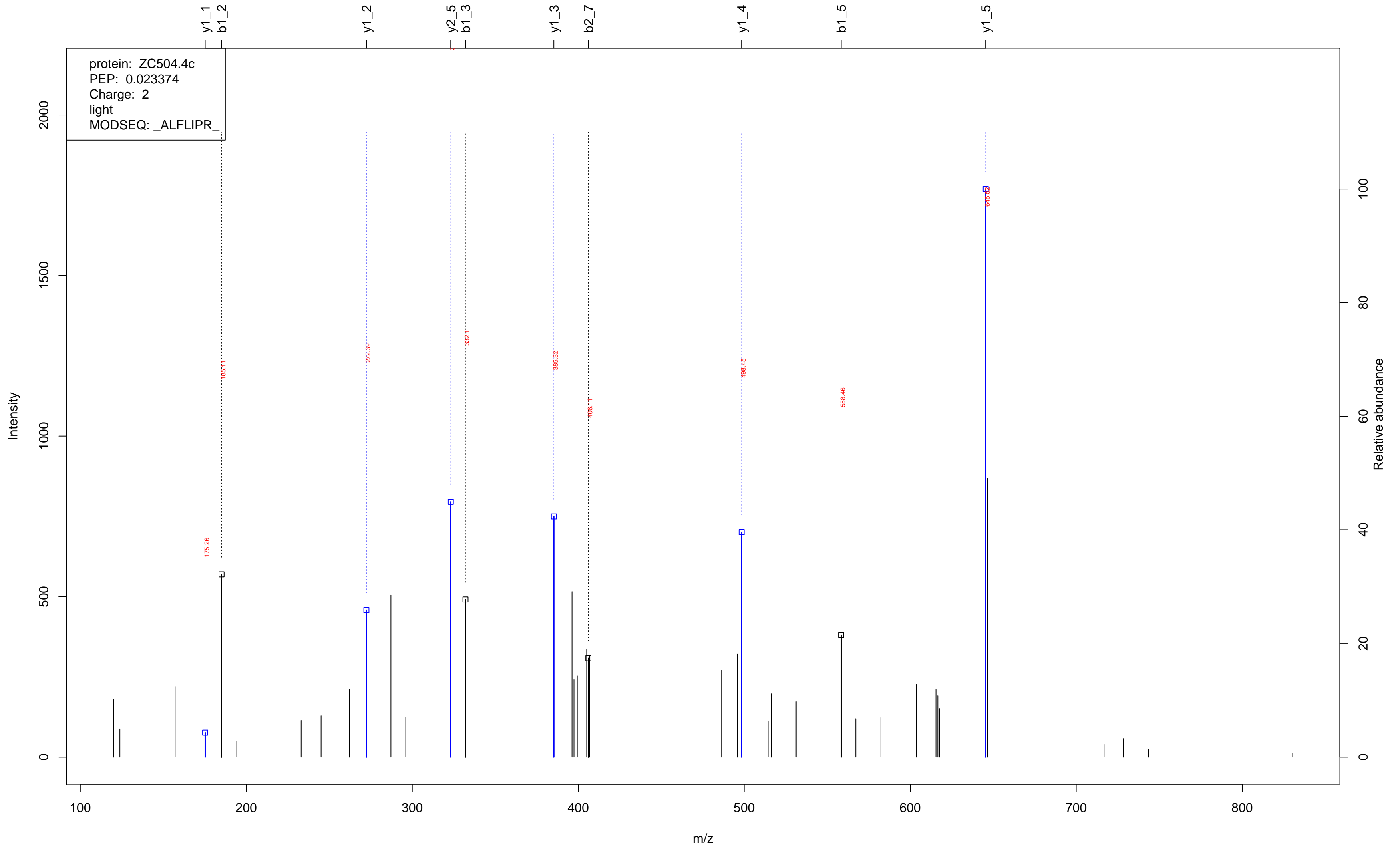
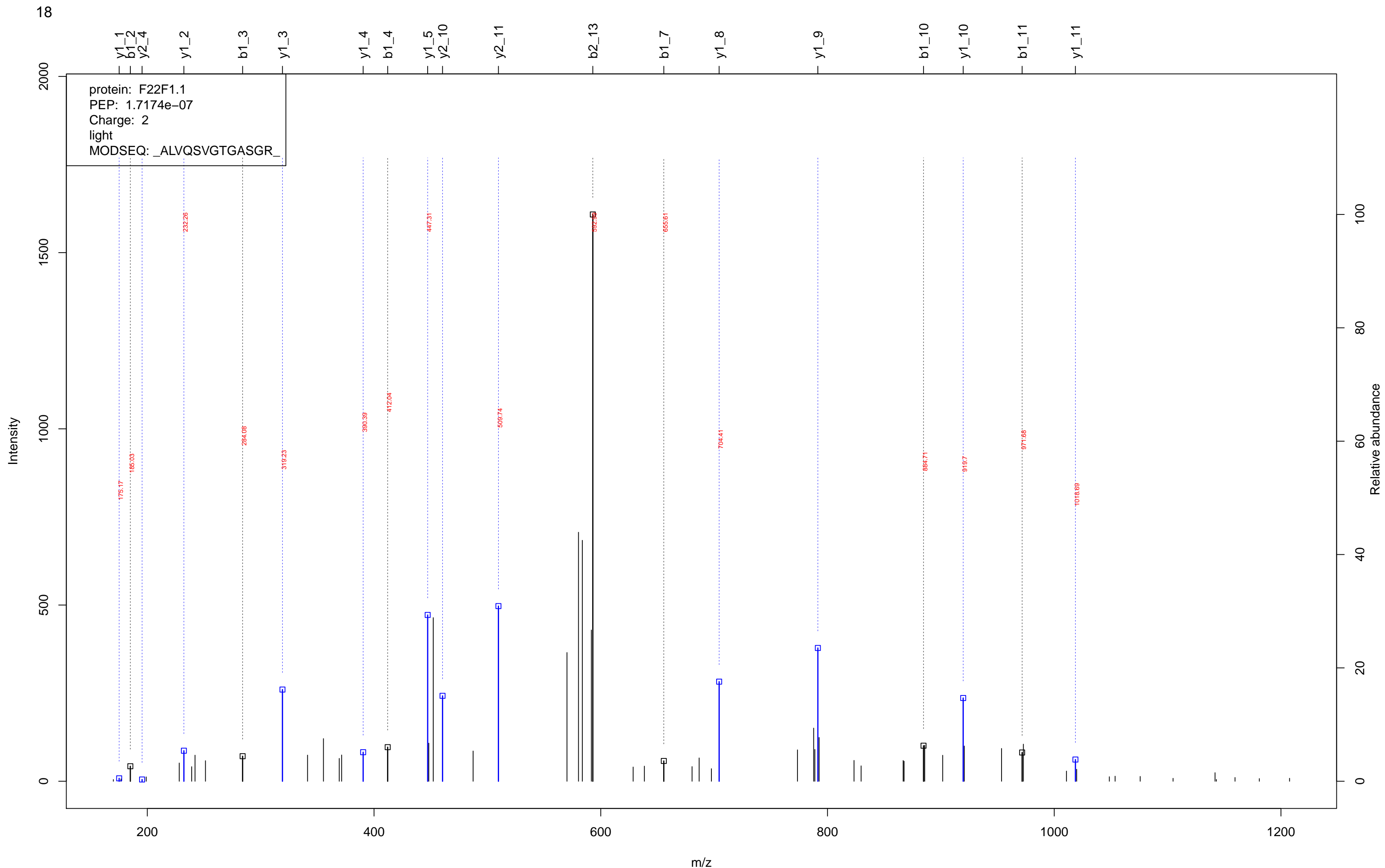
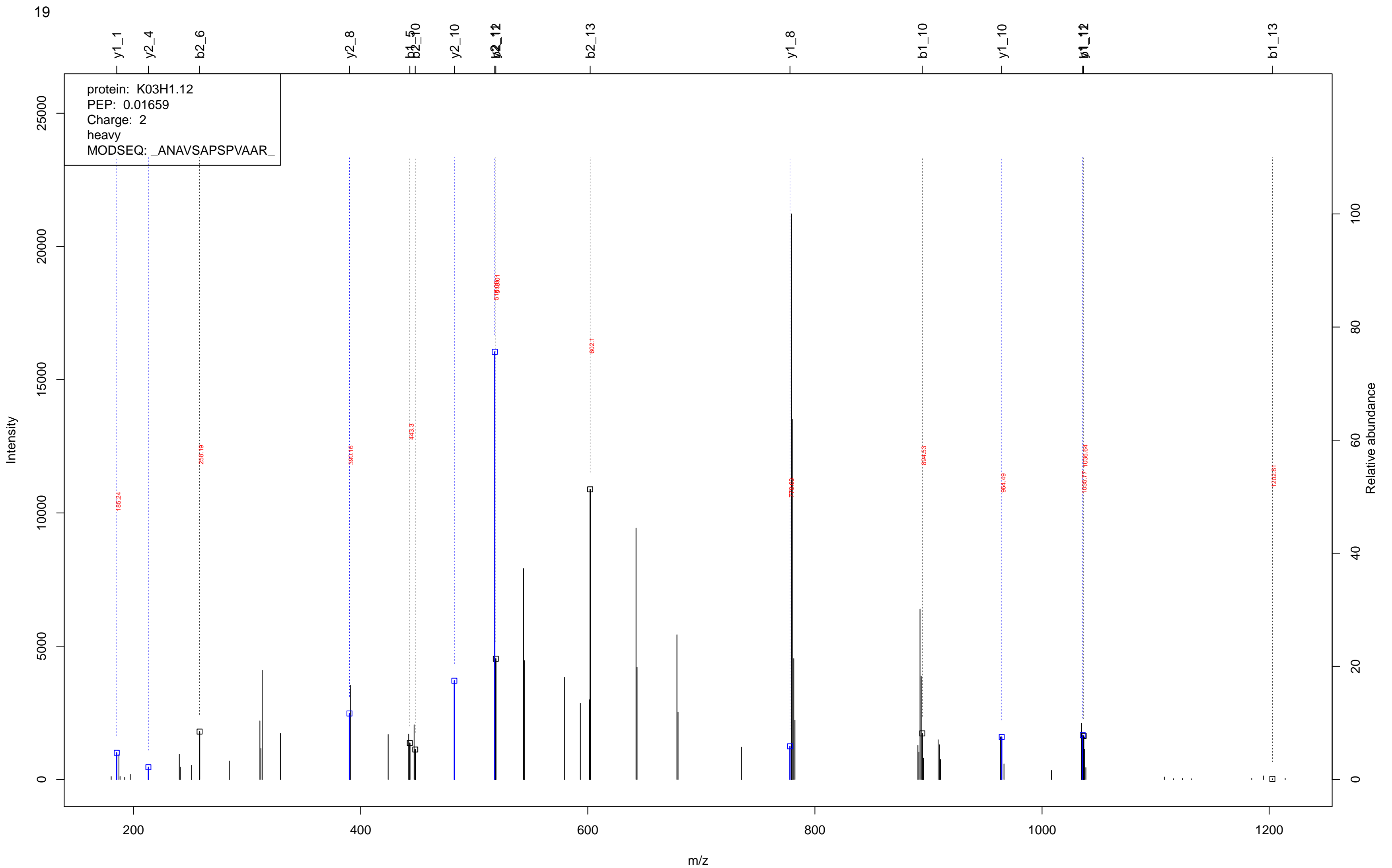
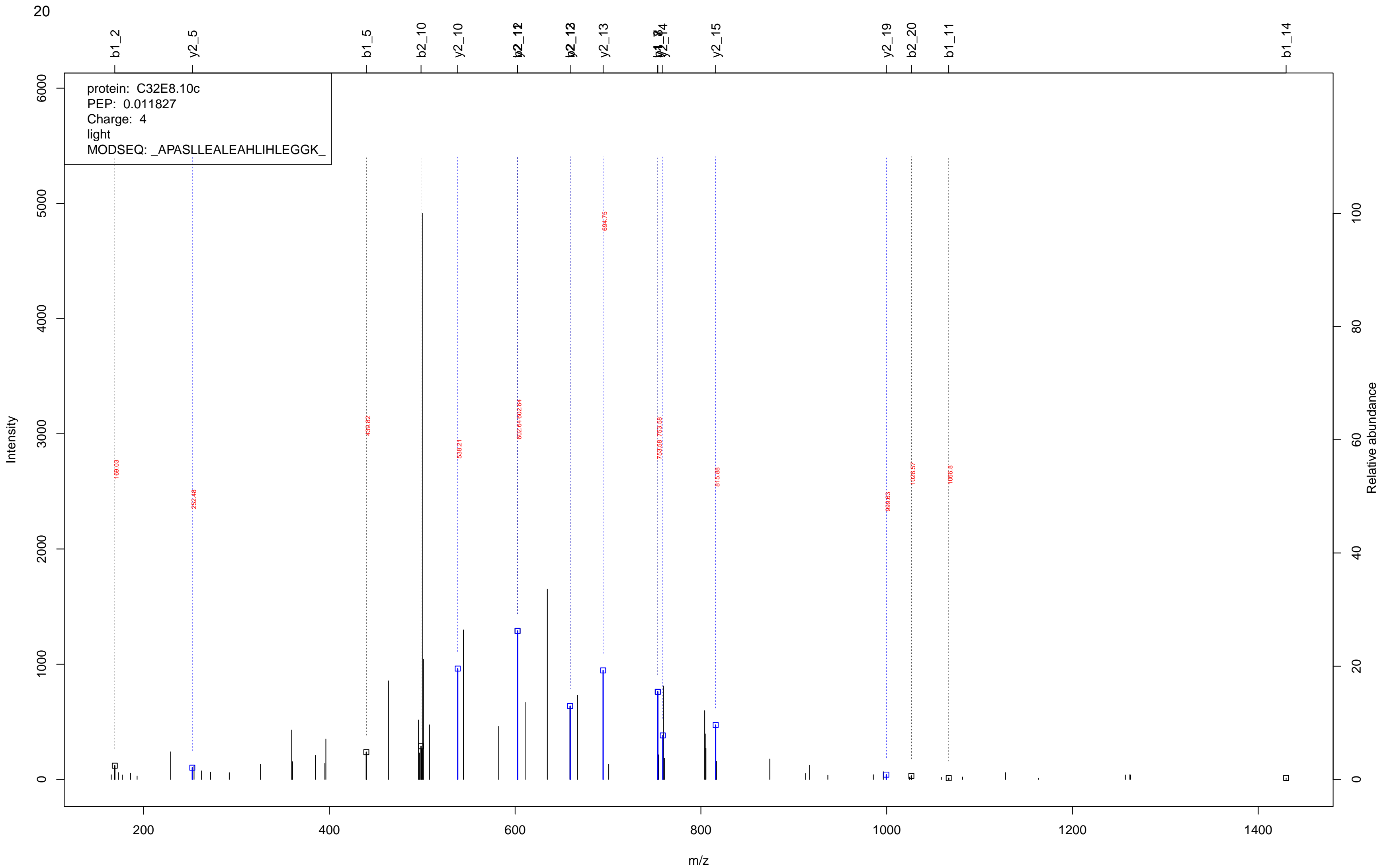


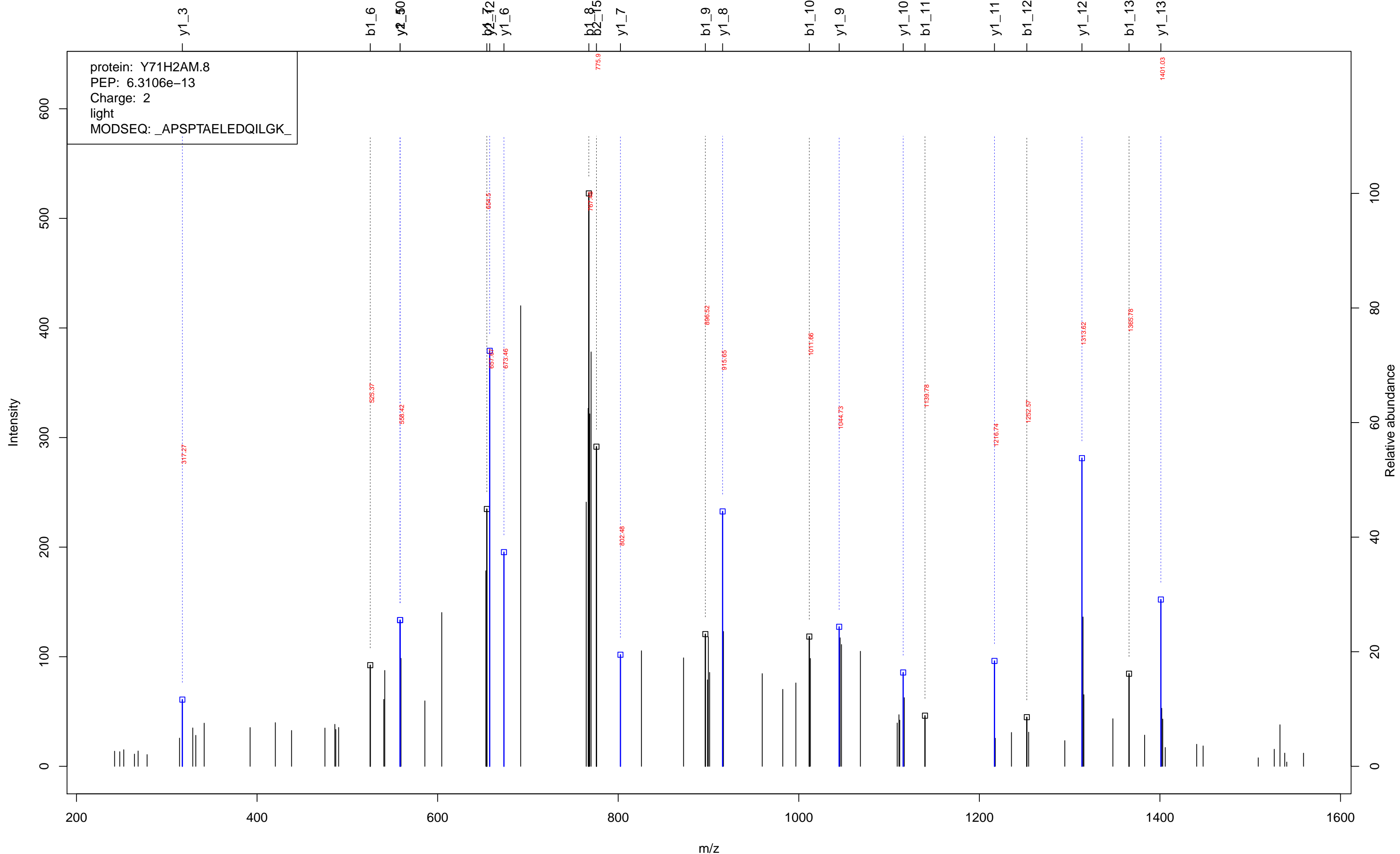
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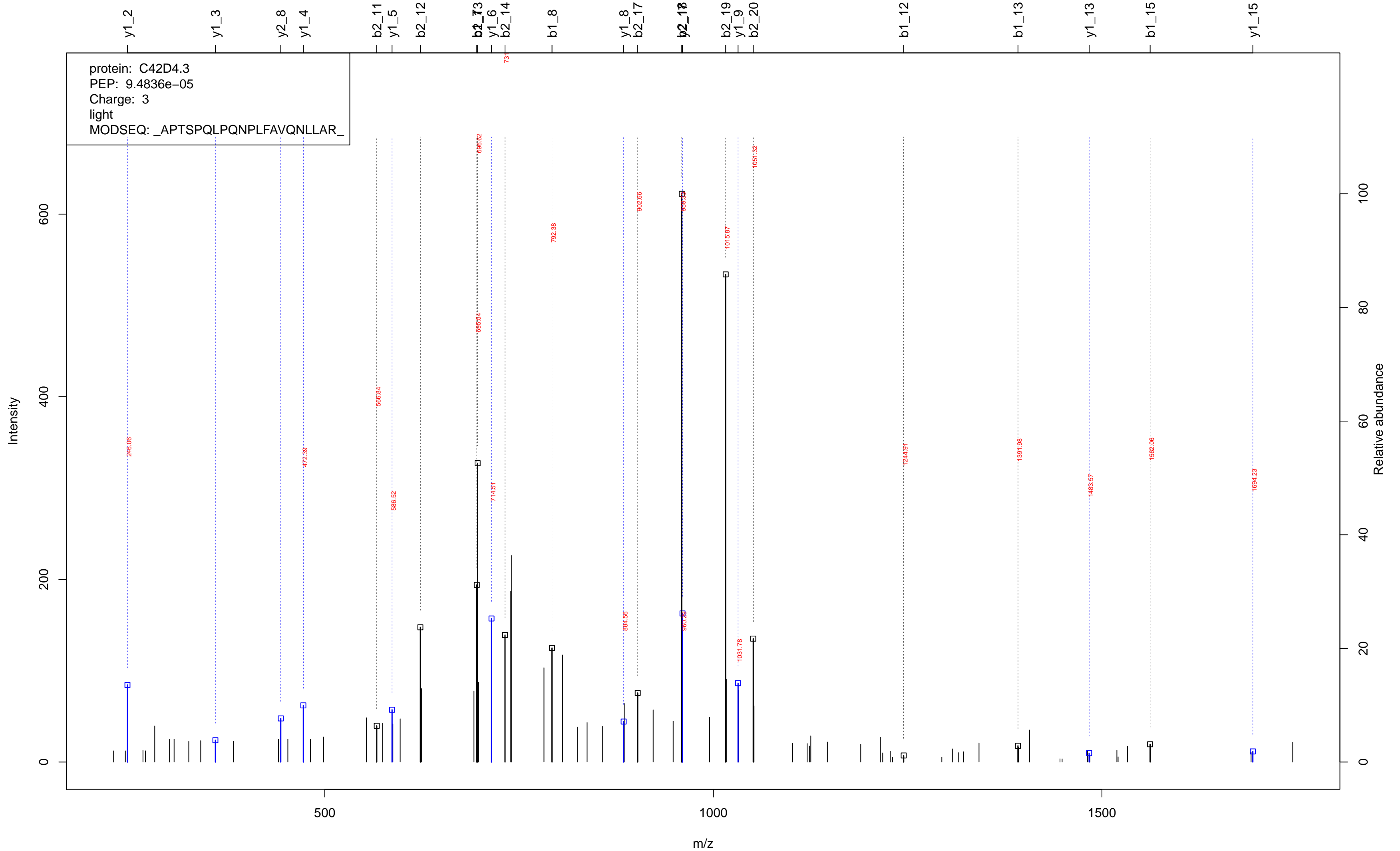


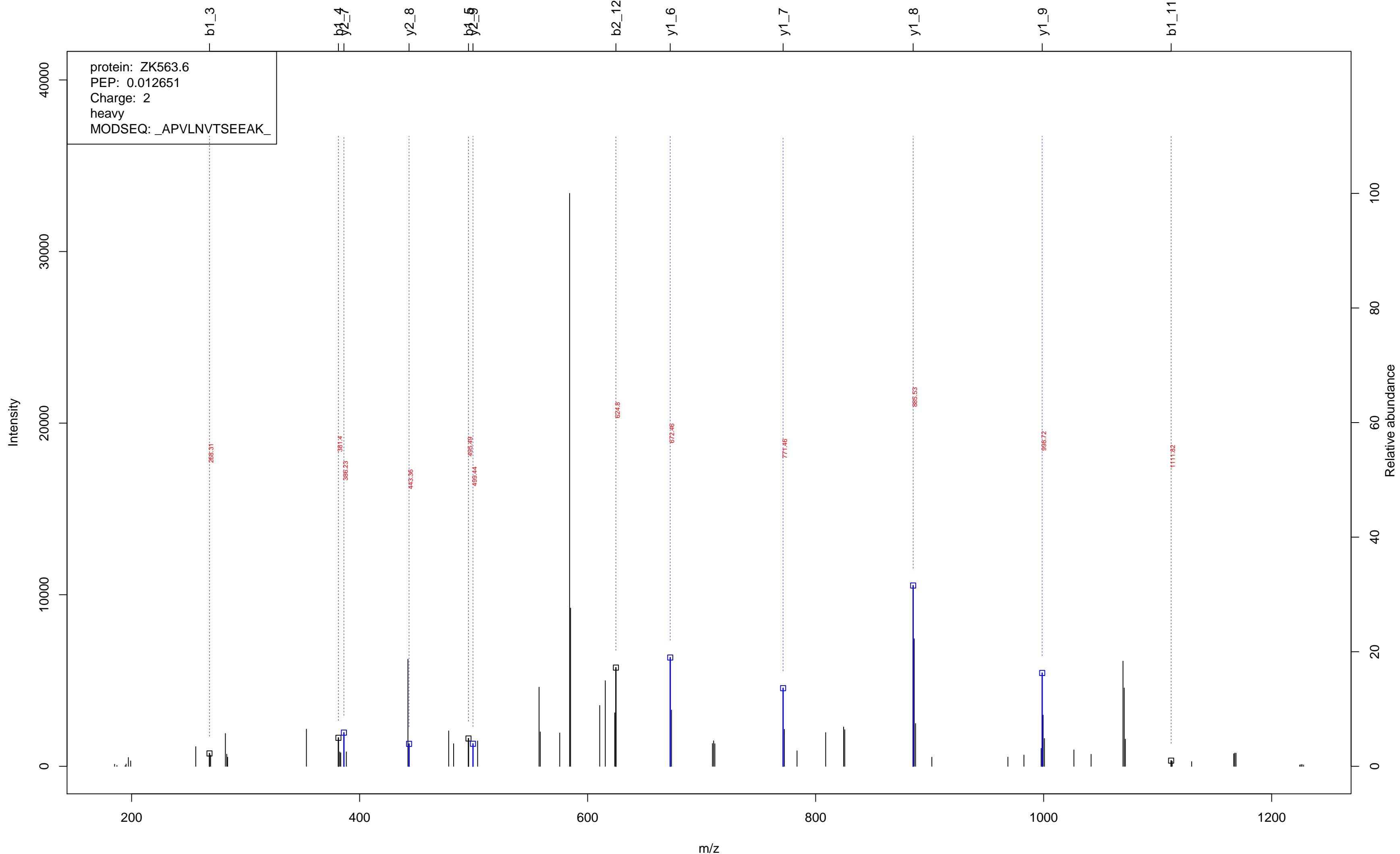


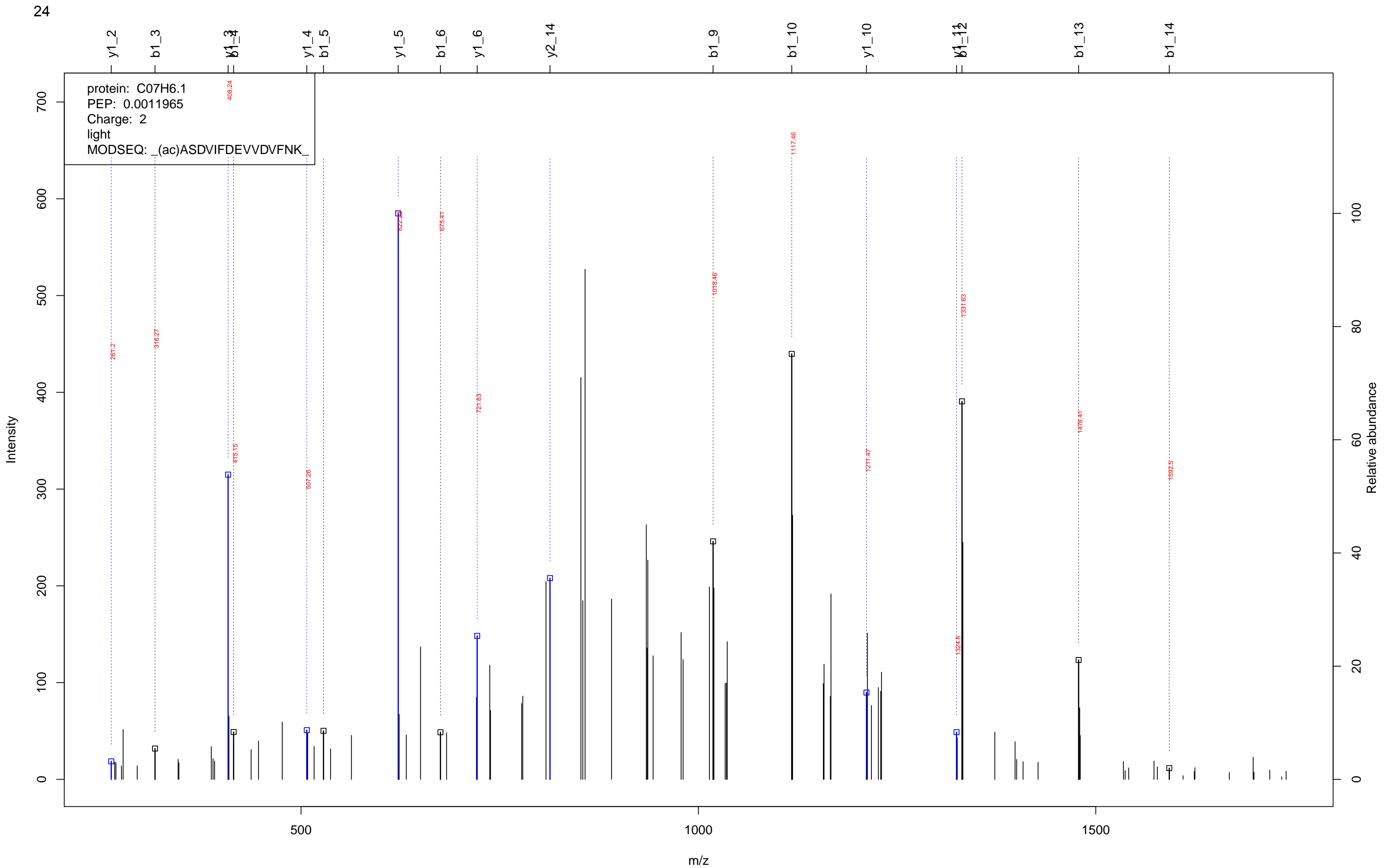


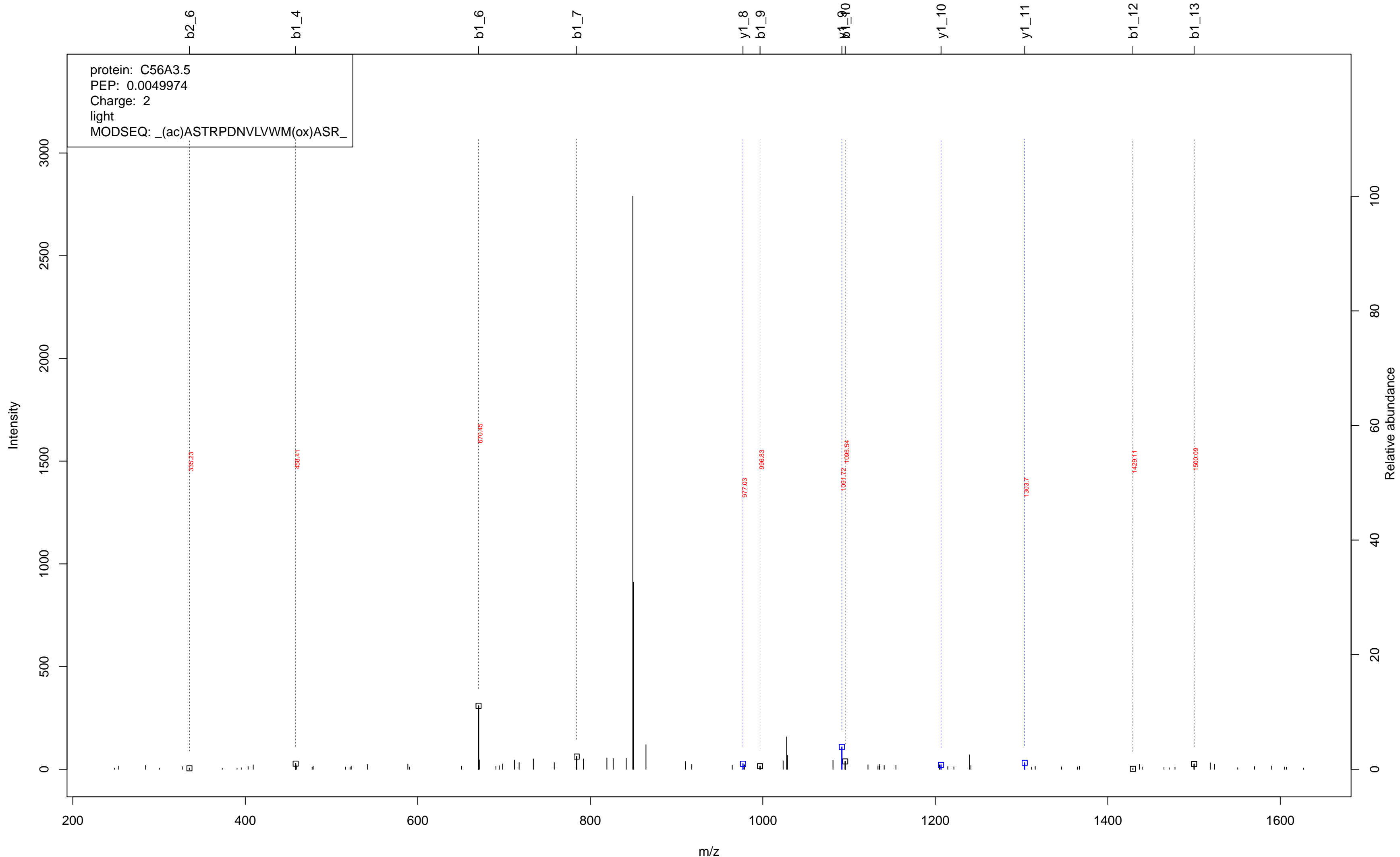


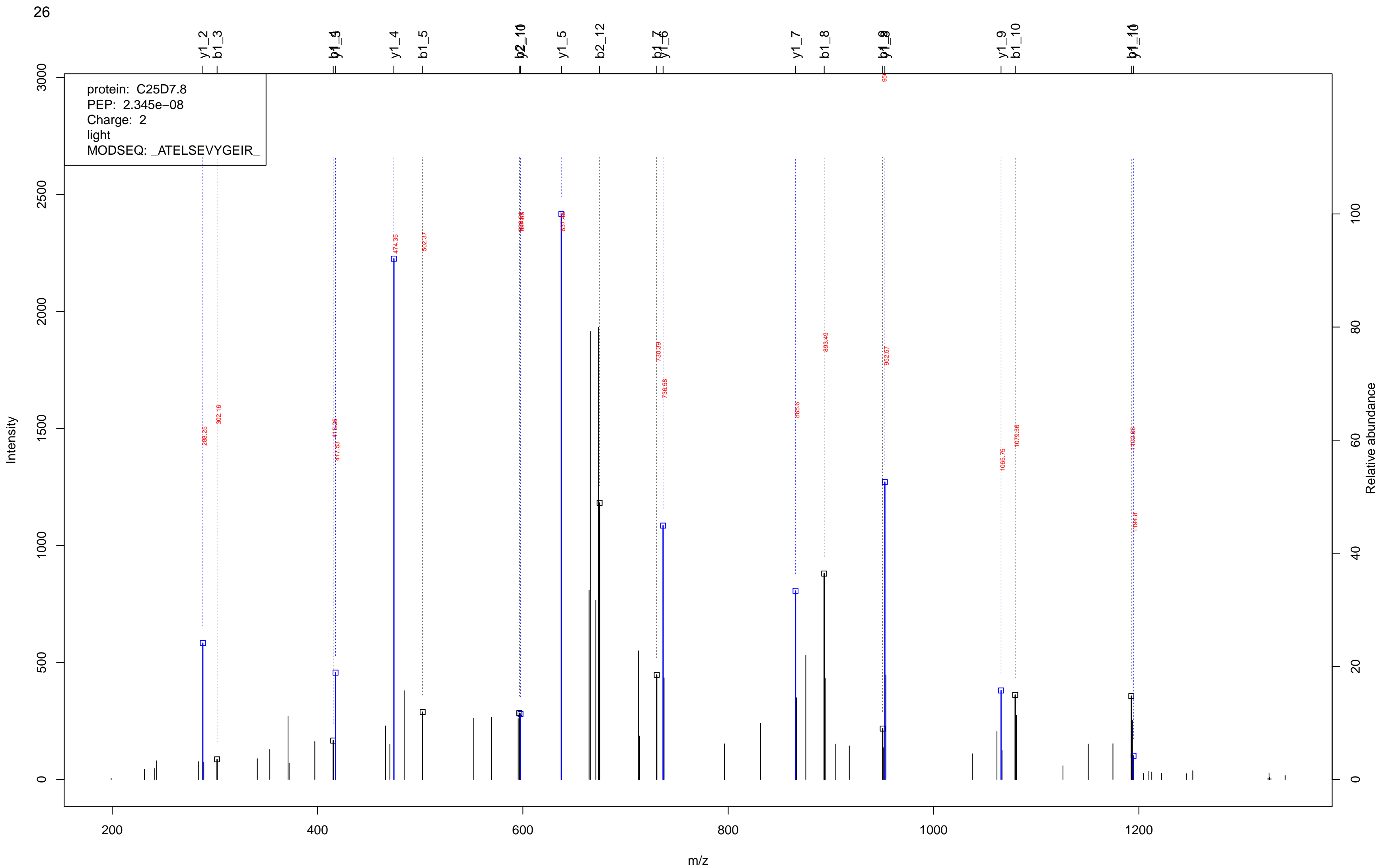


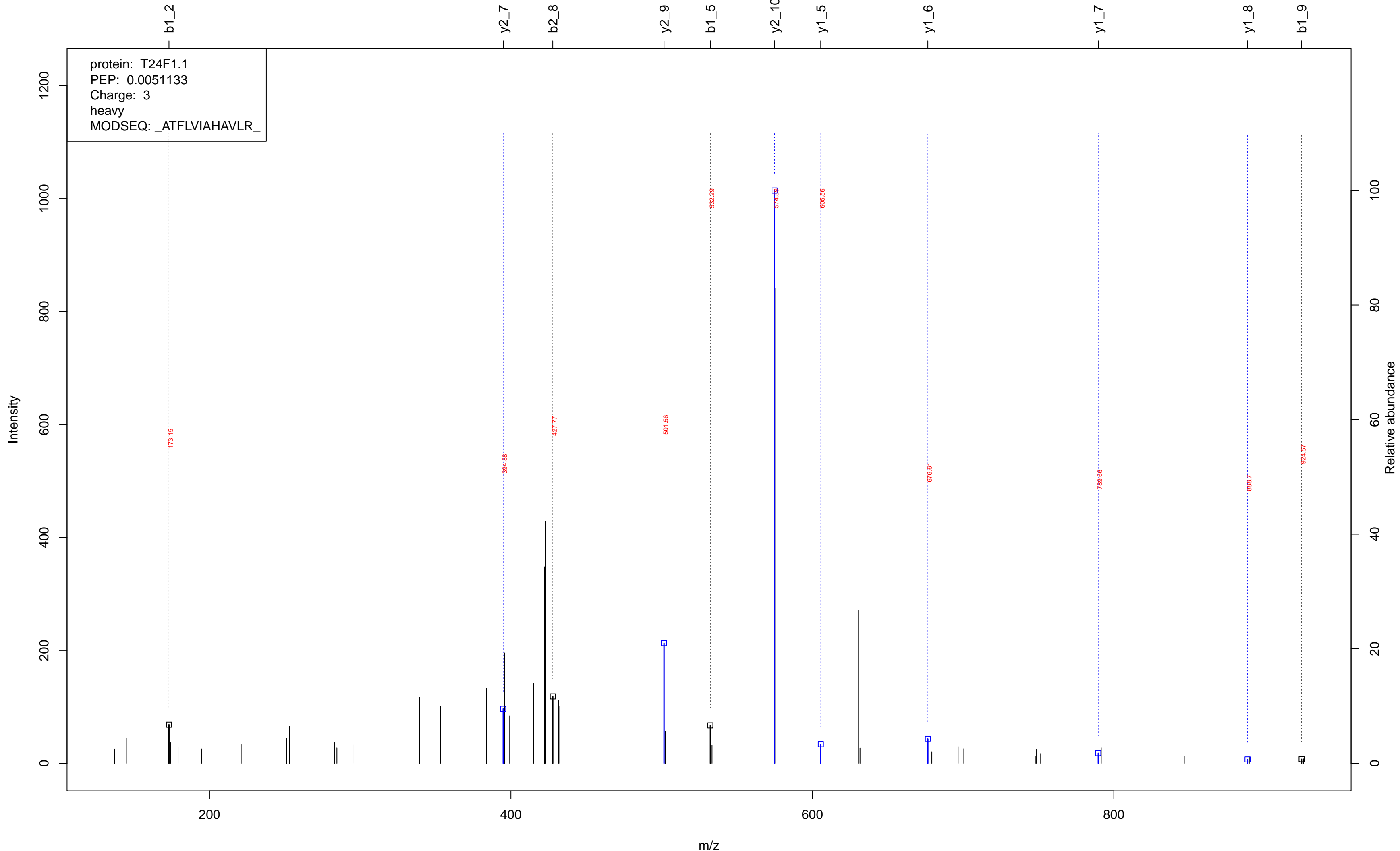


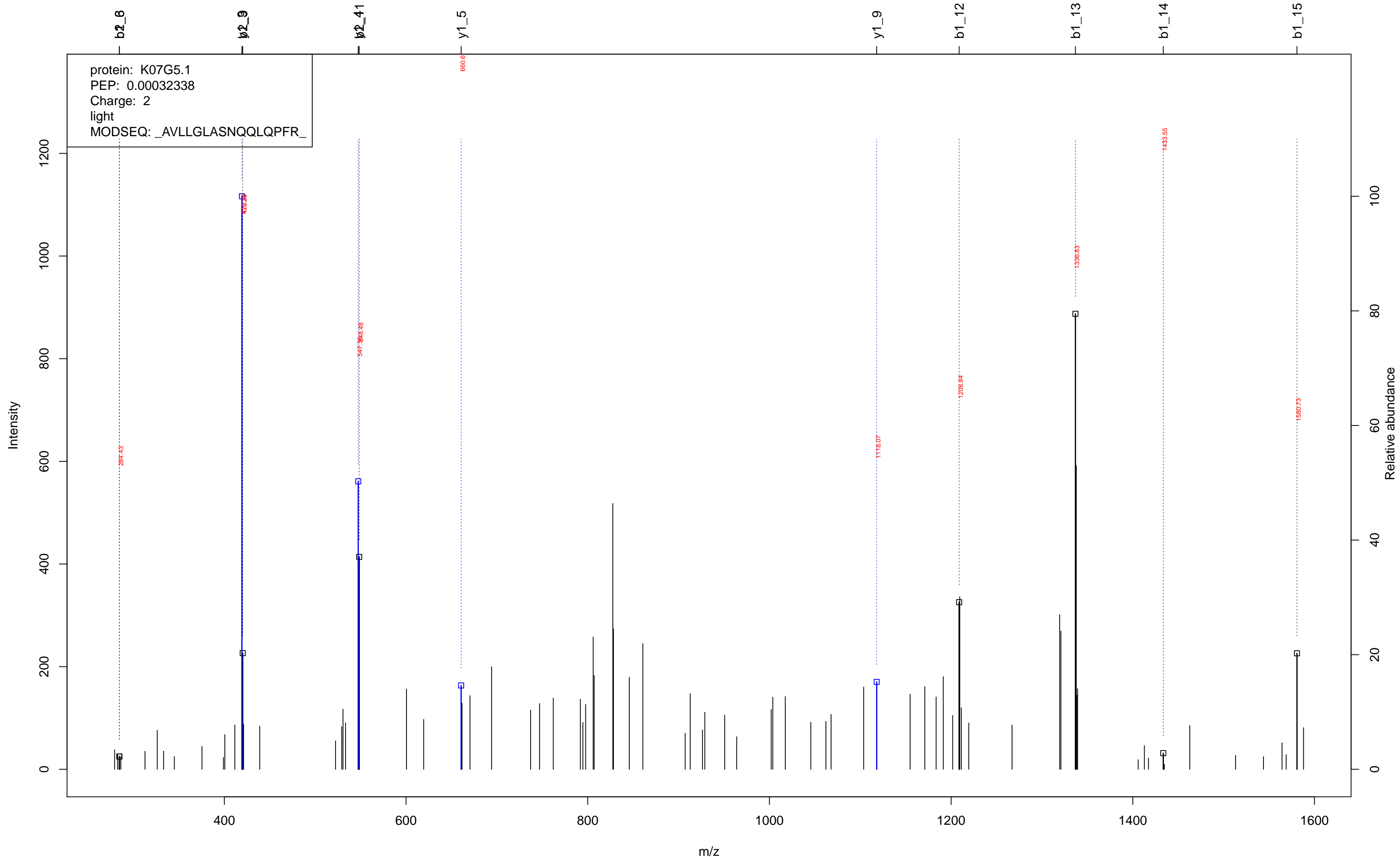


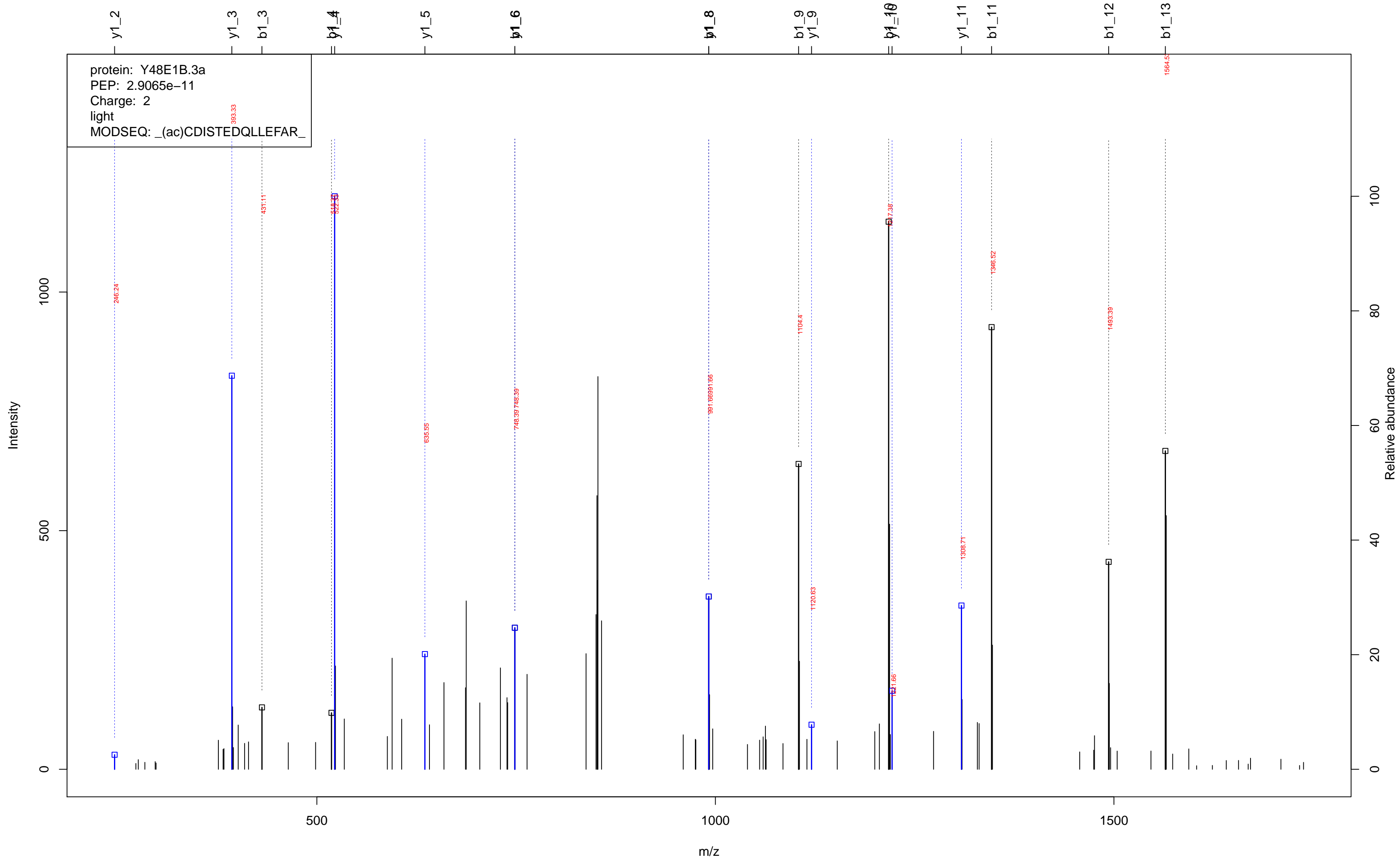


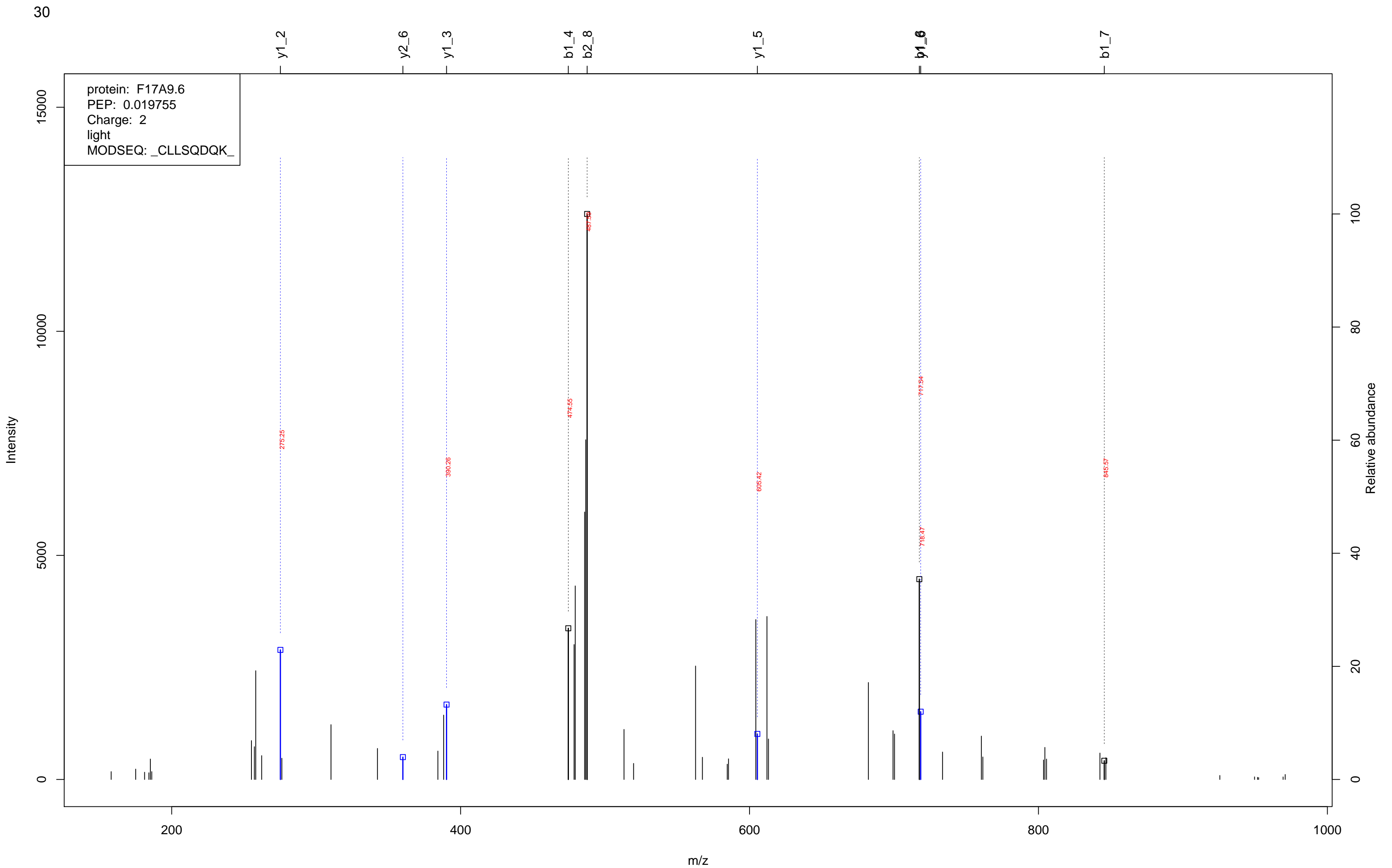


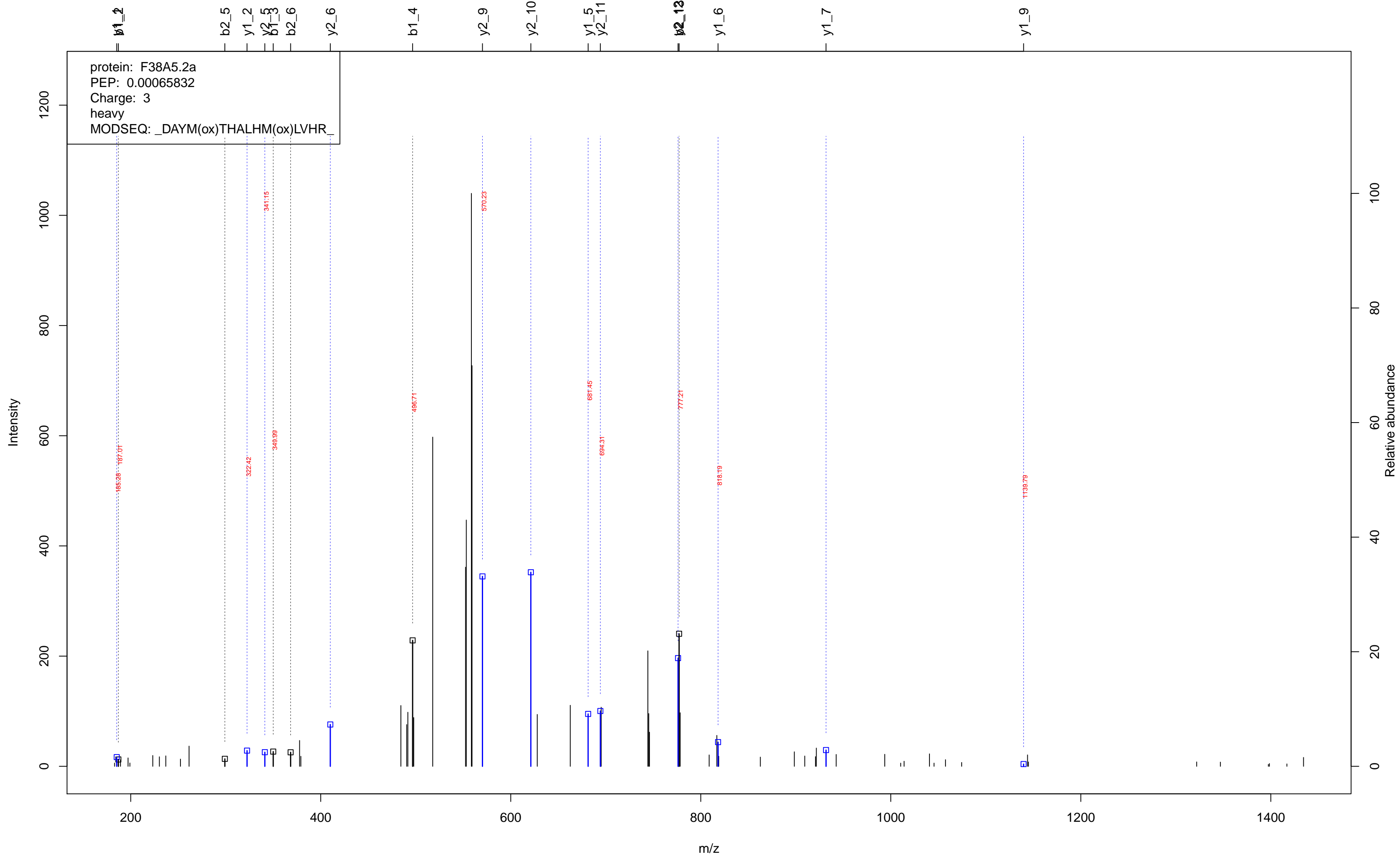


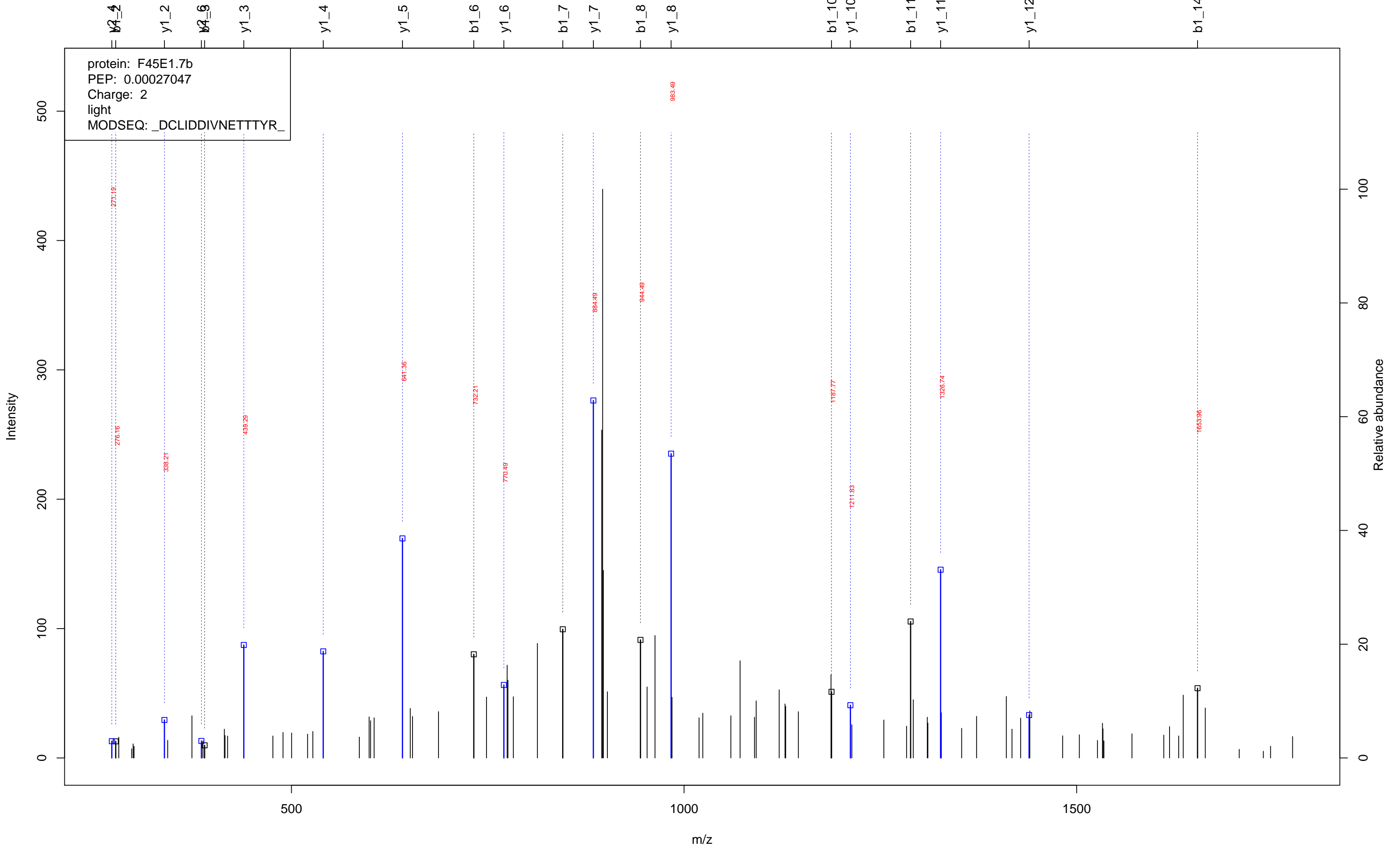


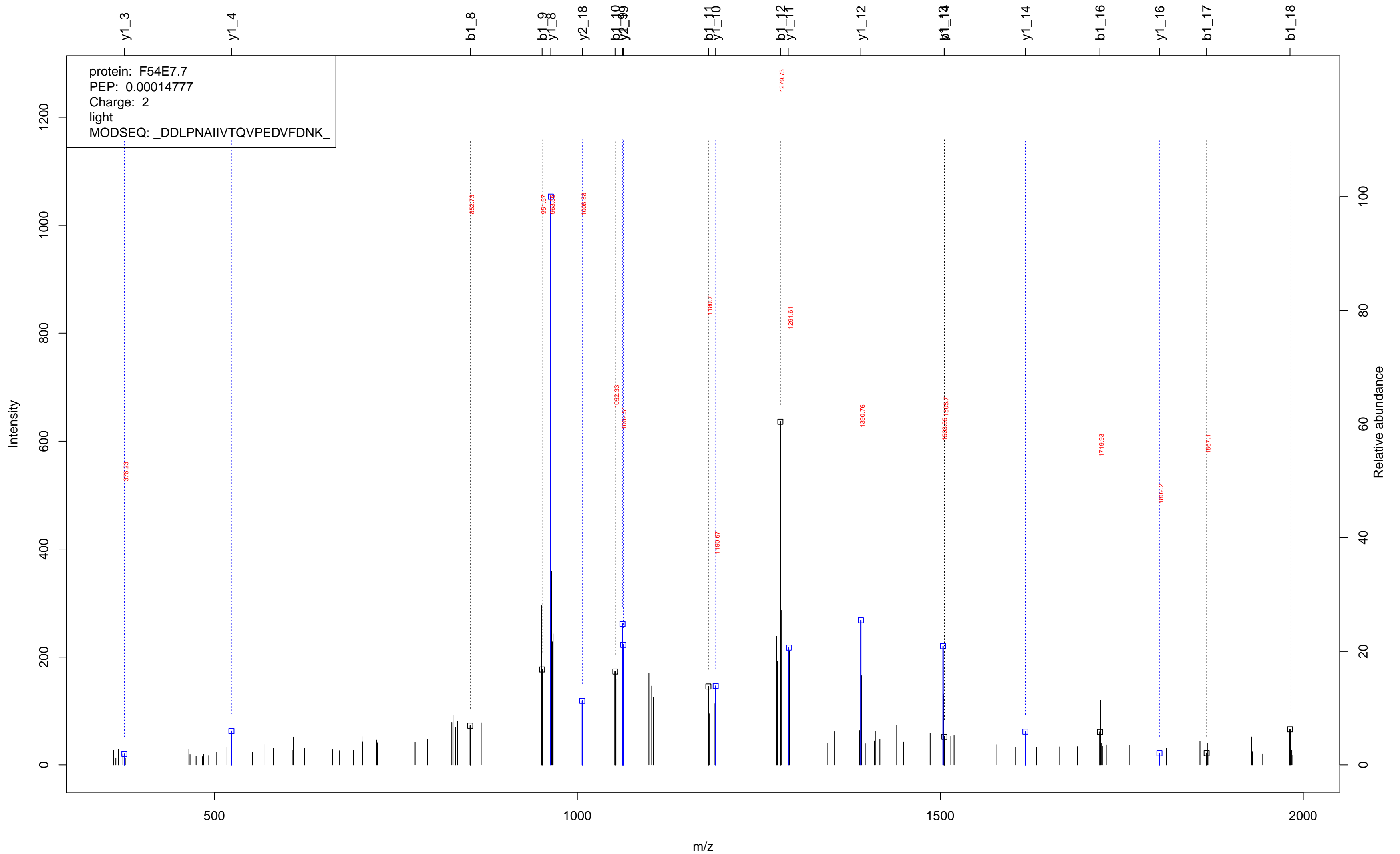


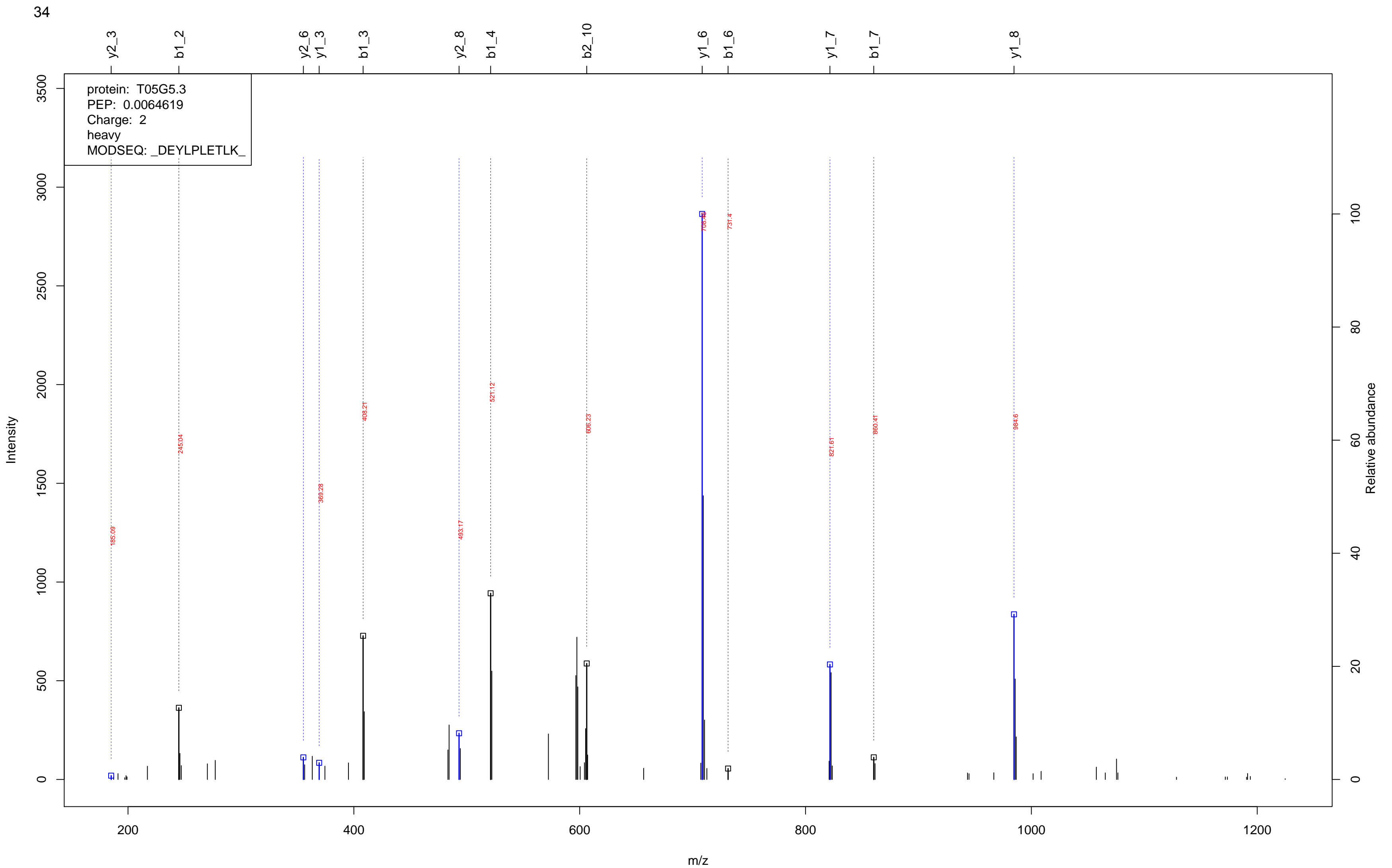


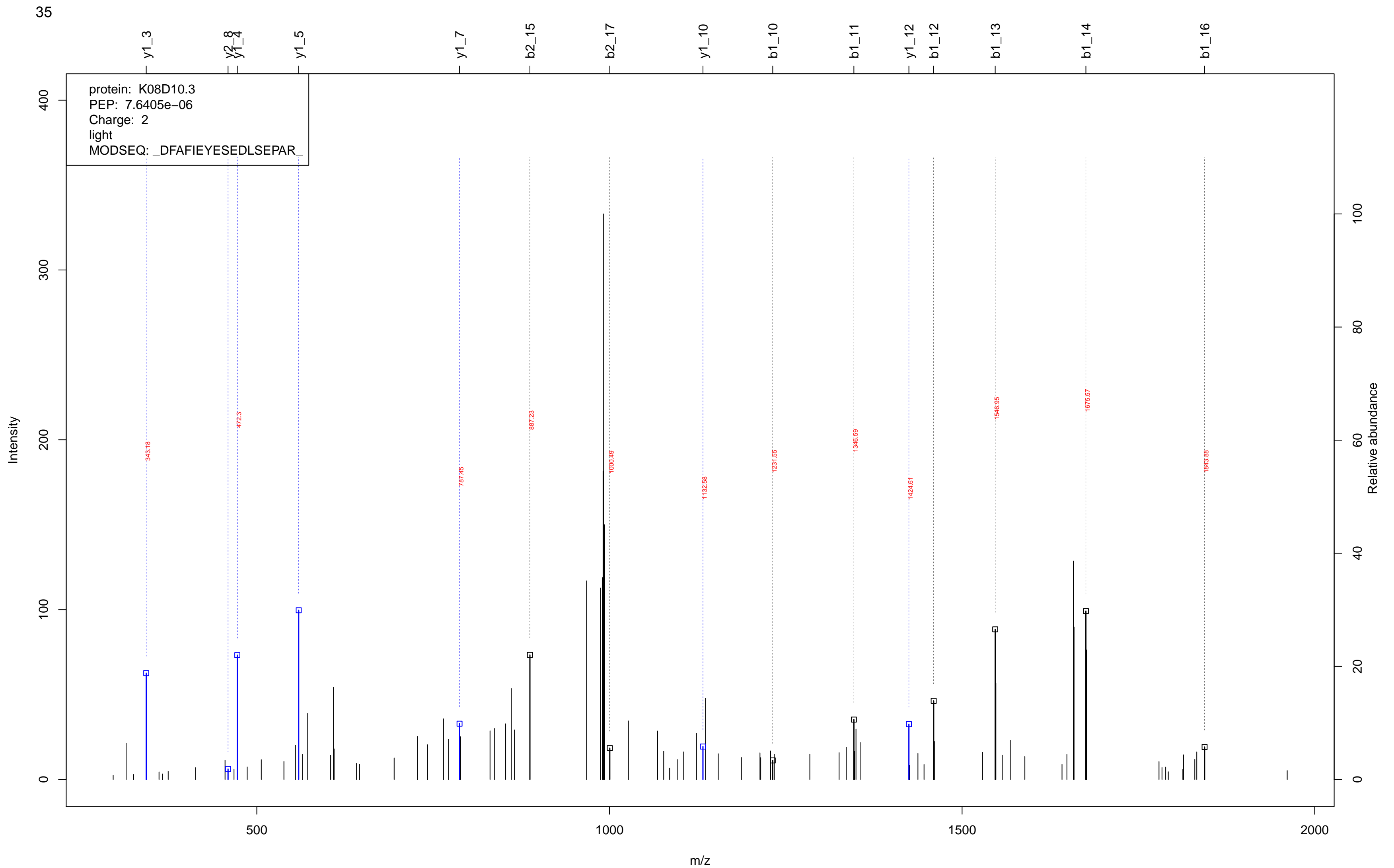


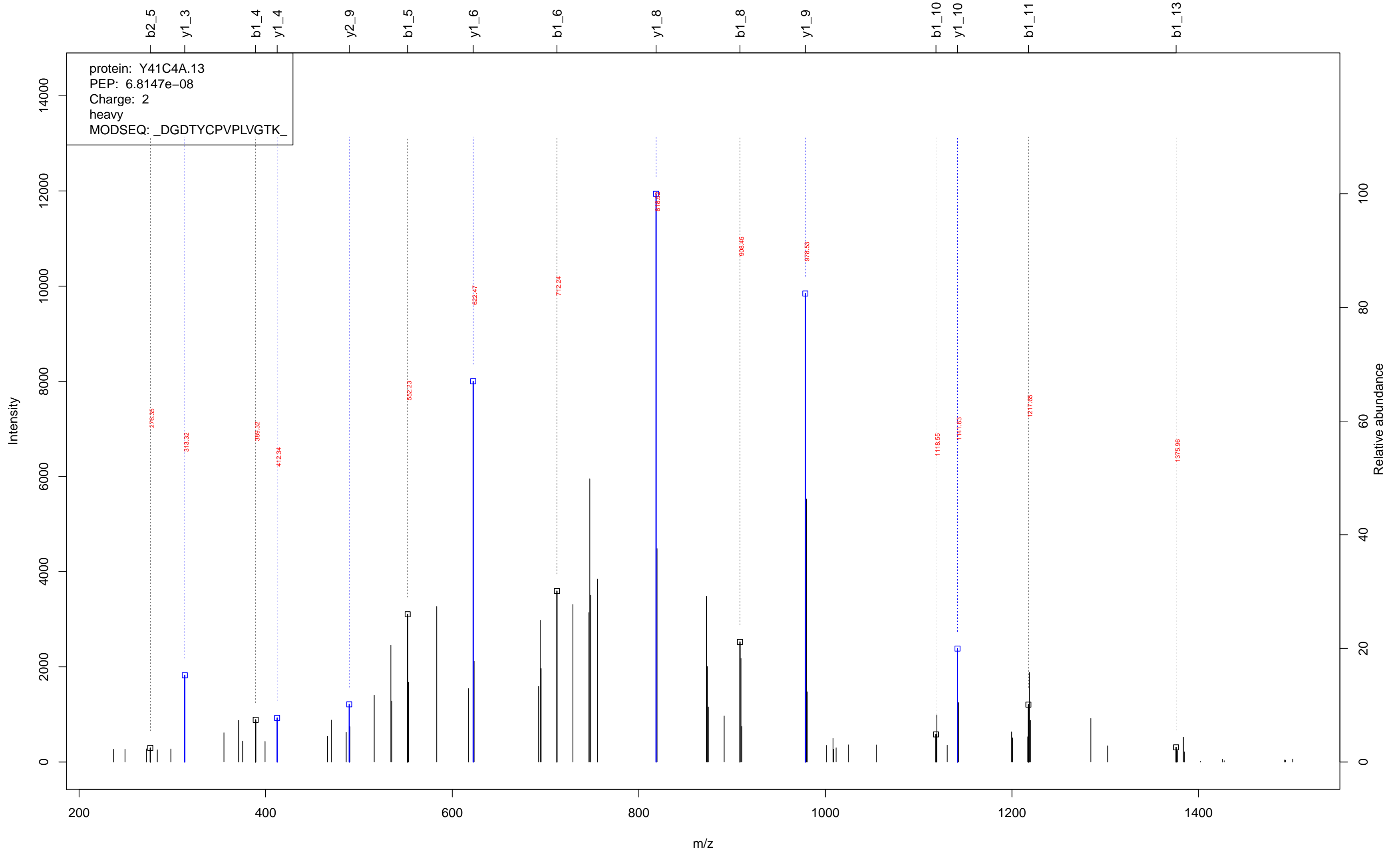


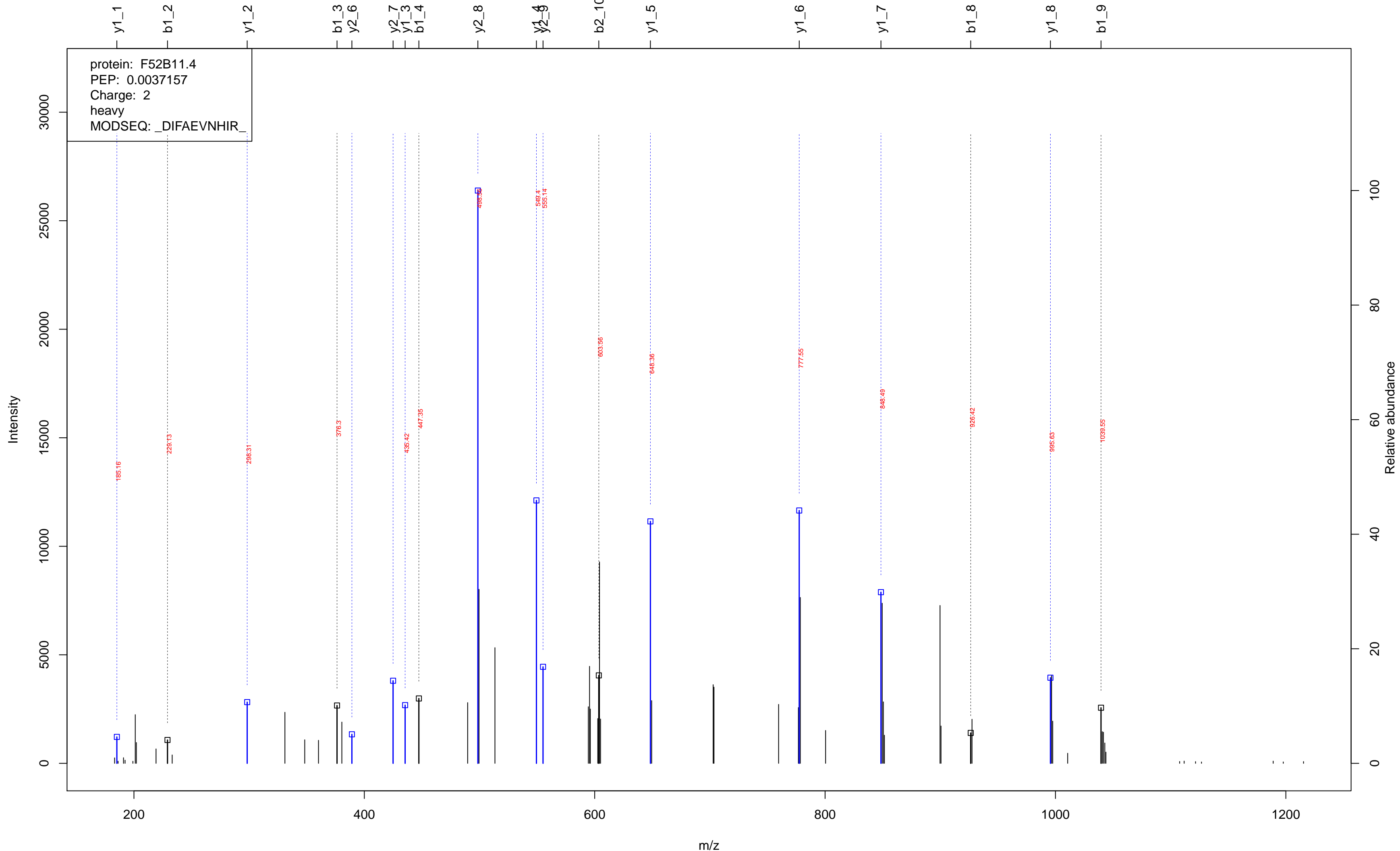


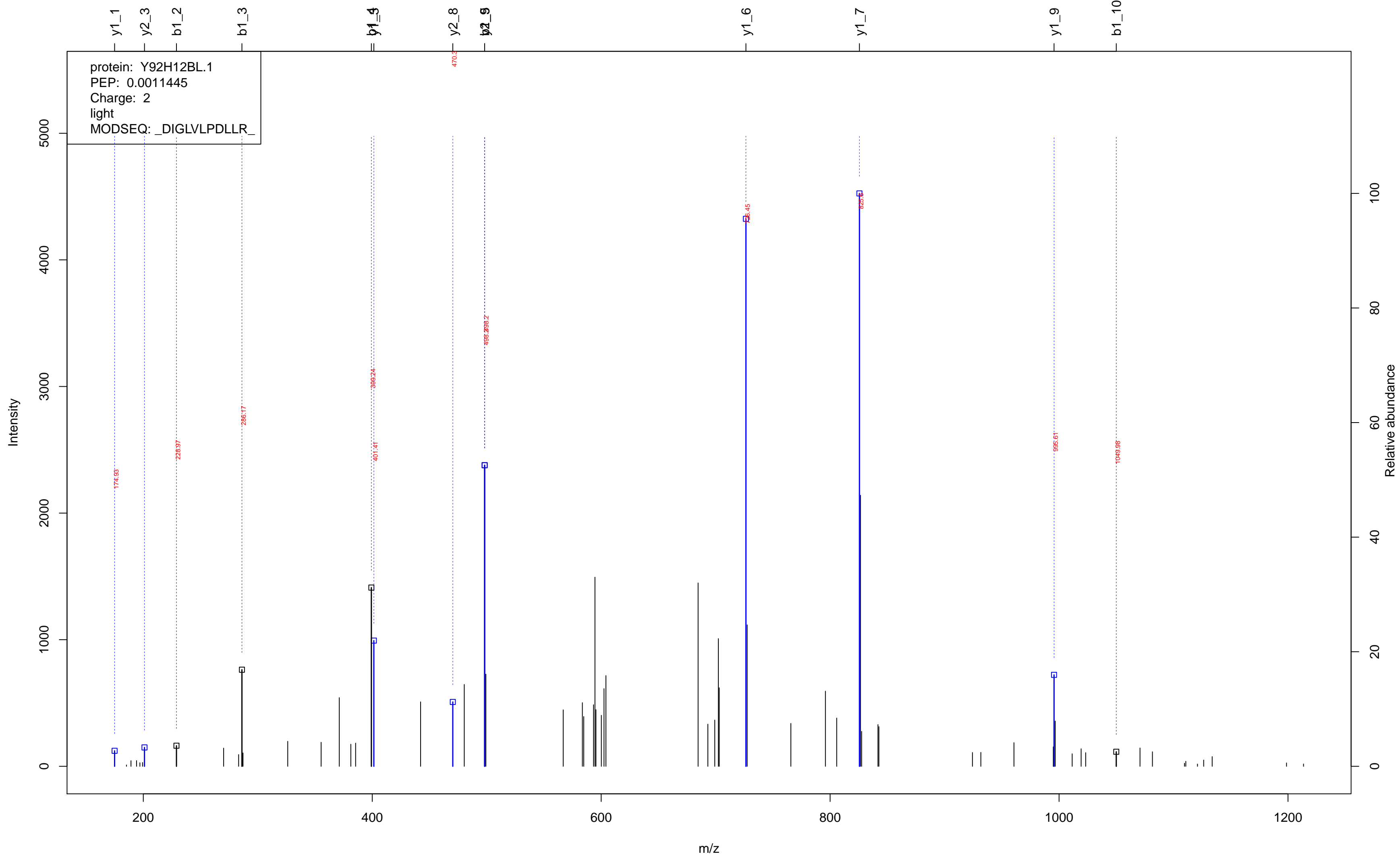




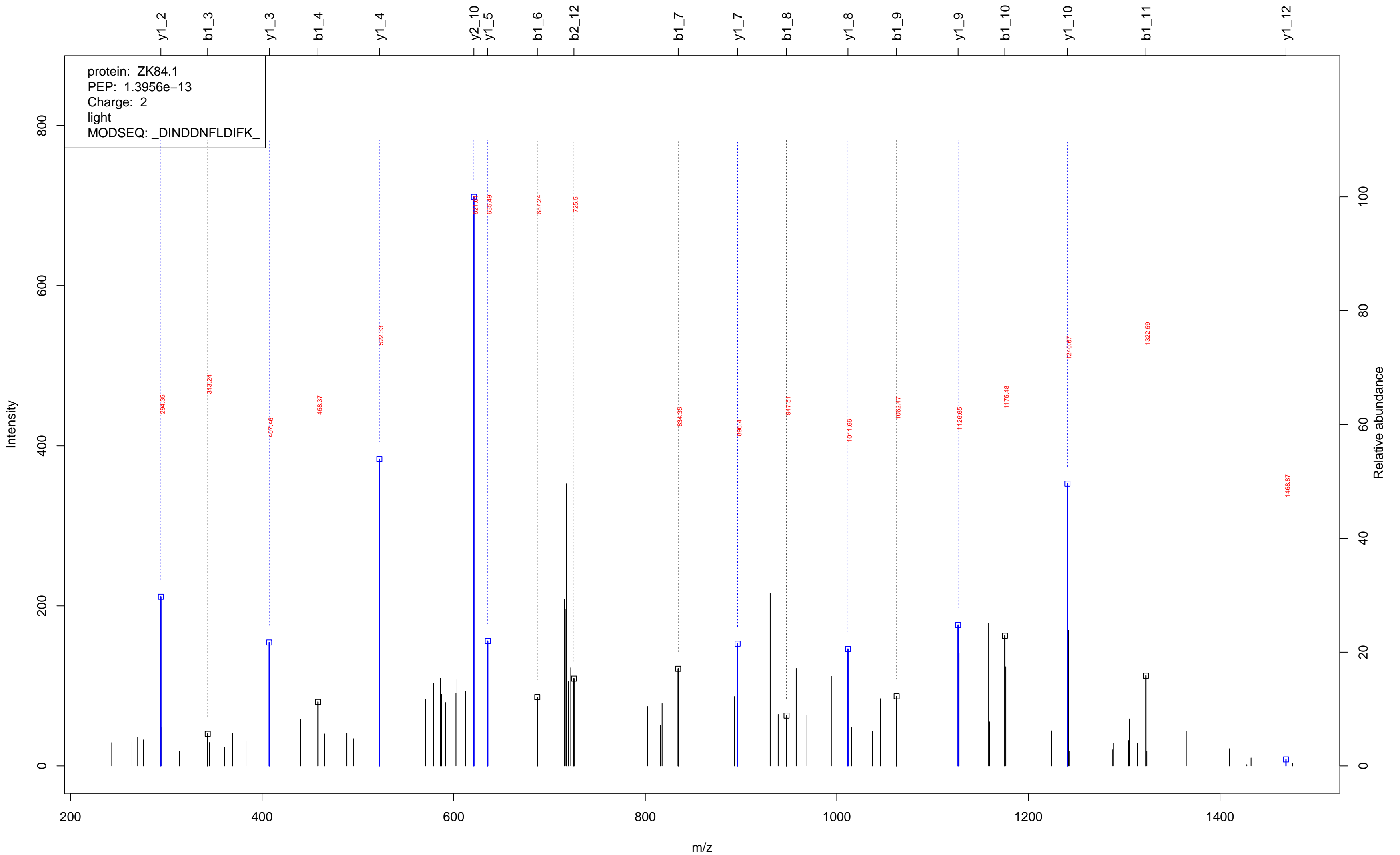


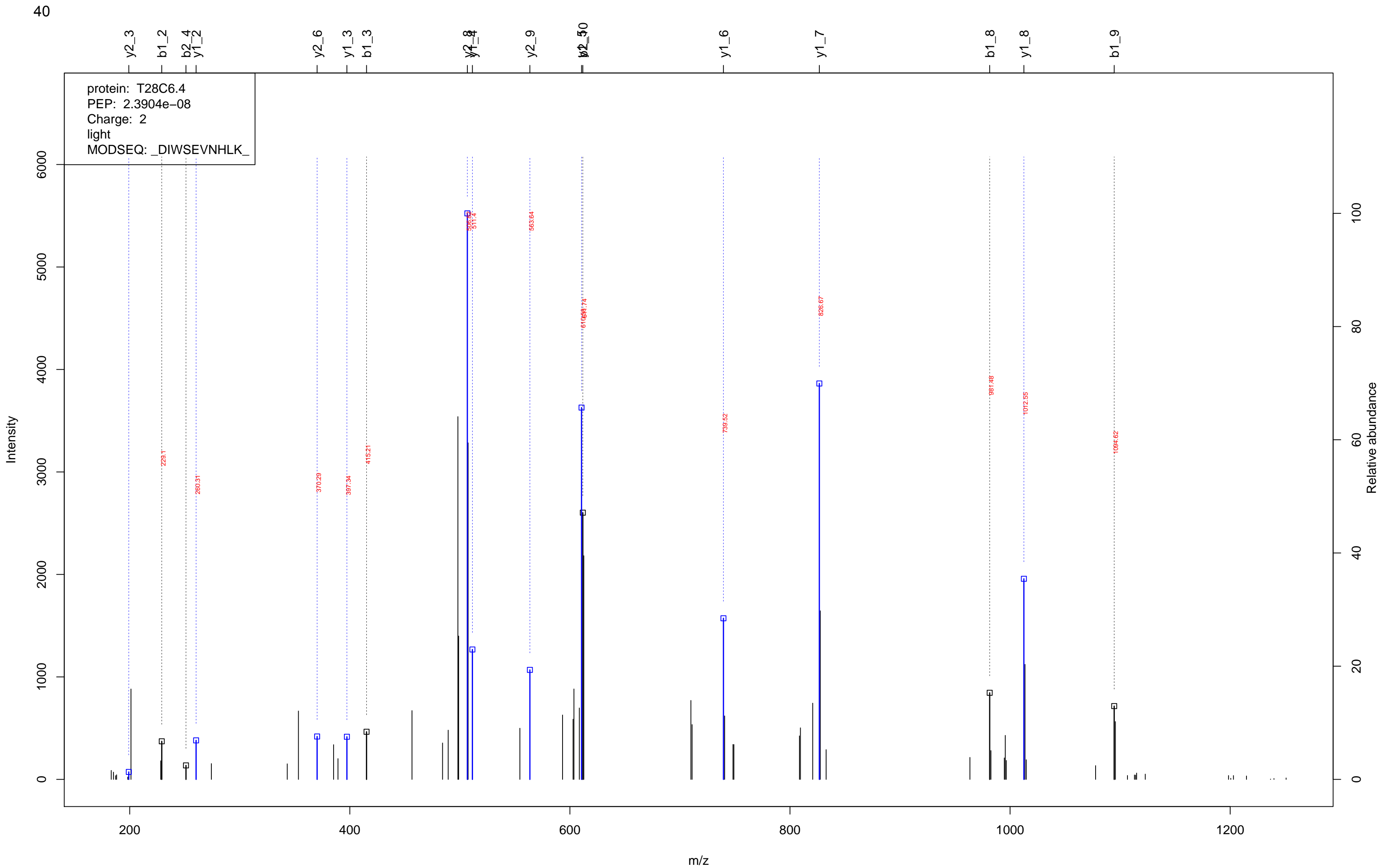


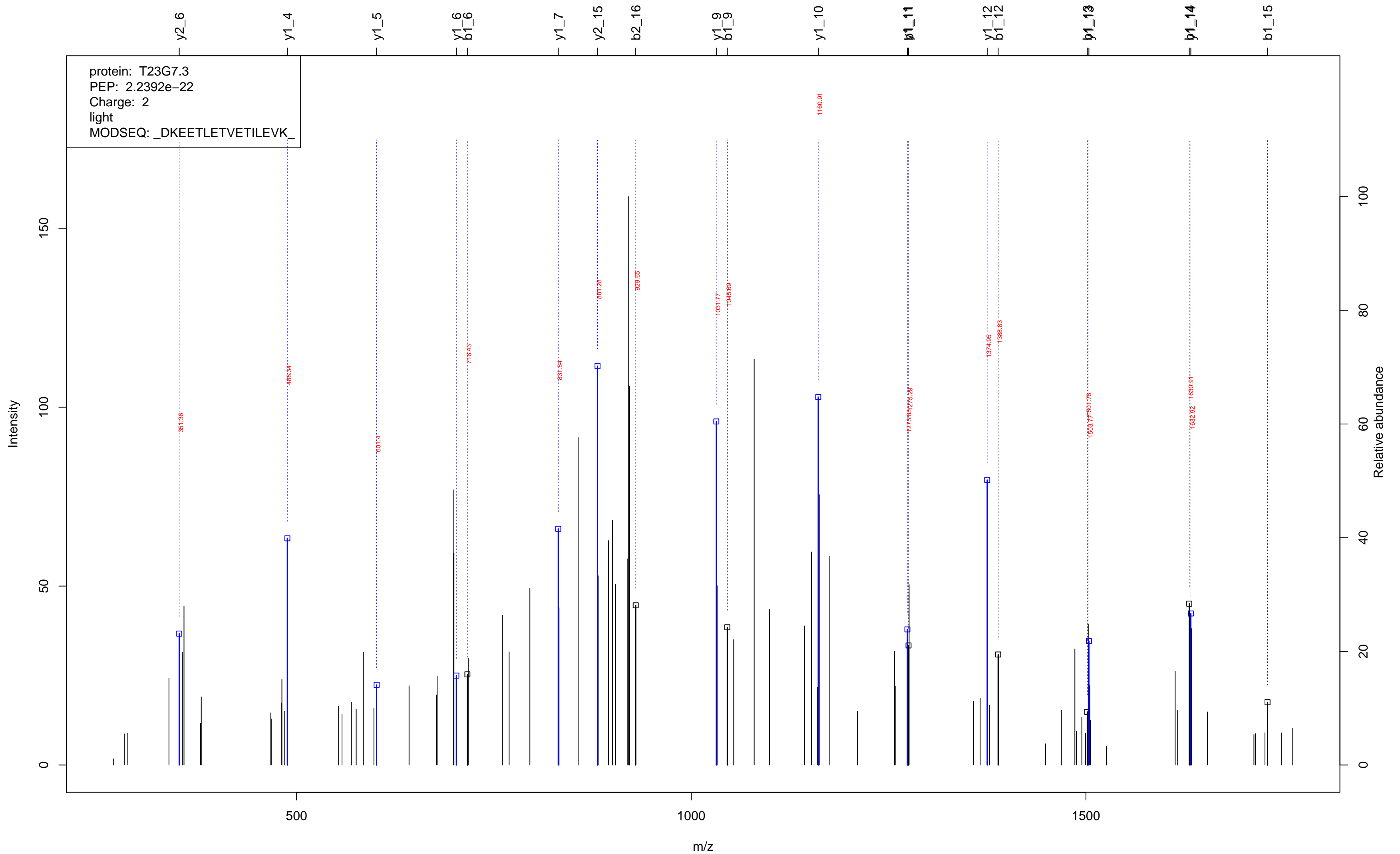


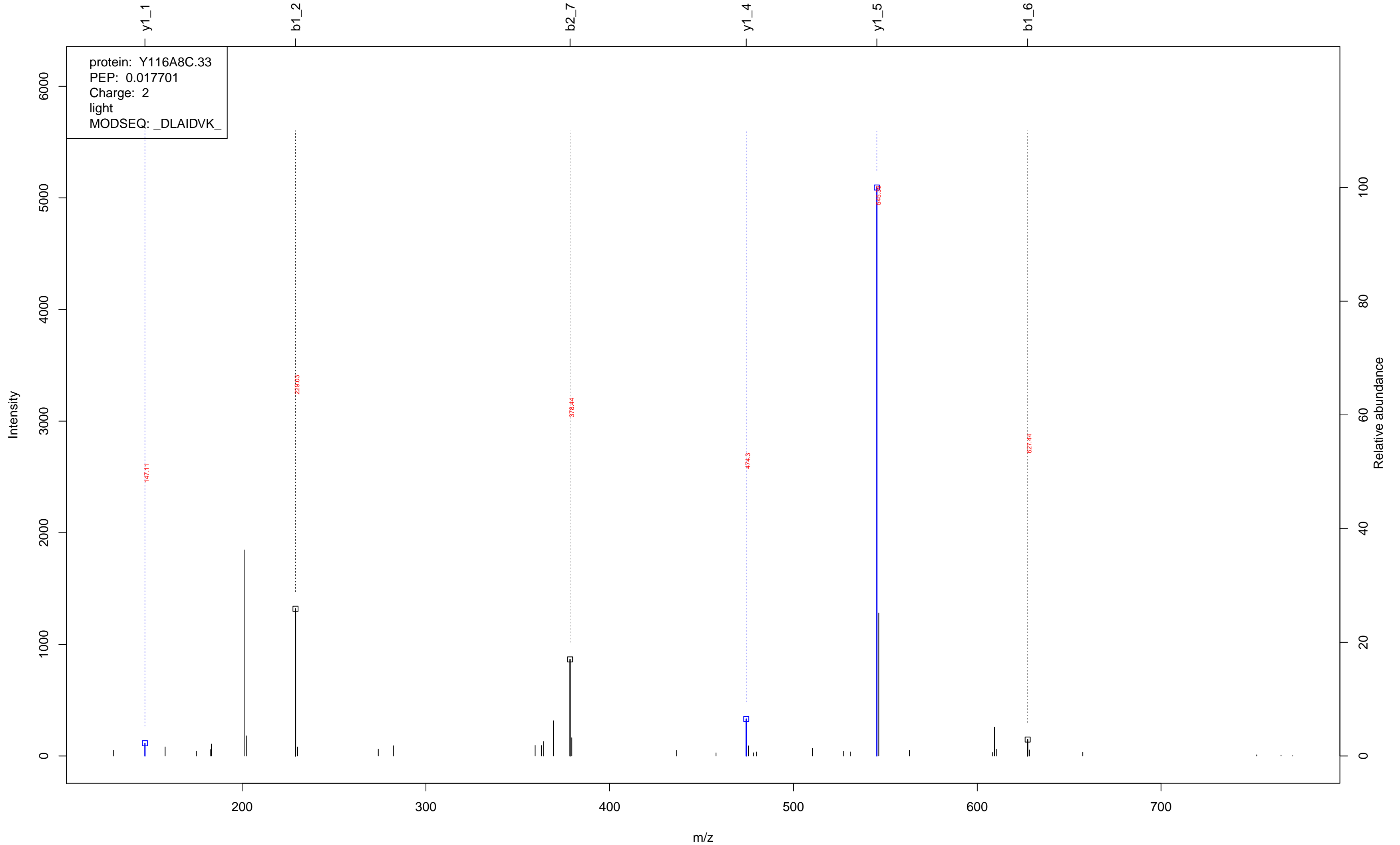


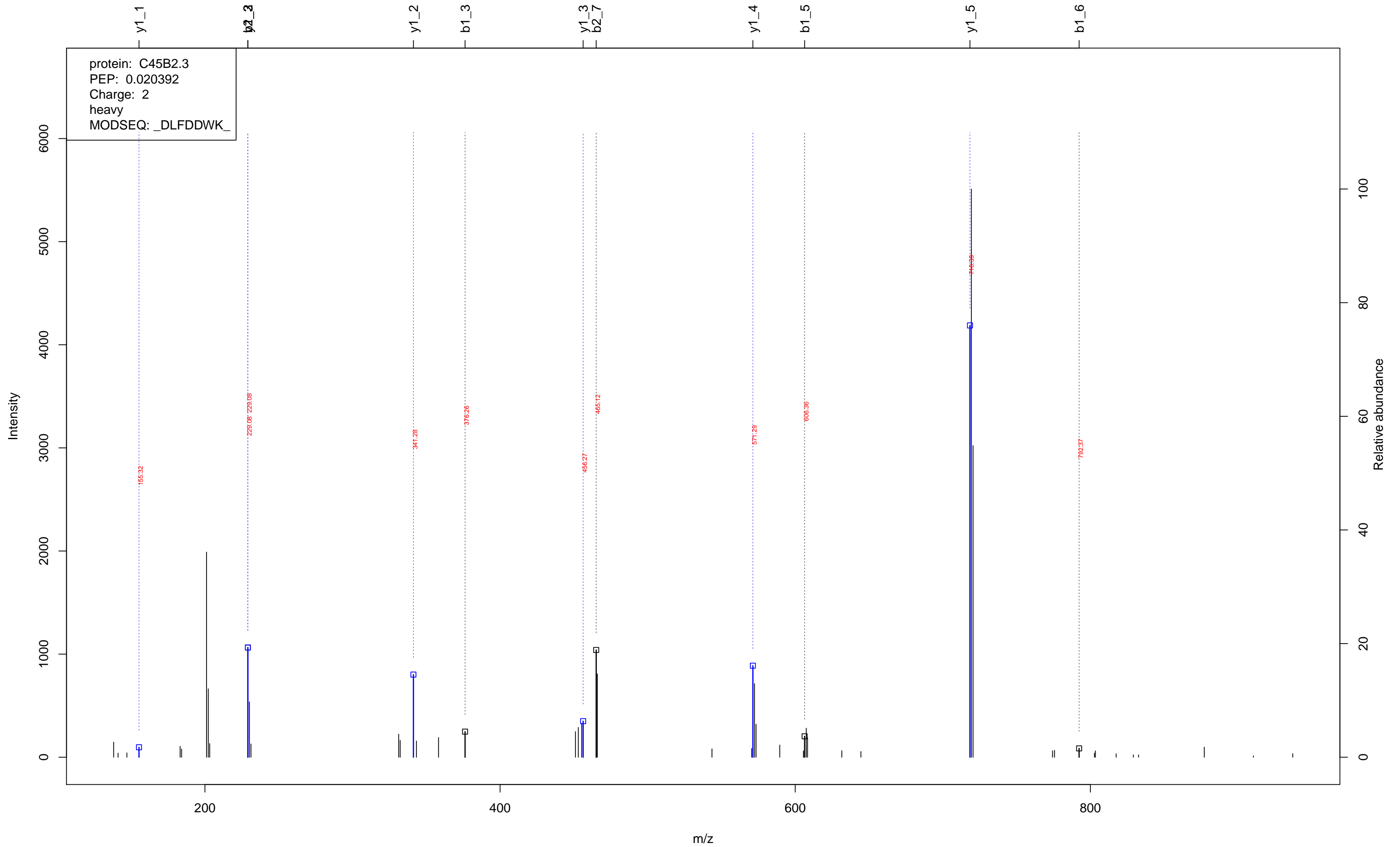
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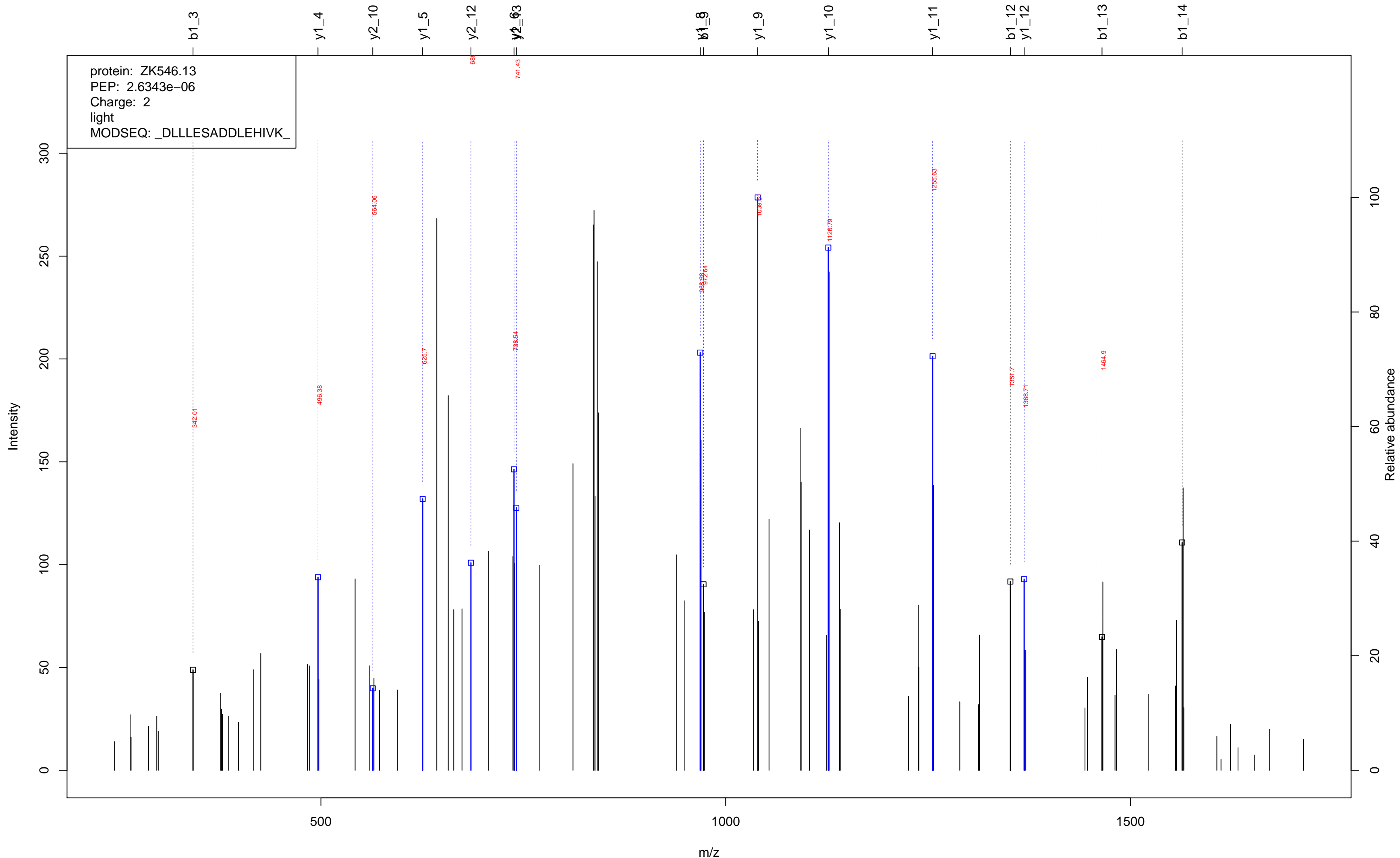


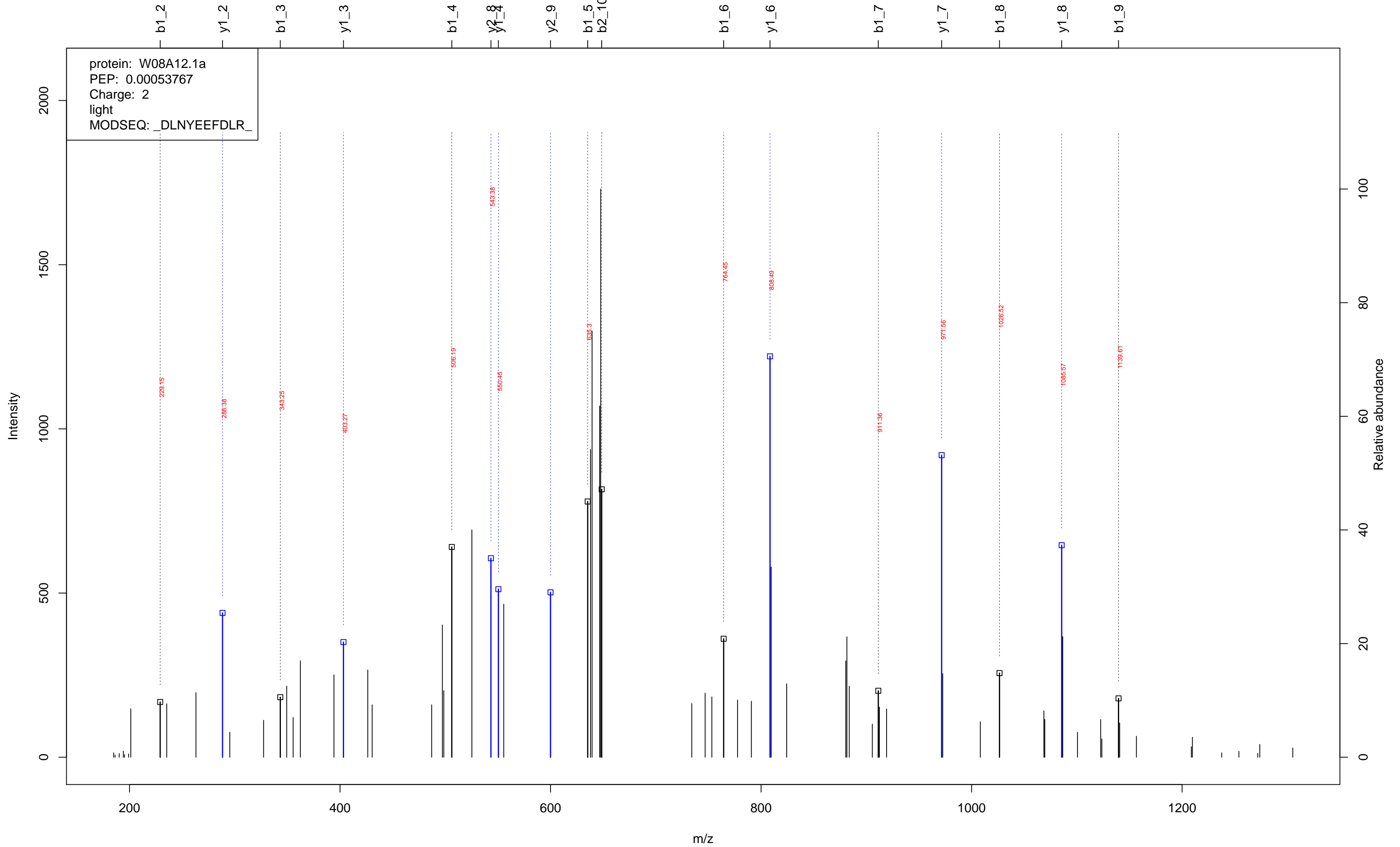


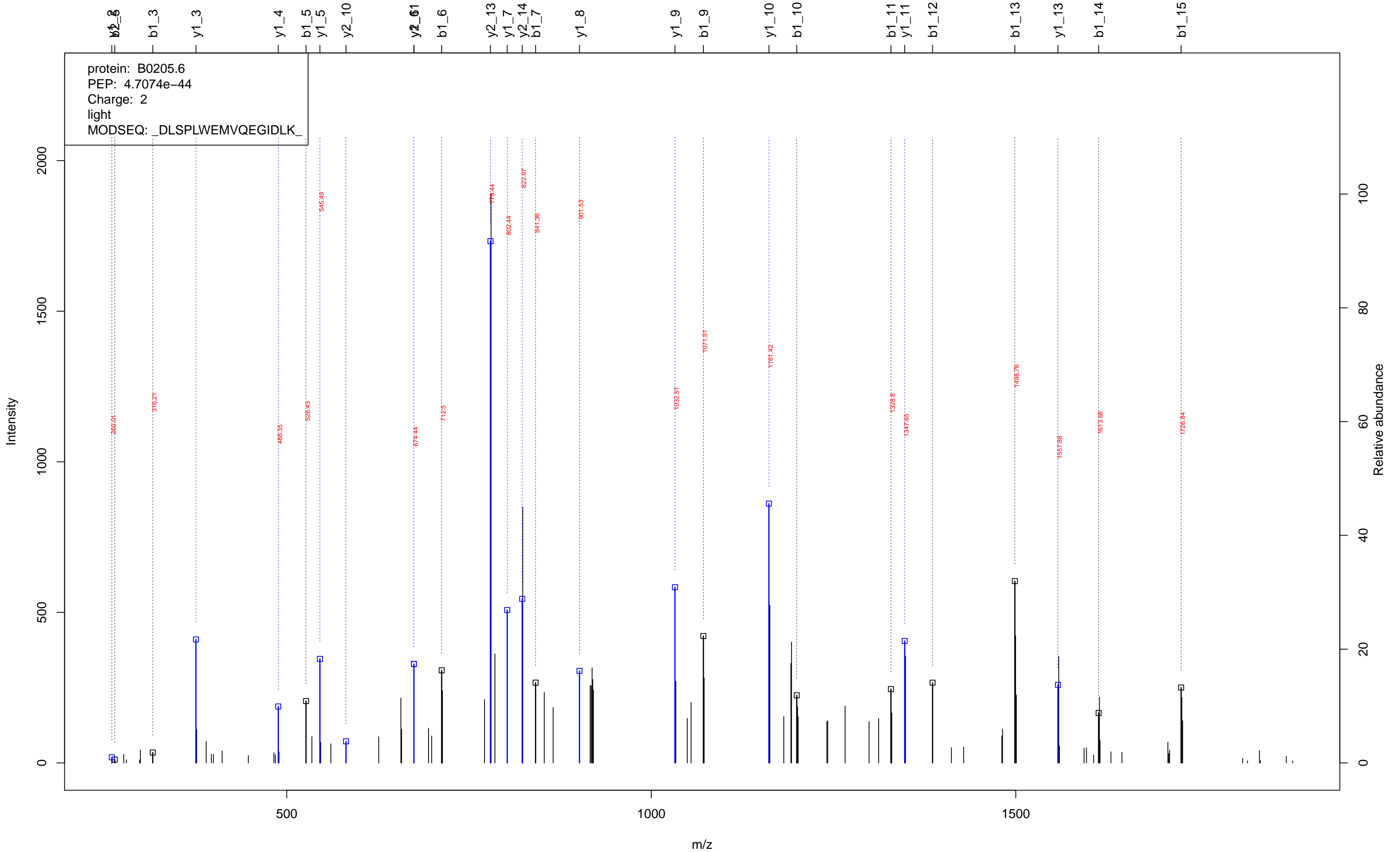


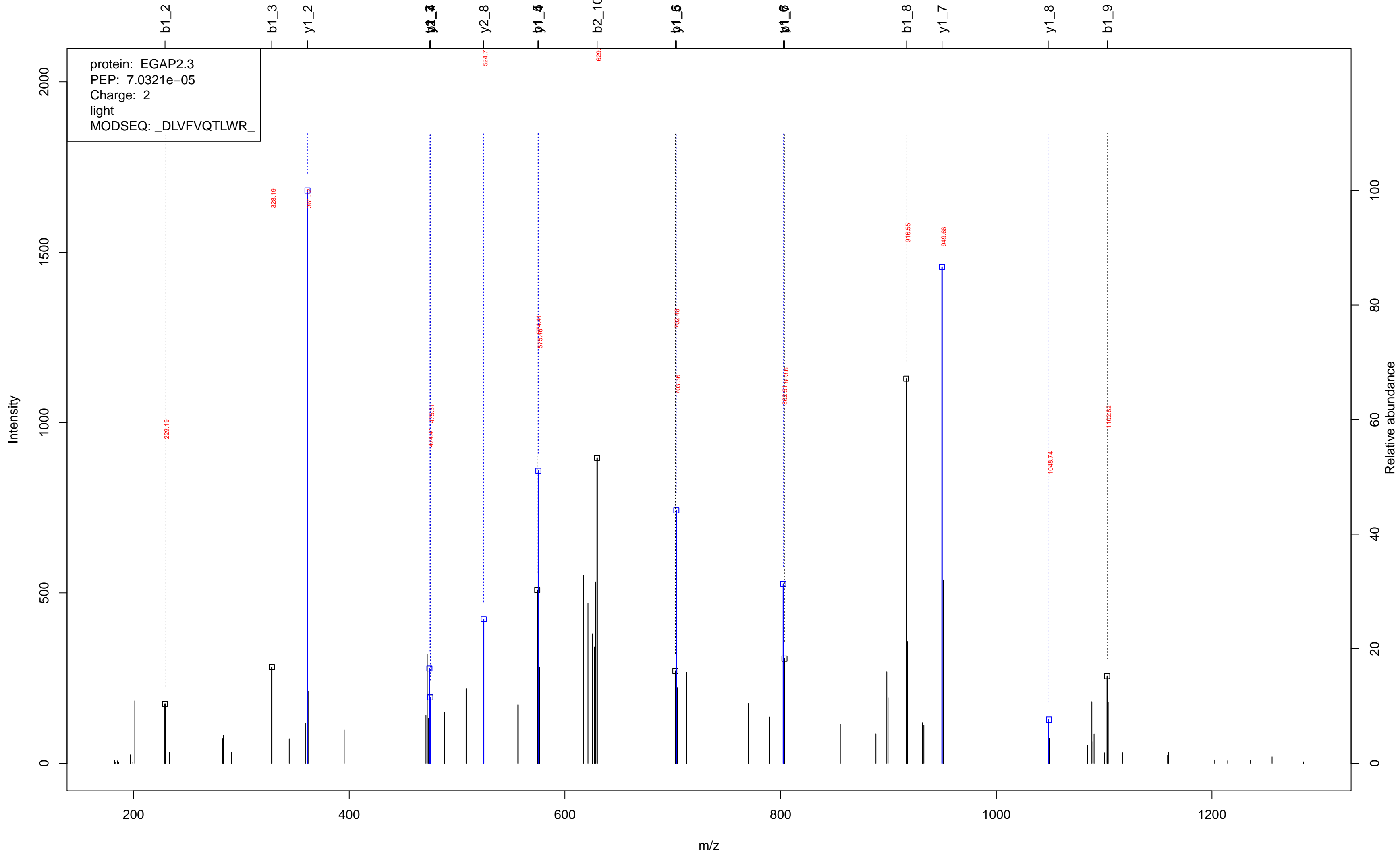


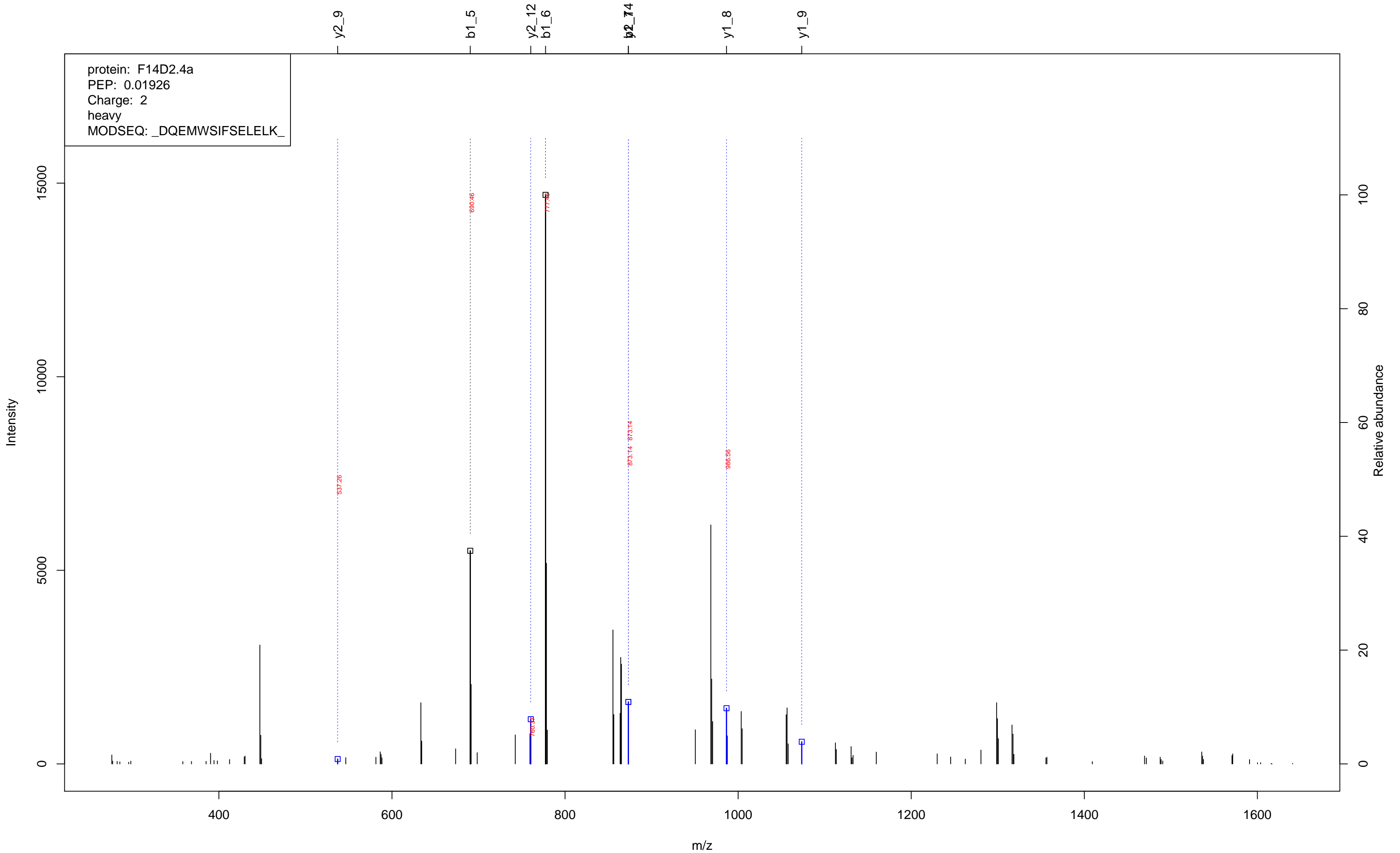


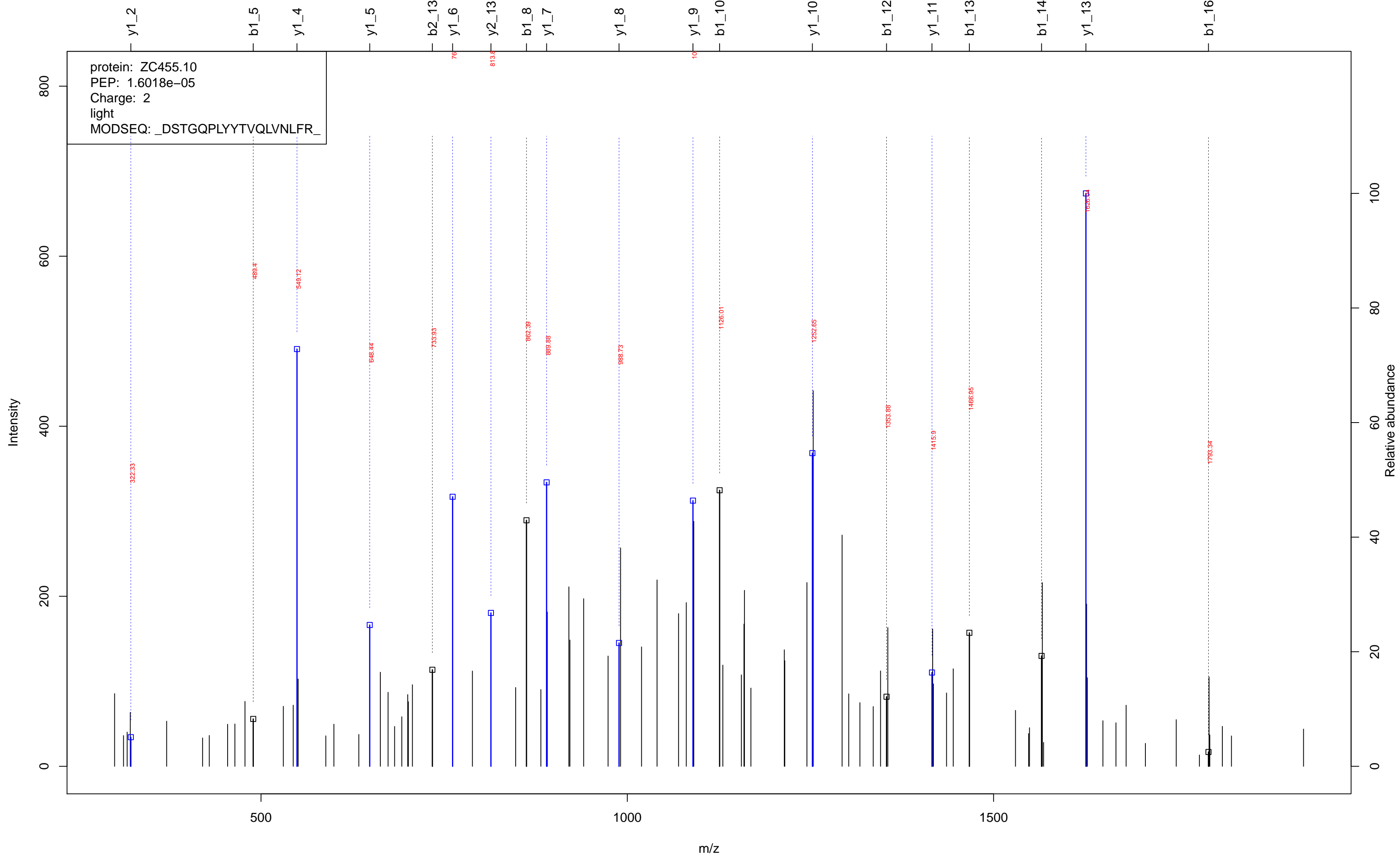


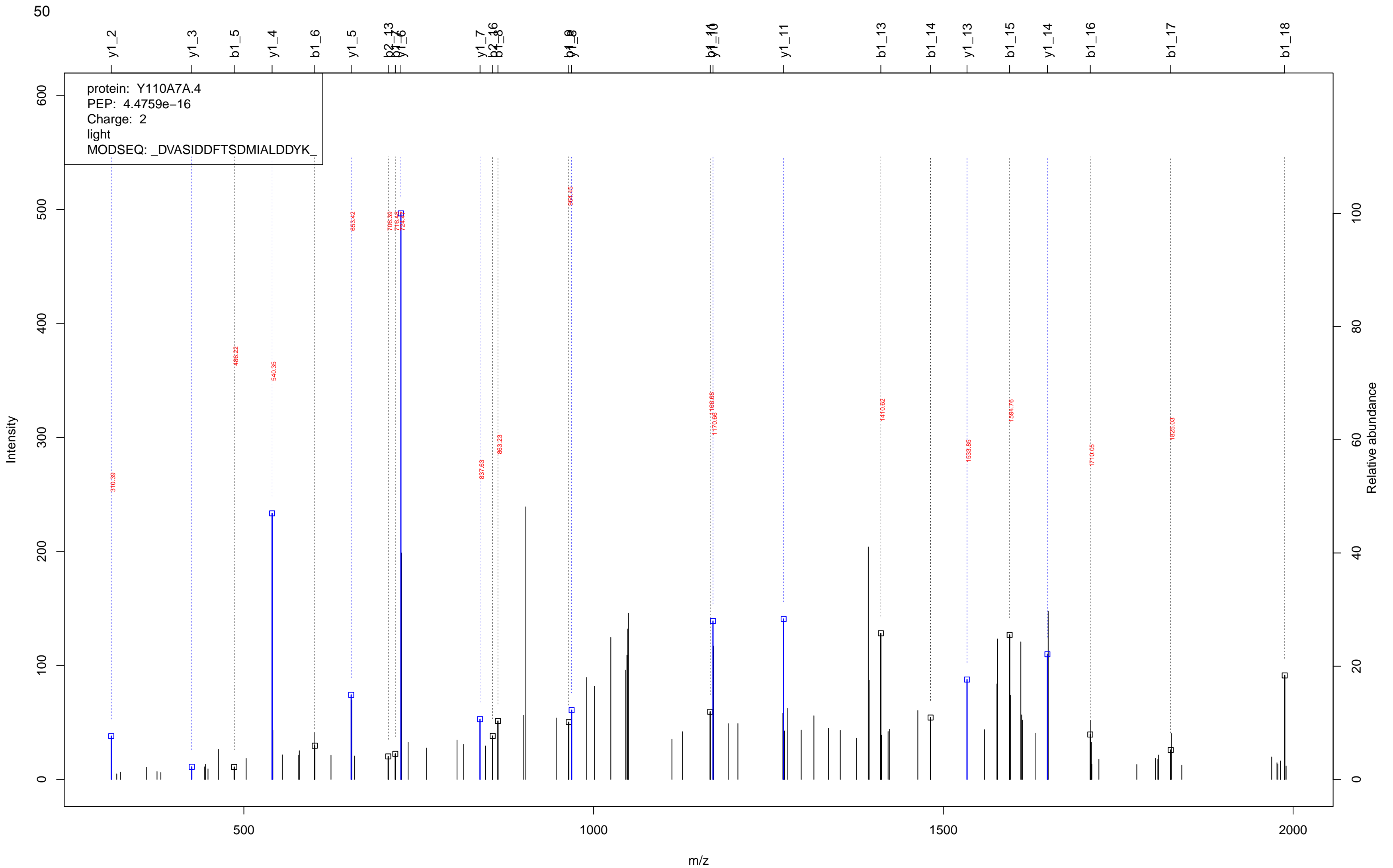


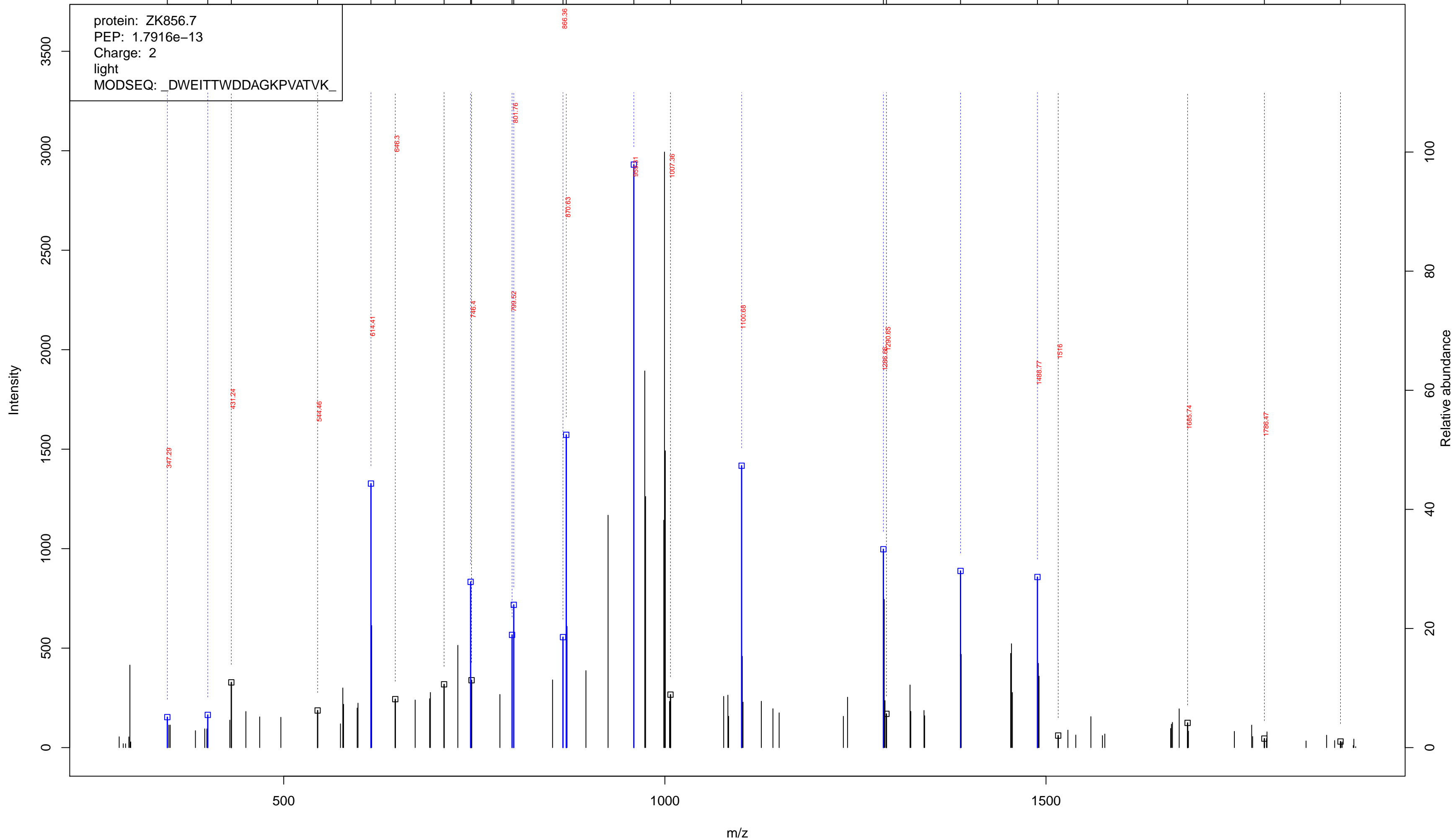


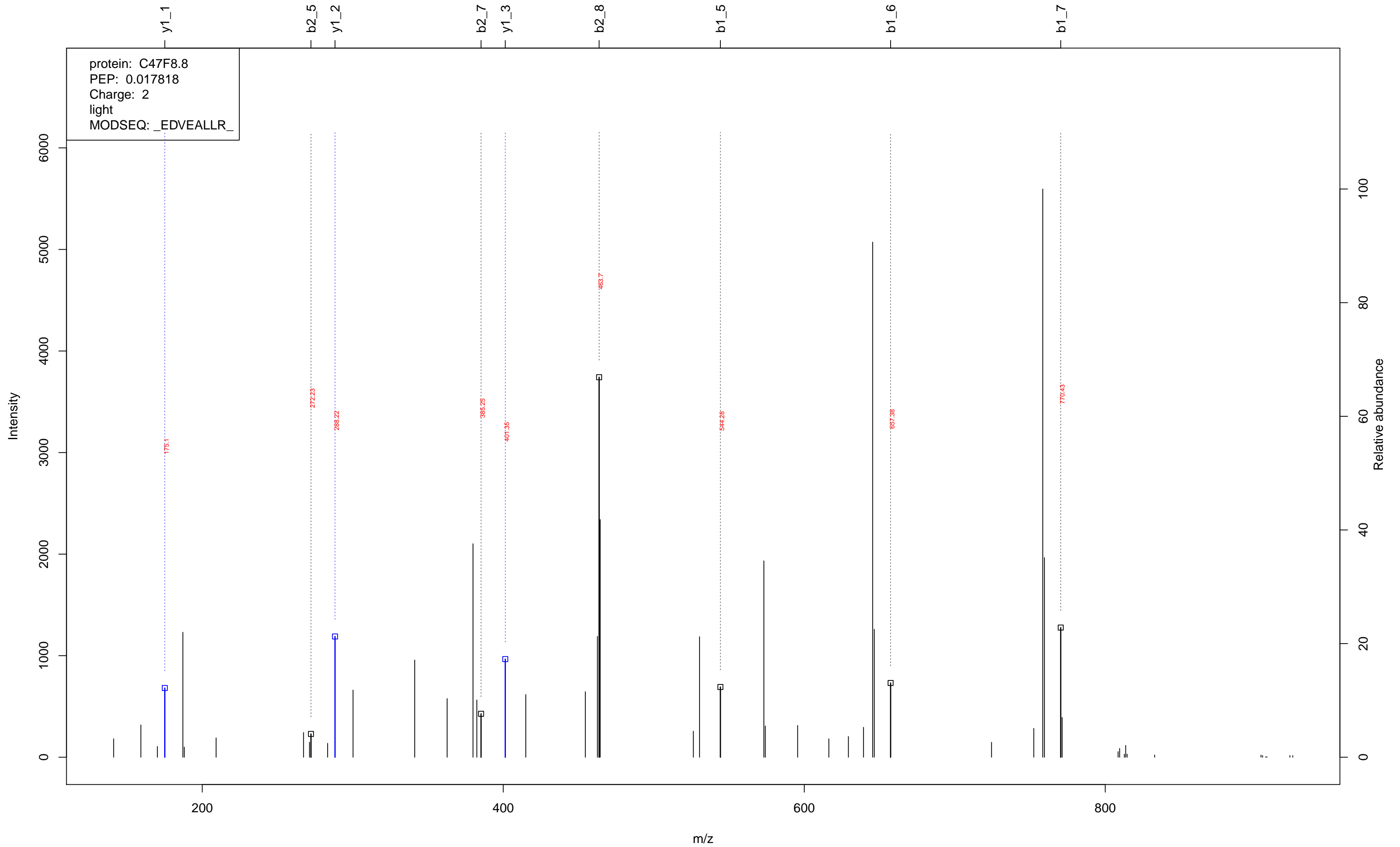


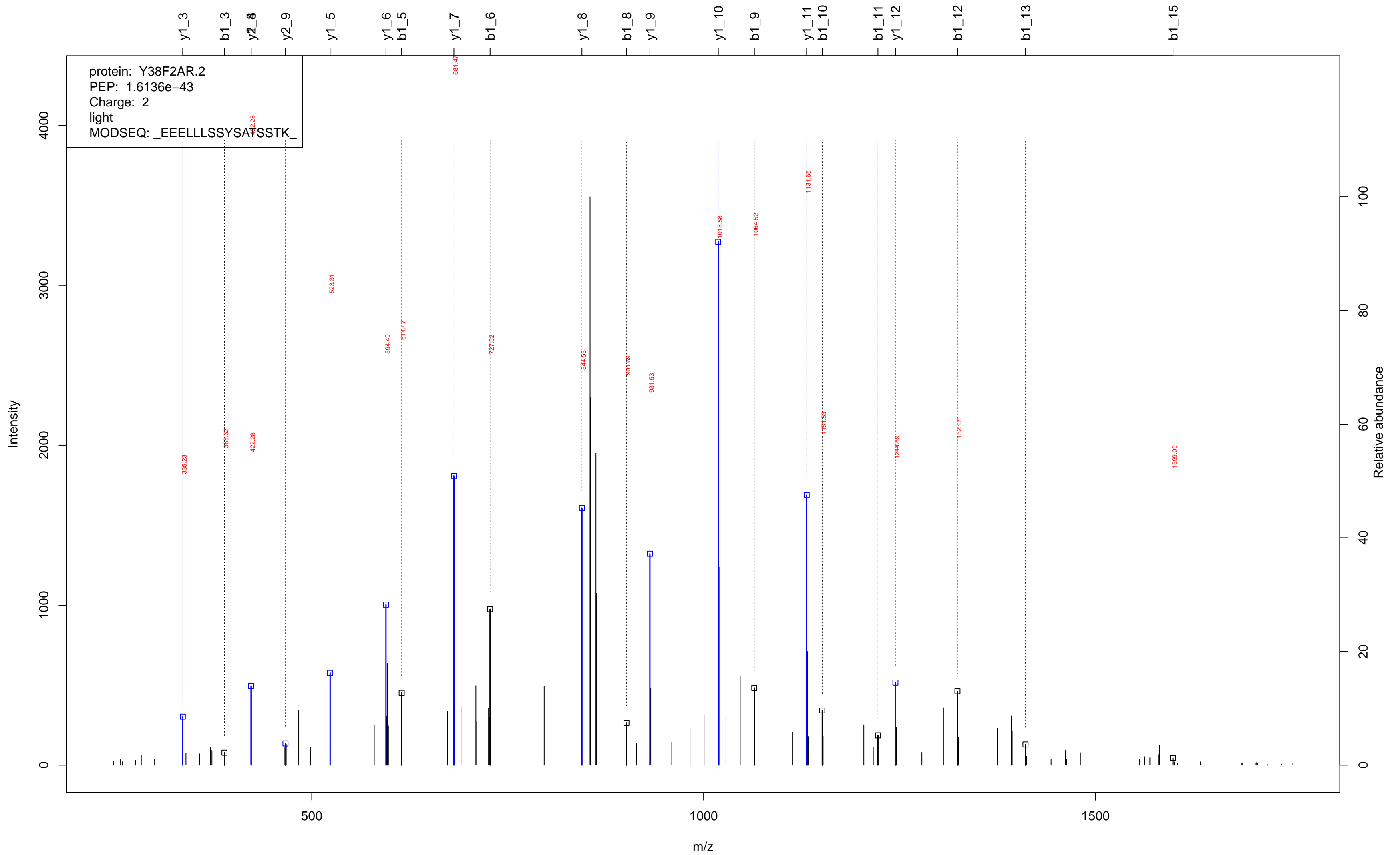


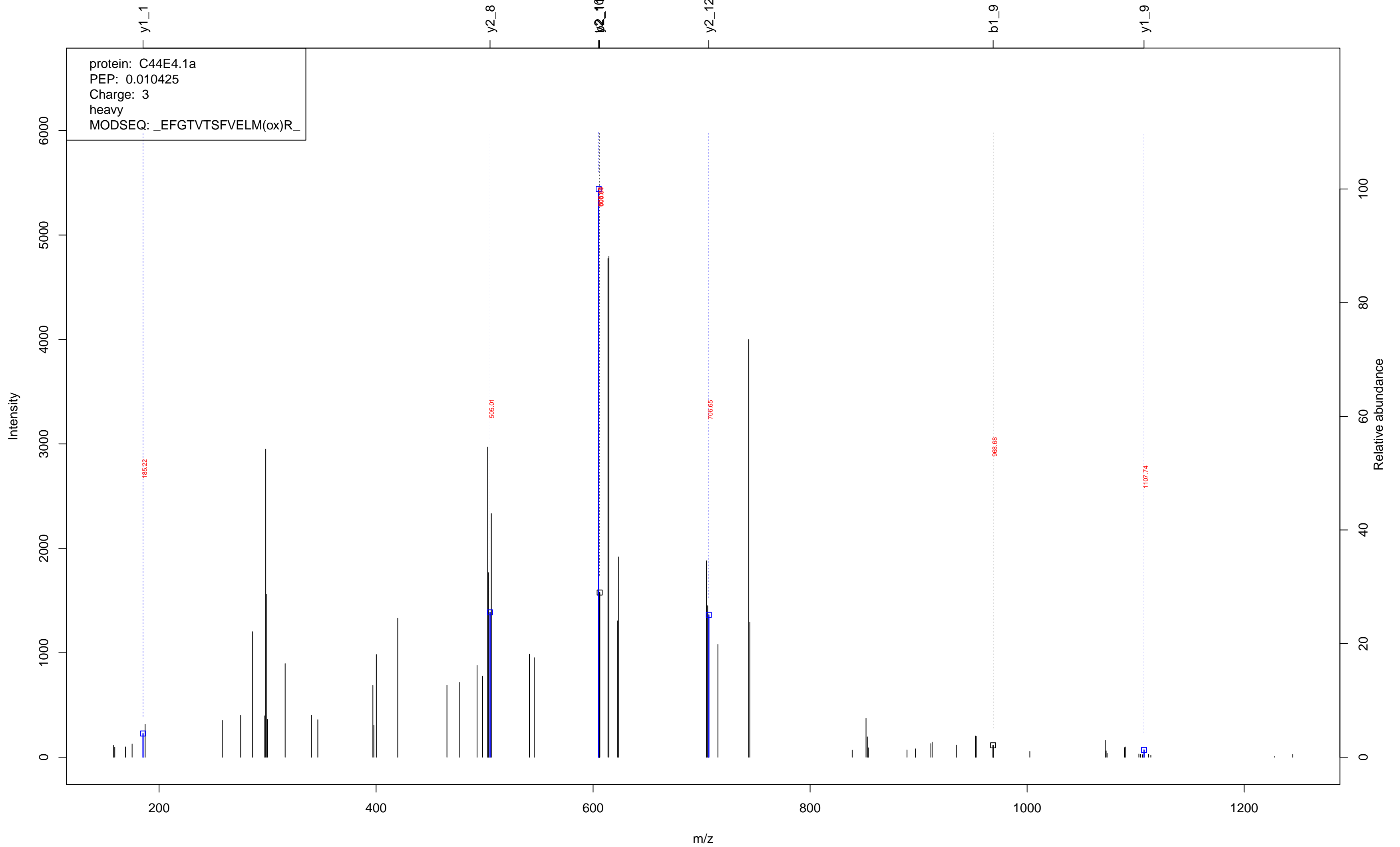


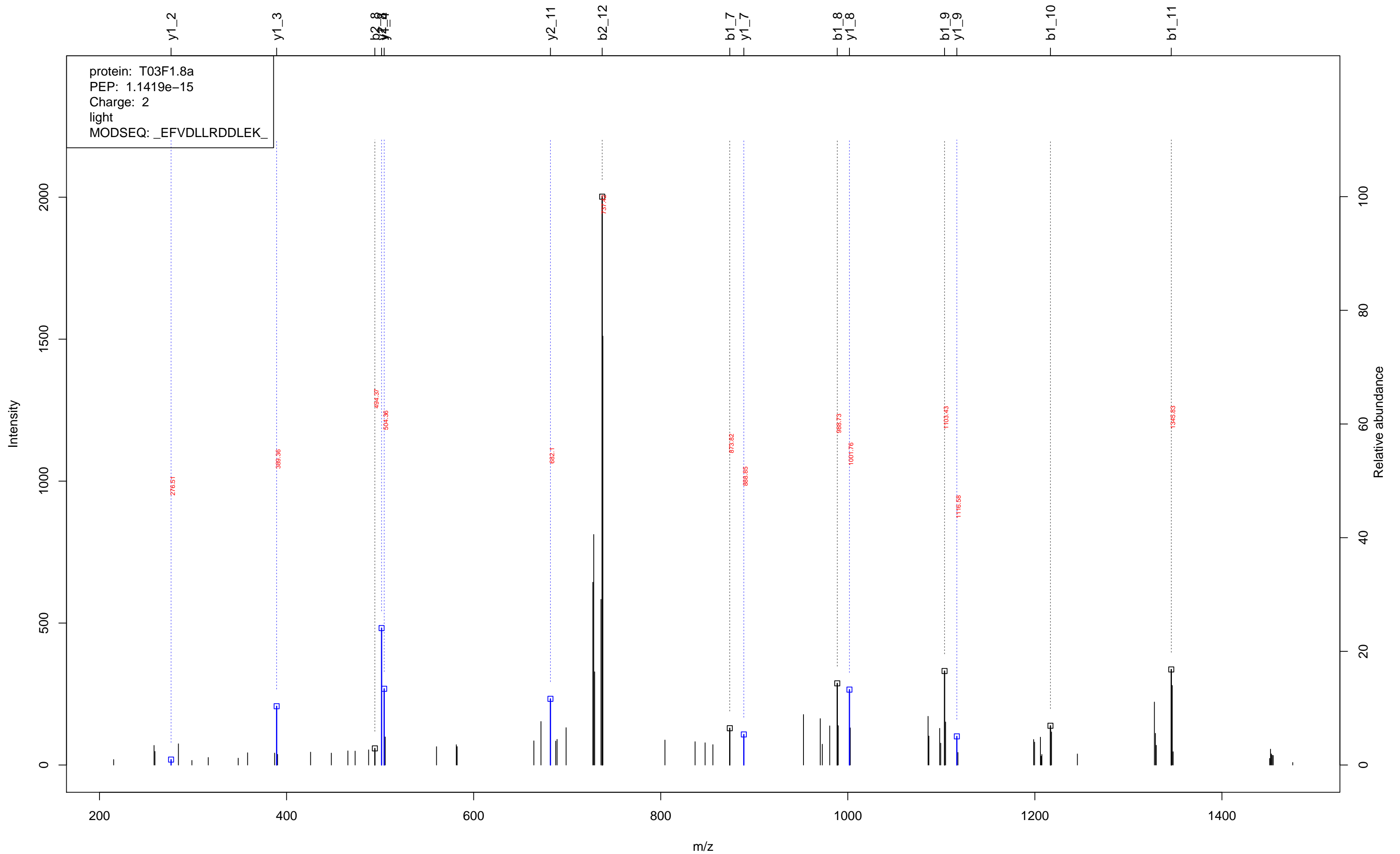


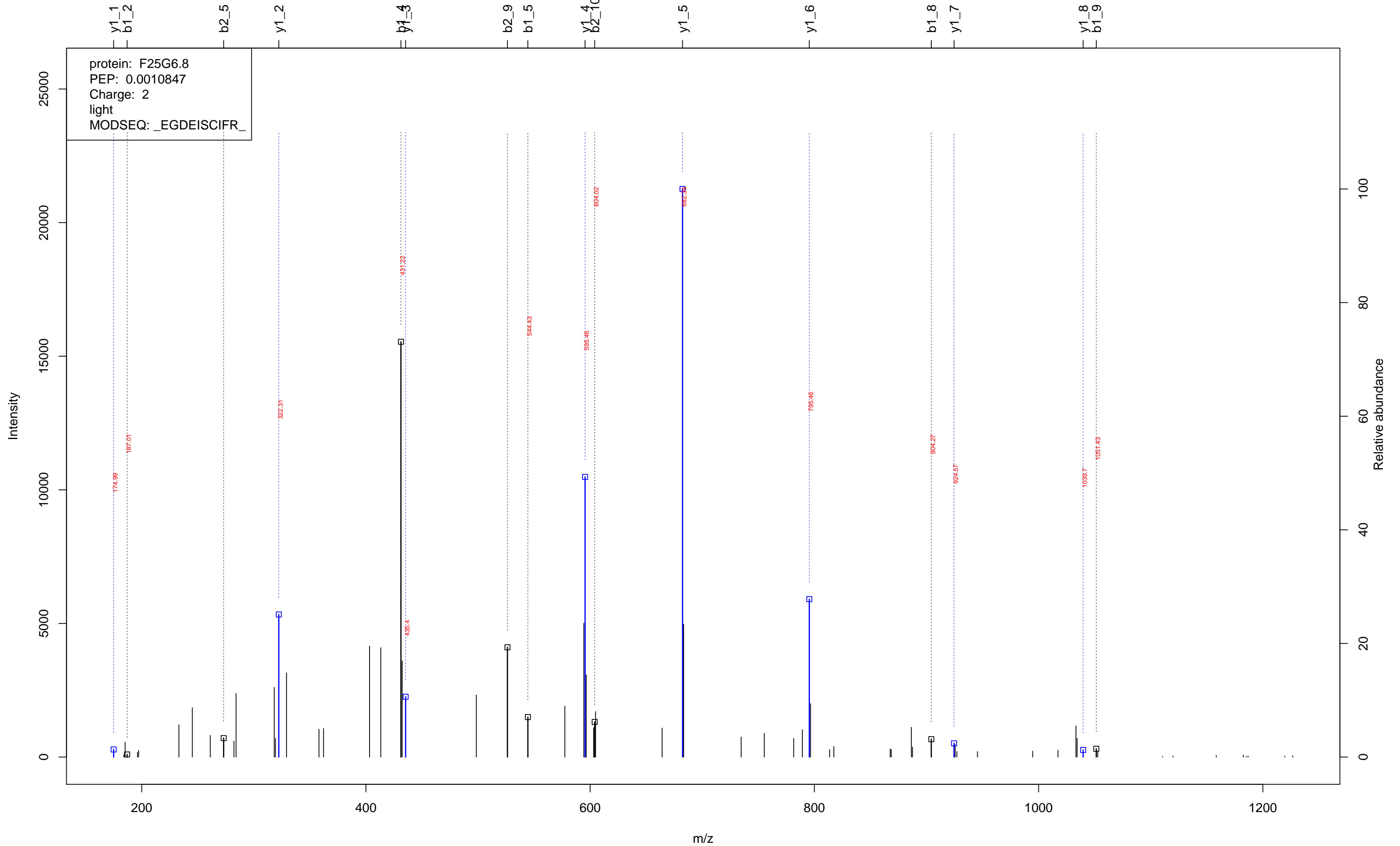


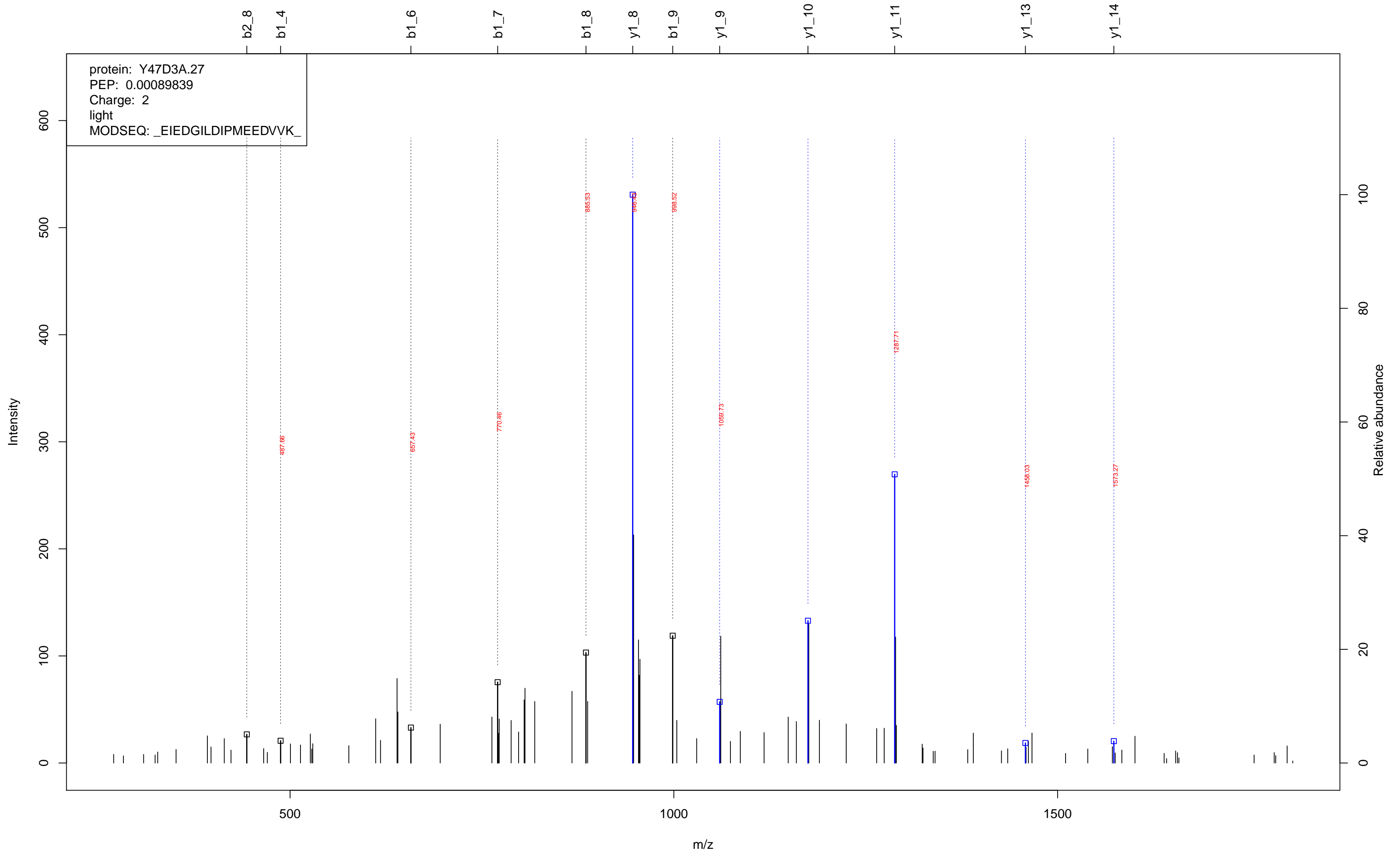


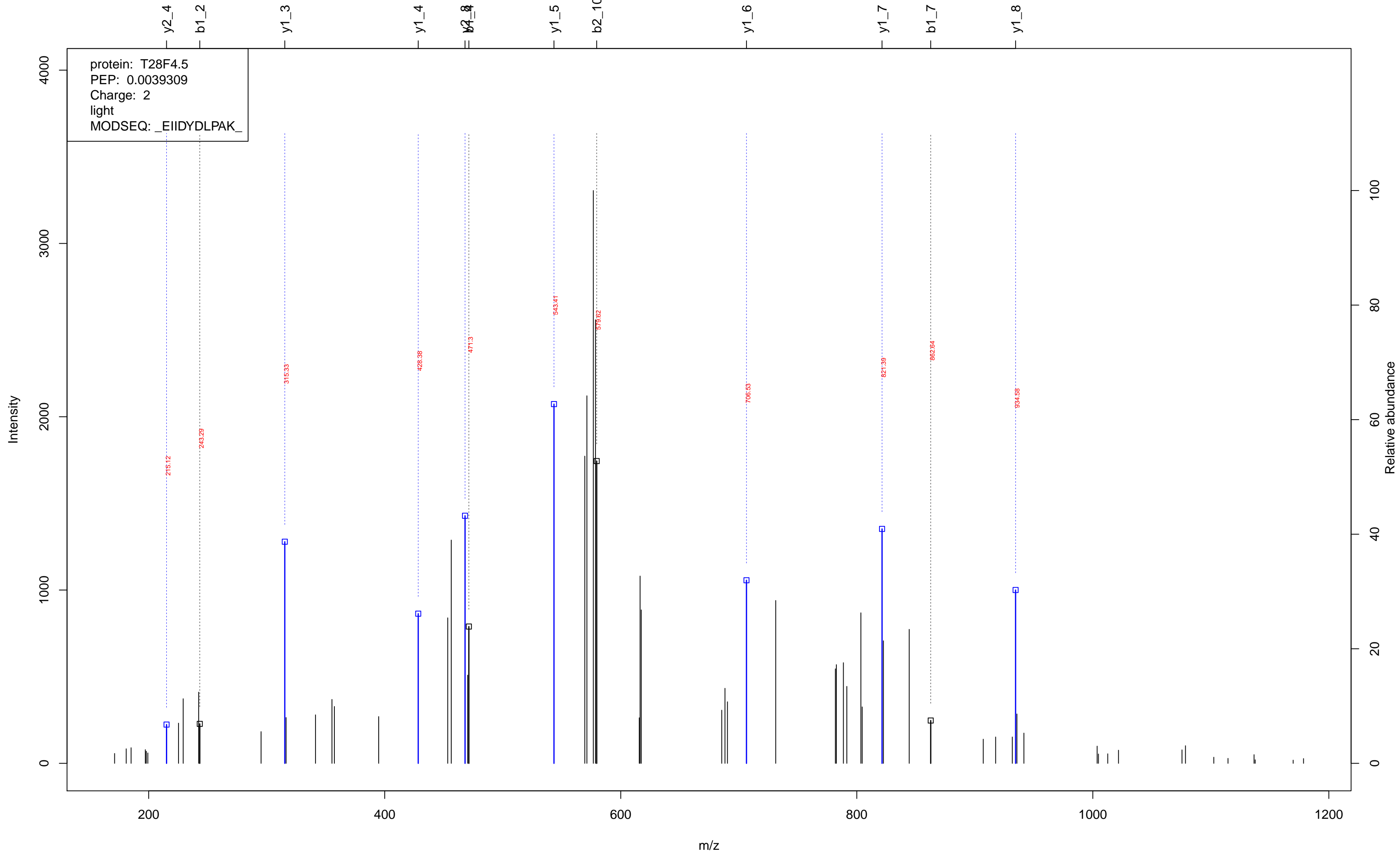


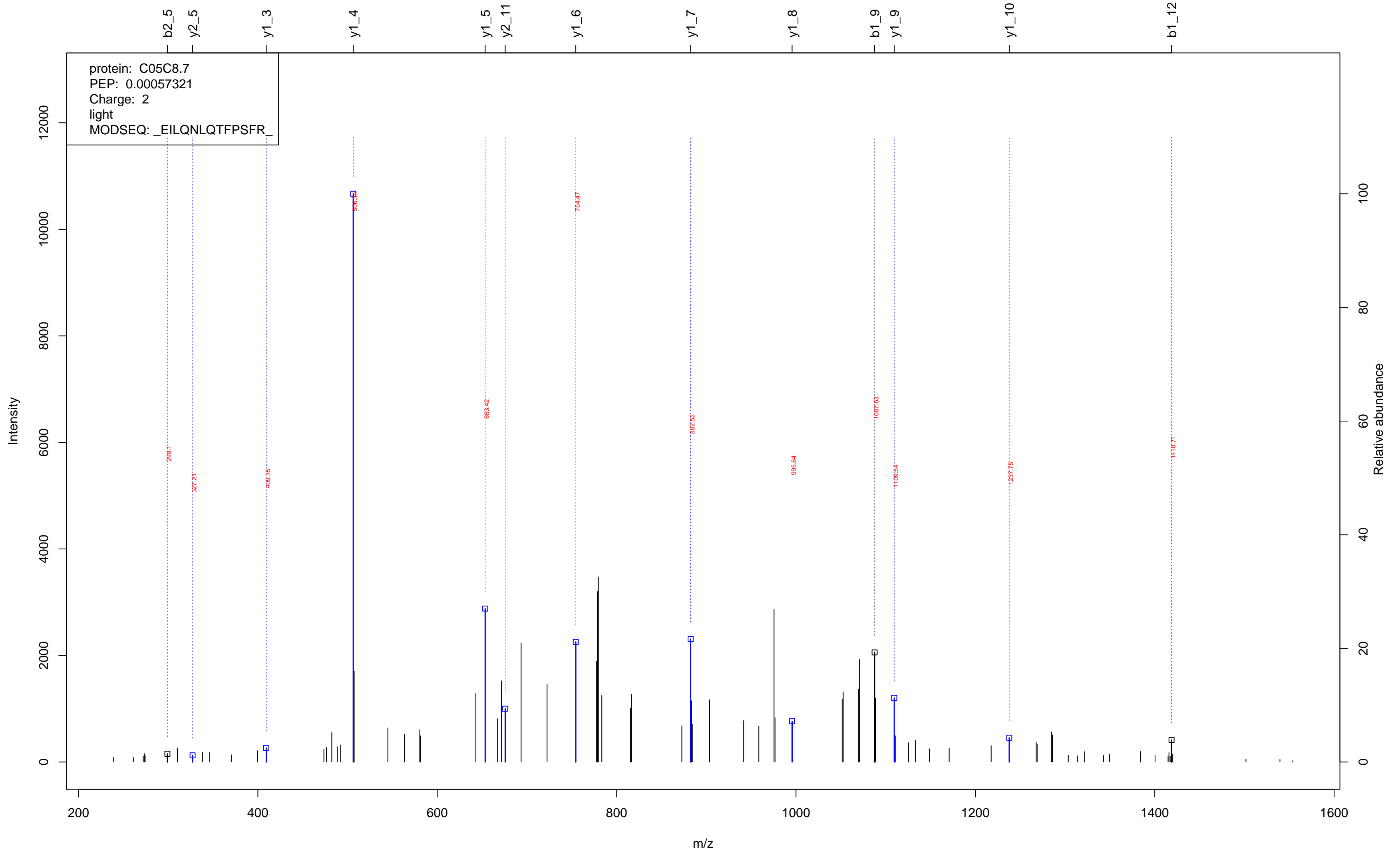


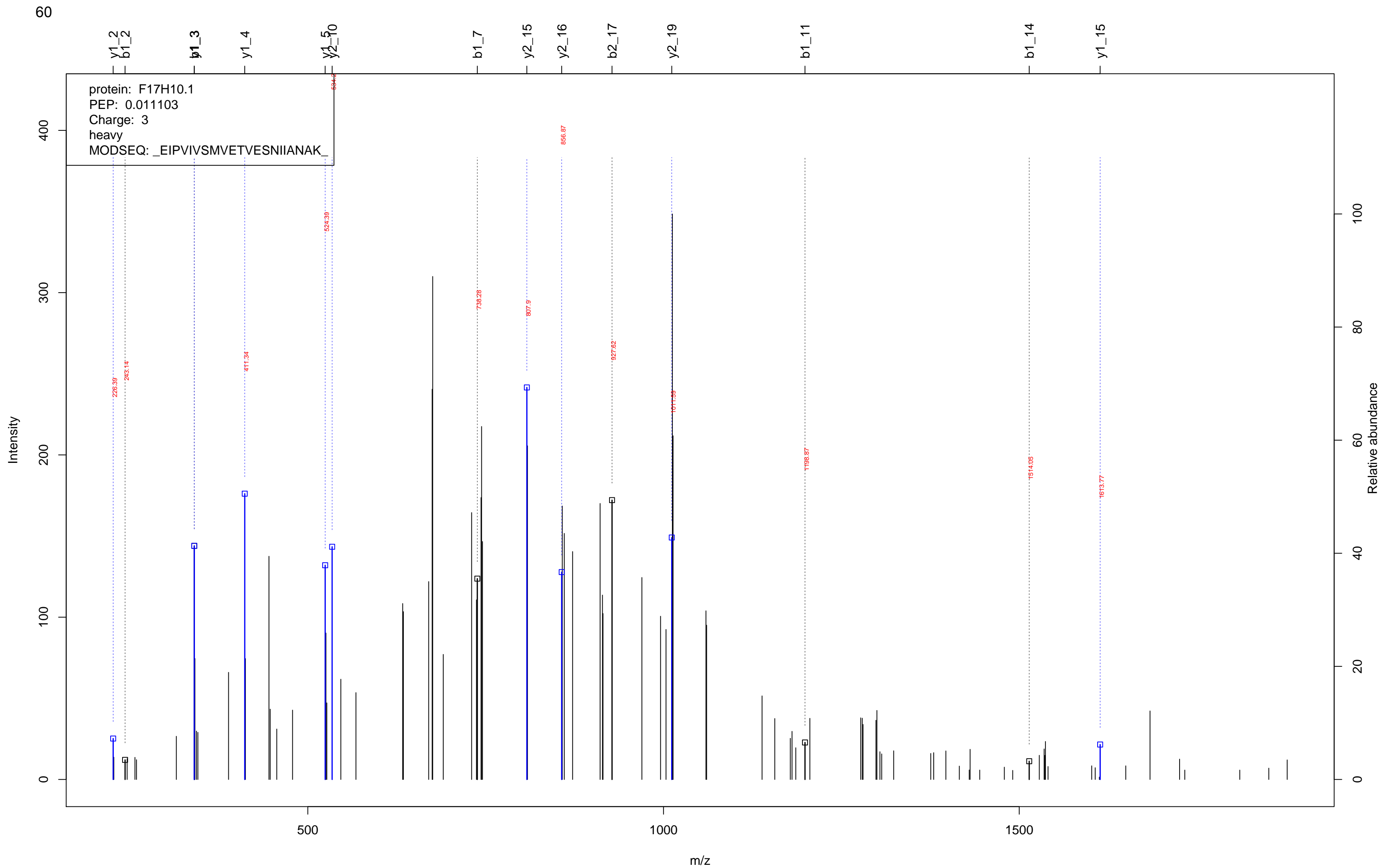


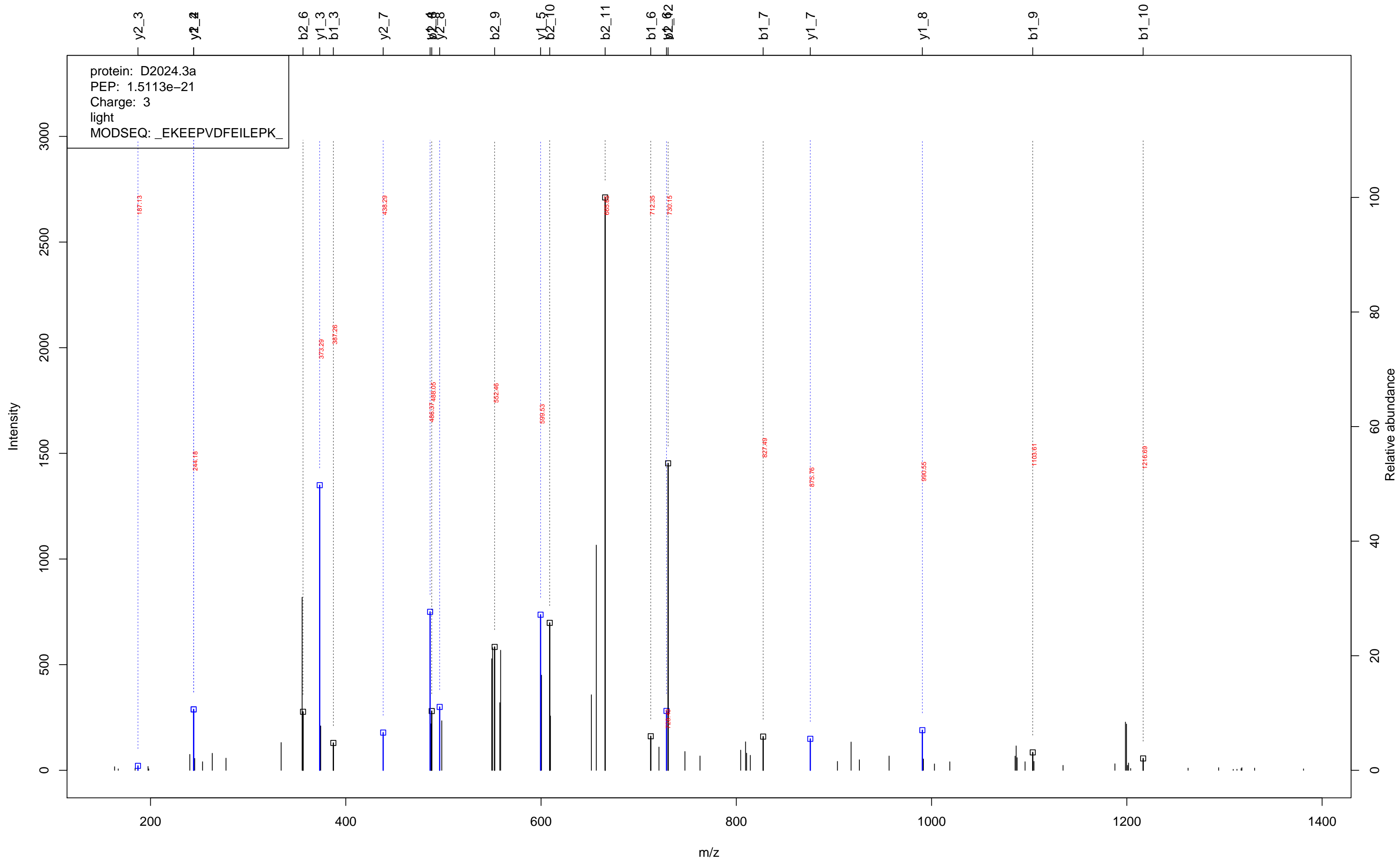


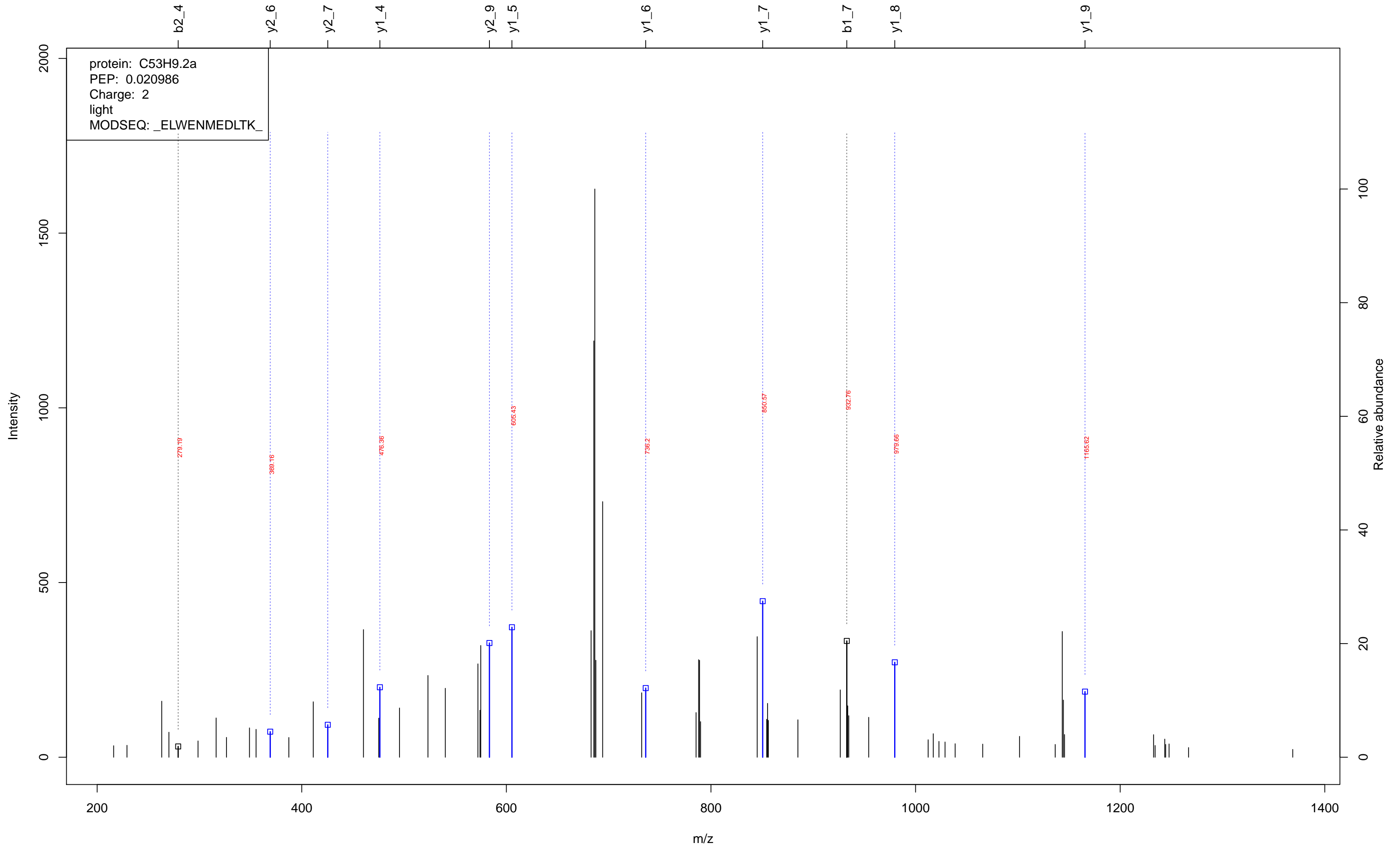


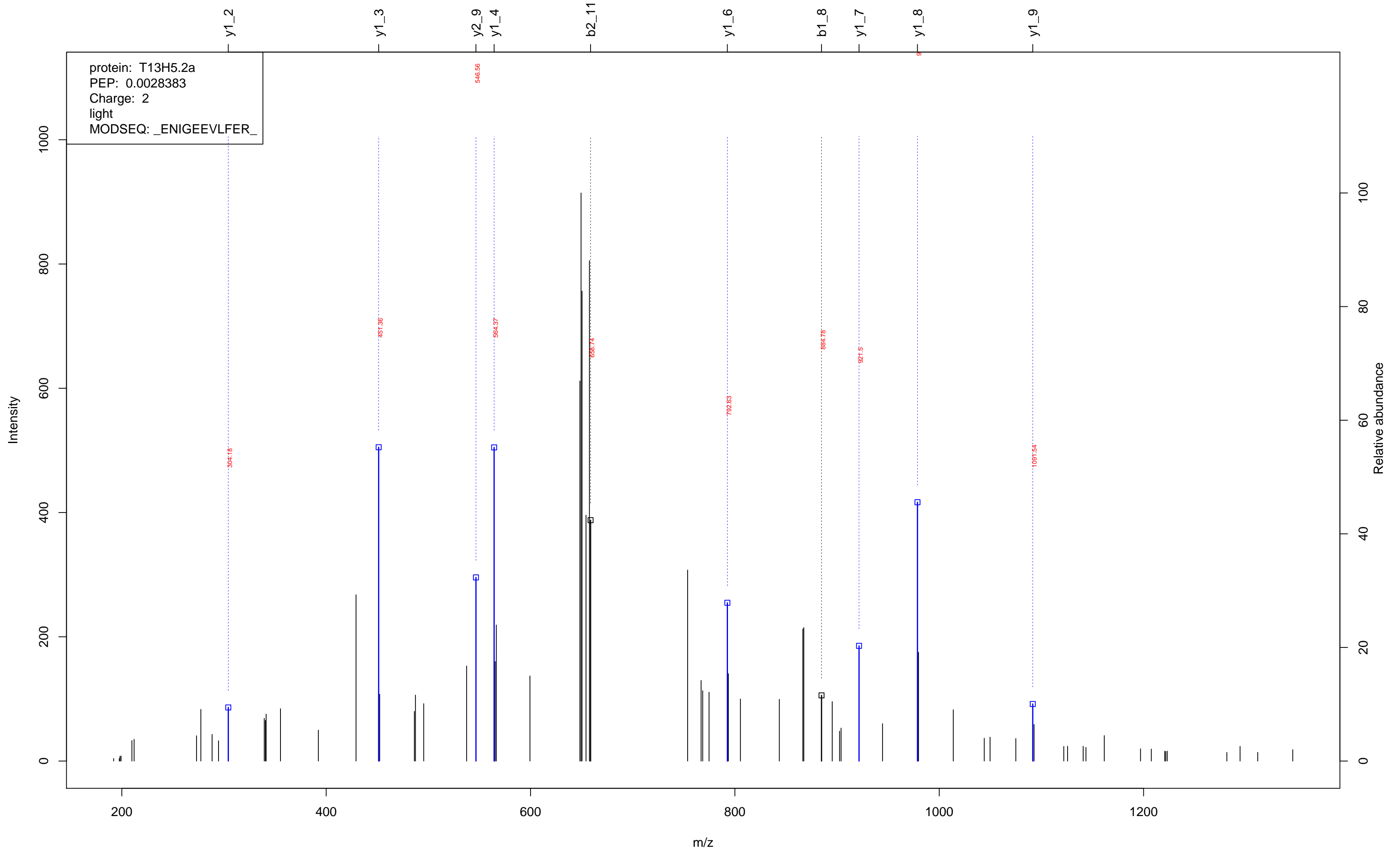


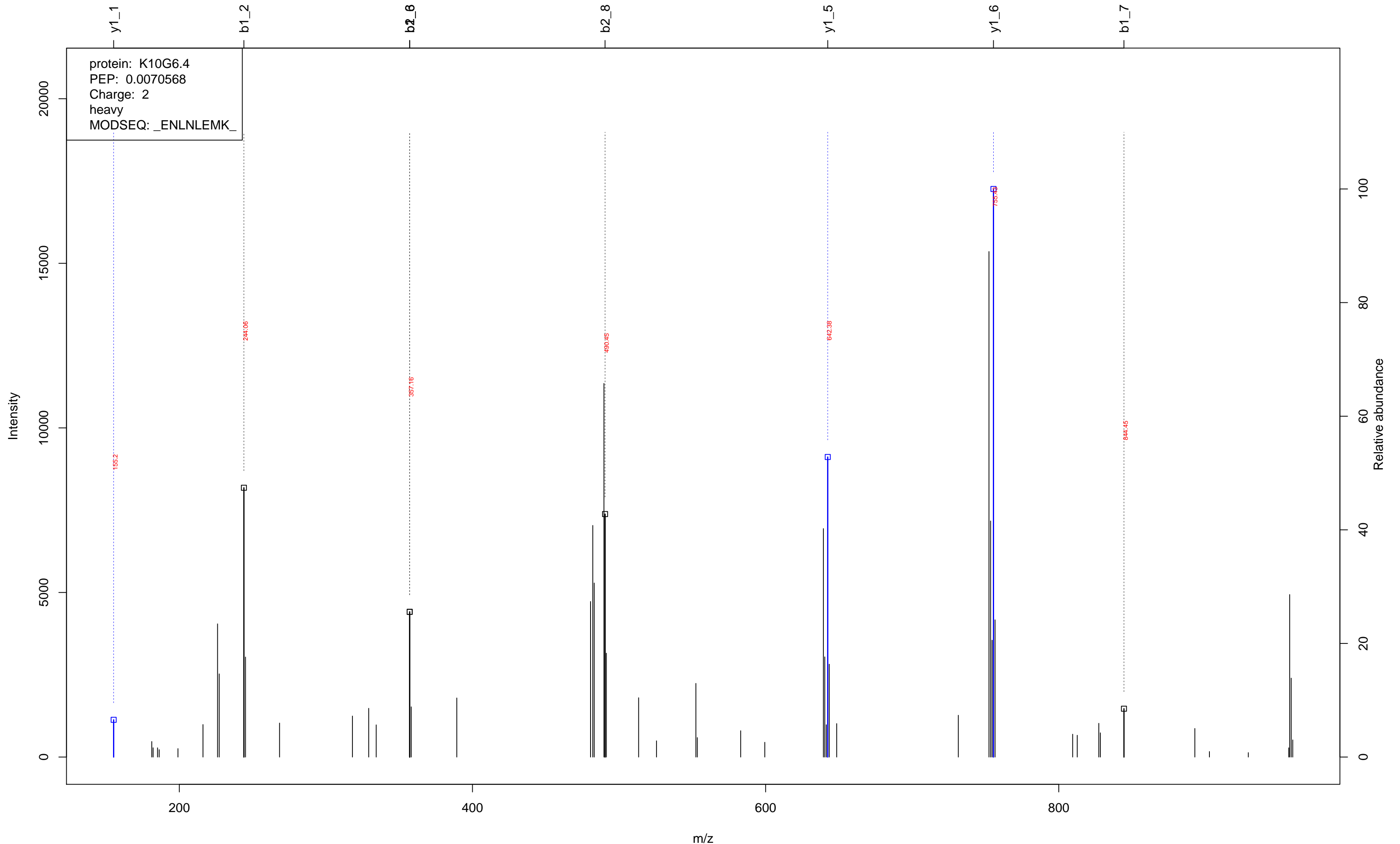


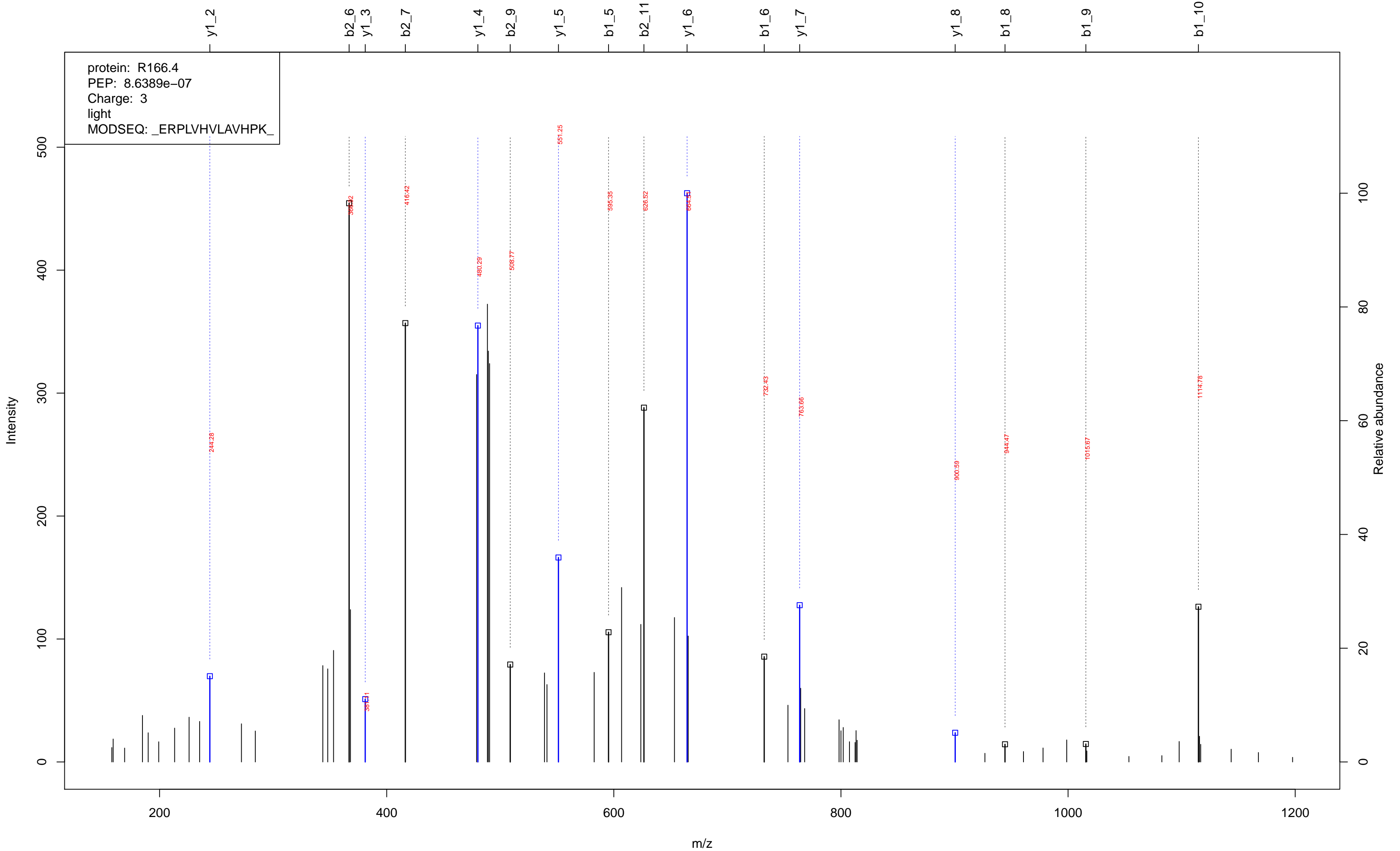


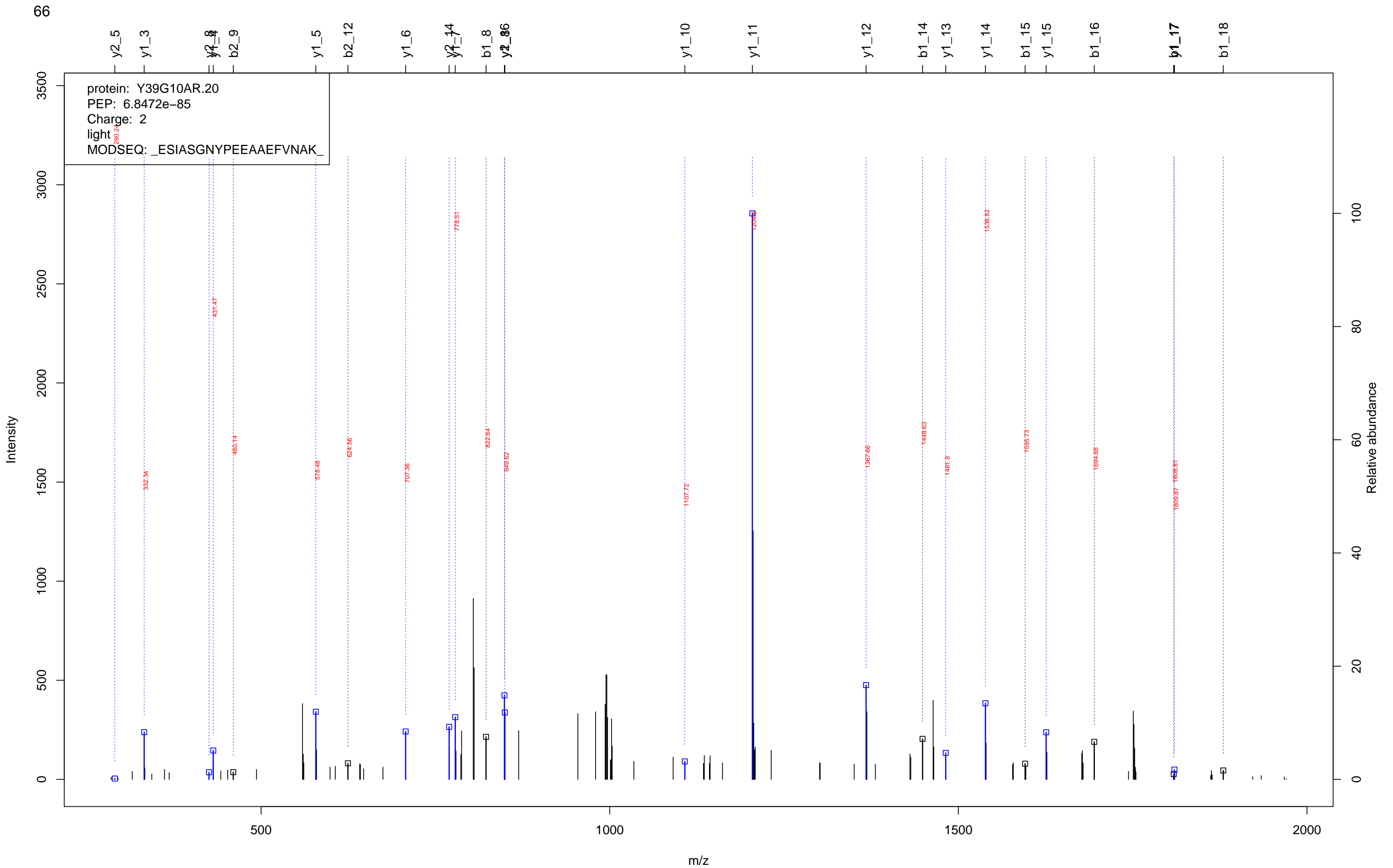


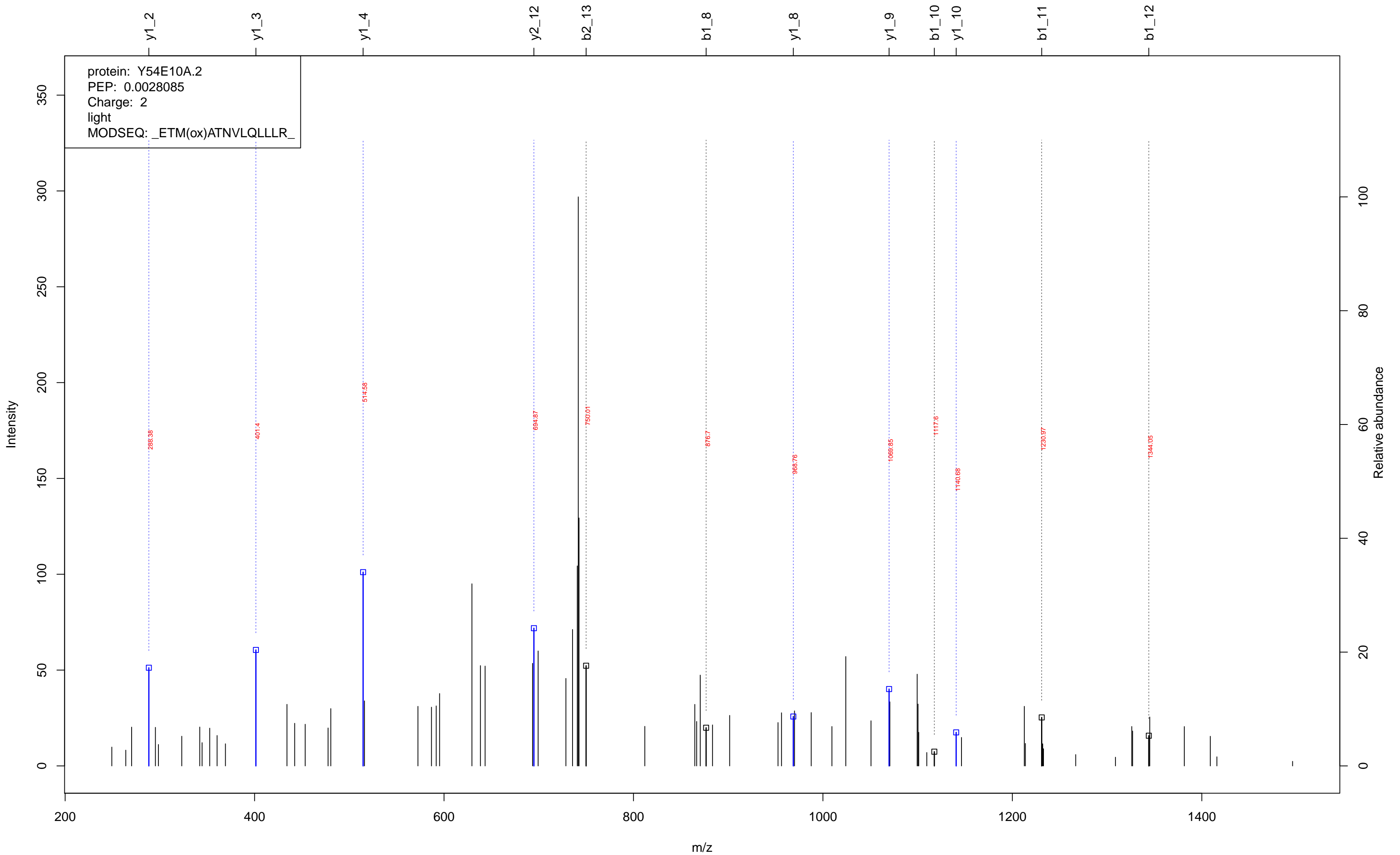


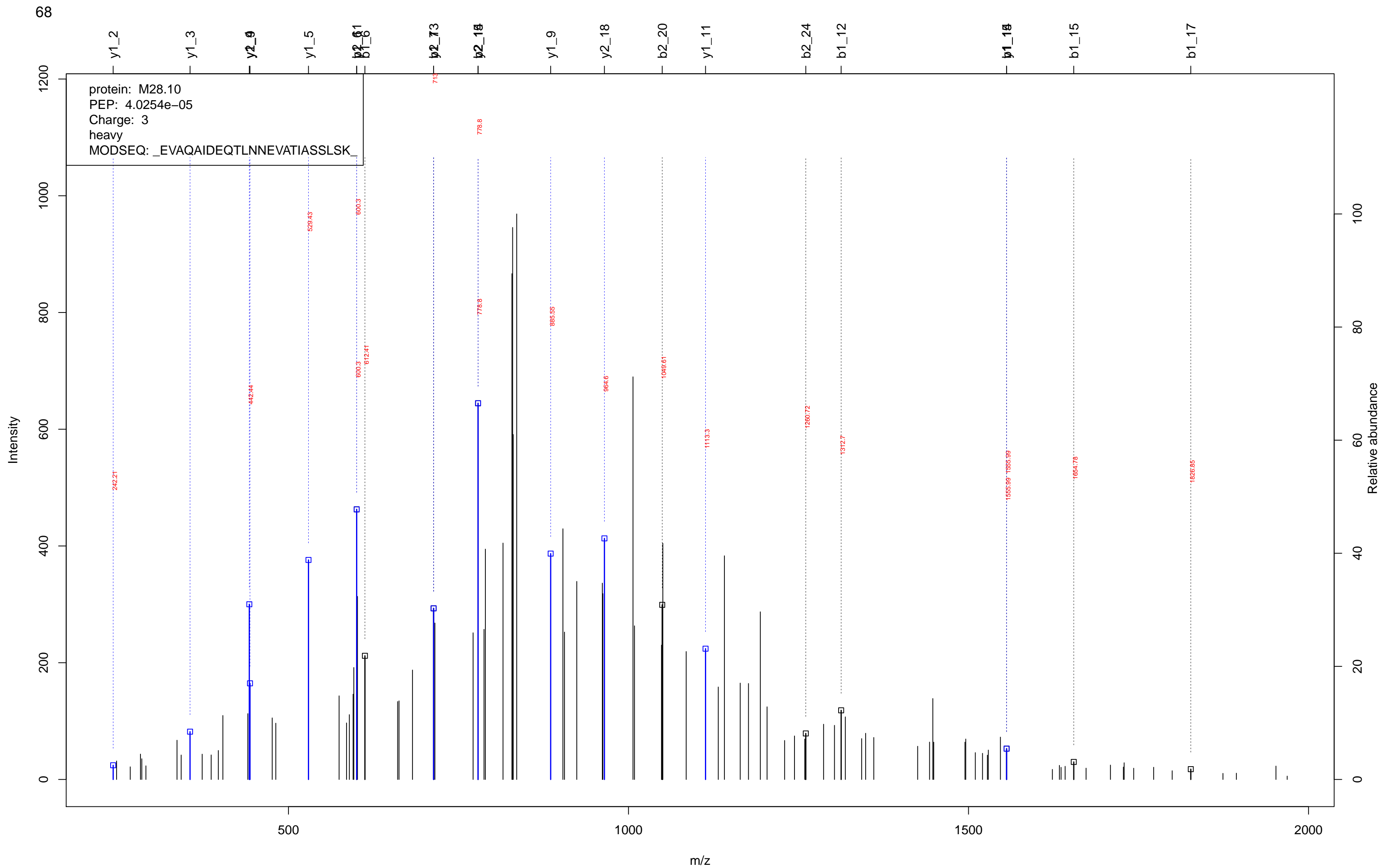


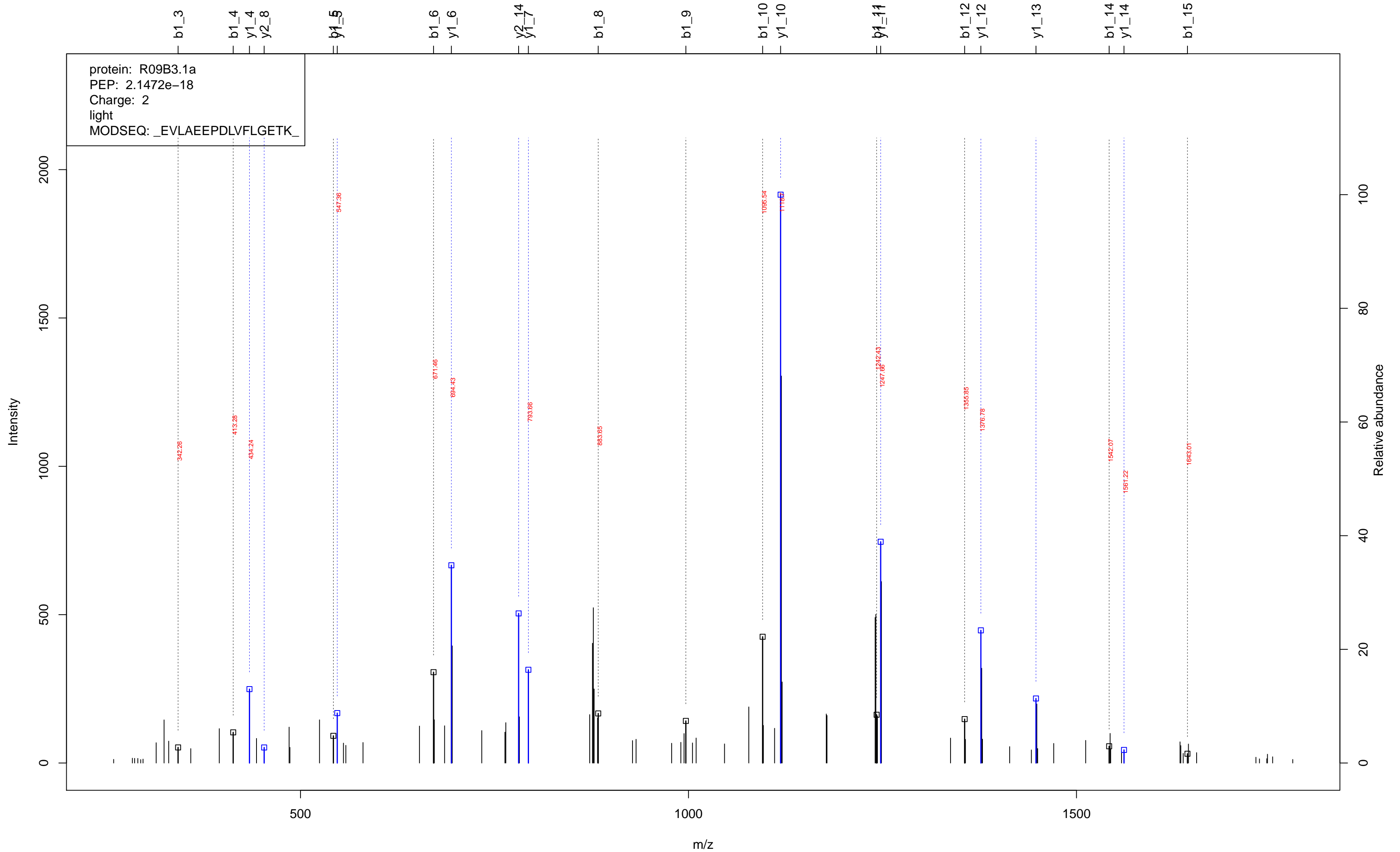


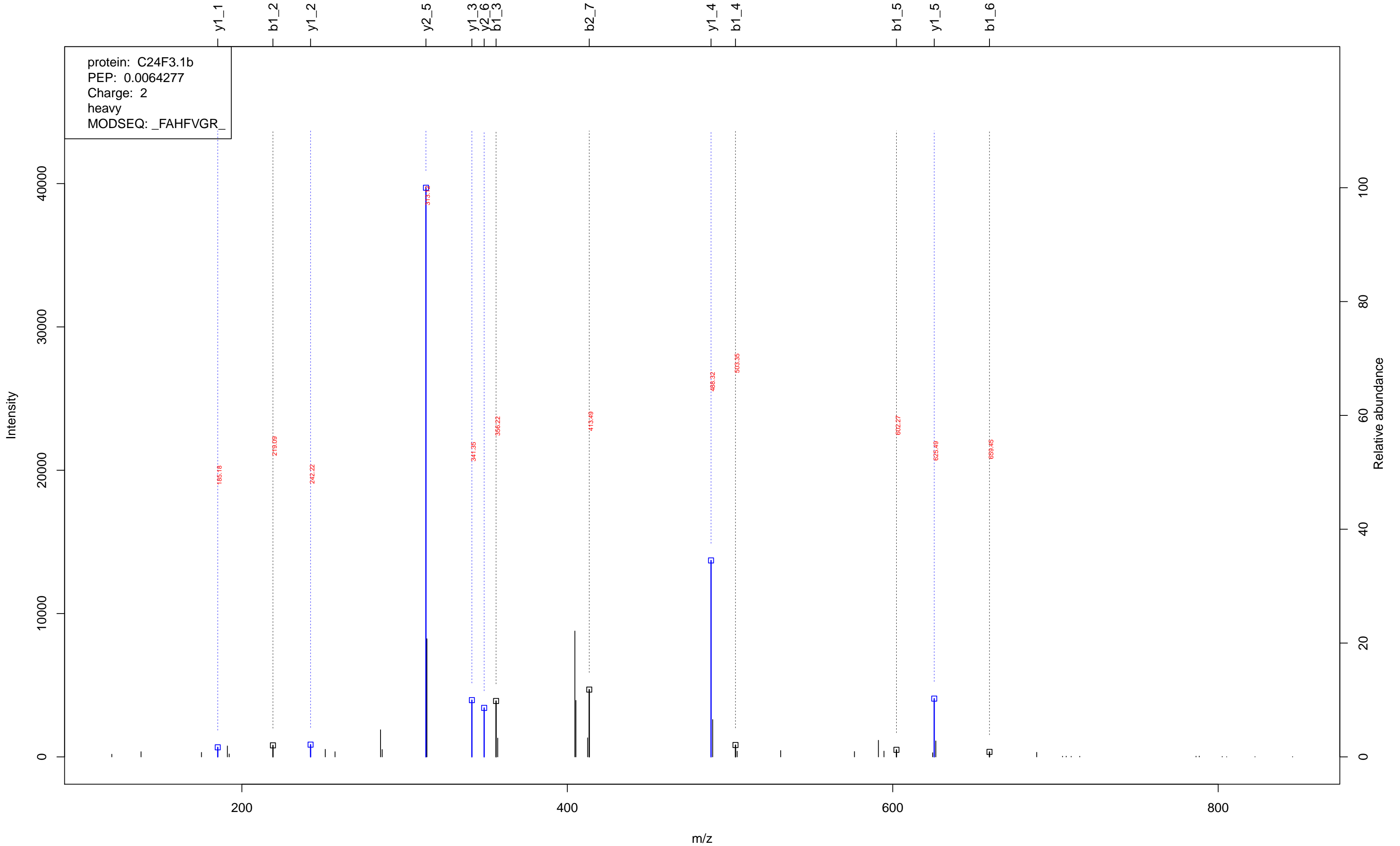


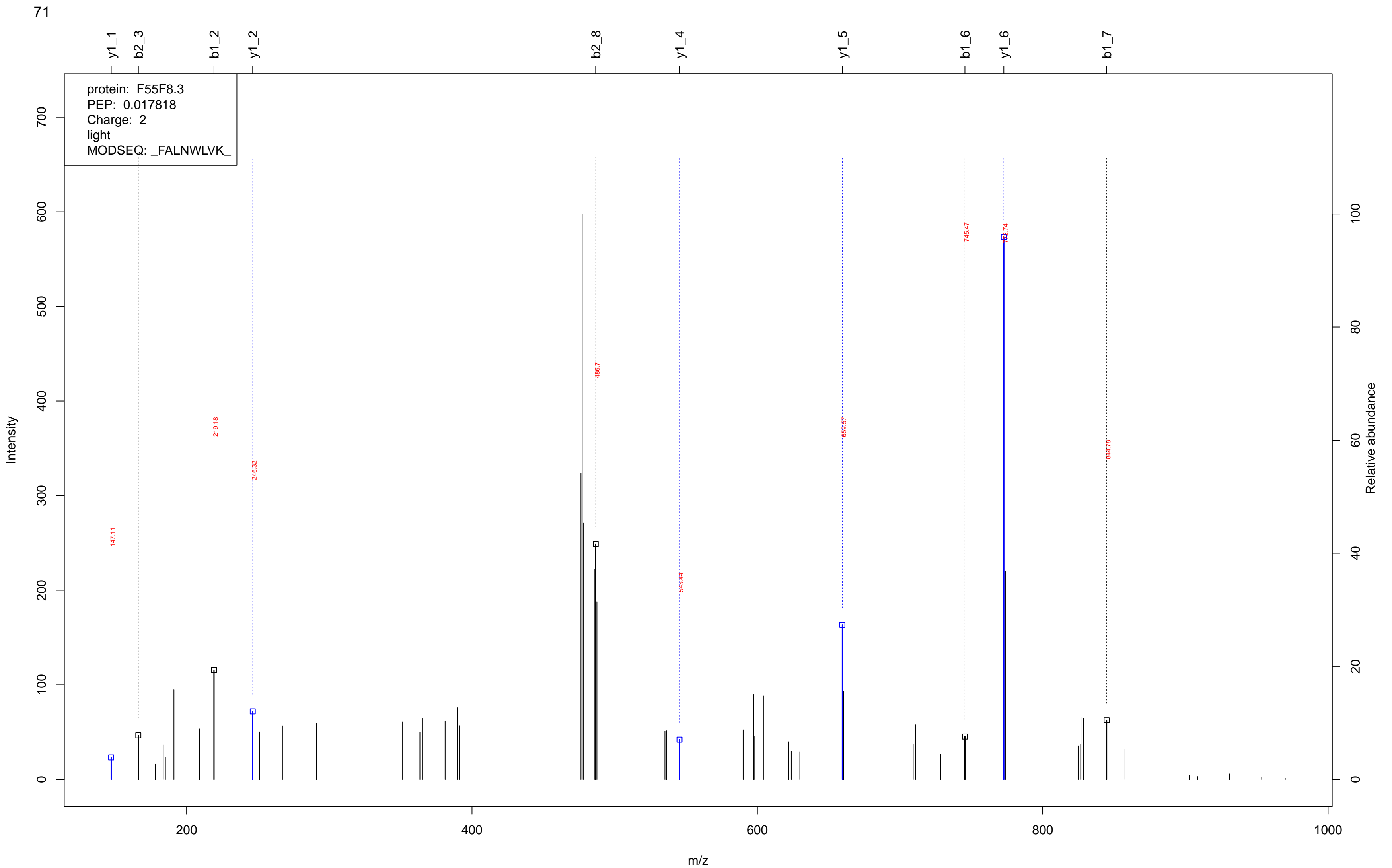


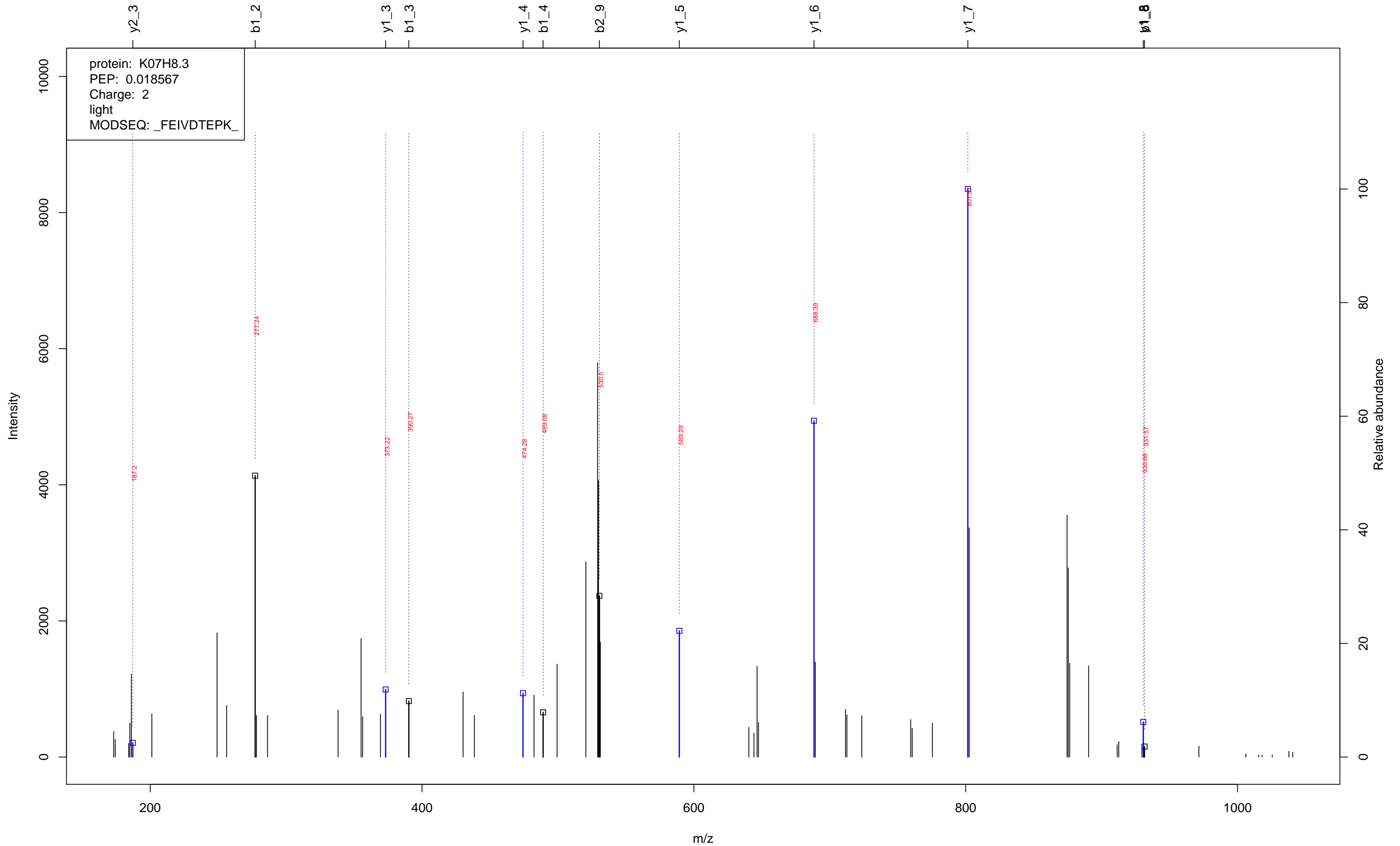


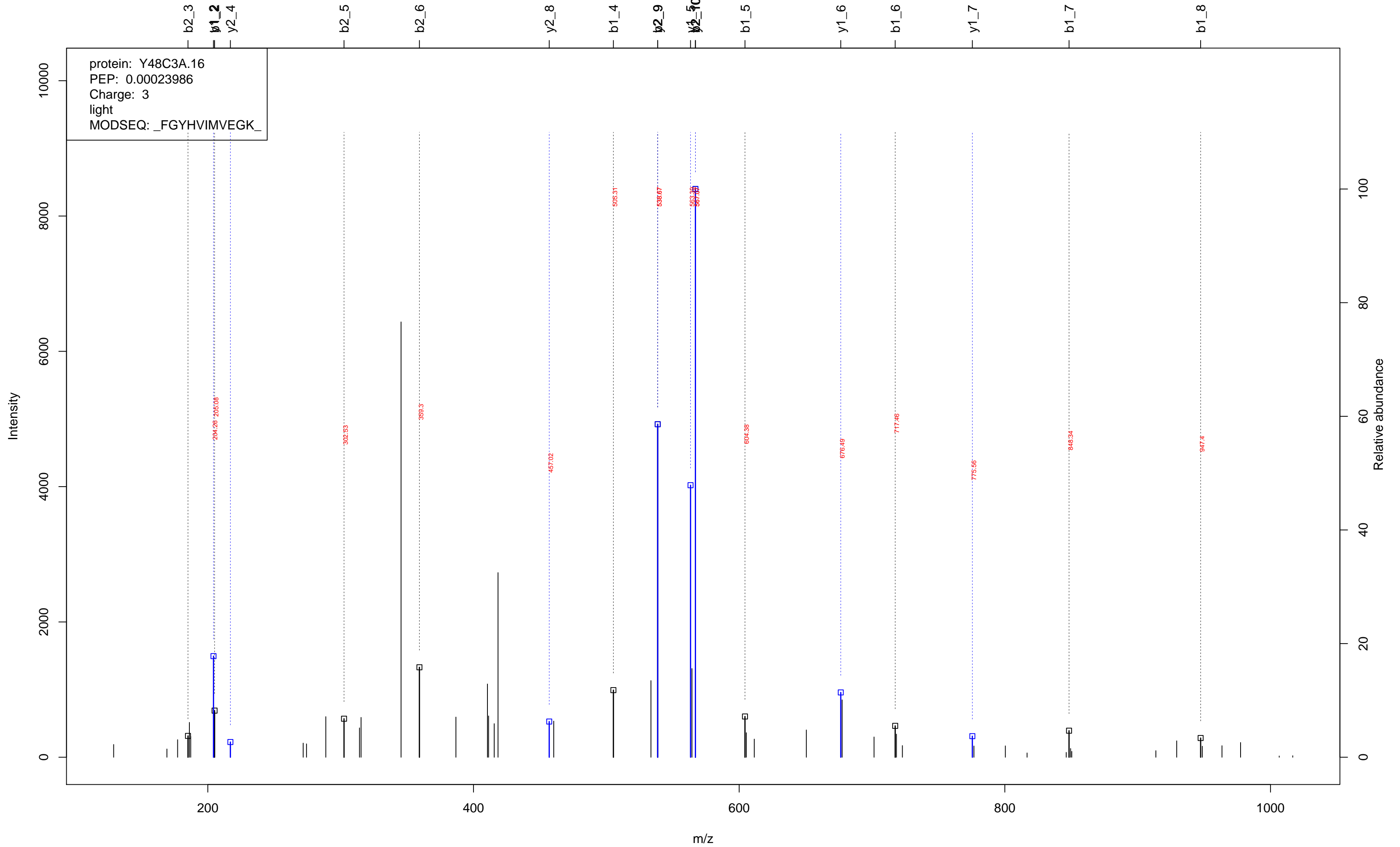


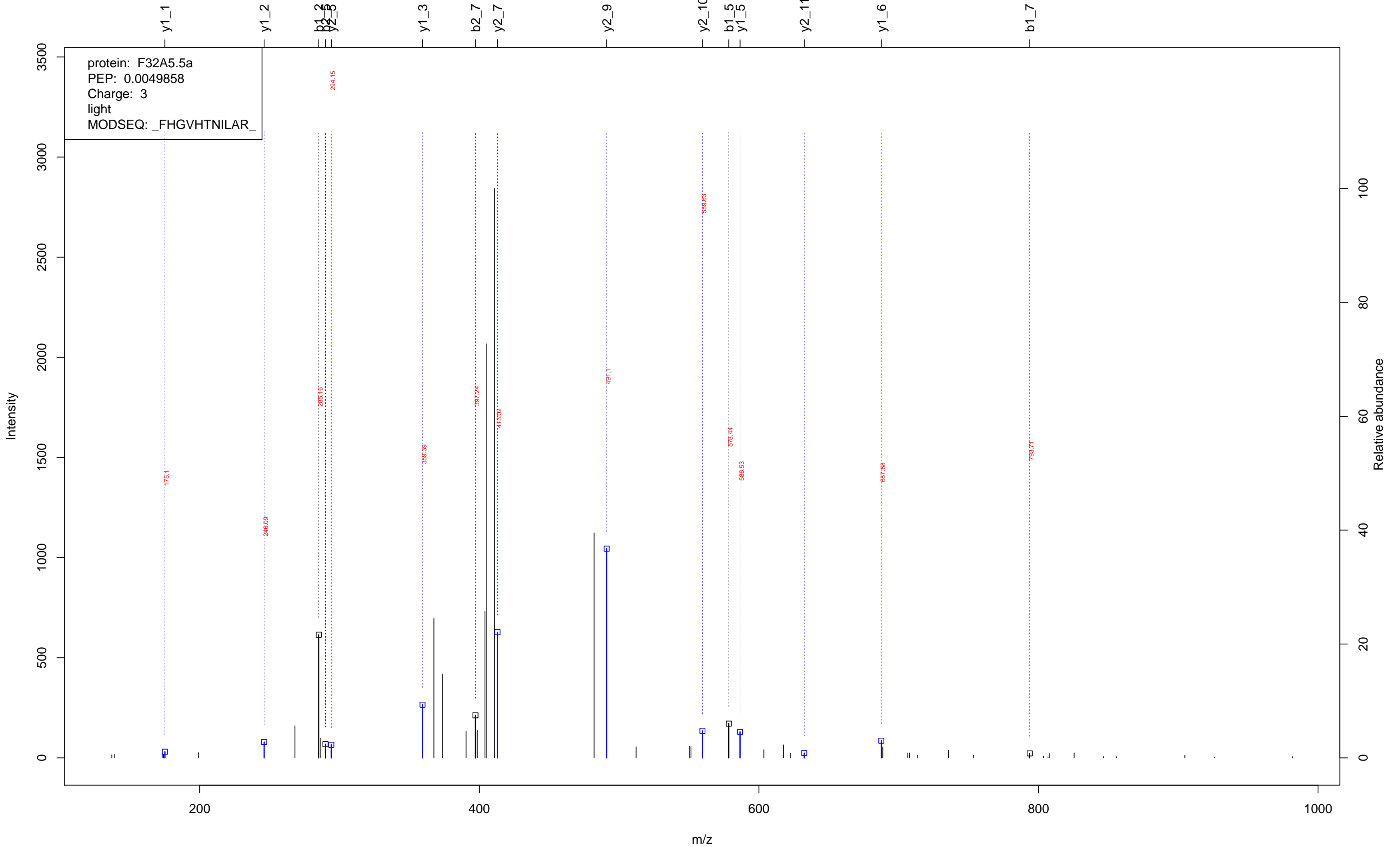


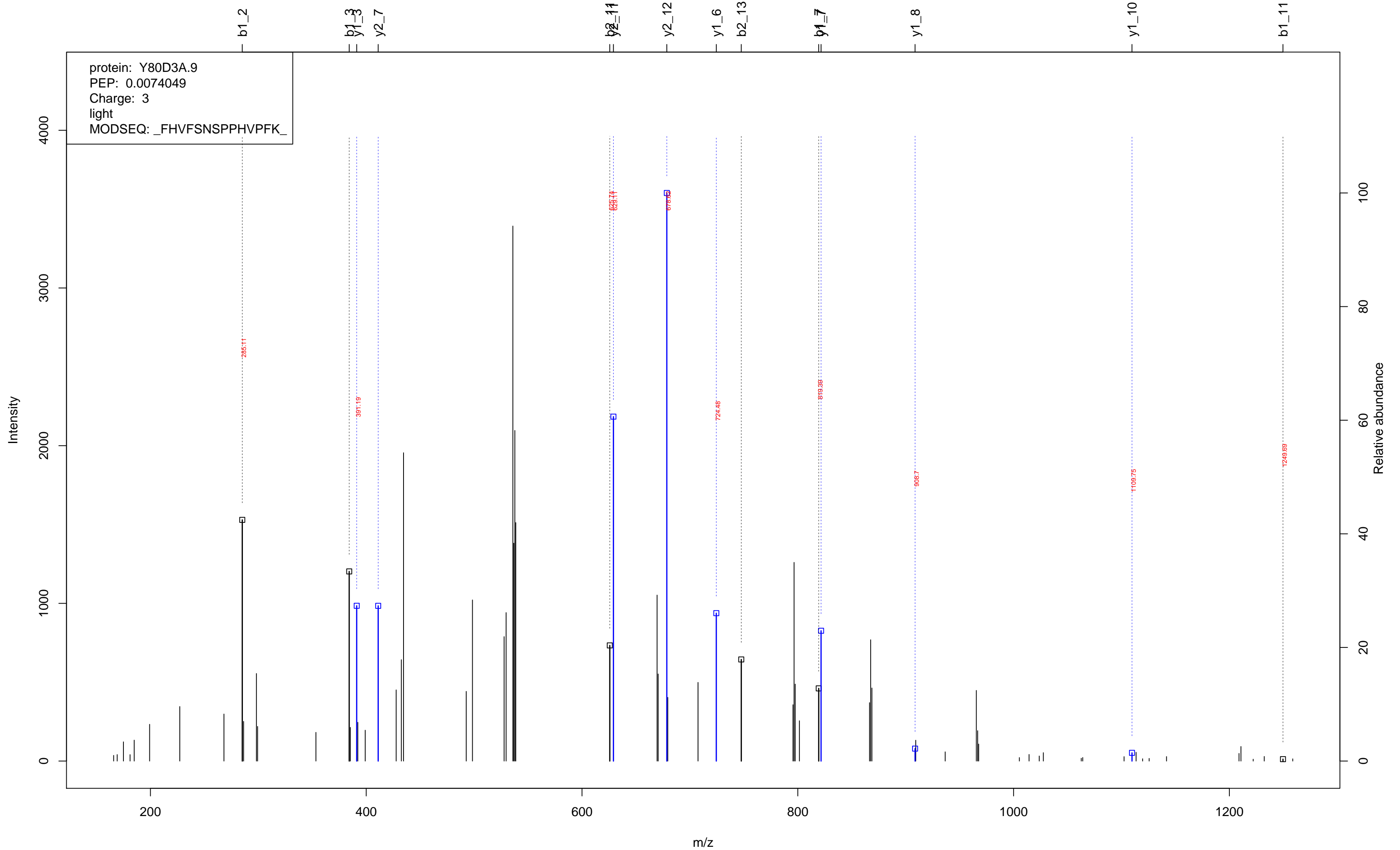


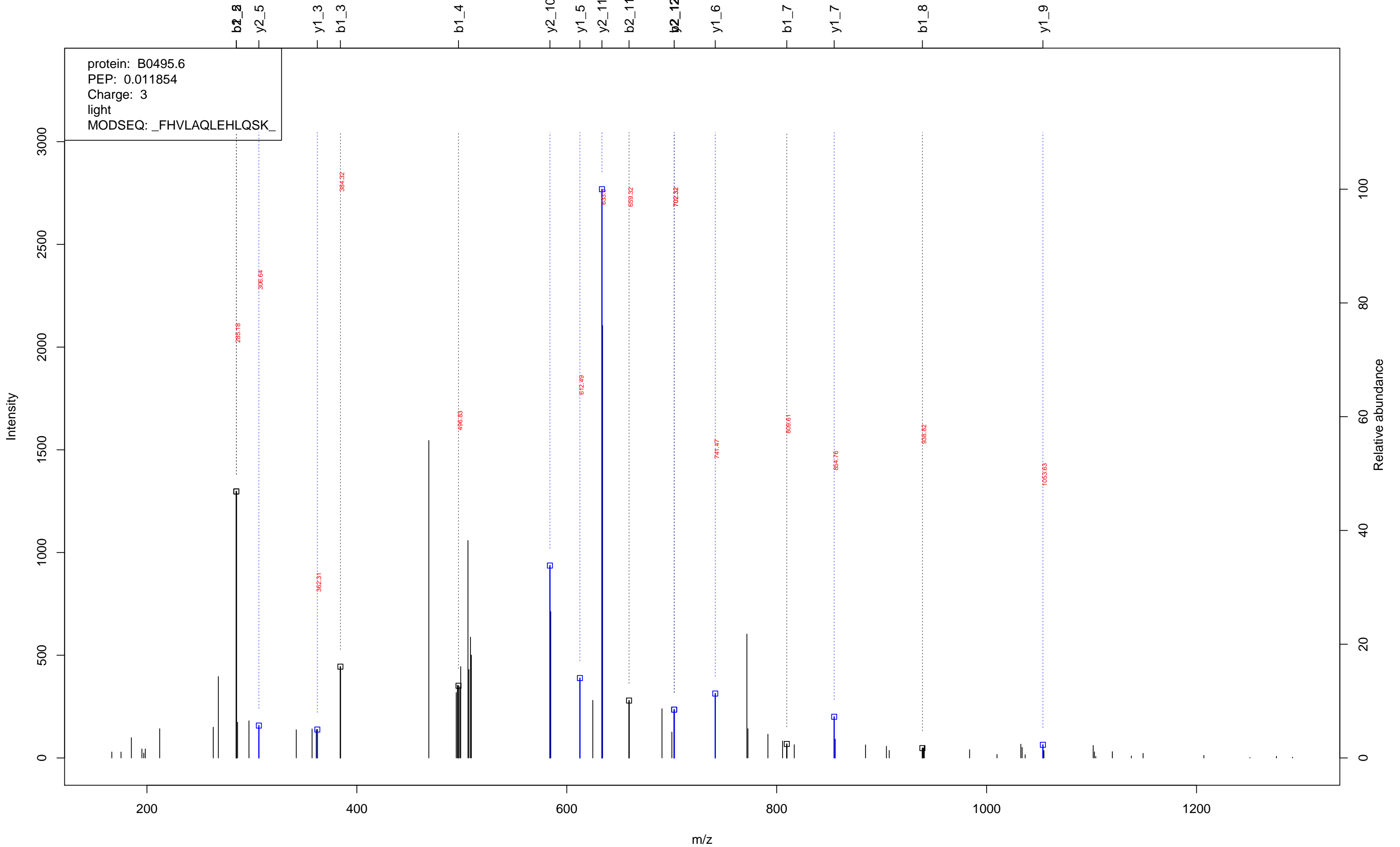


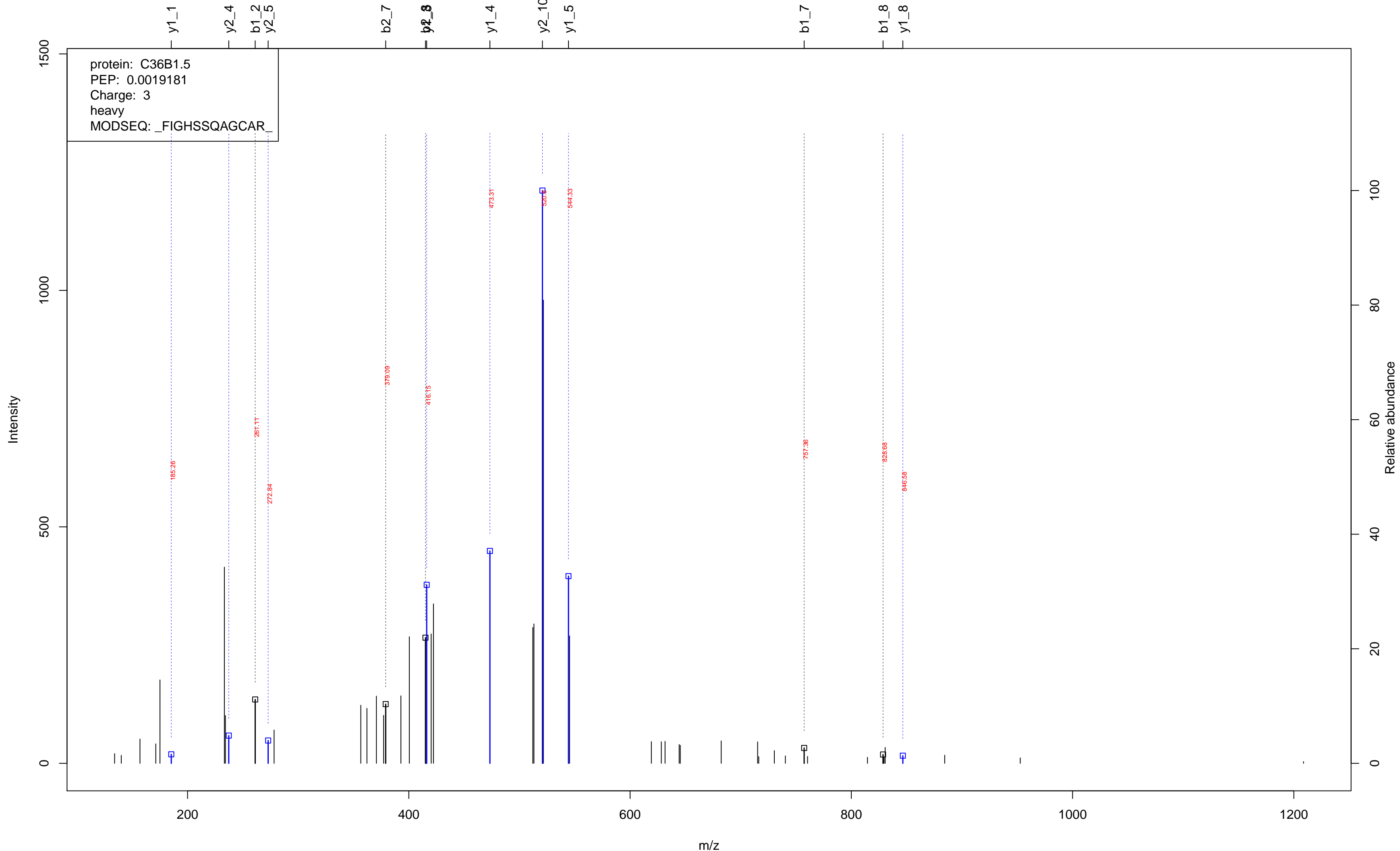


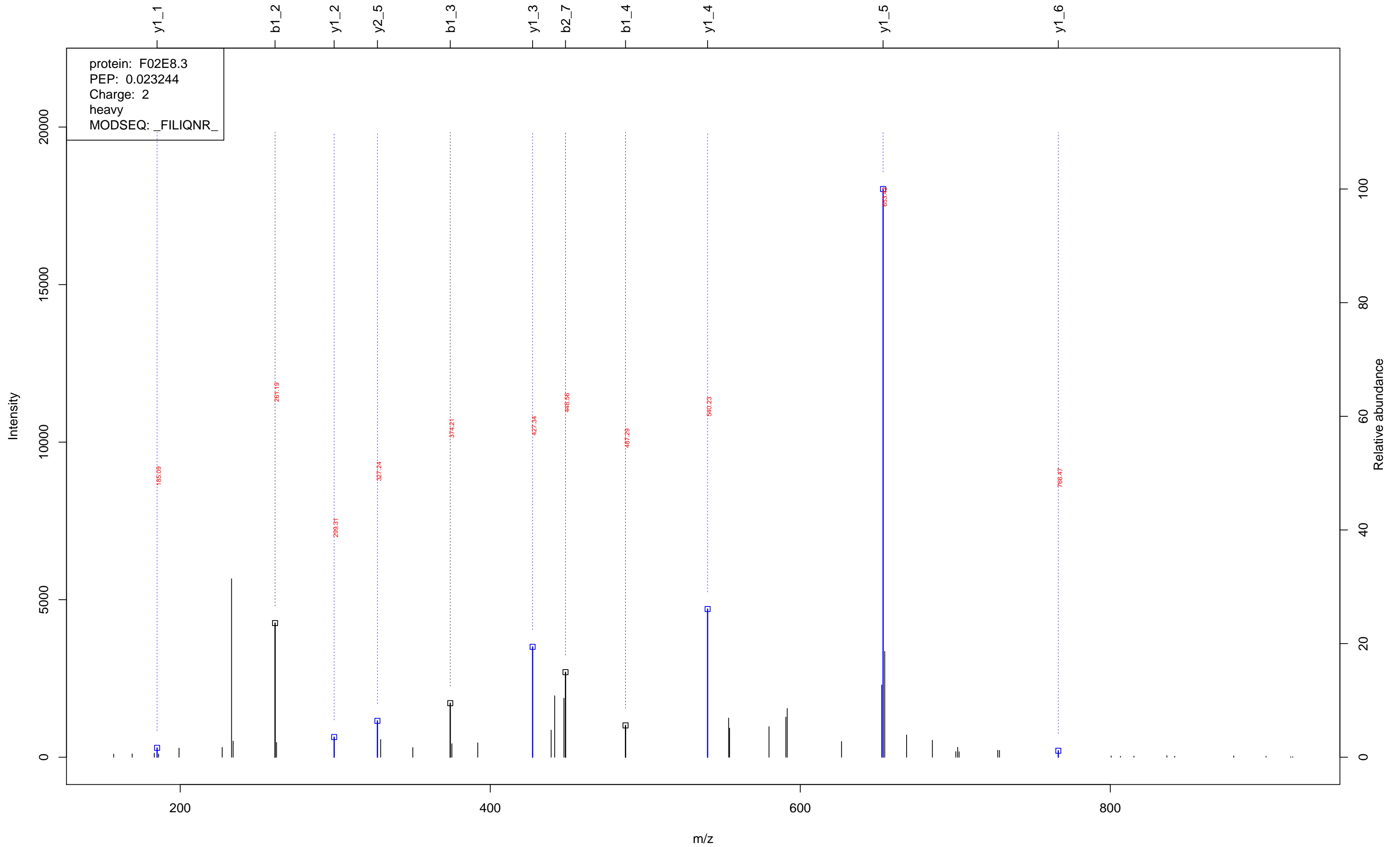


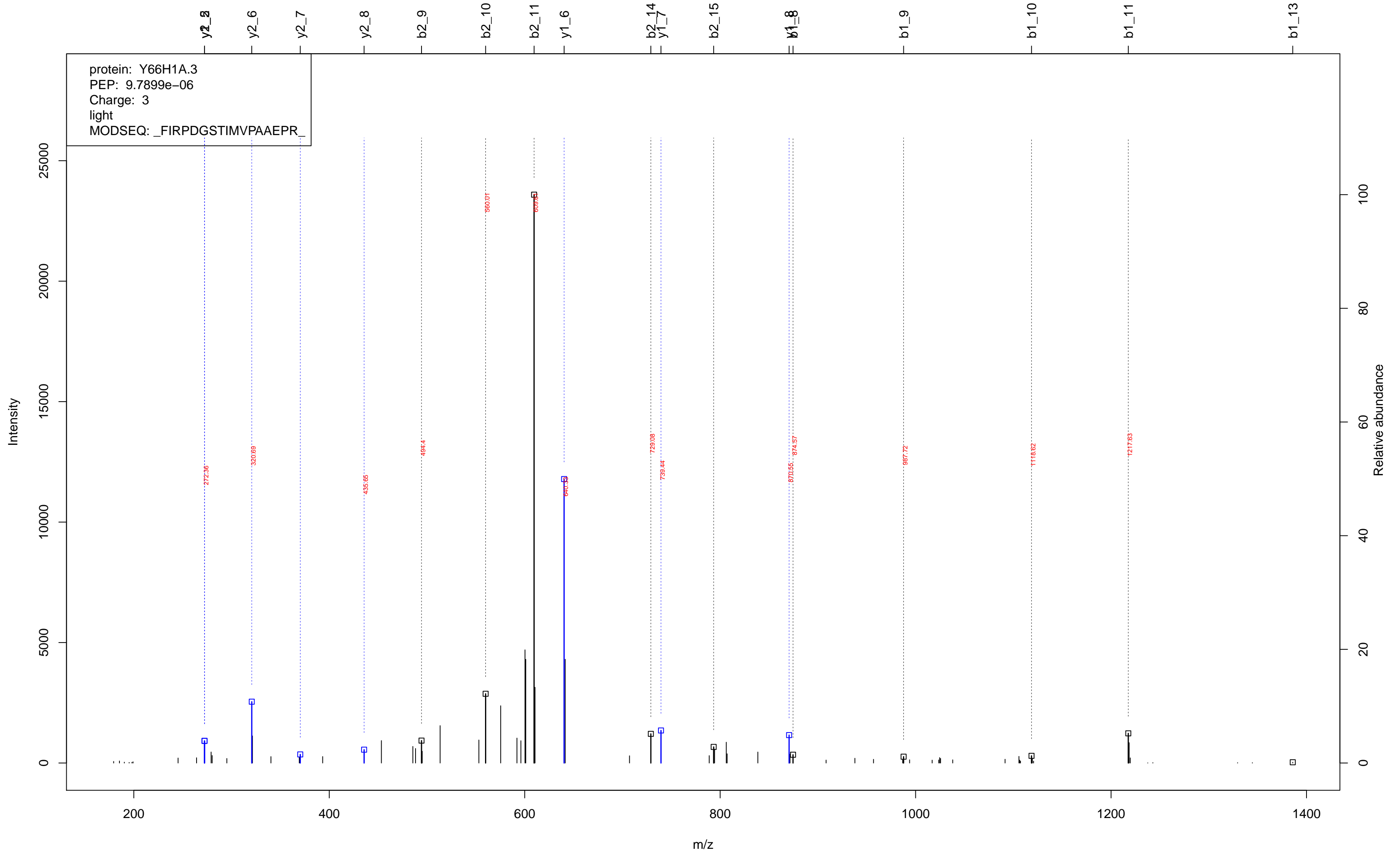


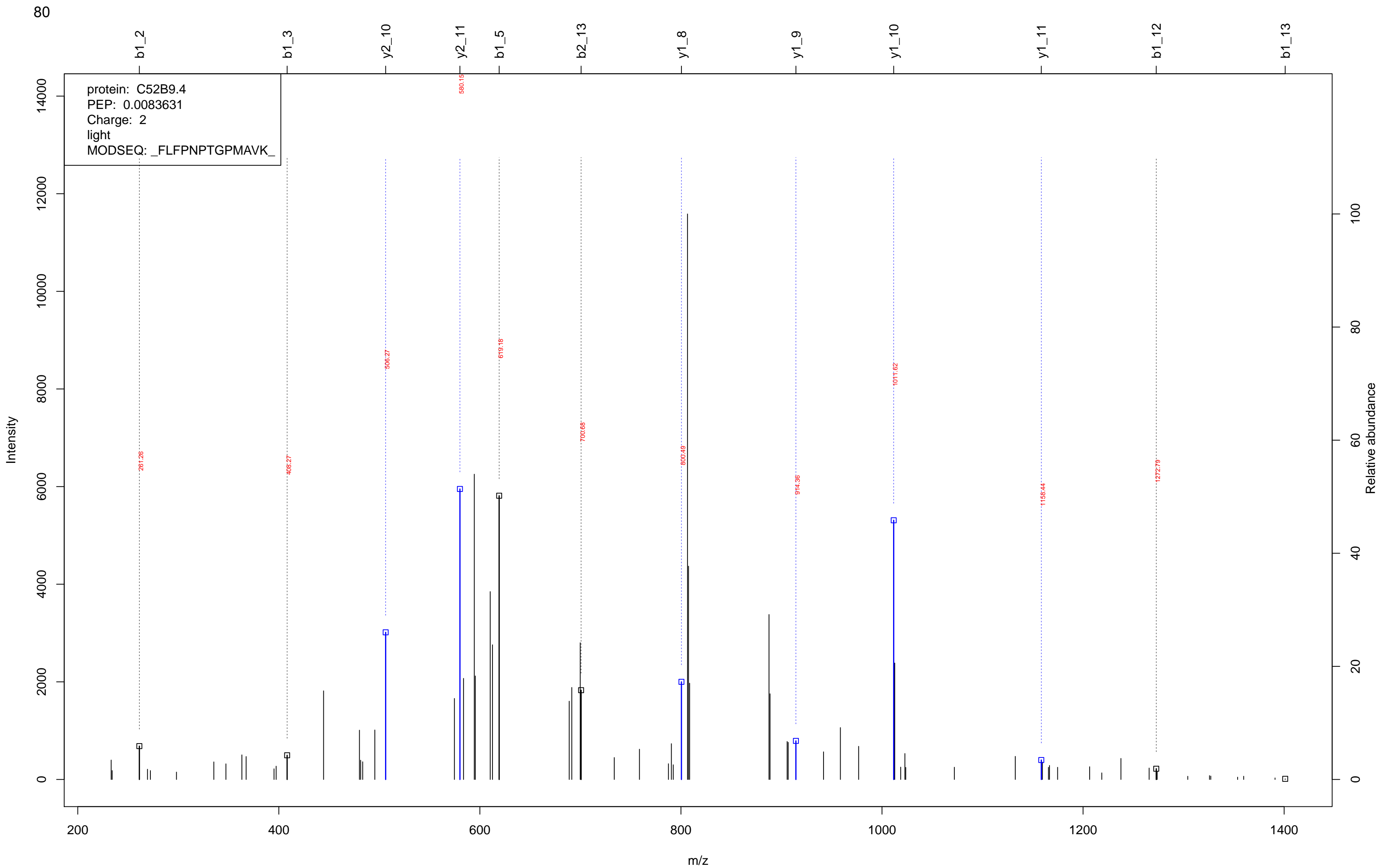


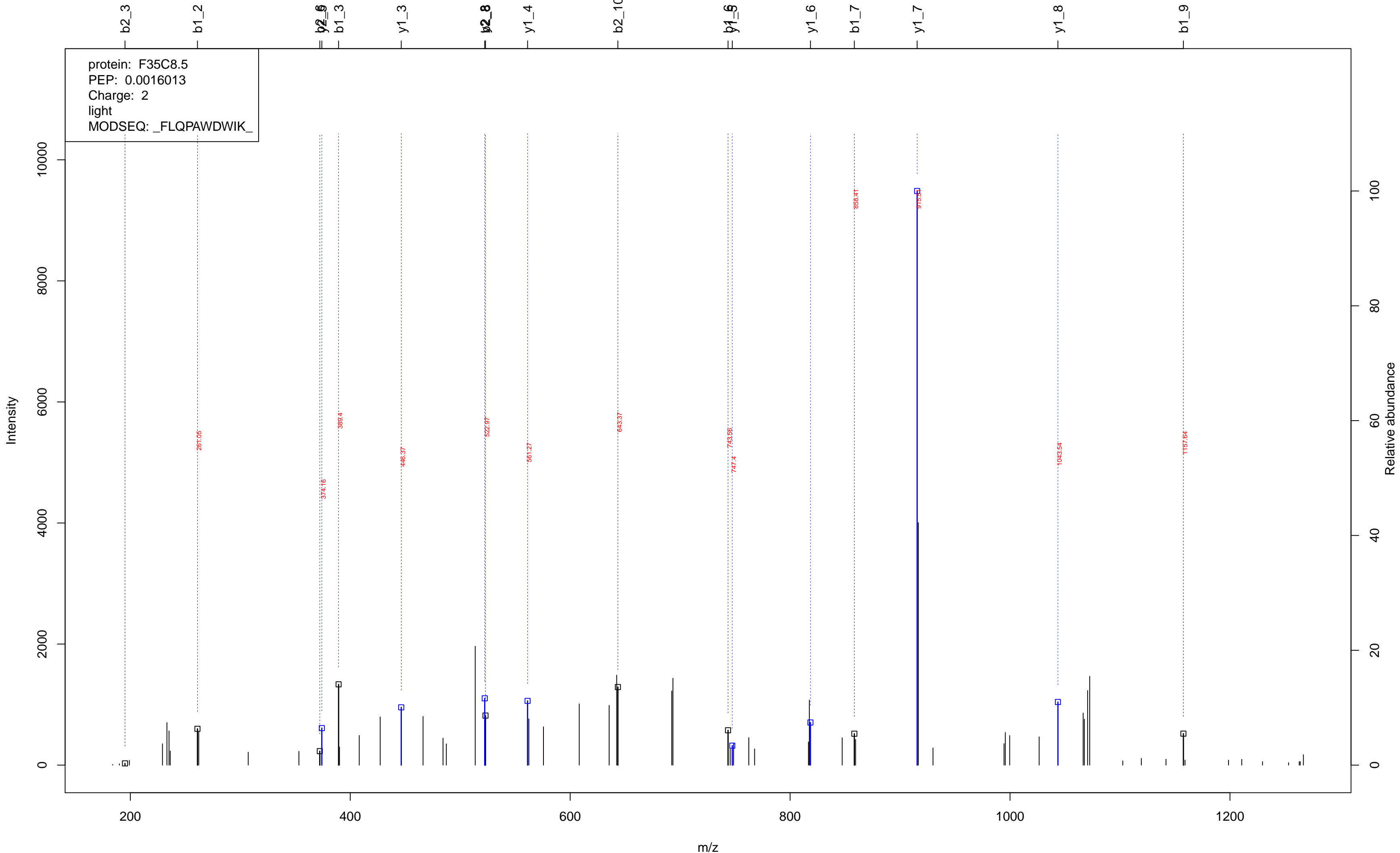


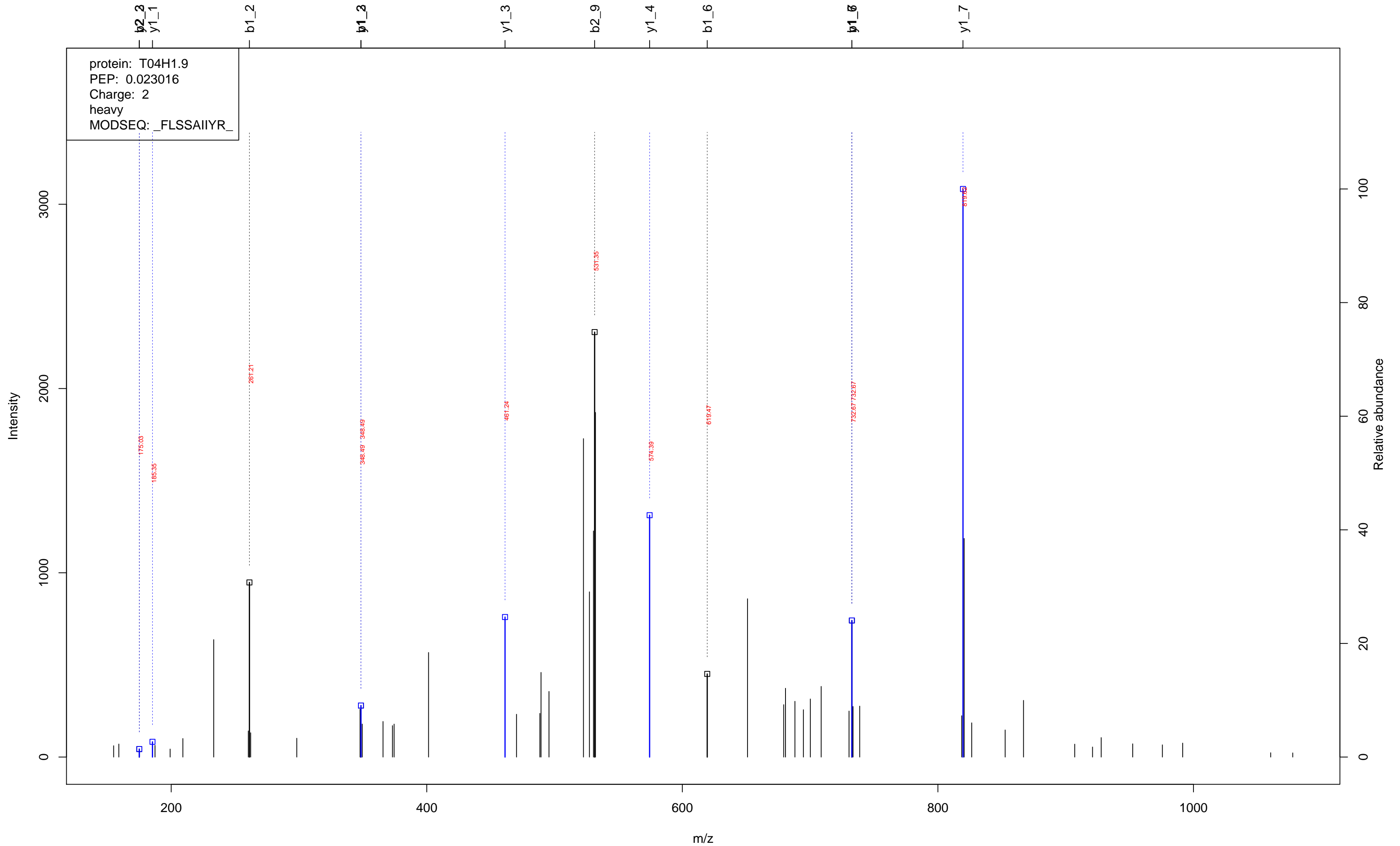


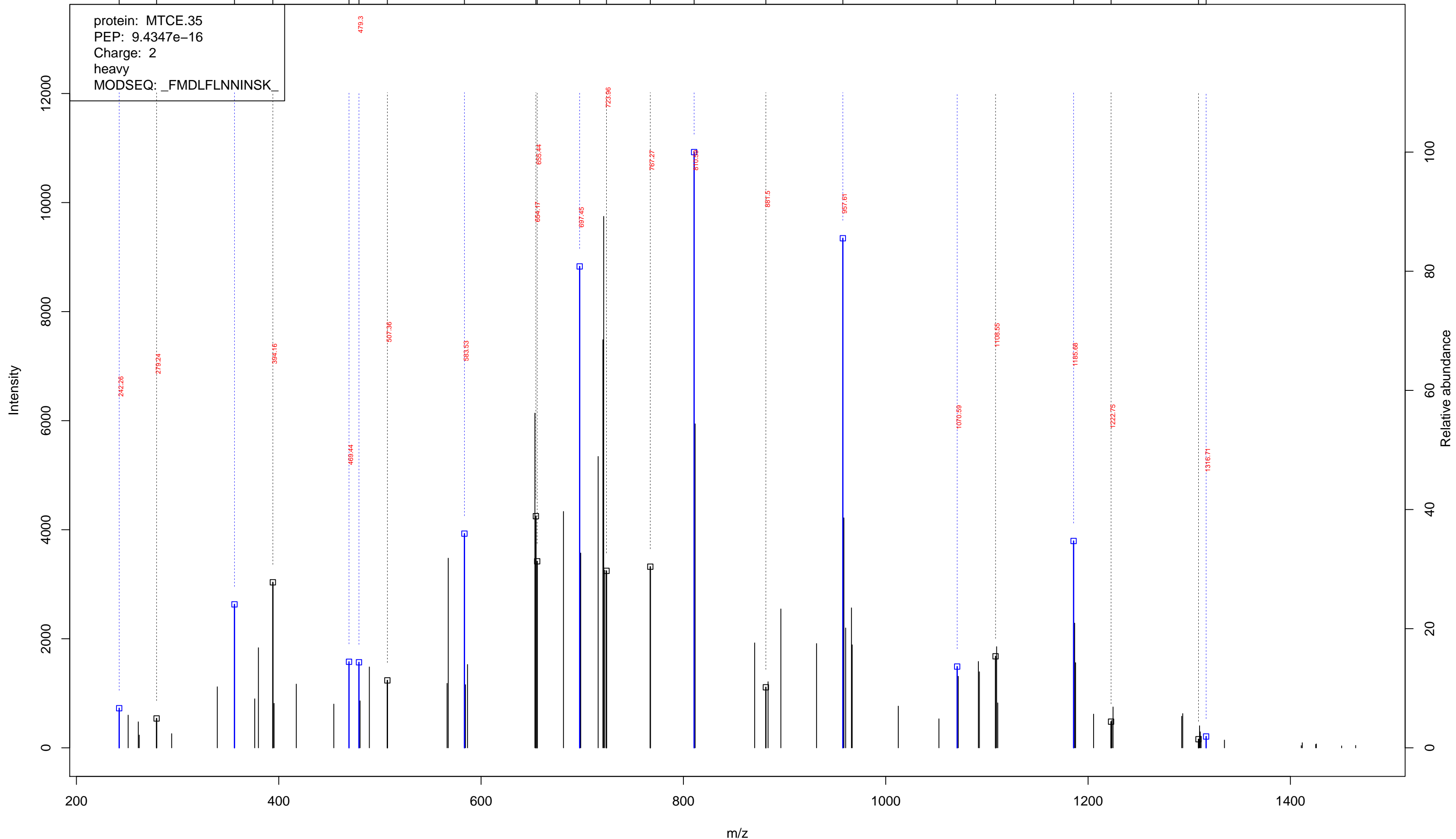


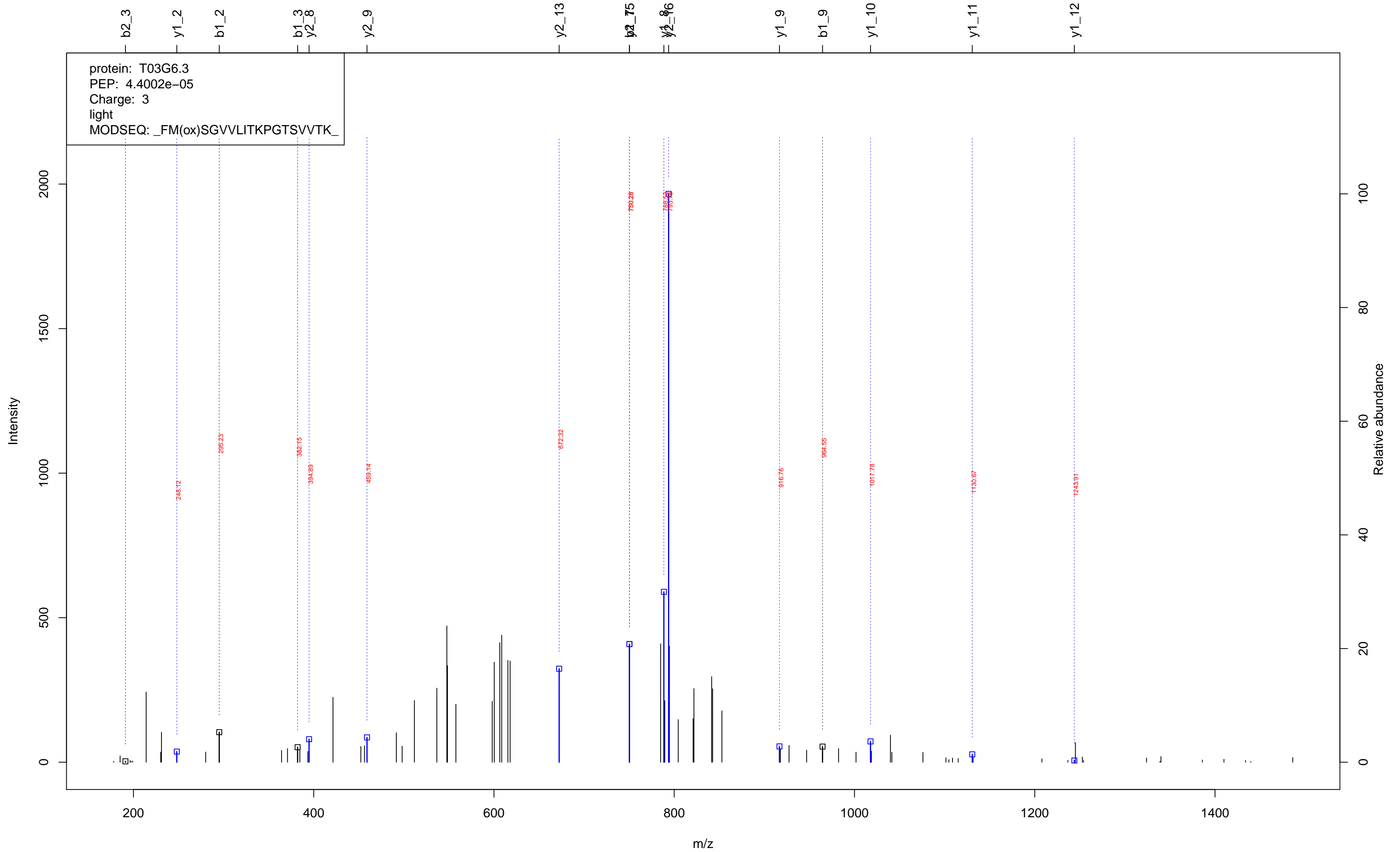


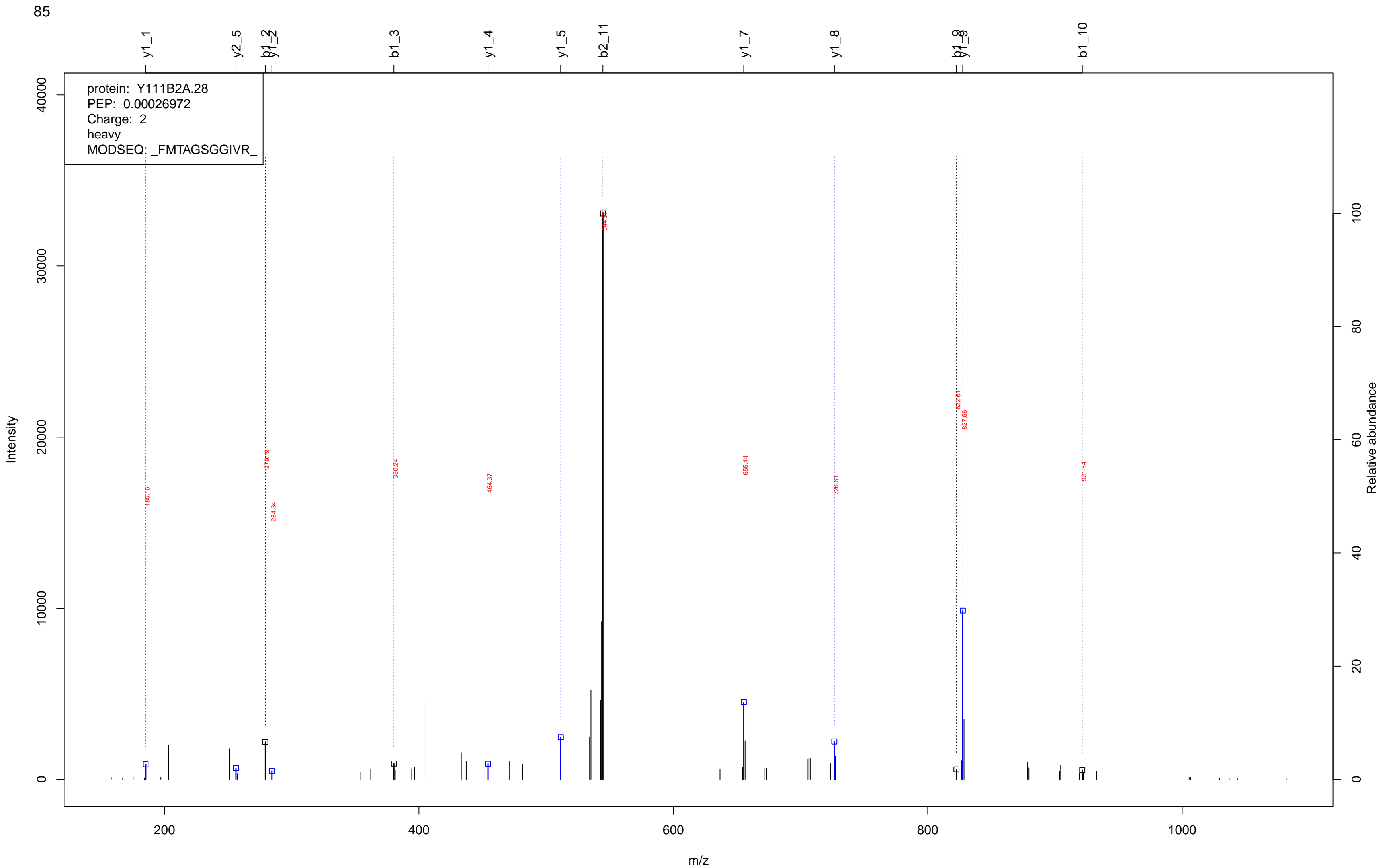


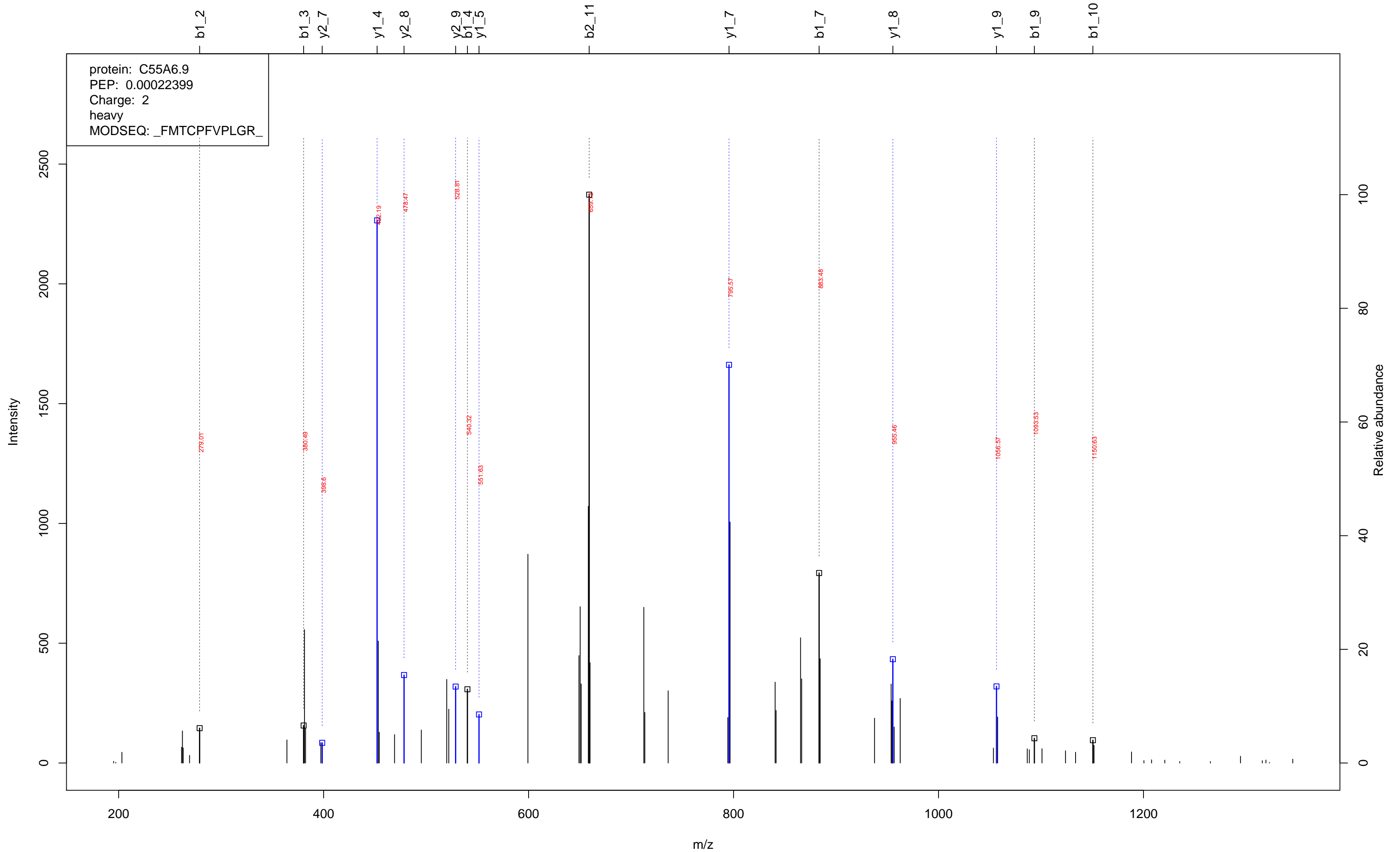


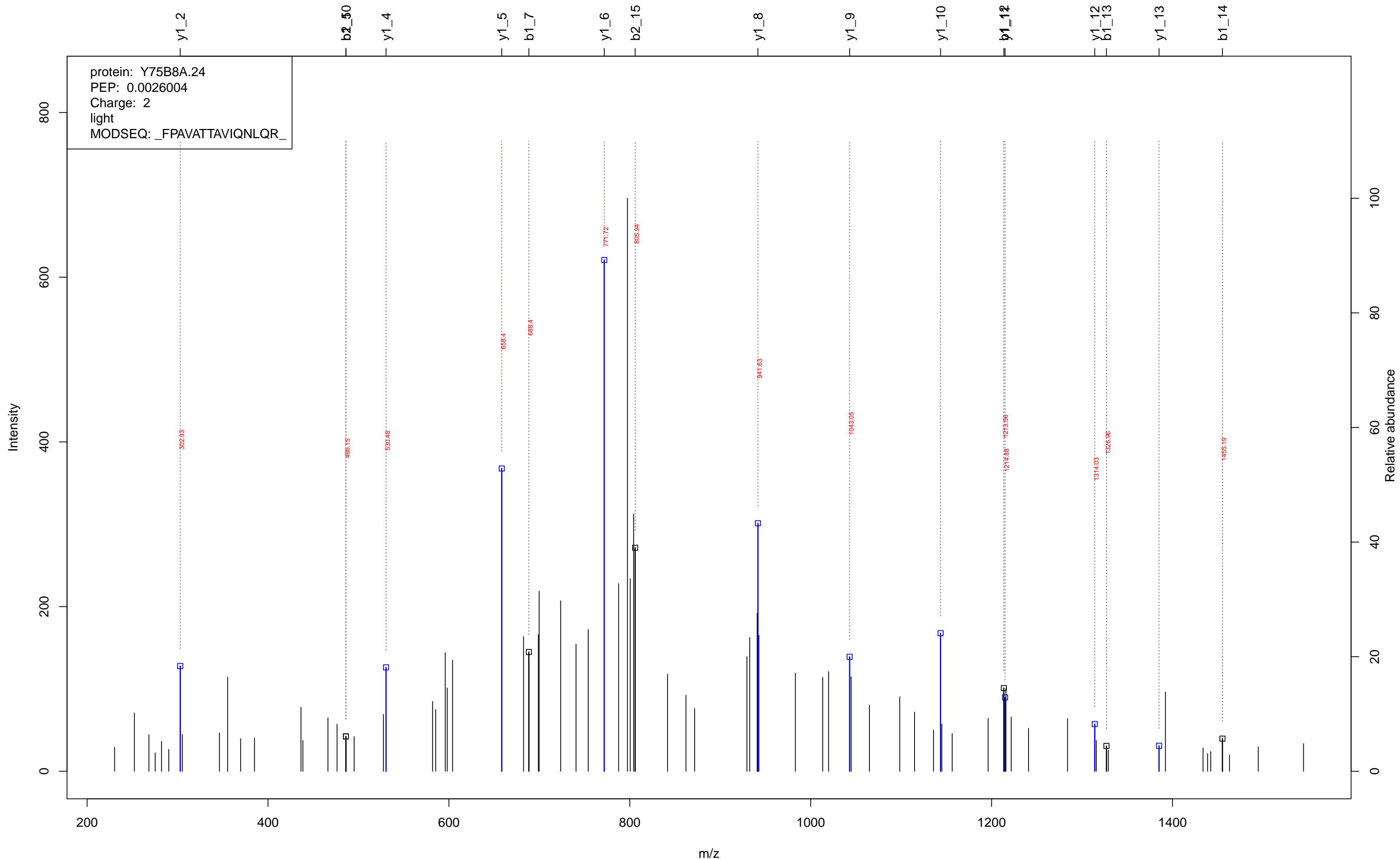


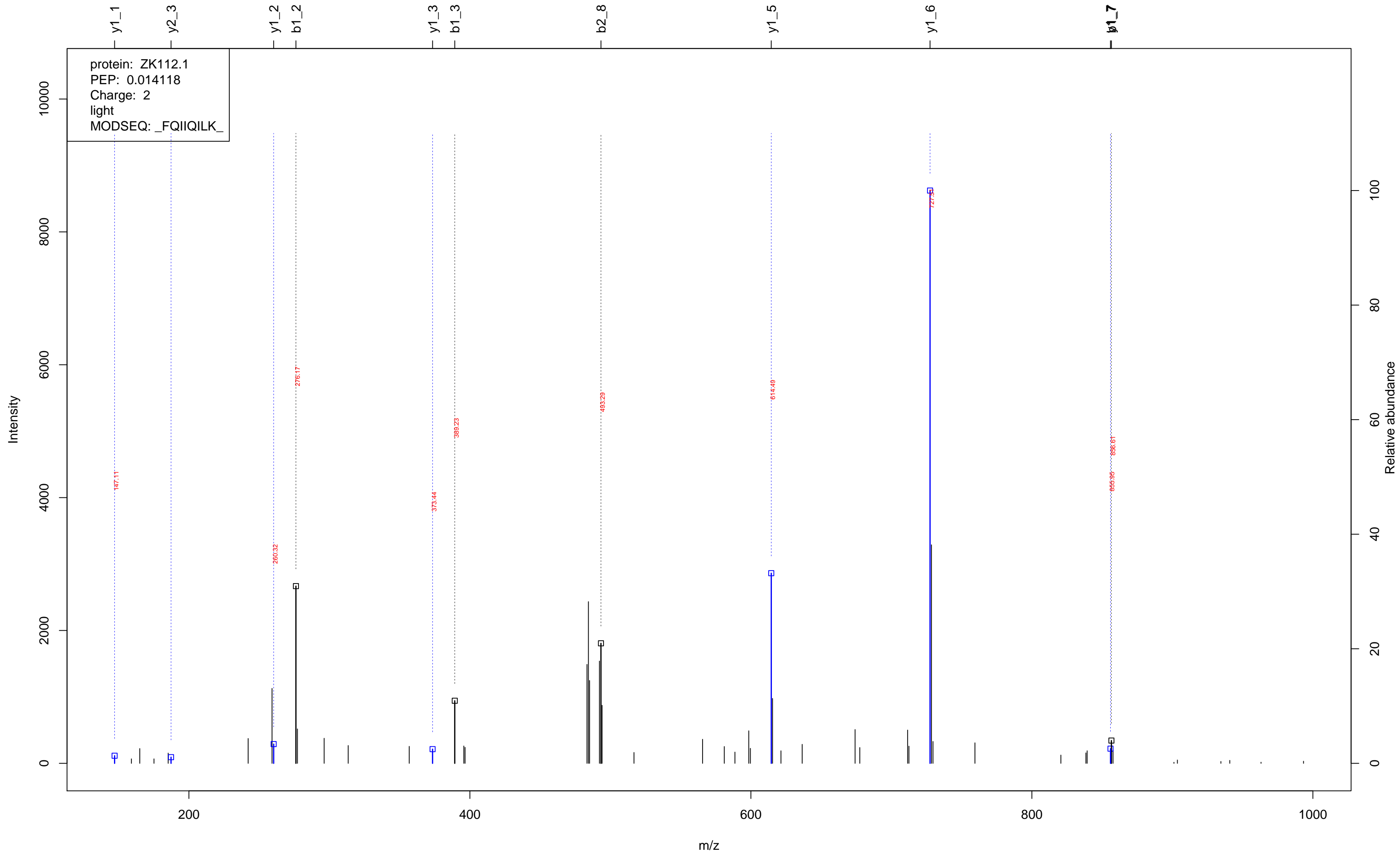


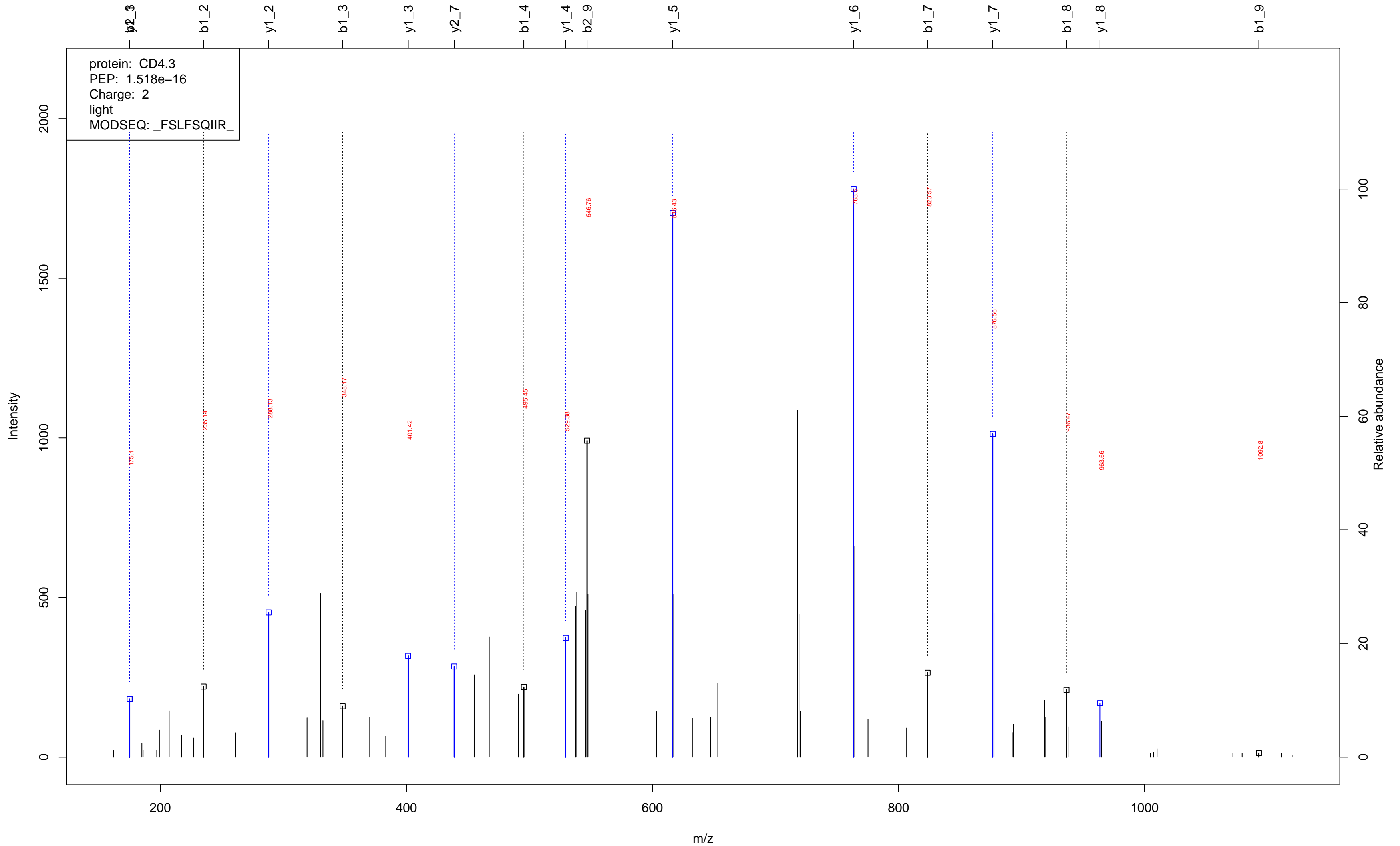




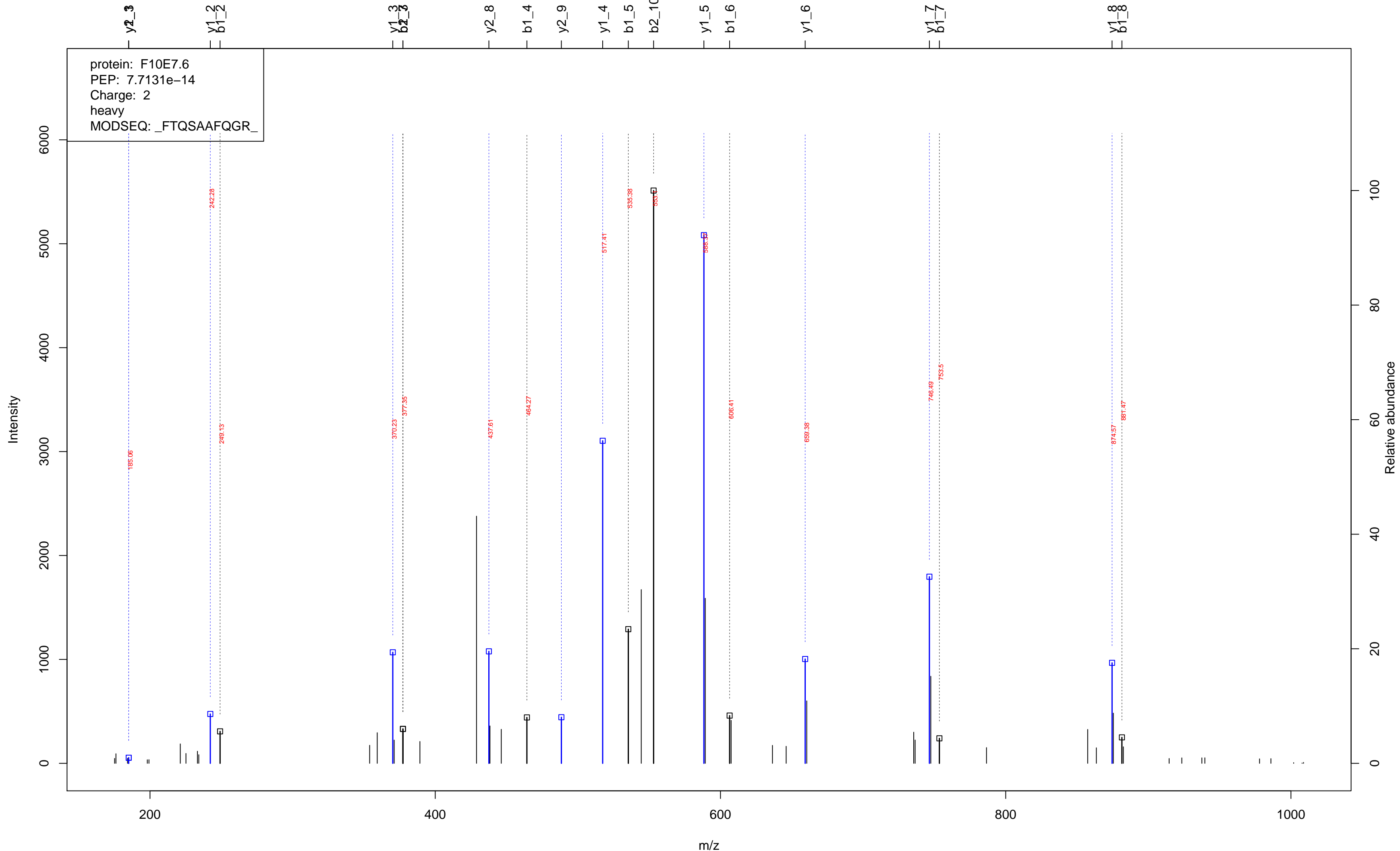


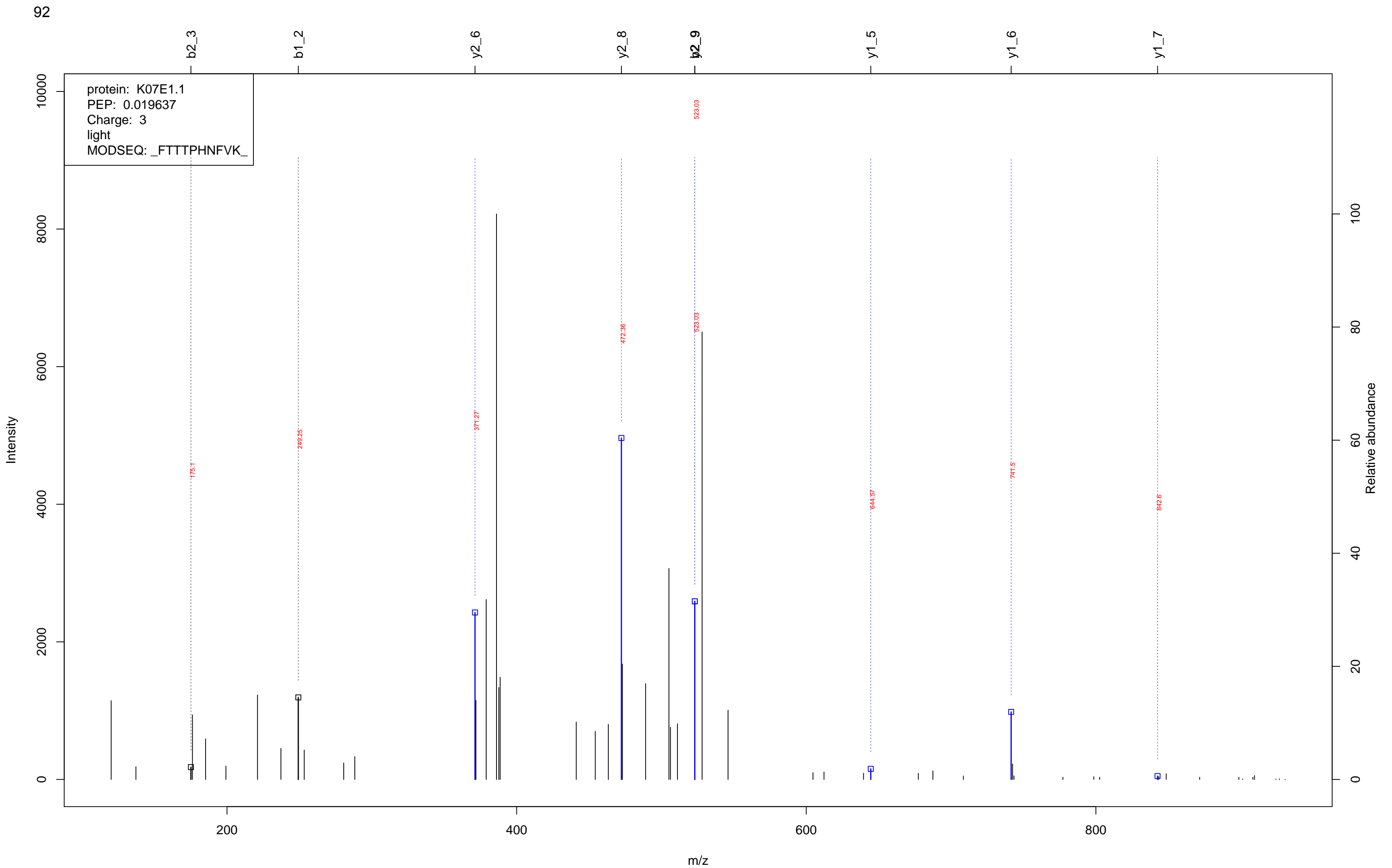


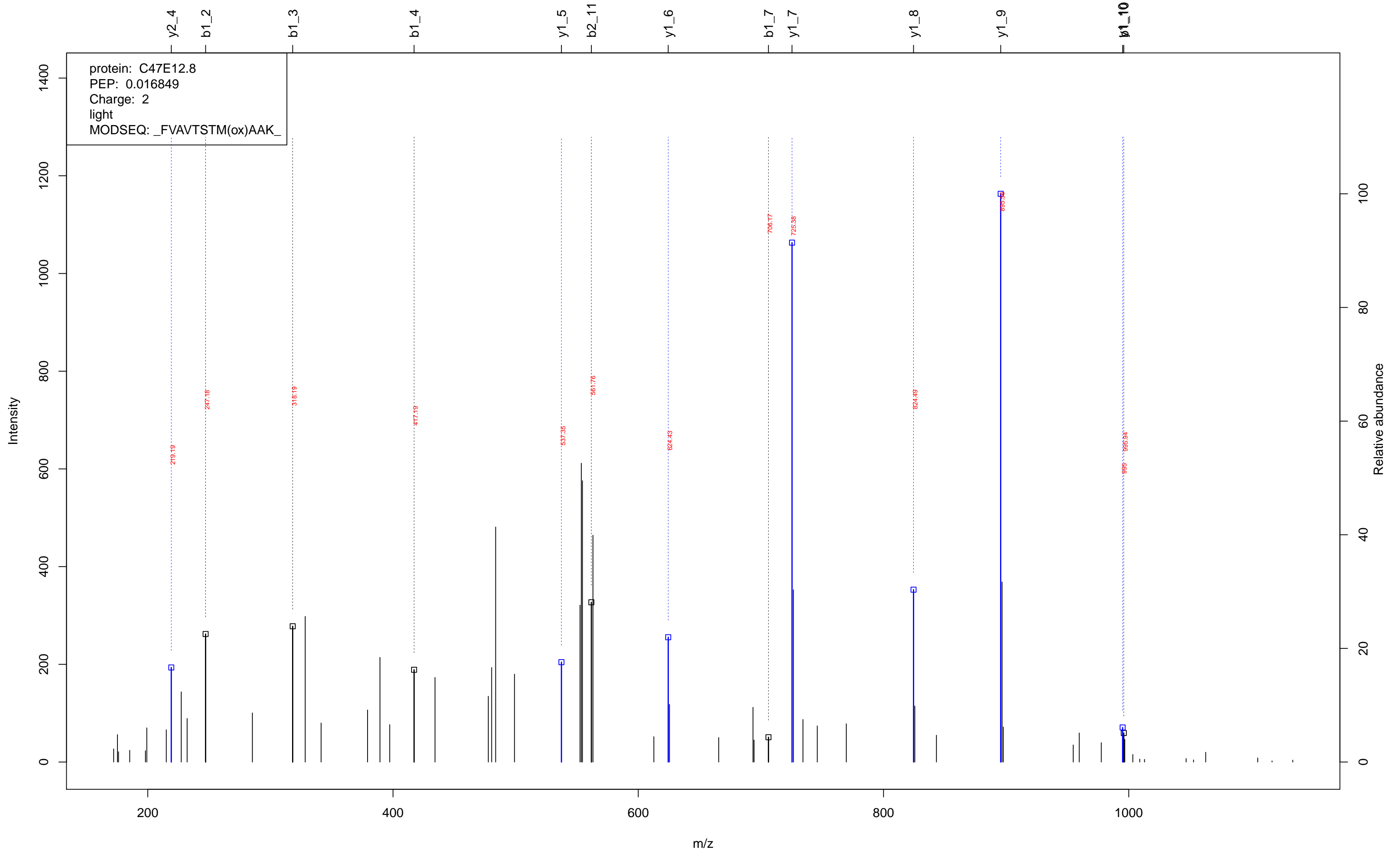


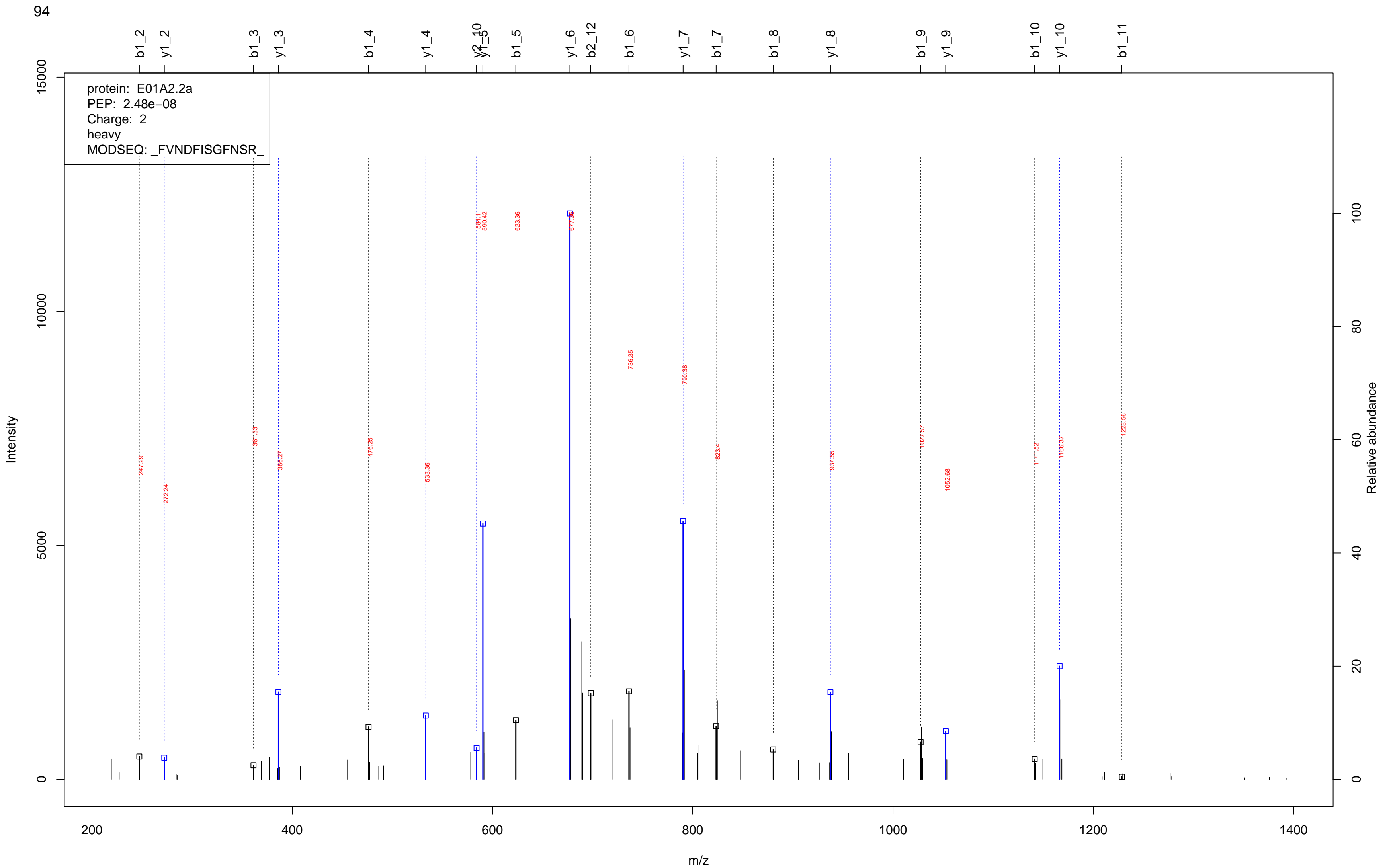


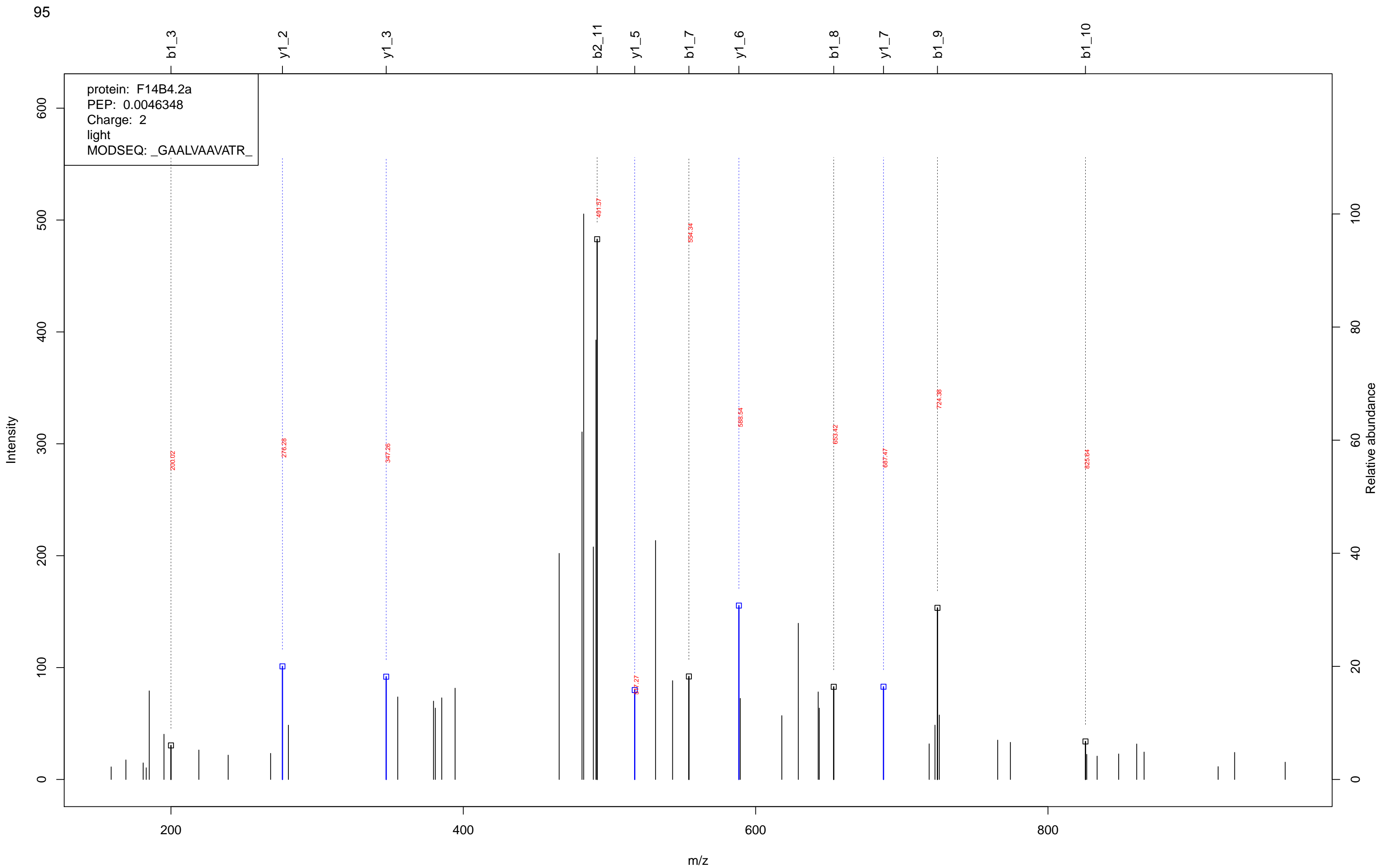


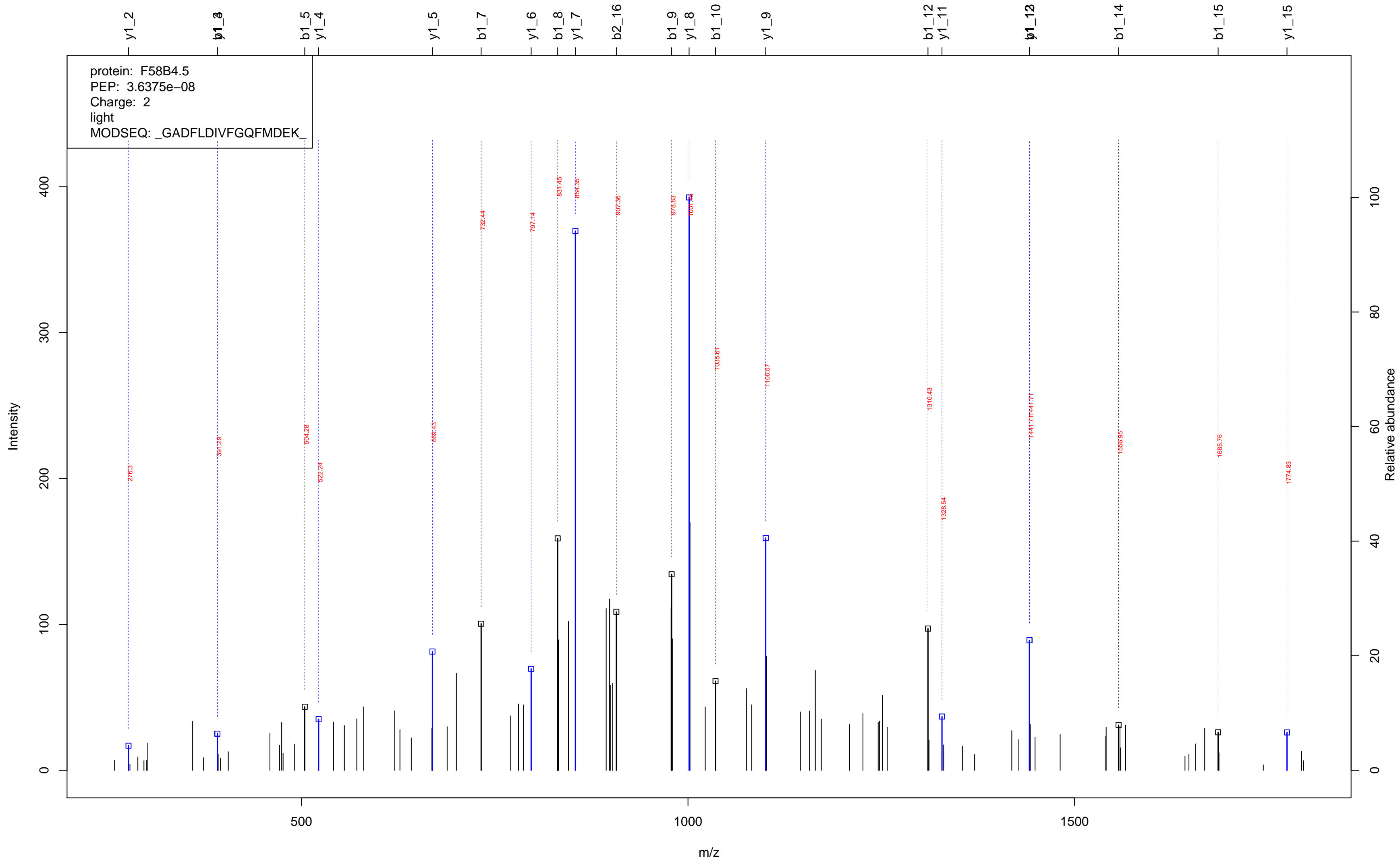


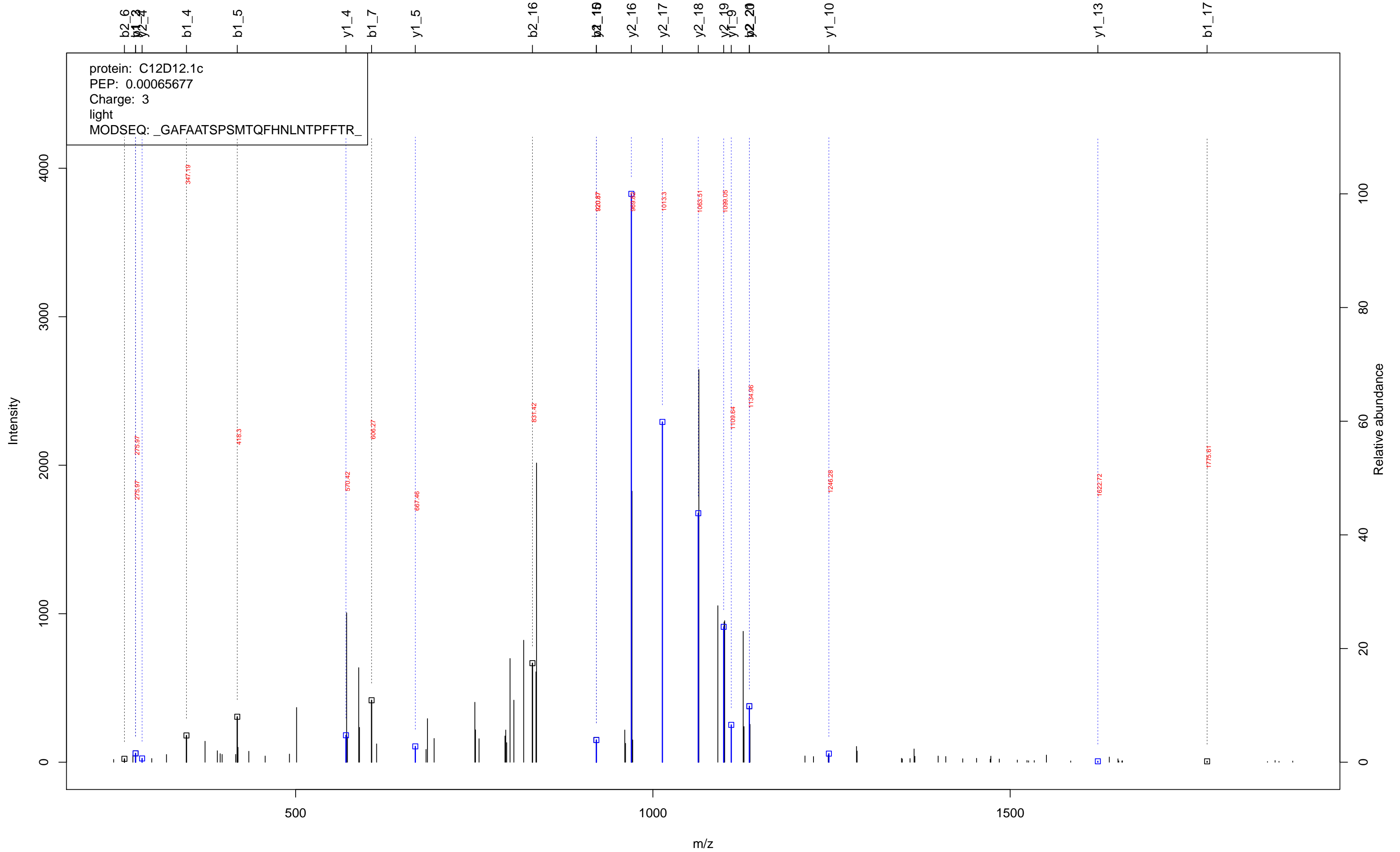


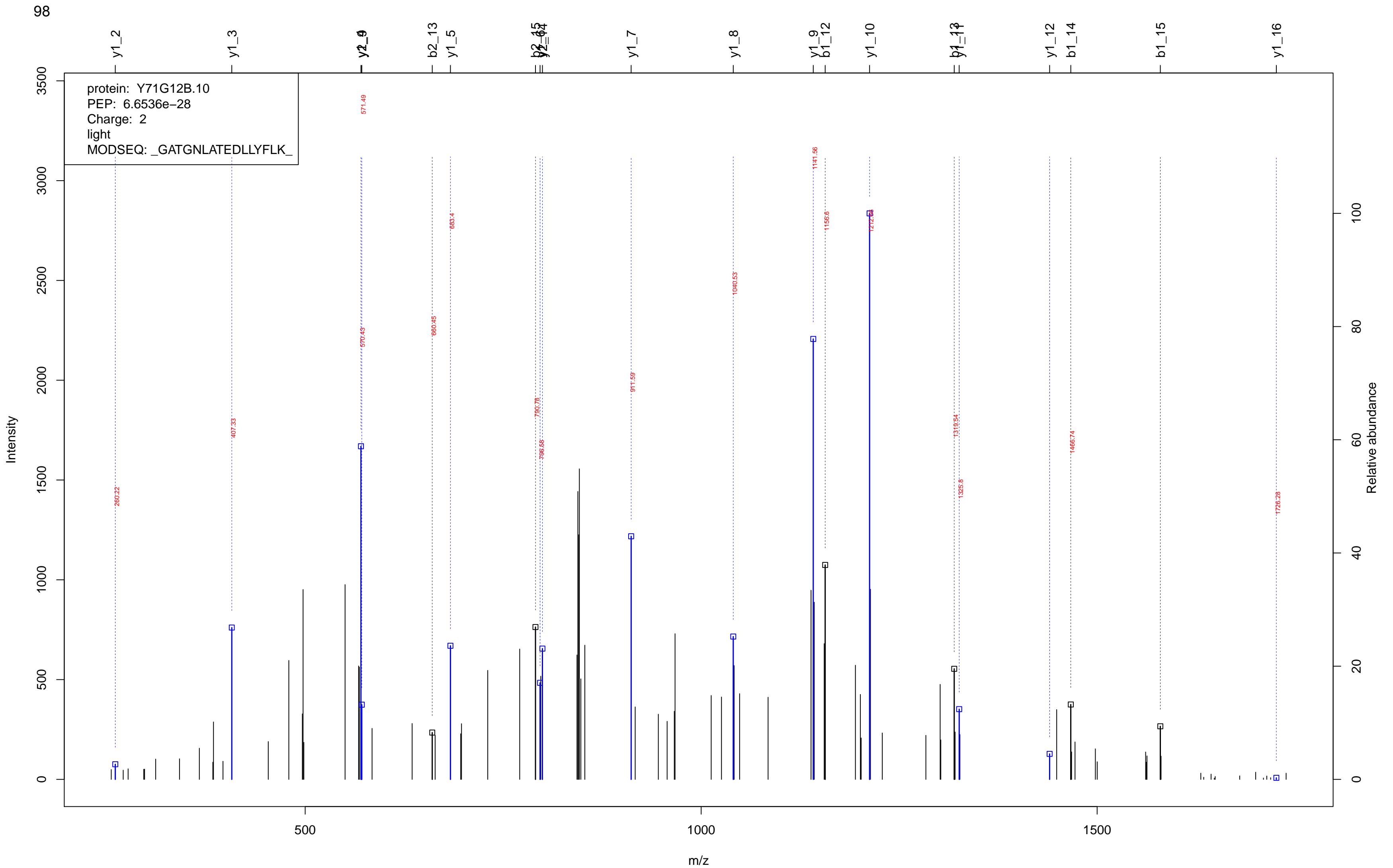


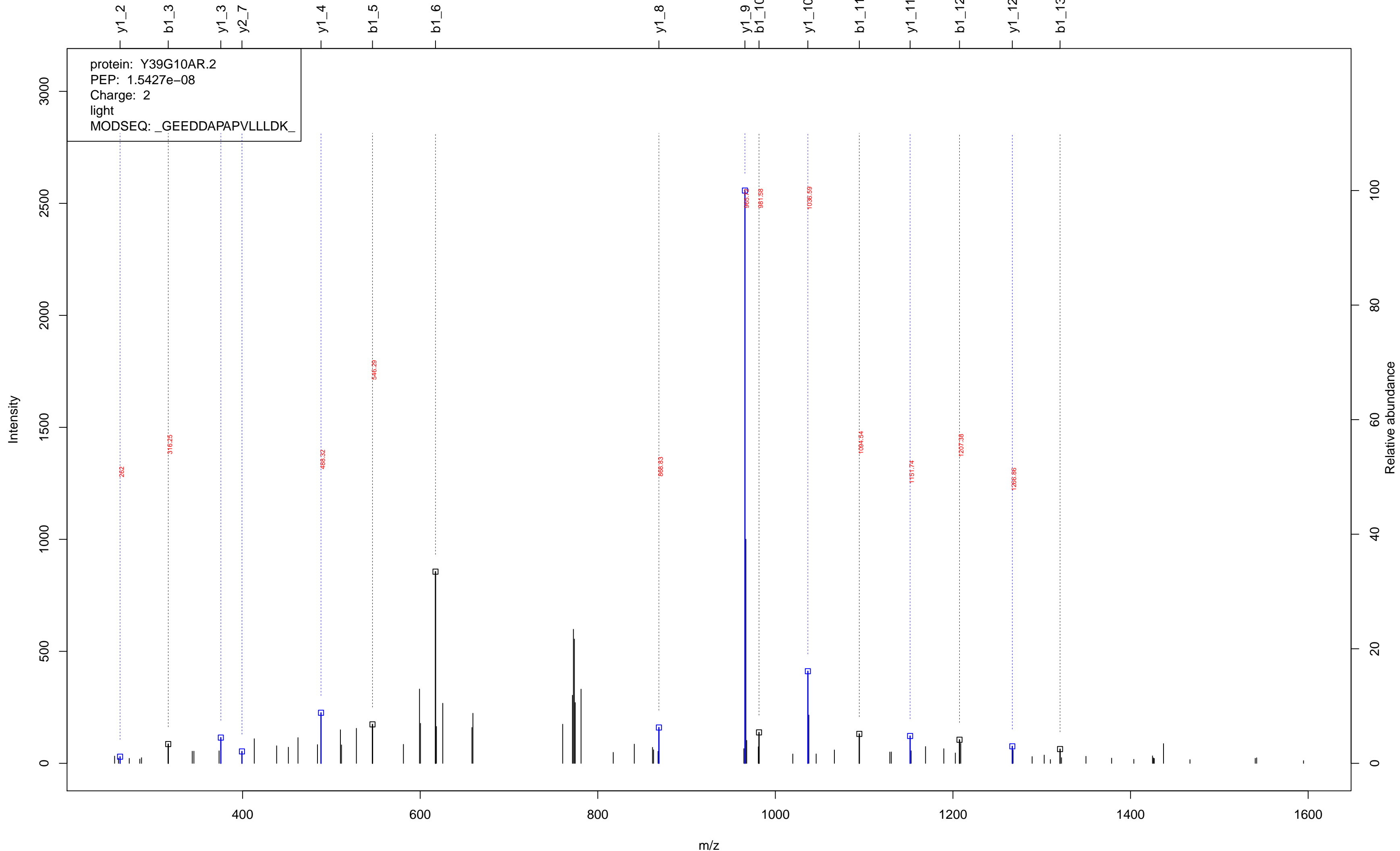


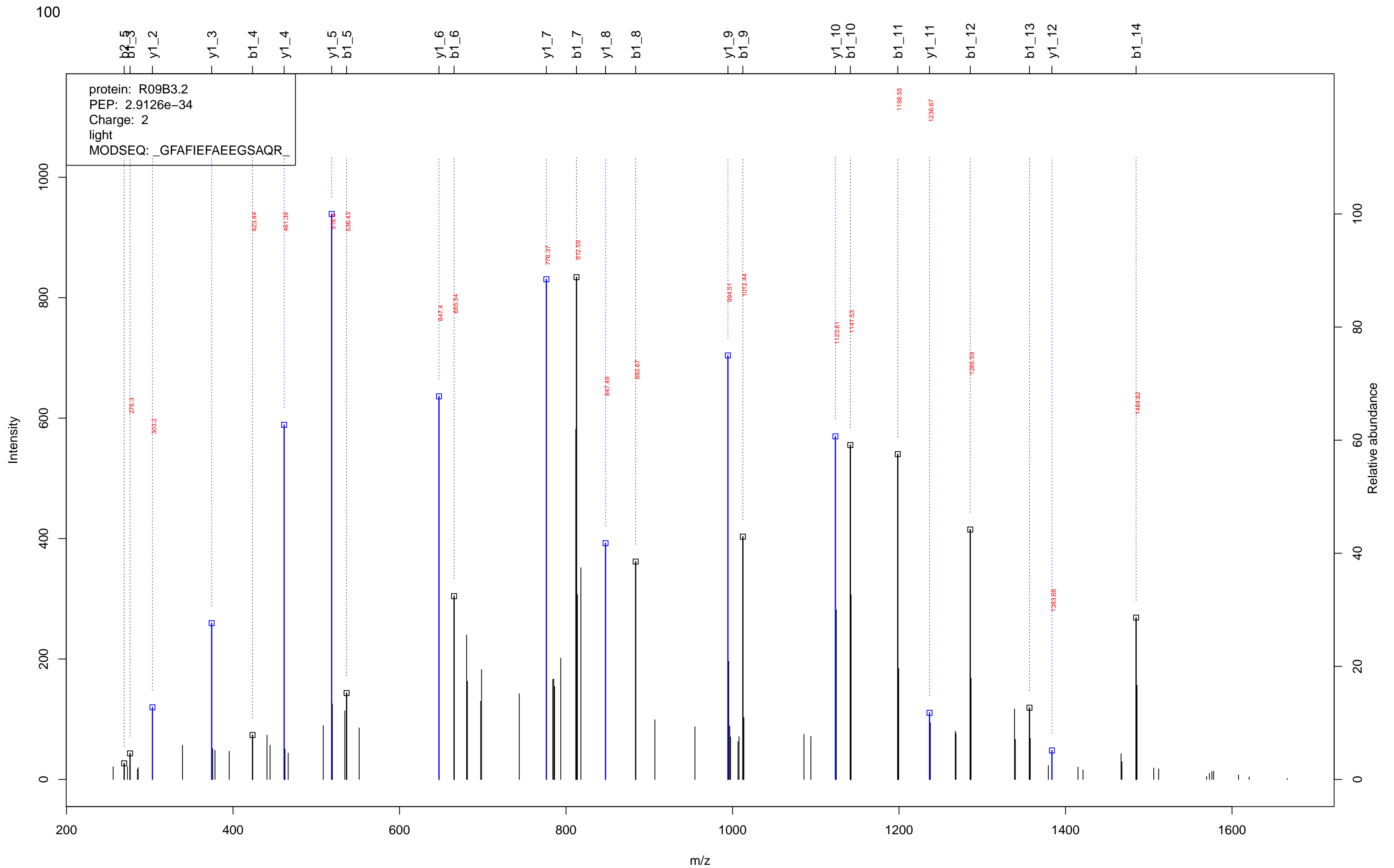


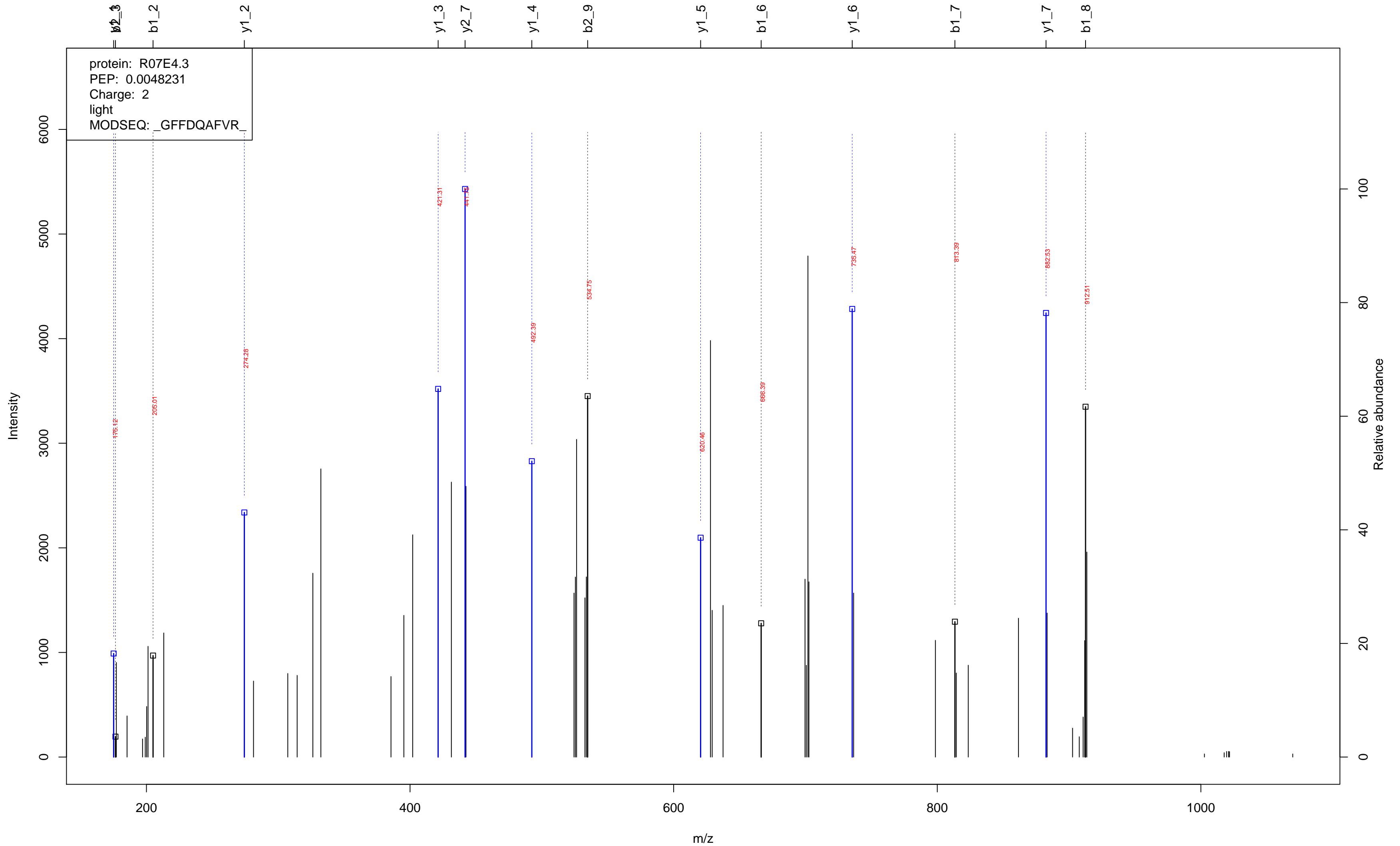


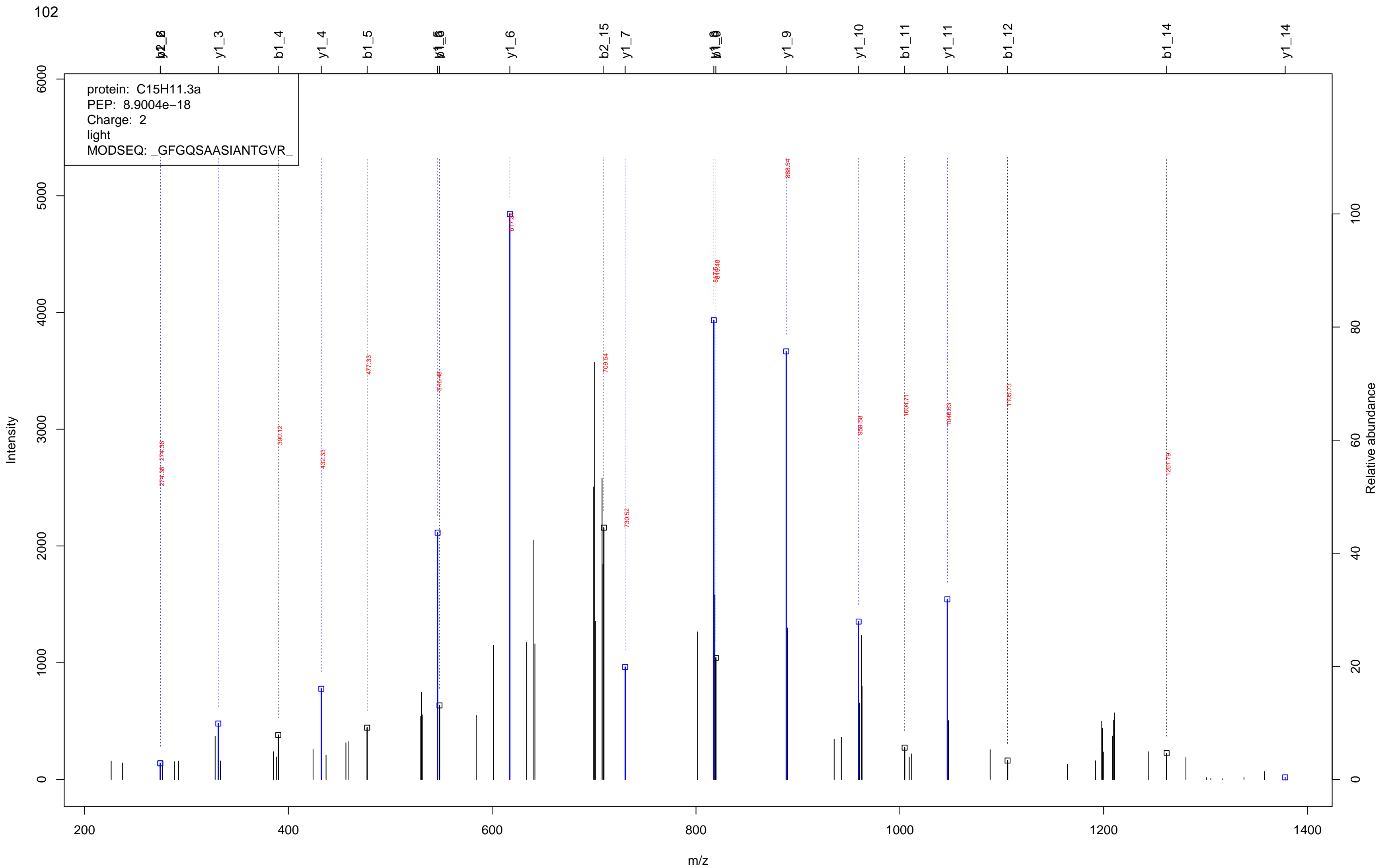


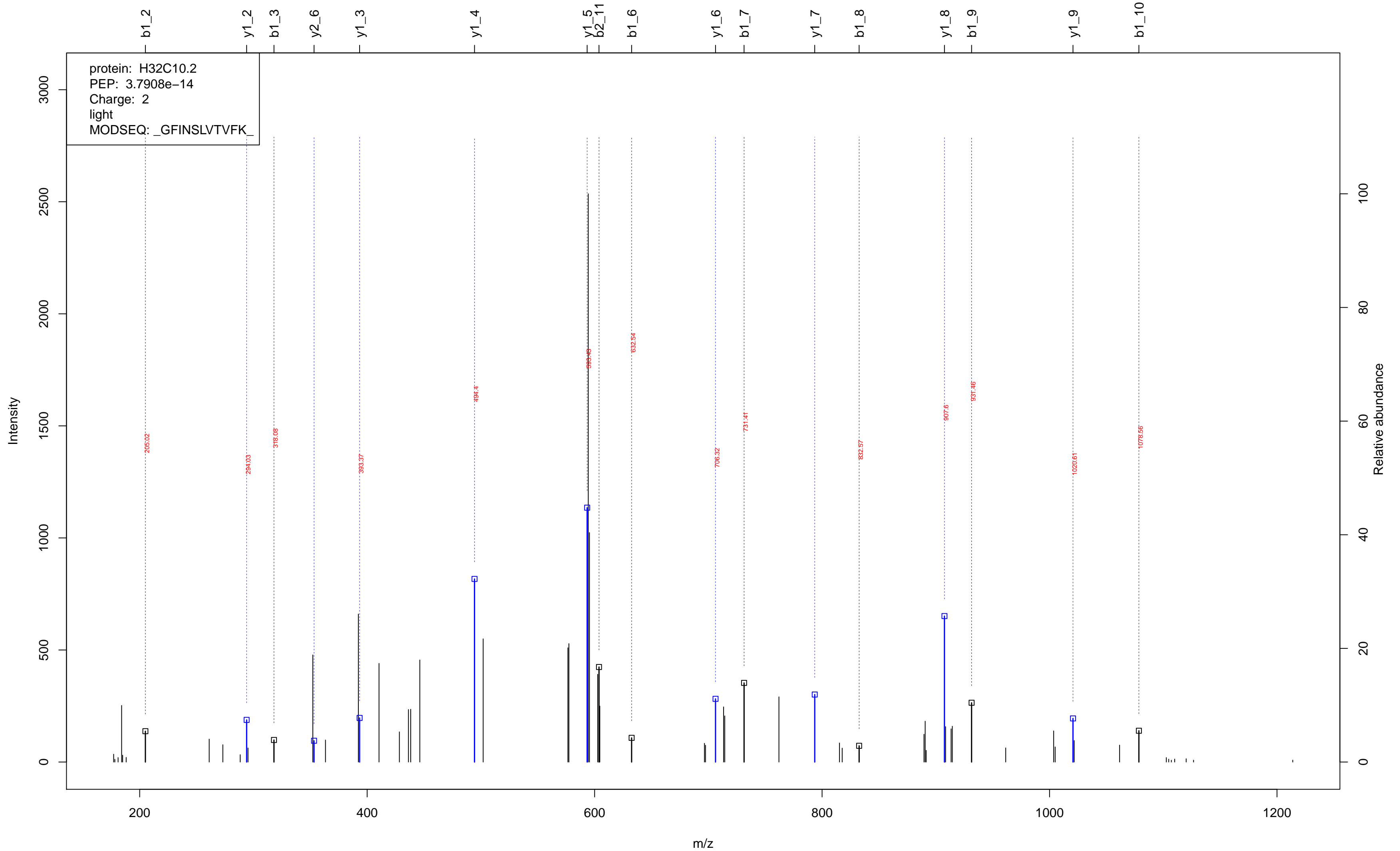


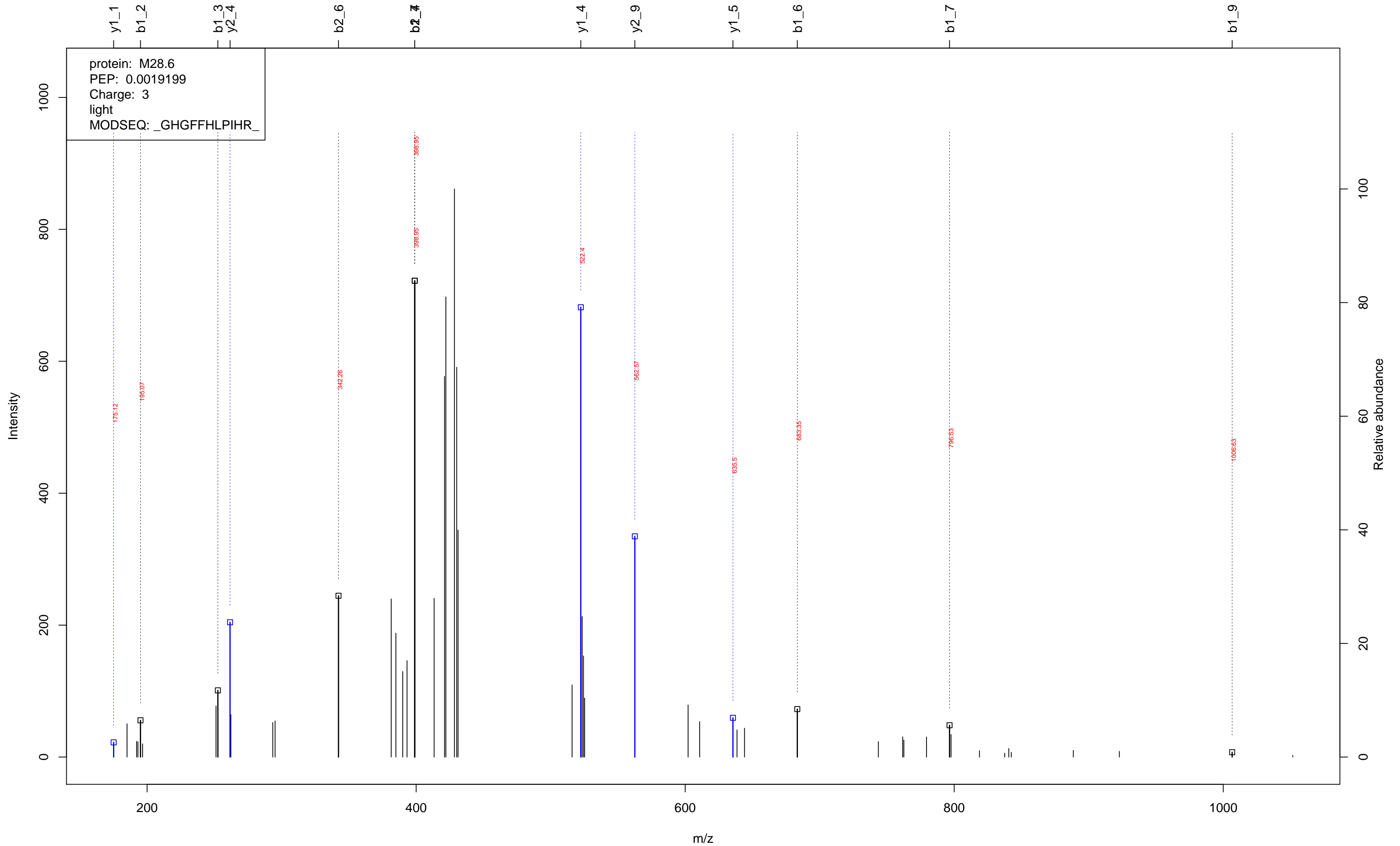


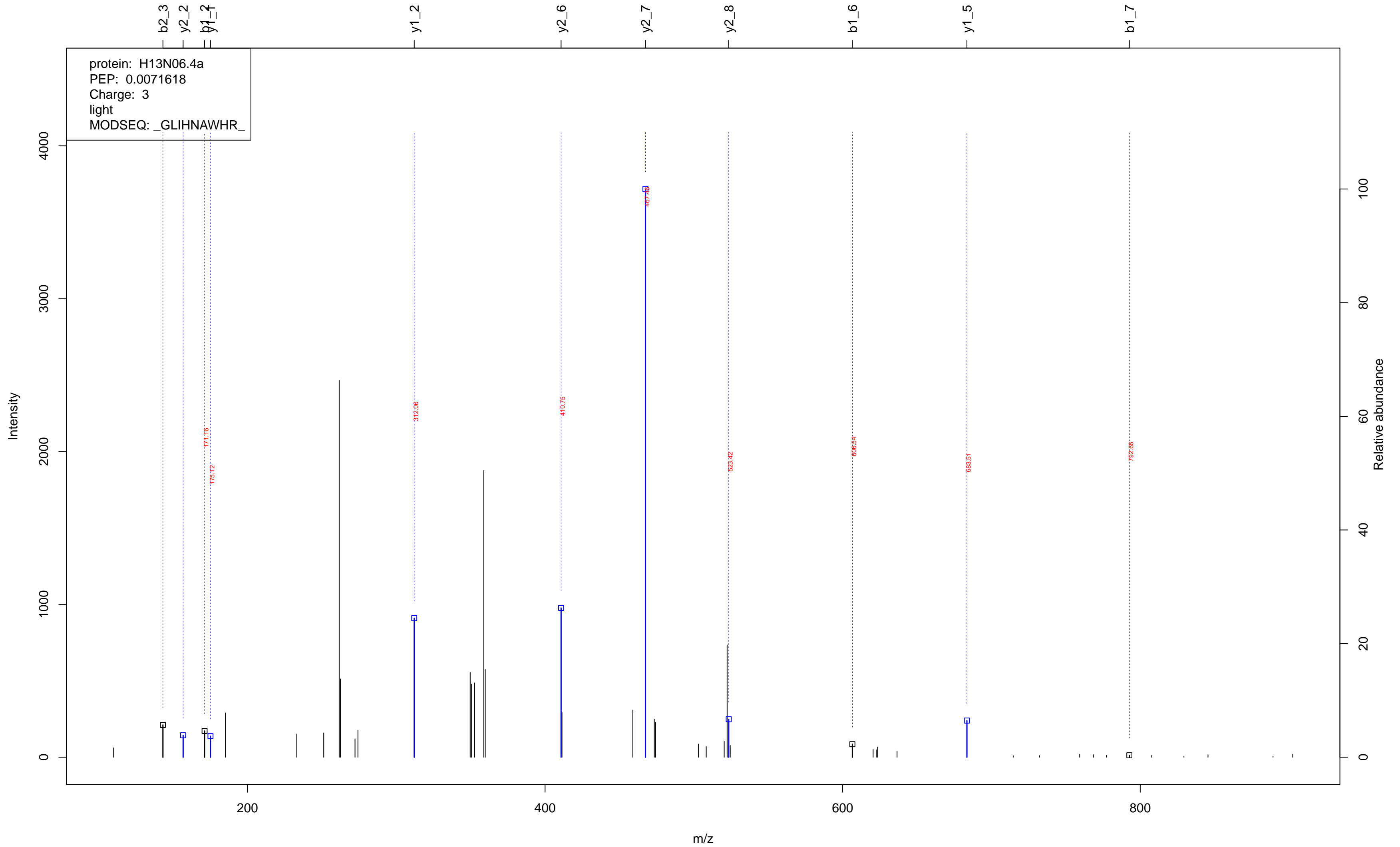


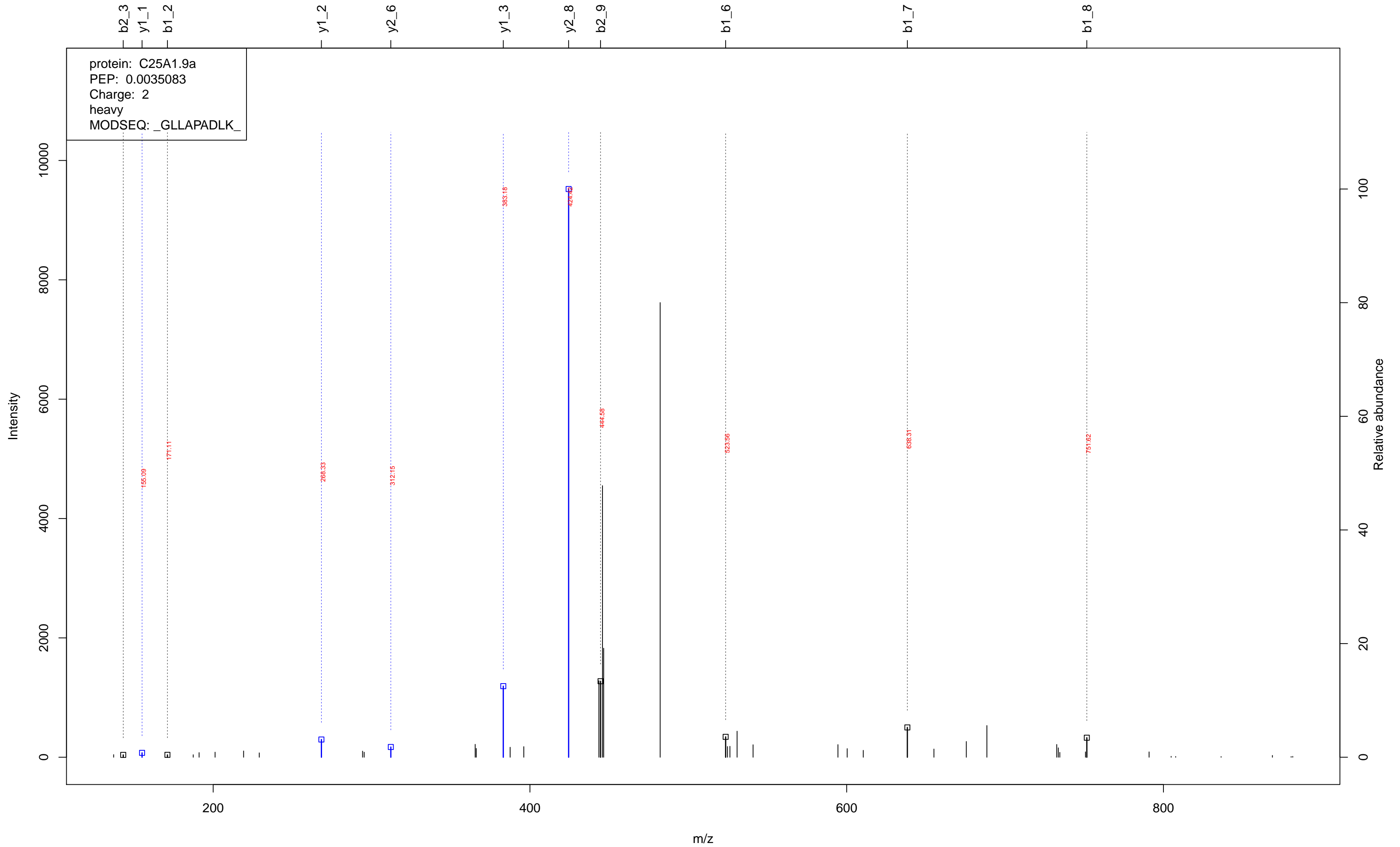


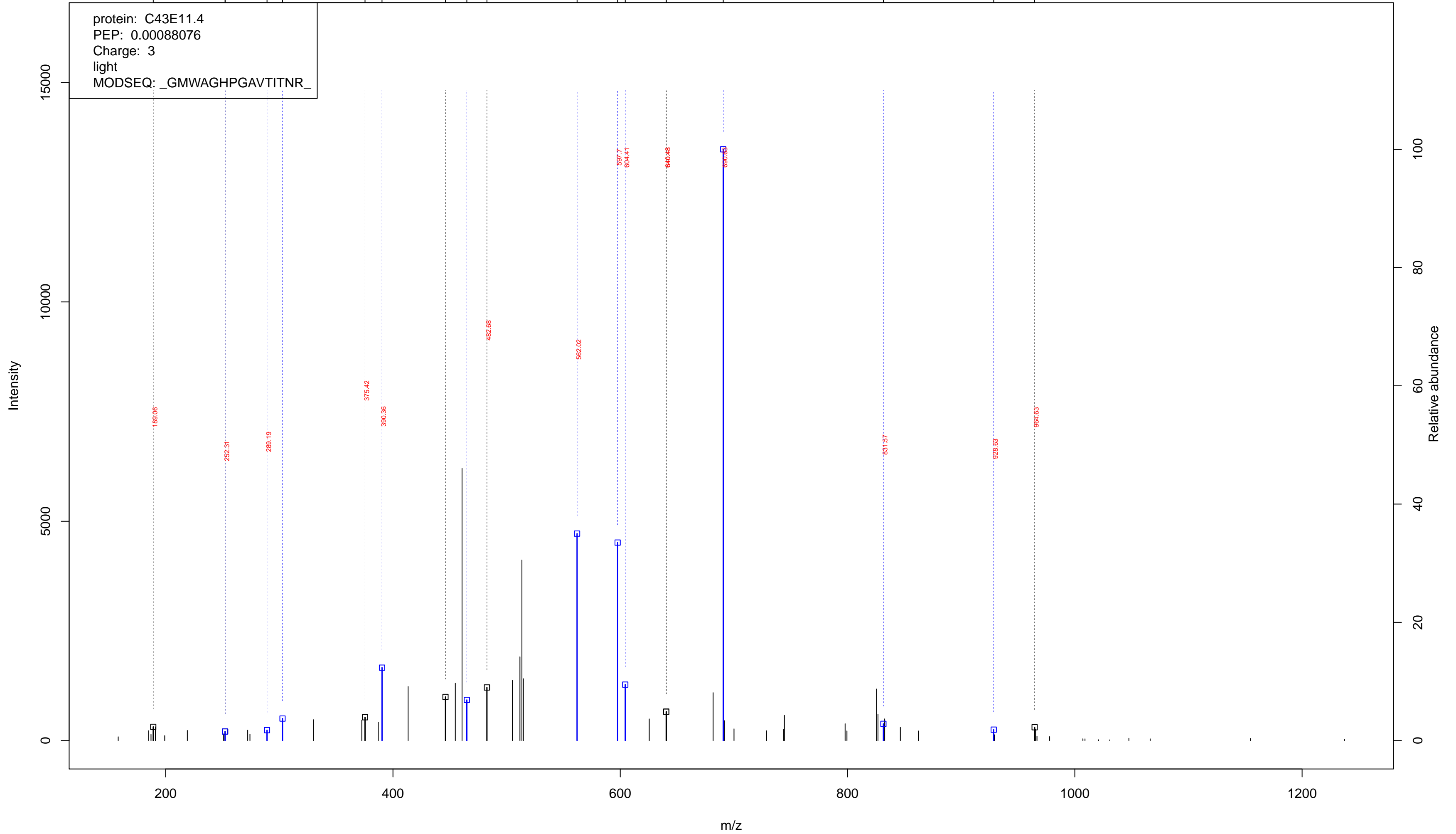


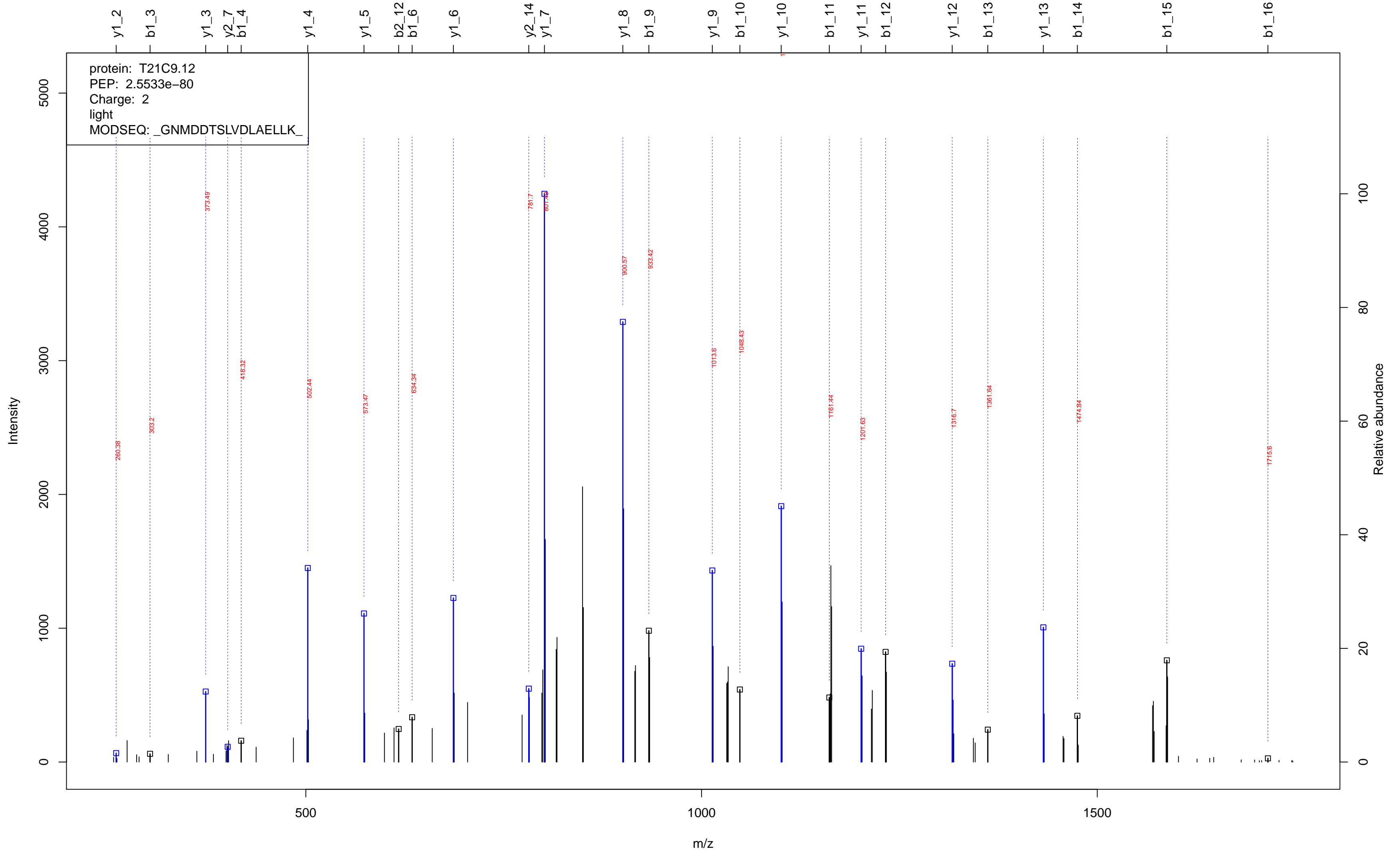


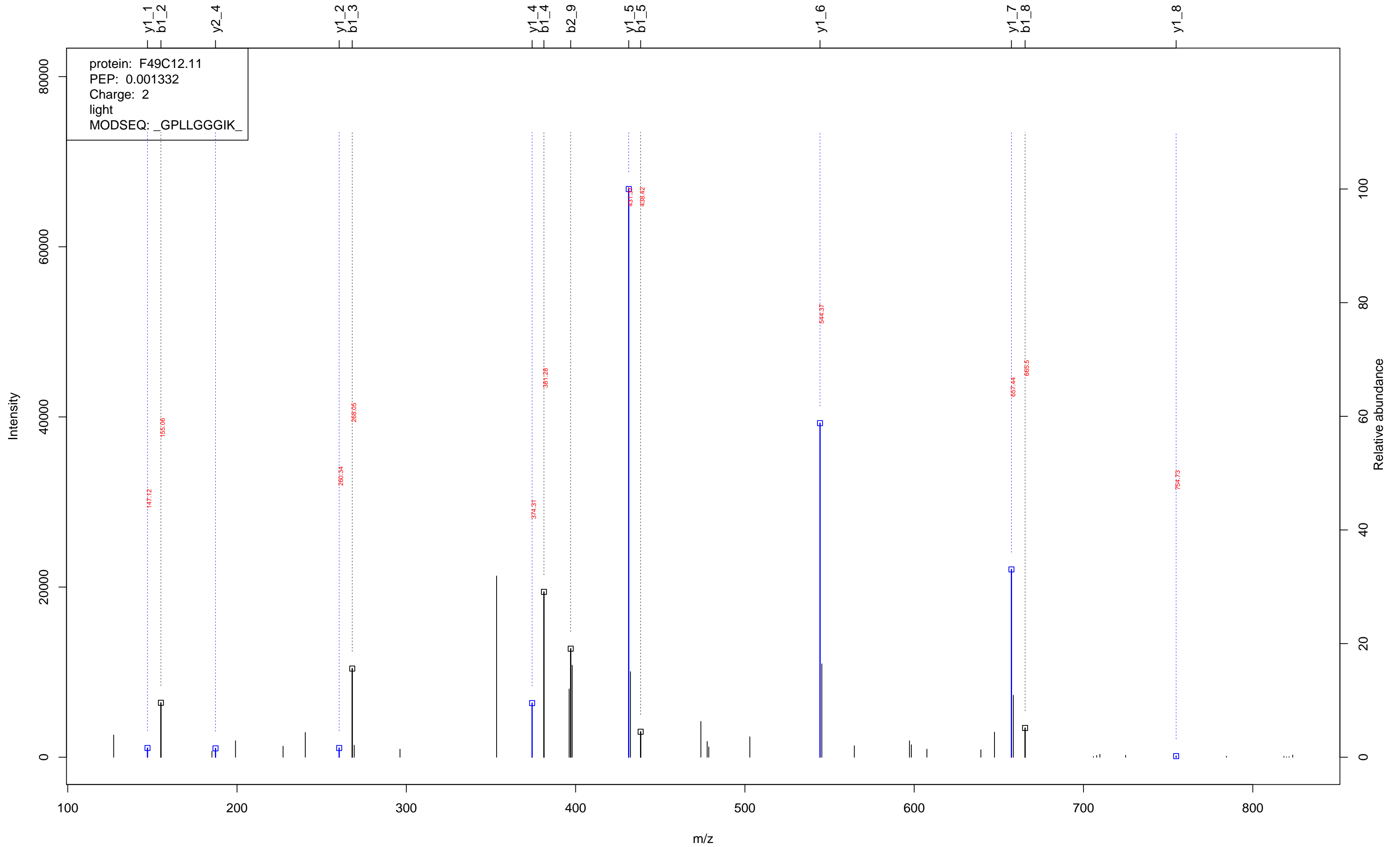


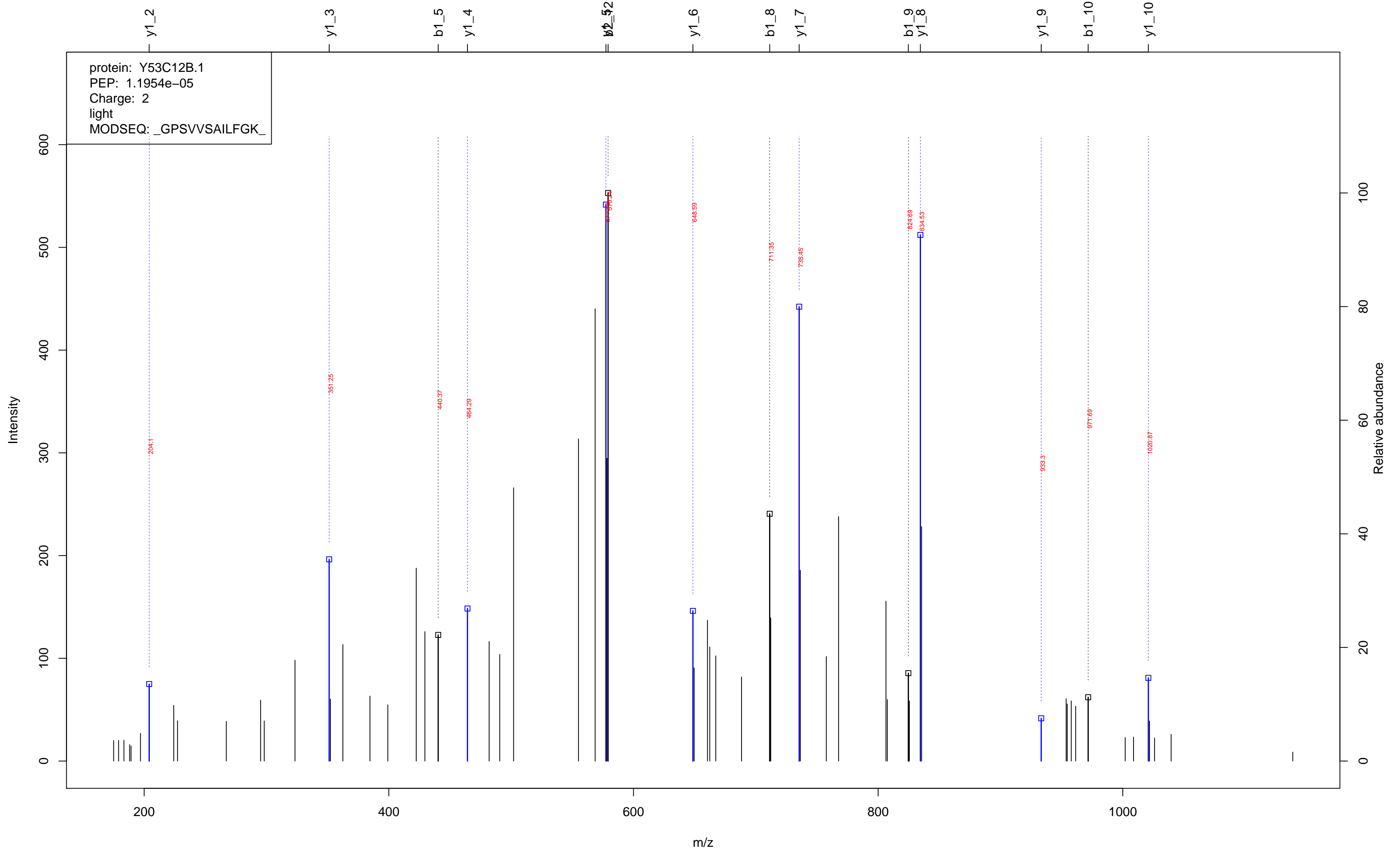


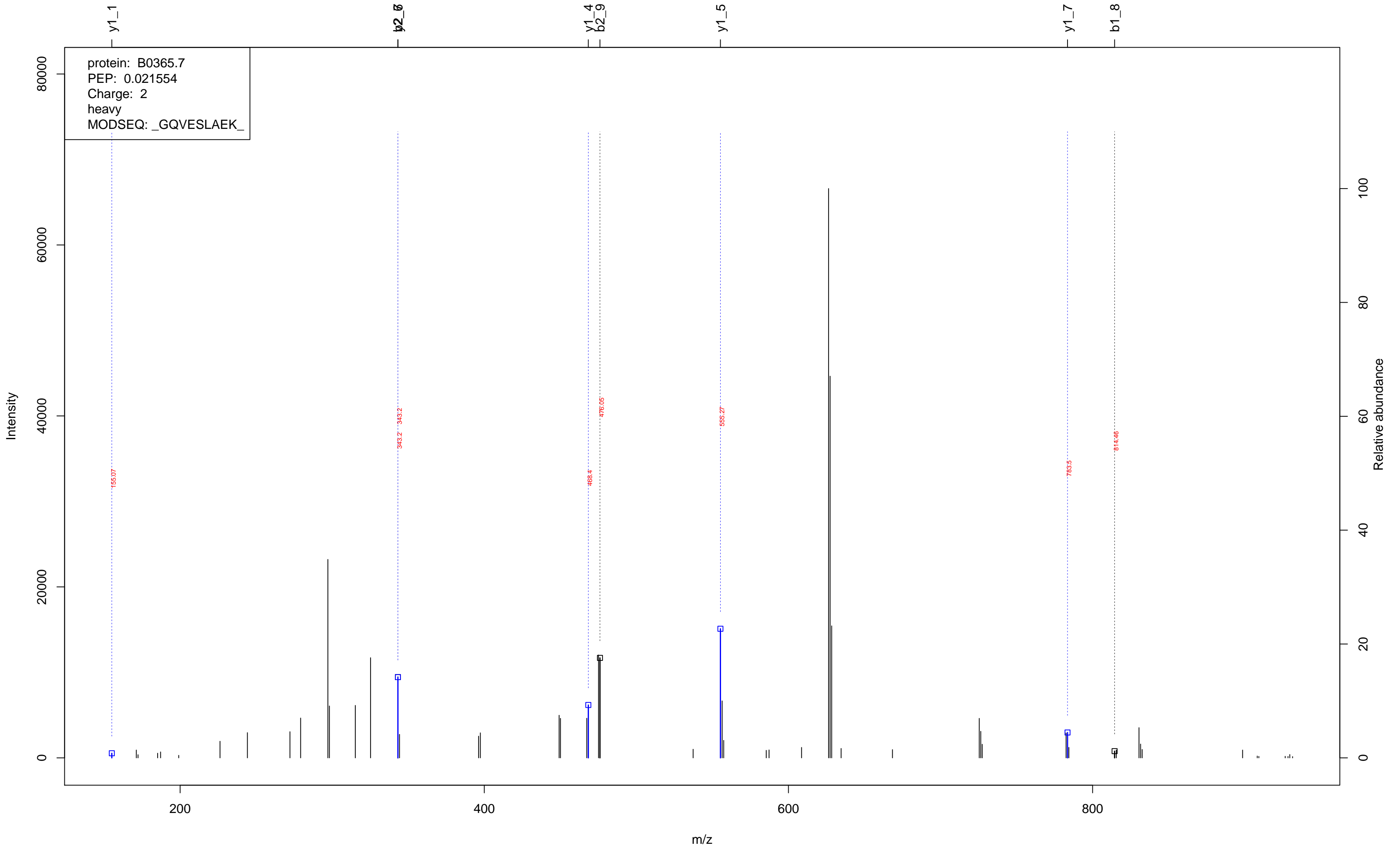


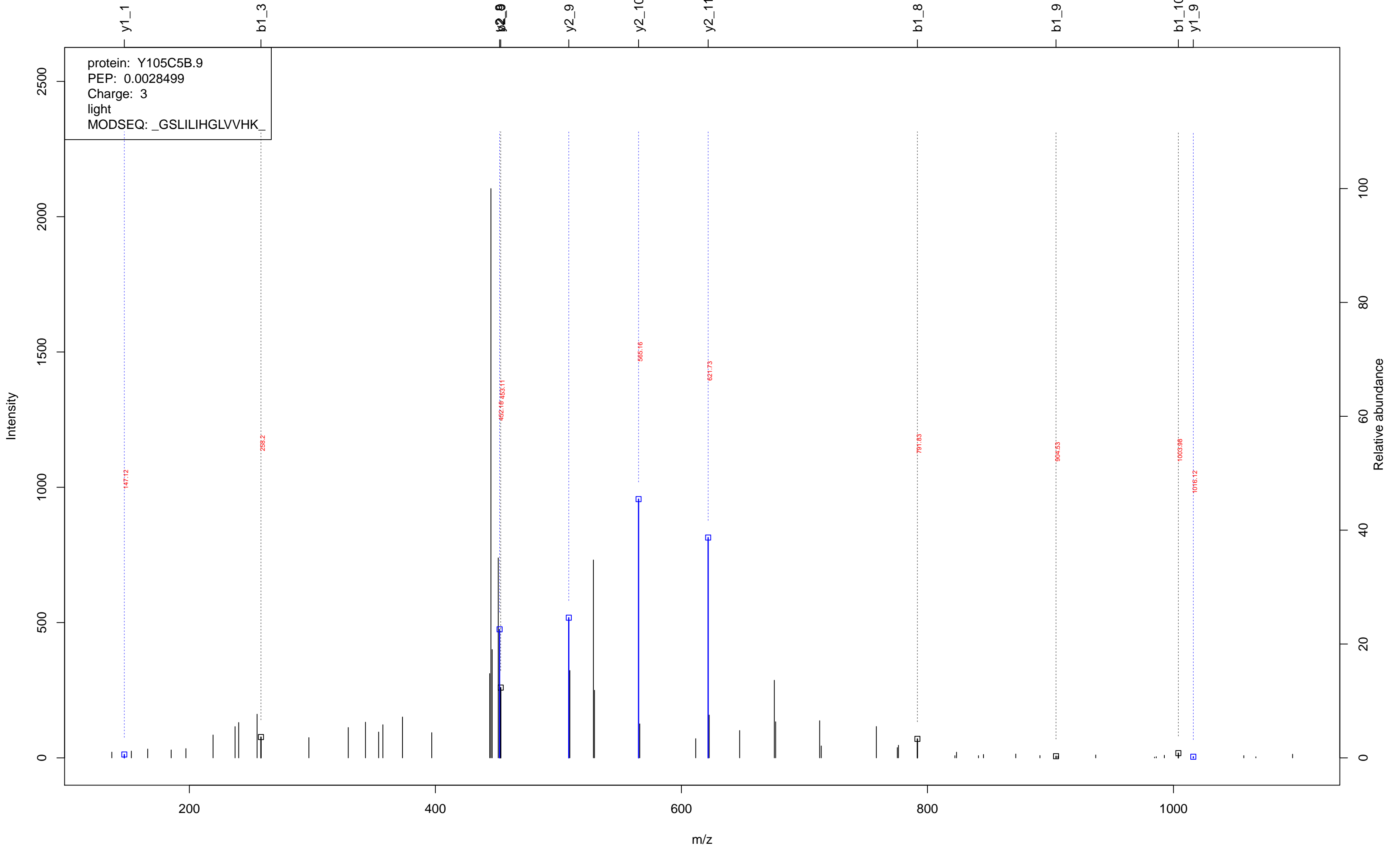


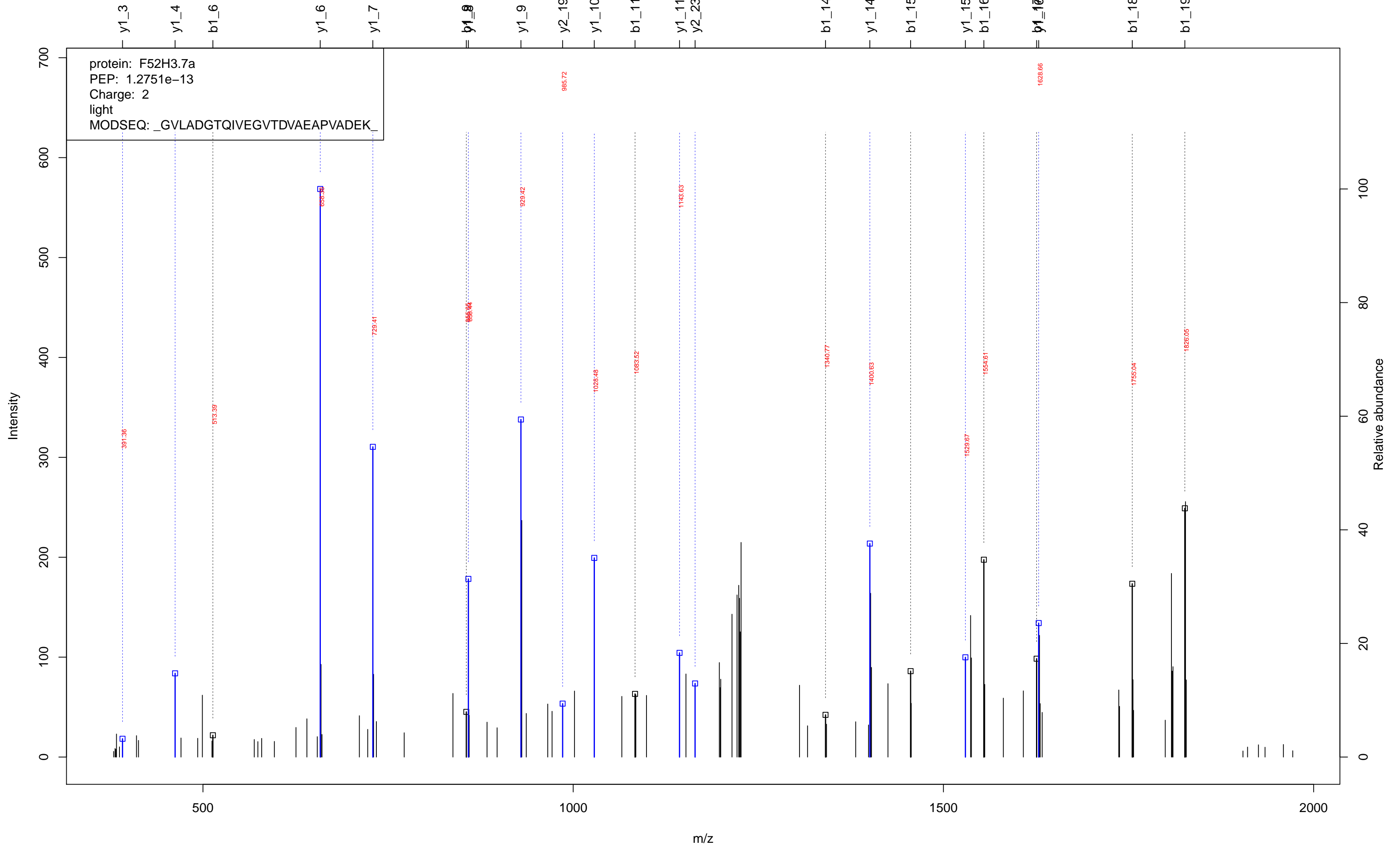


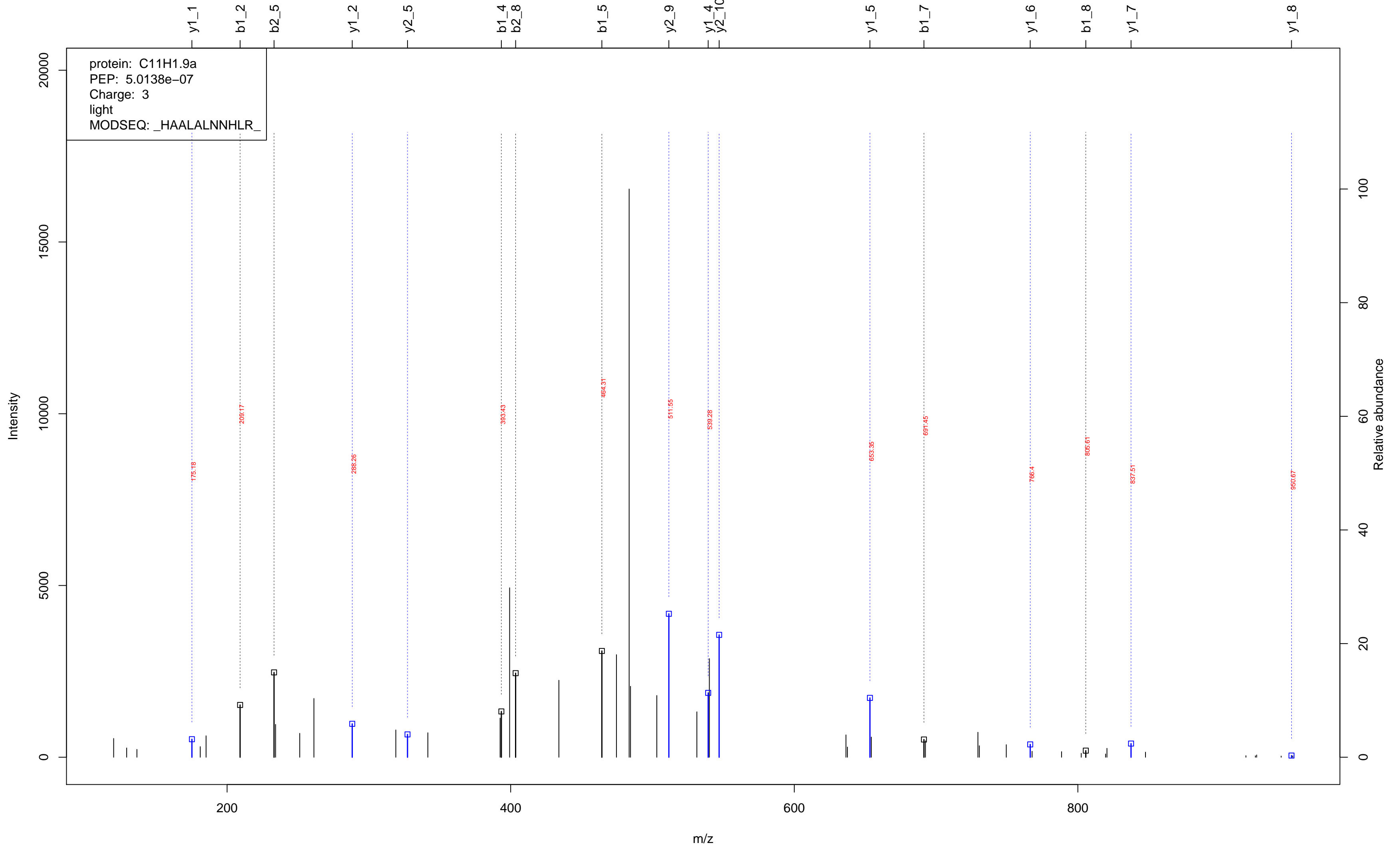


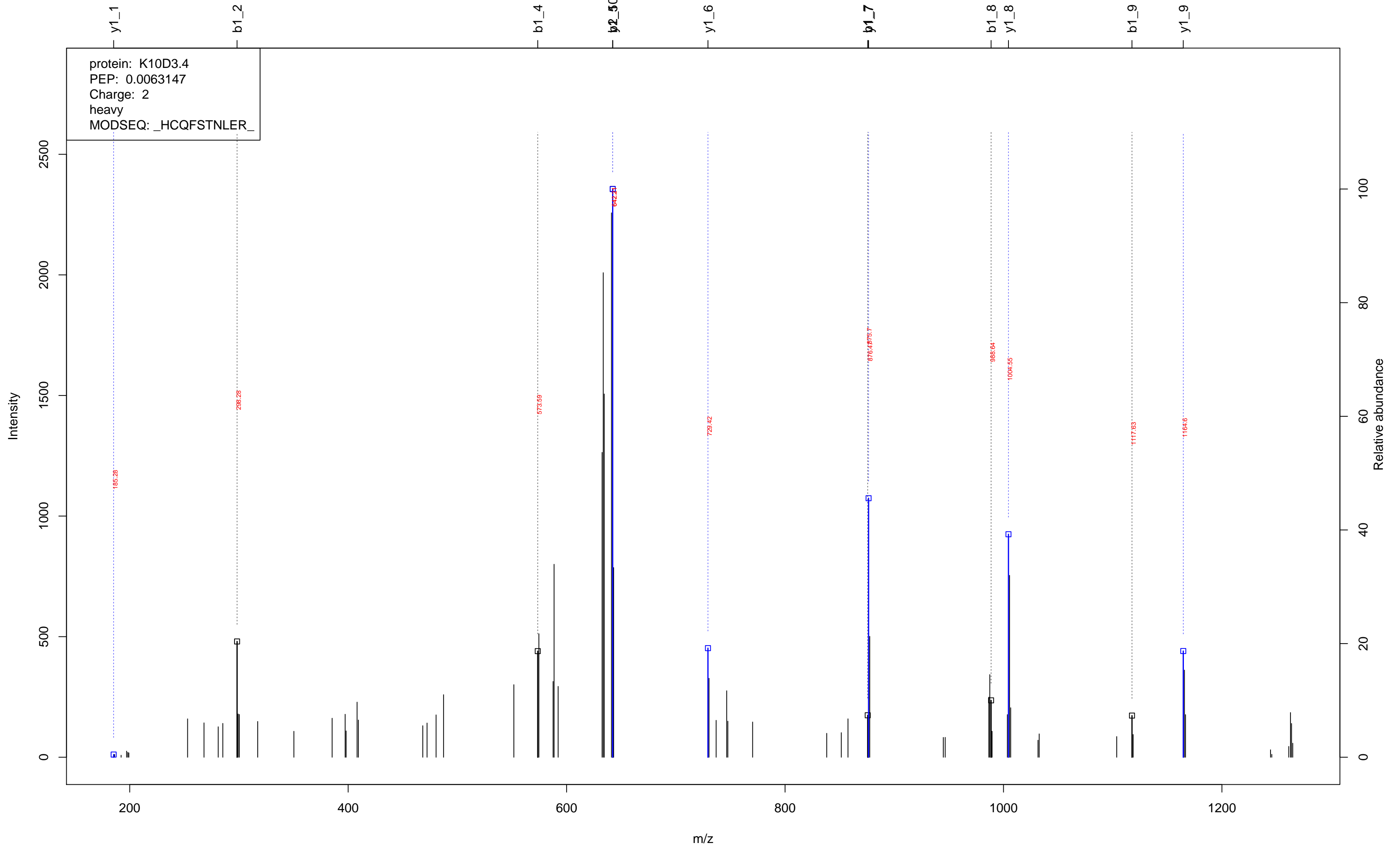












y1_1
b1_2

b1_3
y1_2

b2_8

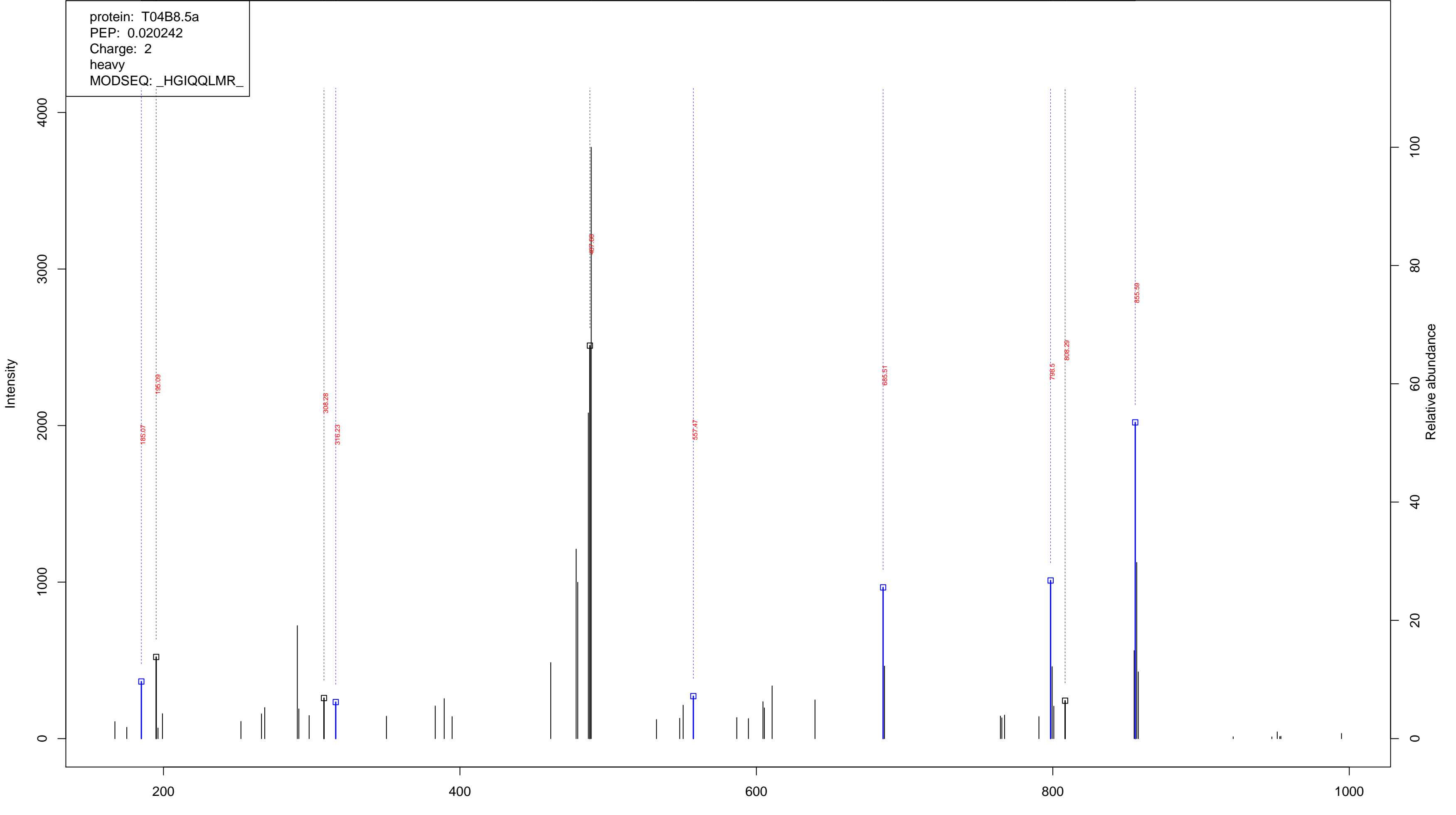
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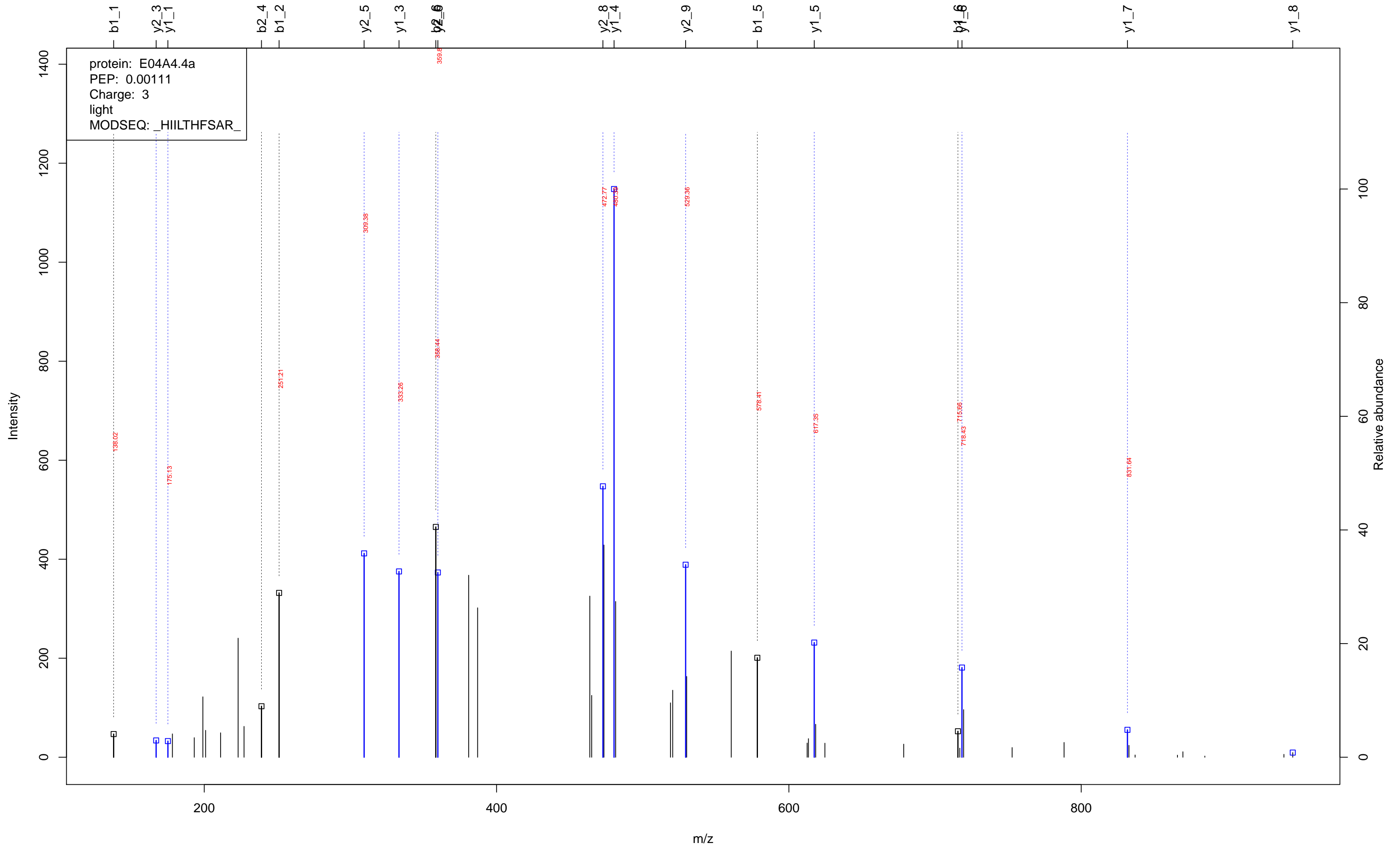
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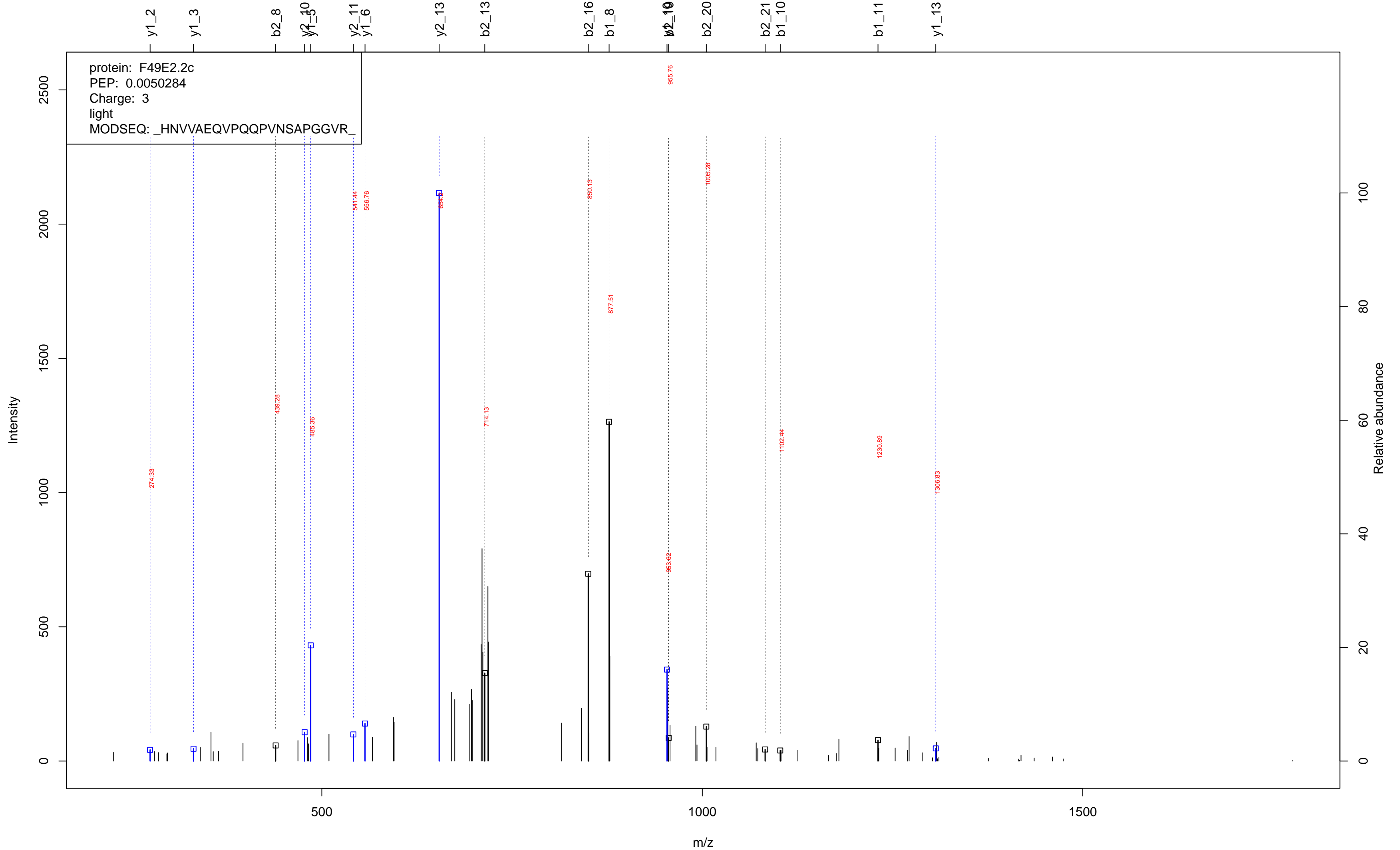
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b1_7

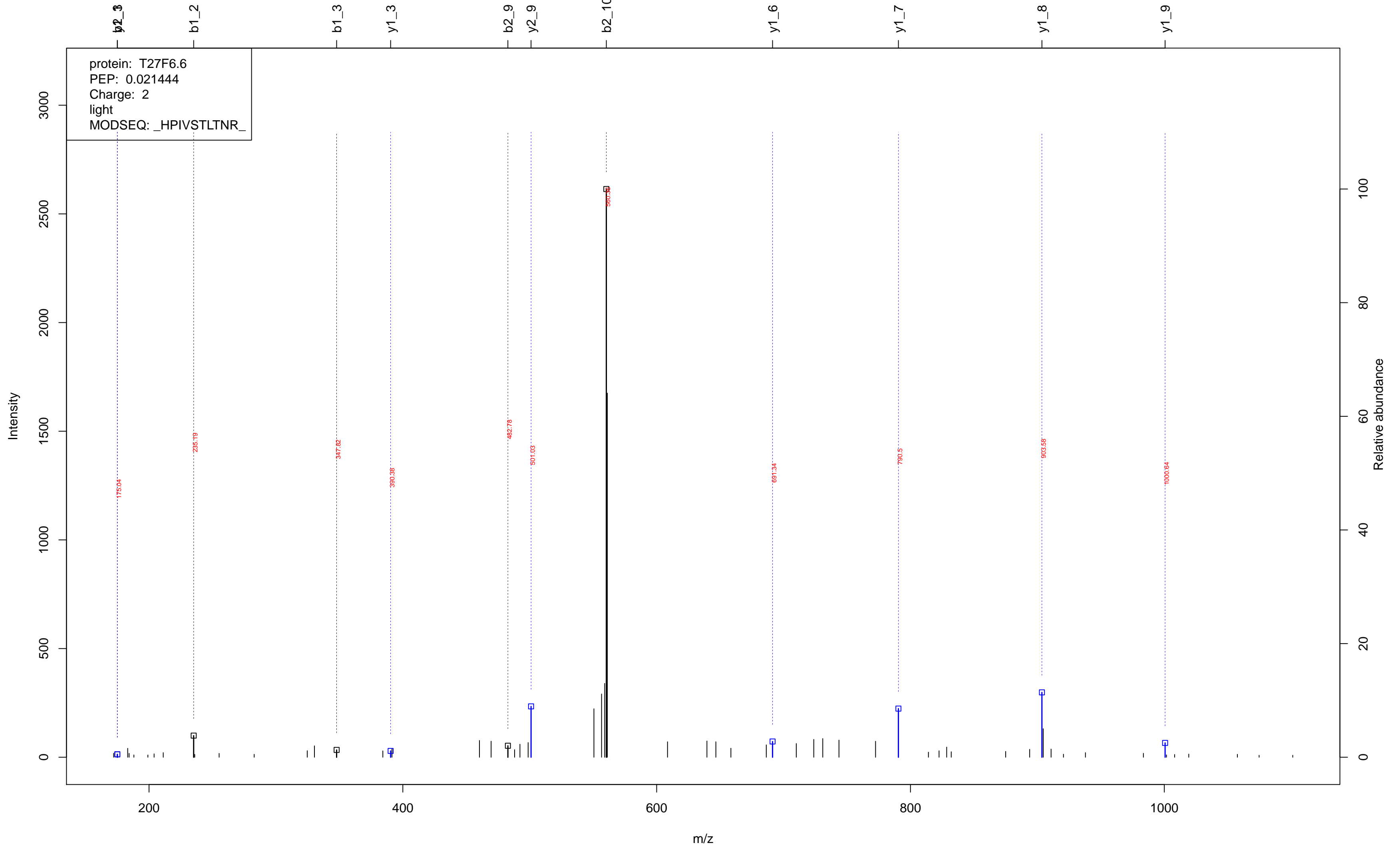
y1_7

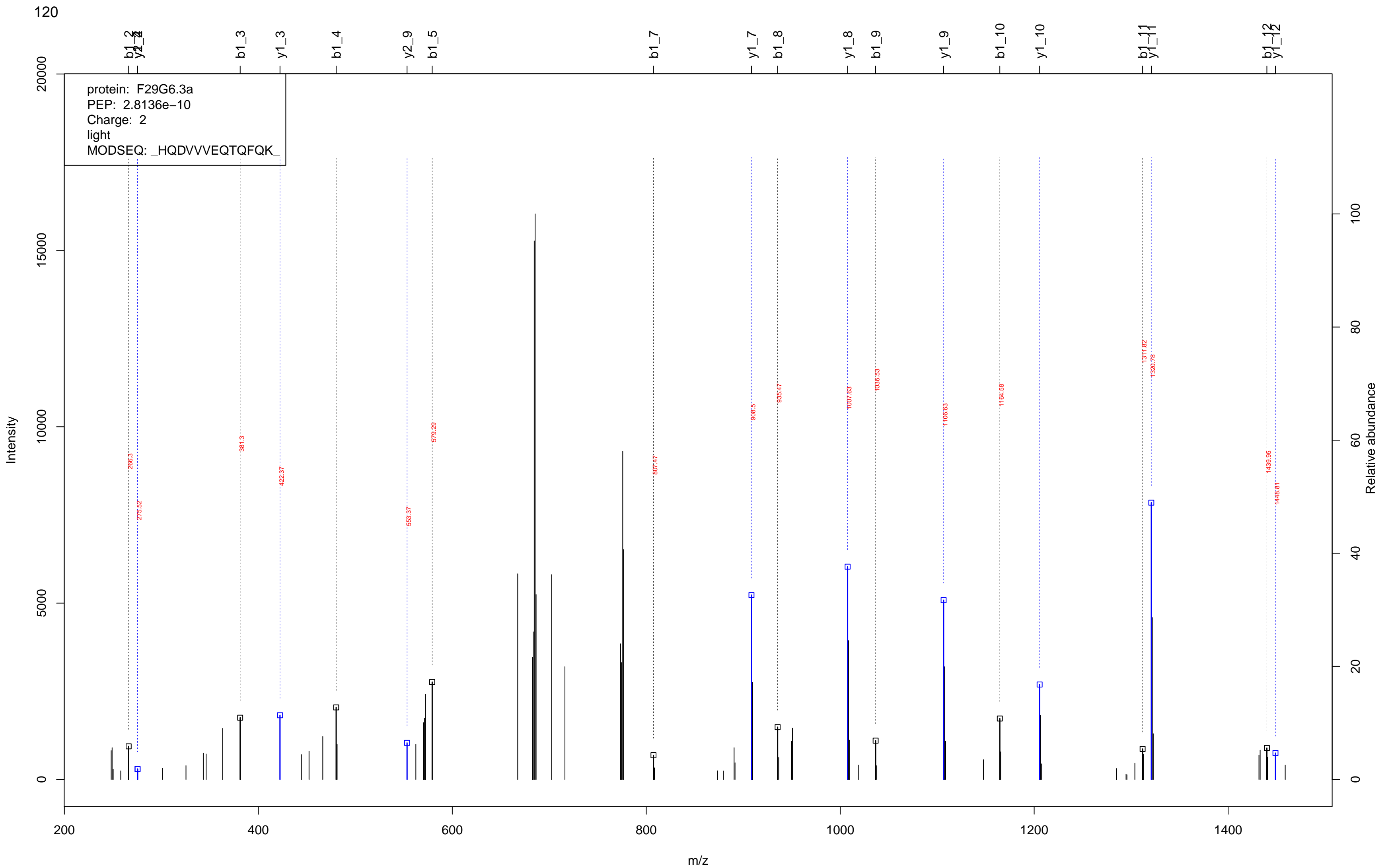
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Charge: 2
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MODSEQ: _HGIQQLMR_

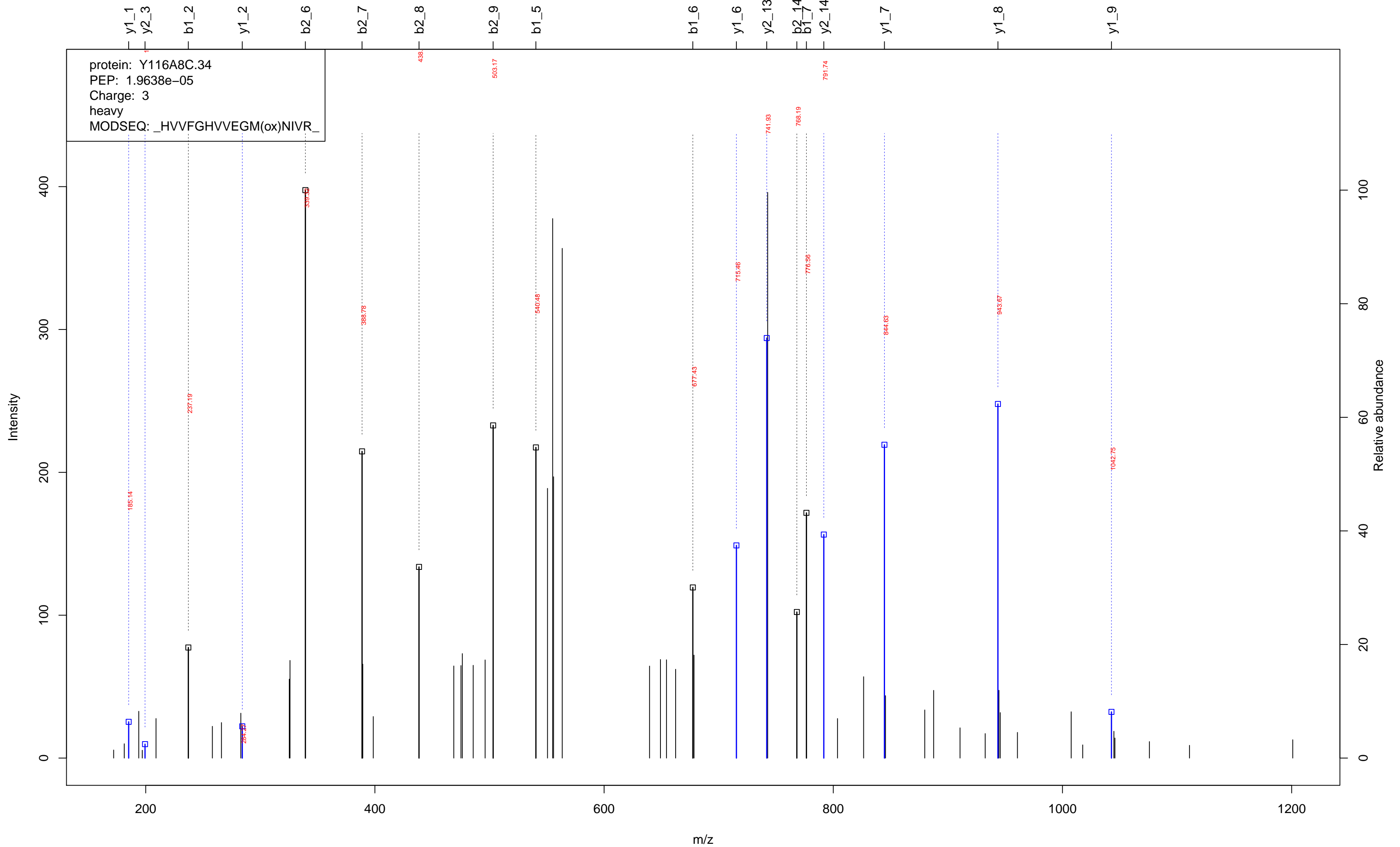


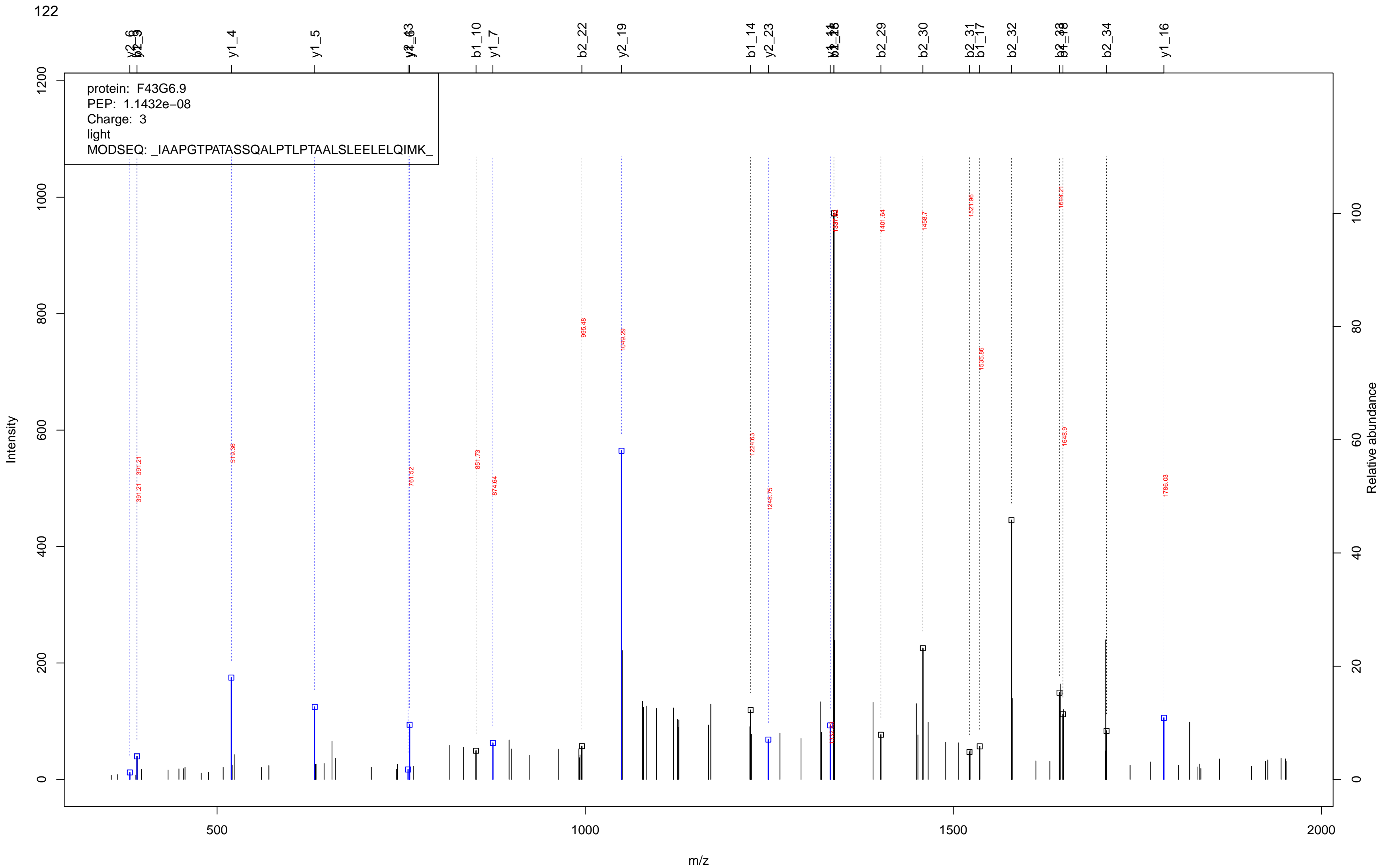


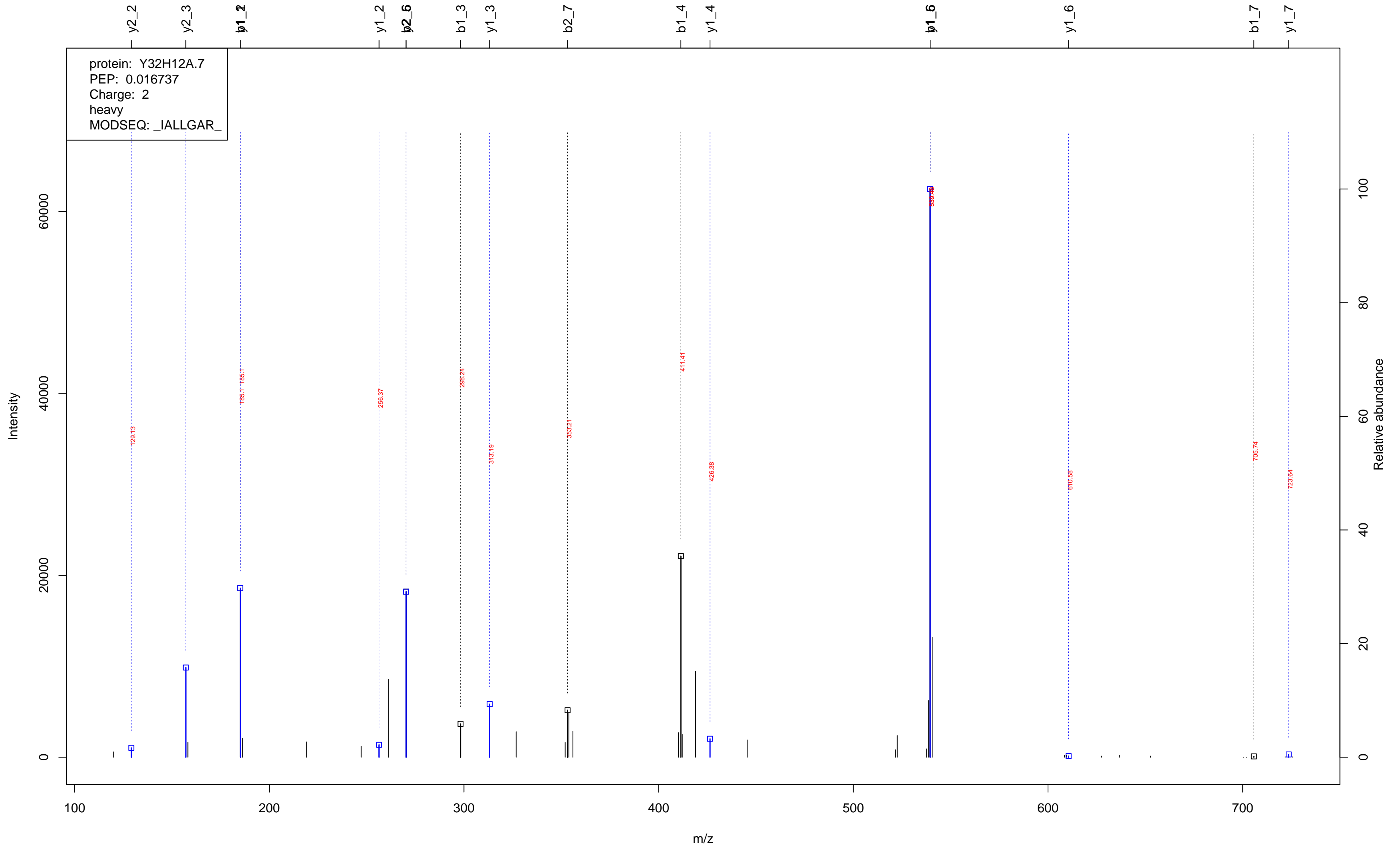


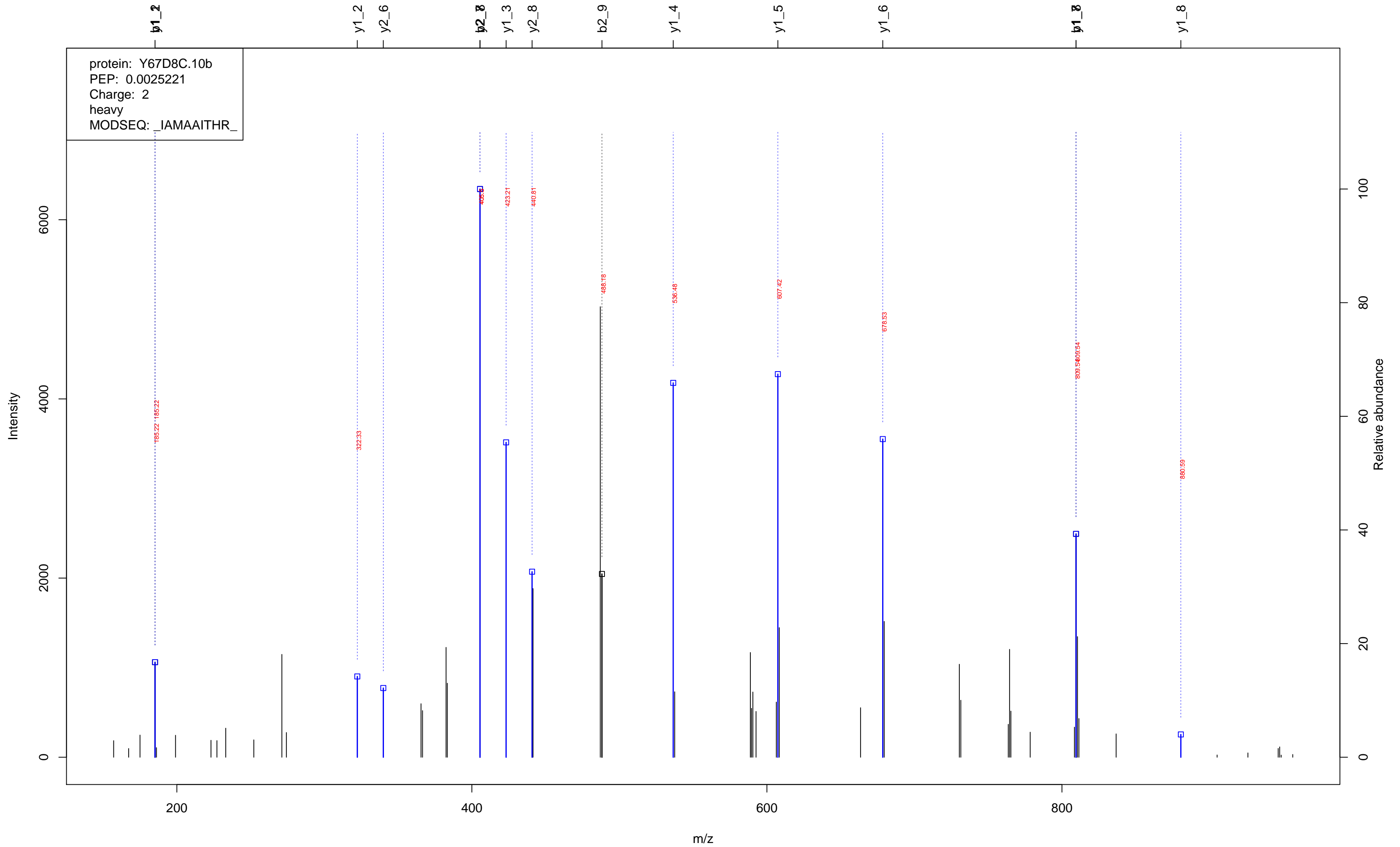


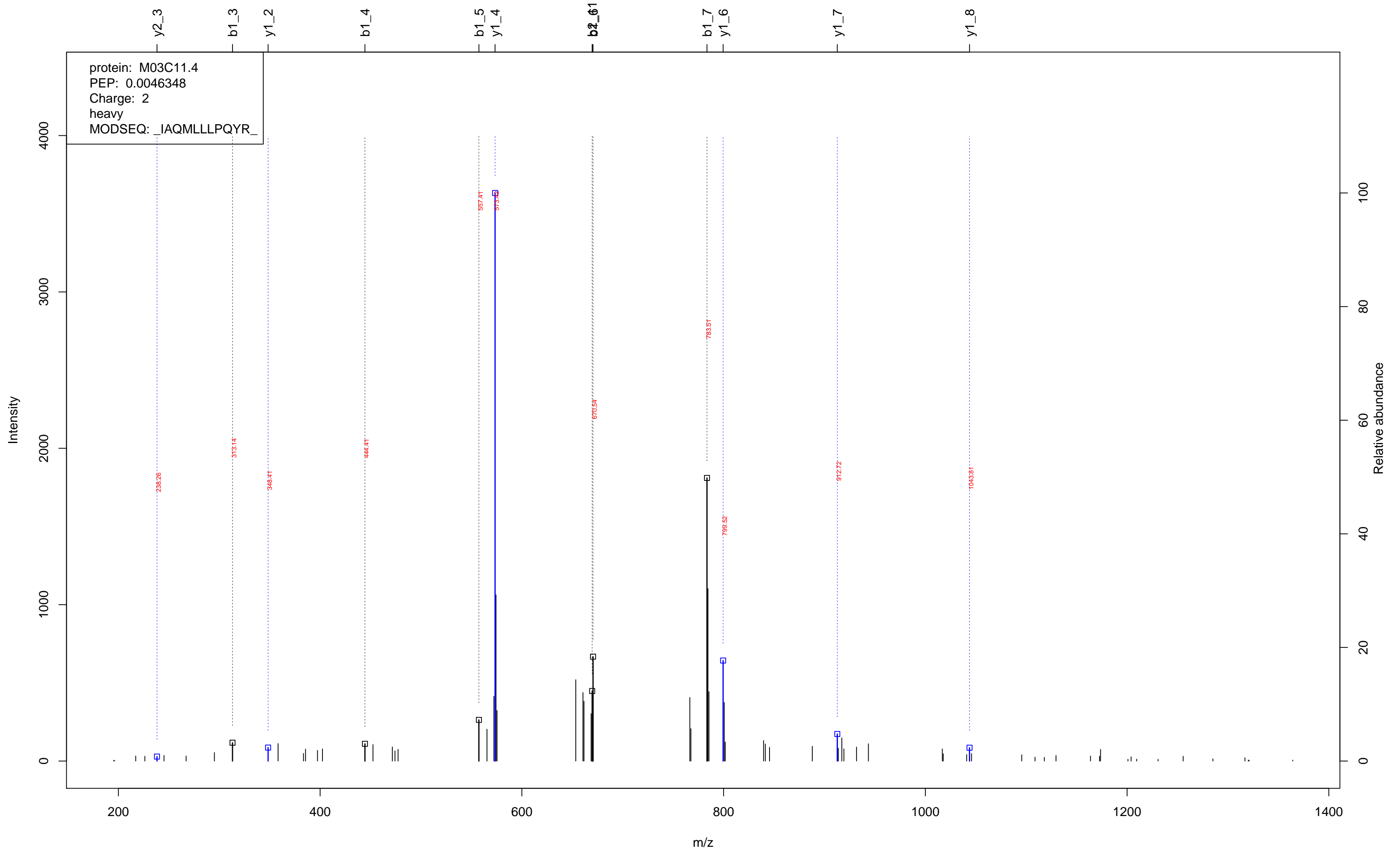


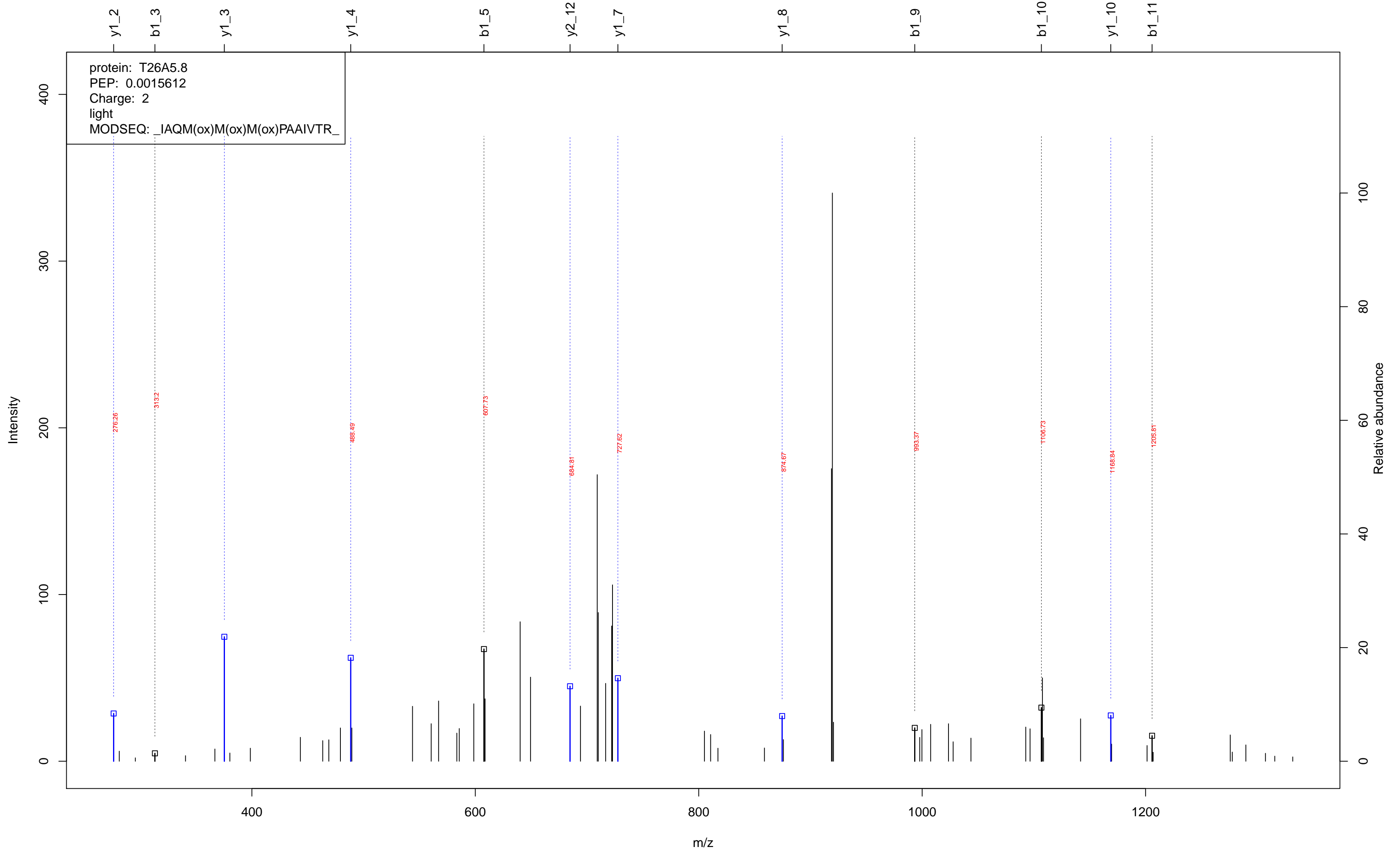


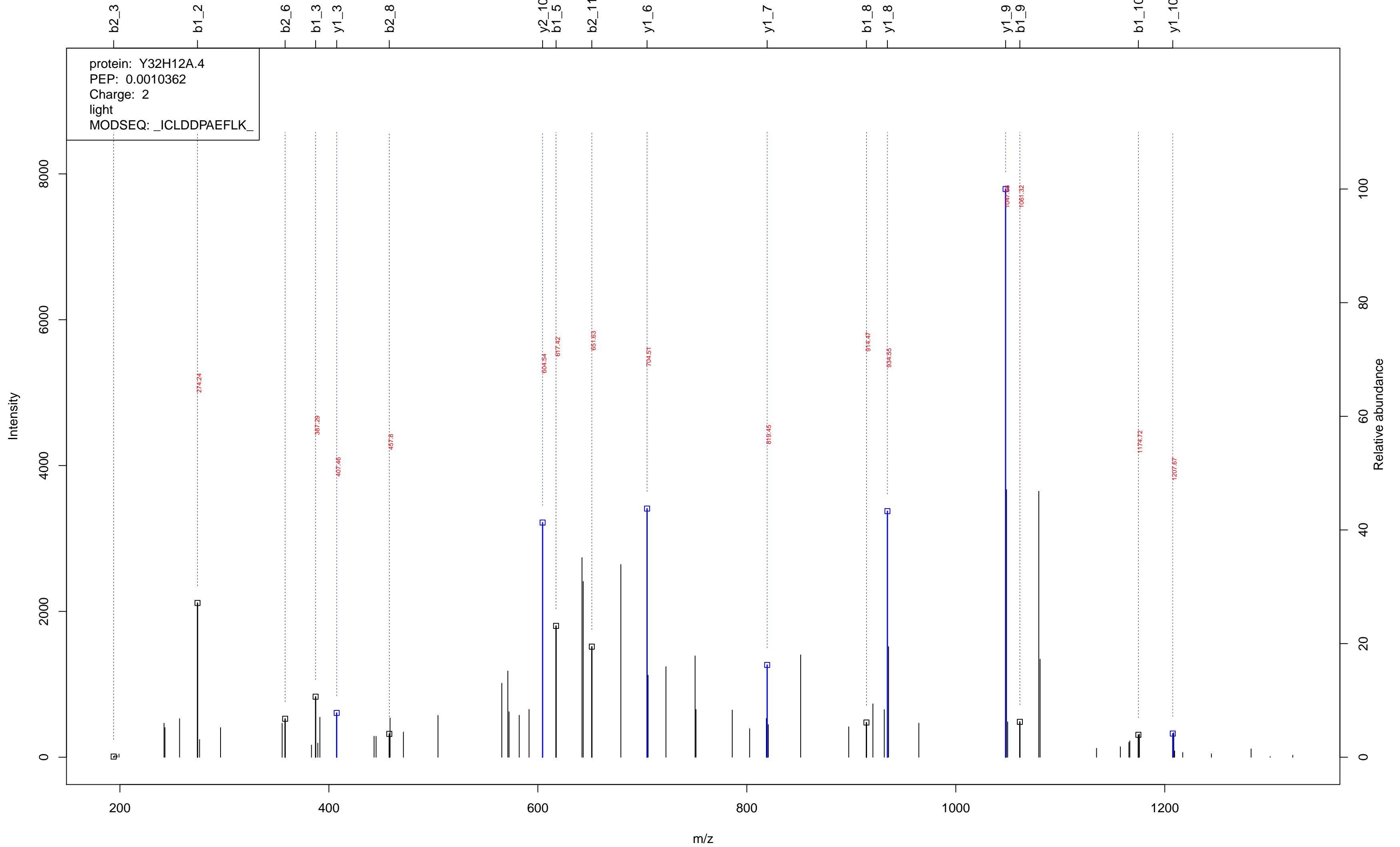


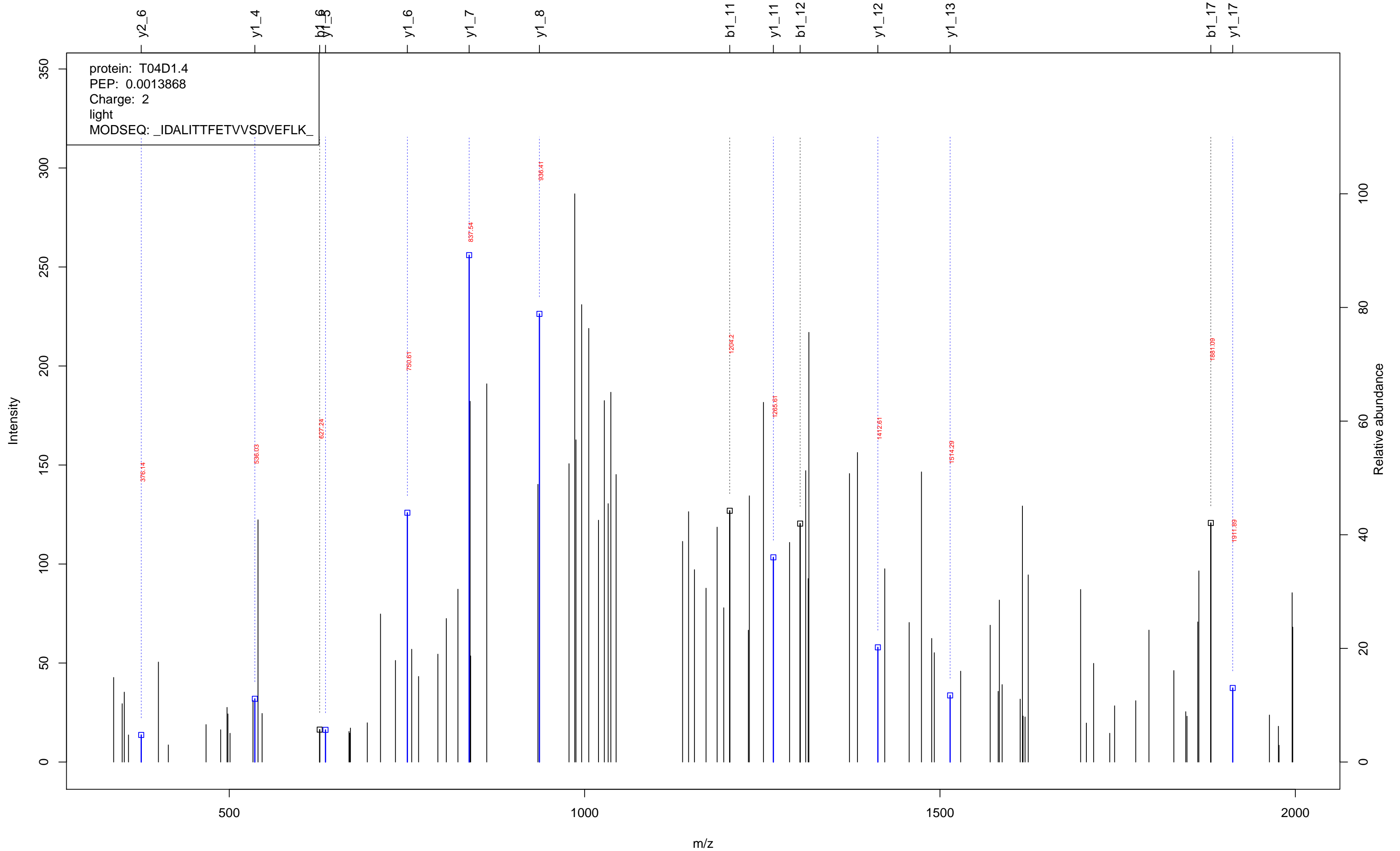


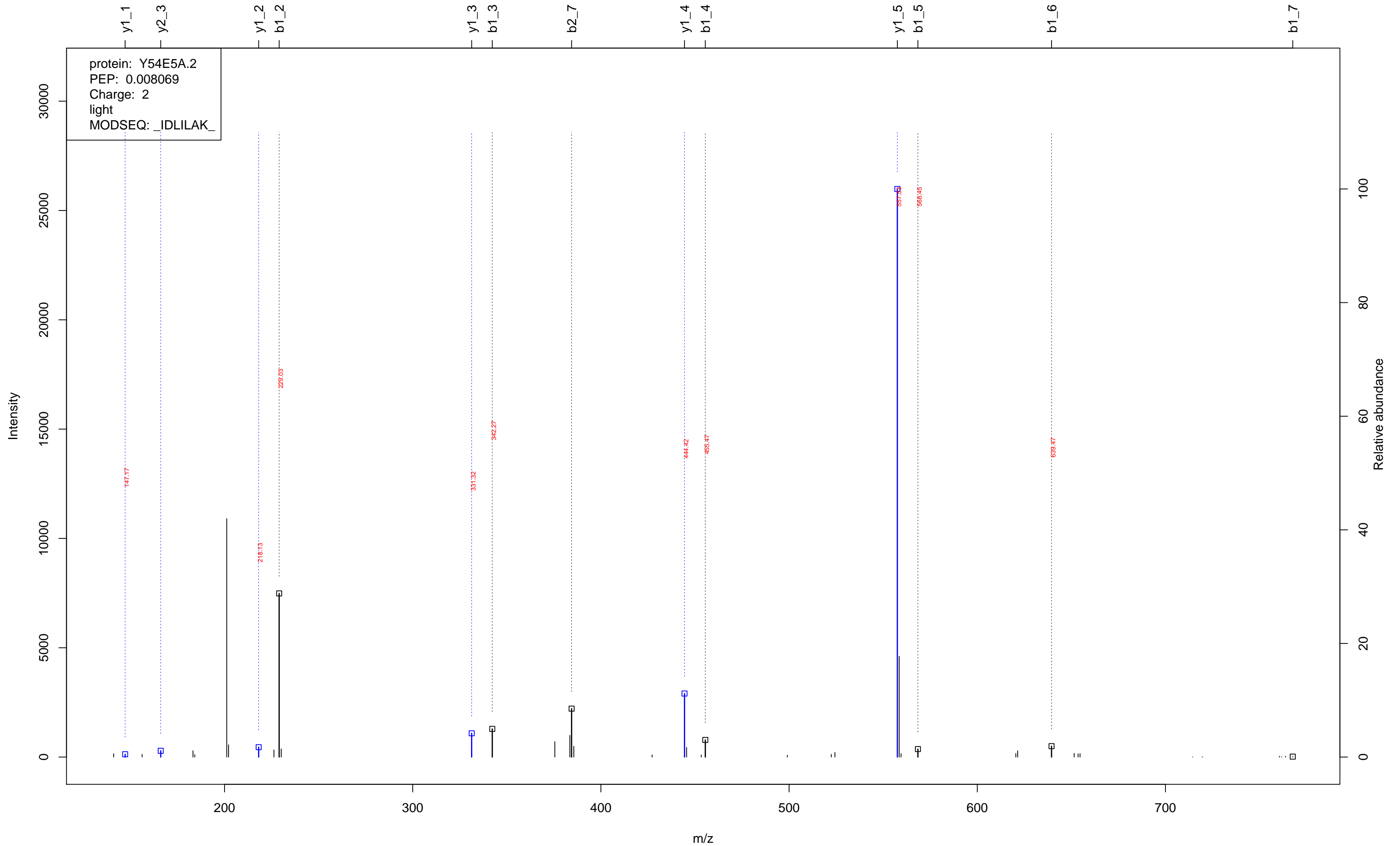




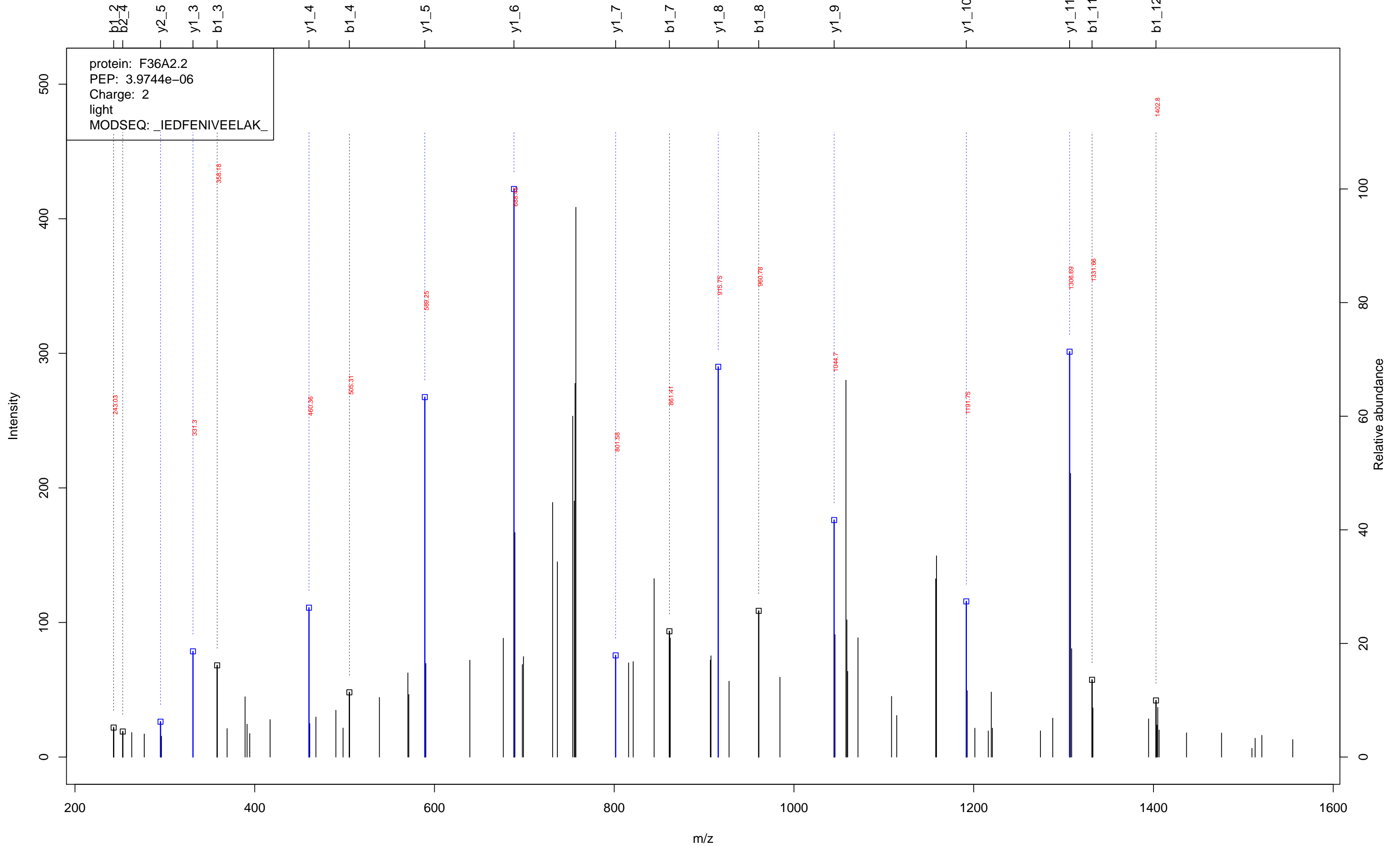


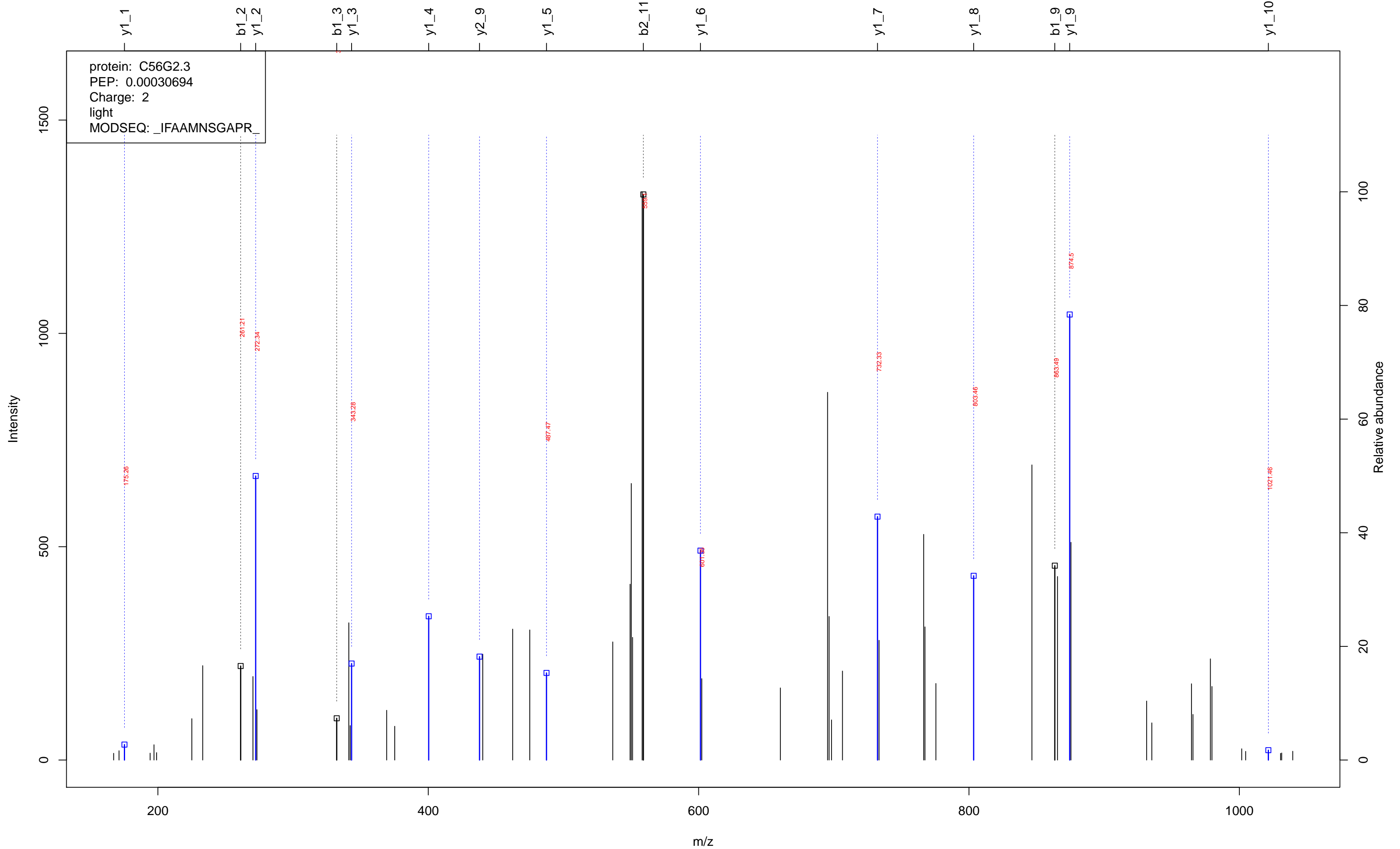


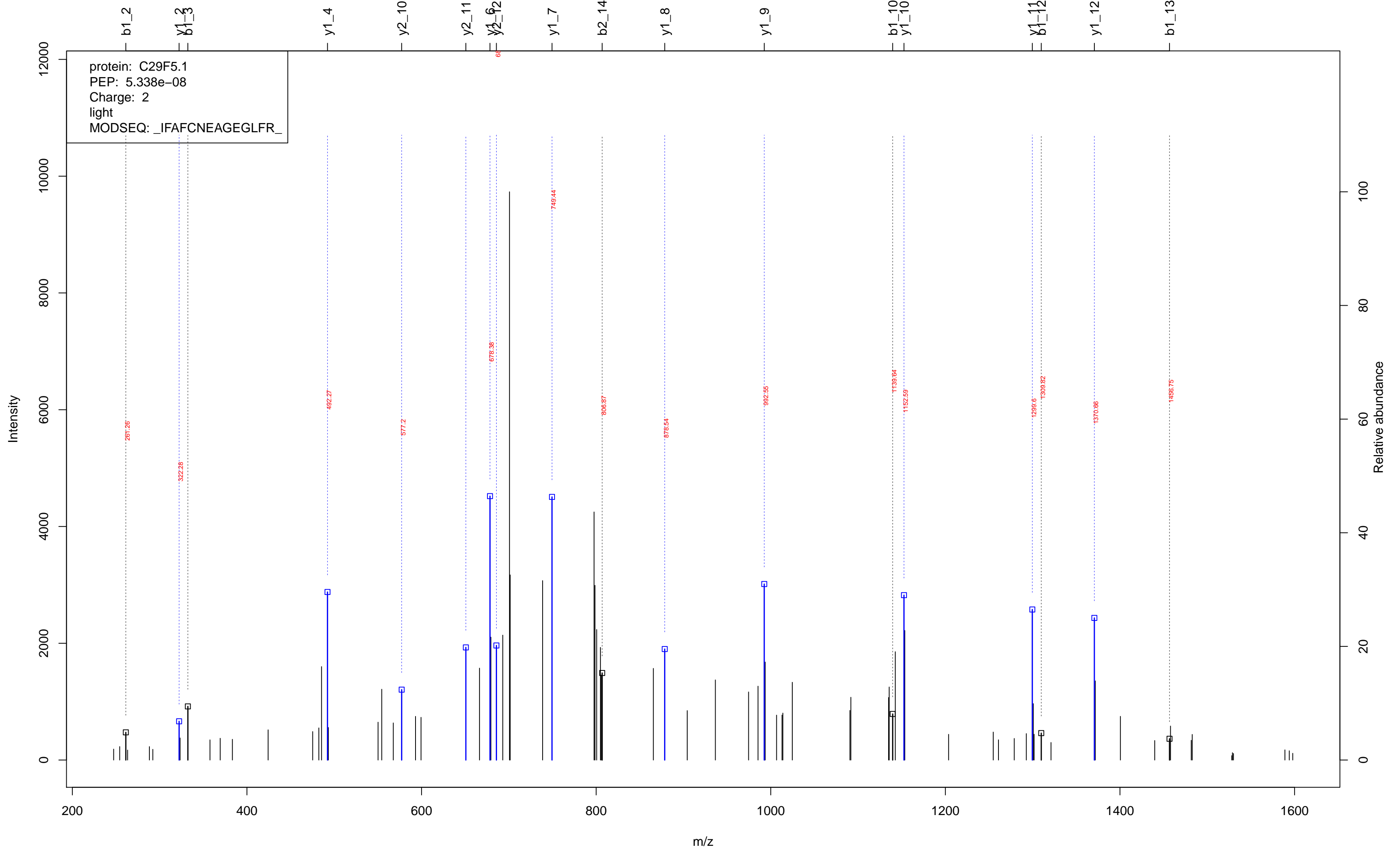


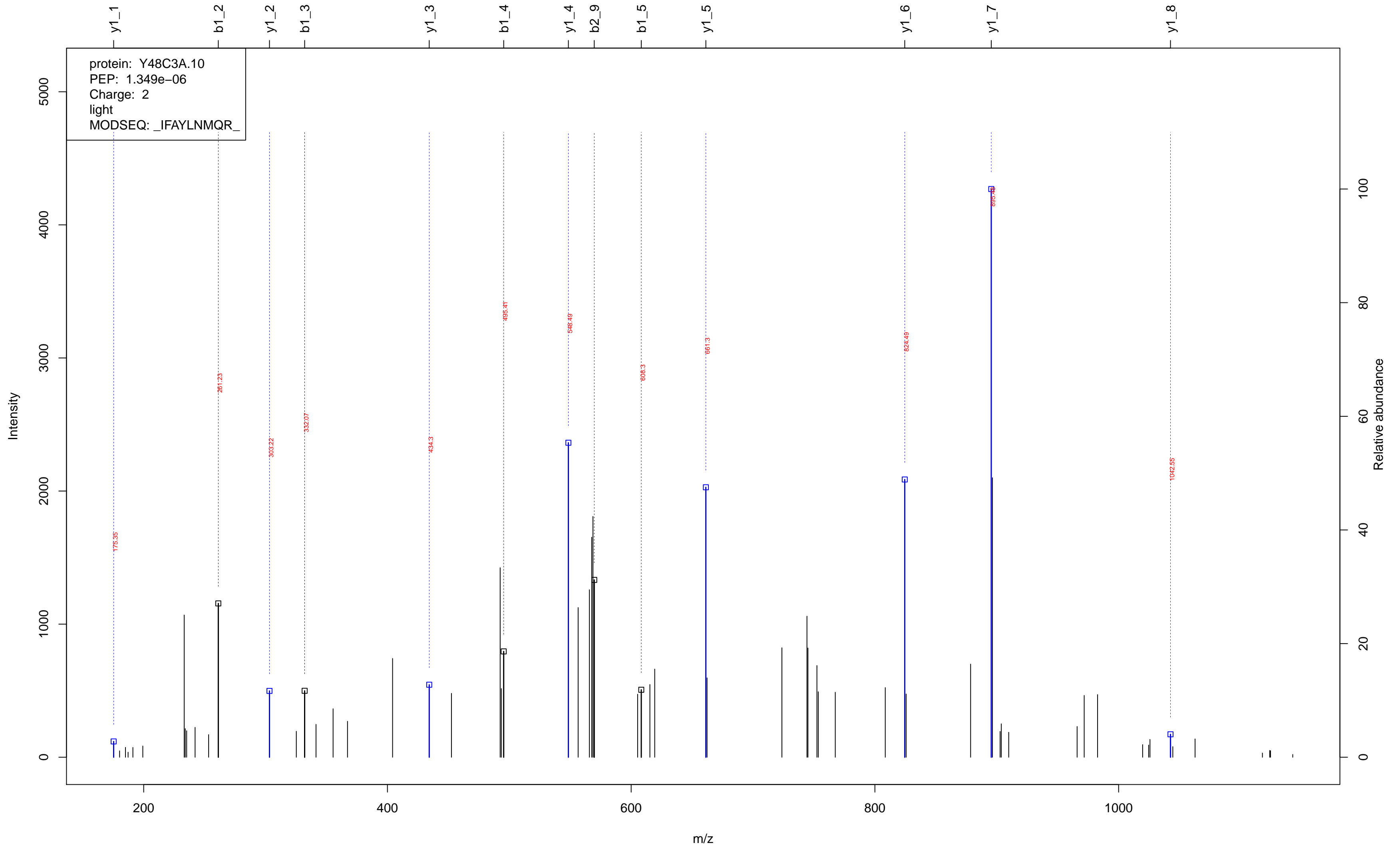


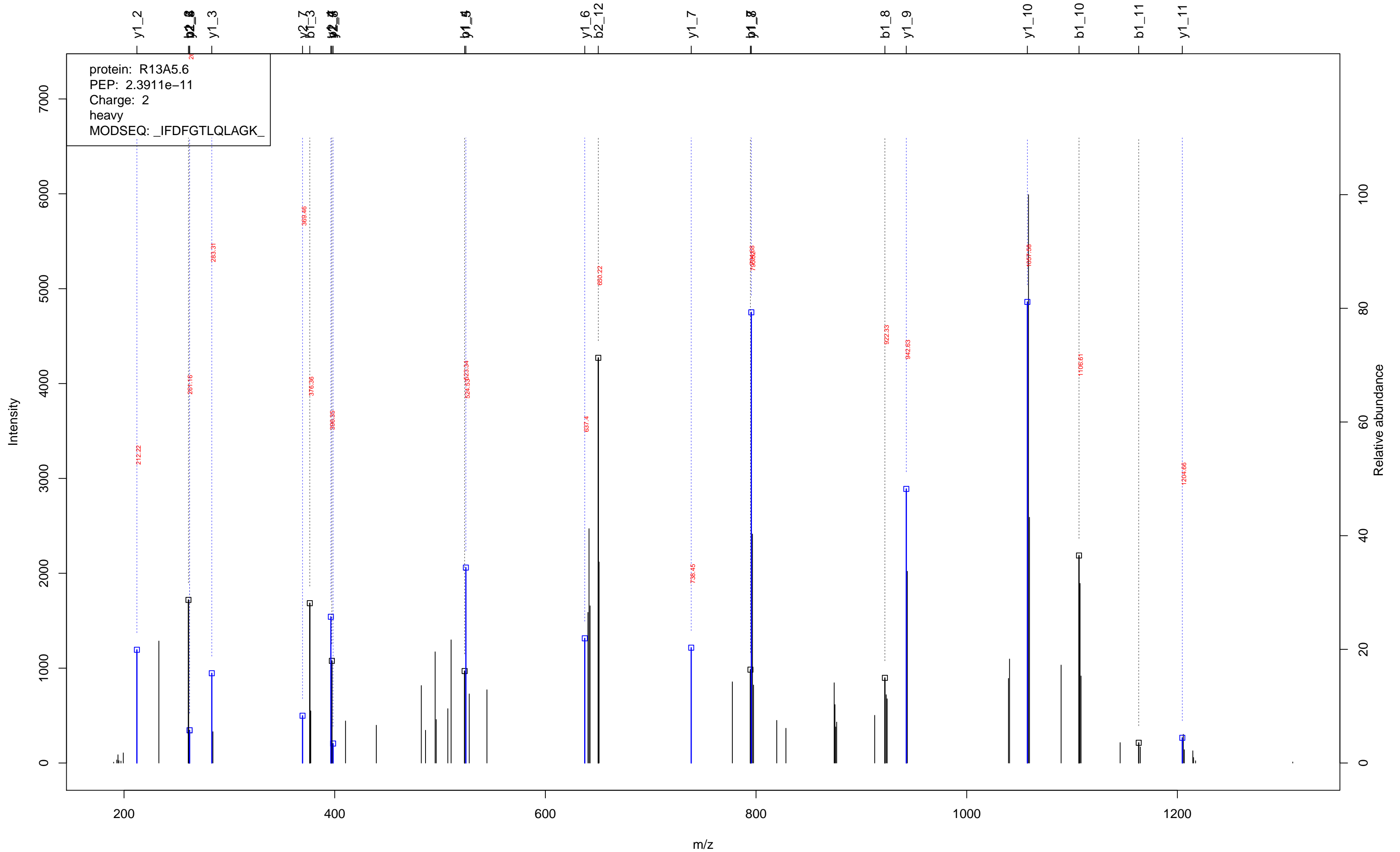
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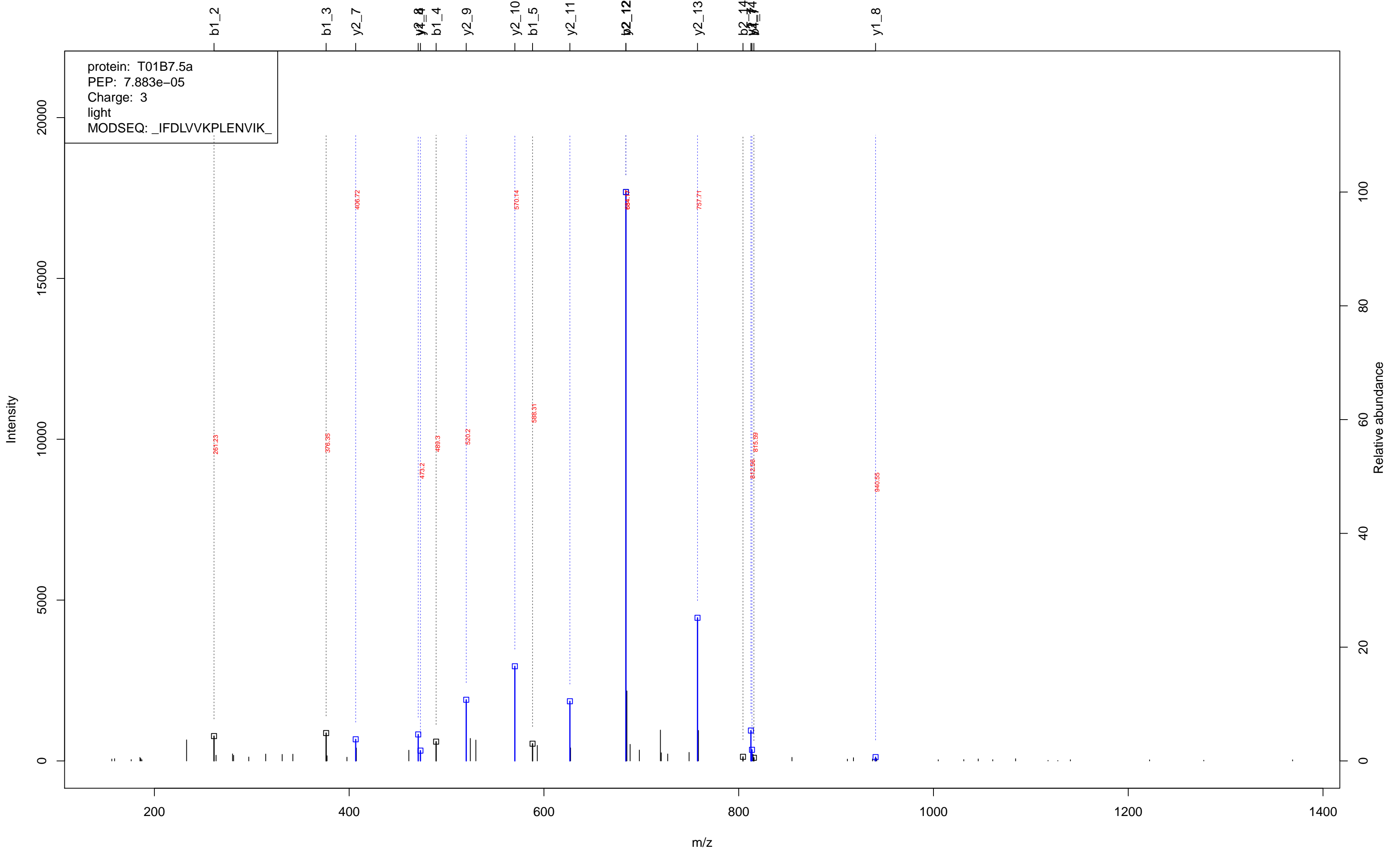


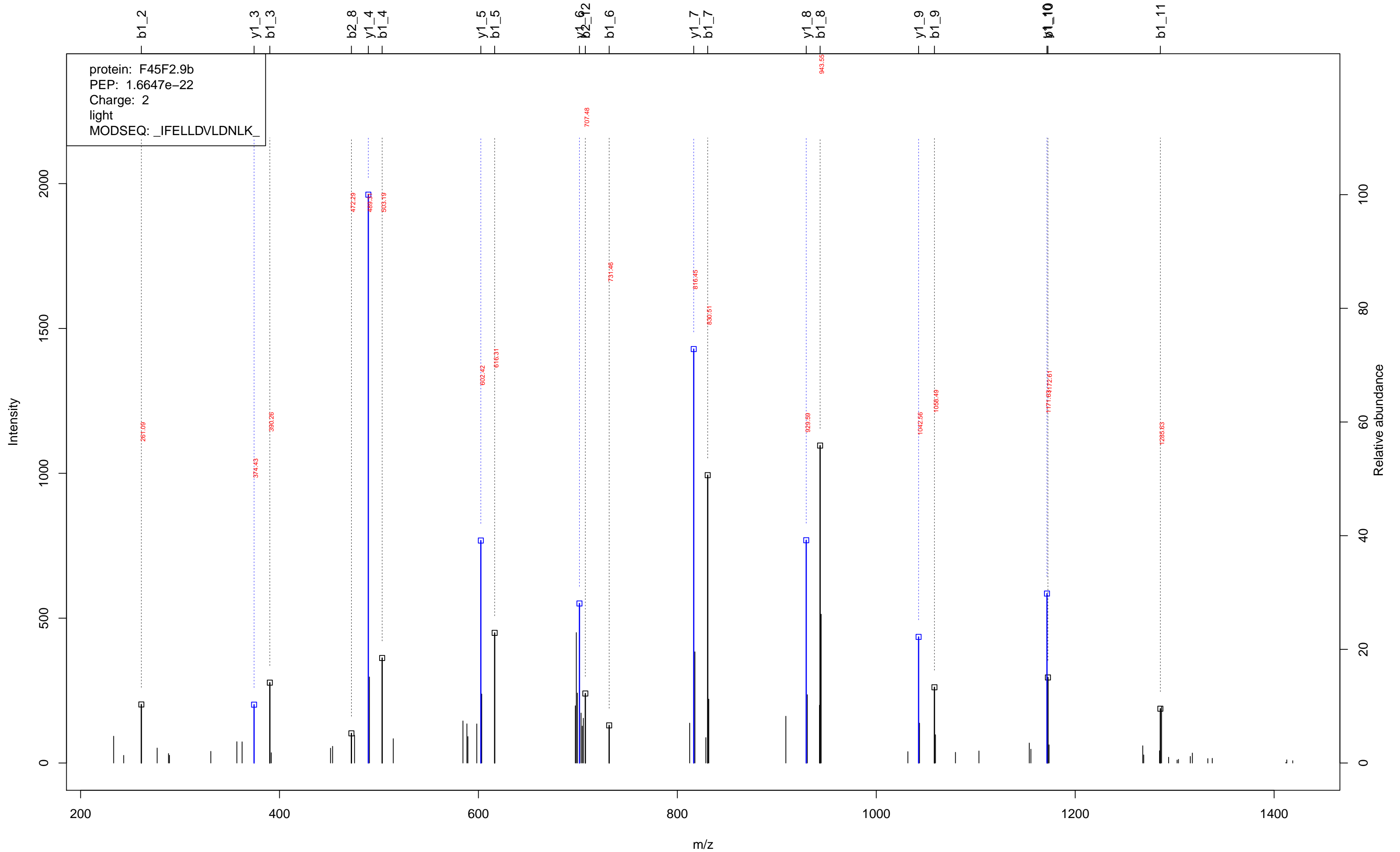


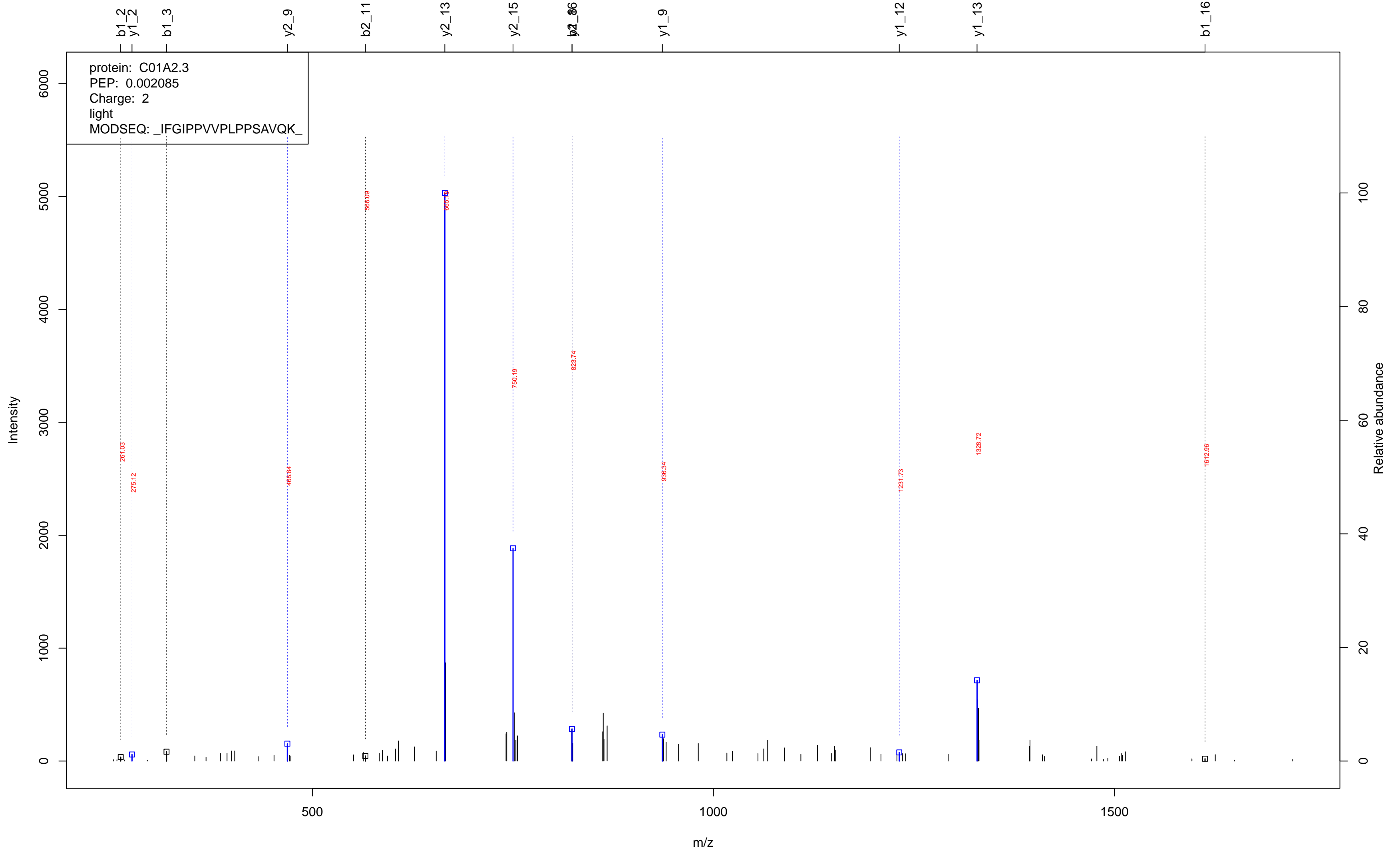


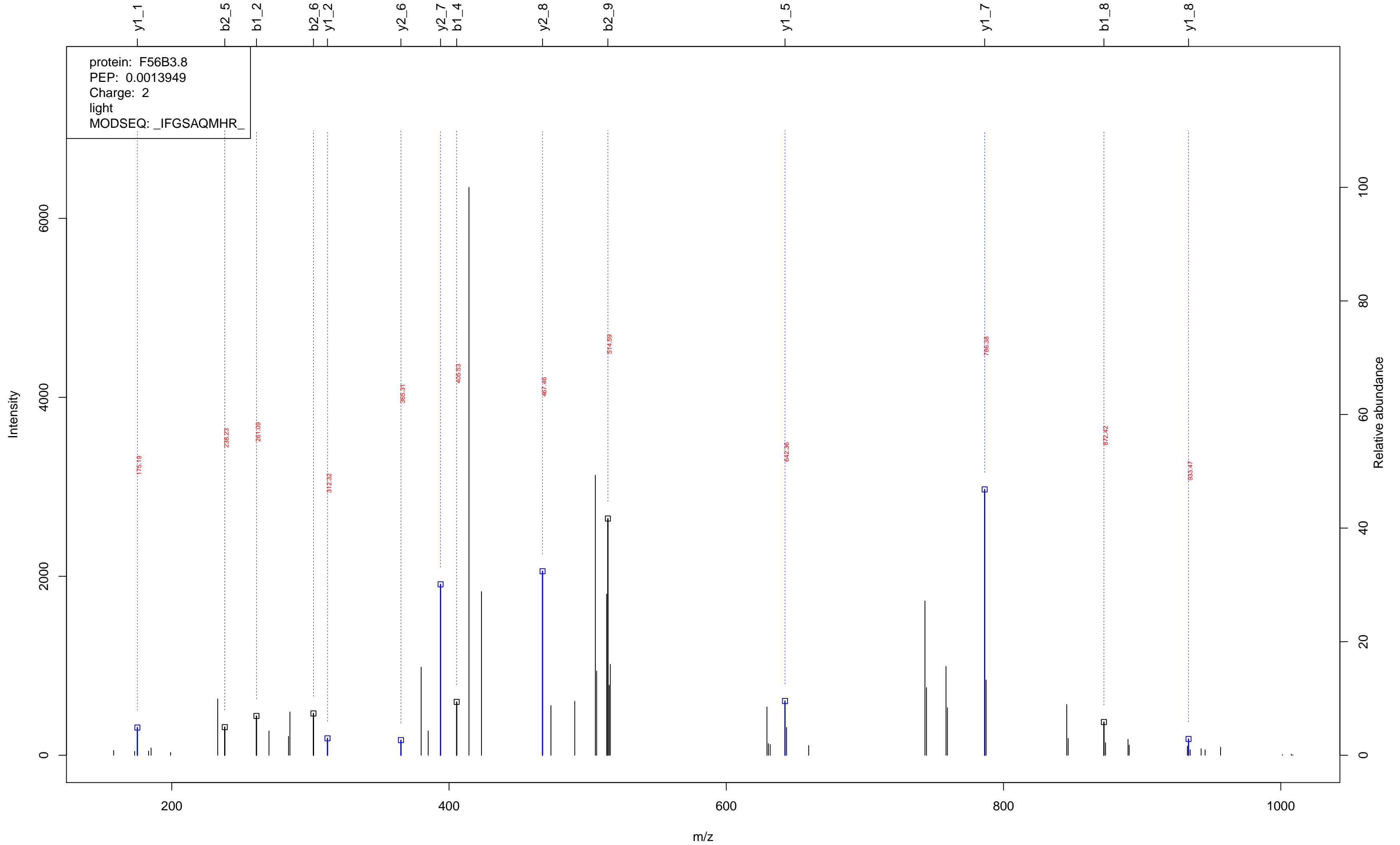


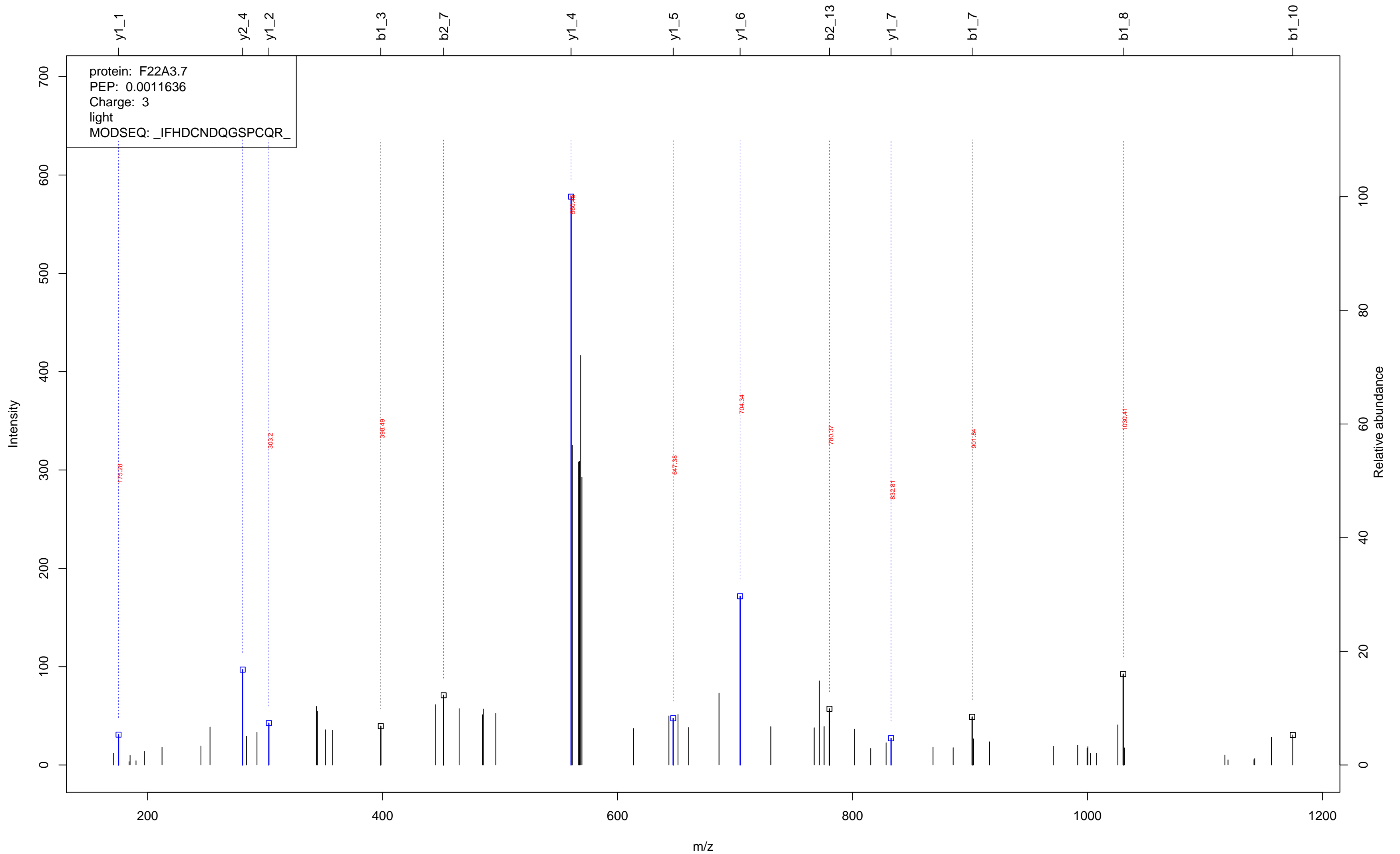


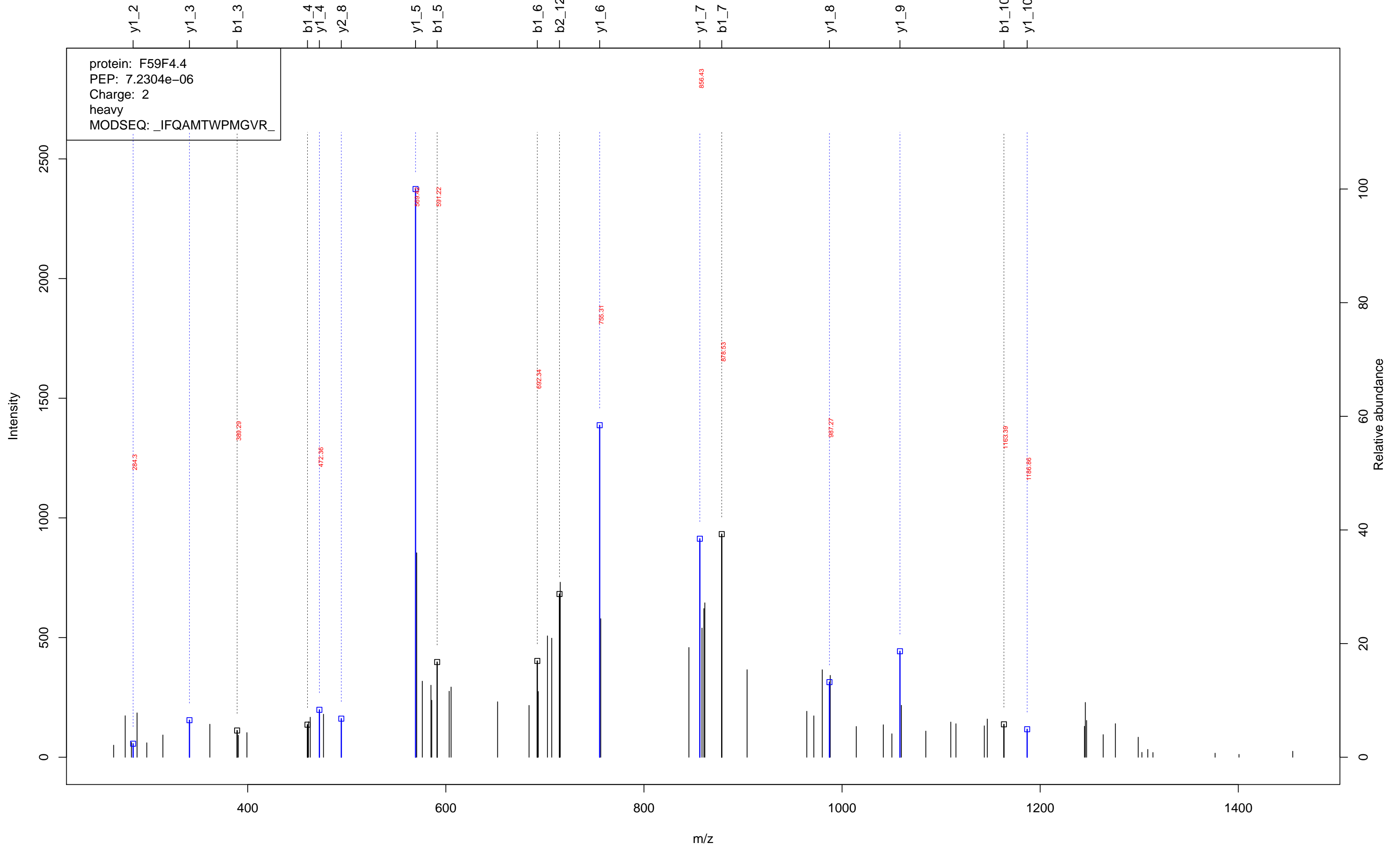


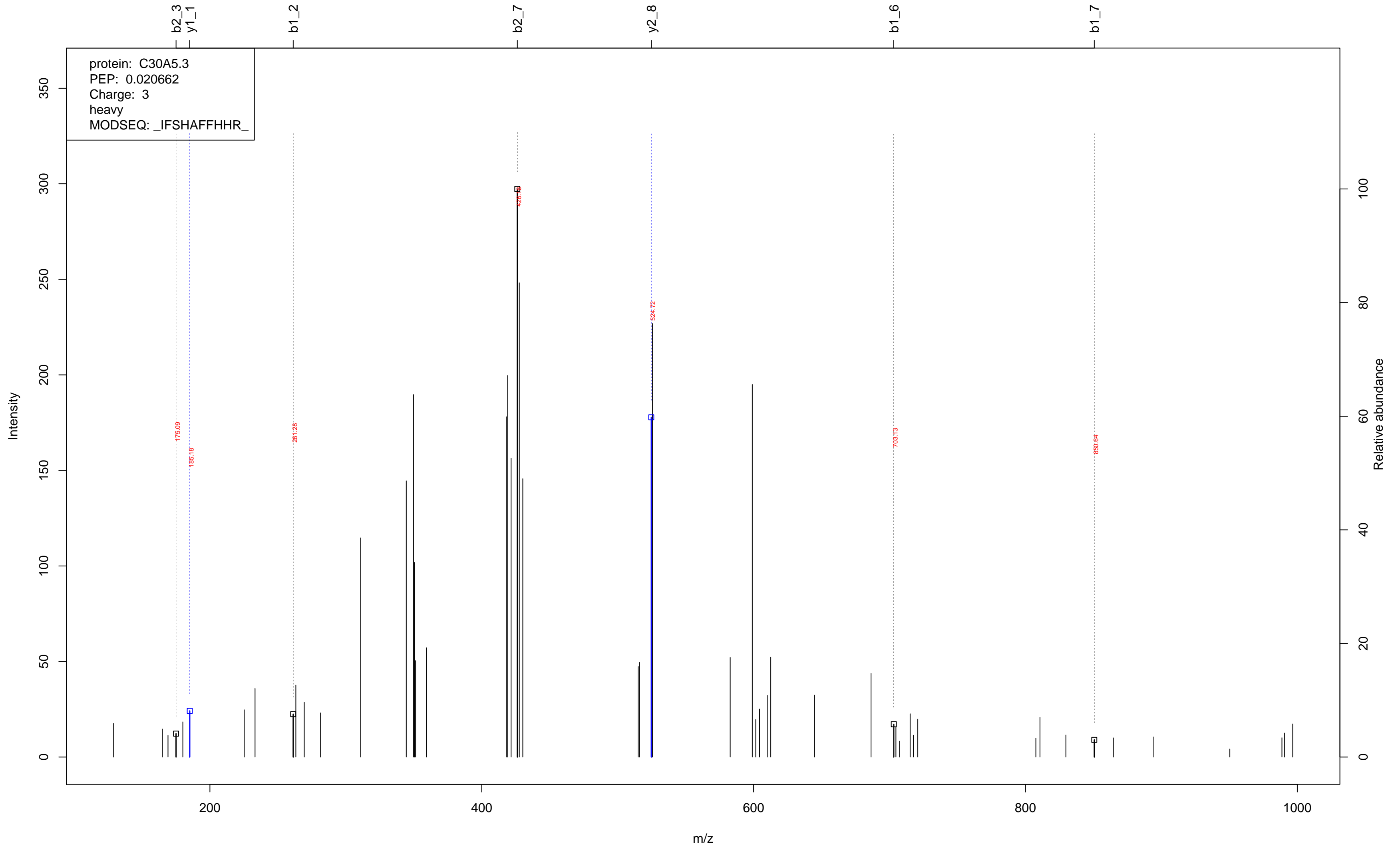


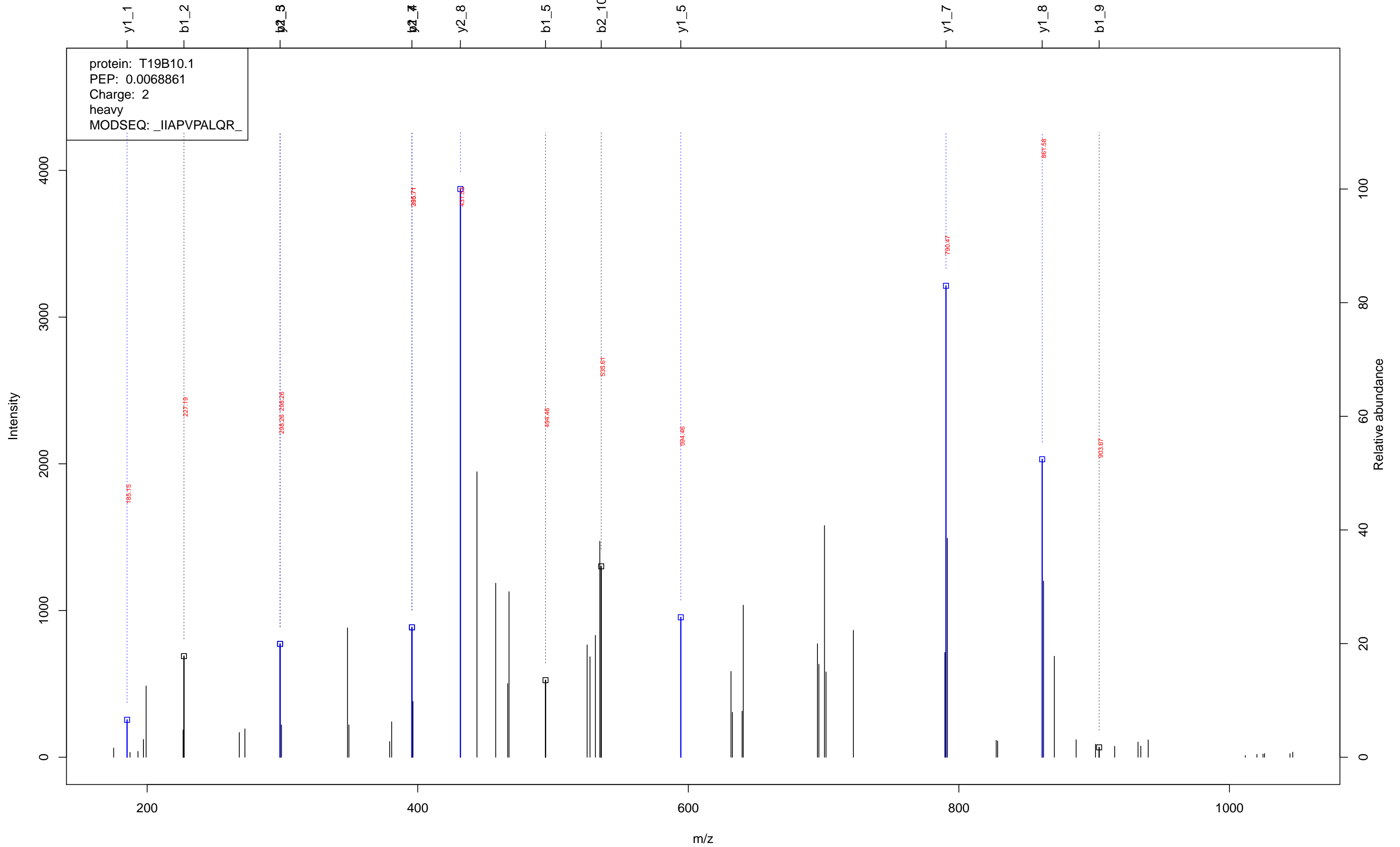




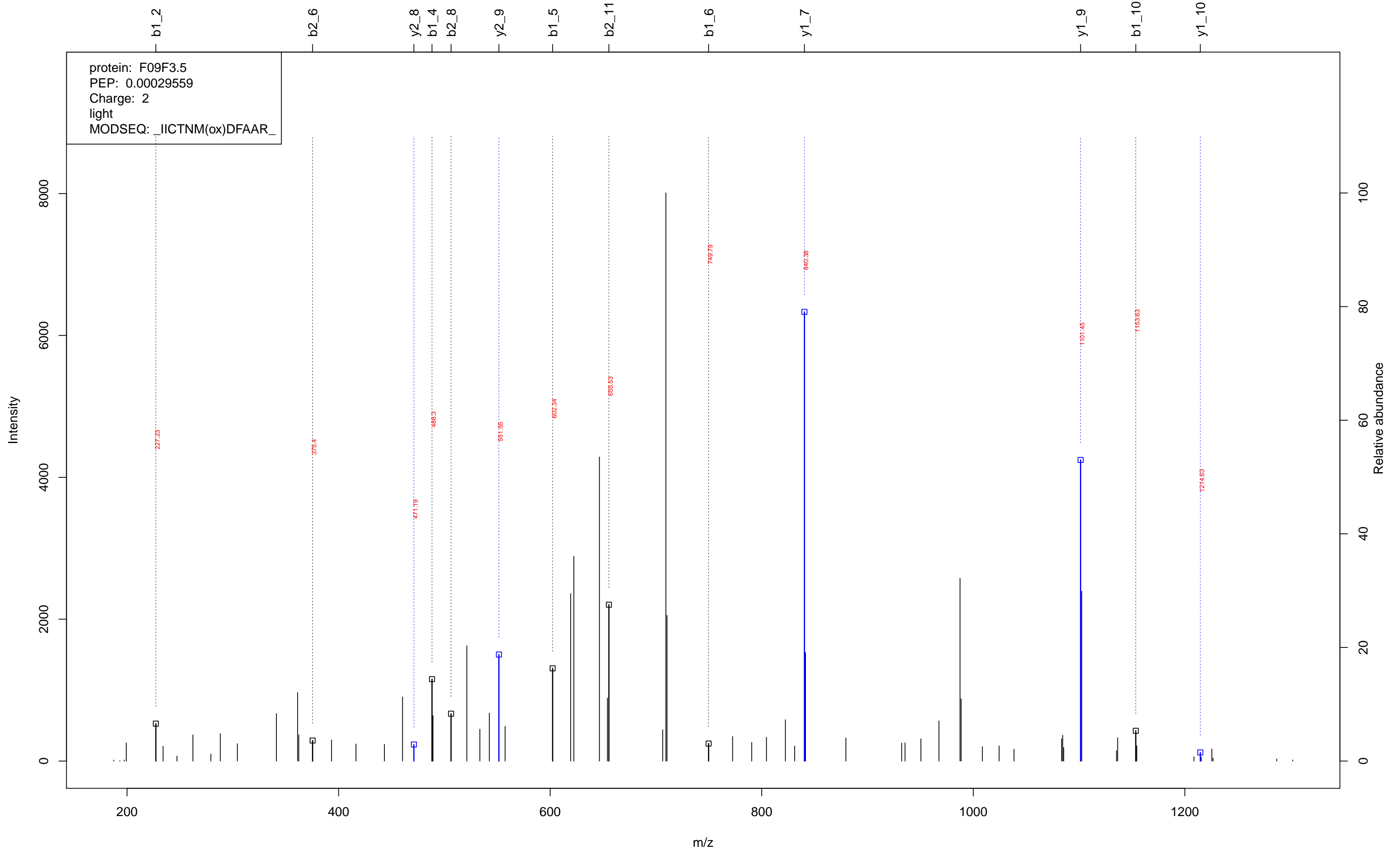


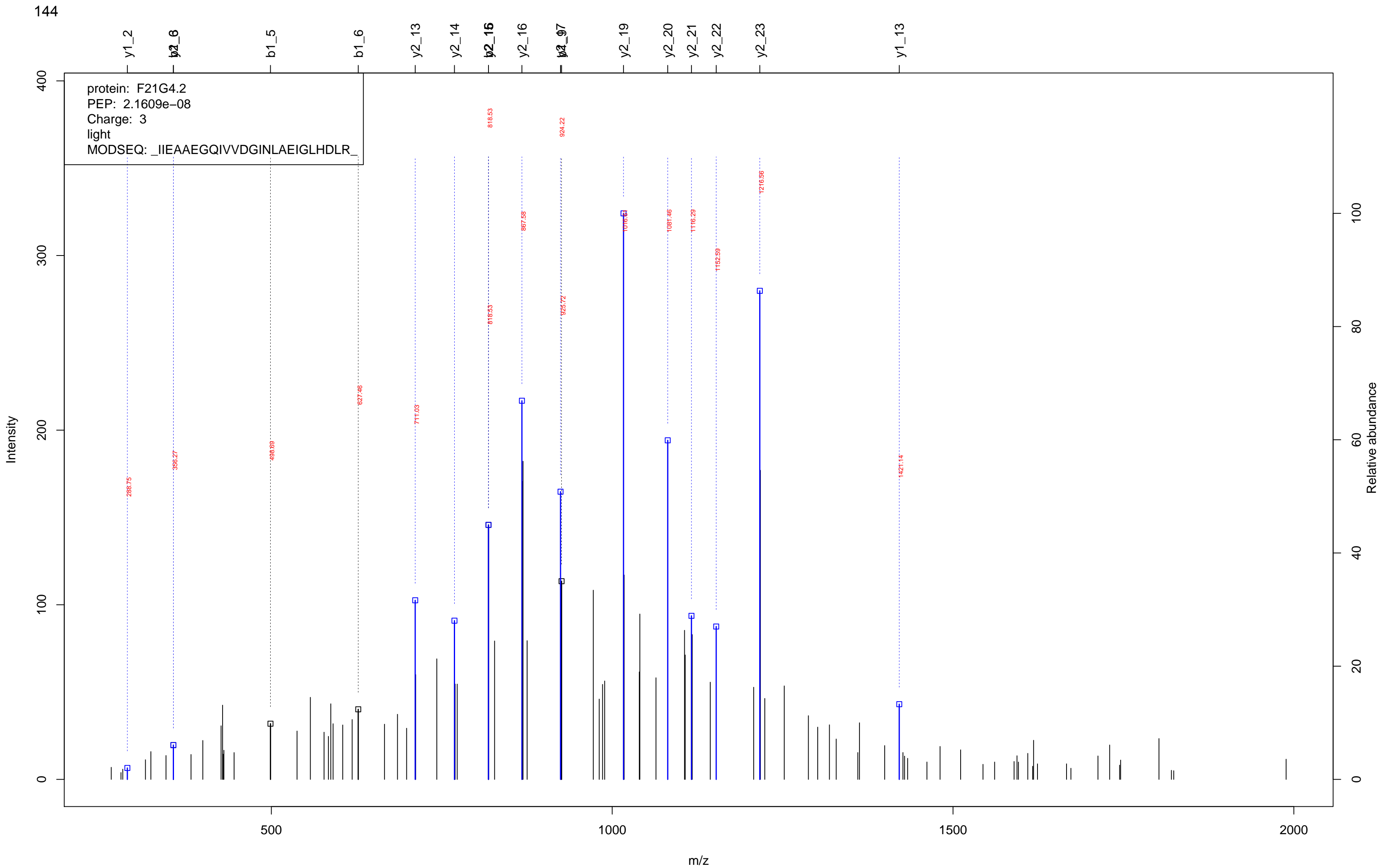


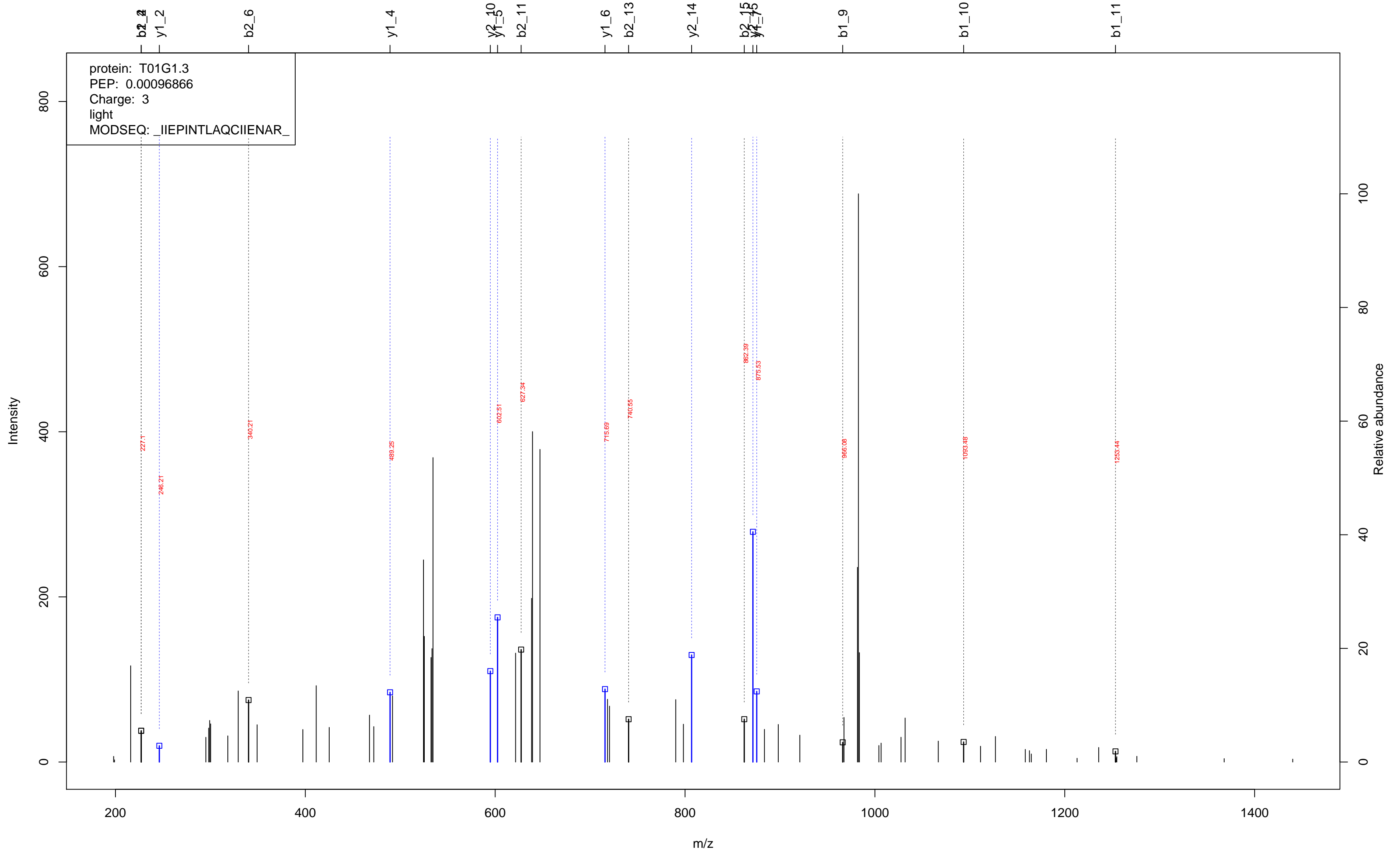


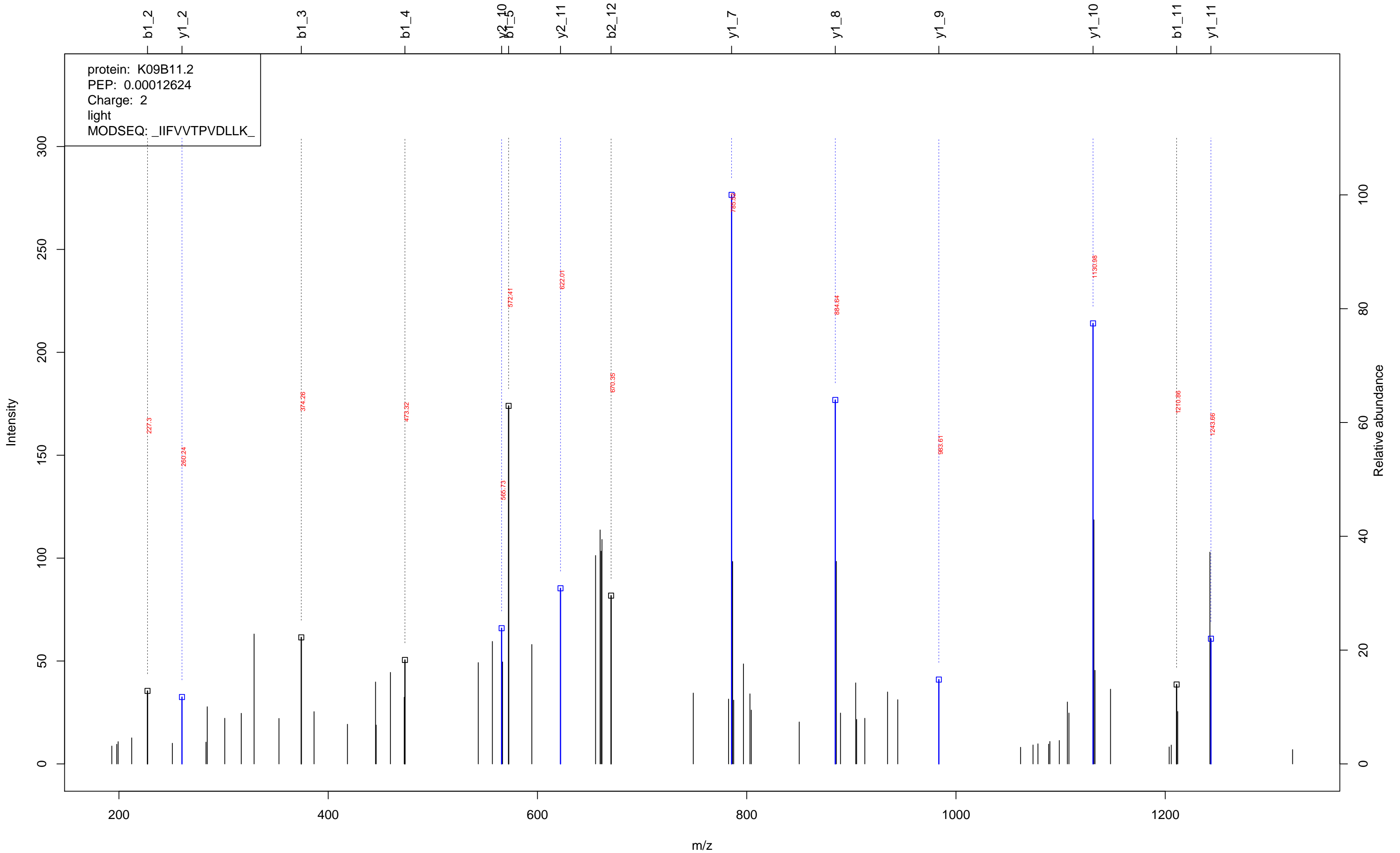


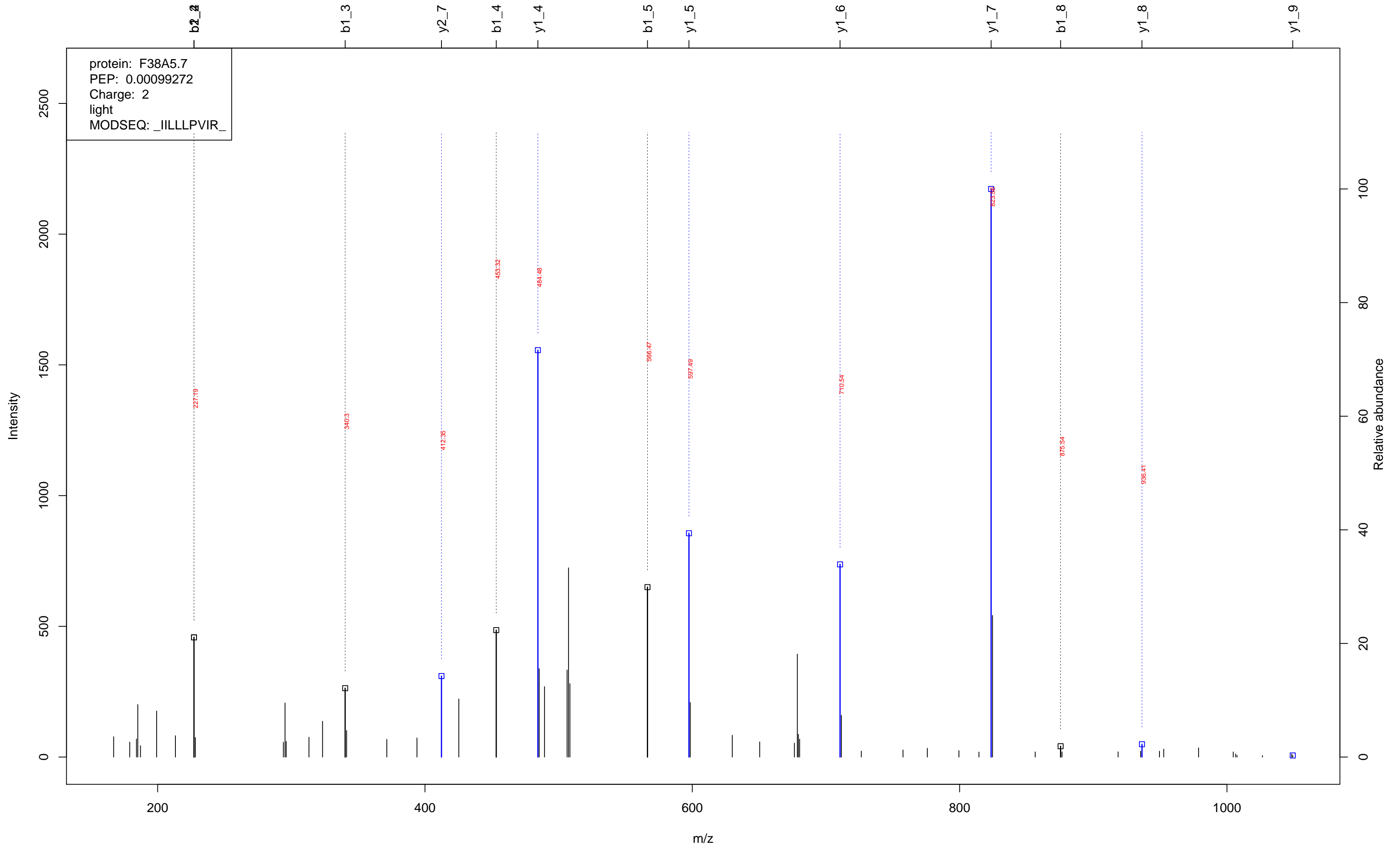
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Charge: 2
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MODSEQ: _IAPVPALQR_

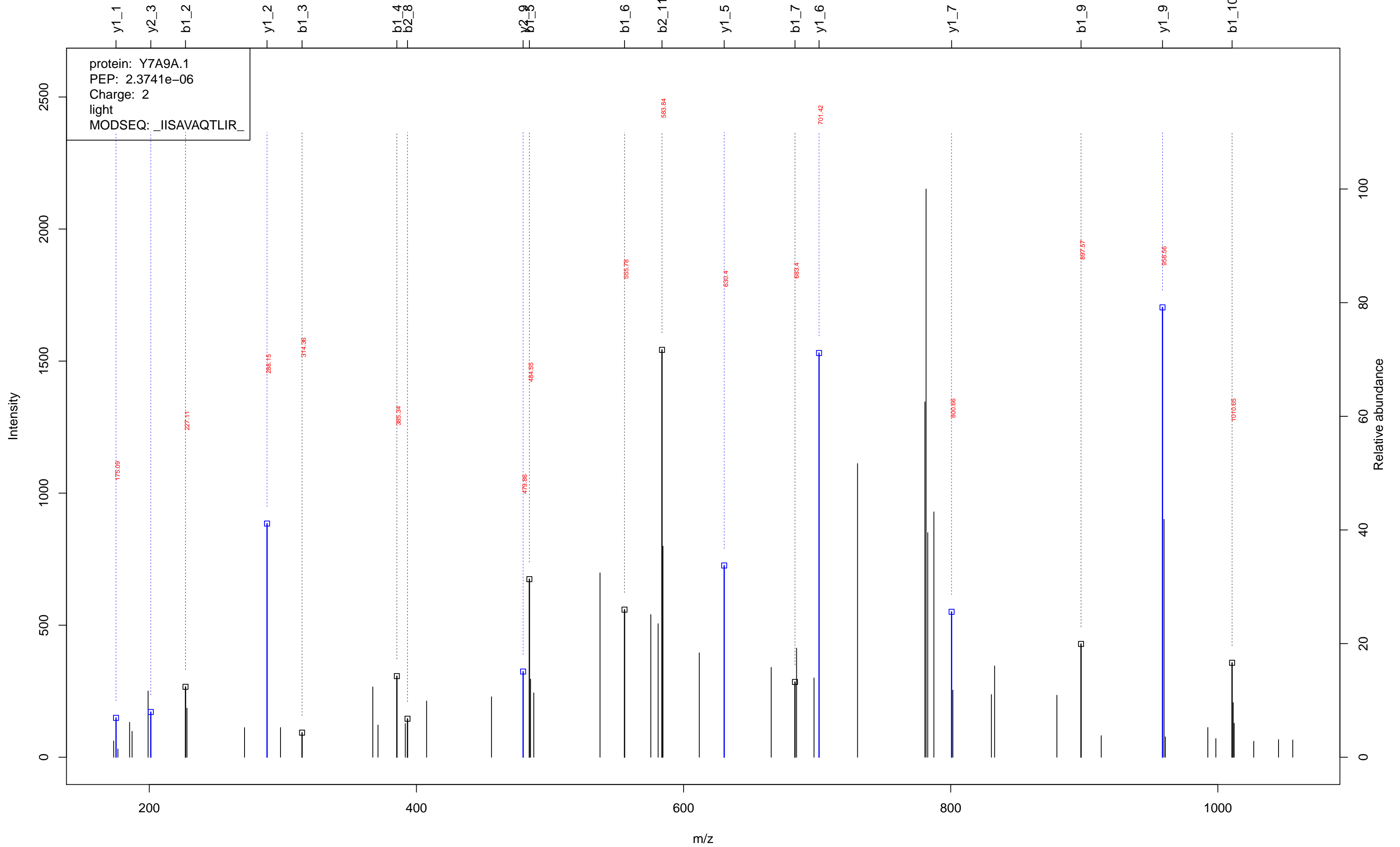


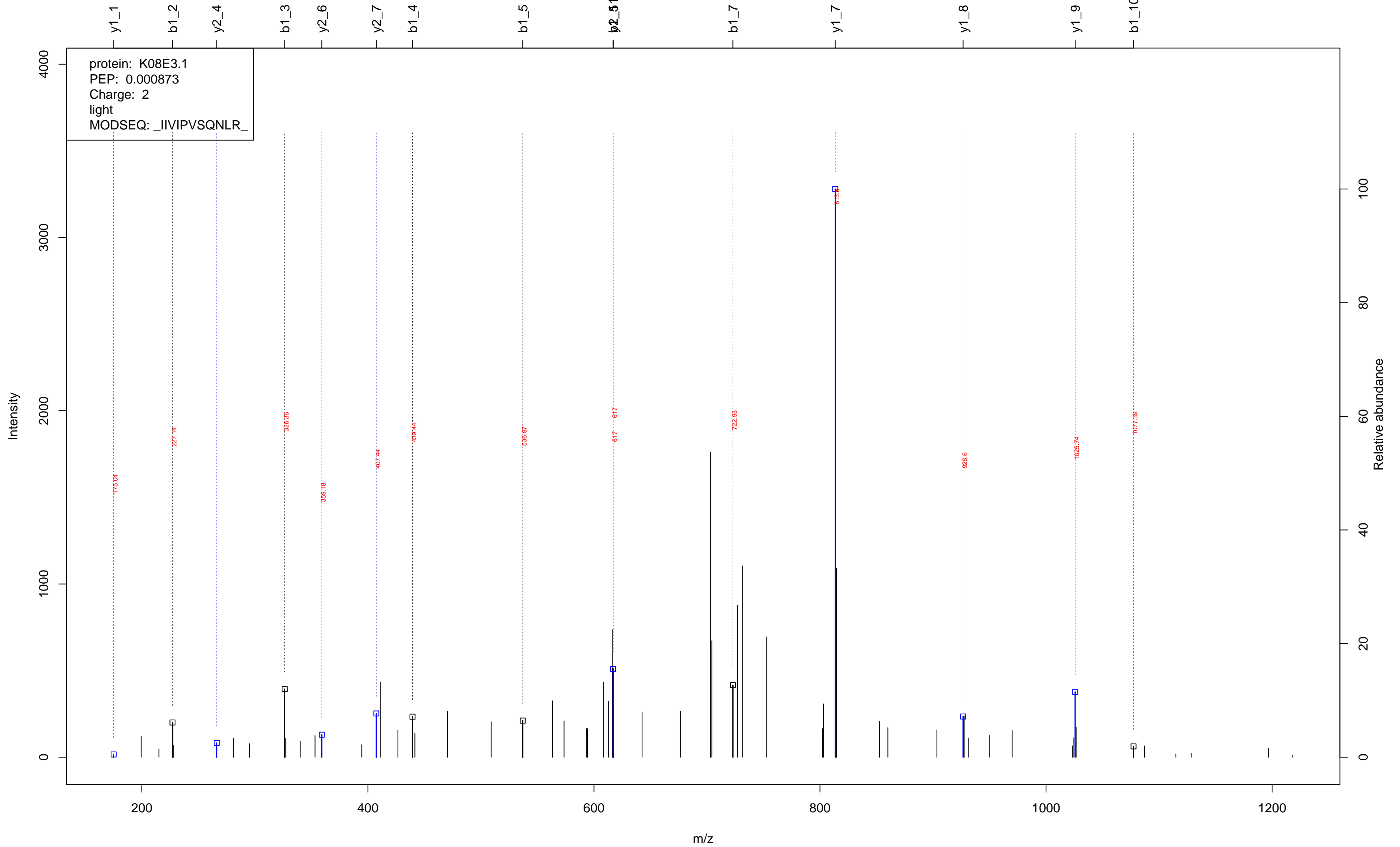


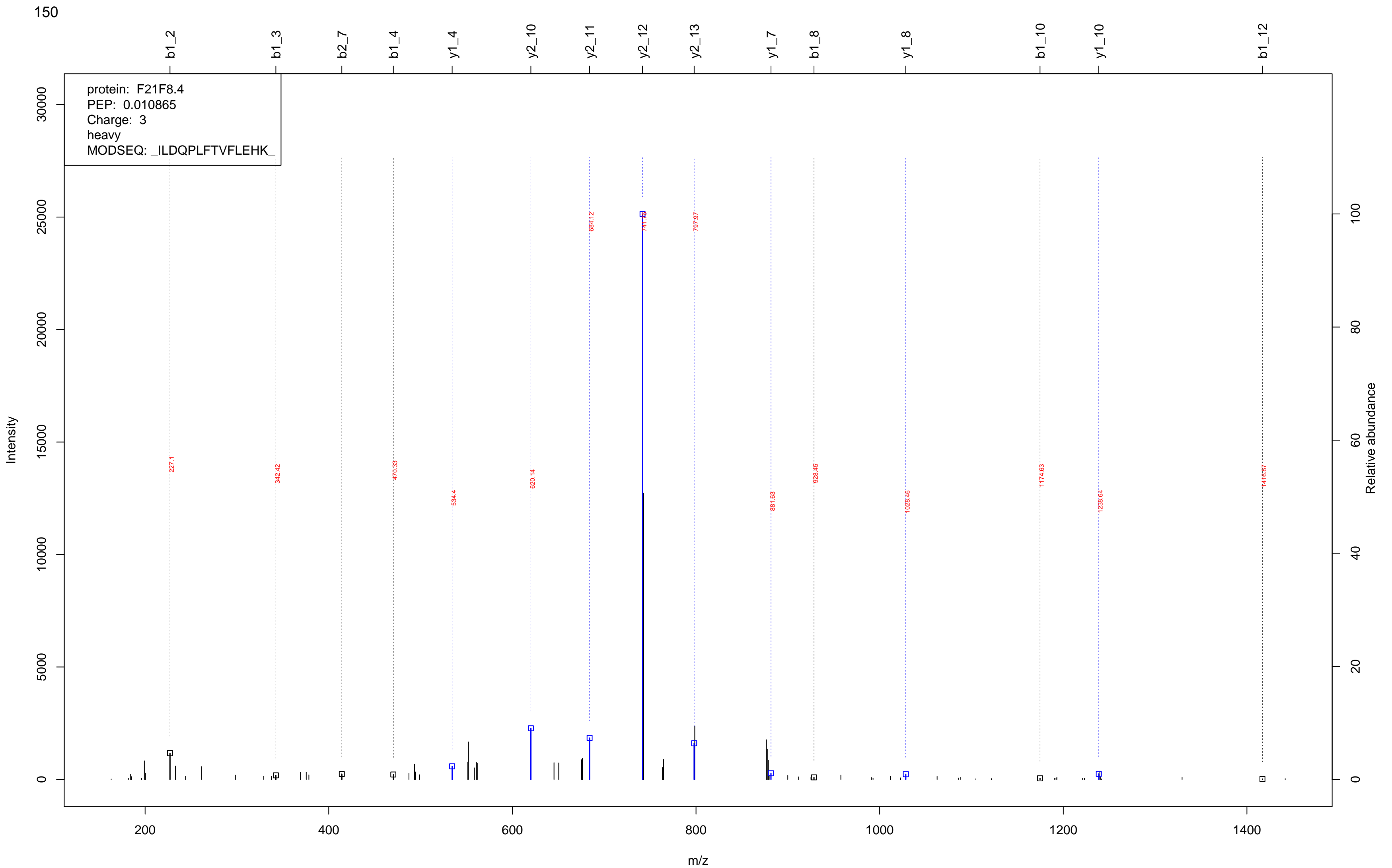


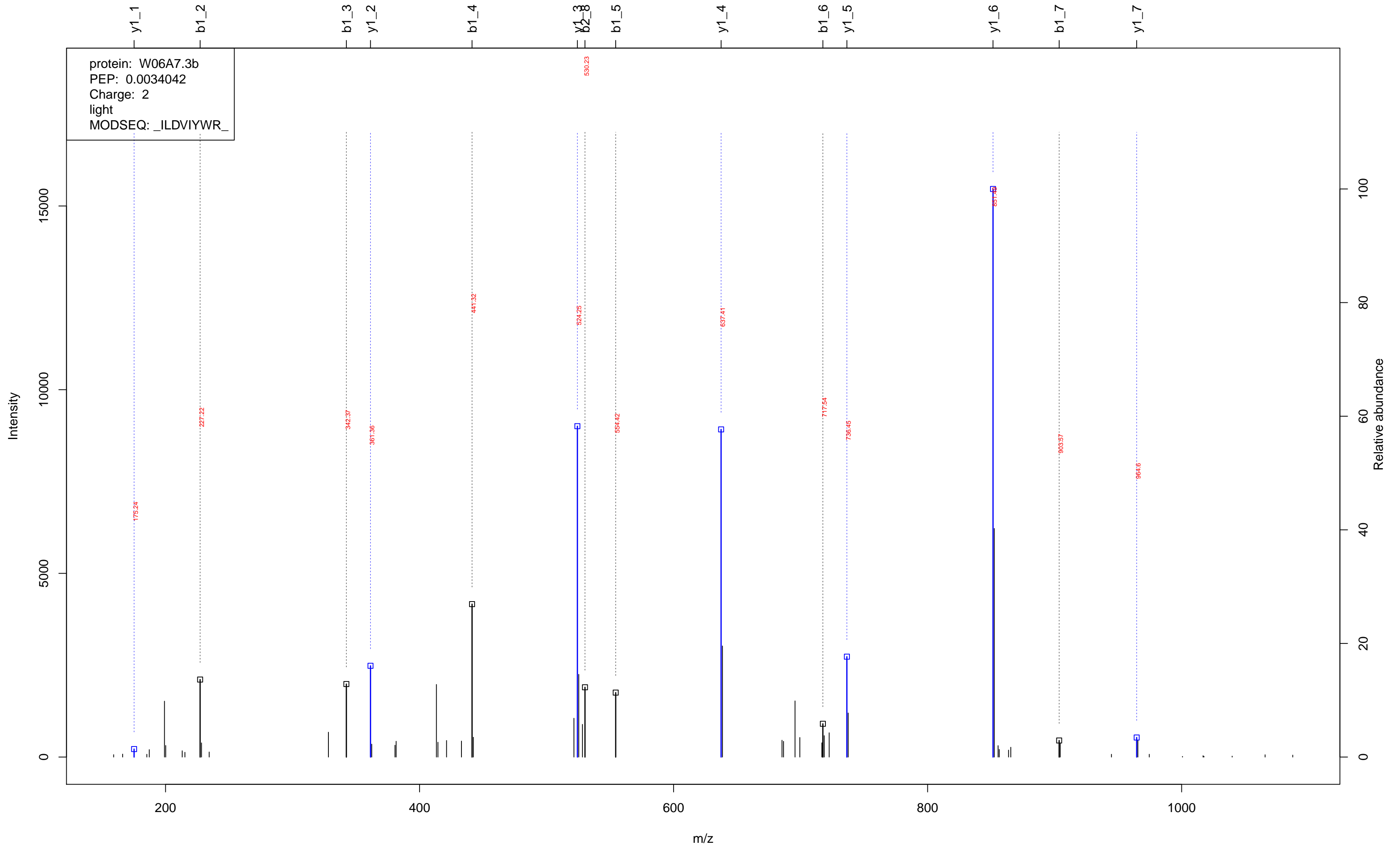


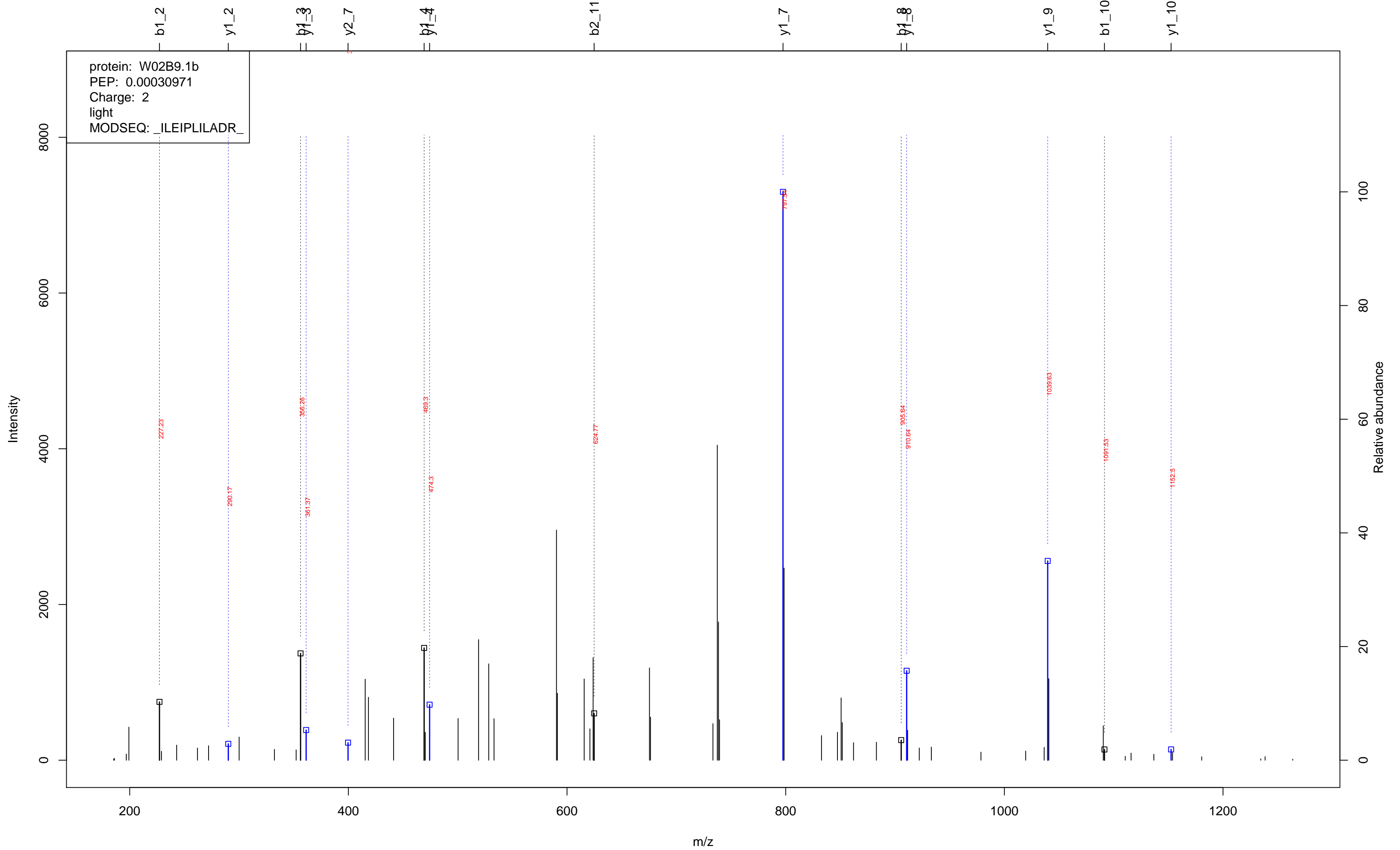


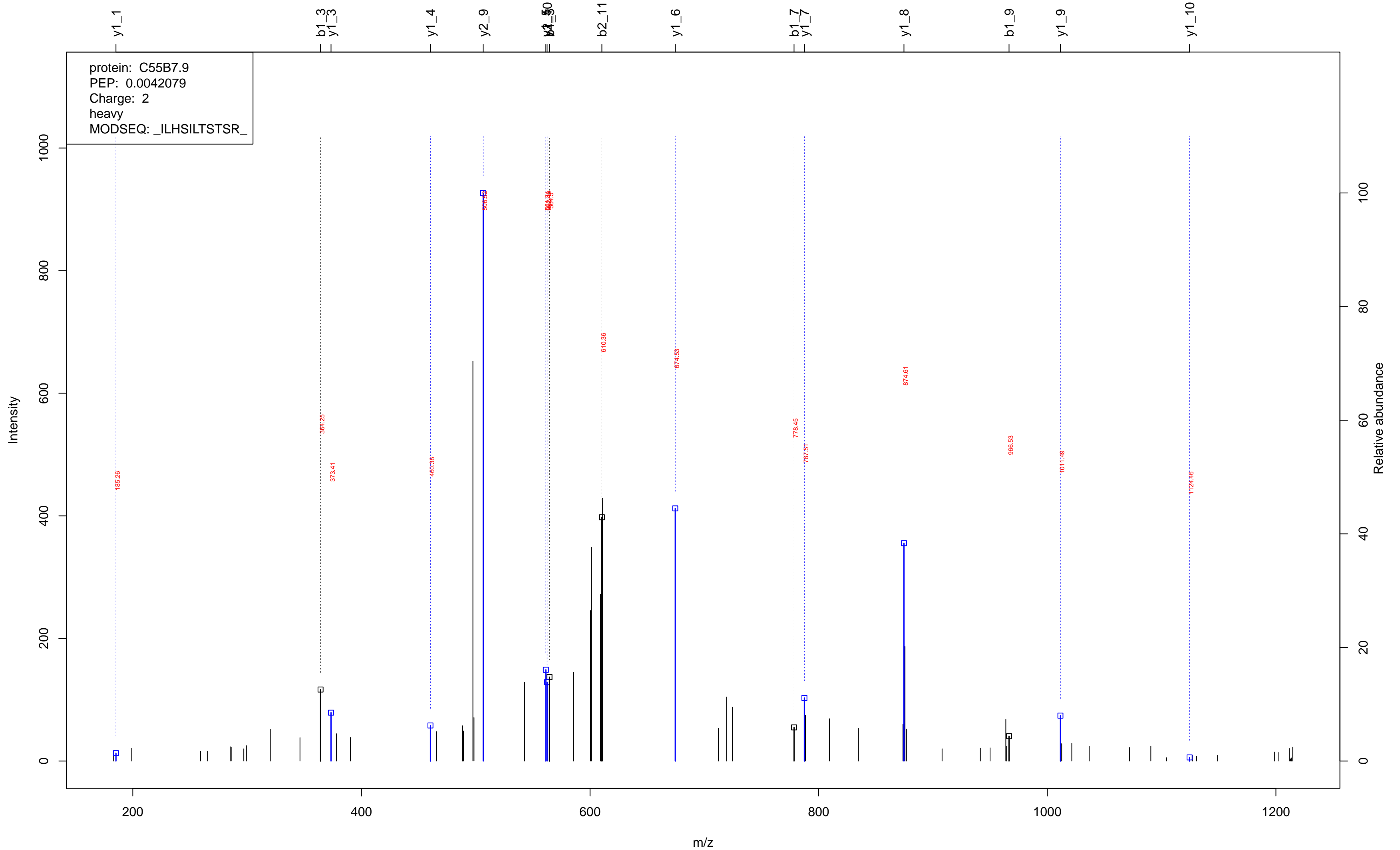






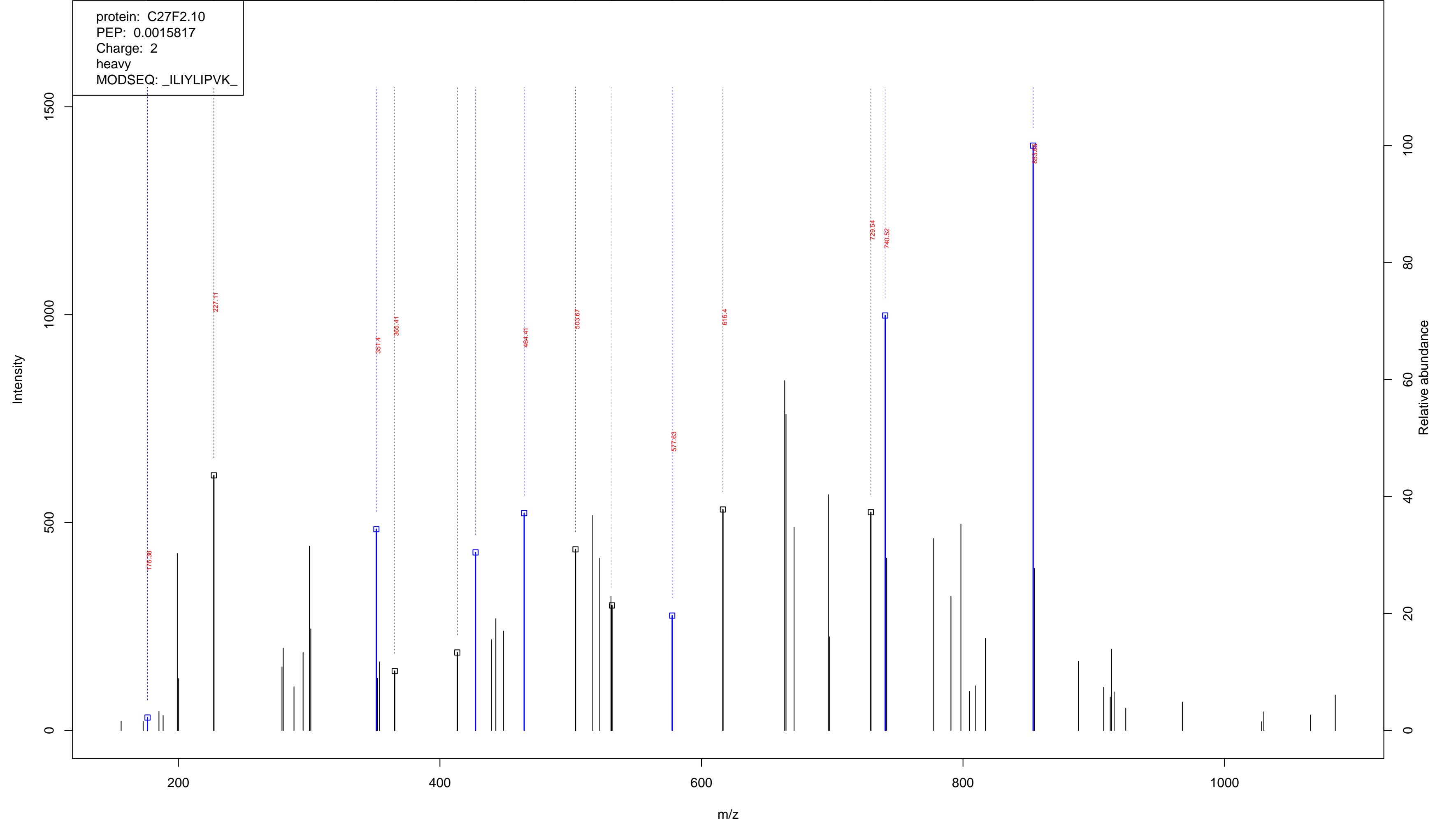


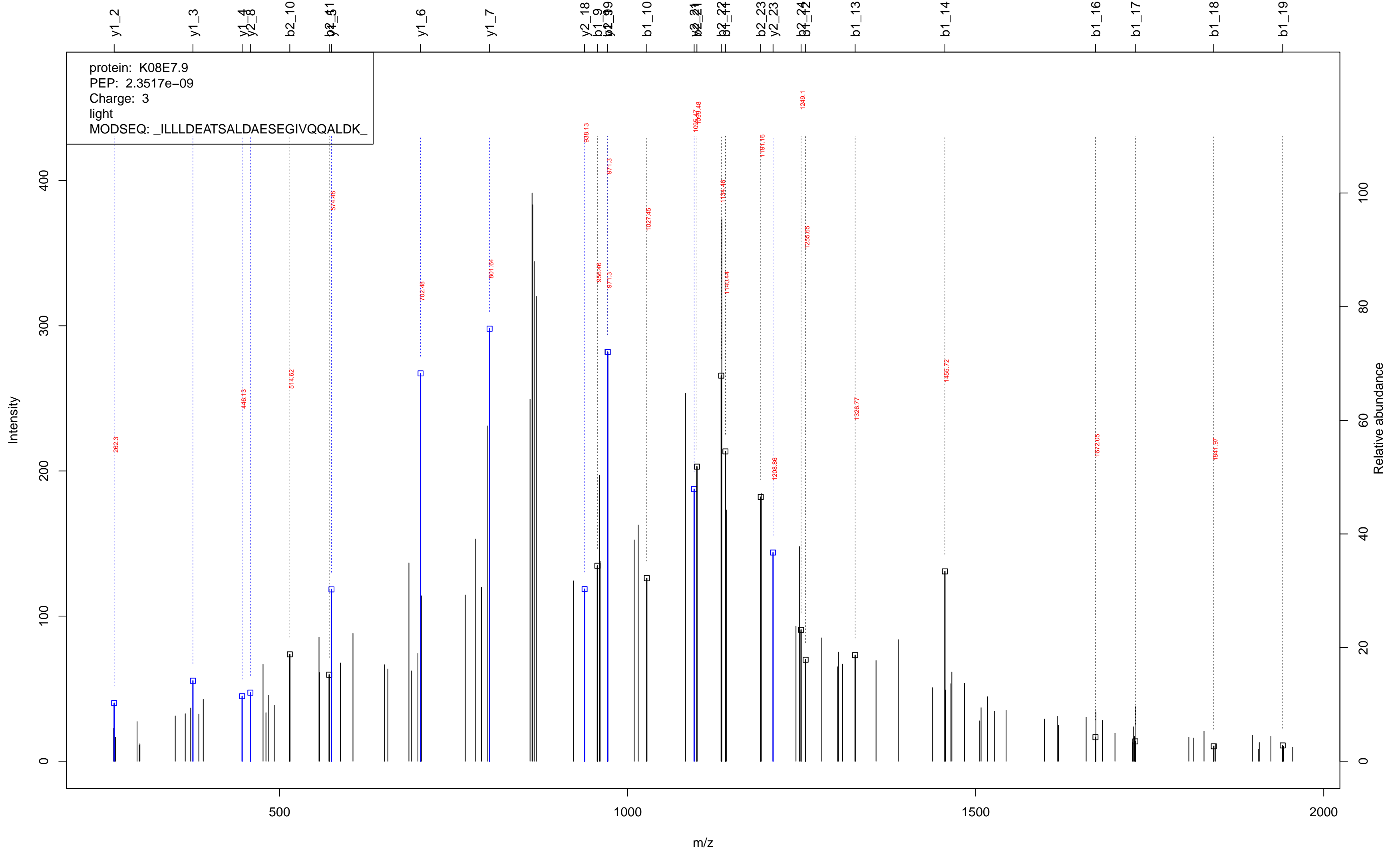




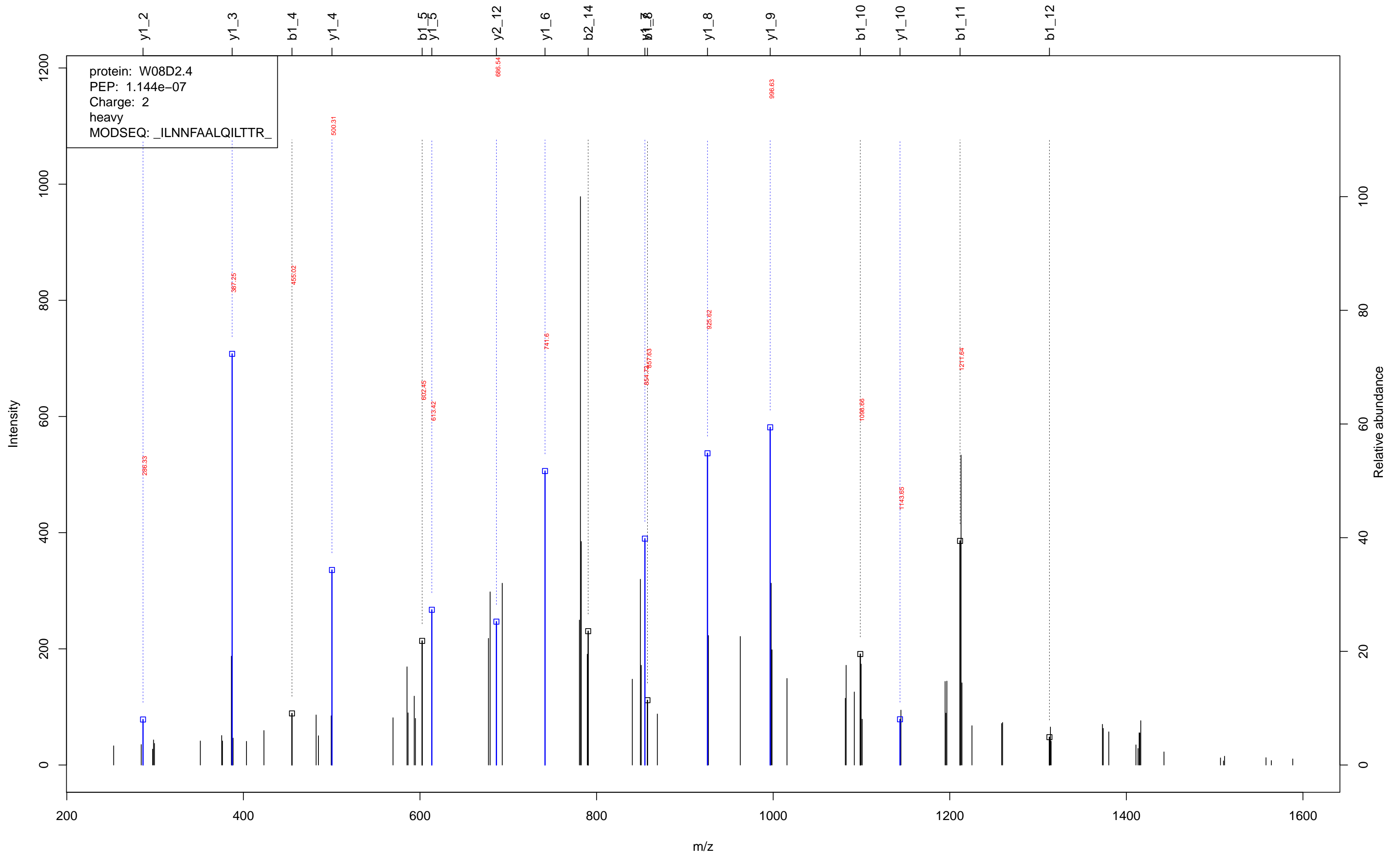
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protein: C27F2.10
PEP: 0.0015817
Charge: 2
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MODSEQ: _ILIYLIPVK_



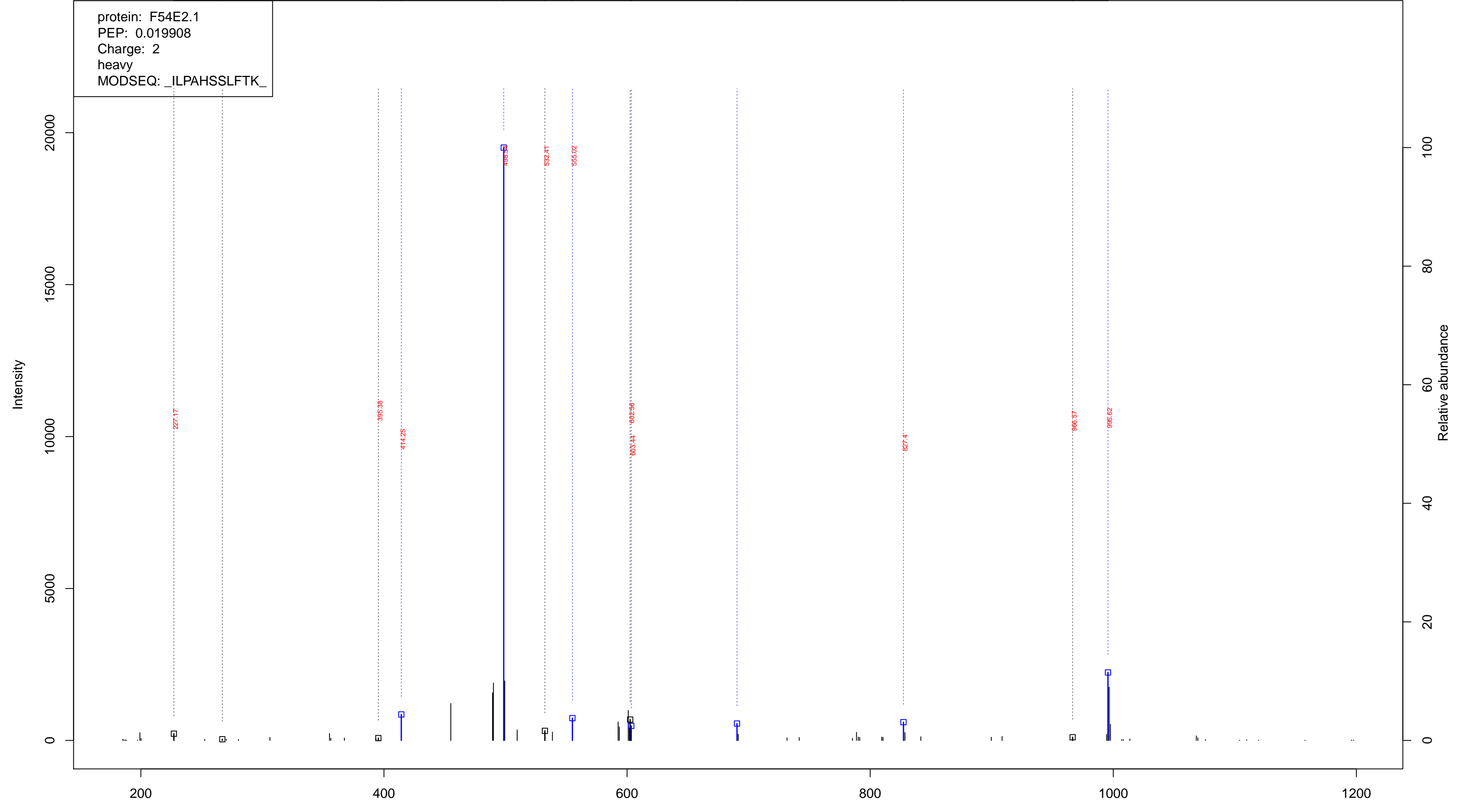


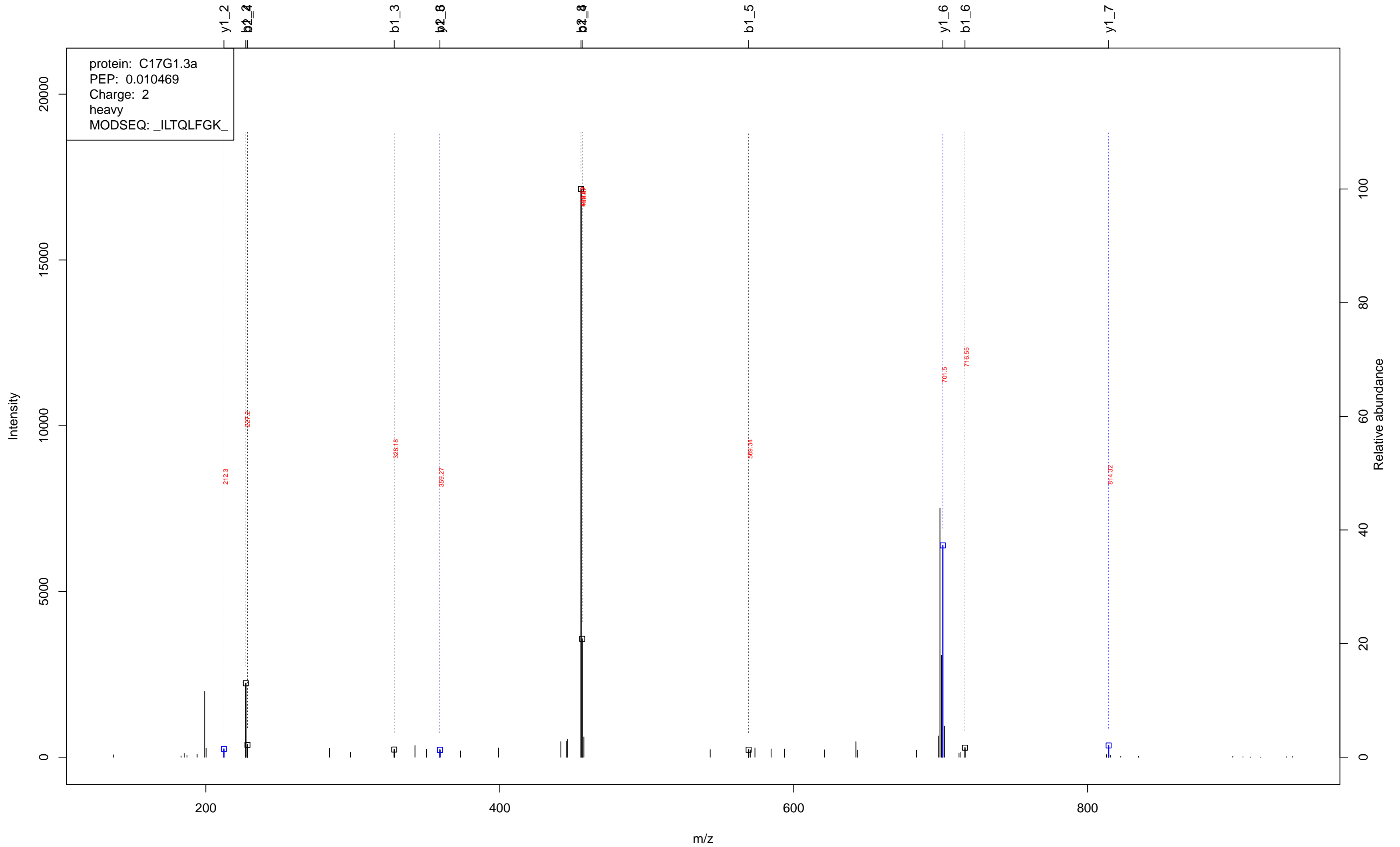
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Charge: 3
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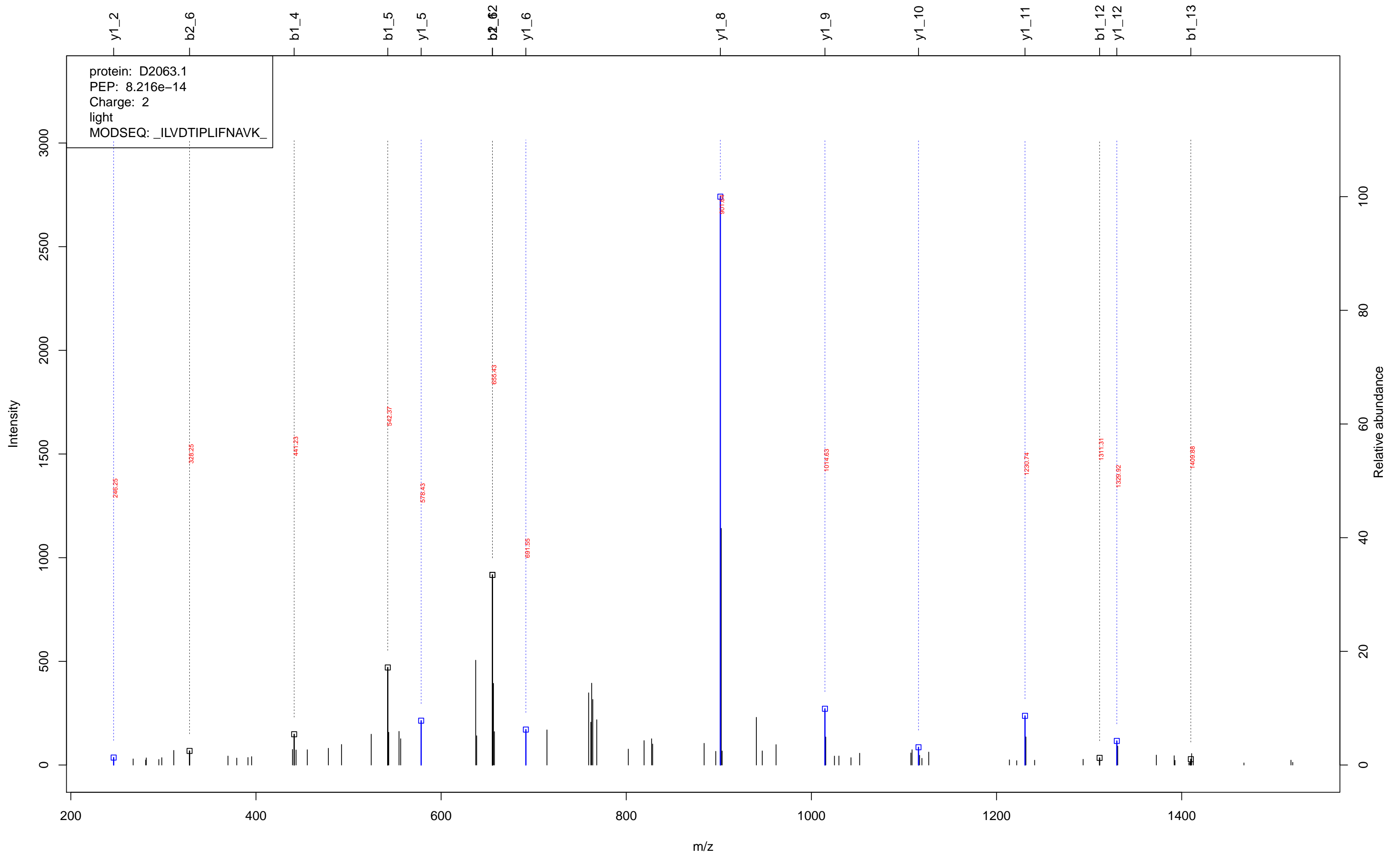


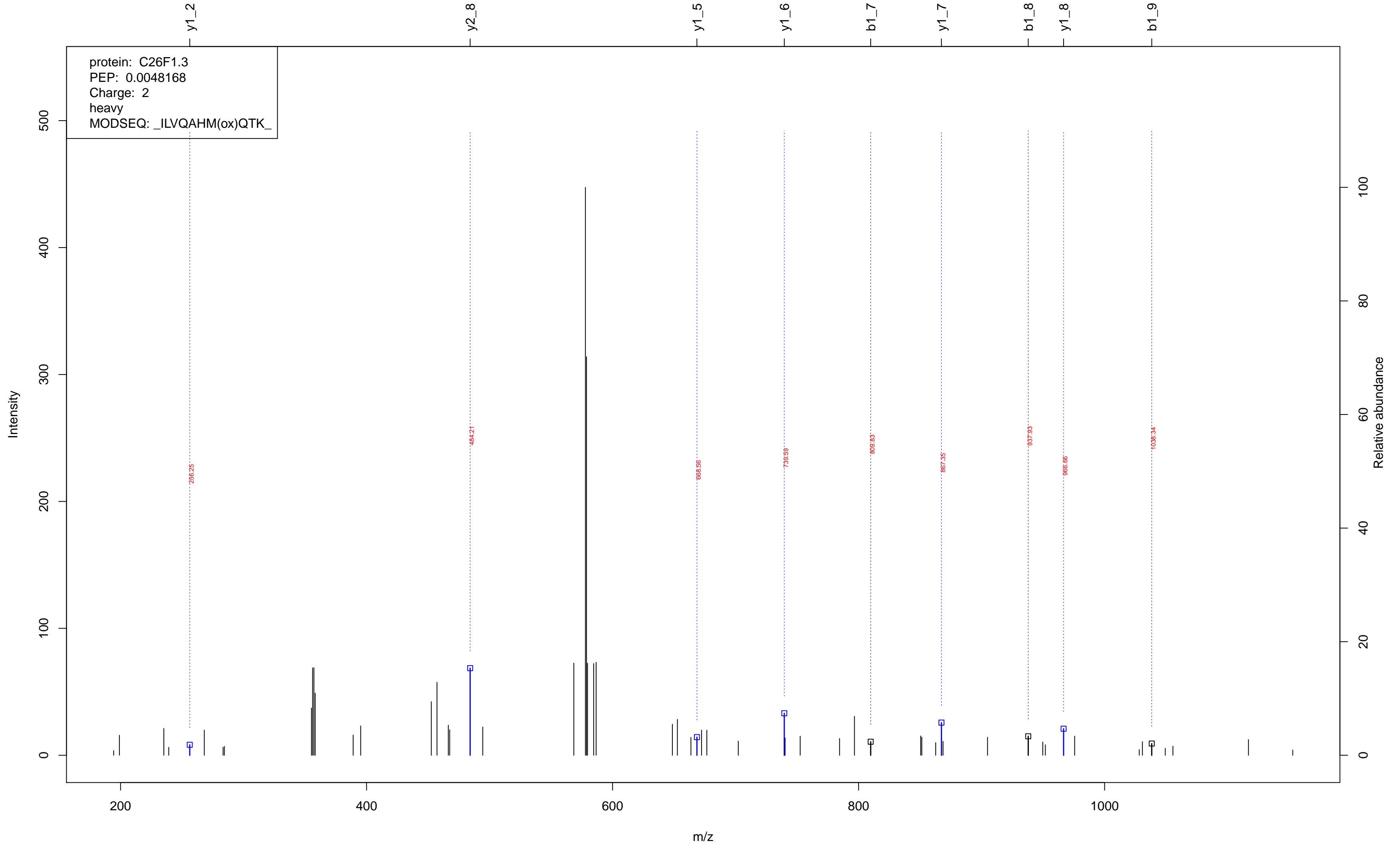
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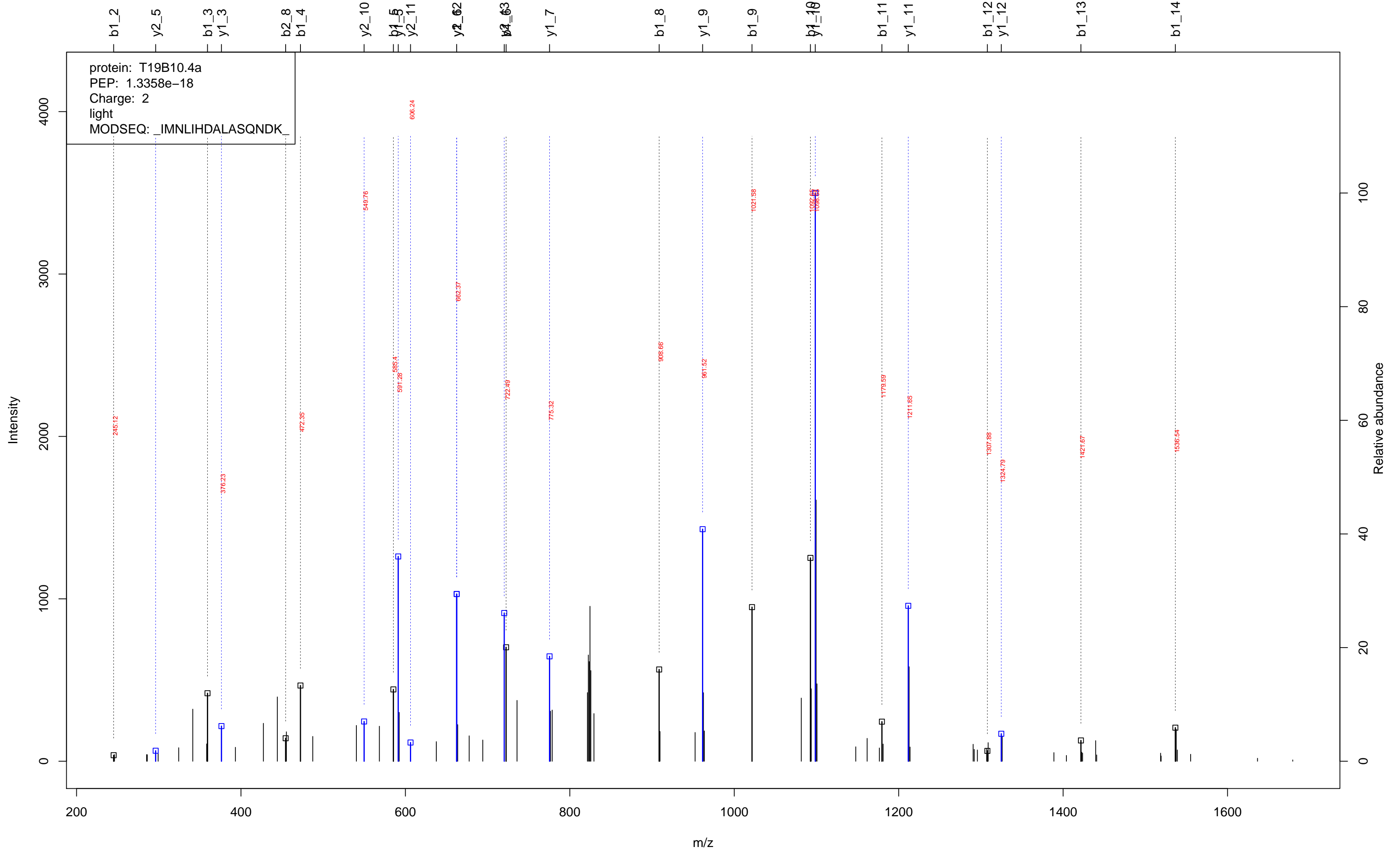
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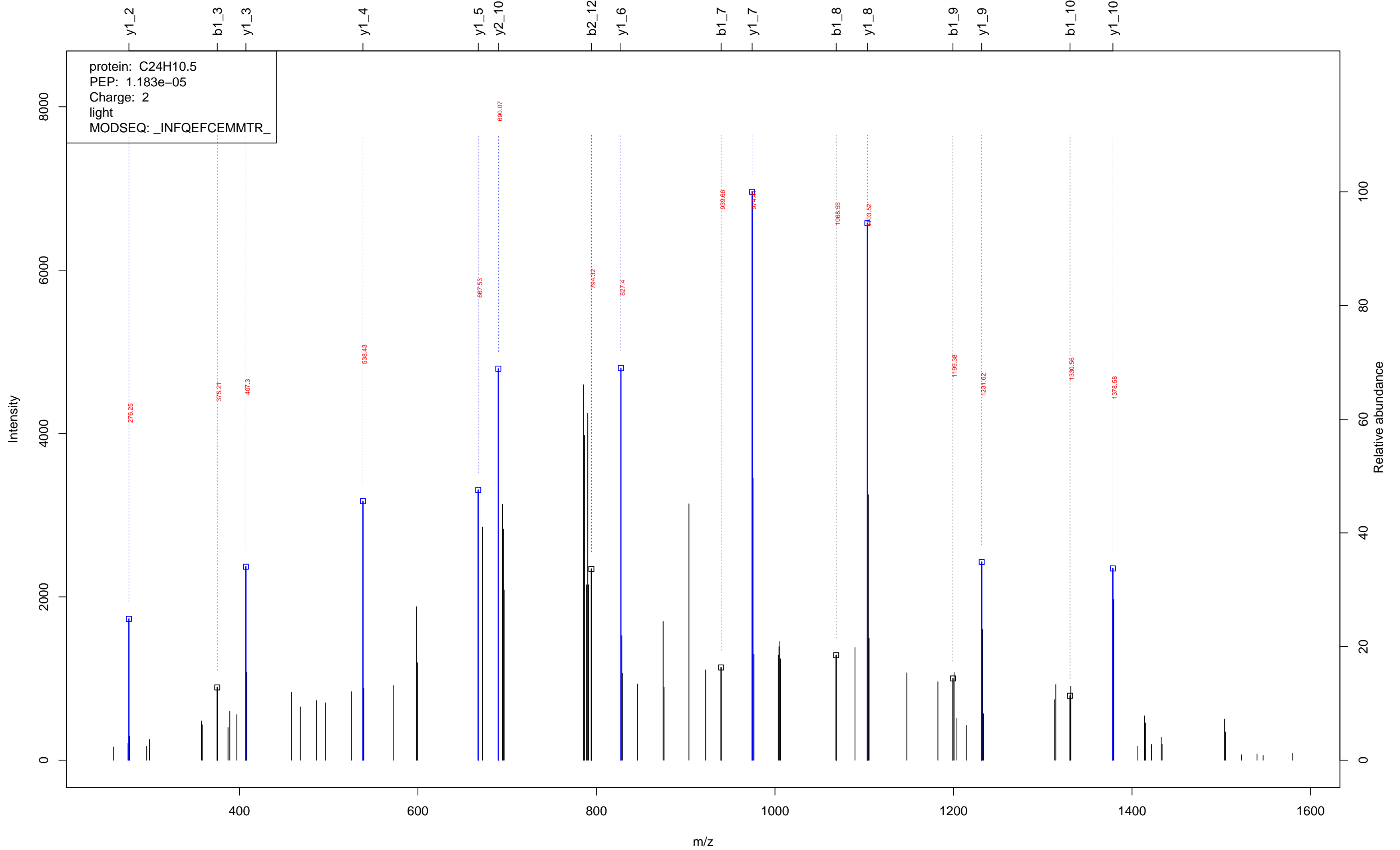


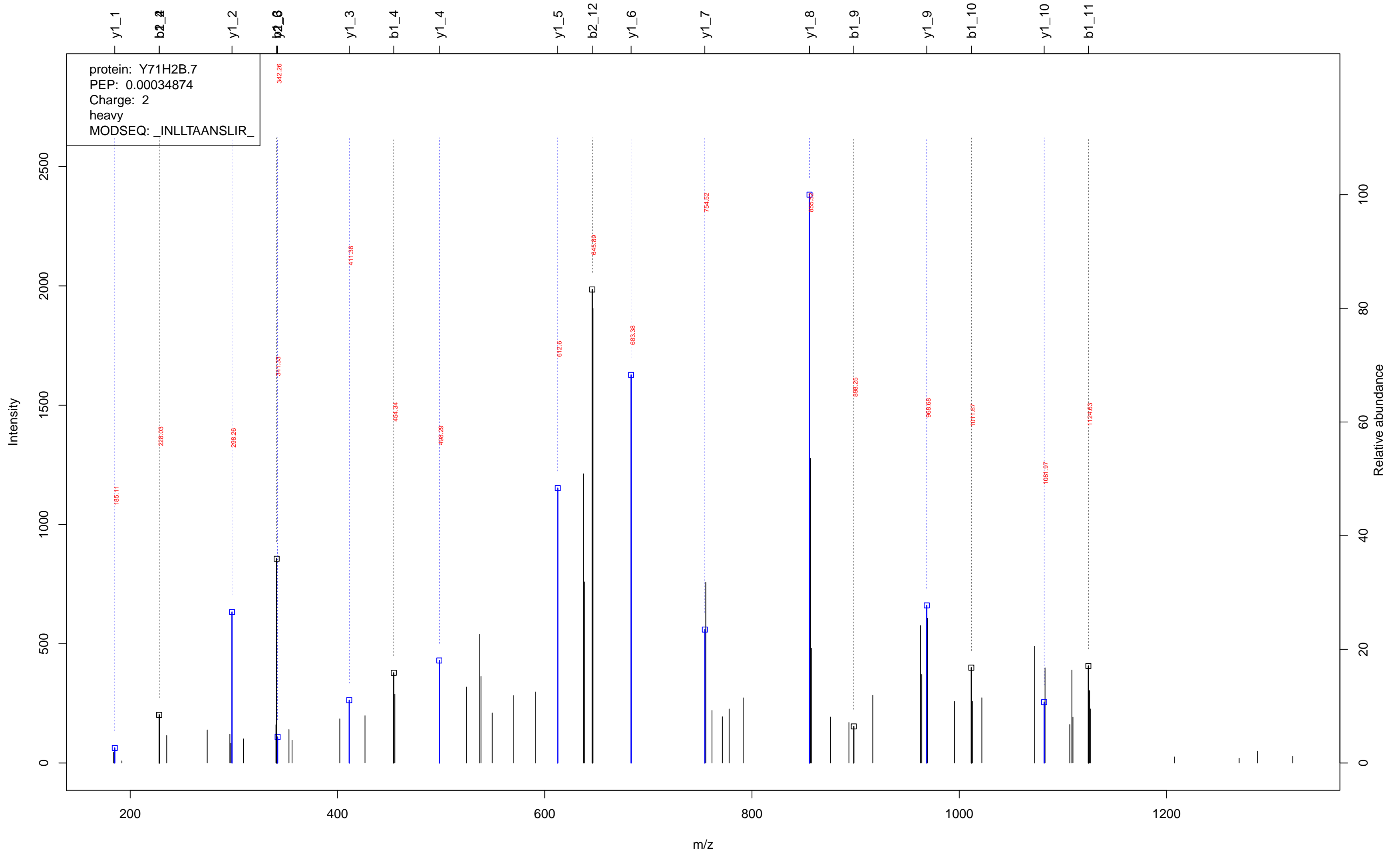


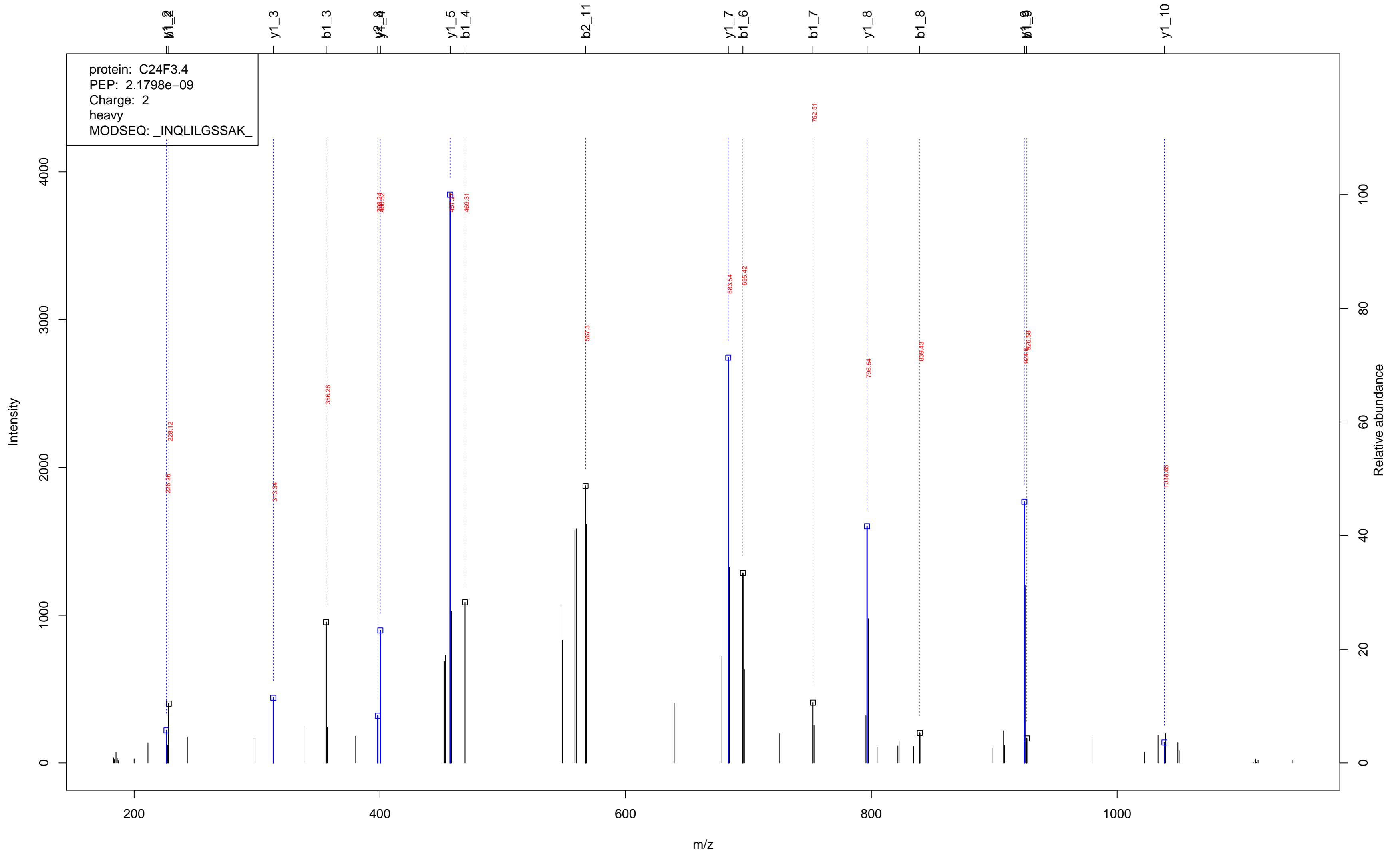


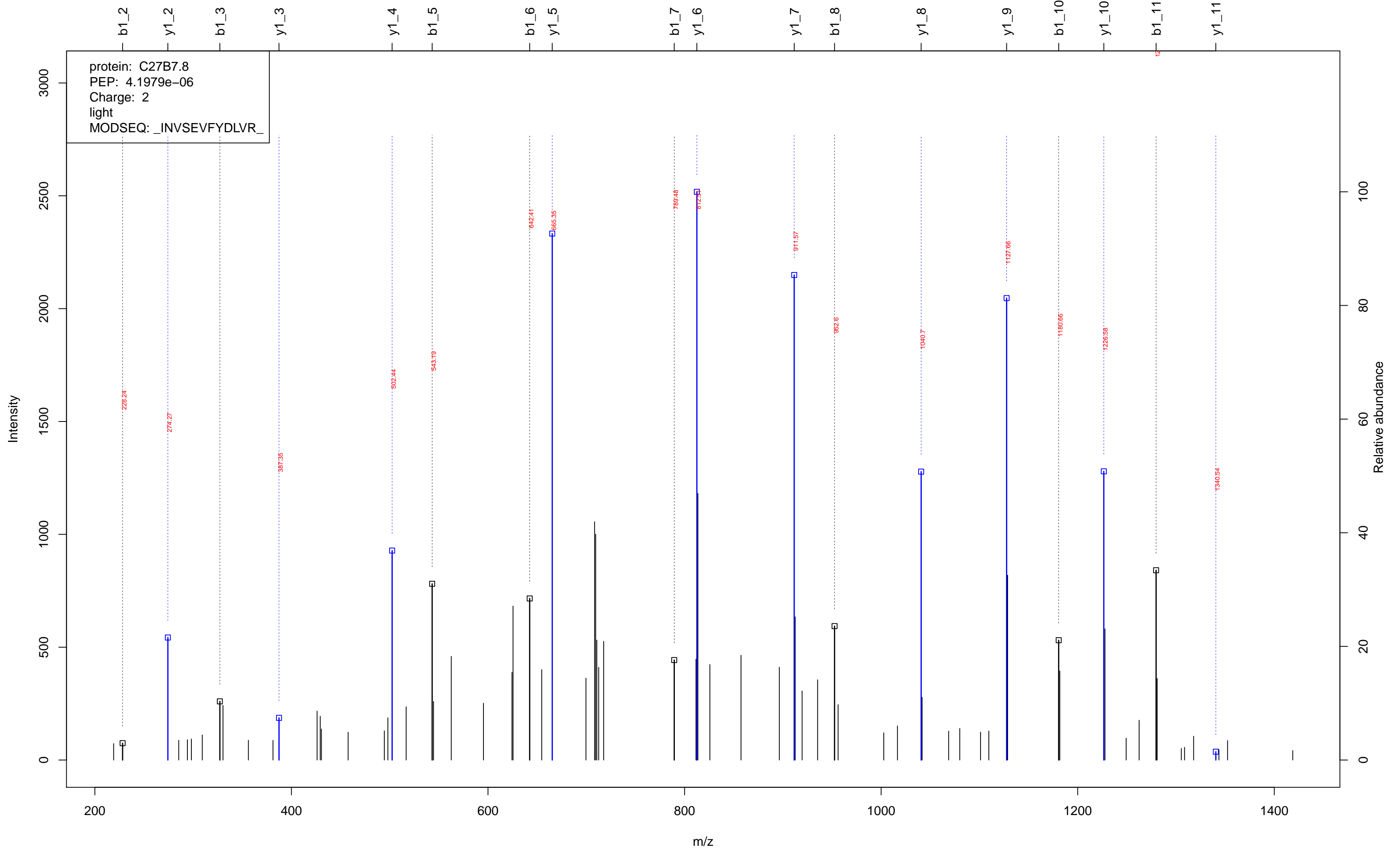


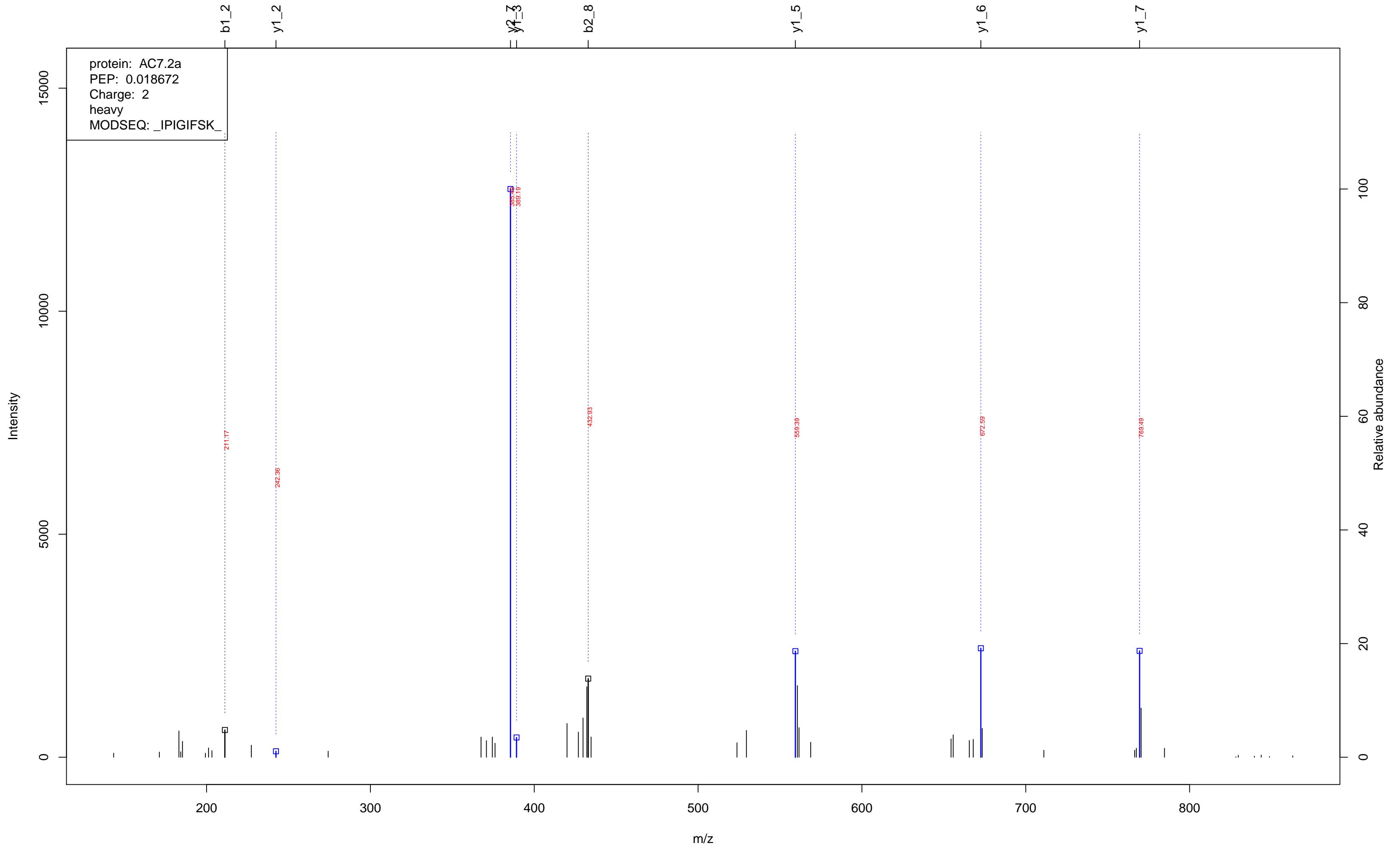


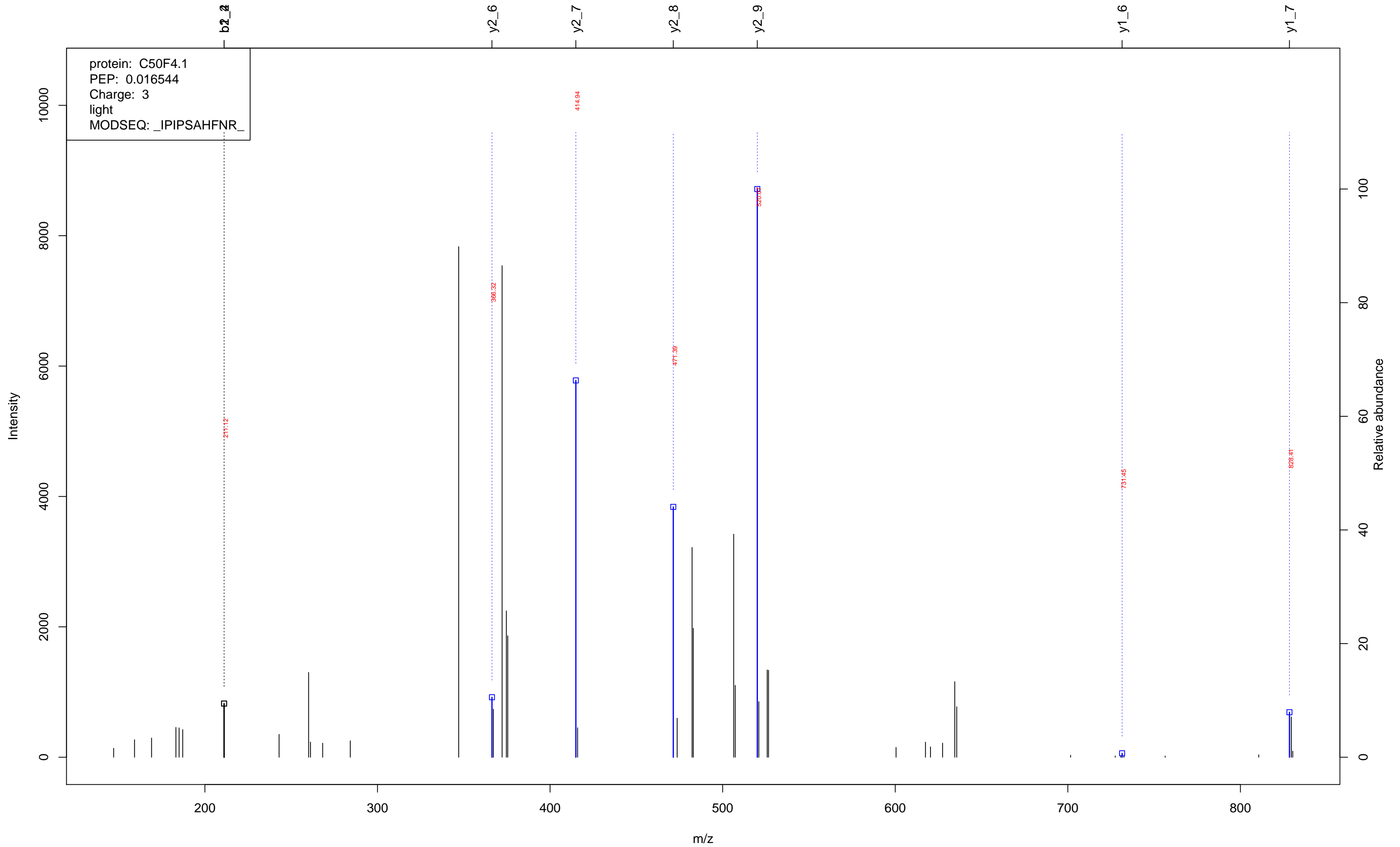


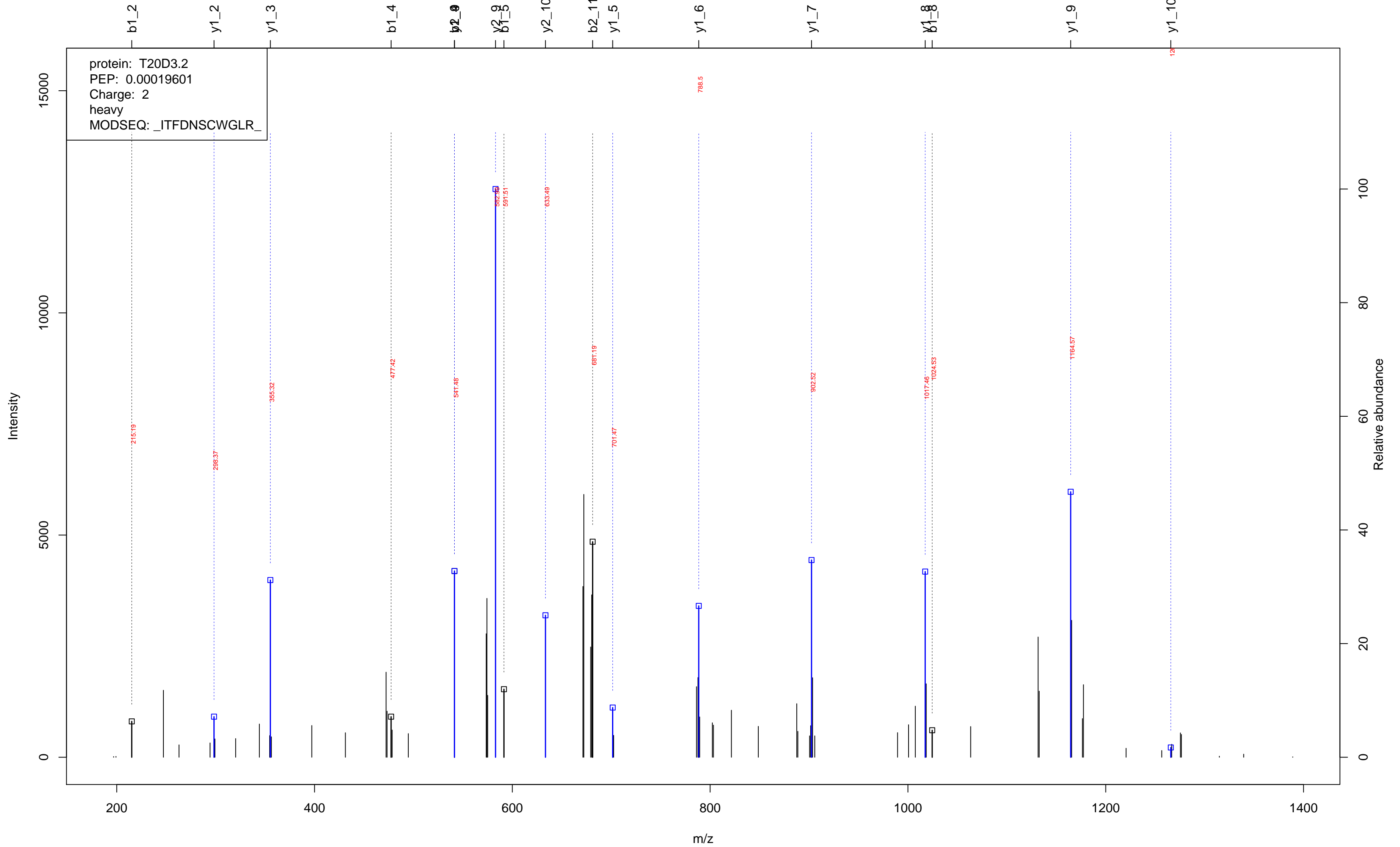


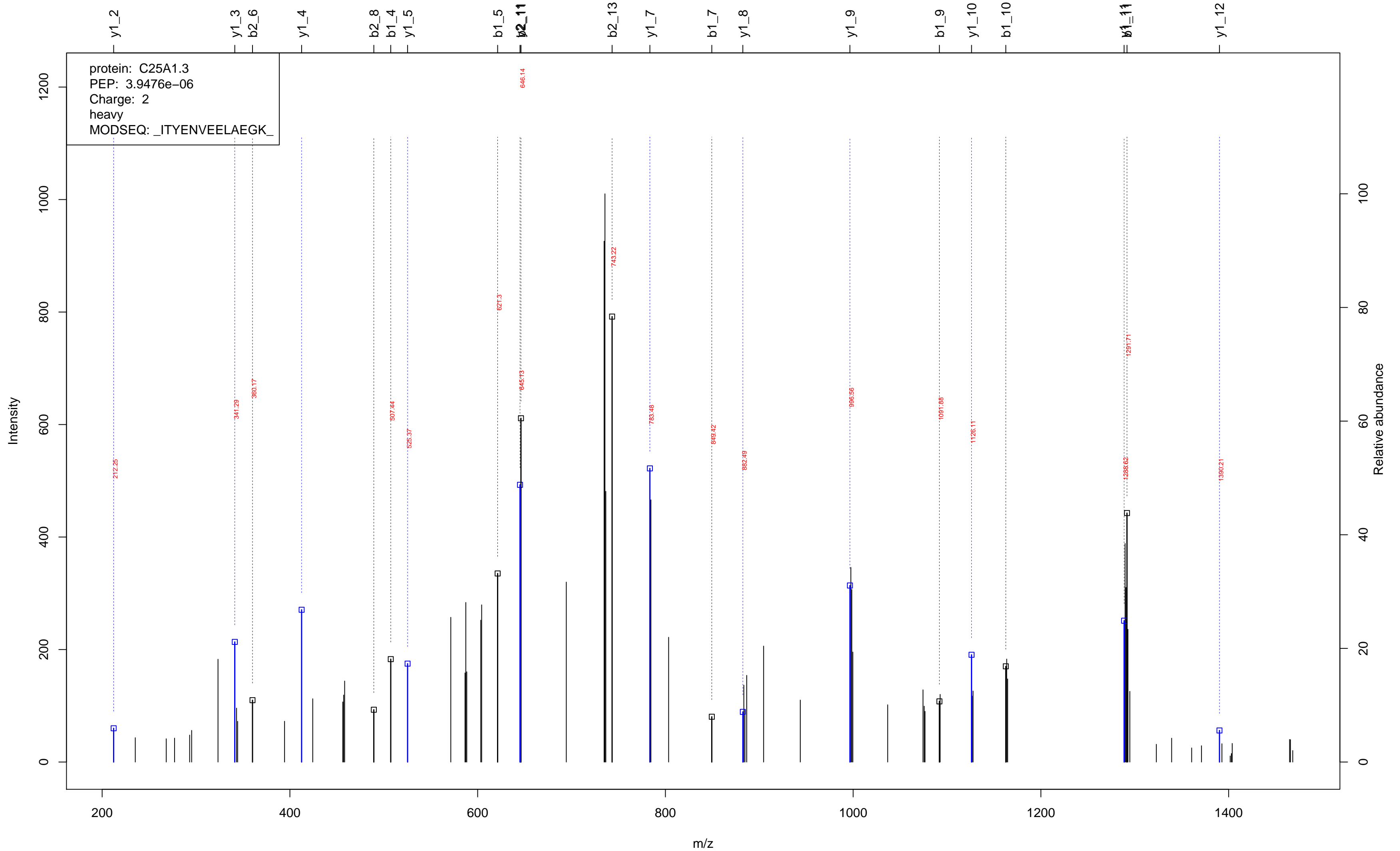


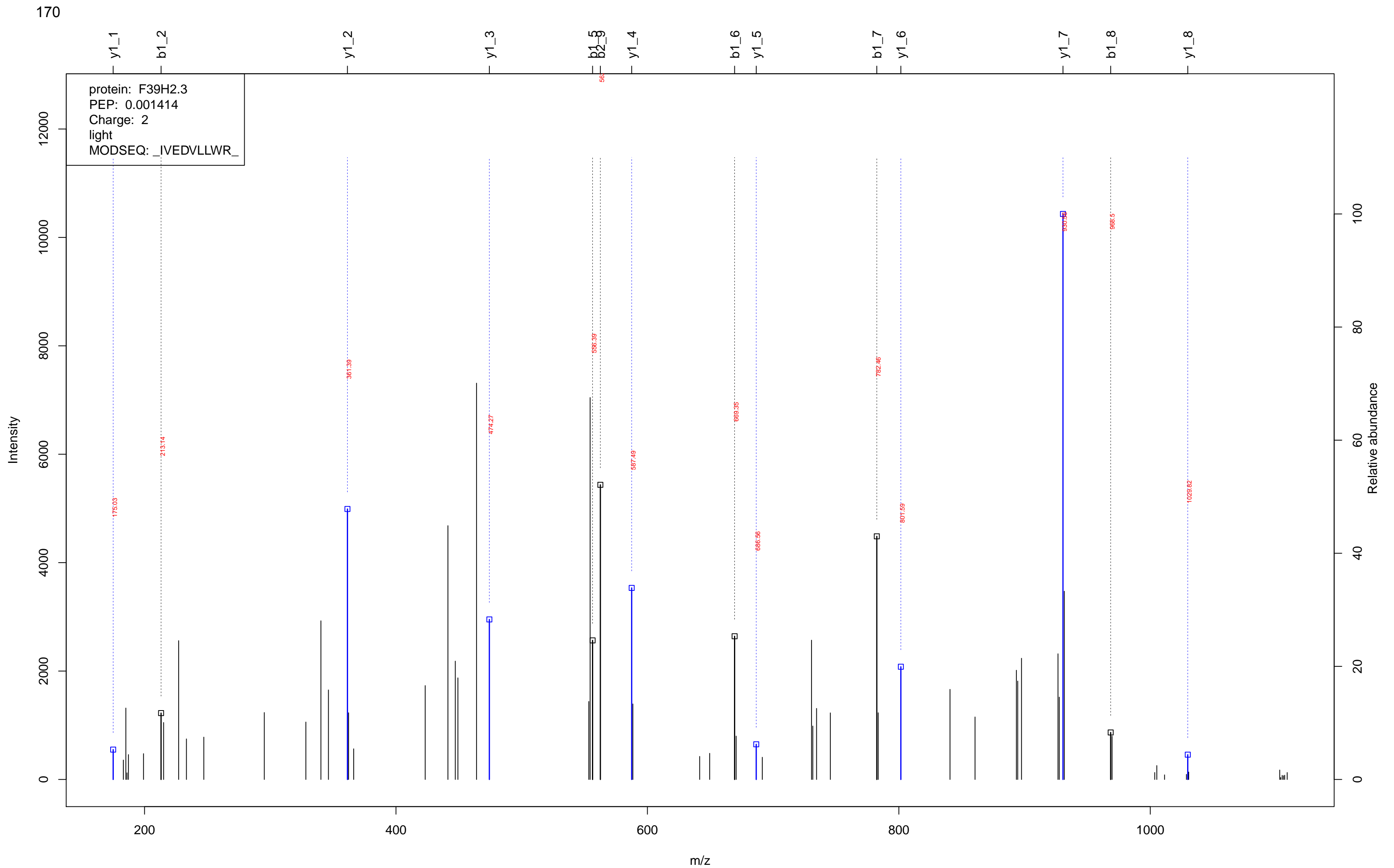


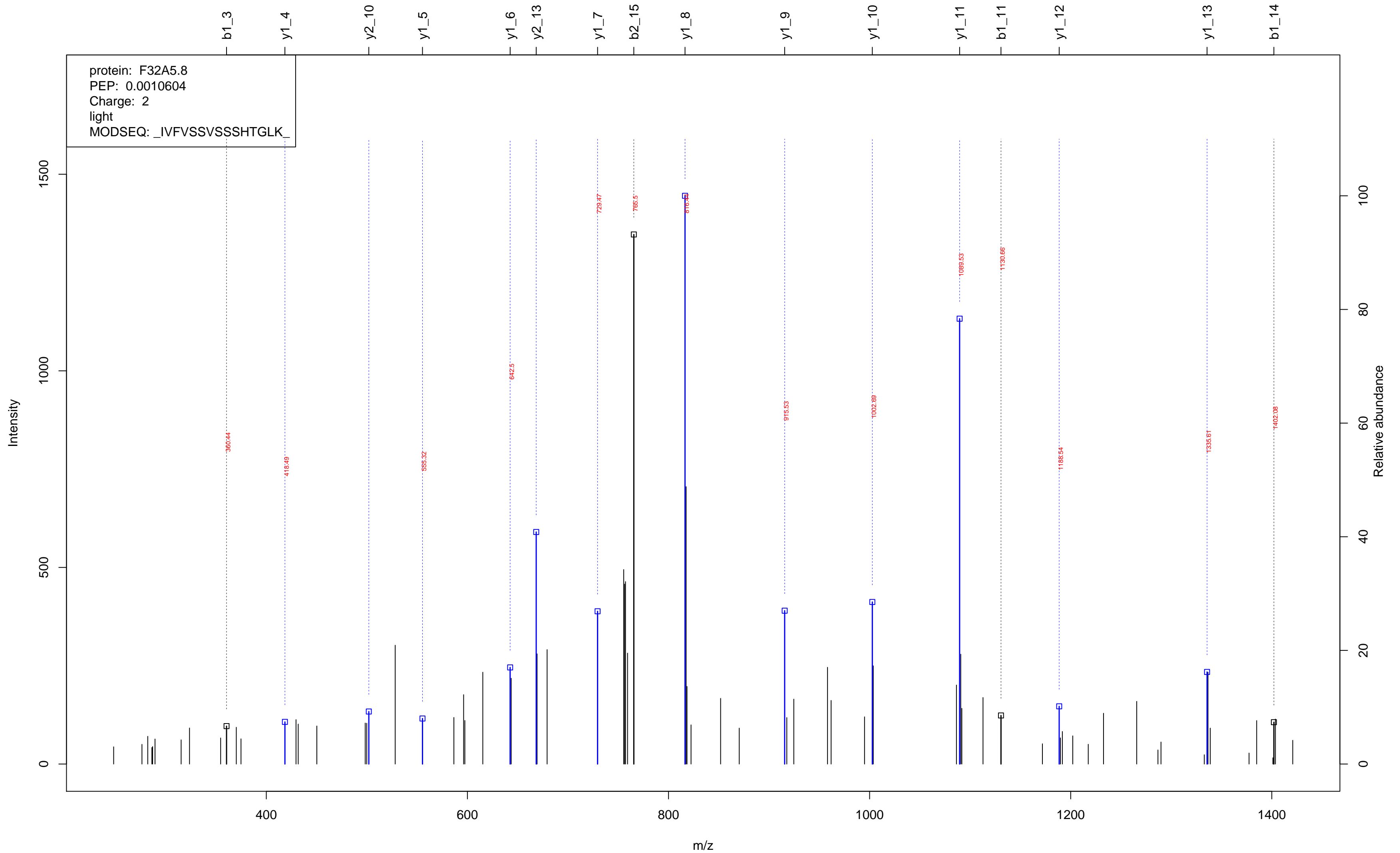


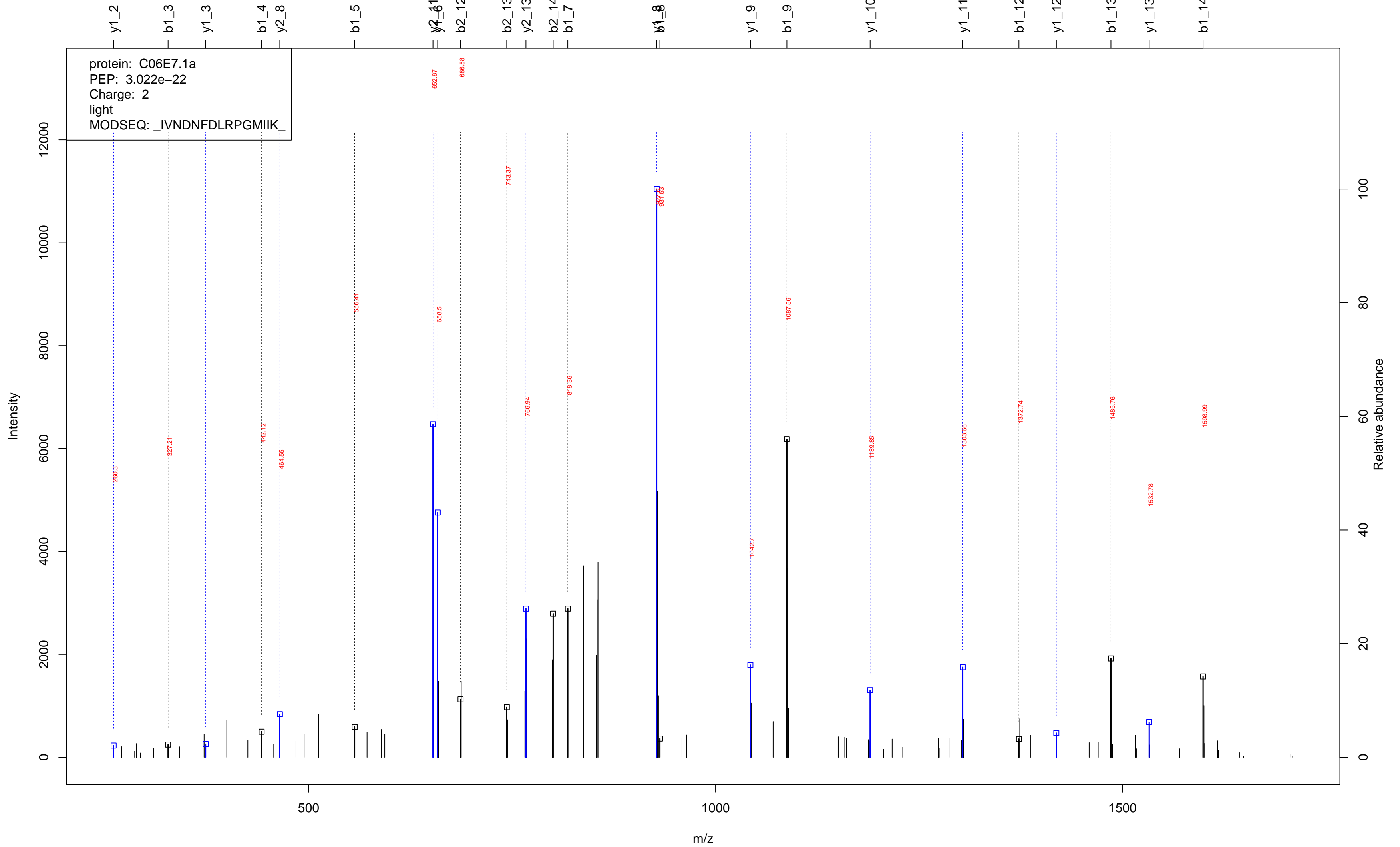


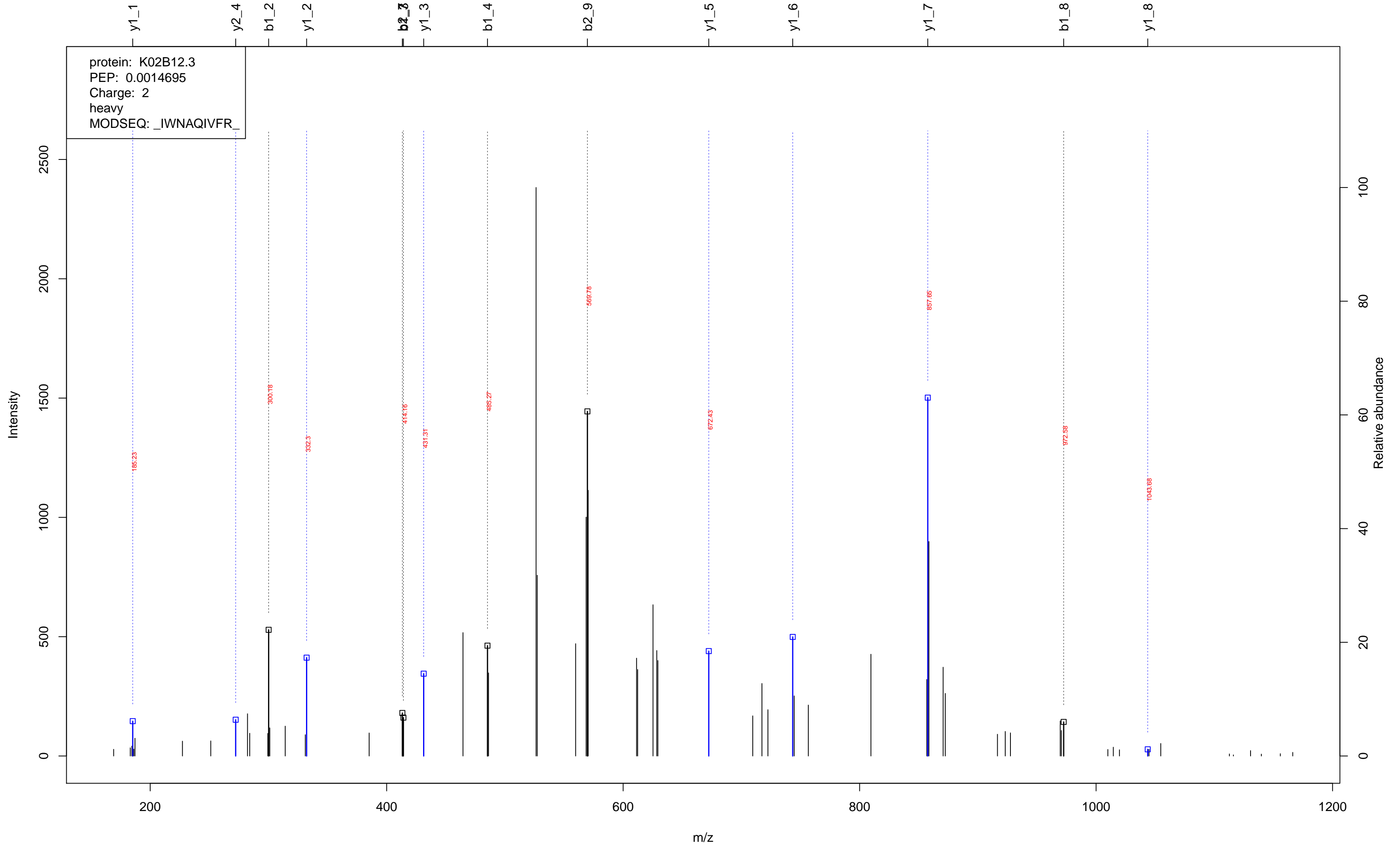


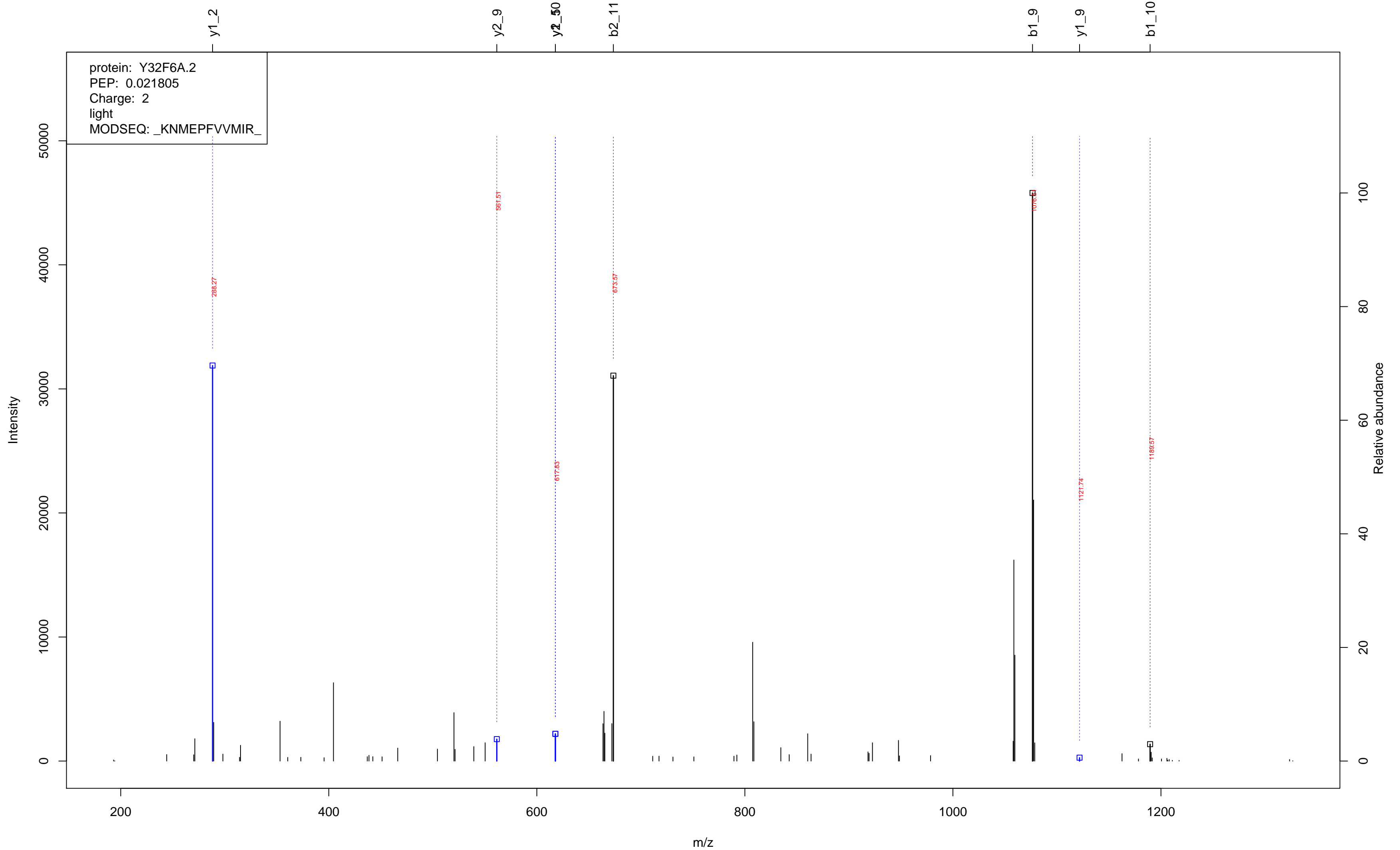


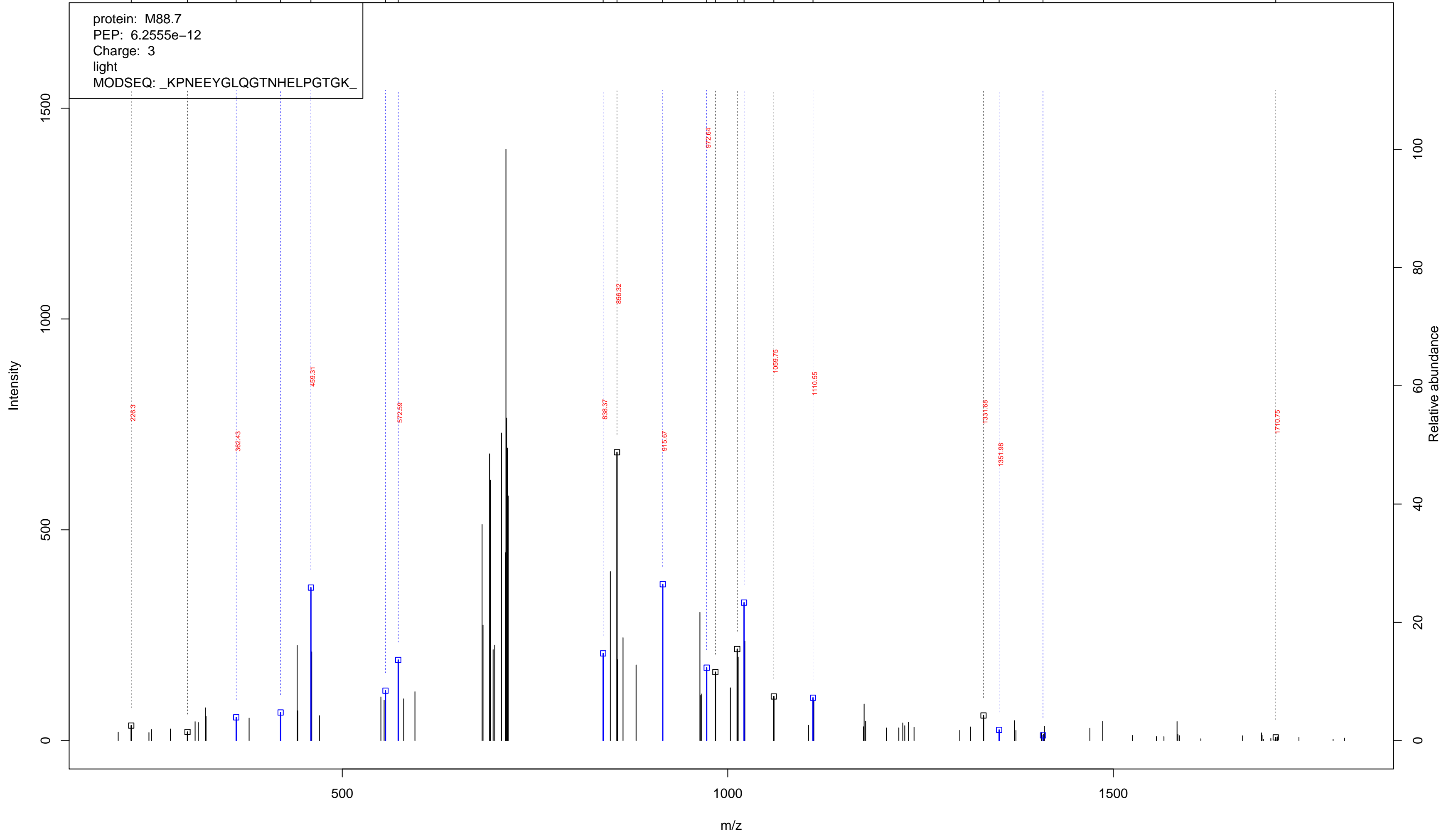


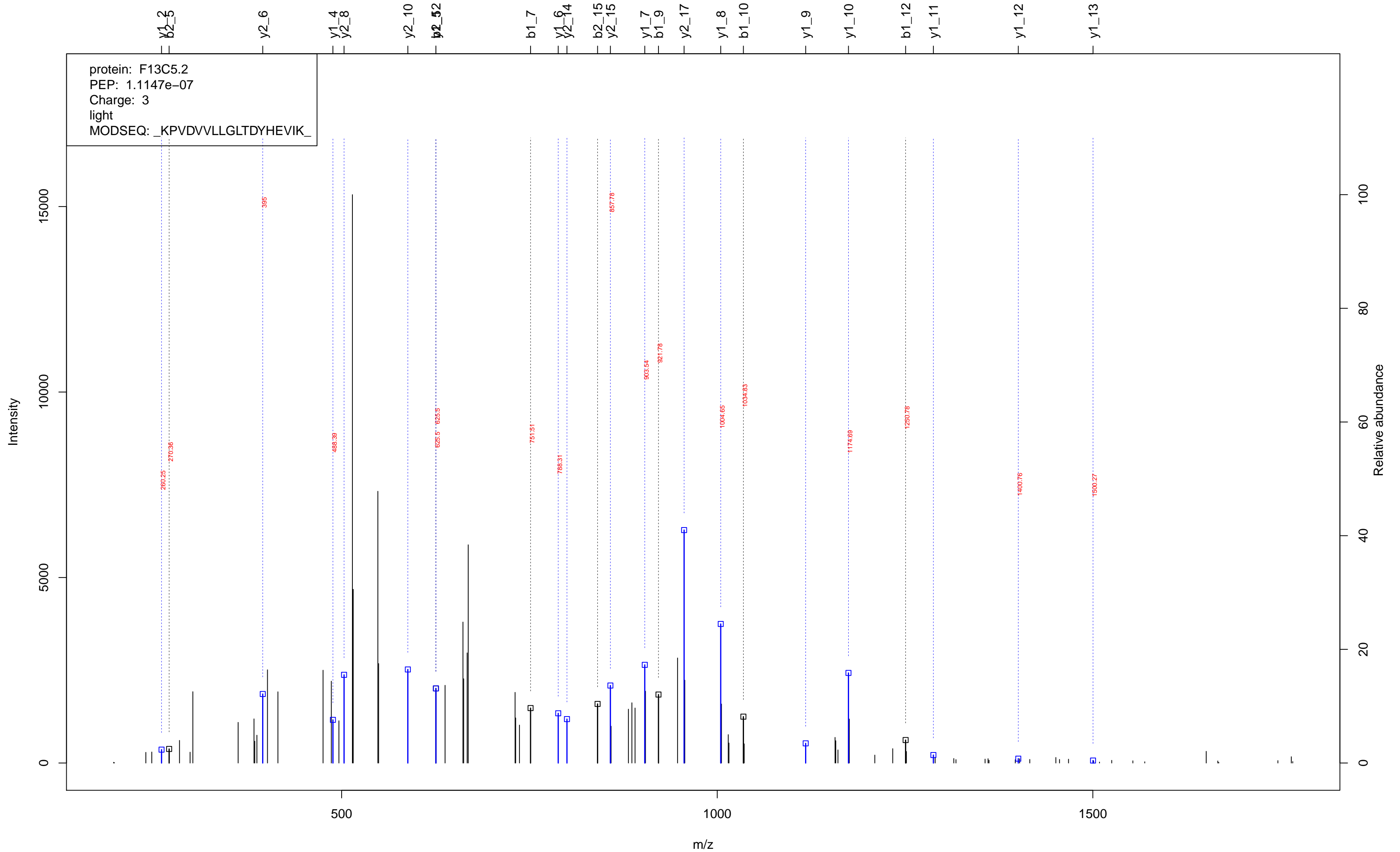


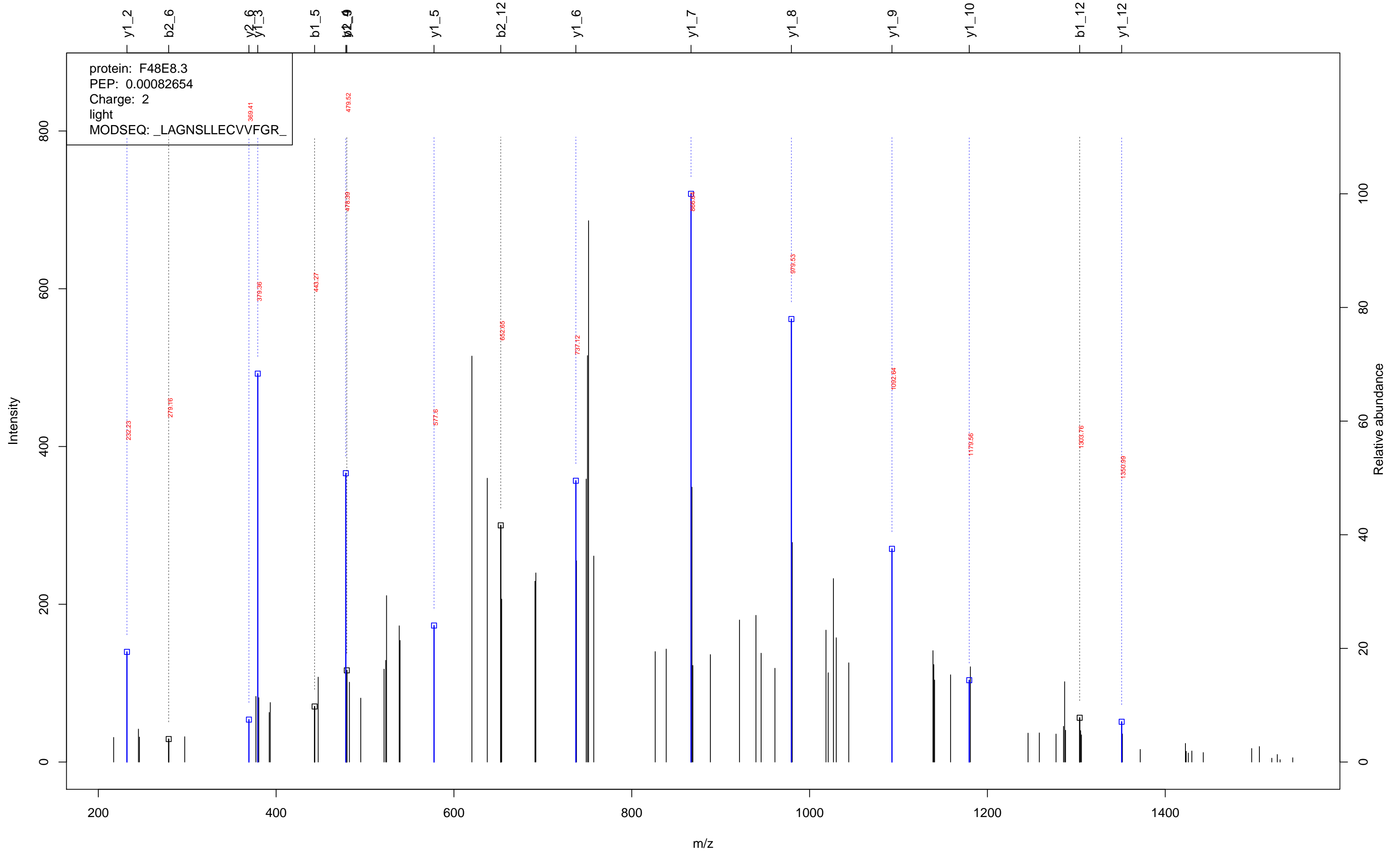


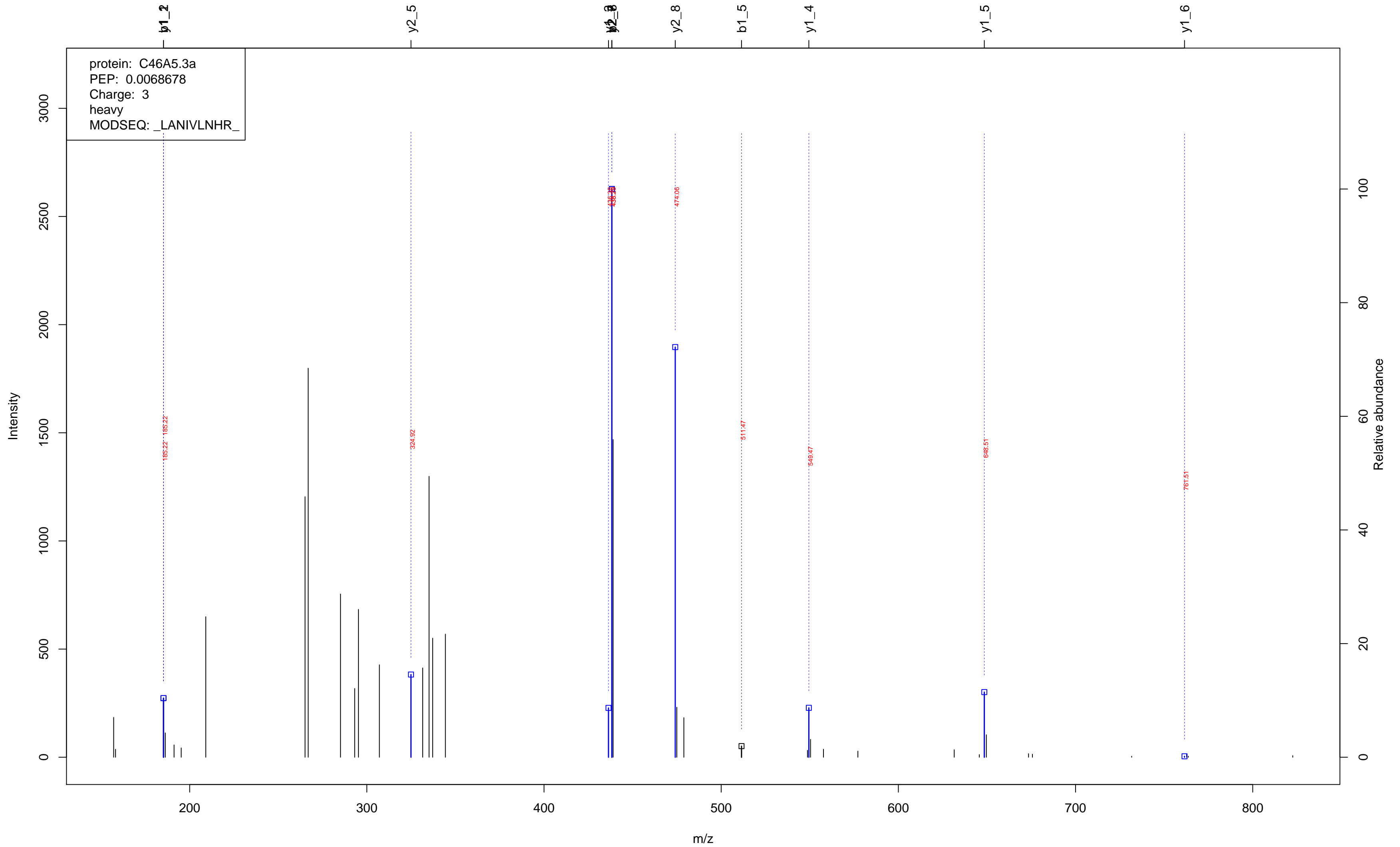


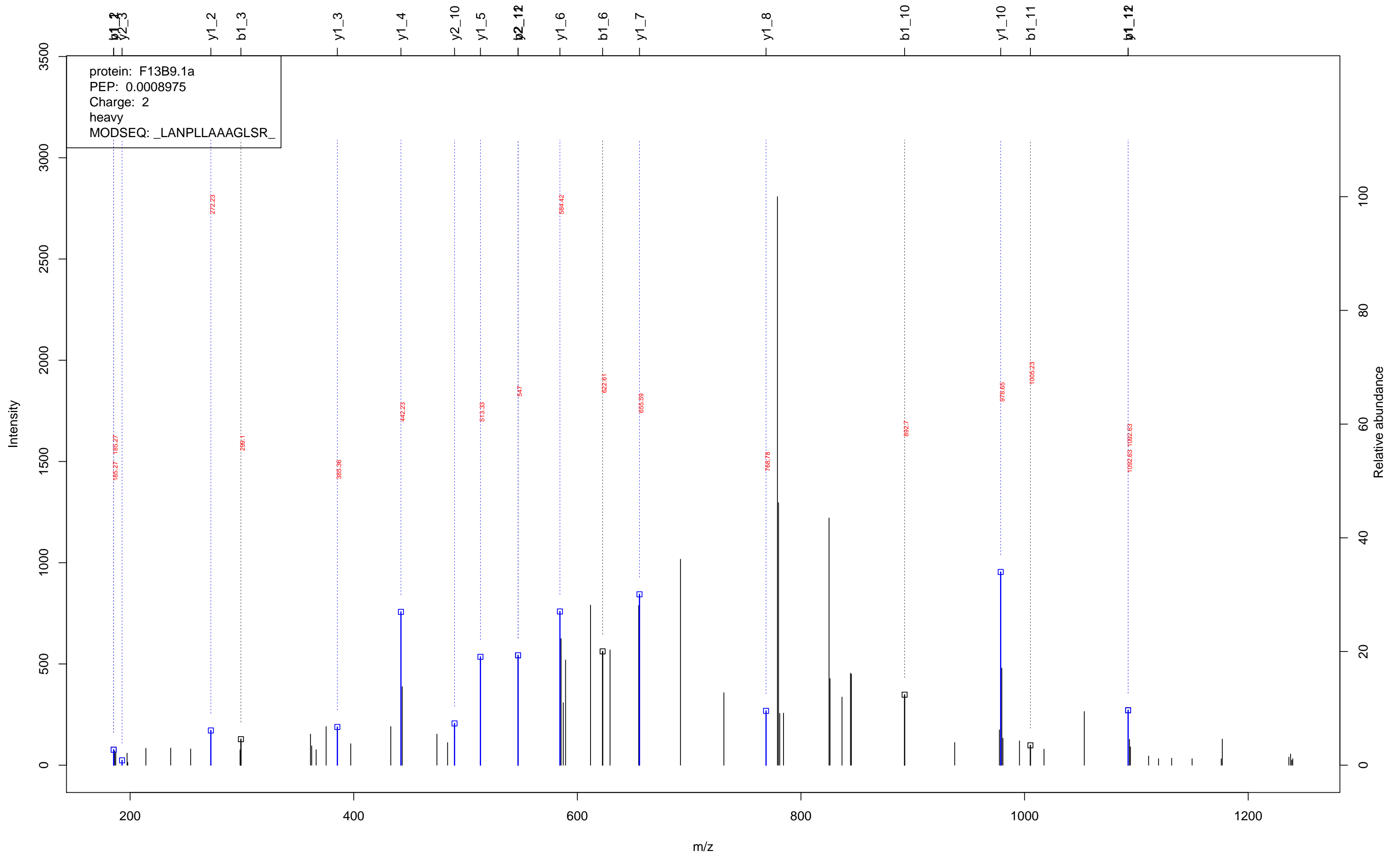








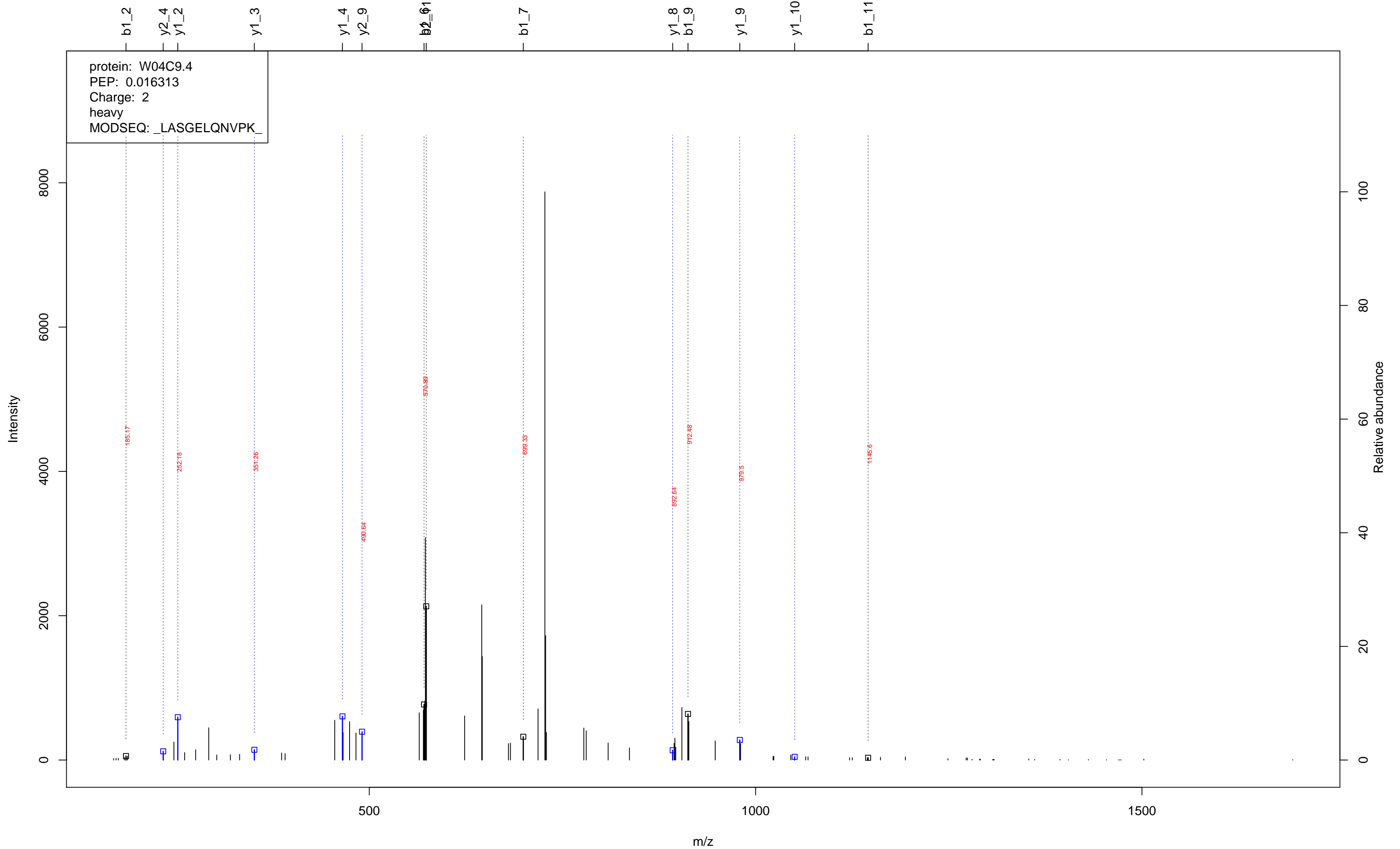


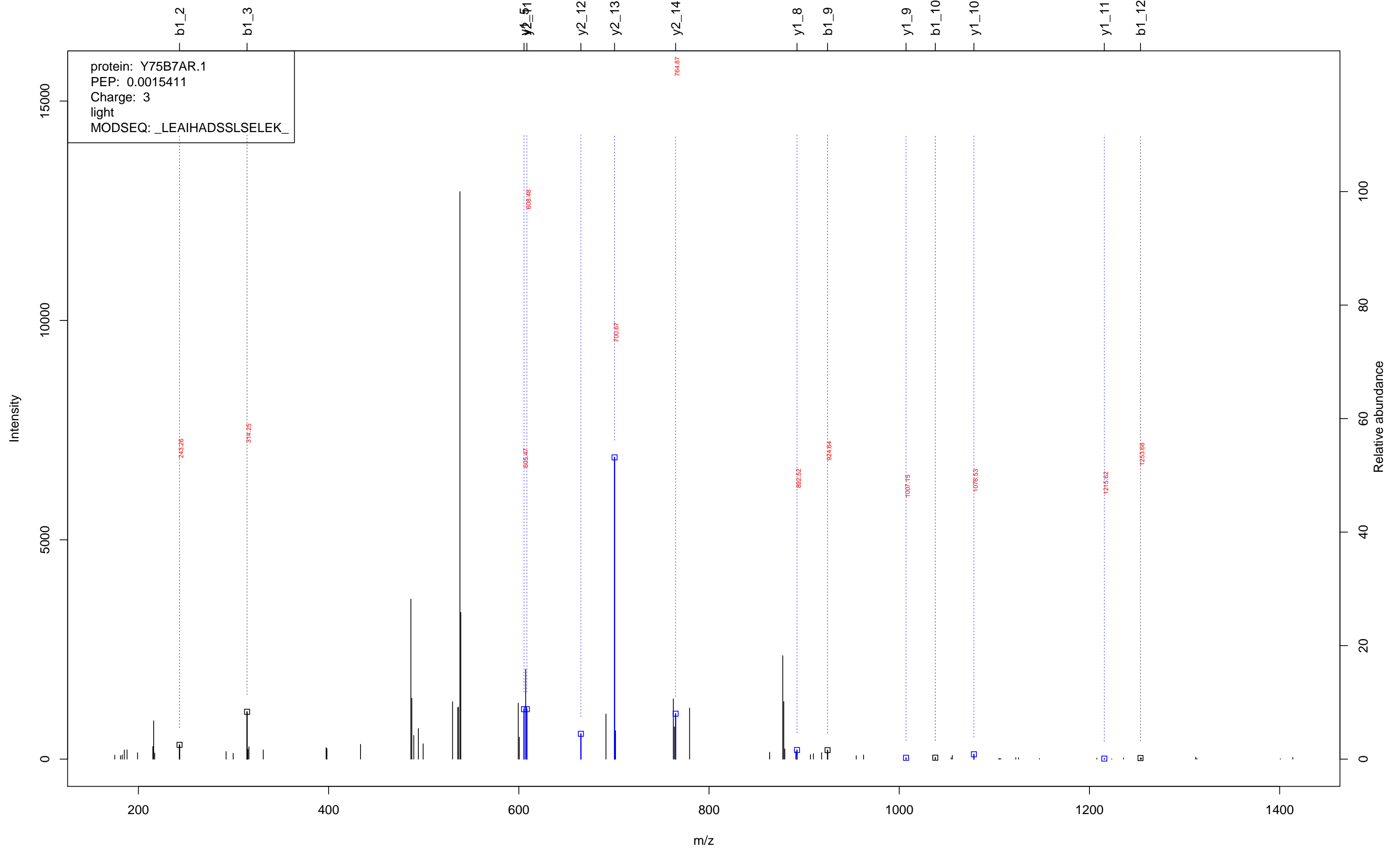


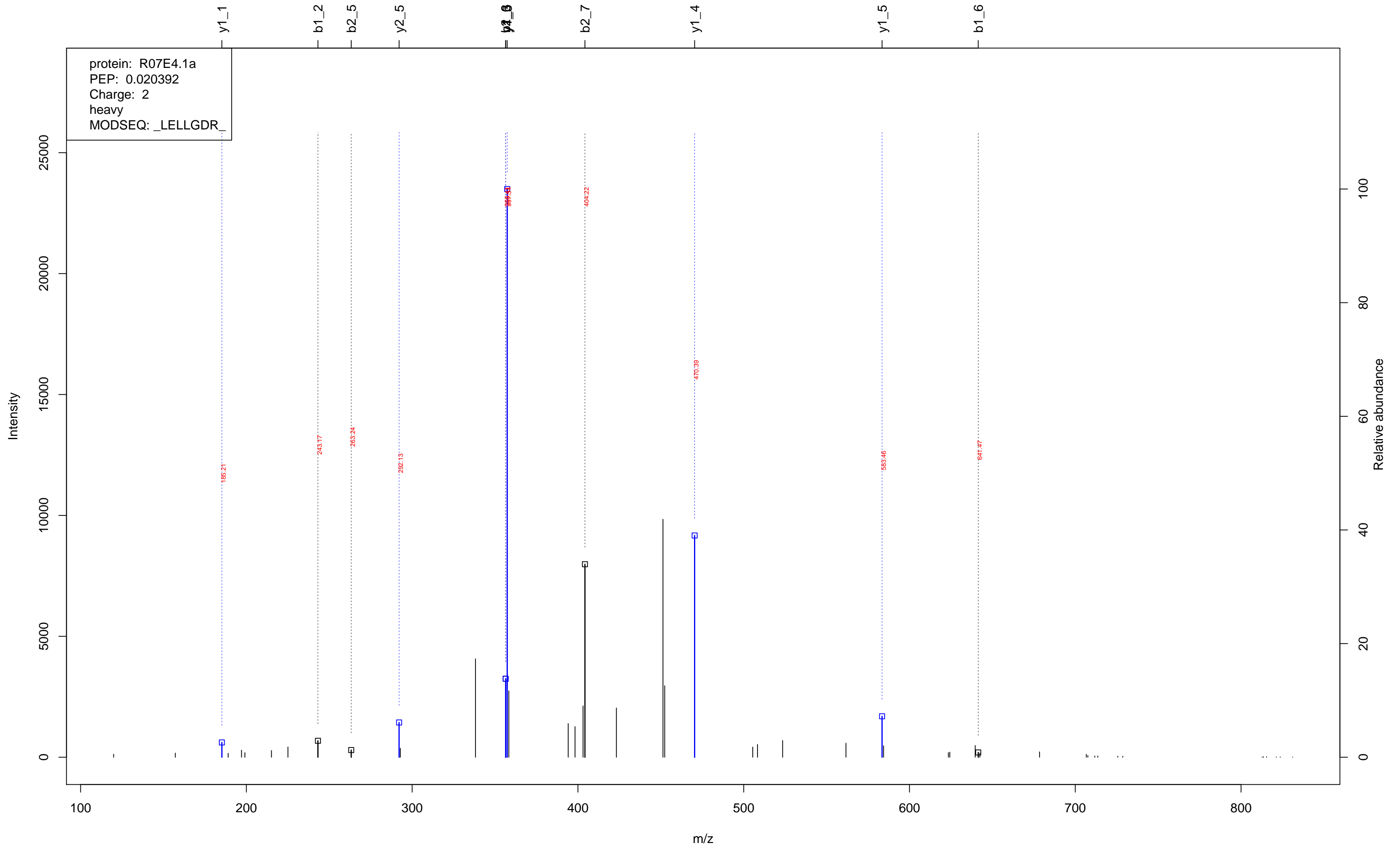
b1_3
y2_3
y1_2
b1_3
y1_3
y1_4
y2_10
y1_5
b2_12
y1_6
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y1_7
y1_8
b1_10
y1_10
b1_11
b1_12

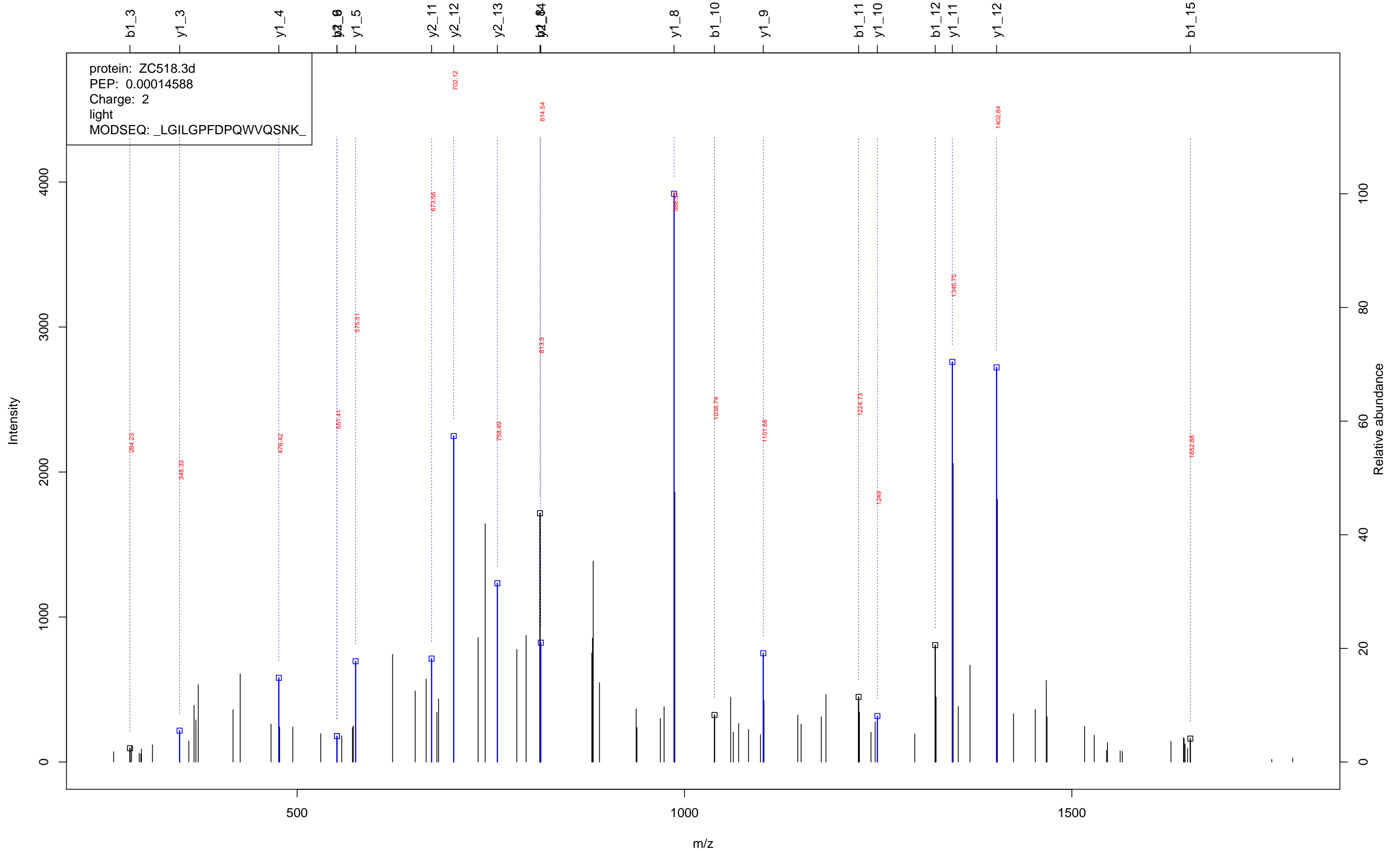
185.27
186.27
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299.1
385.36
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622.61
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978.65
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1092.63
1092.63

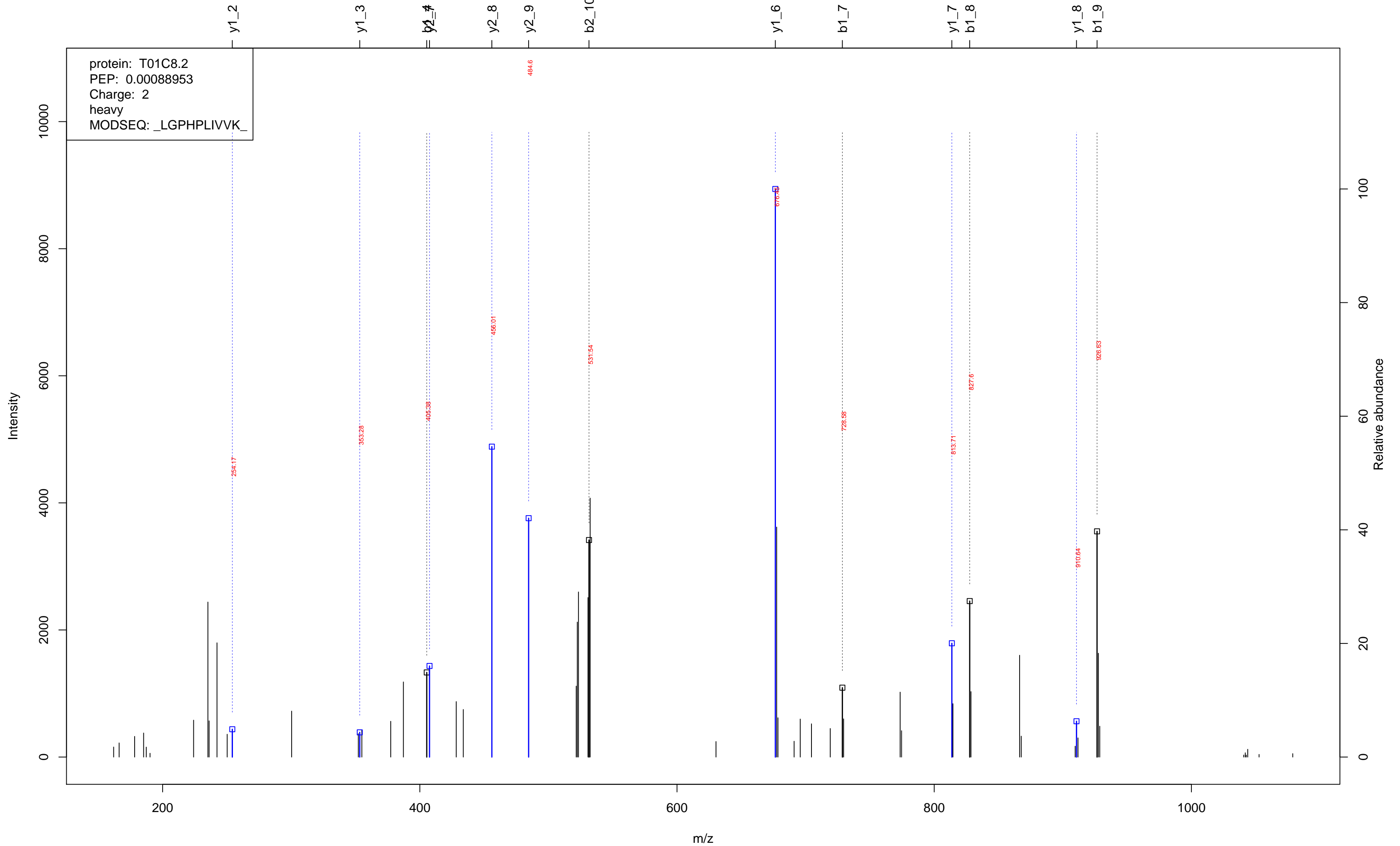
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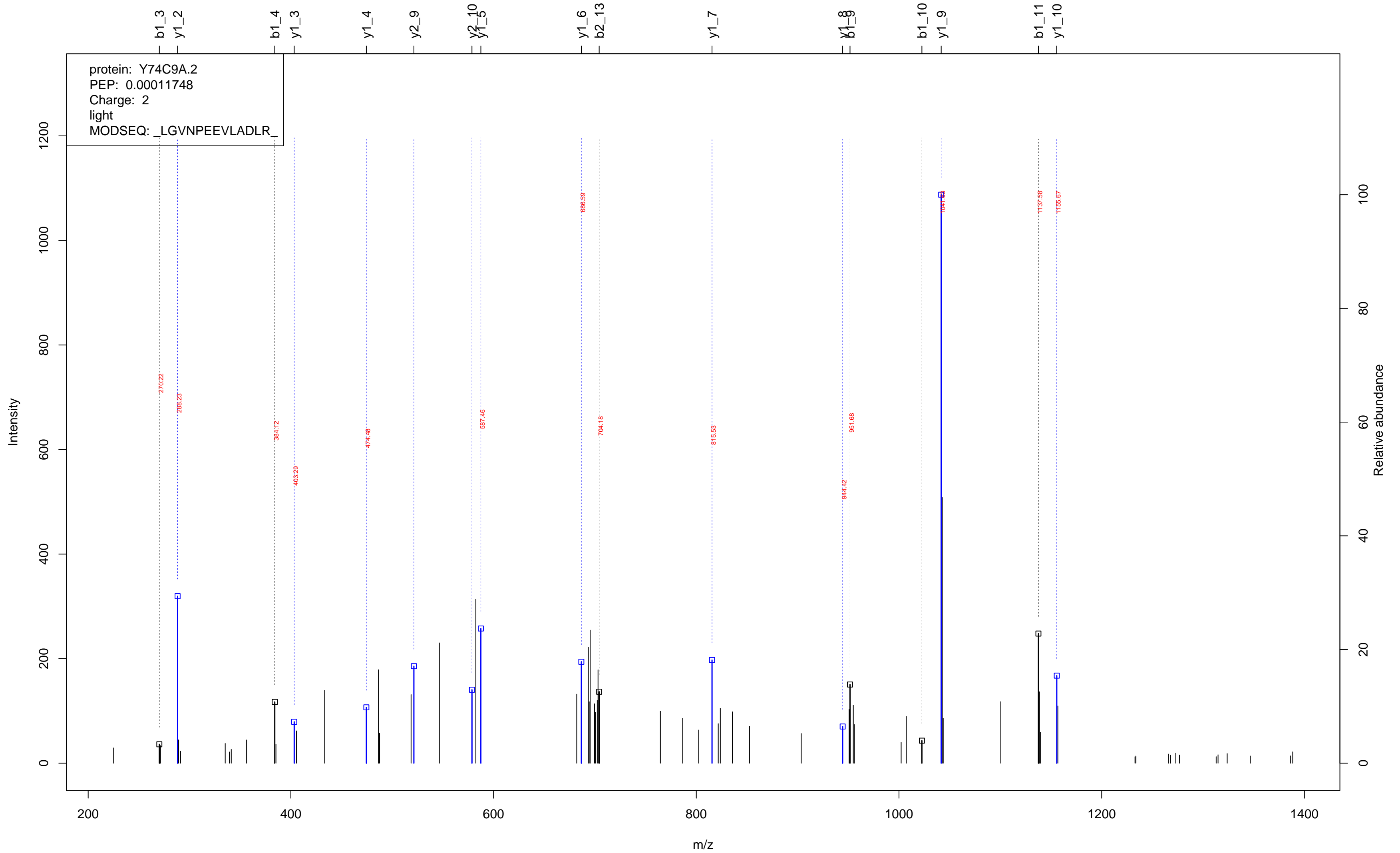


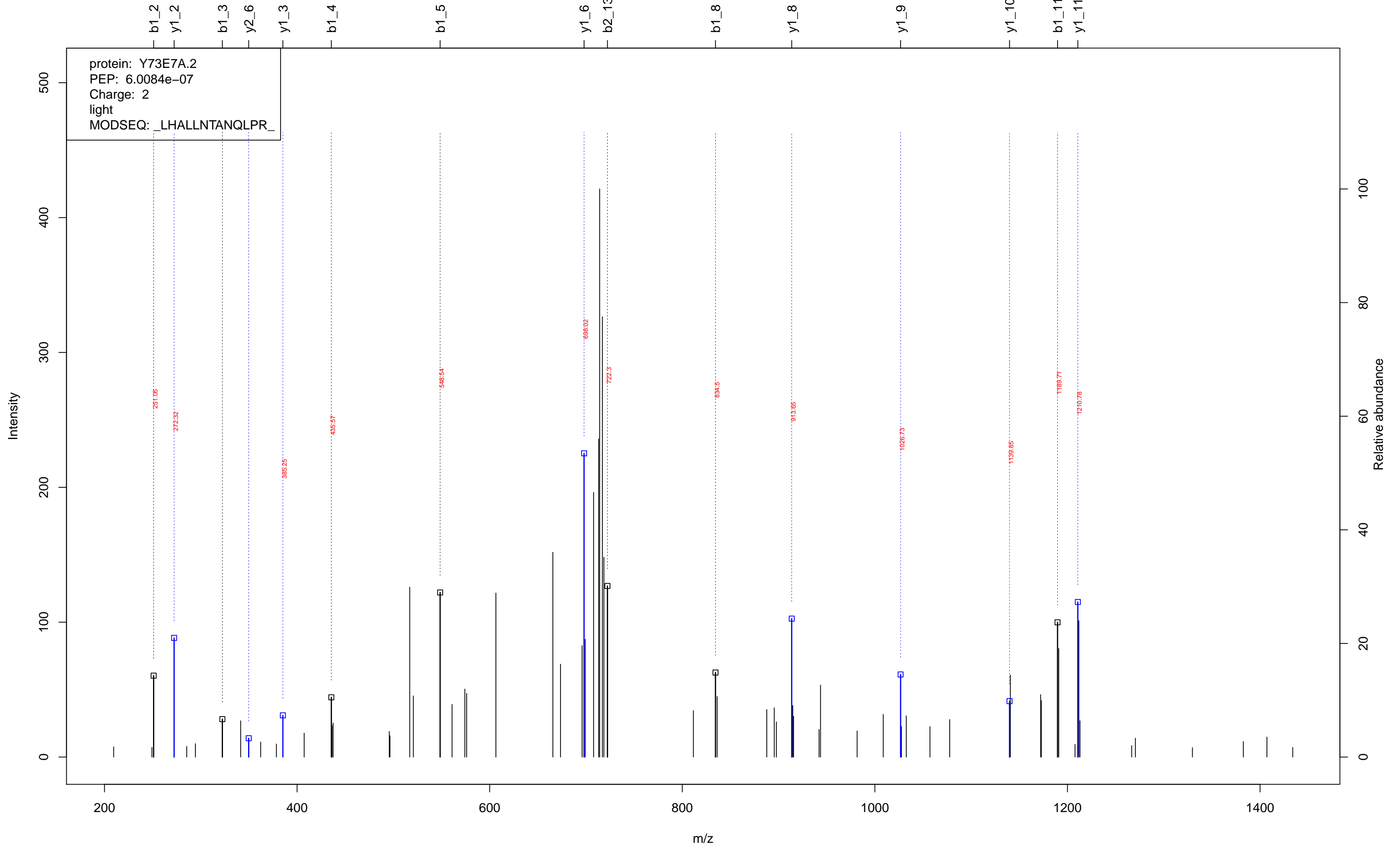


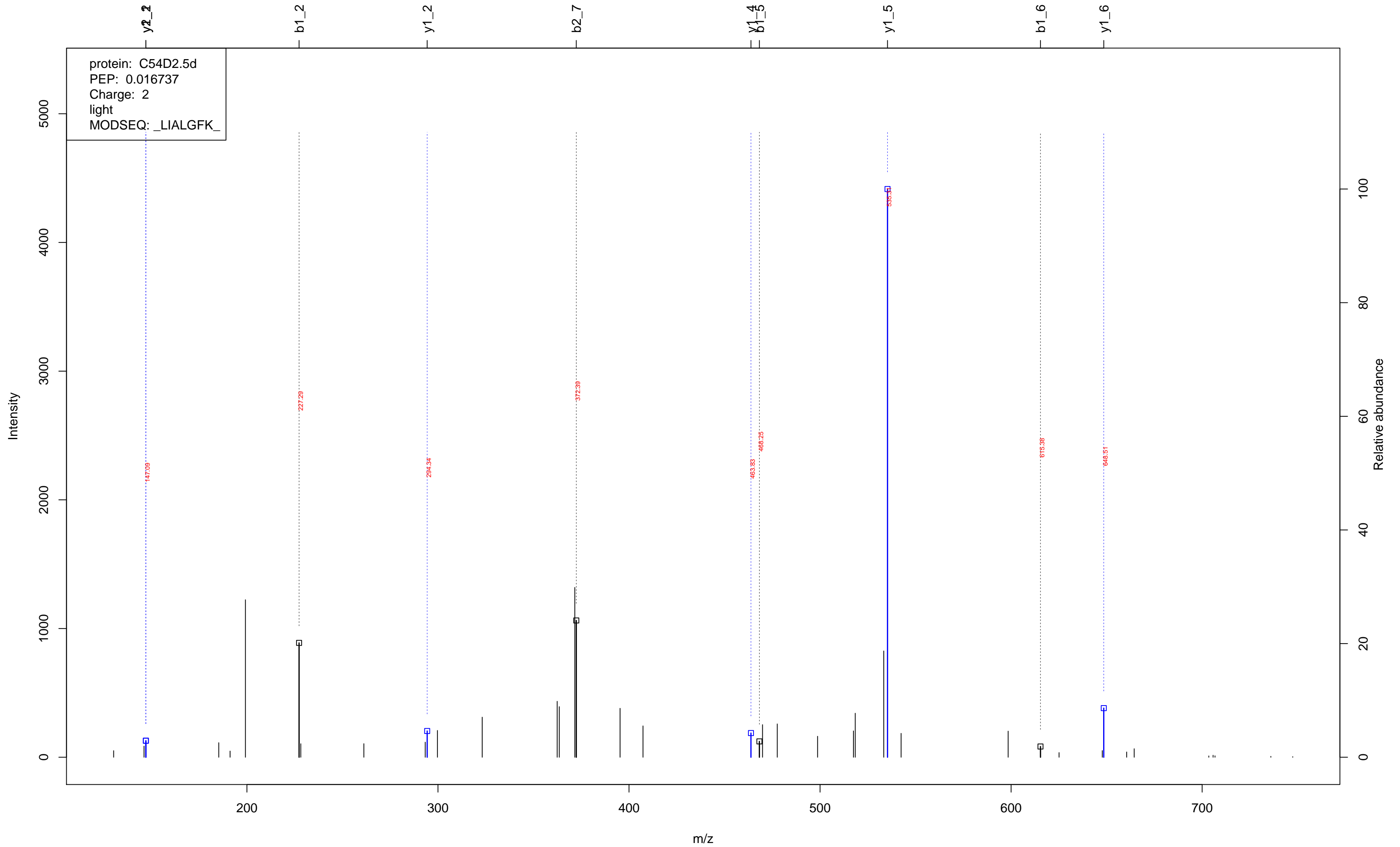






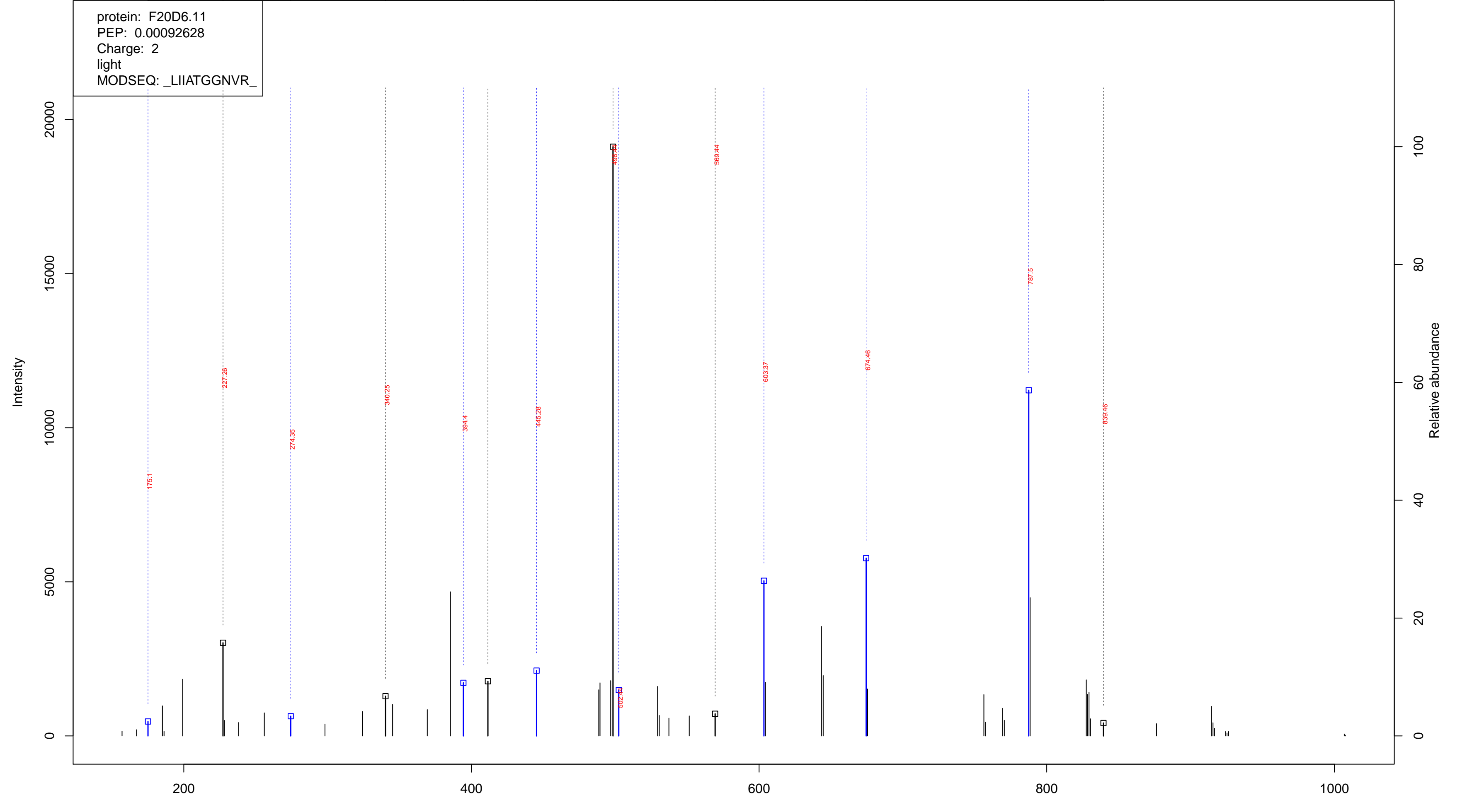


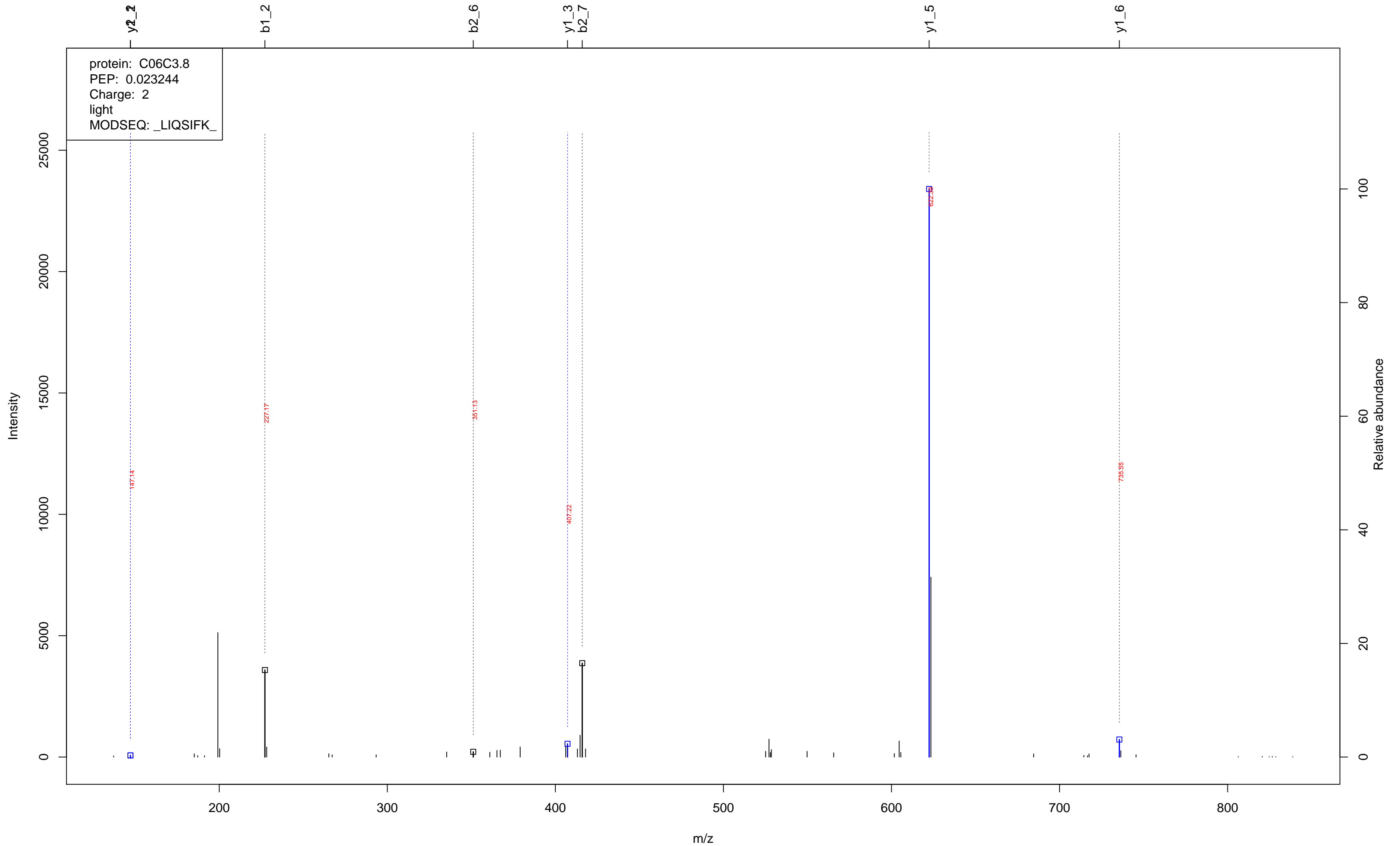


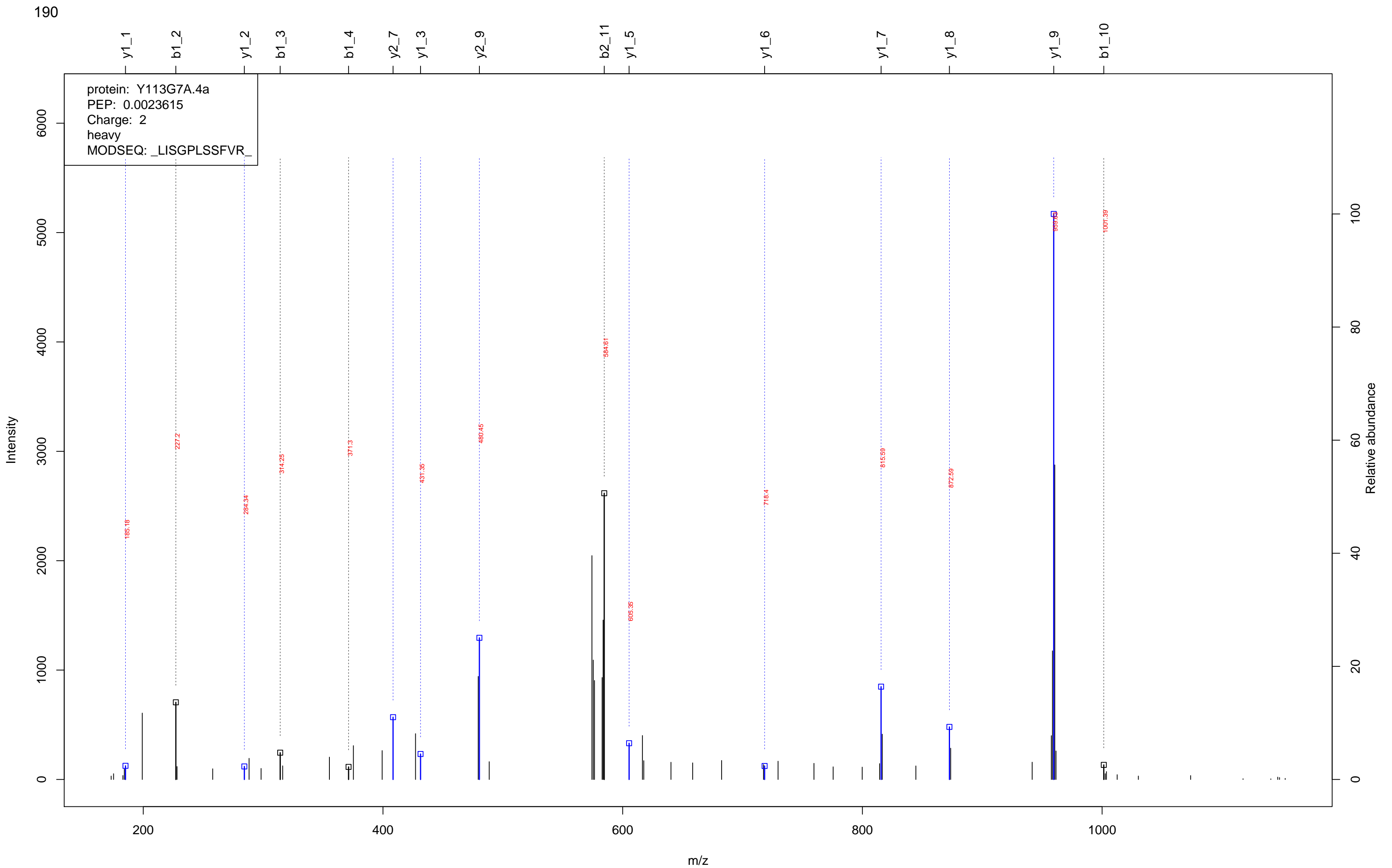


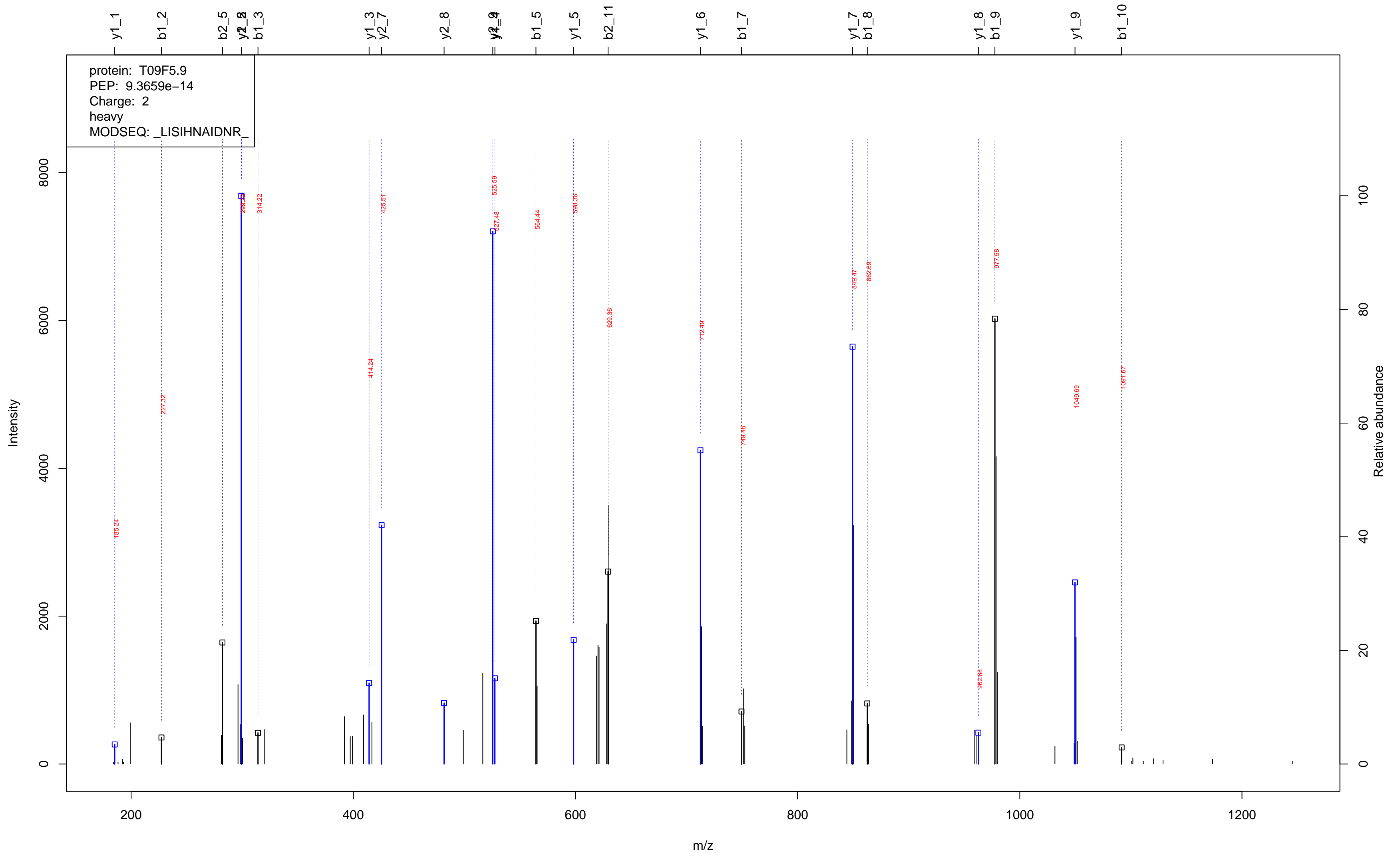
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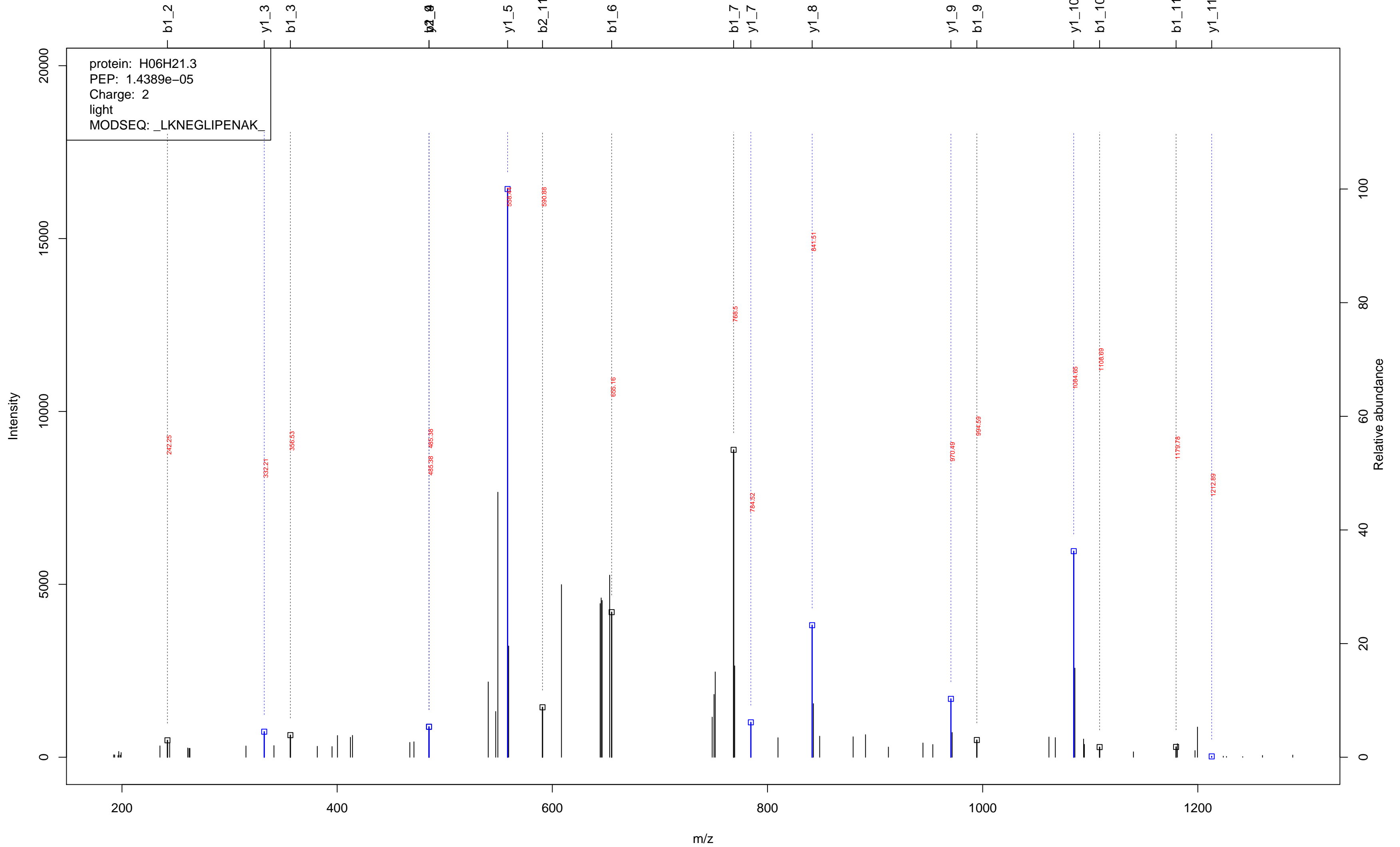
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Charge: 2
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MODSEQ: _LIATGGNVR_

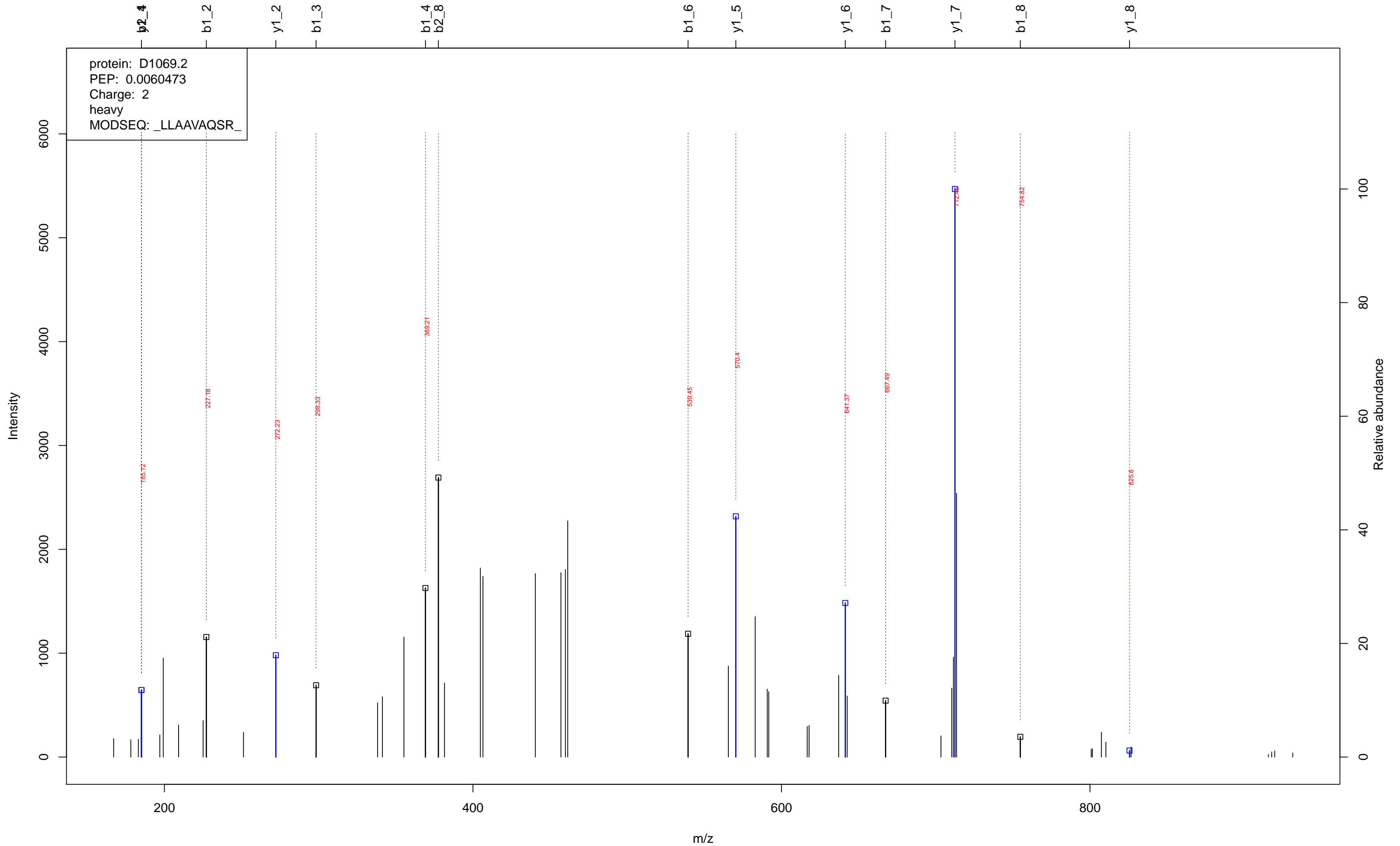


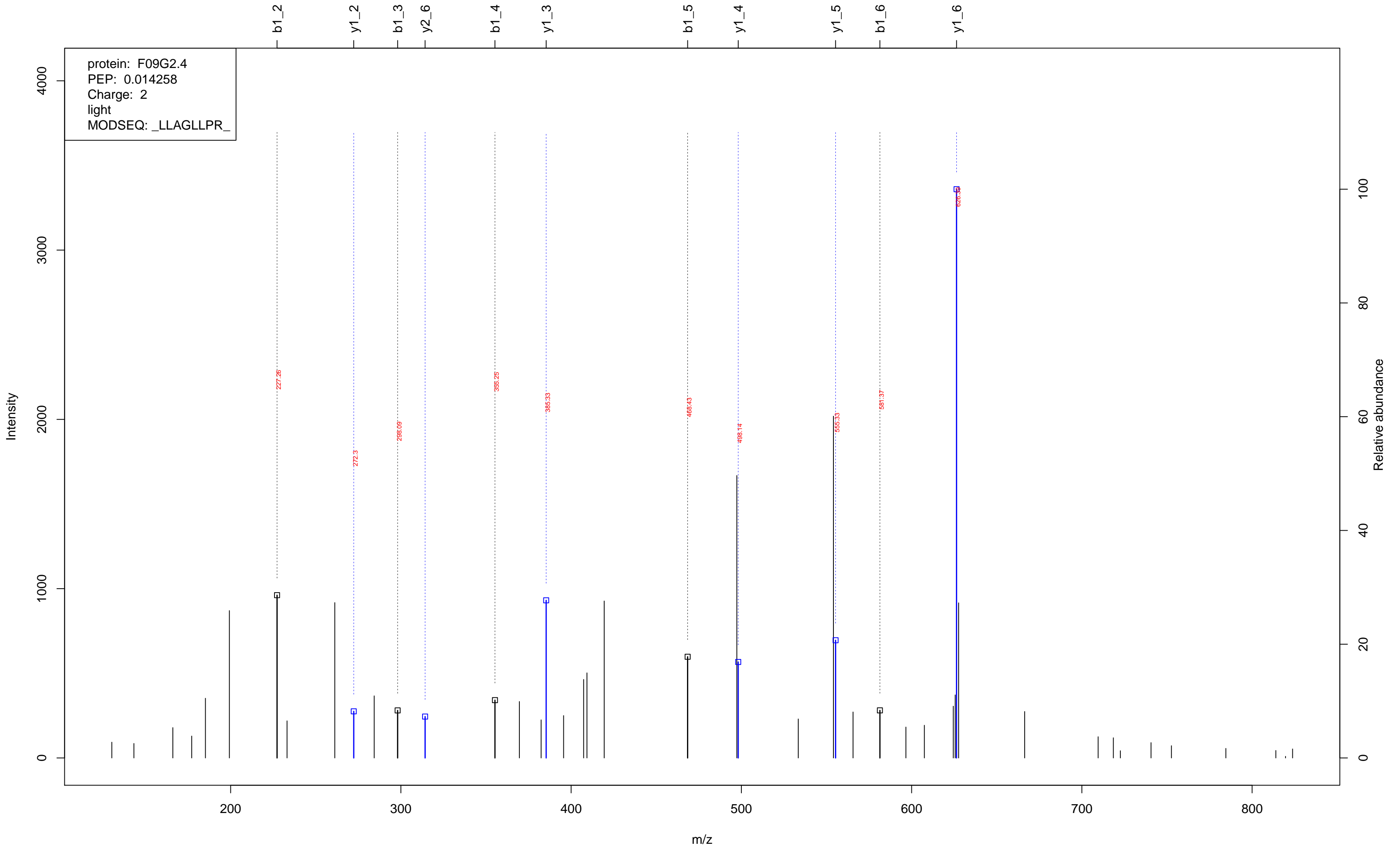


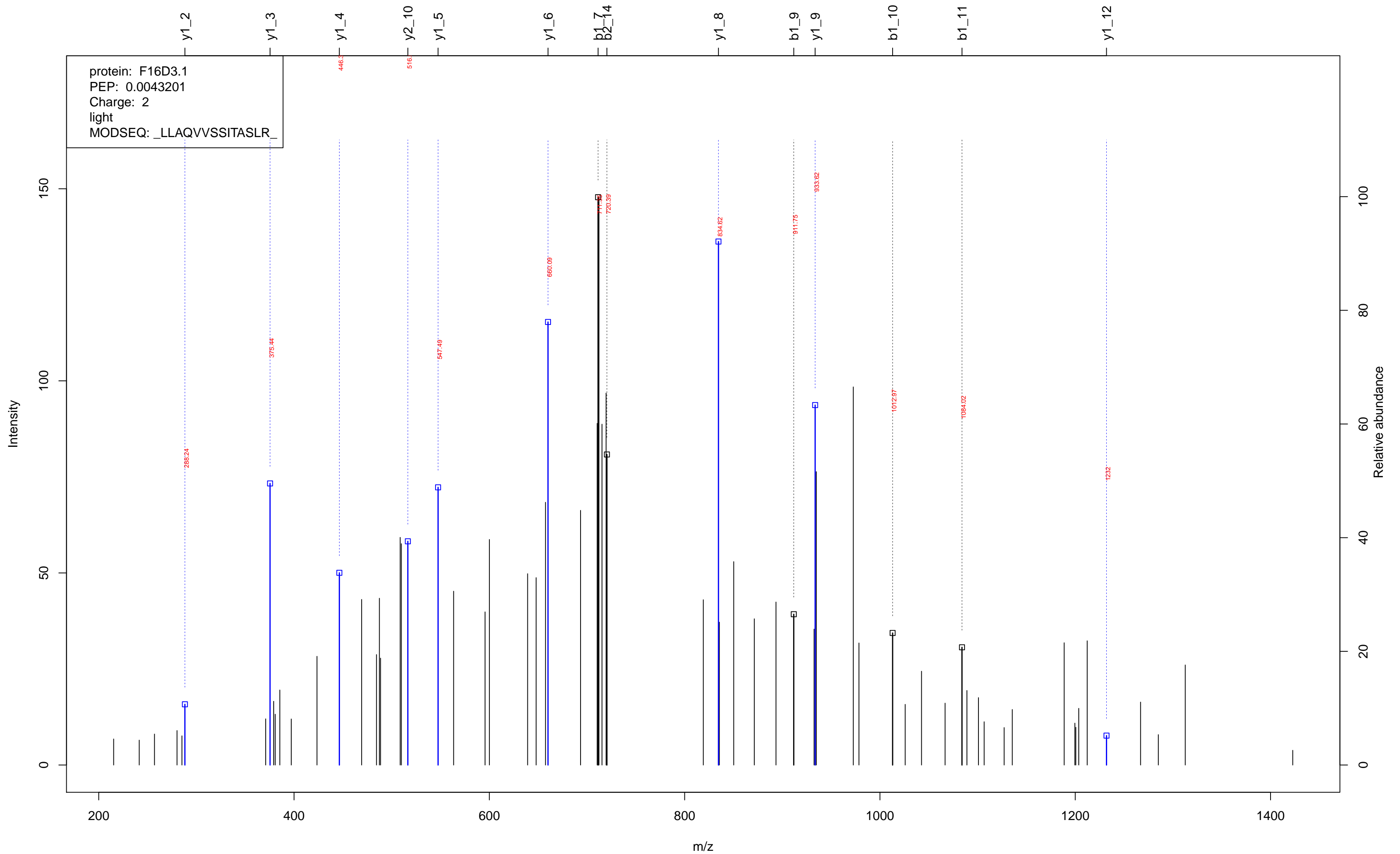


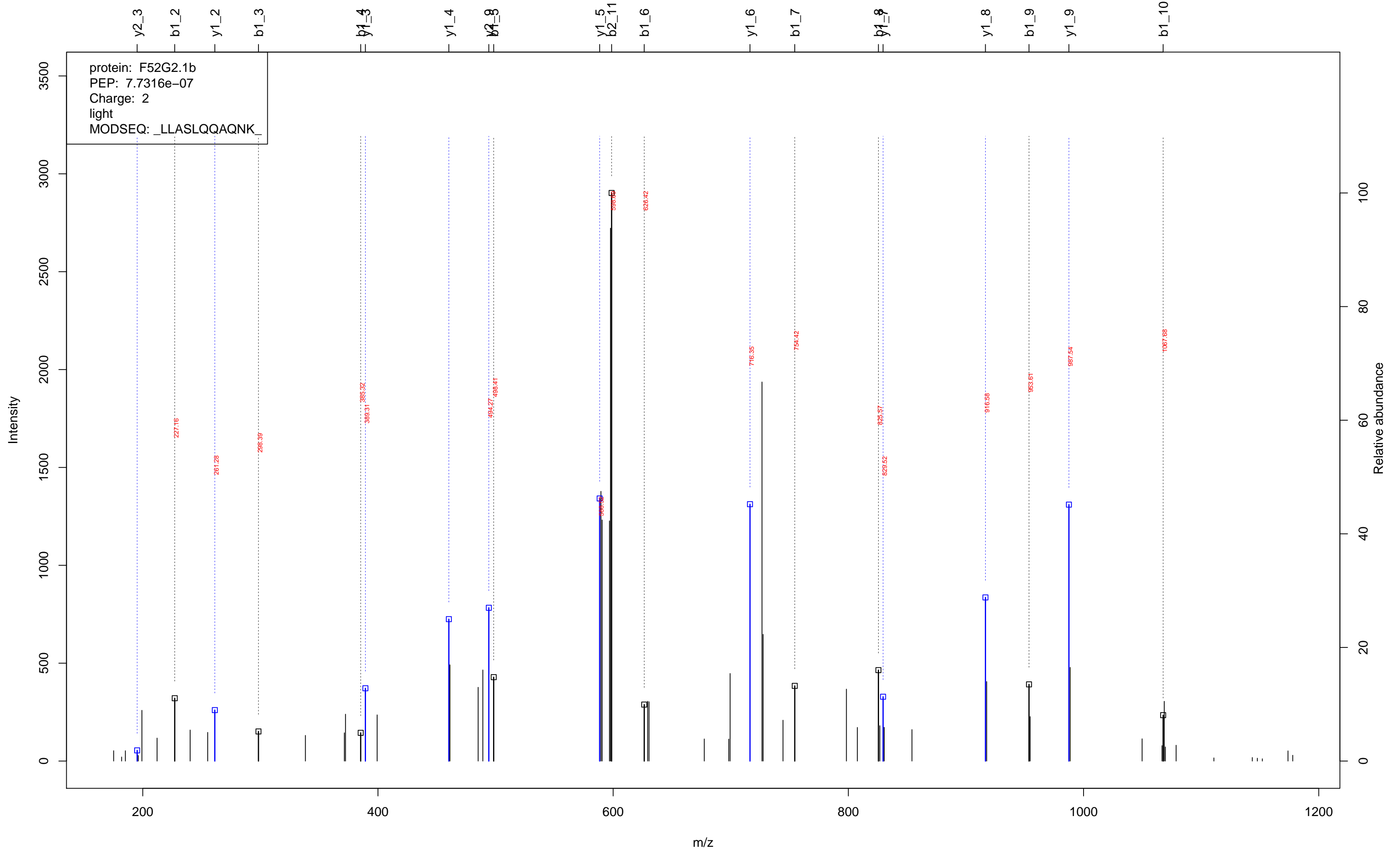


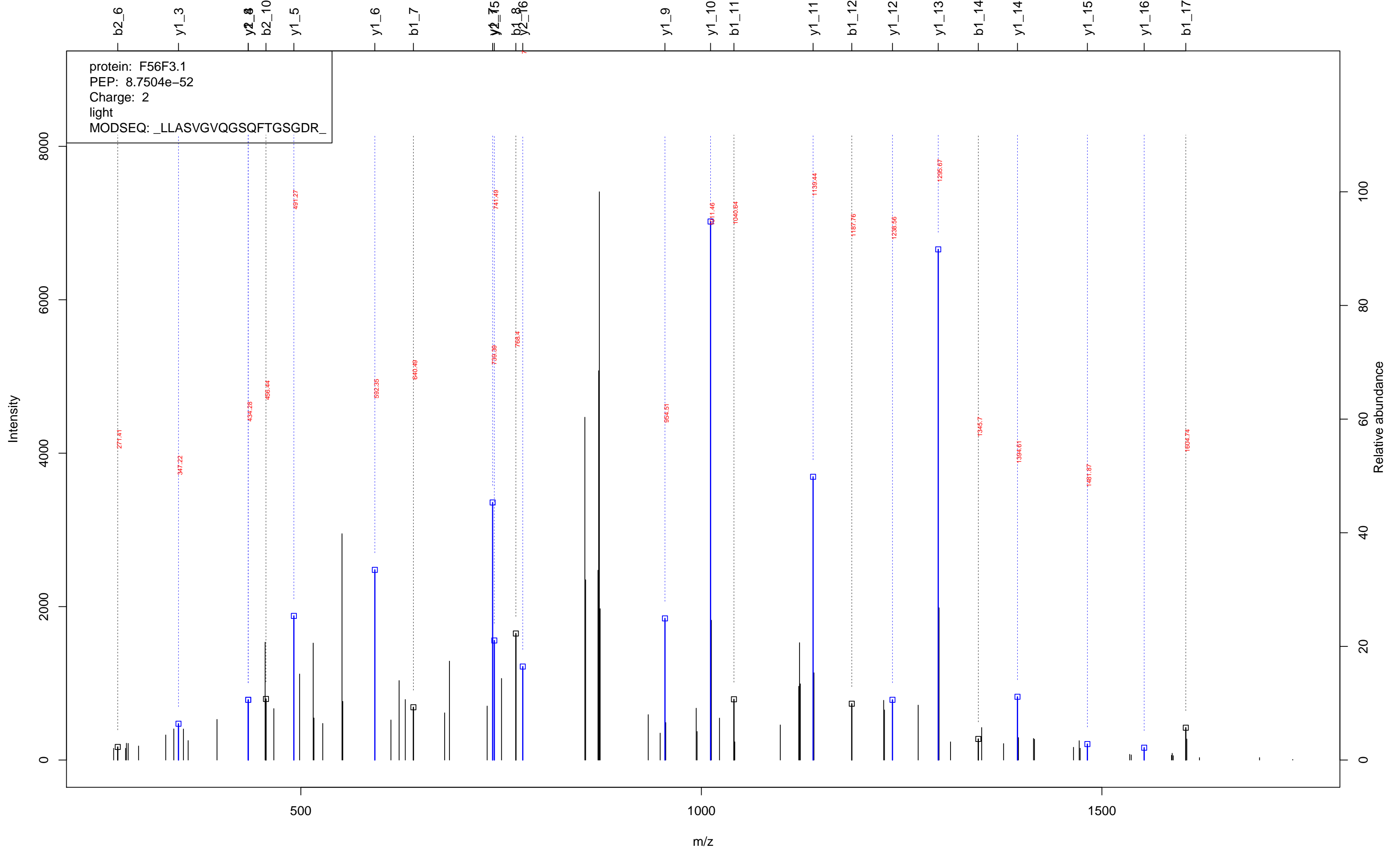


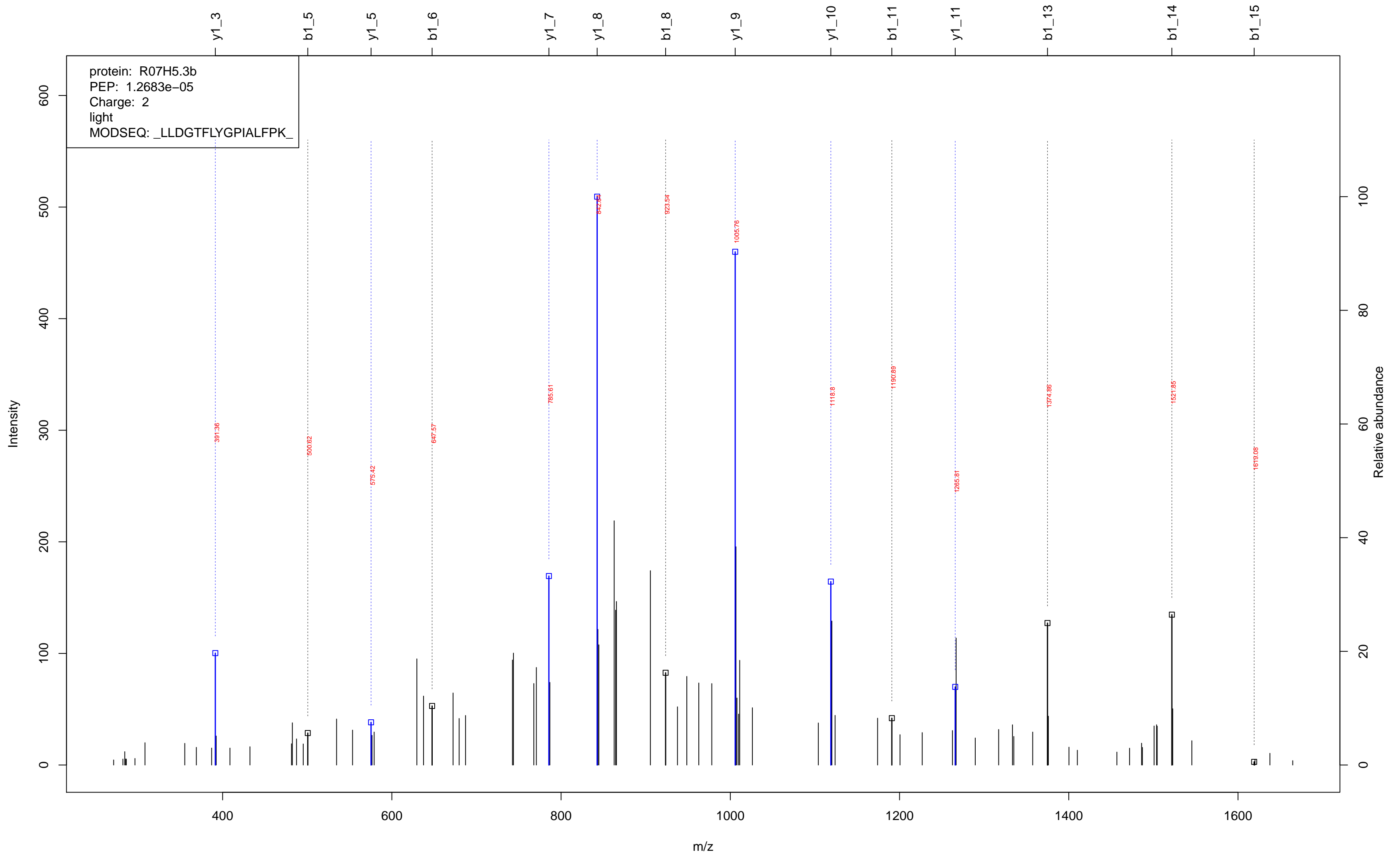


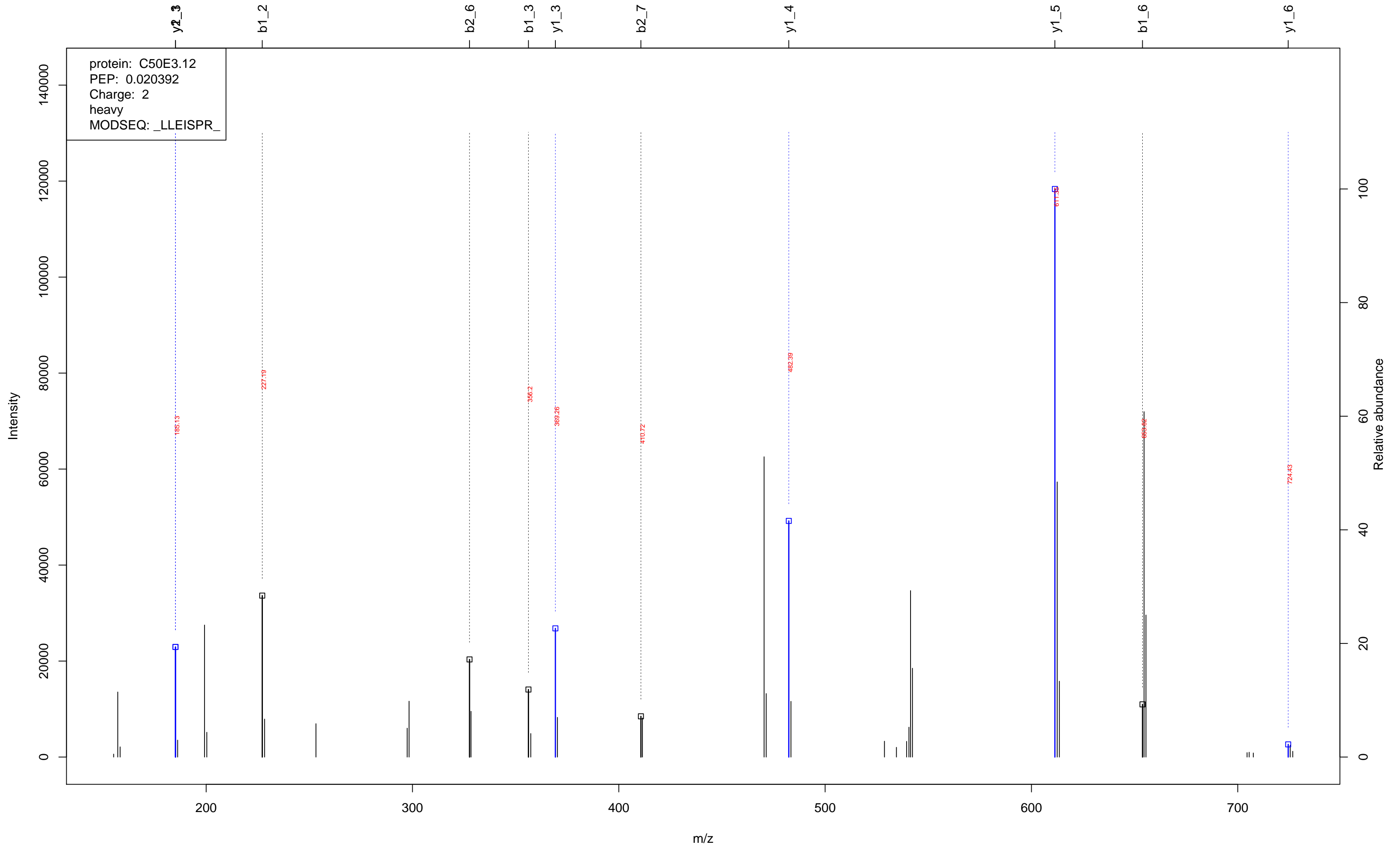


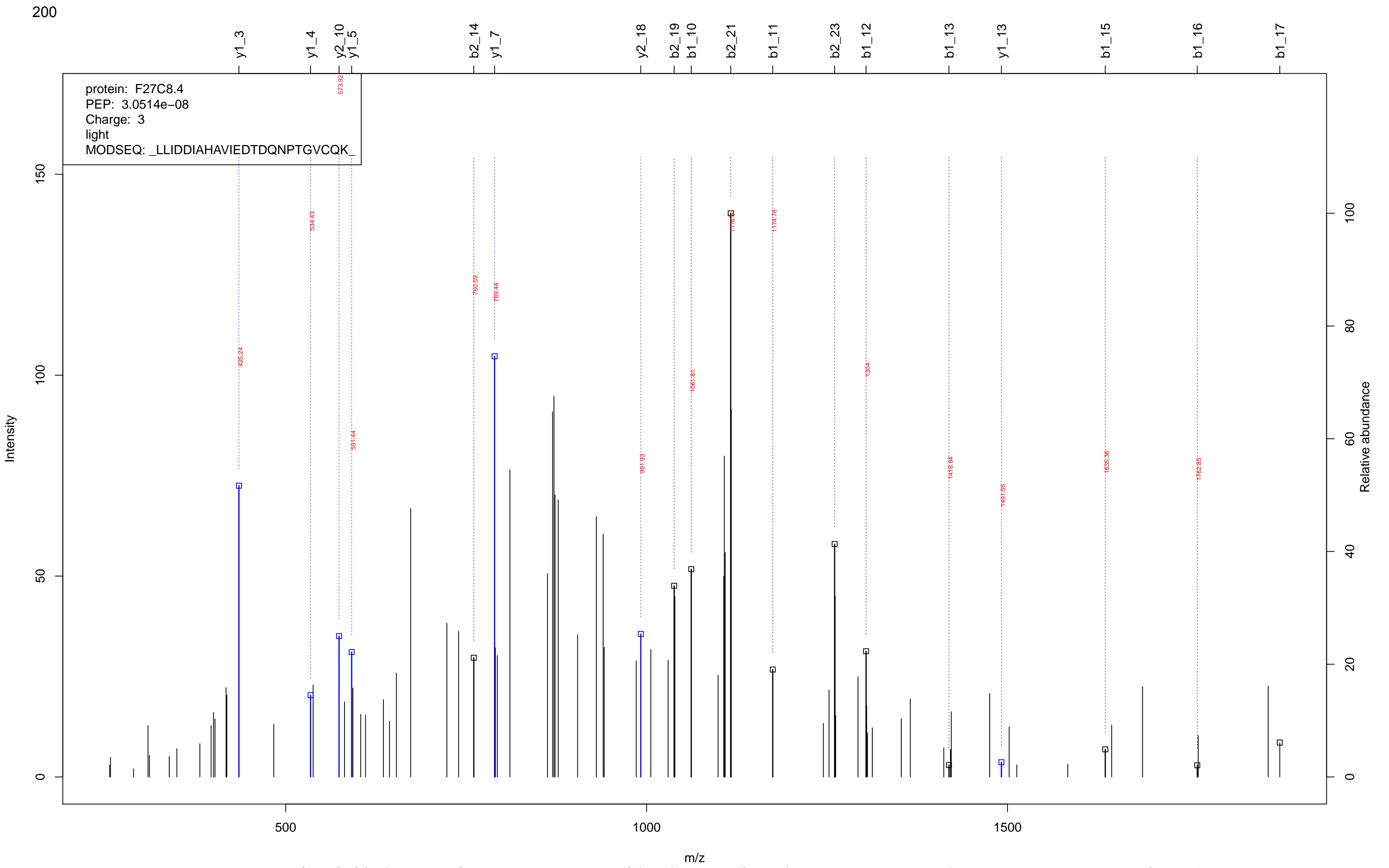


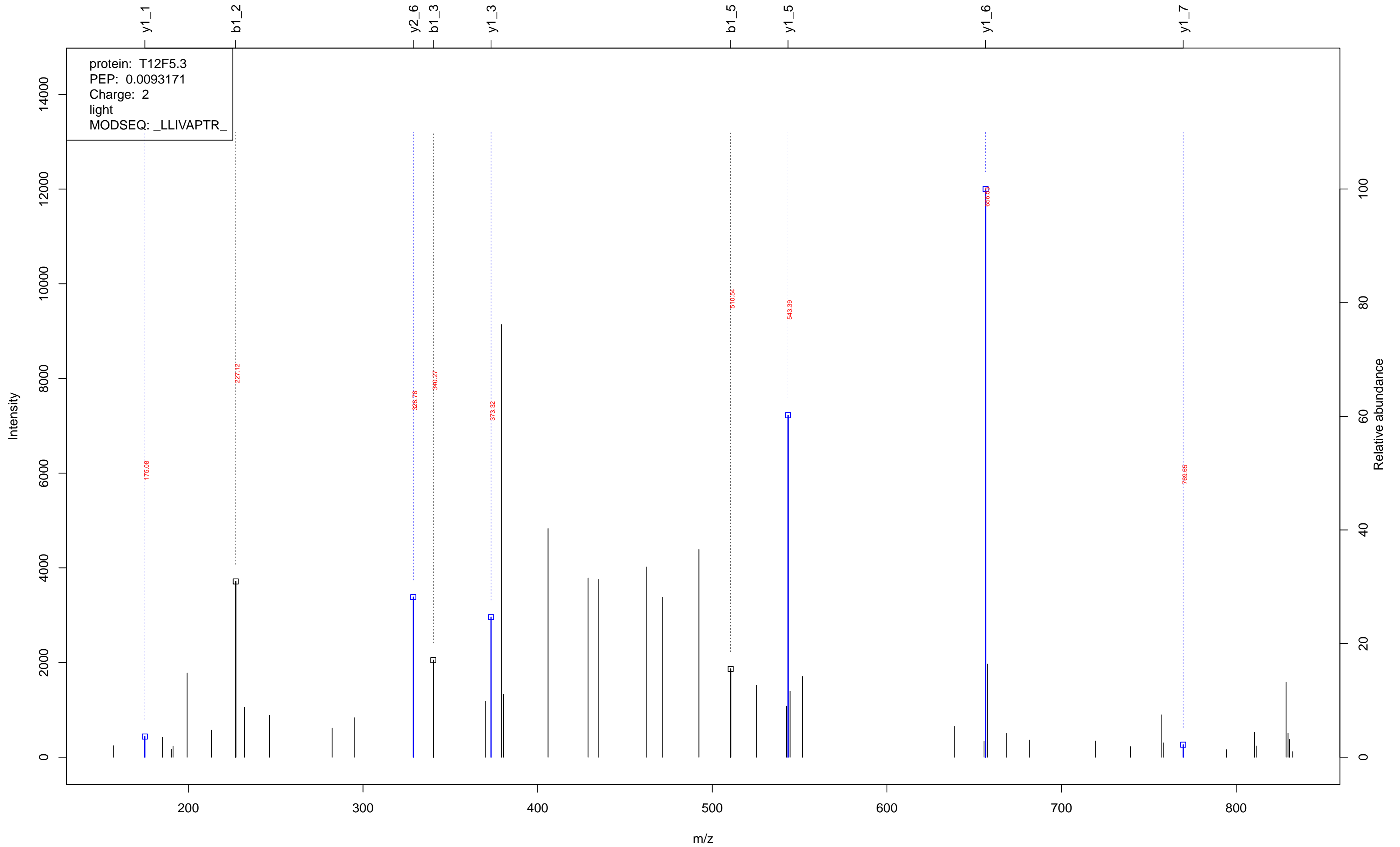


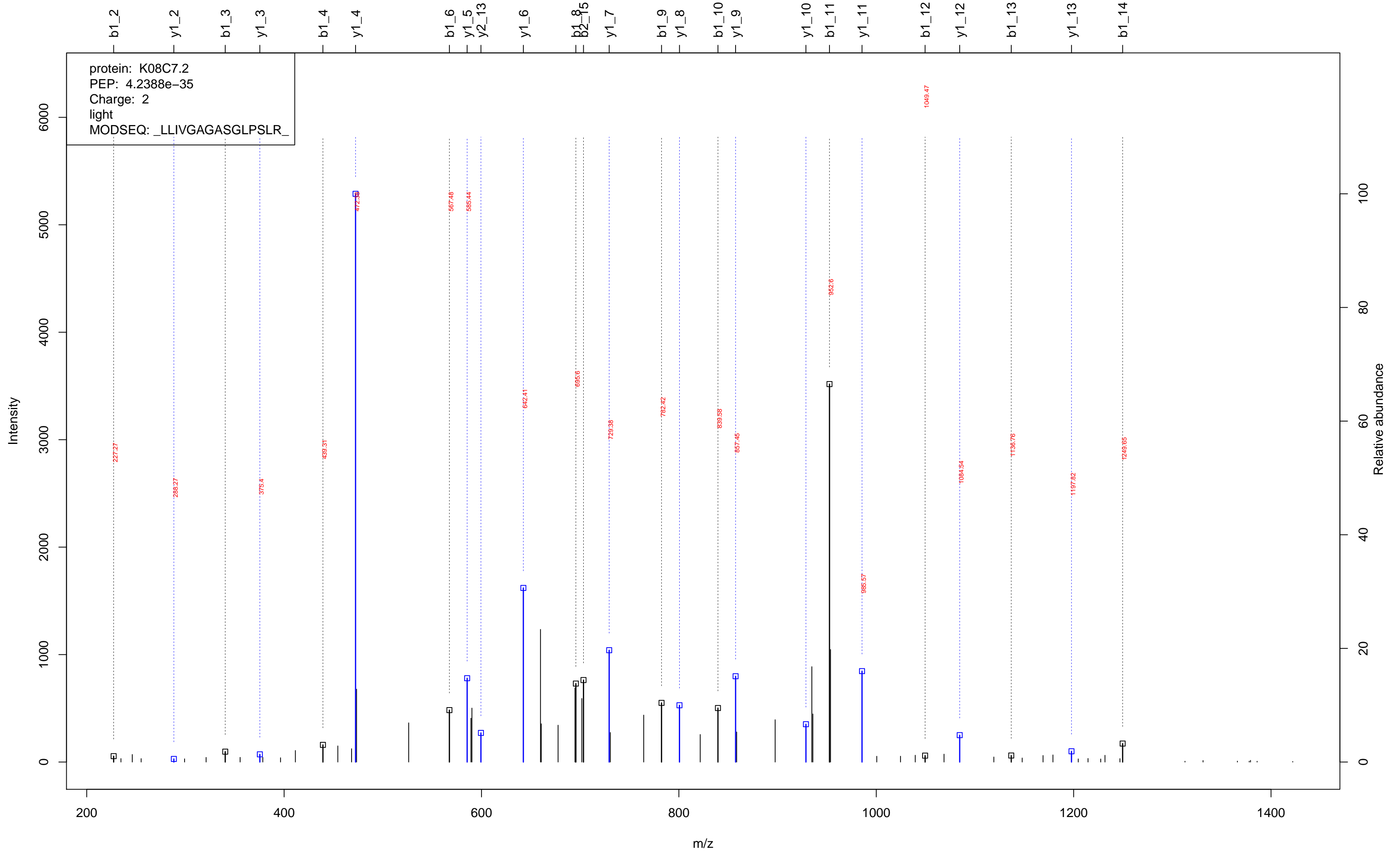


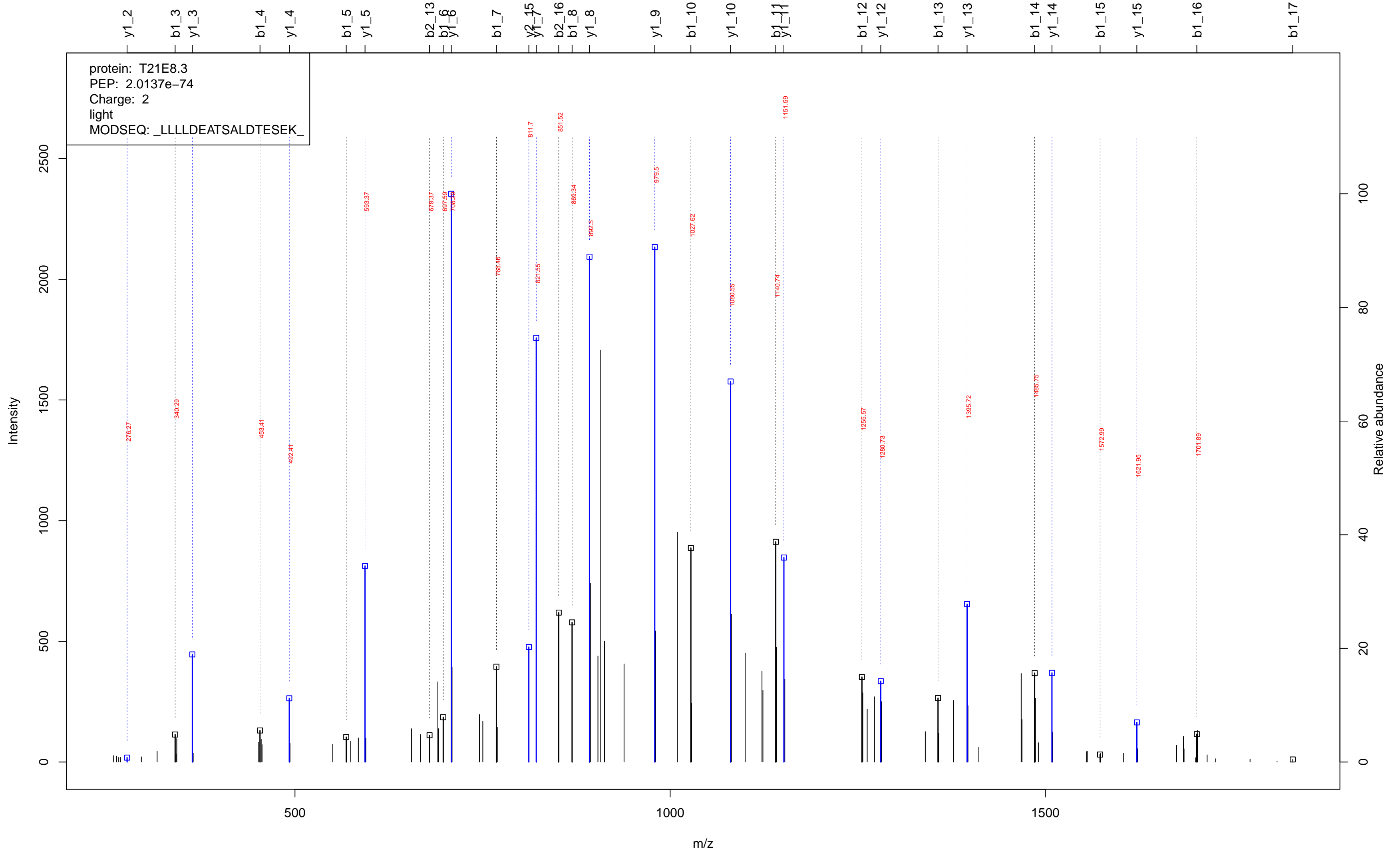


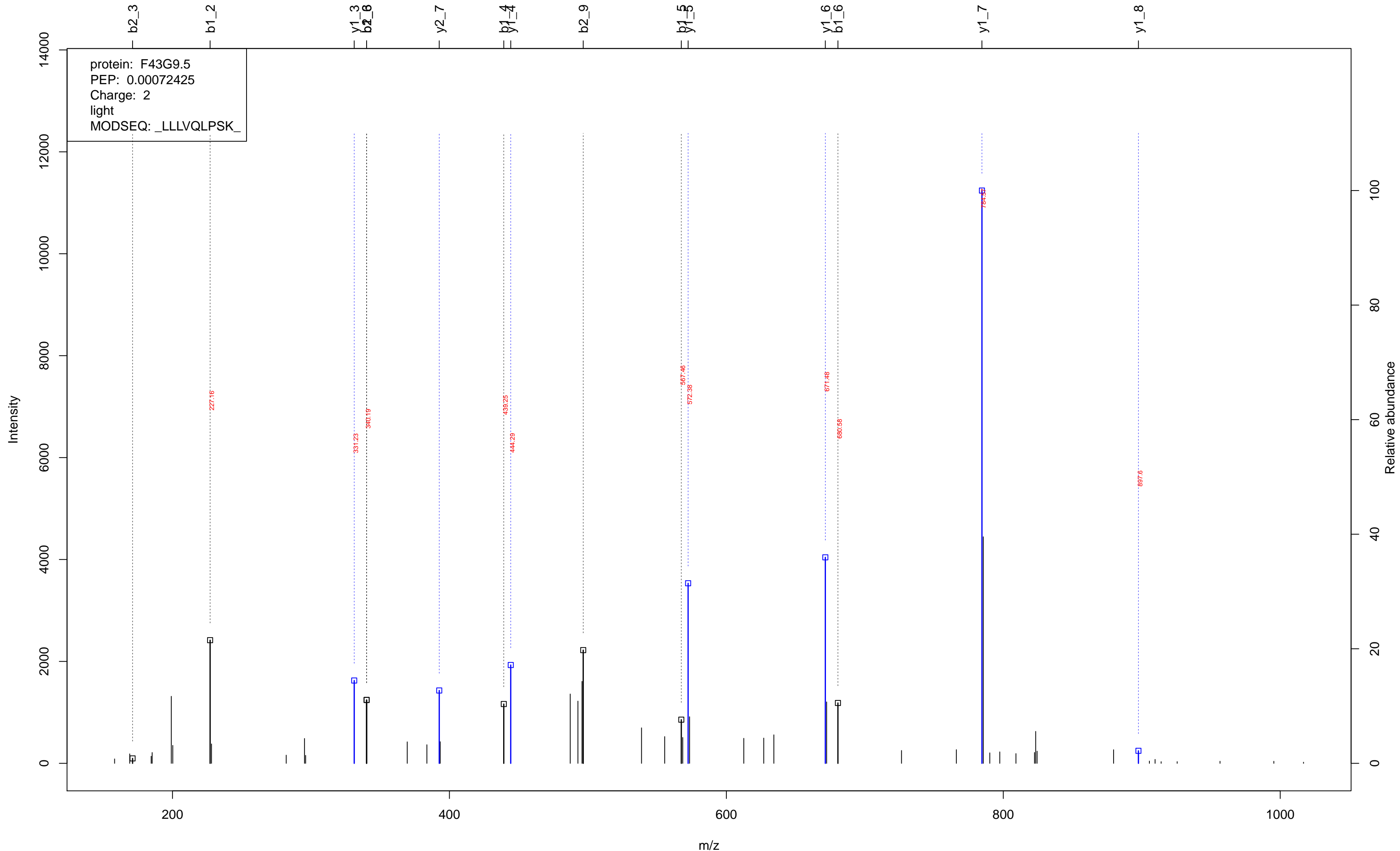


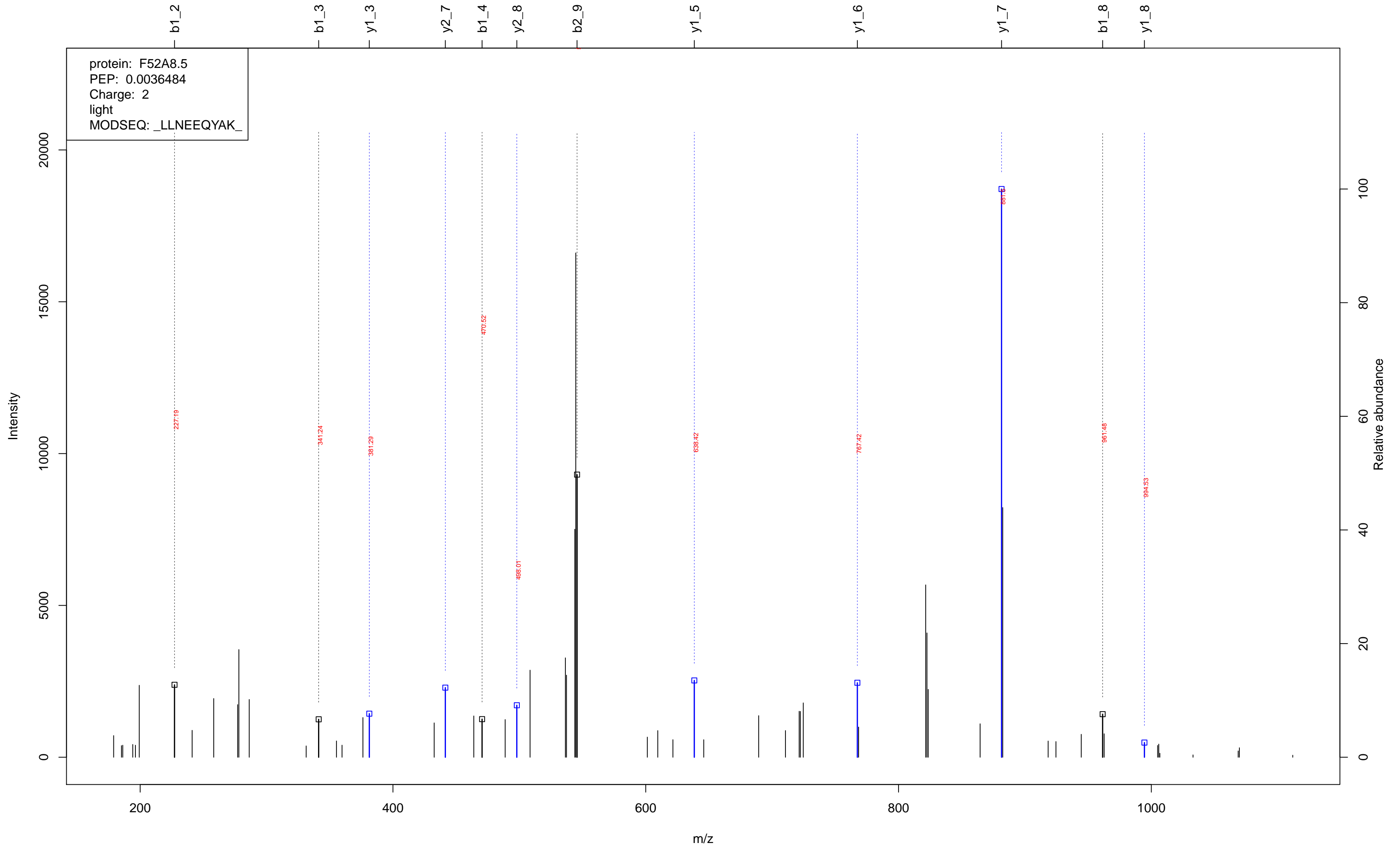


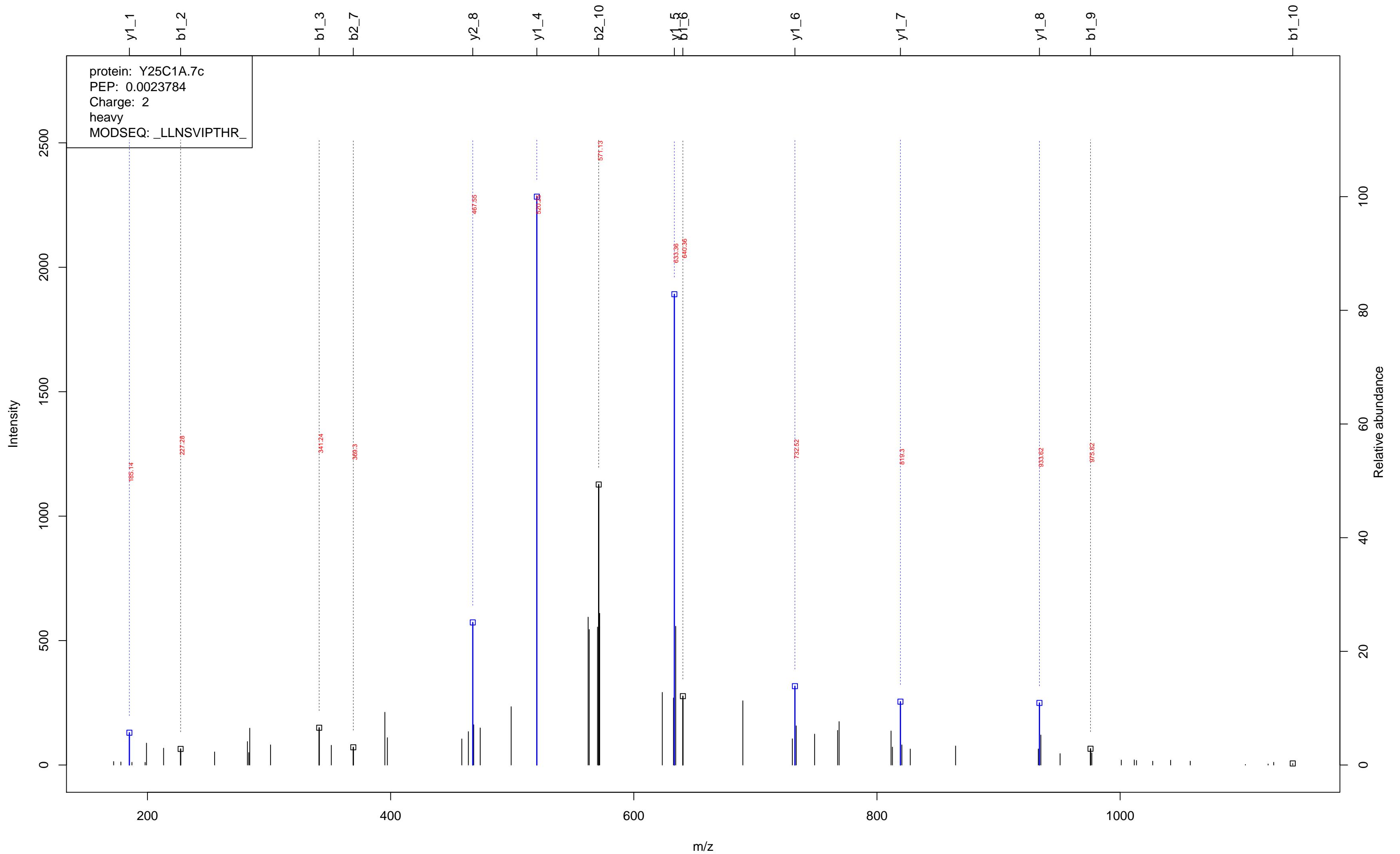


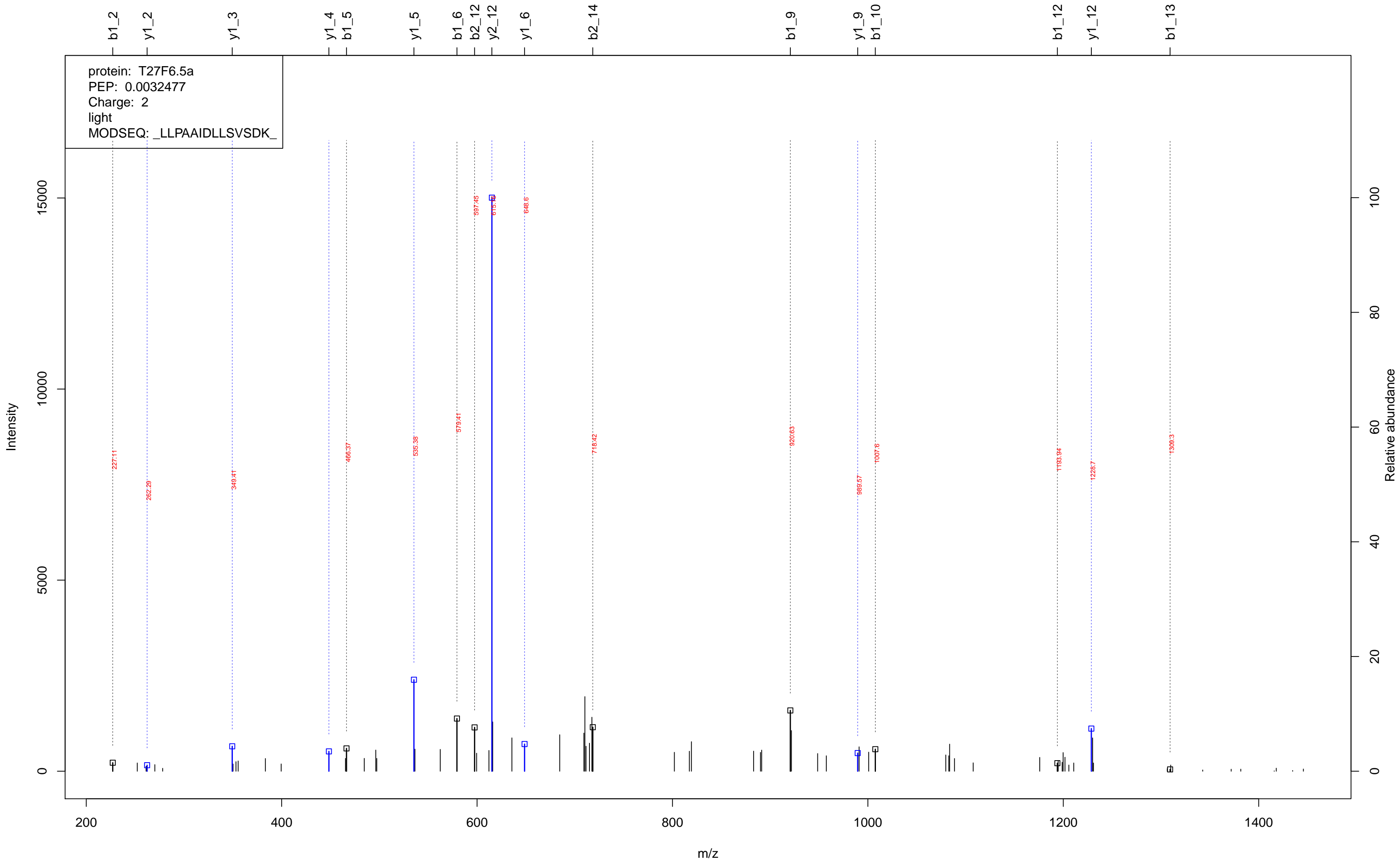


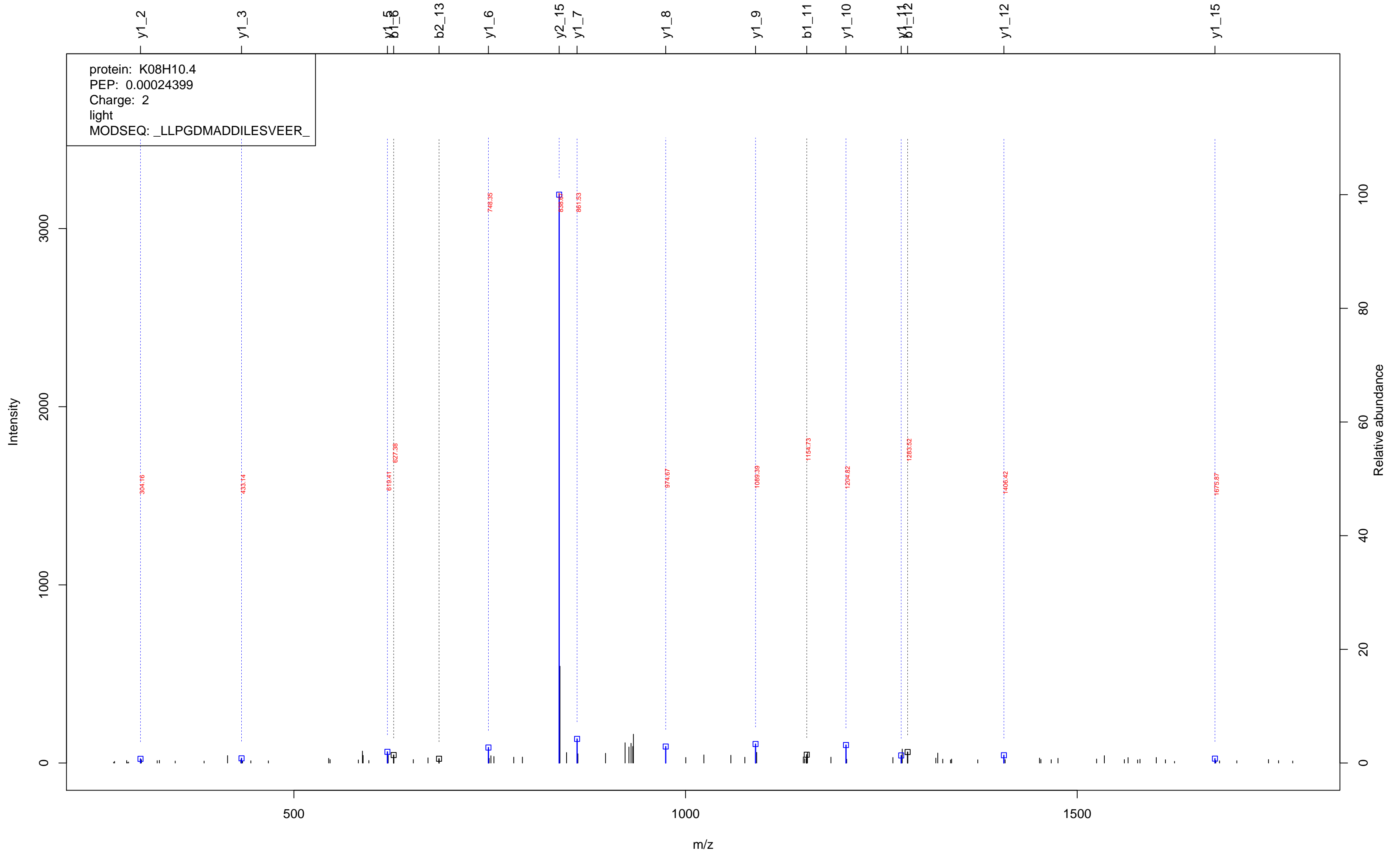


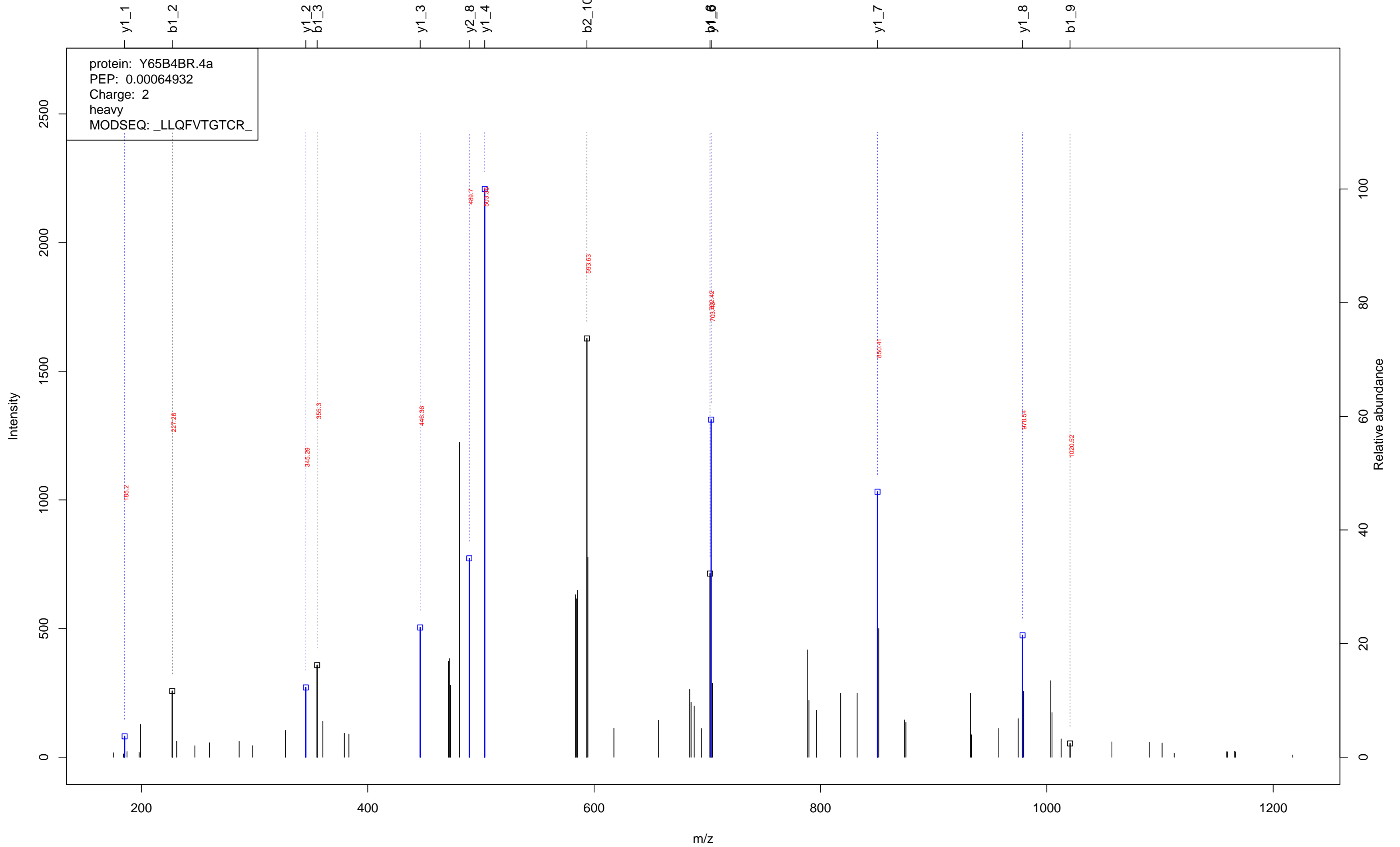


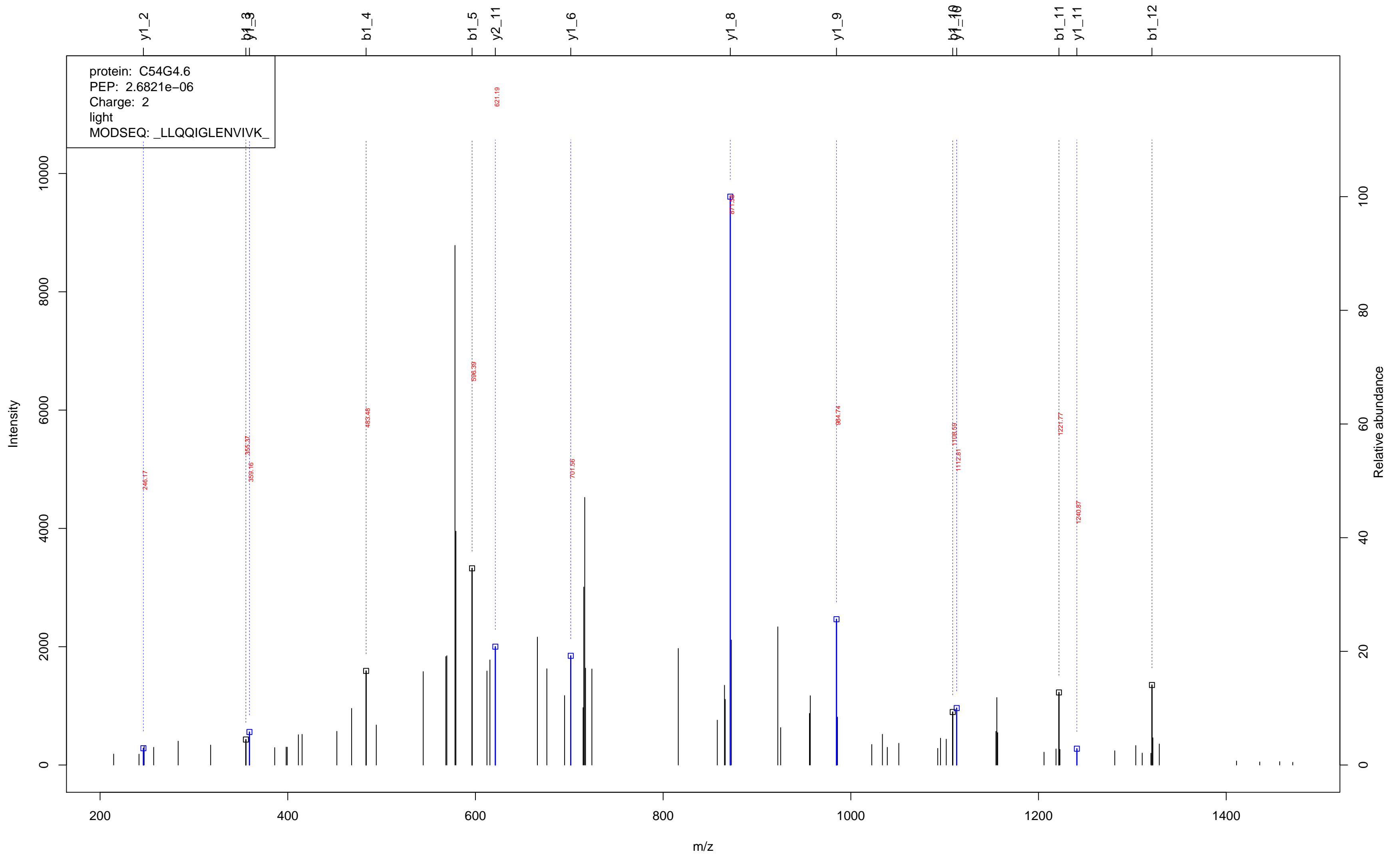


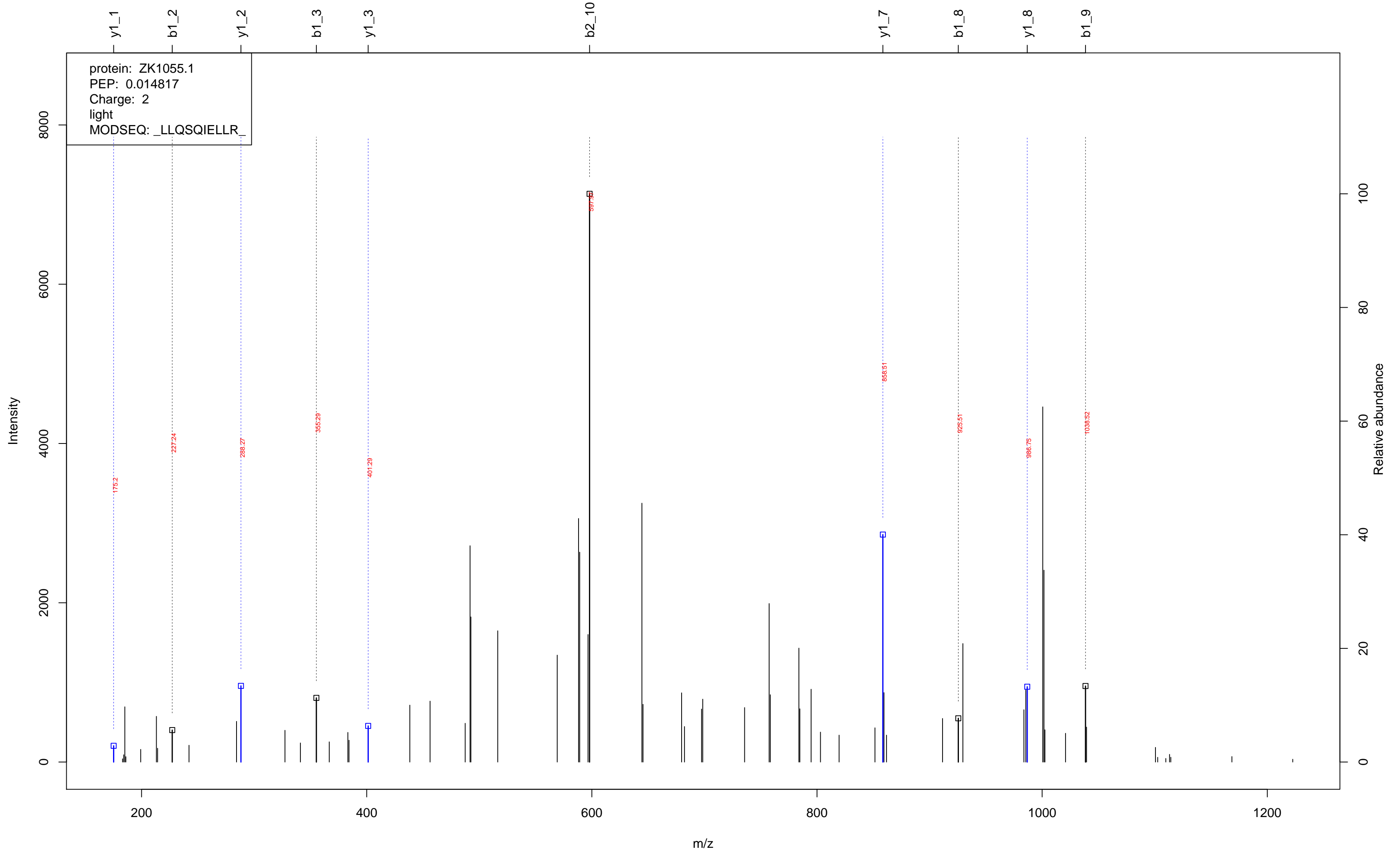


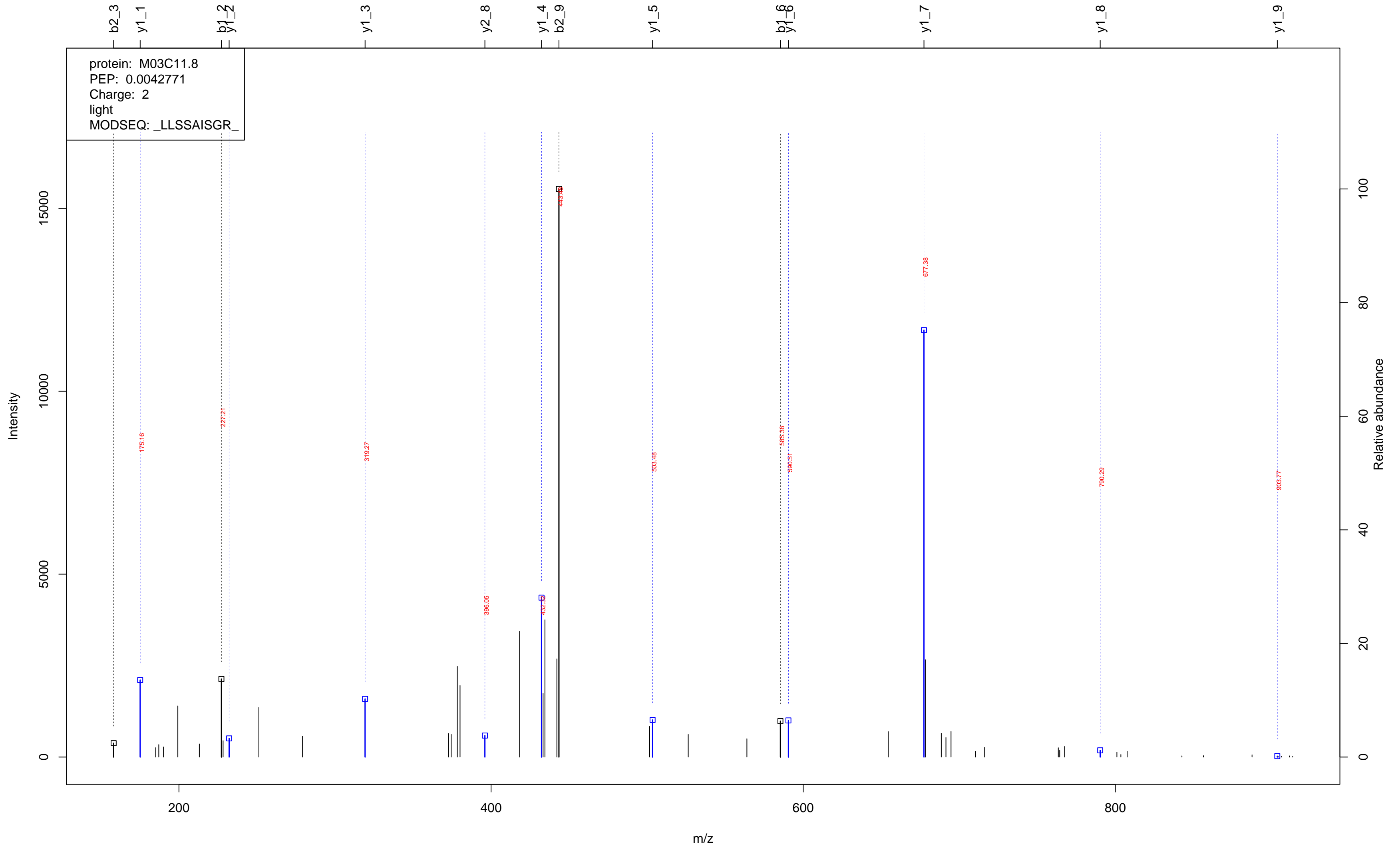


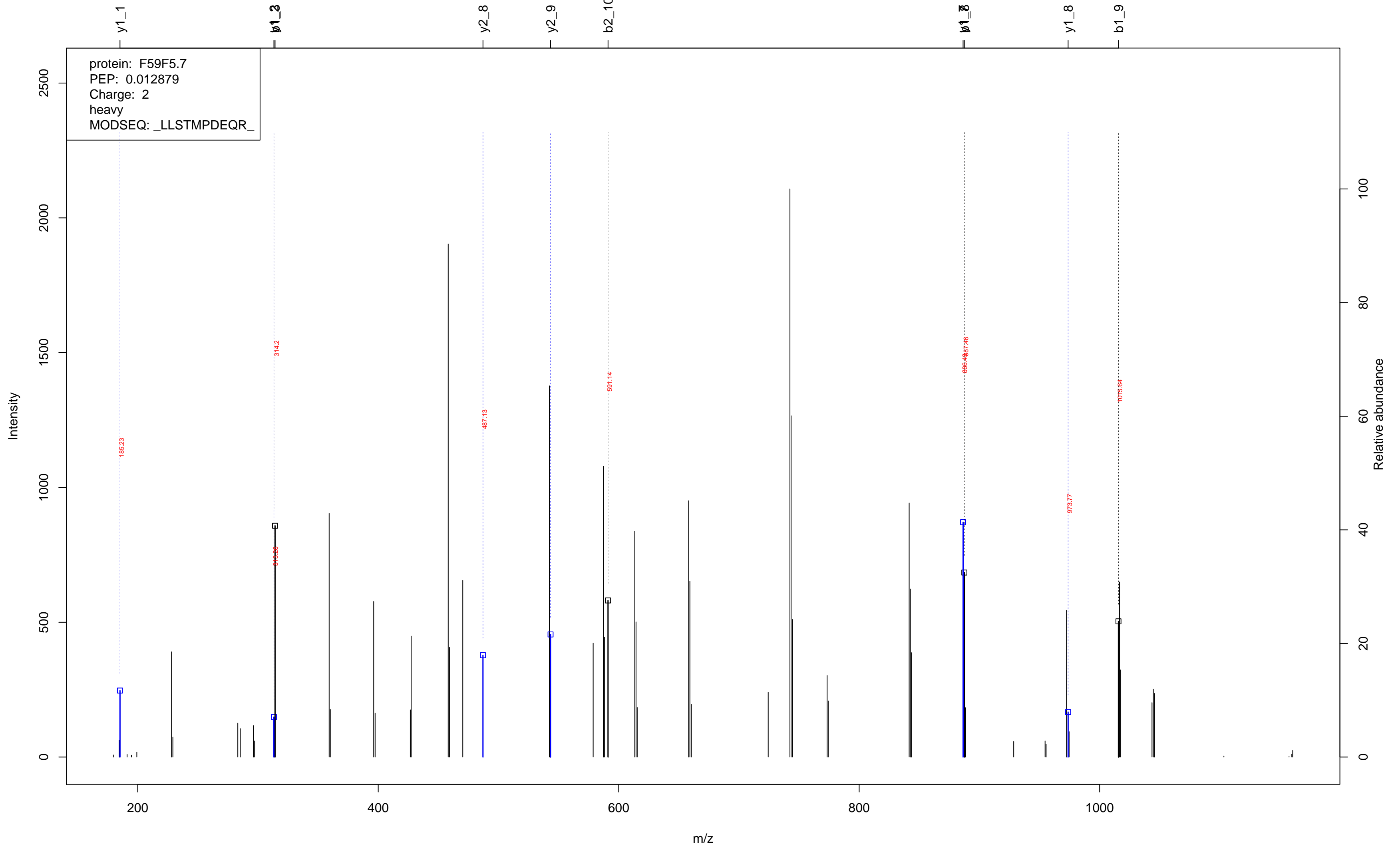


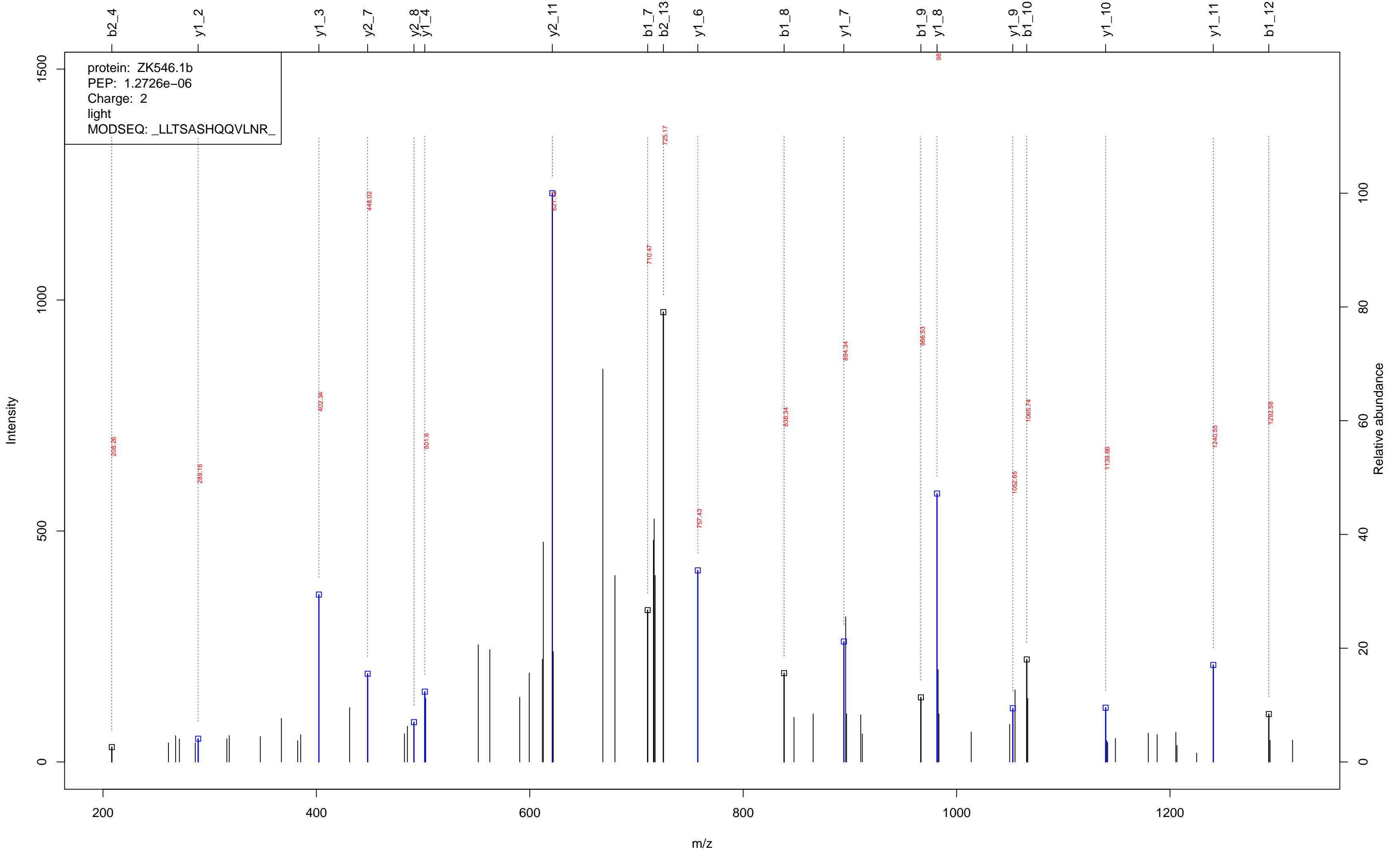


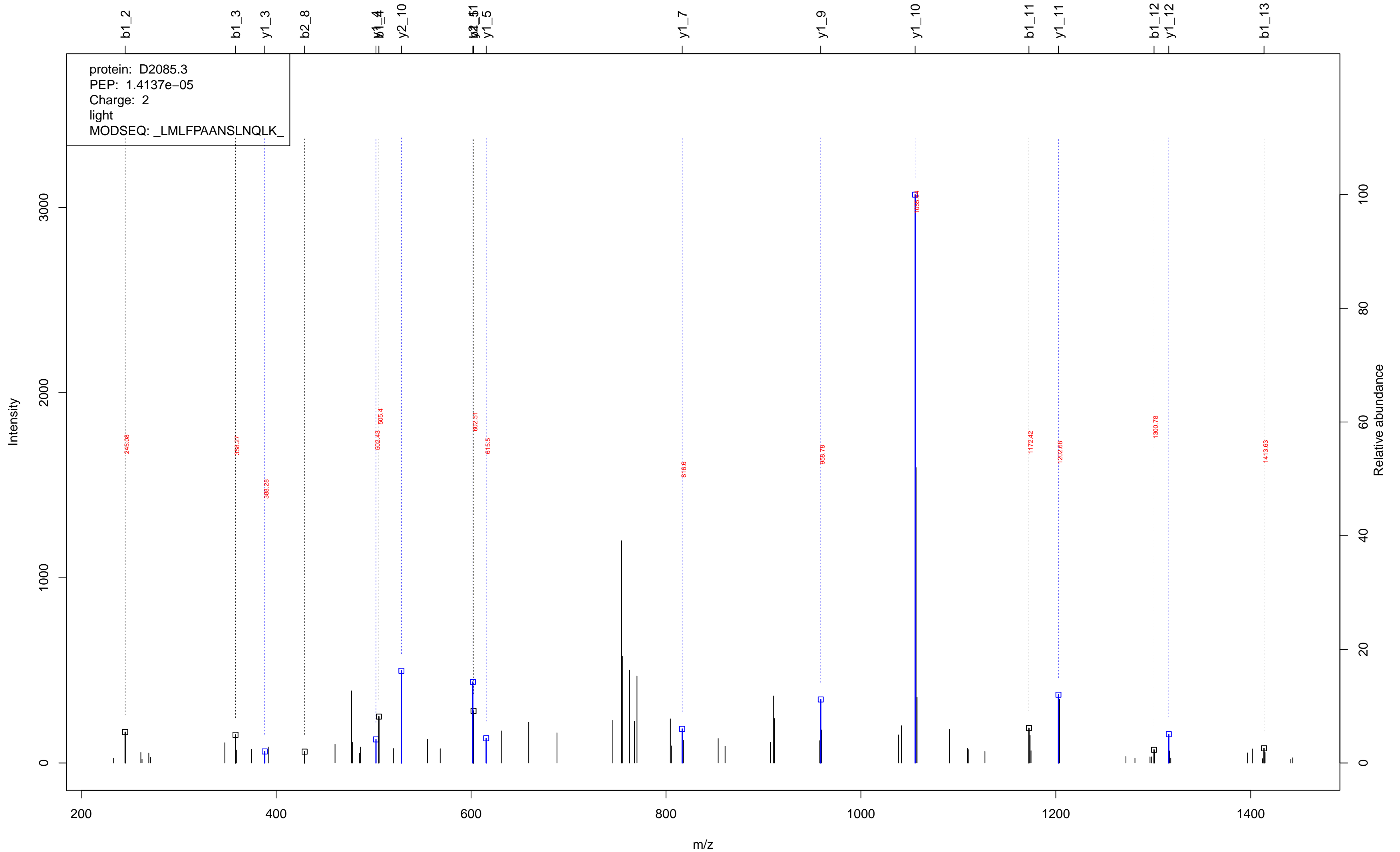


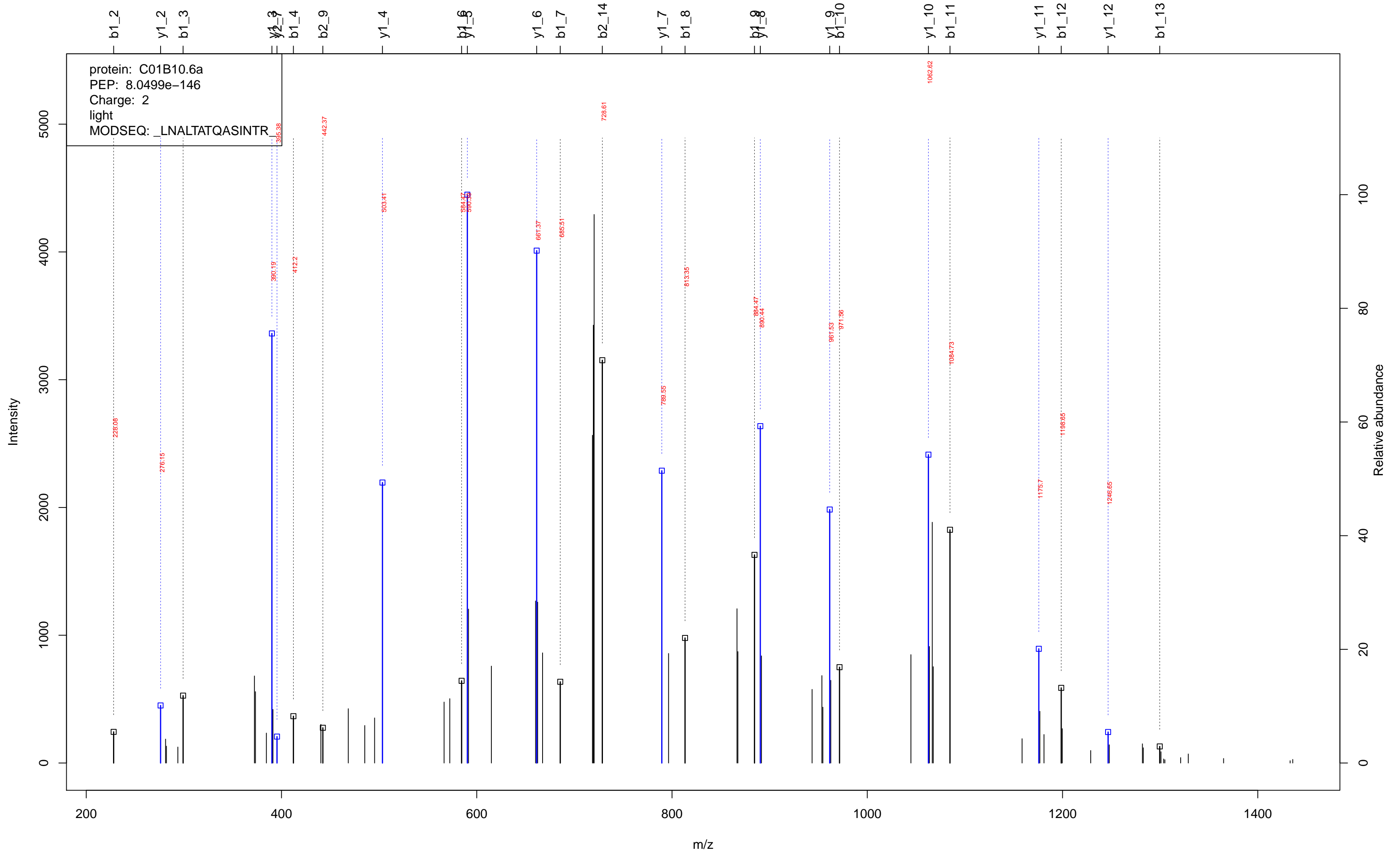


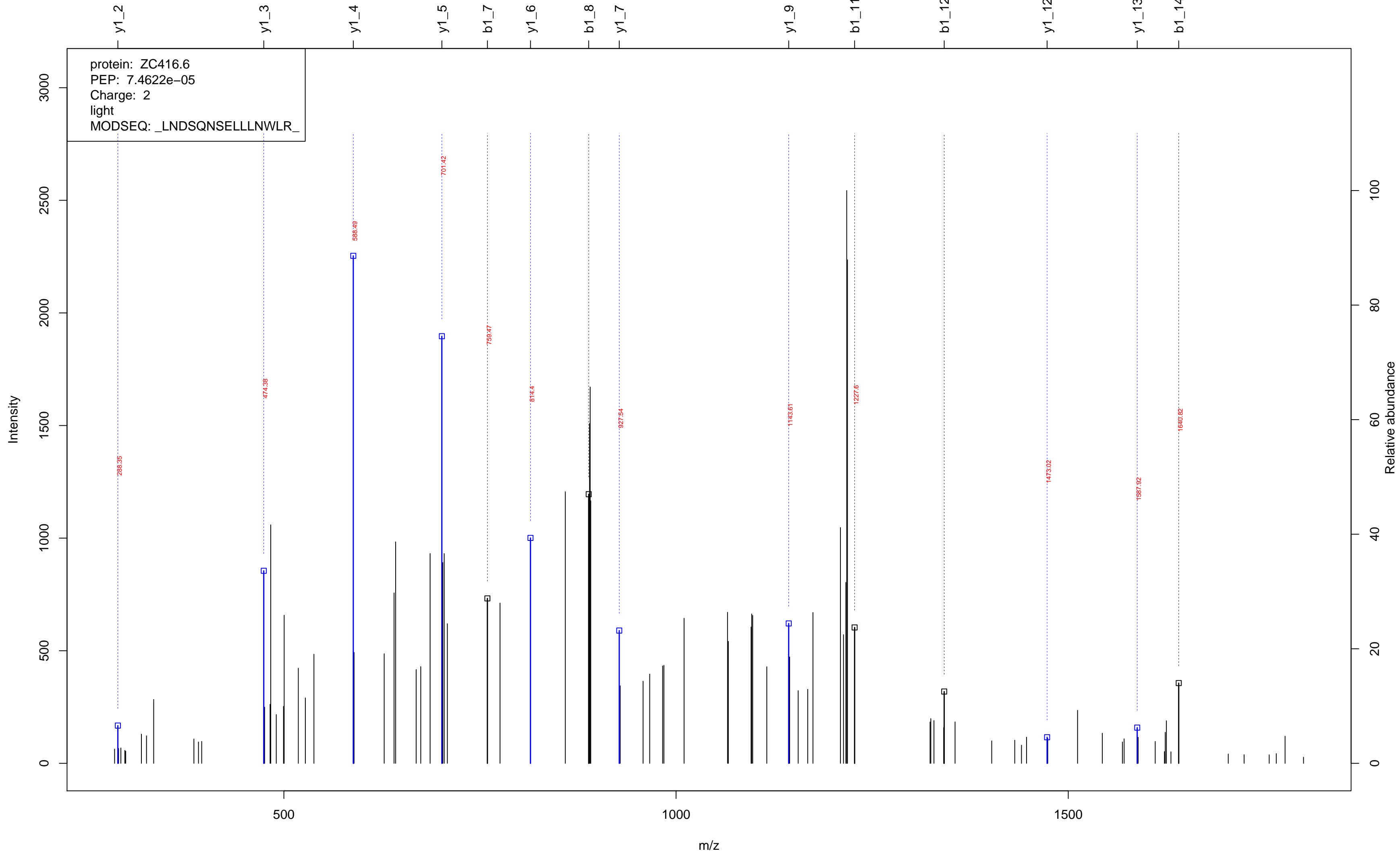


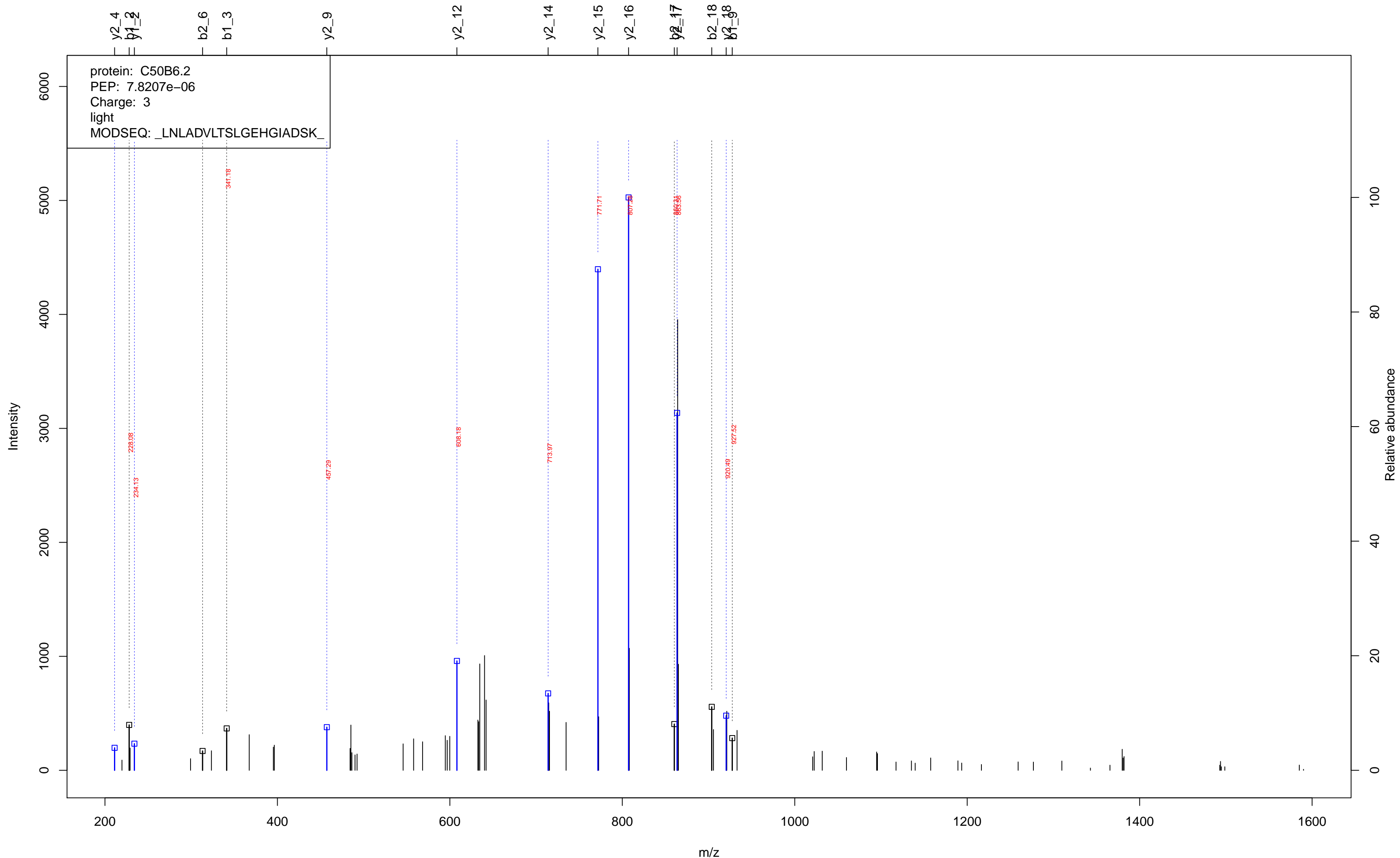


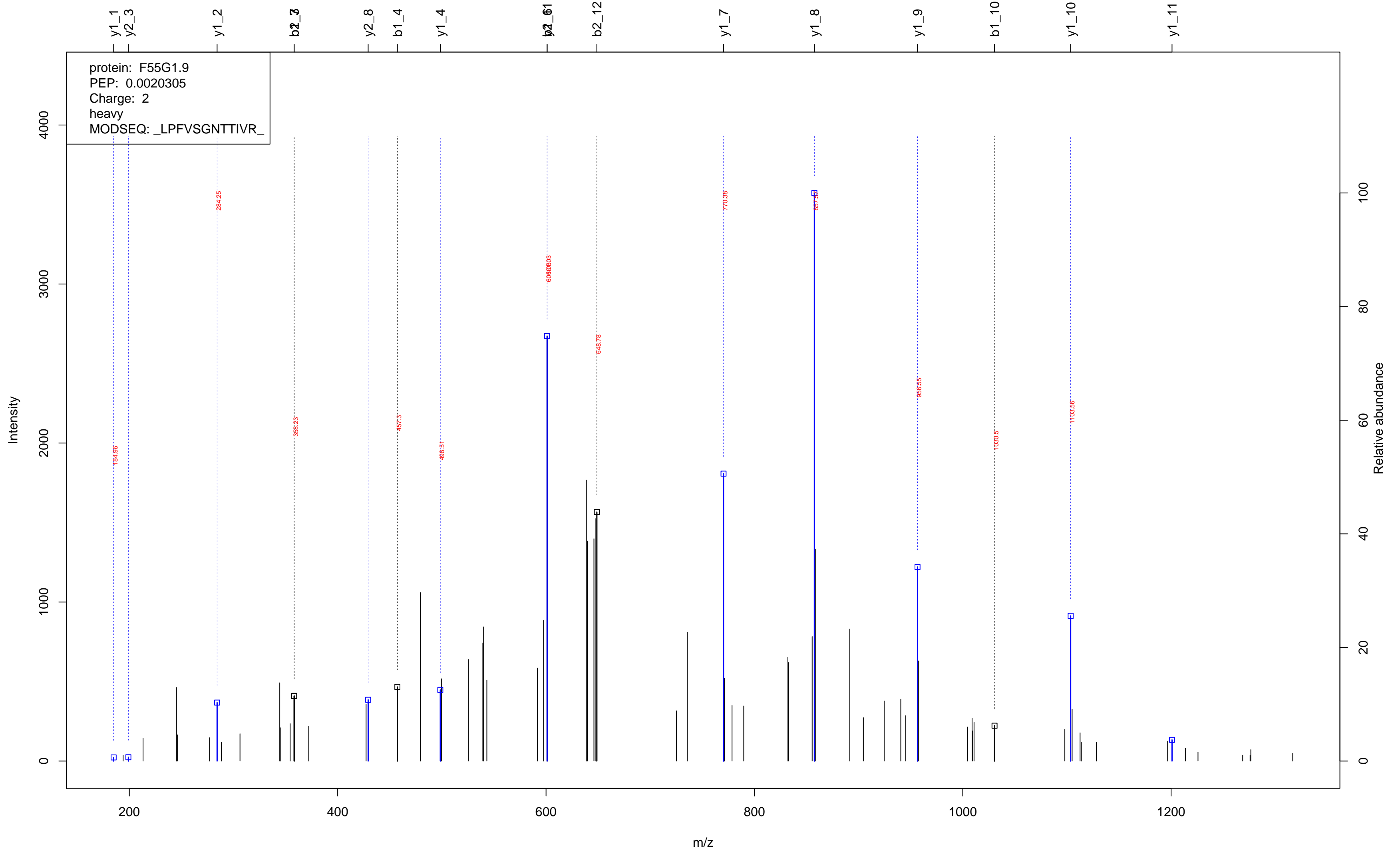


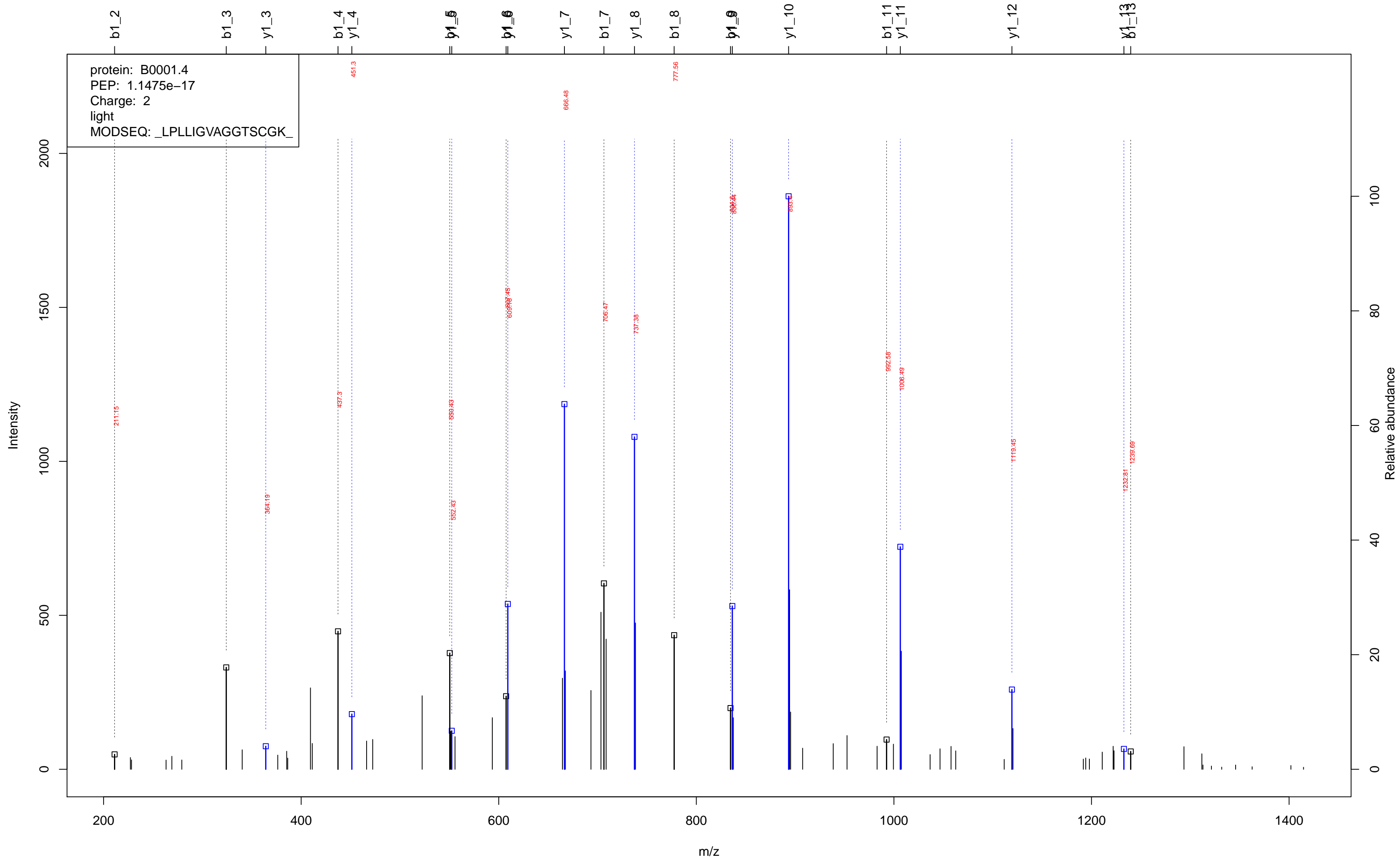


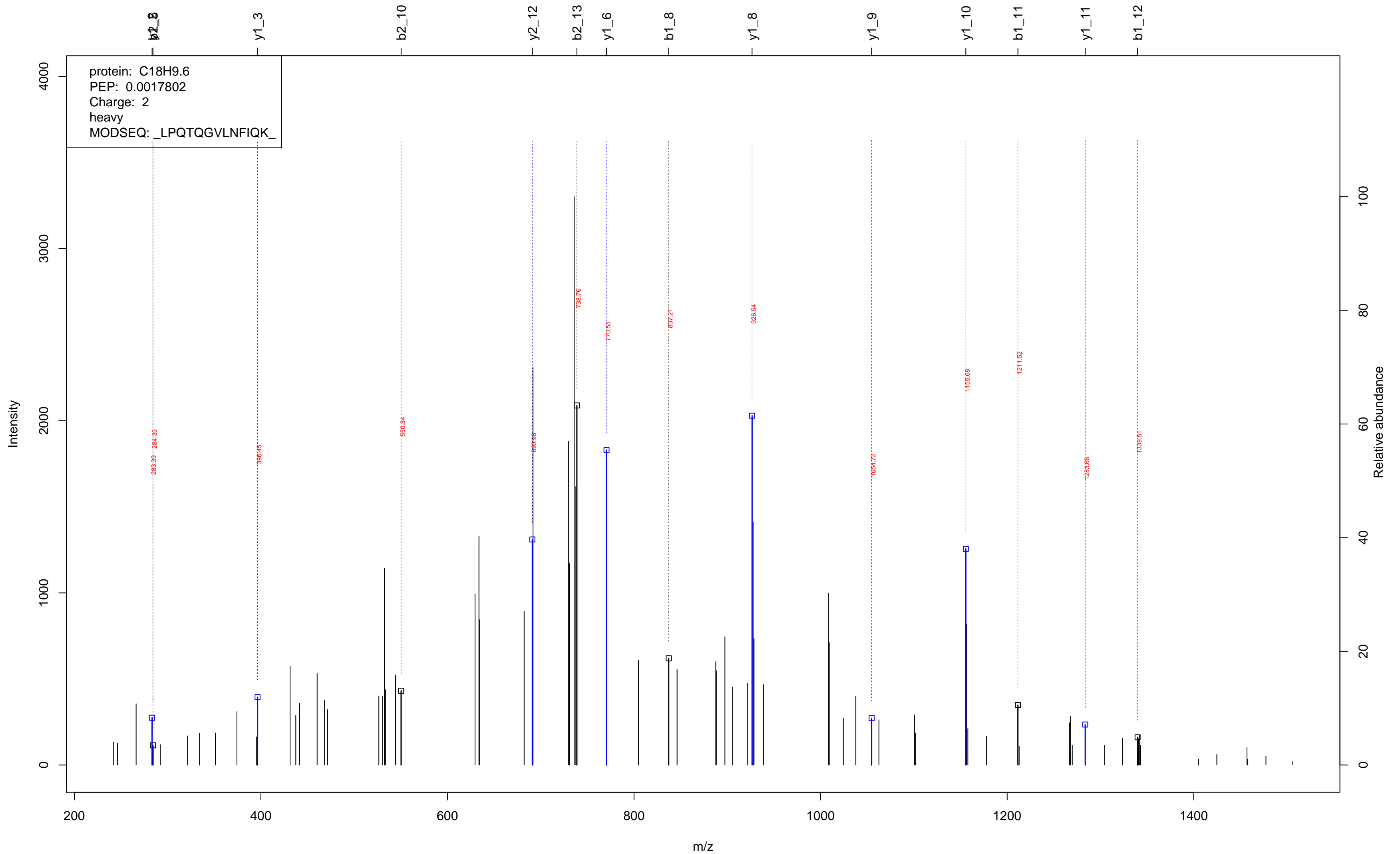






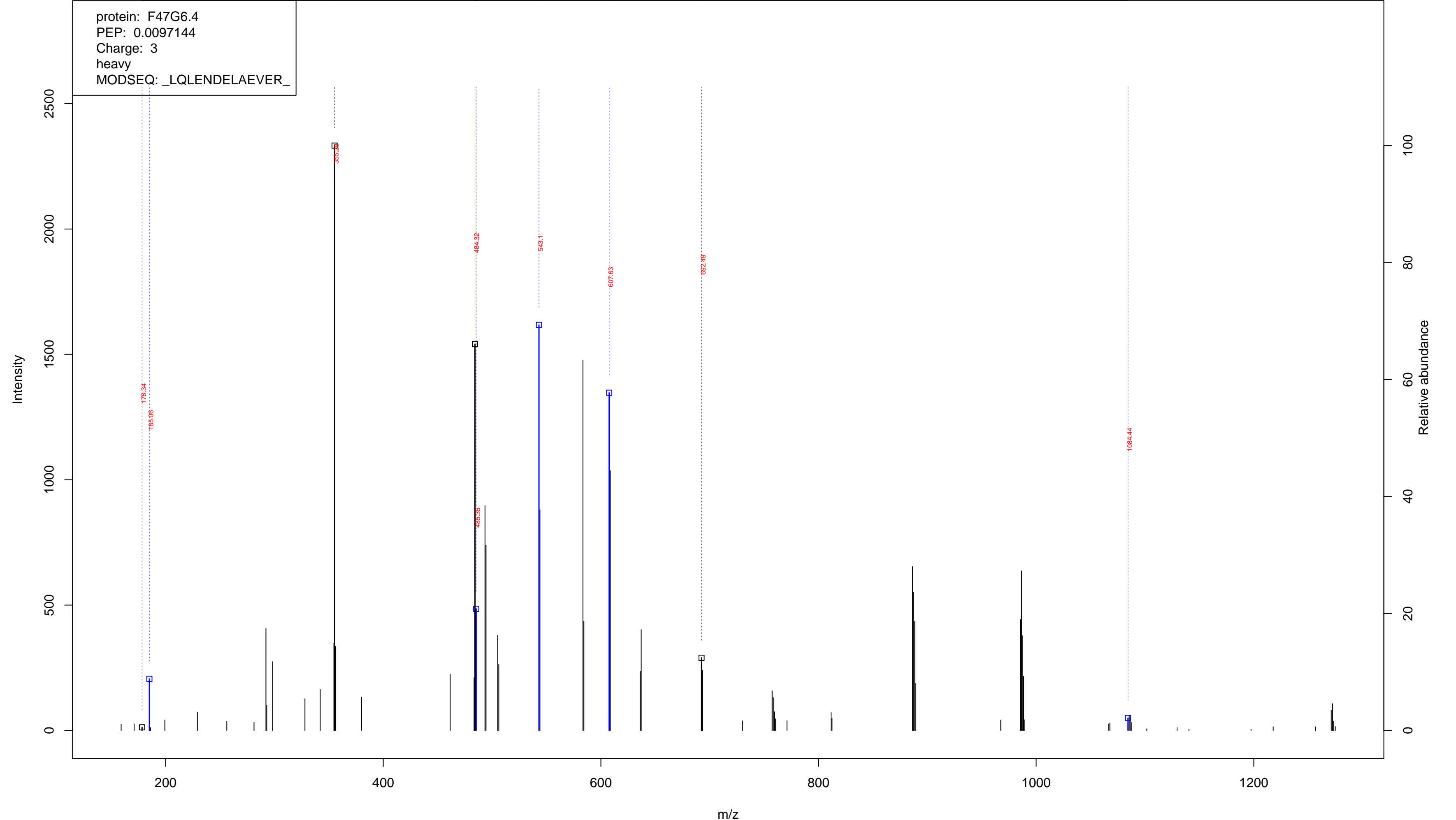


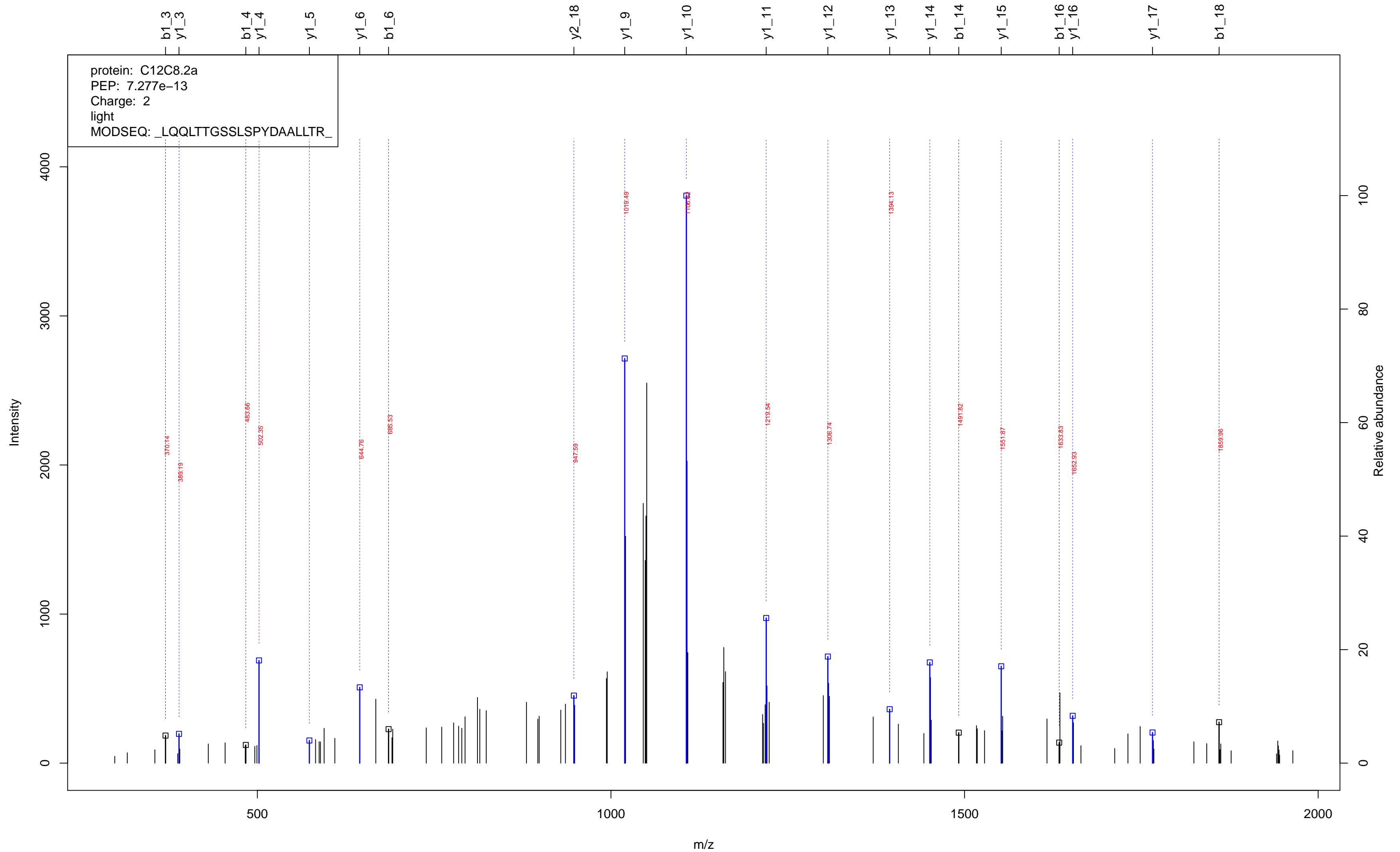


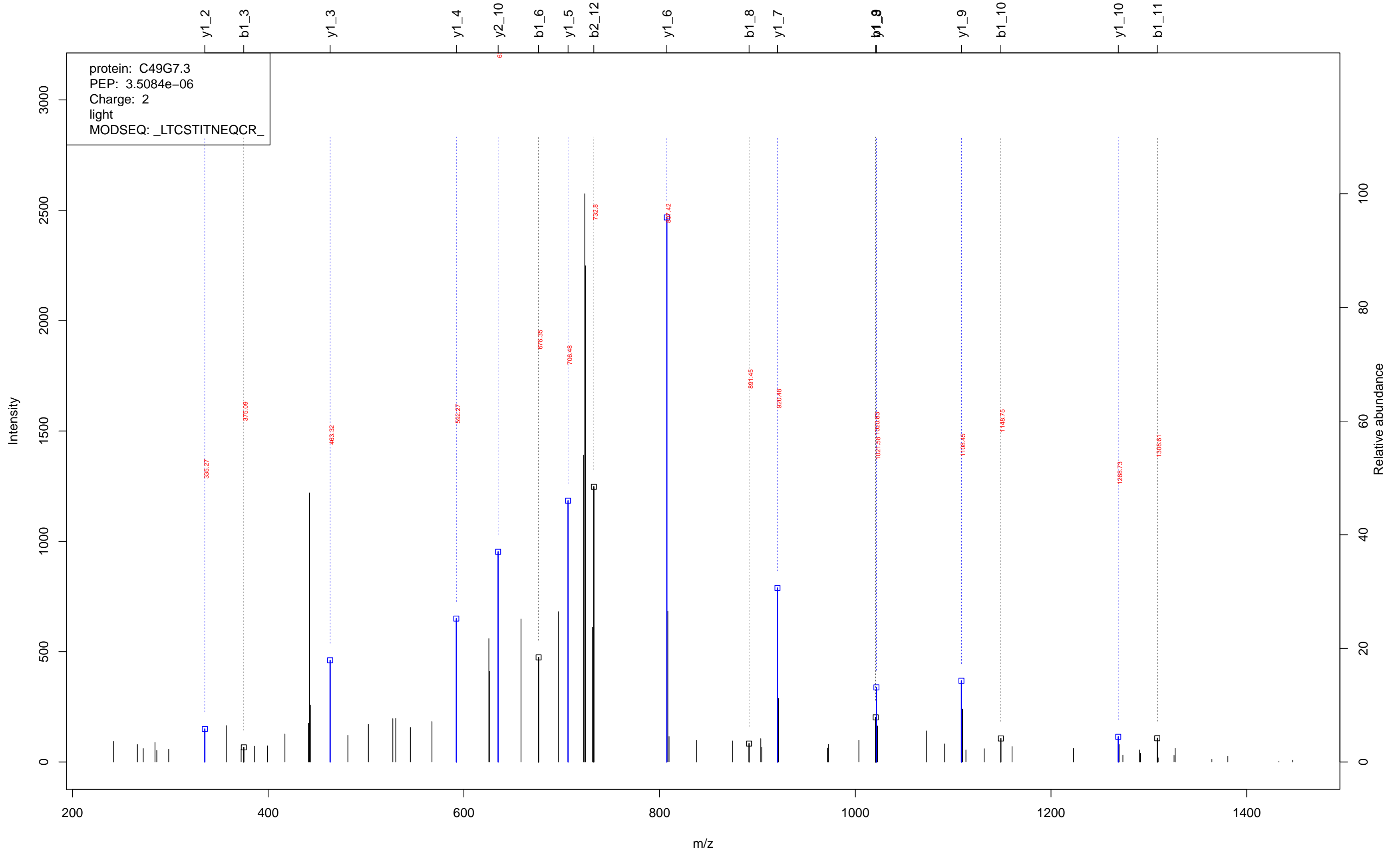


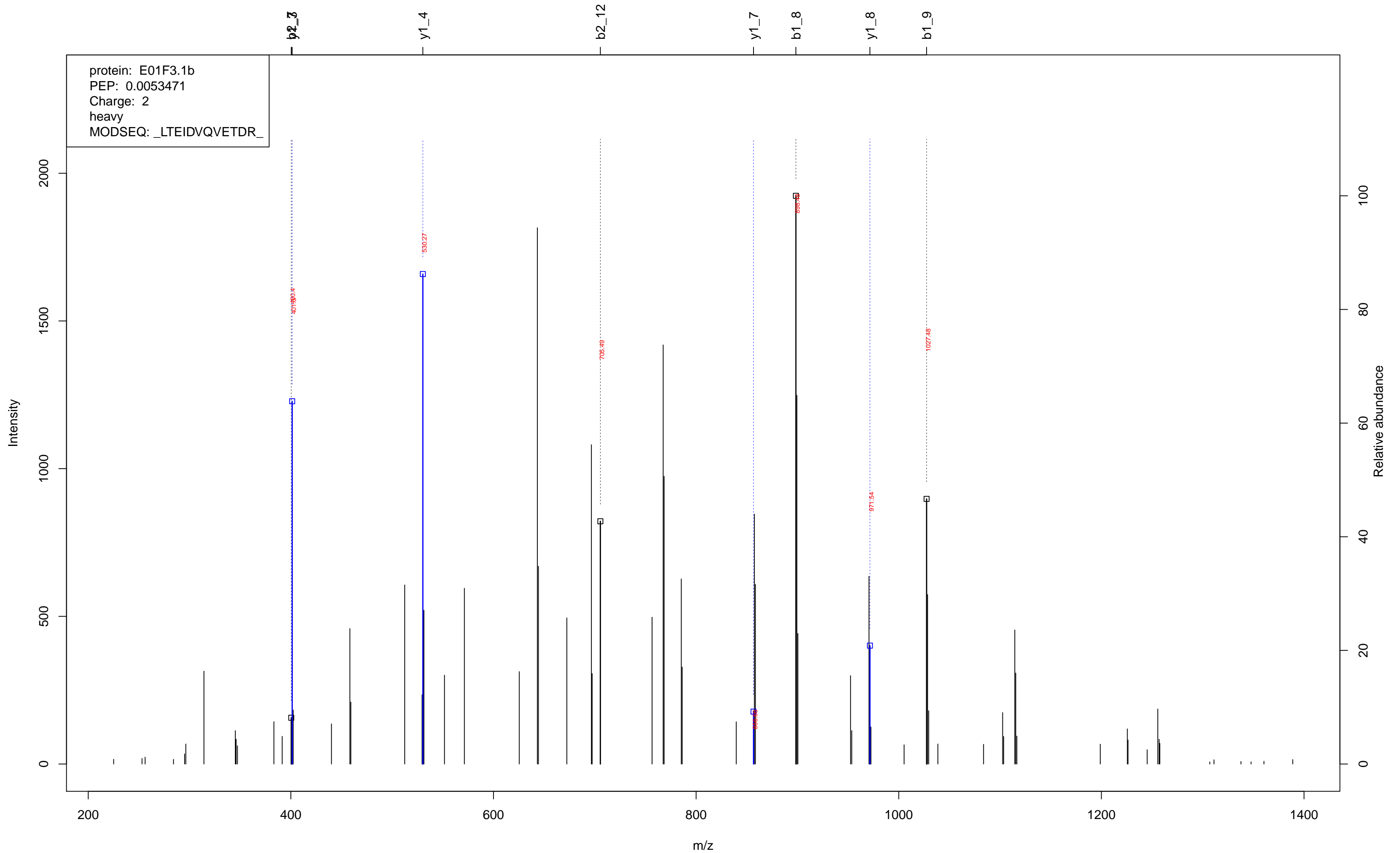
b1_3
y1_3
b1_3
b1_8
y2_9
y2_10
b2_12
y1_9

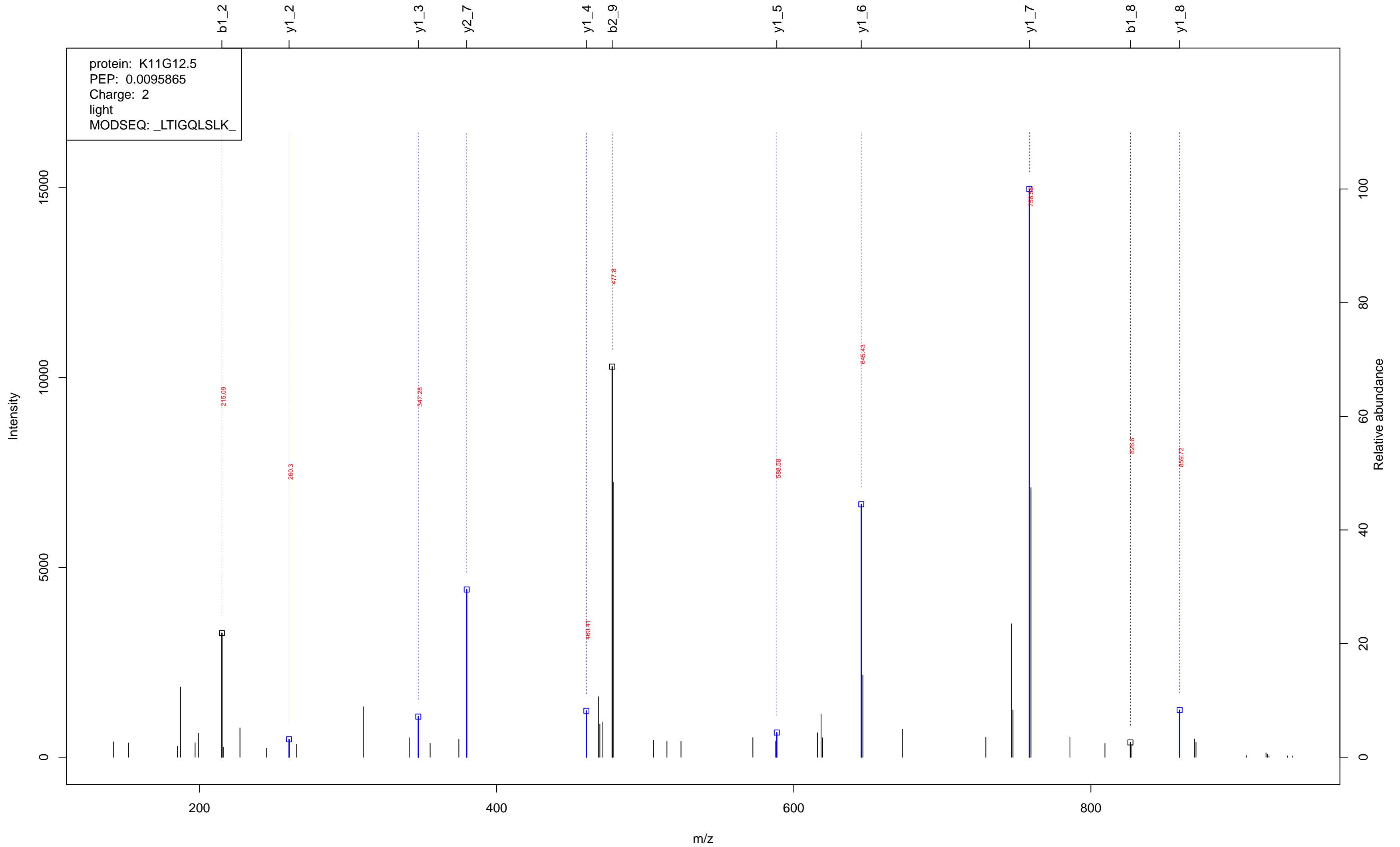
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PEP: 0.0097144
Charge: 3
heavy
MODSEQ: _LQLENDELAEVER_

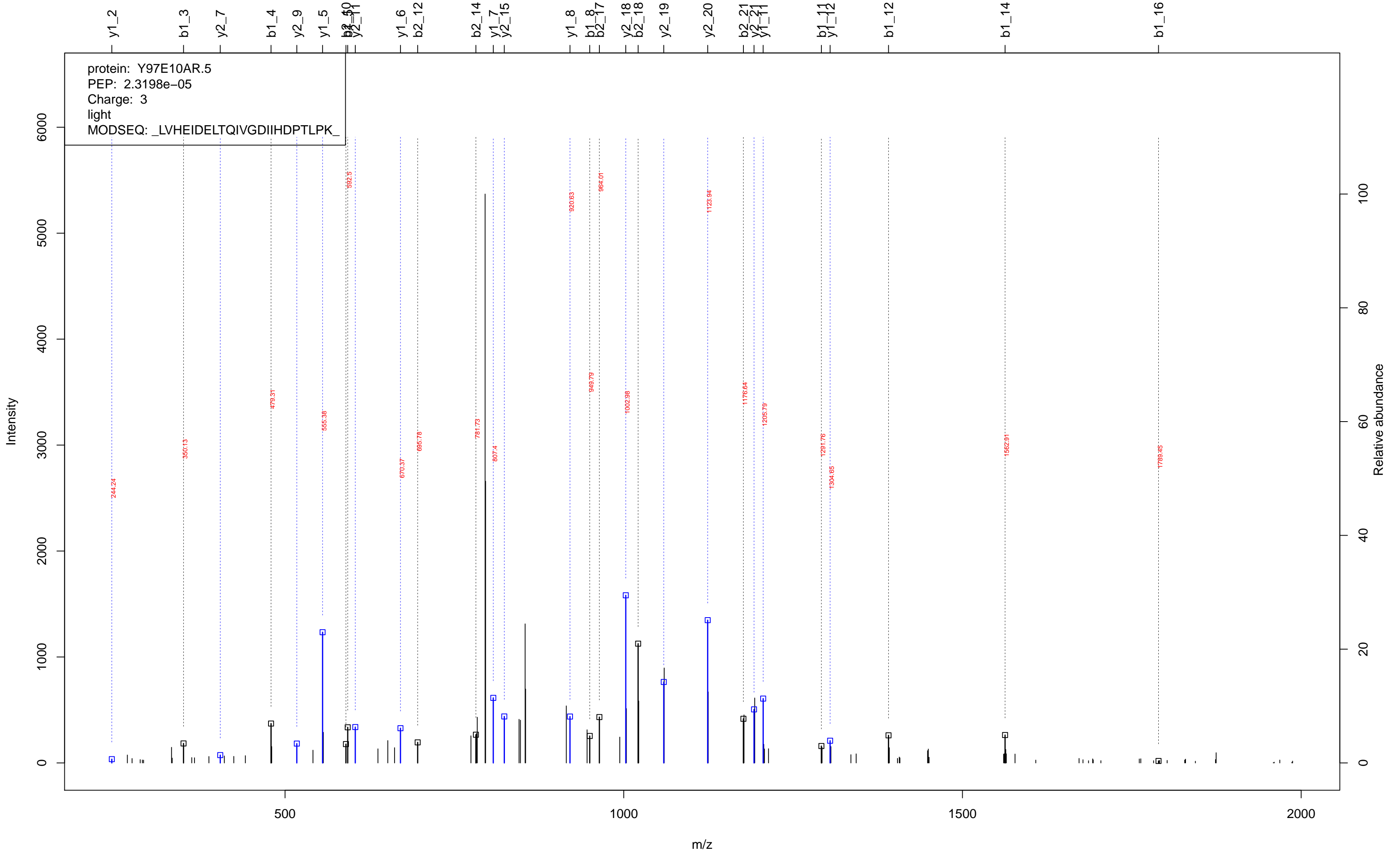


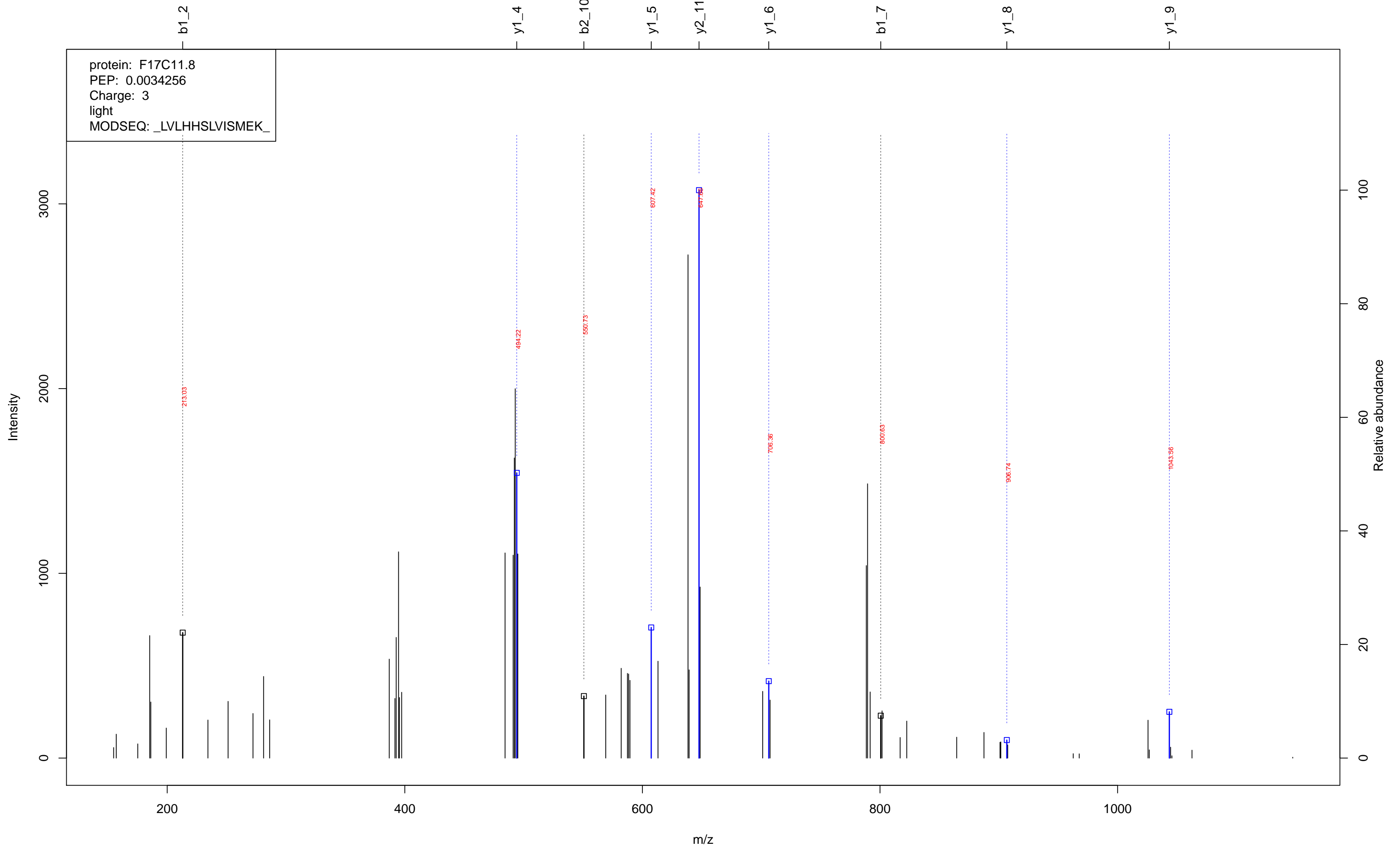


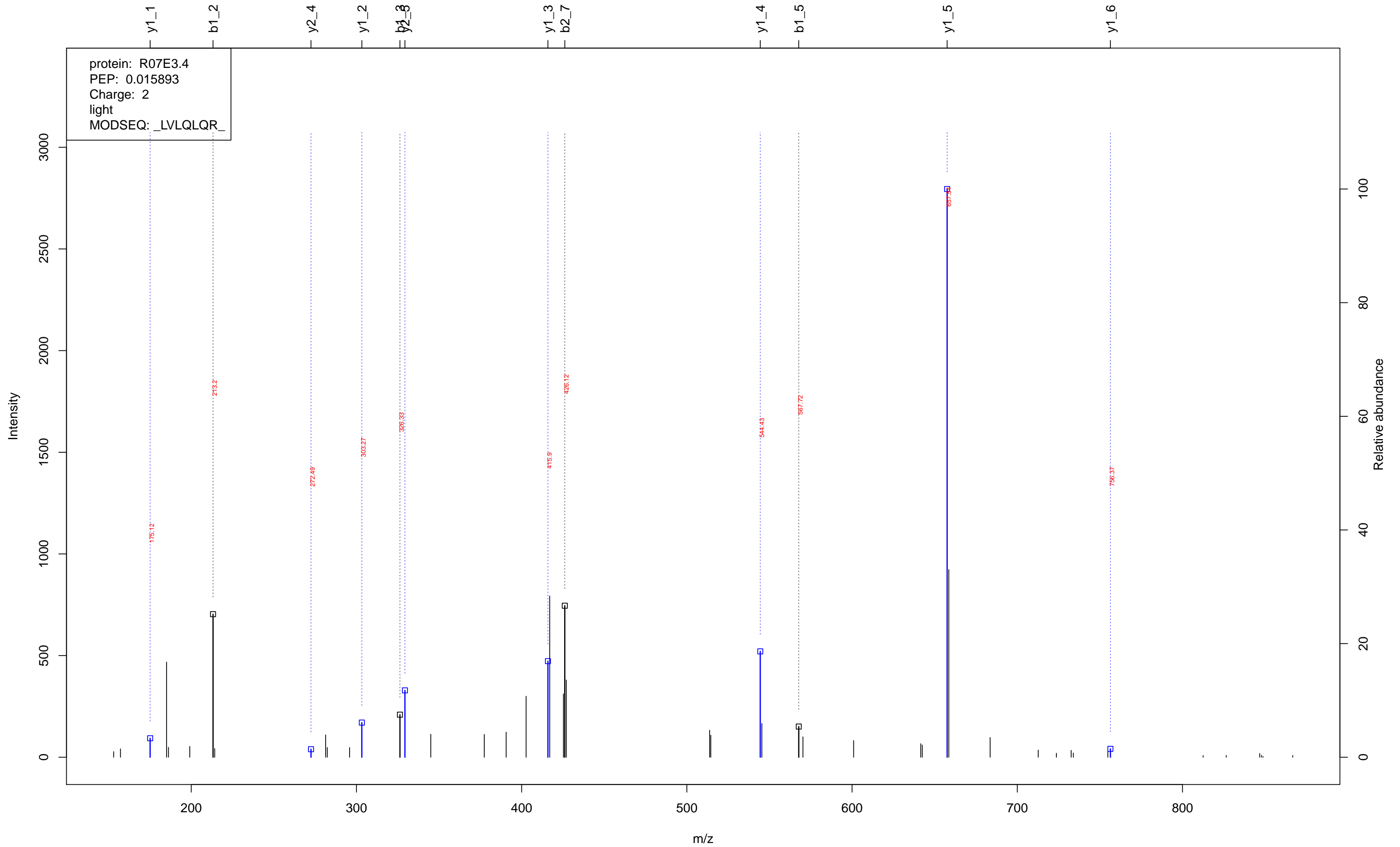


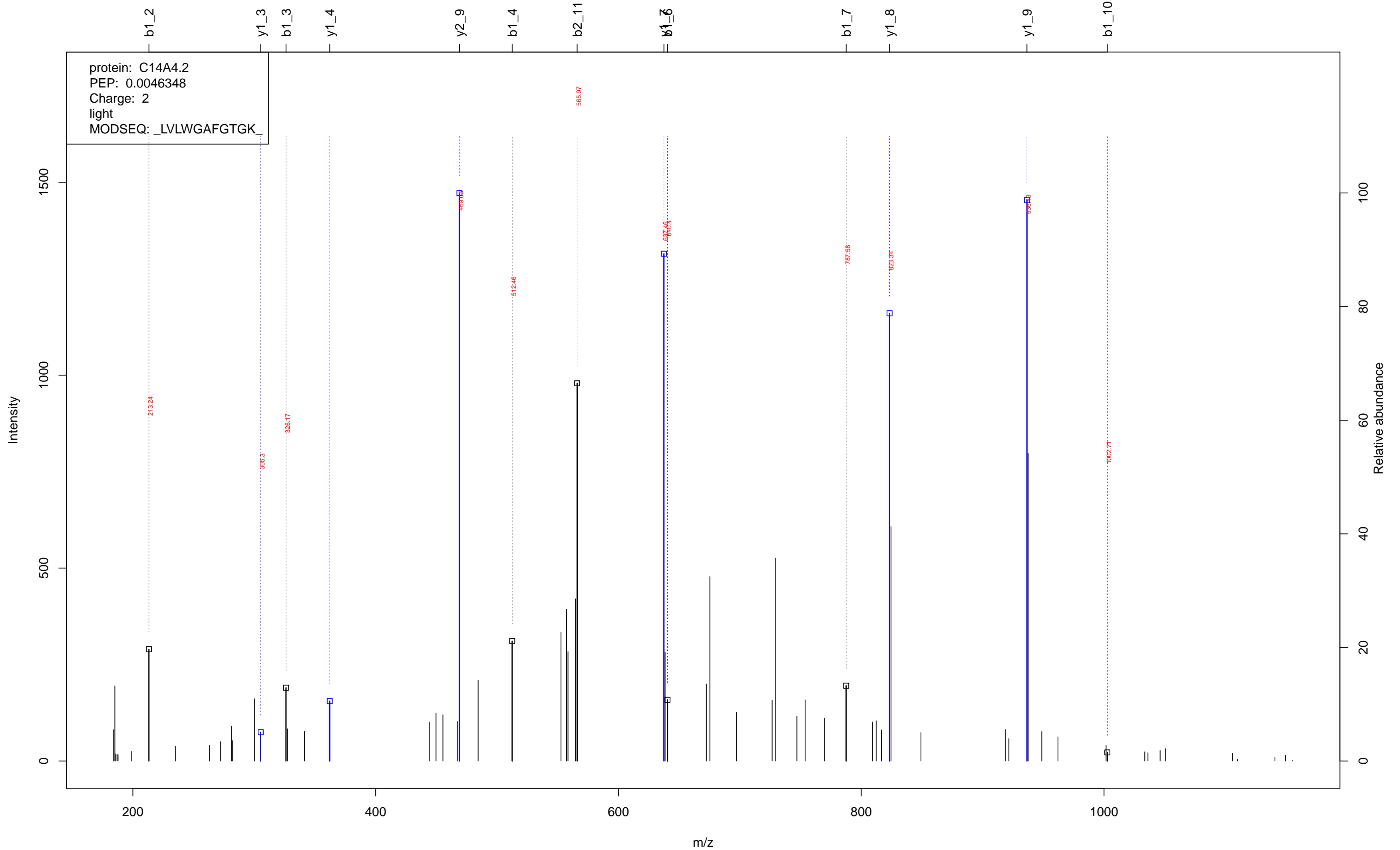


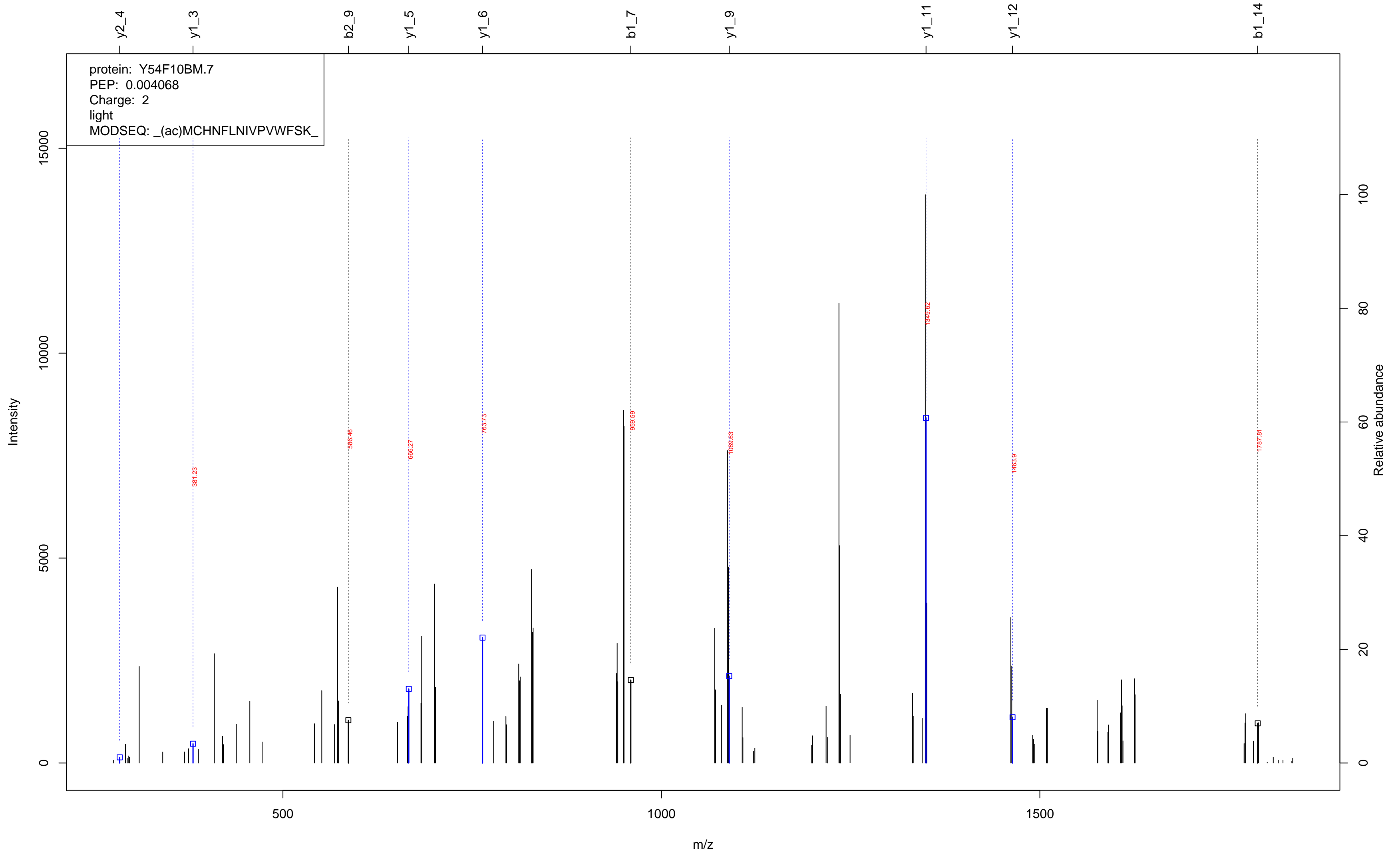


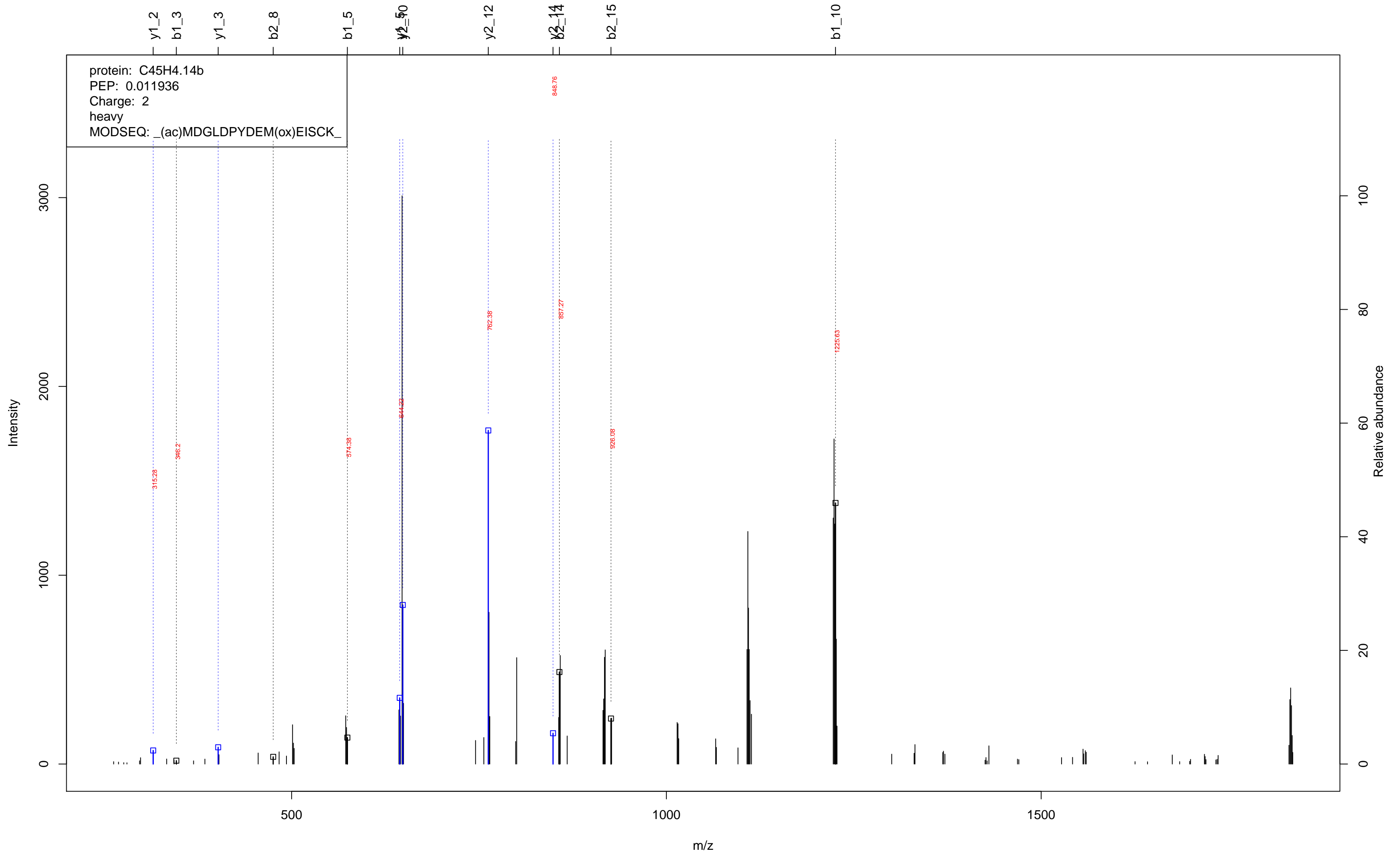


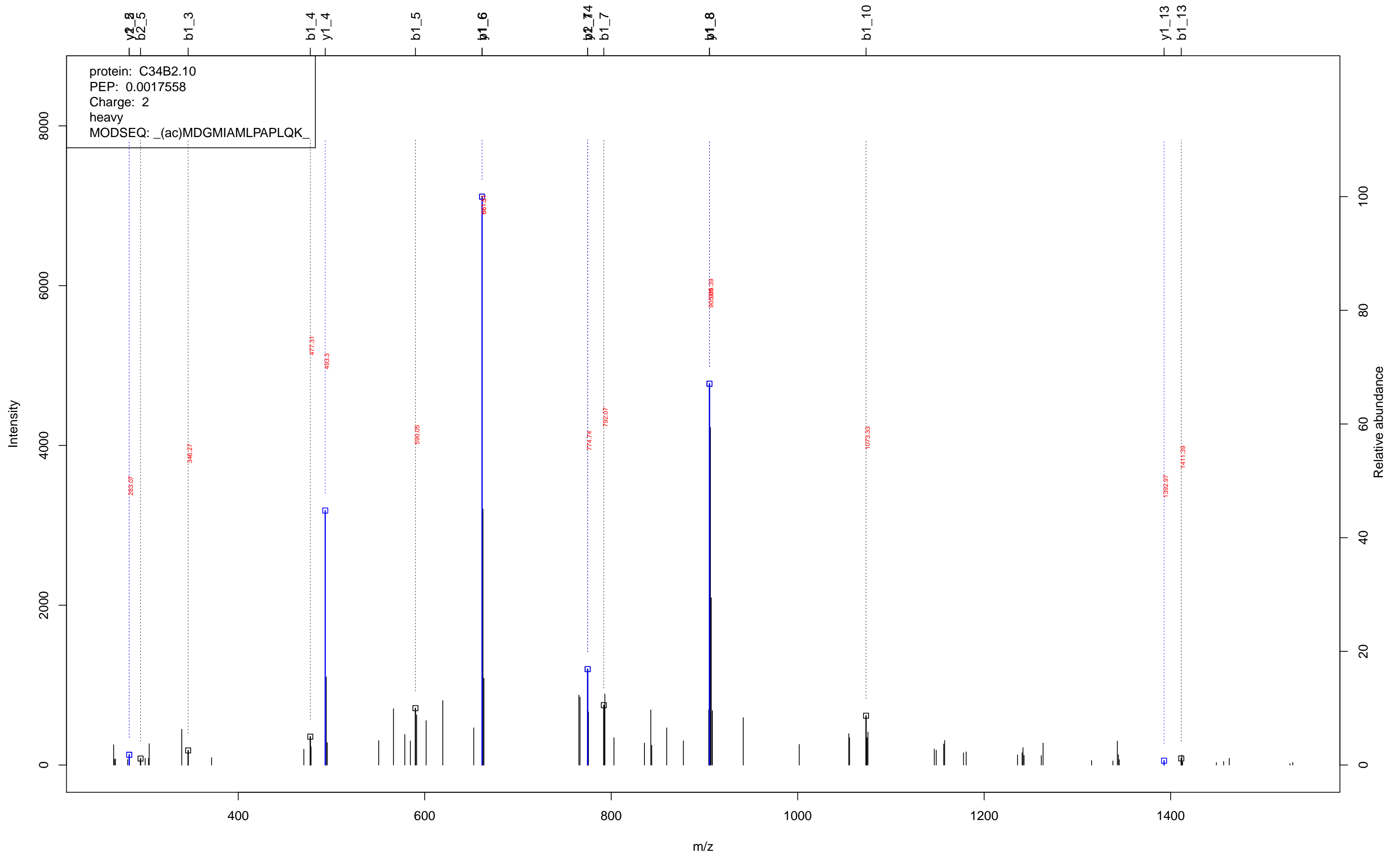


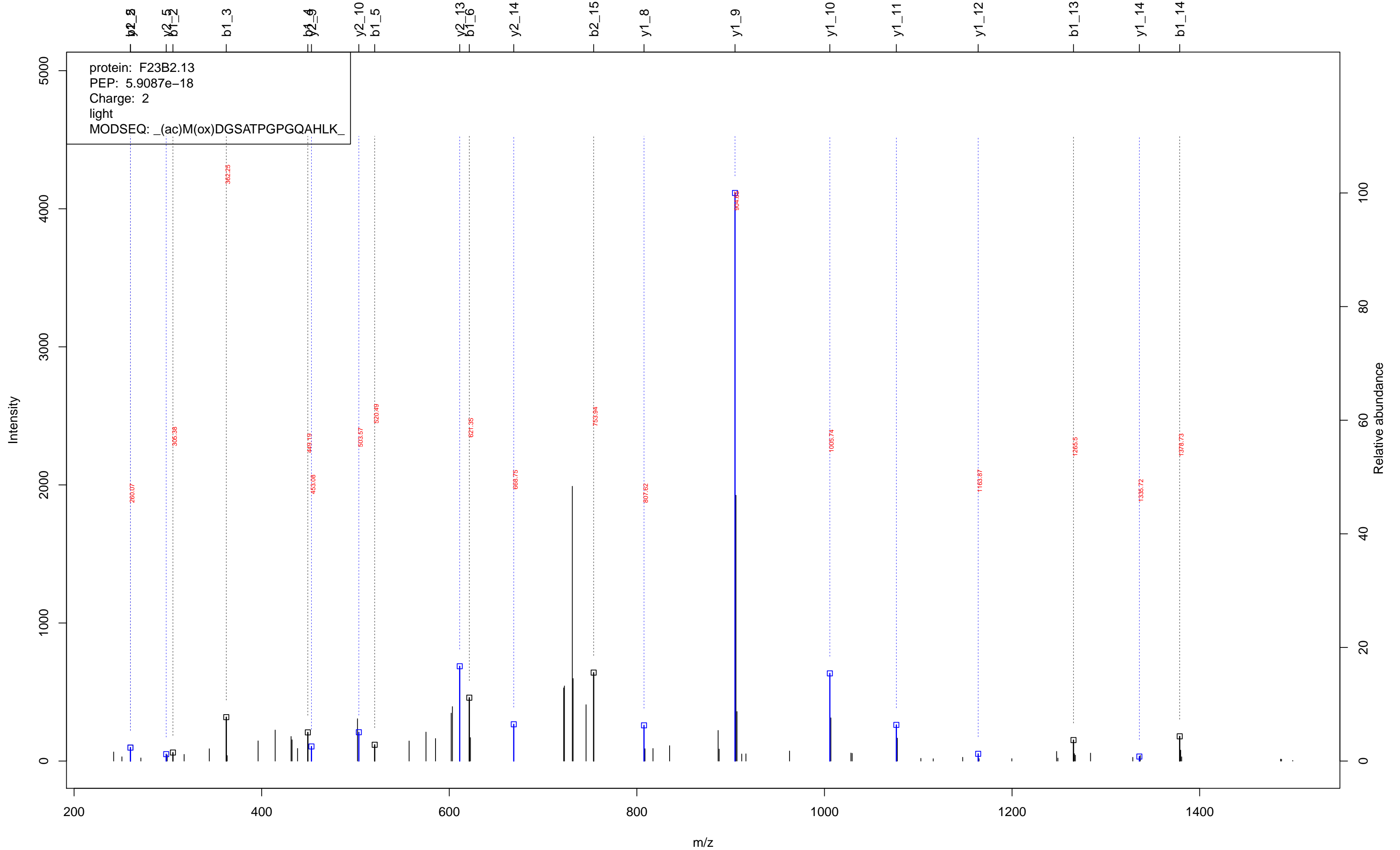


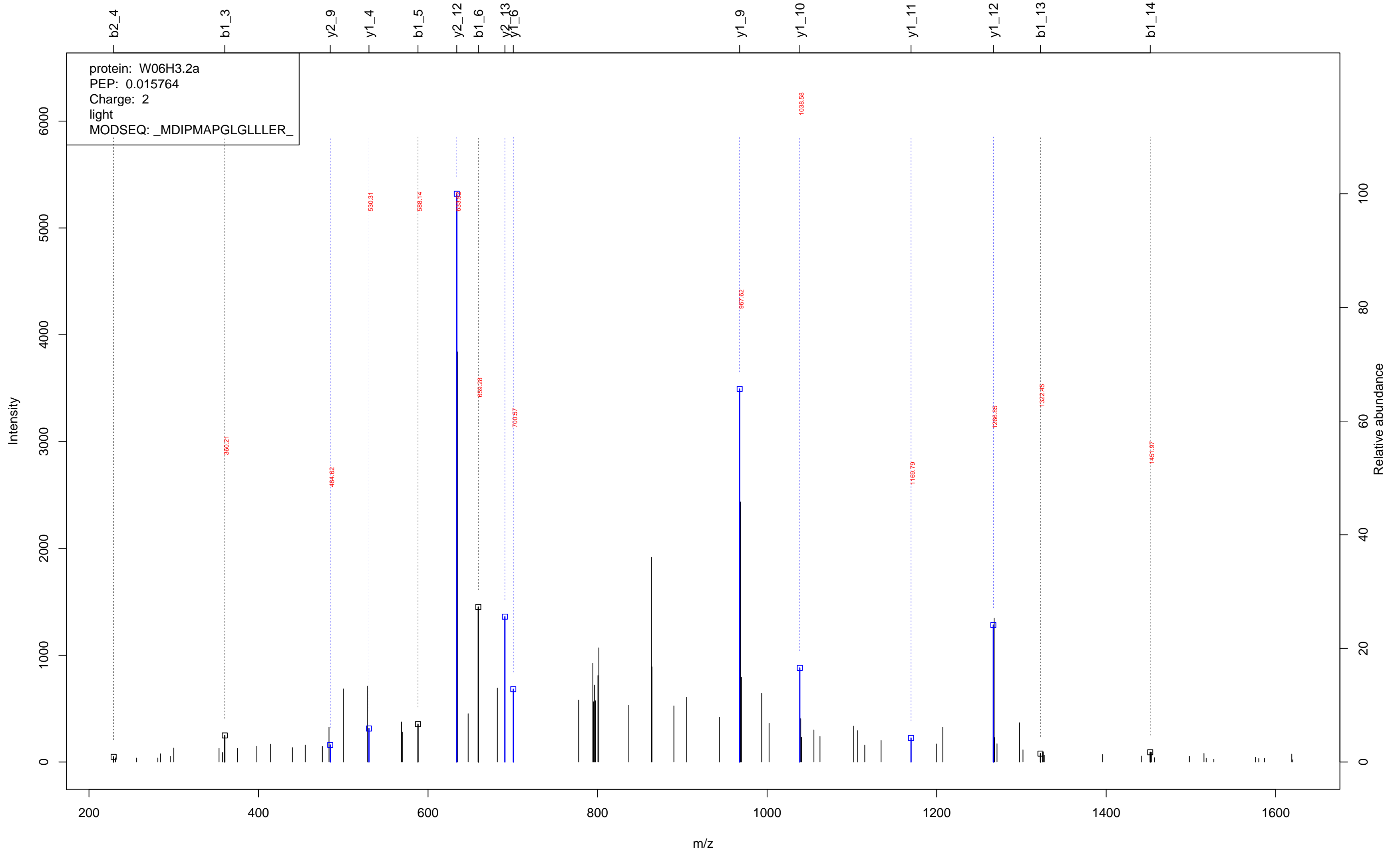


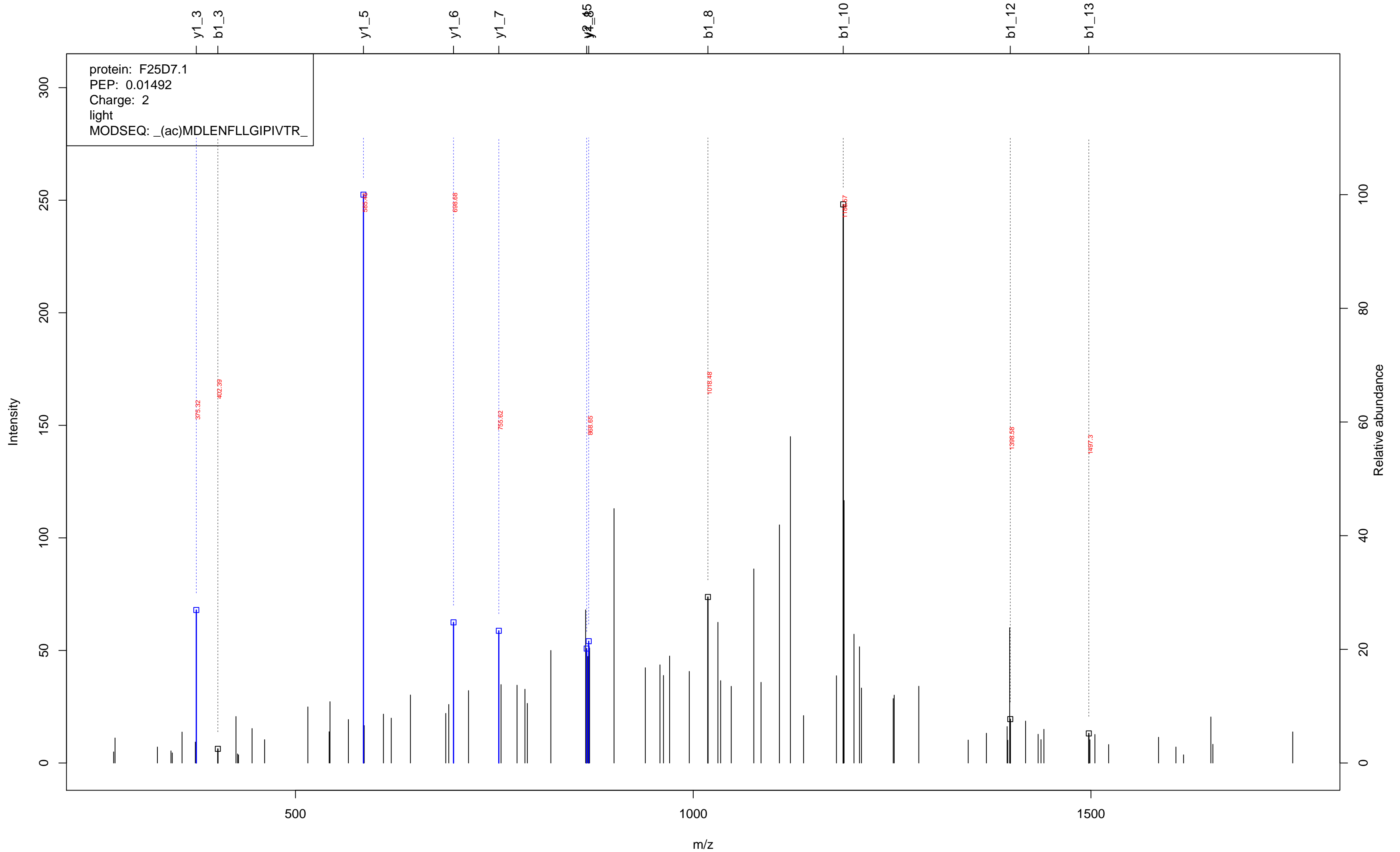


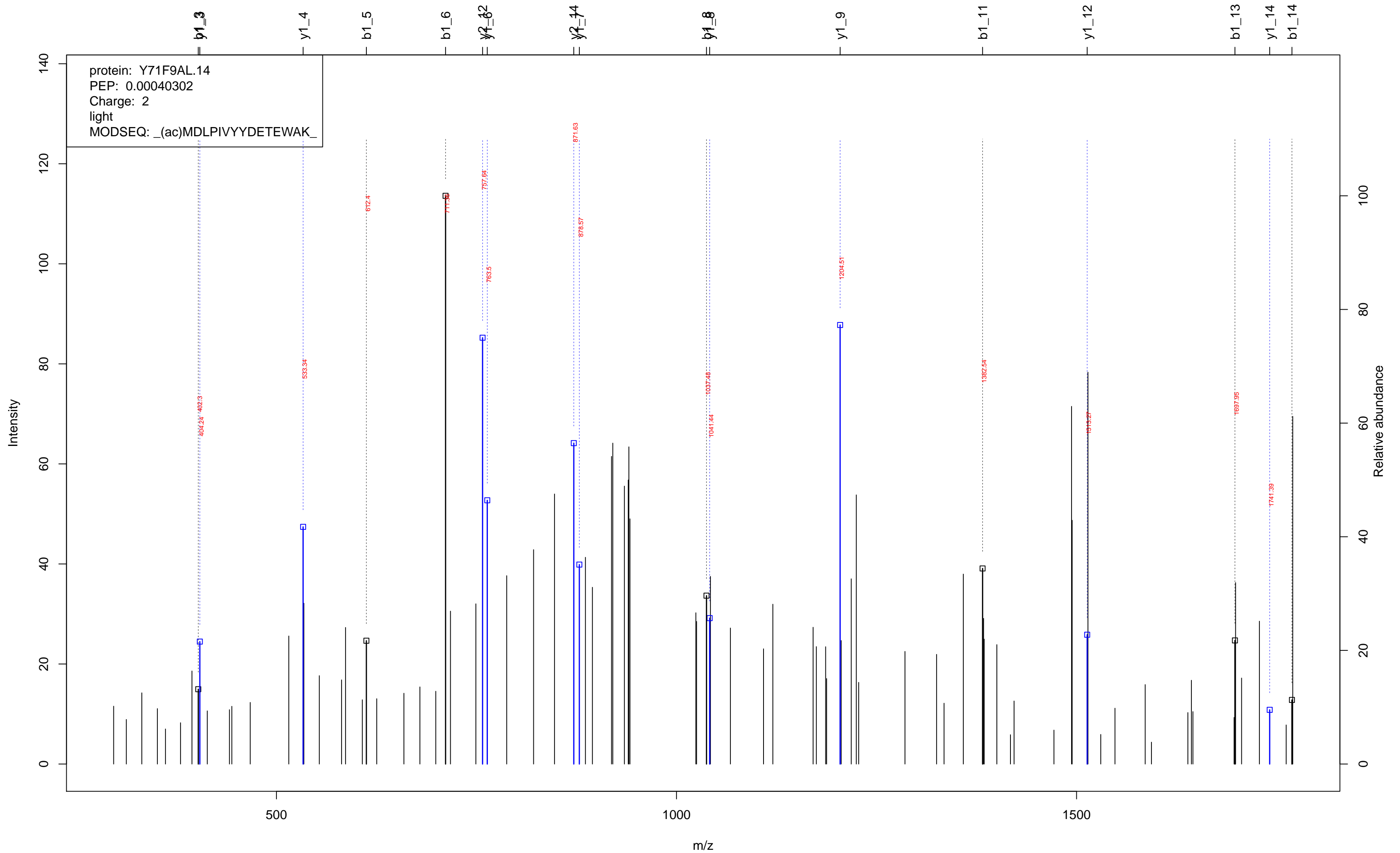


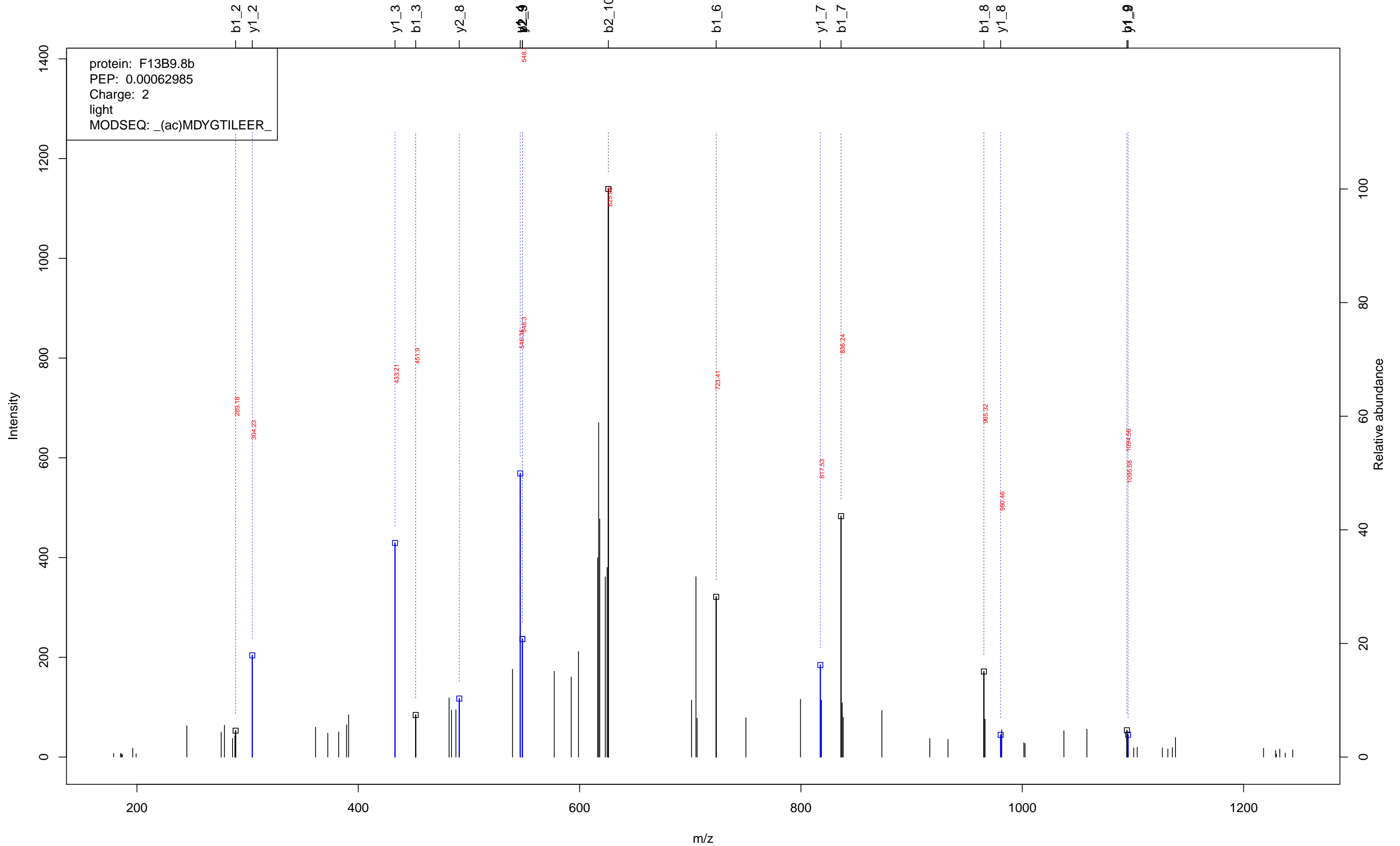


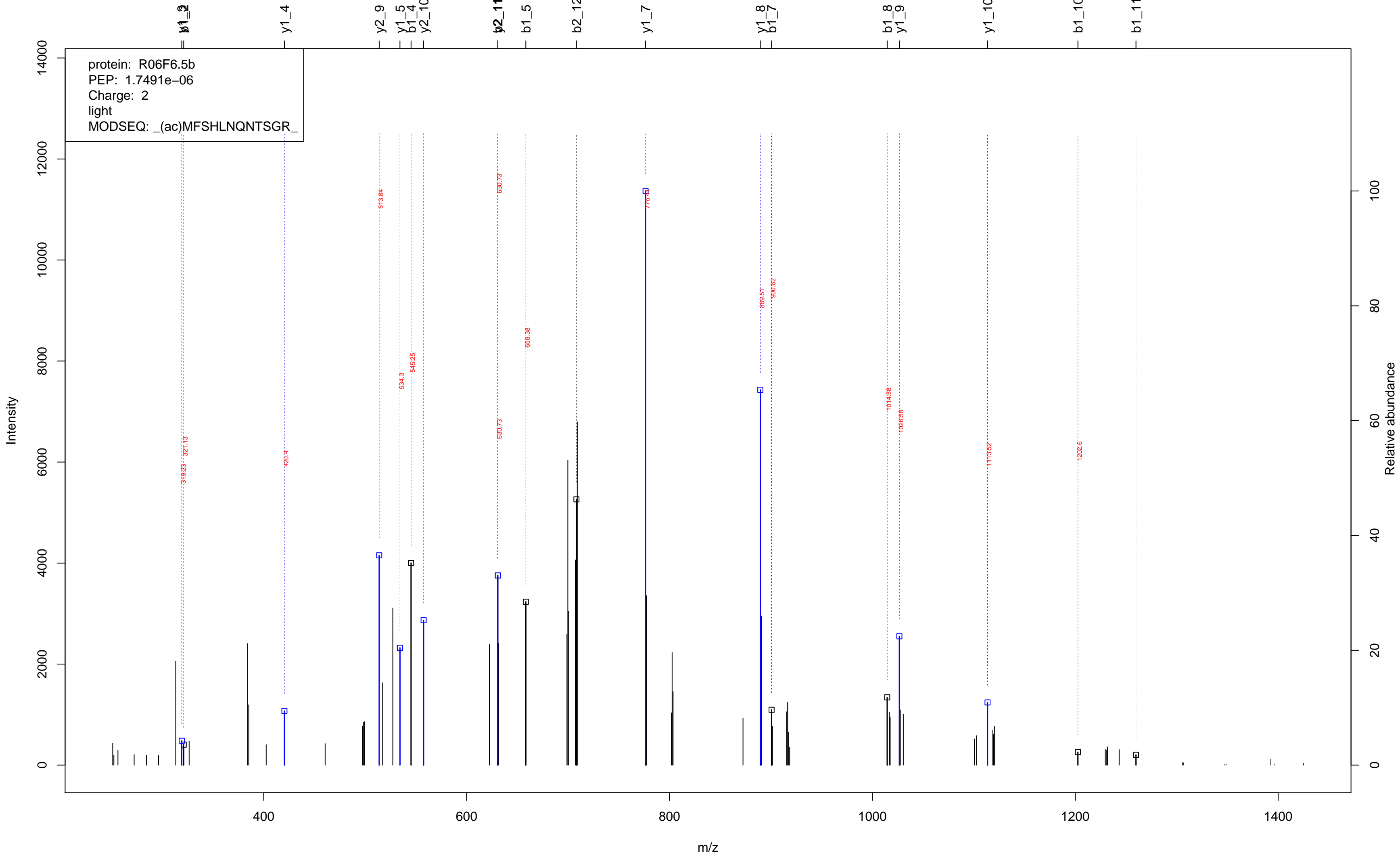


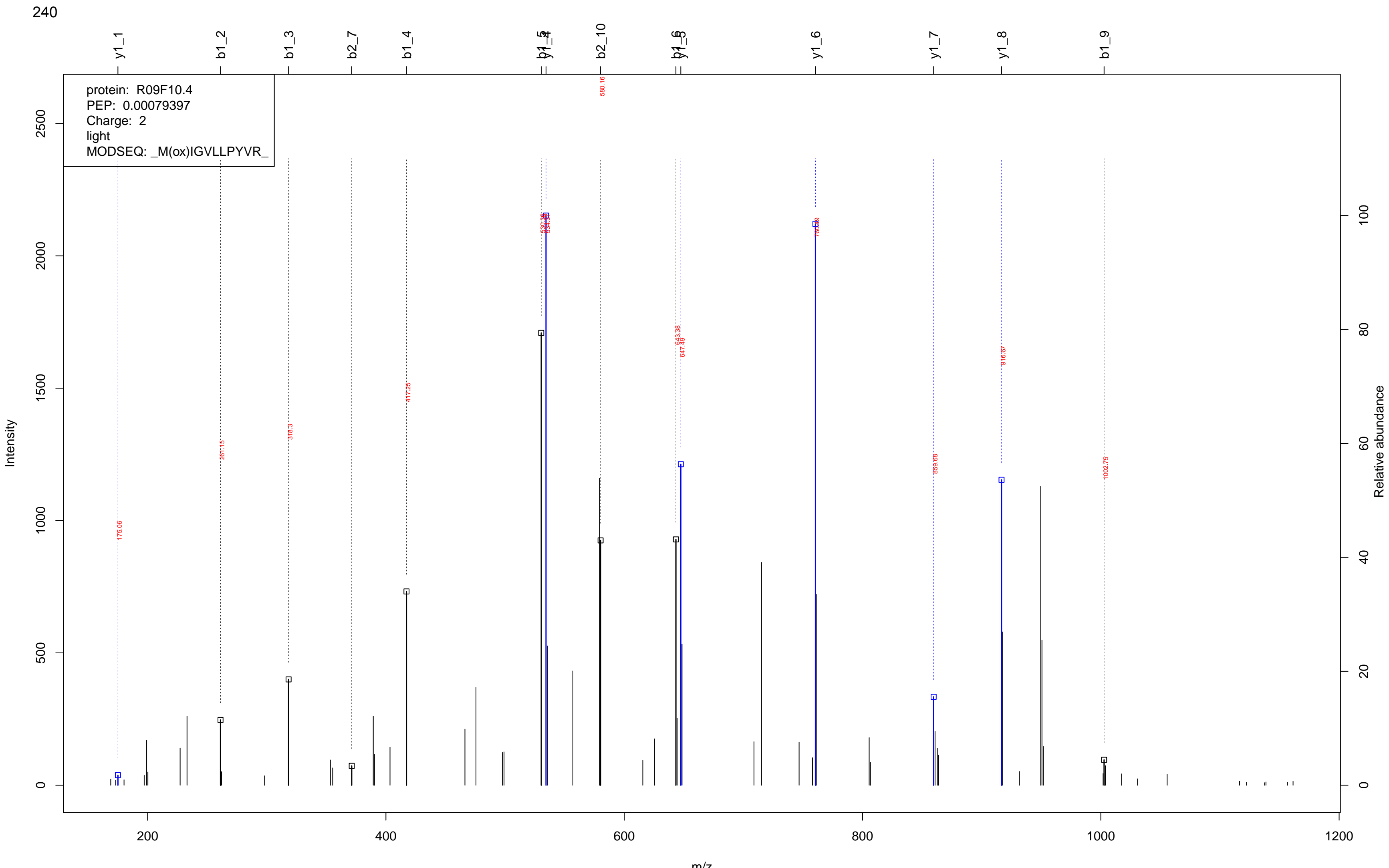




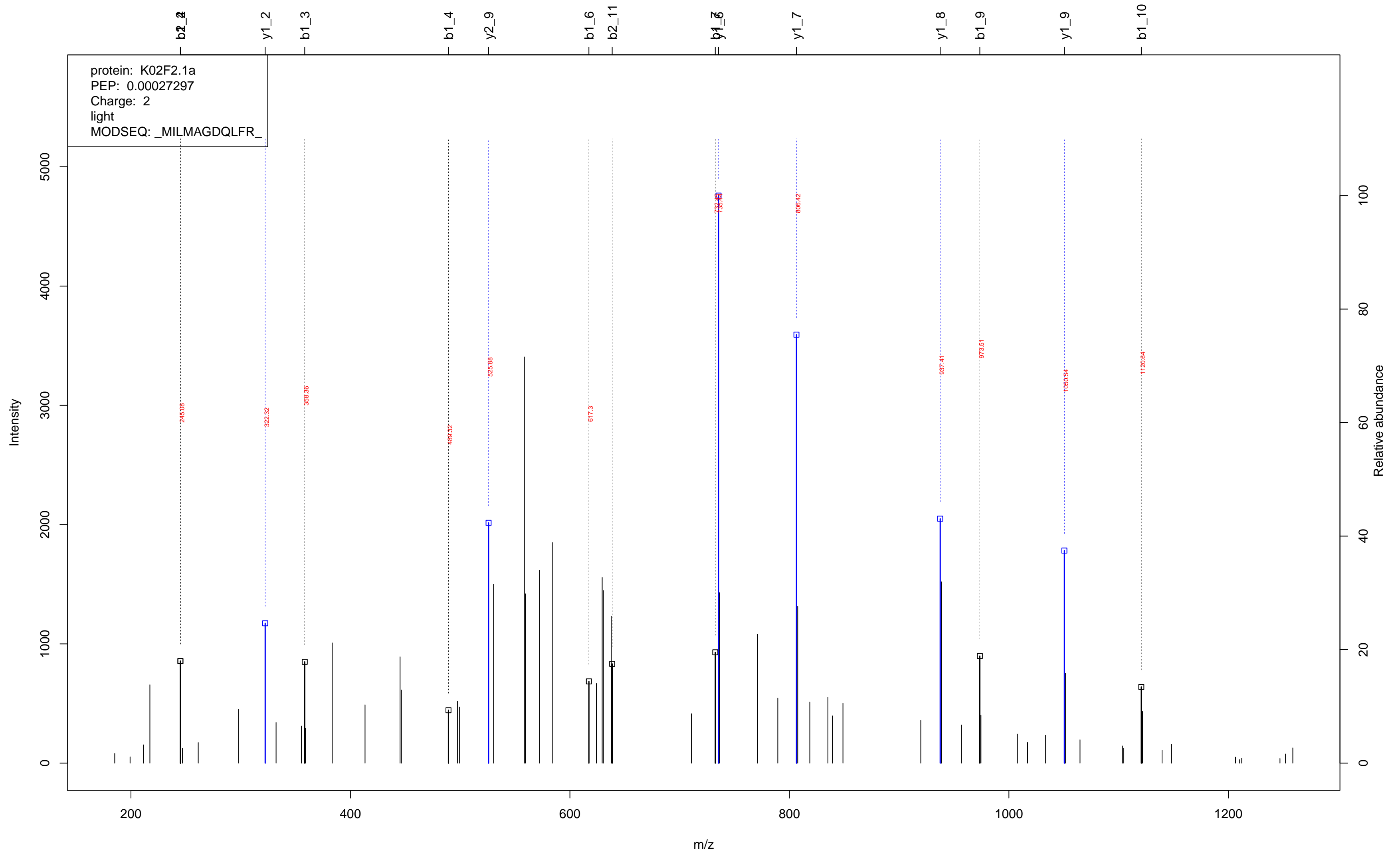


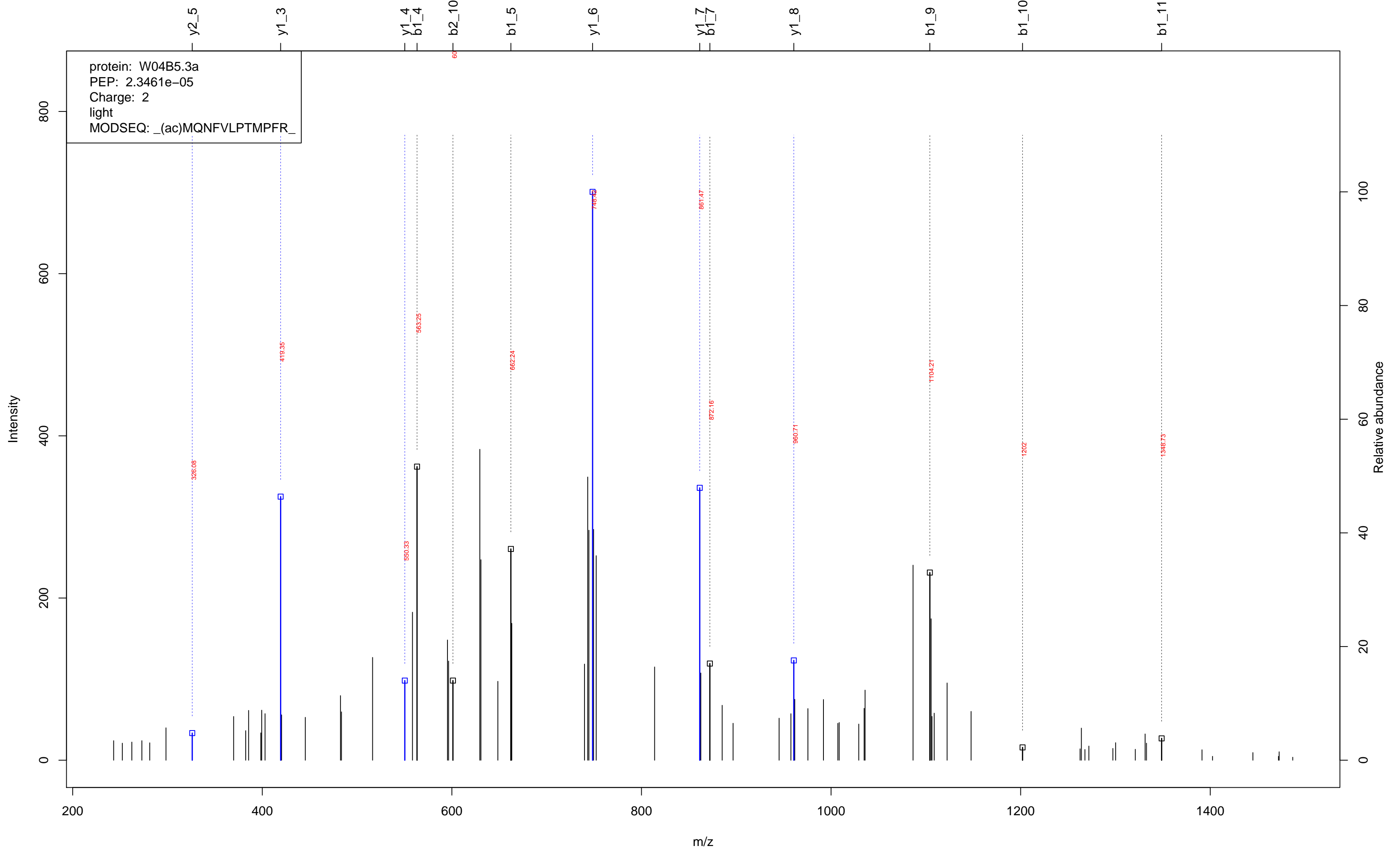


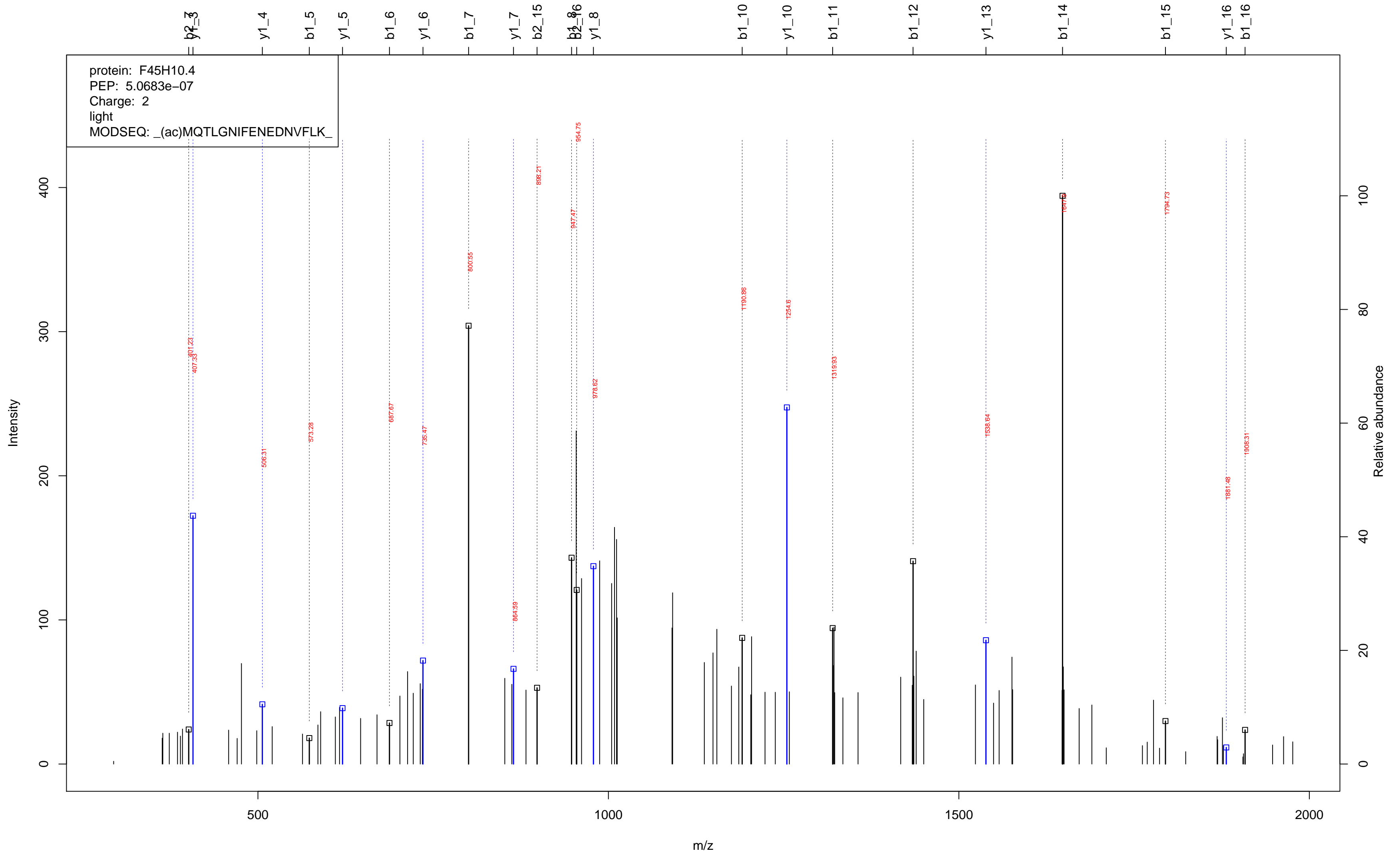


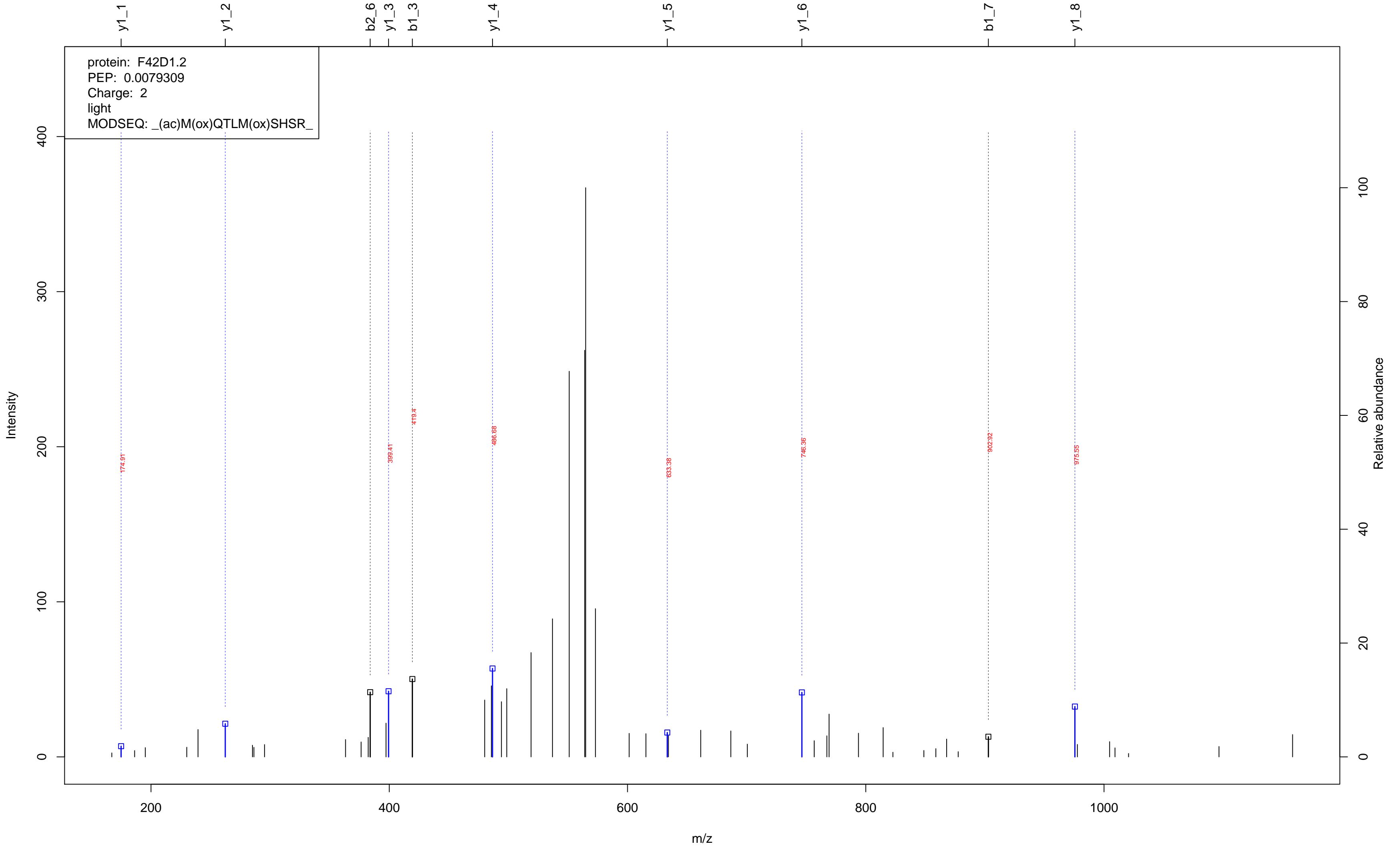


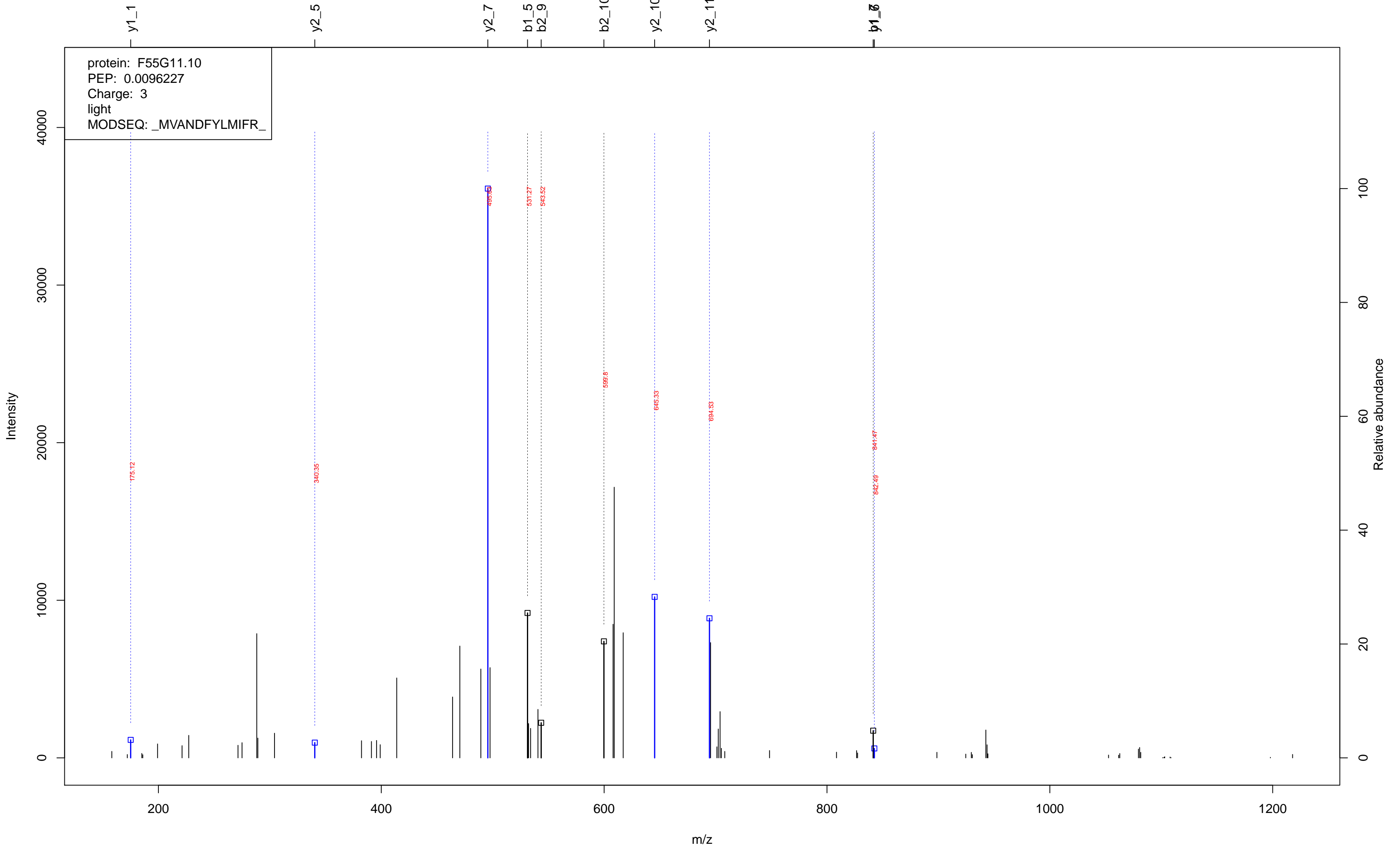
MIGVLLPYVR / File181476 Spectrum7287 scans: 4760 [S:/p743/Proteomics/ORBI_2/cpanse_20160211_peakplot/20121012_12_38to40ExclList_N2hCBI.RAW]

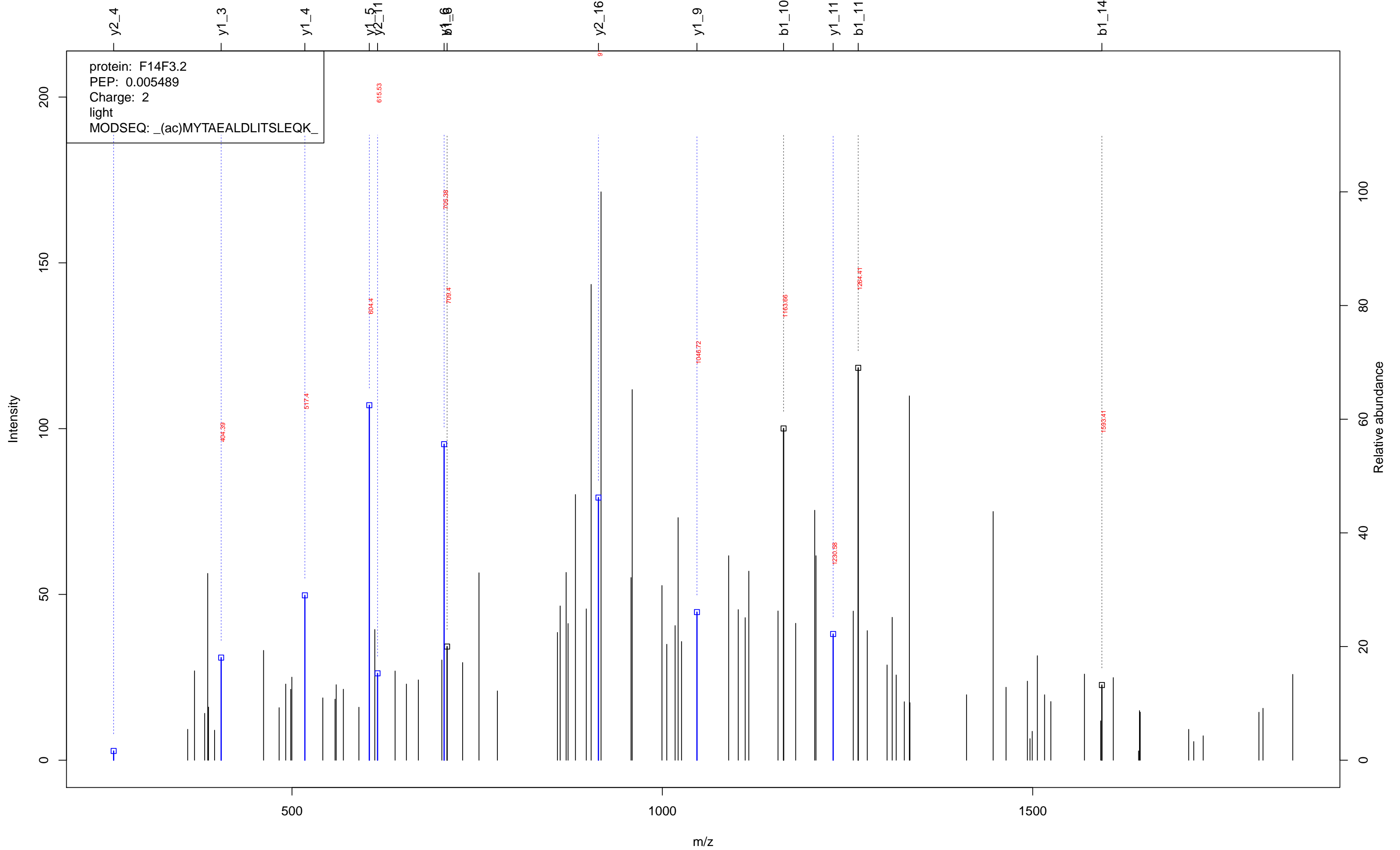


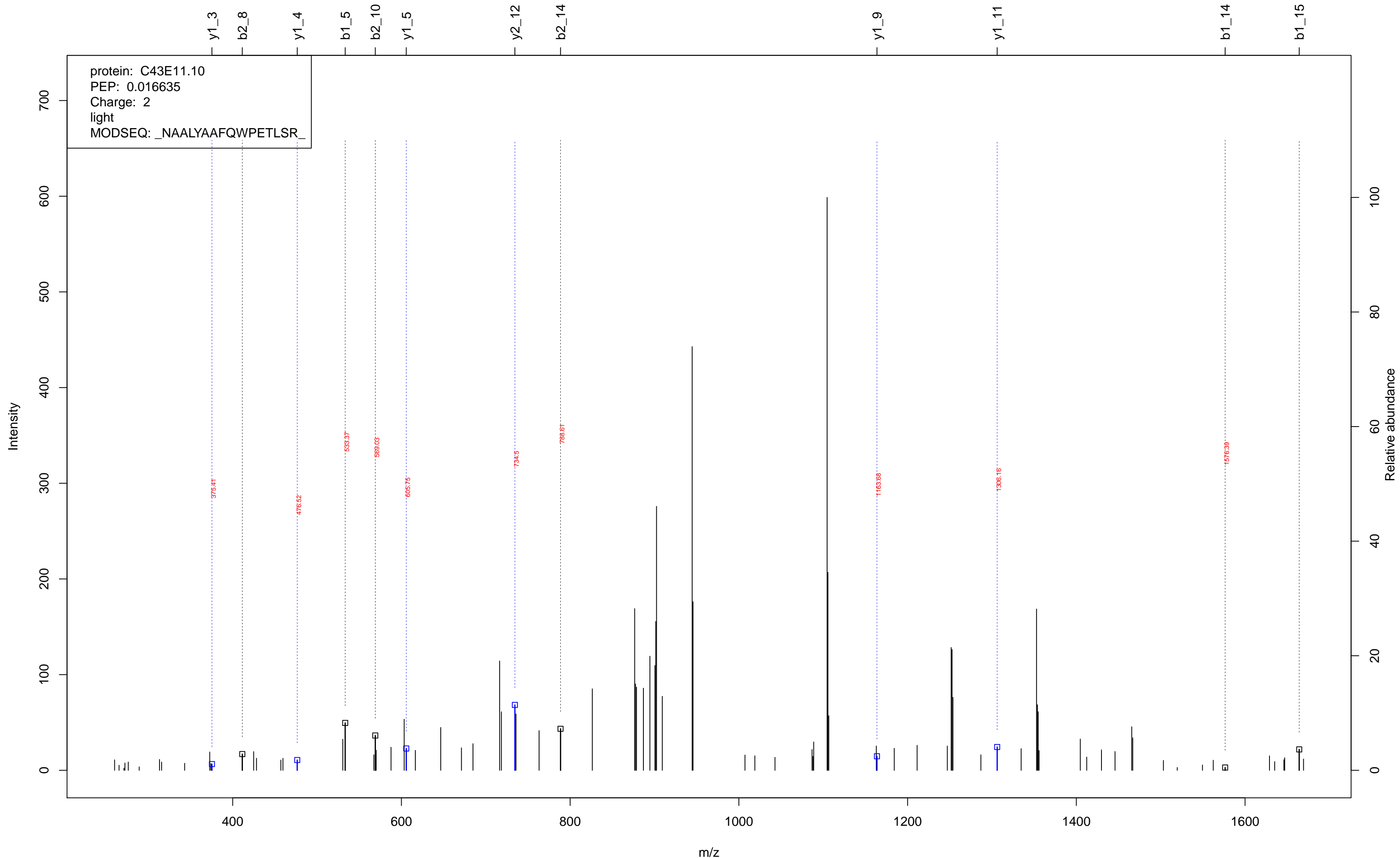


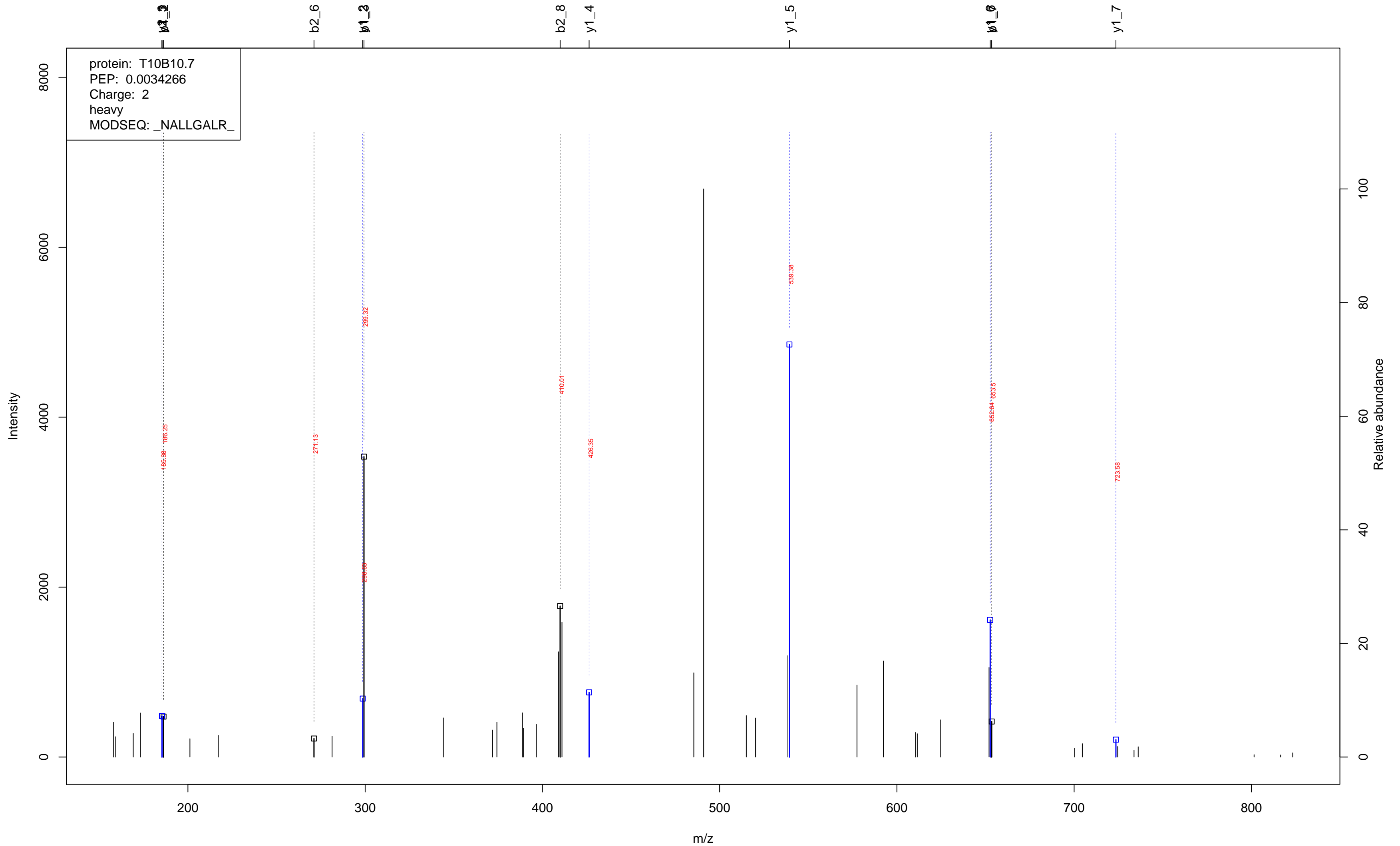


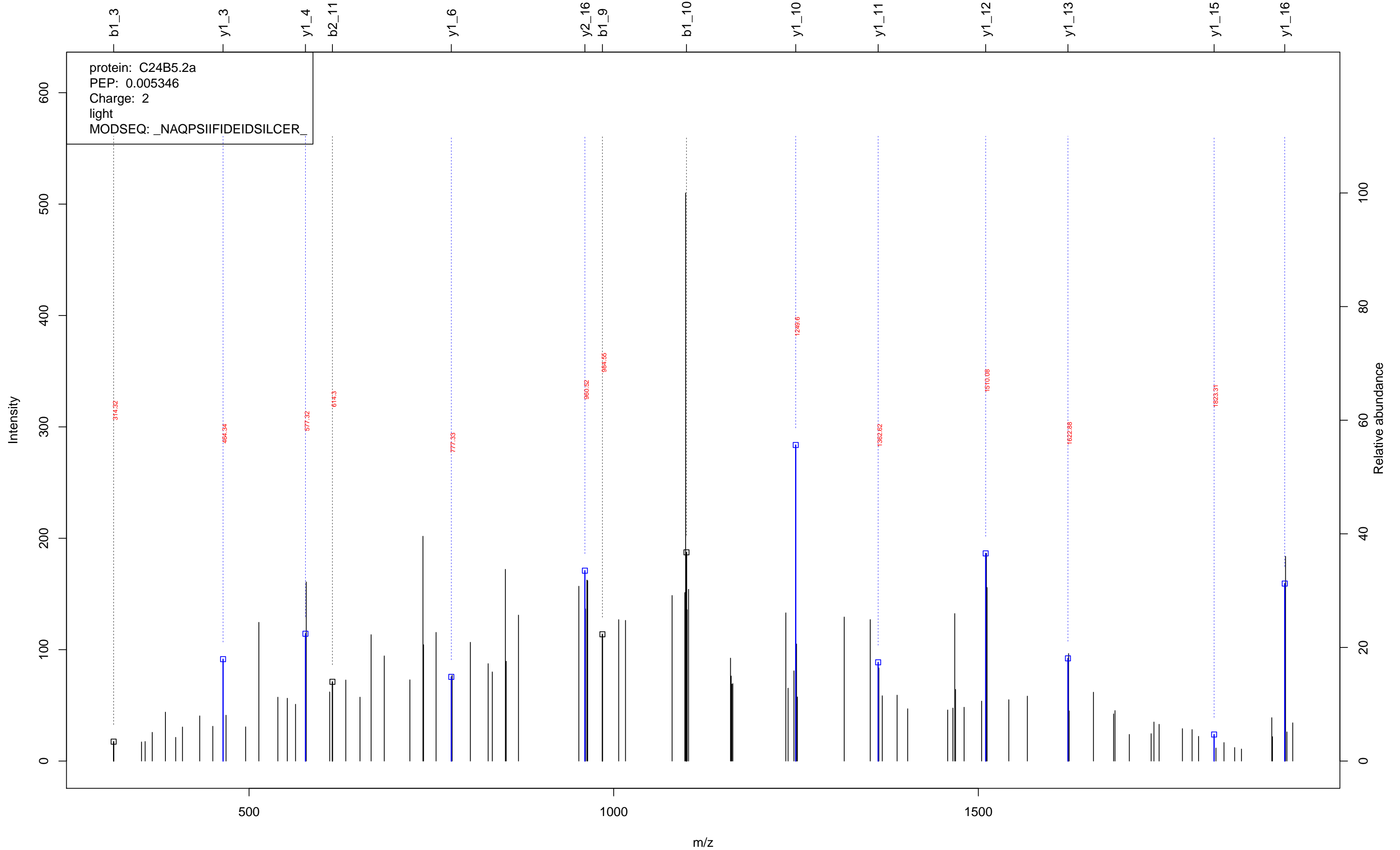












250

y1_1

y2_2

y1_3

b1_4

b2_9

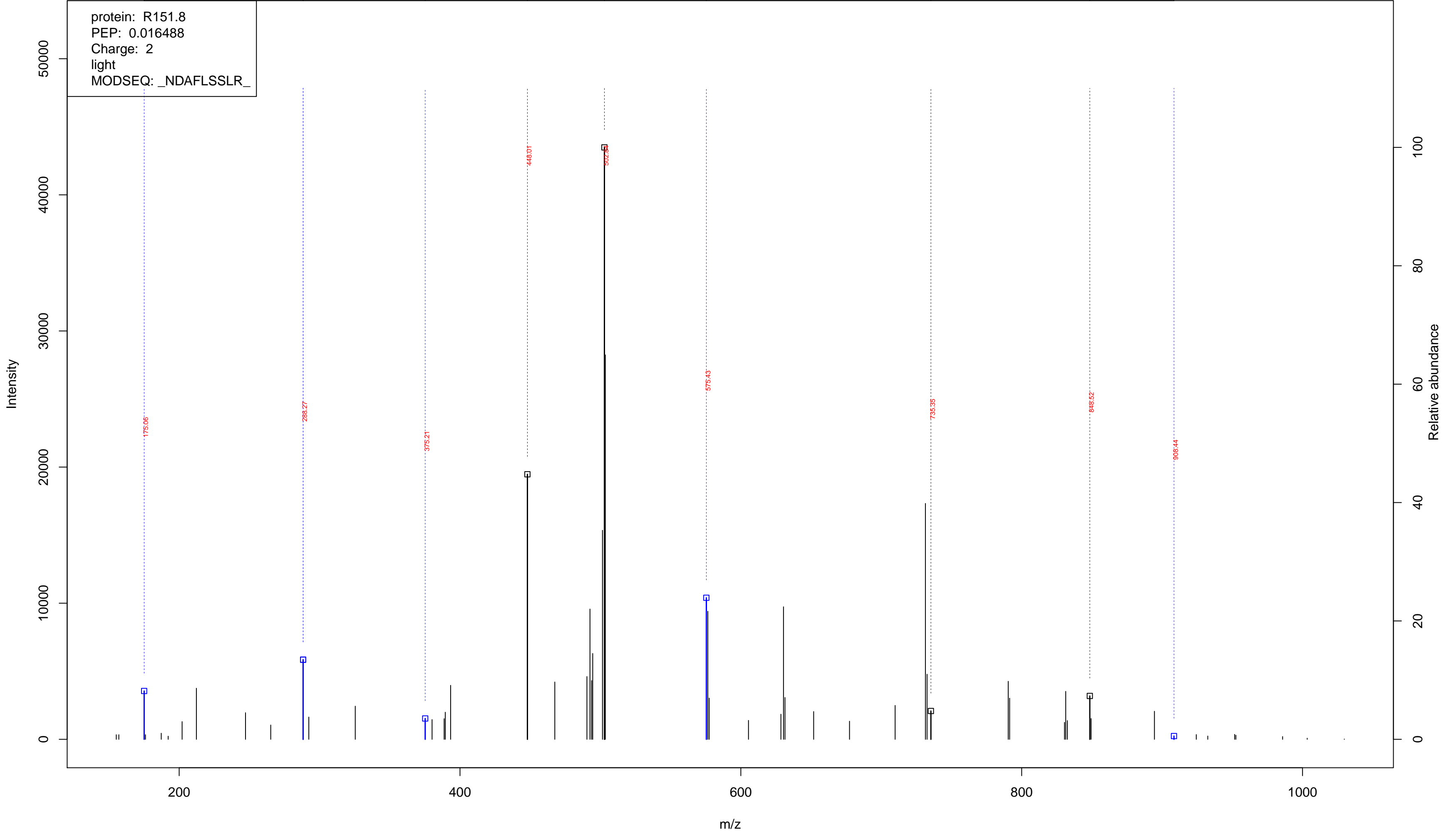
y1_5

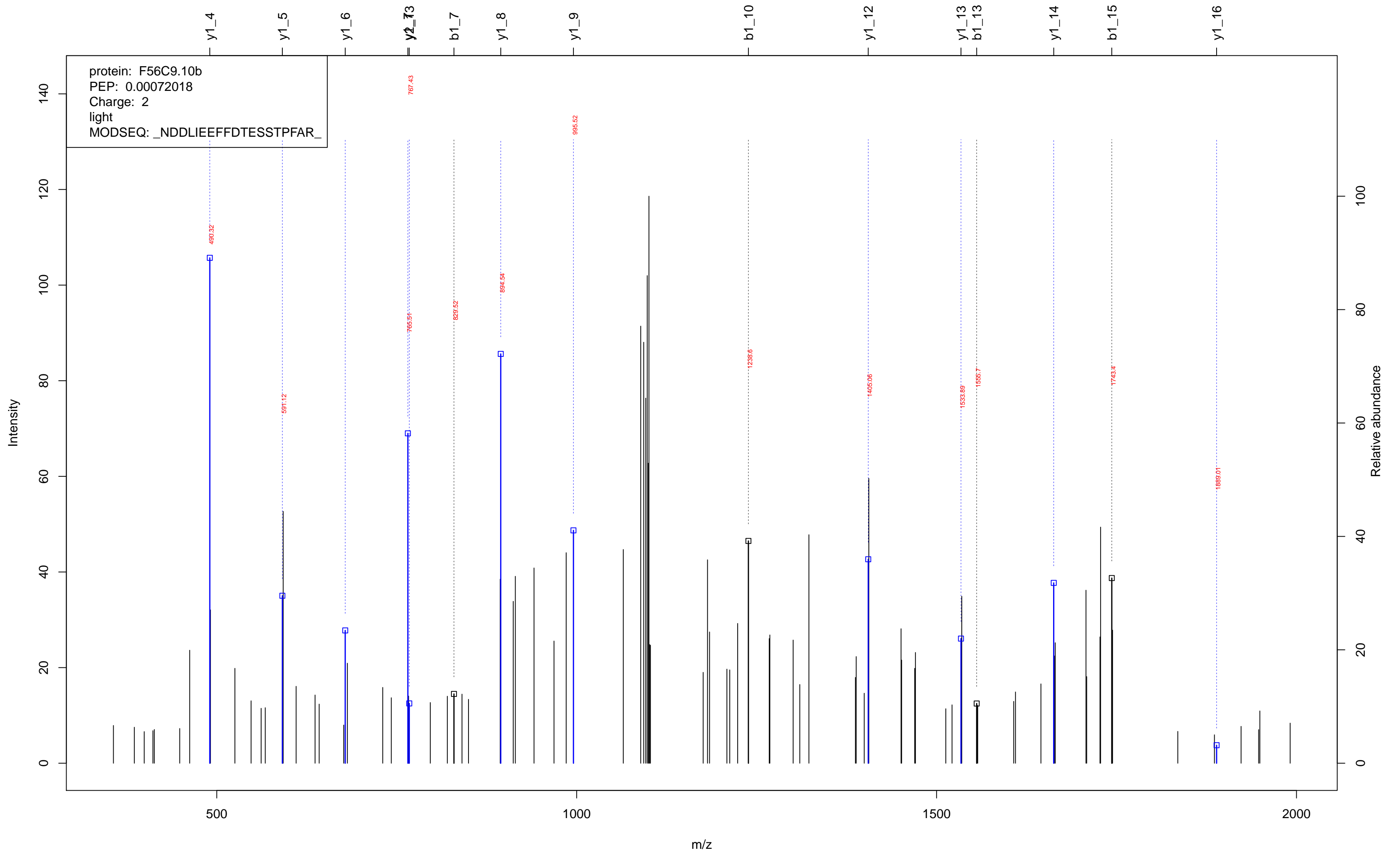
b1_7

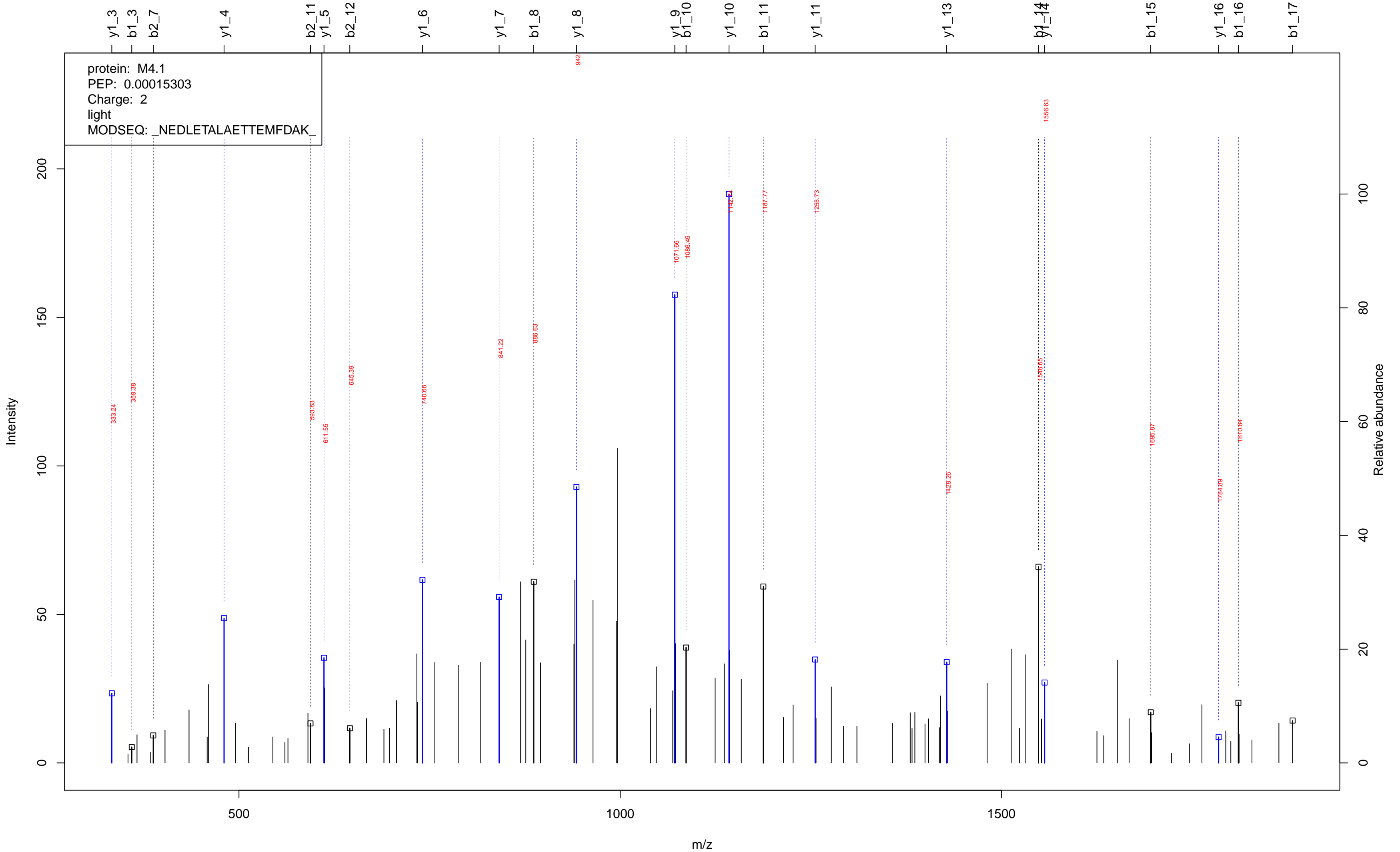
b1_8

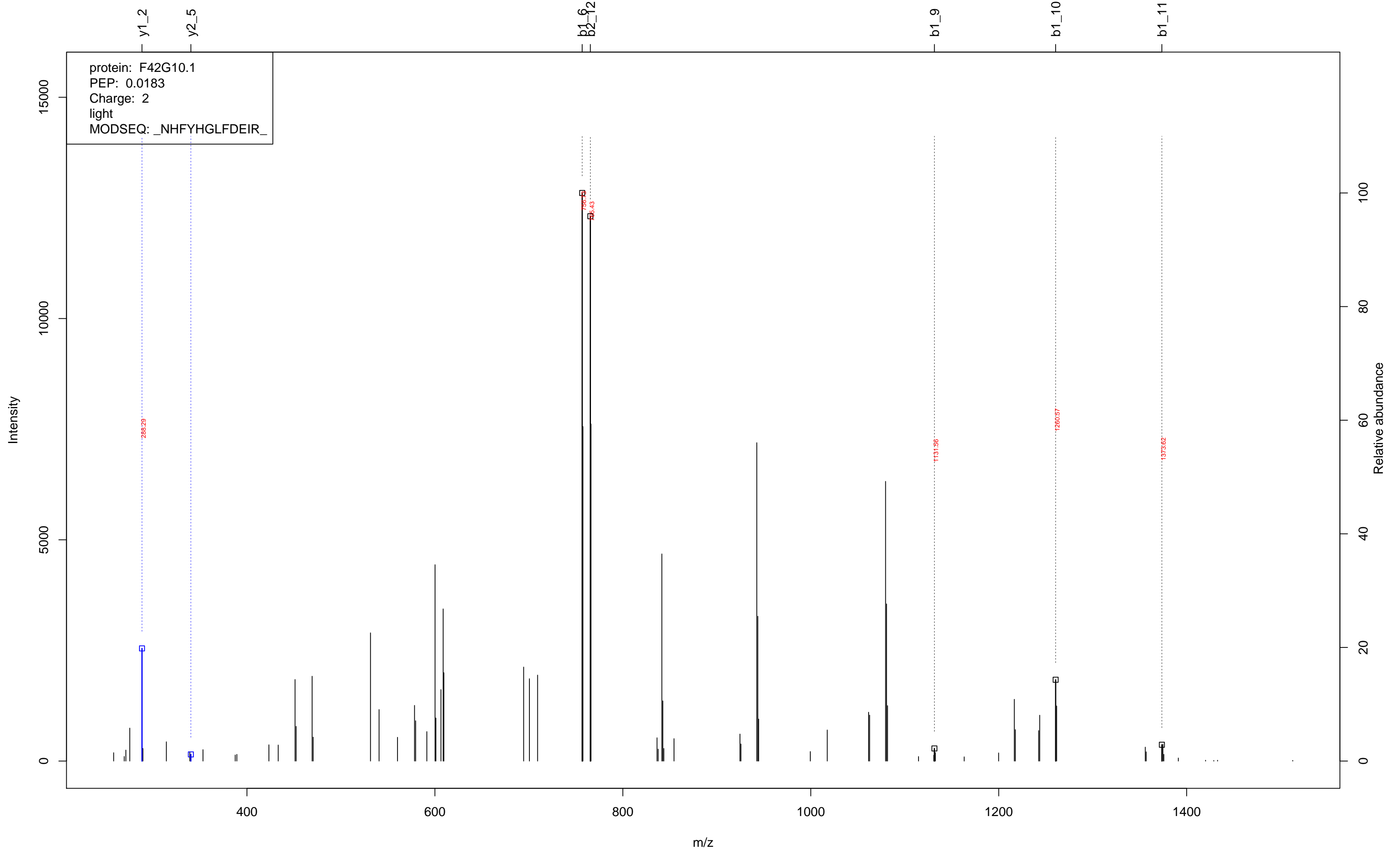
y1_8

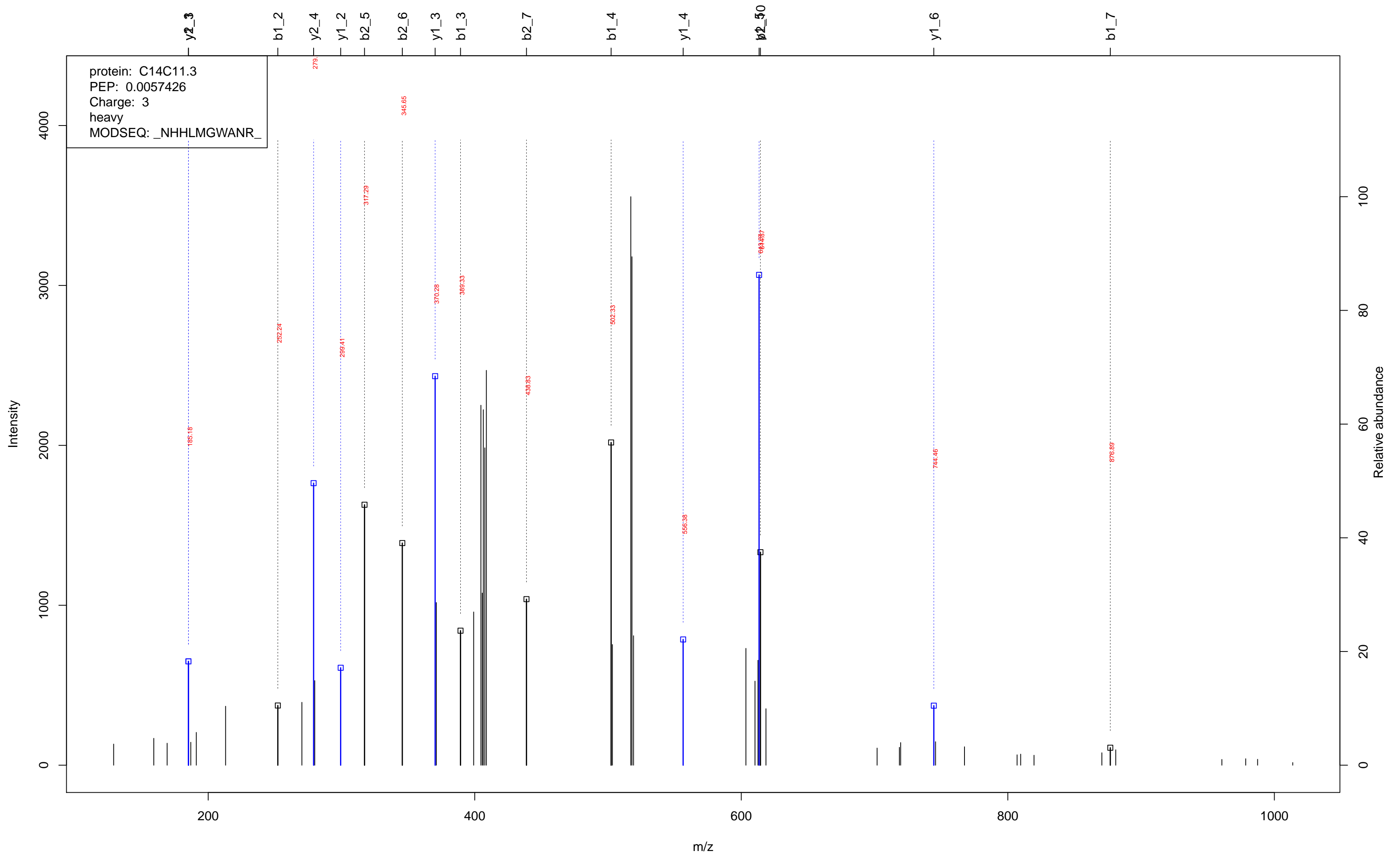
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PEP: 0.016488
Charge: 2
light
MODSEQ: _NDAFLSSLR_

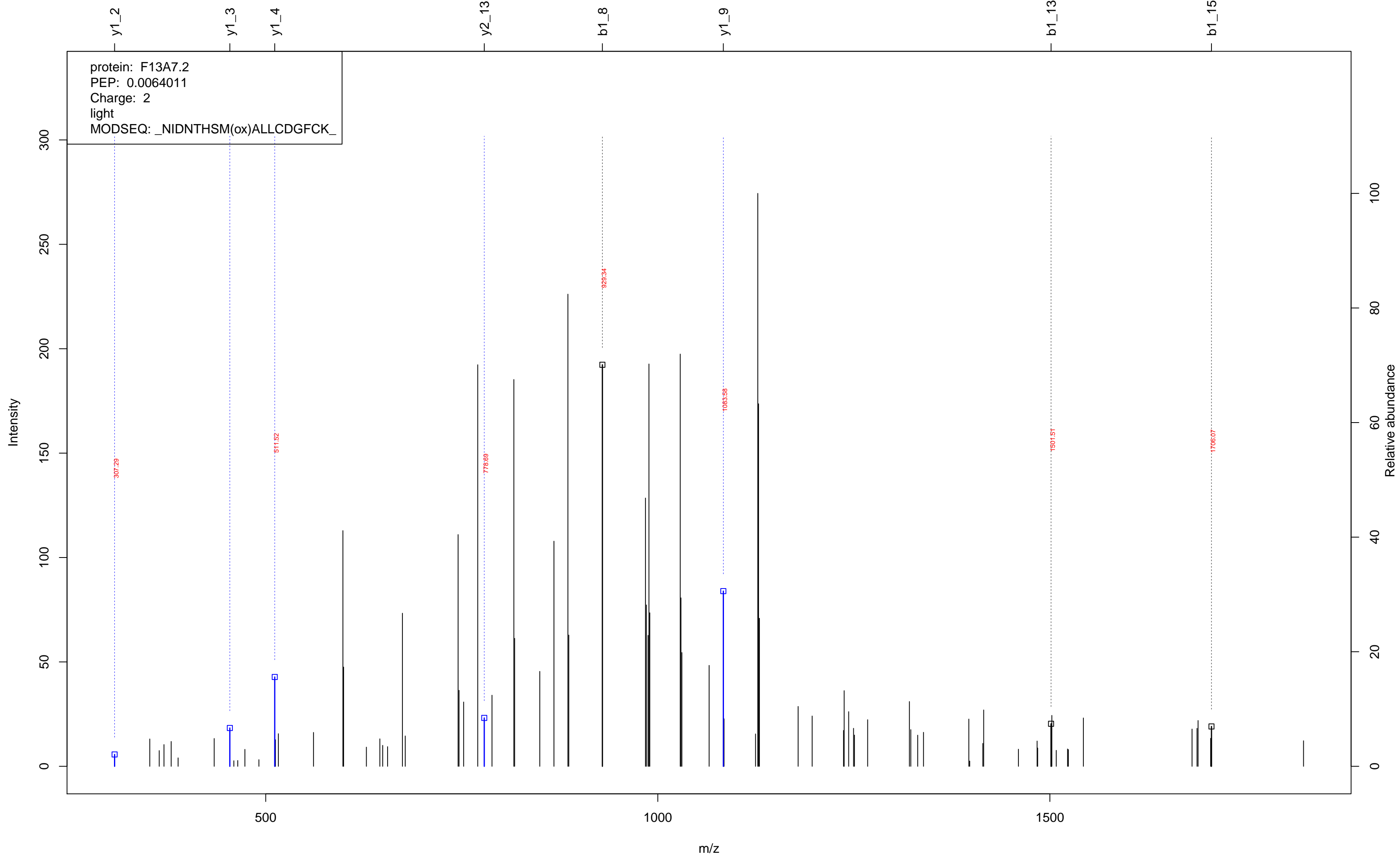


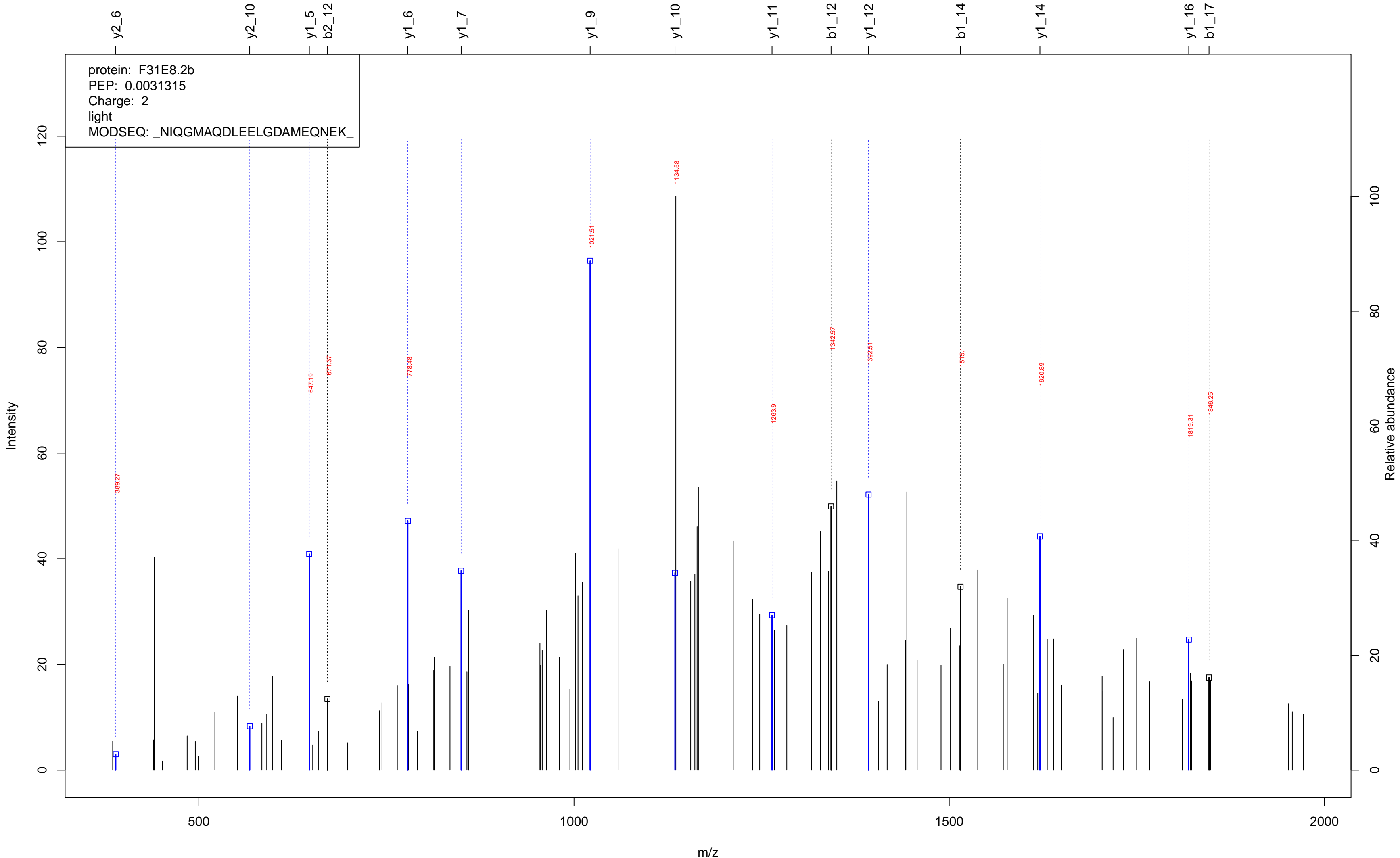


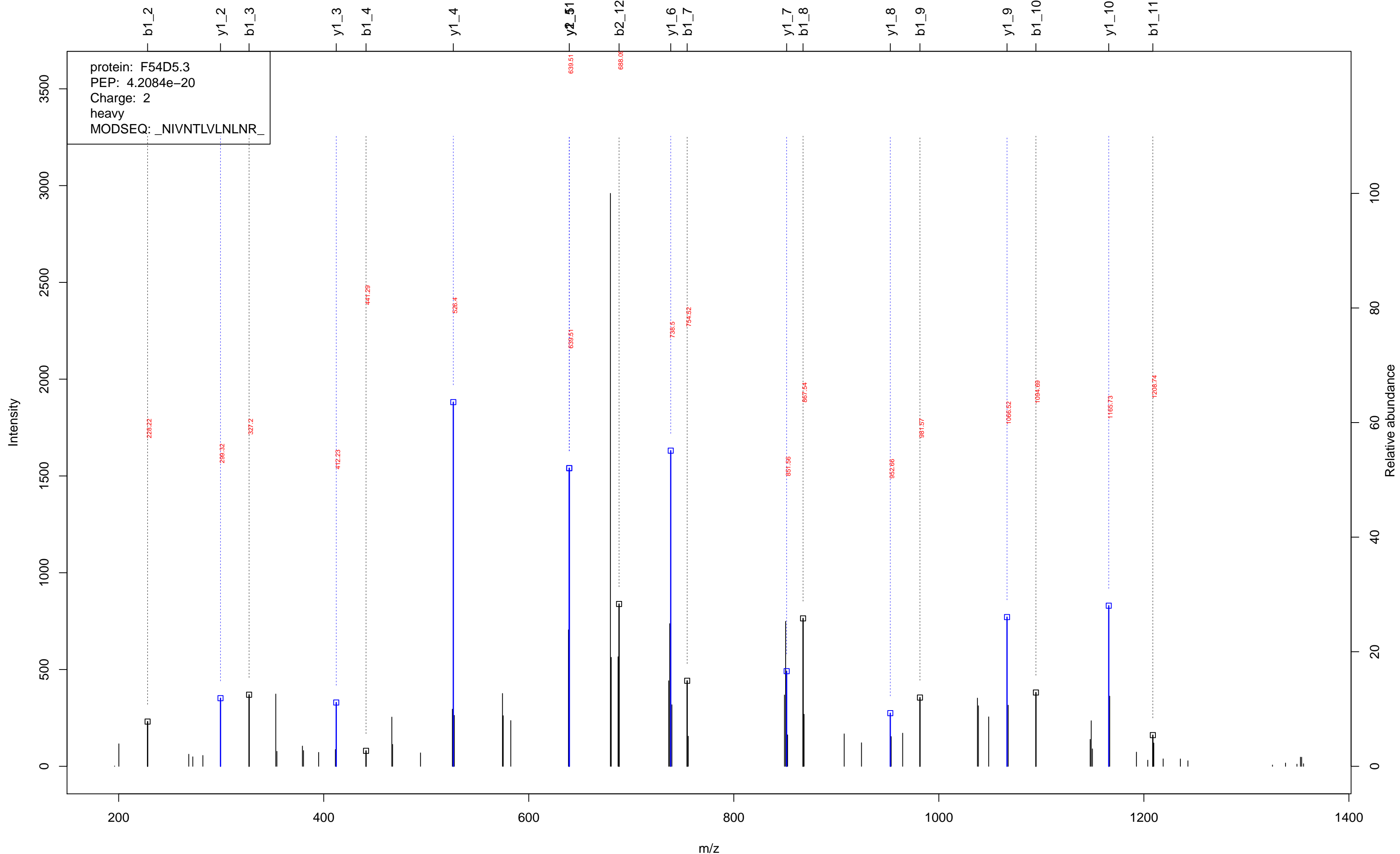


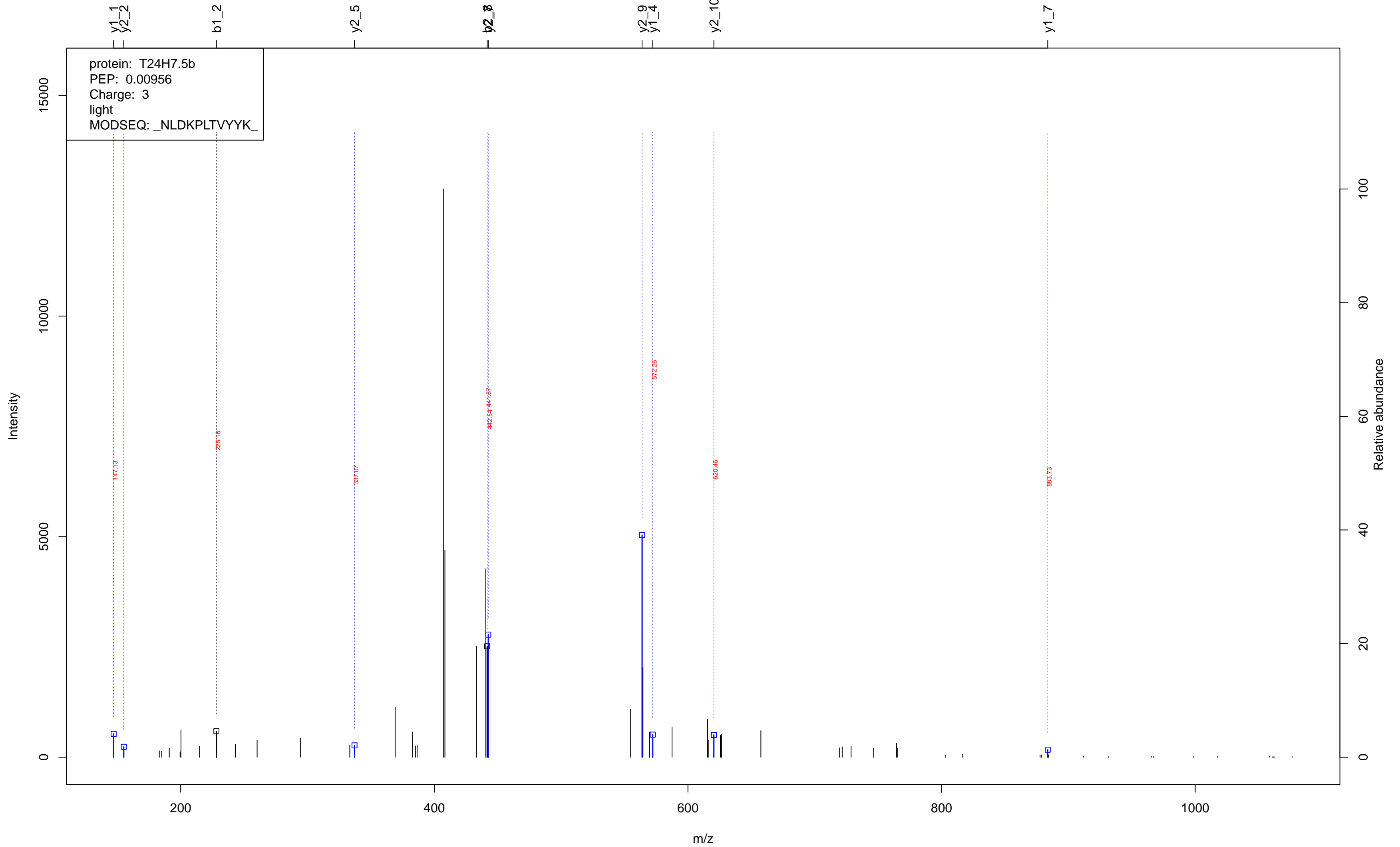


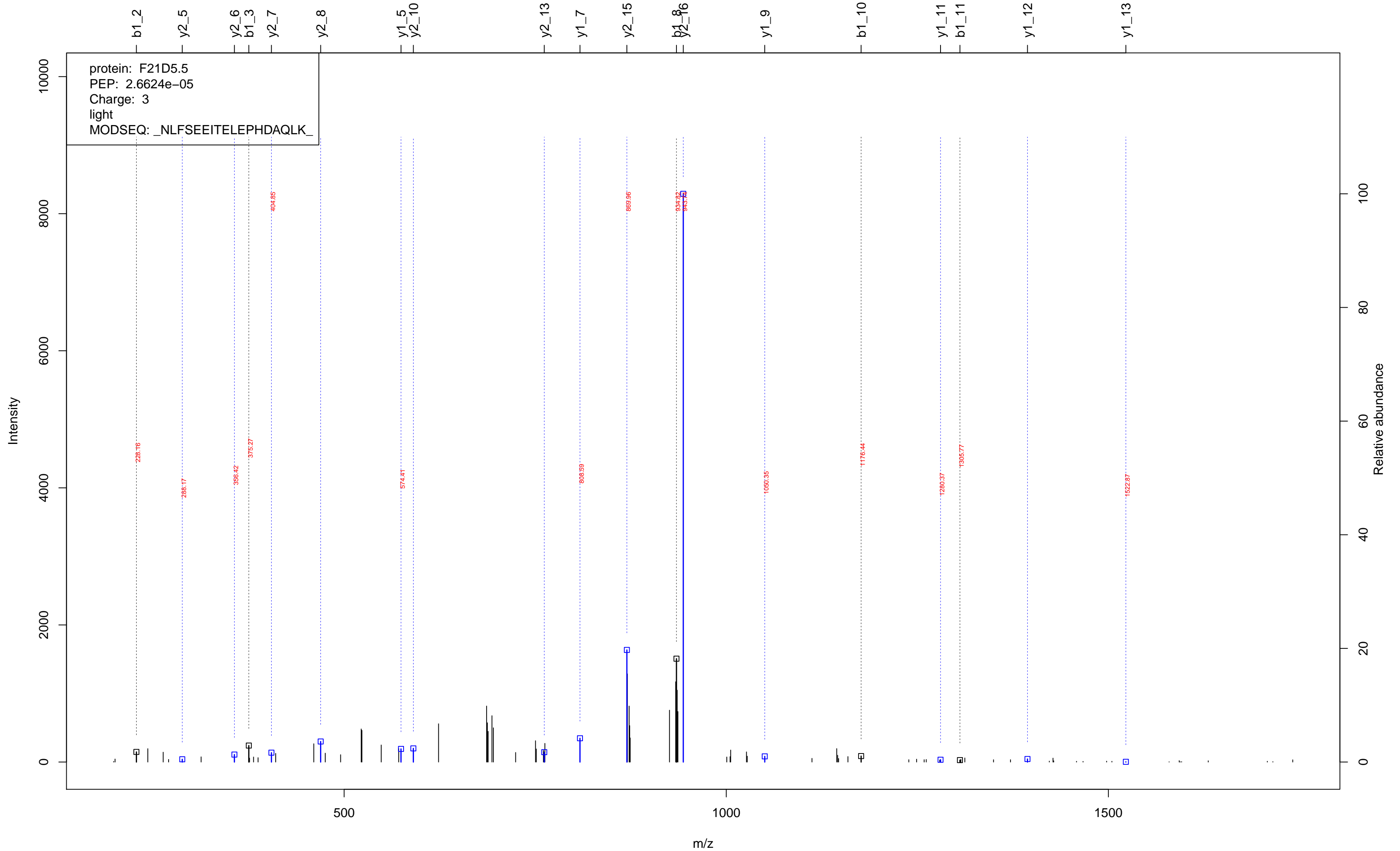






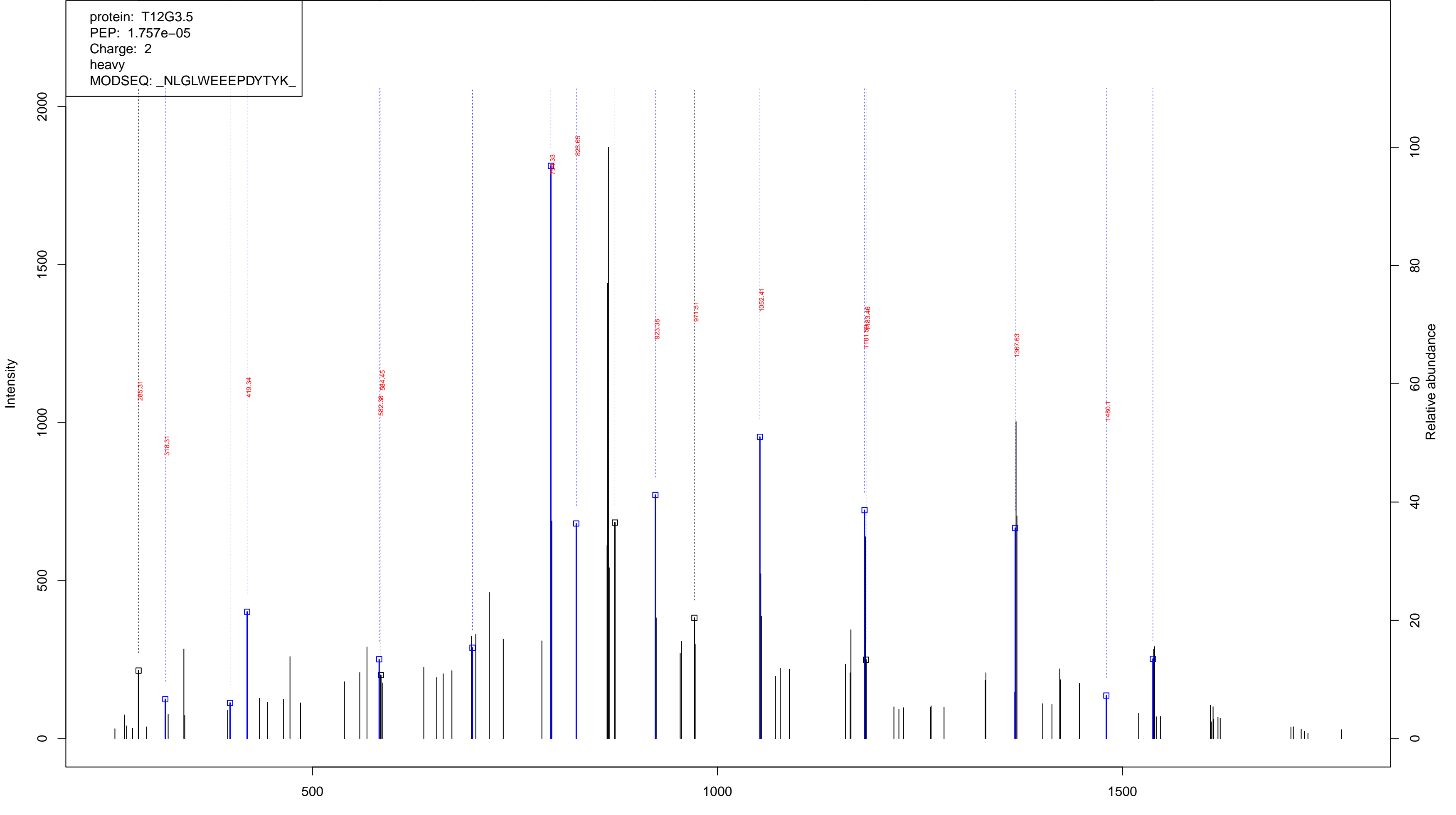


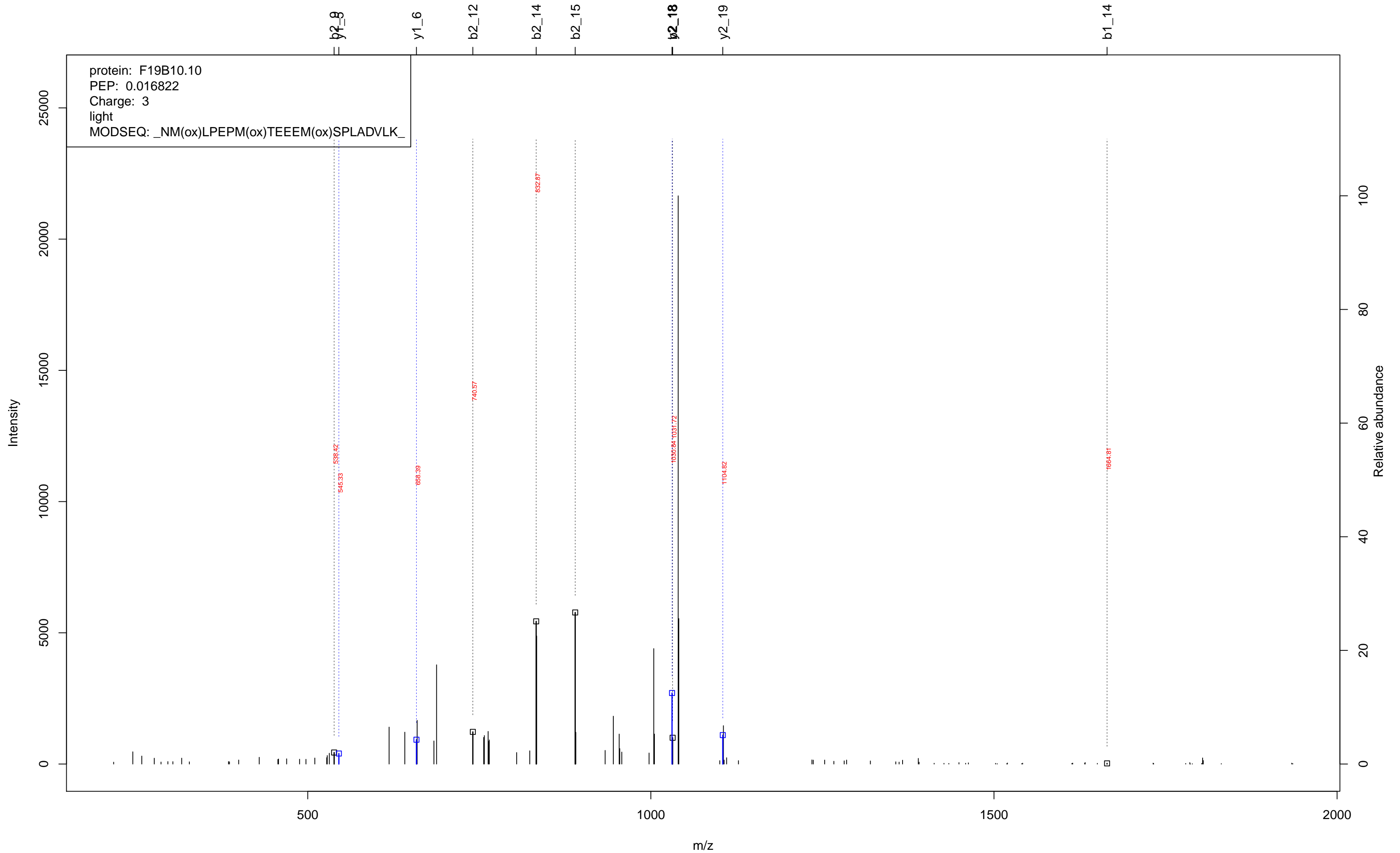


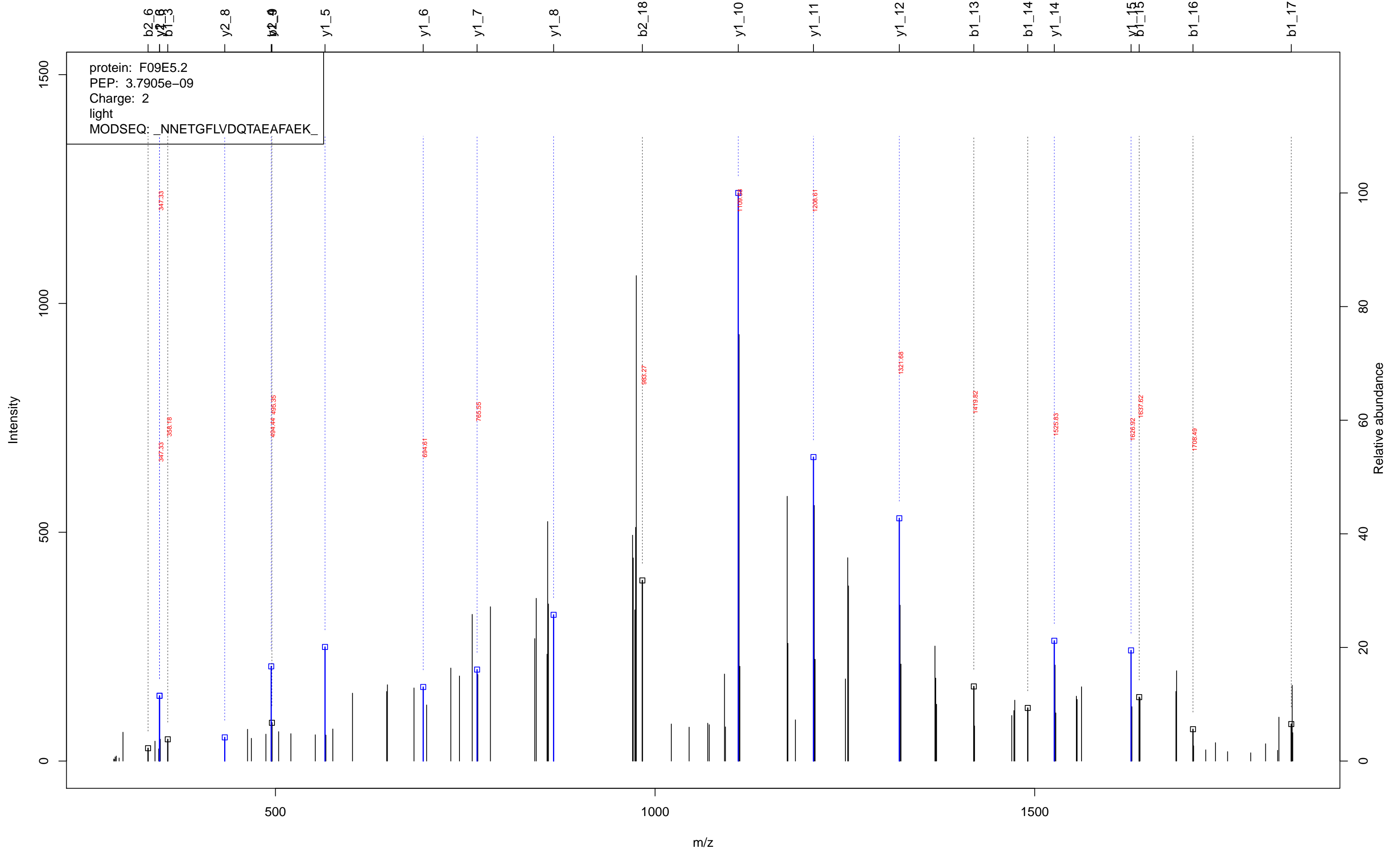


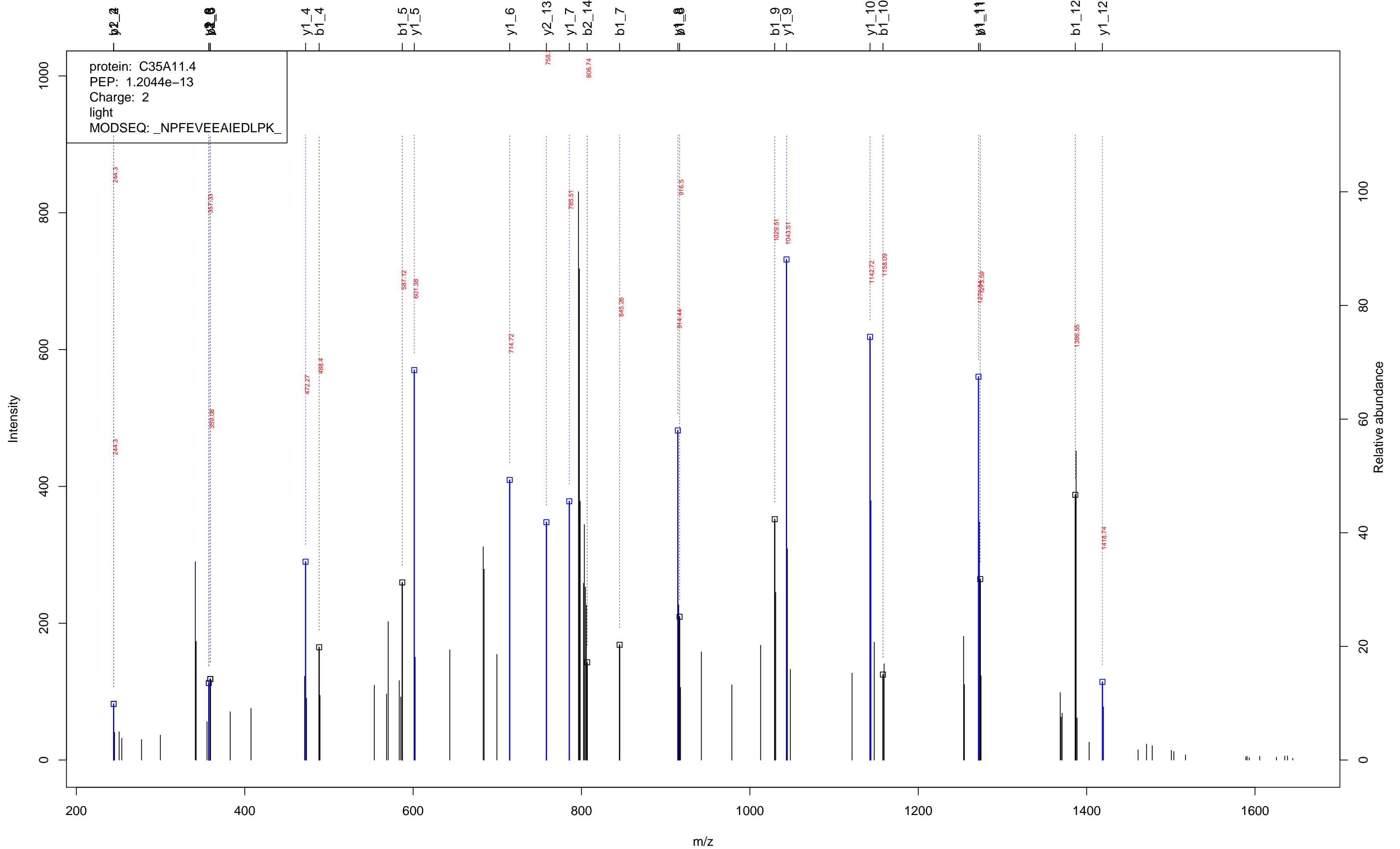
b1_3 y1_2 b2_6 y1_3 b1_4 y1_5 y1_6 y2_13 b2_14 y1_7 b1_8 y1_8 b1_90 y1_10 y1_11 y1_12

protein: T12G3.5
PEP: 1.757e-05
Charge: 2
heavy
MODSEQ: _NLGLWEEEPDYTYK_



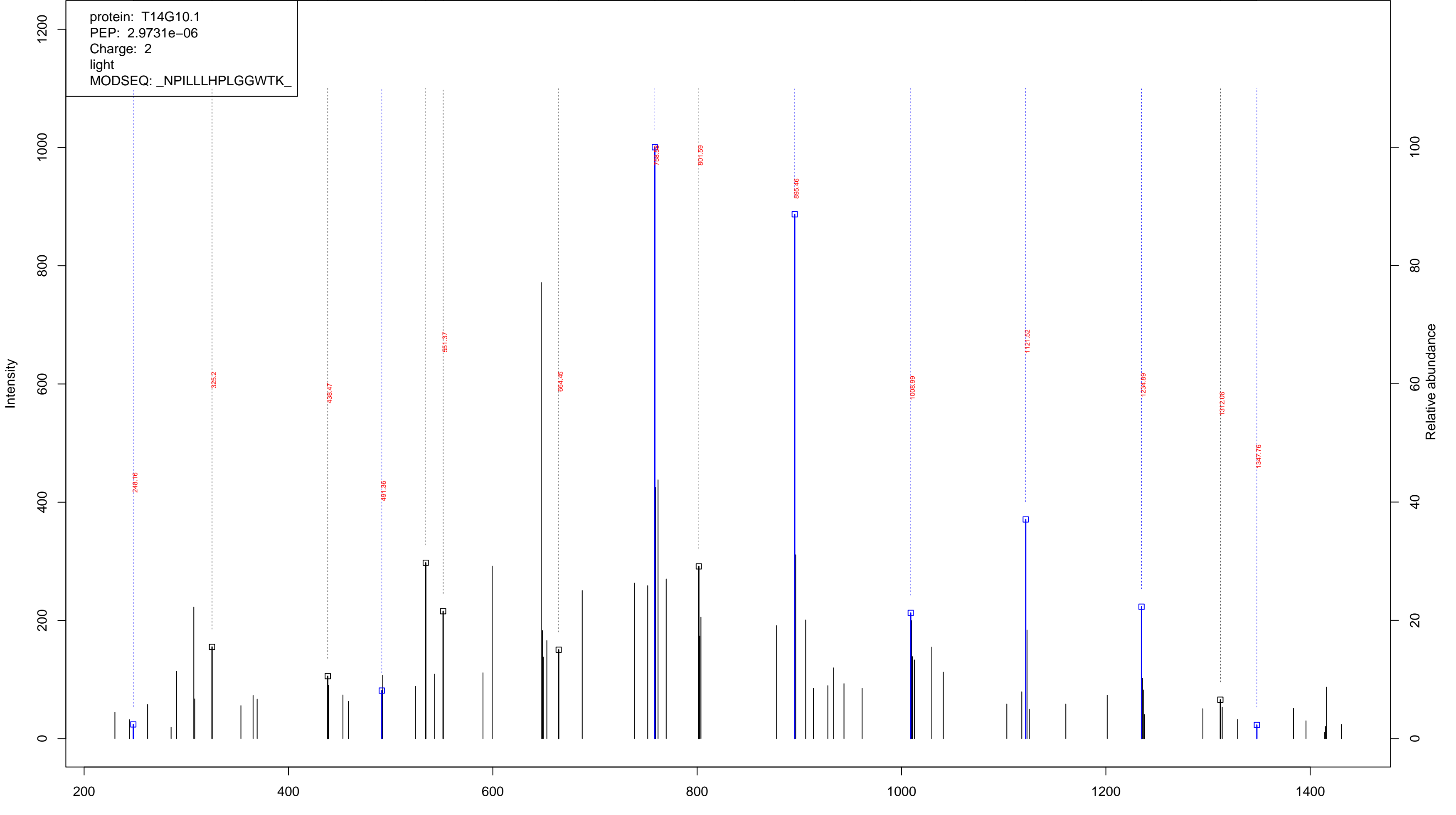


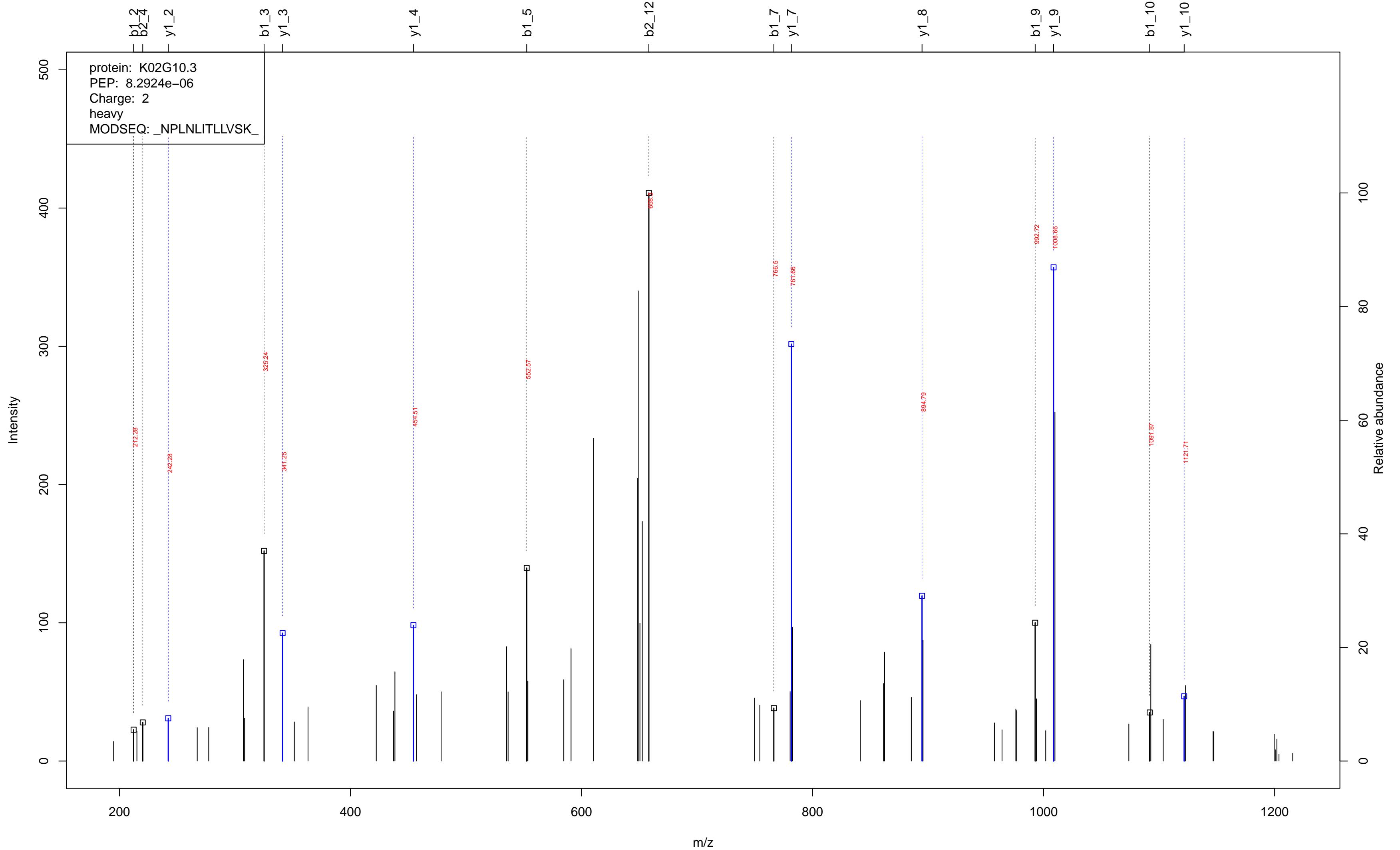


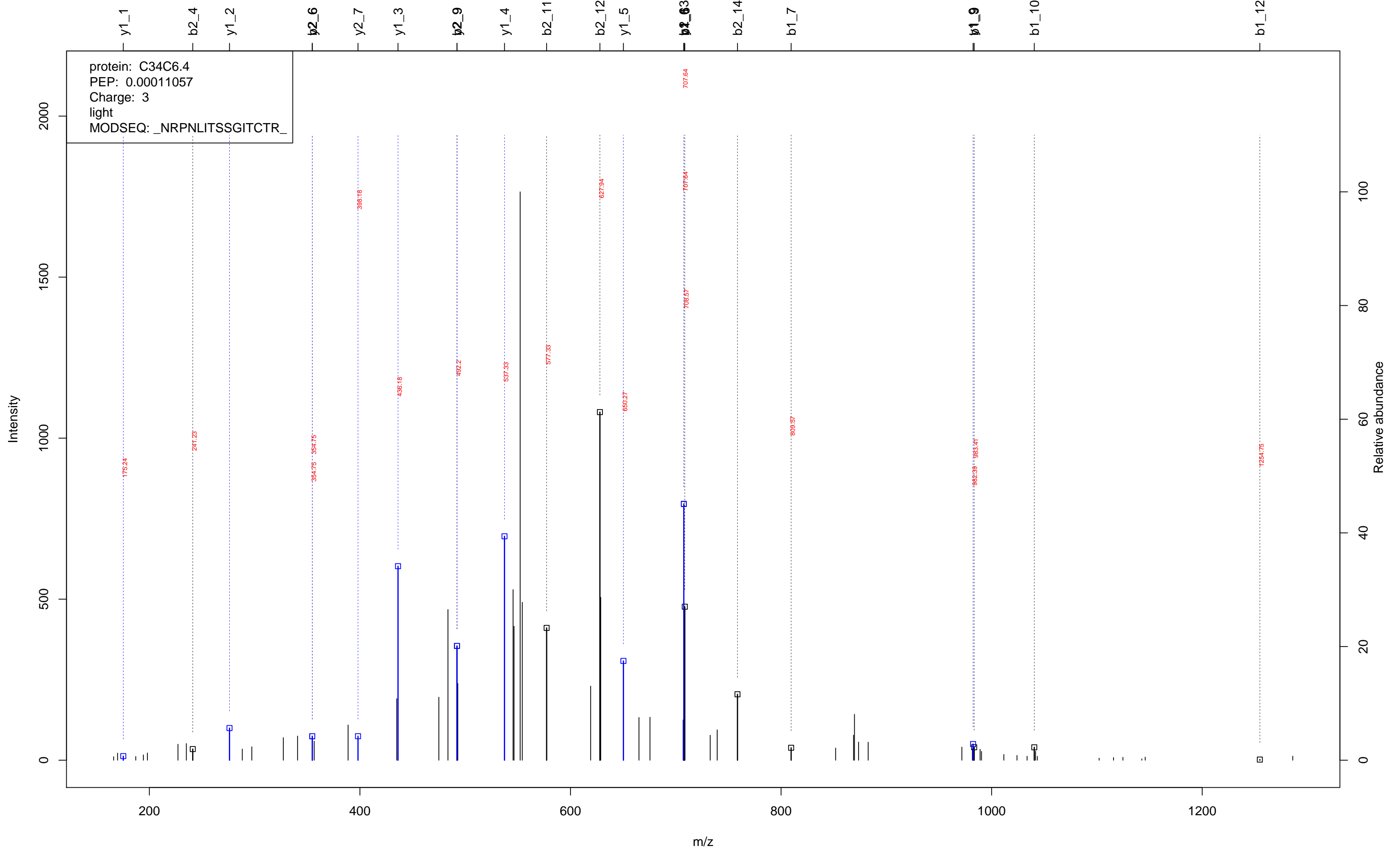


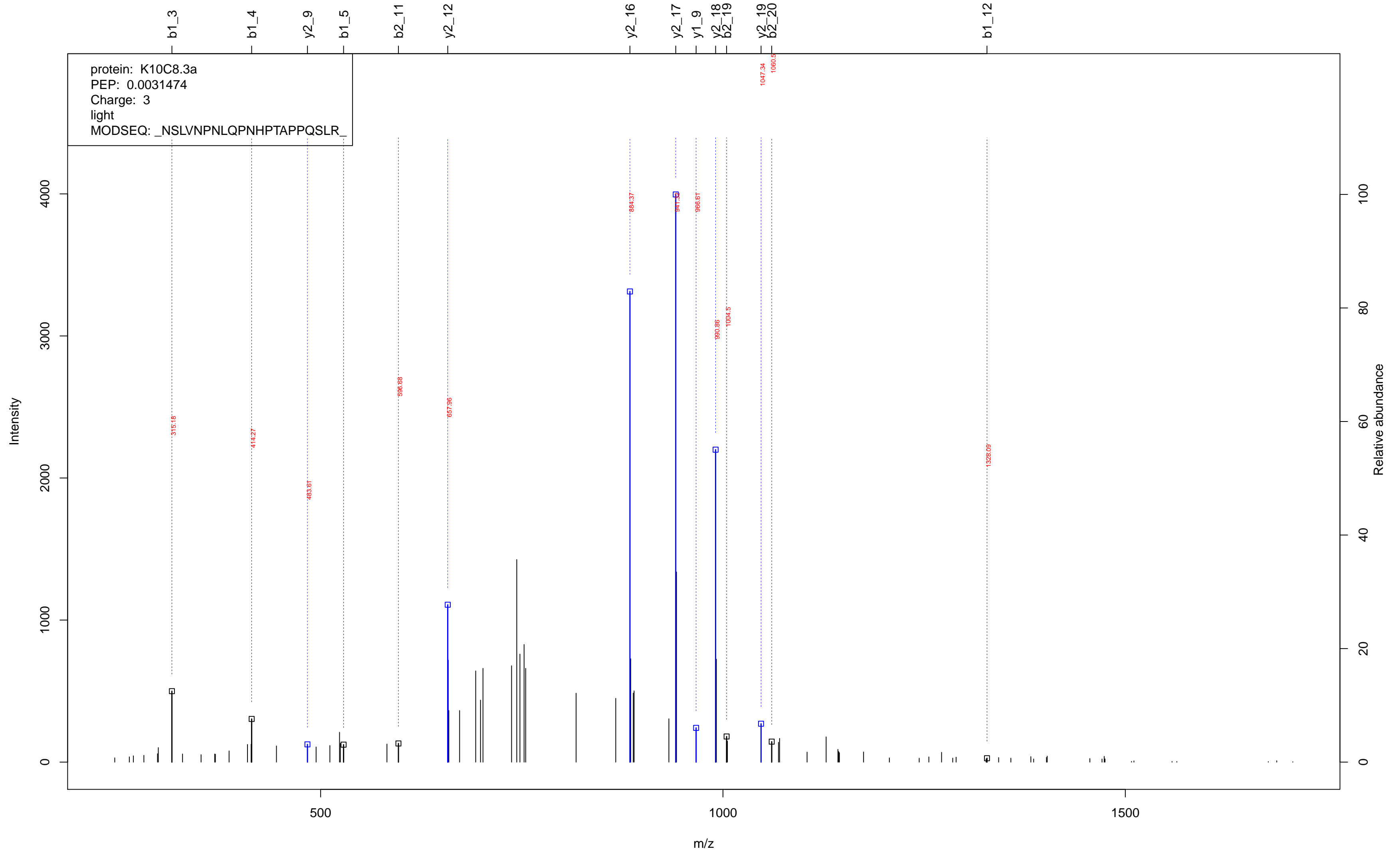
y1_2 b1_3 b1_4 y1_4 b2_10 b1_5 b1_6 y1_7 b1_7 y1_8 y1_9 y1_10 y1_11 b1_12 y1_12

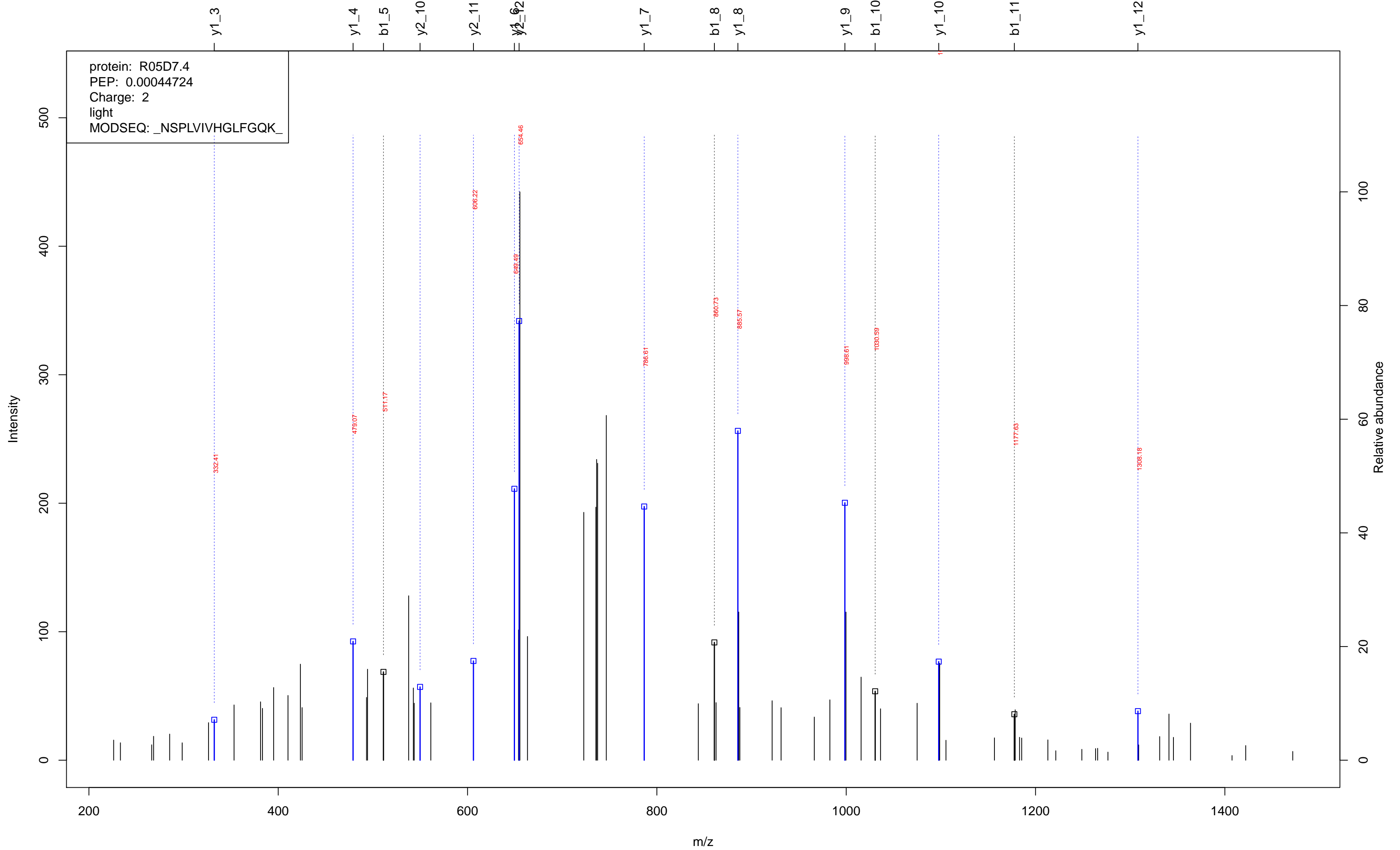
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Charge: 2
light
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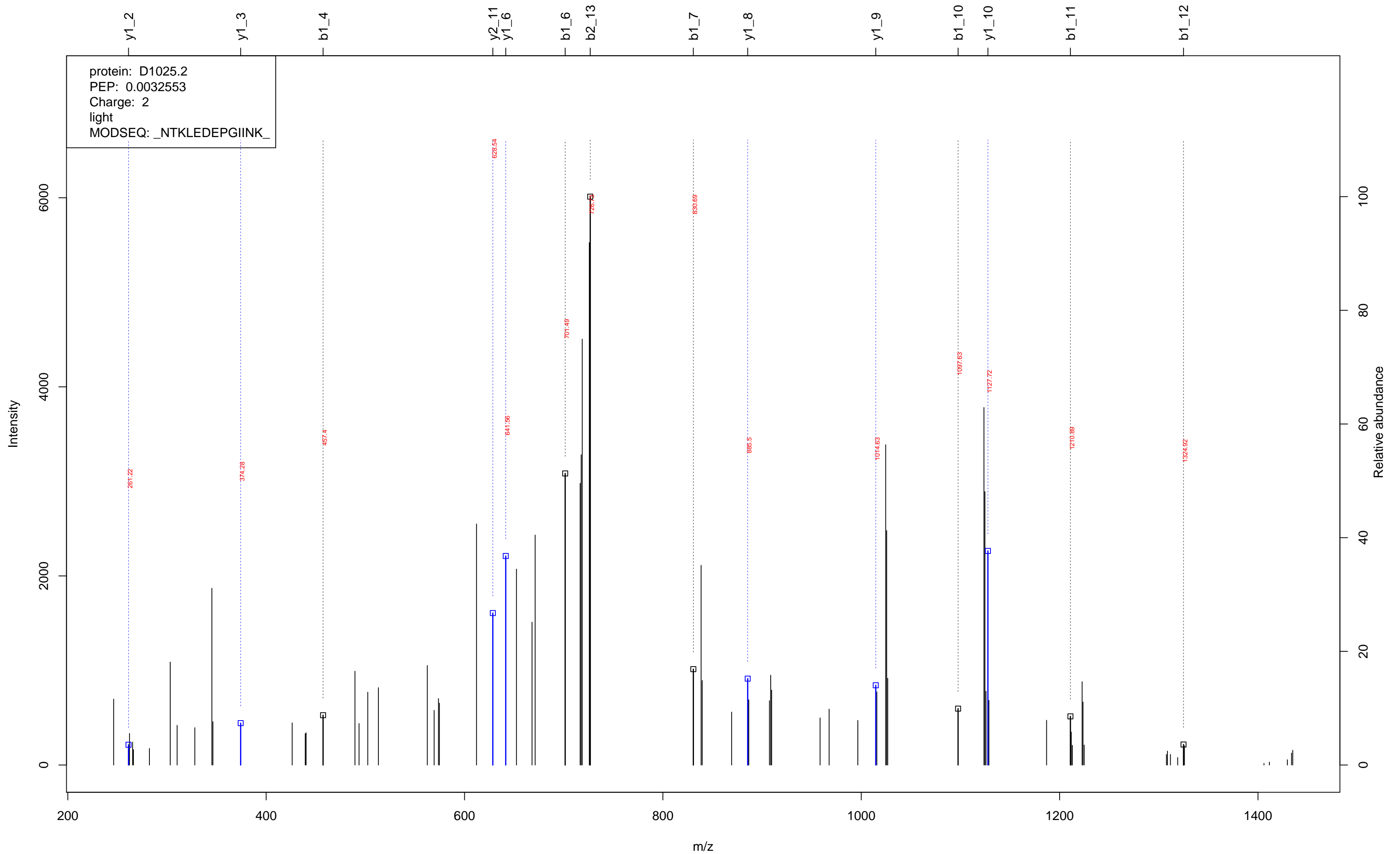




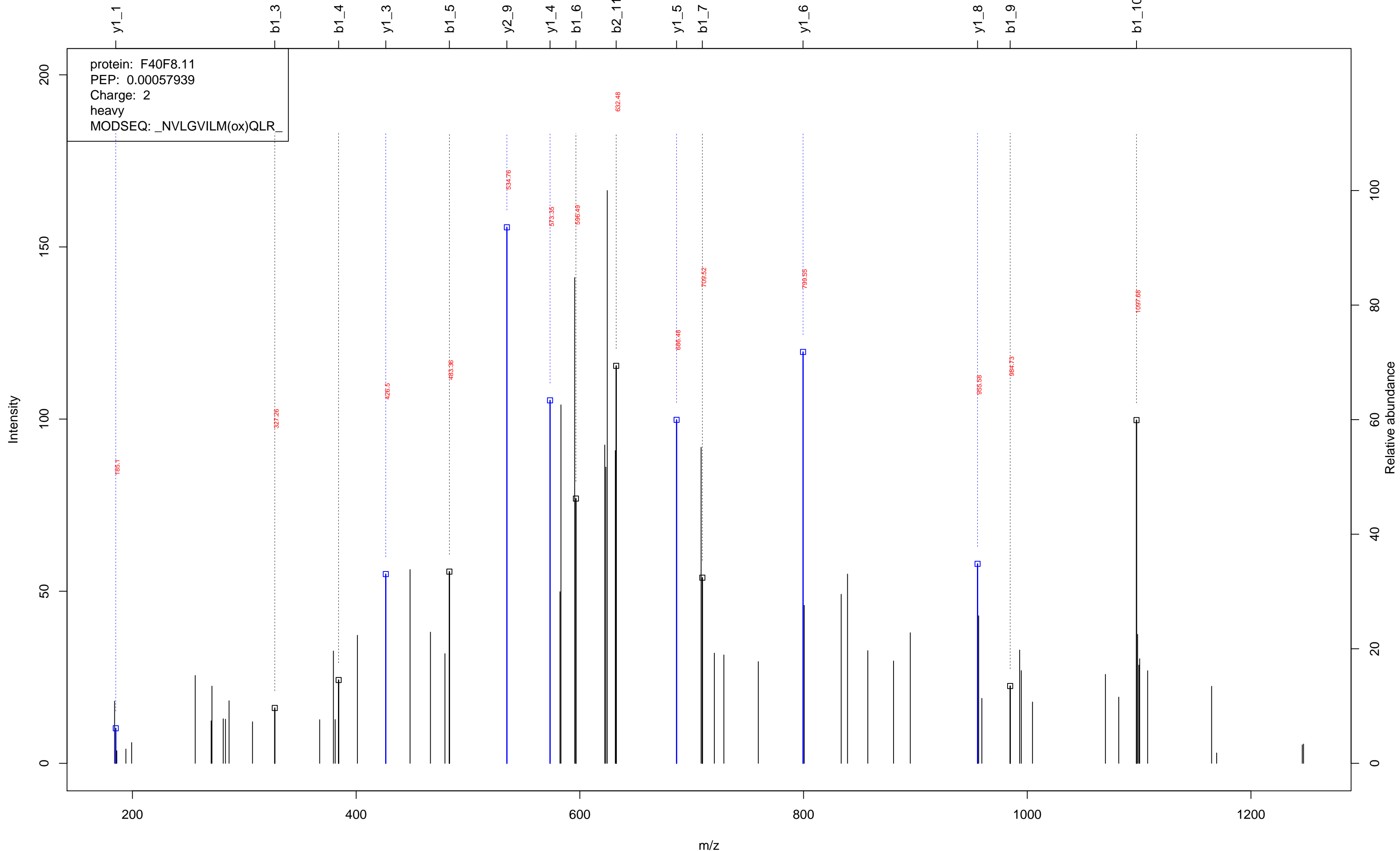


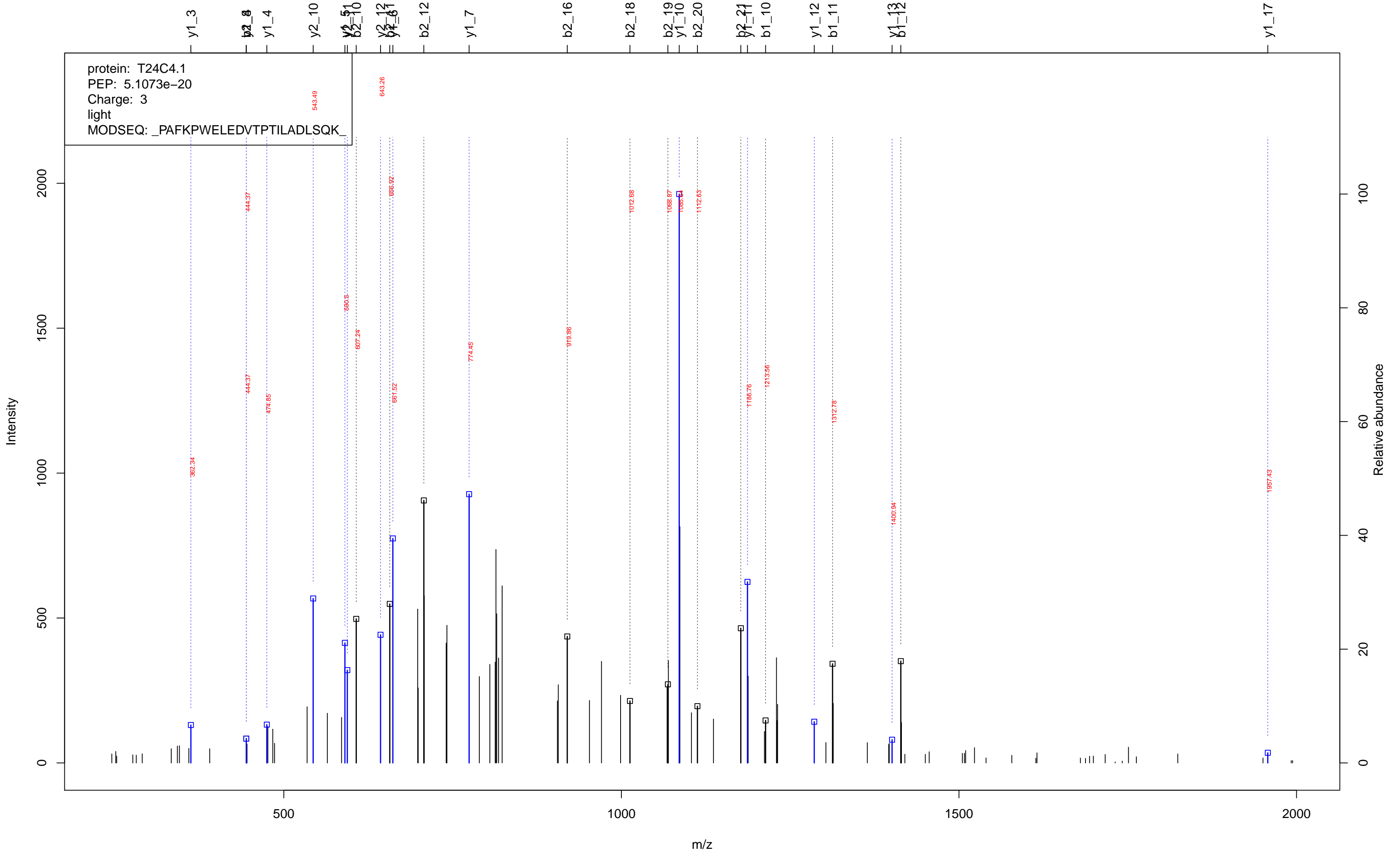


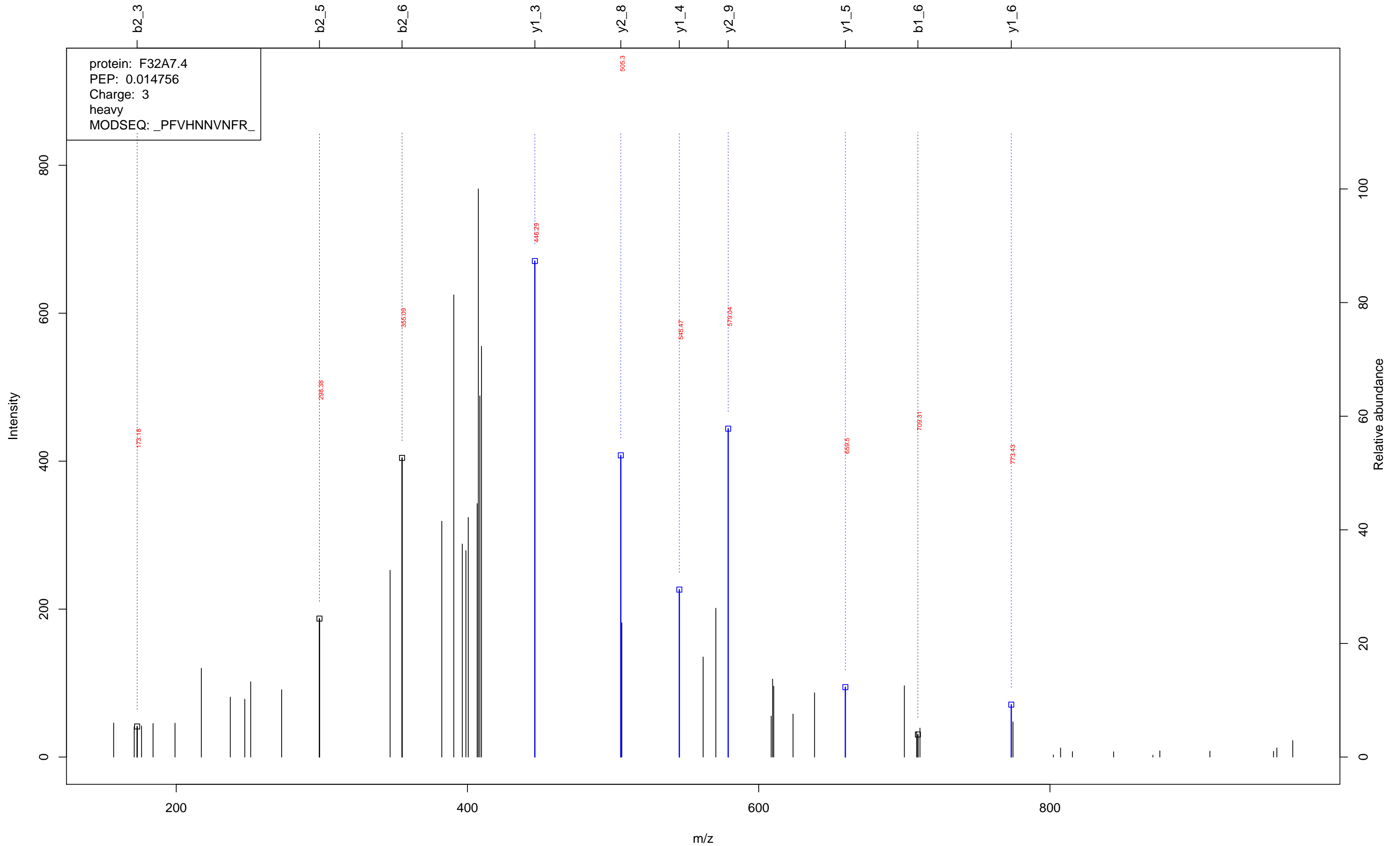


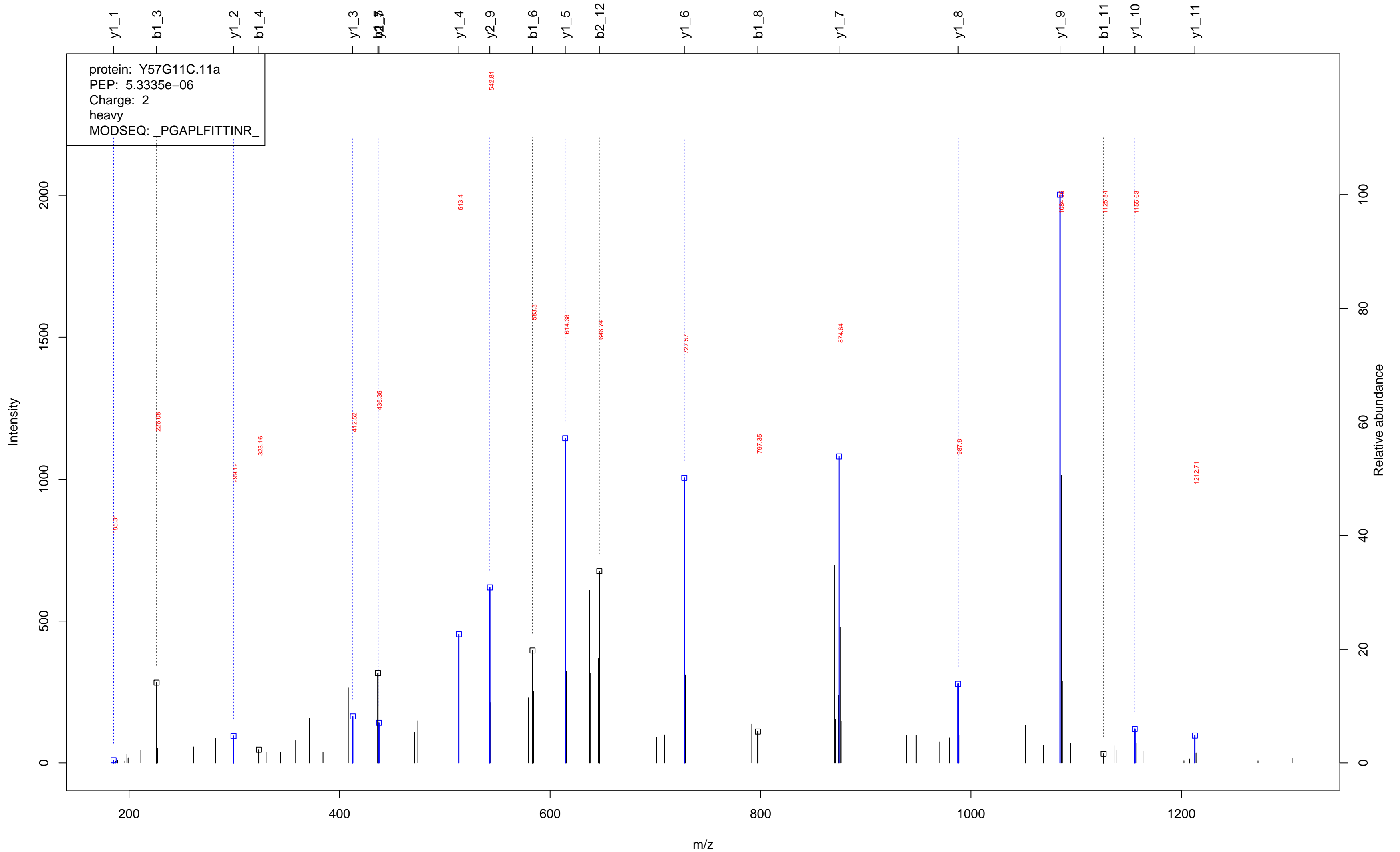


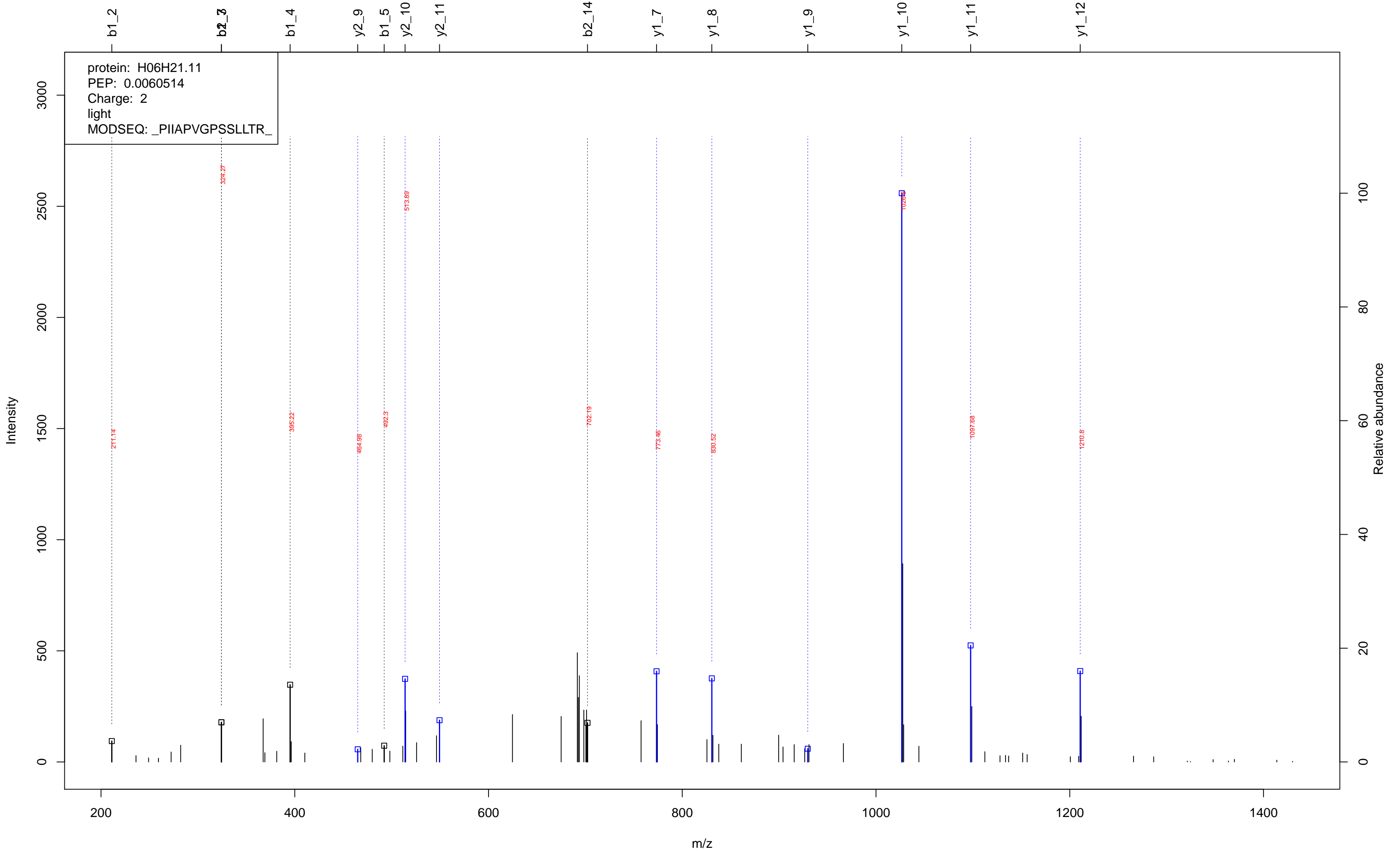
270

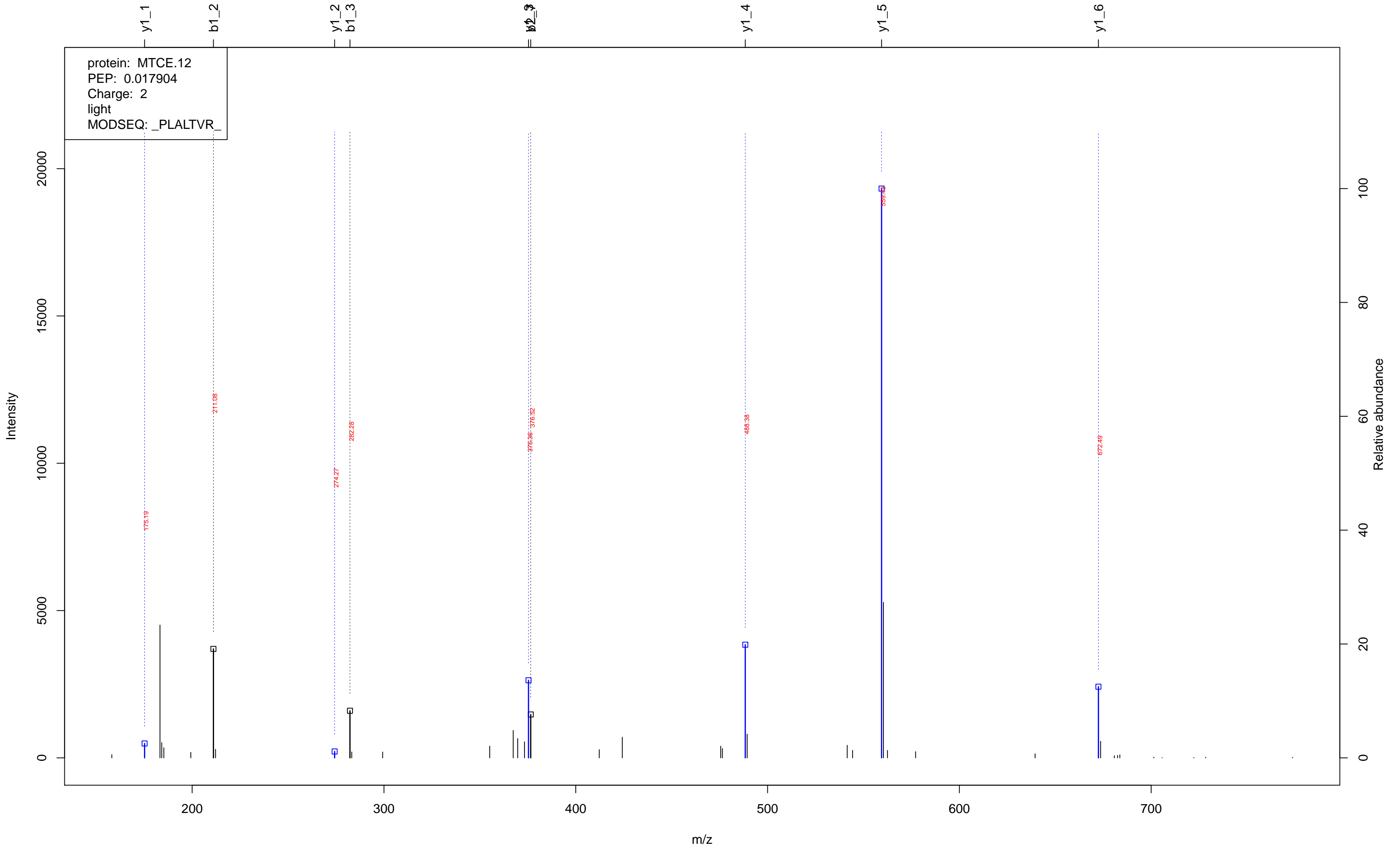


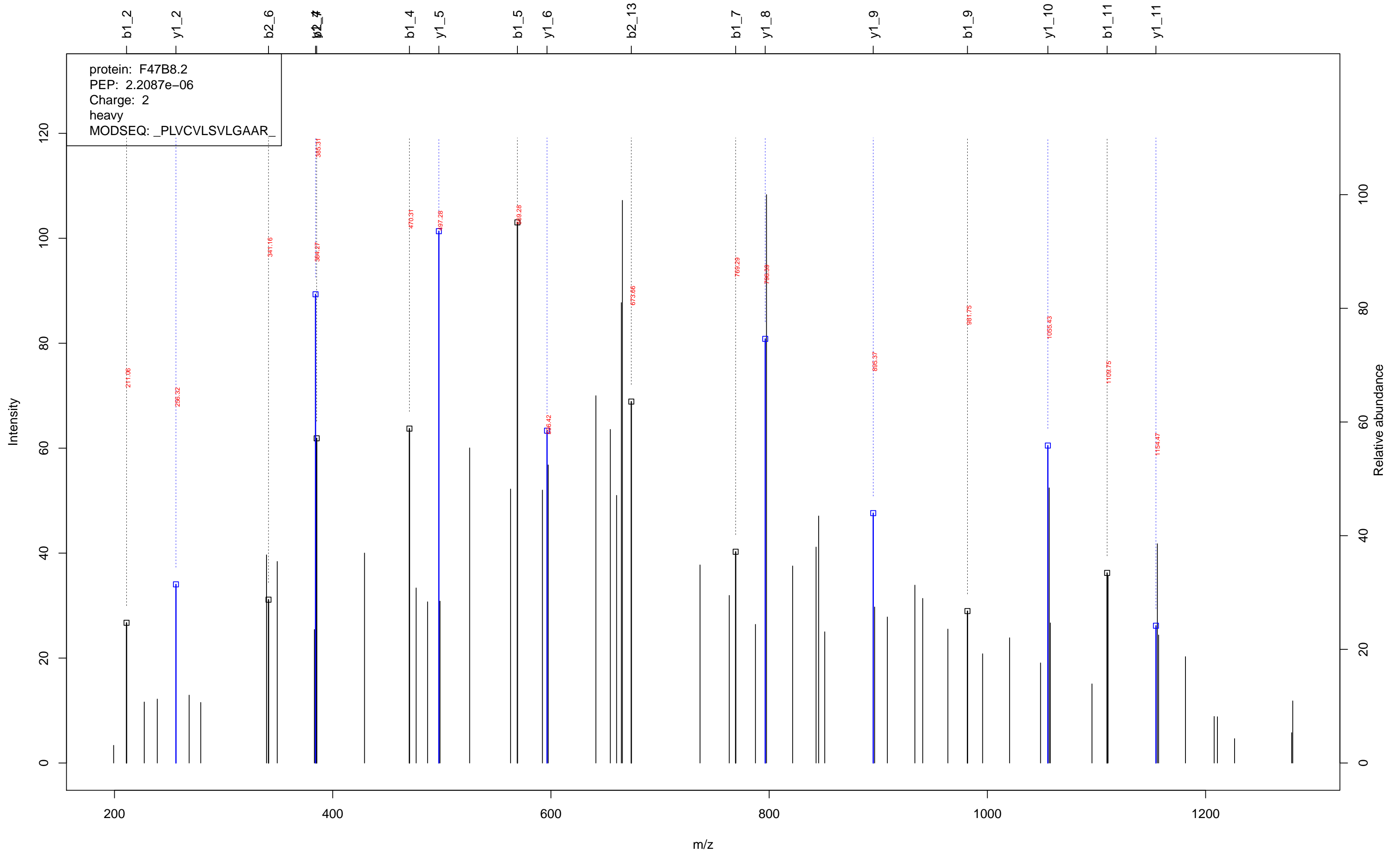


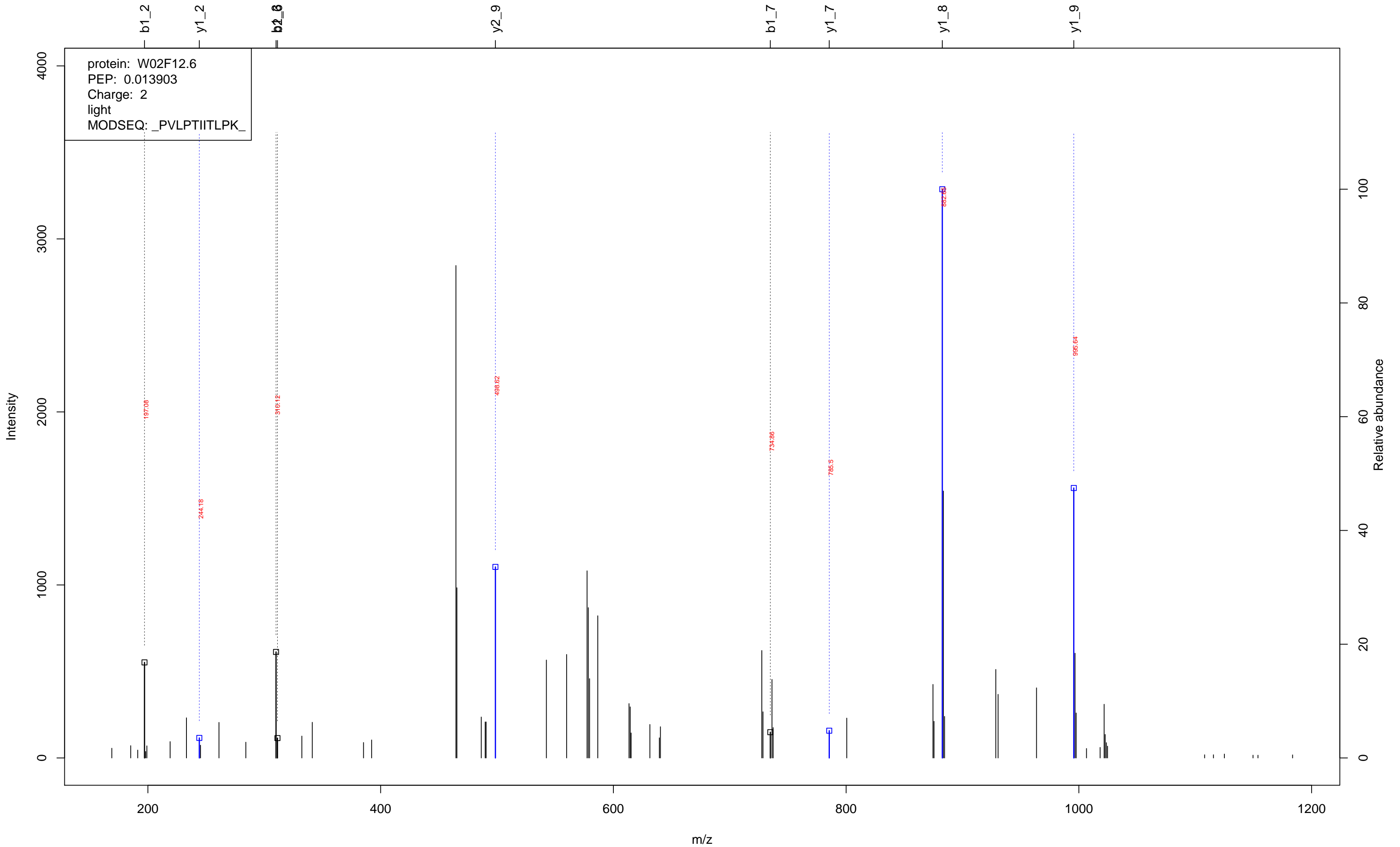


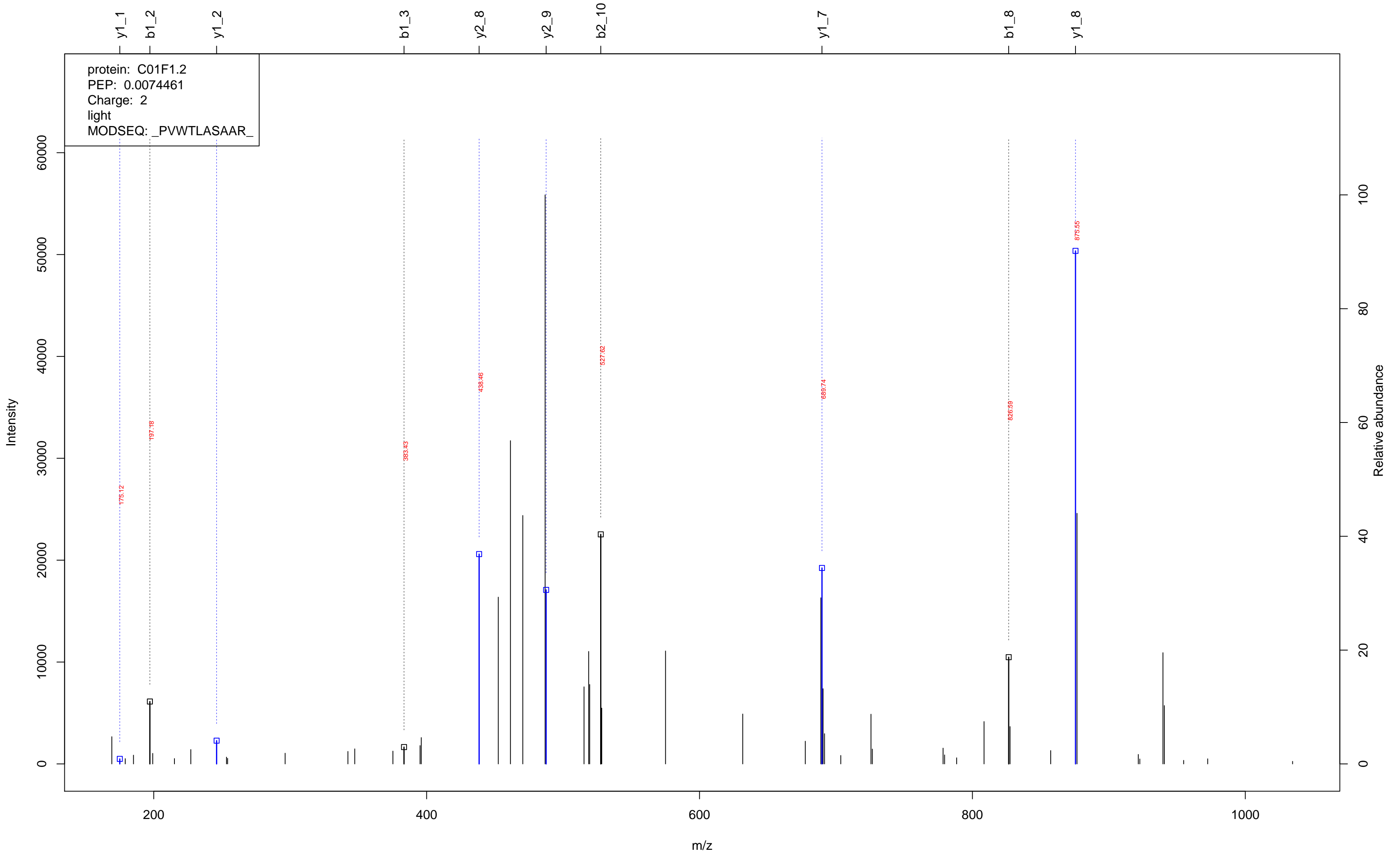


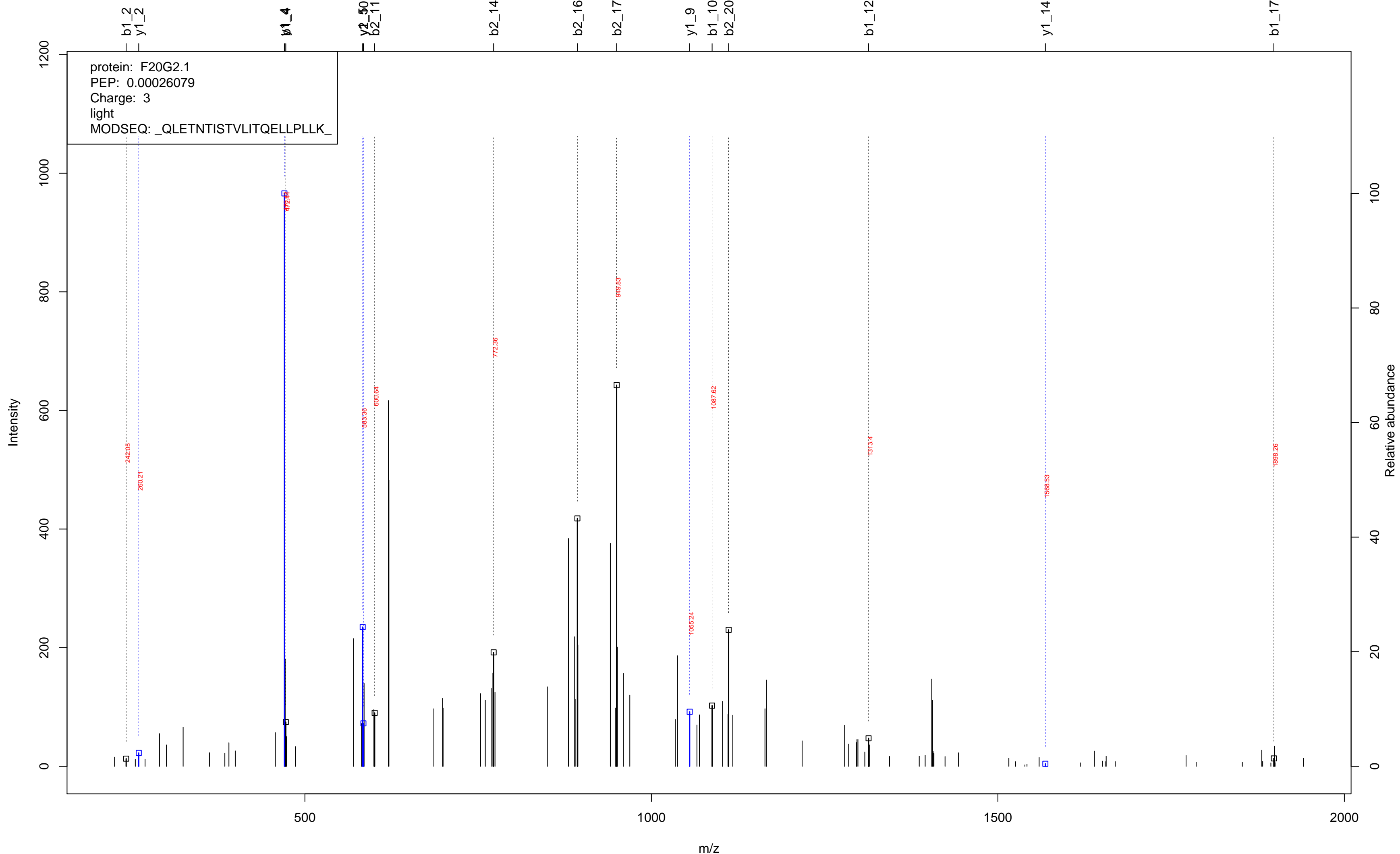


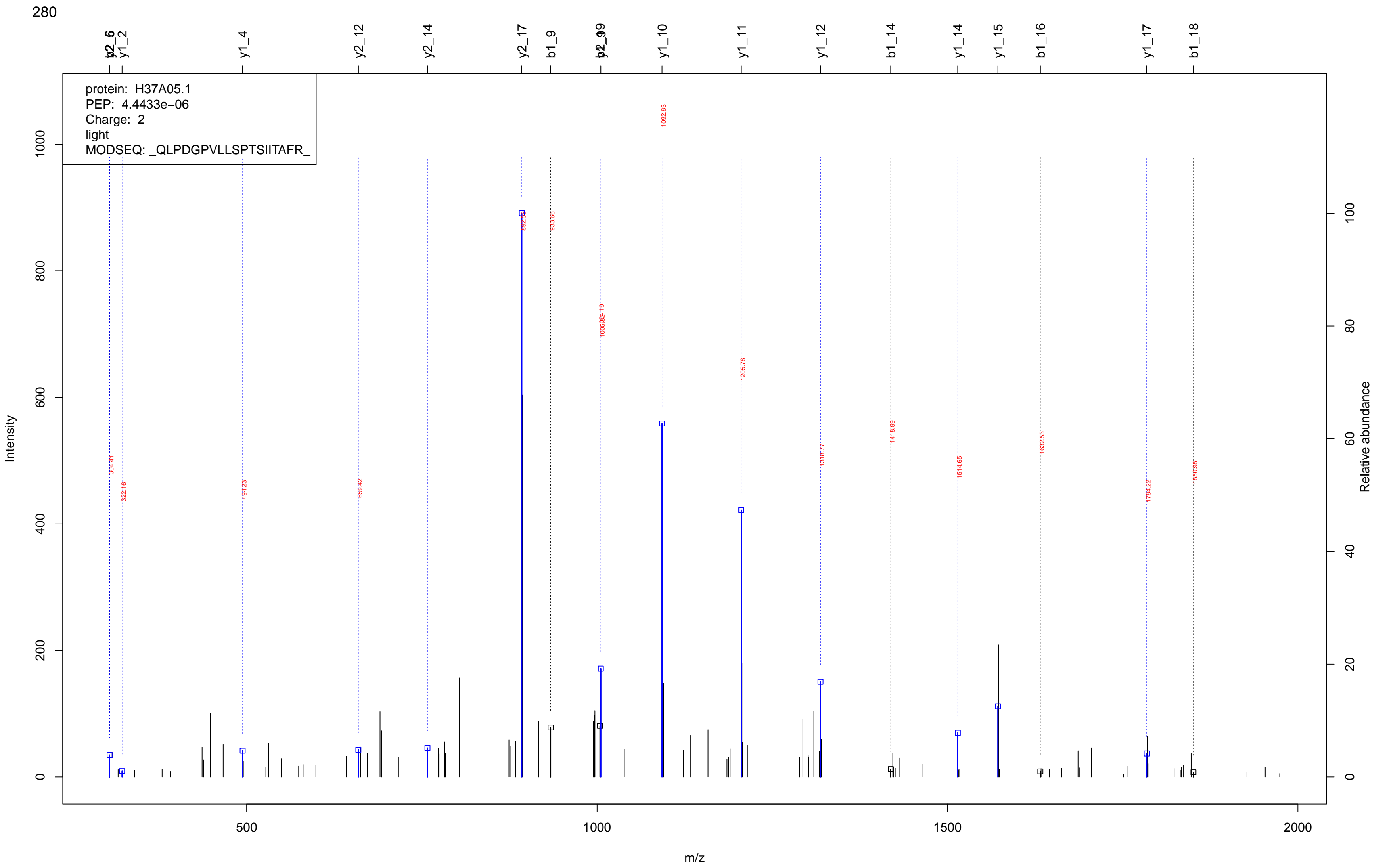


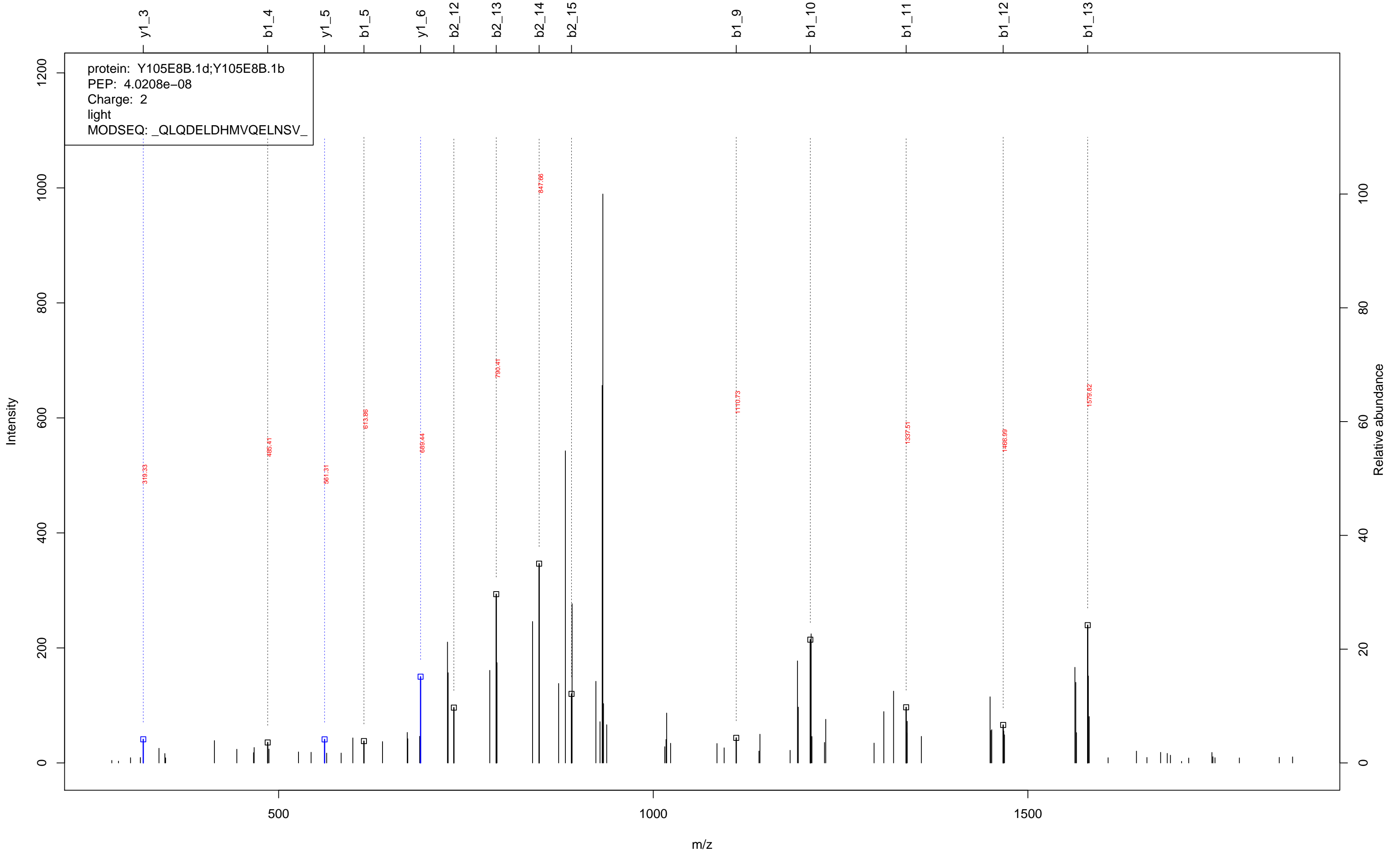


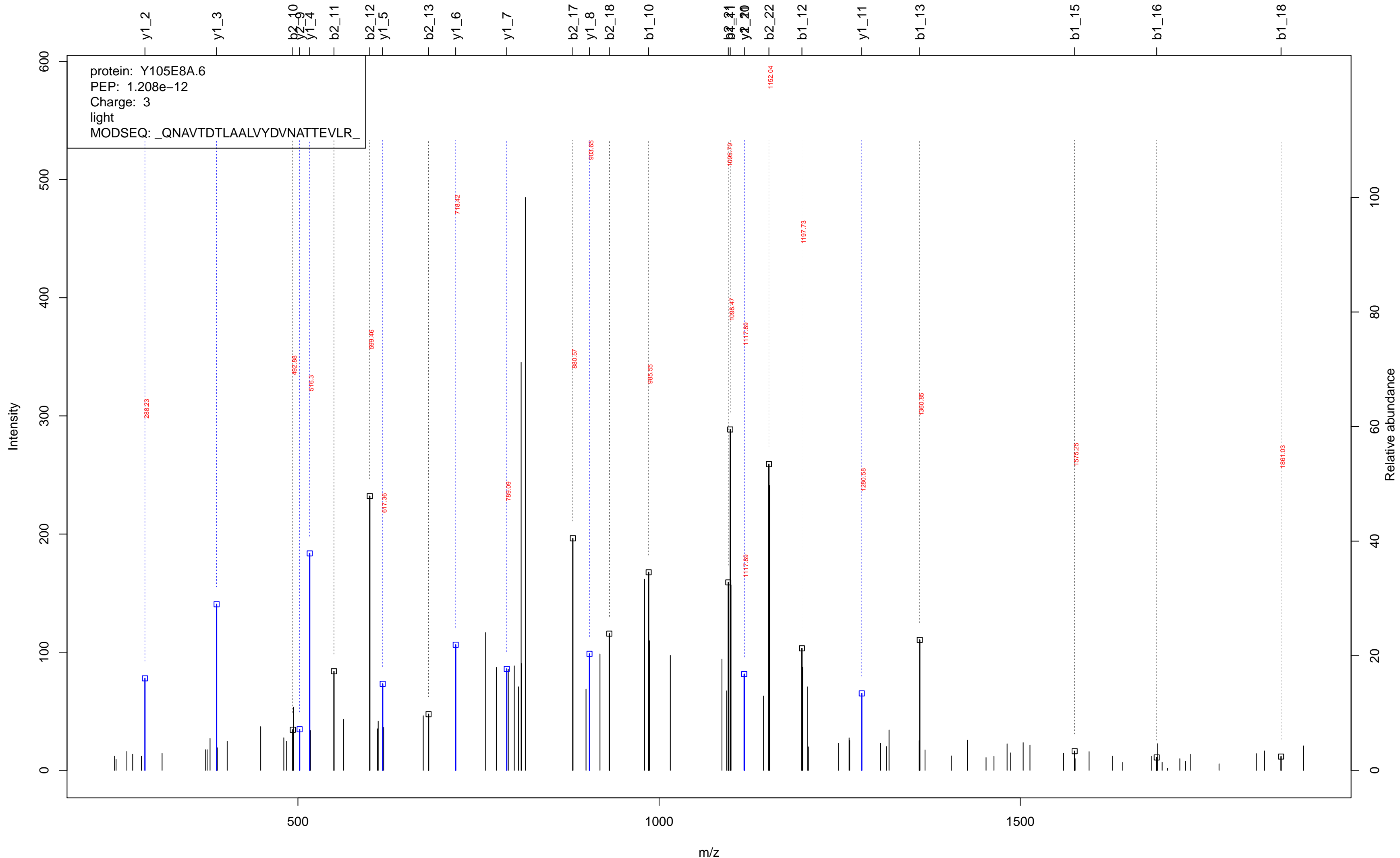


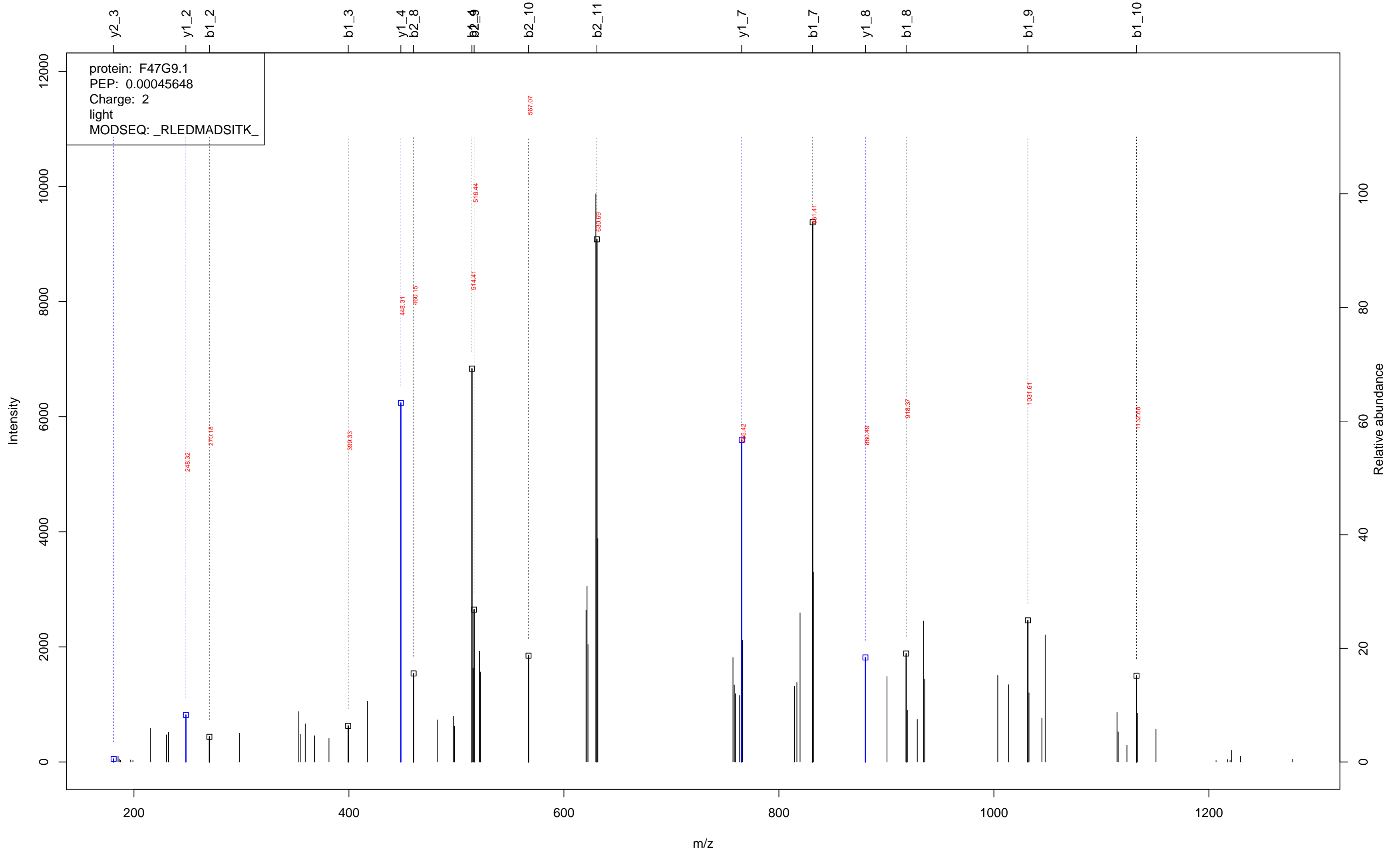


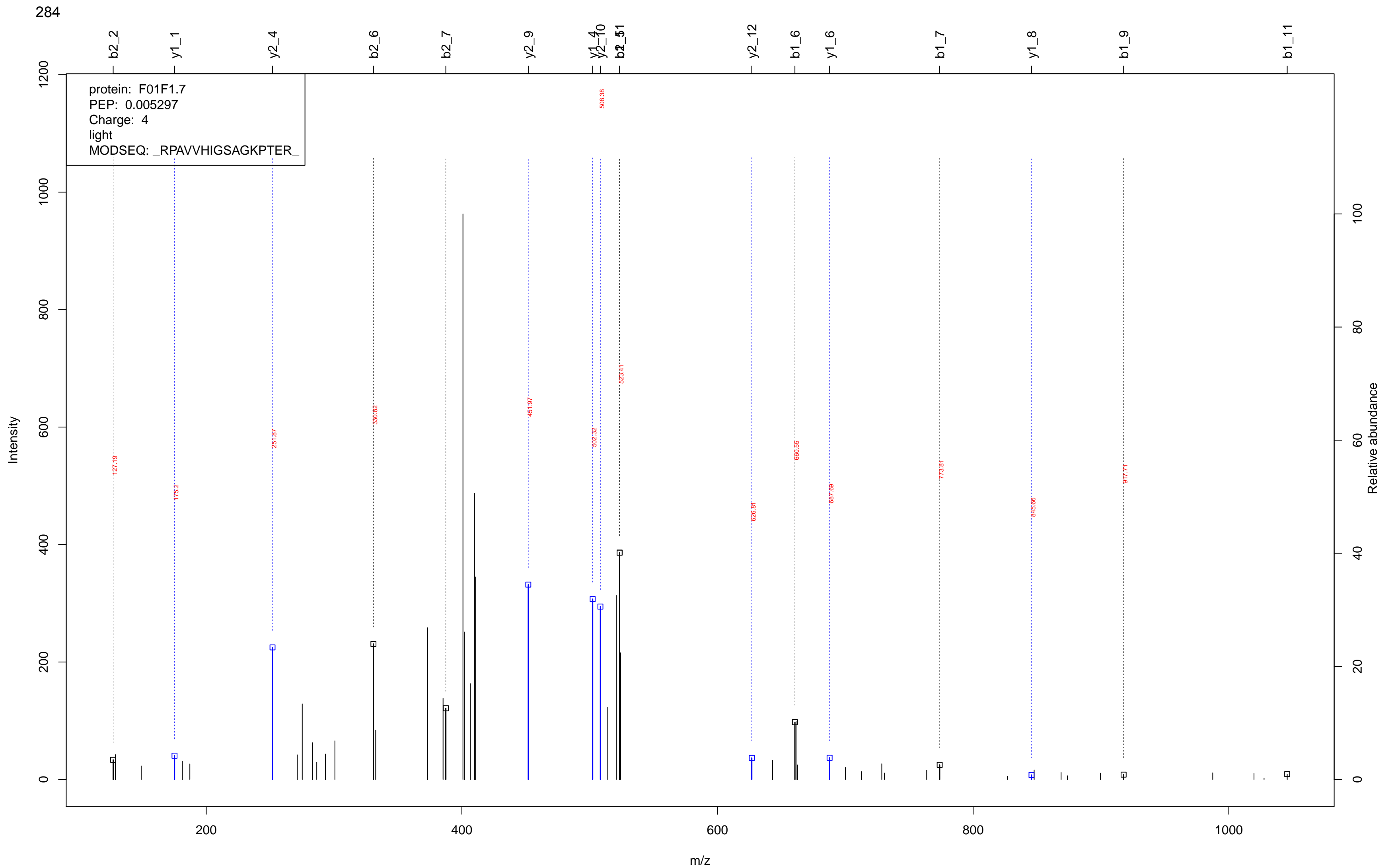


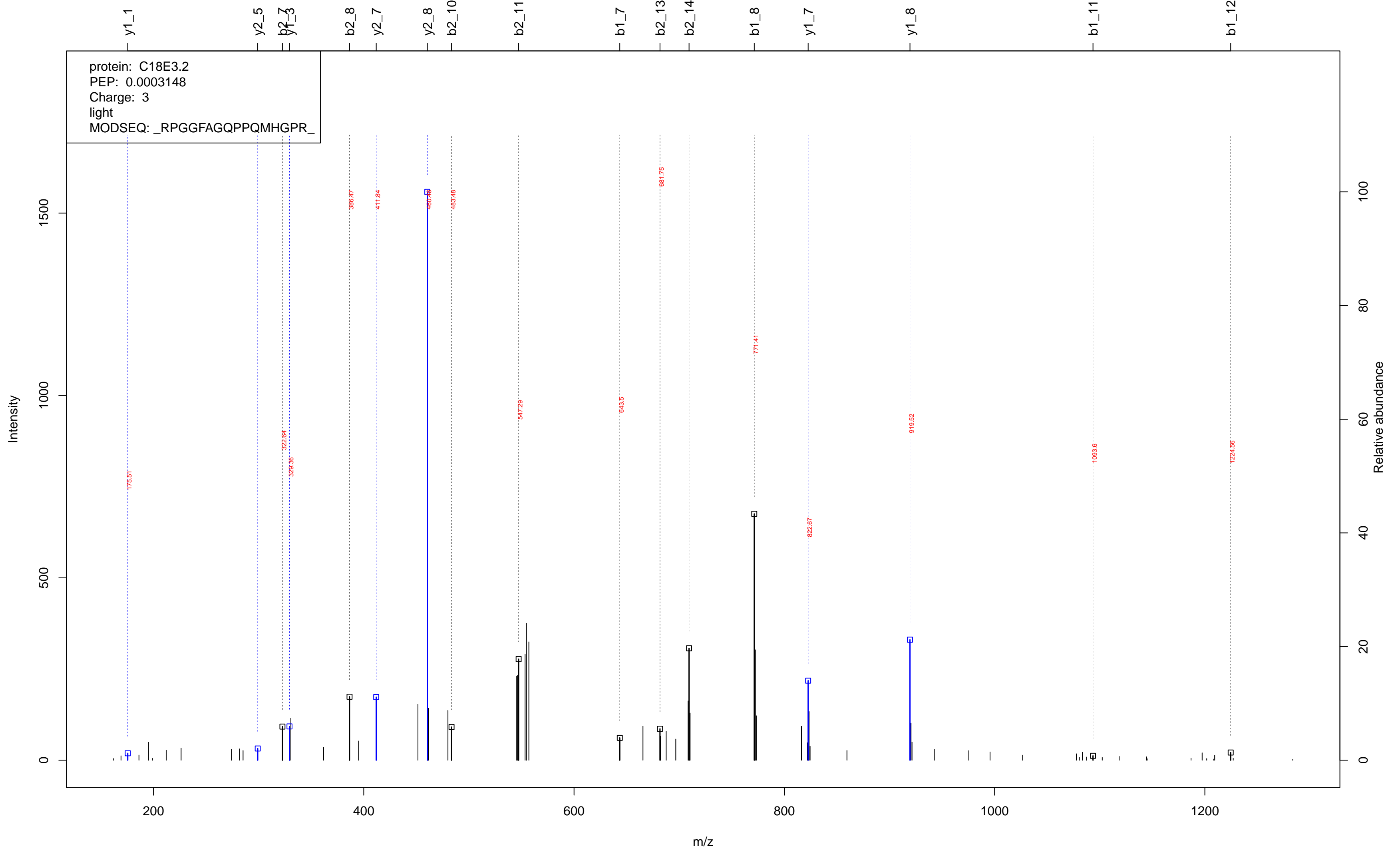












y2_4

y1_3

b2_7

y1_4

b2_11

y4_51

b2_12

b2_13

y1_6

b2_14

b1_7

b2_15

b2_16

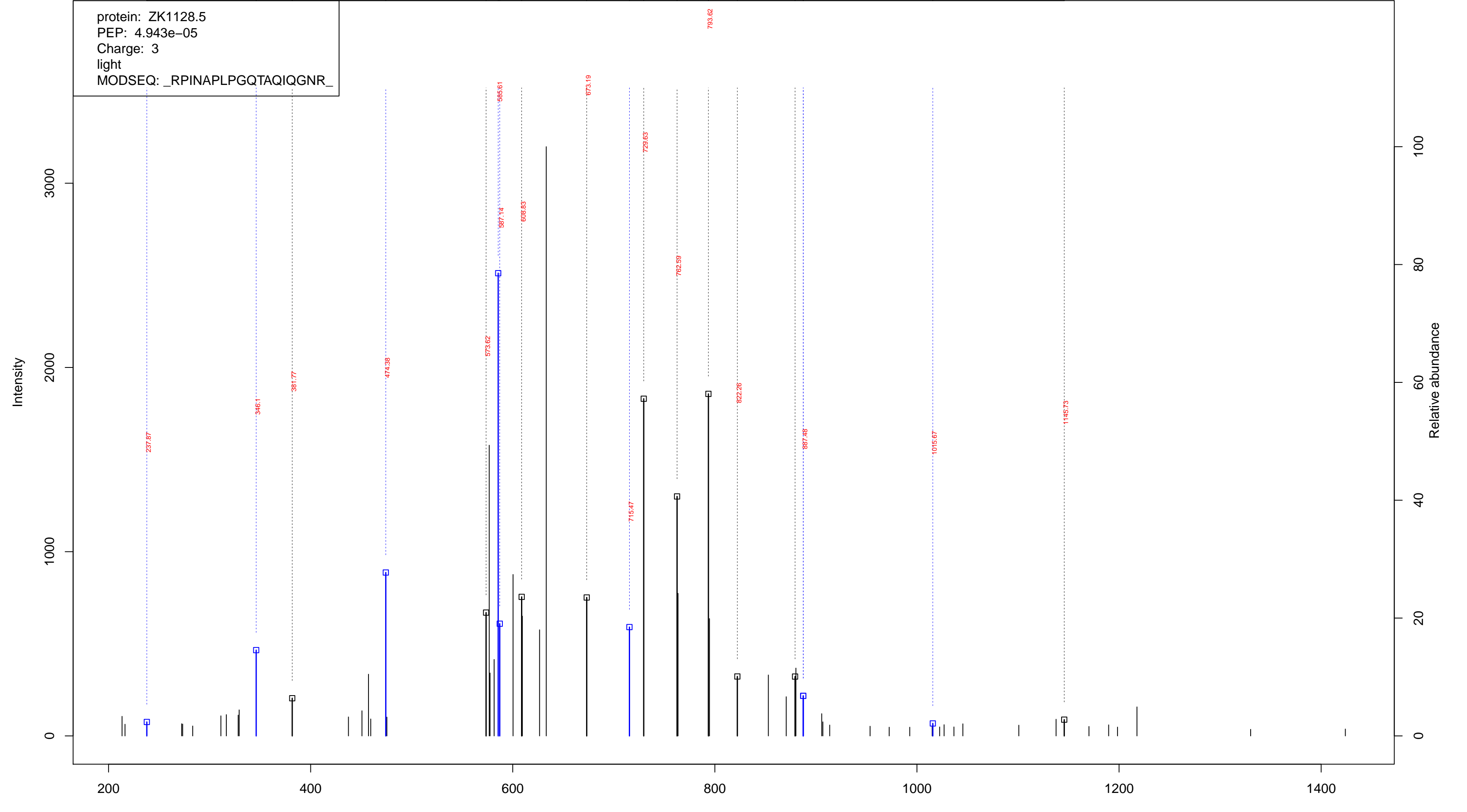
b2_17

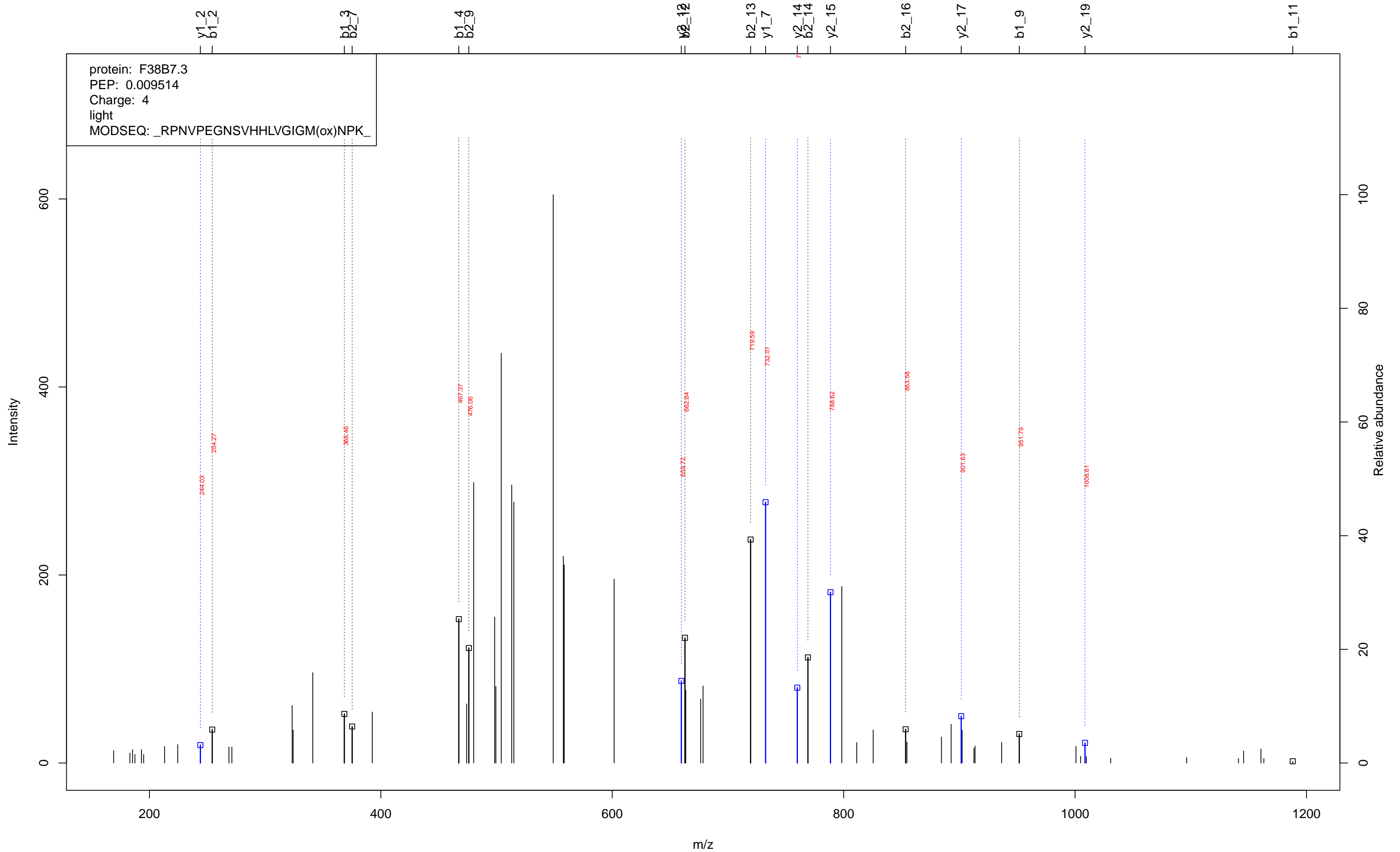
y4_87

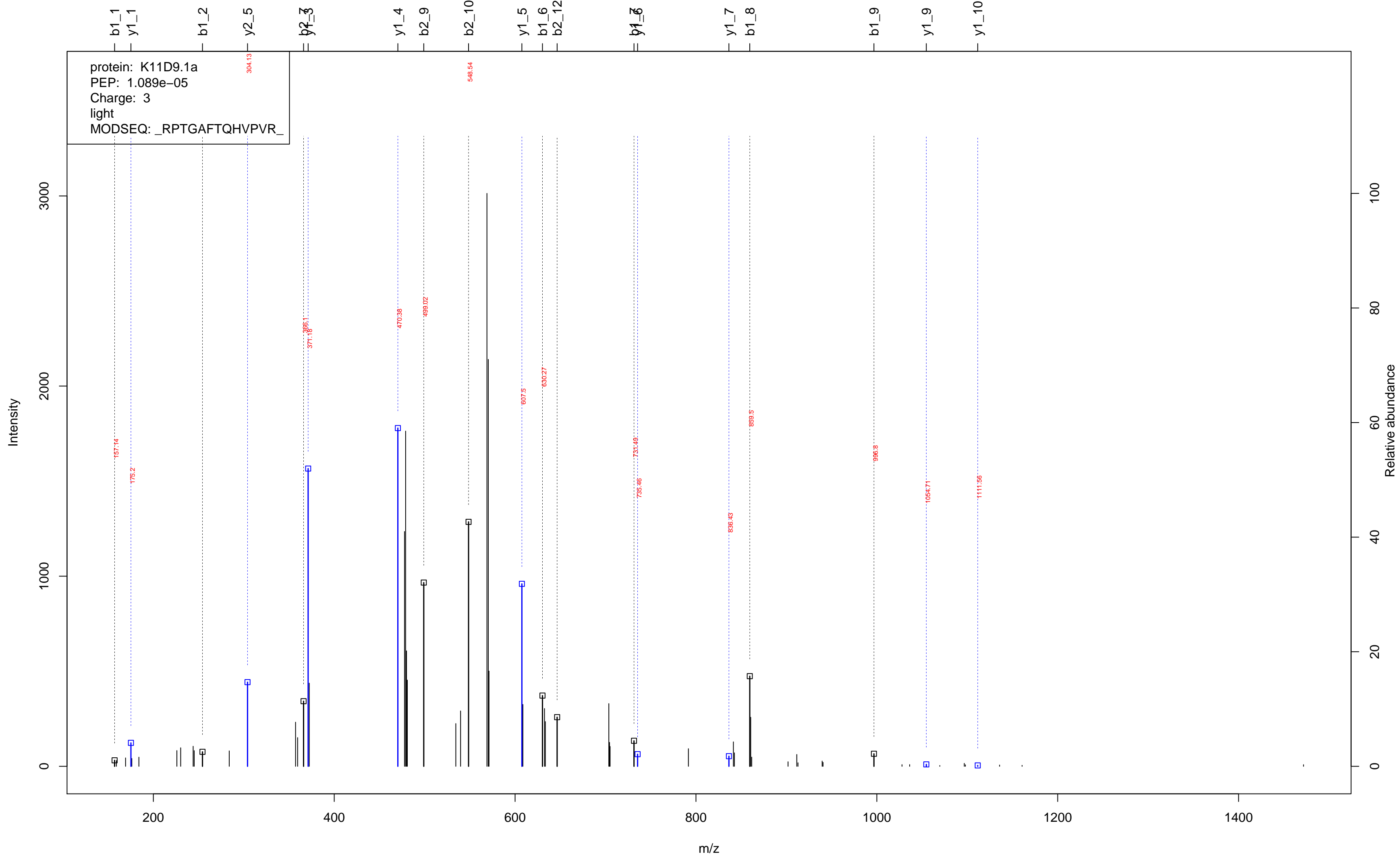
y1_9

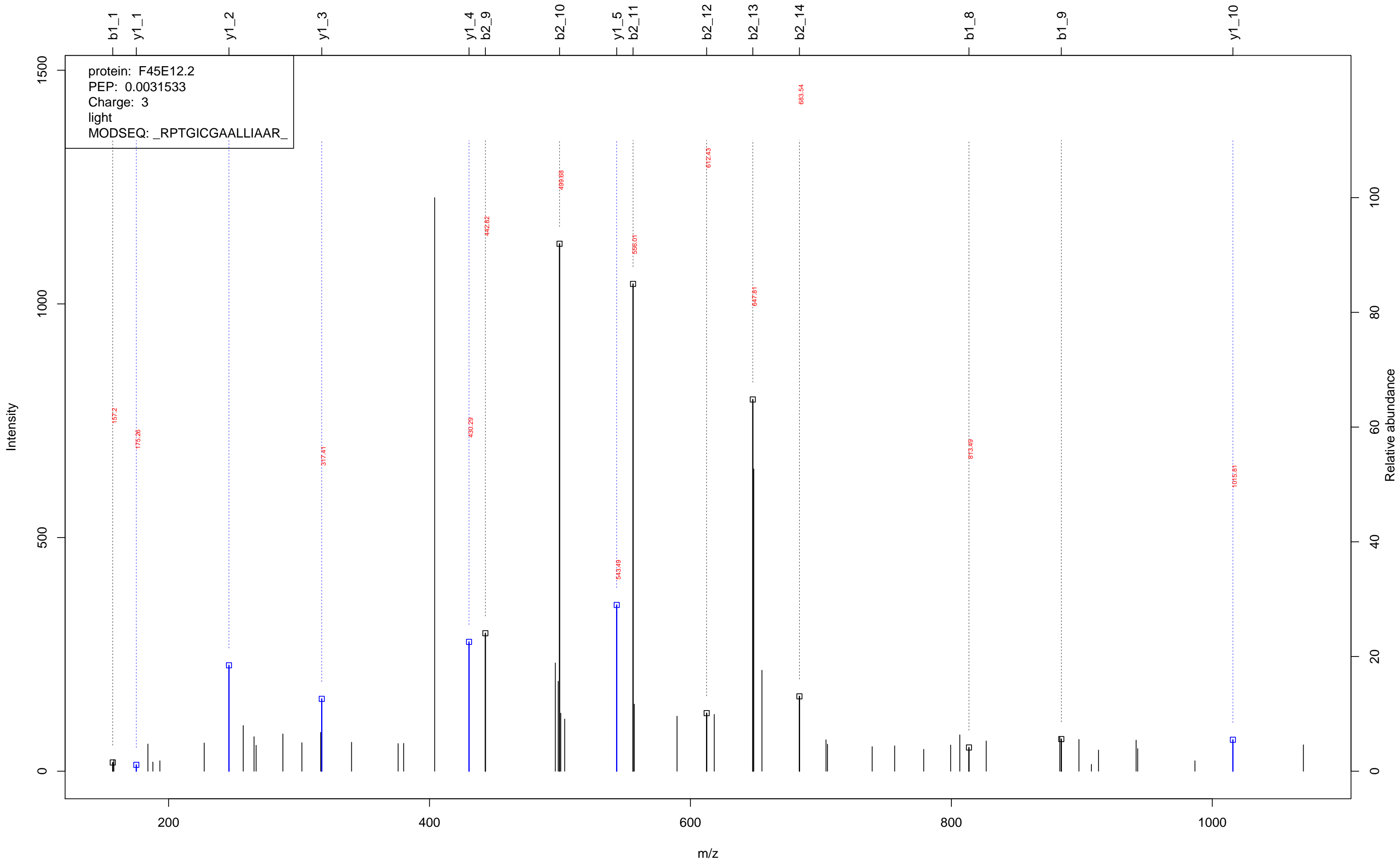
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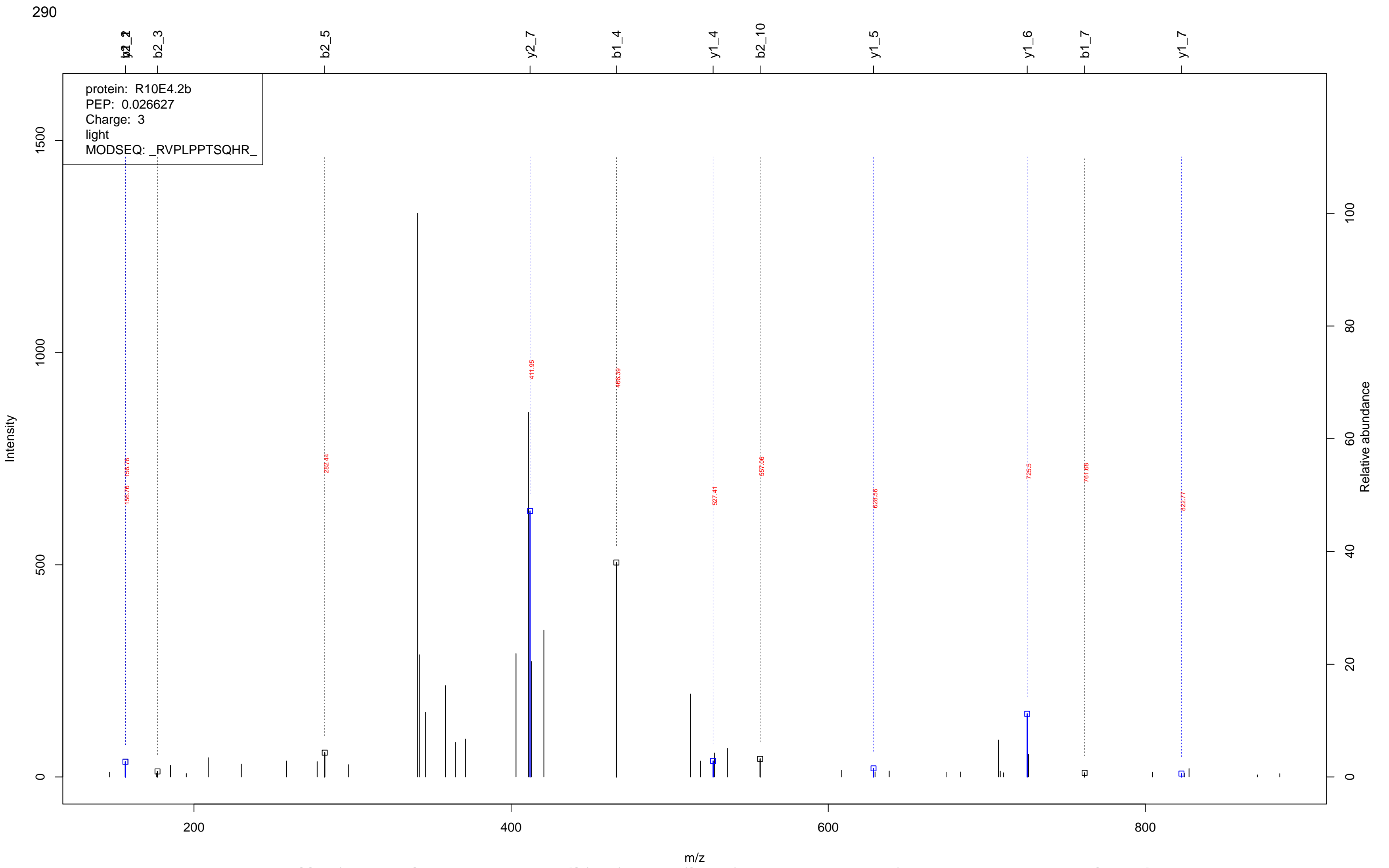
protein: ZK1128.5
PEP: 4.943e-05
Charge: 3
light
MODSEQ: _RPINAPLPGQTAQIQGNR_

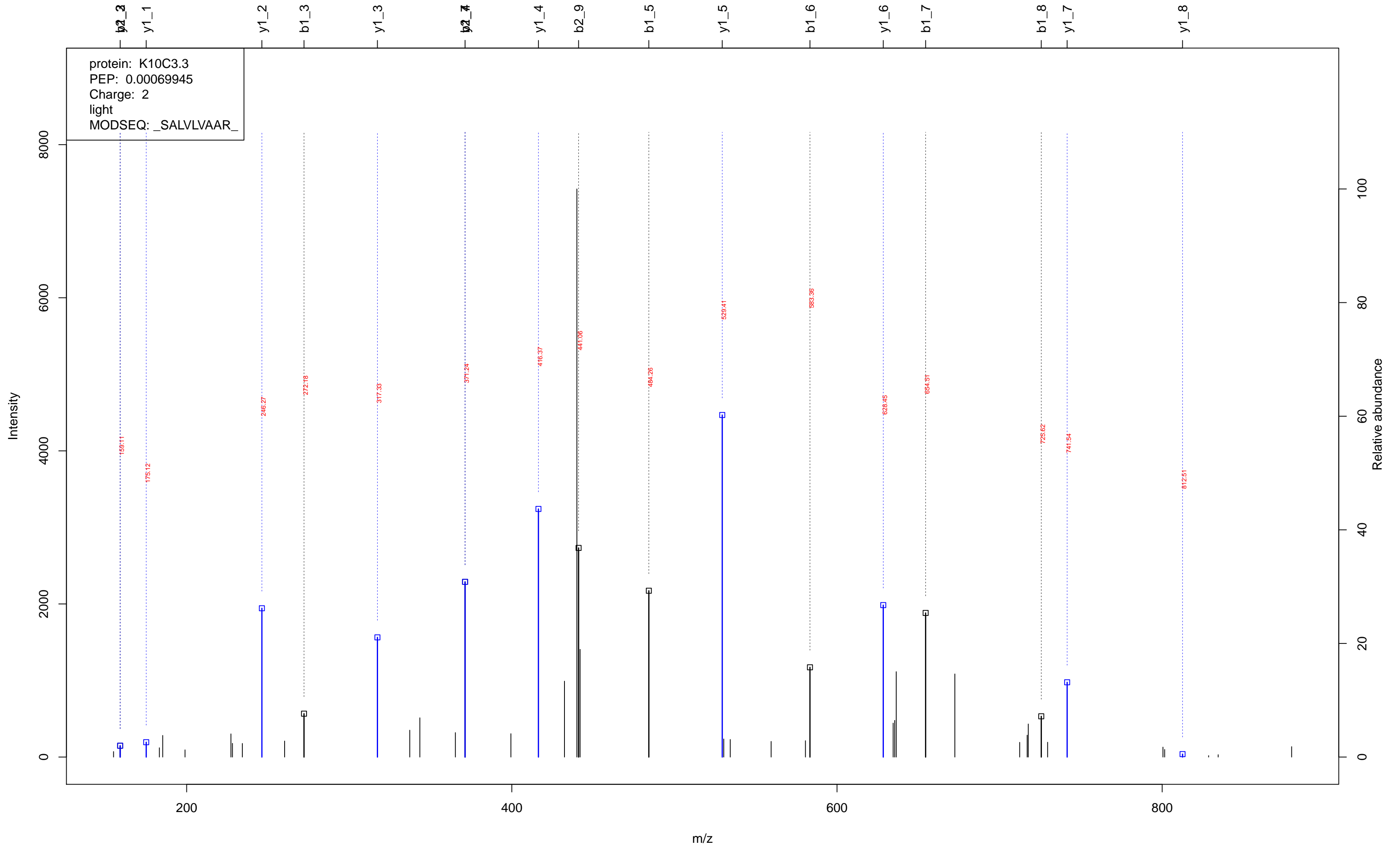


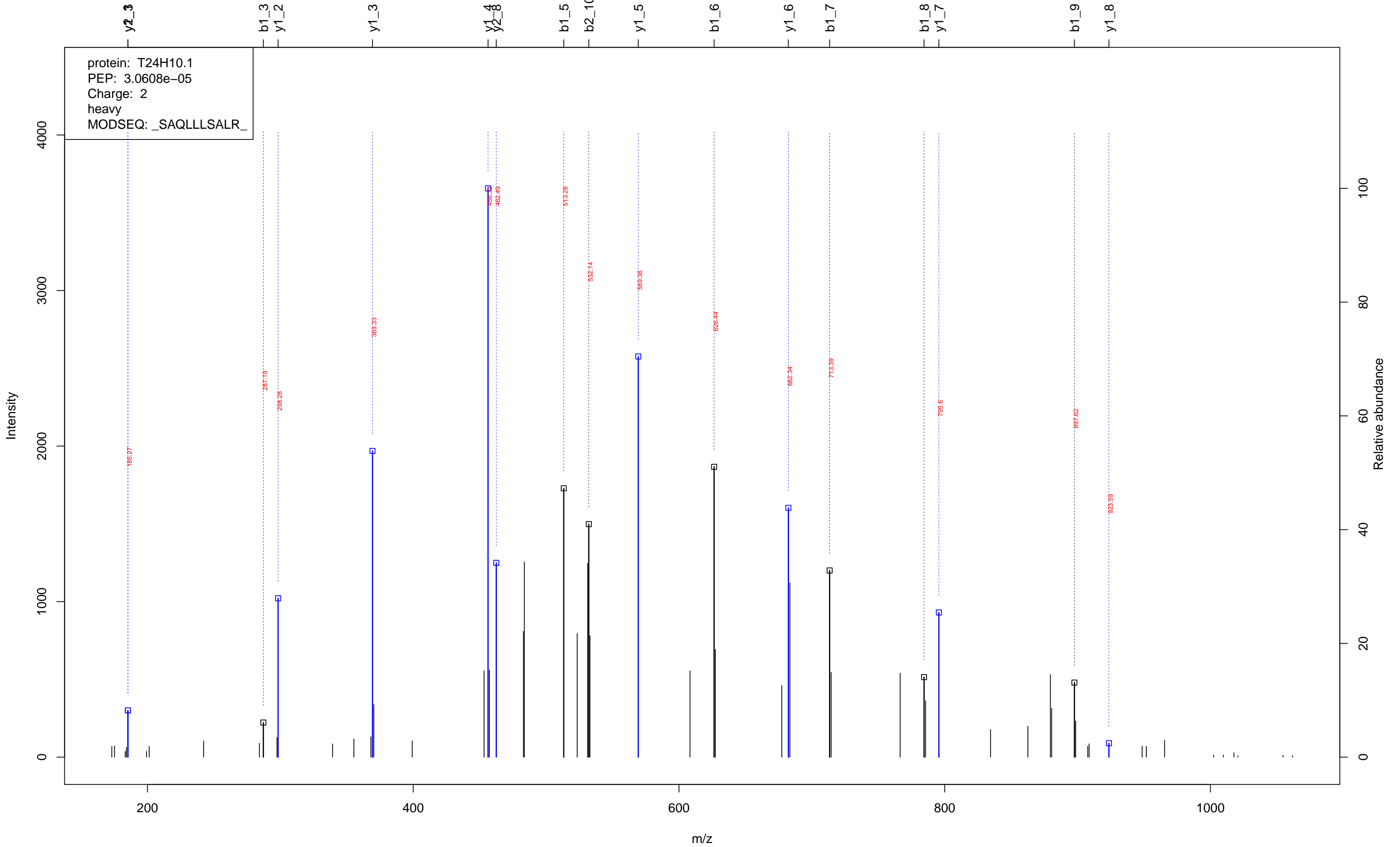


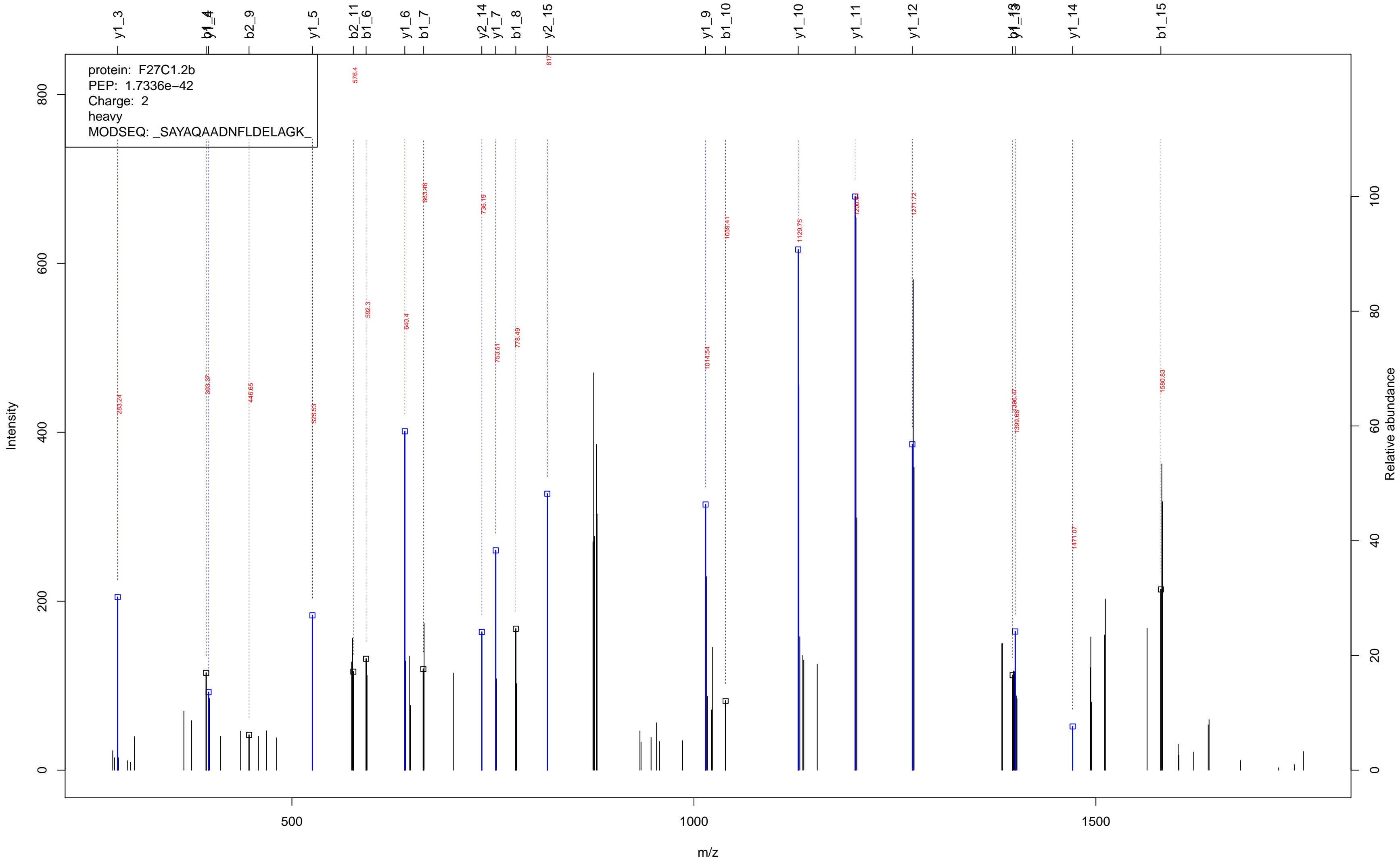


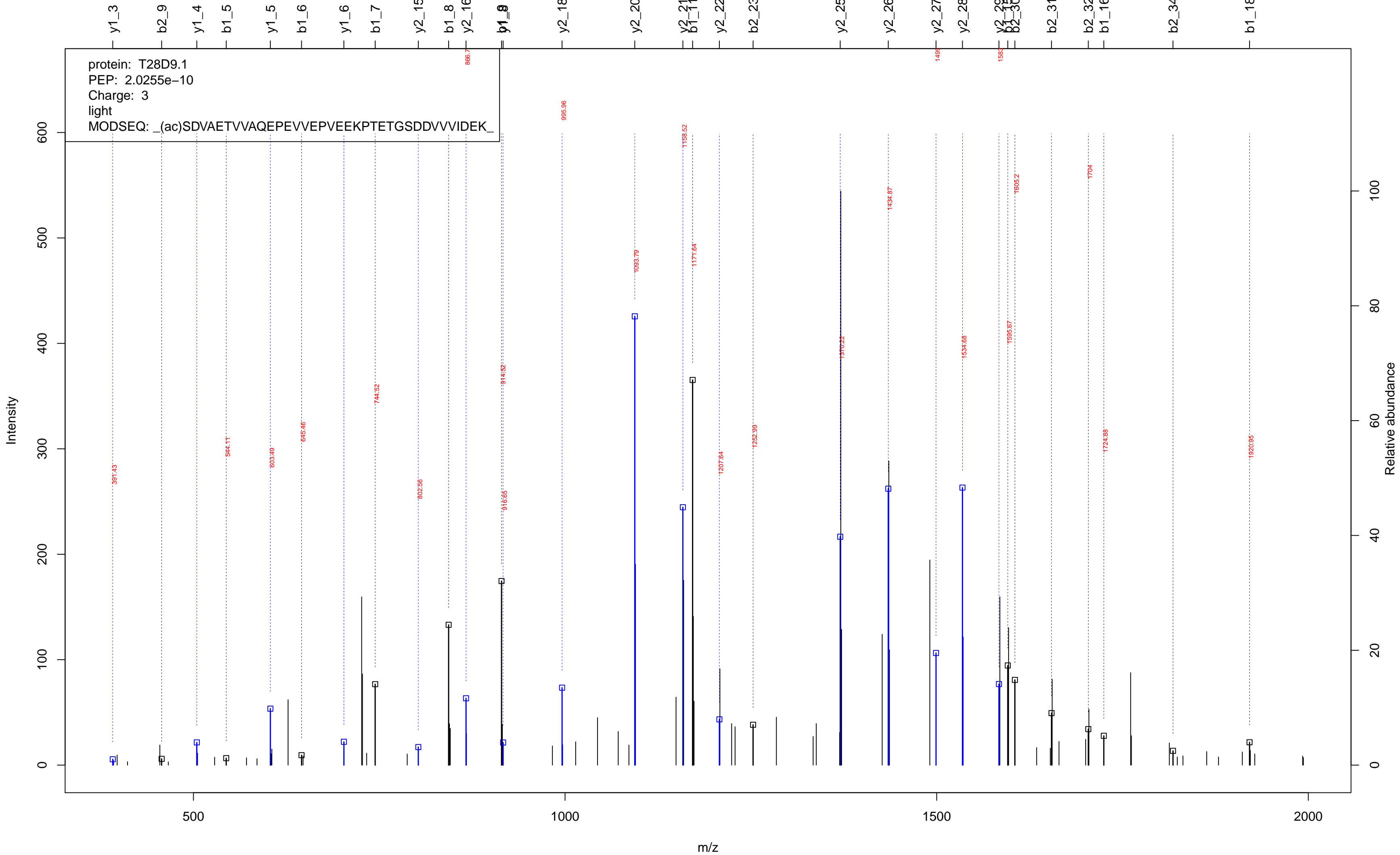


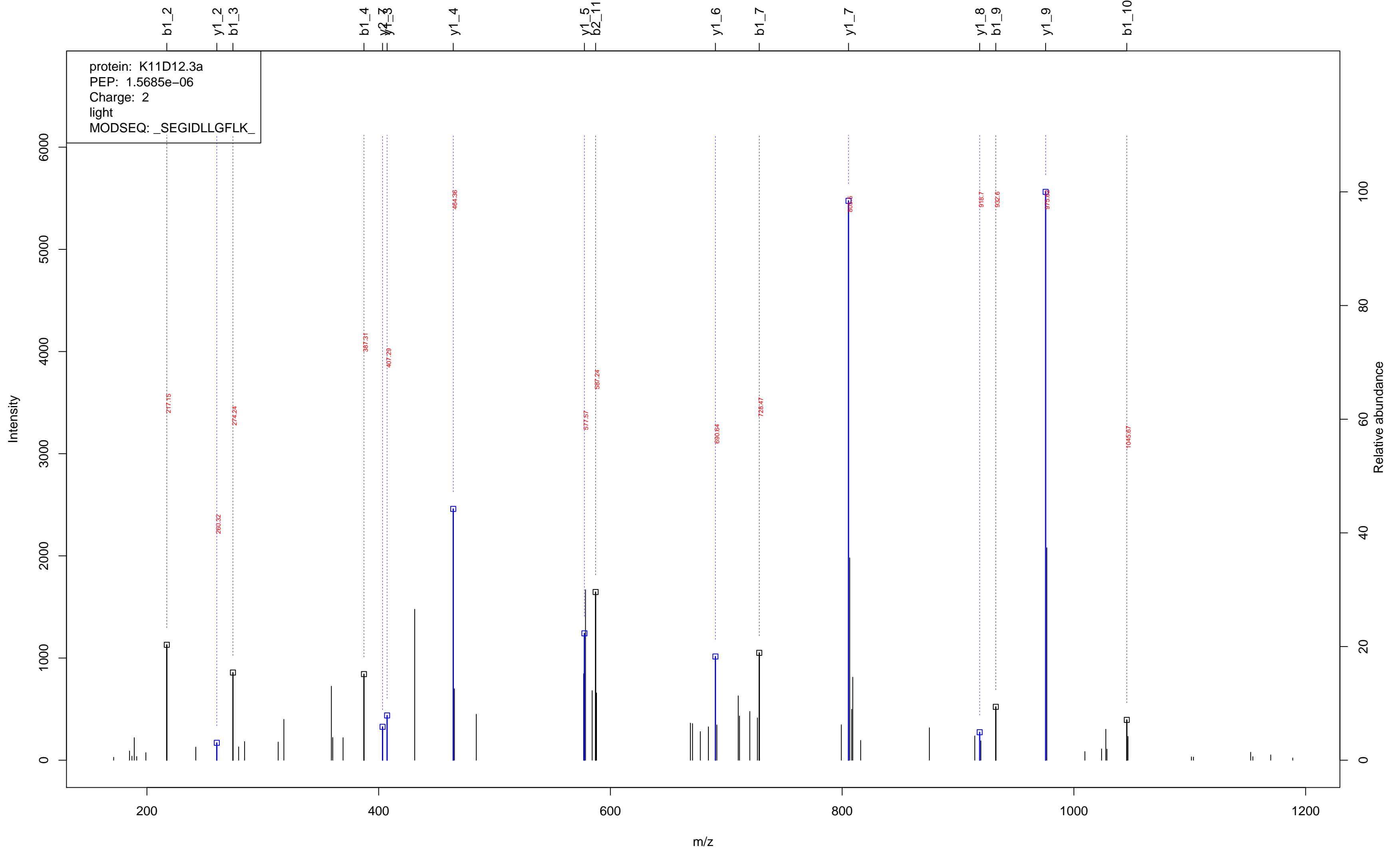


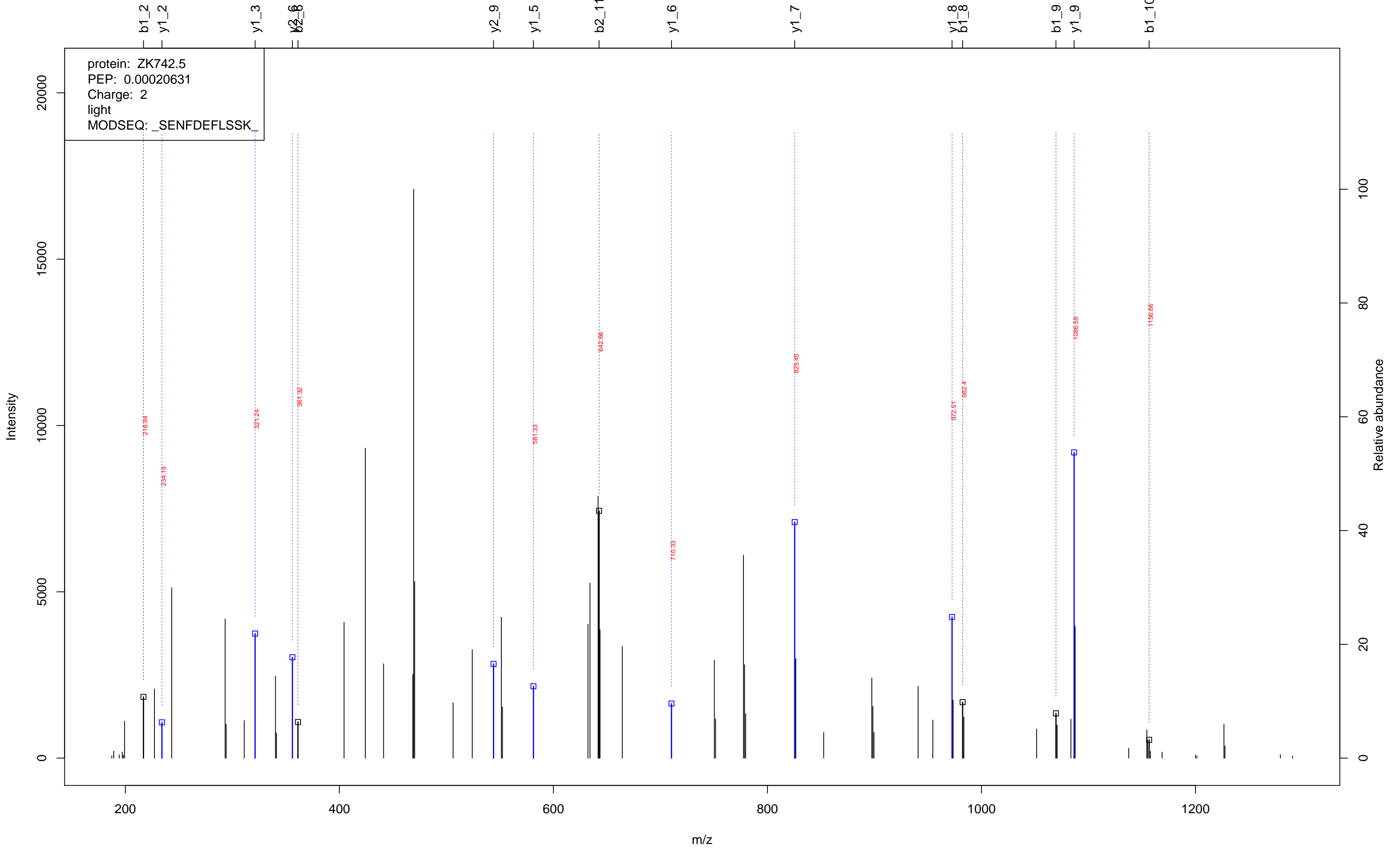


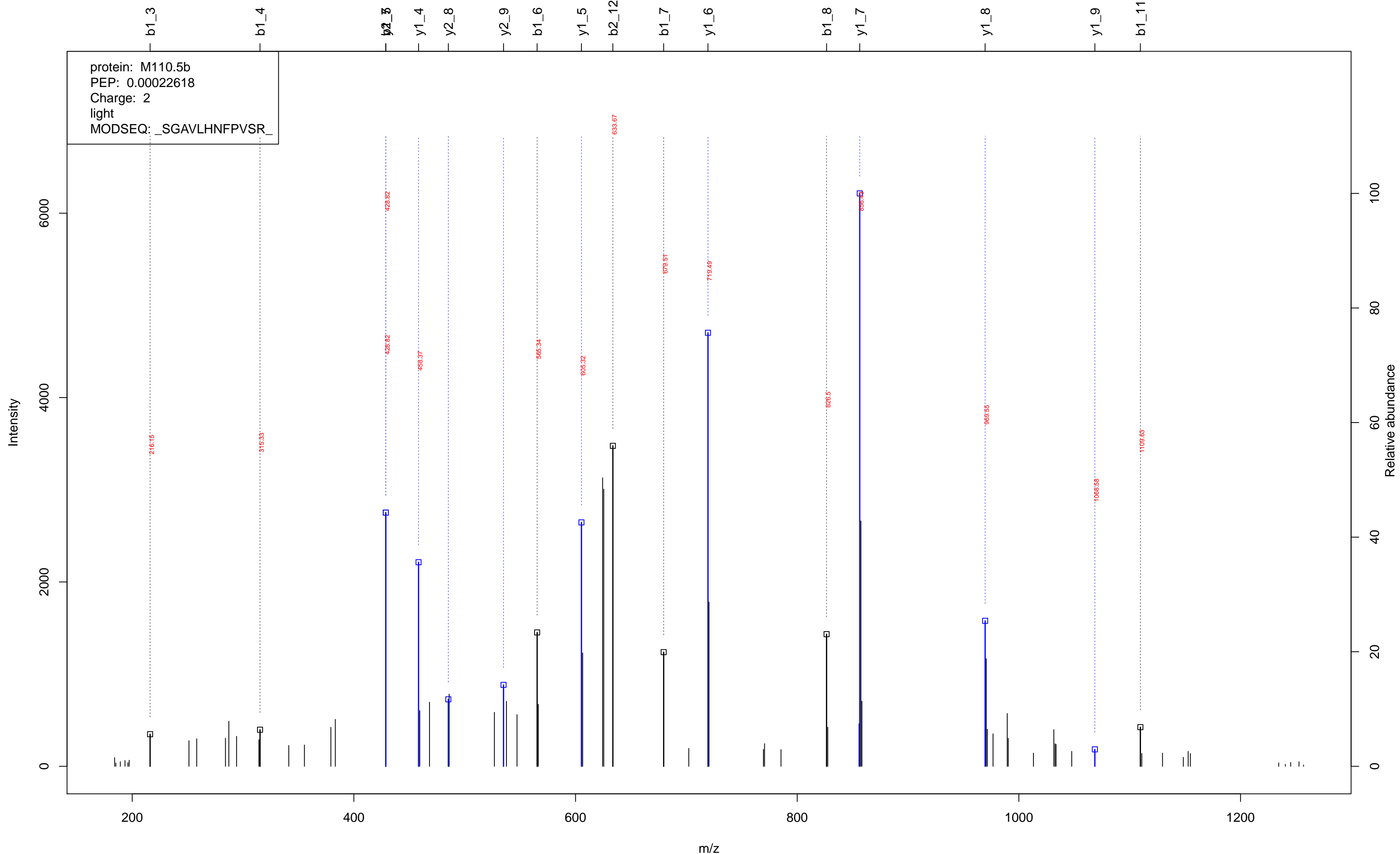






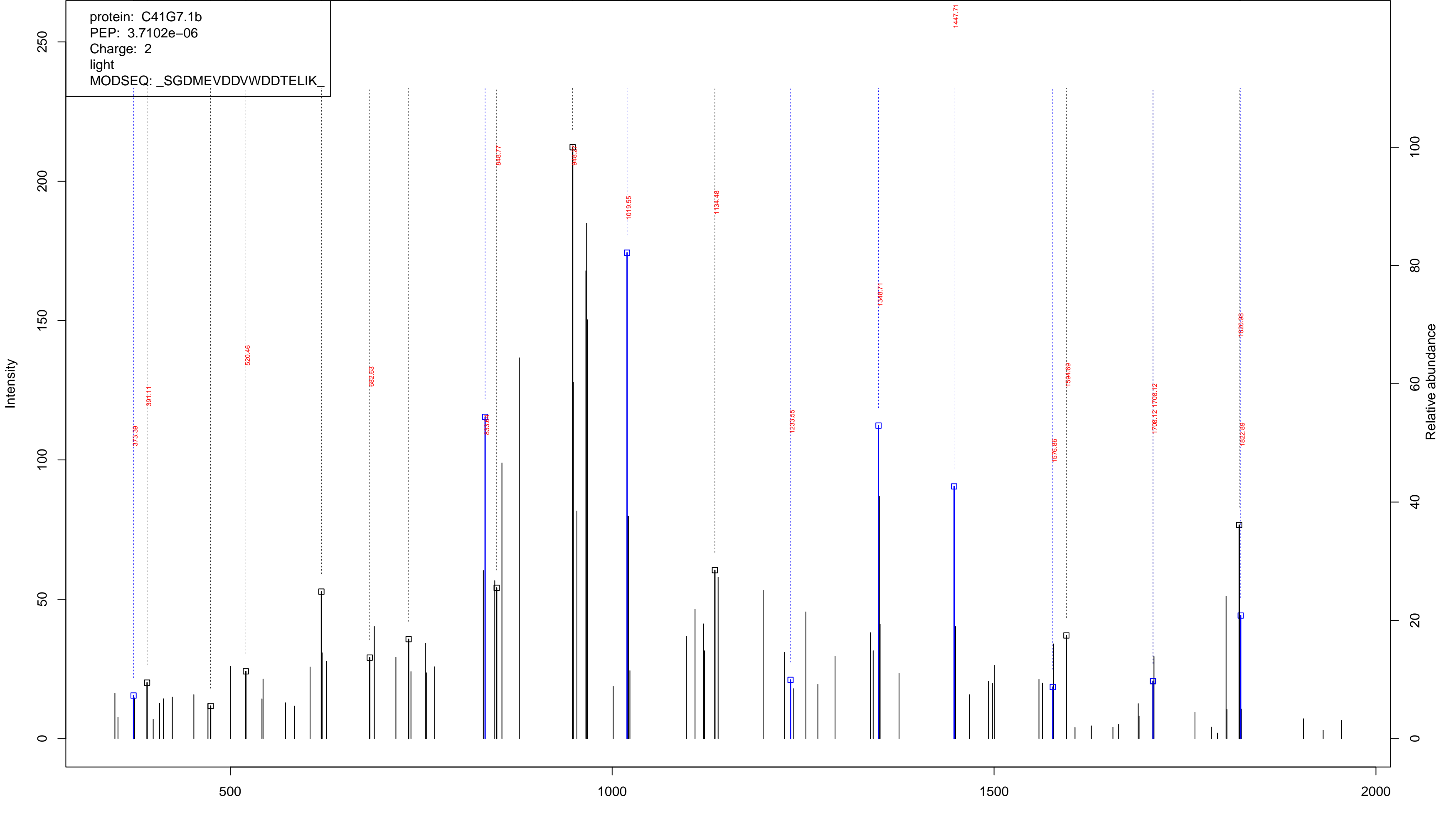






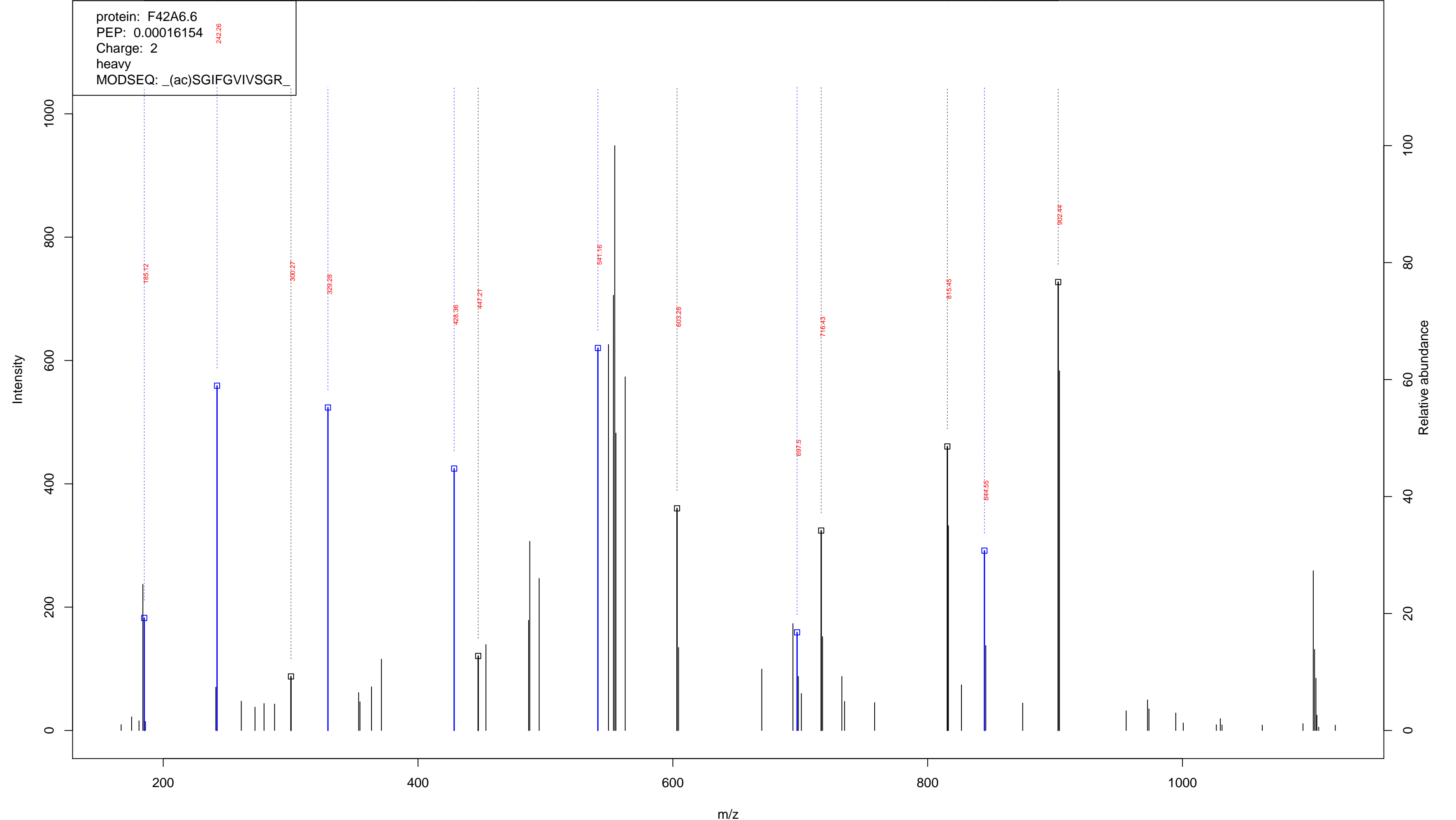
y1_3
b1_4
b2_9
b1_5
b1_6
b2_12
b2_13
y1_7
b1_8
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y1_11
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y1_13
b1_14
b1_15
b1_16

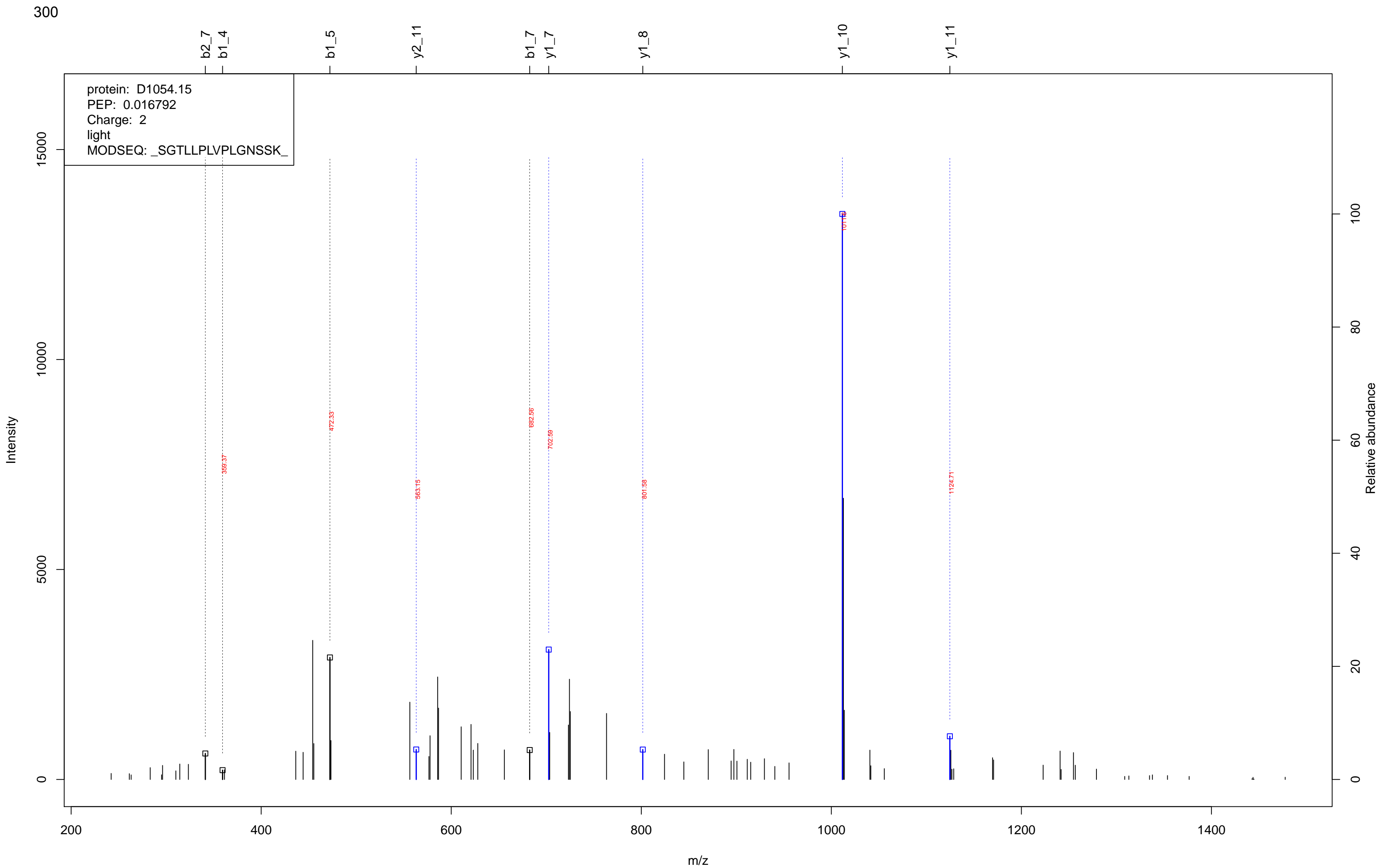
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Charge: 2
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MODSEQ: _SGDMEVDDVWDDTELIK_

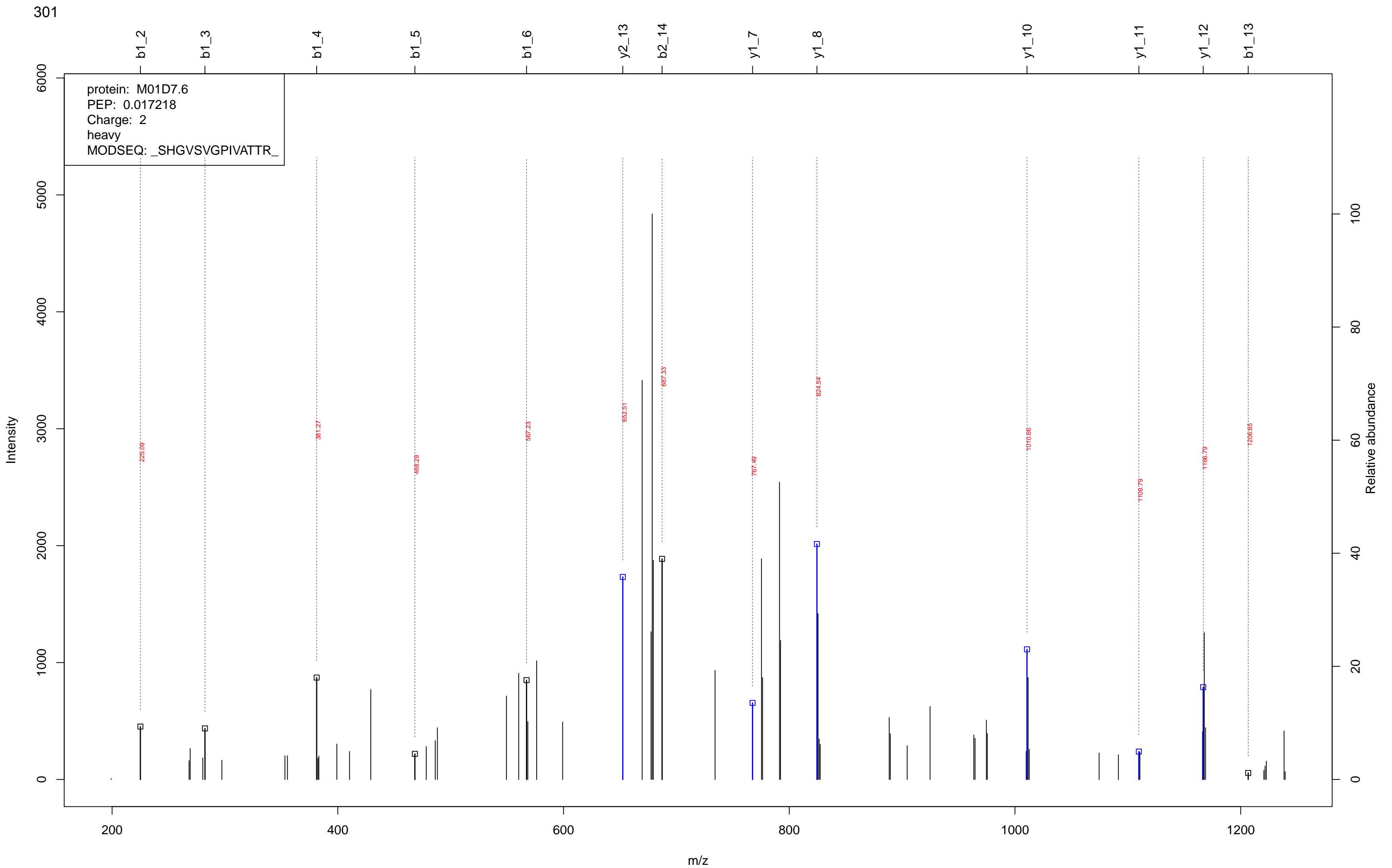


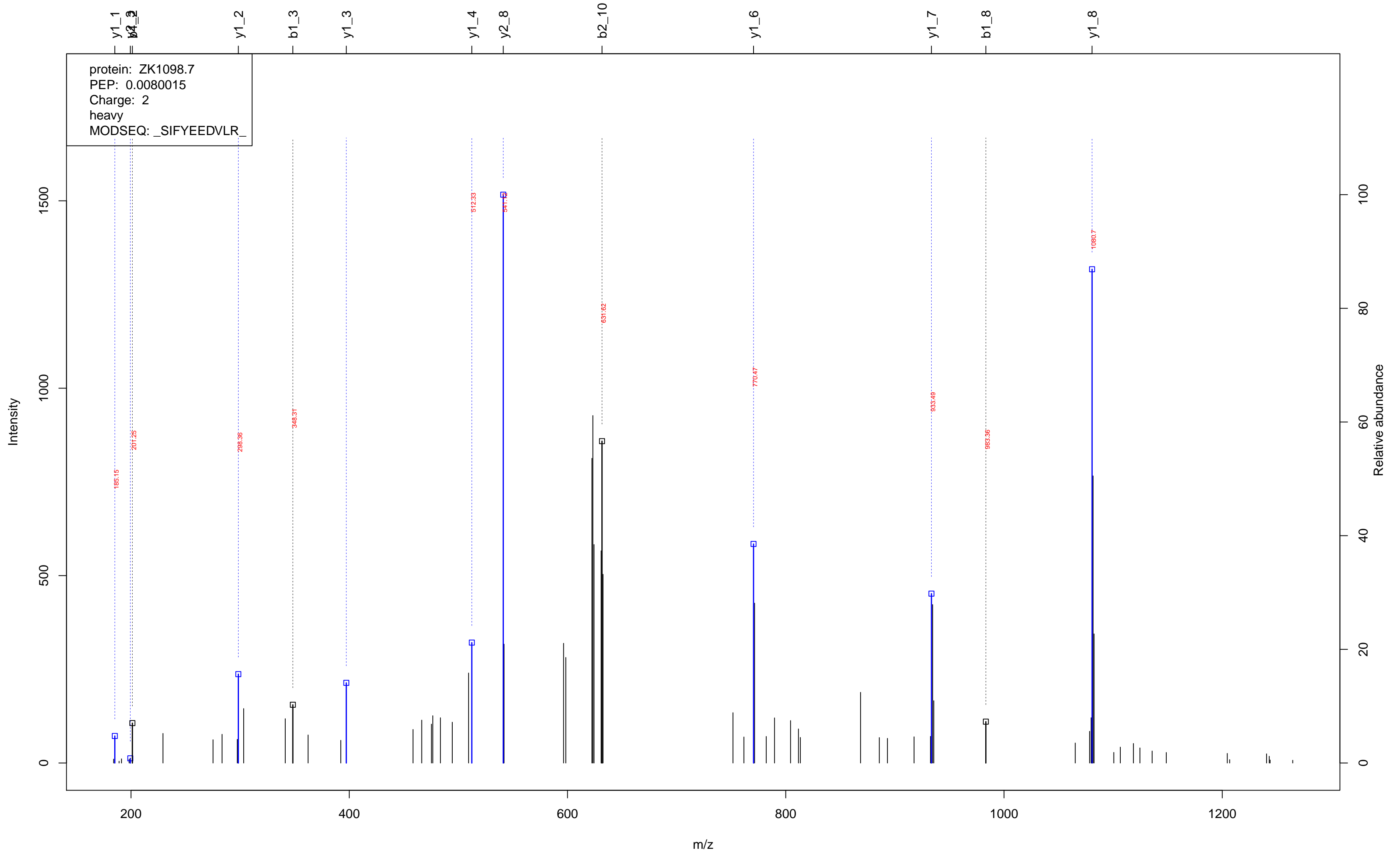
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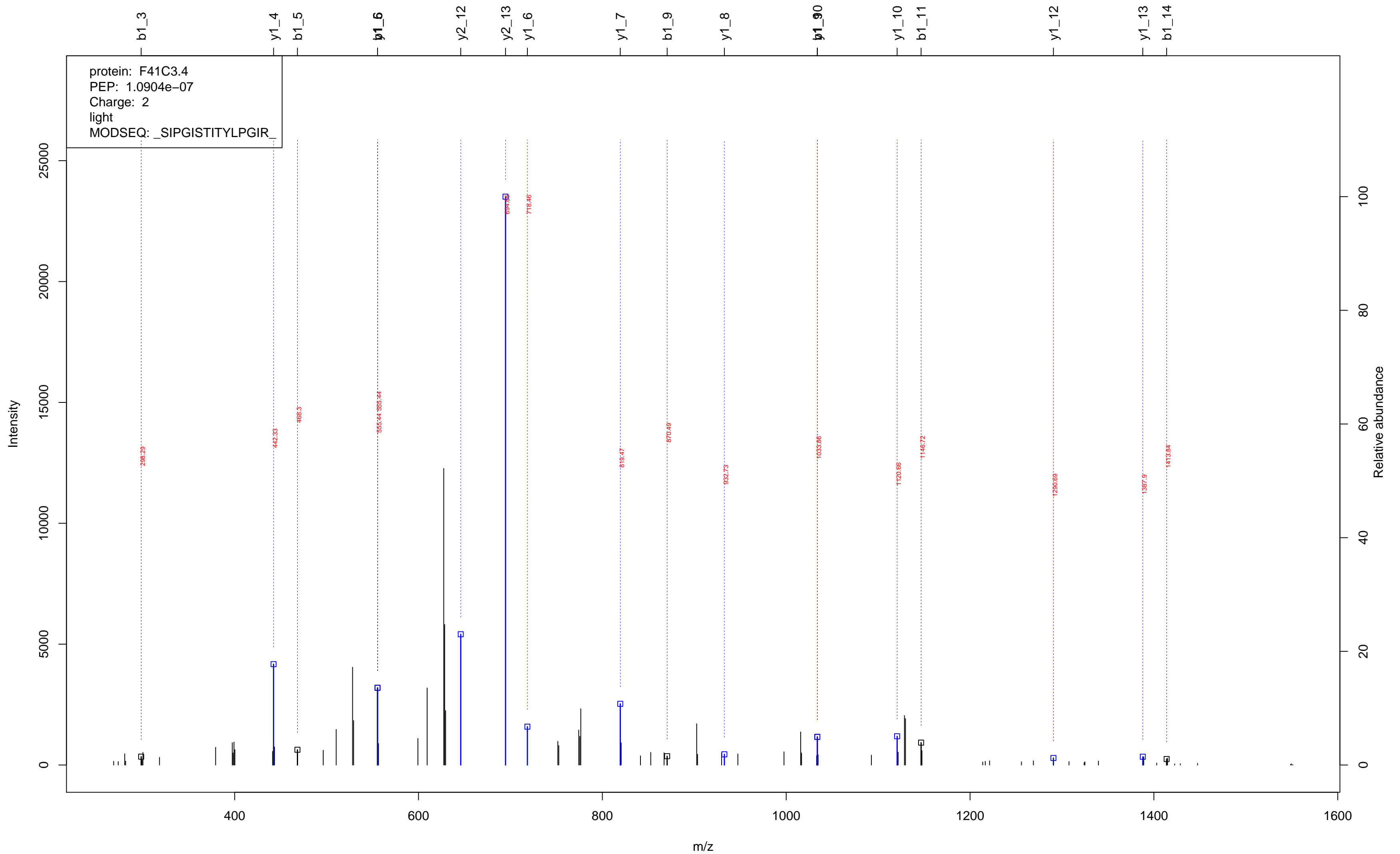
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PEP: 0.00016154
Charge: 2
heavy
MODSEQ: _(ac)SGIFGVIVSGR_

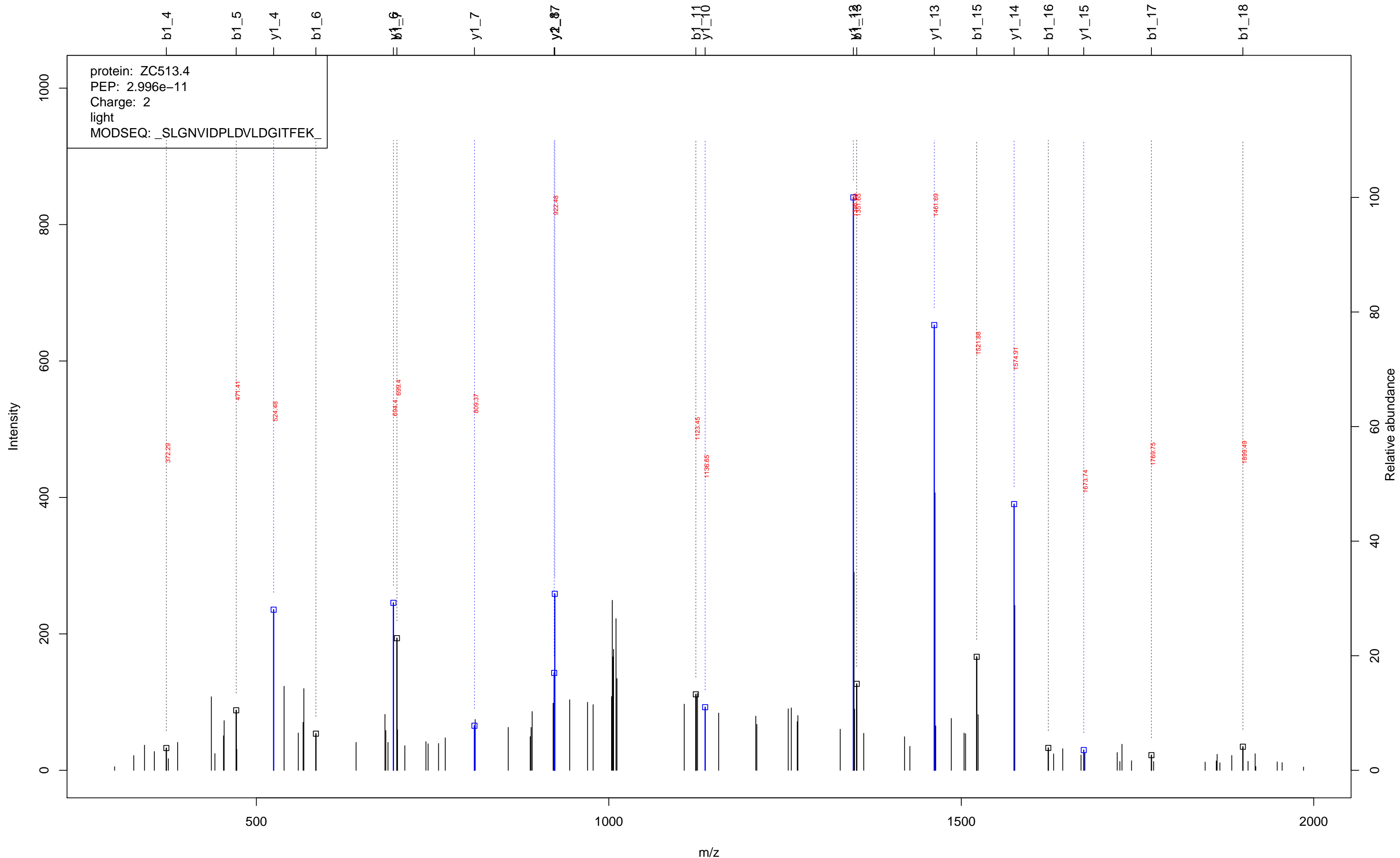


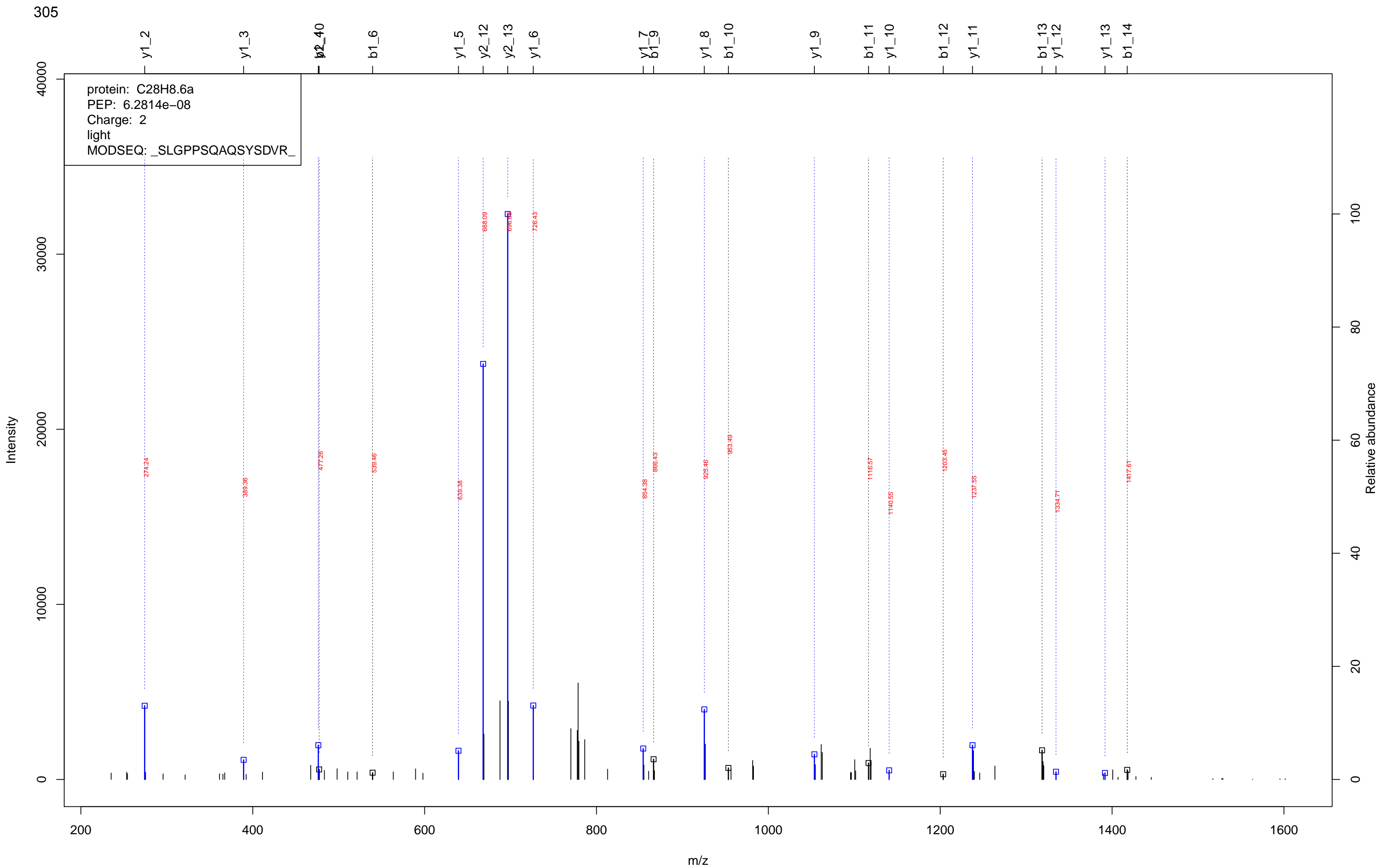


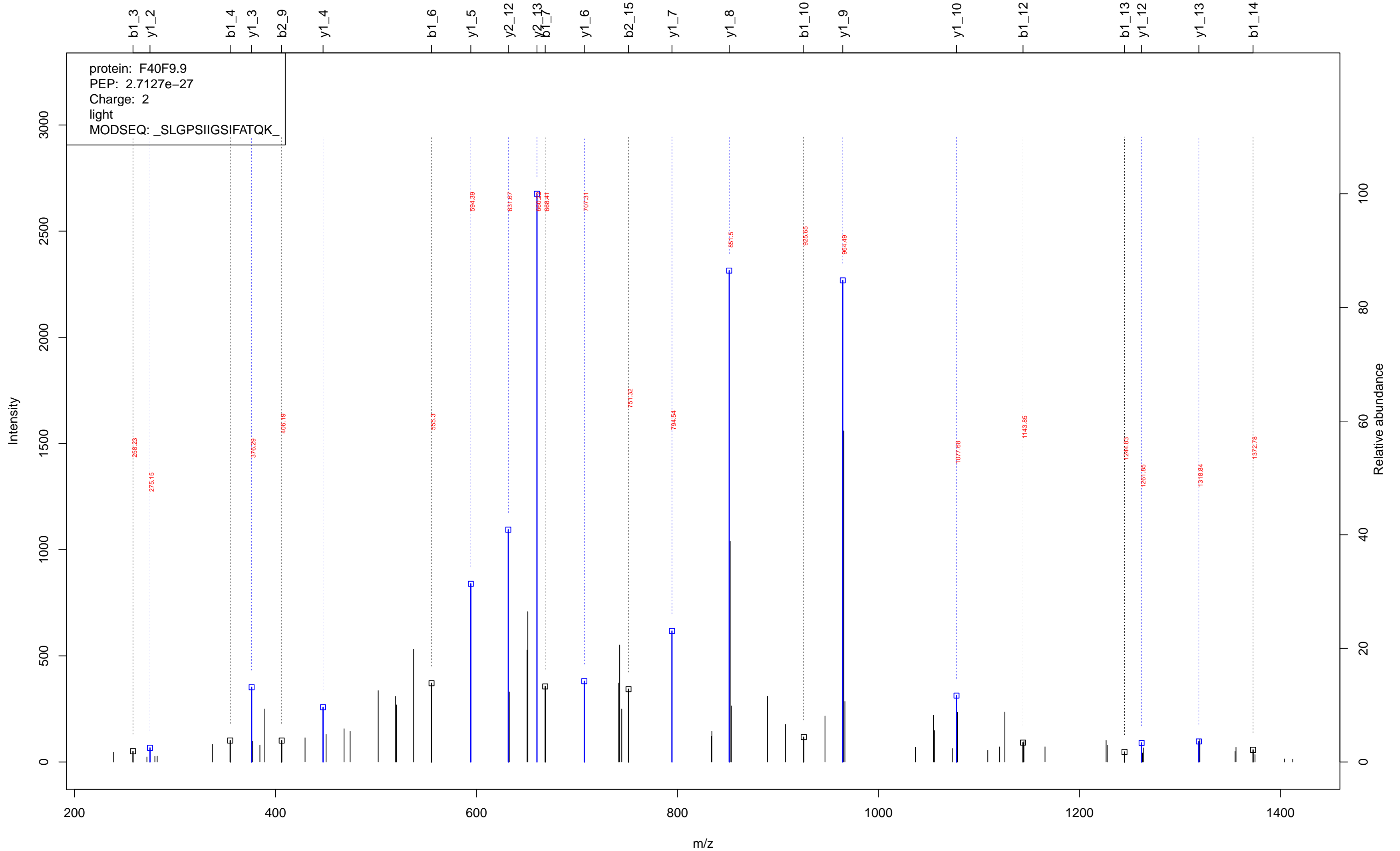


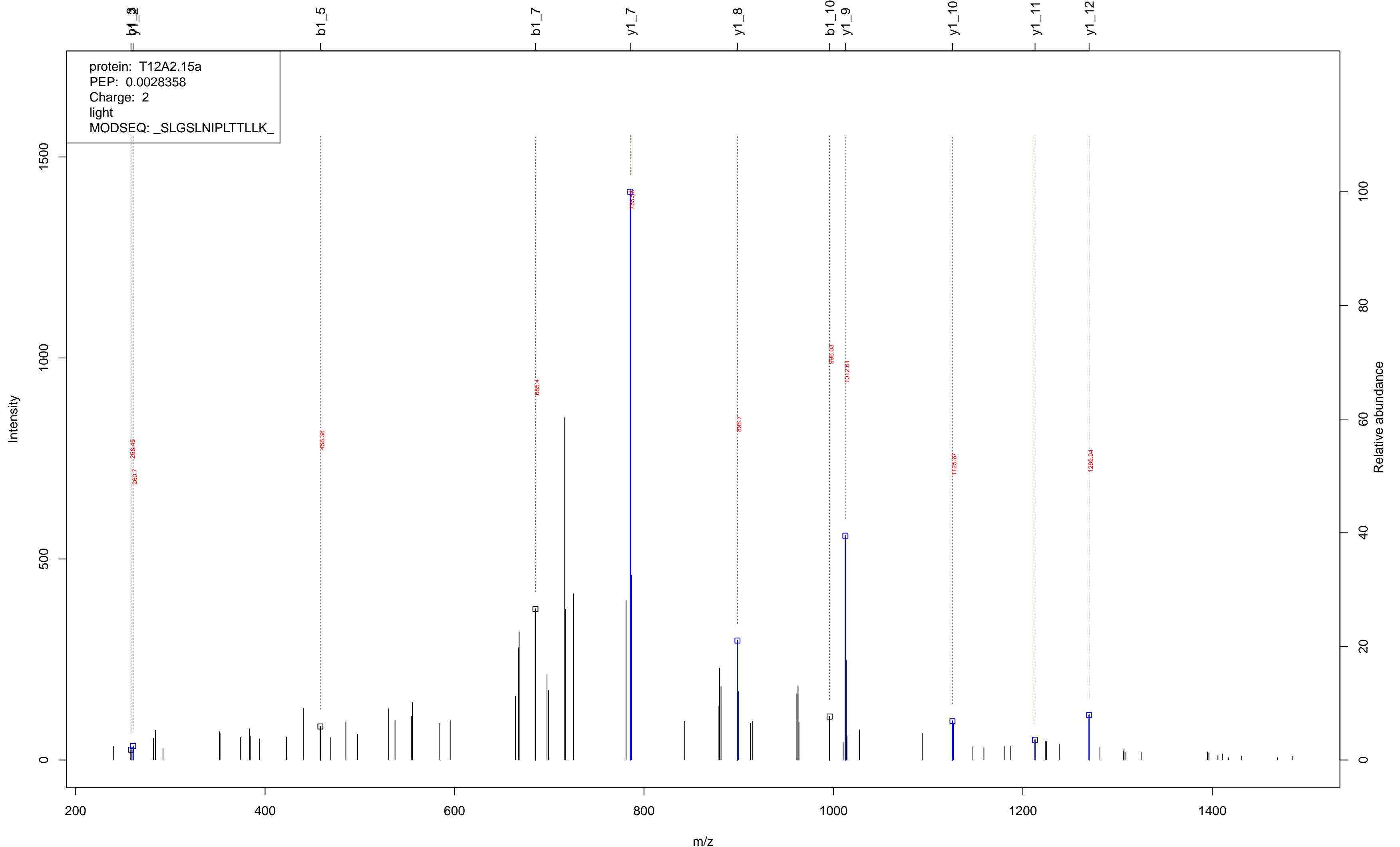


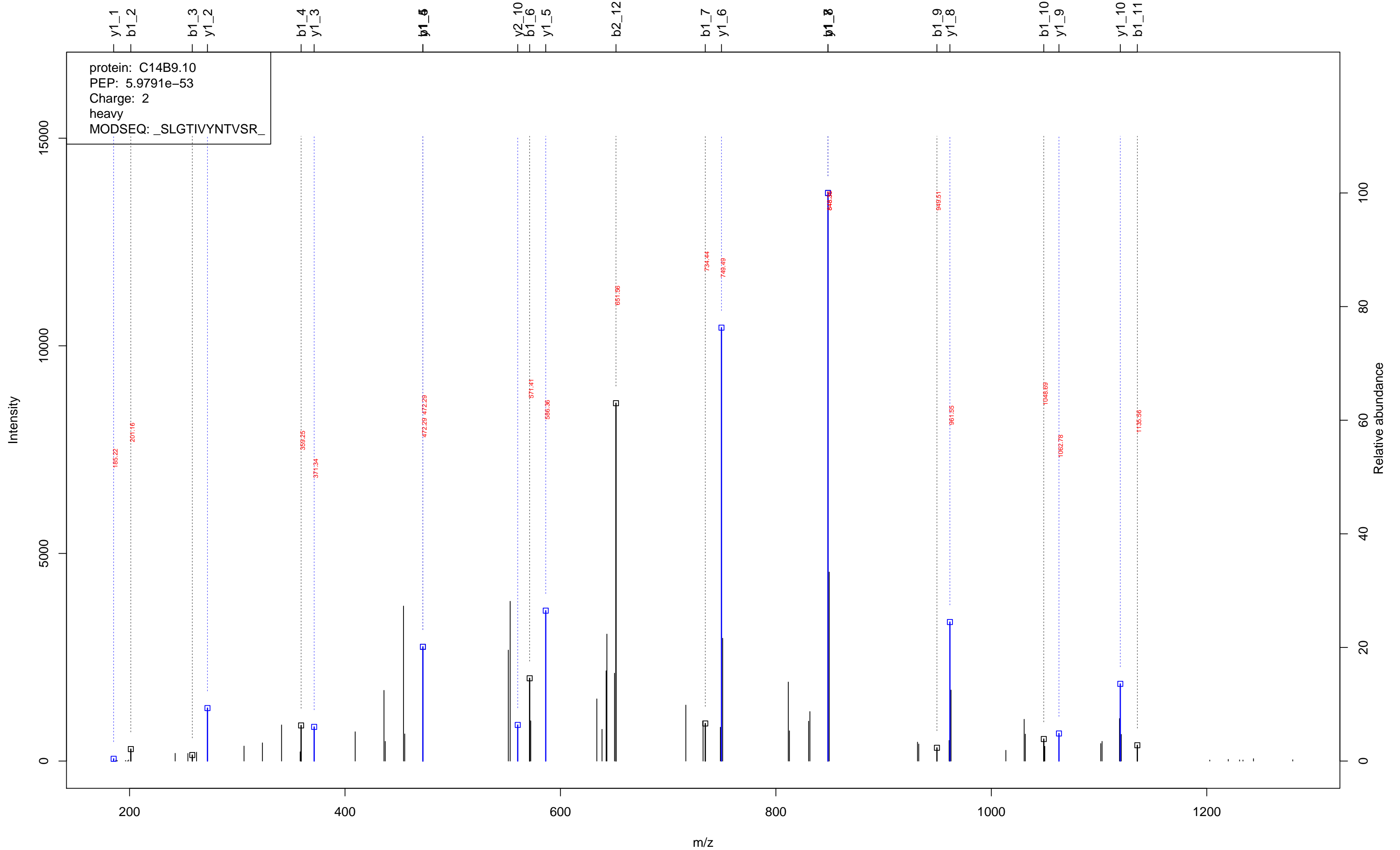


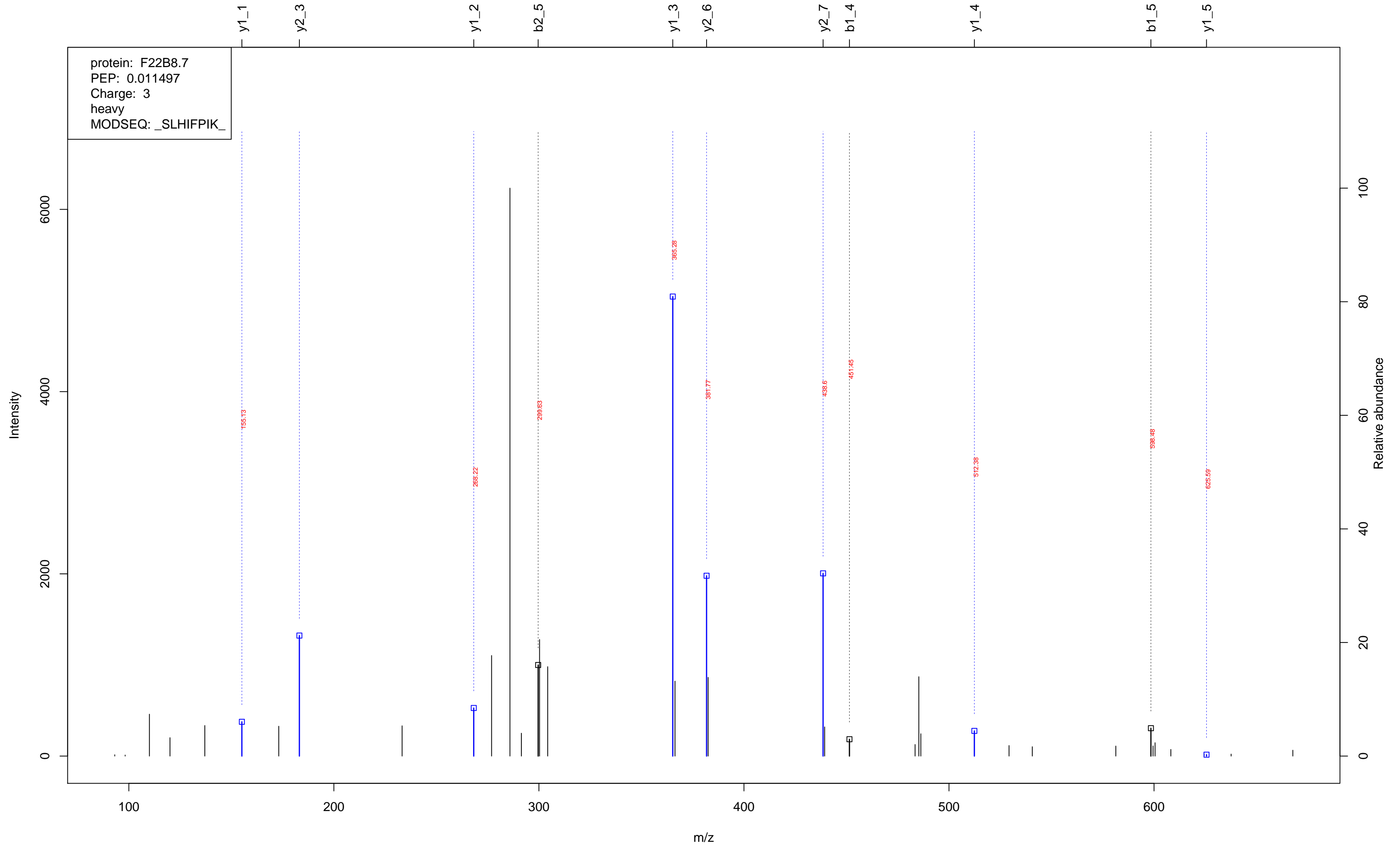


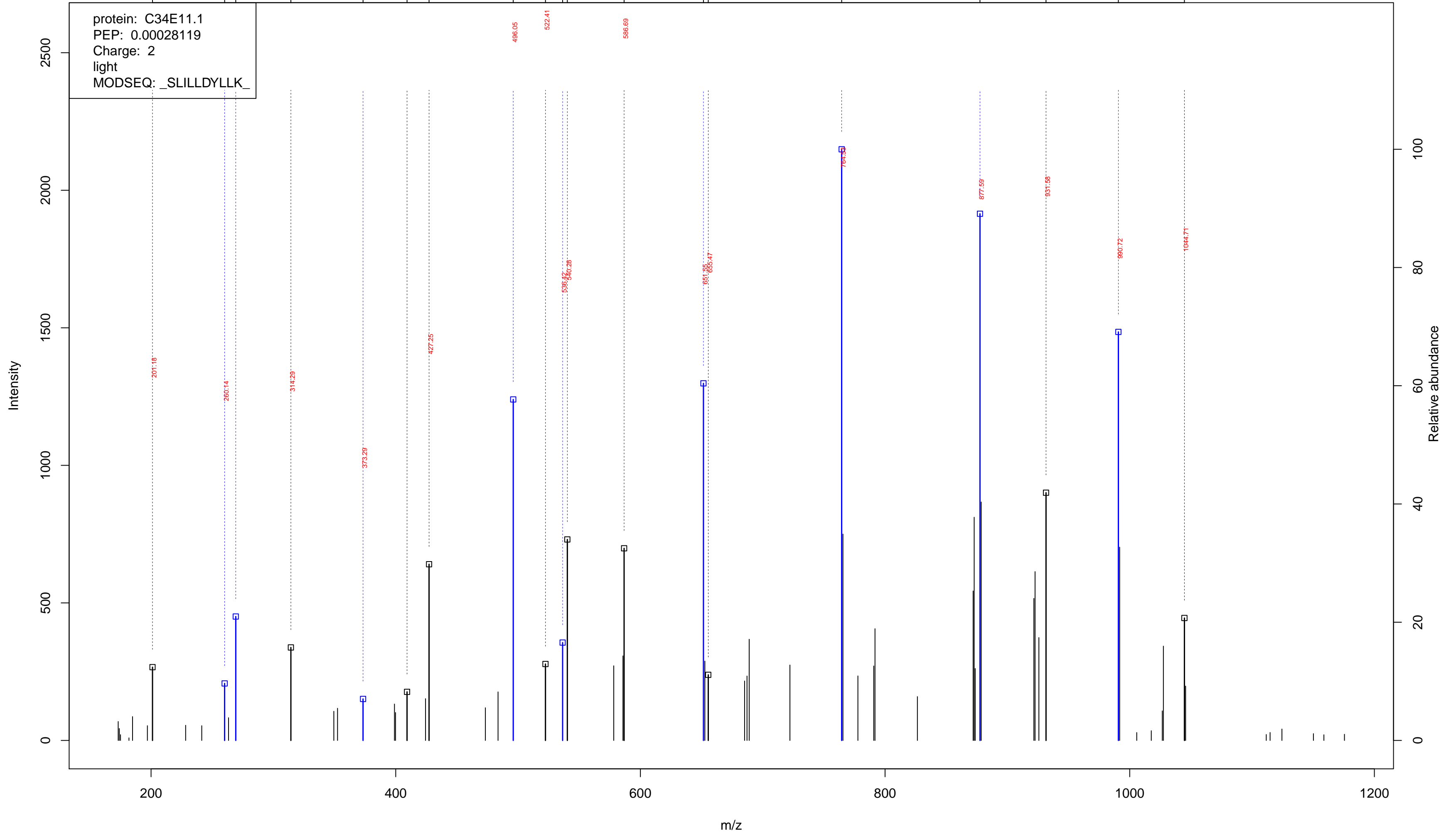




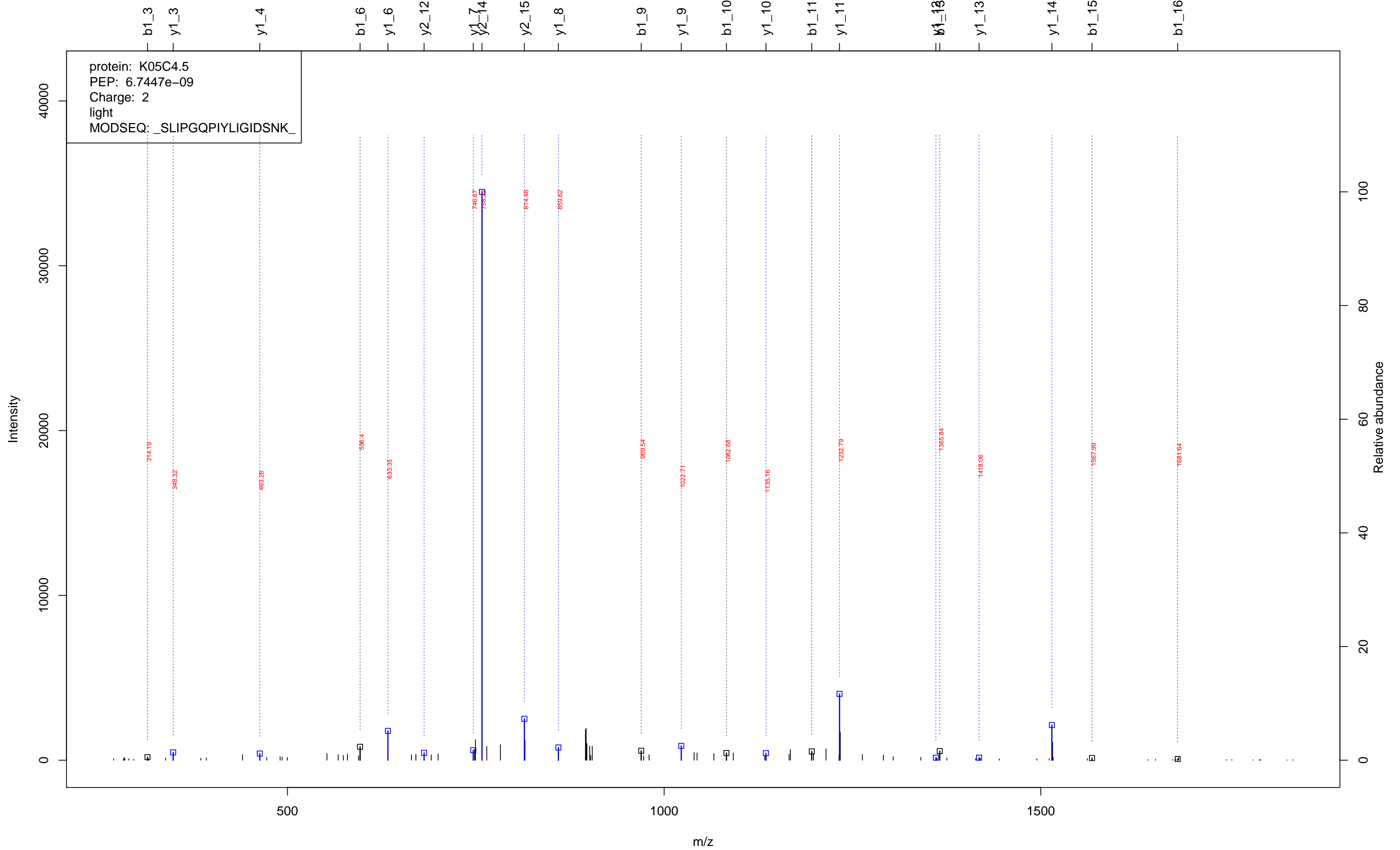


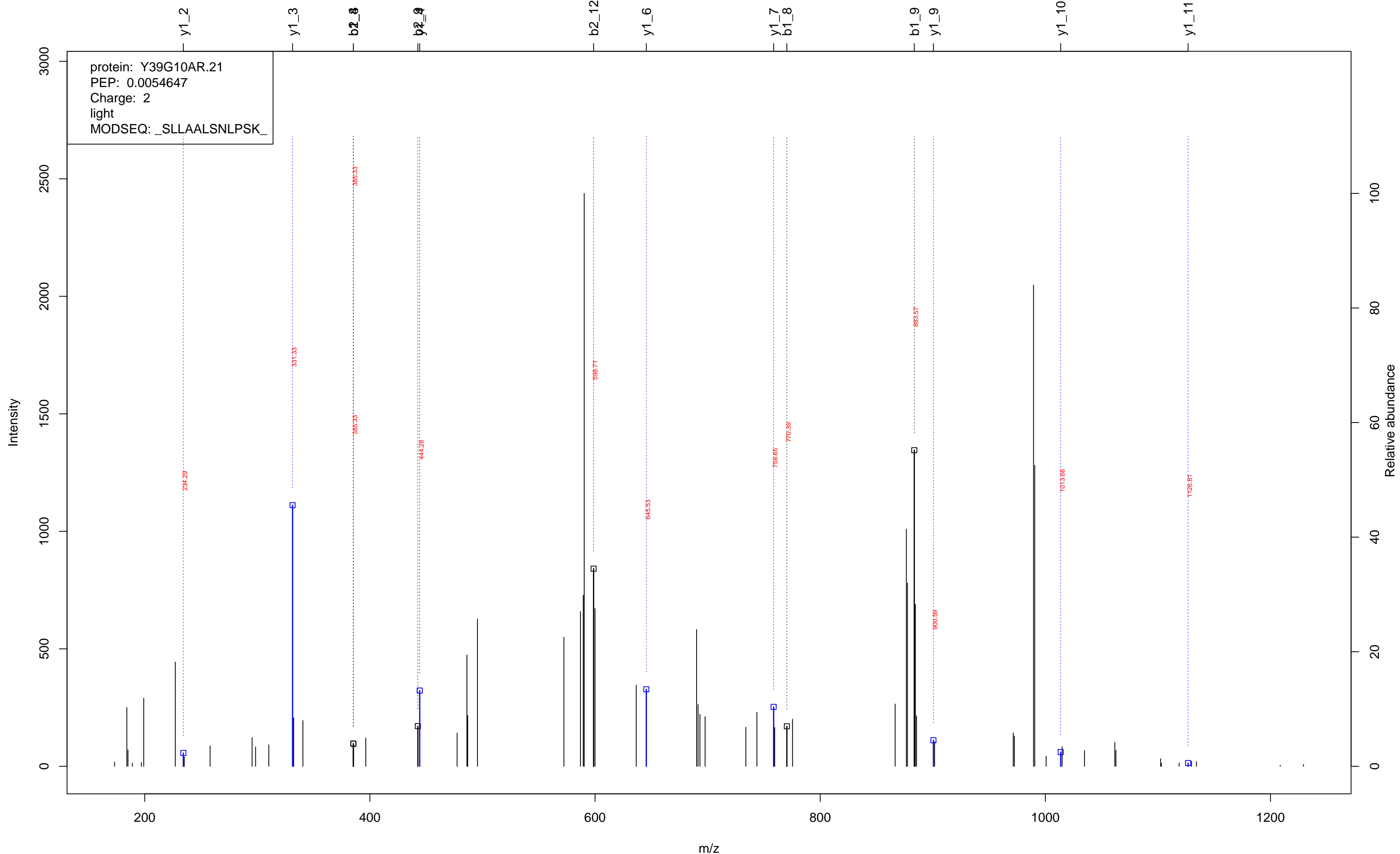


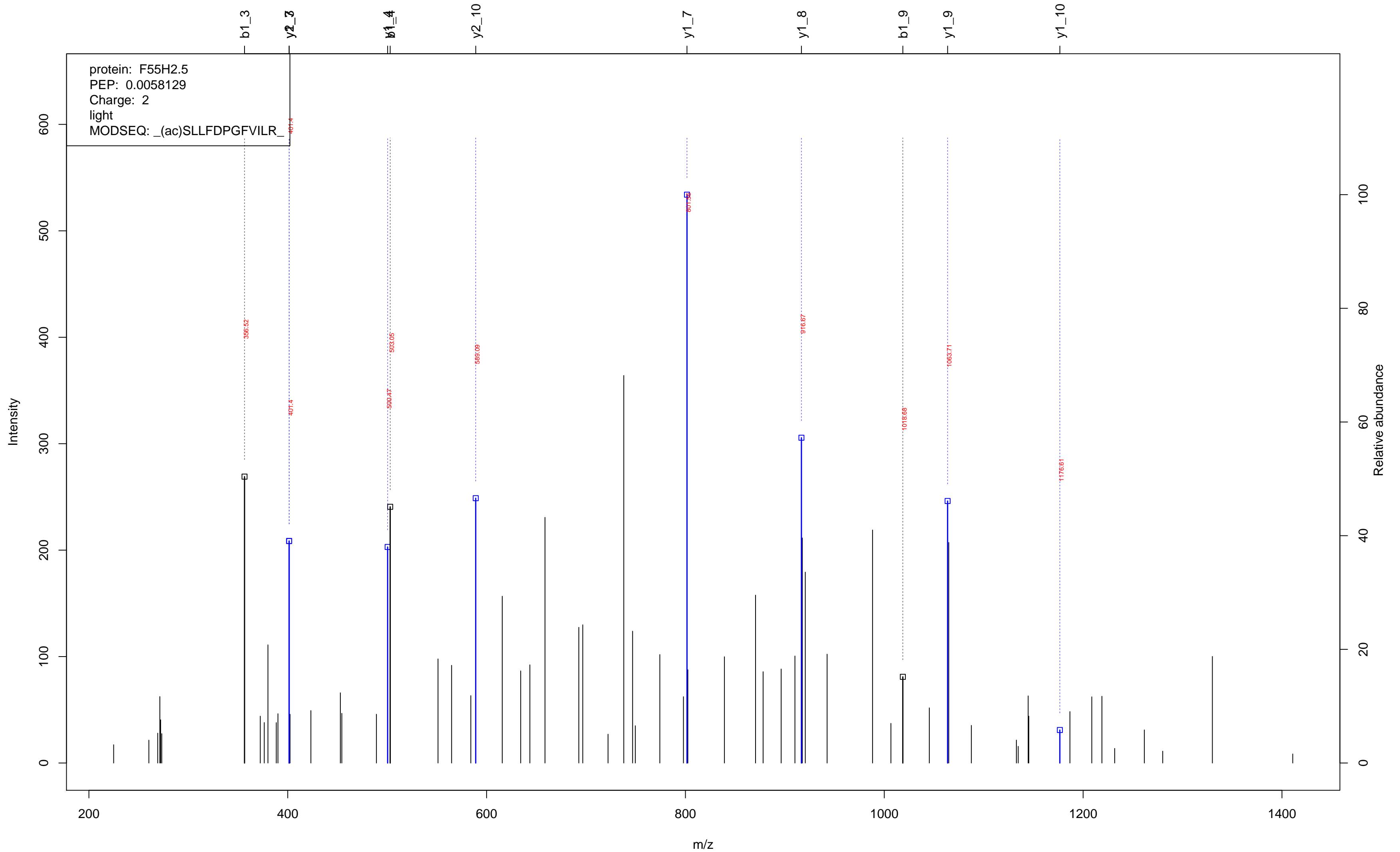


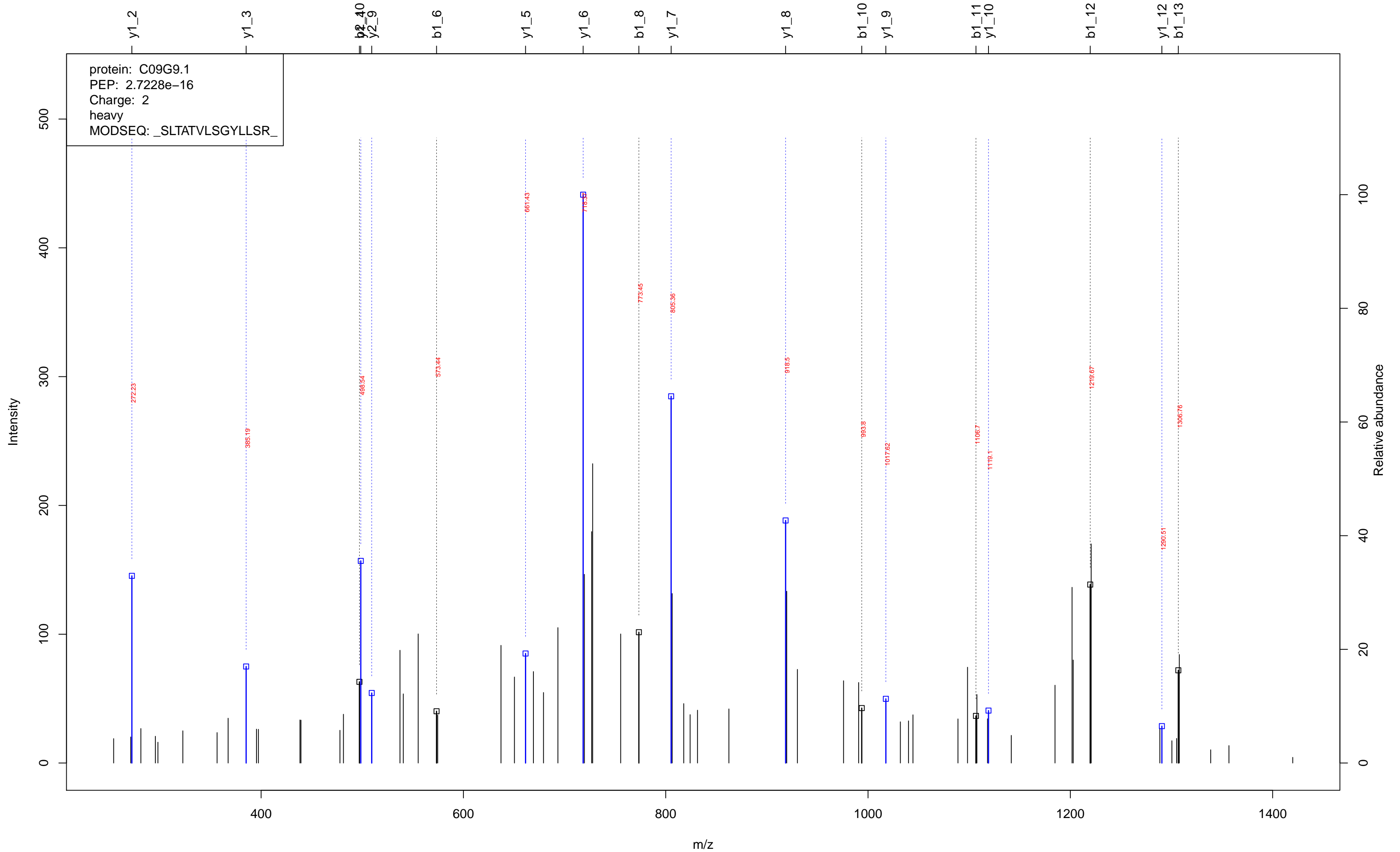


protein: C34E11.1
PEP: 0.00028119
Charge: 2
light
MODSEQ: _SLILLDYLLK_





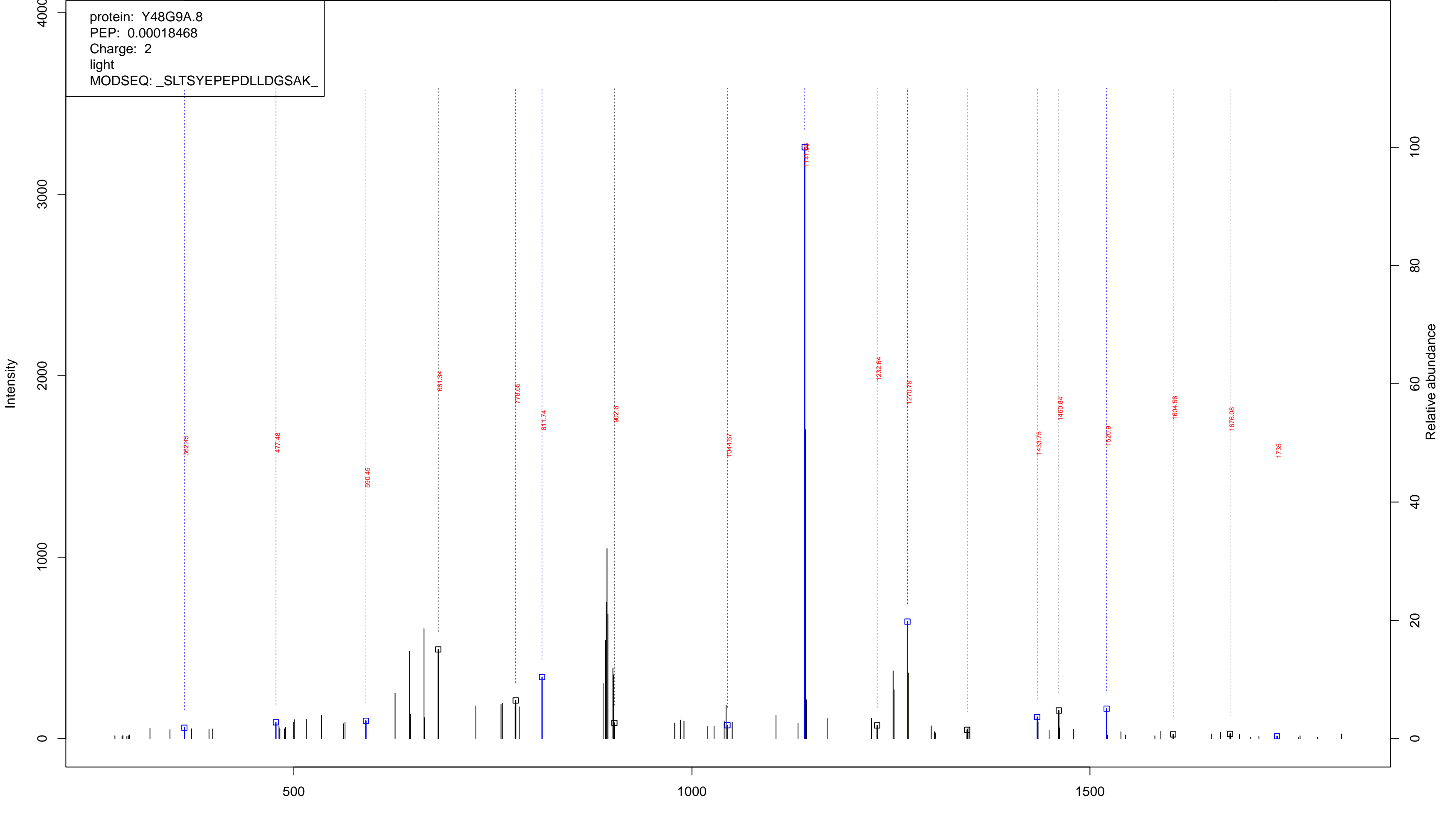


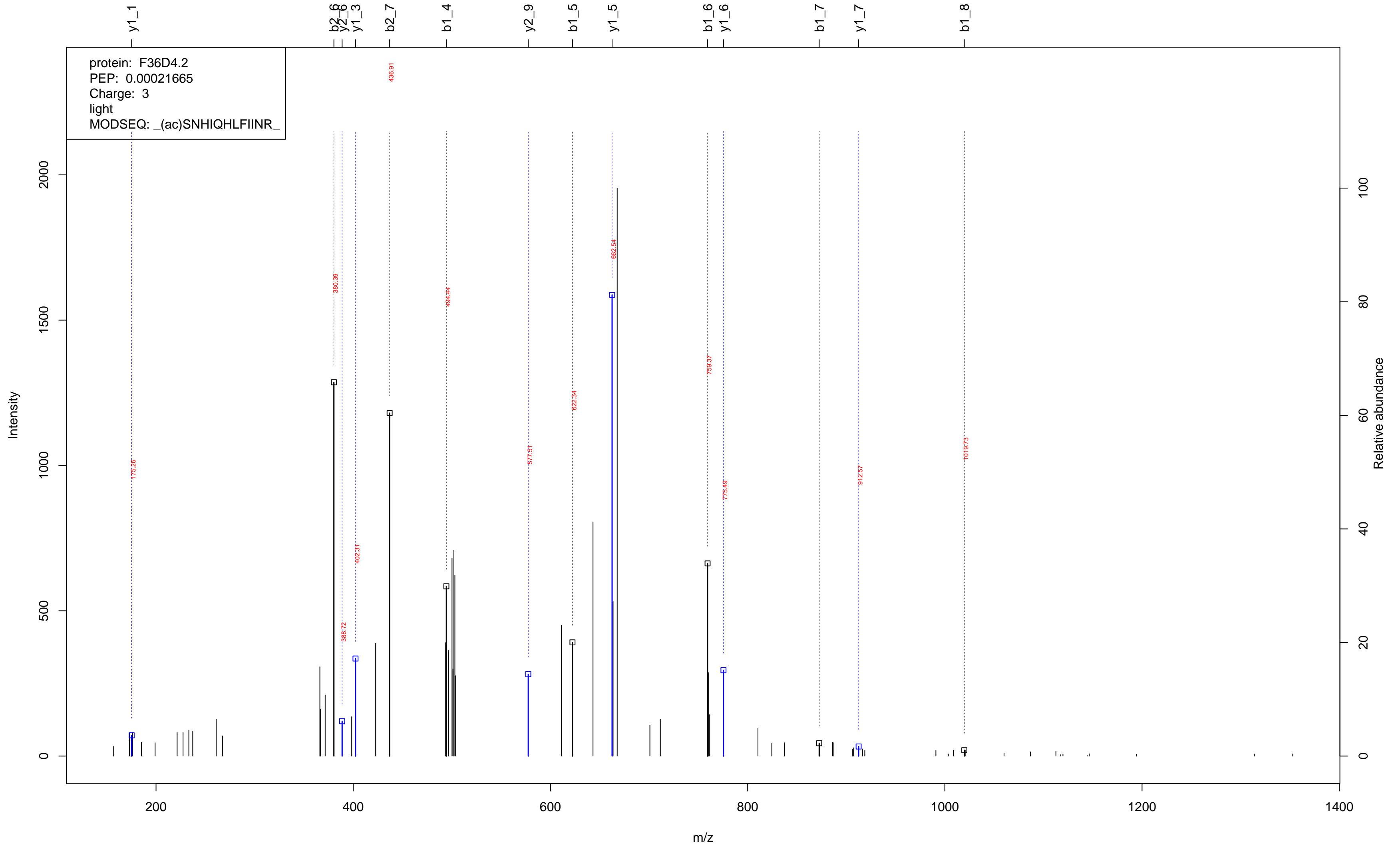


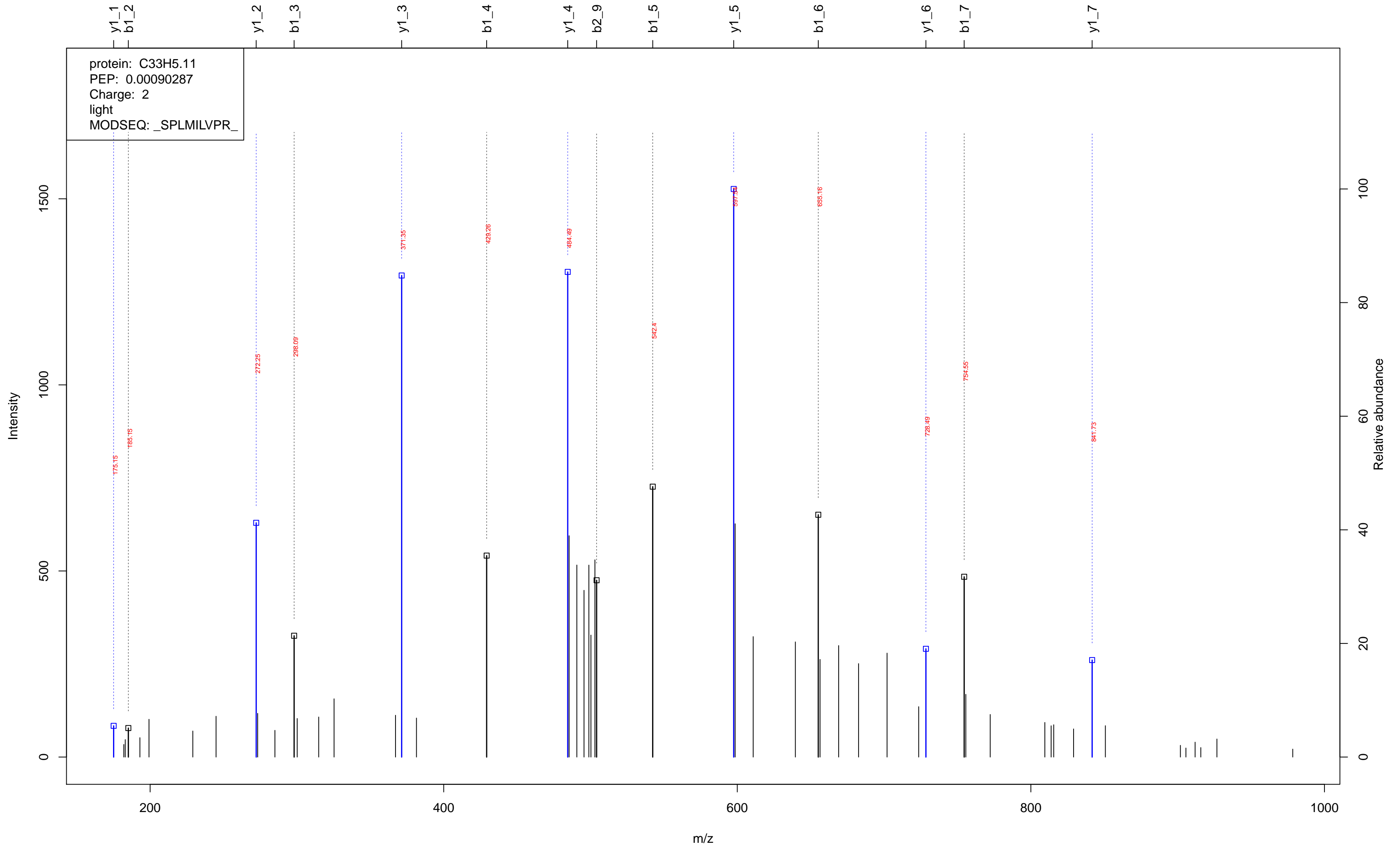
315

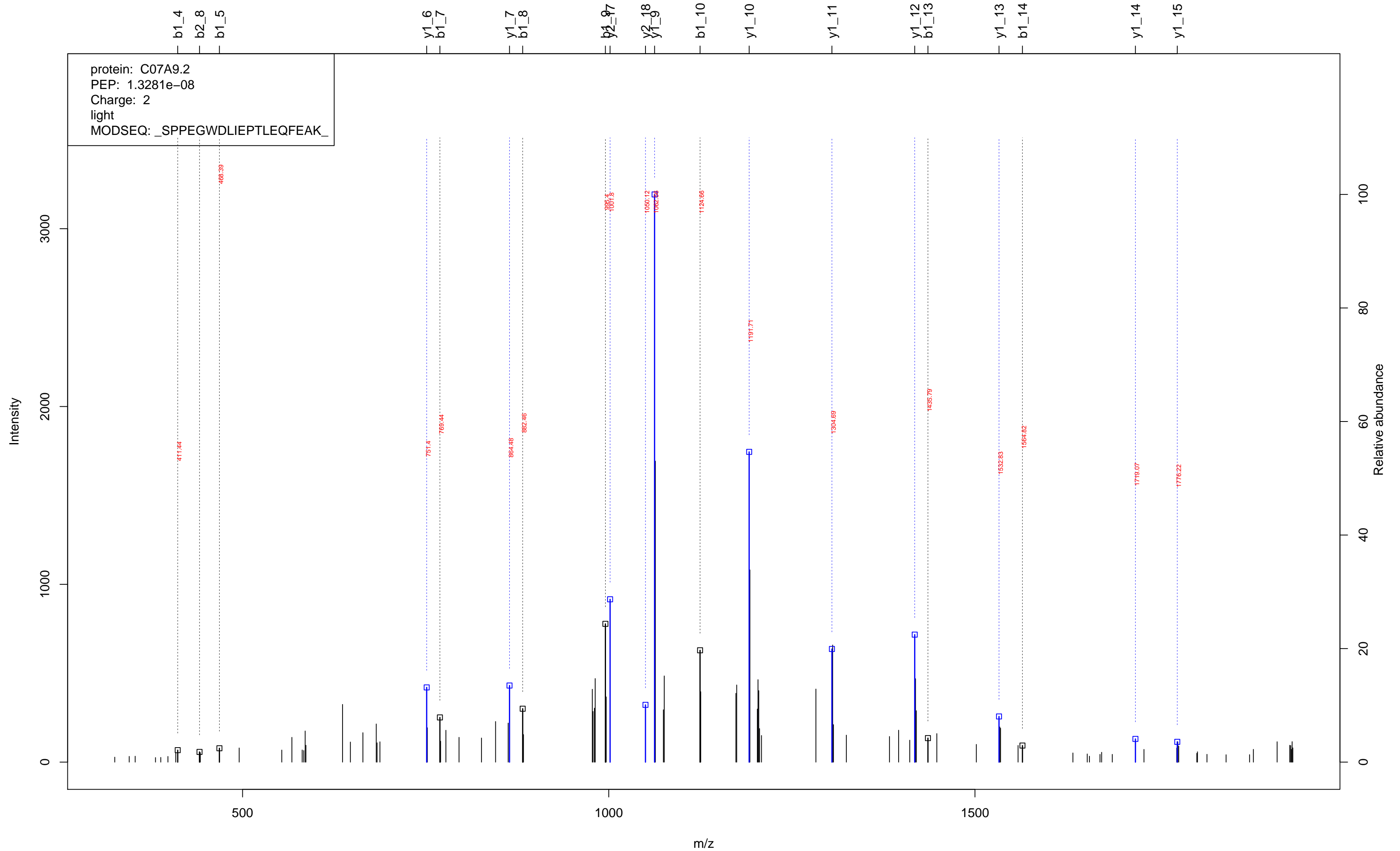
y1_4 y1_5 y1_6 b1_6 b1_7 y2_15 b2_17 y1_10 y1_11 b1_11 y1_12 b1_12 y1_13 b1_13 y1_14 b1_15 b1_16 y1_16

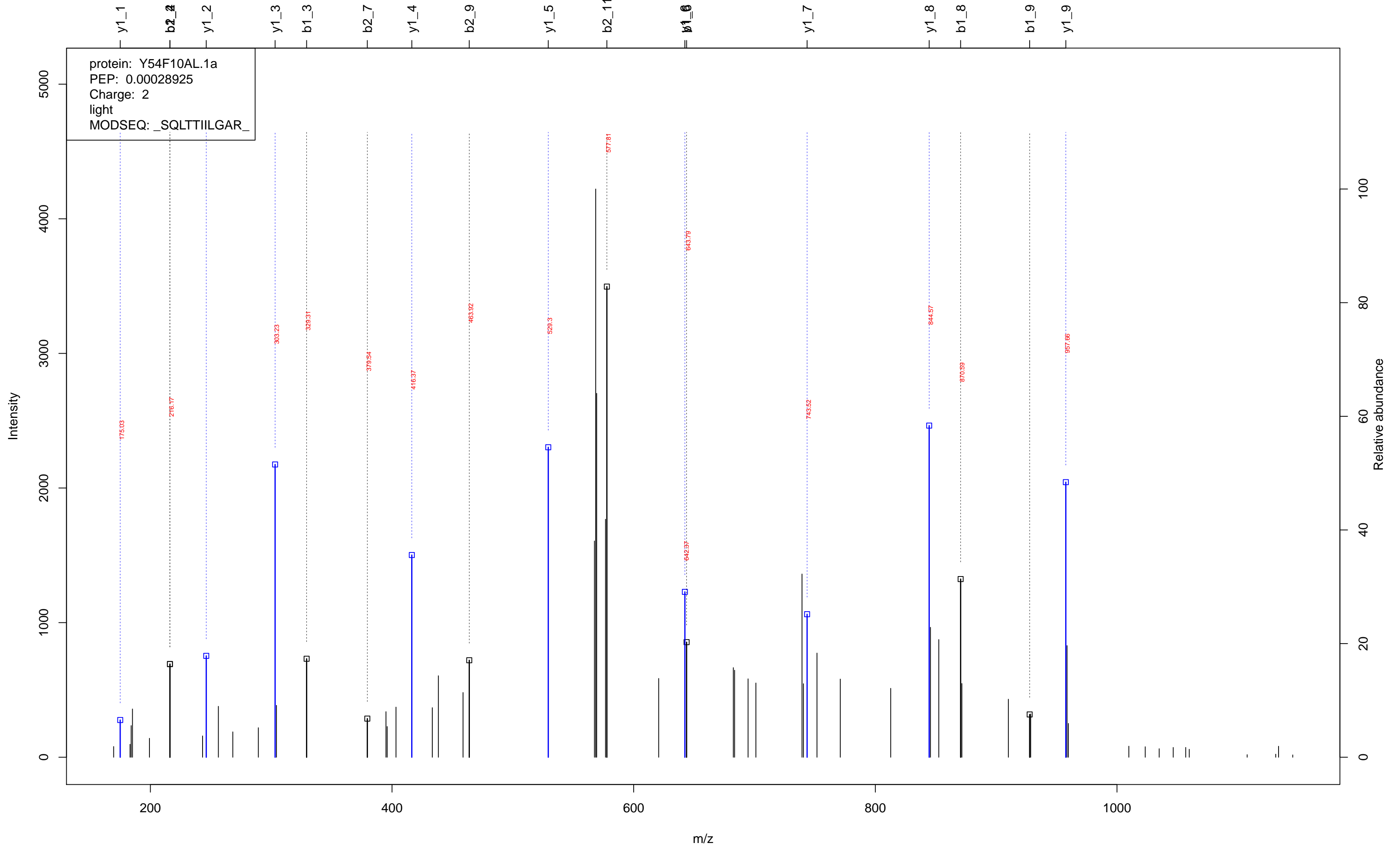
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PEP: 0.00018468
Charge: 2
light
MODSEQ: _SLTSYEPEPDLLDGSAK_

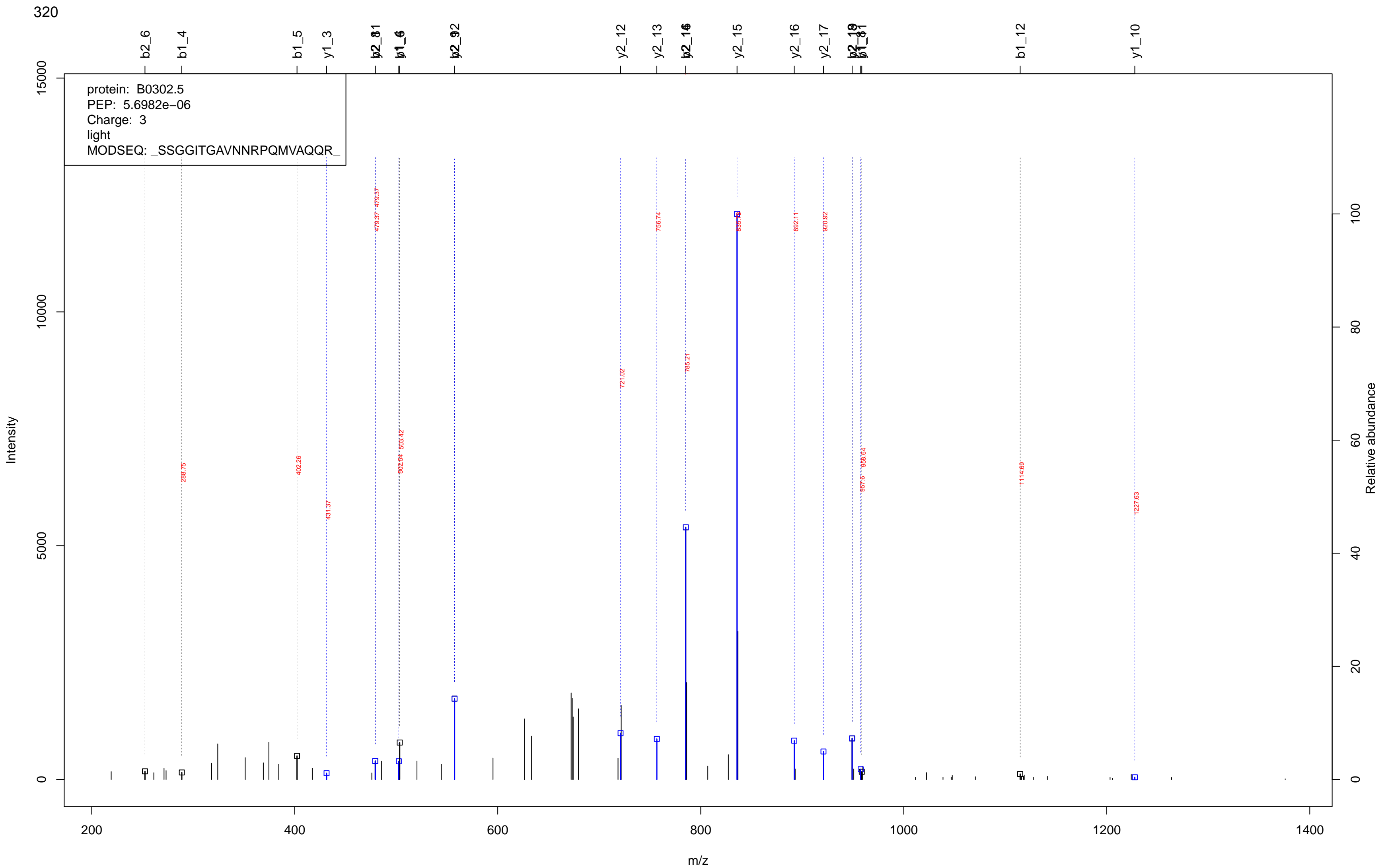


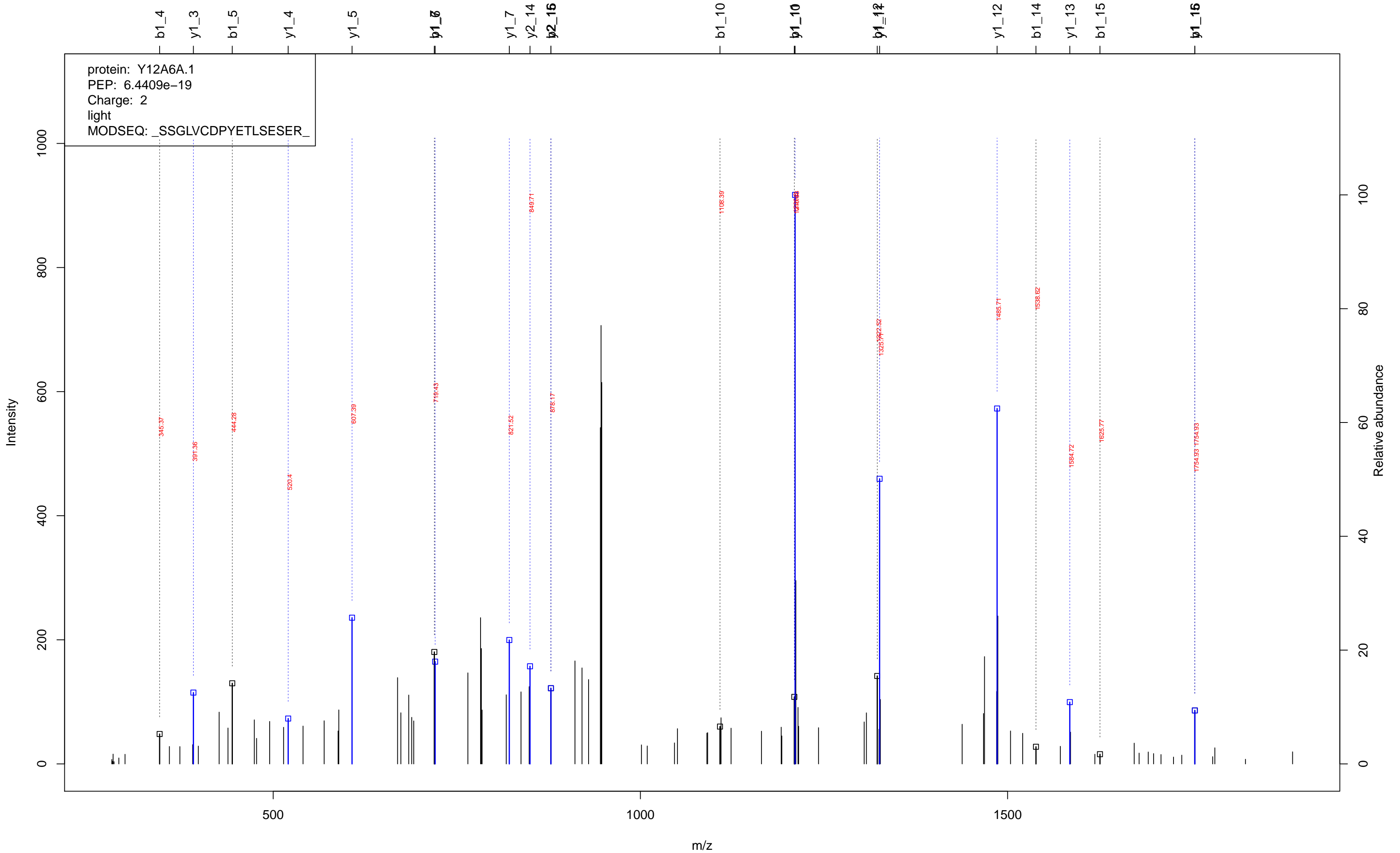


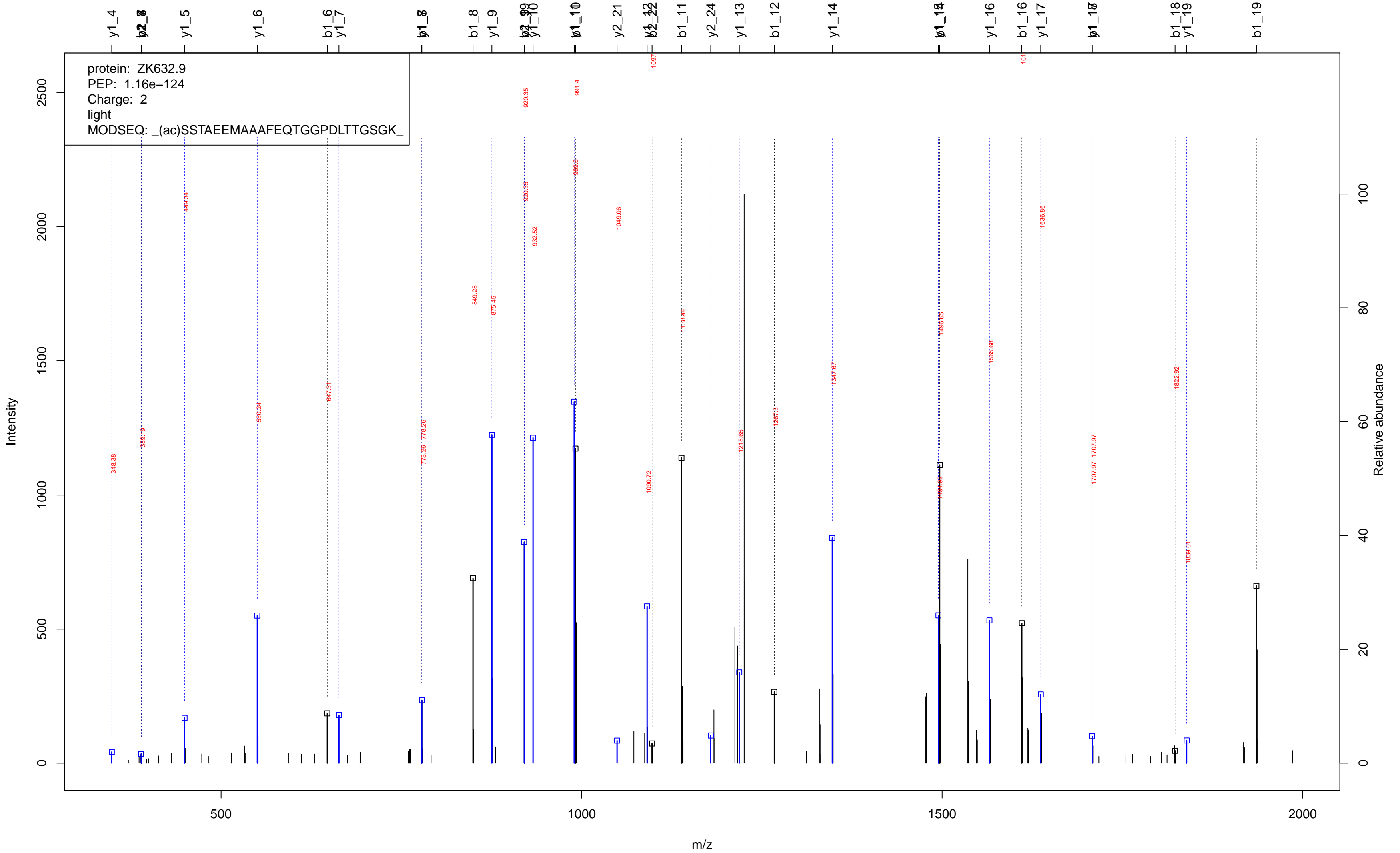


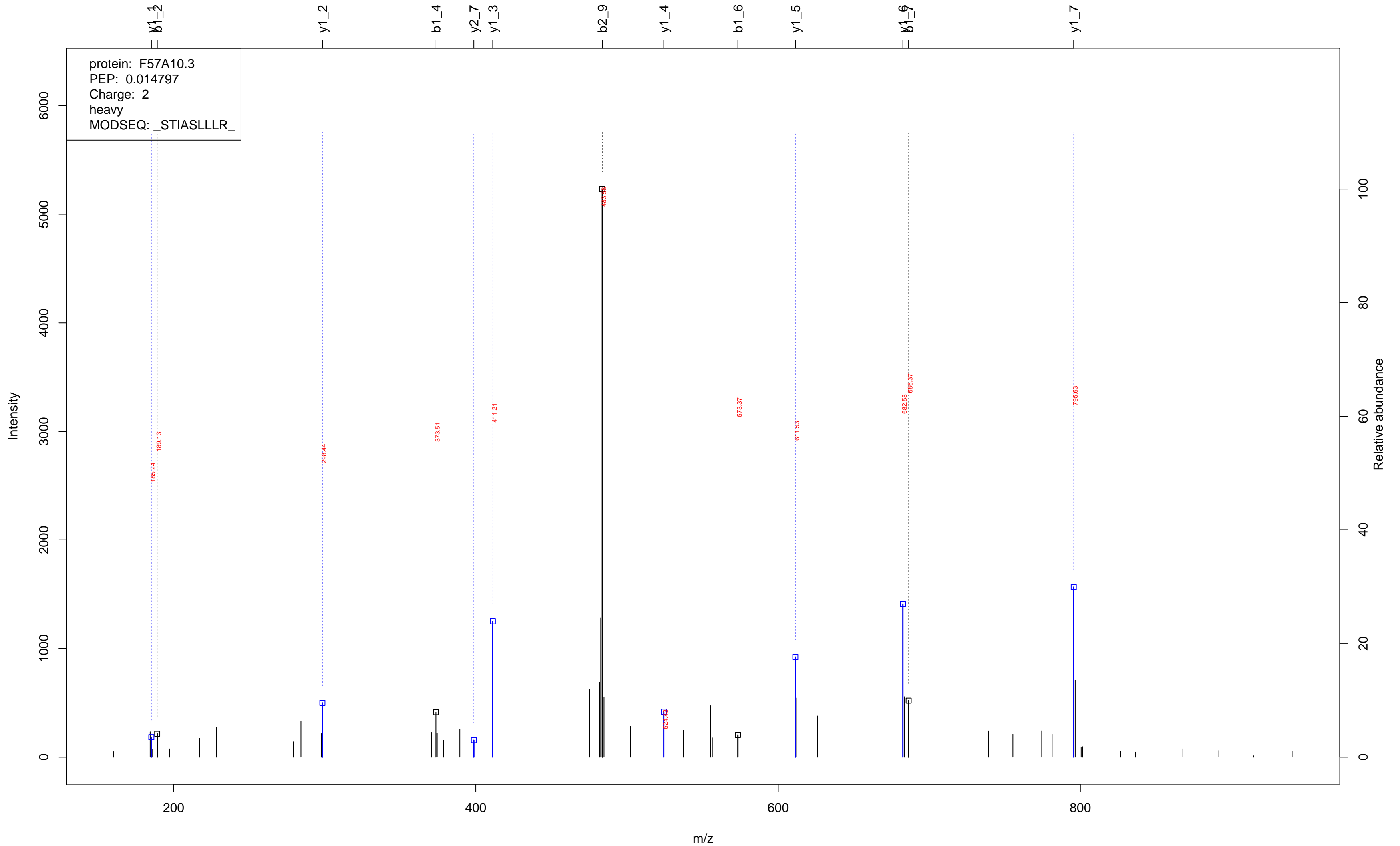


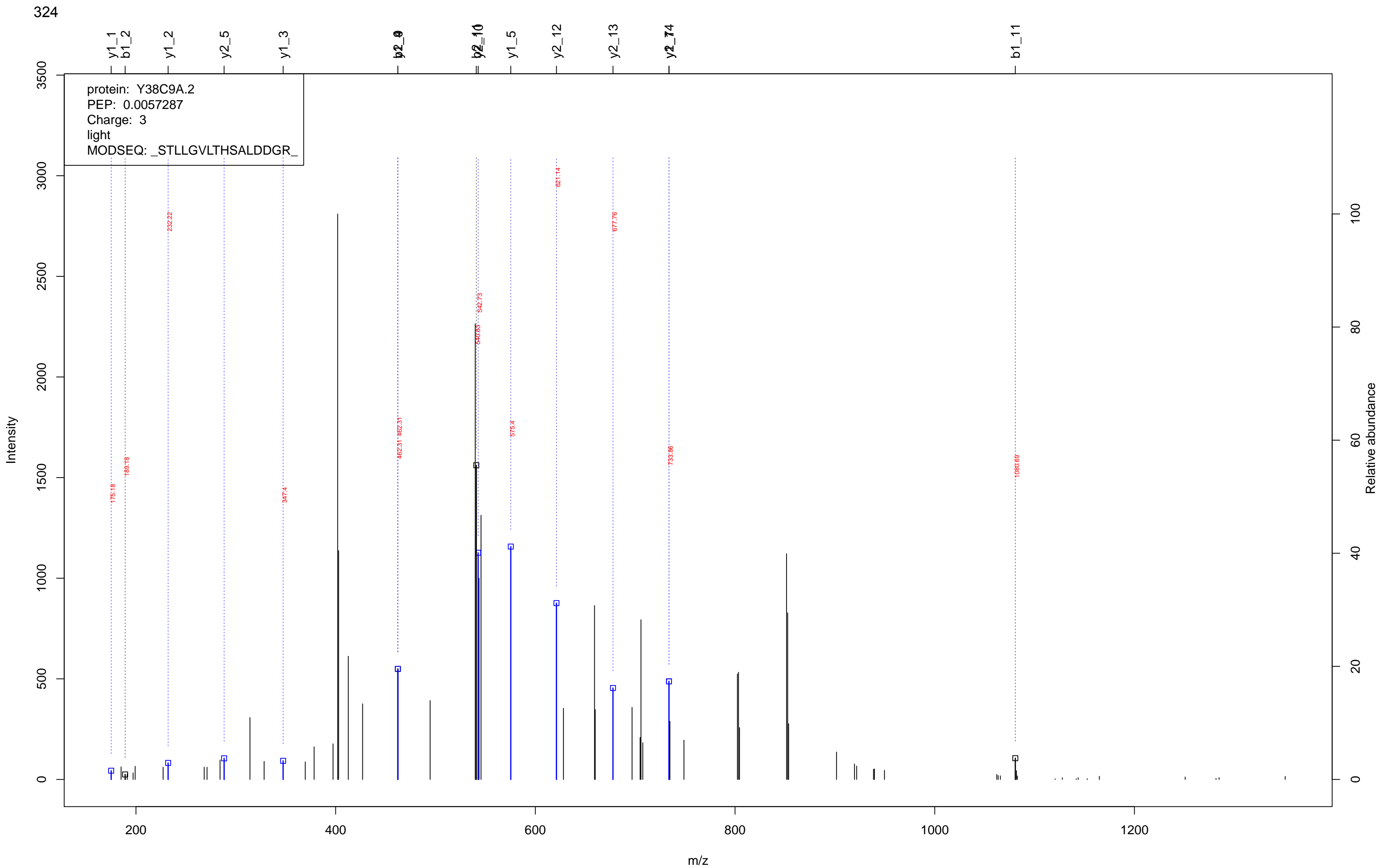


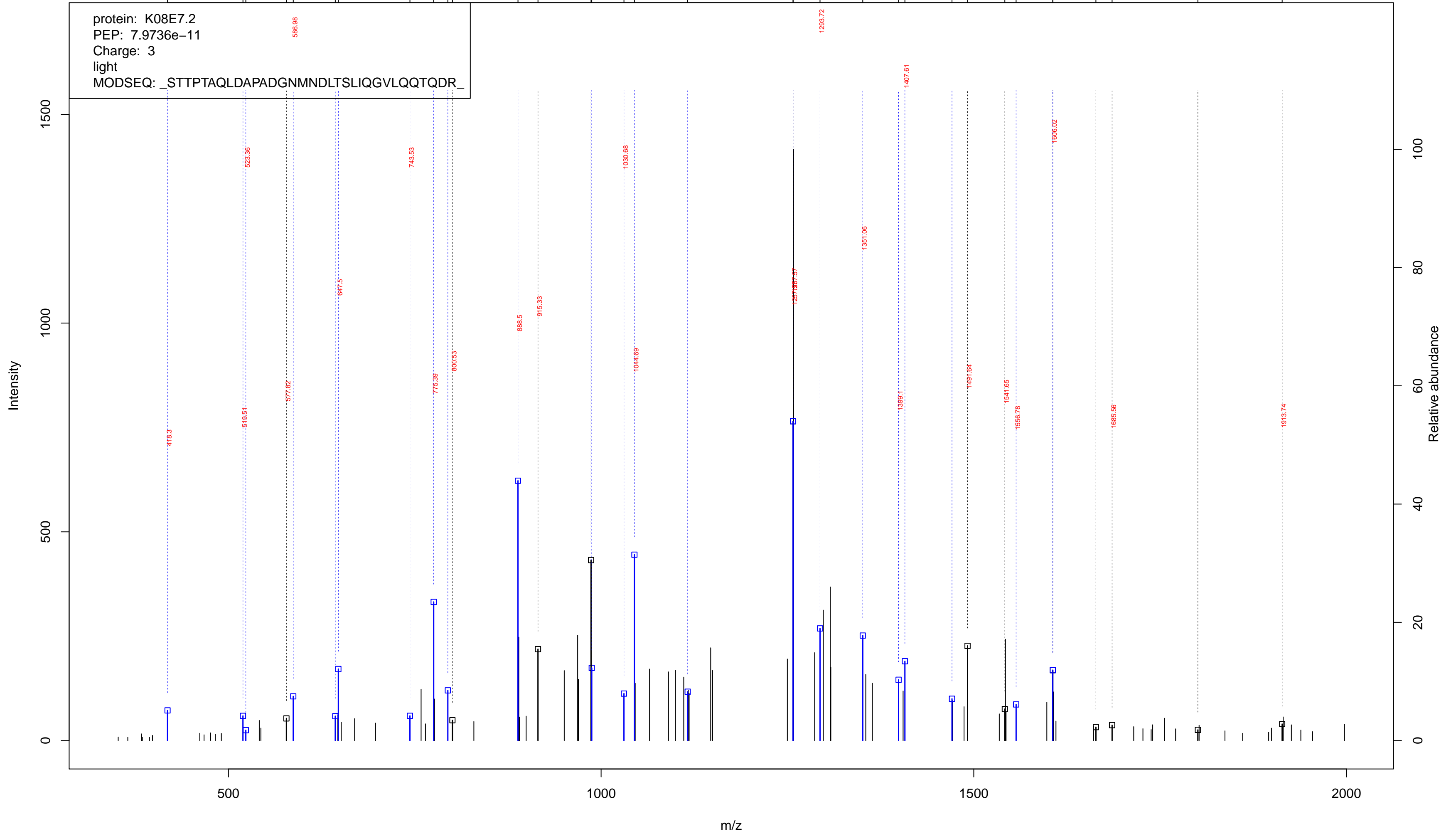


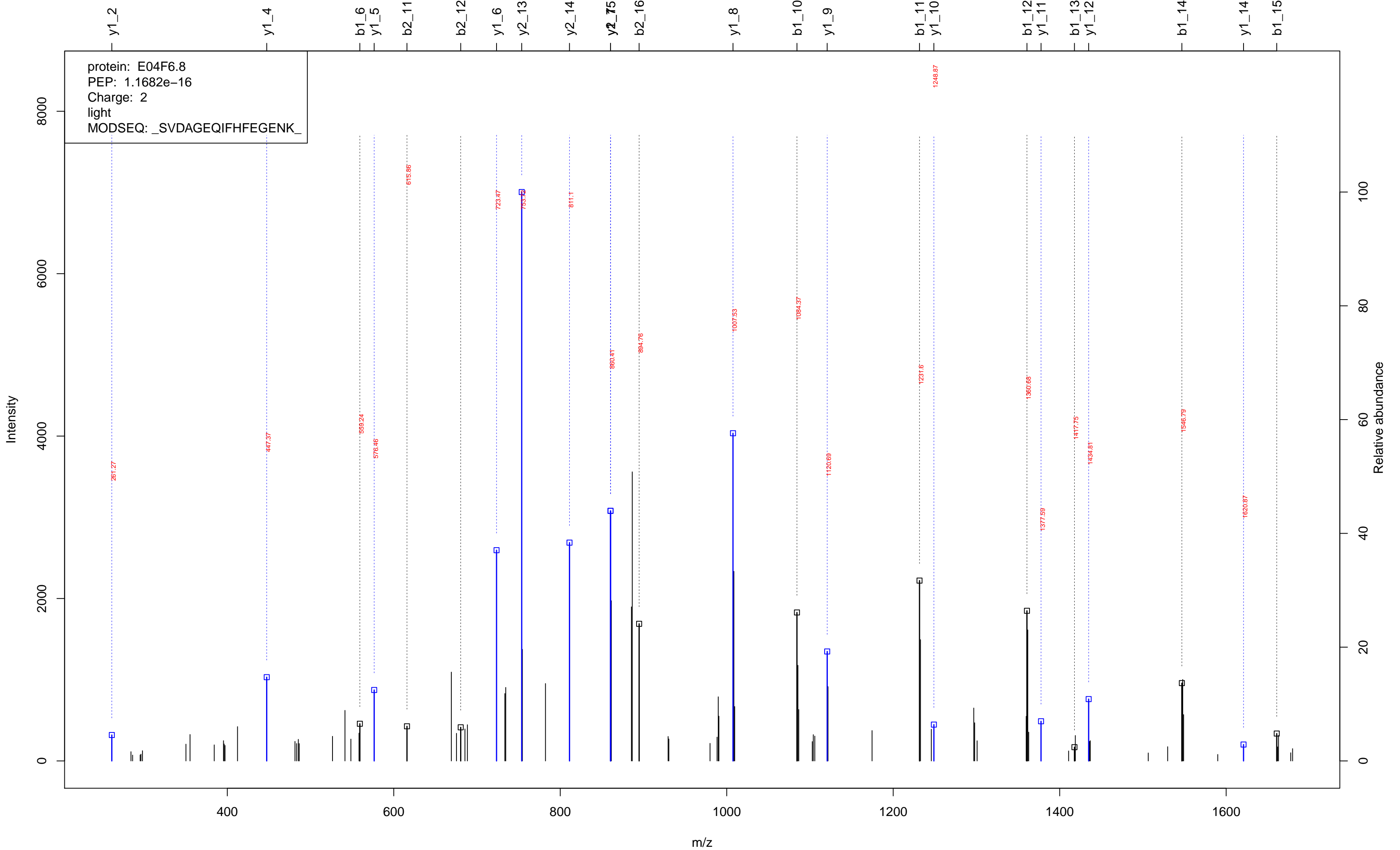


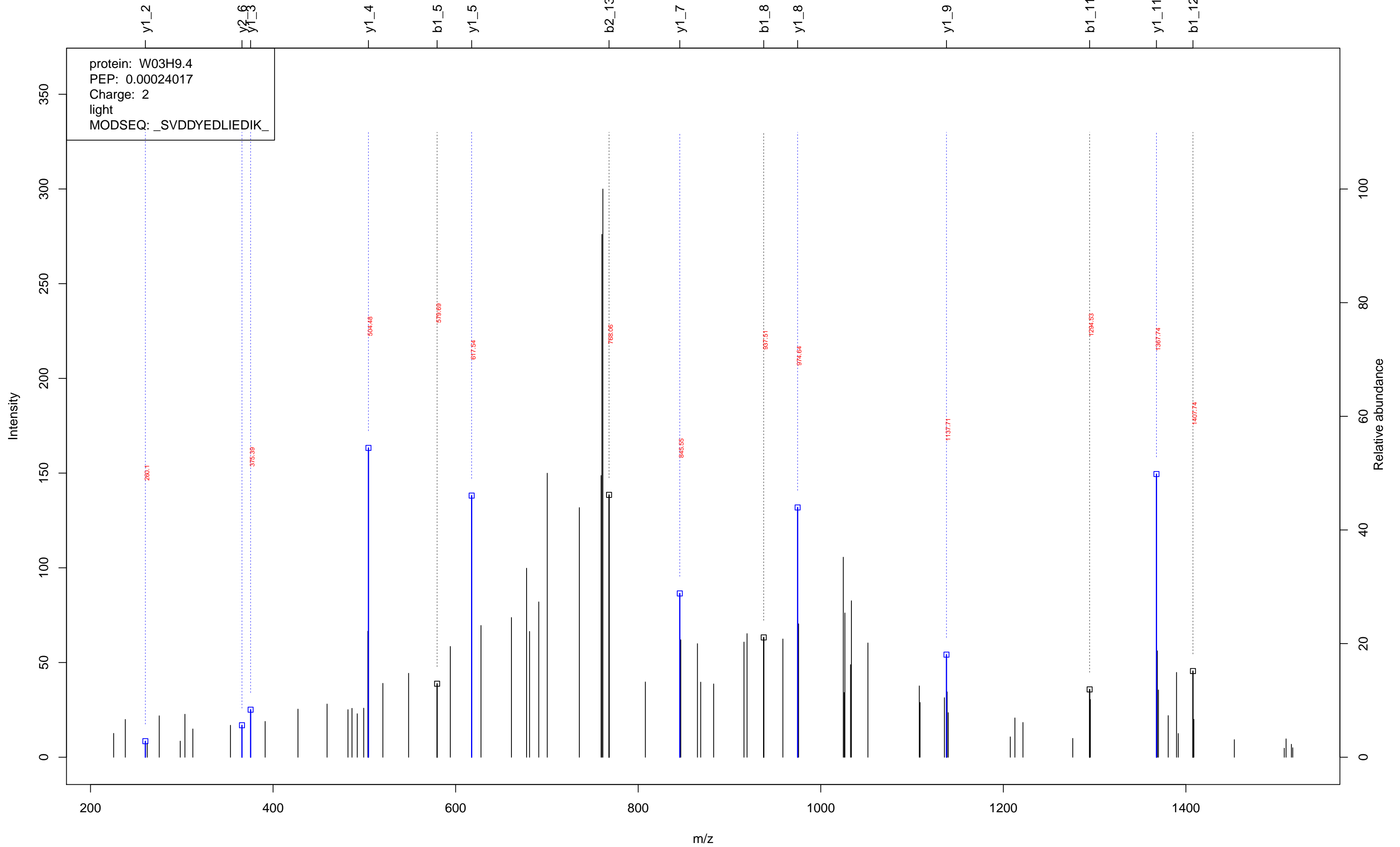


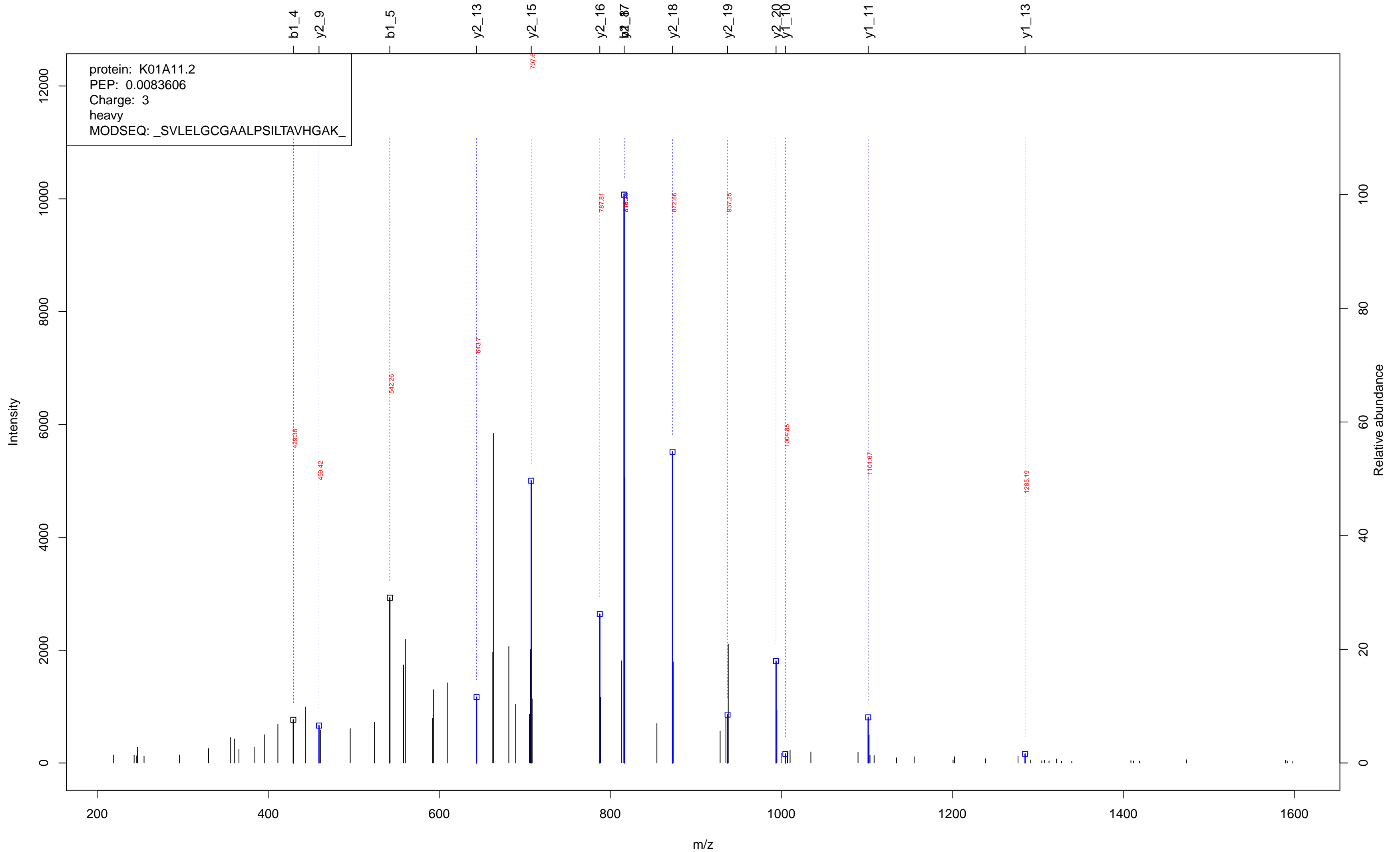






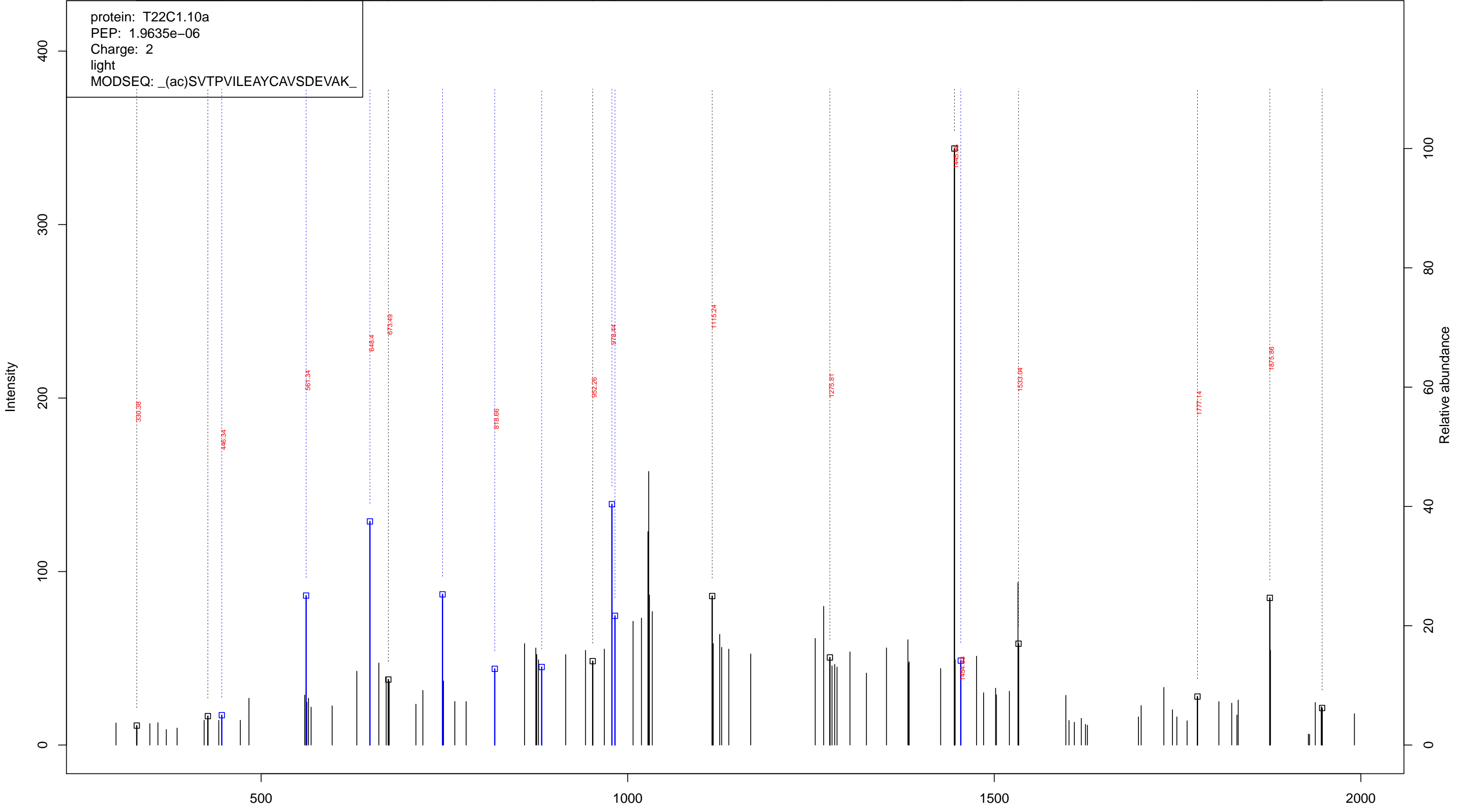


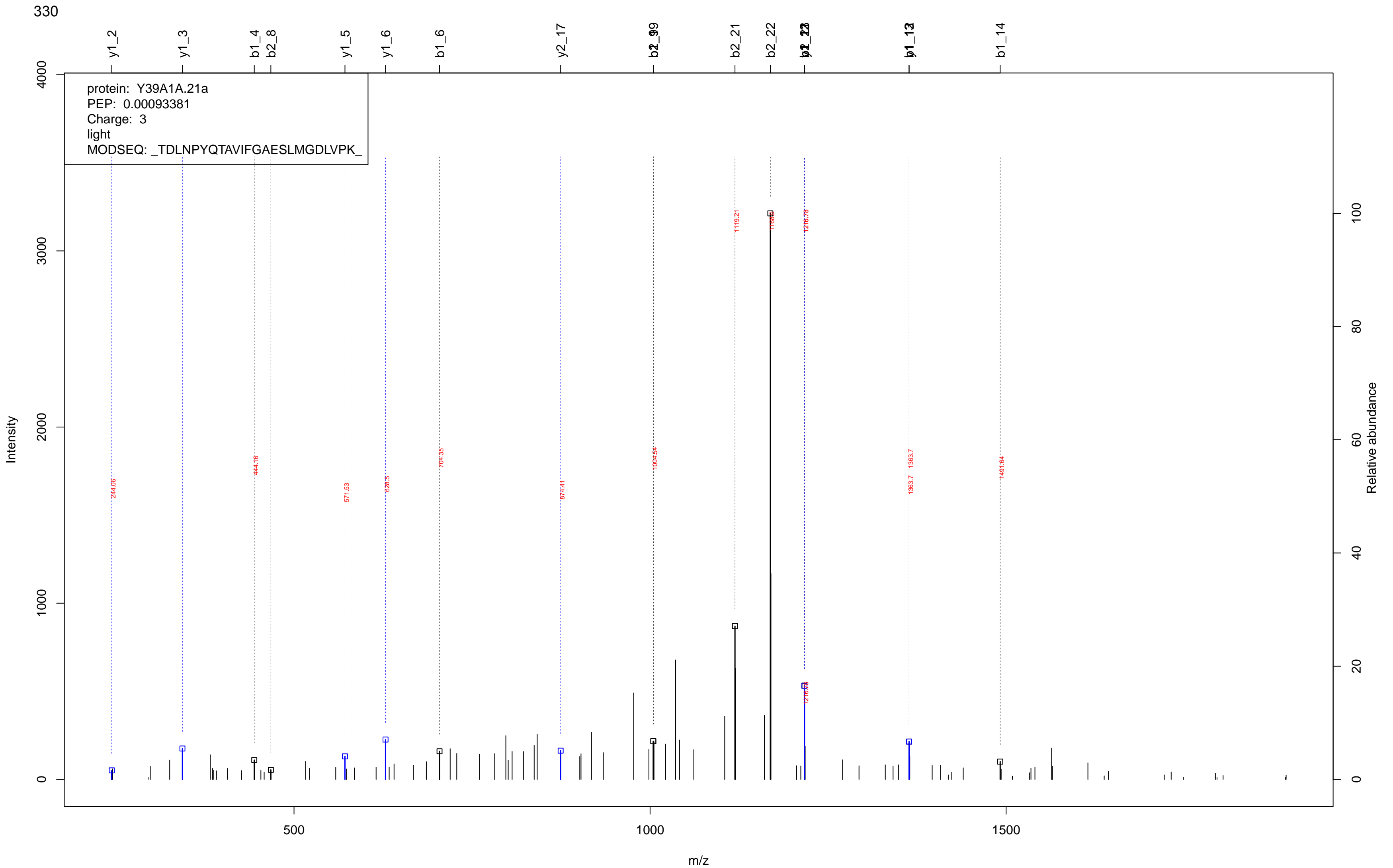


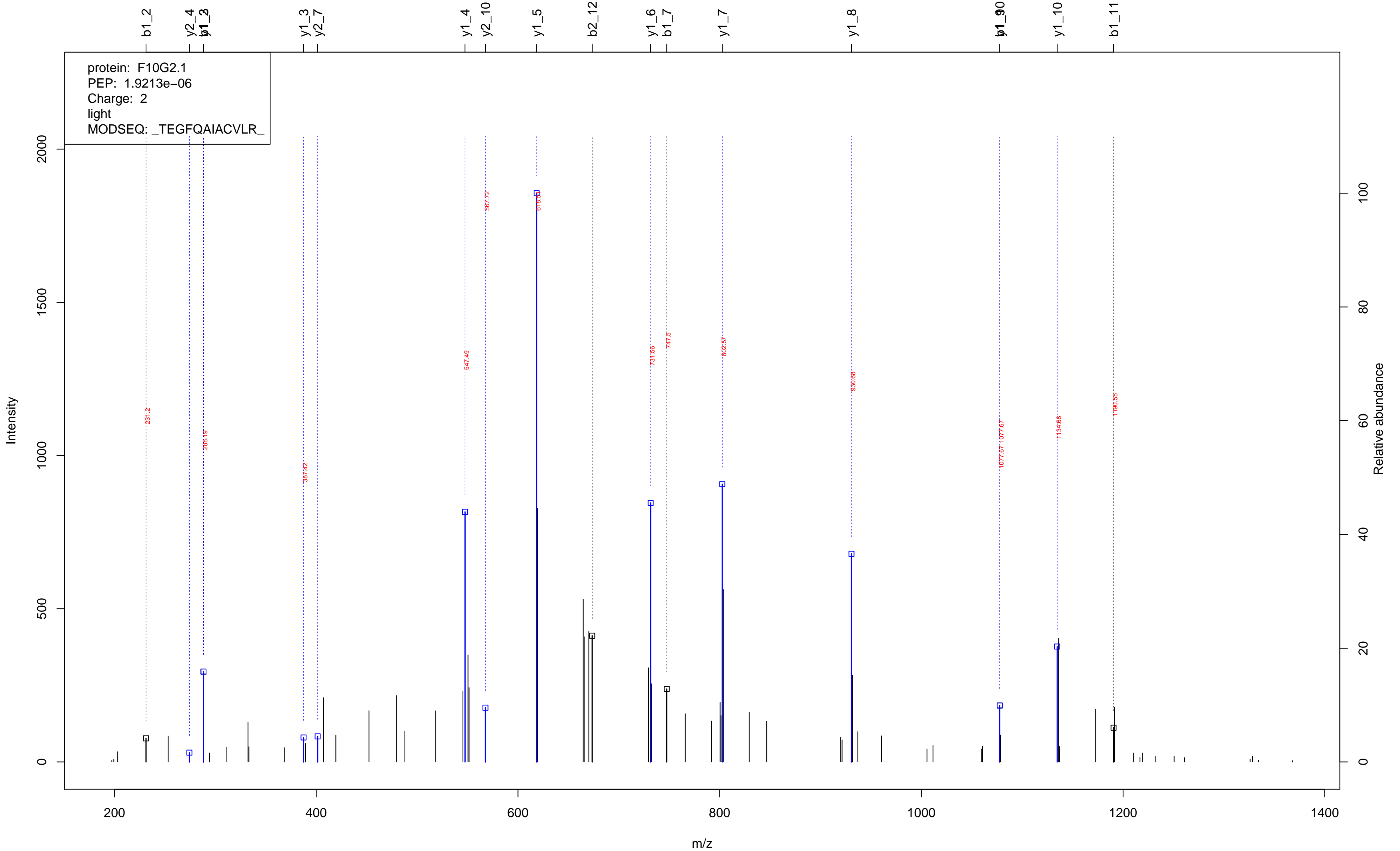


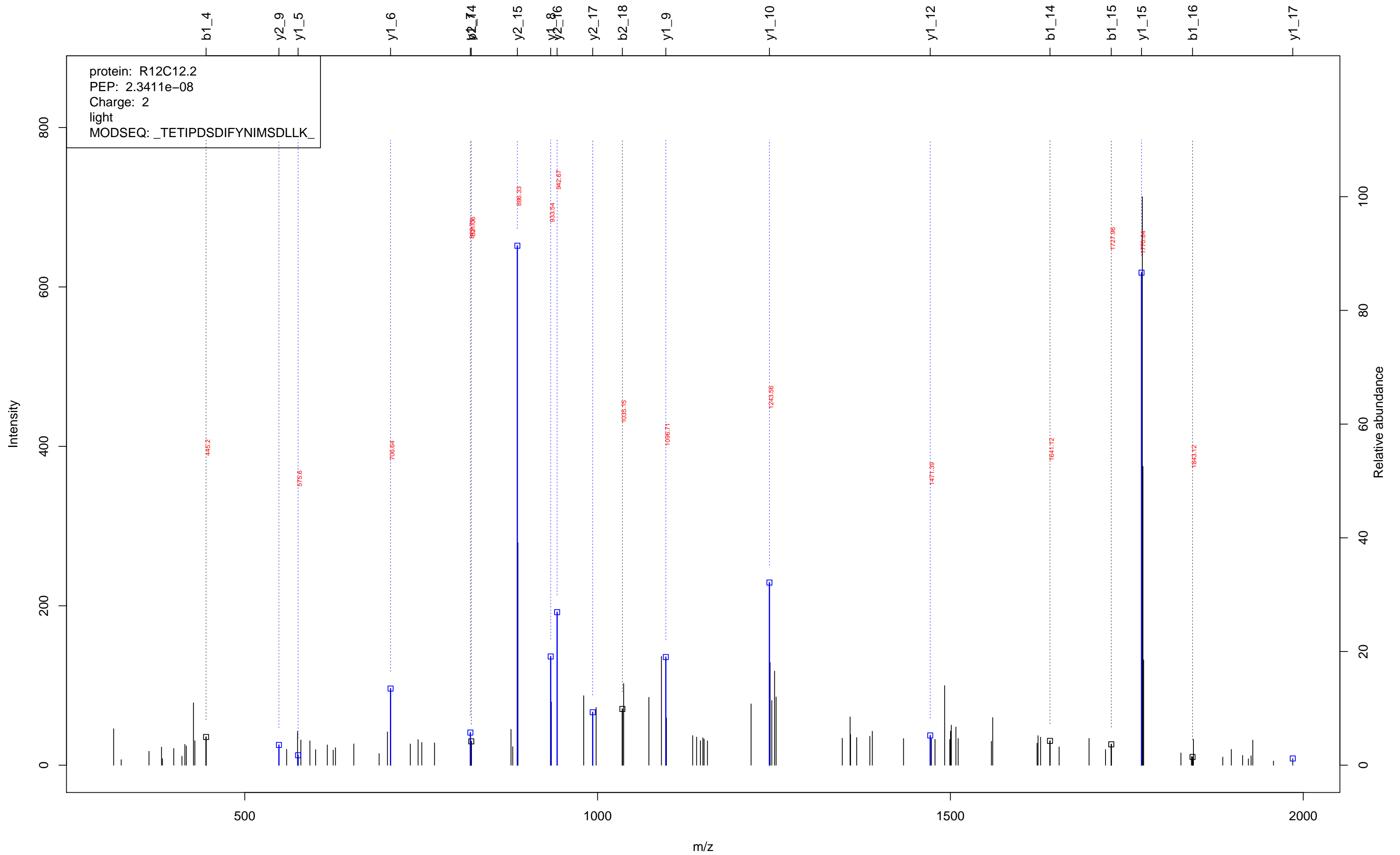
b1_3 b1_4 y1_4 y1_5 y1_6 b2_12 y1_7 y1_8 y2_16 b1_9 y2_98 b1_10 b1_11 b1_13 b1_14 b1_16 b1_17 b1_18

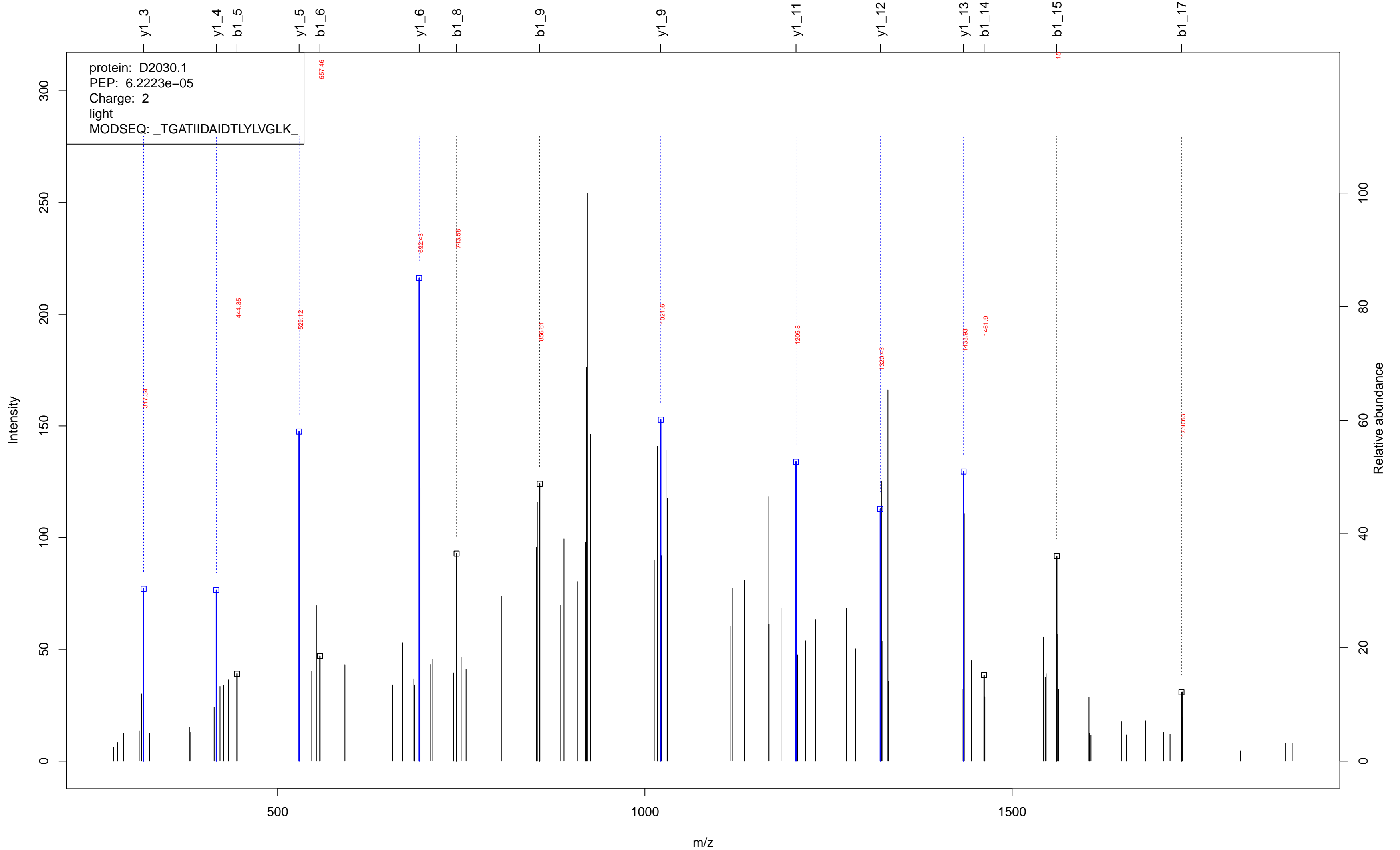
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PEP: 1.9635e-06
Charge: 2
light
MODSEQ: _(ac)SVTPVILEAYCAVSDEVAK_

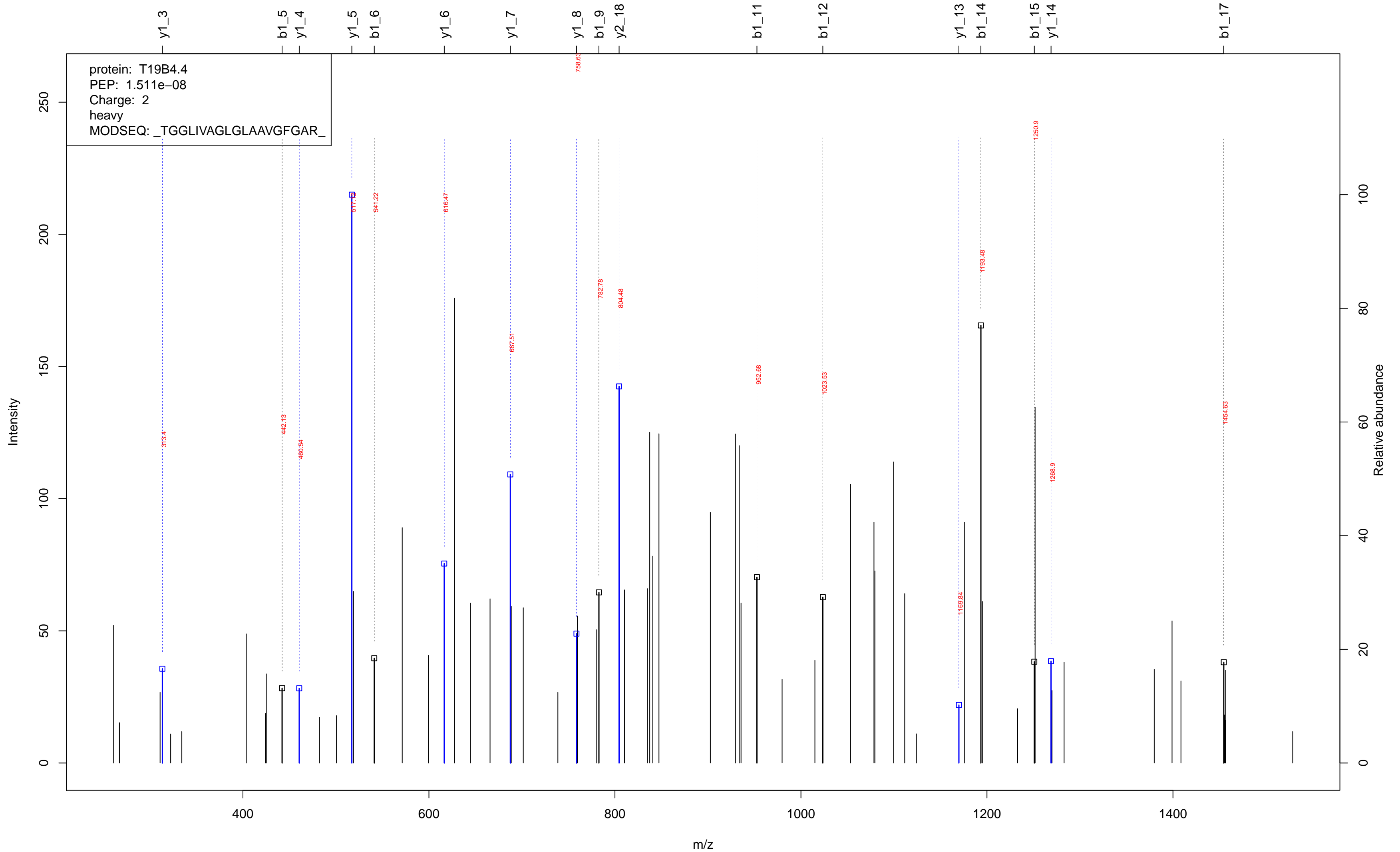


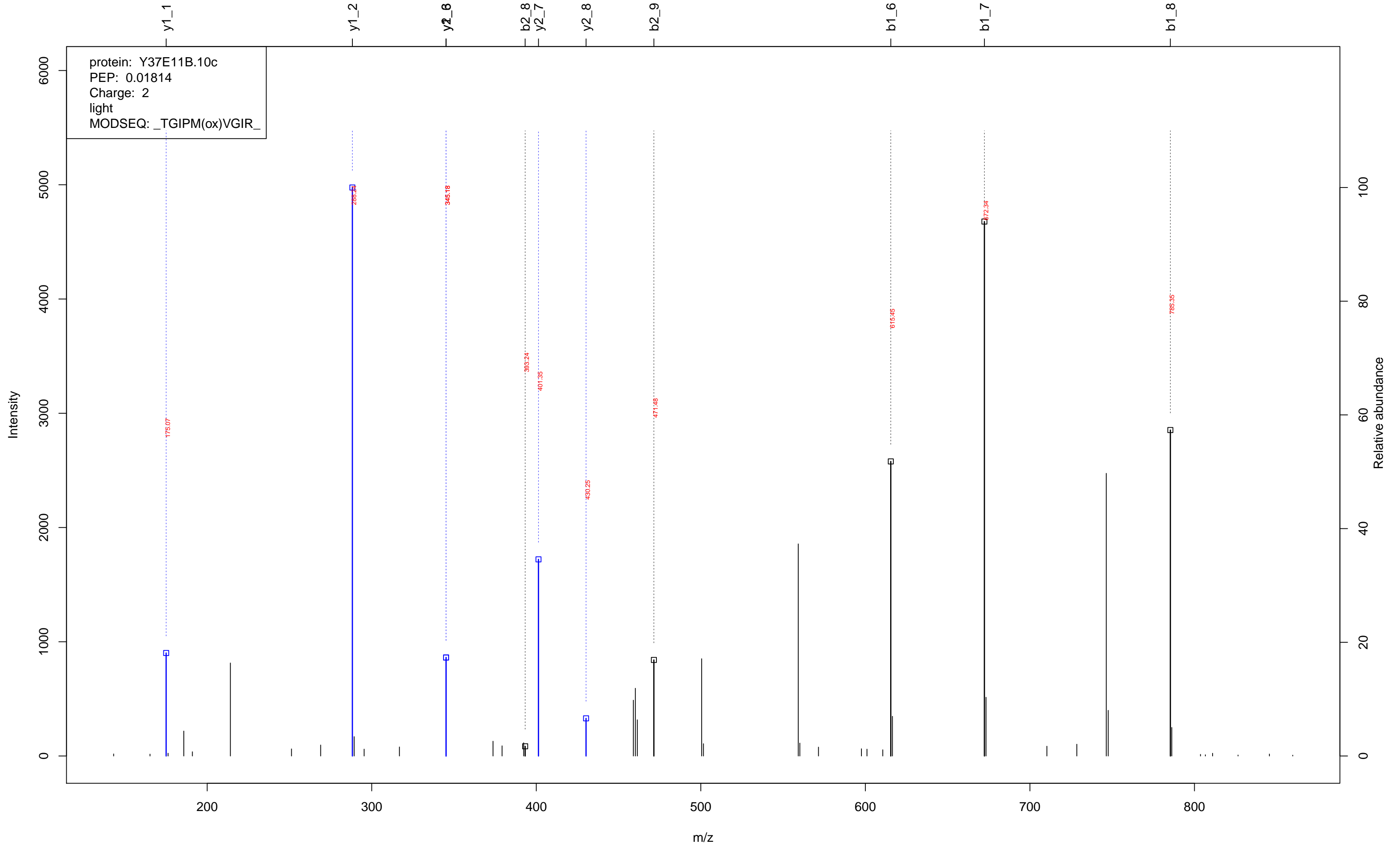


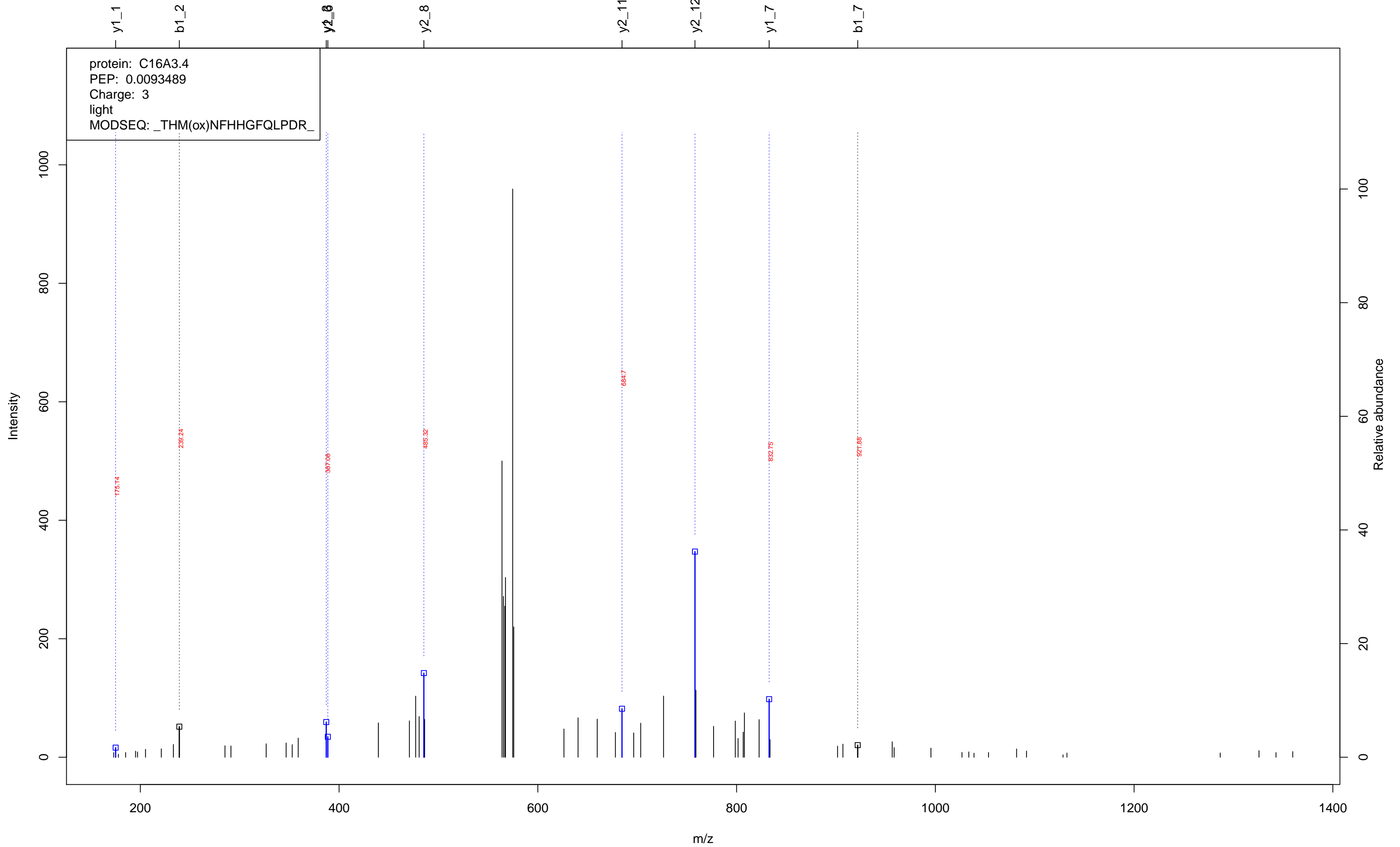


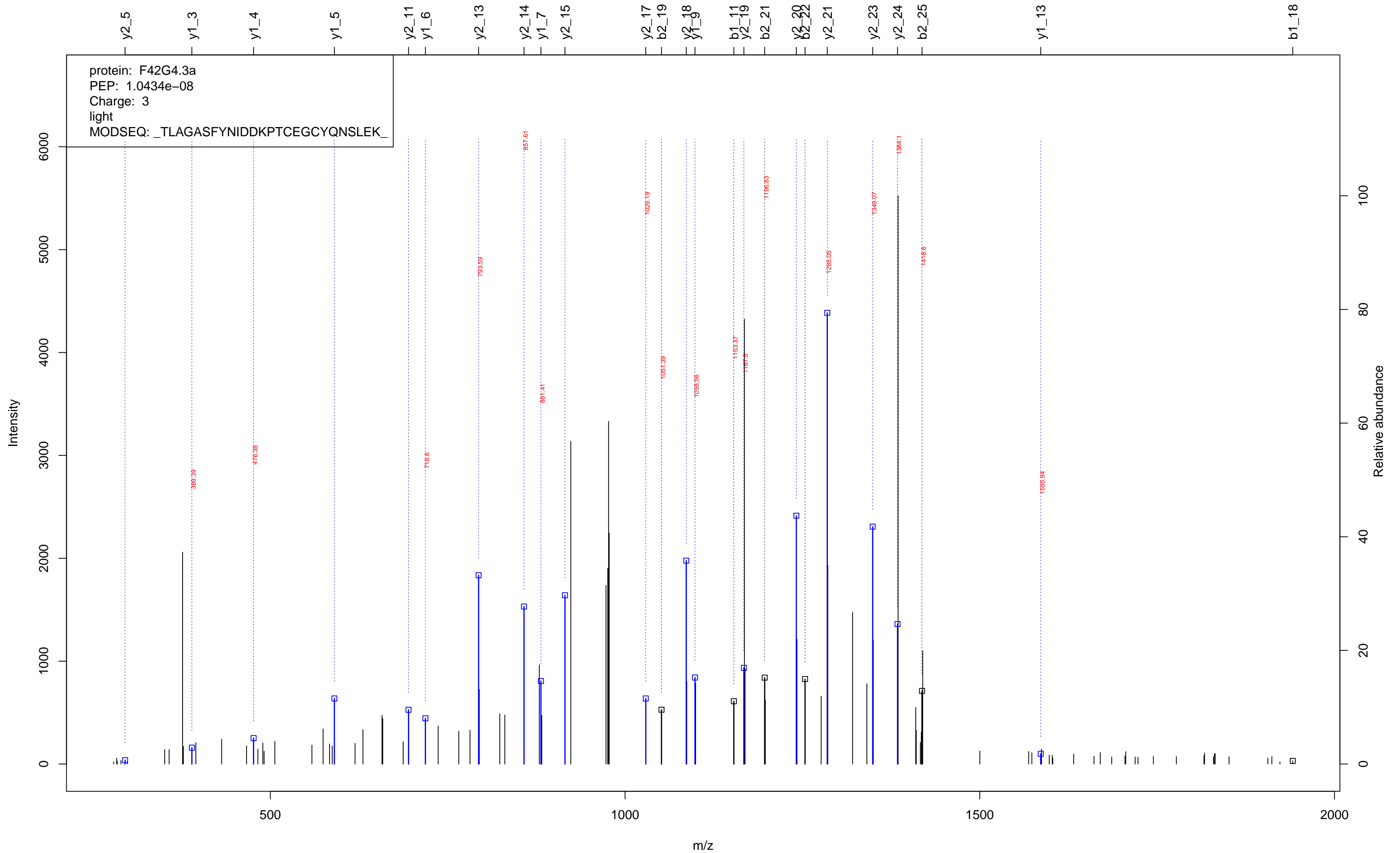


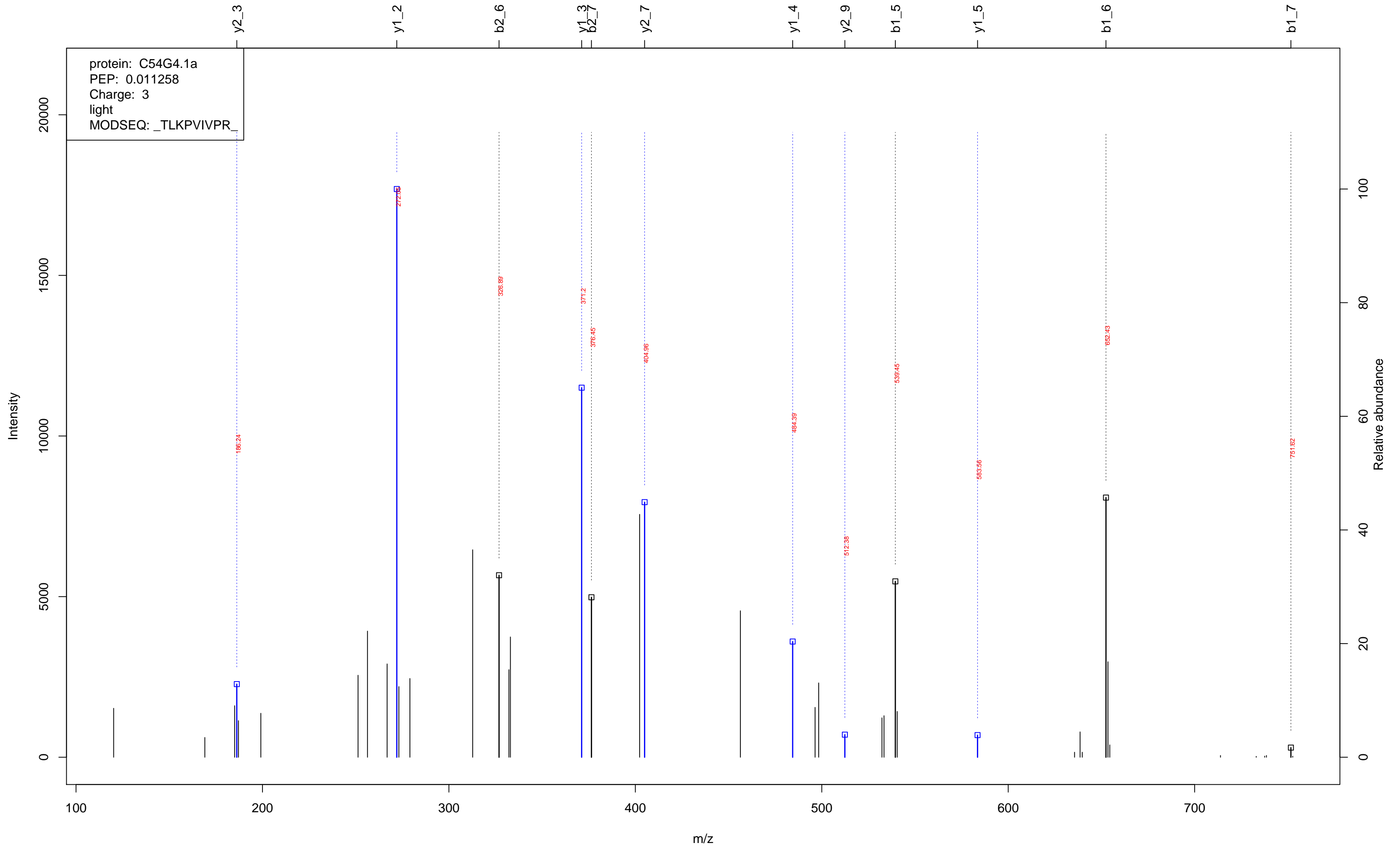


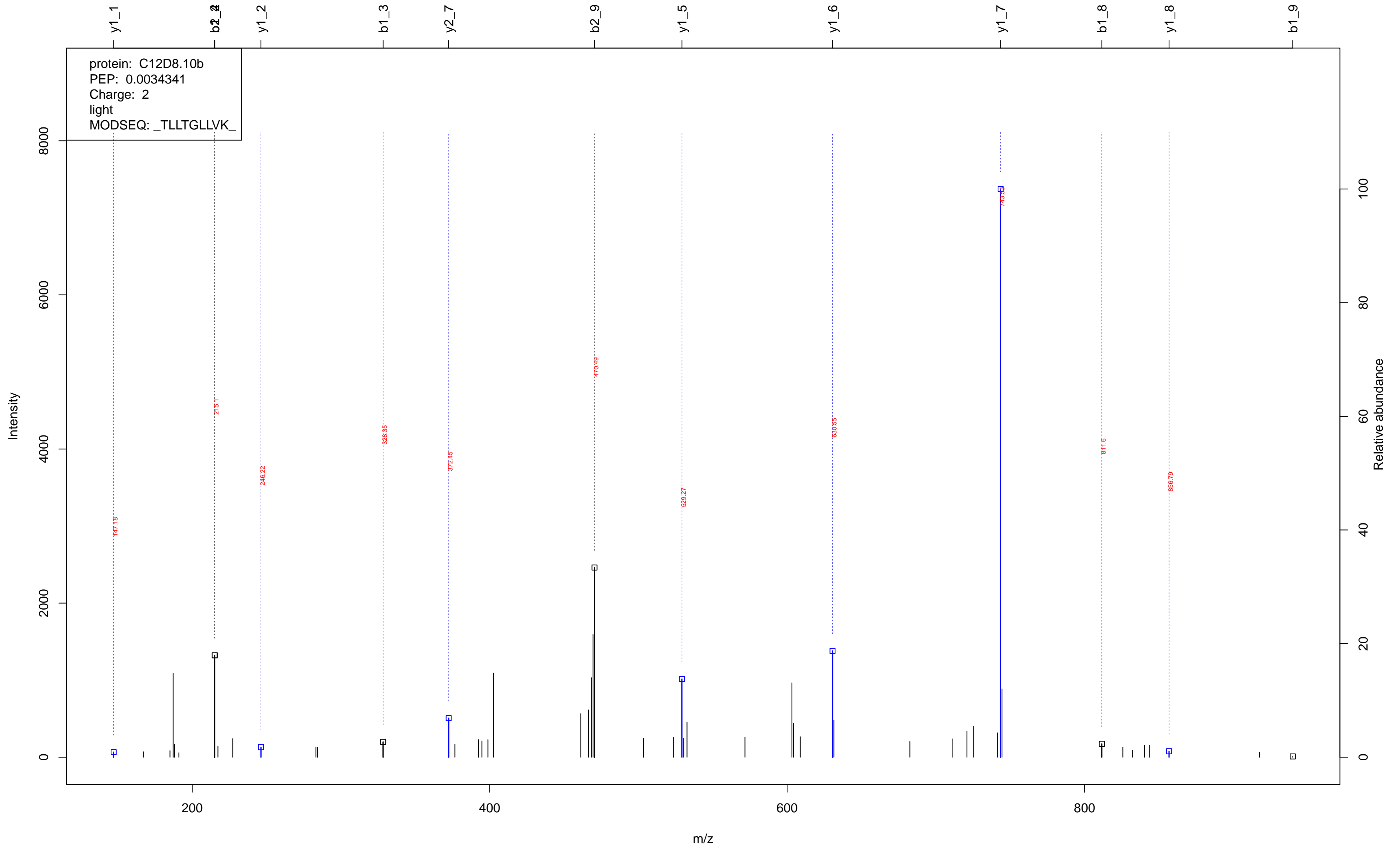












340

y1_1

b1_2

y1_2

b2_6

y1_3

y2_8

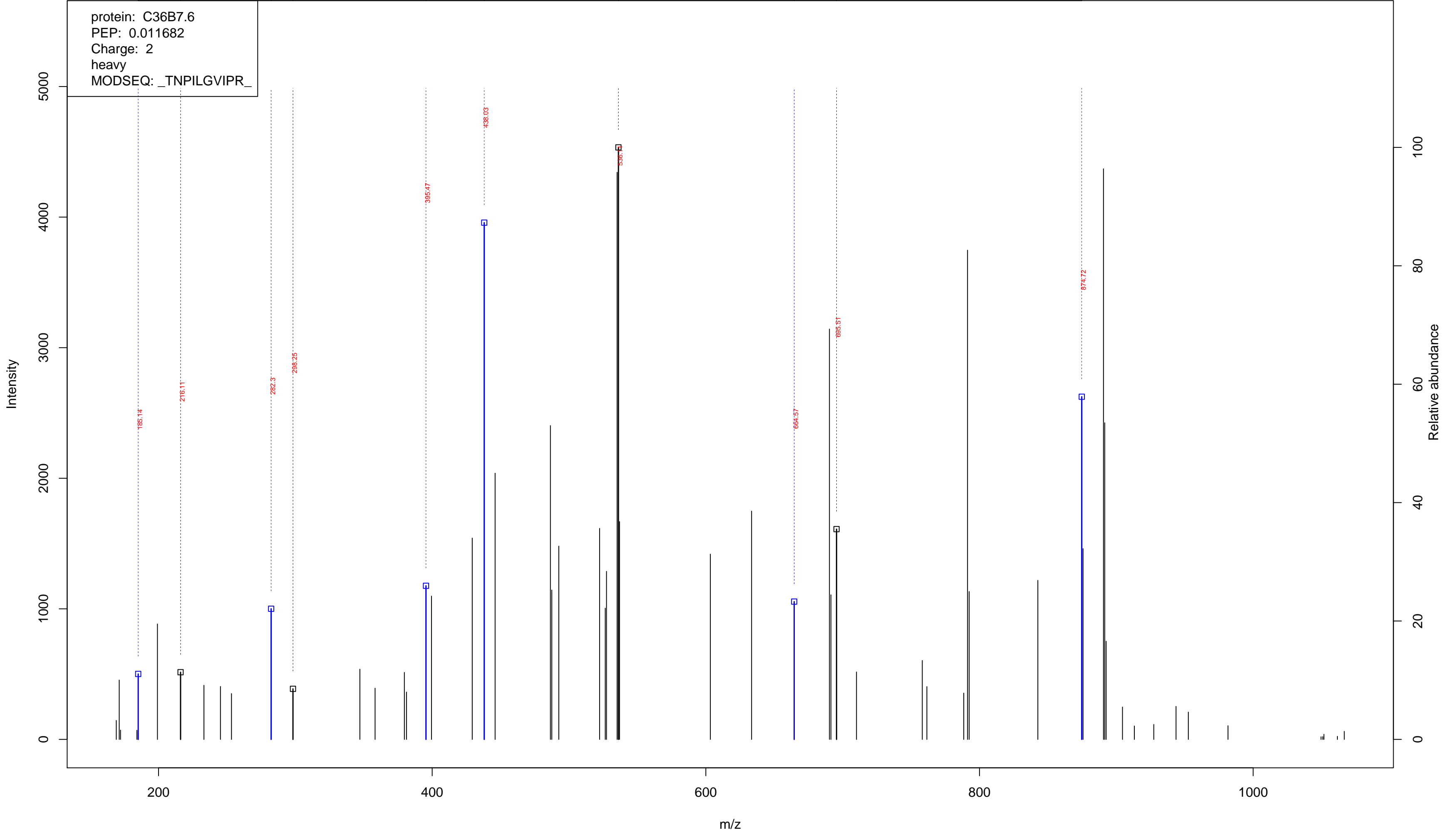
b2_10

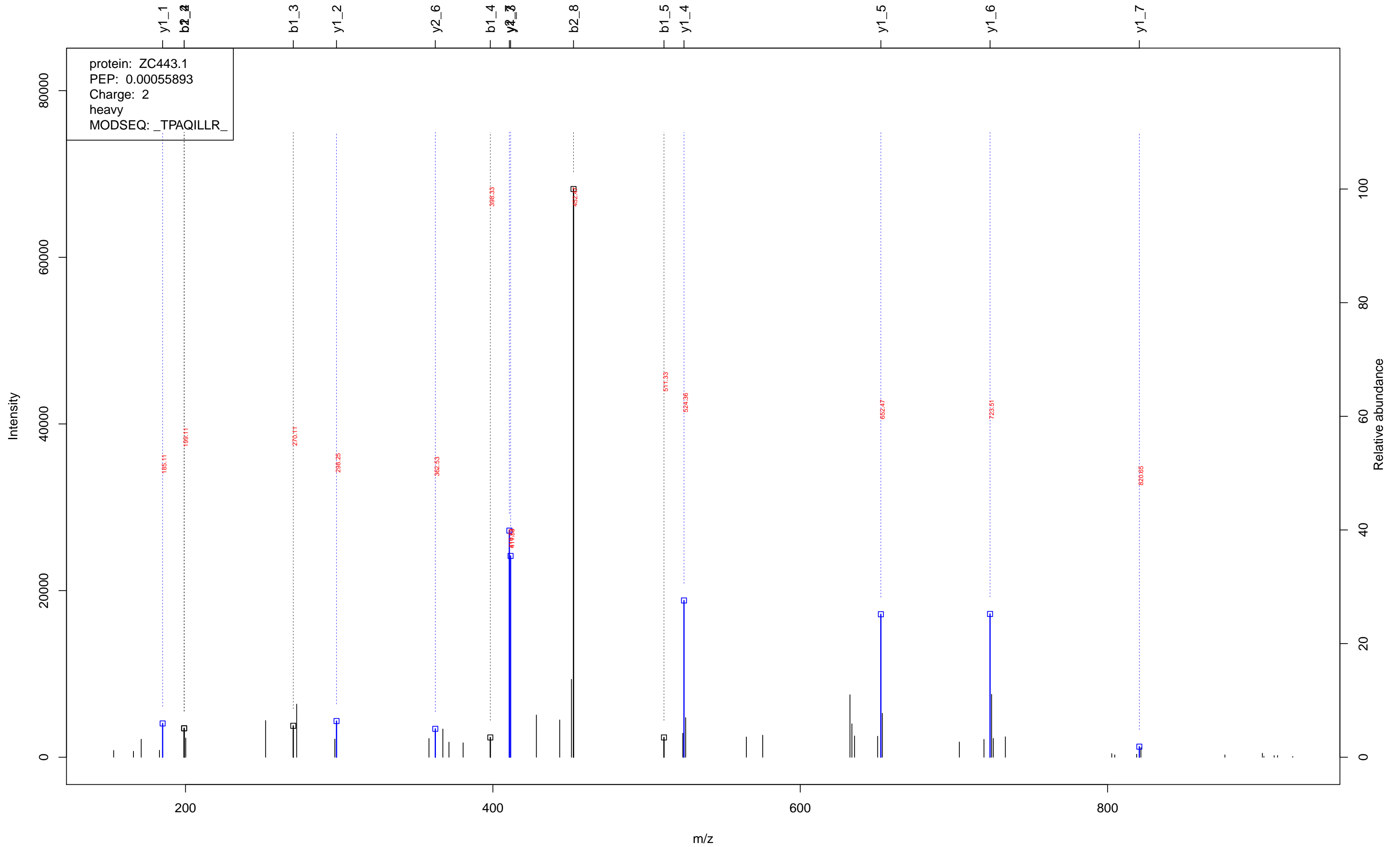
y1_6

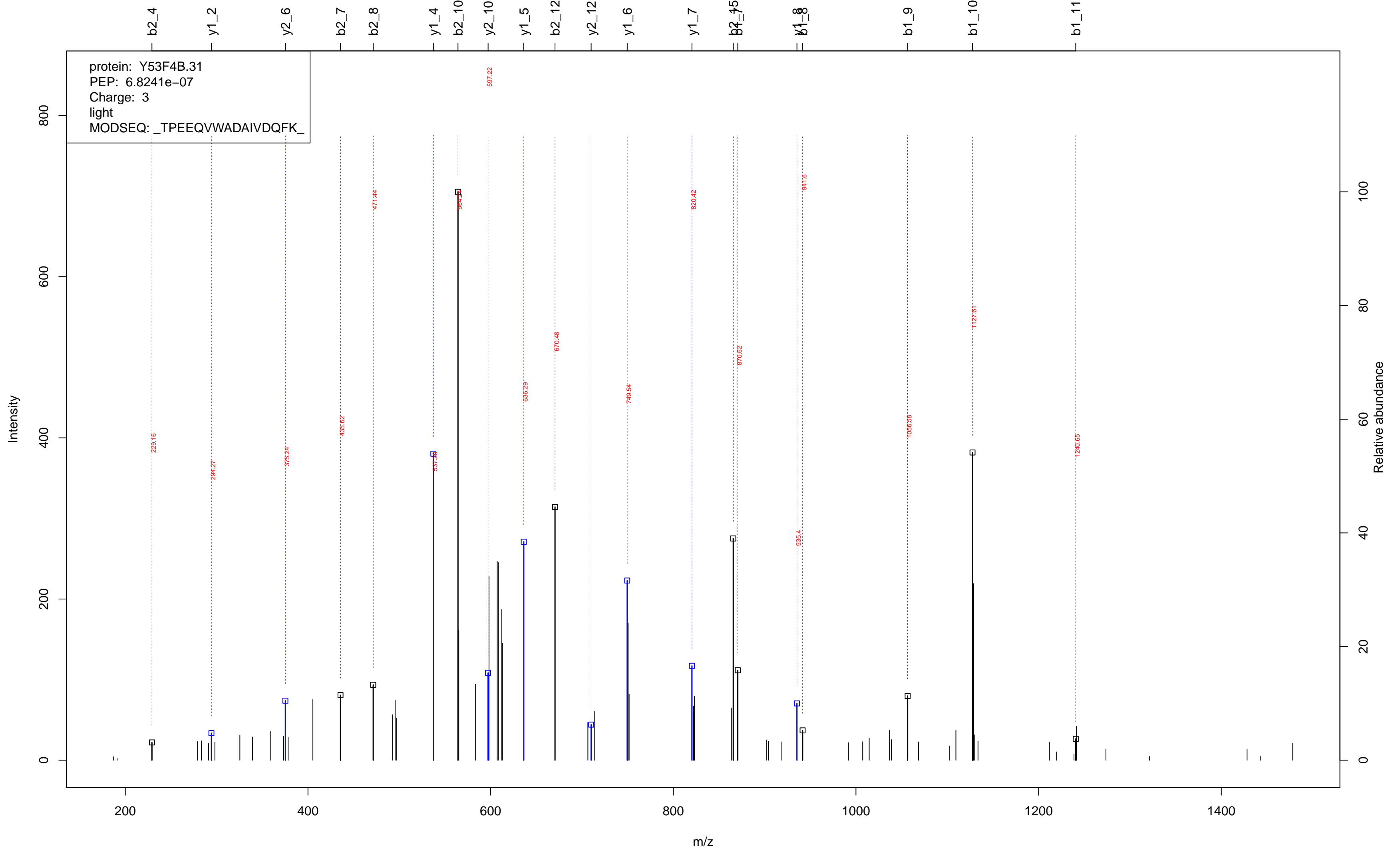
b1_7

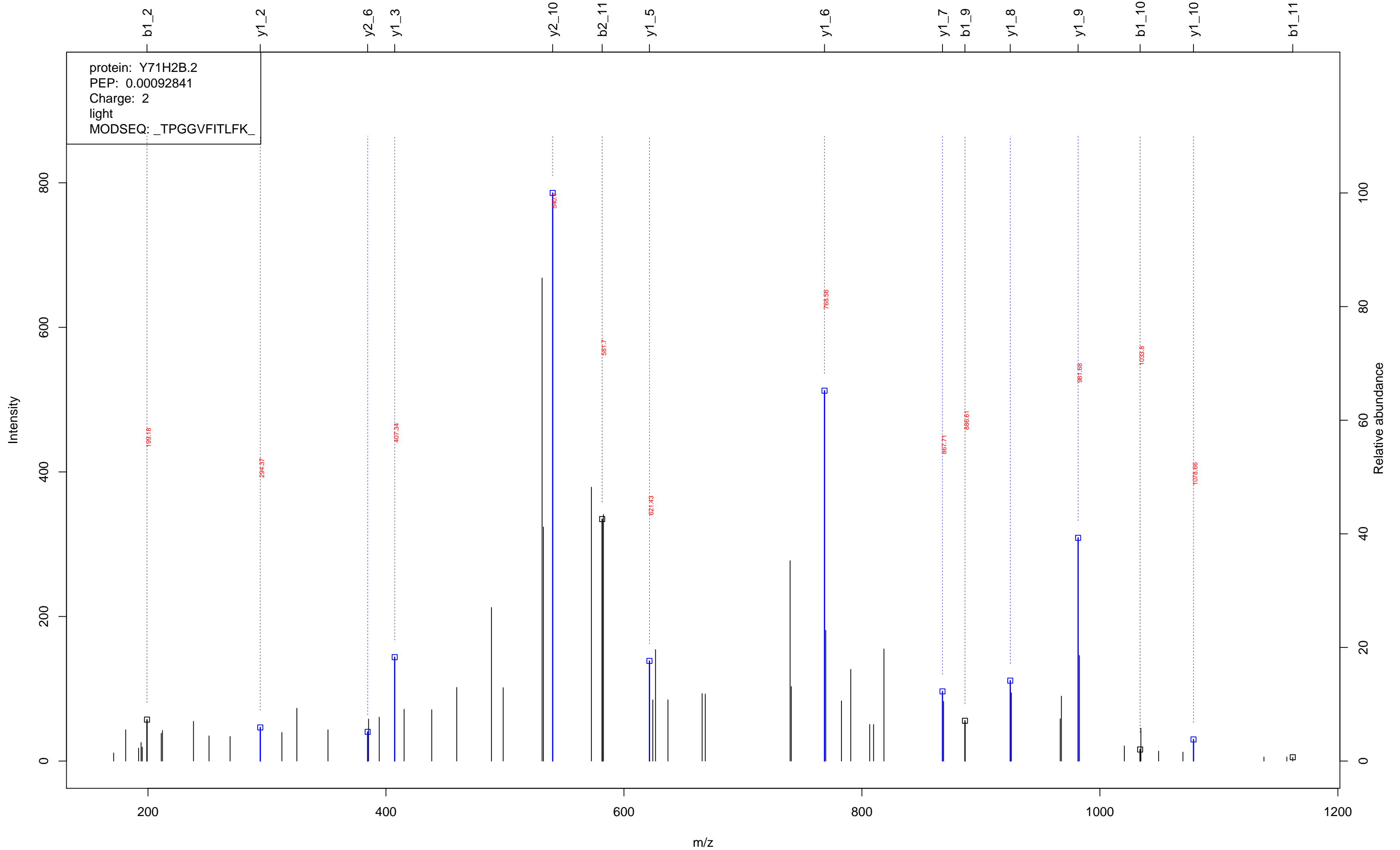
y1_8

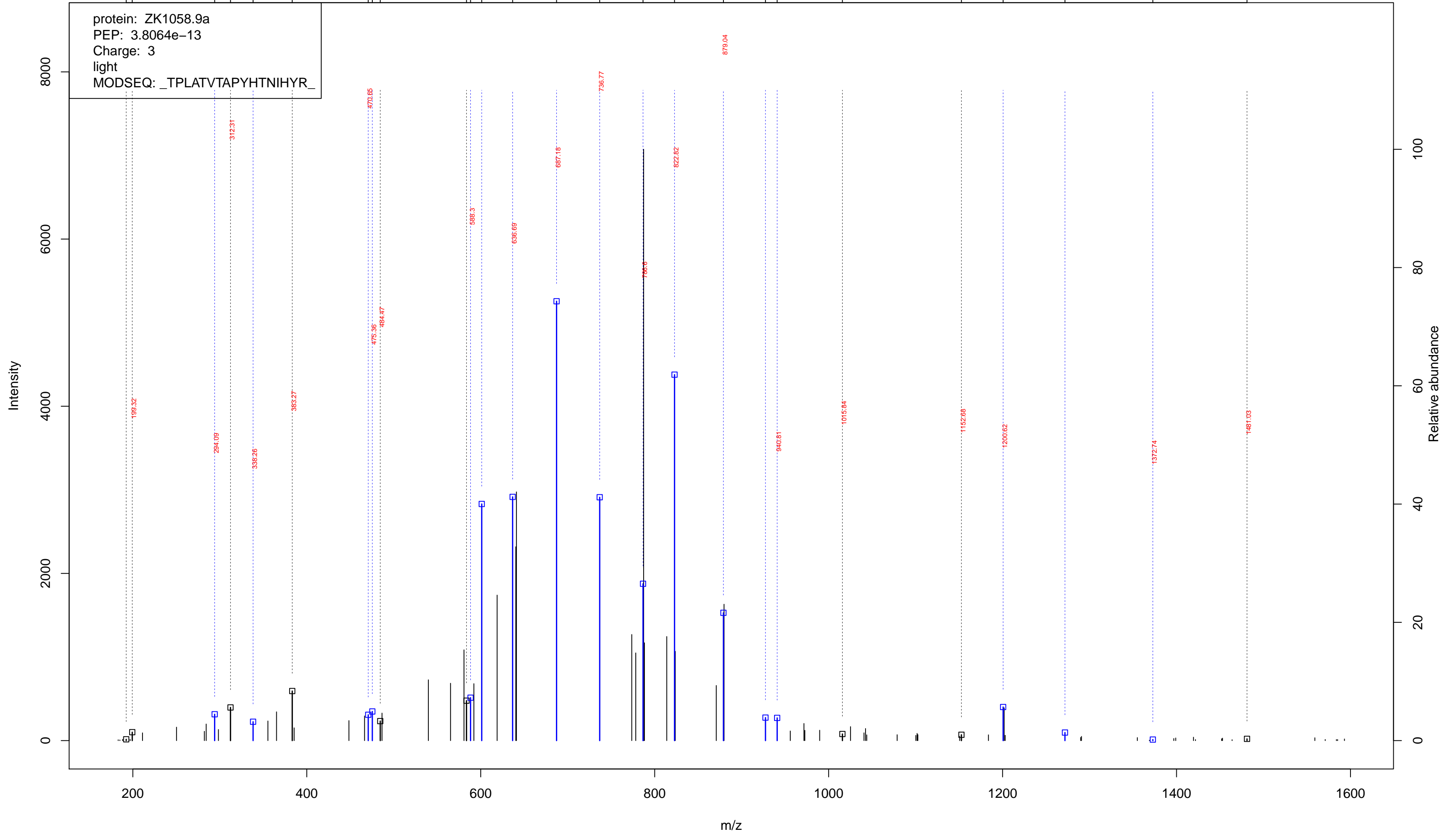
protein: C36B7.6
PEP: 0.011682
Charge: 2
heavy
MODSEQ: _TNPILGVIPR_



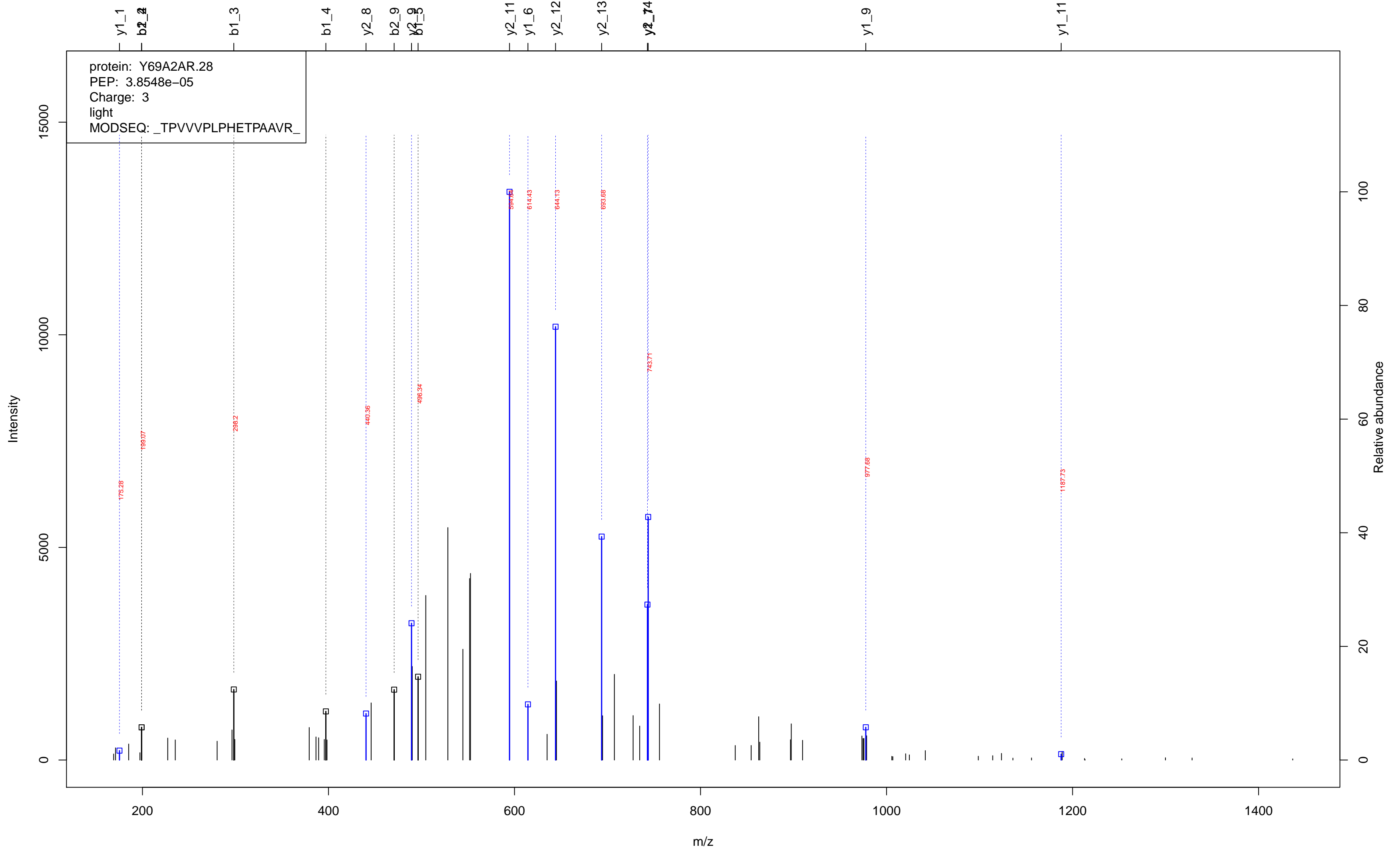


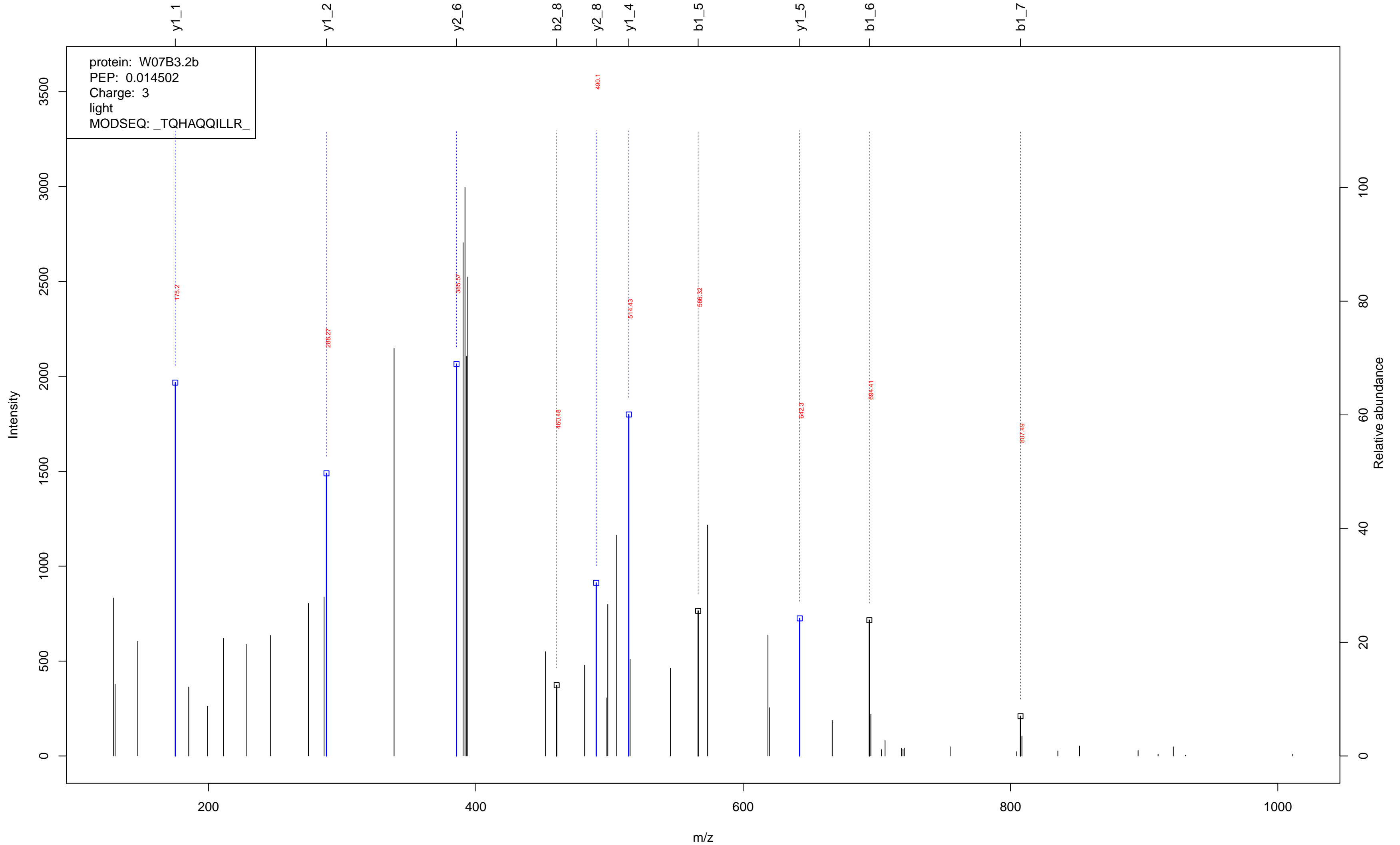


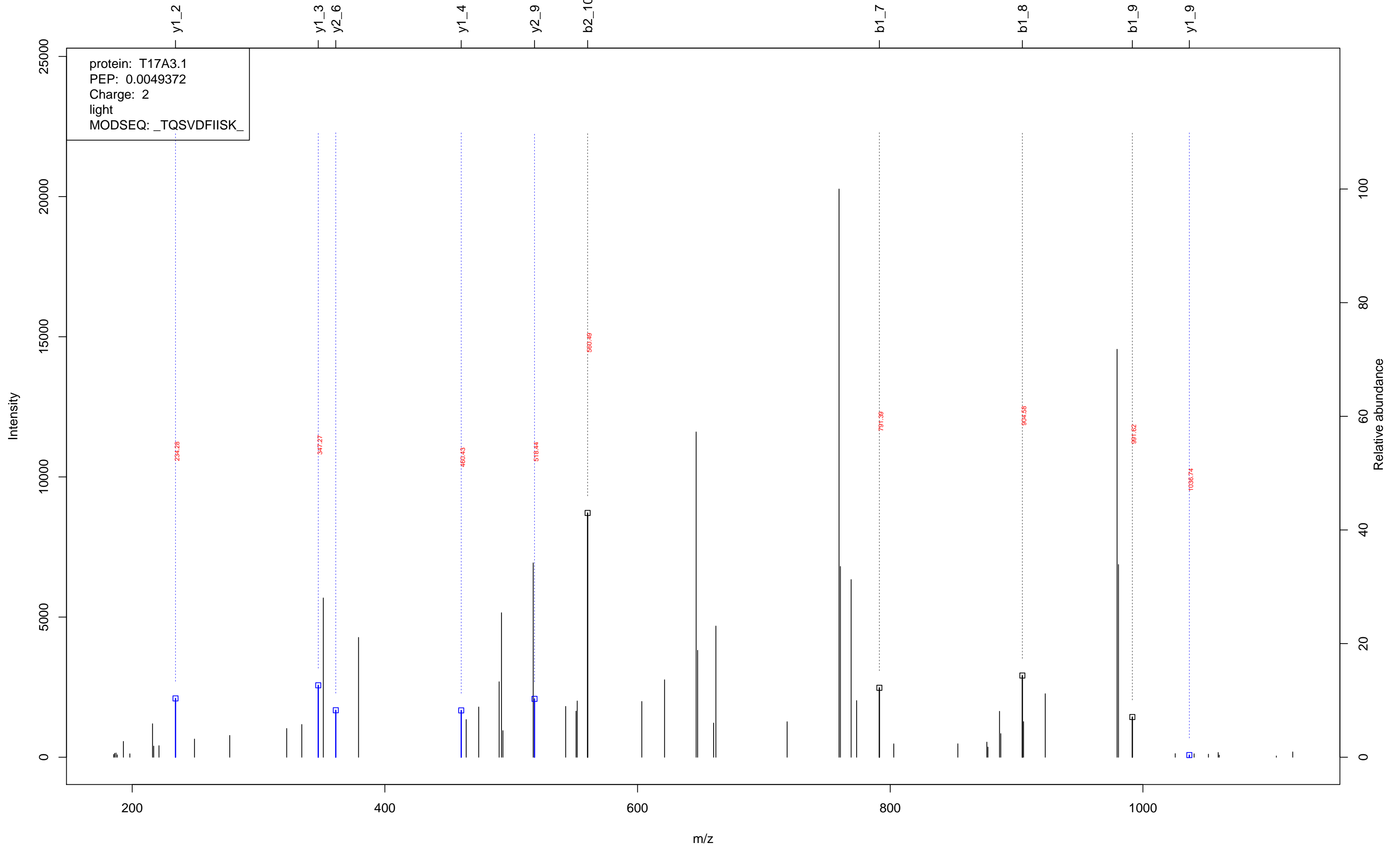


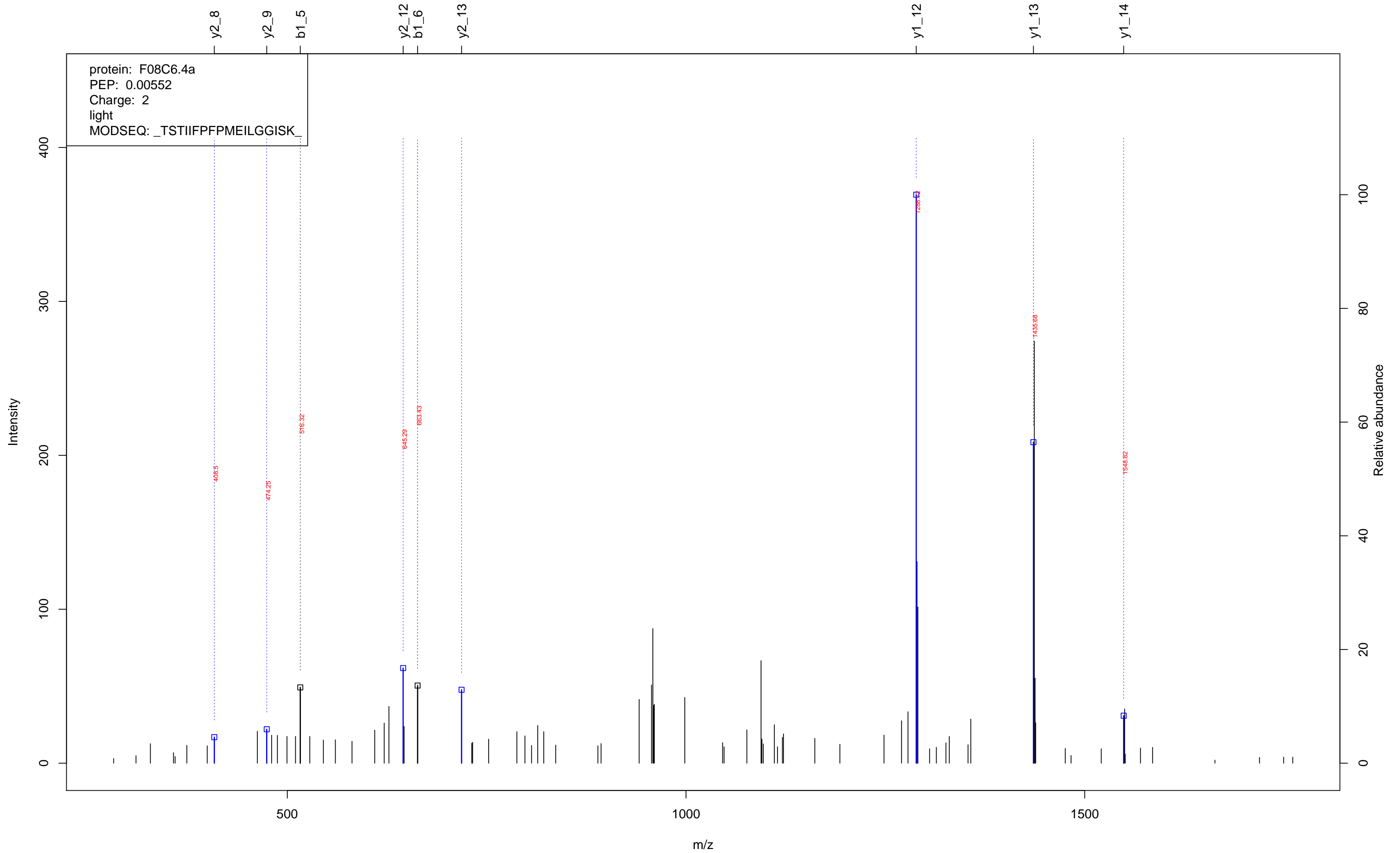


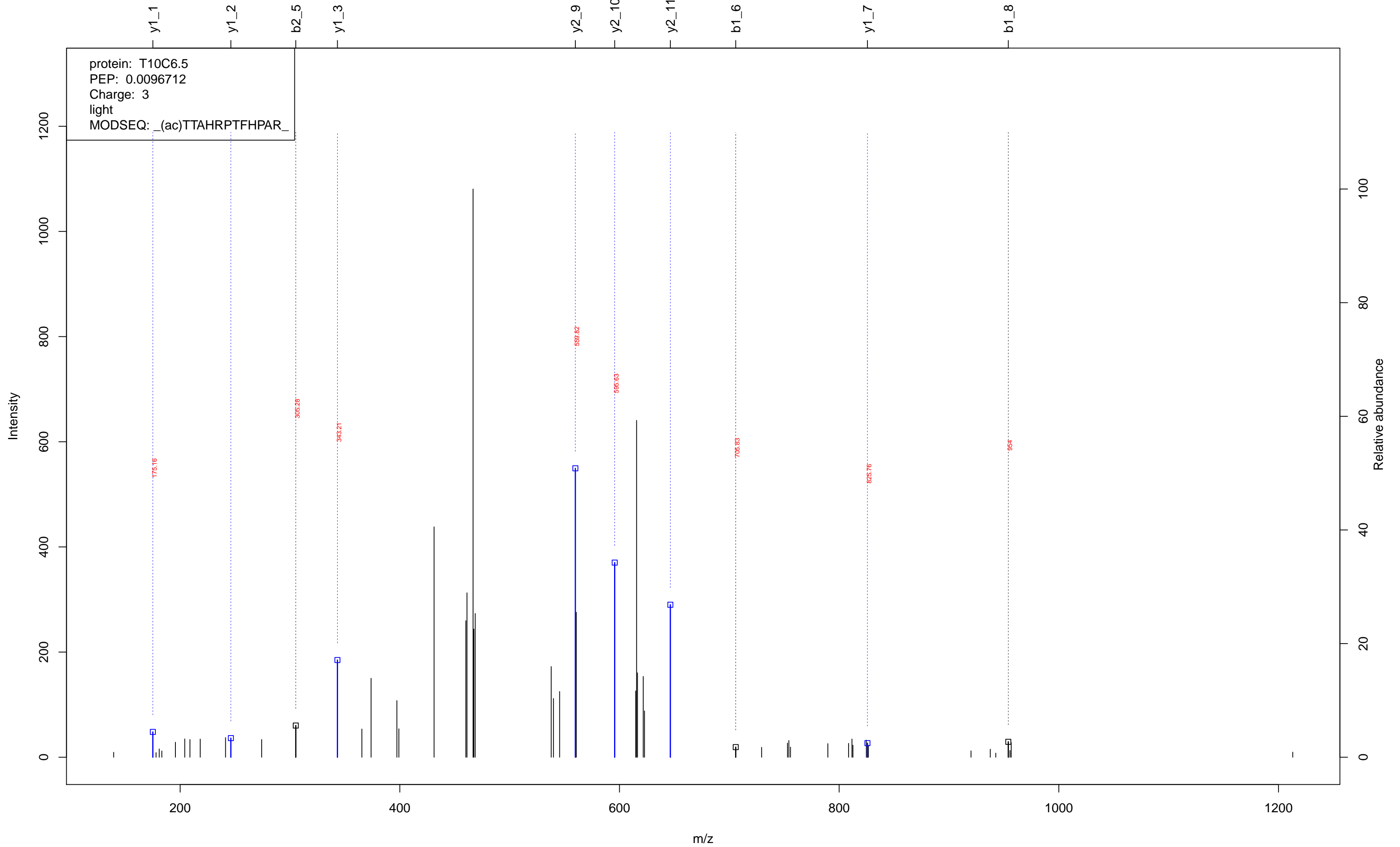
protein: ZK1058.9a
PEP: 3.8064e-13
Charge: 3
light
MODSEQ: _TPLATVTAPYHTNIHYR_

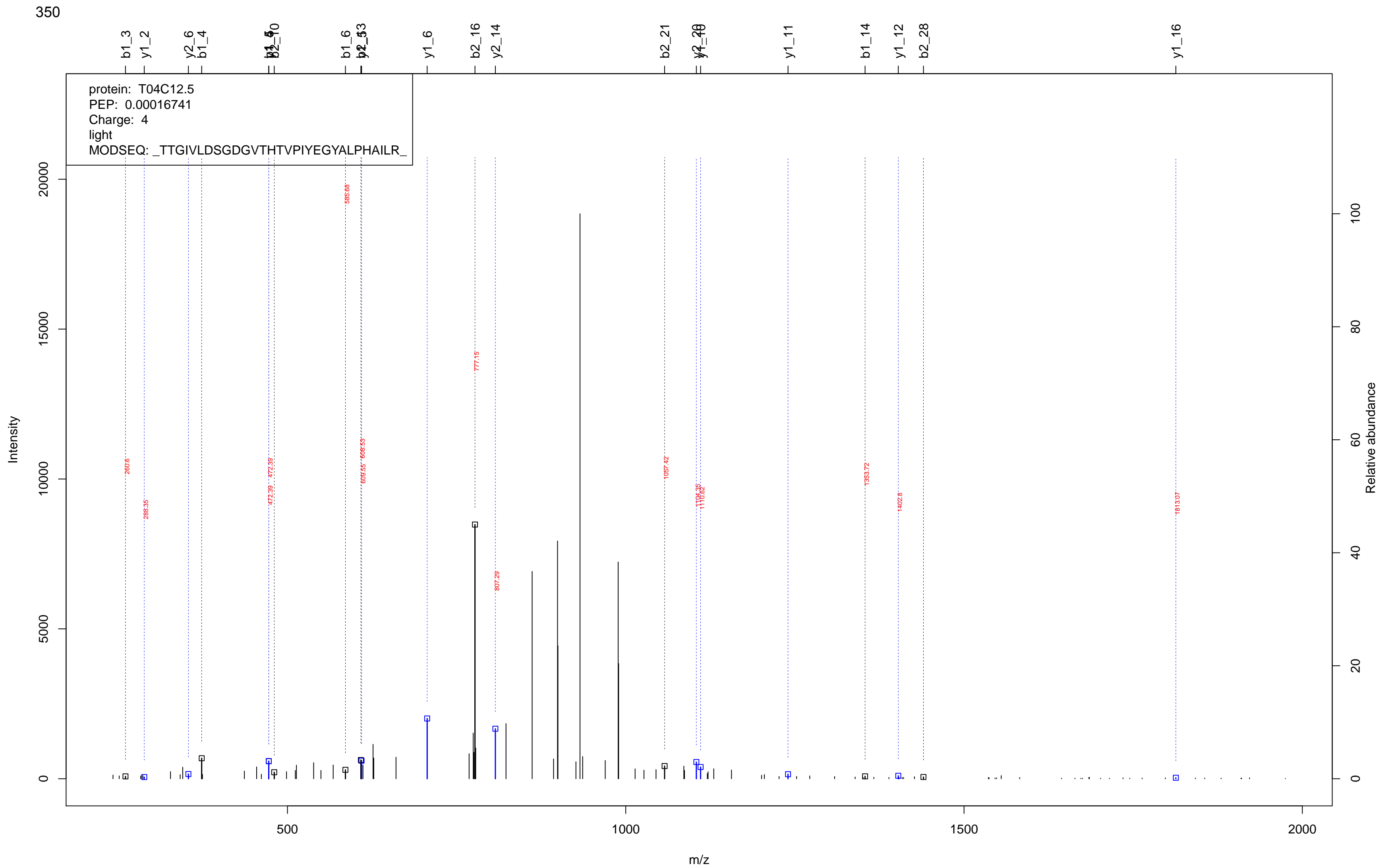


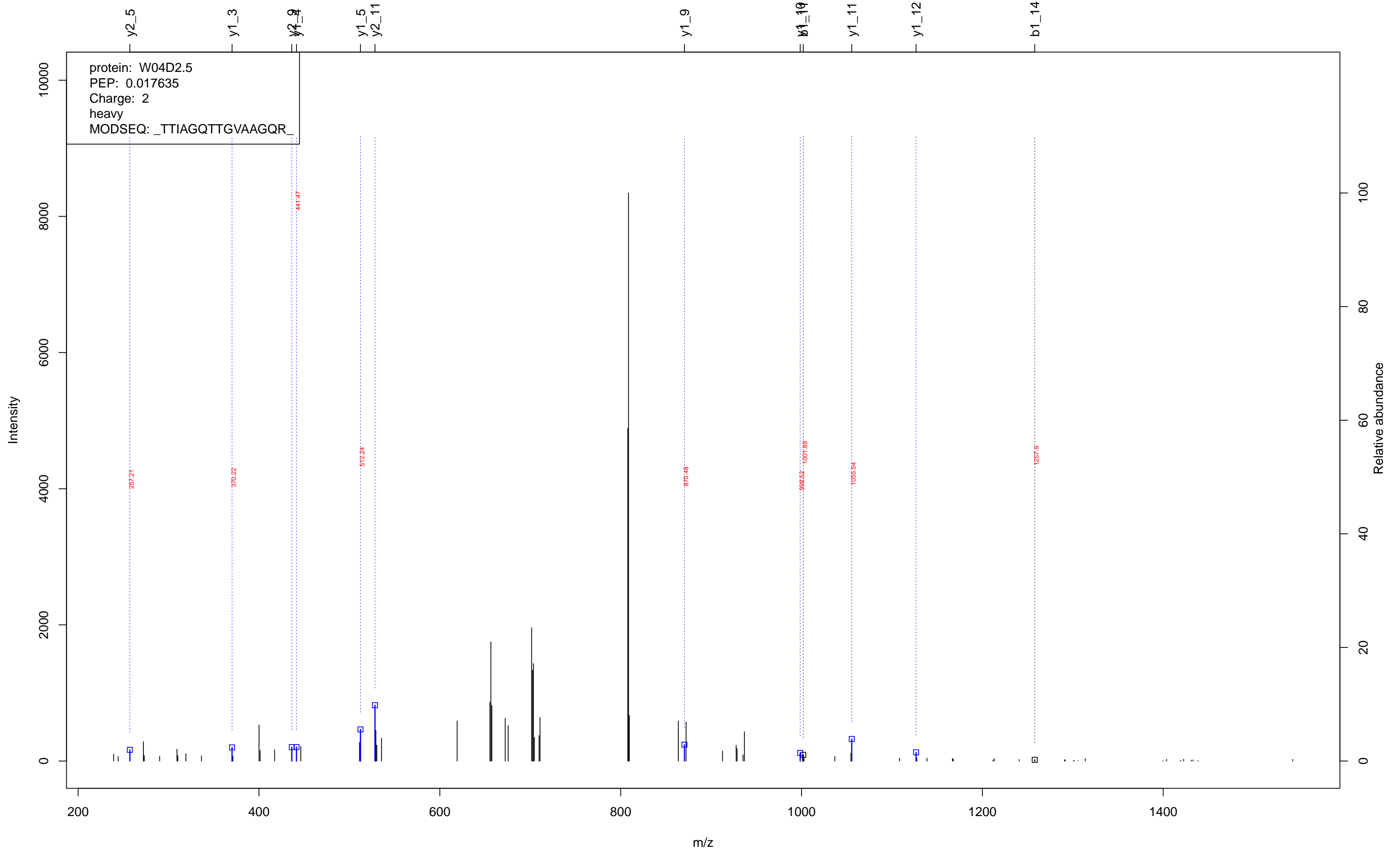


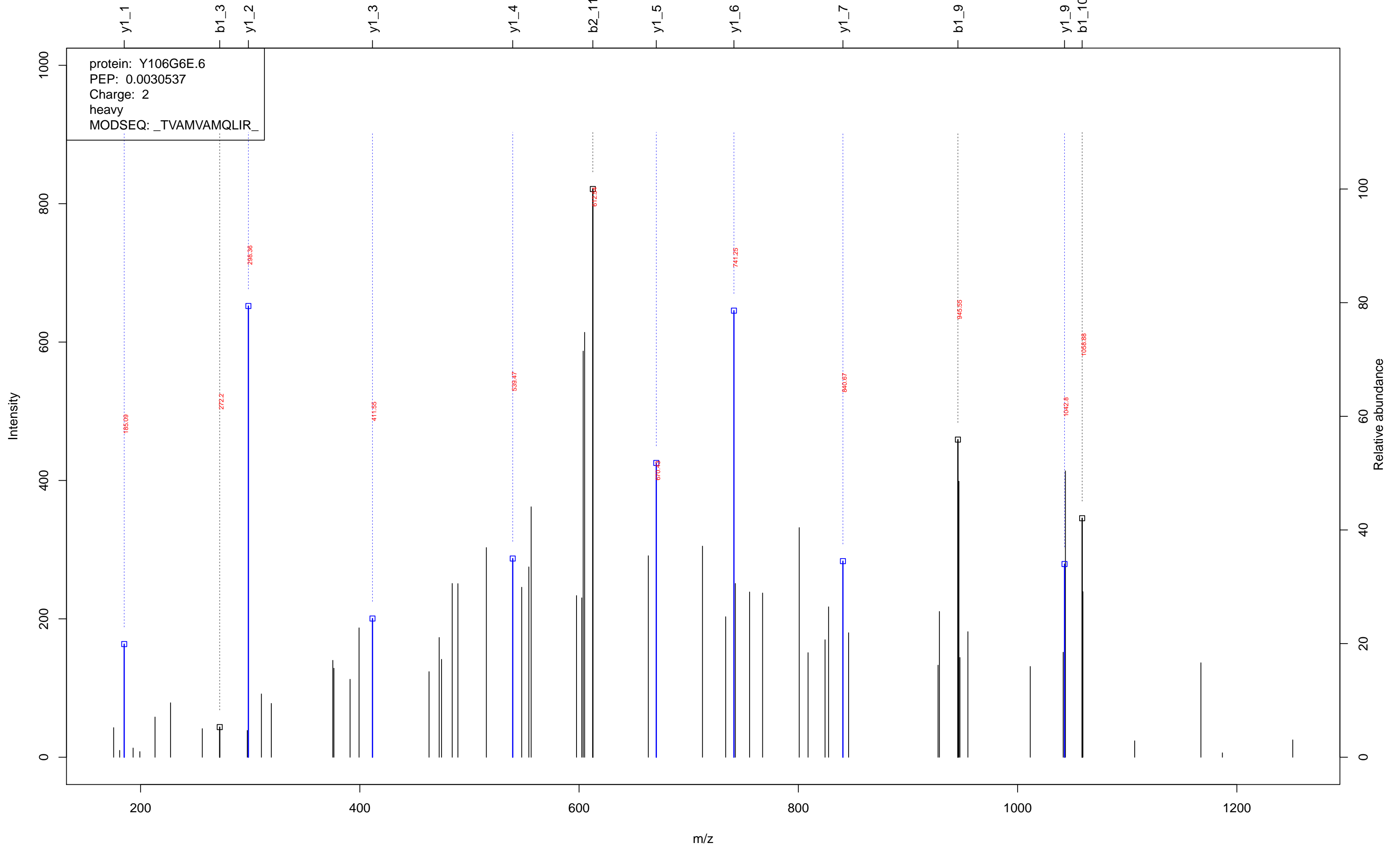




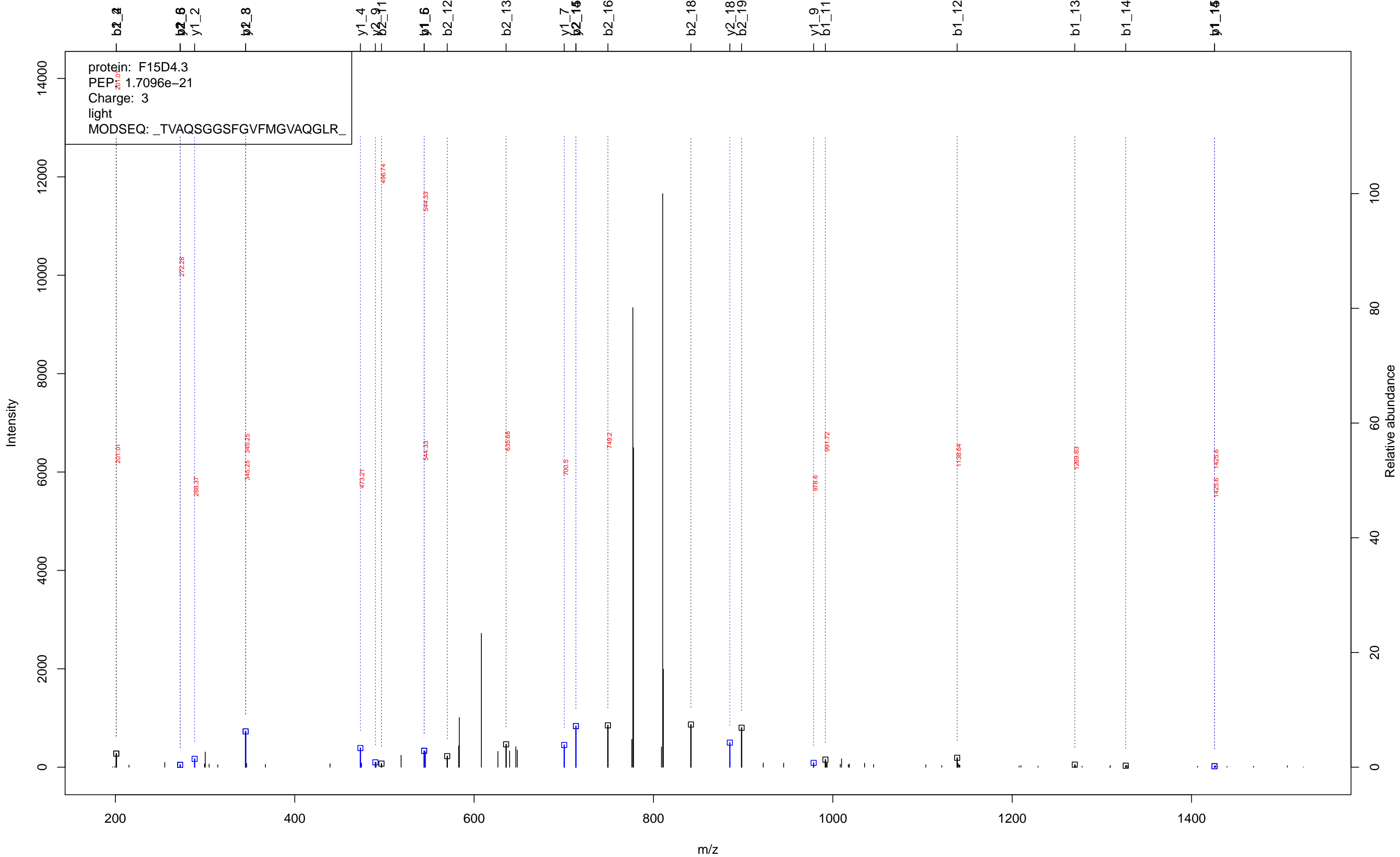


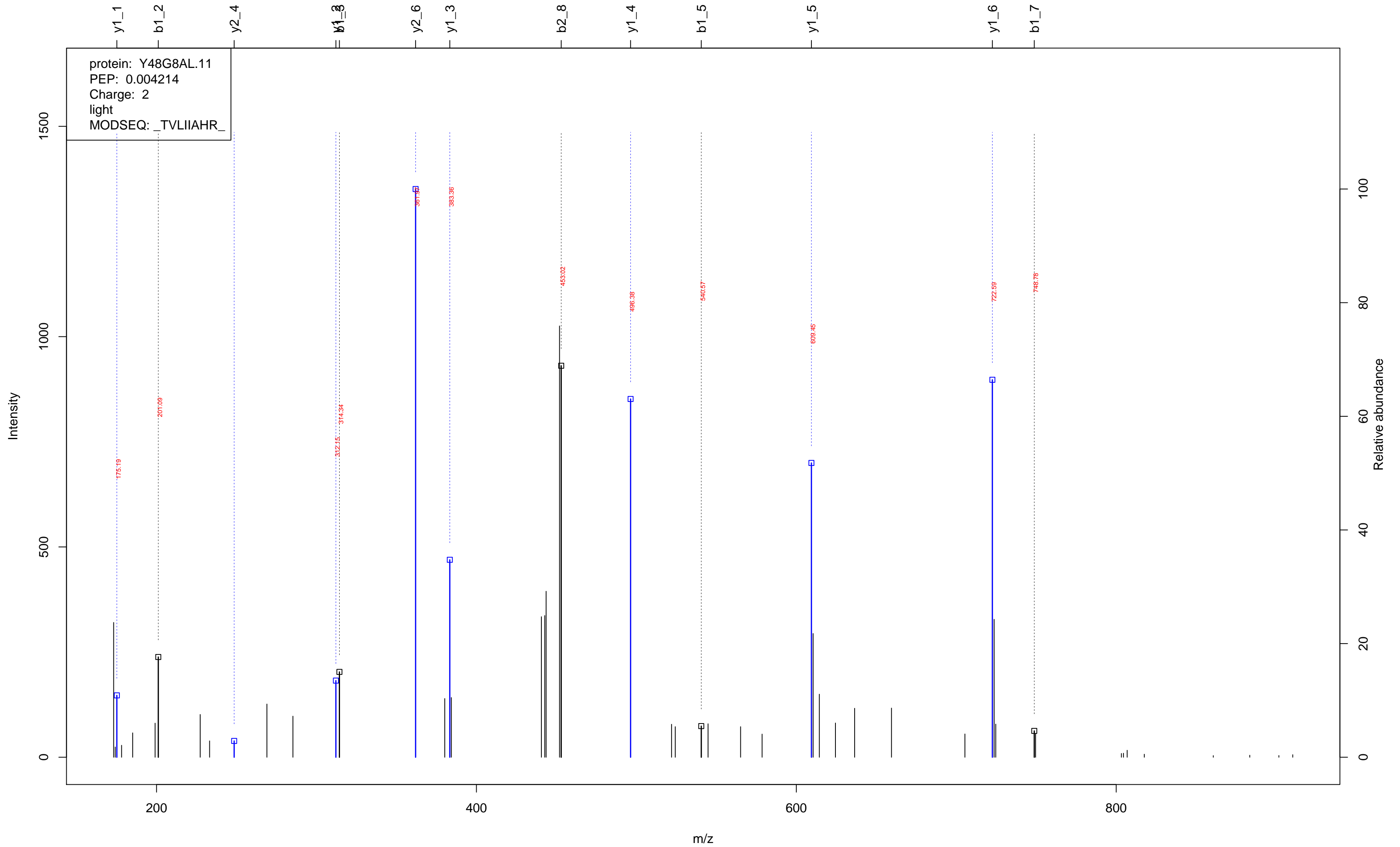


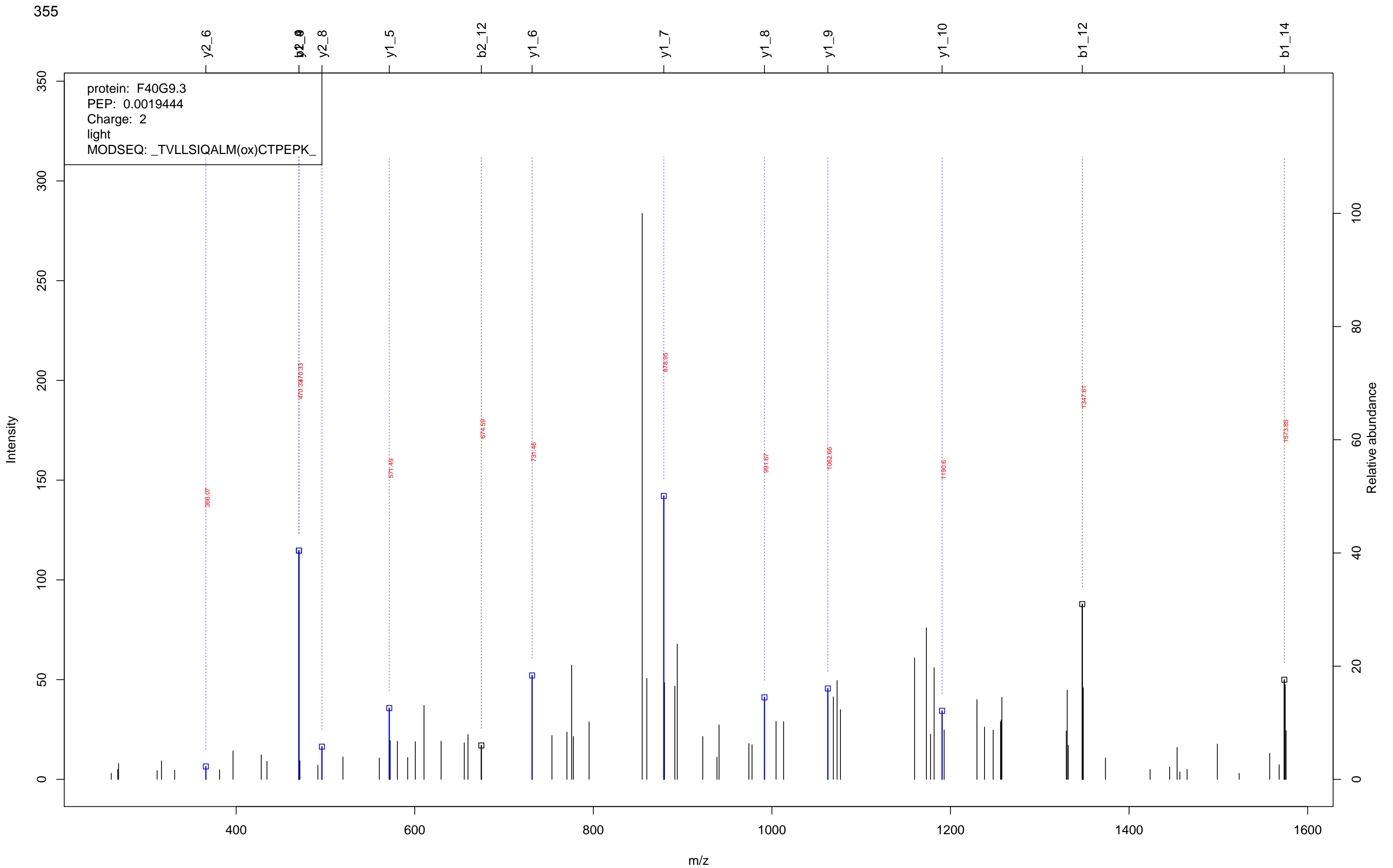


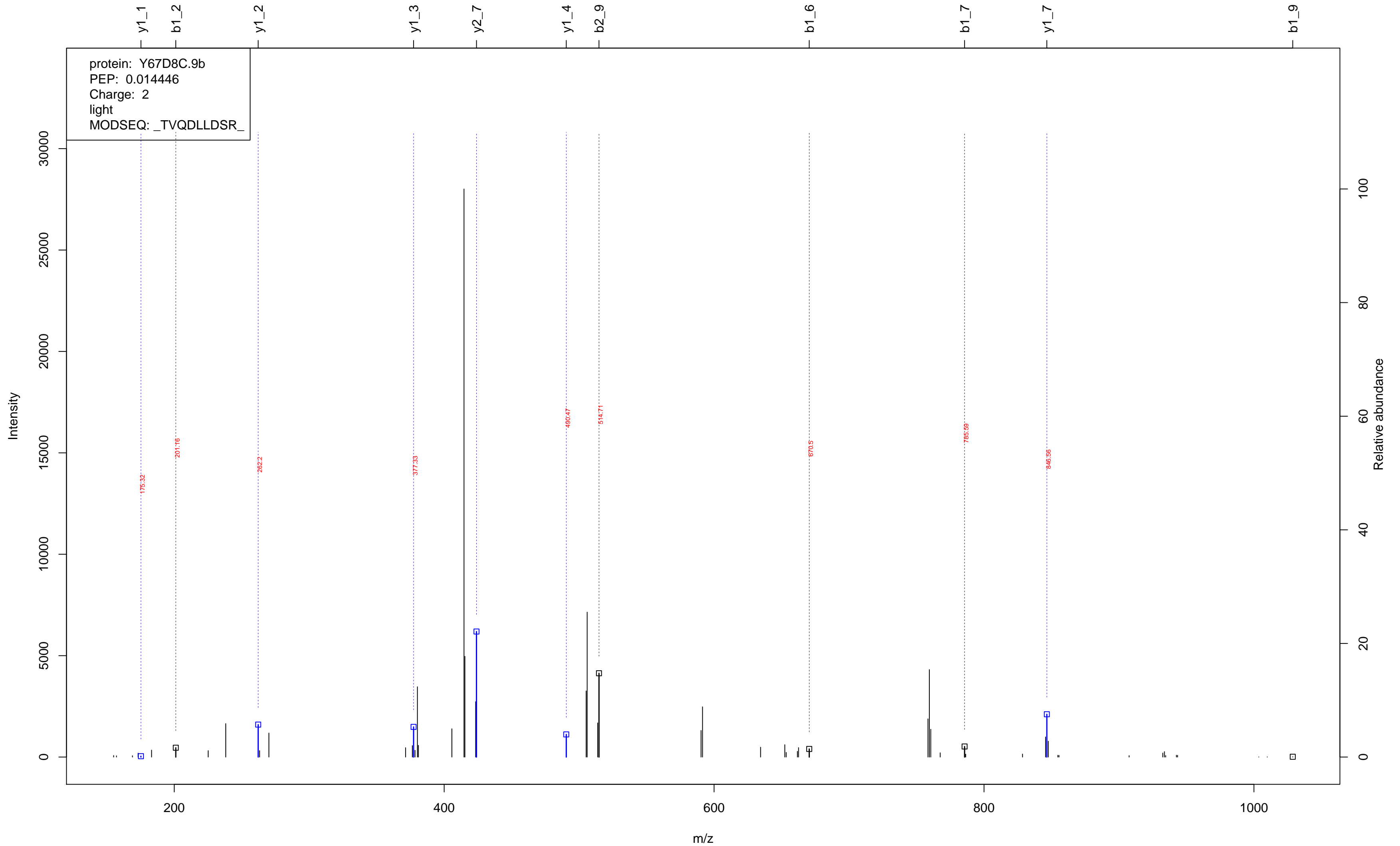


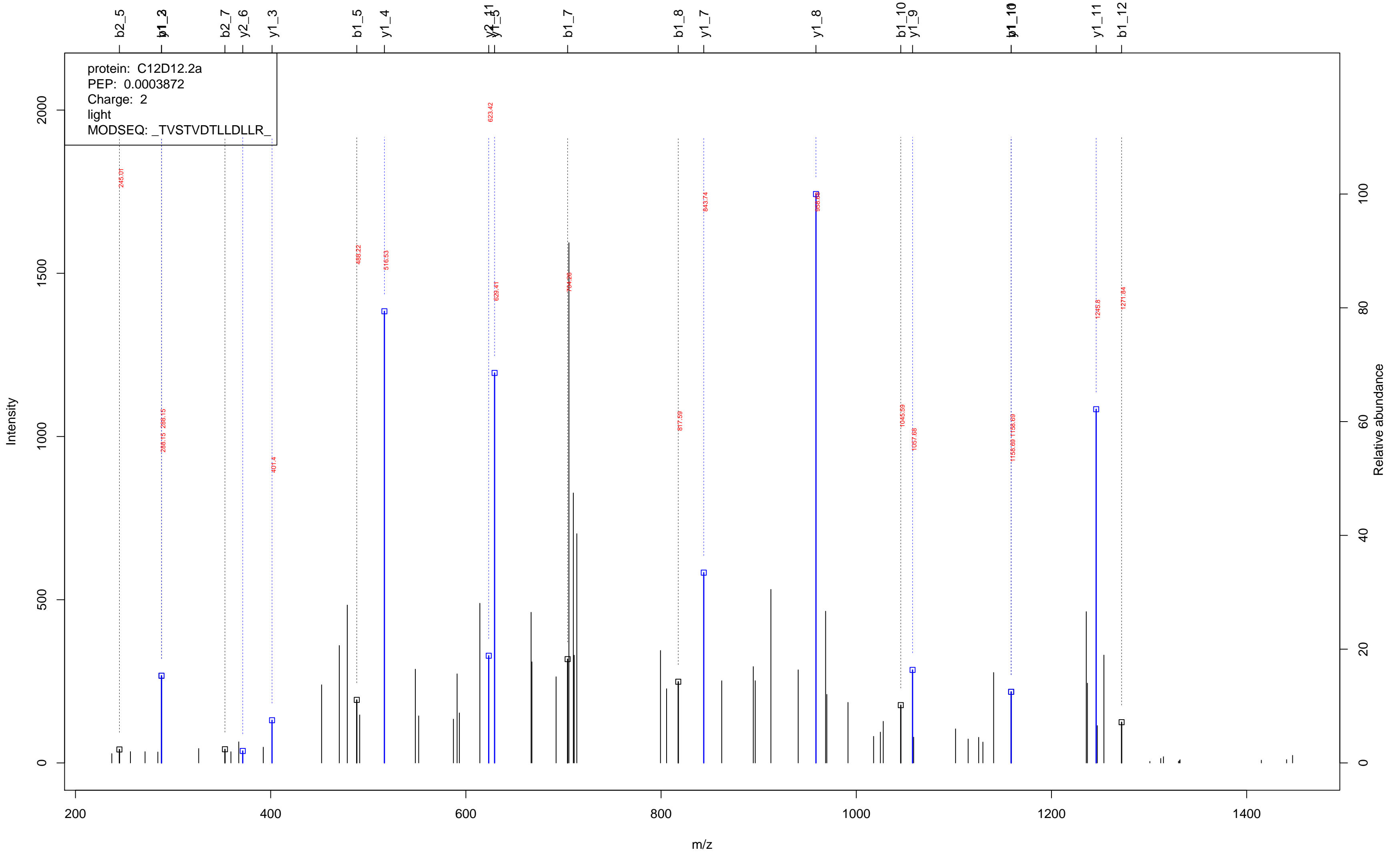
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PEP: 0.0030537
Charge: 2
heavy
MODSEQ: _TVAMVAMQLIR_

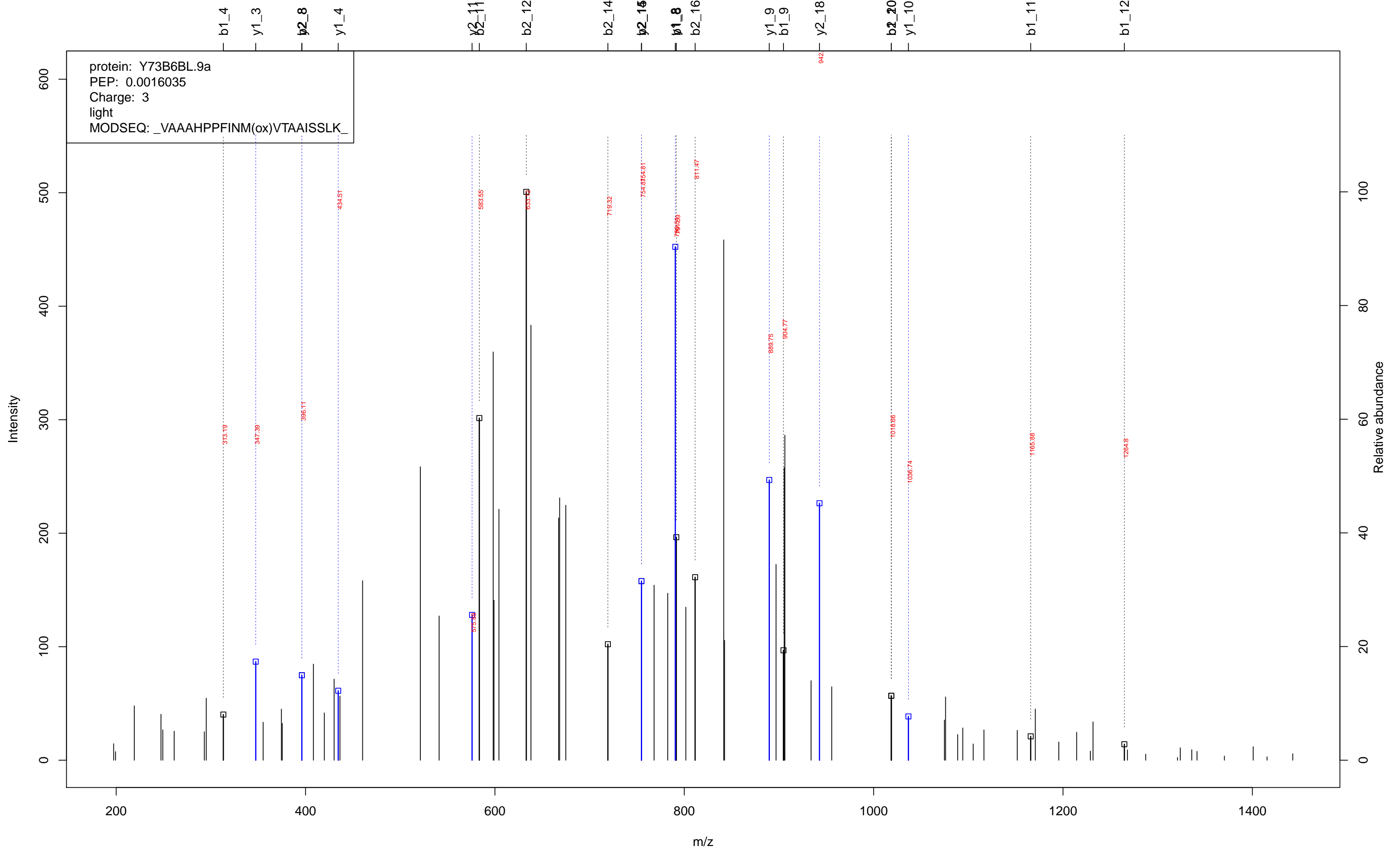


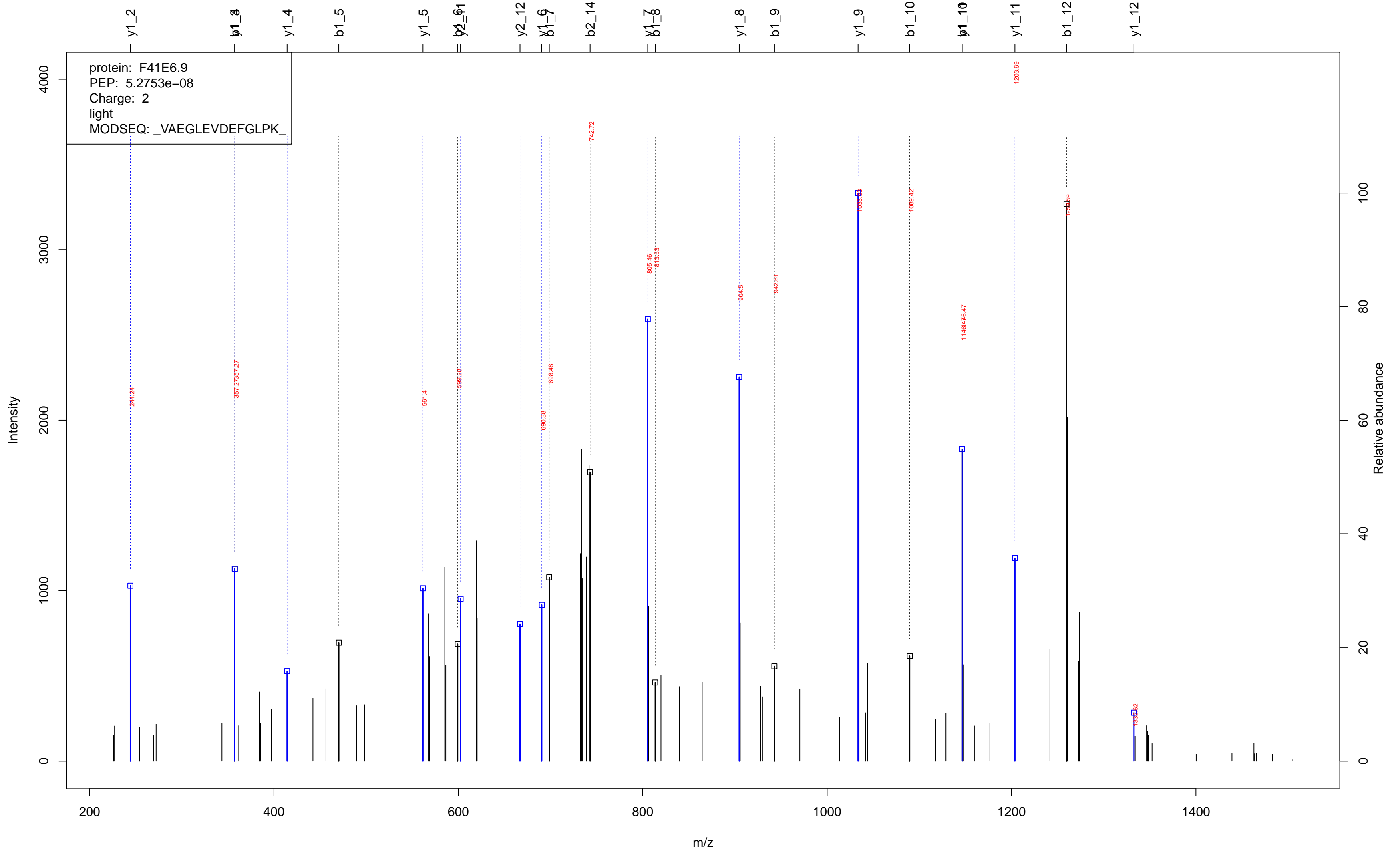


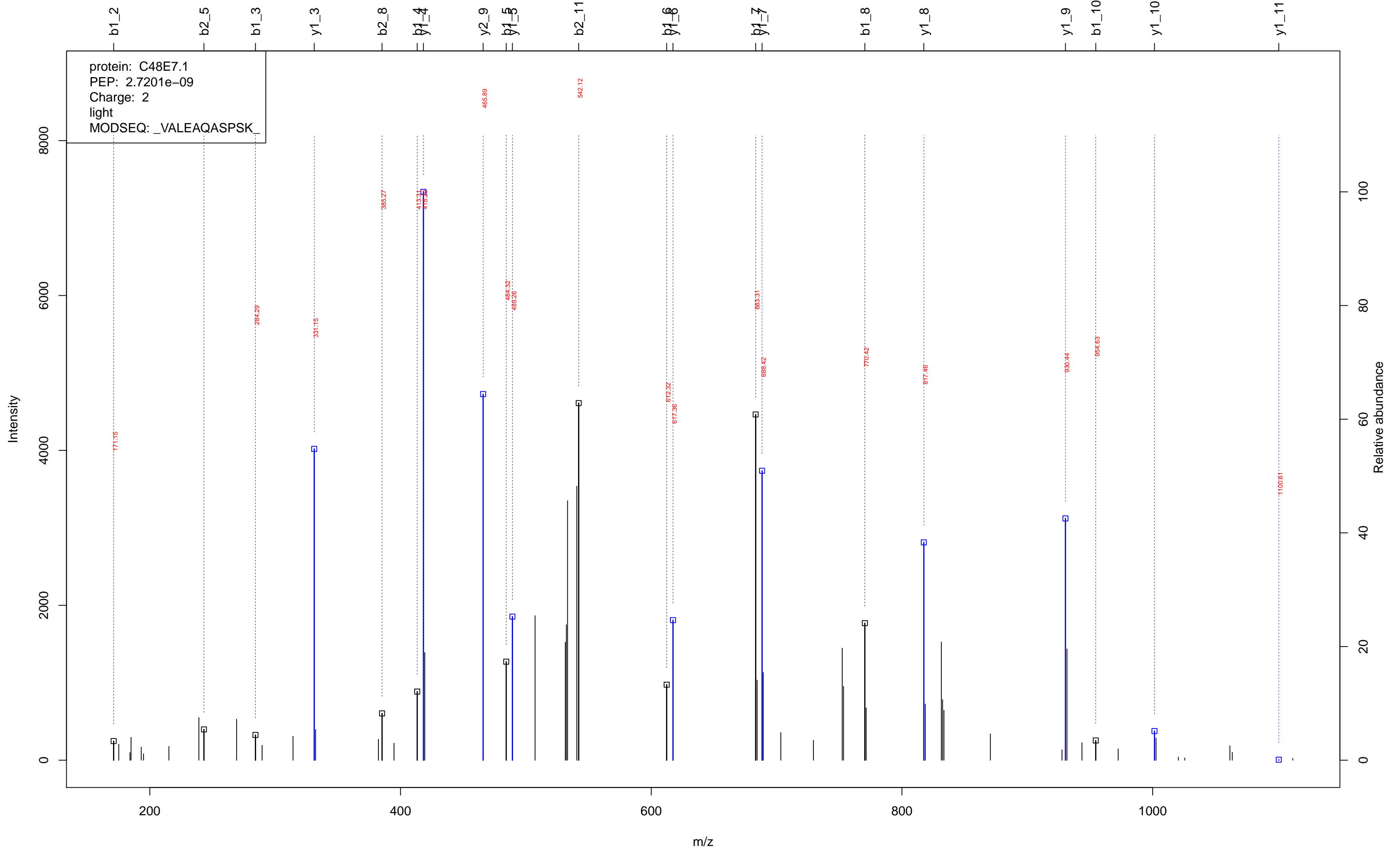


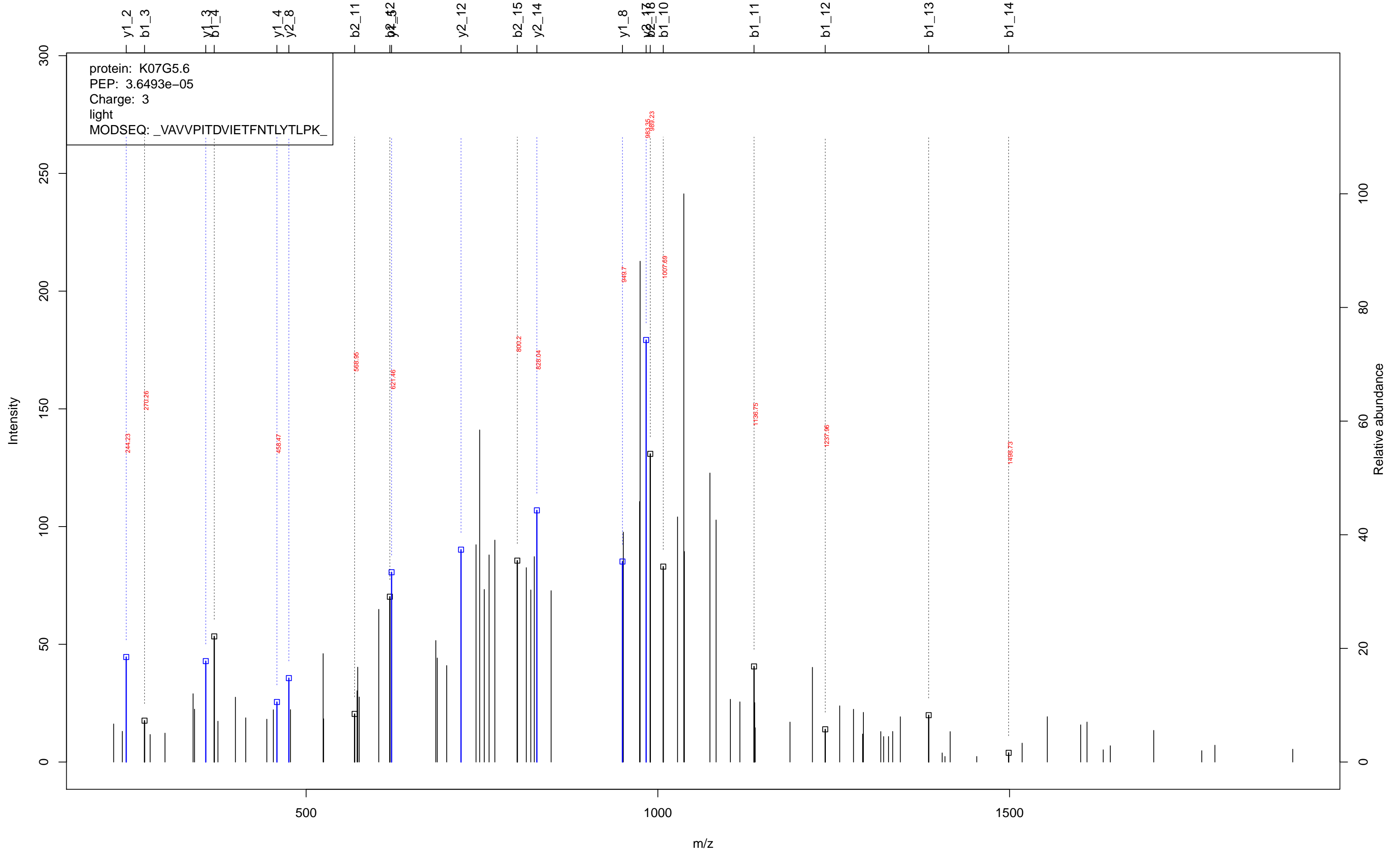


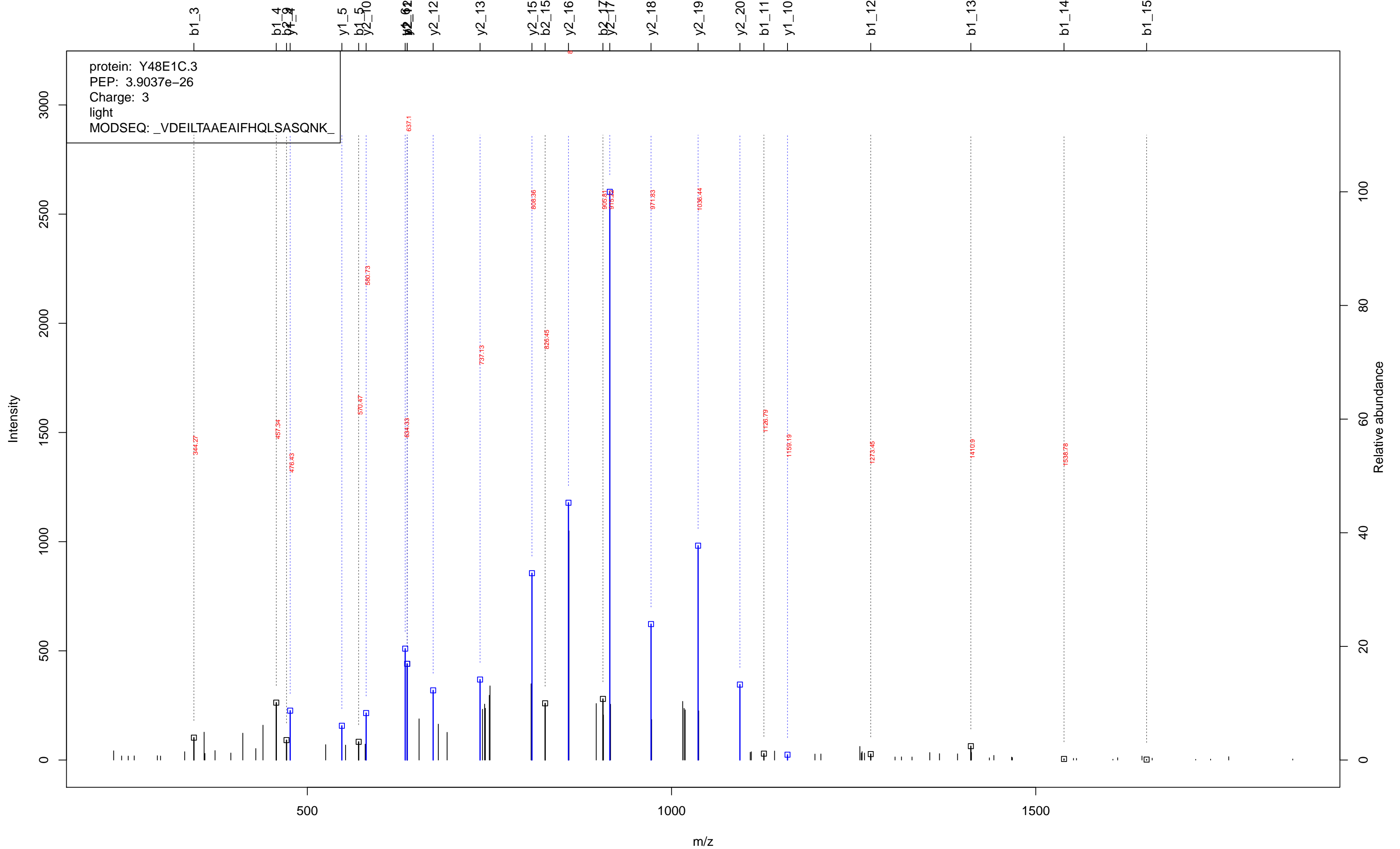






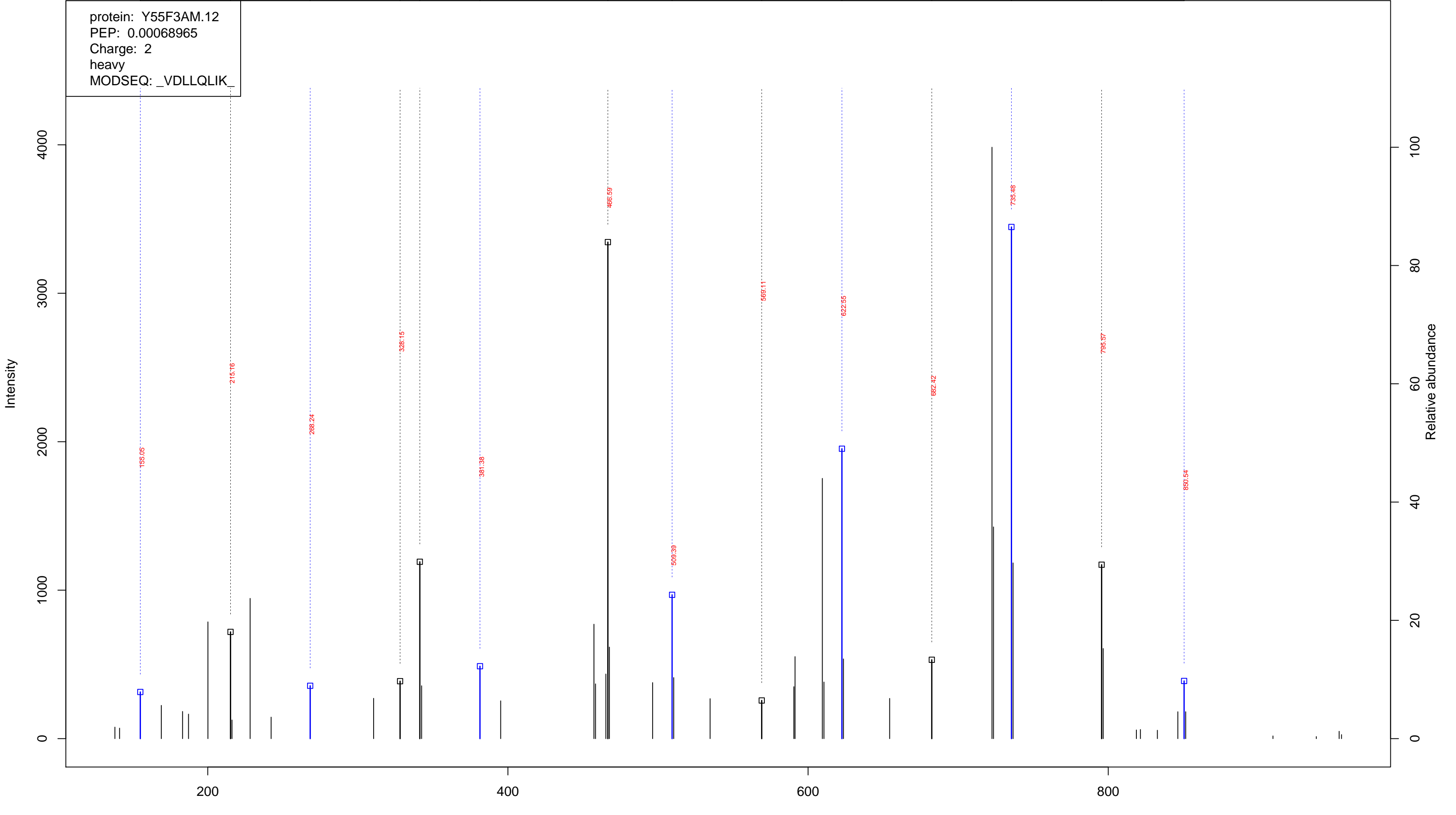


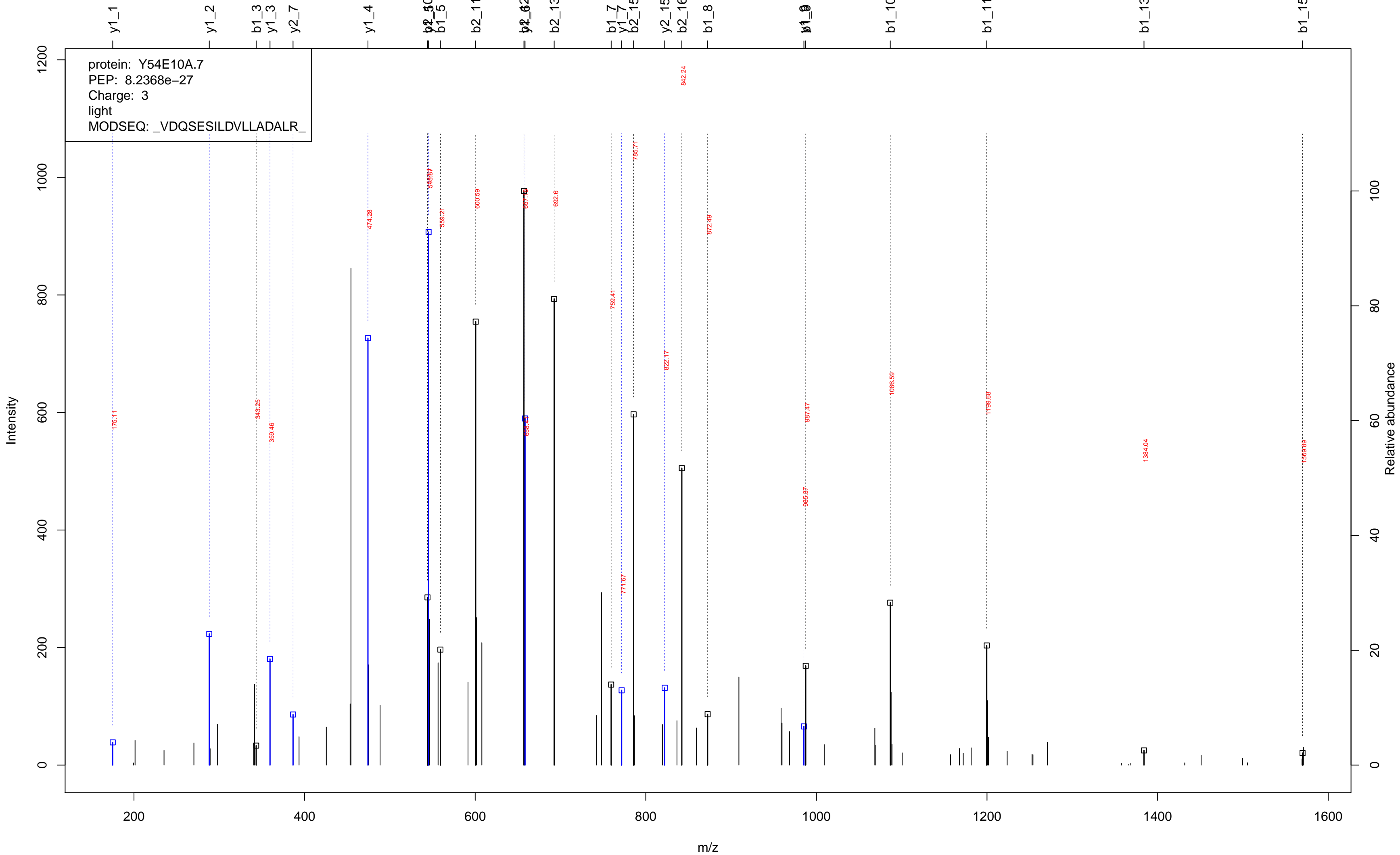


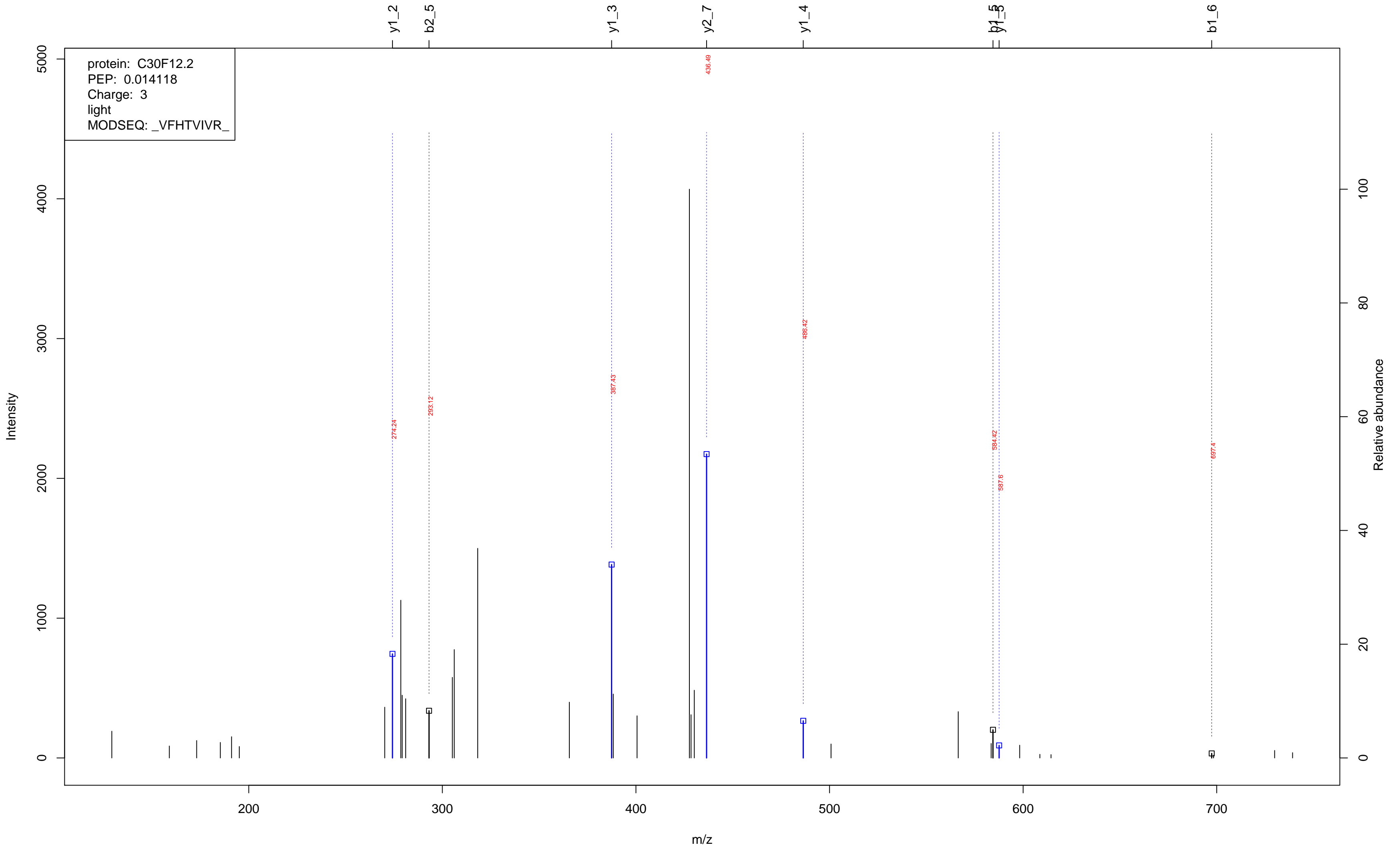


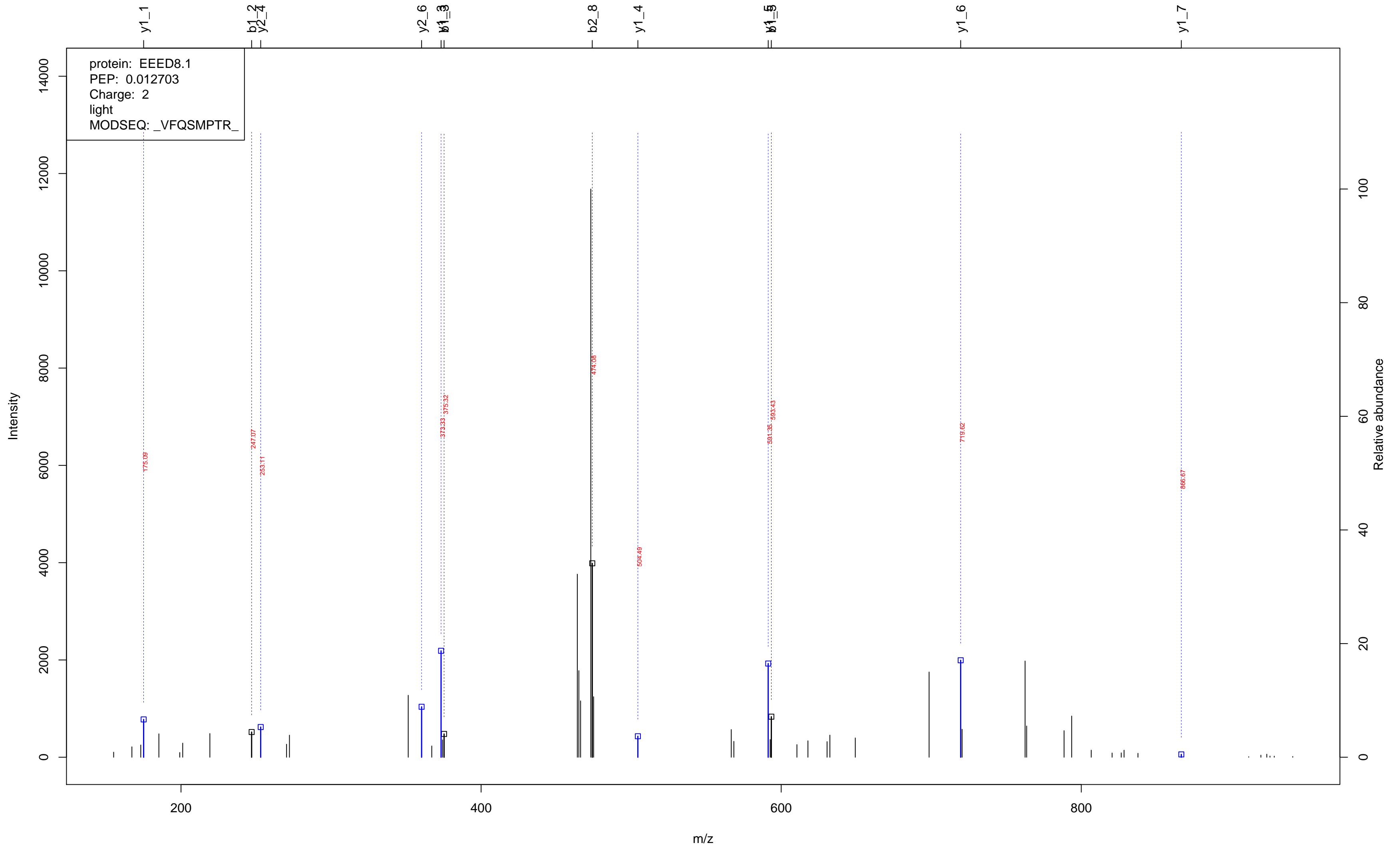
y1_1 b1_2 y1_2 b1_3 b2_6 y1_3 b2_8 y1_4 b1_5 y1_5 b1_6 y1_6 b1_7 y1_7

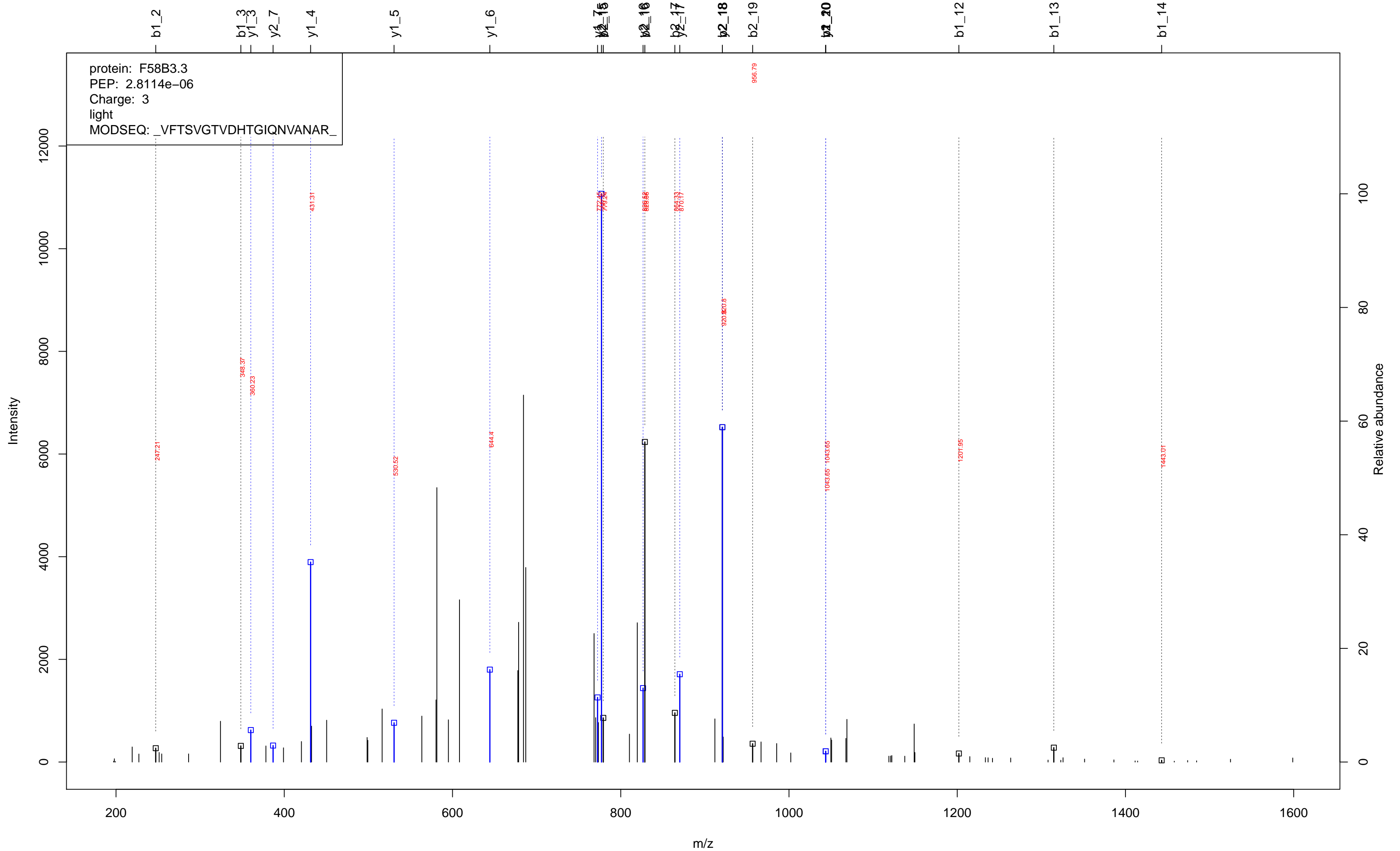
protein: Y55F3AM.12
PEP: 0.00068965
Charge: 2
heavy
MODSEQ: _VDLLQLIK_

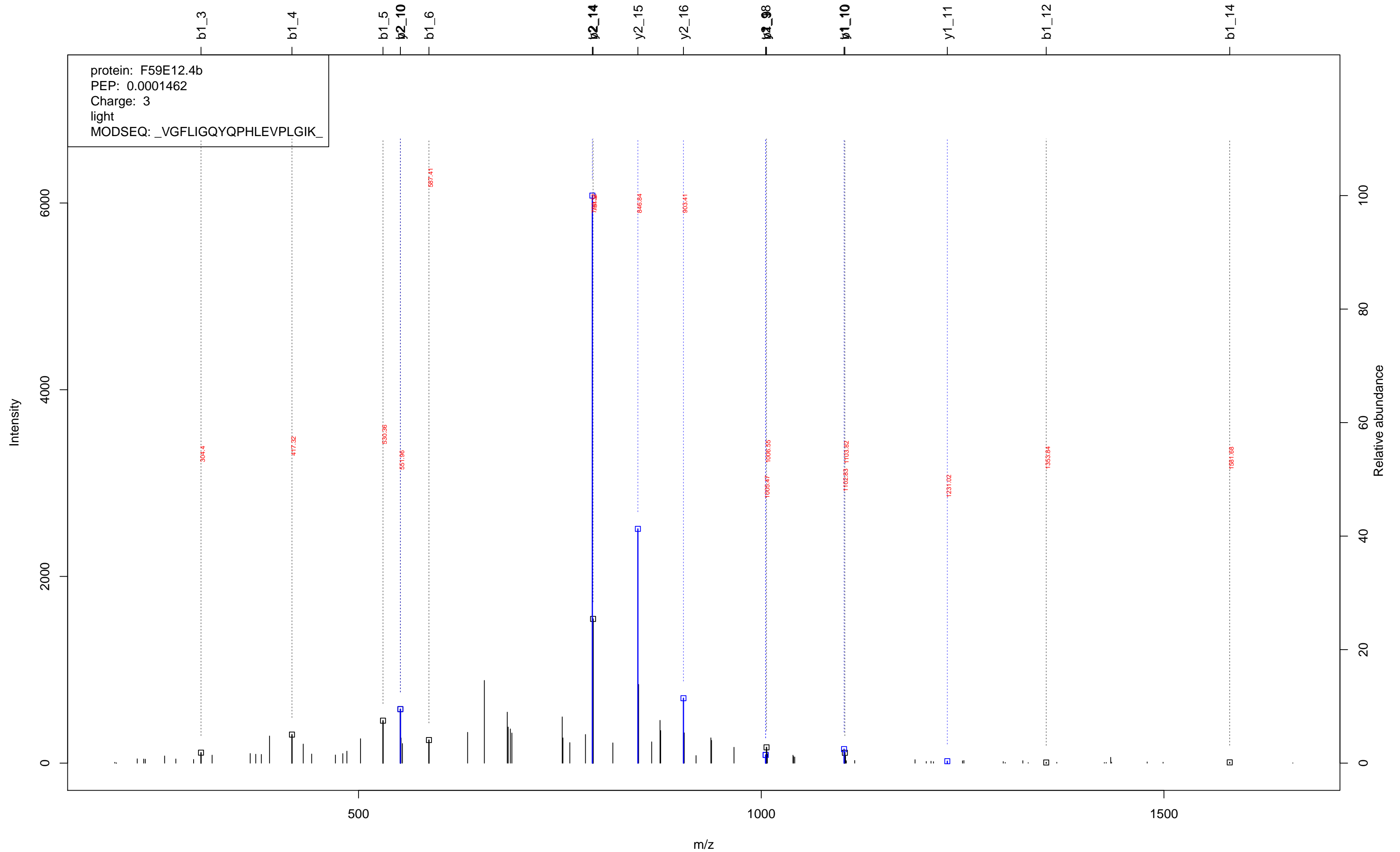


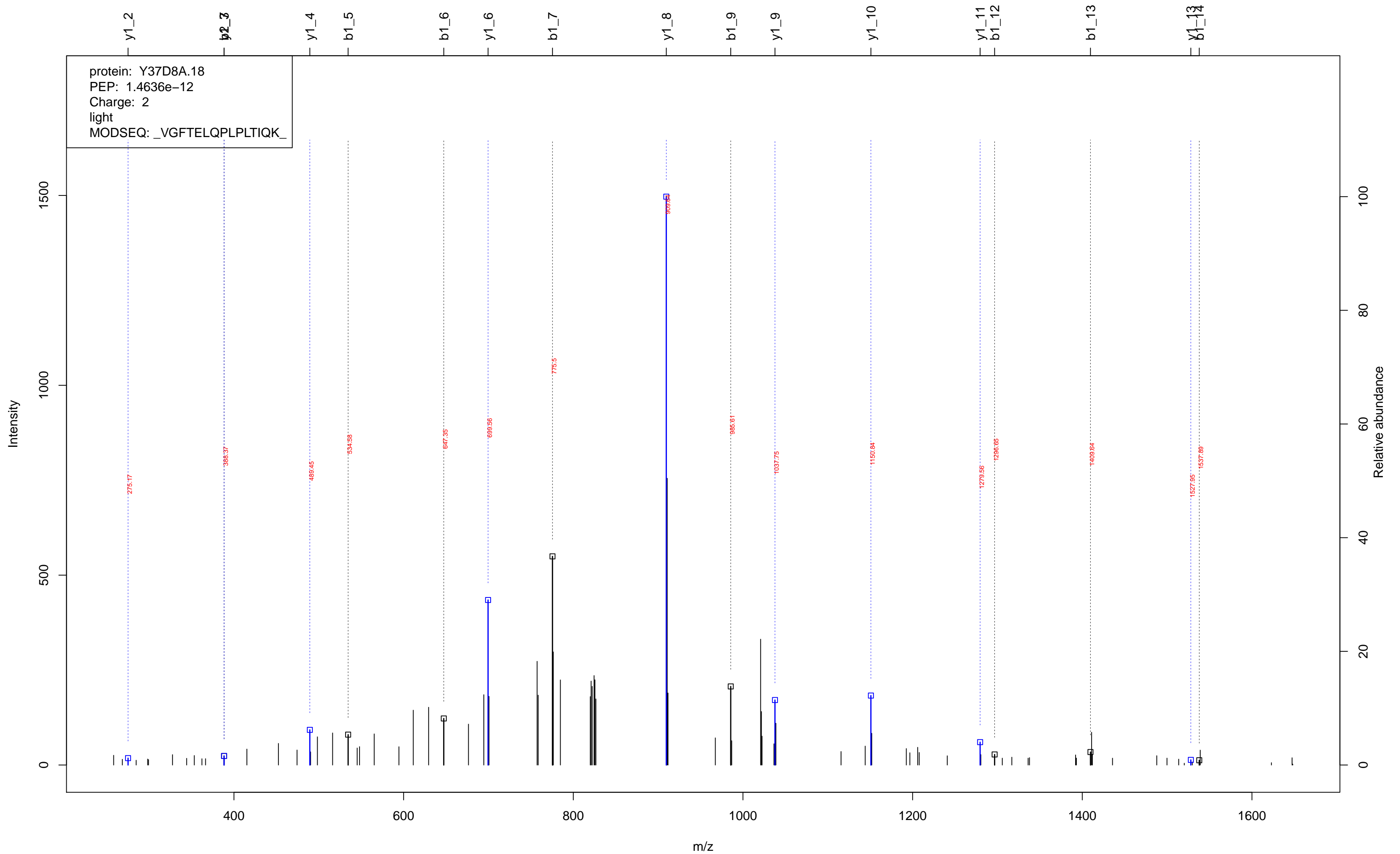


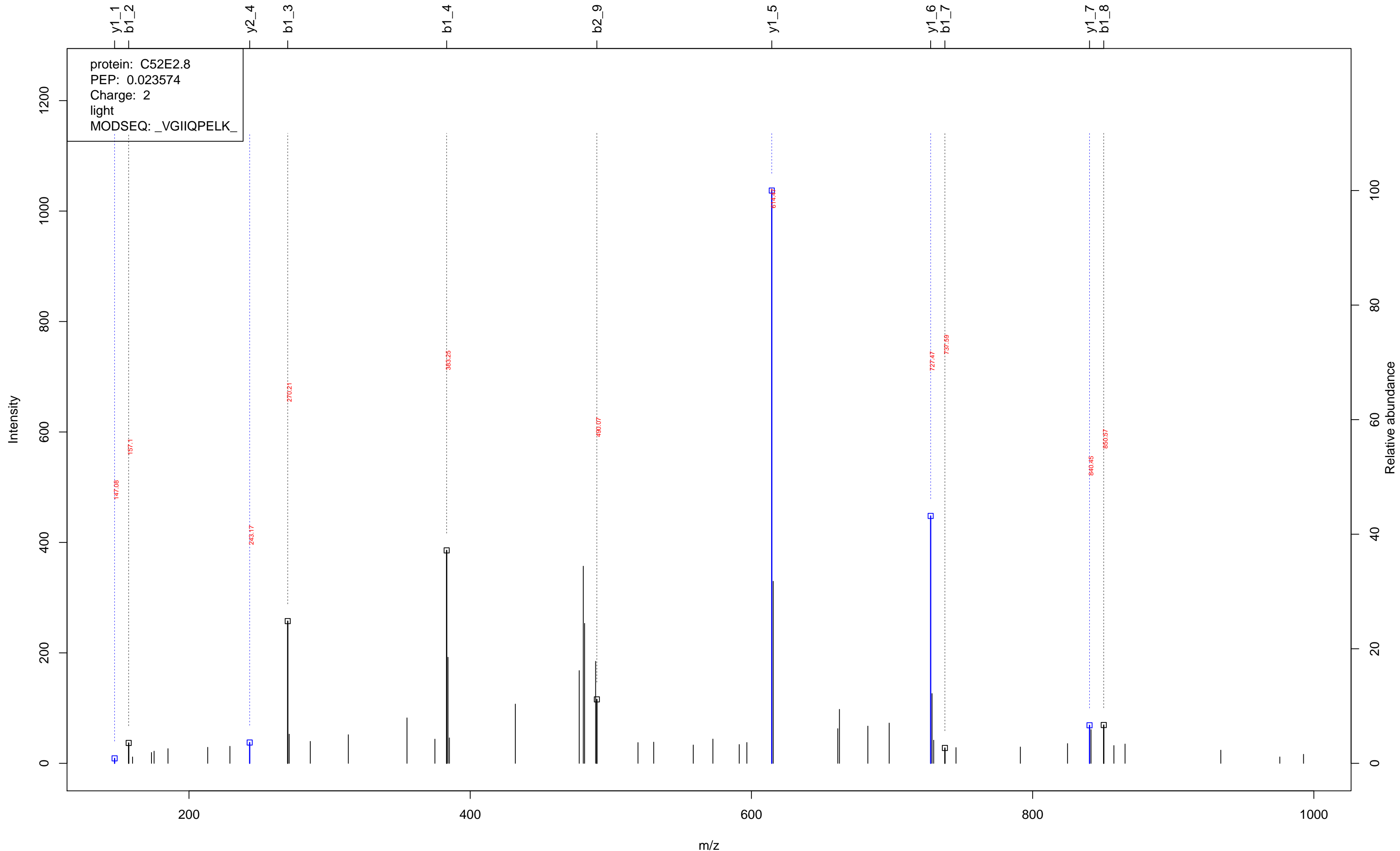












y1_1

y1_2

b2_5

y2_6

b2_7

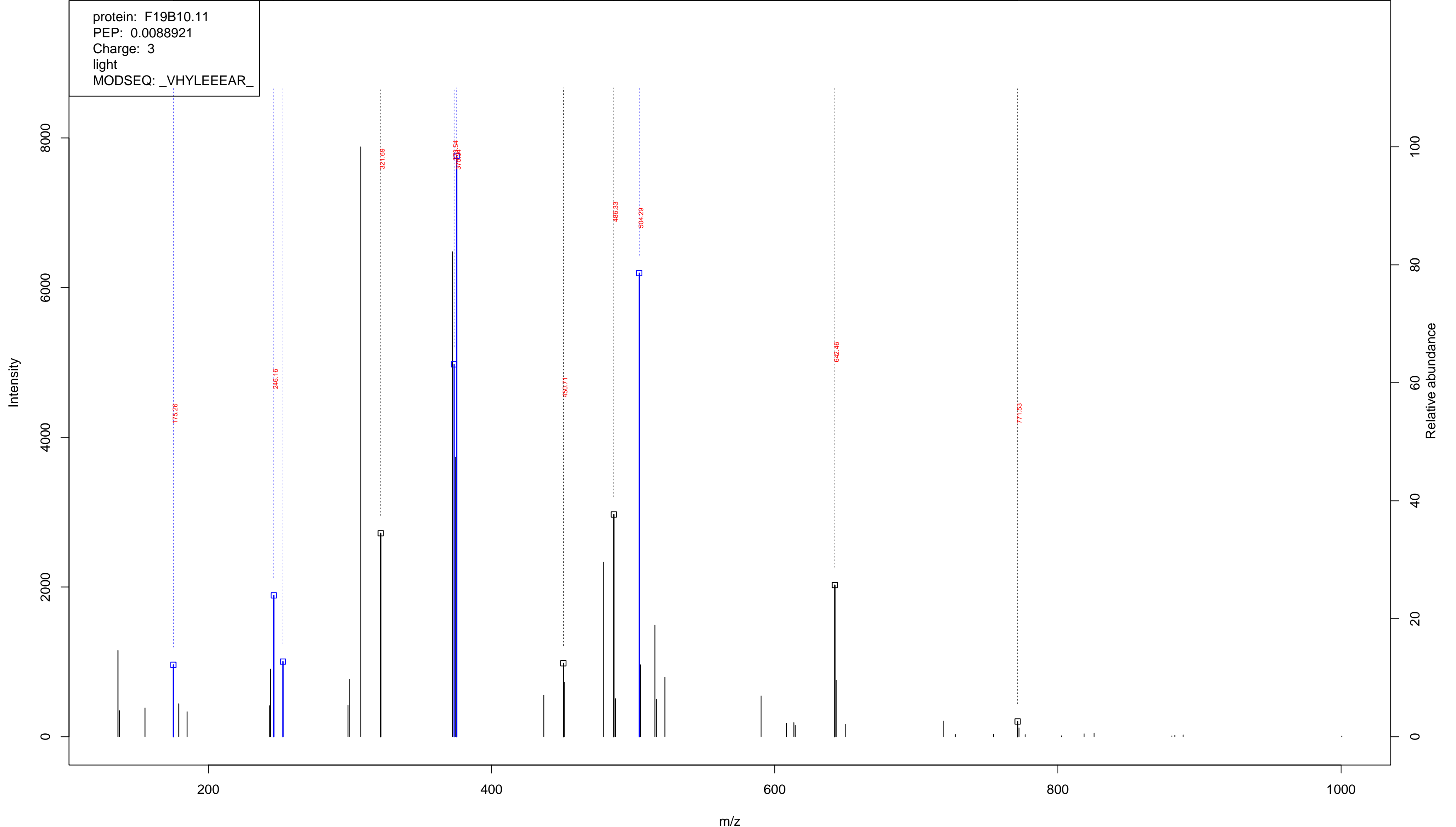
b2_8

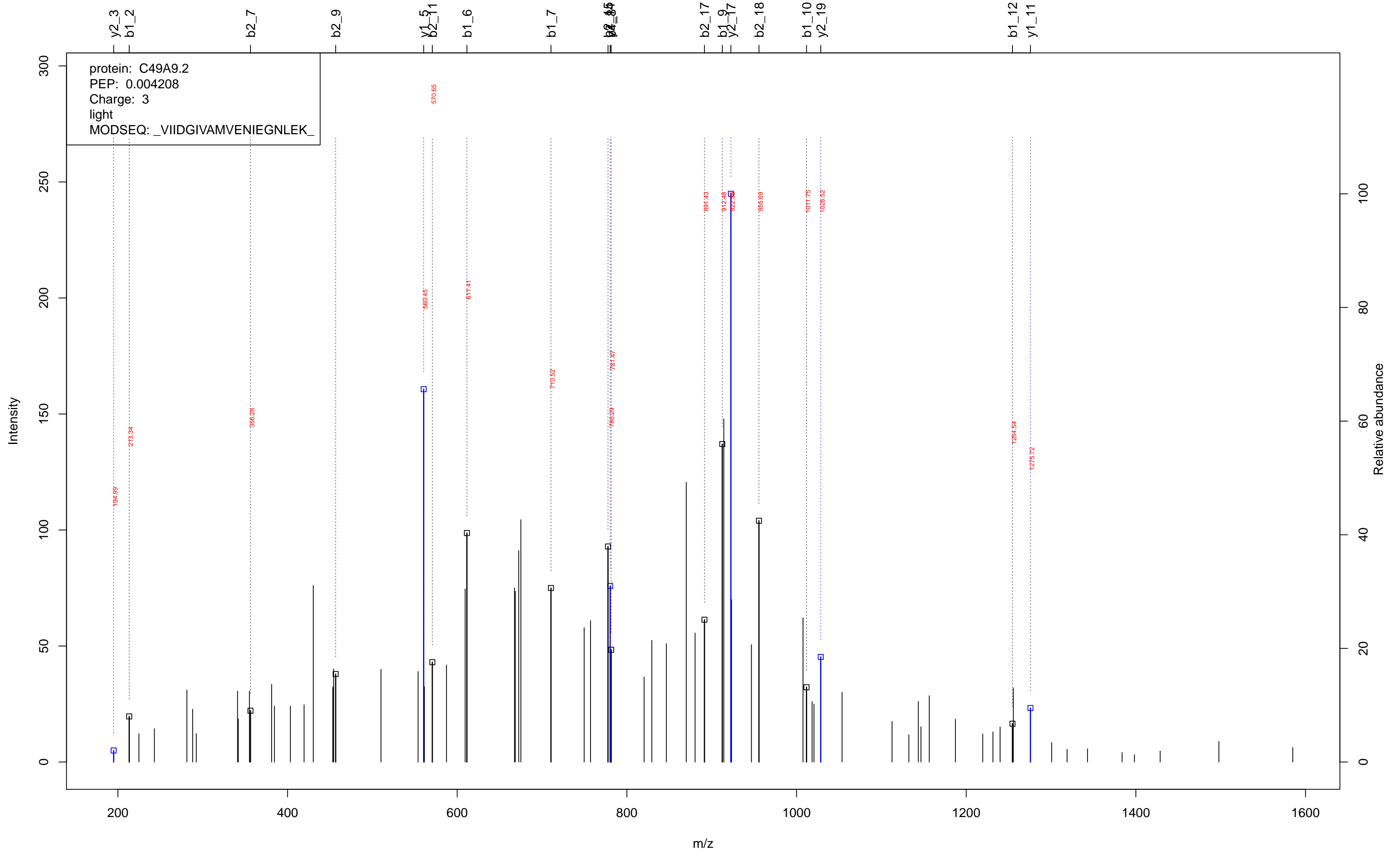
y1_4

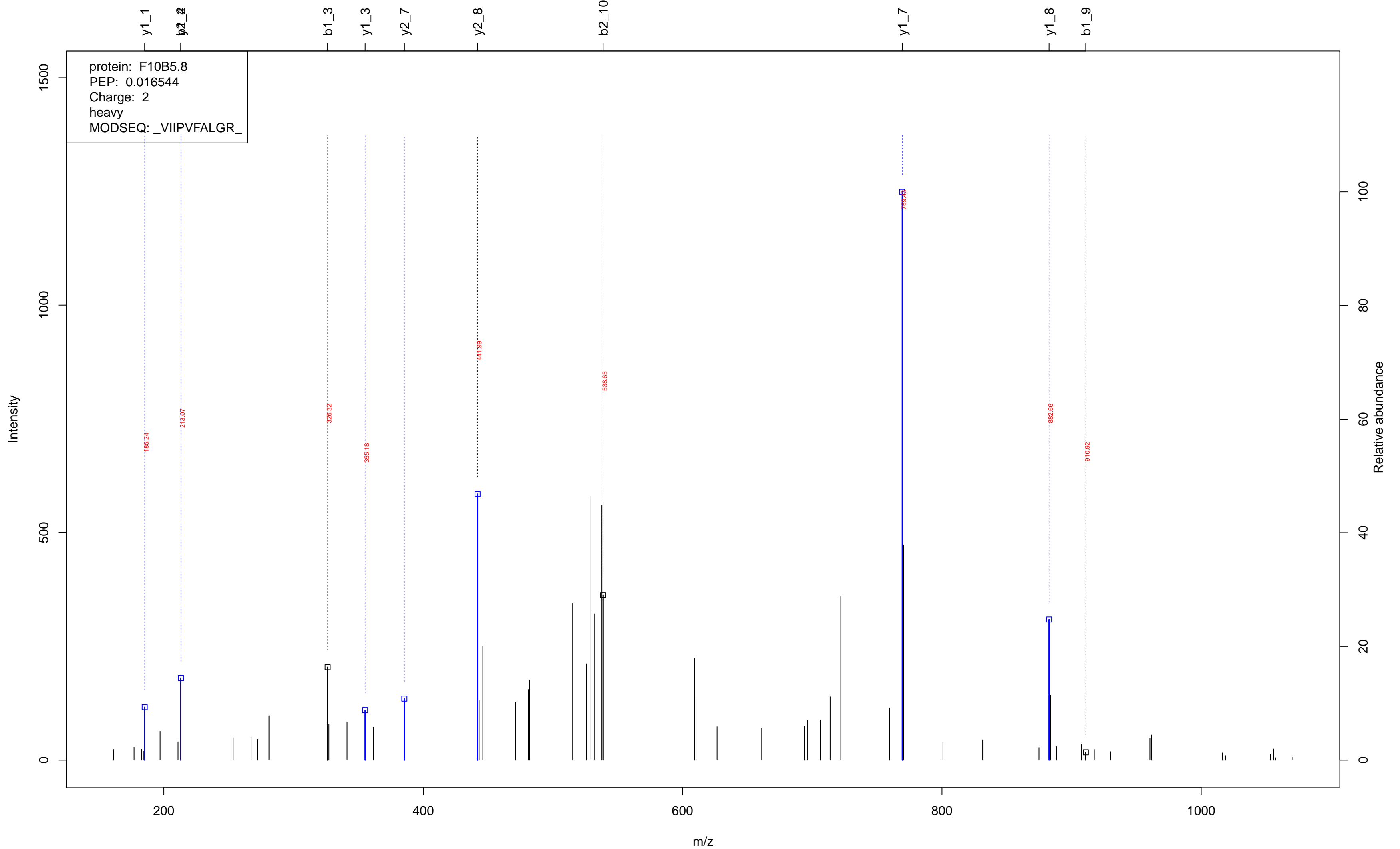
b1_5

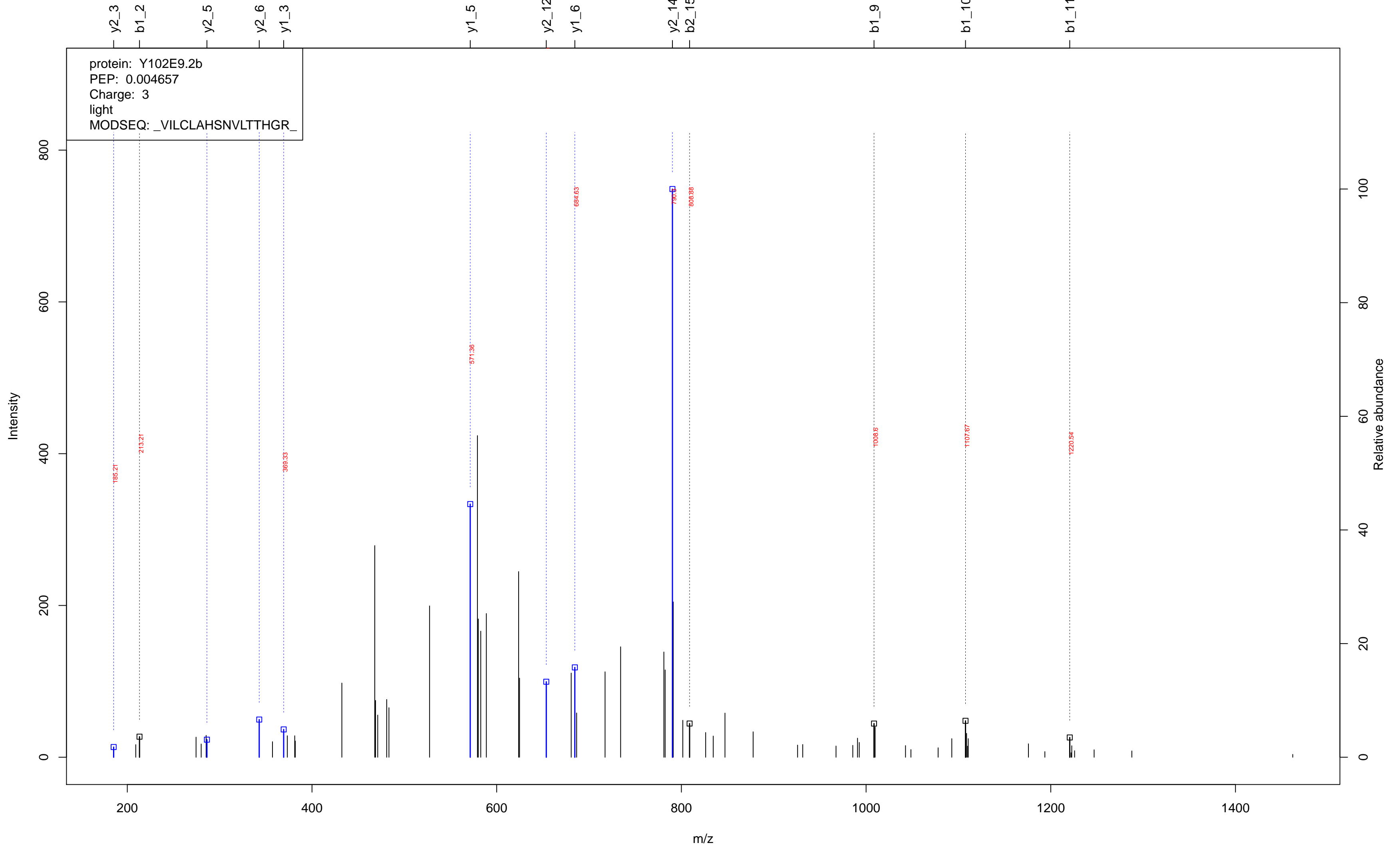
b1_6

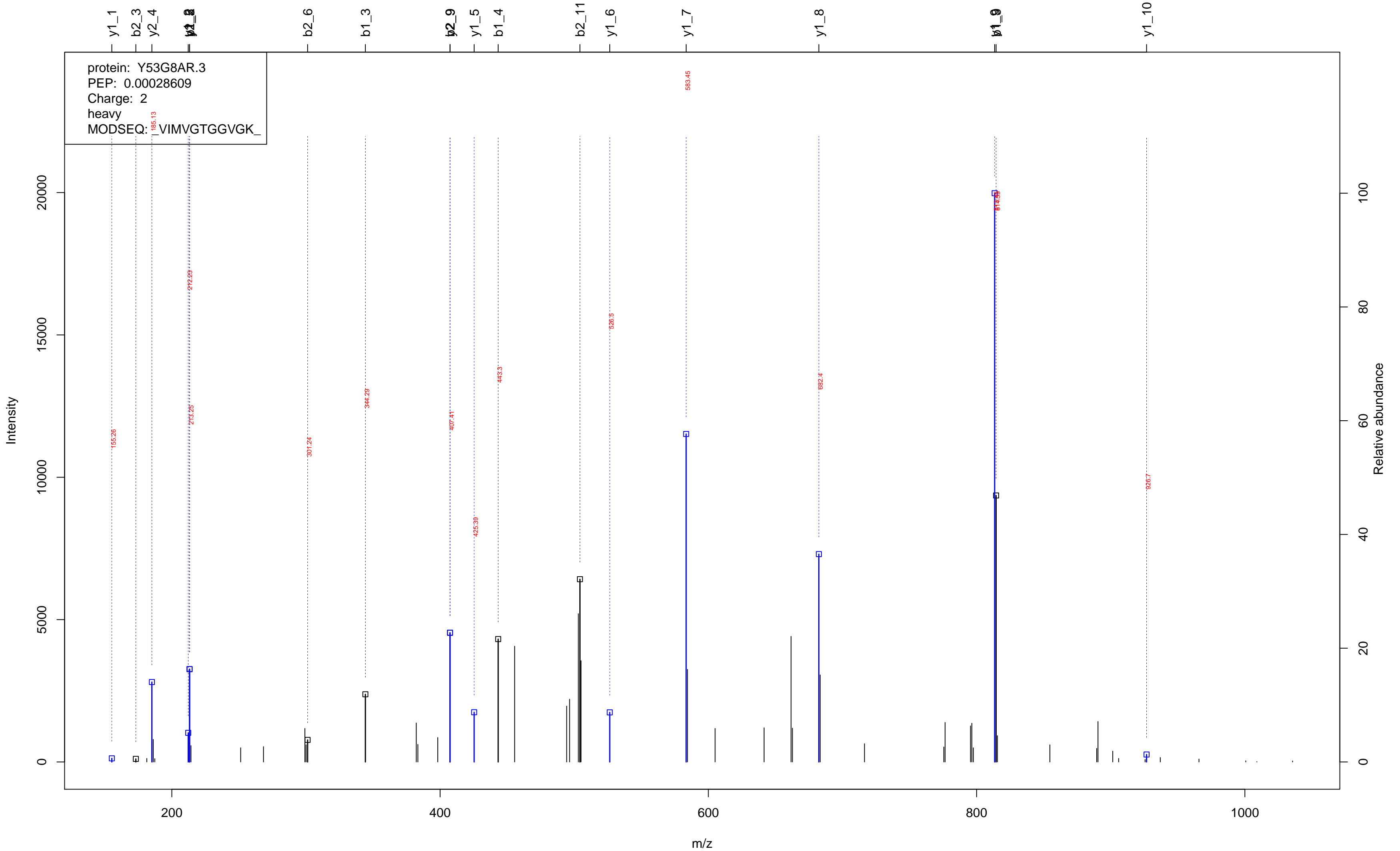
protein: F19B10.11
PEP: 0.0088921
Charge: 3
light
MODSEQ: _VHYLEEEAR_

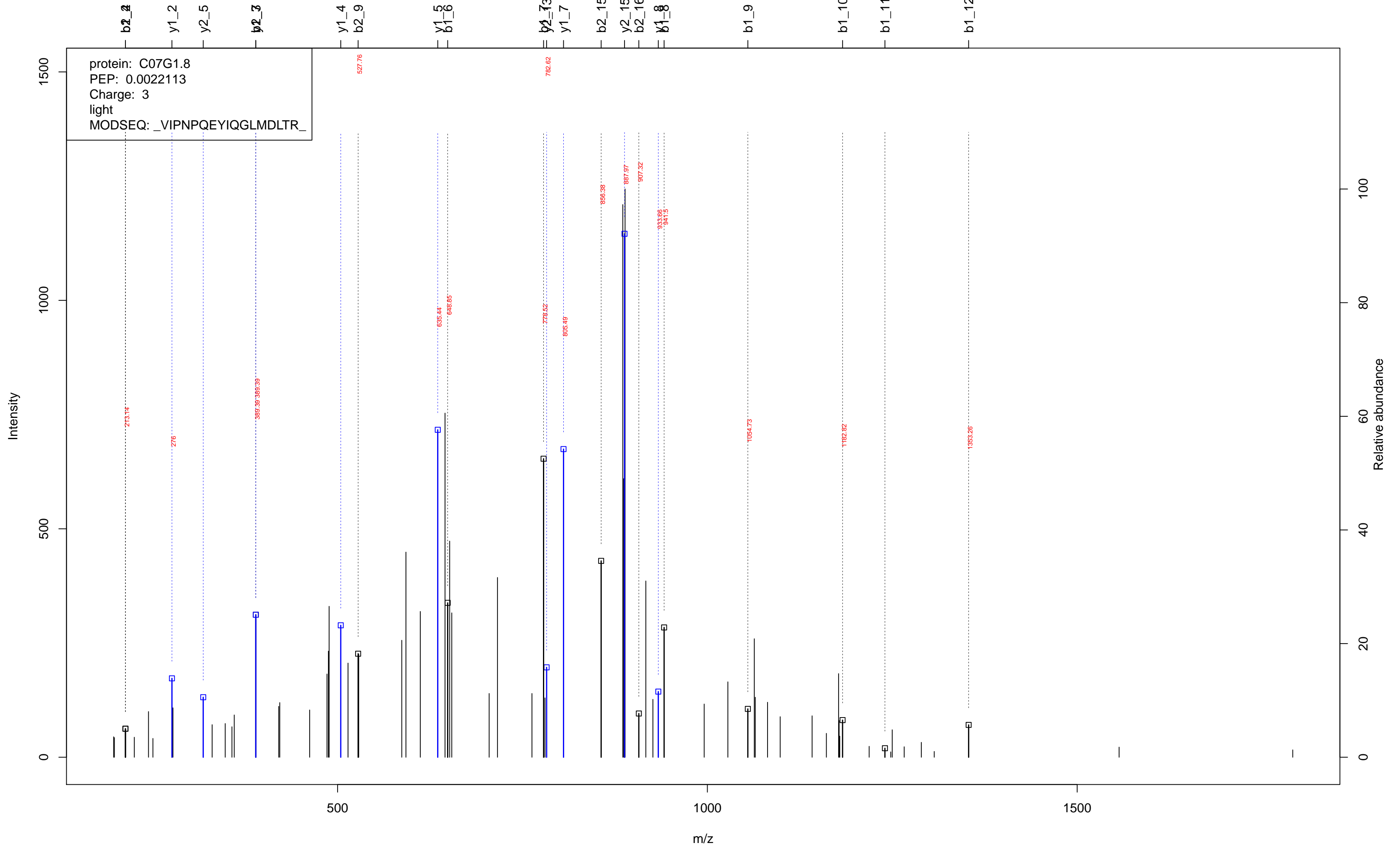


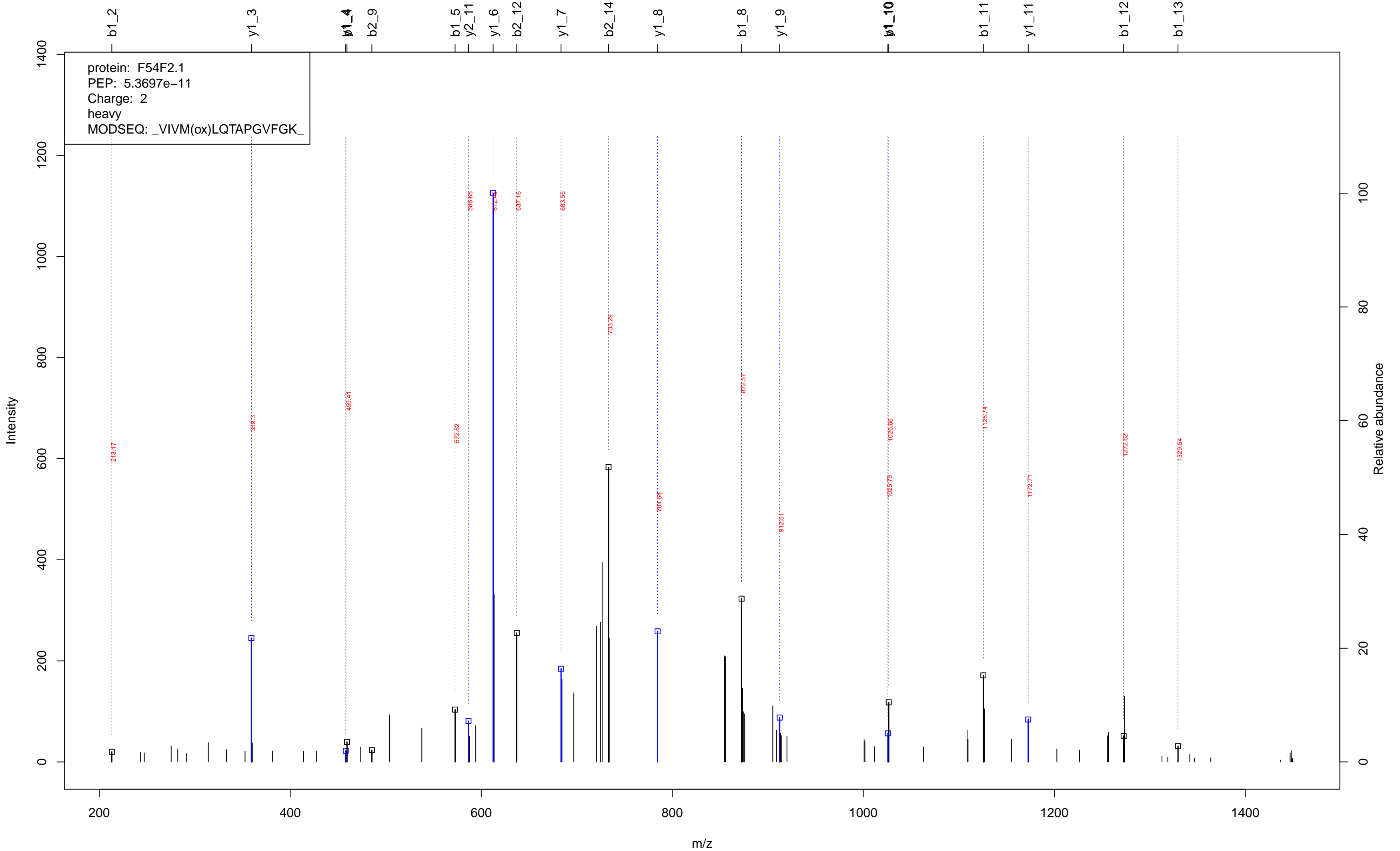


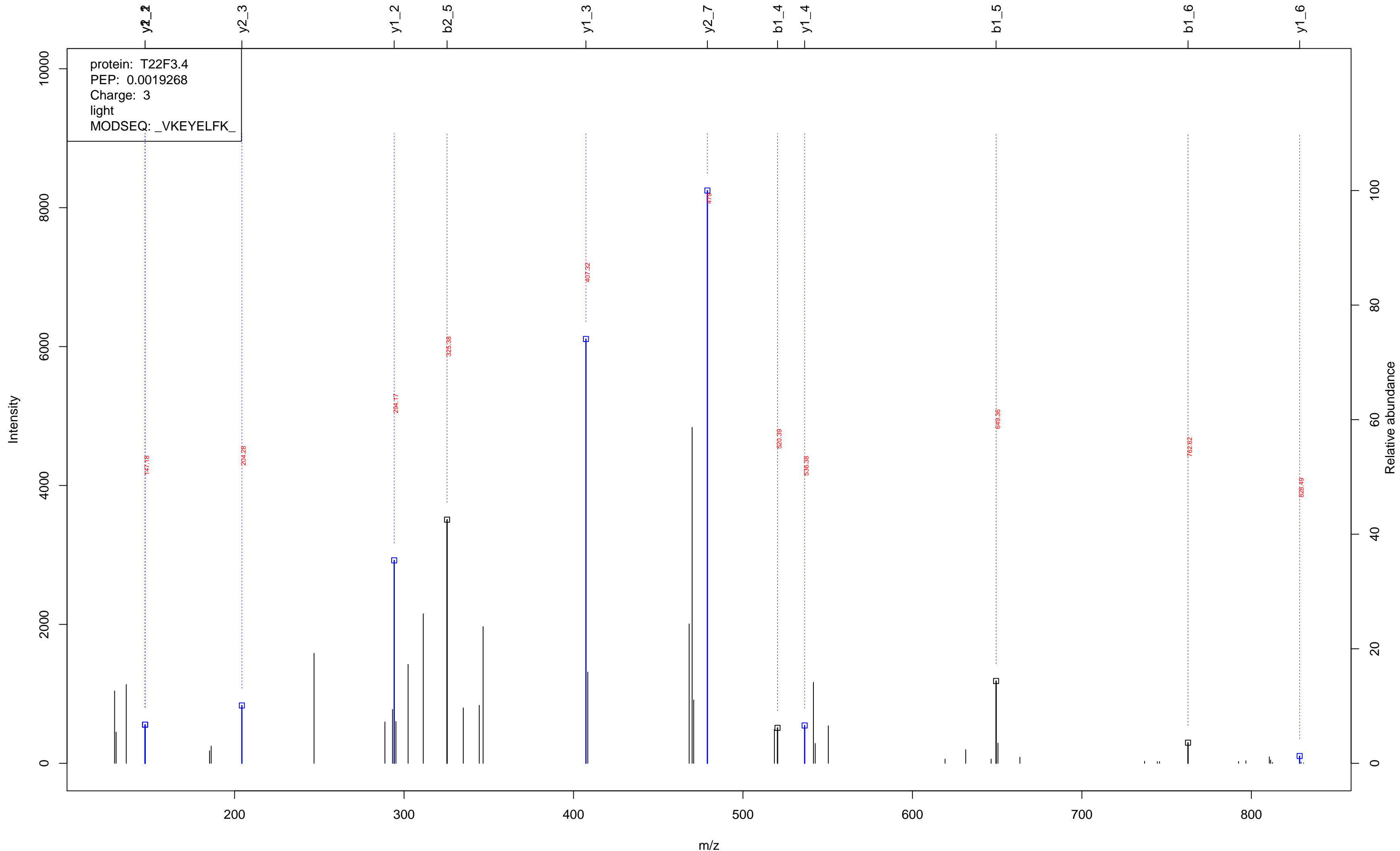


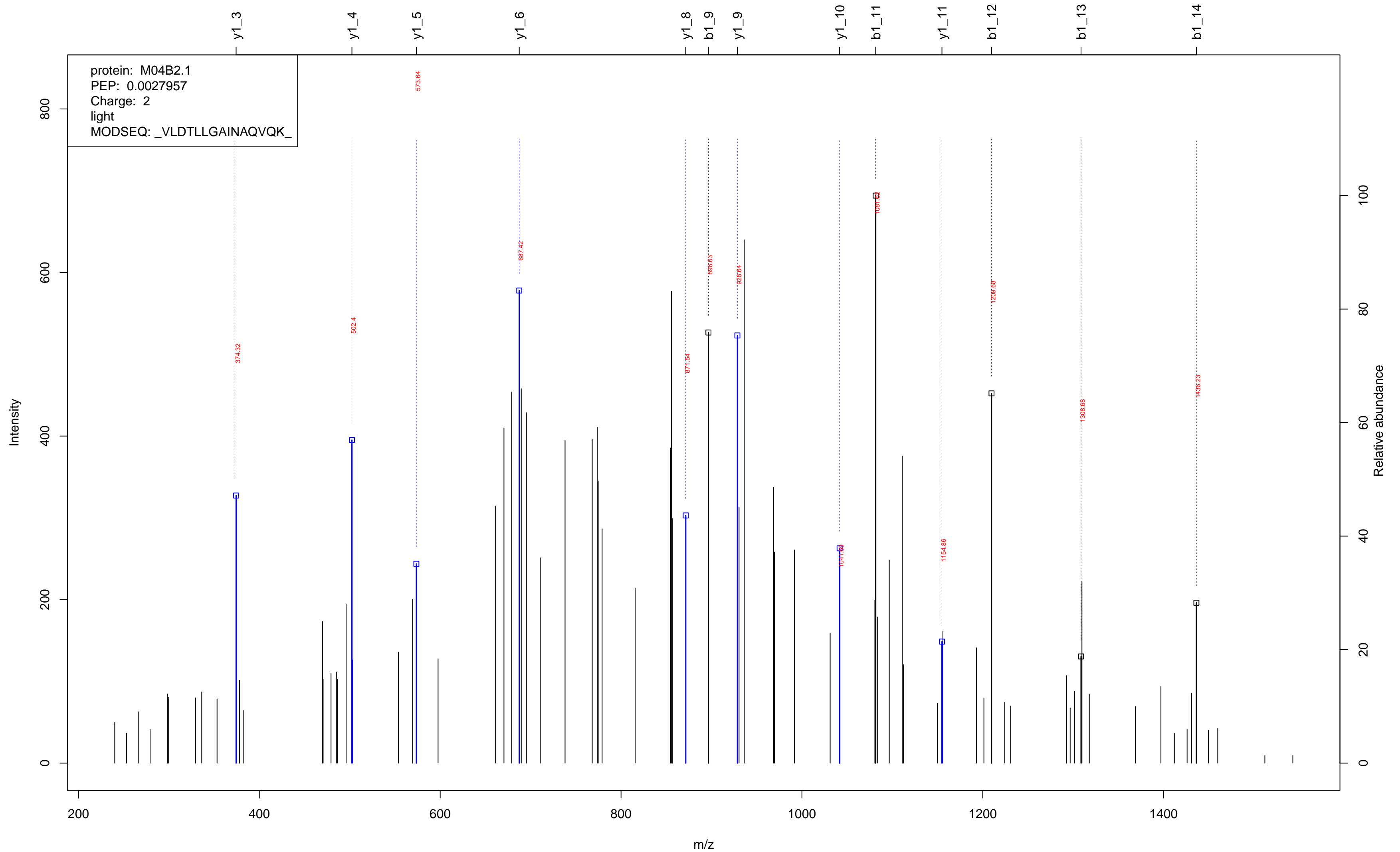








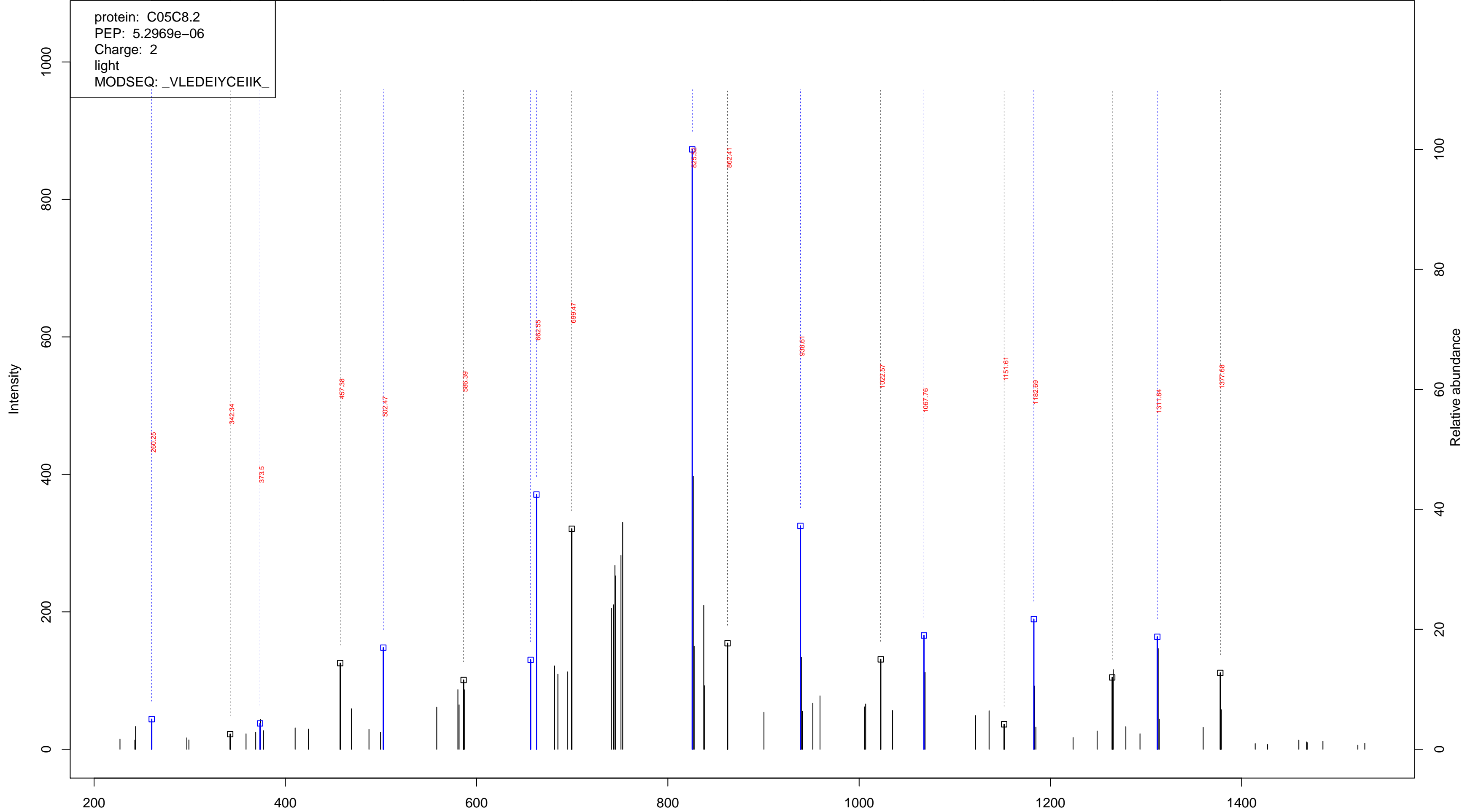


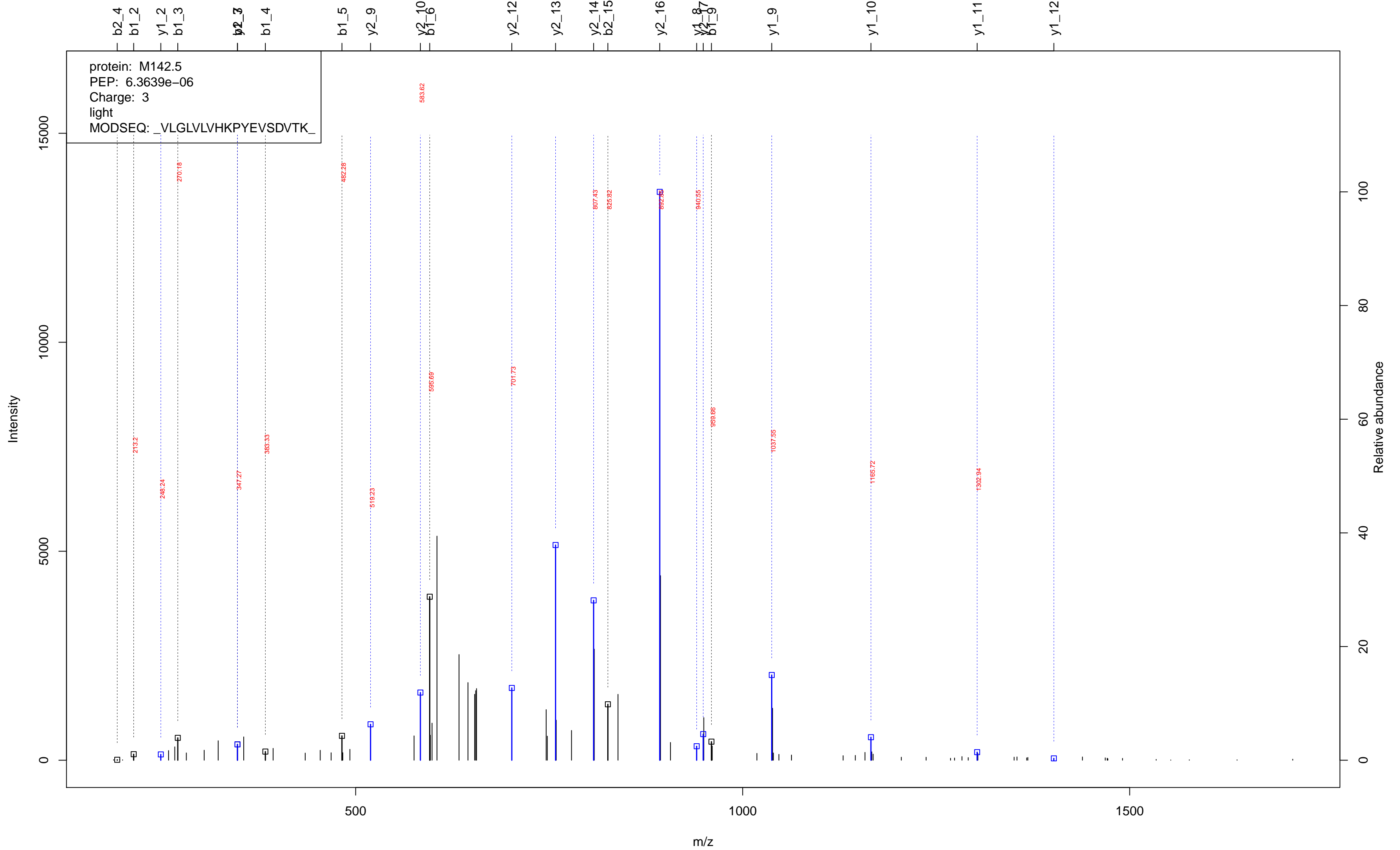


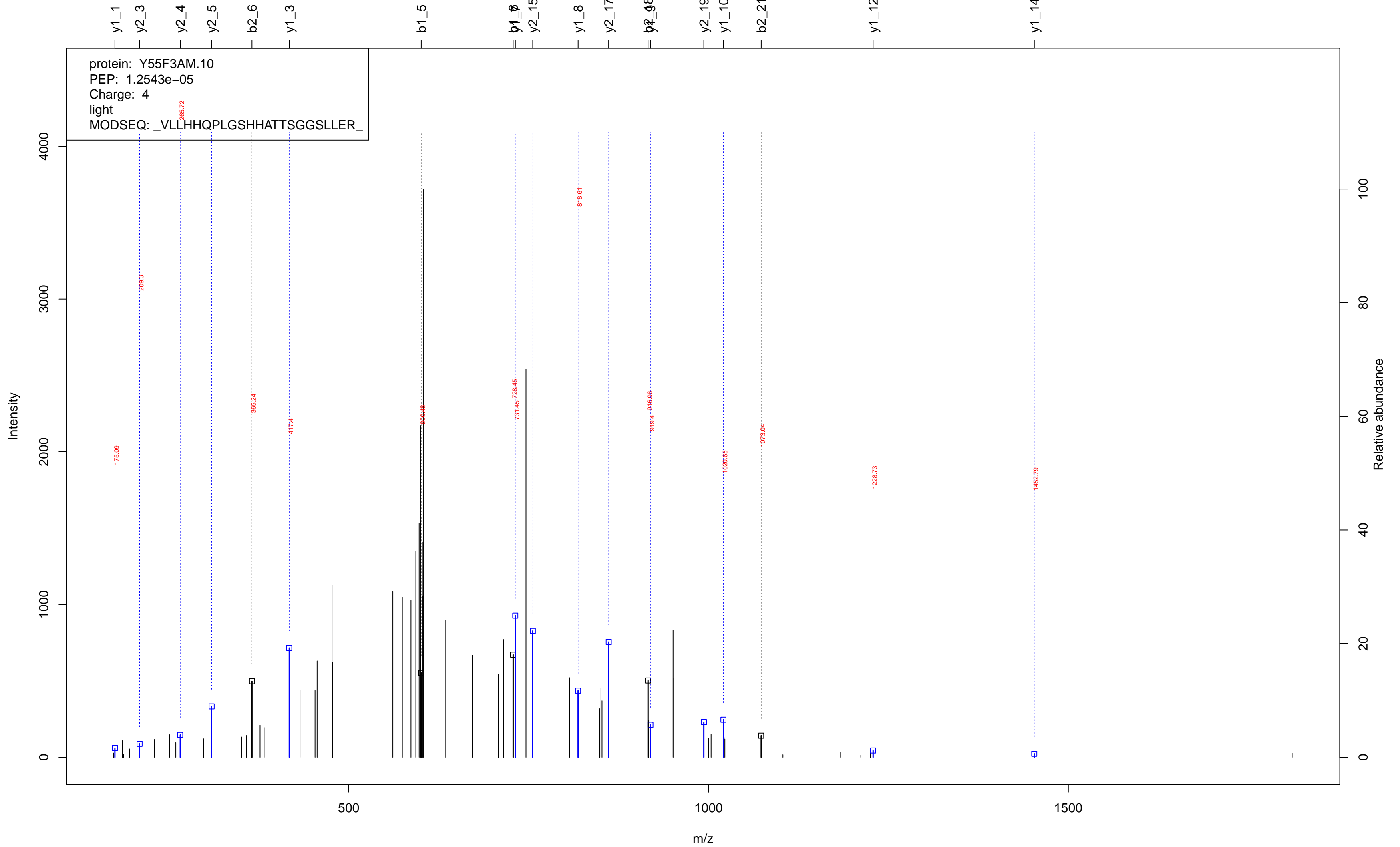
380

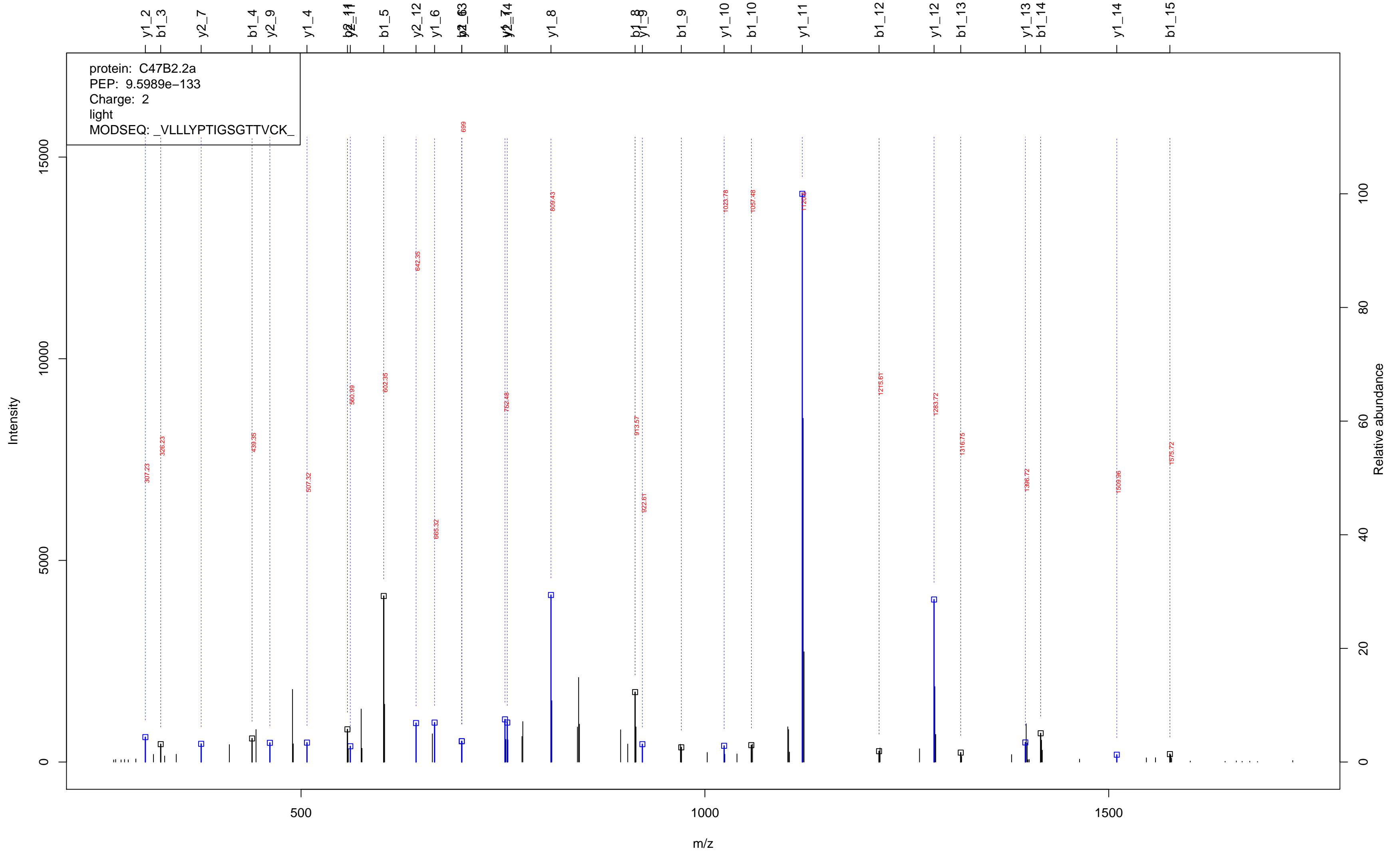
y1_2 b1_3 y1_3 b1_4 y1_4 b1_5 y1_5 b1_6 y1_6 b1_7 y1_7 b1_8 y1_8 b1_9 y1_9 b1_10 y1_10 b1_11

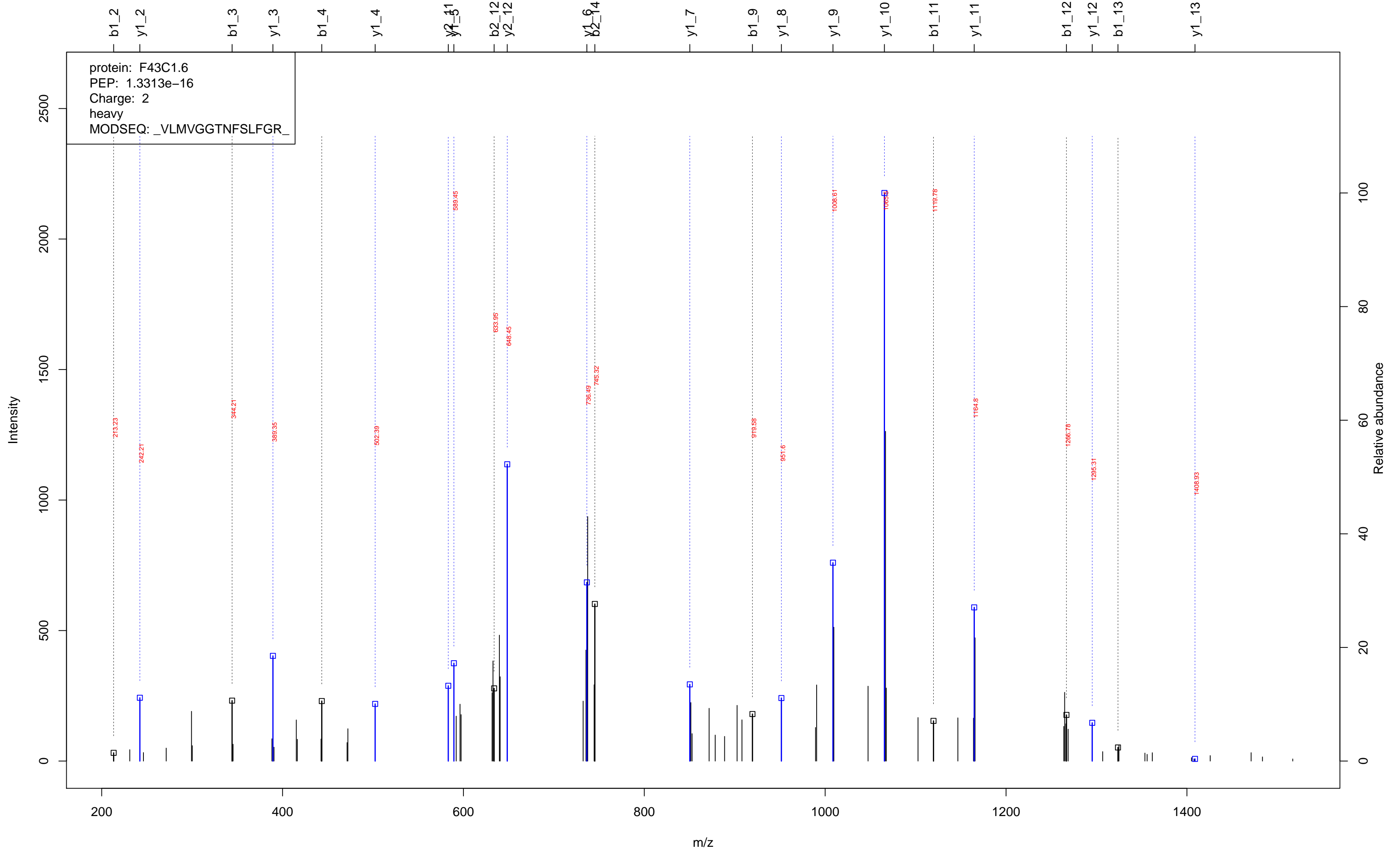
protein: C05C8.2
PEP: 5.2969e-06
Charge: 2
light
MODSEQ: _VLEDEIYCEIIK_

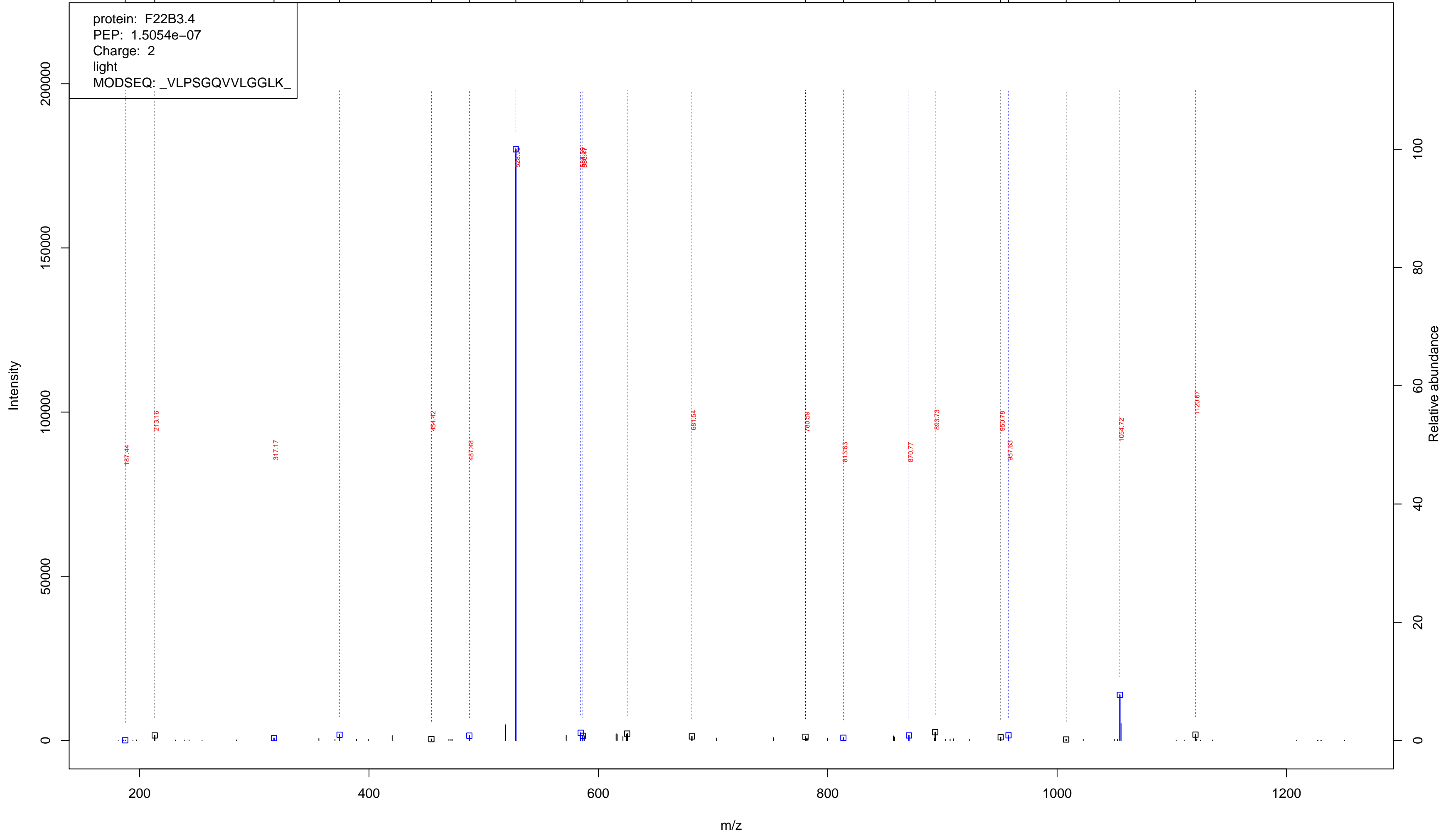


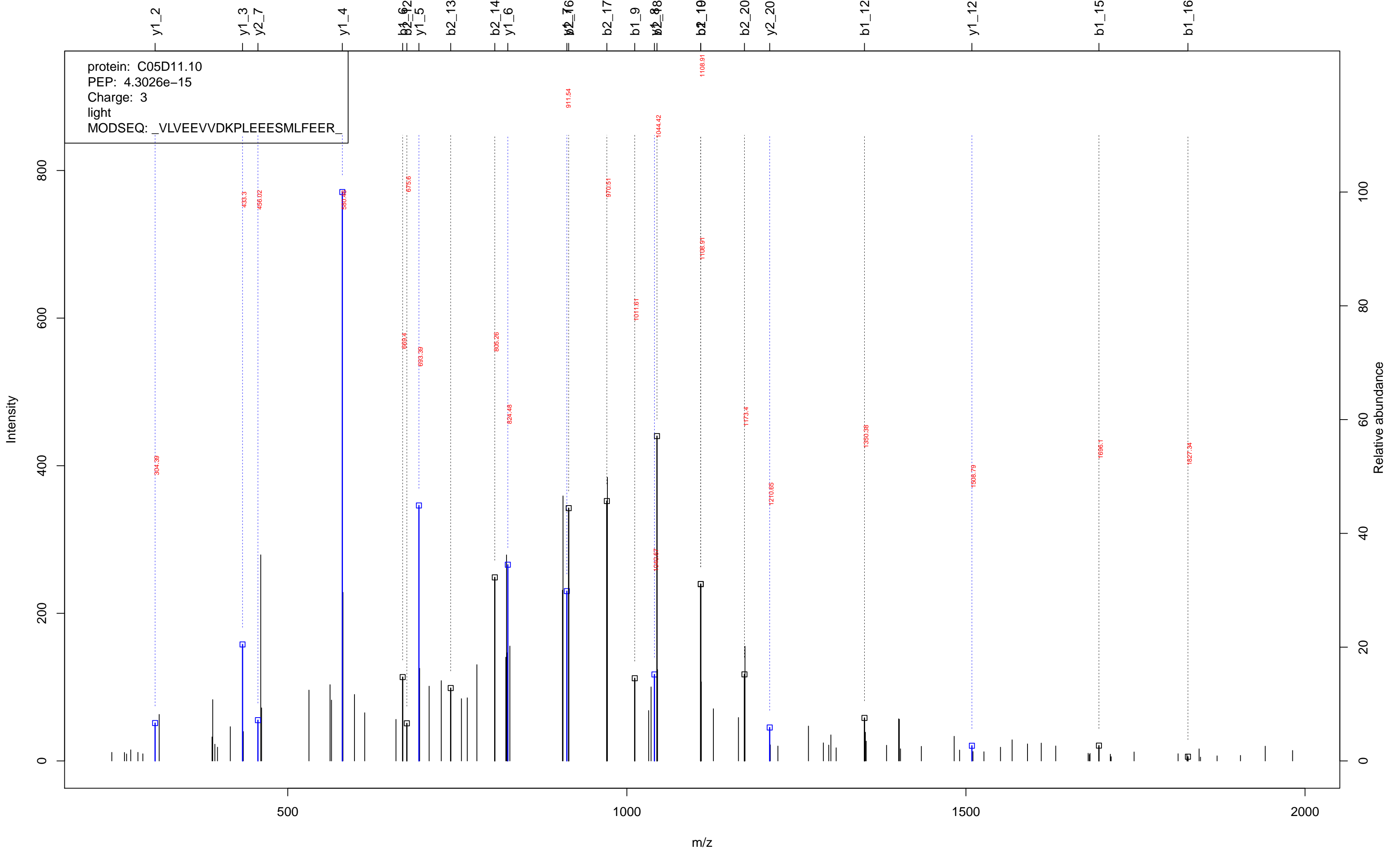


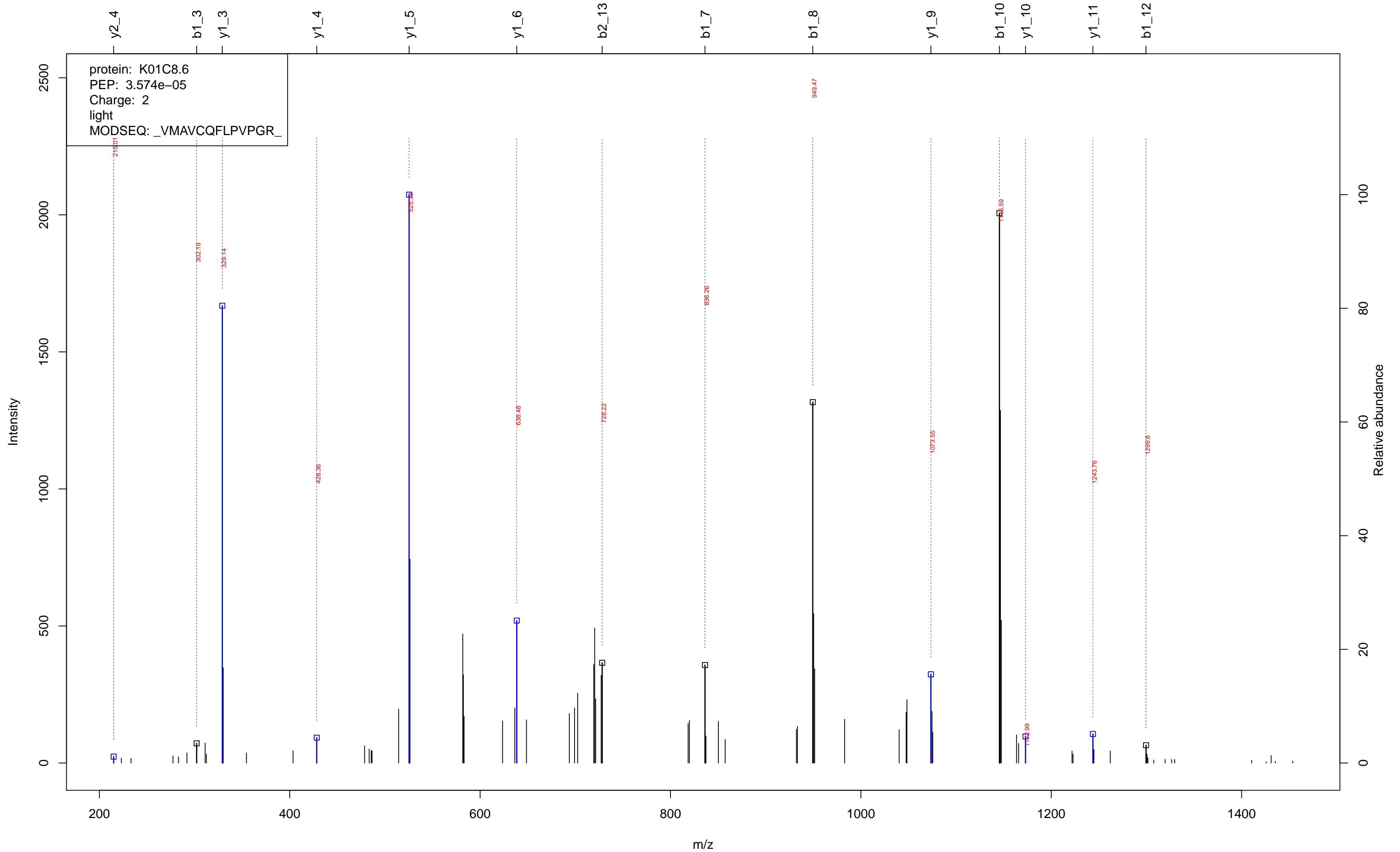


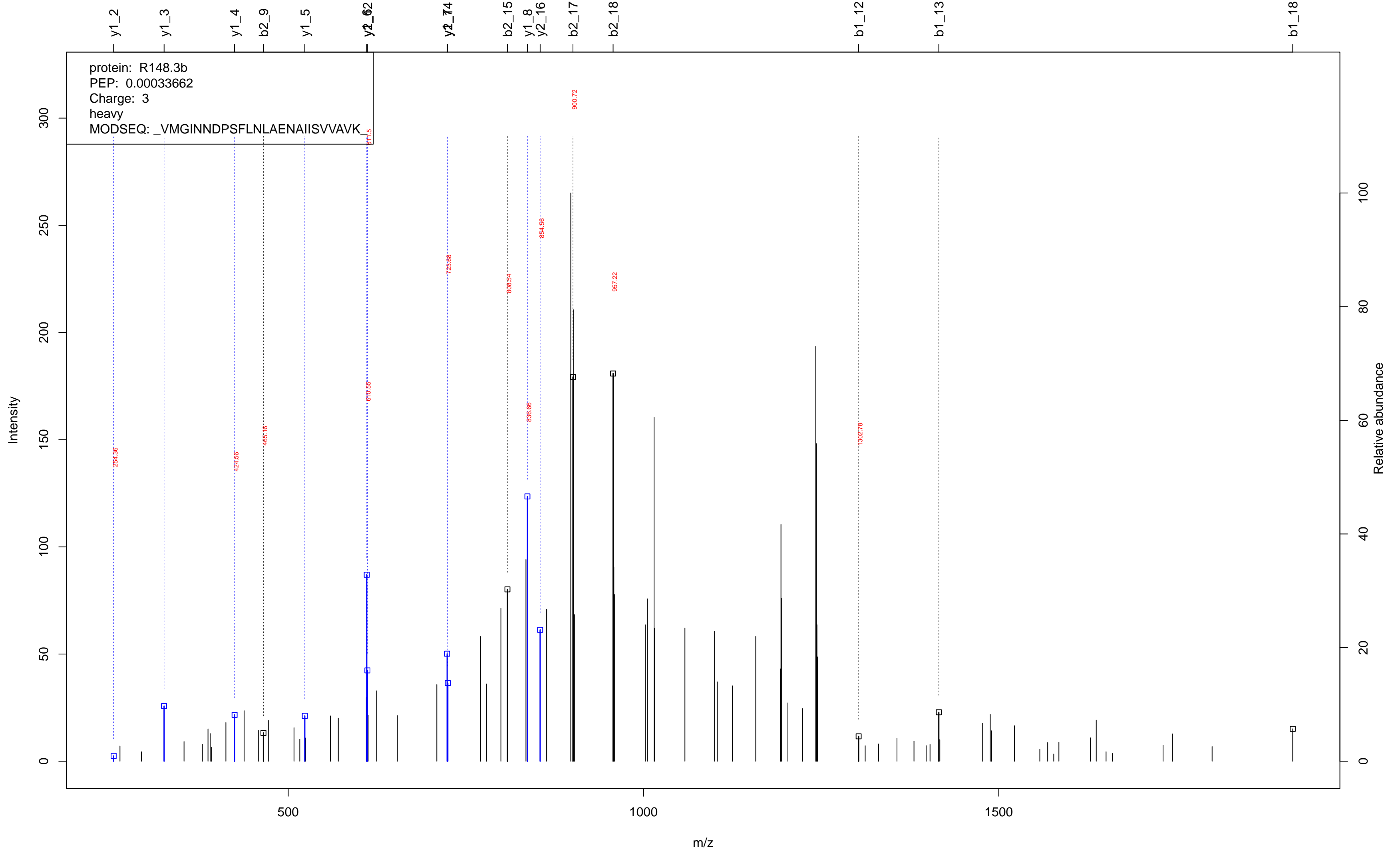


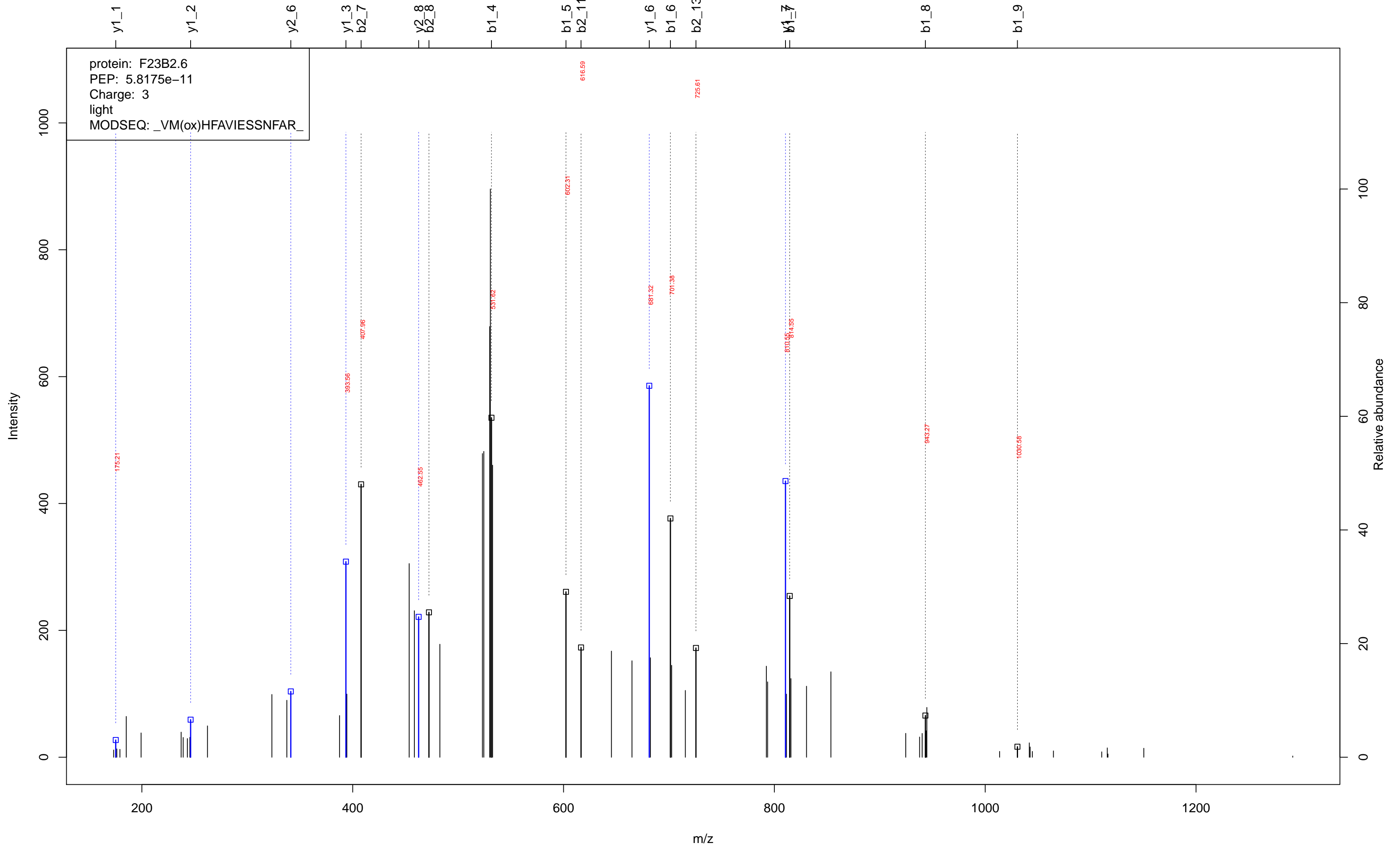


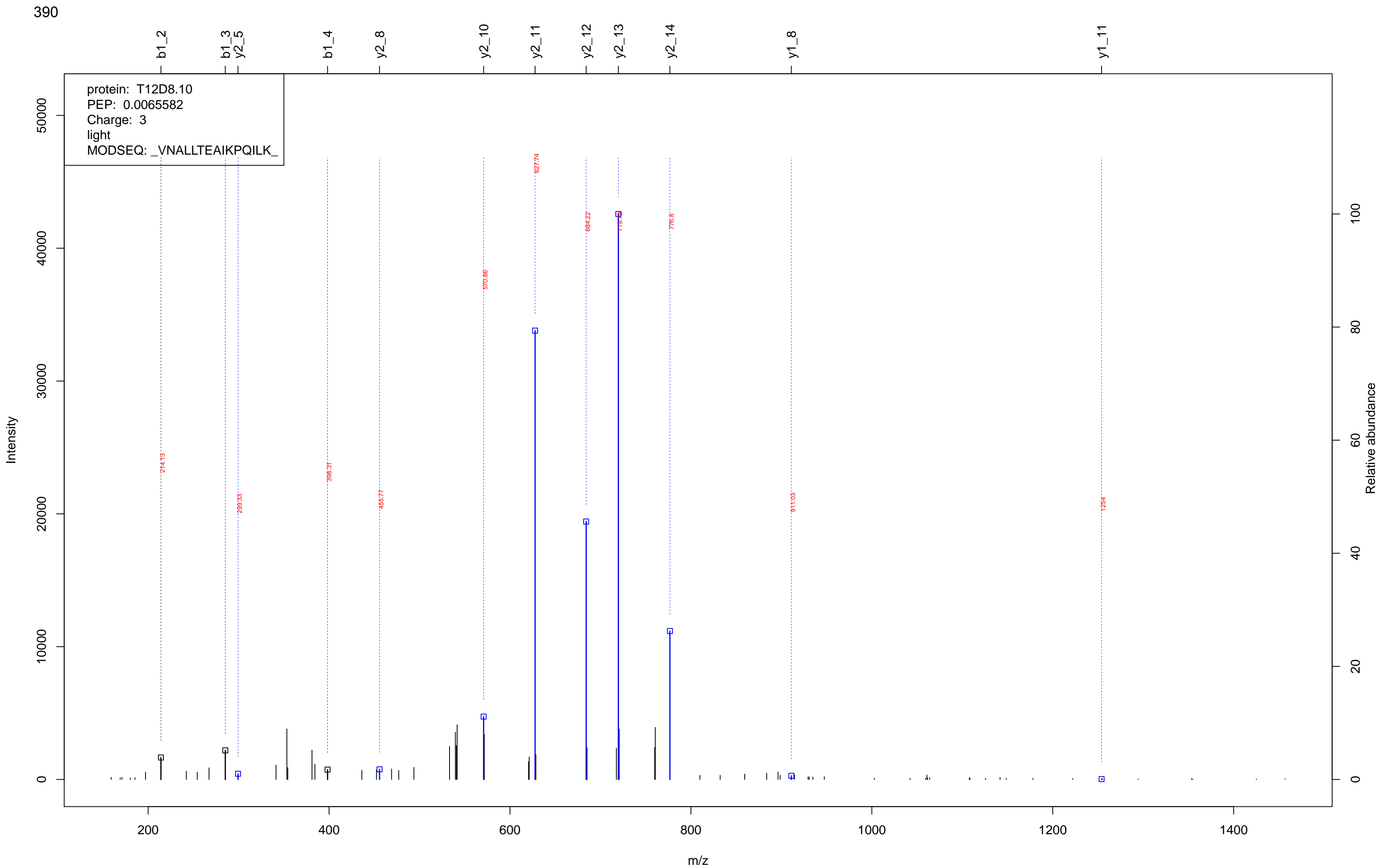


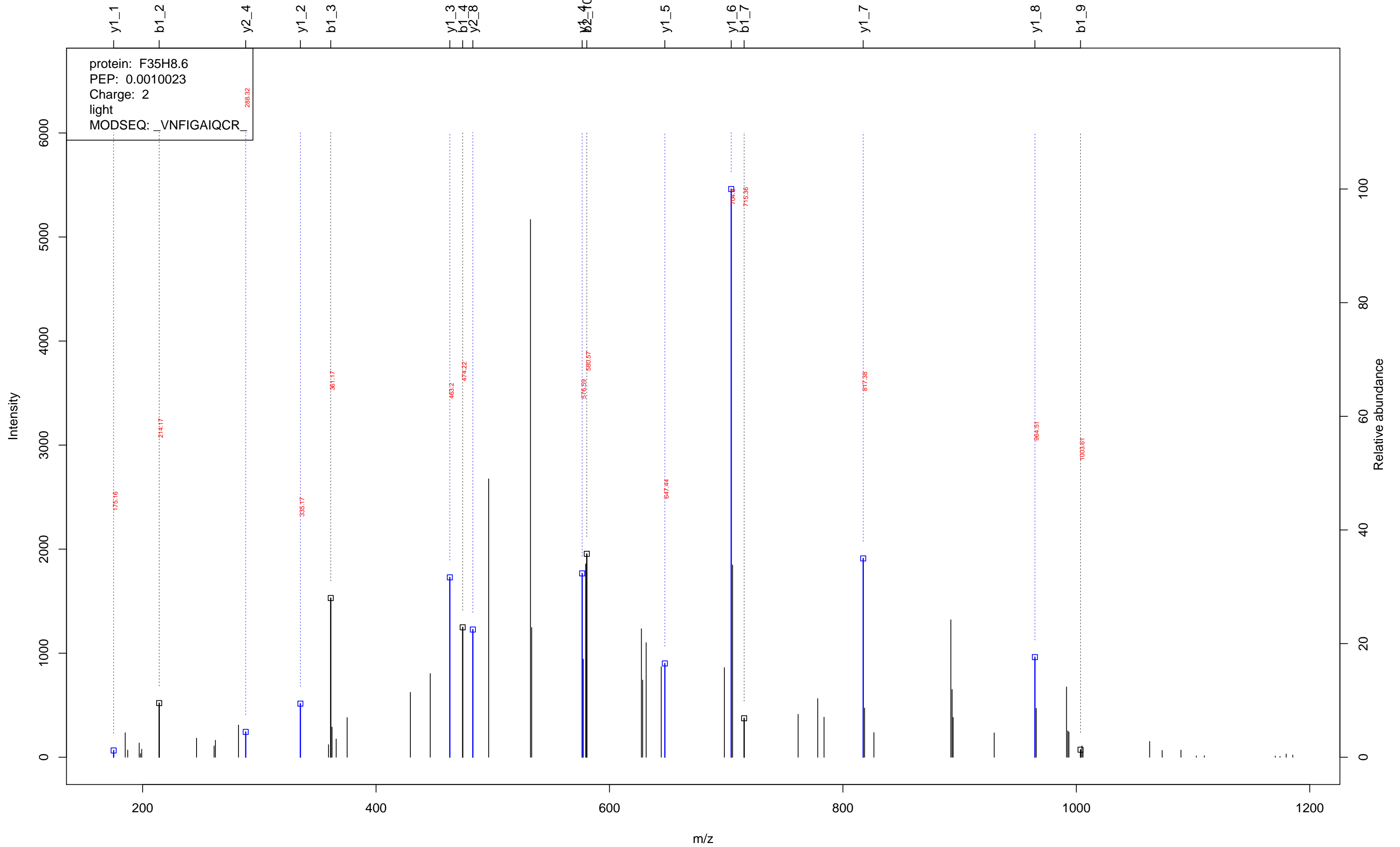


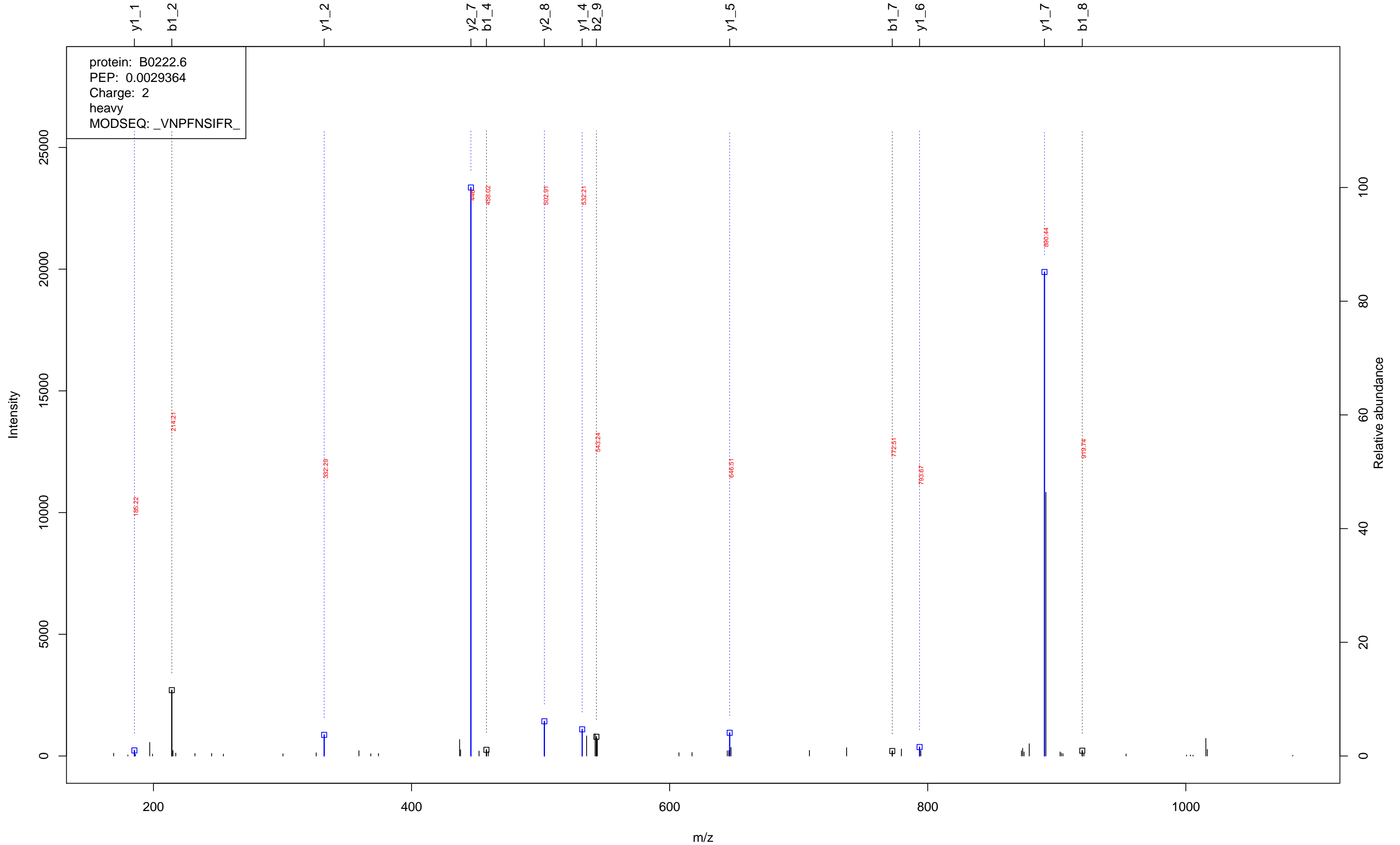


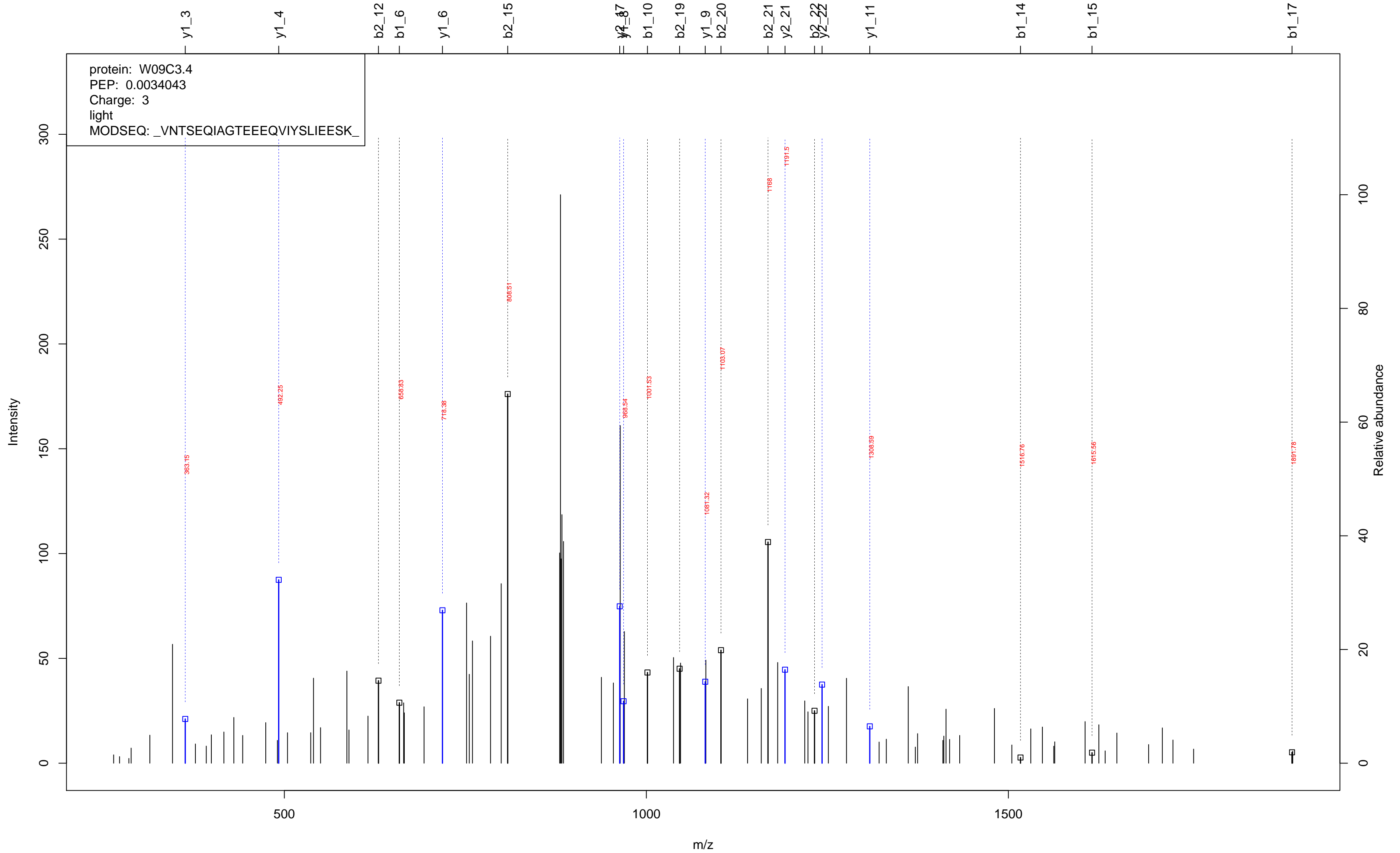


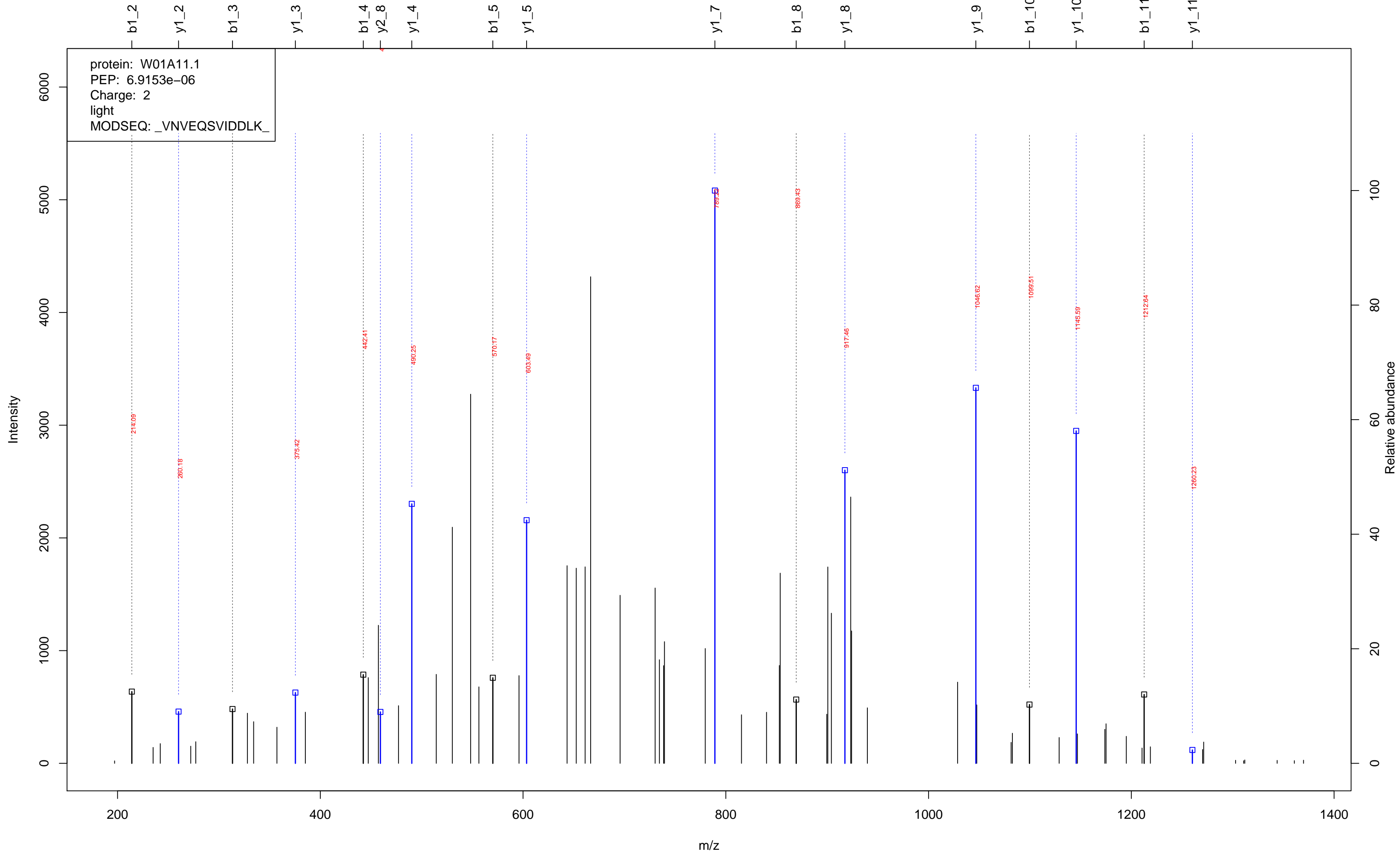


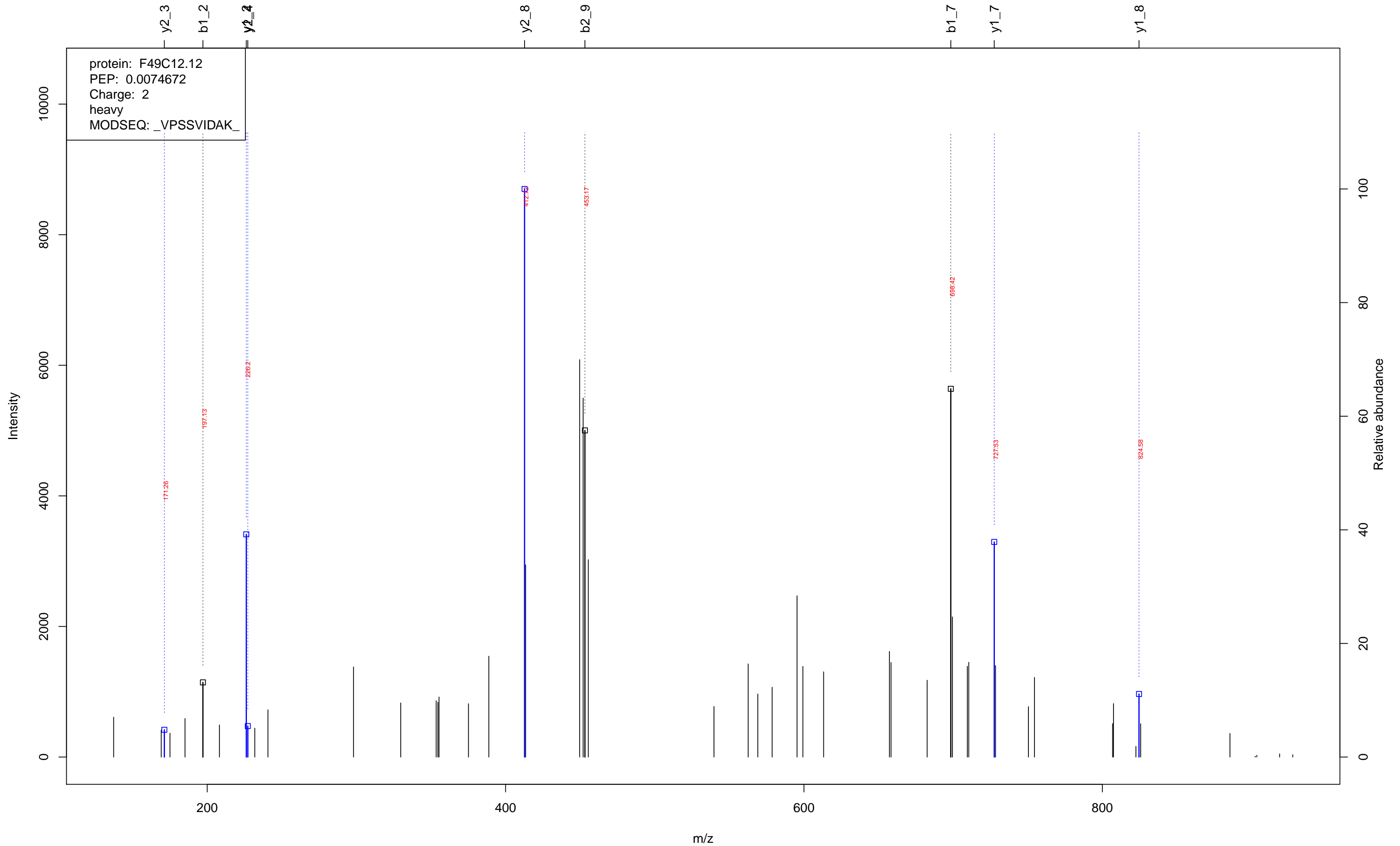


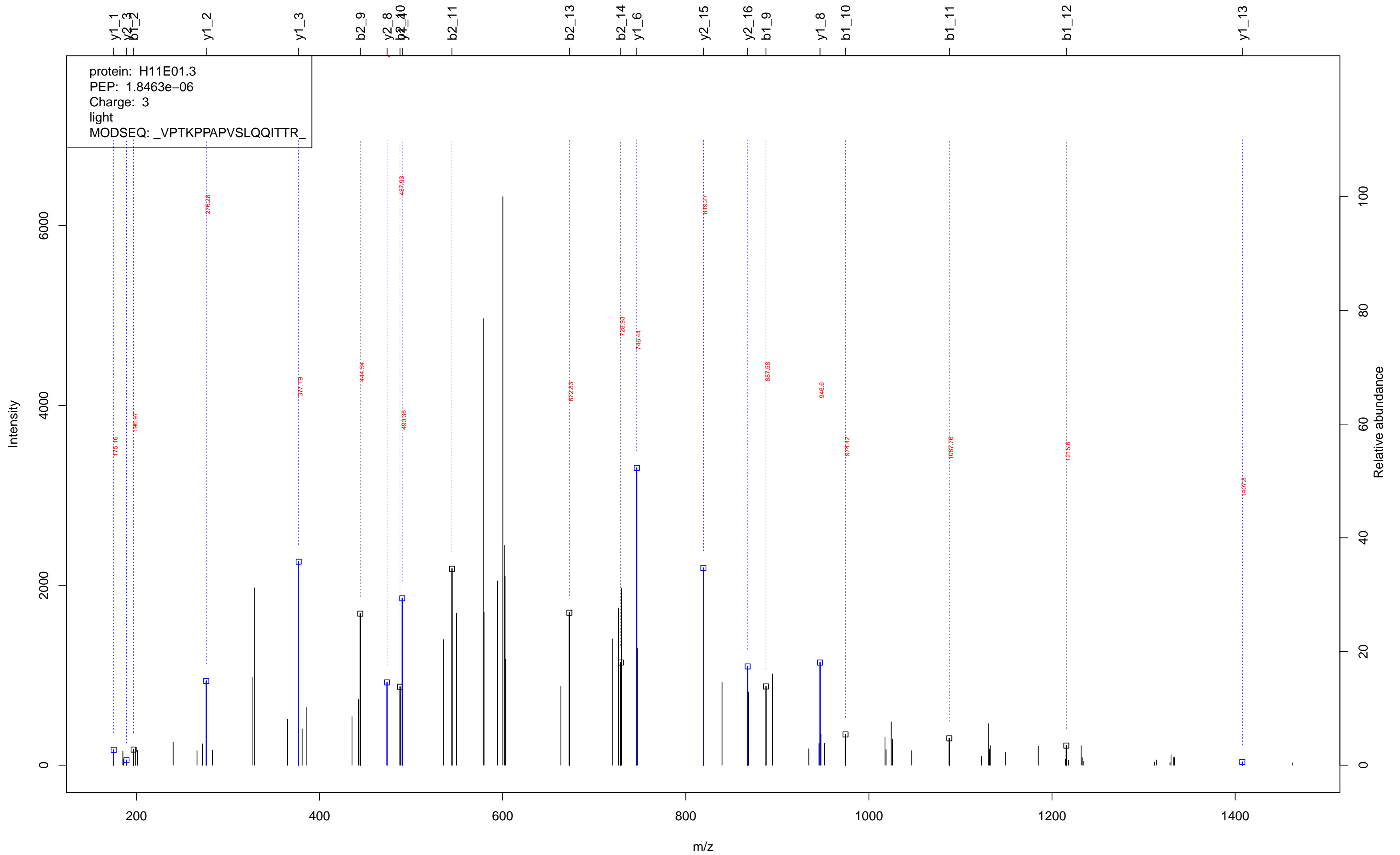


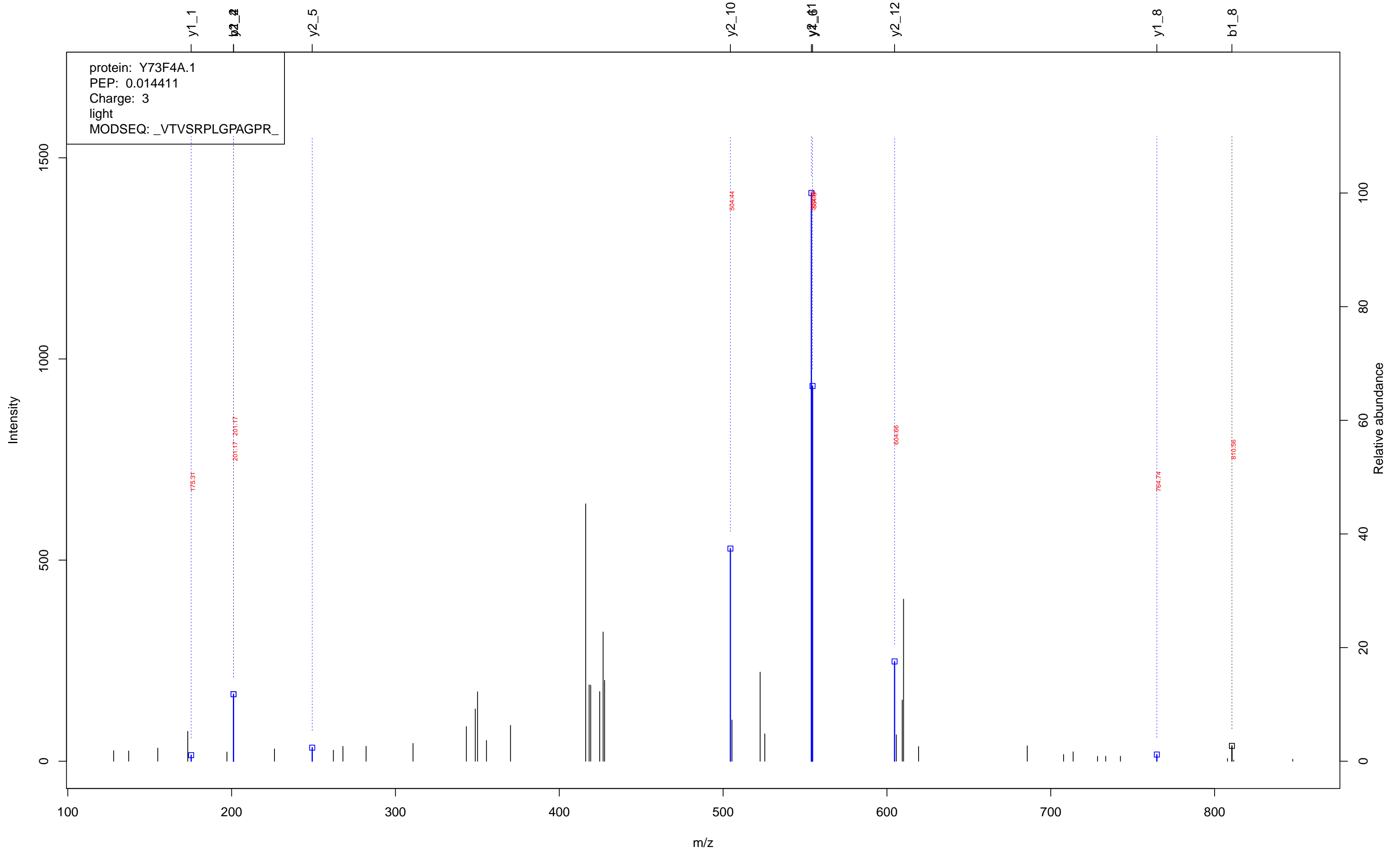


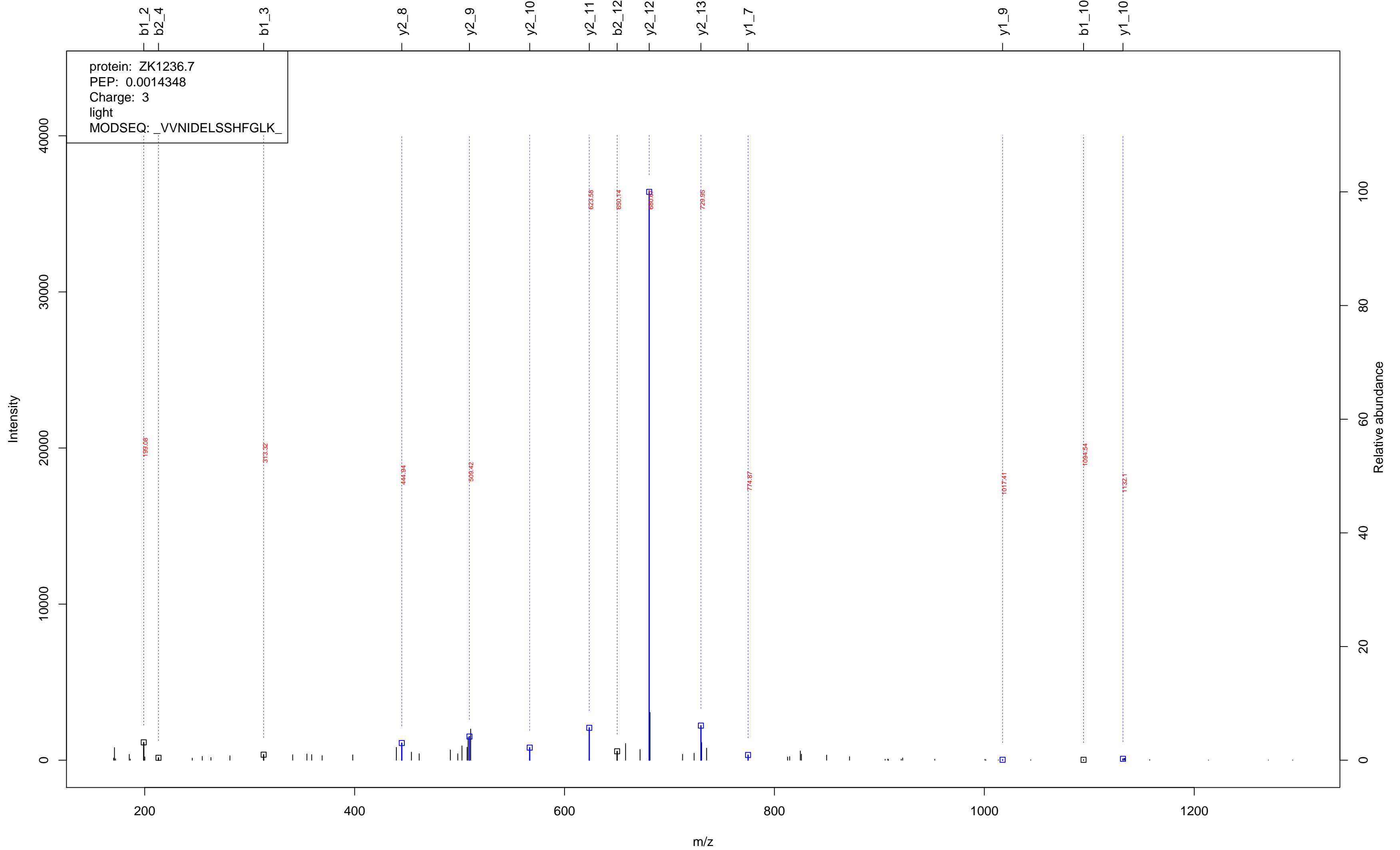


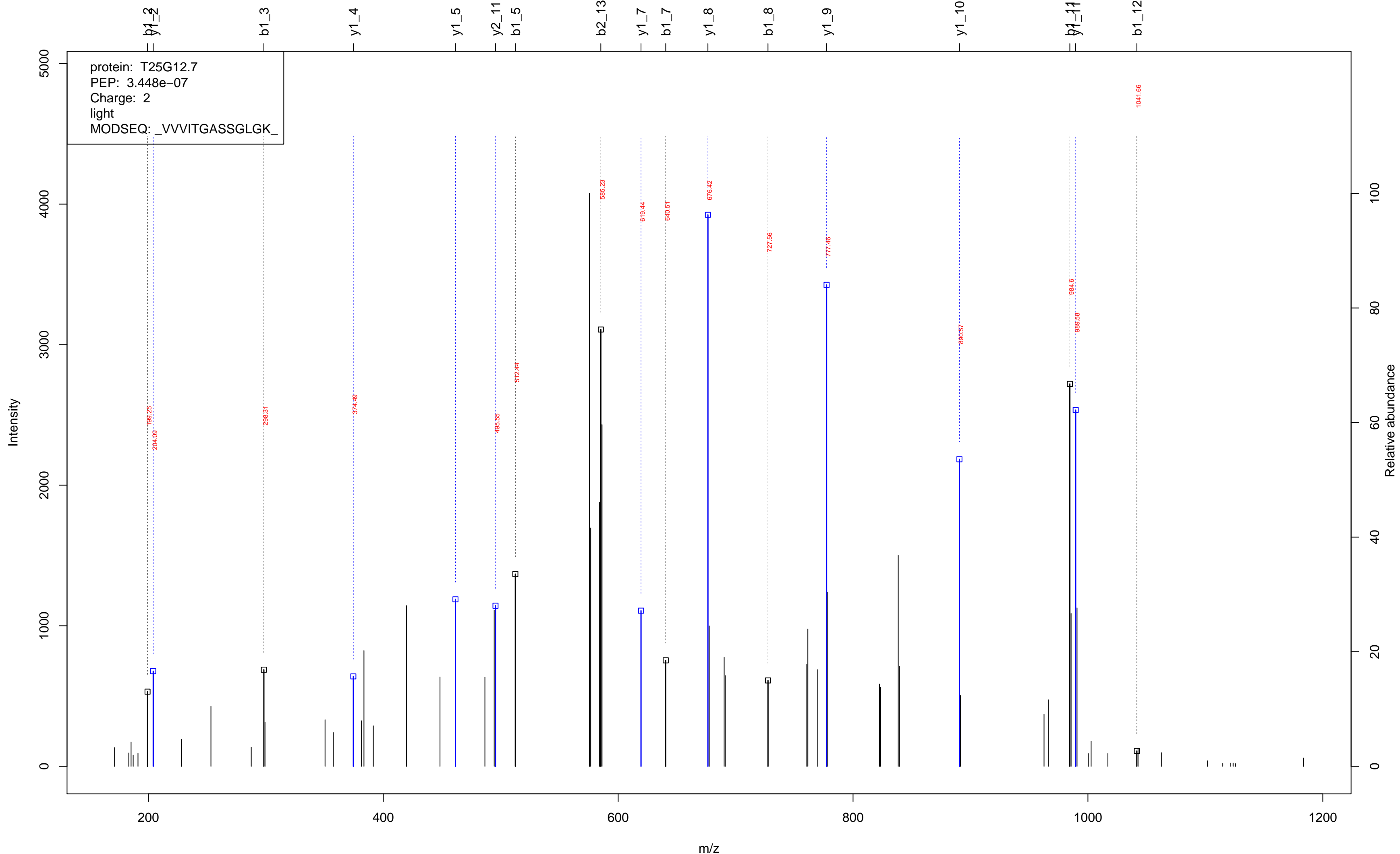


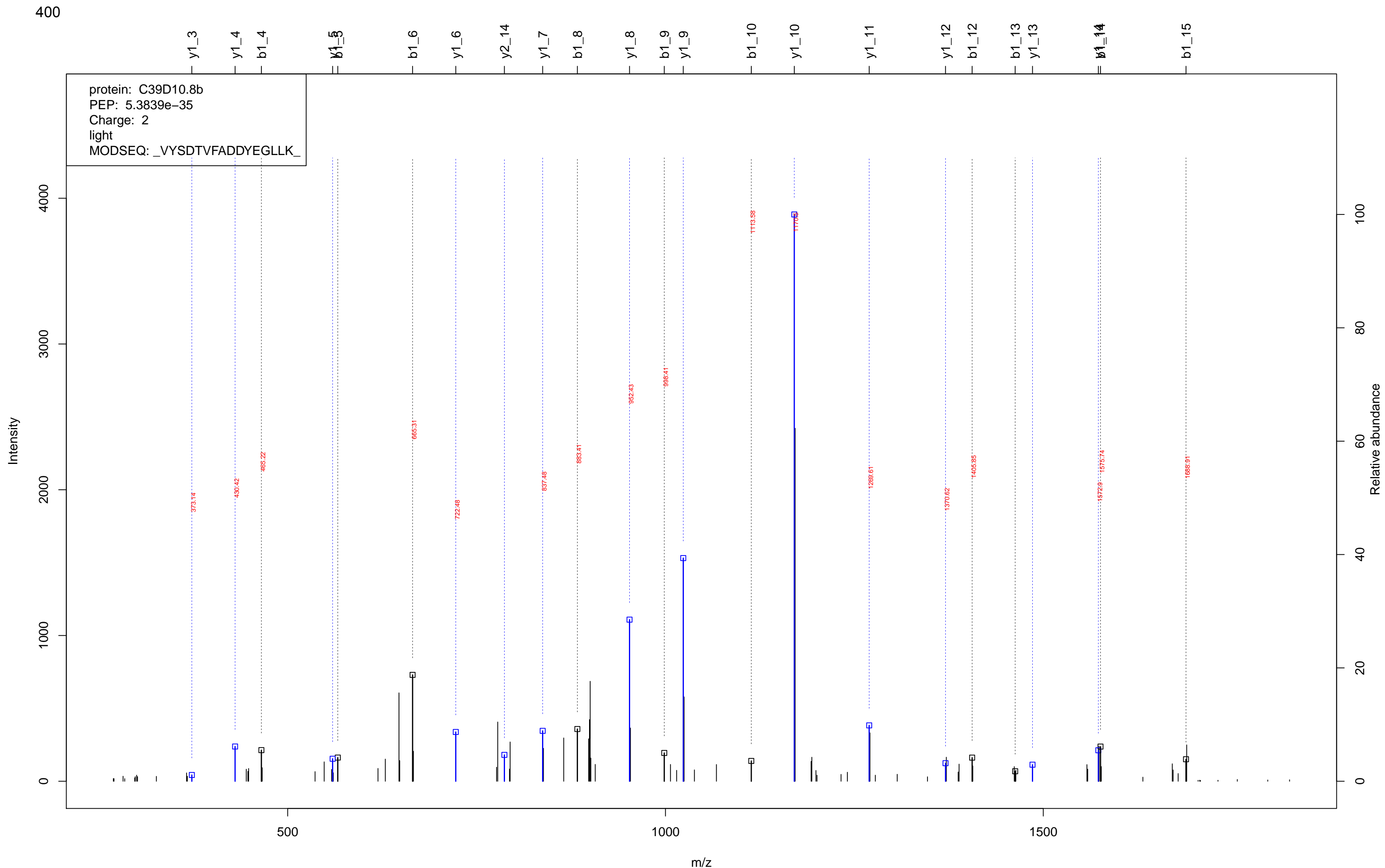


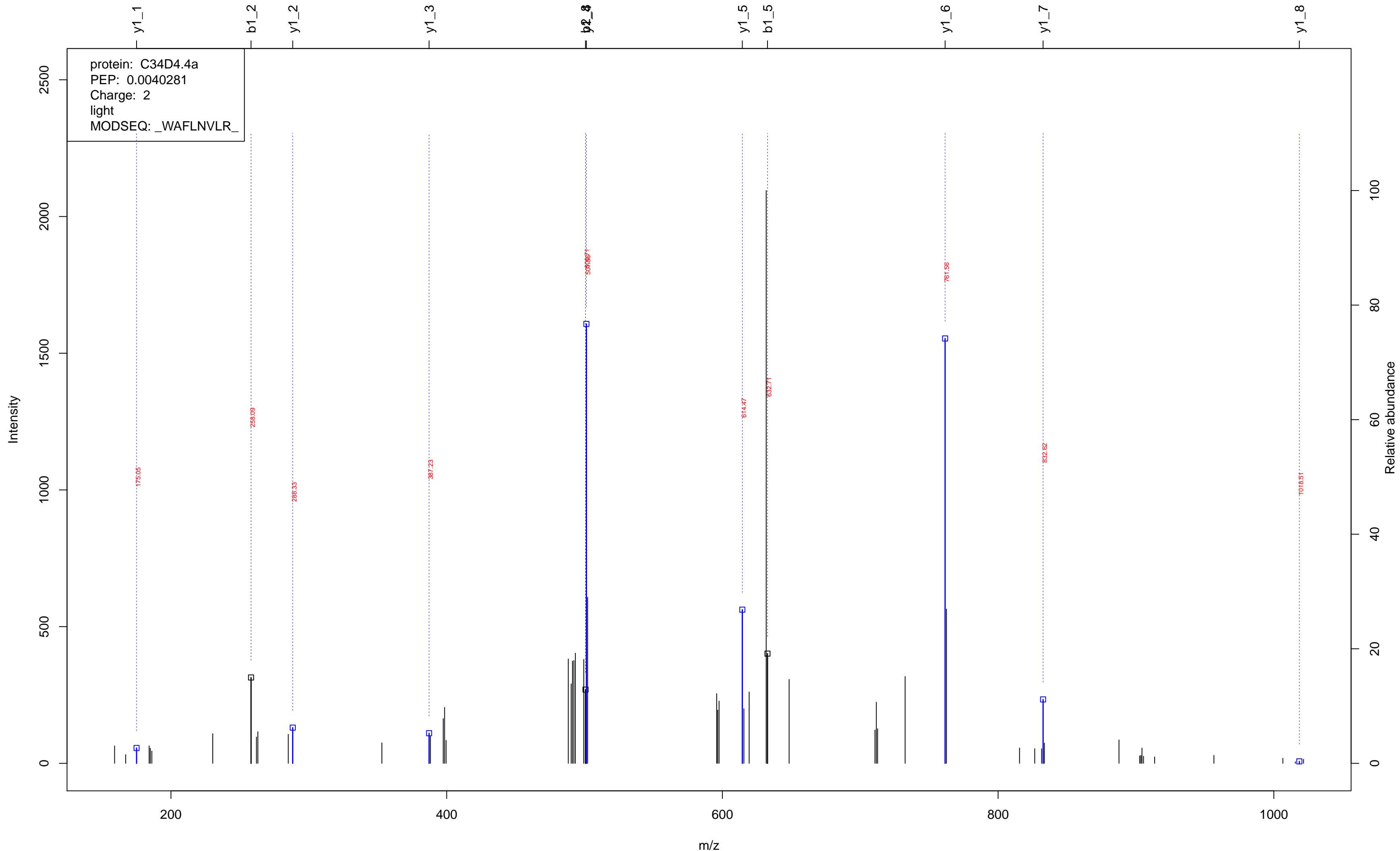






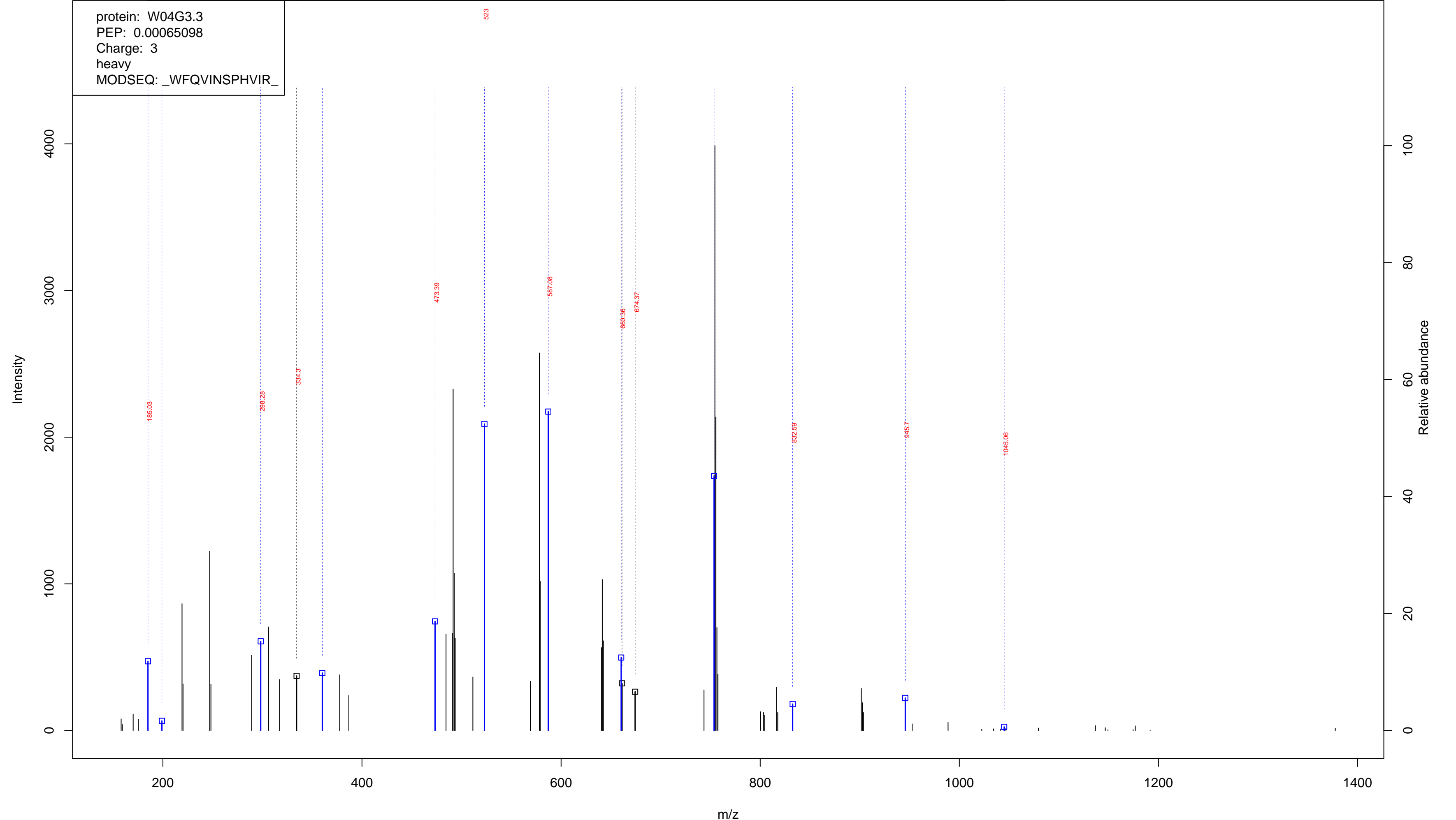






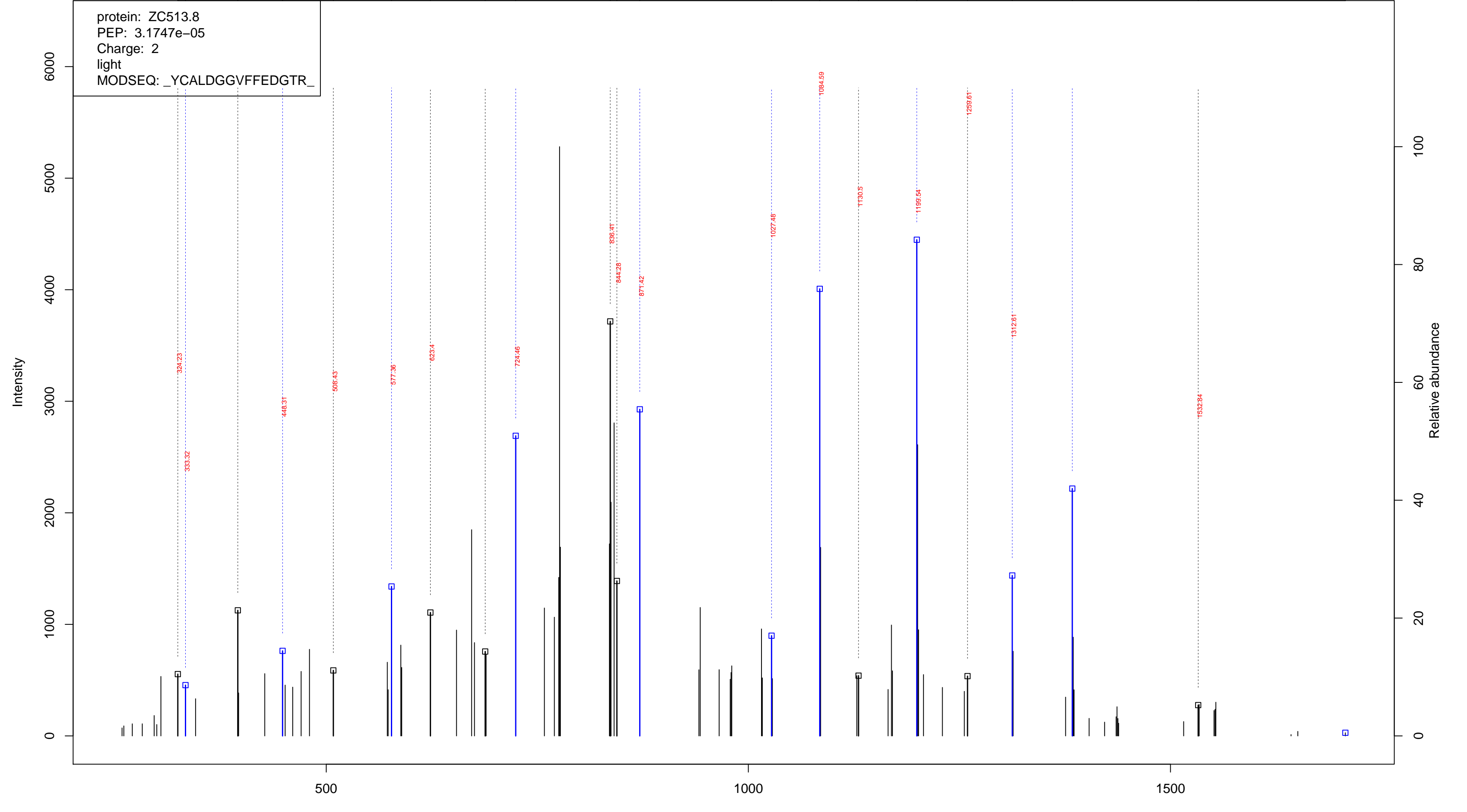
y1_1
y2_3
y1_2
b1_2
y2_6
y2_8
y2_9
y2_10
y2_11
b1_5
y2_12
y1_7
y1_8
y1_9

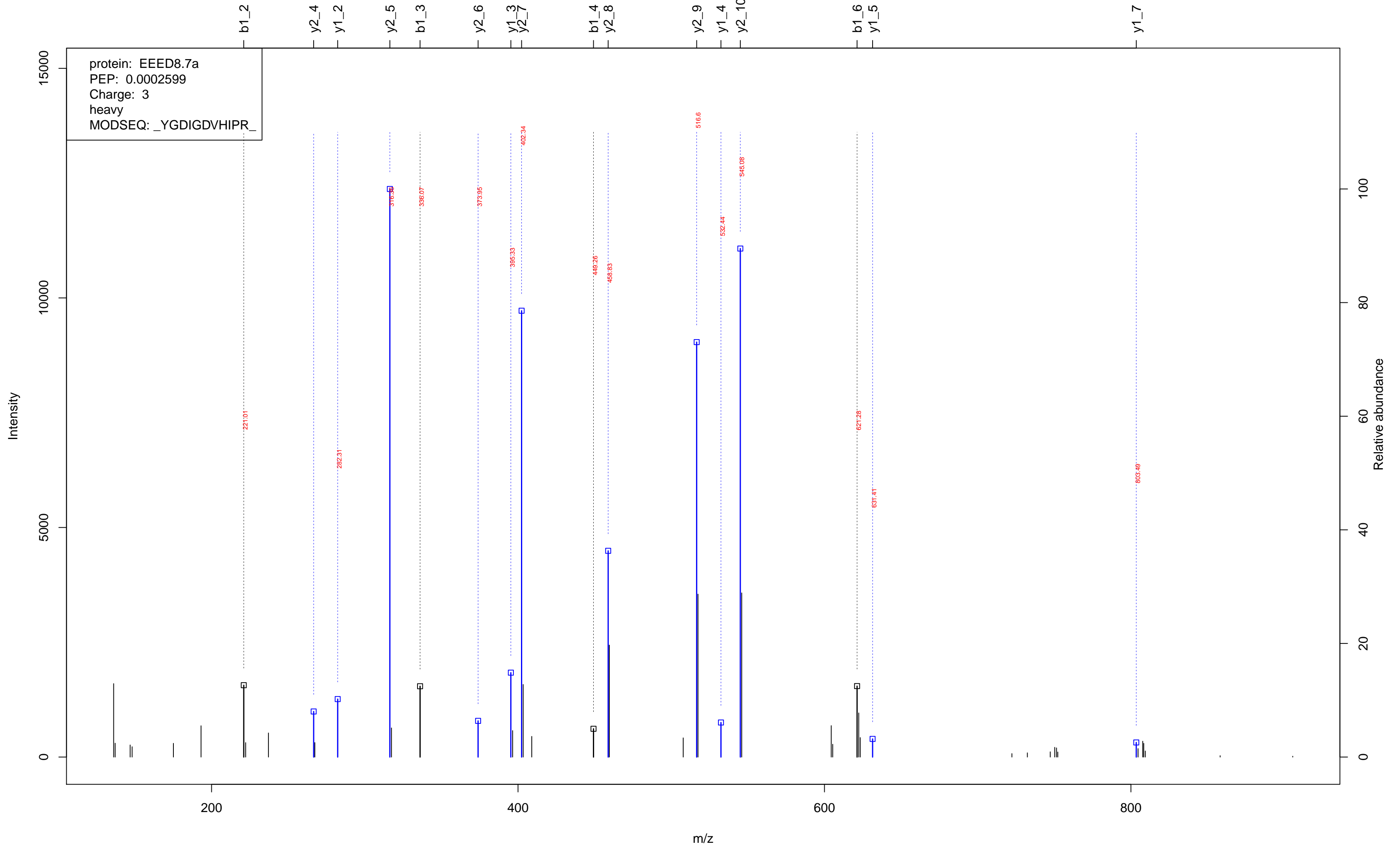
protein: W04G3.3
PEP: 0.00065098
Charge: 3
heavy
MODSEQ: _WFQVINS~~PH~~VIR_

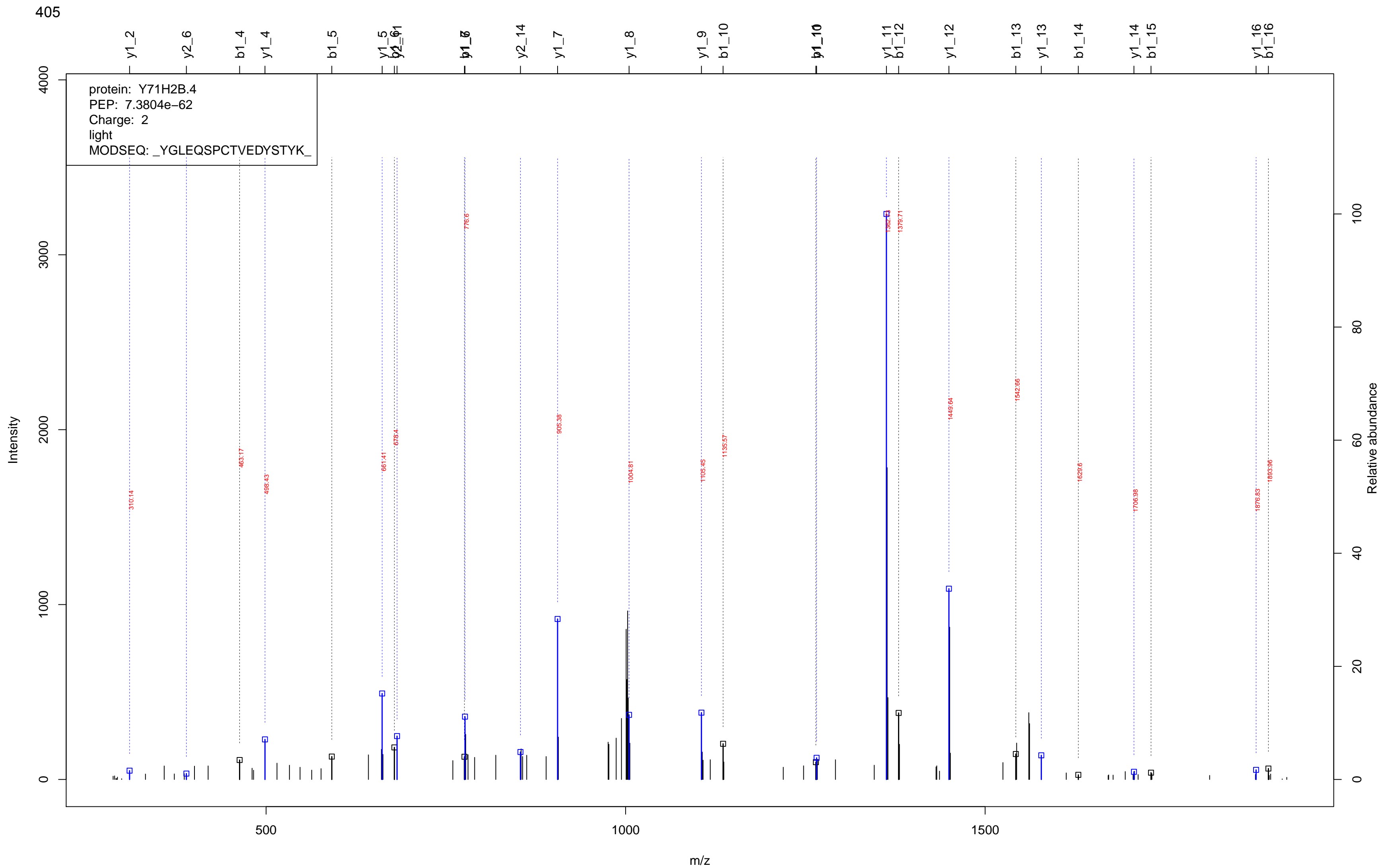


b1_3 y1_3 b1_3 y1_4 b1_4 y1_5 b1_5 b2_12 y1_6 b2_8 b1_5 y1_7 y1_9 y1_10 b1_10 y1_11 b1_11 y1_12 y1_13 b1_14 y1_15

protein: ZC513.8
PEP: 3.1747e-05
Charge: 2
light
MODSEQ: _YCALDGGVFFEDGTR_

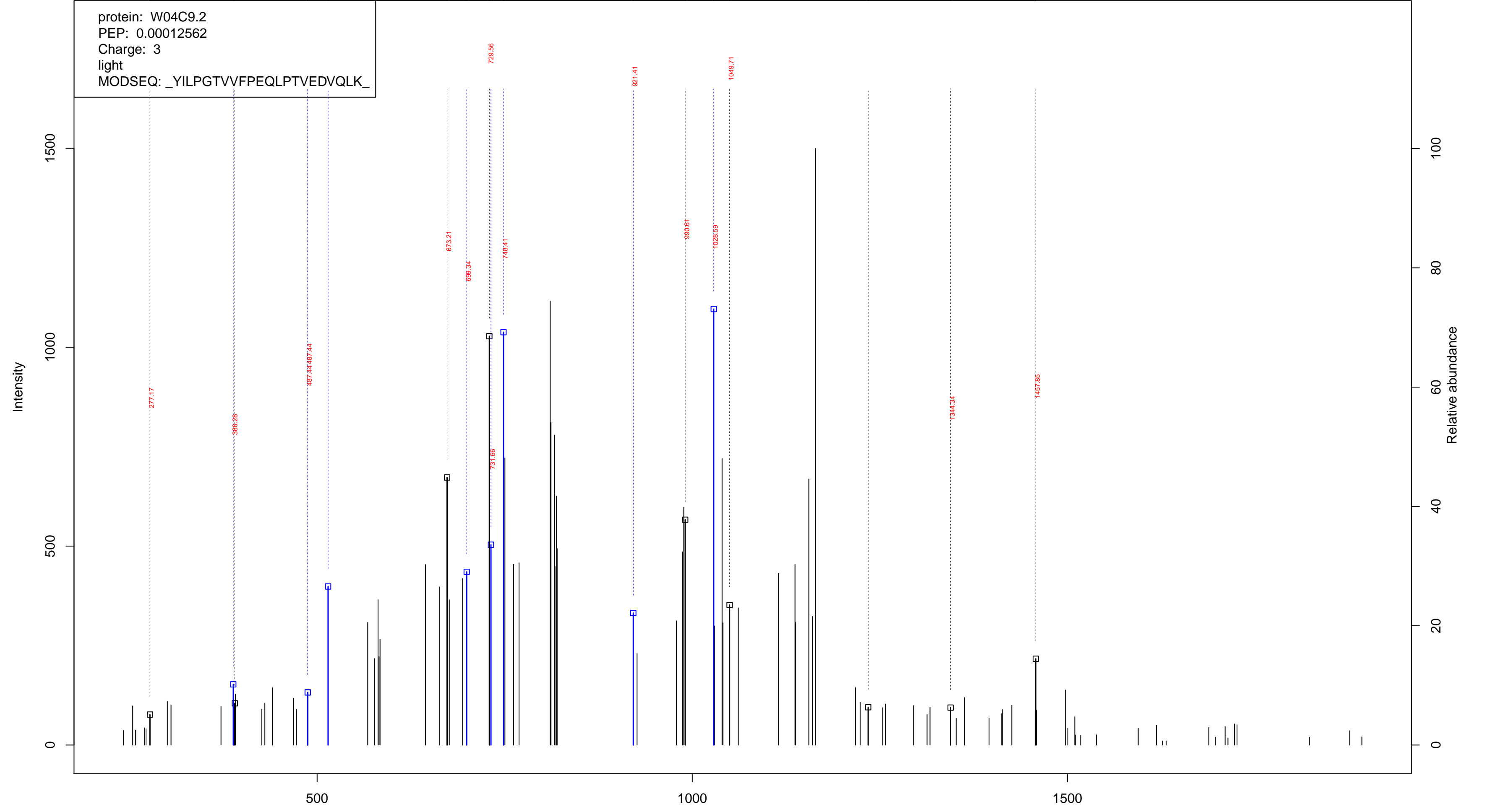






b1_2
b1_3
b1_4
y2_9
b2_12
y2_12
b2_63
y2_13
y2_16
b1_9
y1_9
b2_19
b2_22
b1_12
b1_13

protein: W04C9.2
PEP: 0.00012562
Charge: 3
light
MODSEQ: _YILPGTVVFPEQLPTVEDVQLK_



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