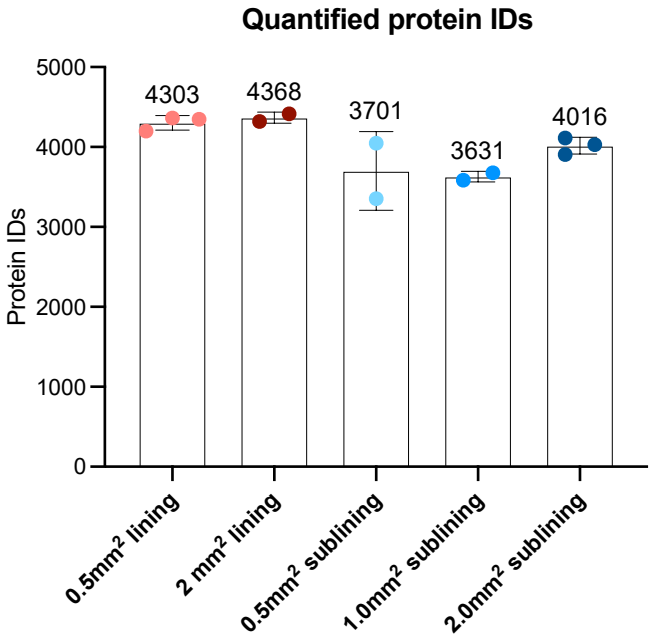
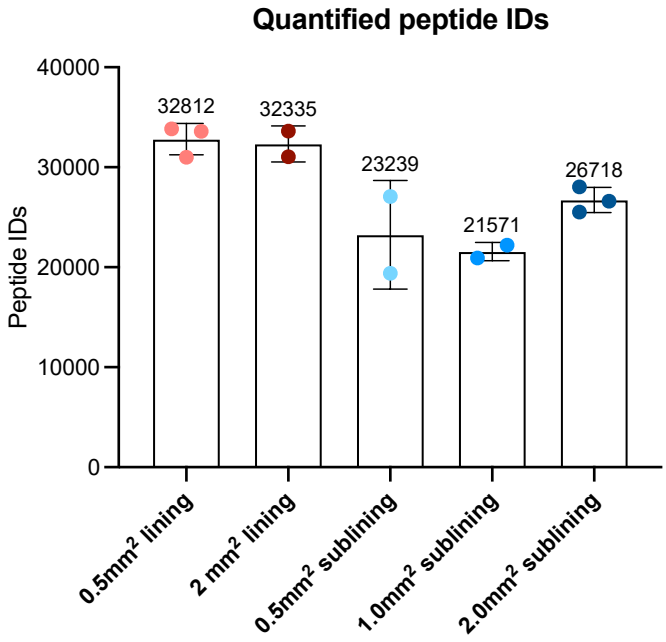
Figure S1. Quantified proteins, peptides and protein sequence coverage of synovium LCMs with varied area sizes

A



B



C

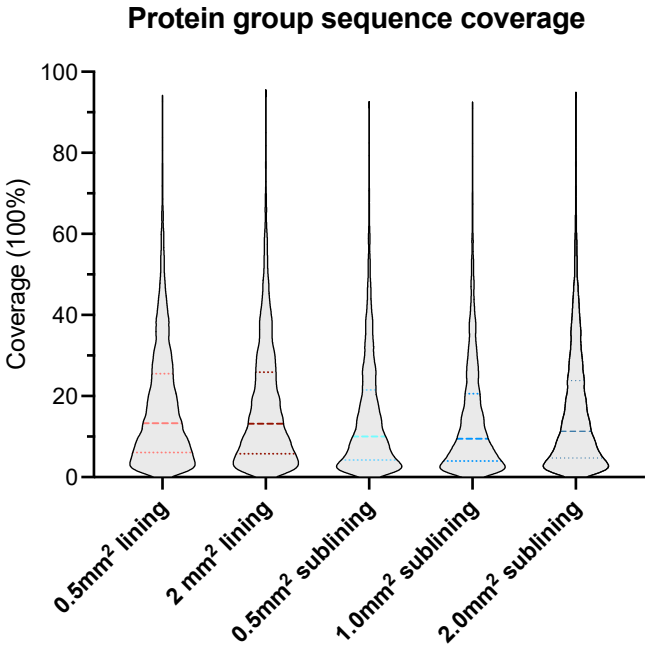


Figure S2. Quantified proteins and peptide ID numbers among region samples

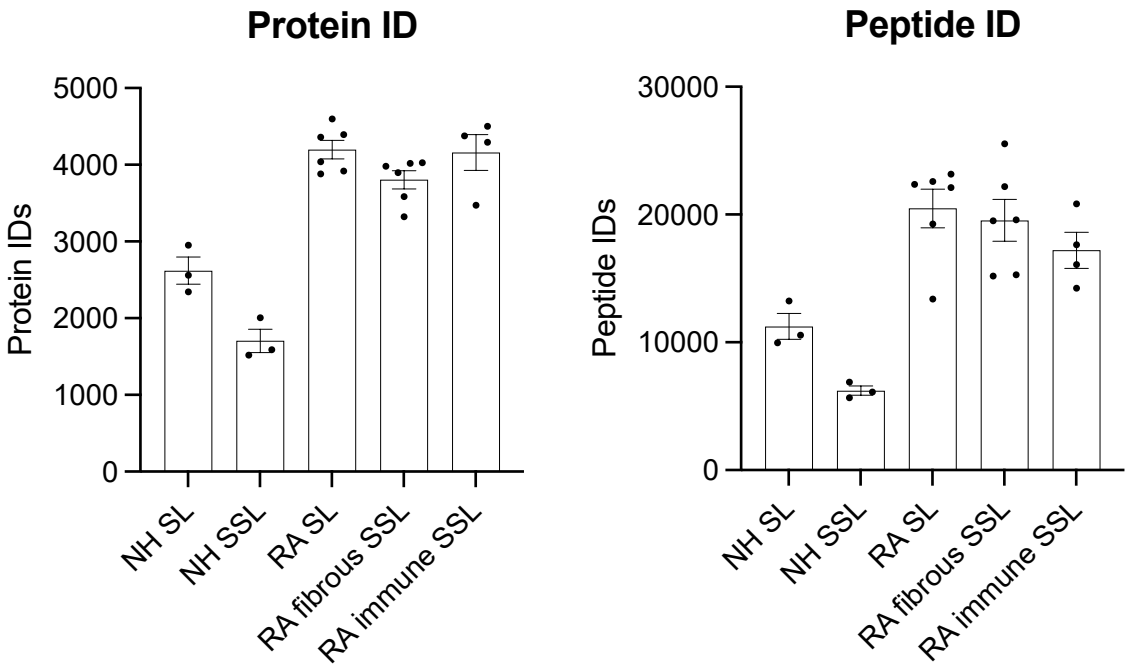


Figure S3. Proteins with maximum PC1 and PC2 loadings from PCA in 7 pairwise region comparisons overlap with differentially expressed proteins

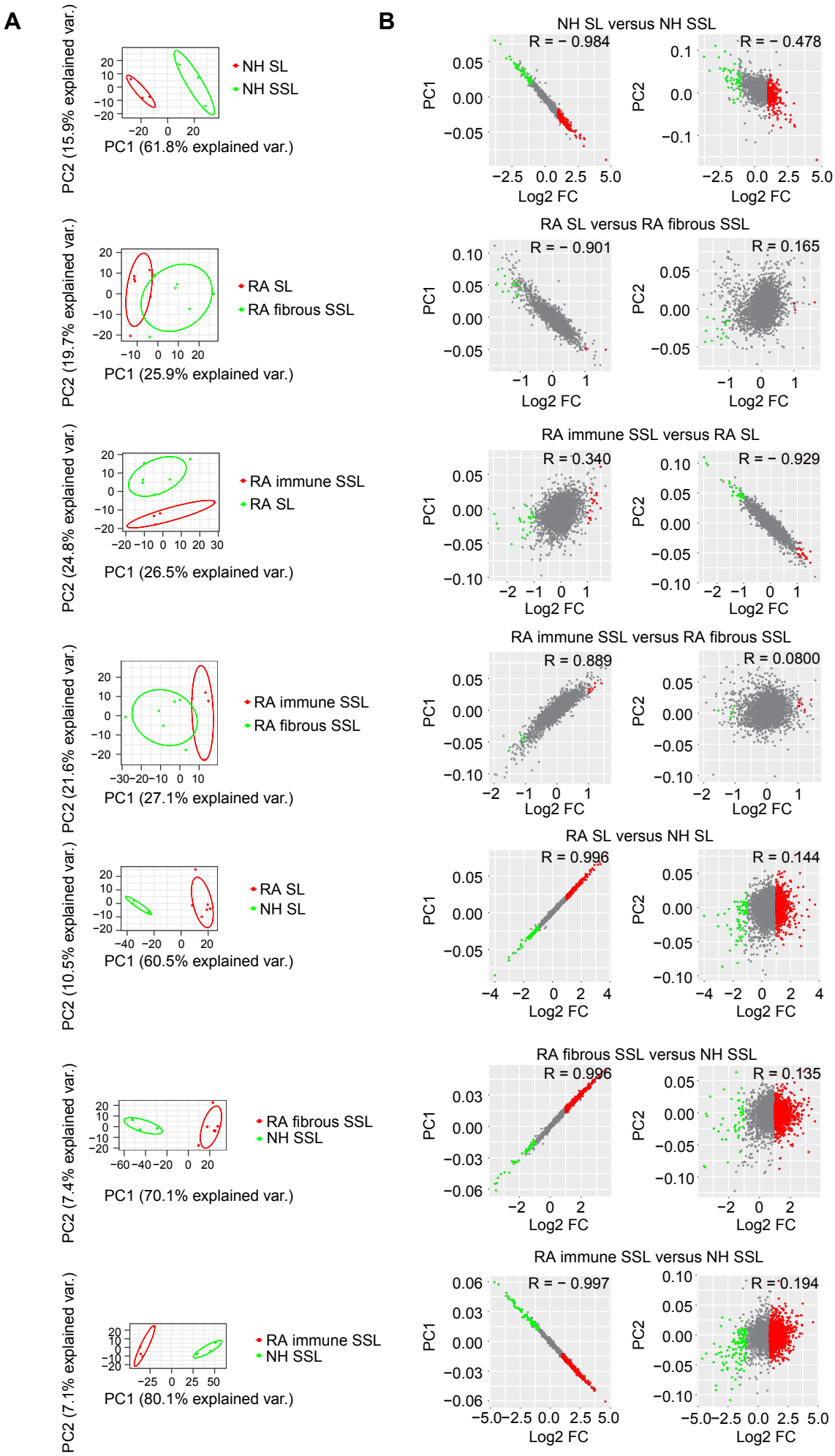


Figure S4. GSEA GO BP summary bubble plotting from protein differential expression (Log2 FC) in respective pairwise comparisons

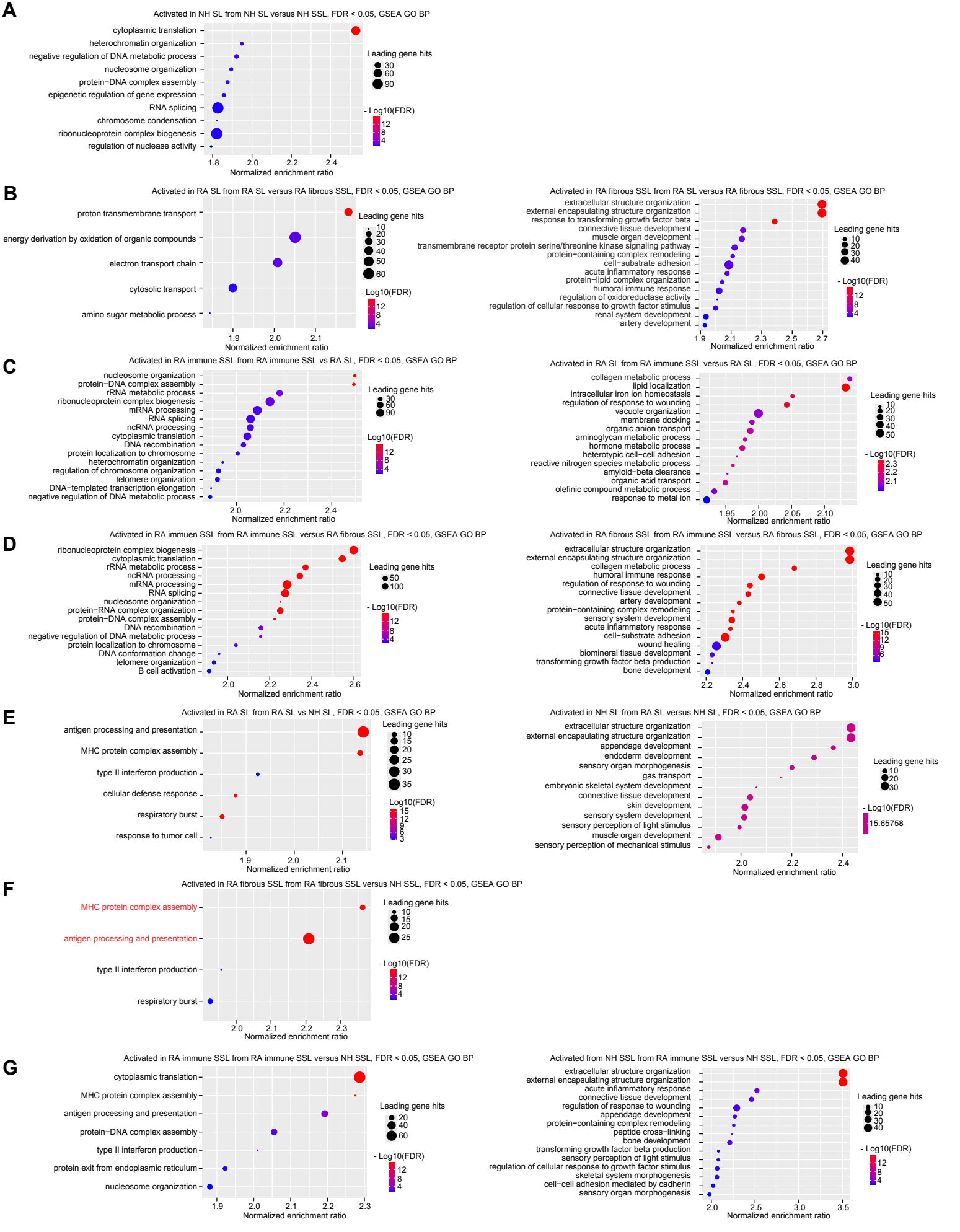


Figure S5. Cell subcluster depletions in different pathological compartments by the Query method integrating LCM spatial proteomics and scRNA-seq transcriptomics

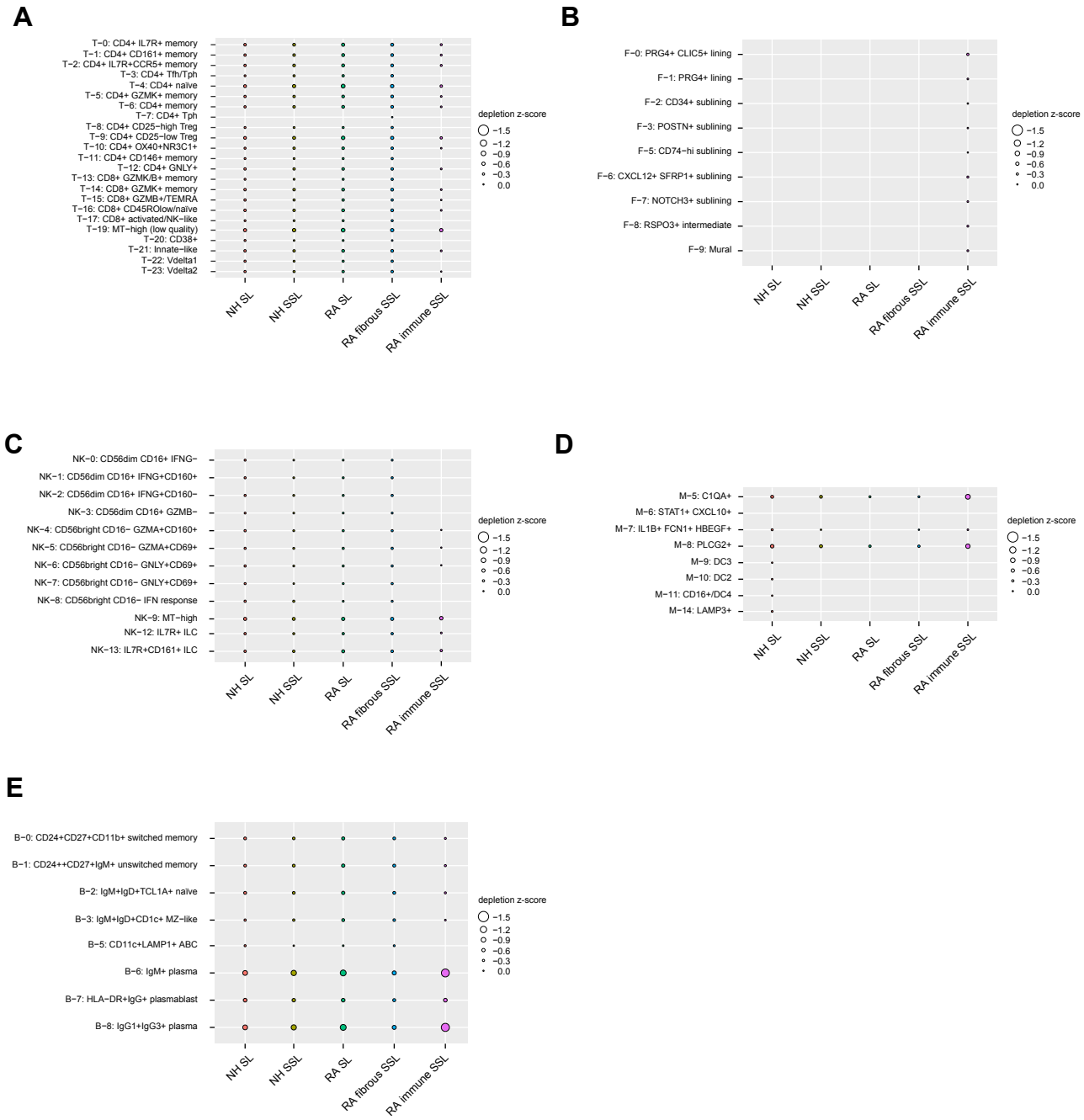
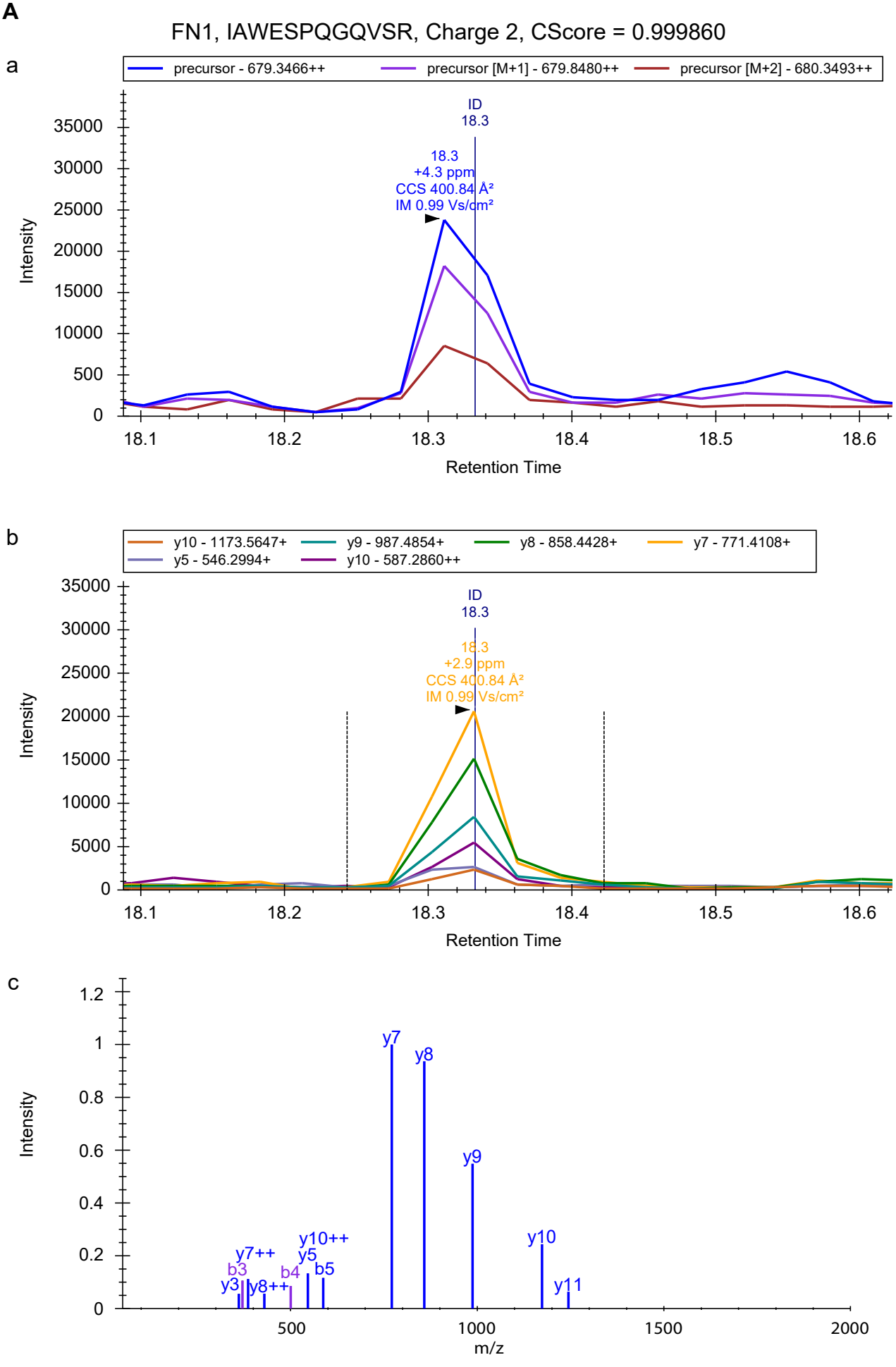


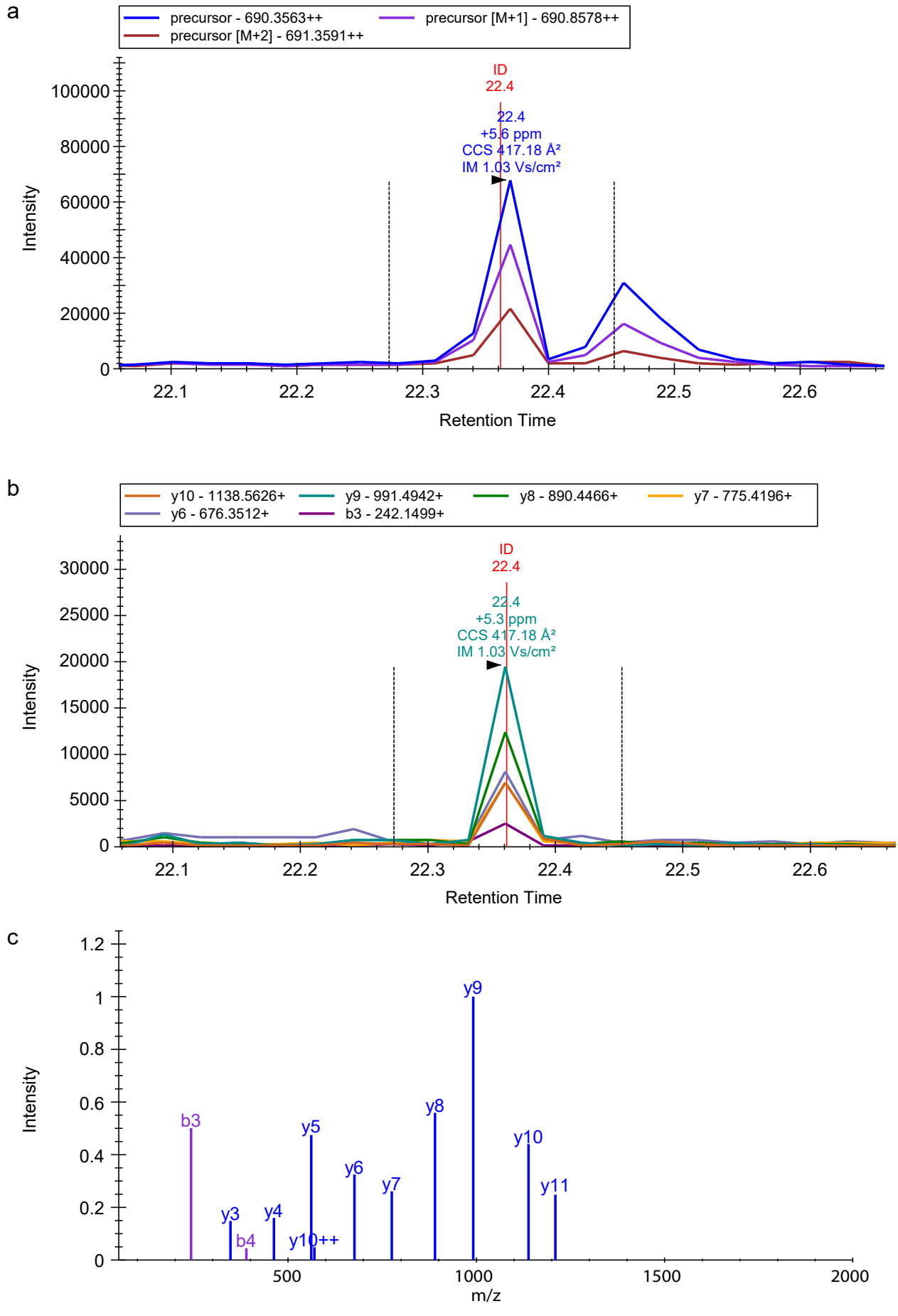
Figure S6: Example MS spectra of several peptides from FN1 and TCIRG1

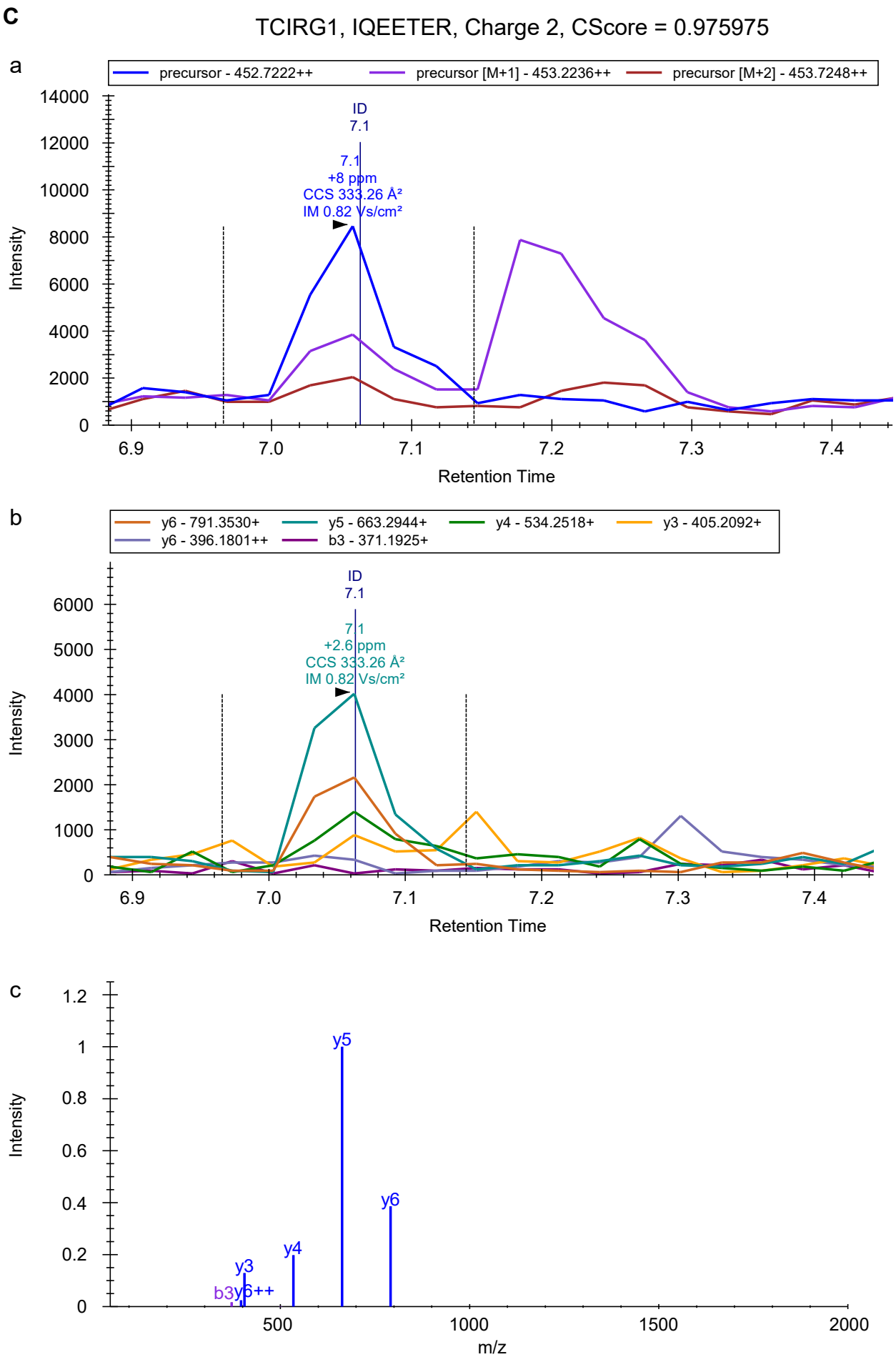
A



B

FN1, GLAFTDVDVDSIK, Charge 2, CScore = 0.999374

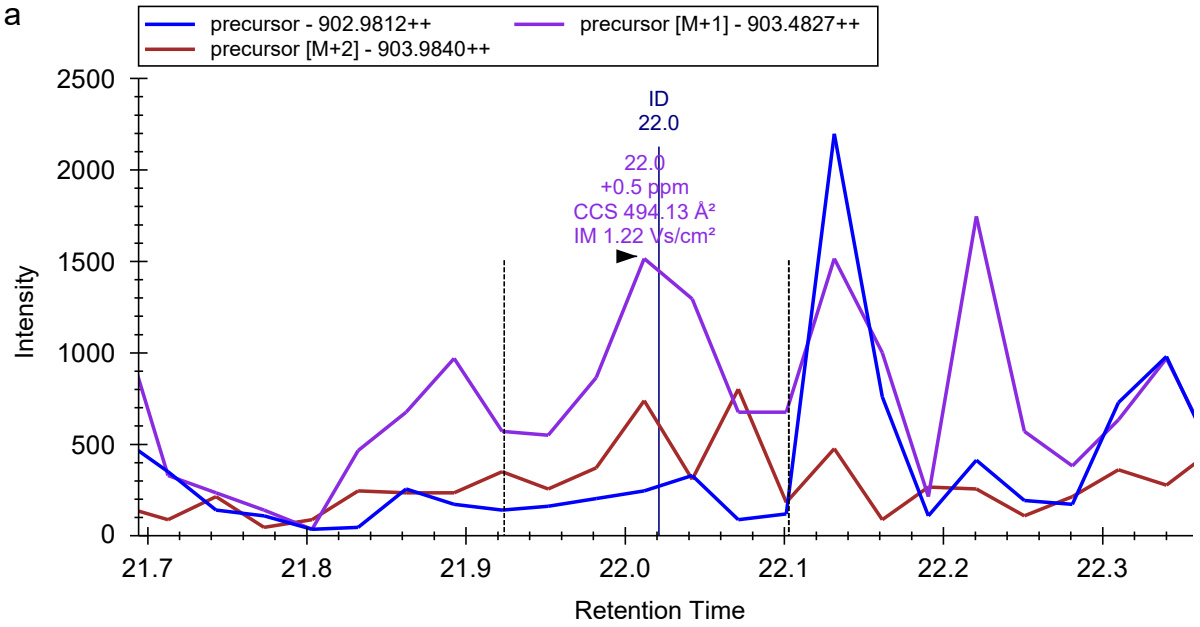



c
TCIRG1, IQEETER, Charge 2, CScore = 0.975975
a
precursor - 452.7222++
precursor [M+1] - 453.2236++
precursor [M+2] - 453.7248++
ID
7.1
7.1
+8 ppm
CCS 333.26 Å²
IM 0.82 Vs/cm²
Intensity
Retention Time
b
y6 - 791.3530+
y5 - 663.2944+
y4 - 534.2518+
y3 - 405.2092+
y6 - 396.1801++
b3 - 371.1925+
ID
7.1
7.1
+2.6 ppm
CCS 333.26 Å²
IM 0.82 Vs/cm²
Intensity
Retention Time
c
y5
y6
y4
y3
b3y6++
Intensity
m/z

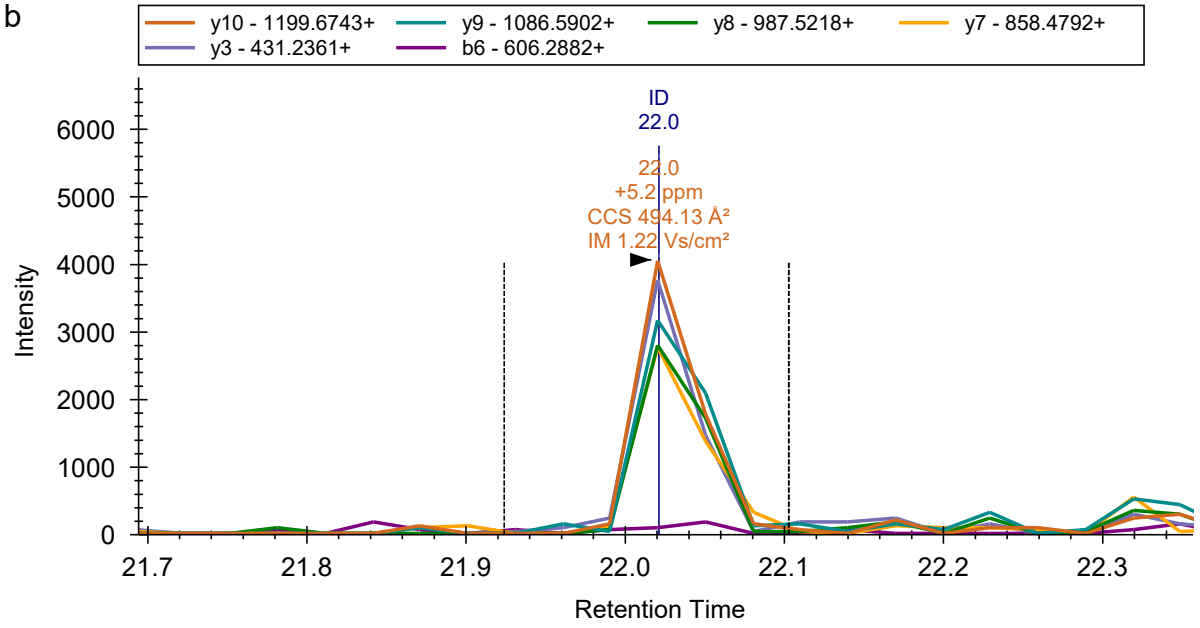
D

FN1, GATYNVIVEALKDQQR, Charge 2, CScore = 0.964173

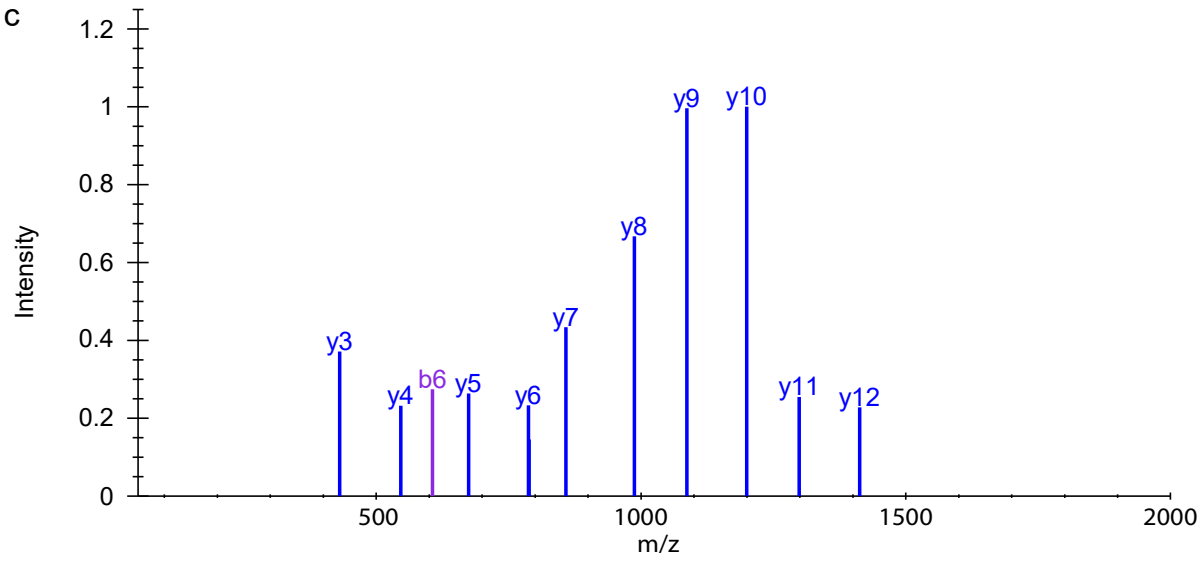
a



b



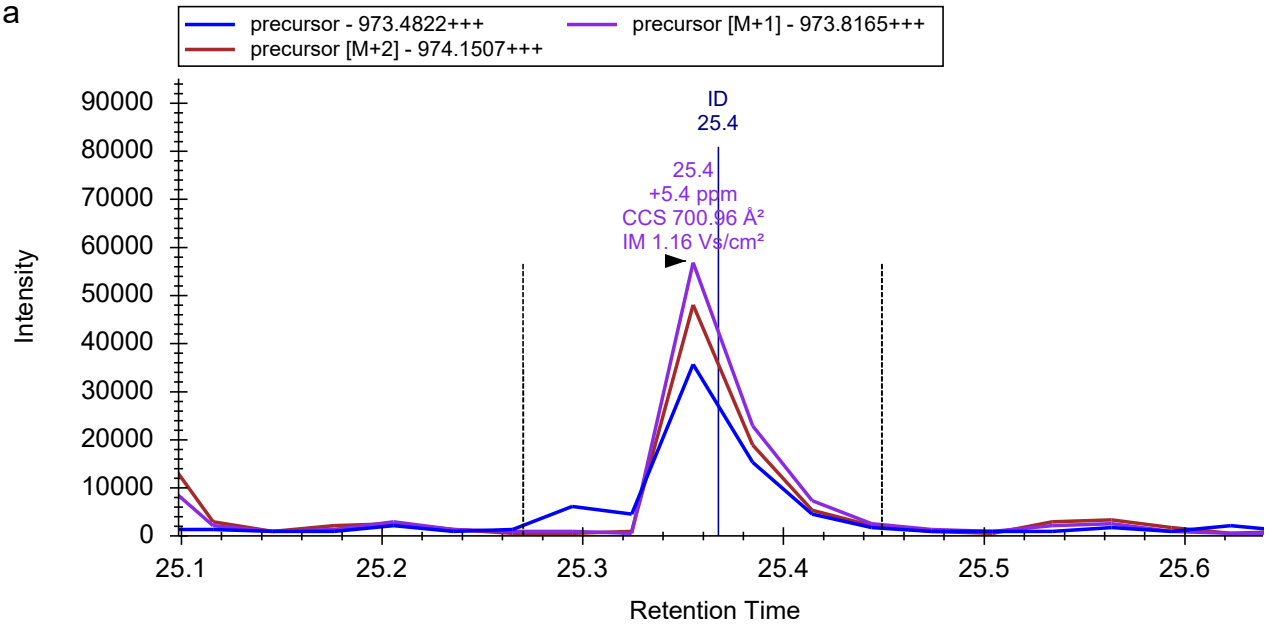
c



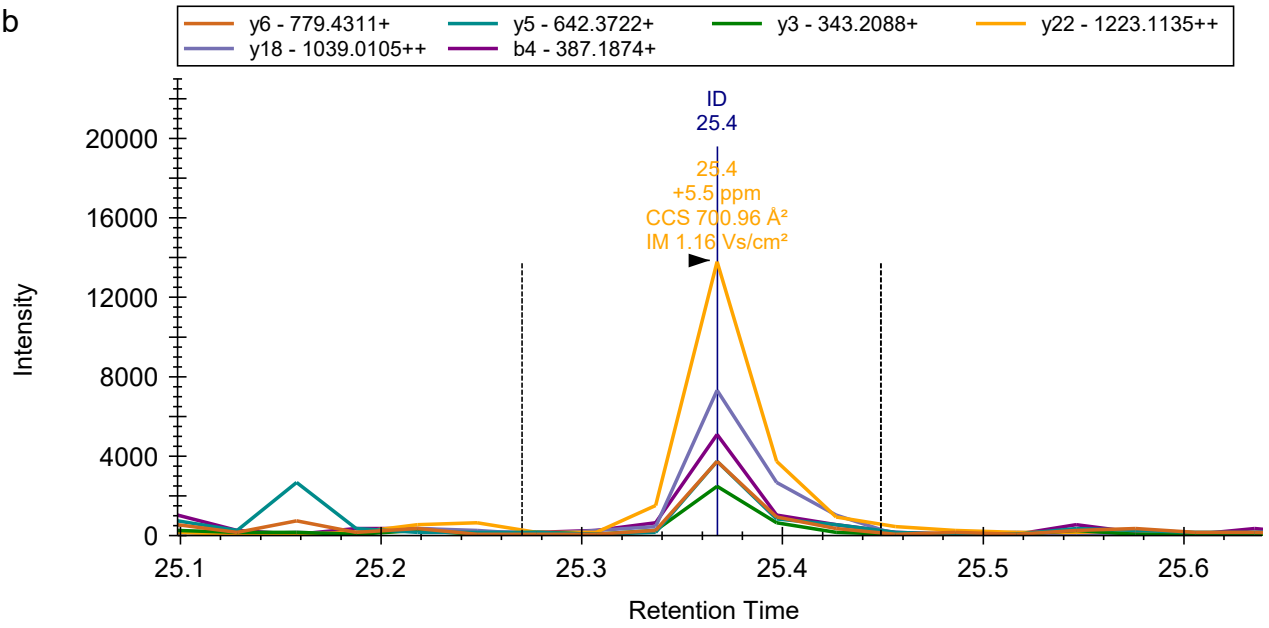
E

FN1, TGLDSPTGIDFSDITANSFTVHWIAPR, Charge 3, CScore = 0.931109

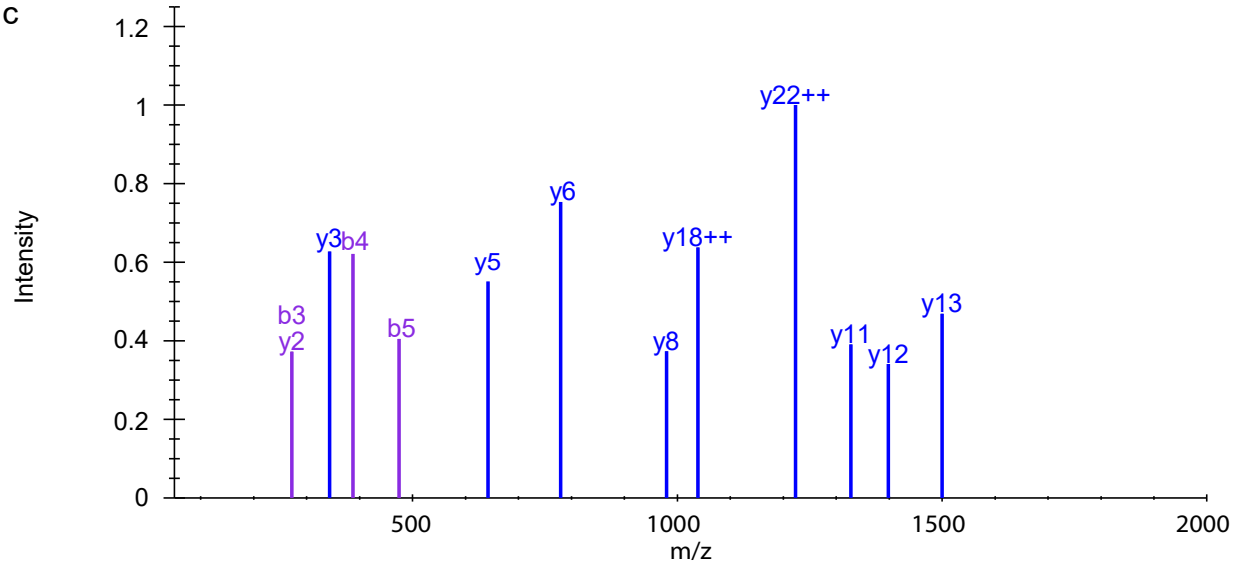
a



b



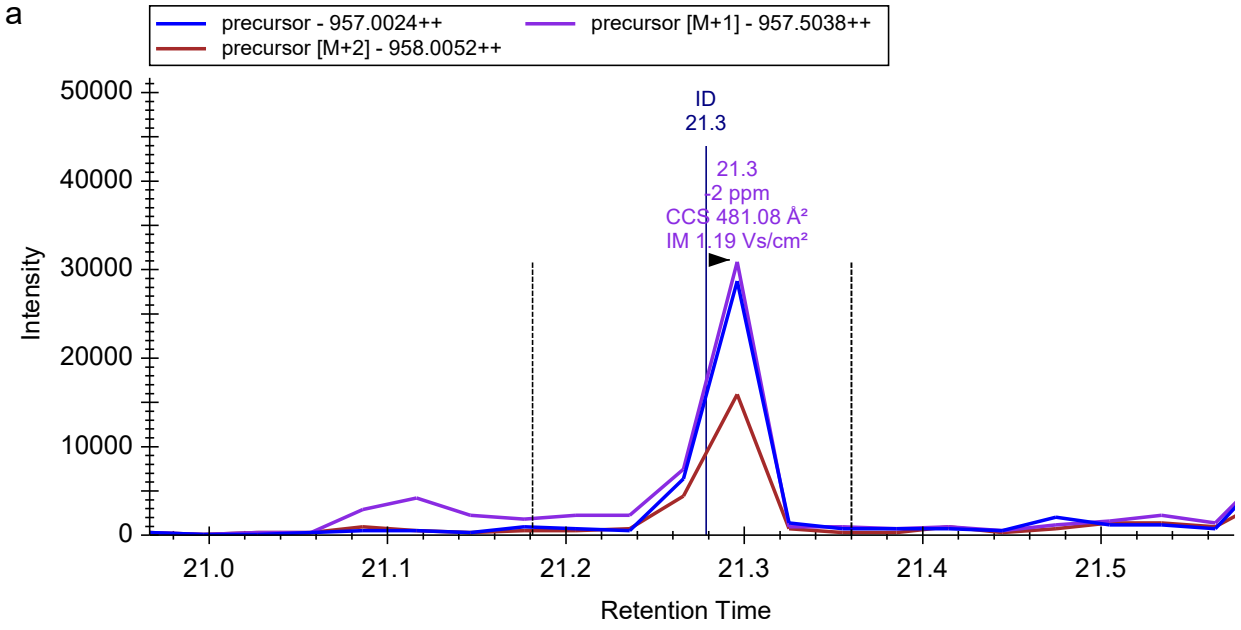
c



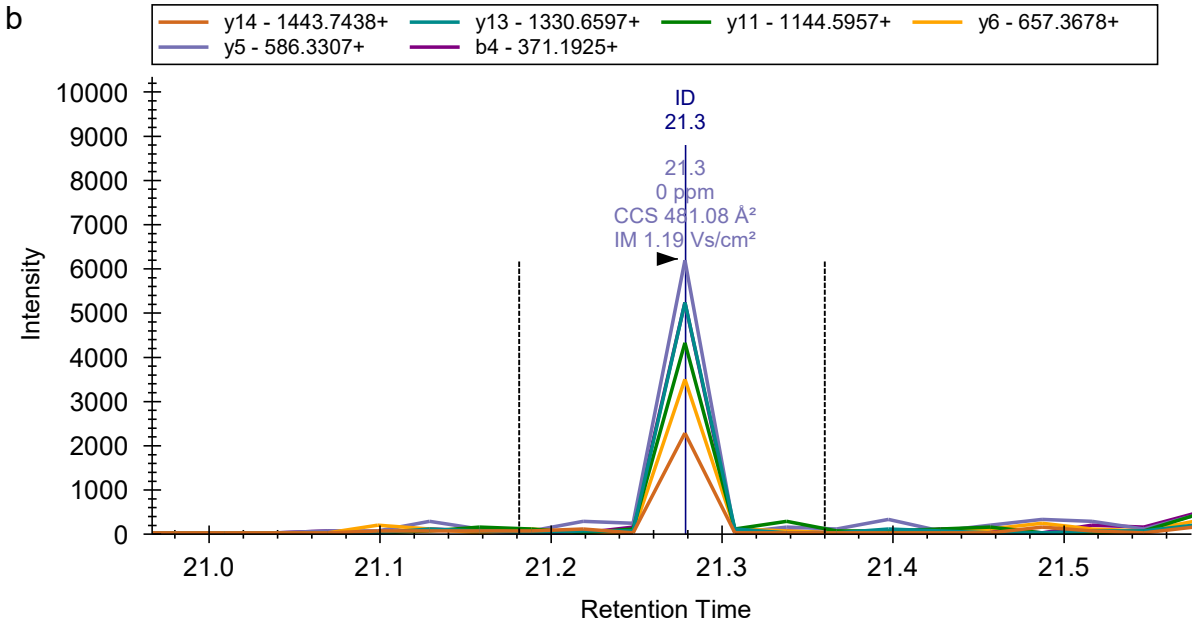
F

FN1, SSPVVIDASTAIDAPSNLR, Charge 2, CScore = 0.888621

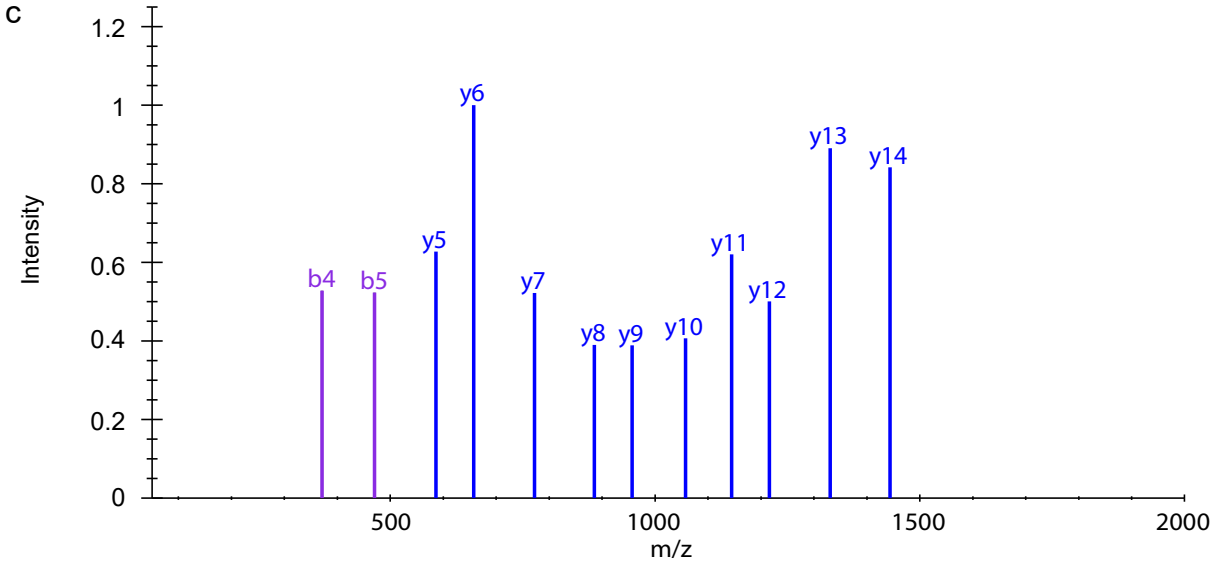
a



b



c



G

TCIRG1, RFVVDVR, Charge 2, CScore = 0.850949

