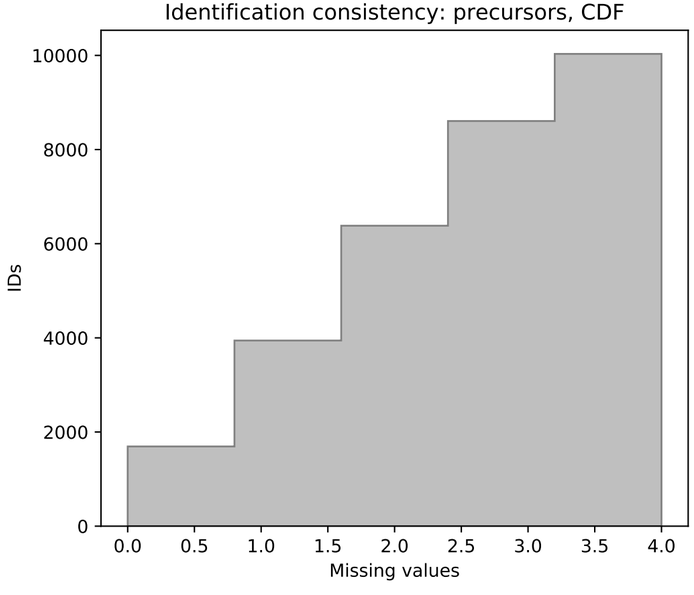
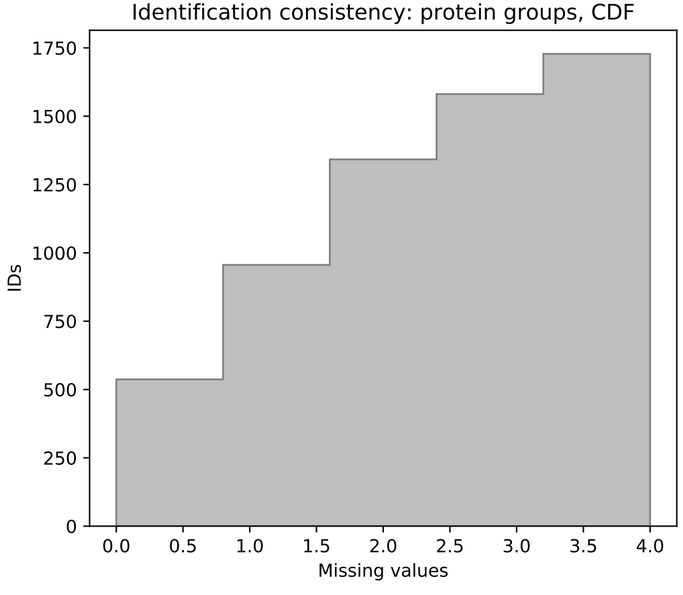
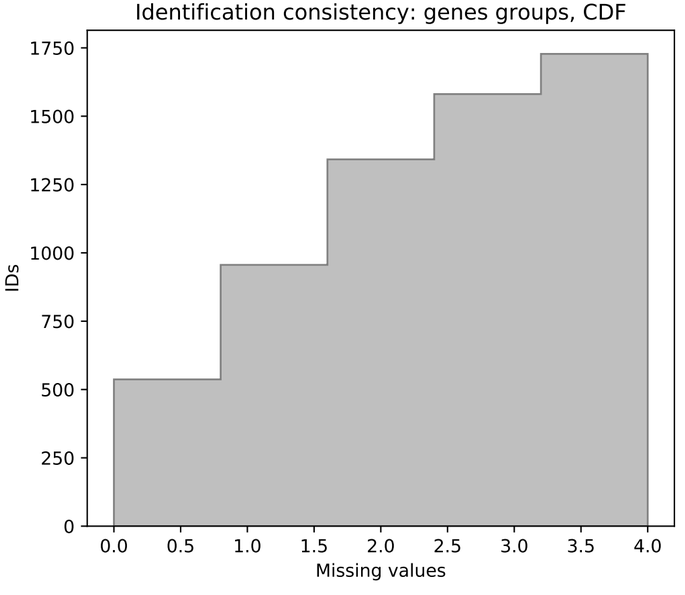
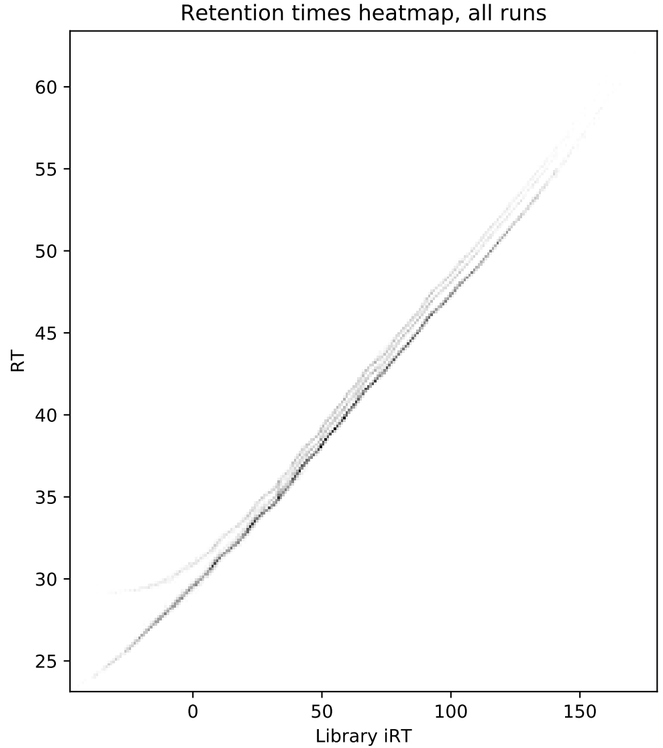
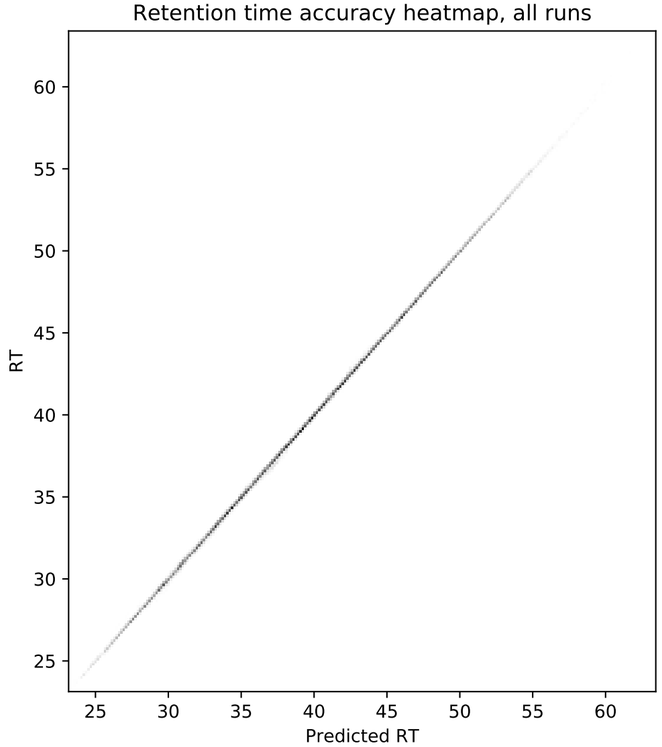
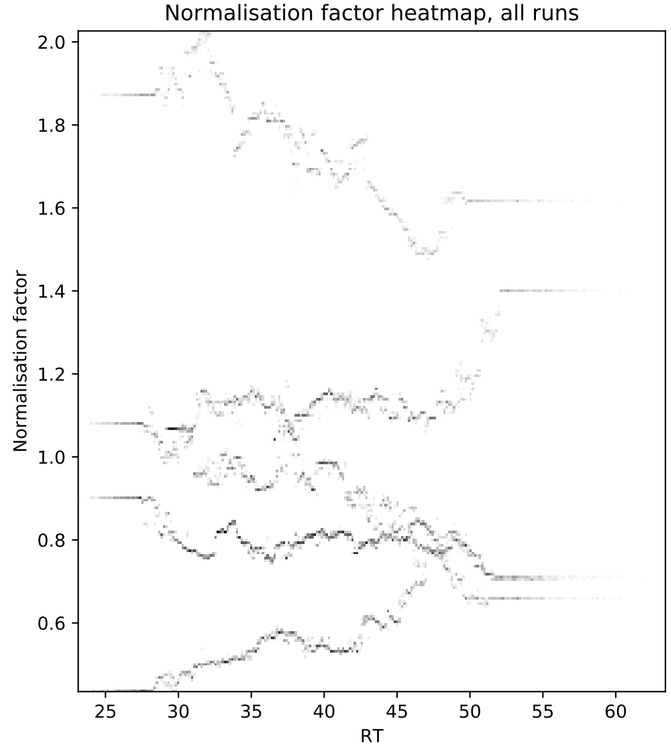

Identification consistency: precursors, CDF
IDs
Missing values
0
2000
4000
6000
8000
10000
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

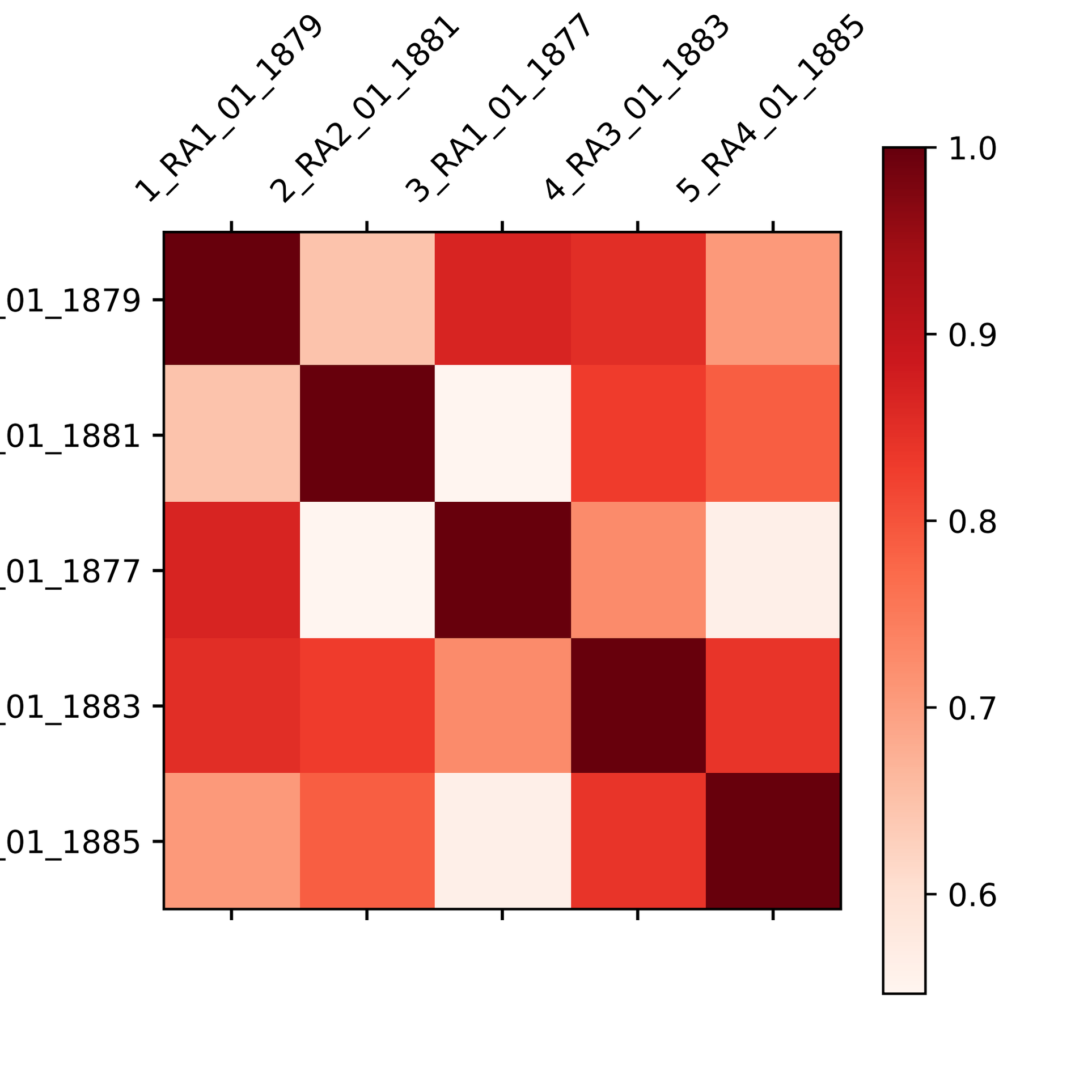

Identification consistency: protein groups, CDF
IDs
Missing values
0
250
500
750
1000
1250
1500
1750
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

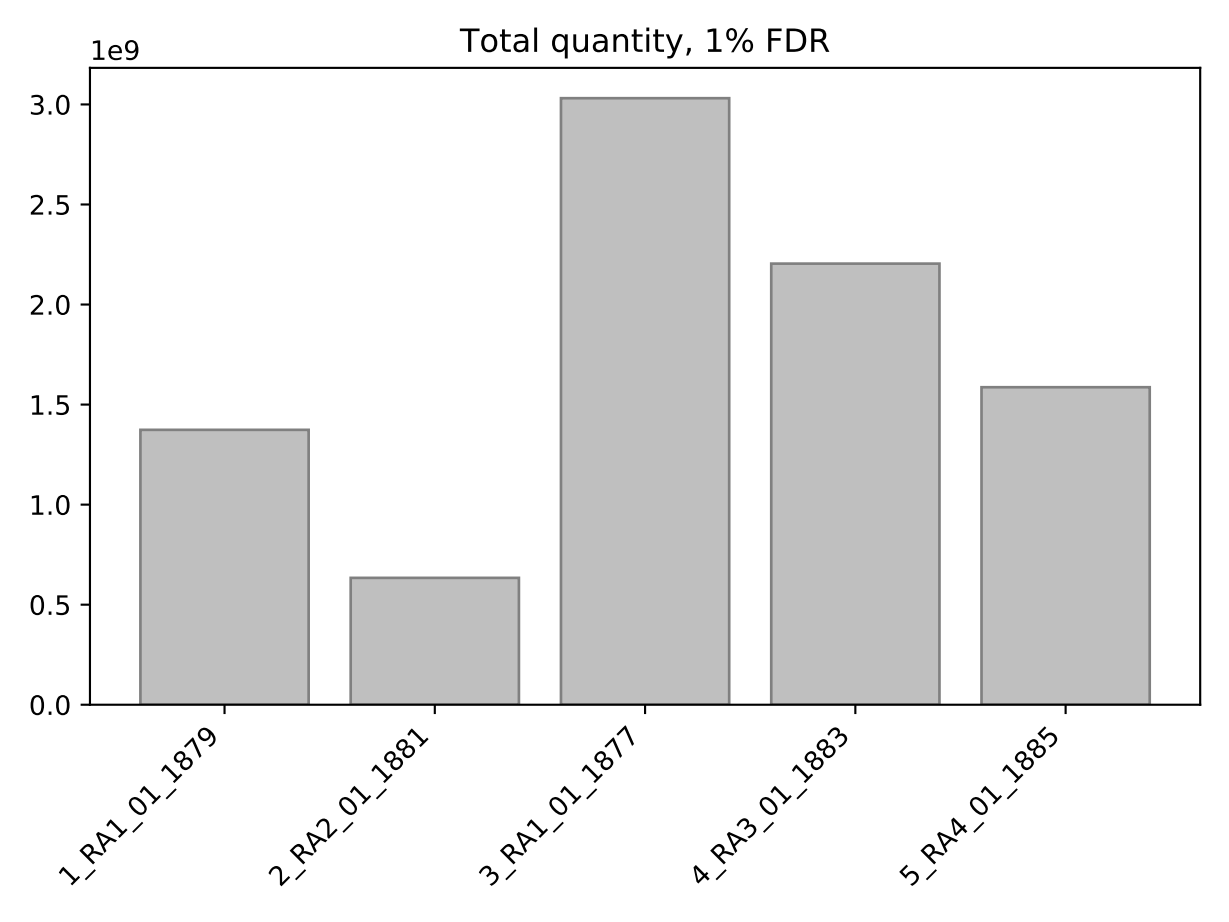

Identification consistency: genes groups, CDF
IDs
Missing values
0
250
500
750
1000
1250
1500
1750
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0

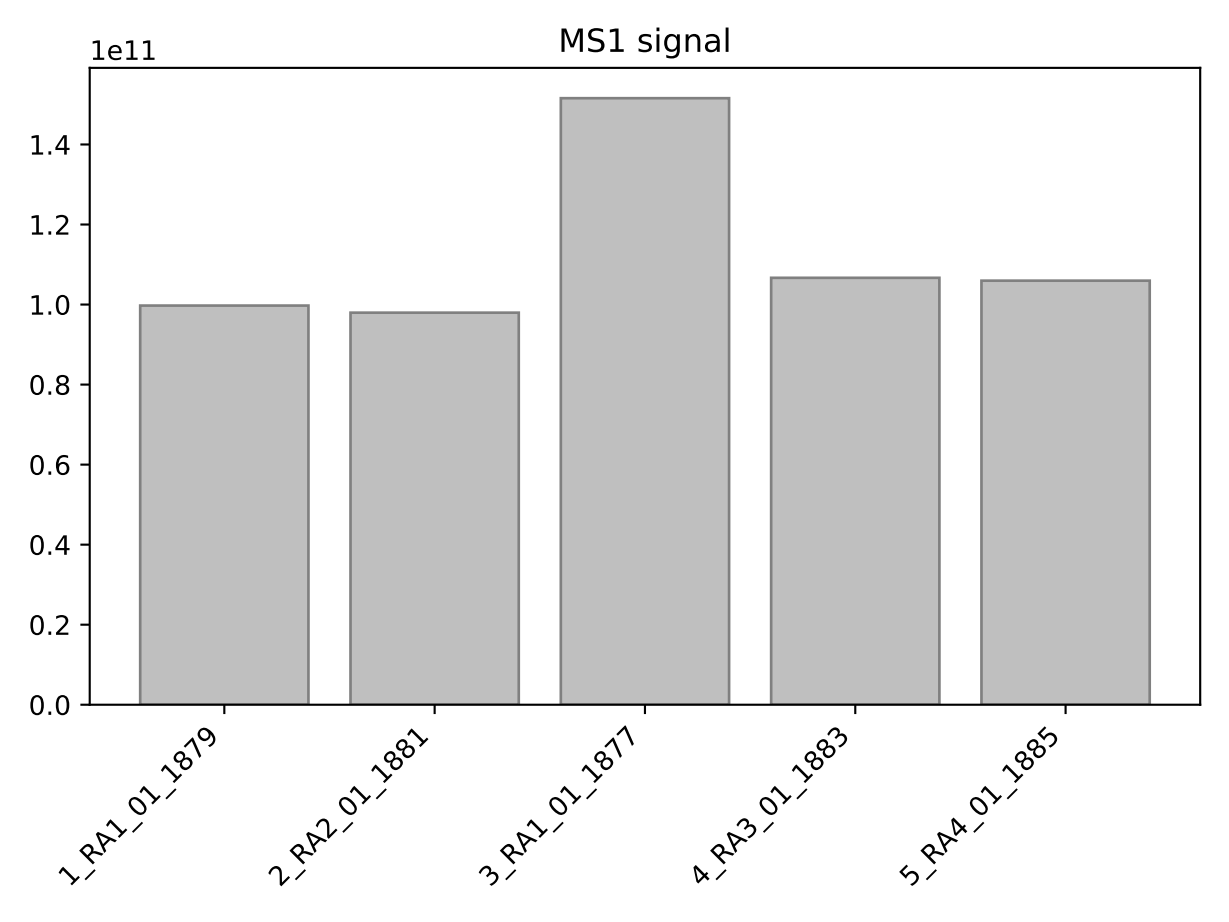

Retention times heatmap, all runs
RT
Library iRT
60
55
50
45
40
35
30
25
0
50
100
150

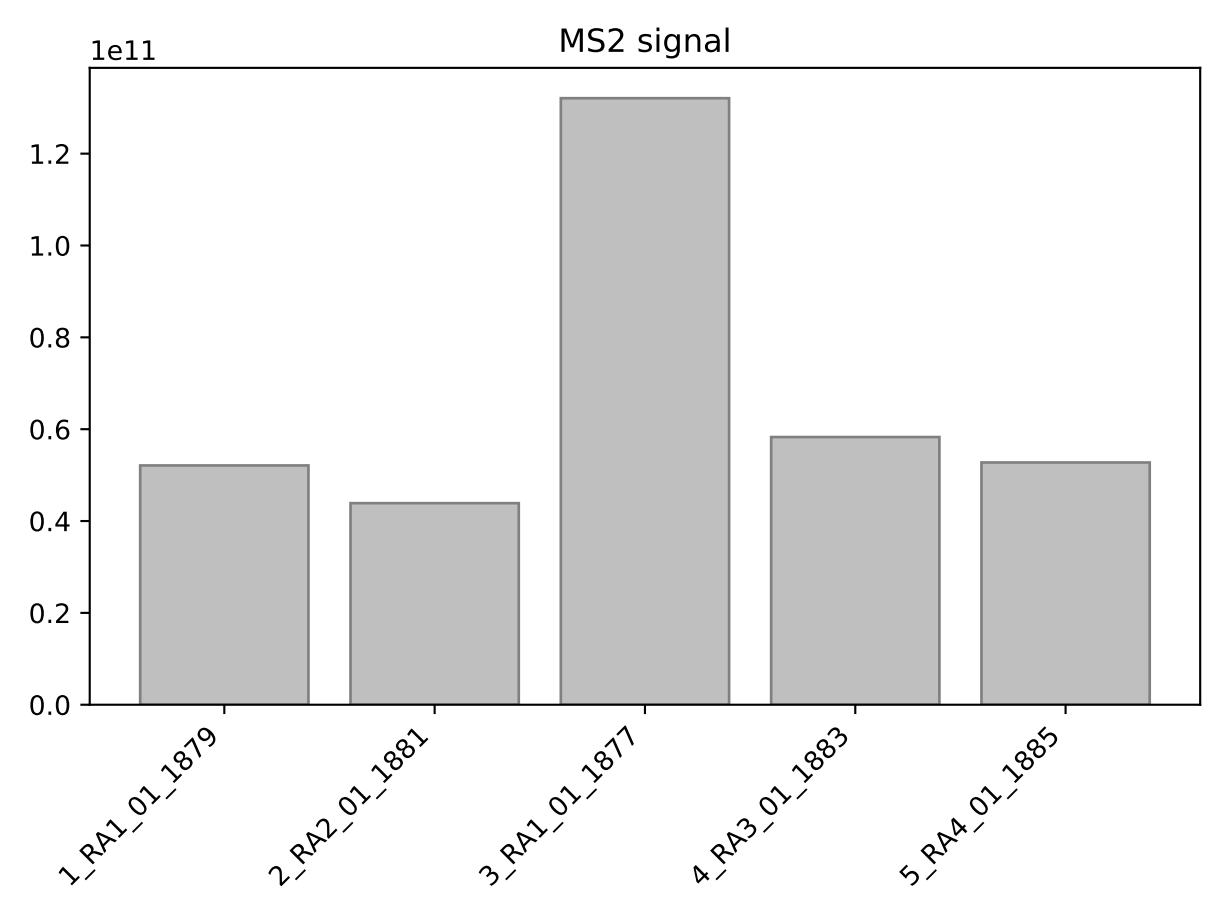

Retention time accuracy heatmap, all runs
RT
Predicted RT
60
55
50
45
40
35
30
25

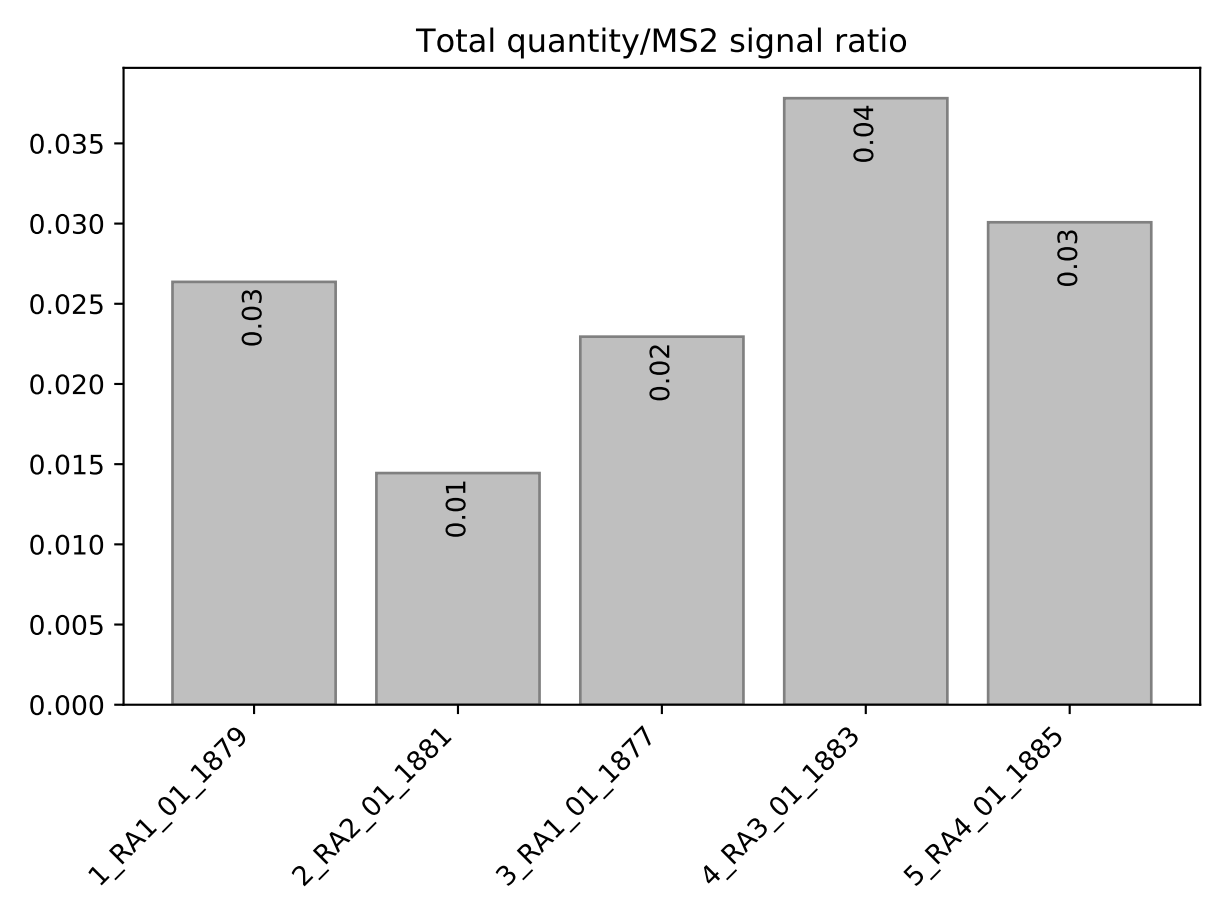

Normalisation factor heatmap, all runs
Normalisation factor
RT
2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6

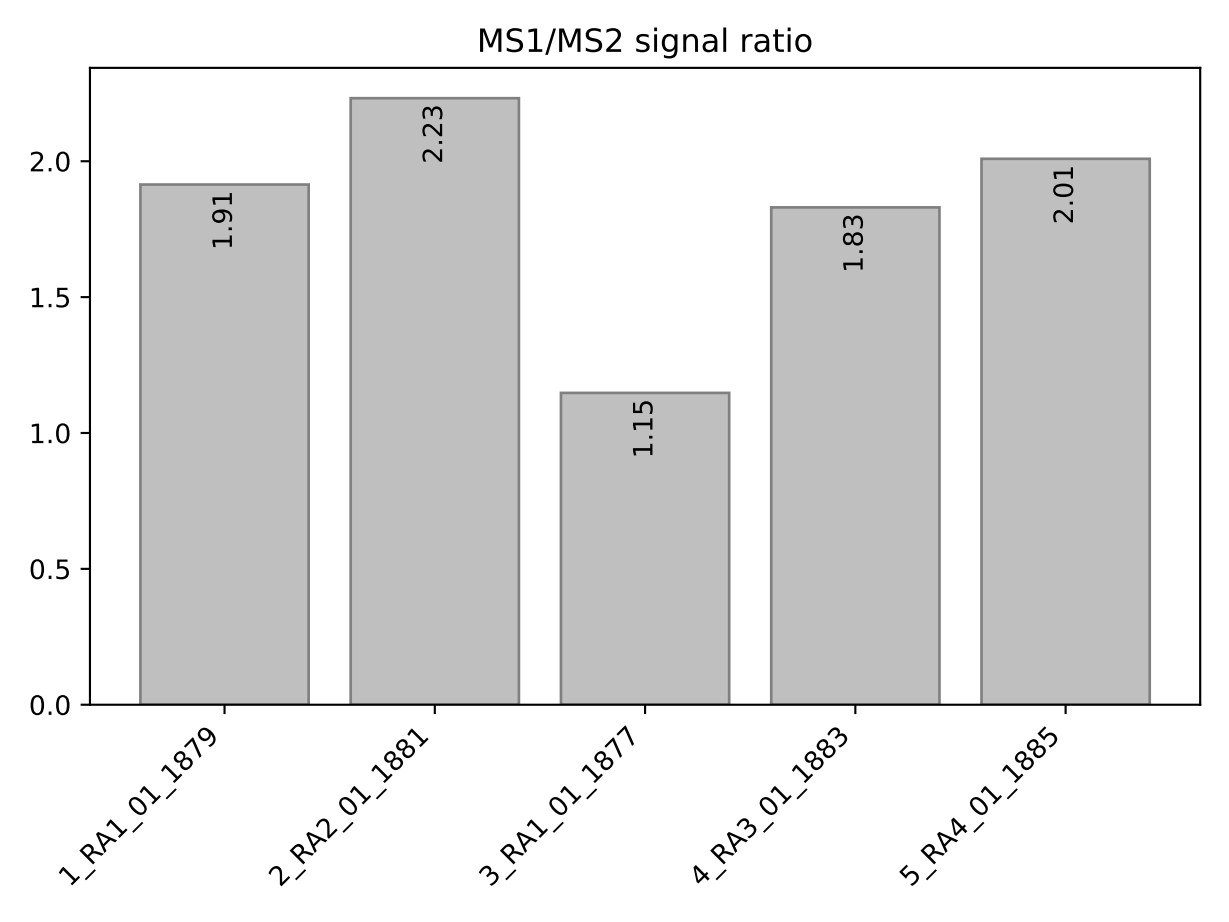

1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885
_01_1879
_01_1881
_01_1877
_01_1883
_01_1885
1.0
0.9
0.8
0.7
0.6

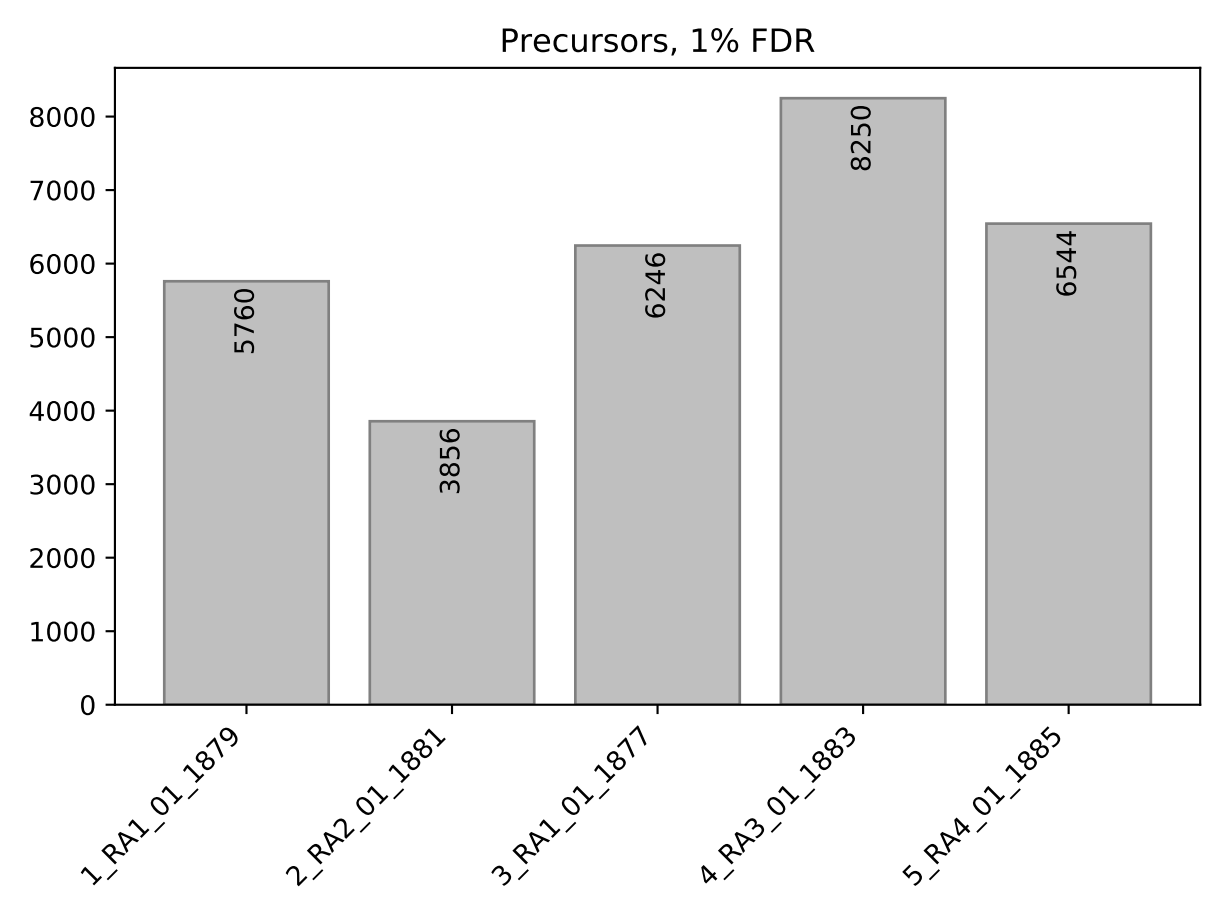

Total quantity, 1% FDR
1e9
3.0
2.5
2.0
1.5
1.0
0.5
0.0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

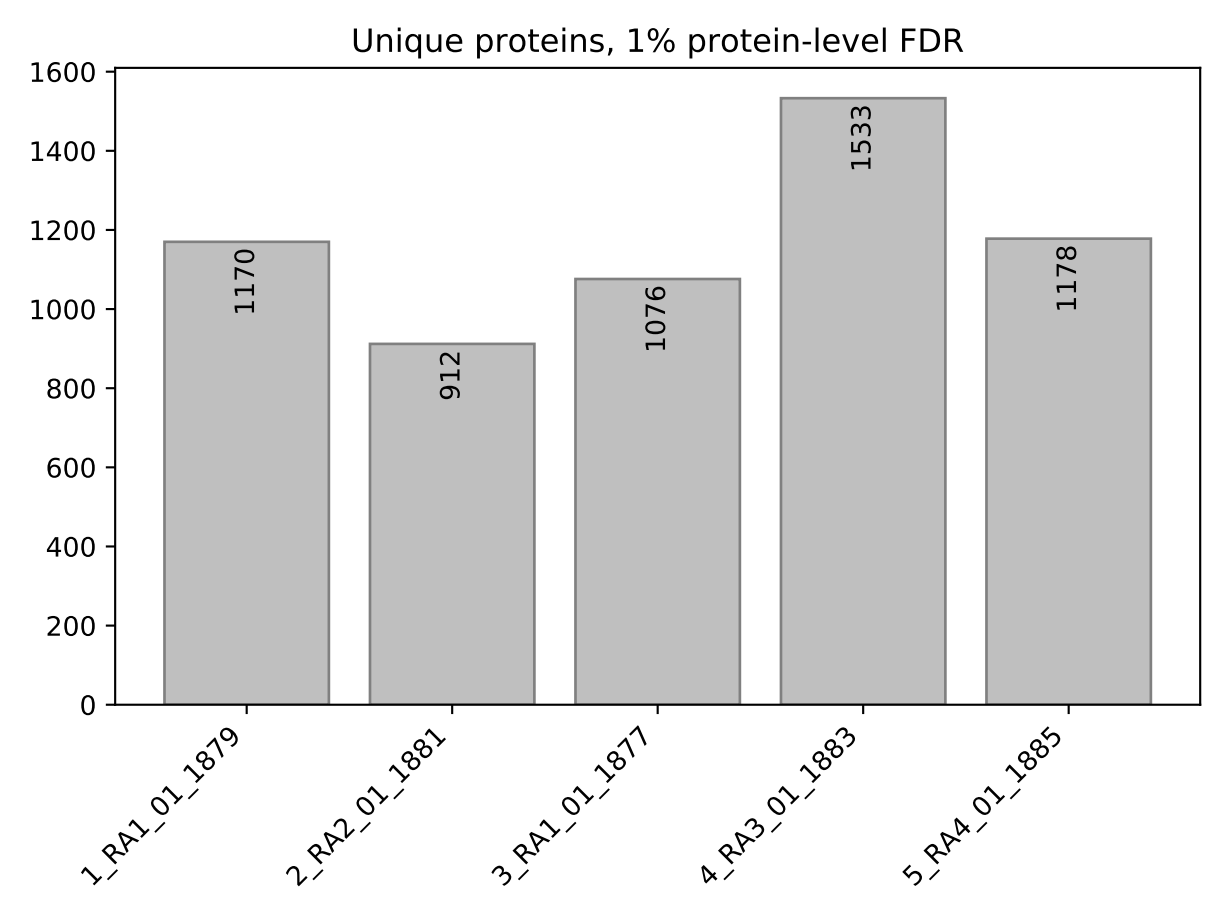

MS1 signal
1e11
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

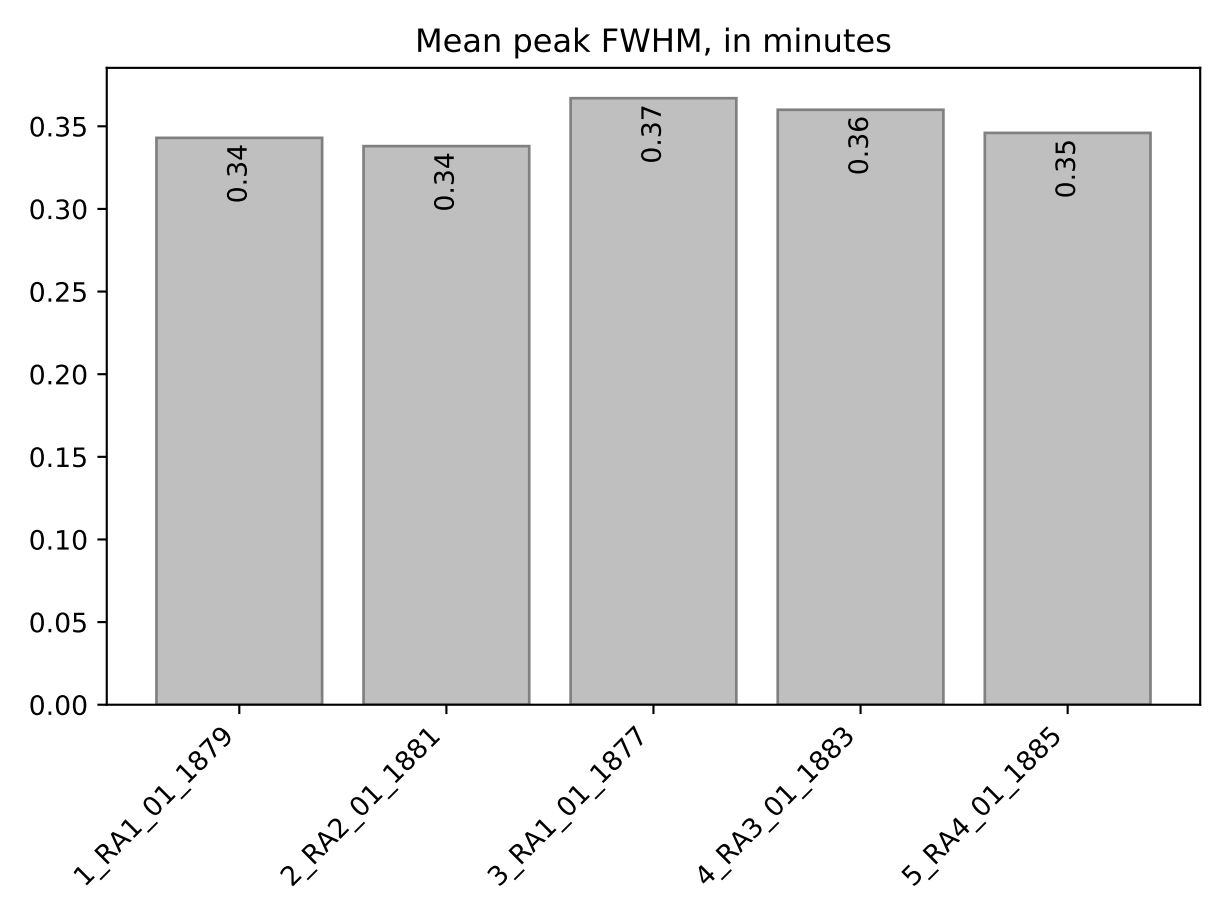

MS2 signal
1e11
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

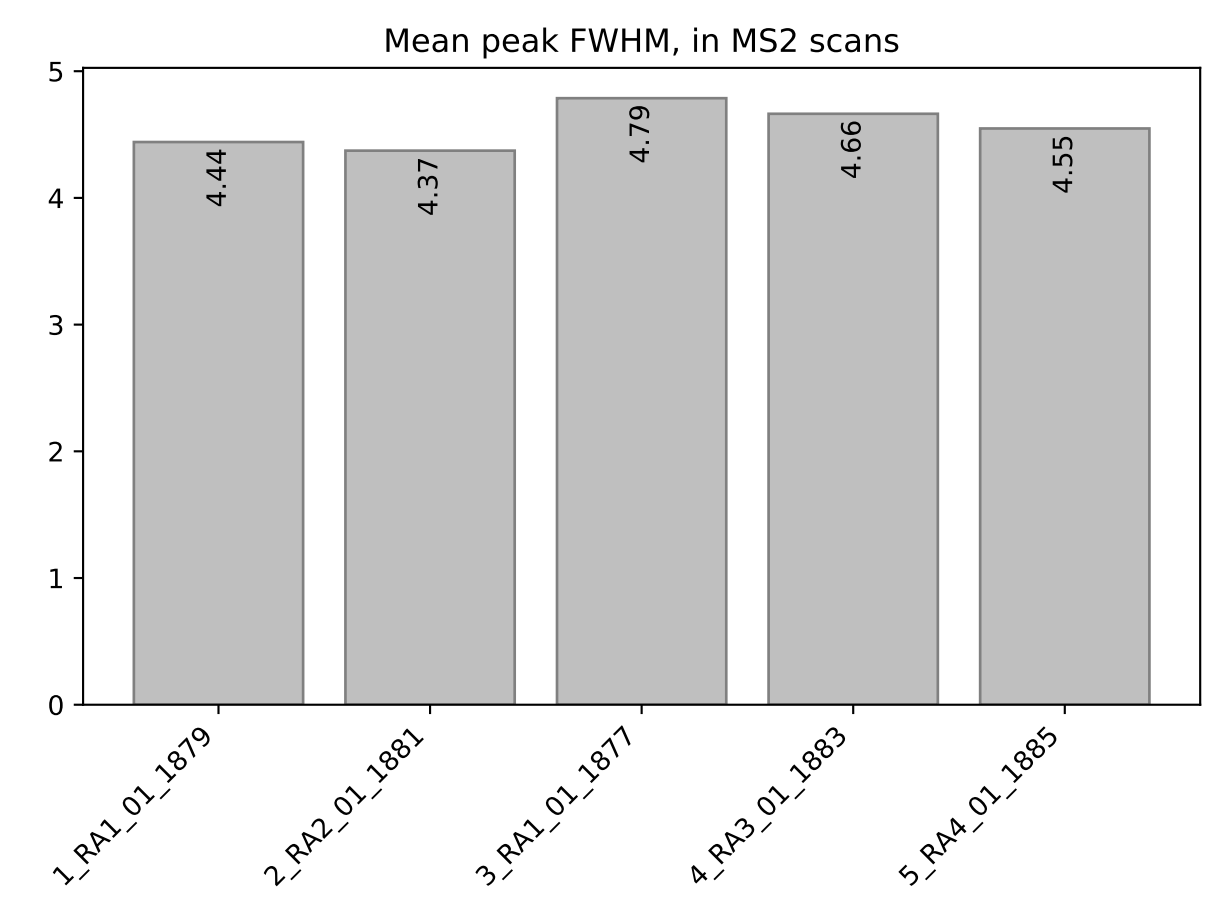

Total quantity/MS2 signal ratio
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0.03
0.01
0.02
0.04
0.03
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

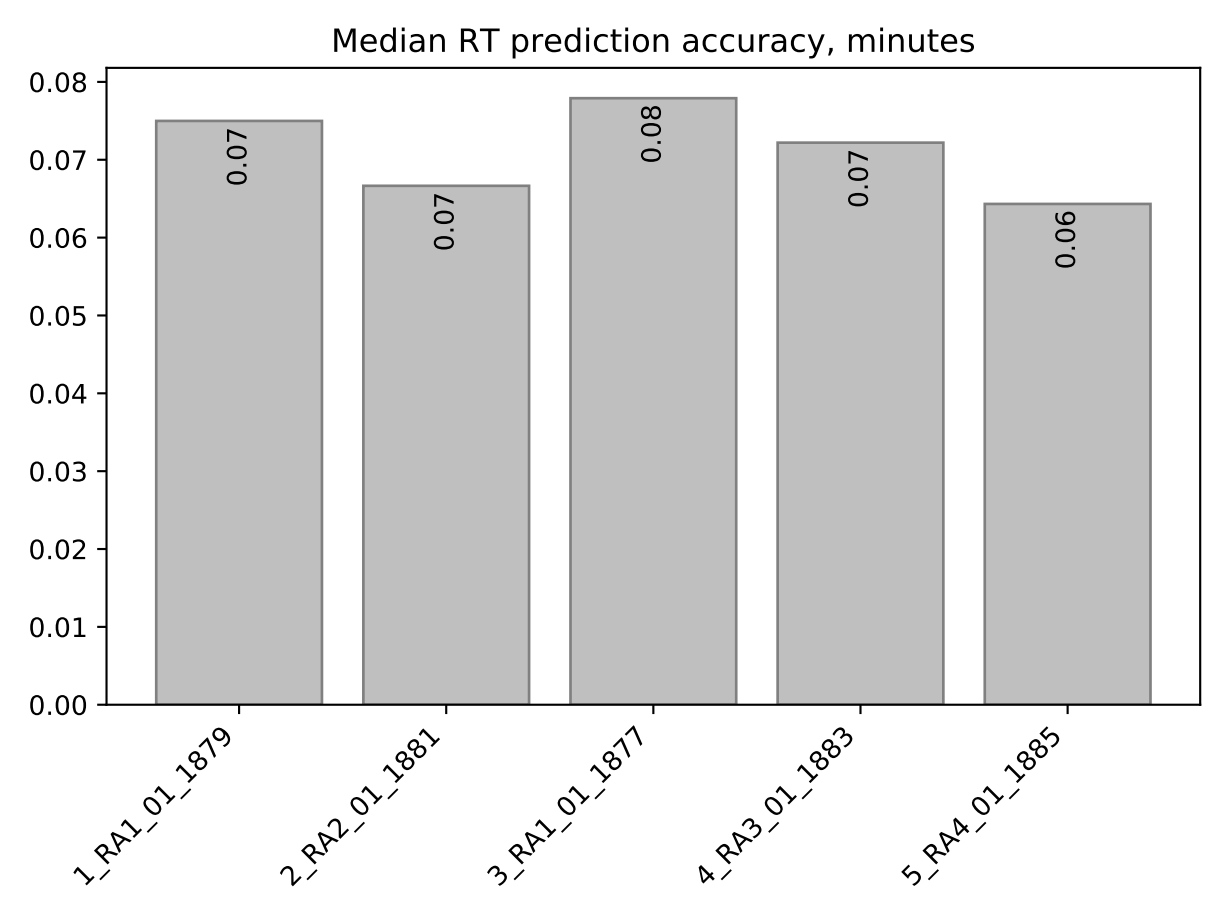

MS1/MS2 signal ratio
2.0
1.5
1.0
0.5
0.0
1.91
2.23
1.15
1.83
2.01
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

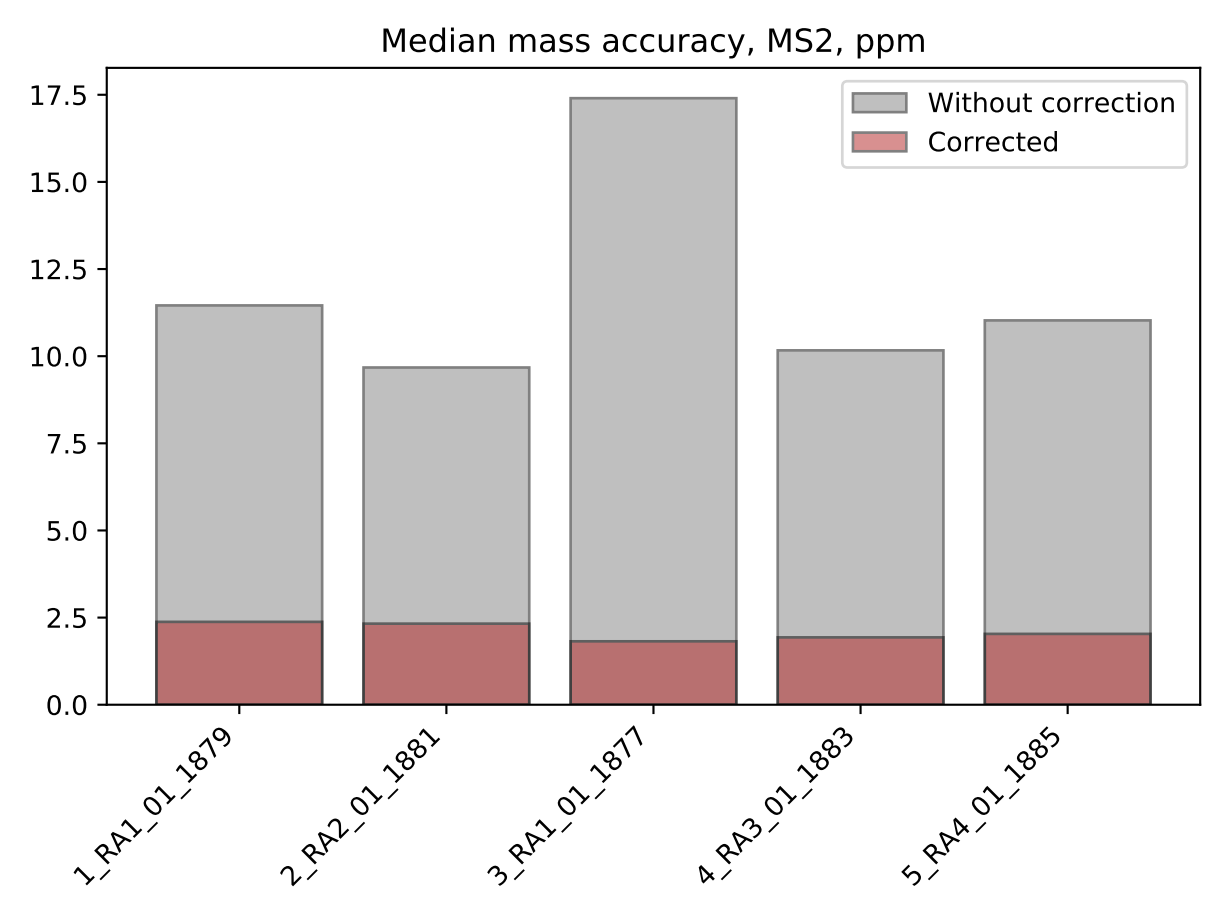

Precursors, 1% FDR
8000
7000
6000
5000
4000
3000
2000
1000
0
5760
3856
6246
8250
6544
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

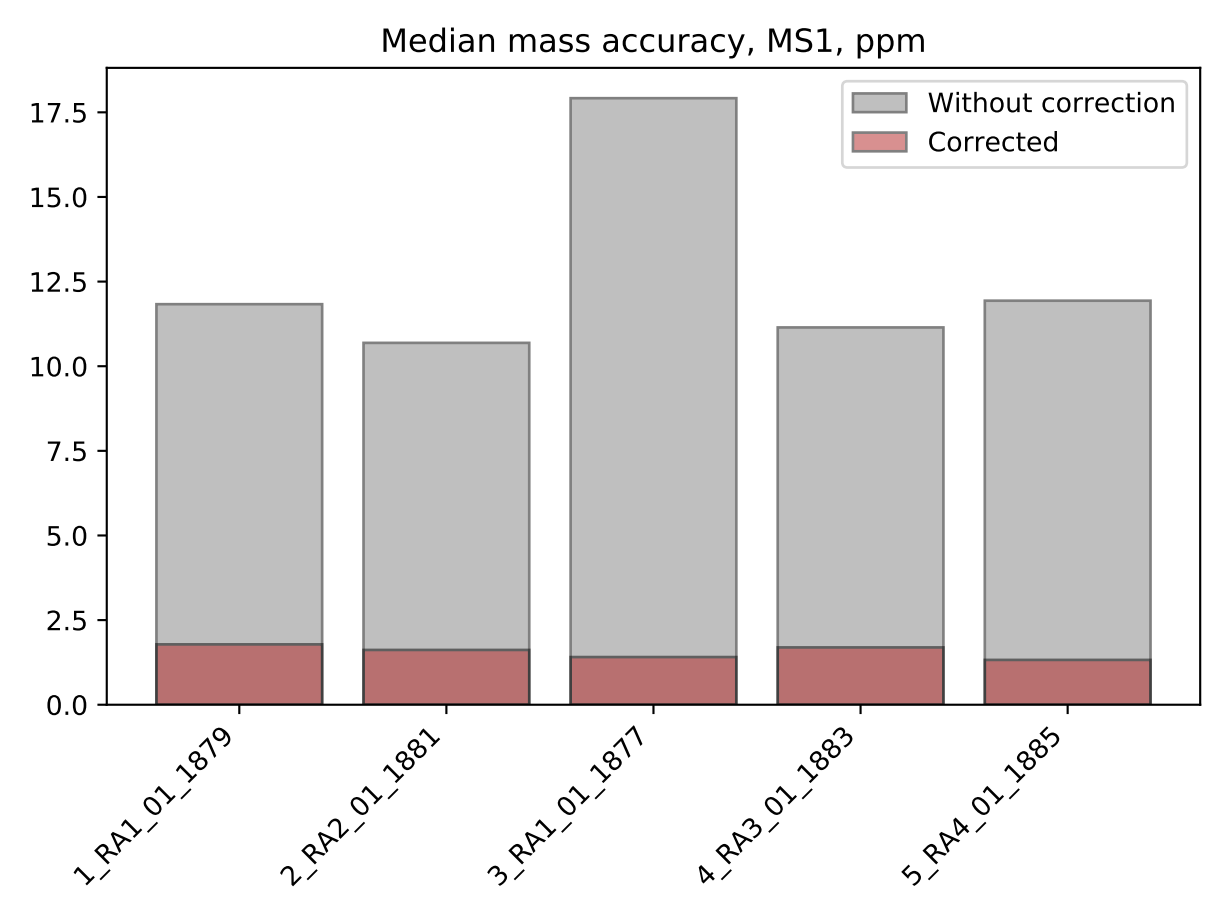

Unique proteins, 1% protein-level FDR
1600
1400
1200
1000
800
600
400
200
0
1170
912
1076
1533
1178
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

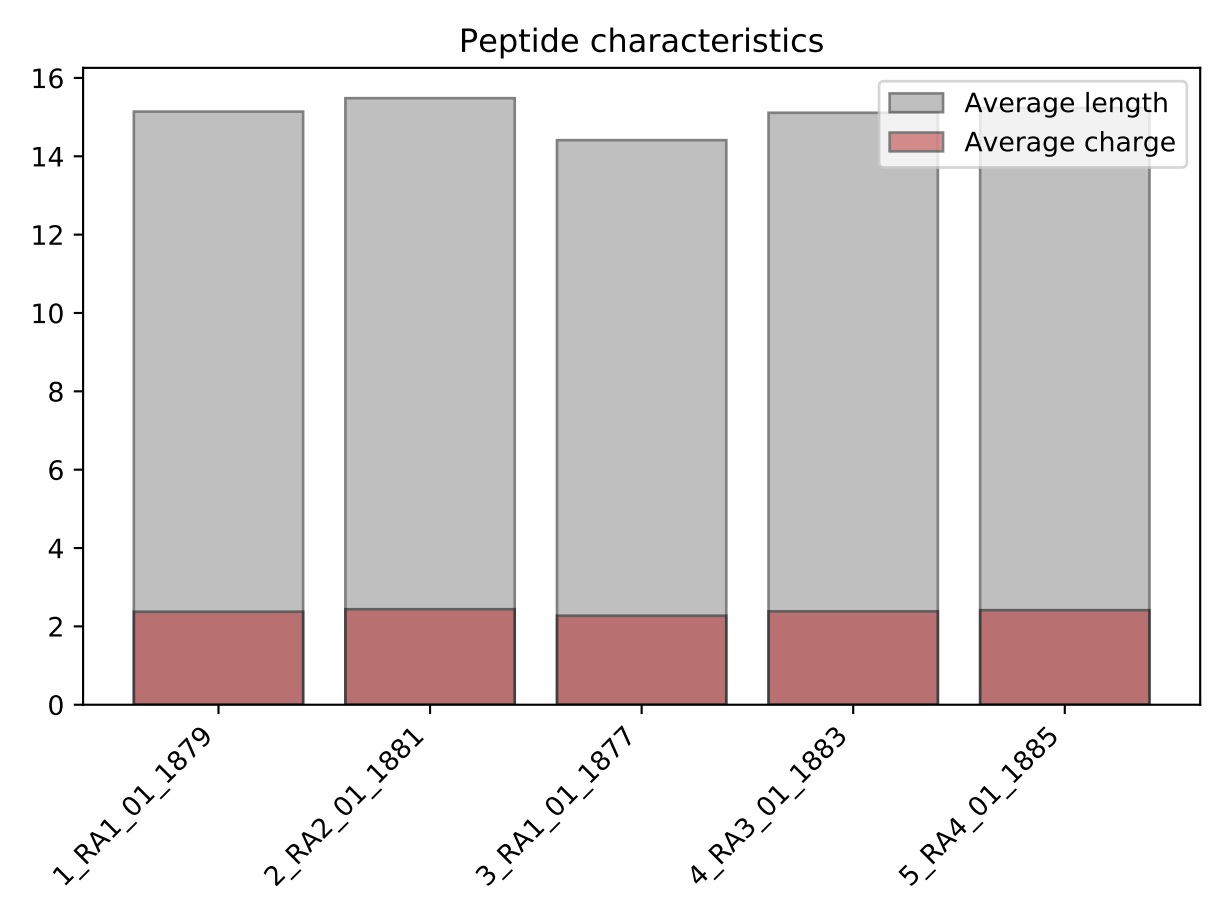

Mean peak FWHM, in minutes
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.34
0.34
0.37
0.36
0.35
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885

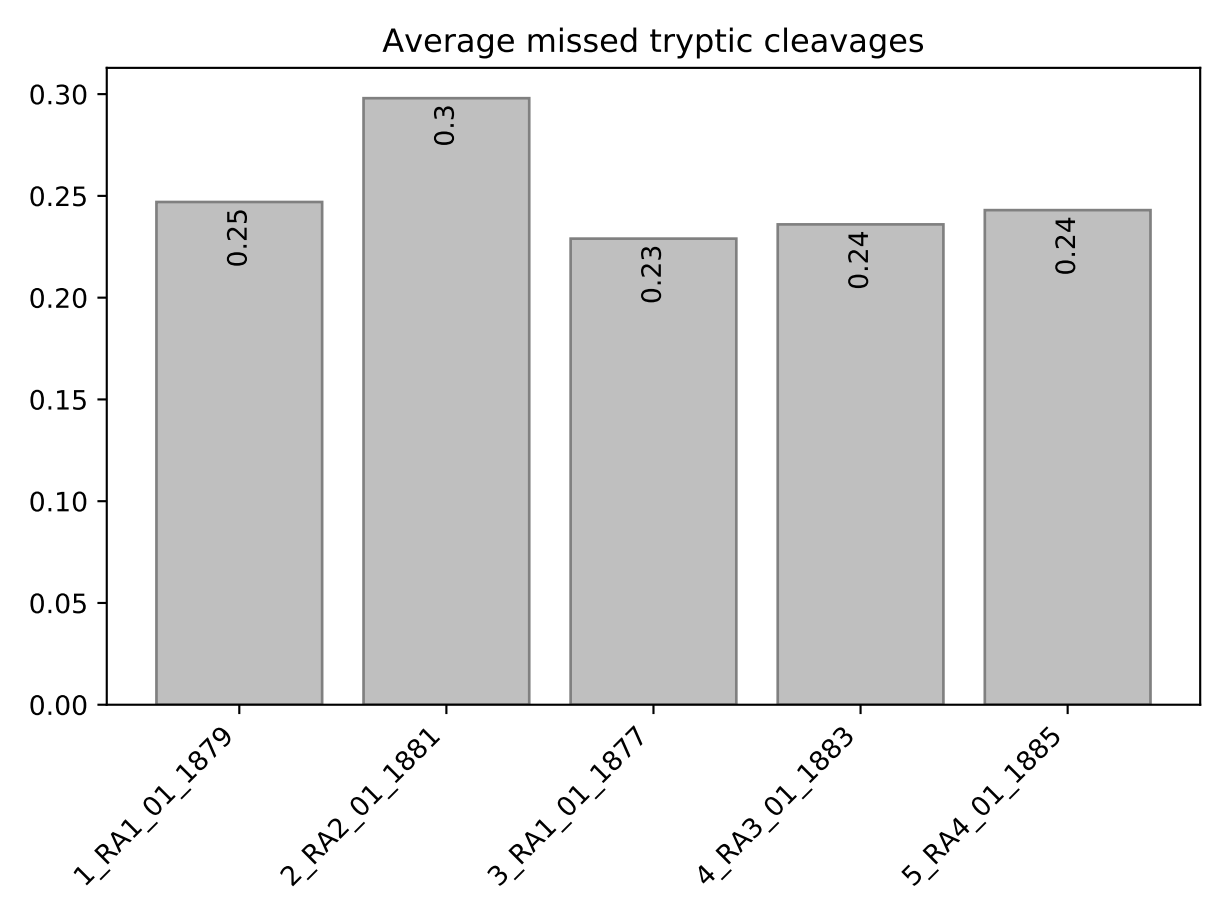

Mean peak FWHM, in MS2 scans
5
4
3
2
1
0
4.44
4.37
4.79
4.66
4.55
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885


Median RT prediction accuracy, minutes
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
0.07
0.07
0.08
0.07
0.06
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885


Median mass accuracy, MS2, ppm
Without correction
Corrected
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885


Median mass accuracy, MS1, ppm
Without correction
Corrected
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885


Peptide characteristics
Average length
Average charge
16
14
12
10
8
6
4
2
0
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885


Average missed tryptic cleavages
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.25
0.3
0.23
0.24
0.24
1_RA1_01_1879
2_RA2_01_1881
3_RA1_01_1877
4_RA3_01_1883
5_RA4_01_1885