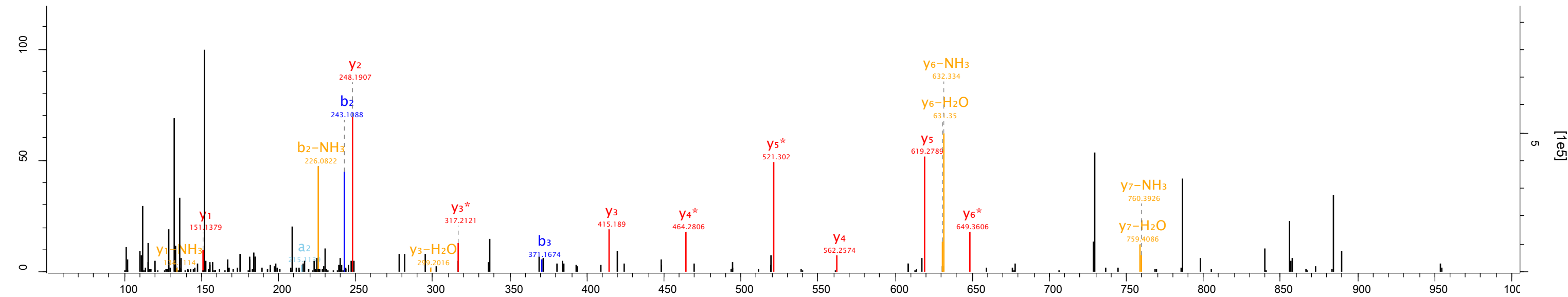
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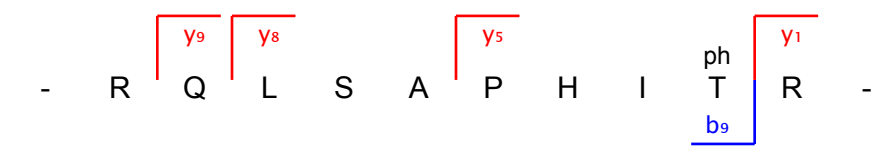
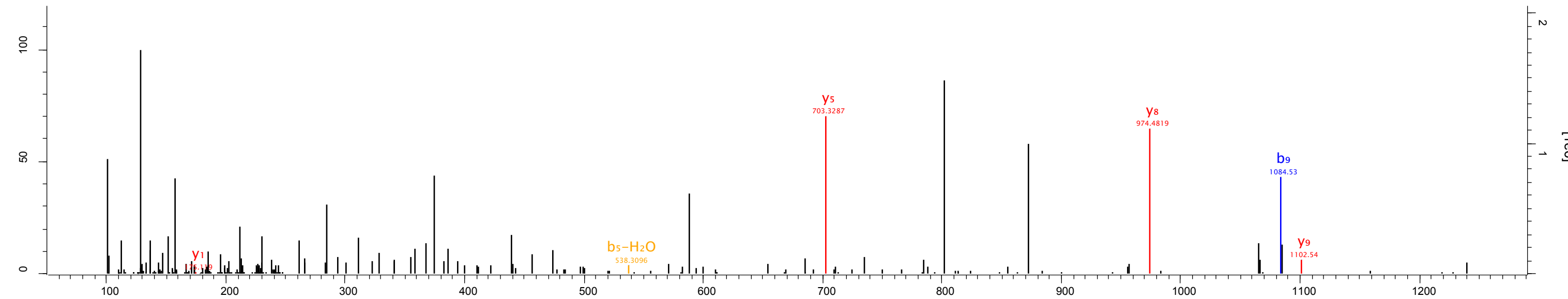
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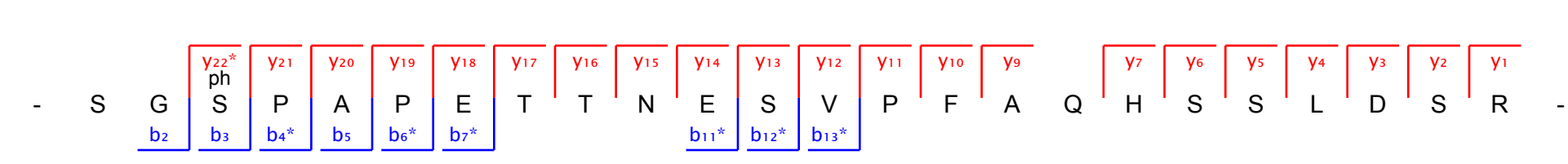
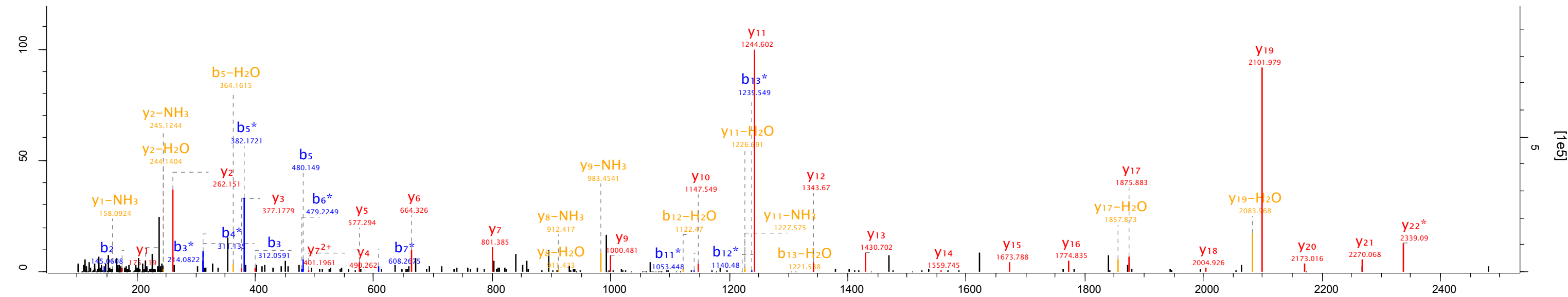
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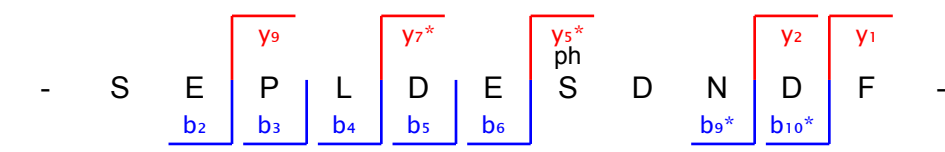
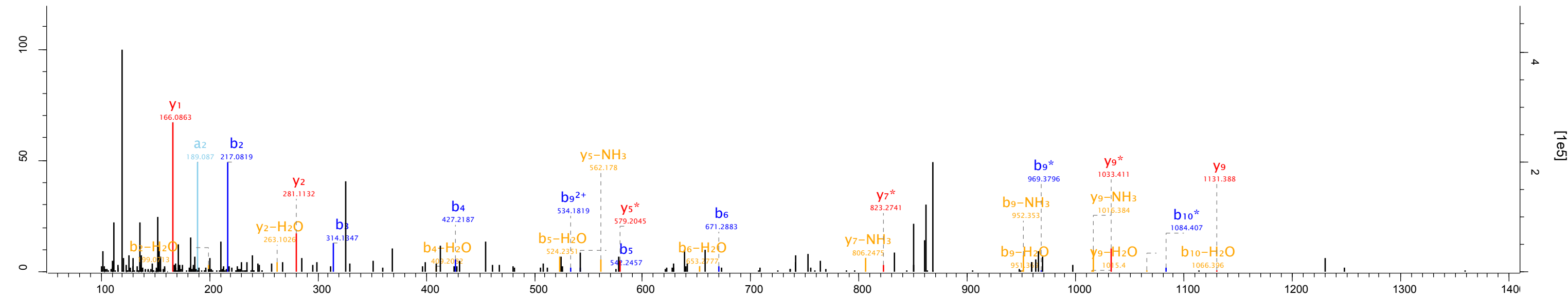
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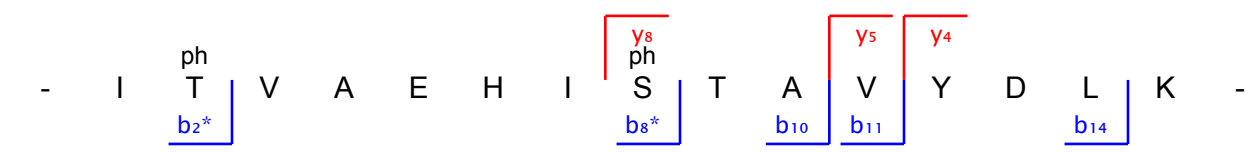
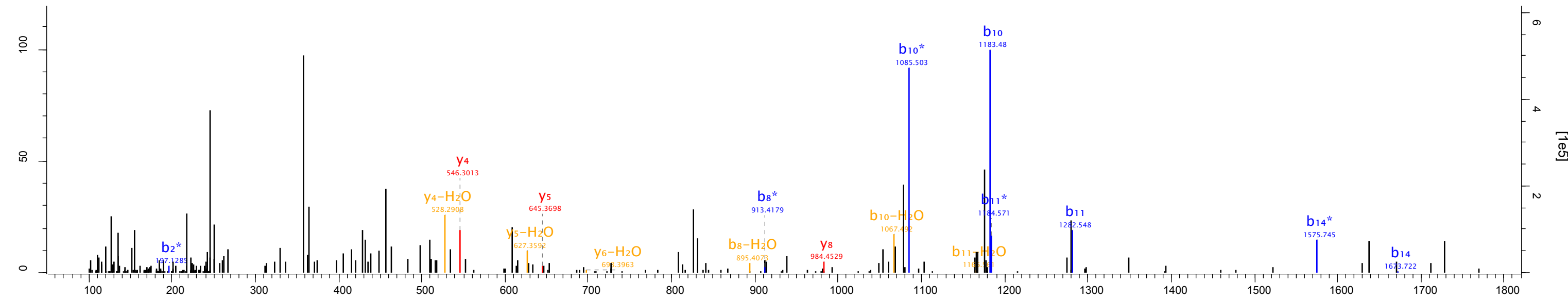
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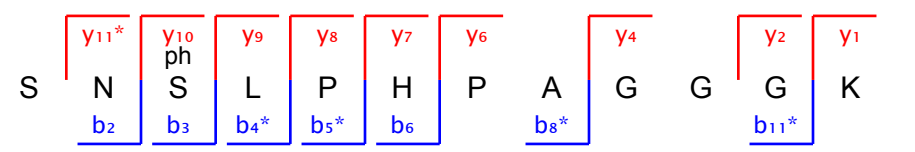
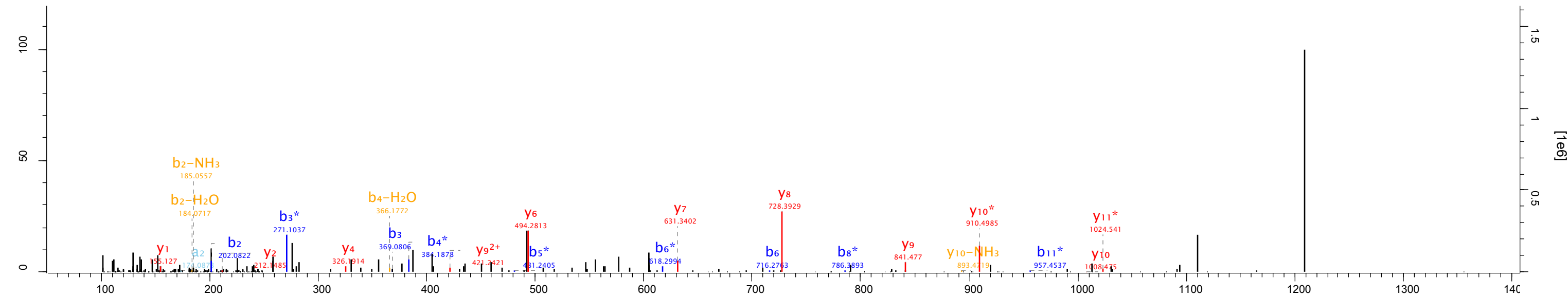
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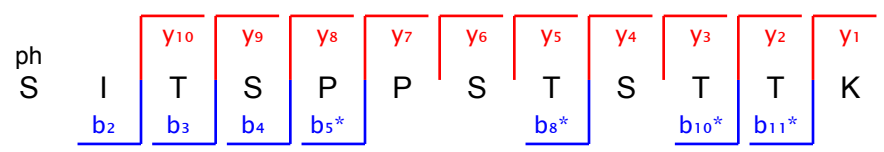
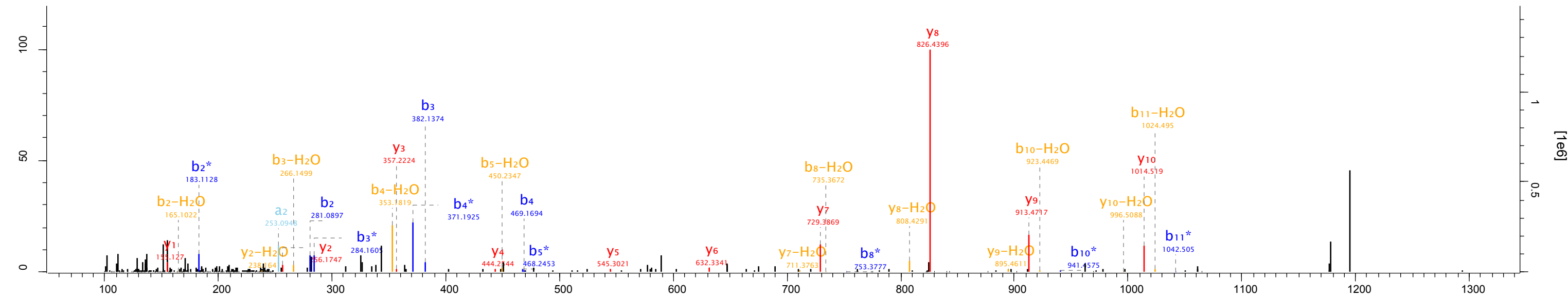
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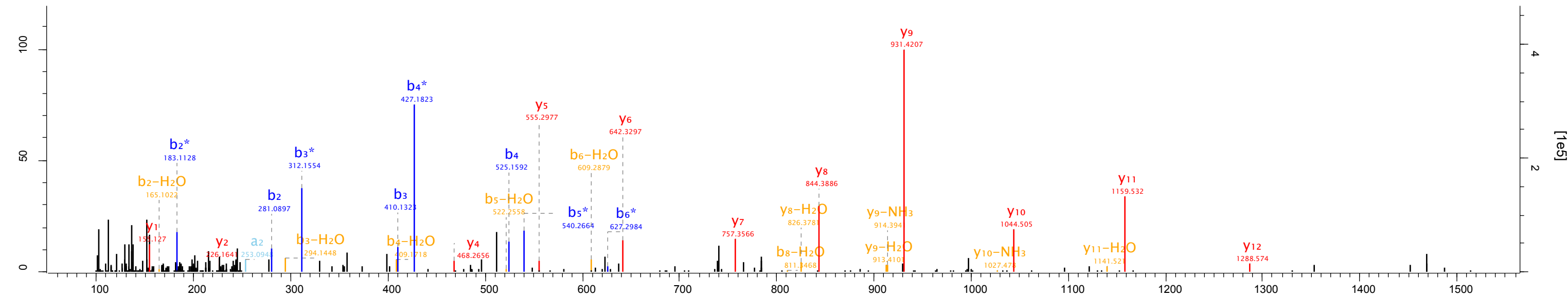
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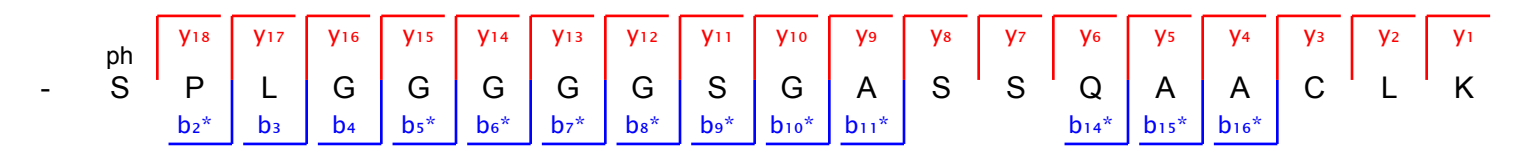
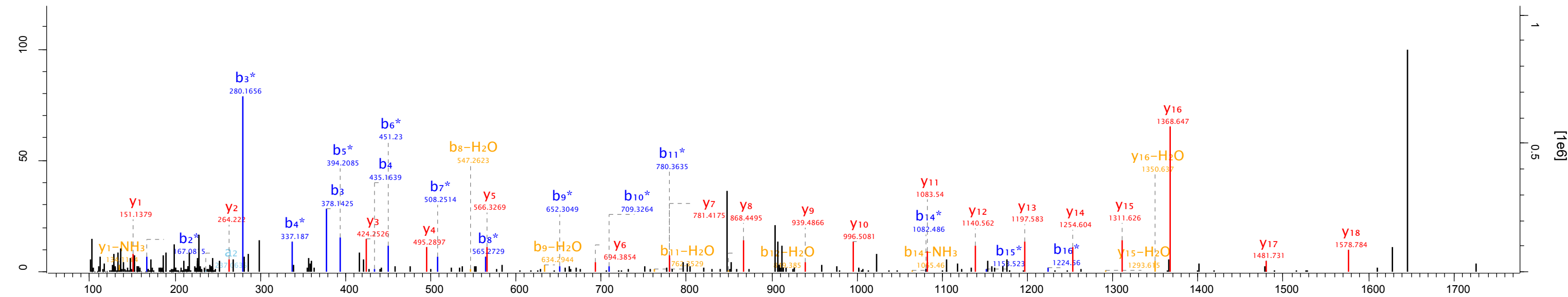
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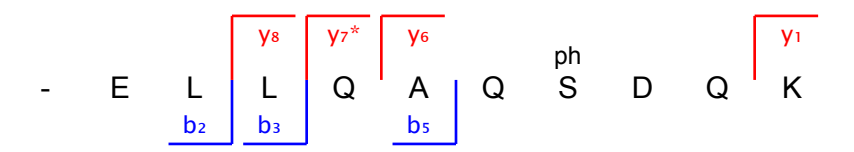
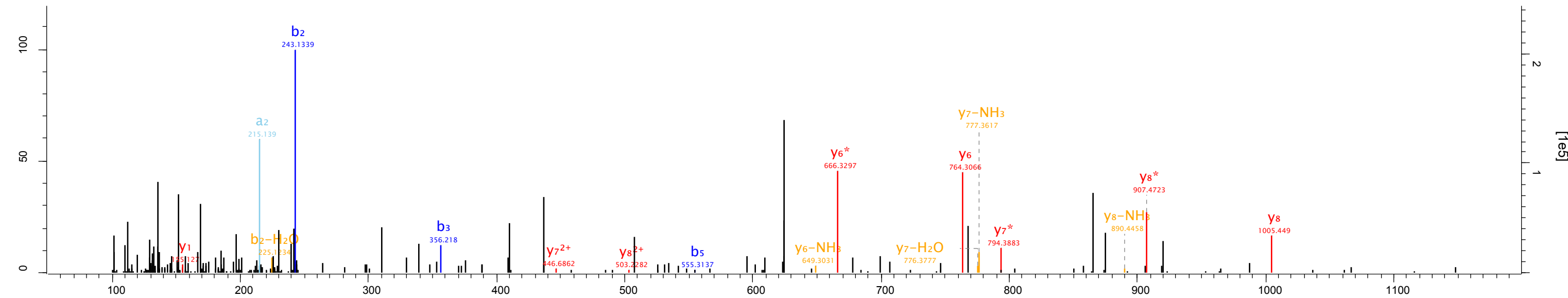
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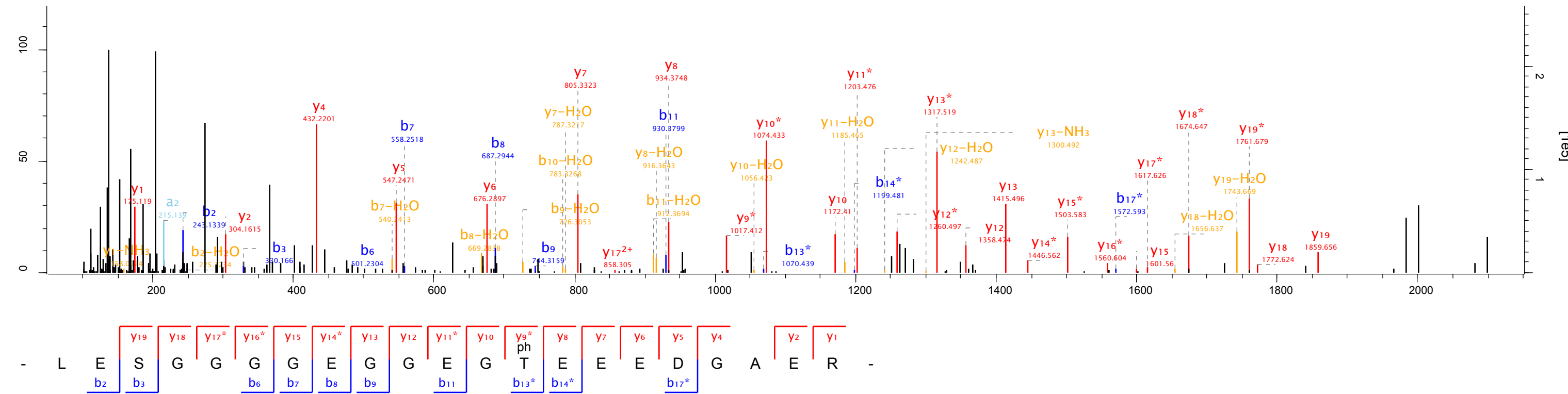


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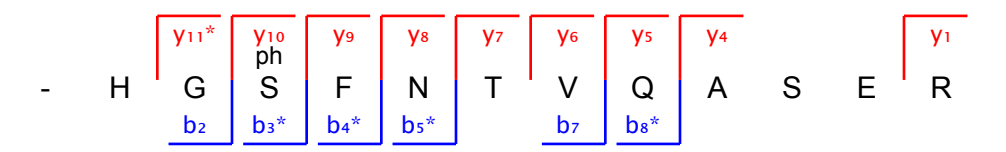
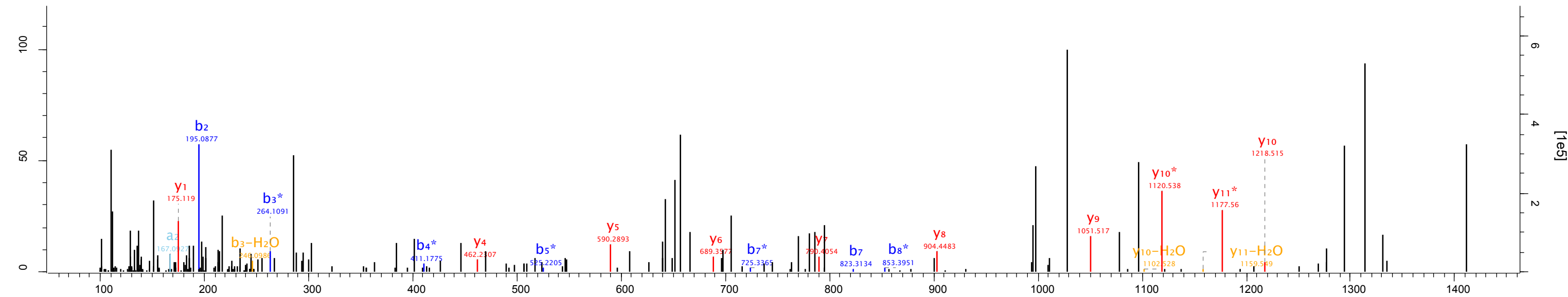


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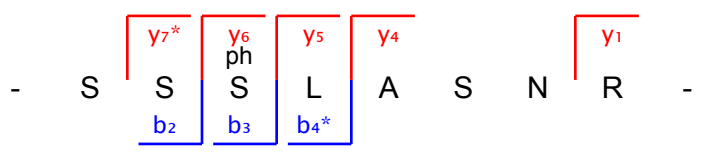
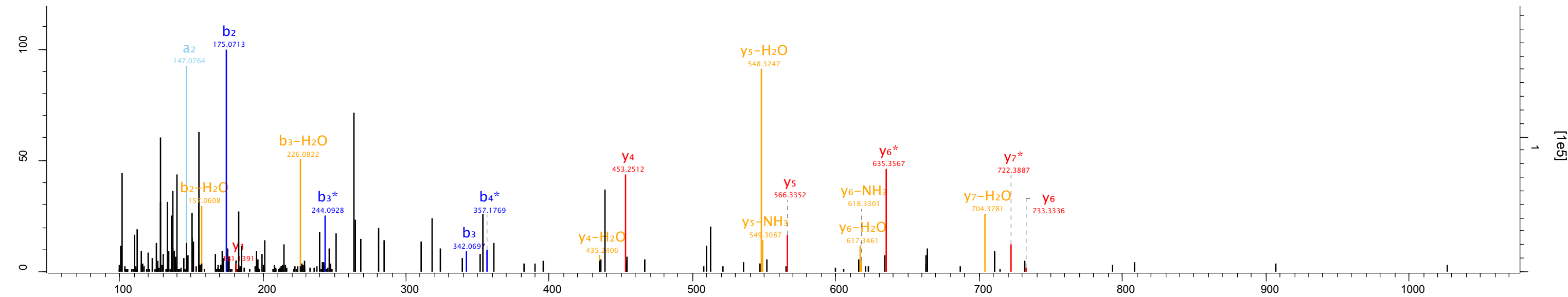




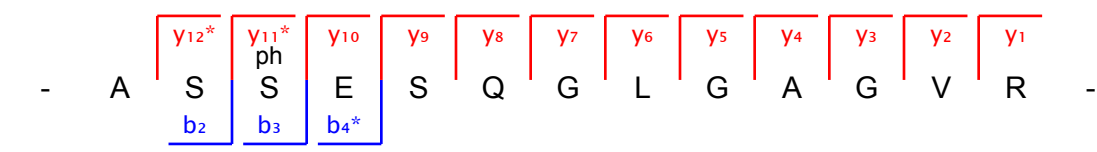
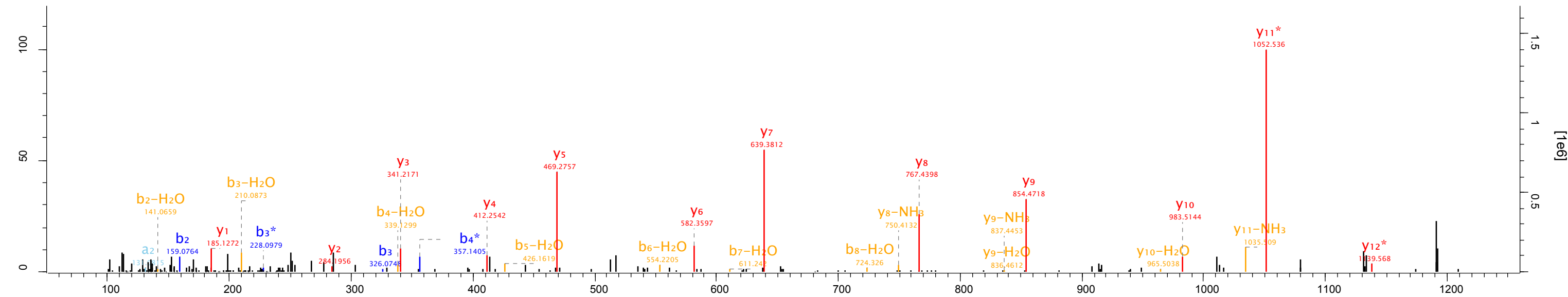
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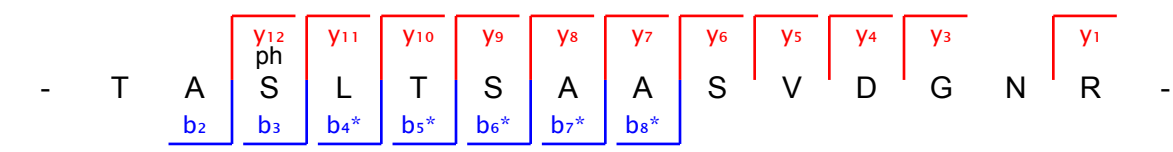
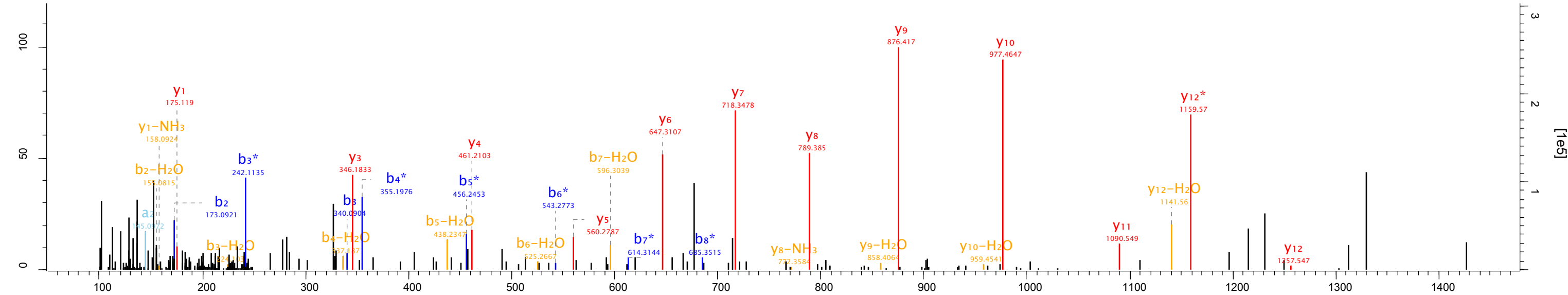
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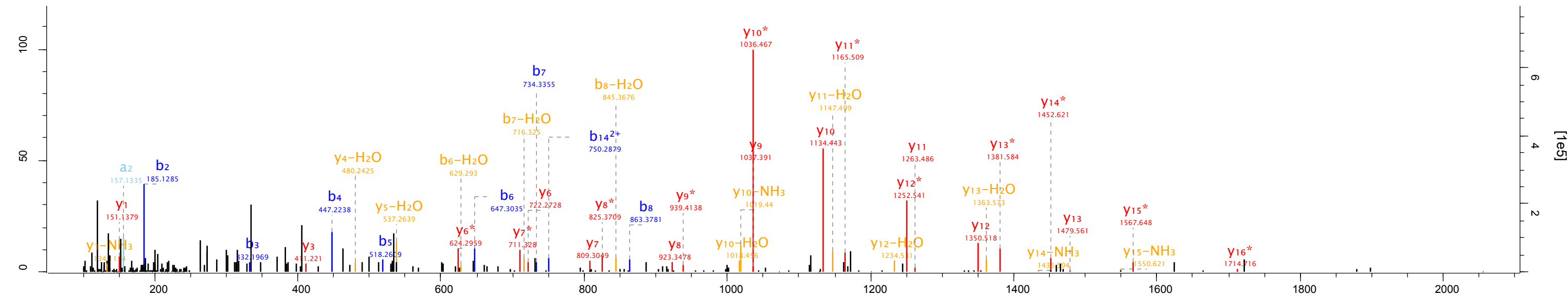
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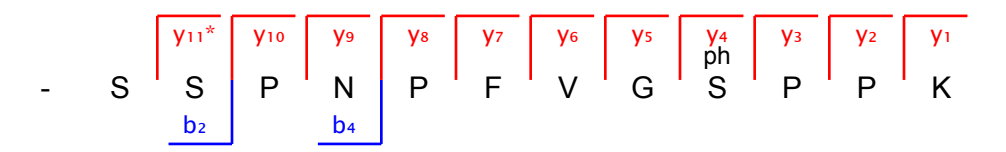
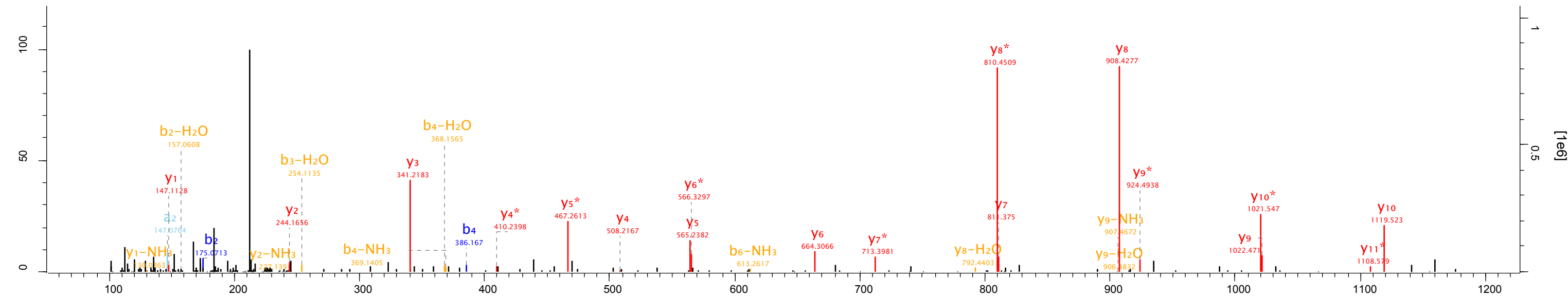
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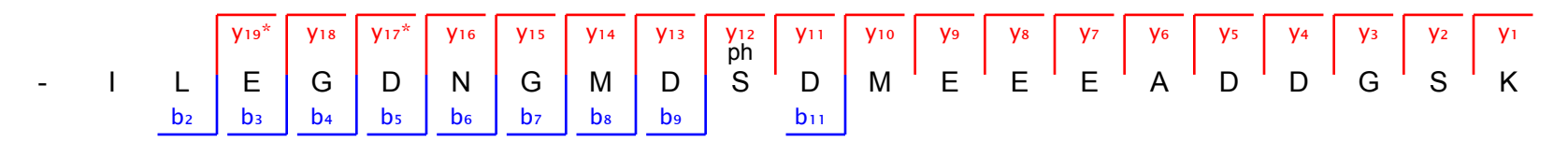
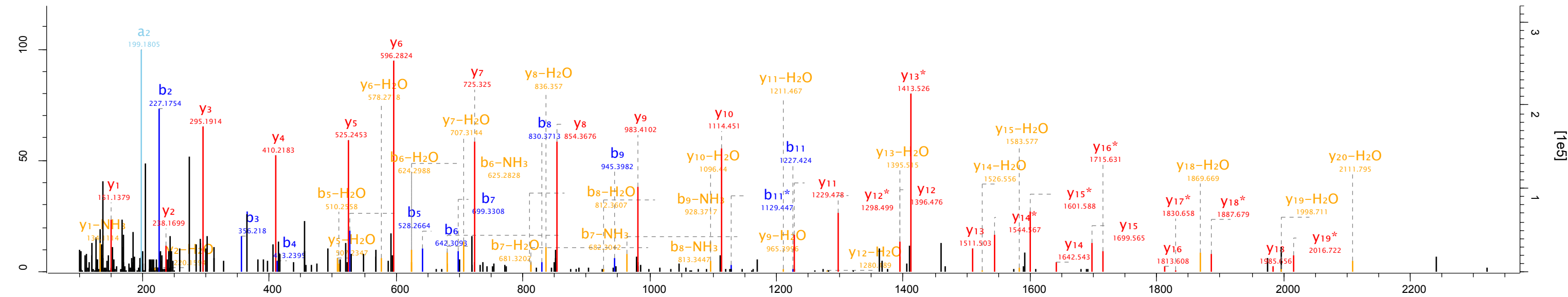
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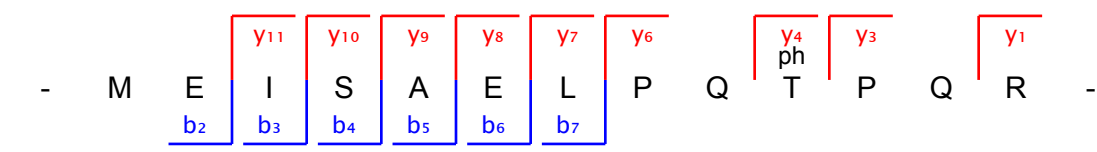
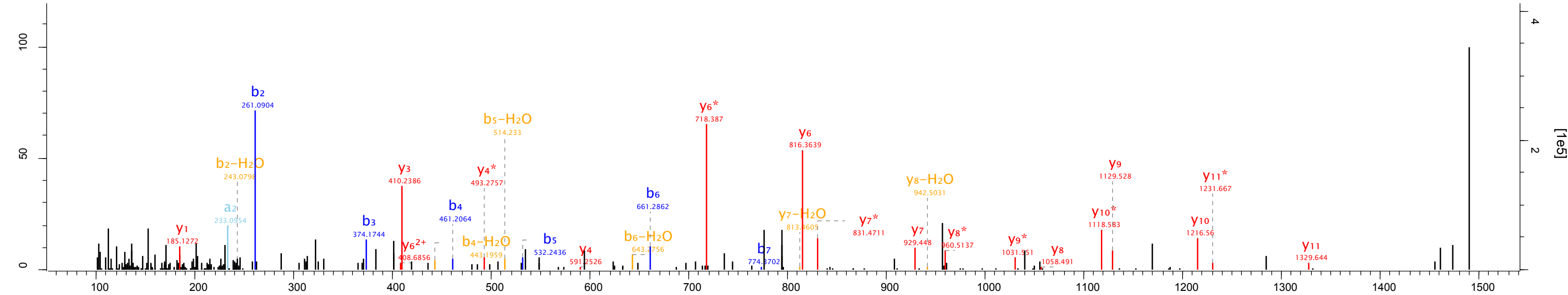
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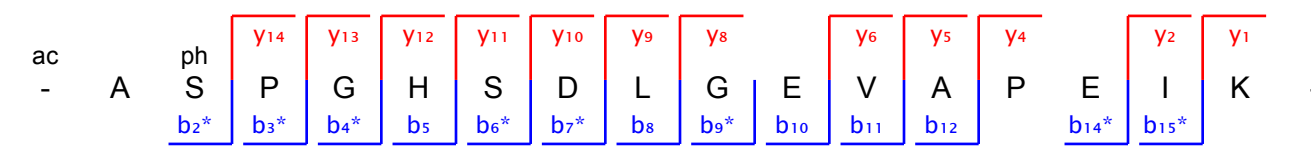
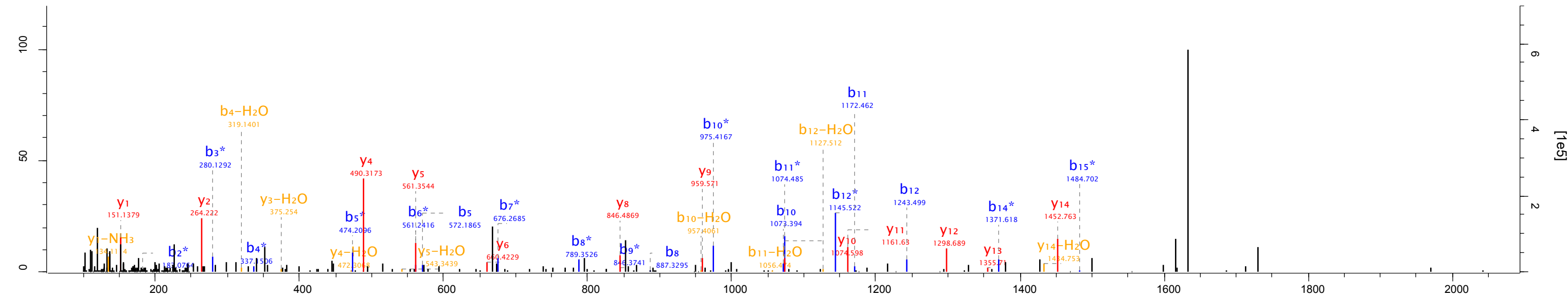
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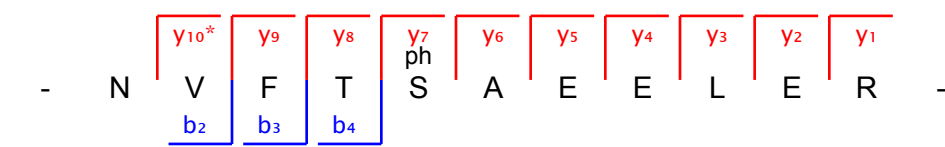
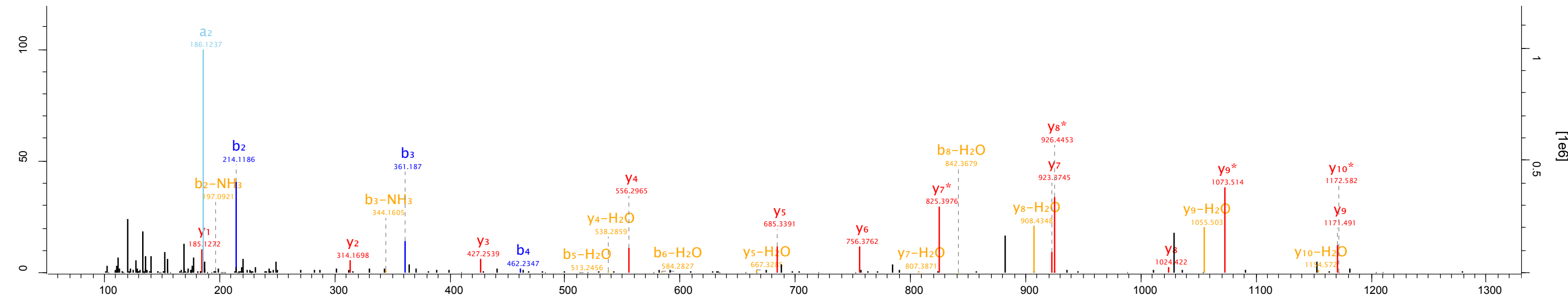


20171215_MaS_33SR_LMH_phospho_06 12559 FTMS; HCD 107.62 795.37 UBR1

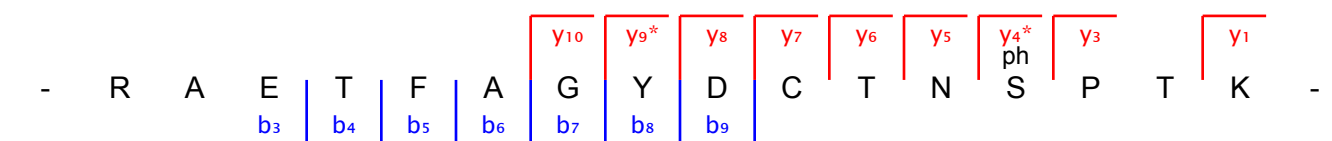
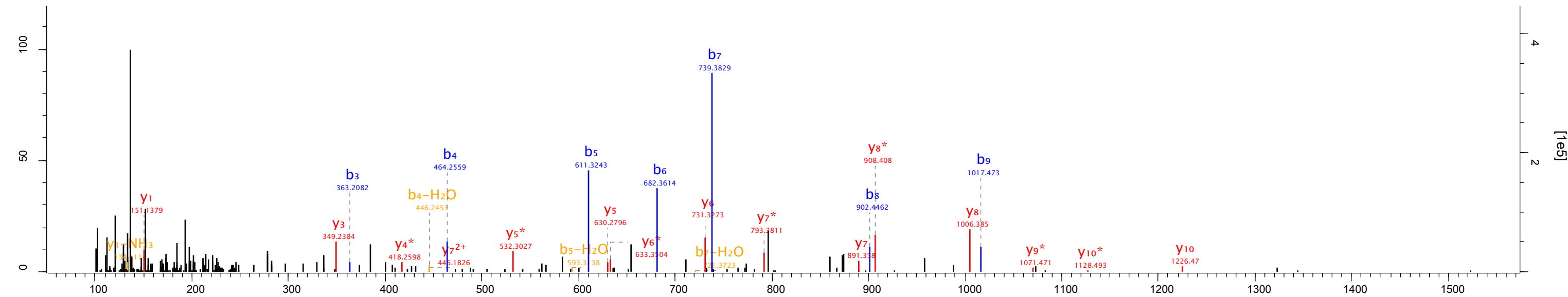


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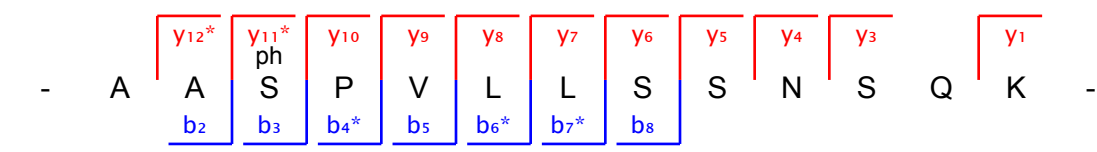
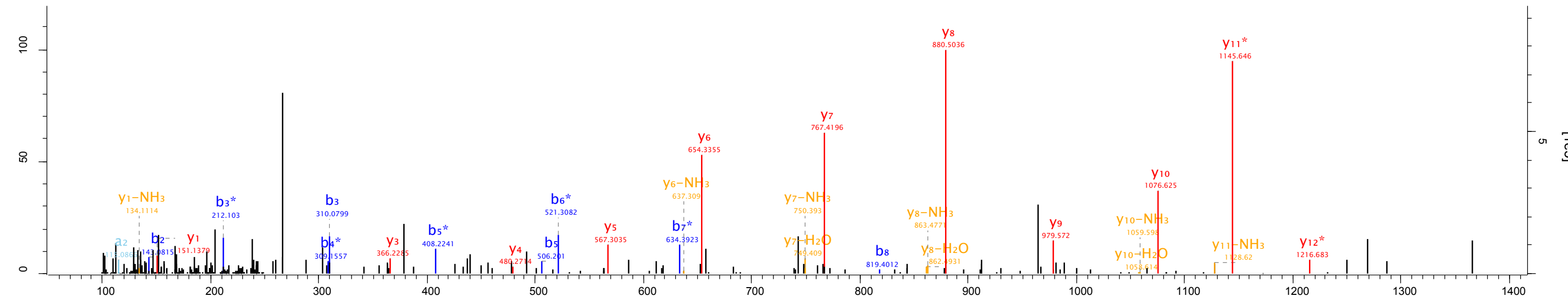


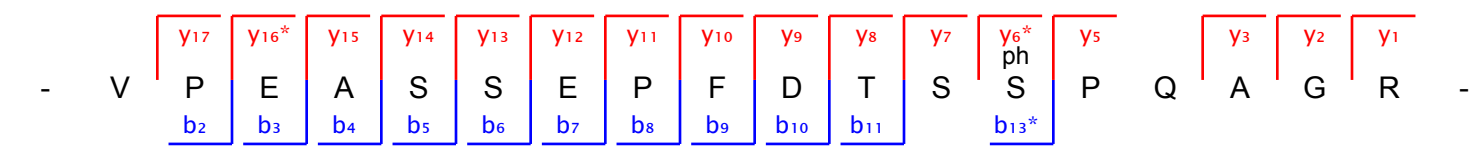
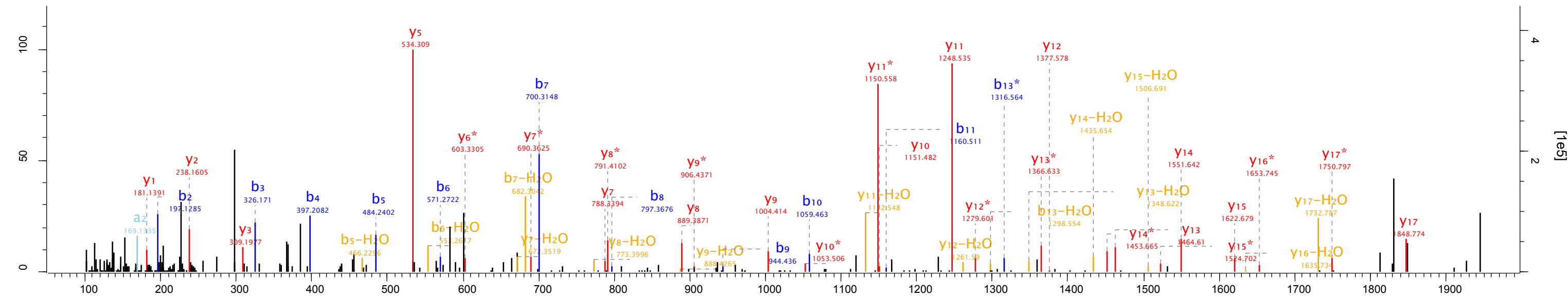


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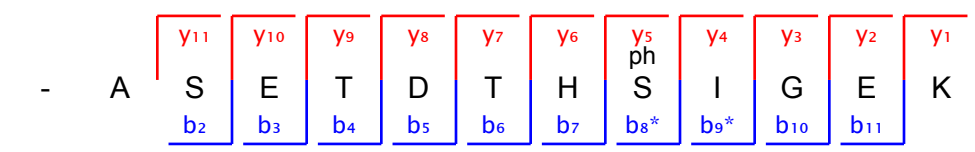
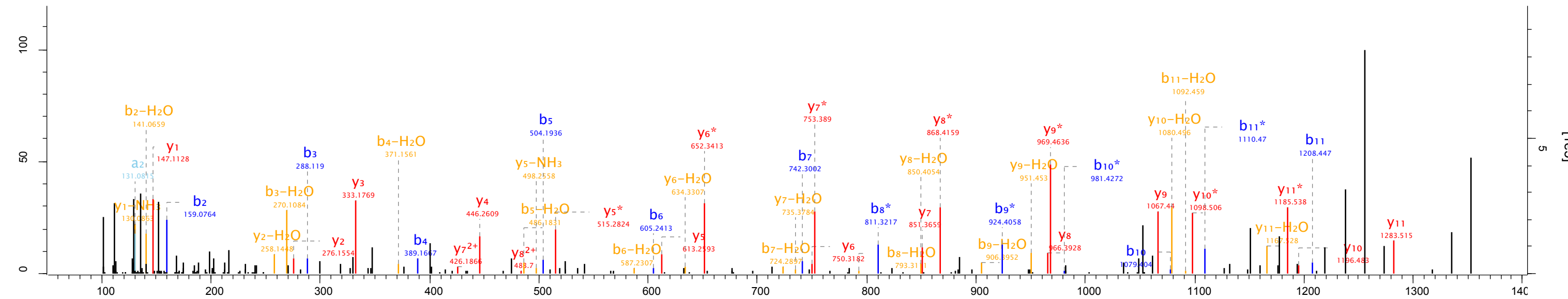
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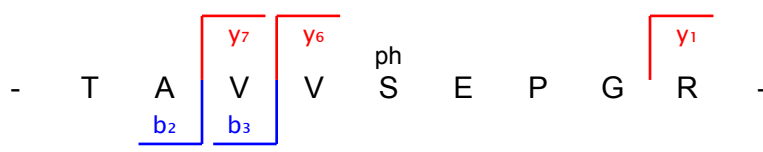
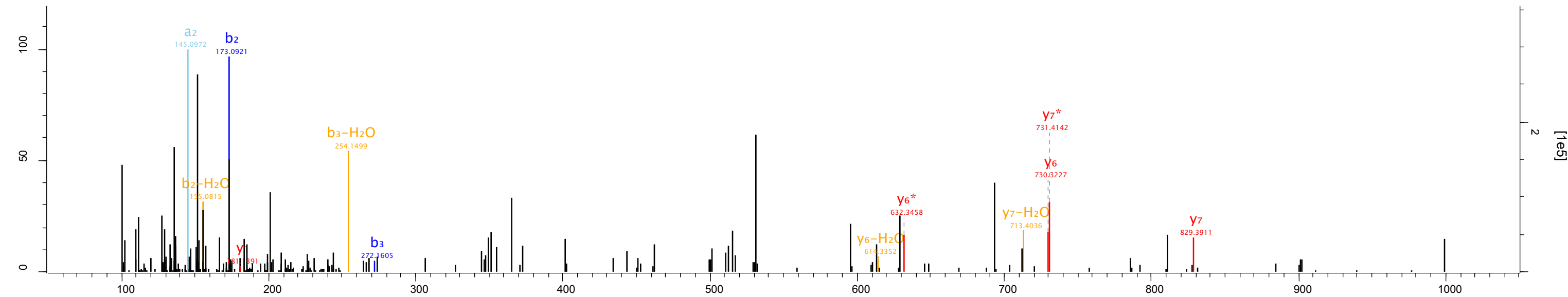


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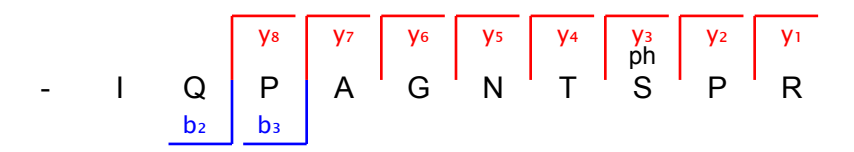
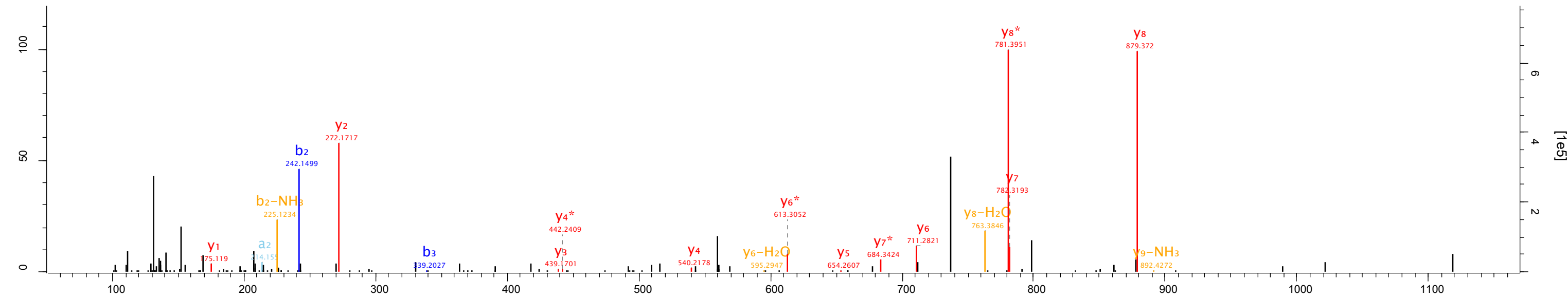
Scan 2339 Method FTMS; HCD Score 253.82 m/z 677.78 Gene names BNIP3



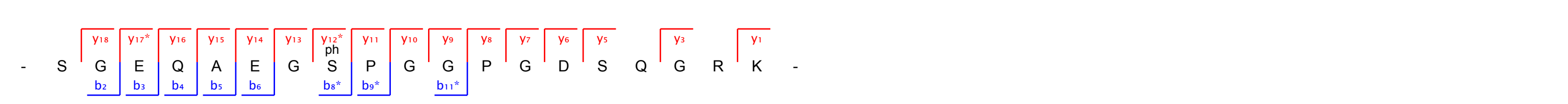
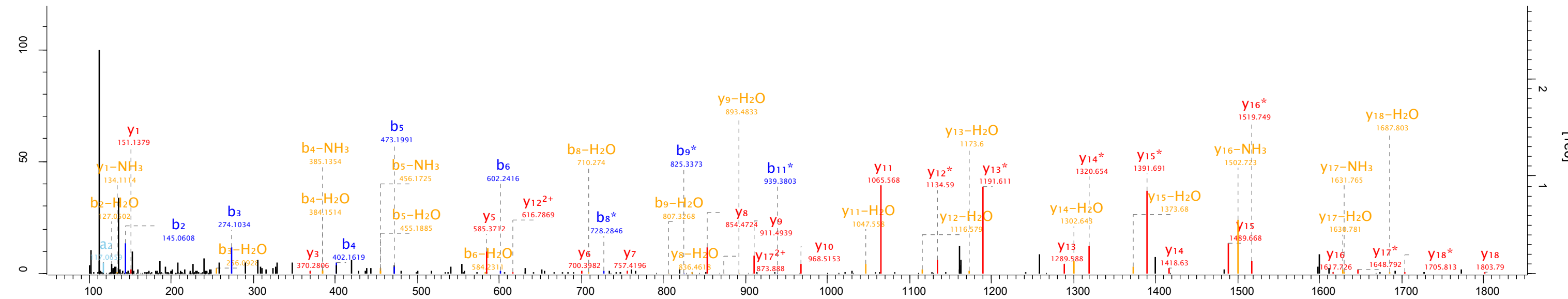
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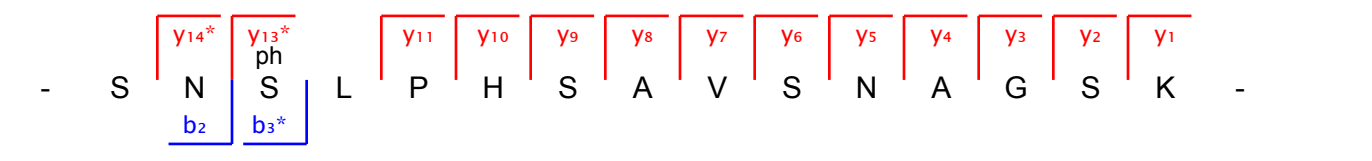
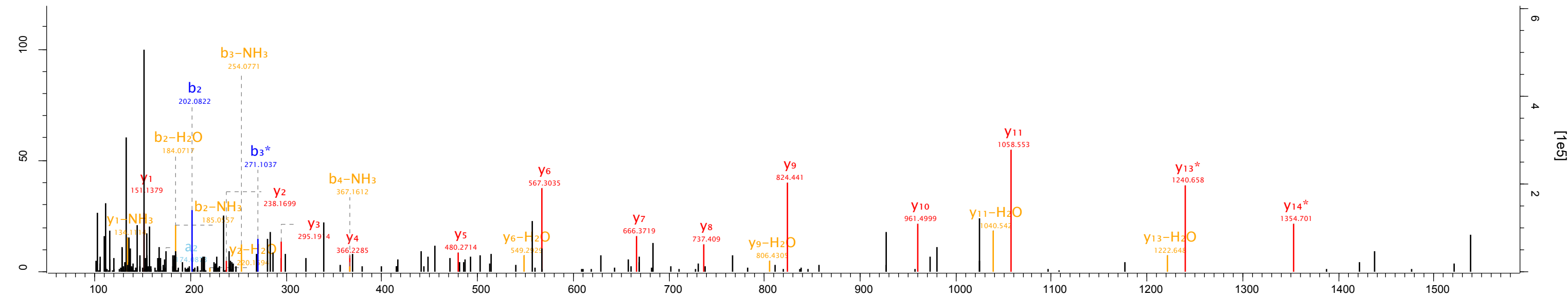
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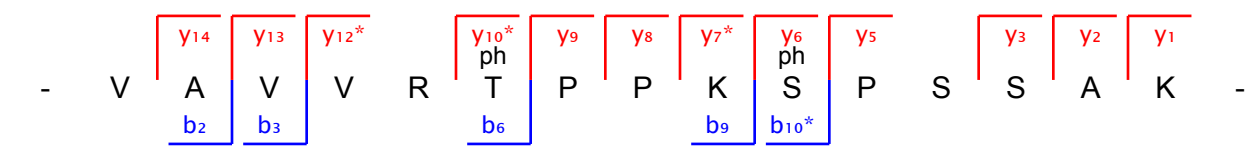
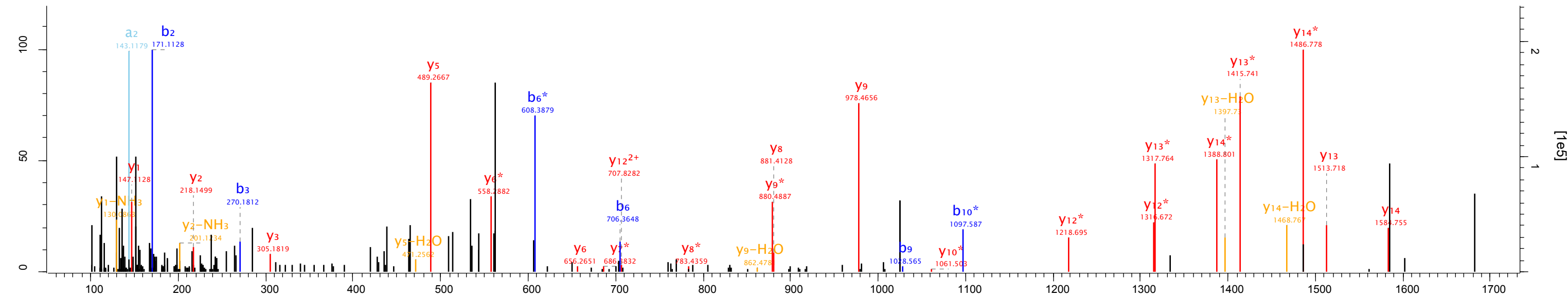
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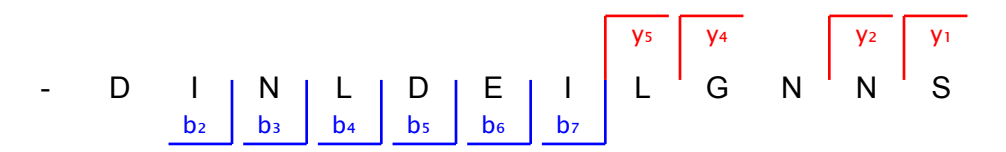
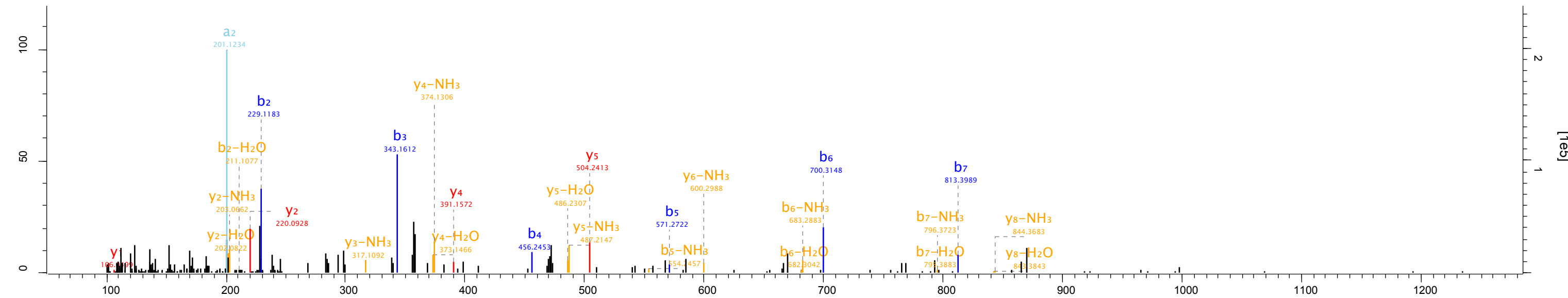
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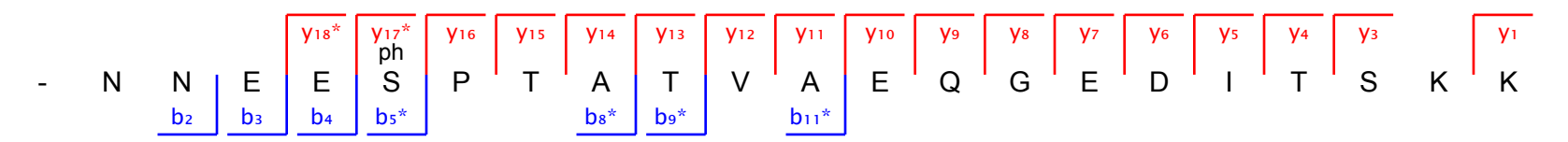
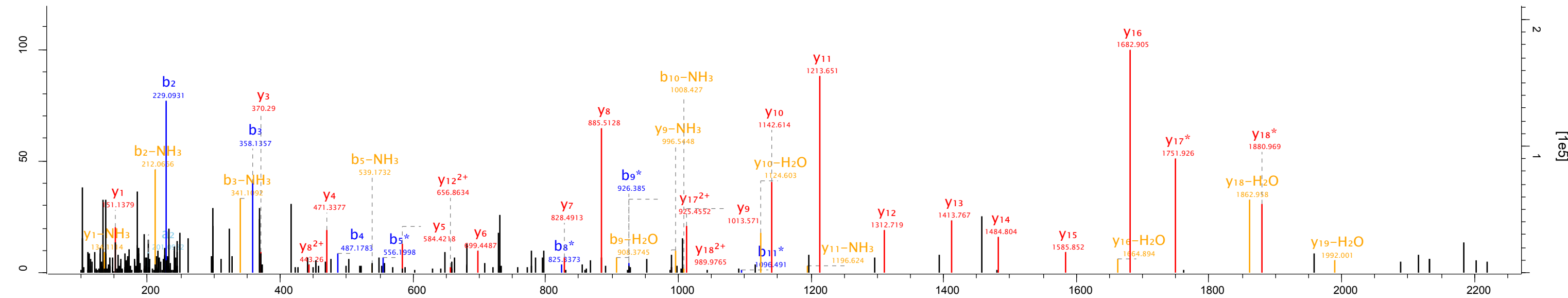


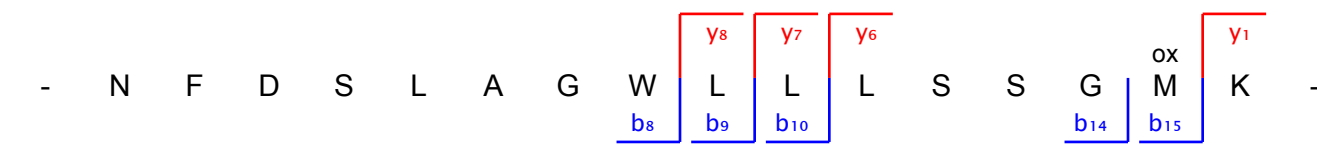
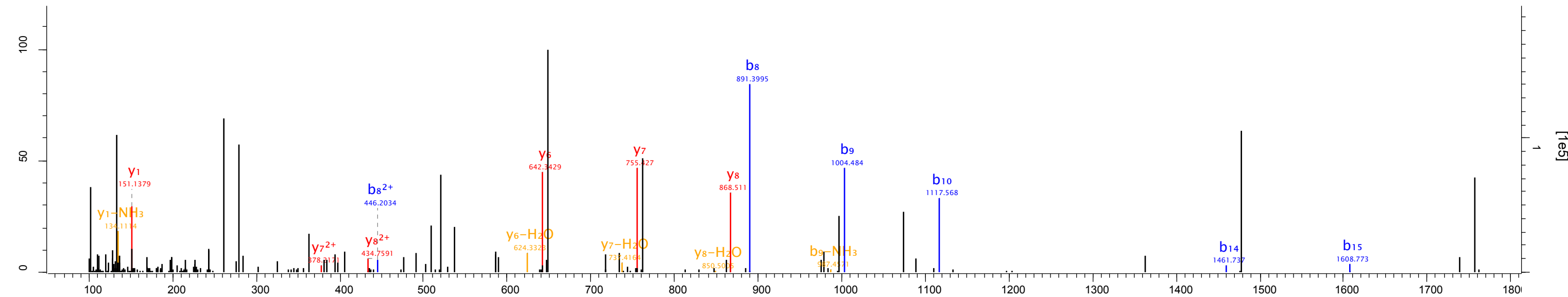
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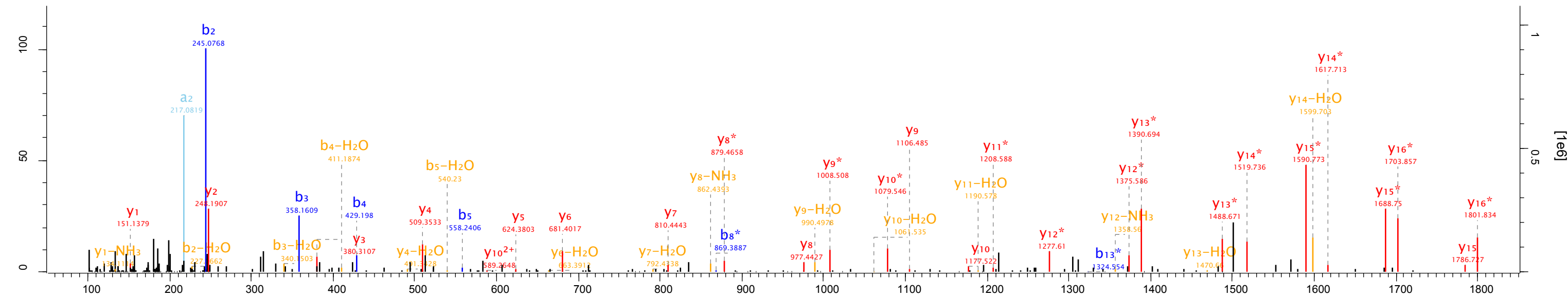
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20171215_MaS_33SR_LMH_phospho2_02

Scan 9319 Method FTMS; HCD Score 112.34 m/z 779.7 Gene names FKBP5

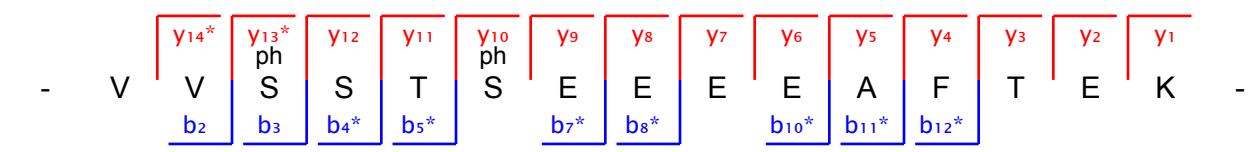
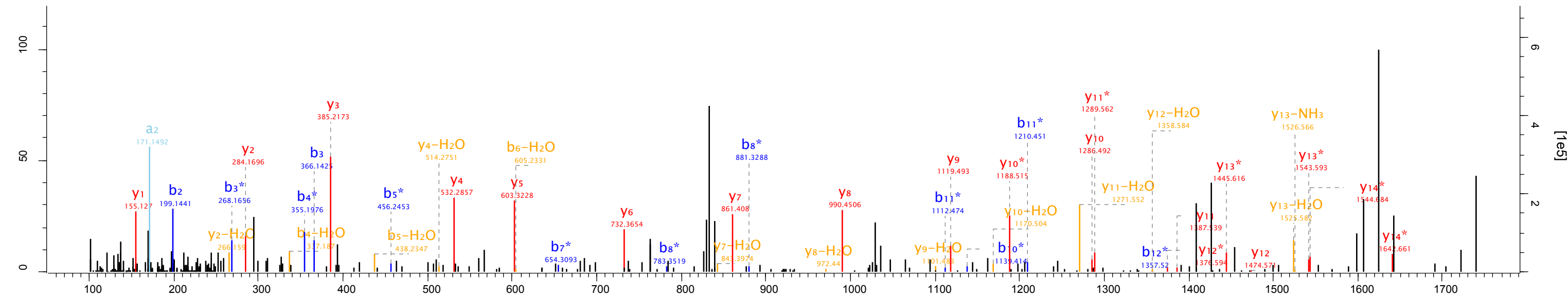




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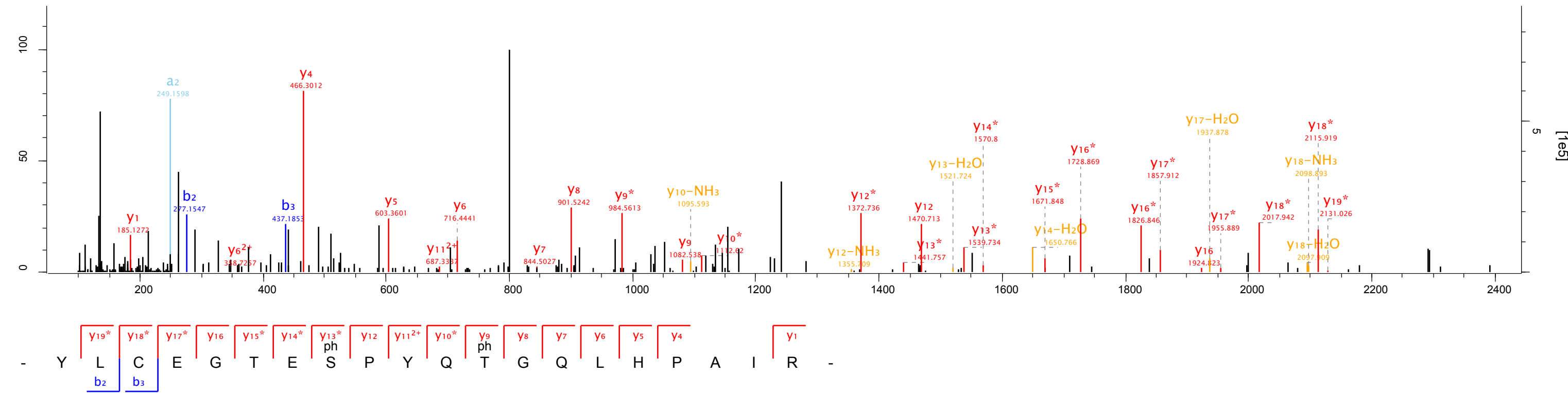
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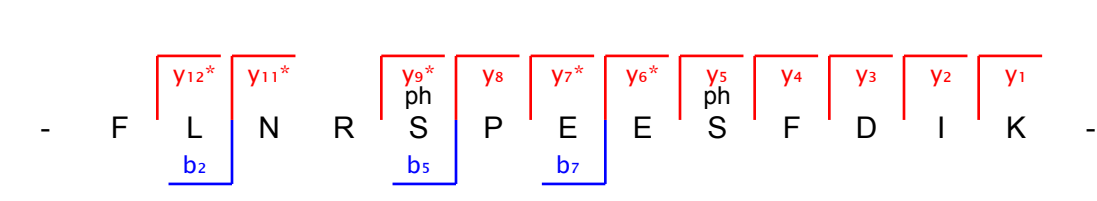
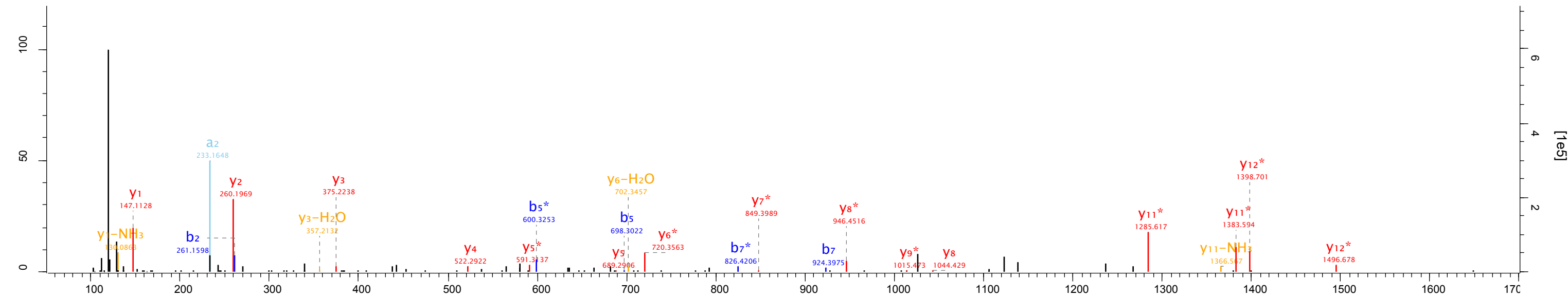
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20171215_MaS_33SR_LMH_phospho2_03

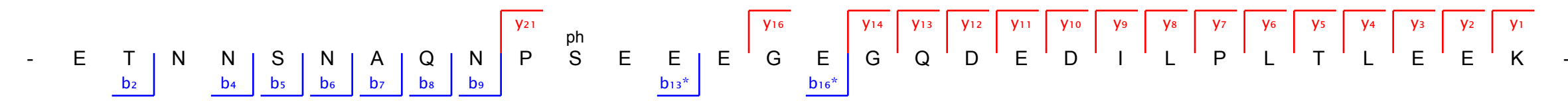
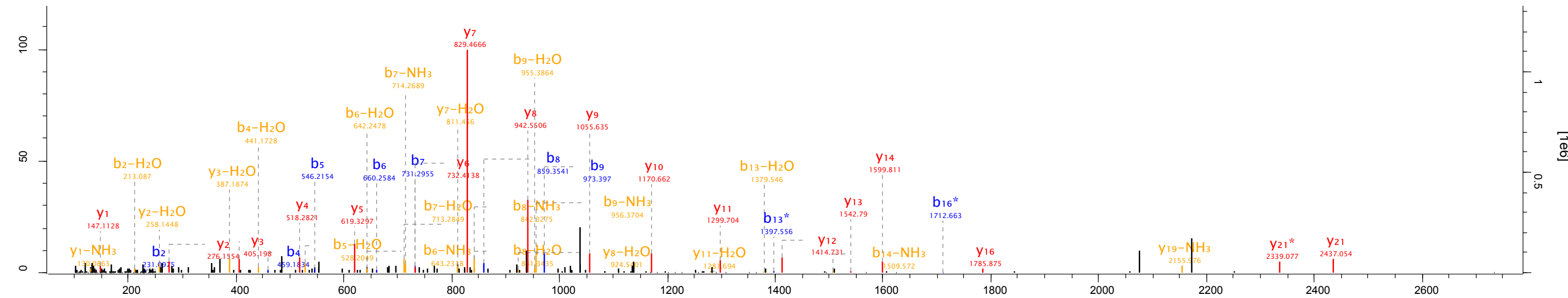
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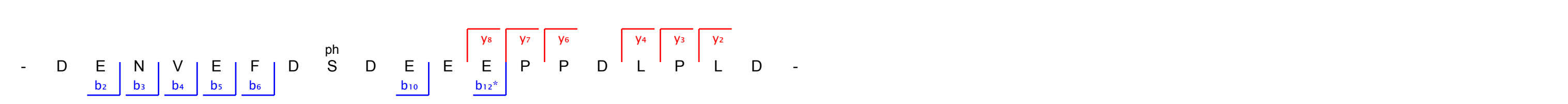
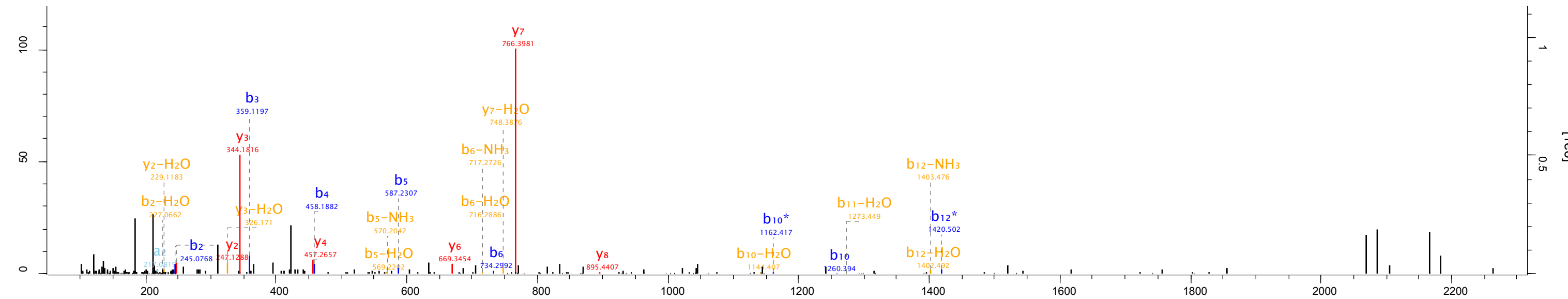
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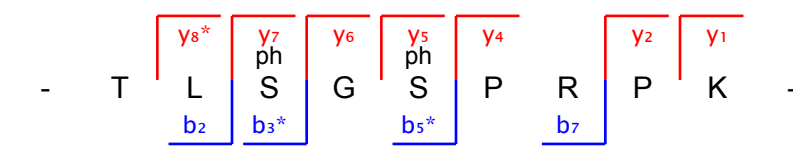
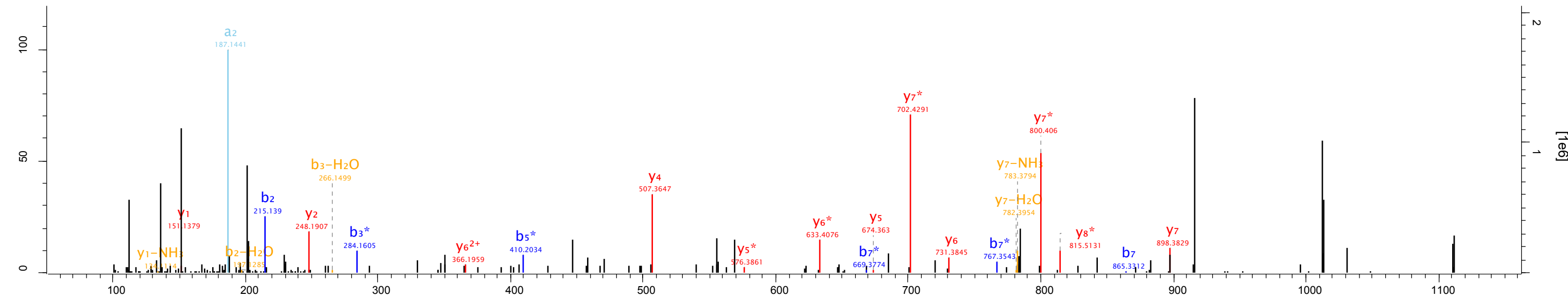
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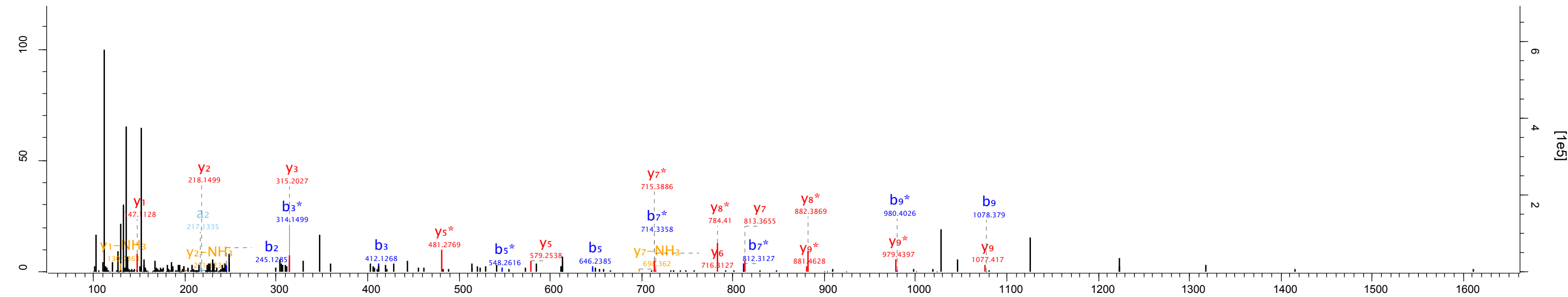
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20171215_MaS_33SR_LMH_phospho2_03

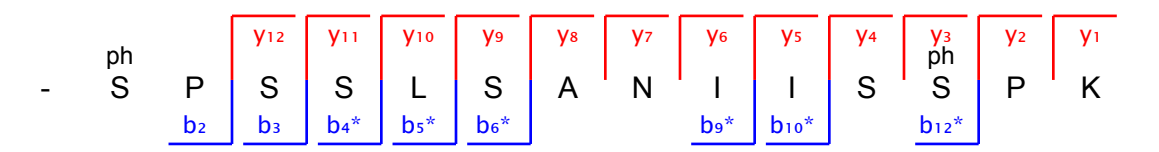
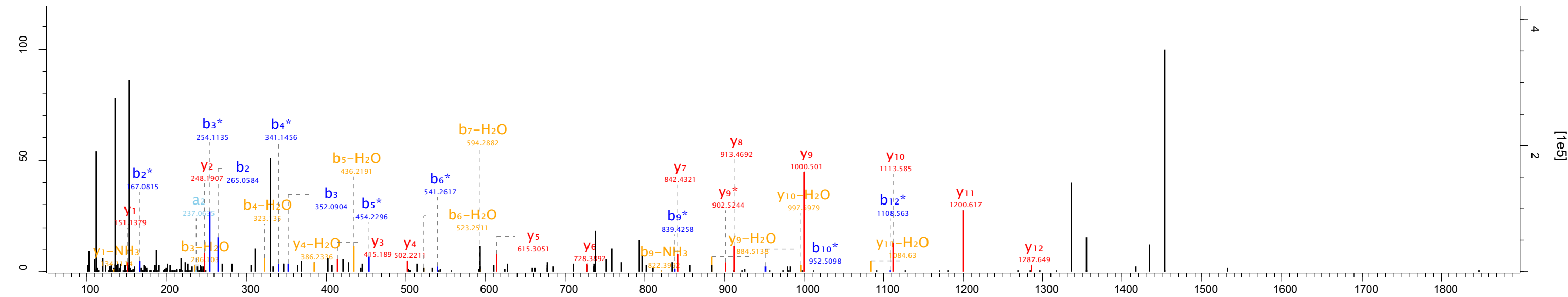
Scan	Method	Score	m/z	Gene names
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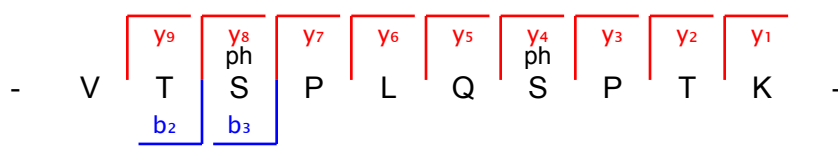
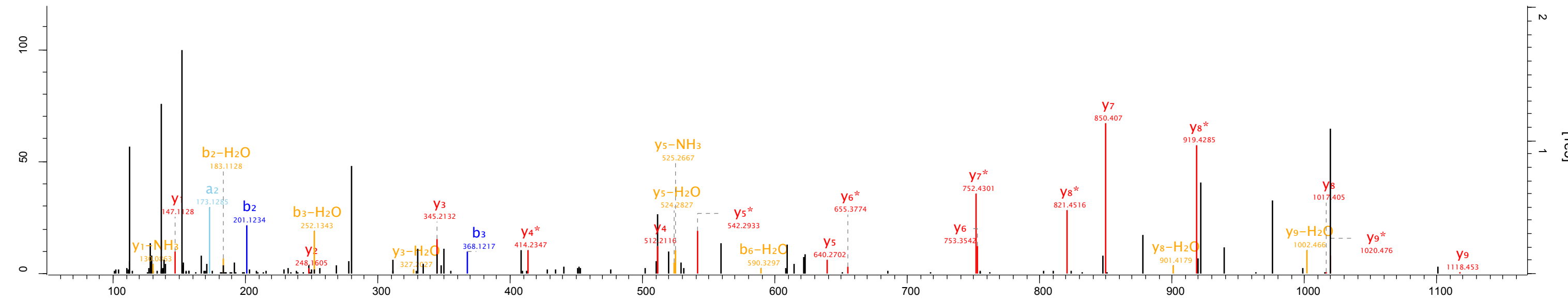


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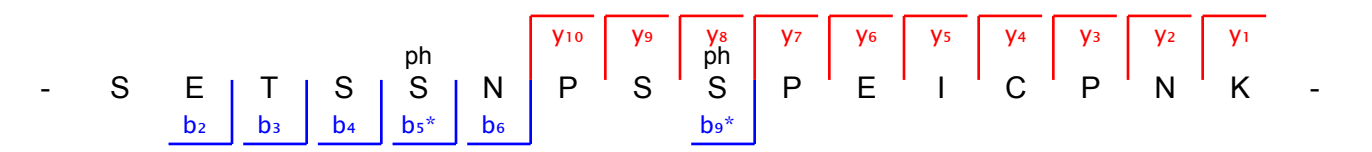
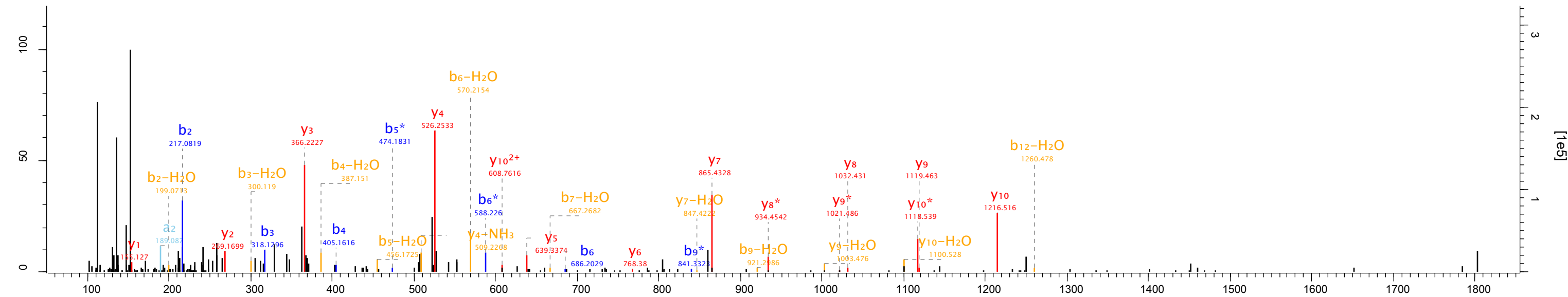


Raw file
20171215_MaS_33SR_LMH_phospho2_04

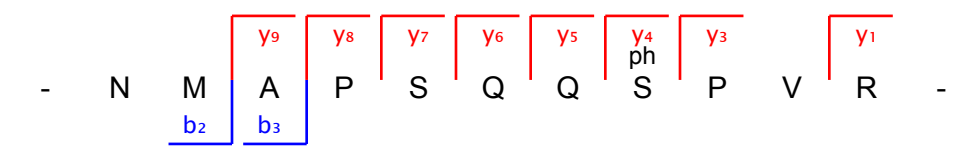
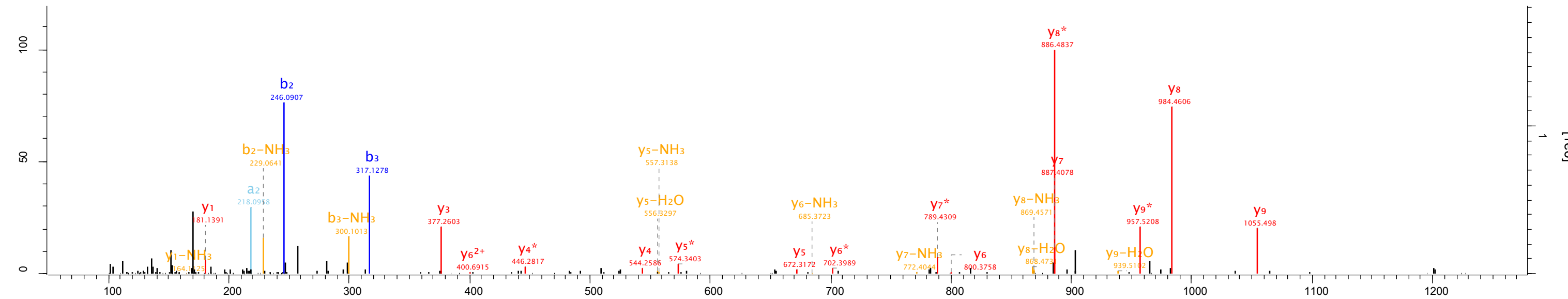
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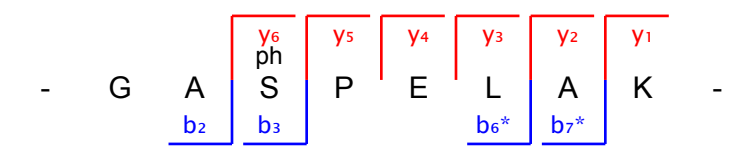
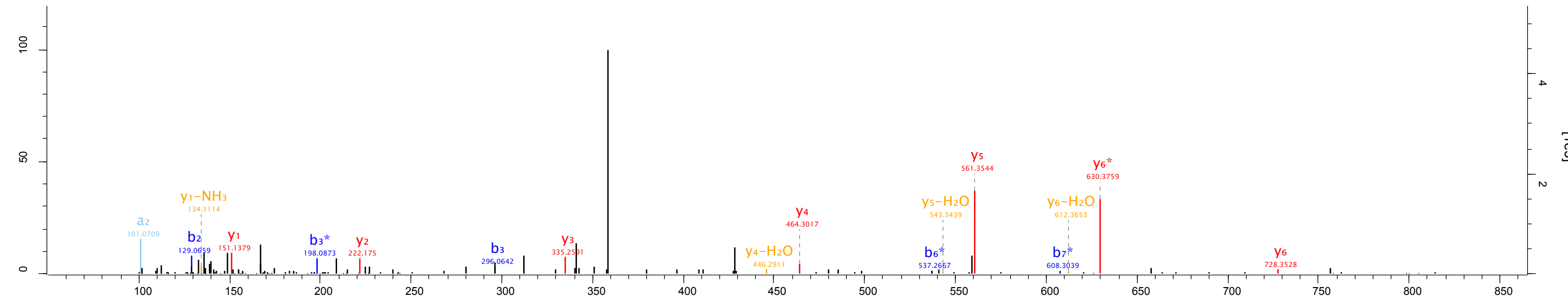
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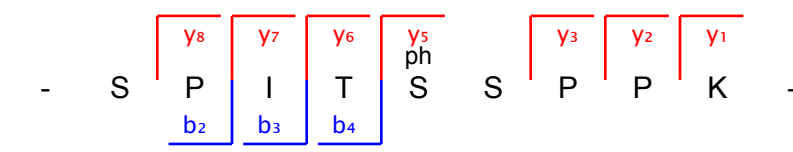
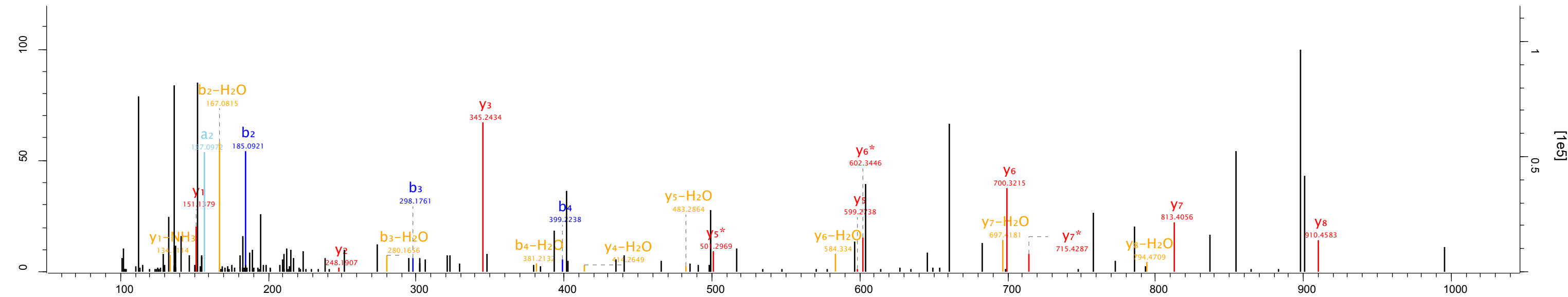
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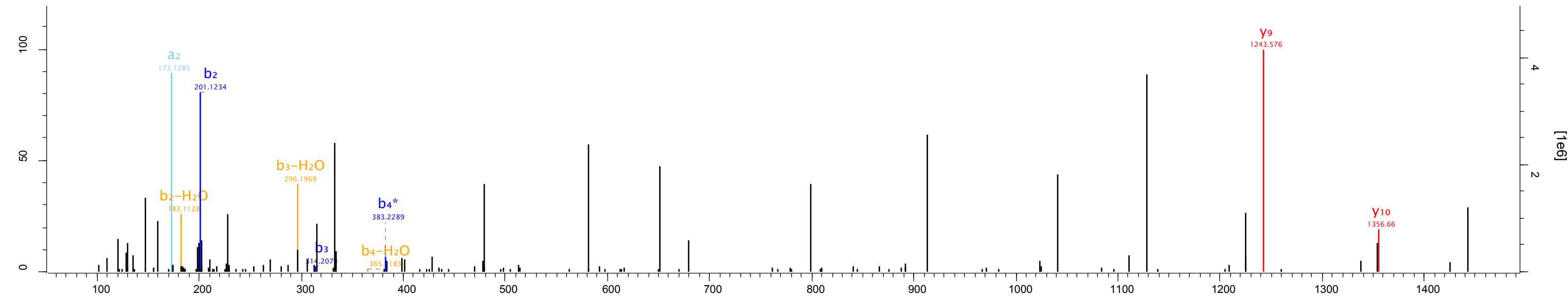
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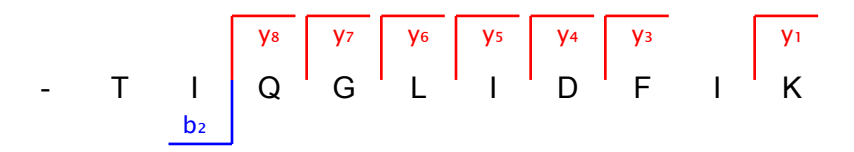
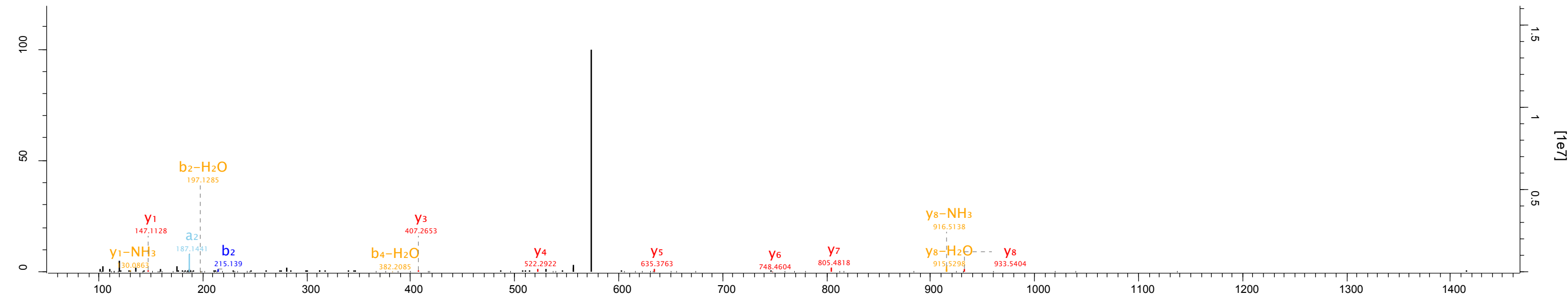
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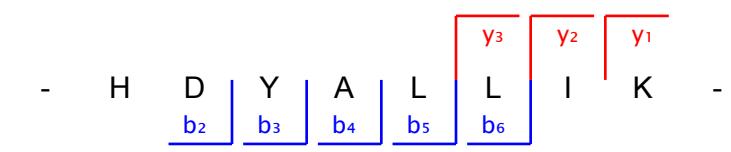
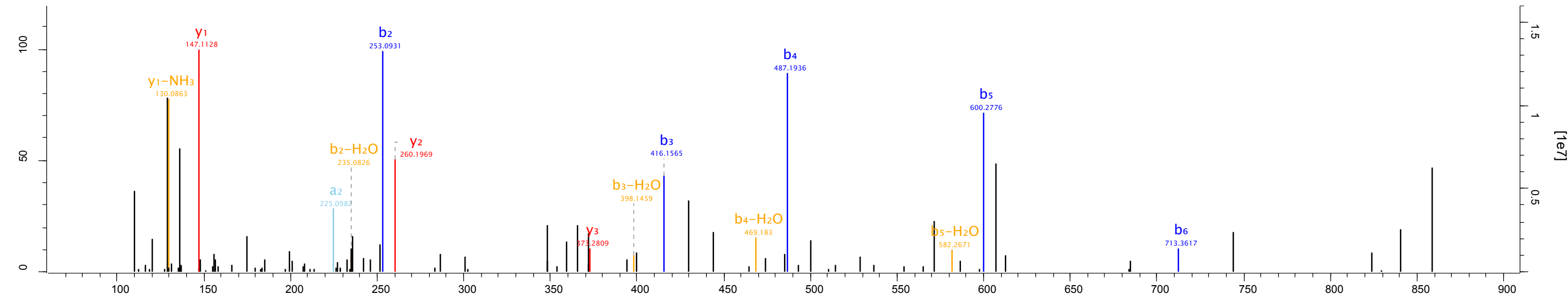
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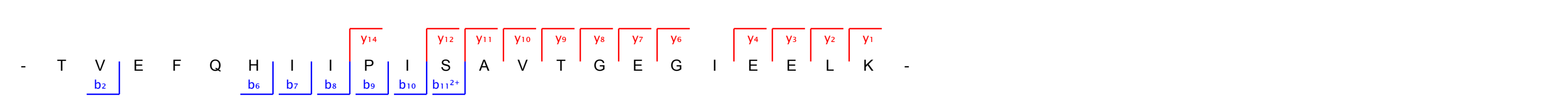
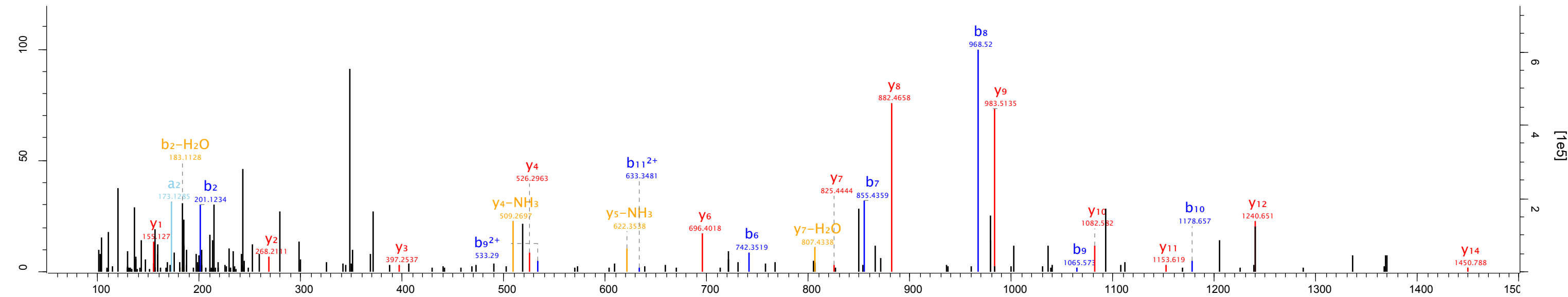
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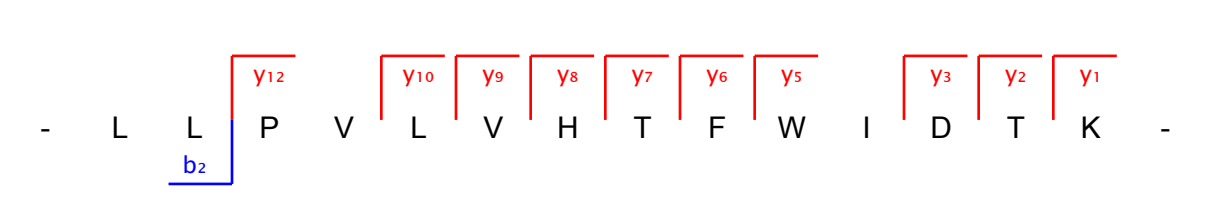
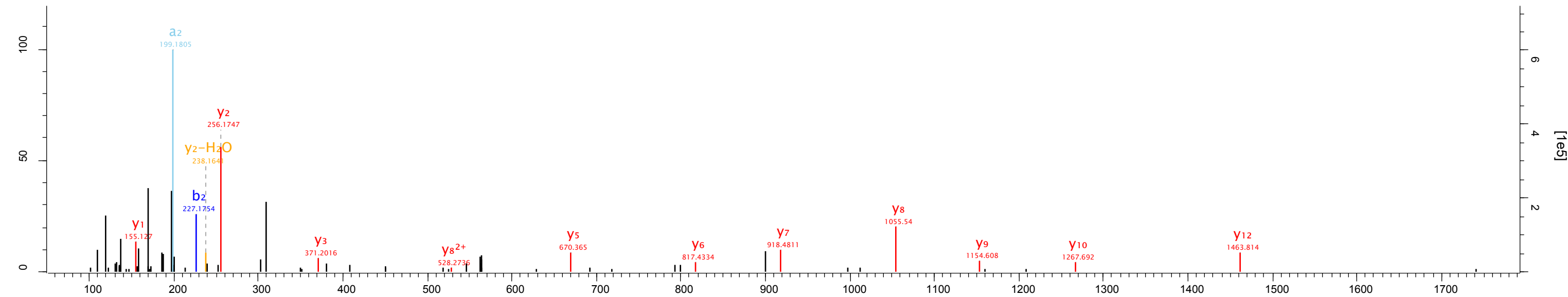
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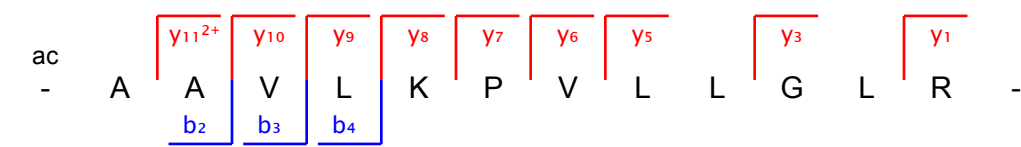
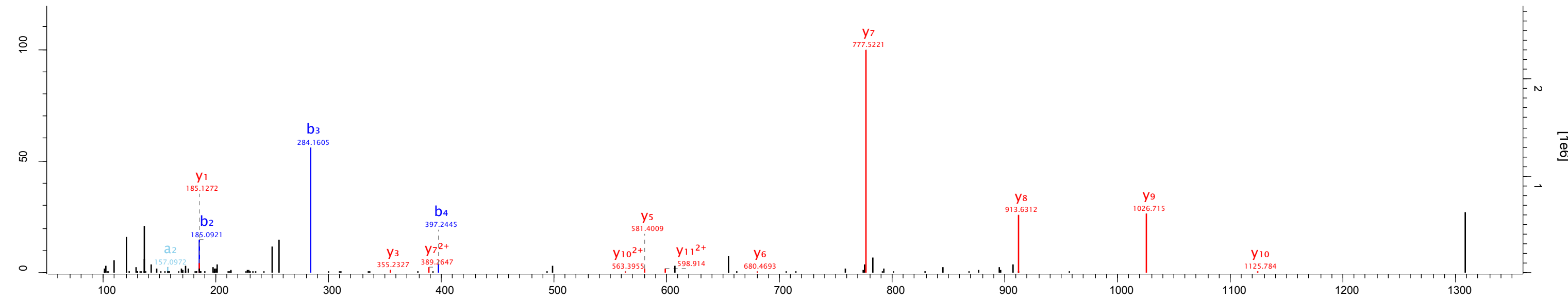
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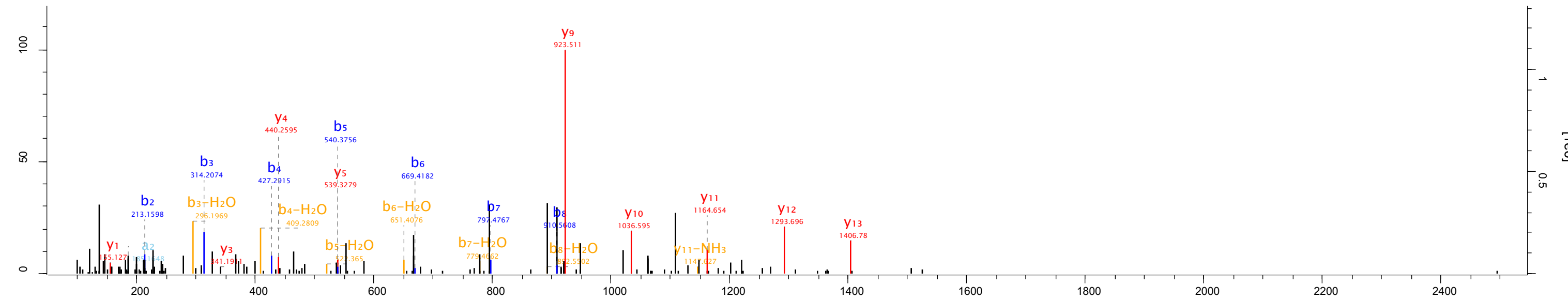
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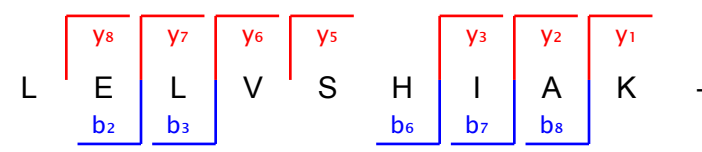
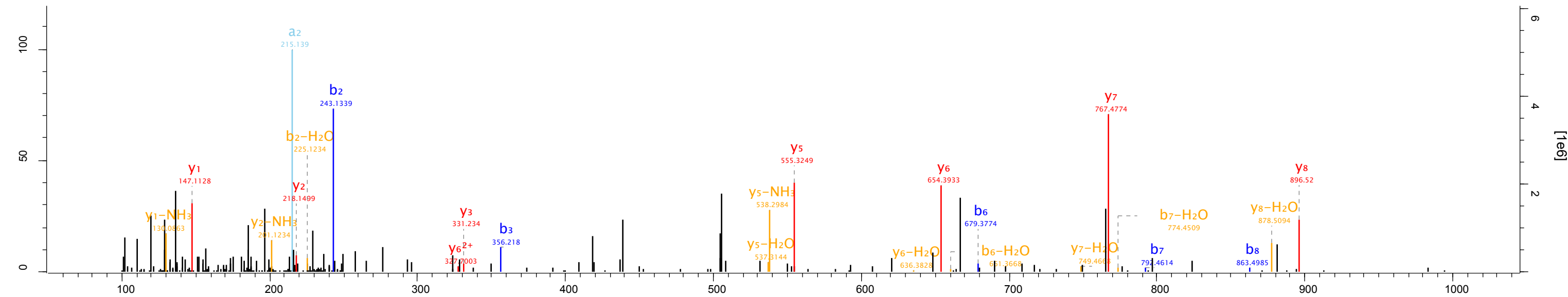
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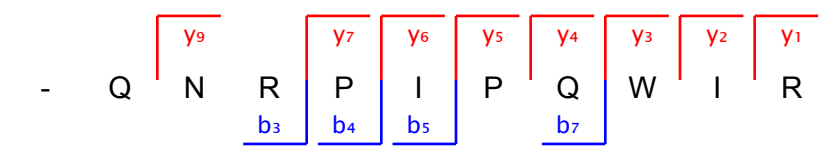
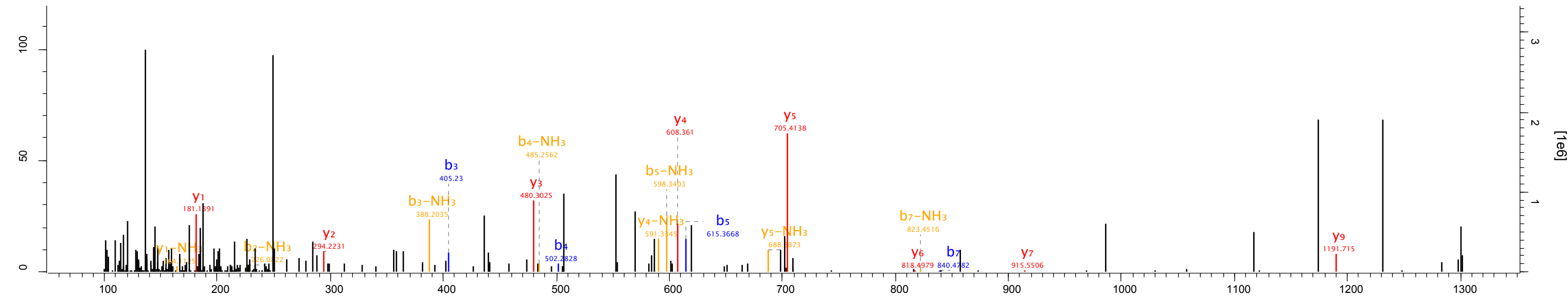
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Raw file 20171215_MaS_33SR_LMH_proteome_01 Scan 14039 Method FTMS; HCD Score 128.57 m/z 505.3



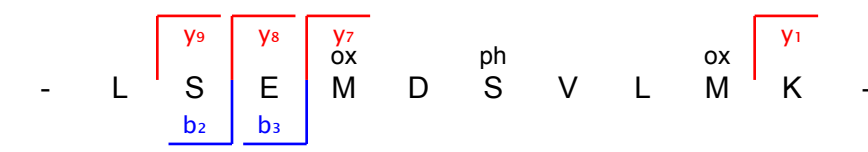
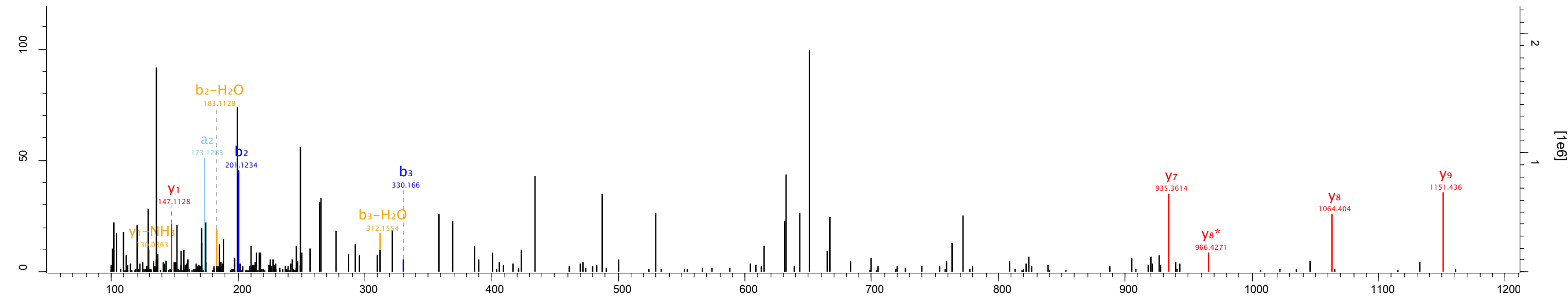
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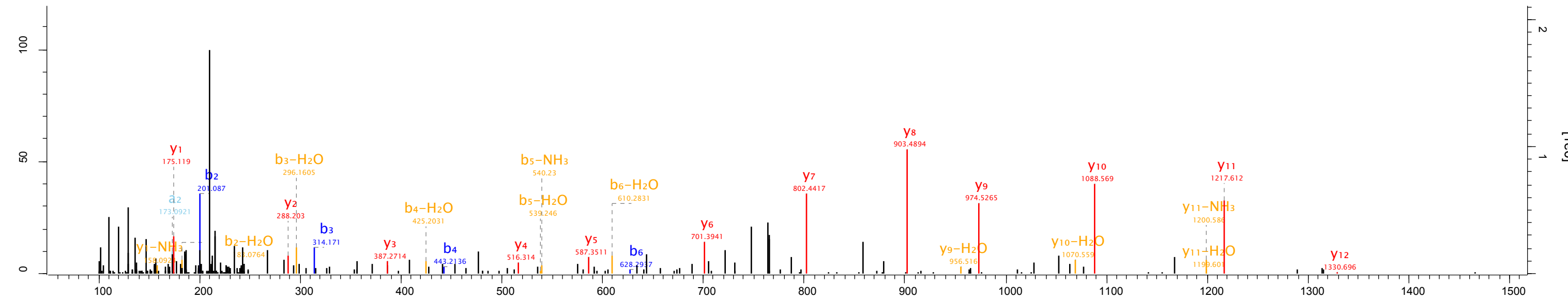
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20171215_MaS_33SR_LMH_proteome_01

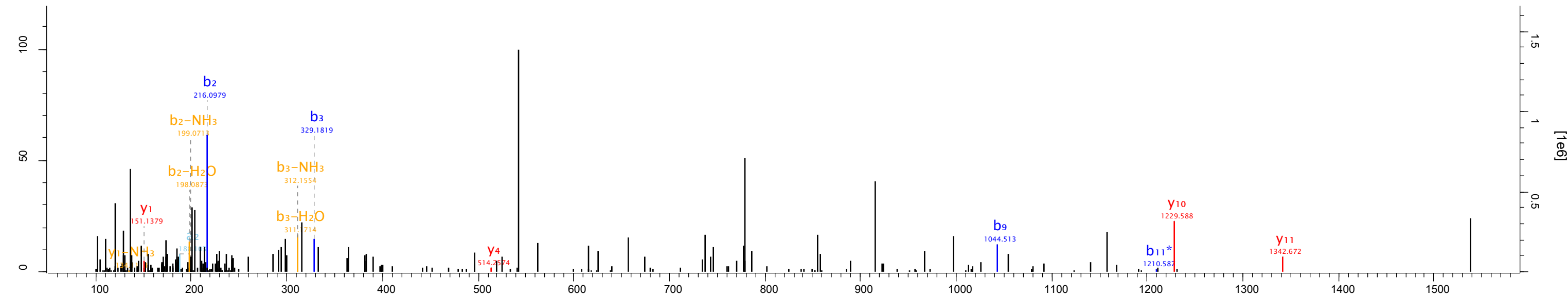
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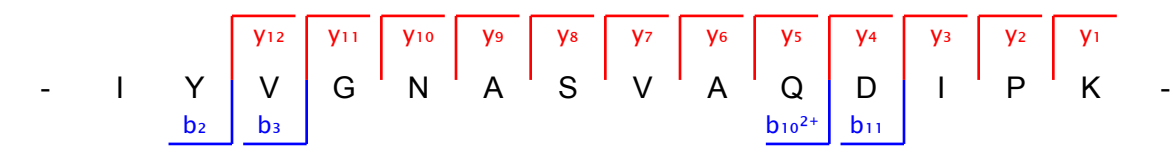
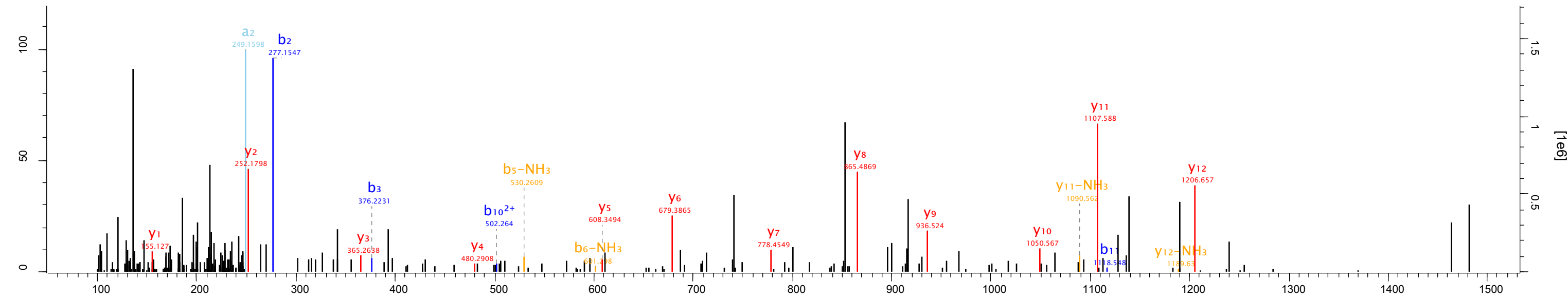
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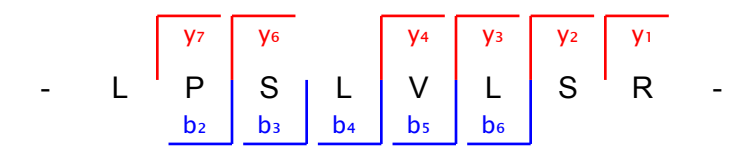
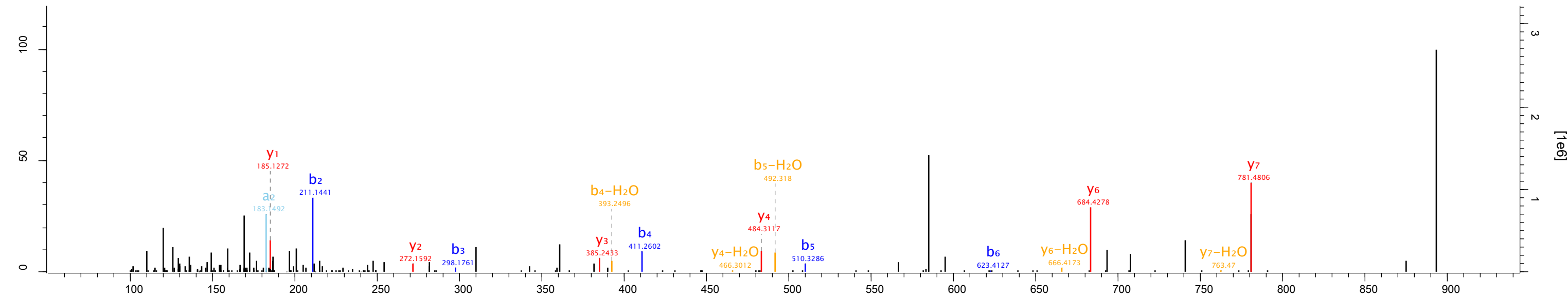
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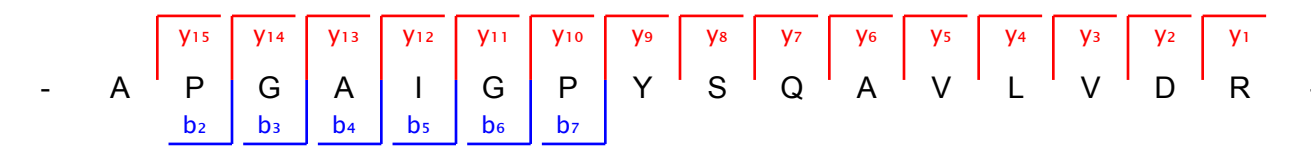
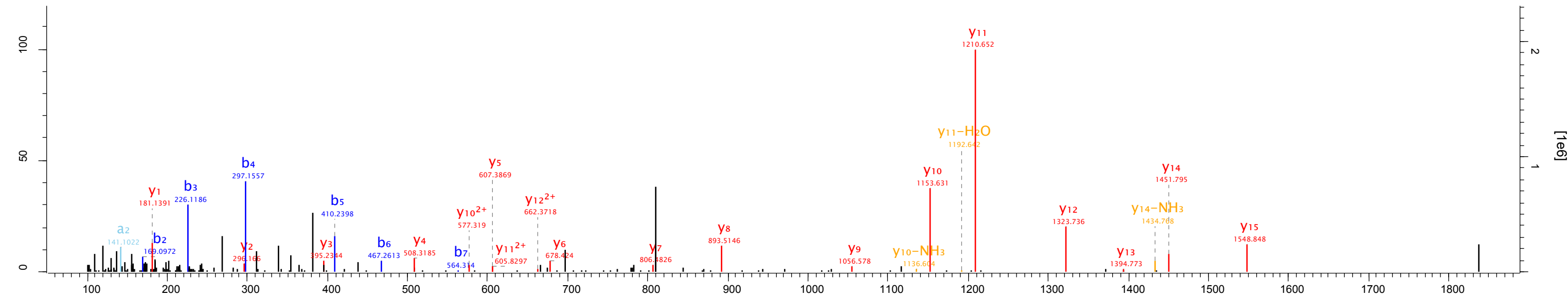
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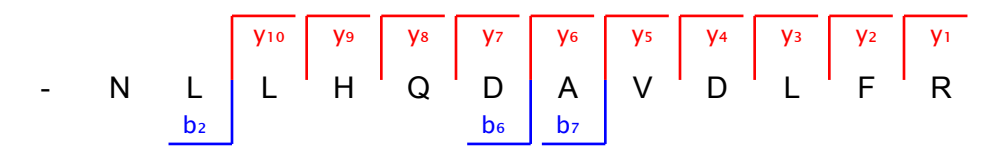
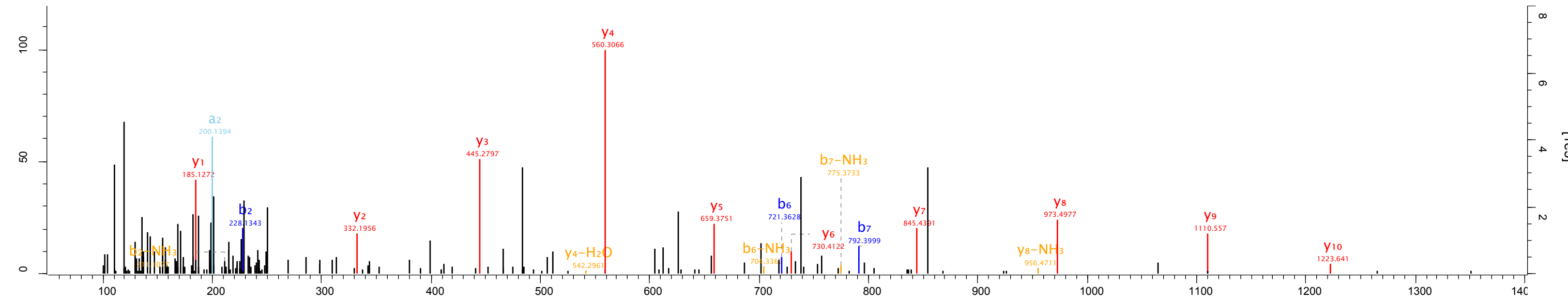
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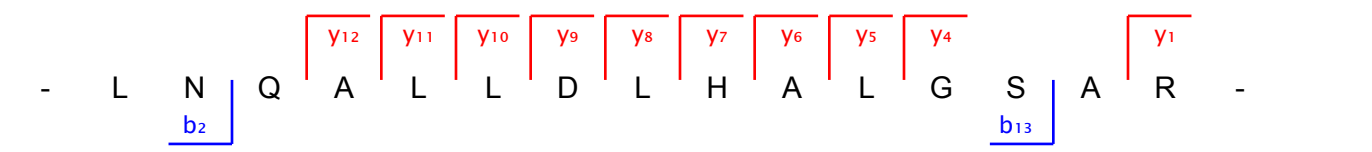
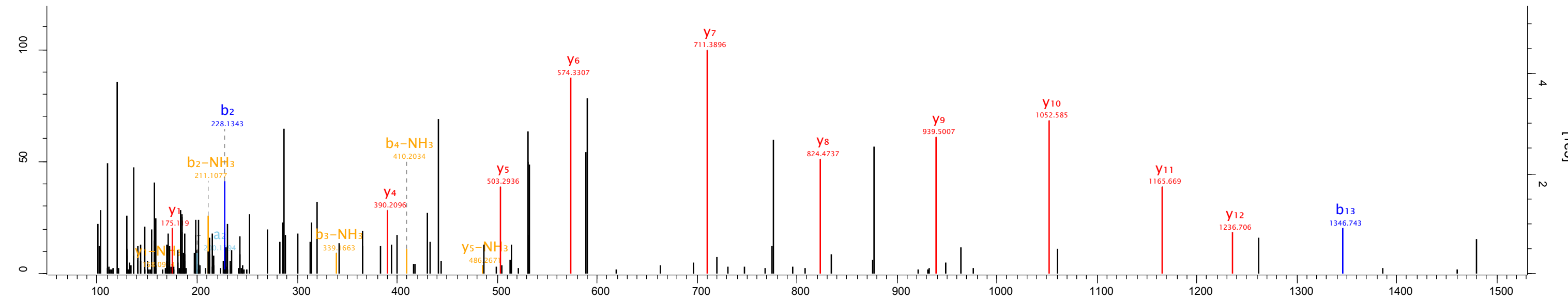
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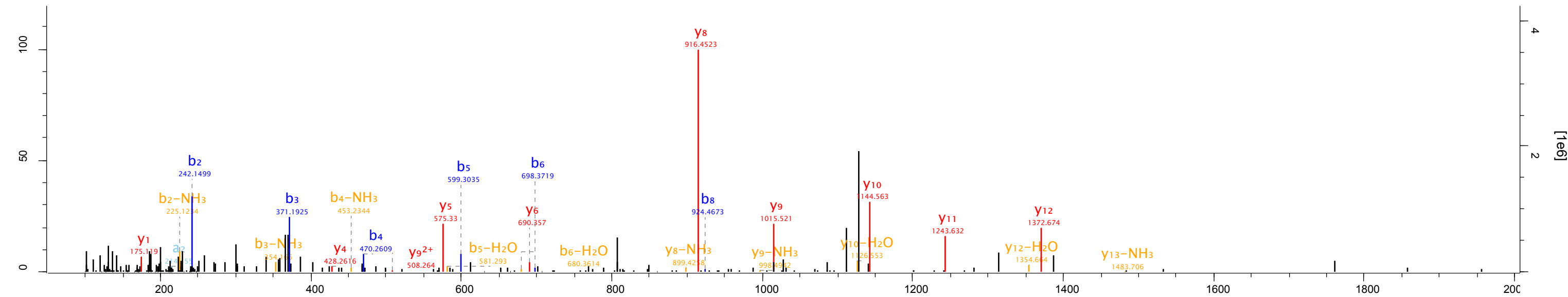
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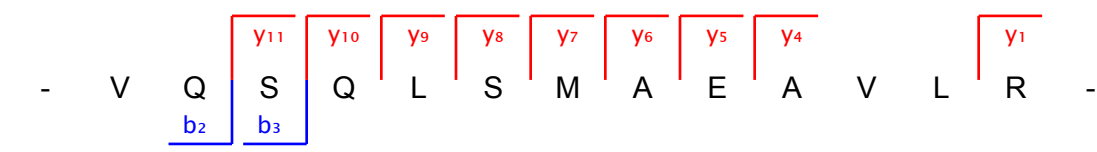
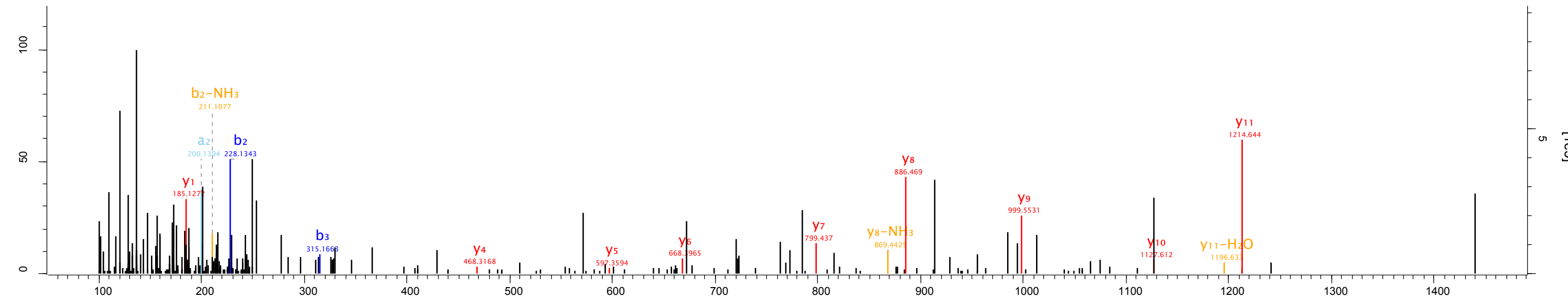
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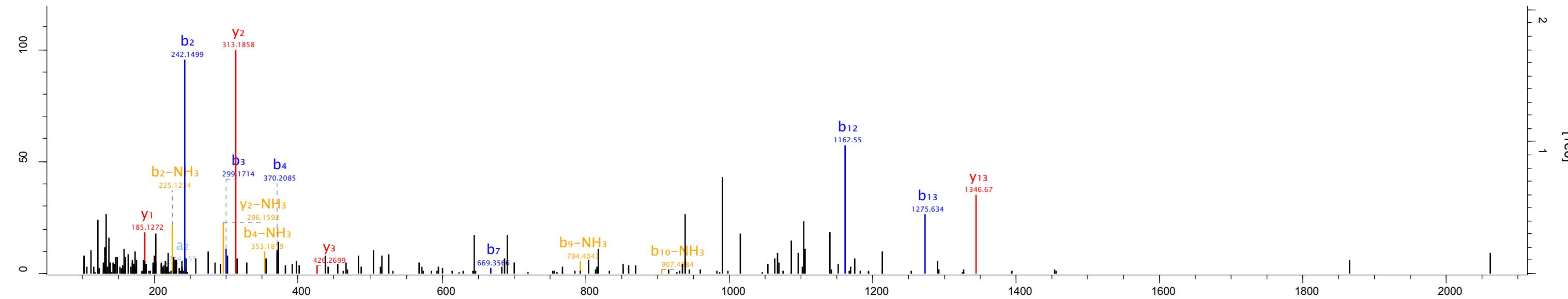
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Scan Method Score m/z Gene names

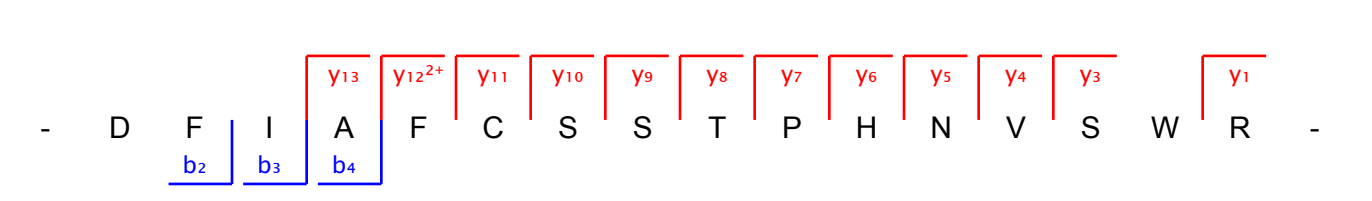
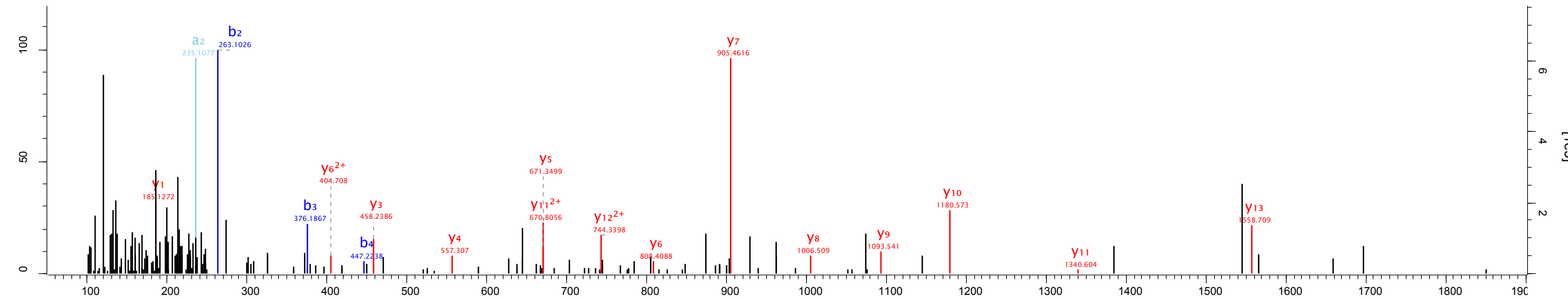
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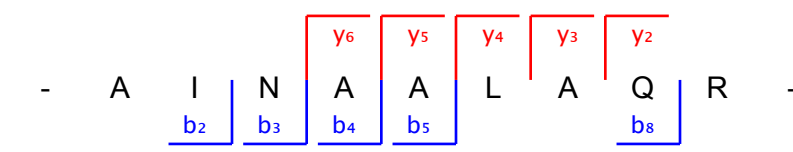
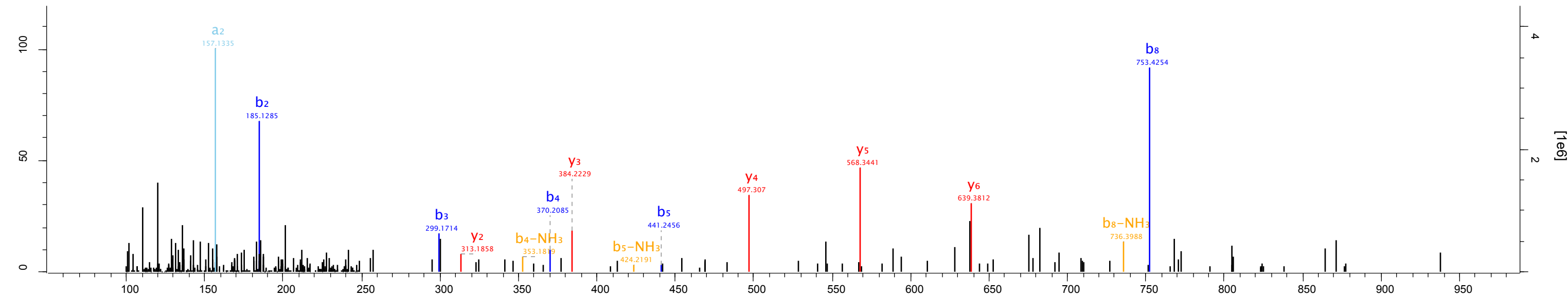
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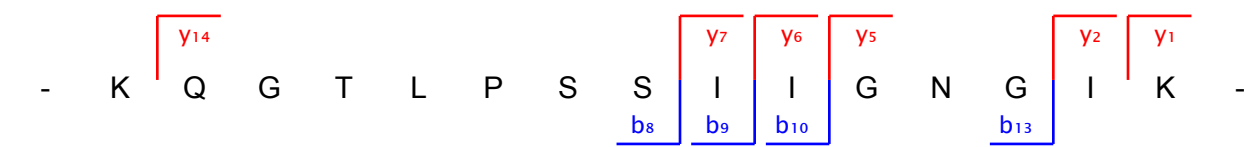
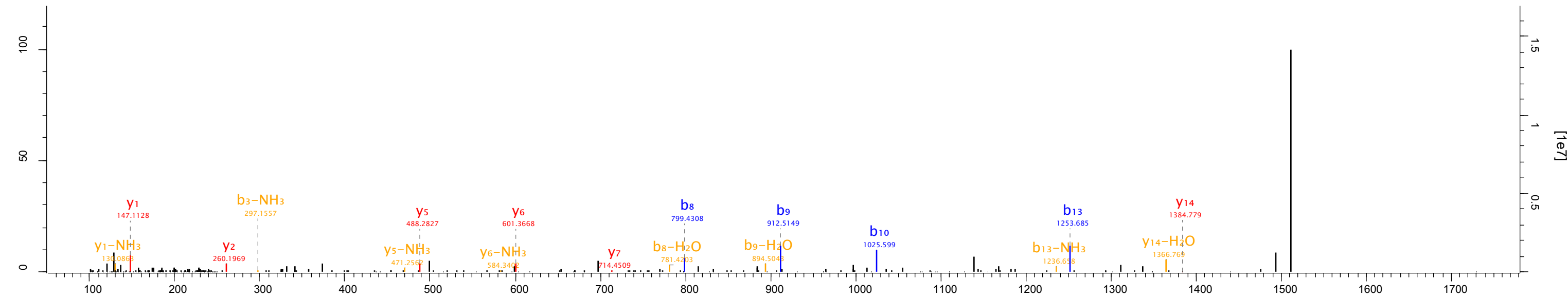


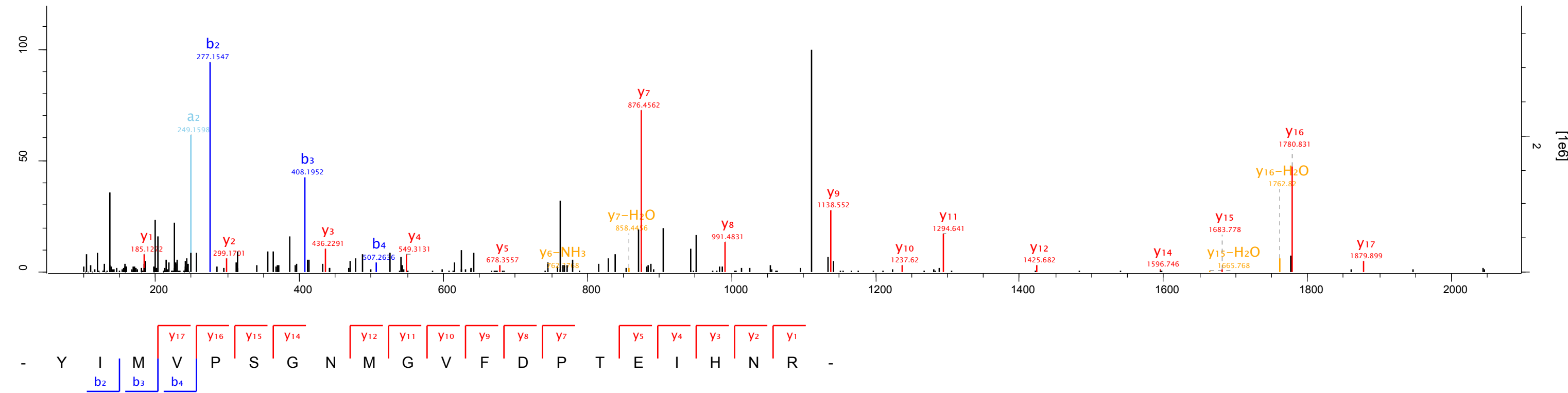
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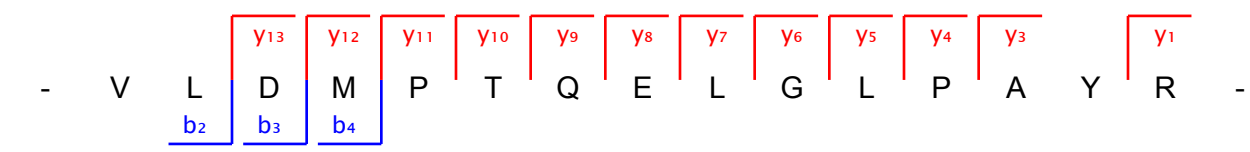
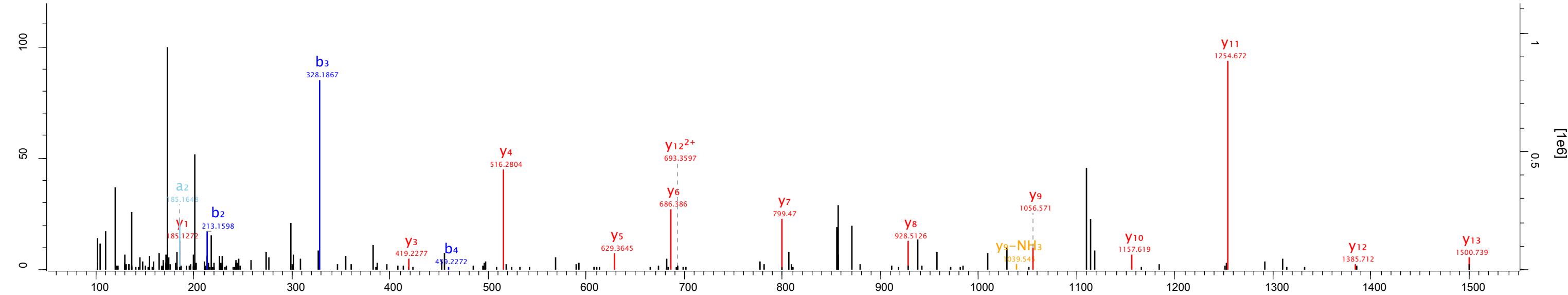




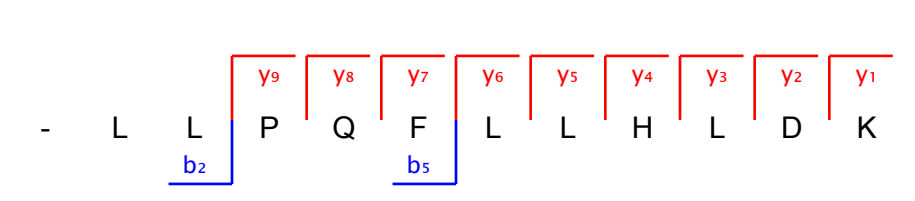
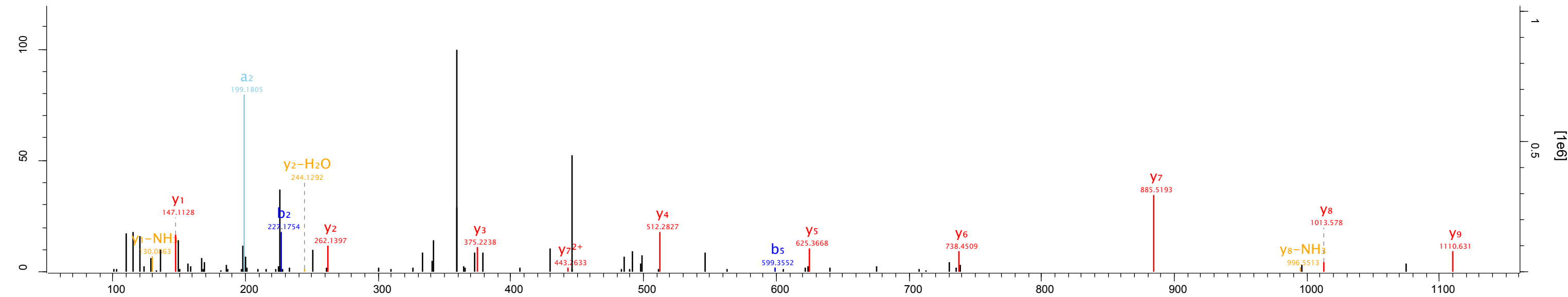
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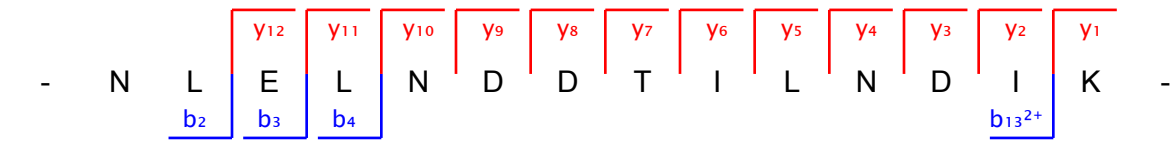
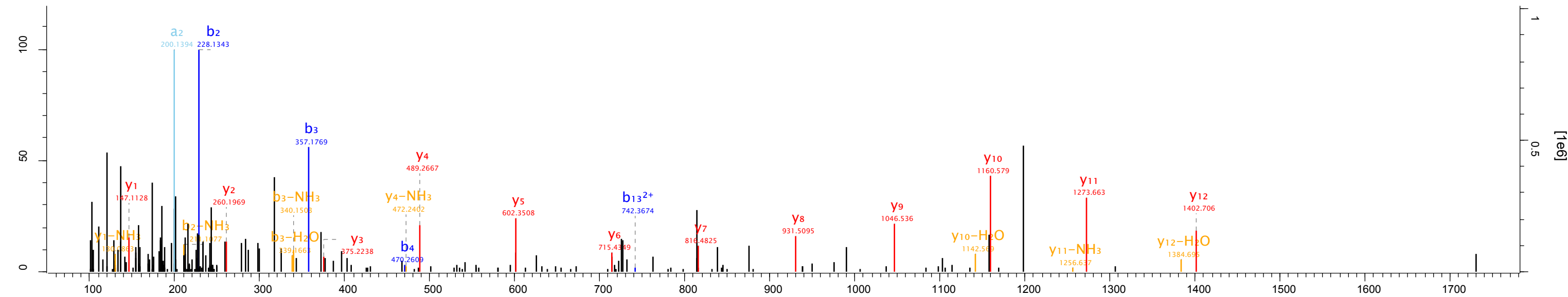
20171215_MaS_33SR_LMH_proteome_01

Scan 89849 Method FTMS; HCD Score 58.72 m/z 856.95 Gene names SARS2



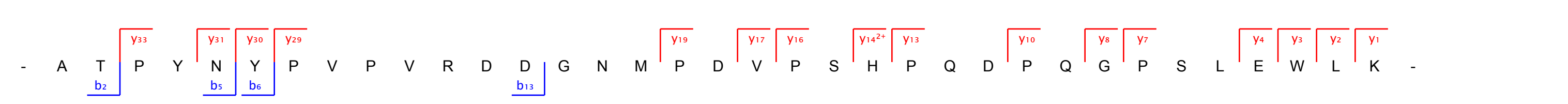
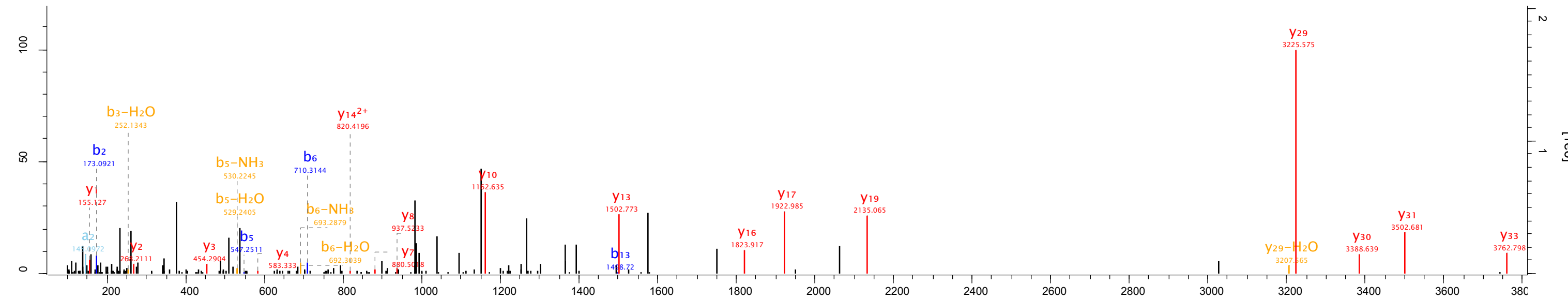
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 Scan: 91209 Method: FTMS; HCD Score: 65.18 m/z: 446.27 Gene names: C9orf41





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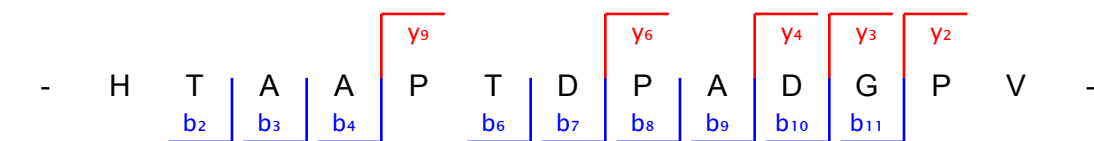
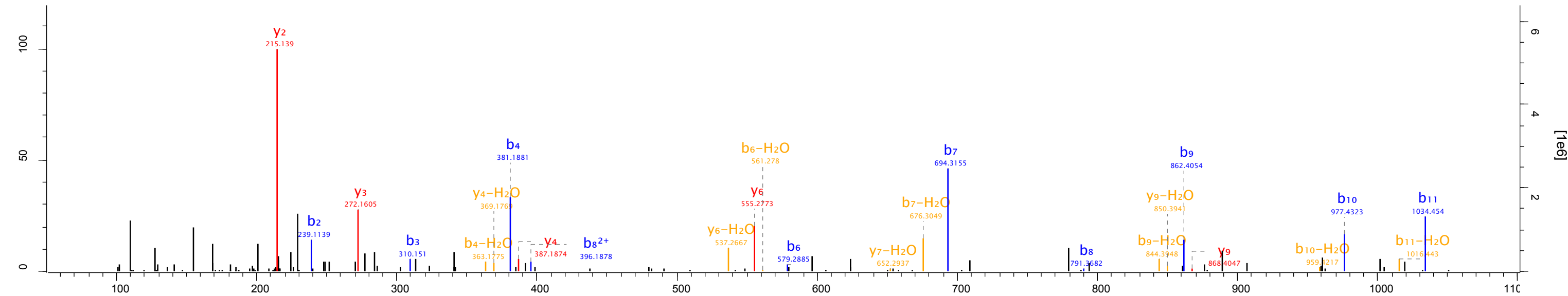
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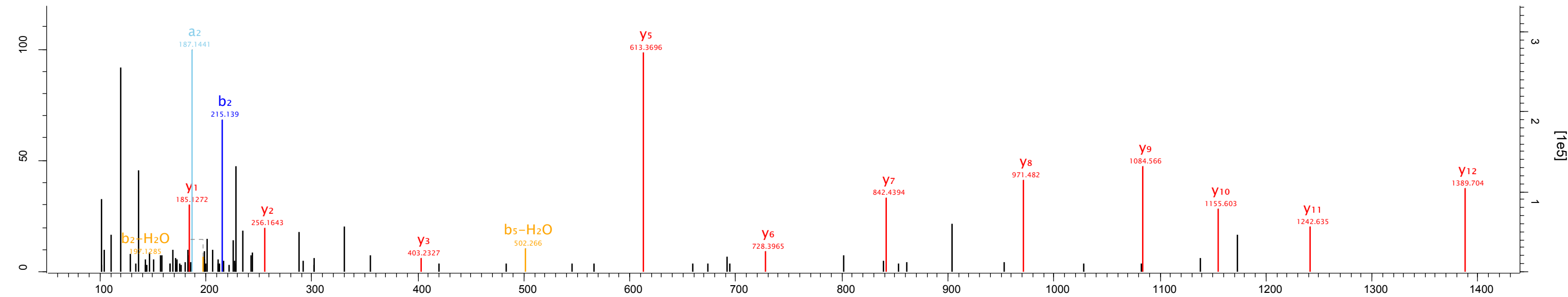
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20171215_MaS_33SR_LMH_proteome_02

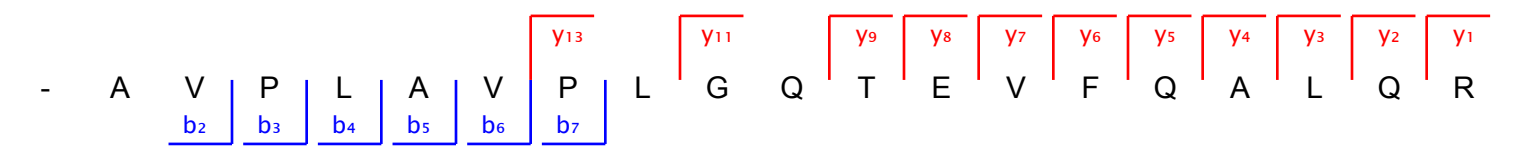
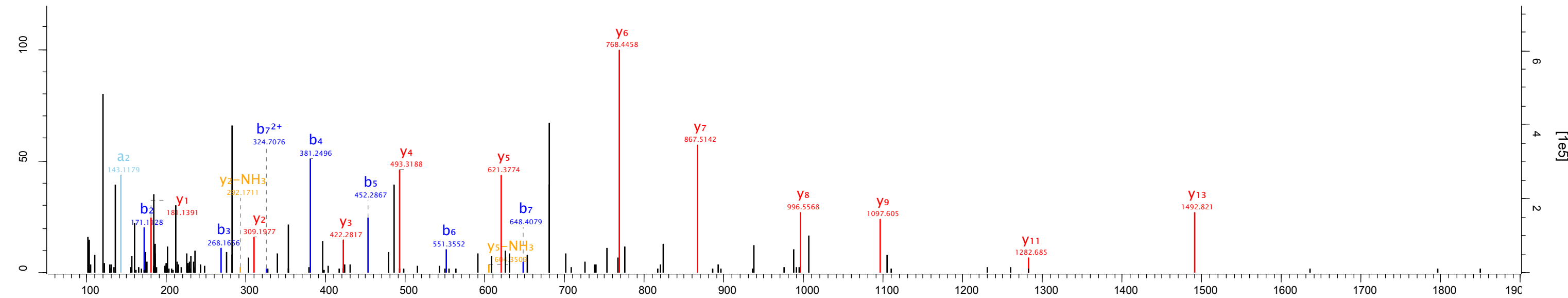
Scan	Method	Score	m/z	Gene names
10069	FTMS; HCD	120.32	624.79	PLP2



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 122489 Method FTMS; HCD Score 53.3 m/z 802.42 Gene names ACOX3

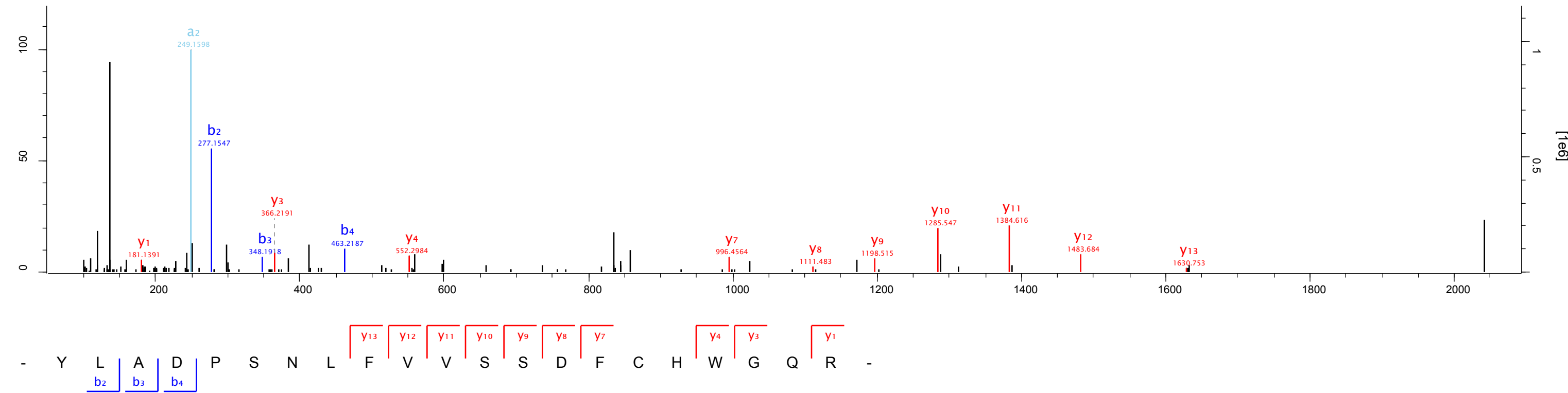


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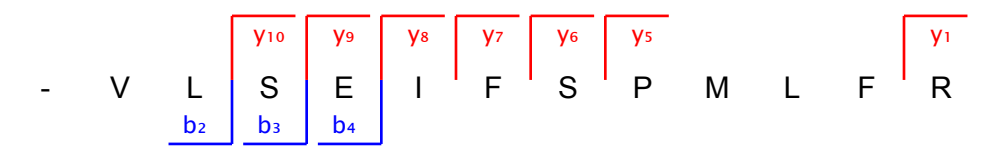
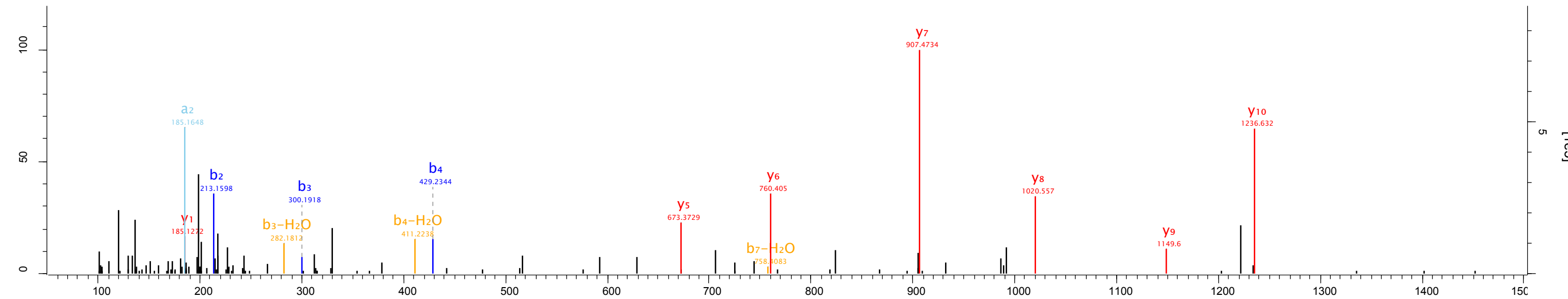


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20171215_MaS_33SR_LMH_proteome_02

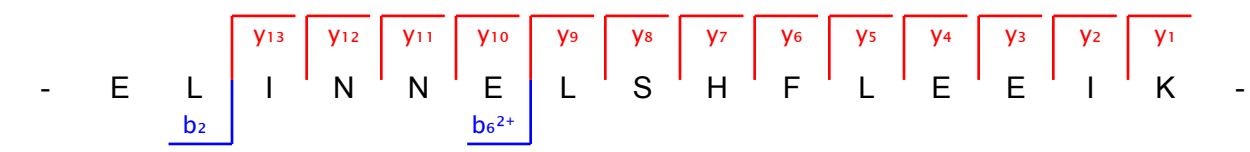
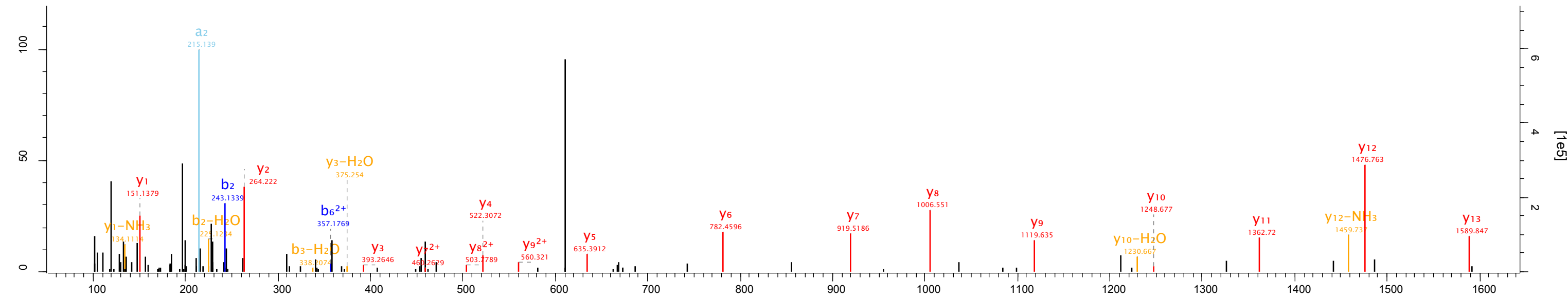
Scan 124579 Method FTMS; HCD Score 43.7 m/z 836.07 Gene names MEMO1



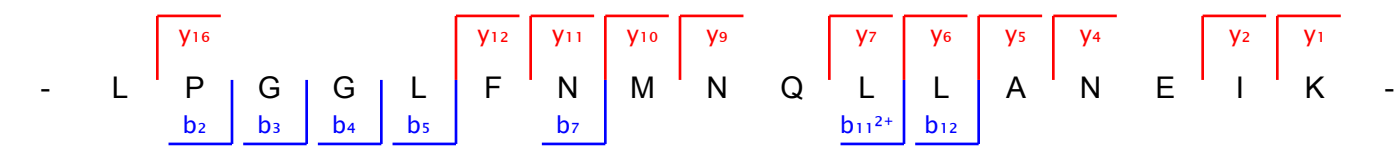
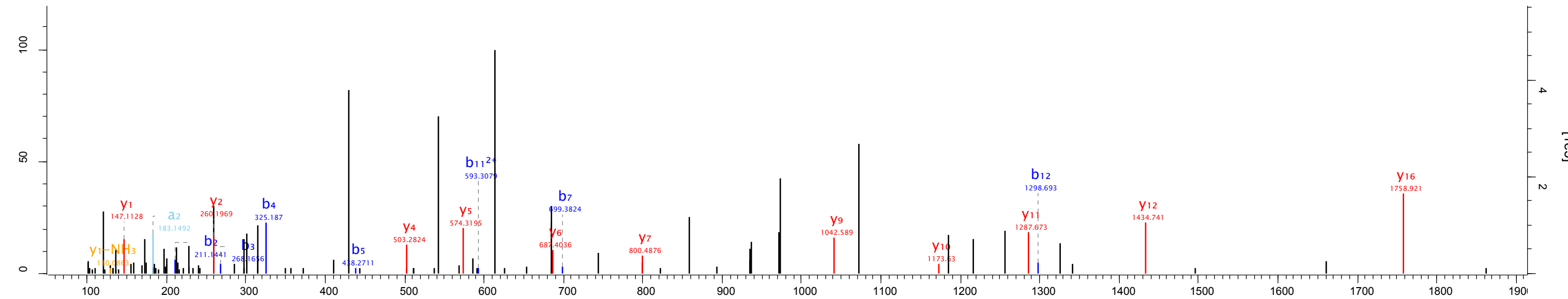
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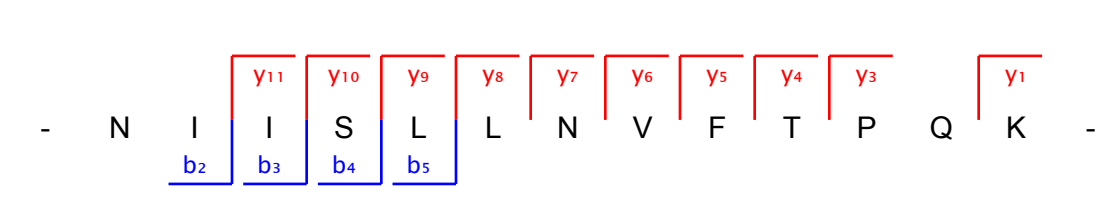
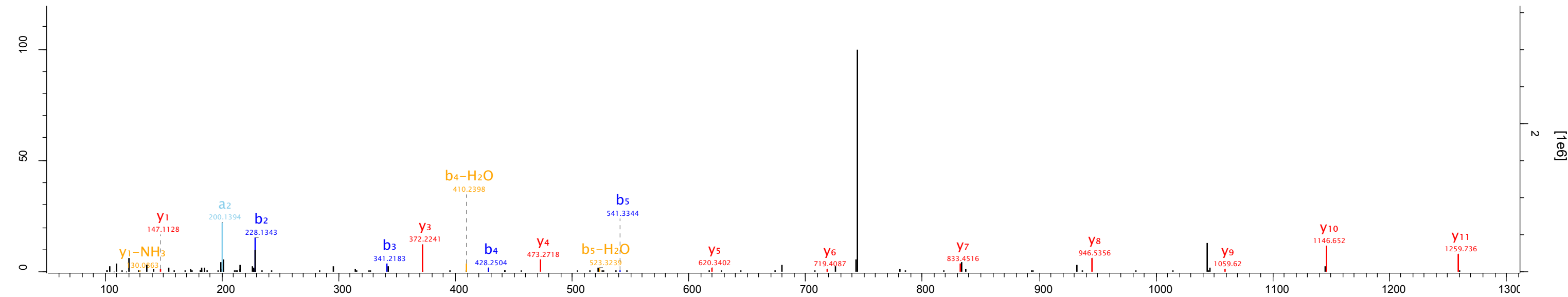
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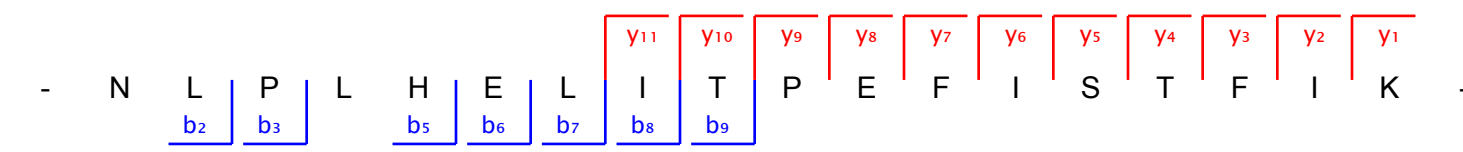
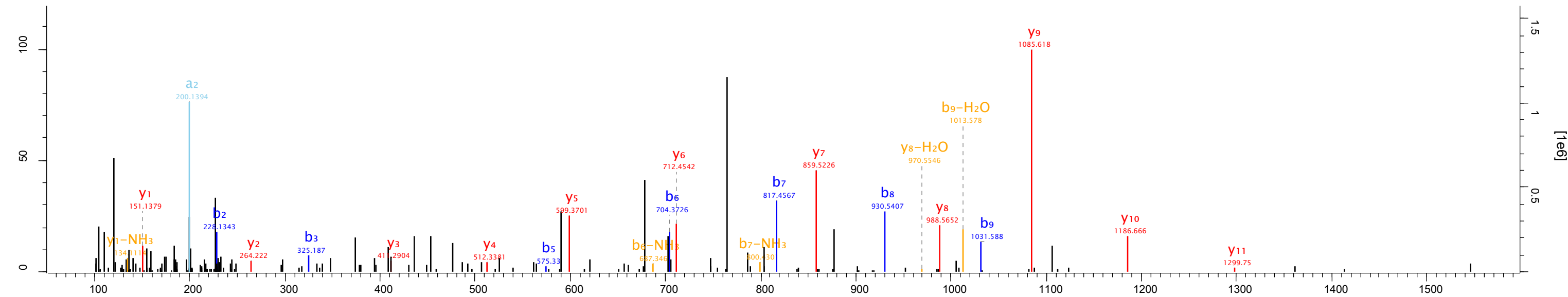
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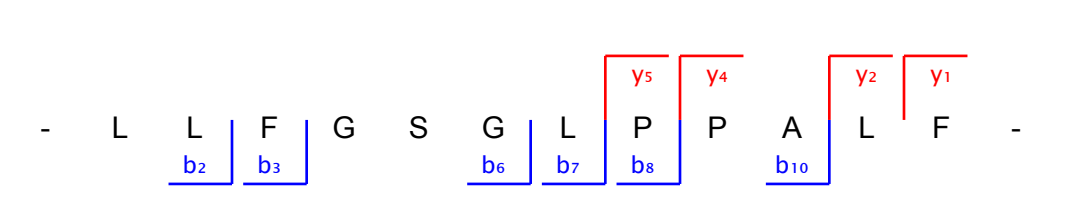
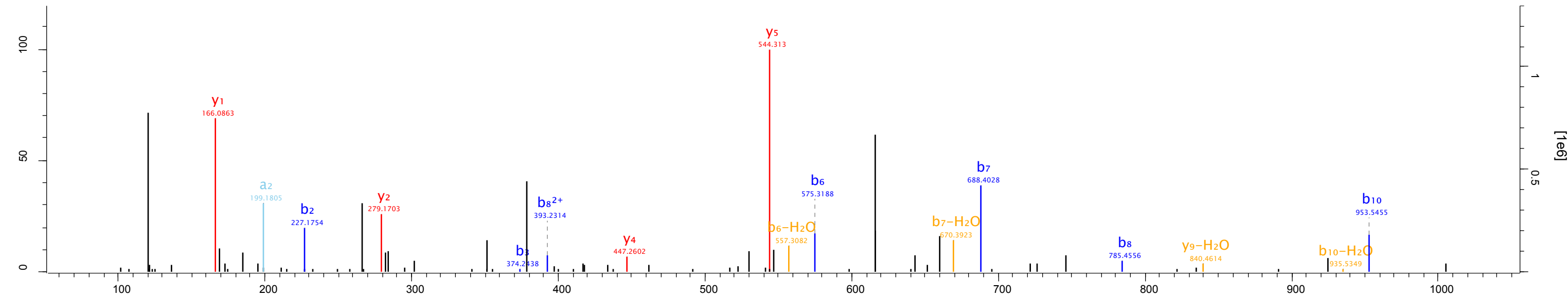
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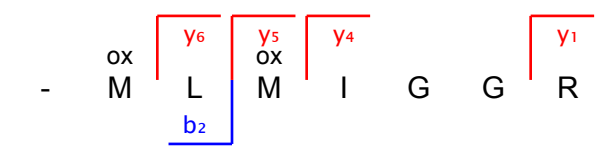
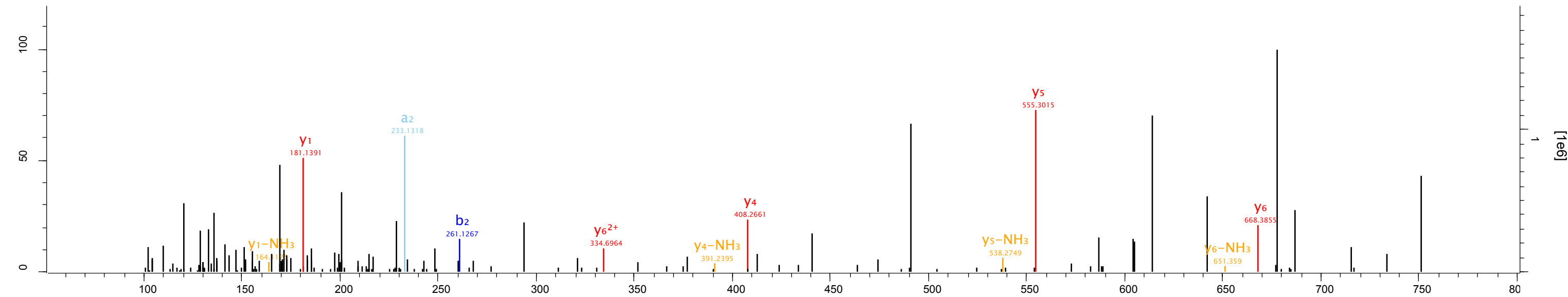
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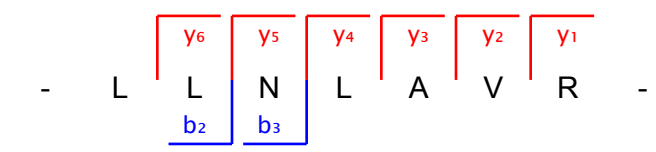
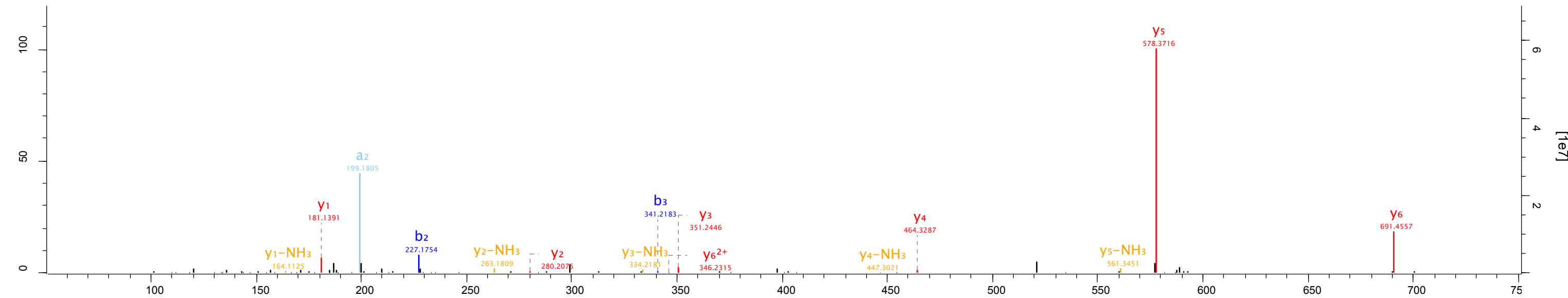


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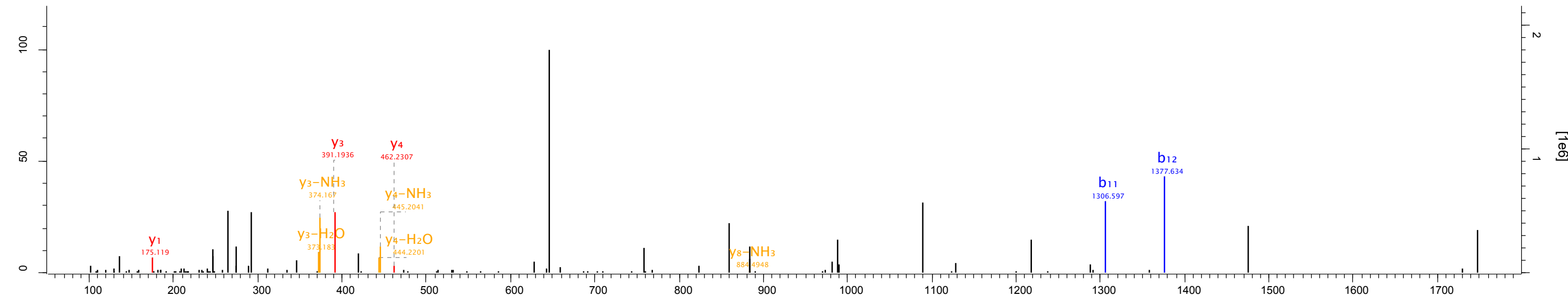


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20171215_MaS_33SR_LMH_proteome_02

Scan 32319 Method FTMS; HCD Score 92.32 m/z 402.77 Gene names KCNK1



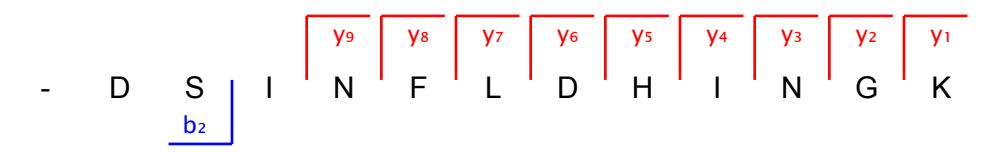
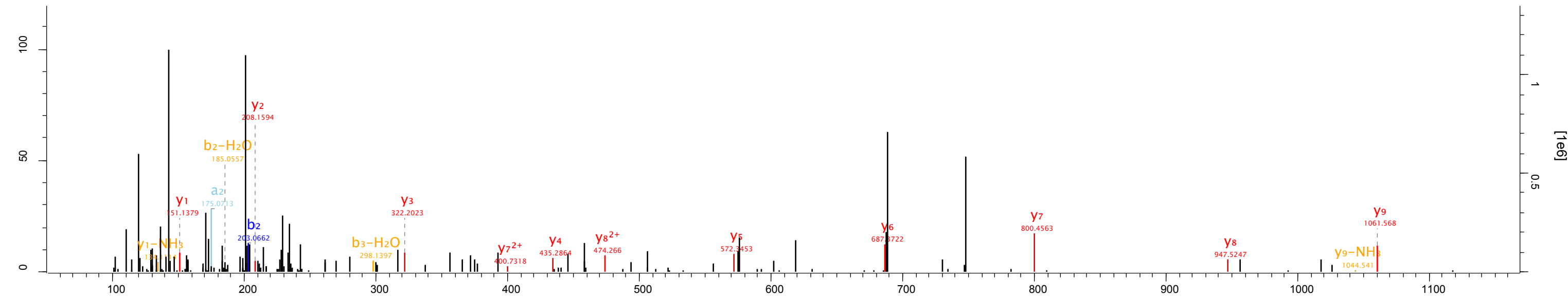
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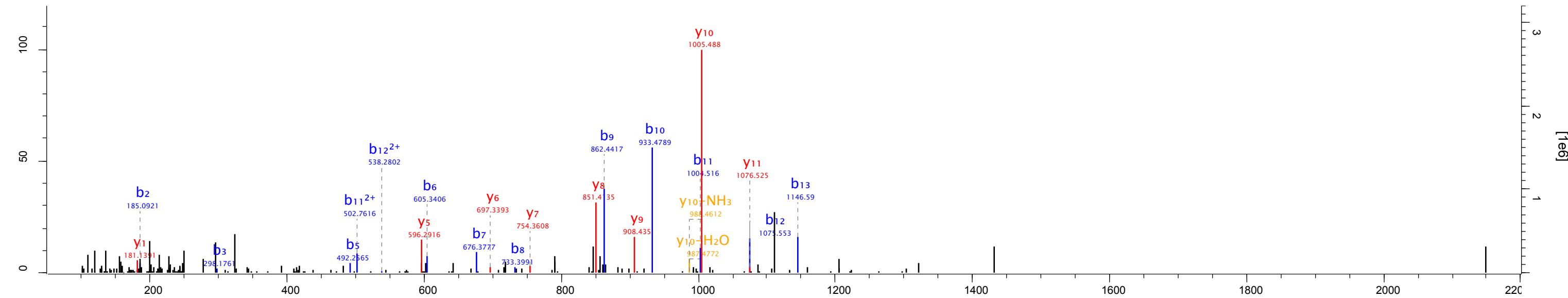
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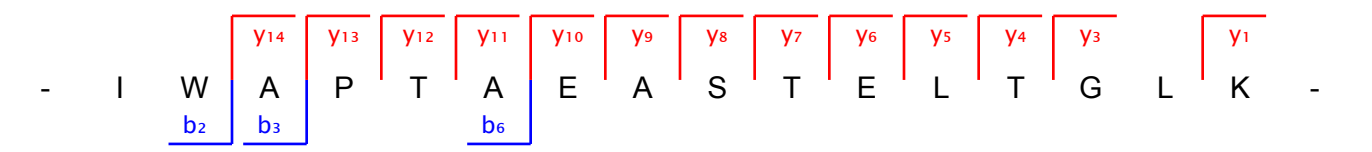
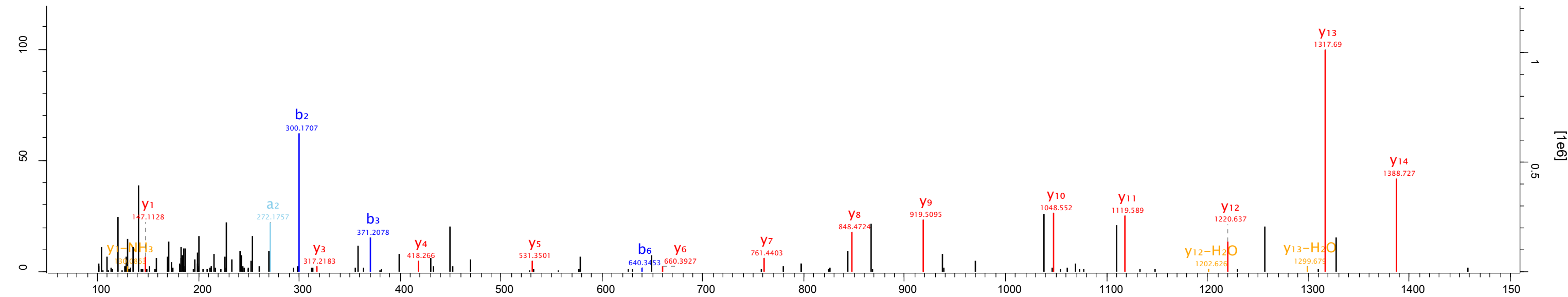
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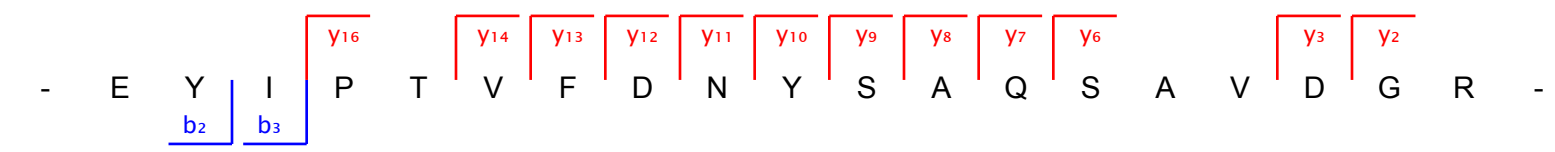
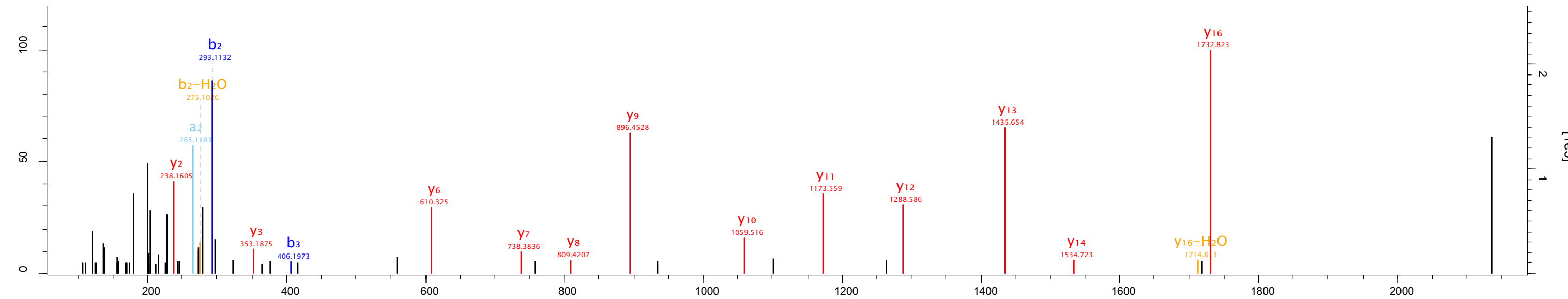
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Fragmentation mapping:
- b2 b3 b5 b6 b7 b8 b9 b10 b11 b12 b13 y11 y10 y9 y8 y7 y6 y5 y1

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Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 83329 Method FTMS; HCD Score 64.7 m/z 1069.51 Gene names RHOG



Raw file 20171215_MaS_33SR_LMH_proteome_02 Scan 88159 Method FTMS; HCD Score 41.91 m/z 877.77 Gene names ERIC-1s;TACC3

