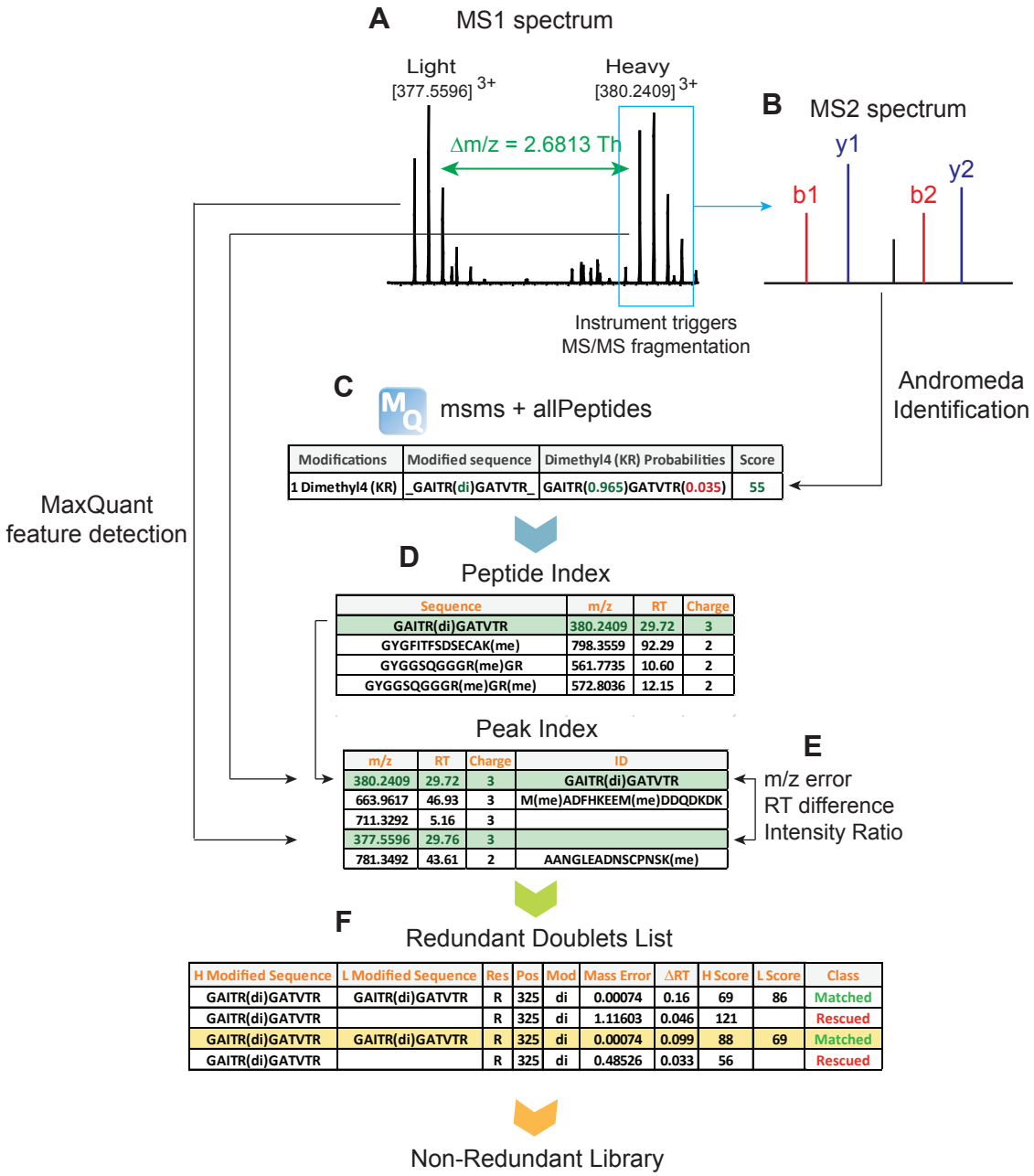
A
MS1 spectrum
Light
[377.5596] 3+
Heavy
[380.2409] 3+
Δm/z = 2.6813 Th
B
MS2 spectrum
y1
y2
b1
b2
Instrument triggers
MS/MS fragmentation
Andromeda
Identification
C
msms + allPeptides
Modifications
Modified sequence
Dimethyl4 (KR) Probabilities
Score
1 Dimethyl4 (KR)
GAITR(di)GATVTR
GAITR(0.965)GATVTR(0.035)
55
MaxQuant
feature detection
D
Peptide Index
Sequence
m/z
RT
Charge
GAITR(di)GATVTR
380.2409
29.72
3
GYGFITFSDSECAK(me)
798.3559
92.29
2
GYGGSQGGGR(me)GR
561.7735
10.60
2
GYGGSQGGGR(me)GR(me)
572.8036
12.15
2
Peak Index
m/z
RT
Charge
ID
380.2409
29.72
3
GAITR(di)GATVTR
663.9617
46.93
3
M(me)ADFHKEEM(me)DDQDKDK
711.3292
5.16
3
377.5596
29.76
3
781.3492
43.61
2
AANGLEADNSCPNSK(me)
E
m/z error
RT difference
Intensity Ratio
F
Redundant Doublets List
H Modified Sequence
L Modified Sequence
Res
Pos
Mod
Mass Error
ΔRT
H Score
L Score
Class
GAITR(di)GATVTR
GAITR(di)GATVTR
R
325
di
0.00074
0.16
69
86
Matched
GAITR(di)GATVTR
R
325
di
1.11603
0.046
121
Rescued
GAITR(di)GATVTR
GAITR(di)GATVTR
R
325
di
0.00074
0.099
88
69
Matched
GAITR(di)GATVTR
R
325
di
0.48526
0.033
56
Rescued
Non-Redundant Library