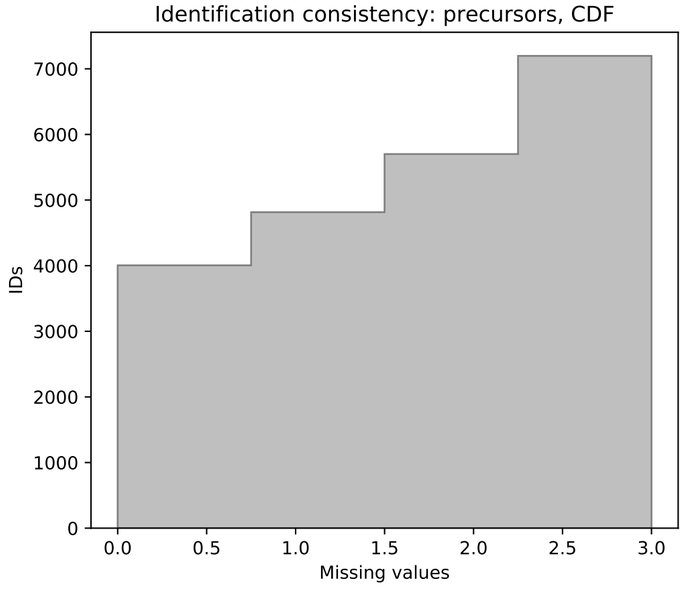
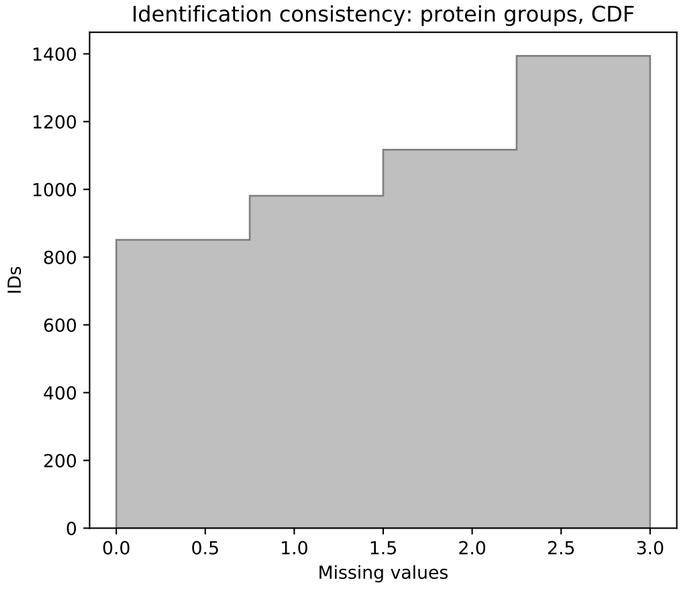
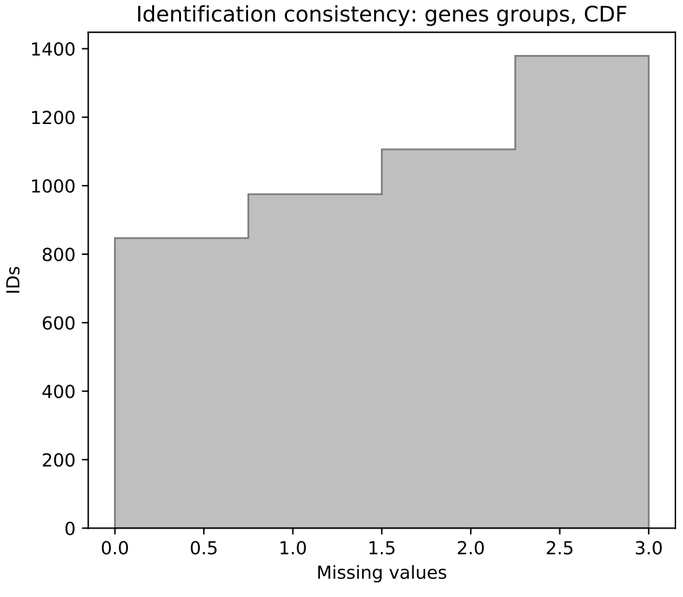
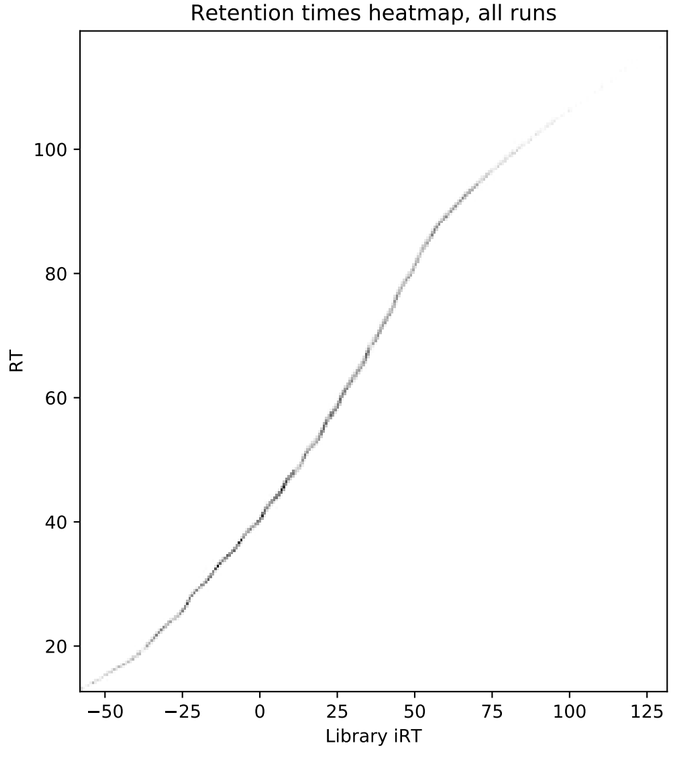
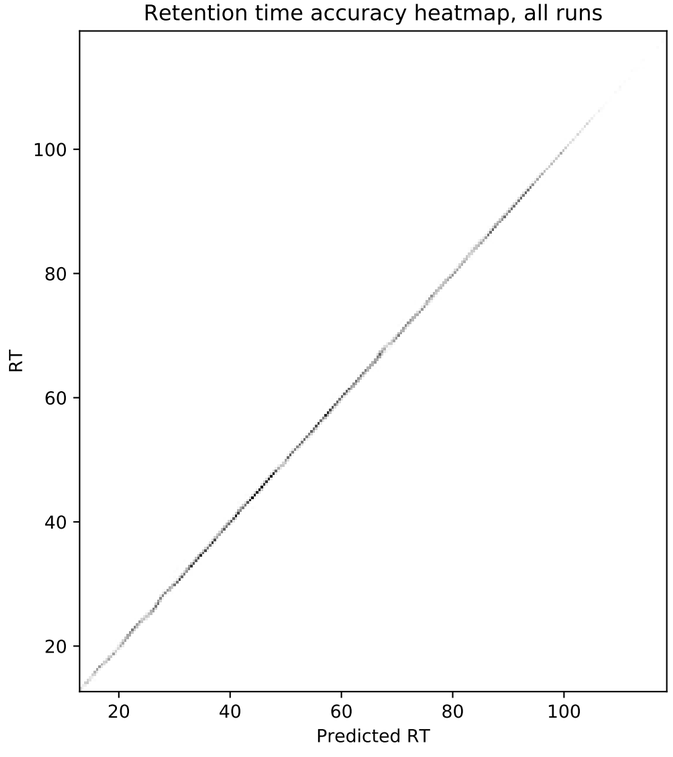
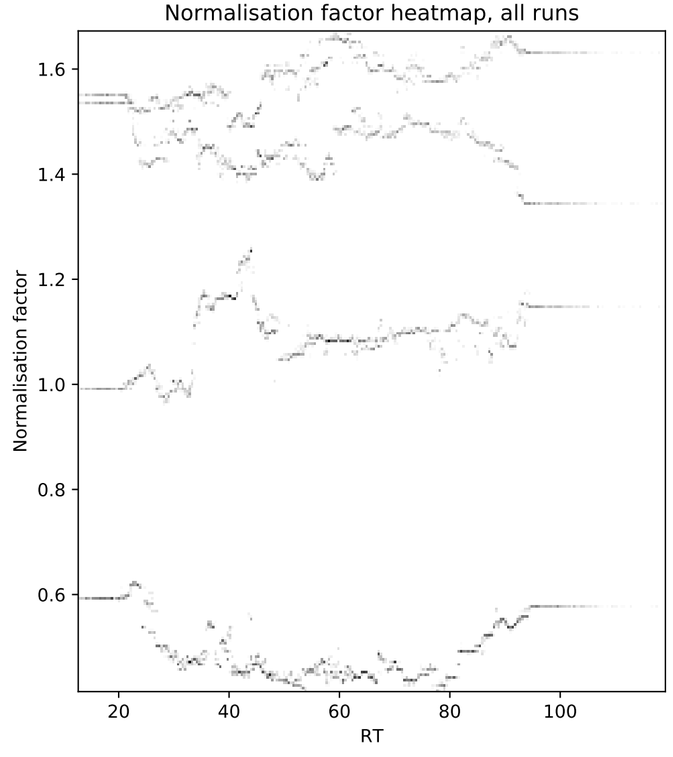

Identification consistency: precursors, CDF
IDs
Missing values
0
1000
2000
3000
4000
5000
6000
7000
0.0
0.5
1.0
1.5
2.0
2.5
3.0

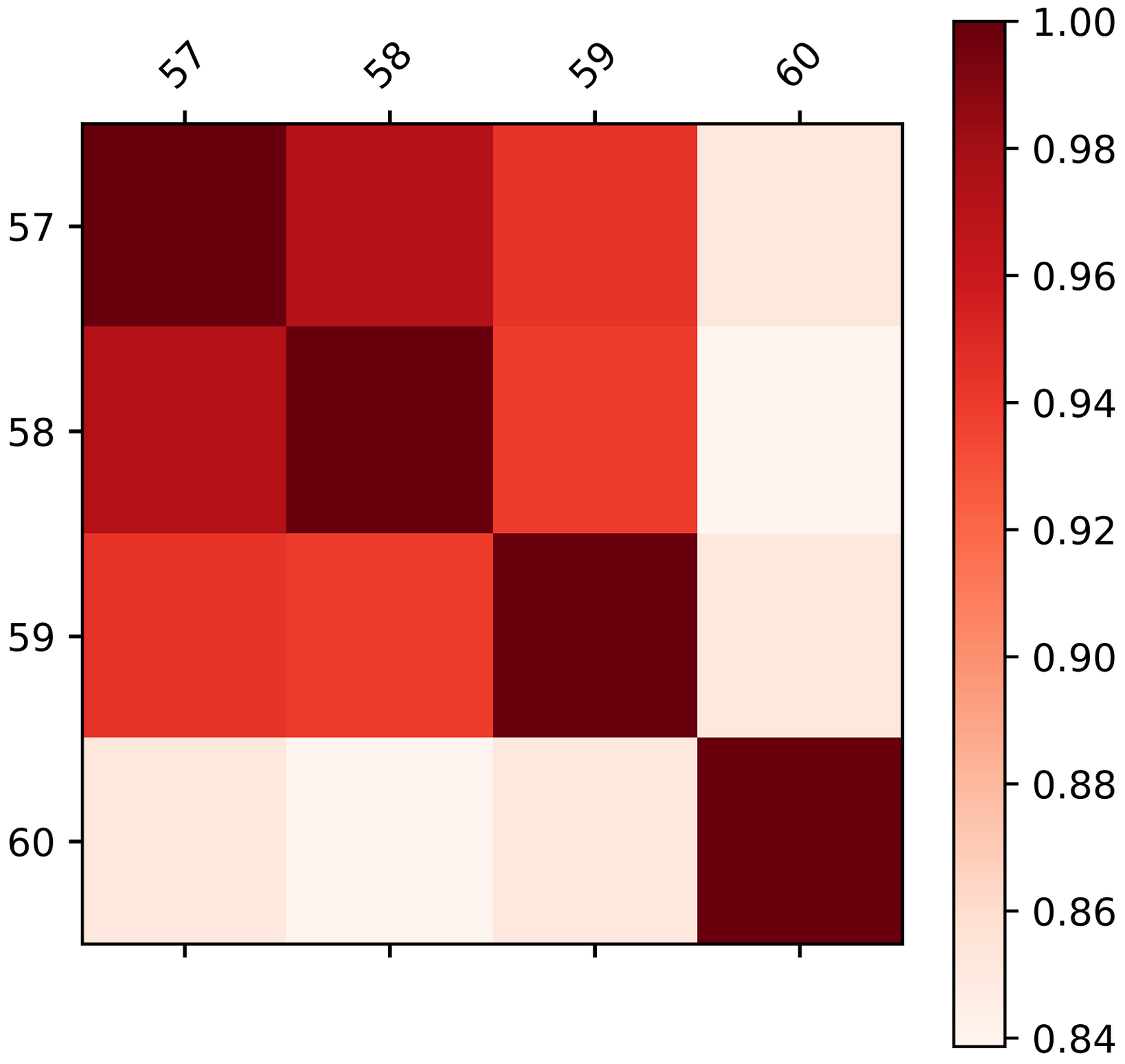

Identification consistency: protein groups, CDF
IDs
Missing values
0
200
400
600
800
1000
1200
1400
0.0
0.5
1.0
1.5
2.0
2.5
3.0

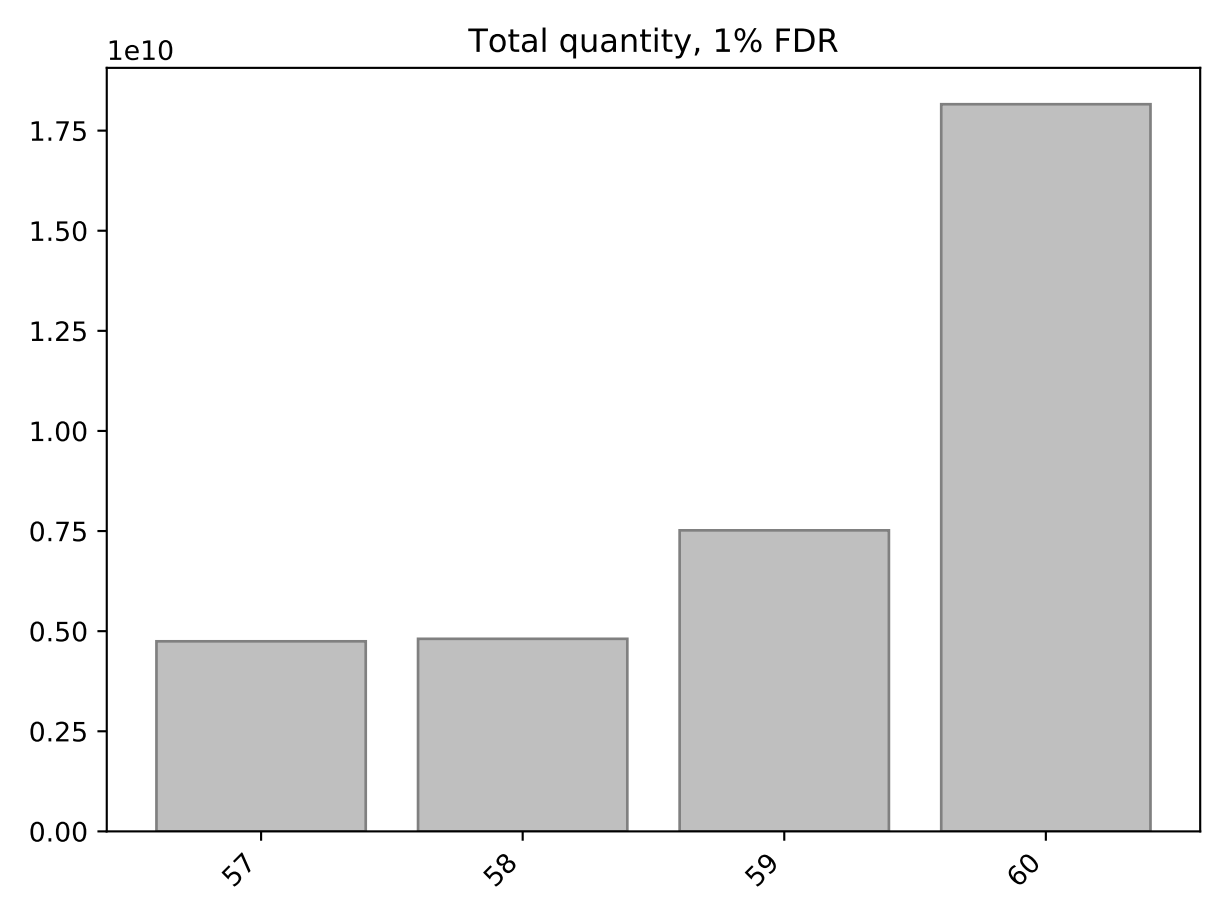

Identification consistency: genes groups, CDF
IDs
Missing values
0
200
400
600
800
1000
1200
1400
0.0
0.5
1.0
1.5
2.0
2.5
3.0

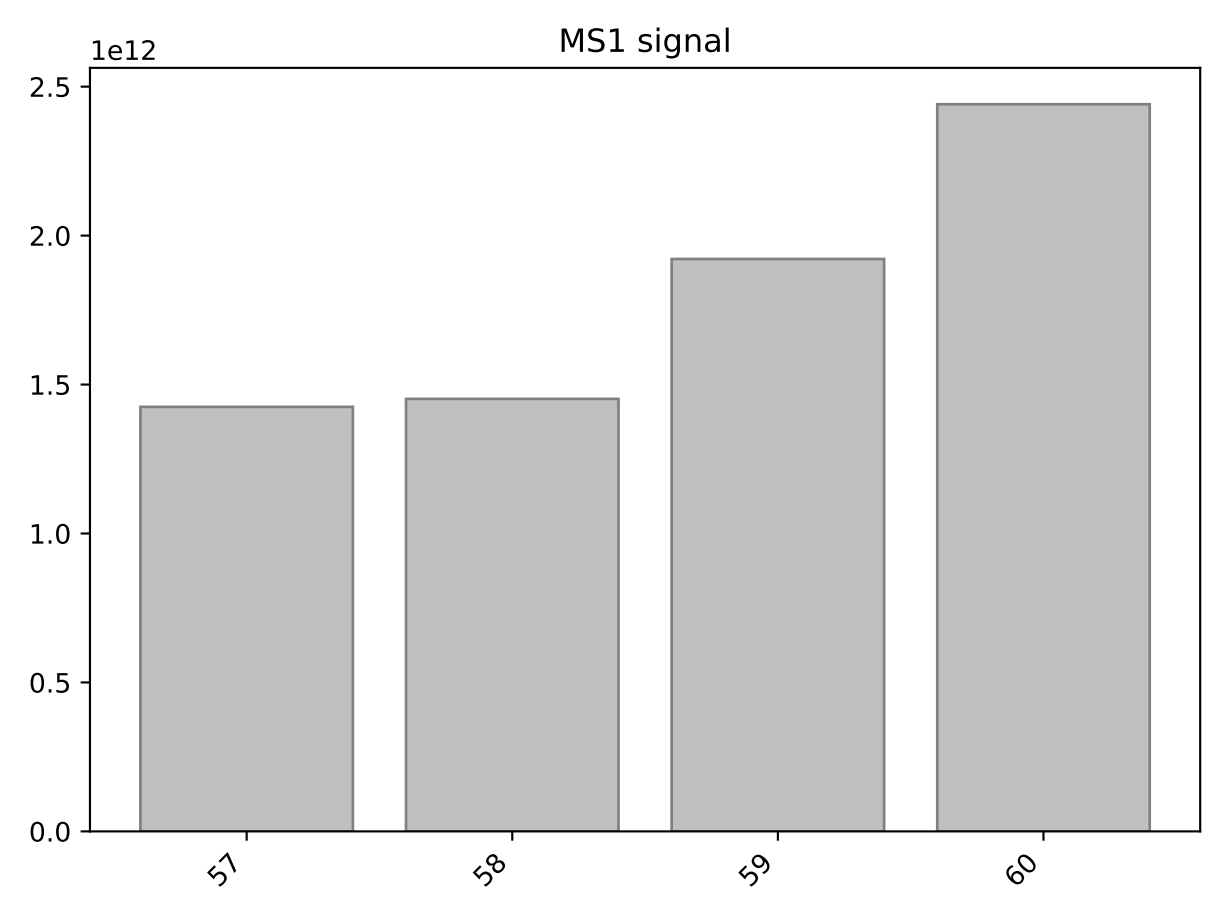

Retention times heatmap, all runs
RT
Library iRT
100
80
60
40
20
−50
−25
0
25
50
75
100
125

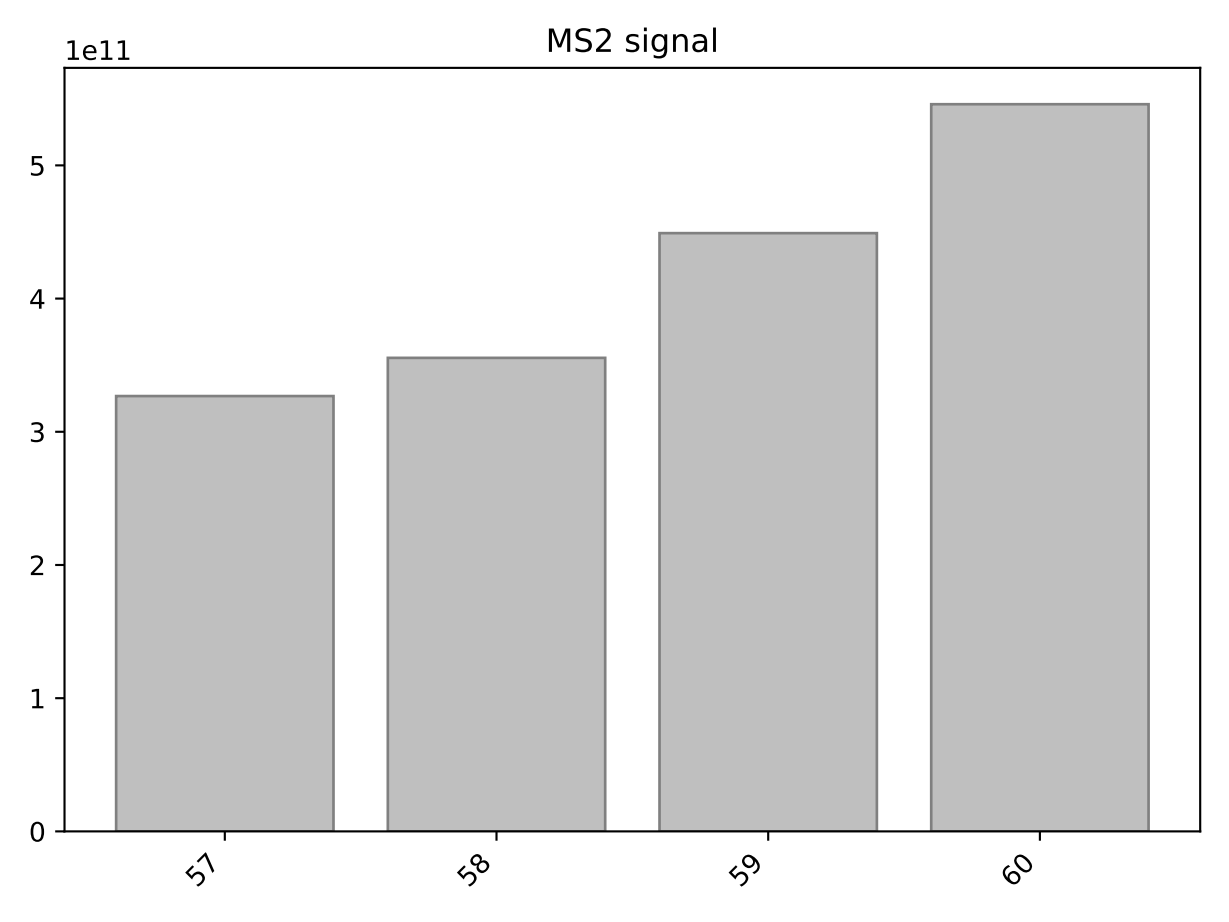

Retention time accuracy heatmap, all runs
RT
Predicted RT
100
80
60
40
20
20
40
60
80
100

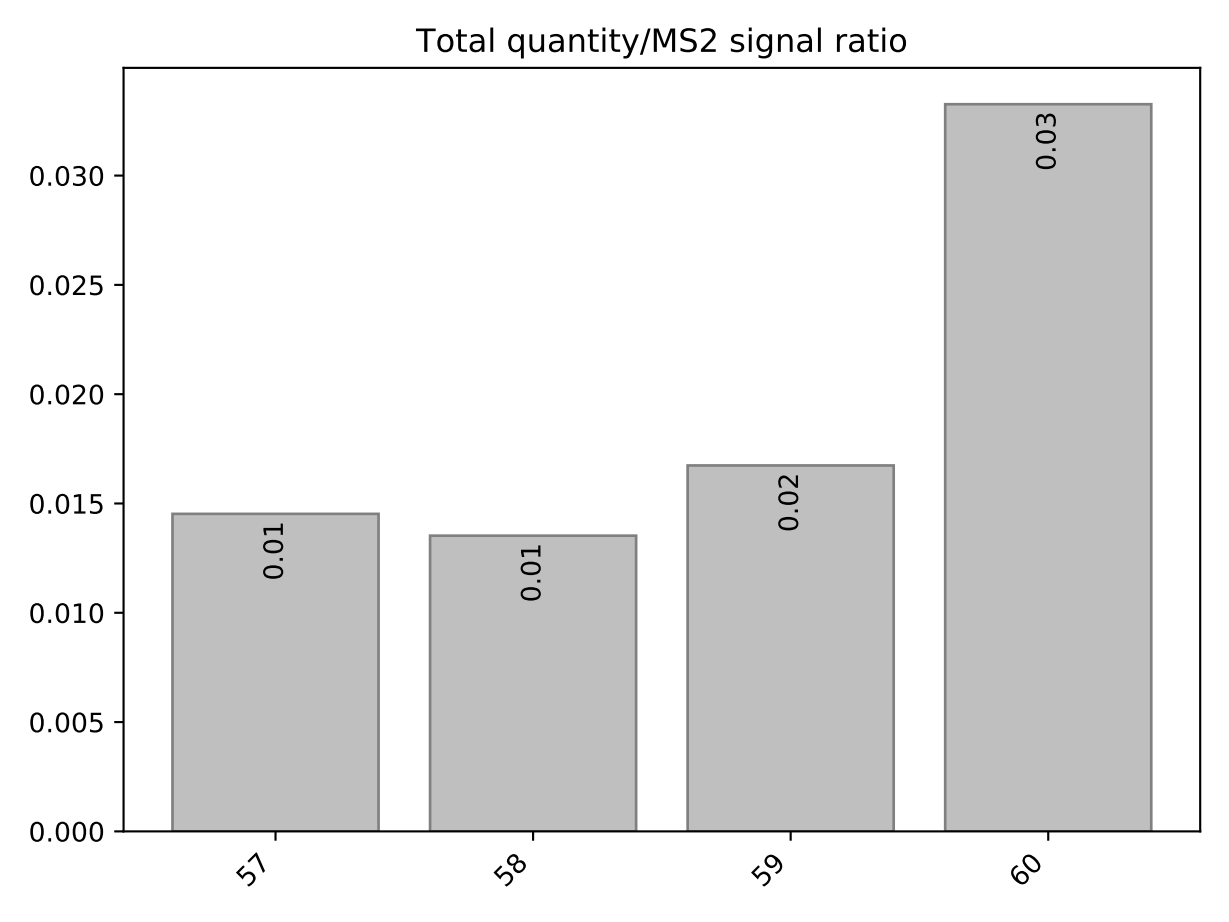

Normalisation factor heatmap, all runs
Normalisation factor
RT
1.6
1.4
1.2
1.0
0.8
0.6
20
40
60
80
100

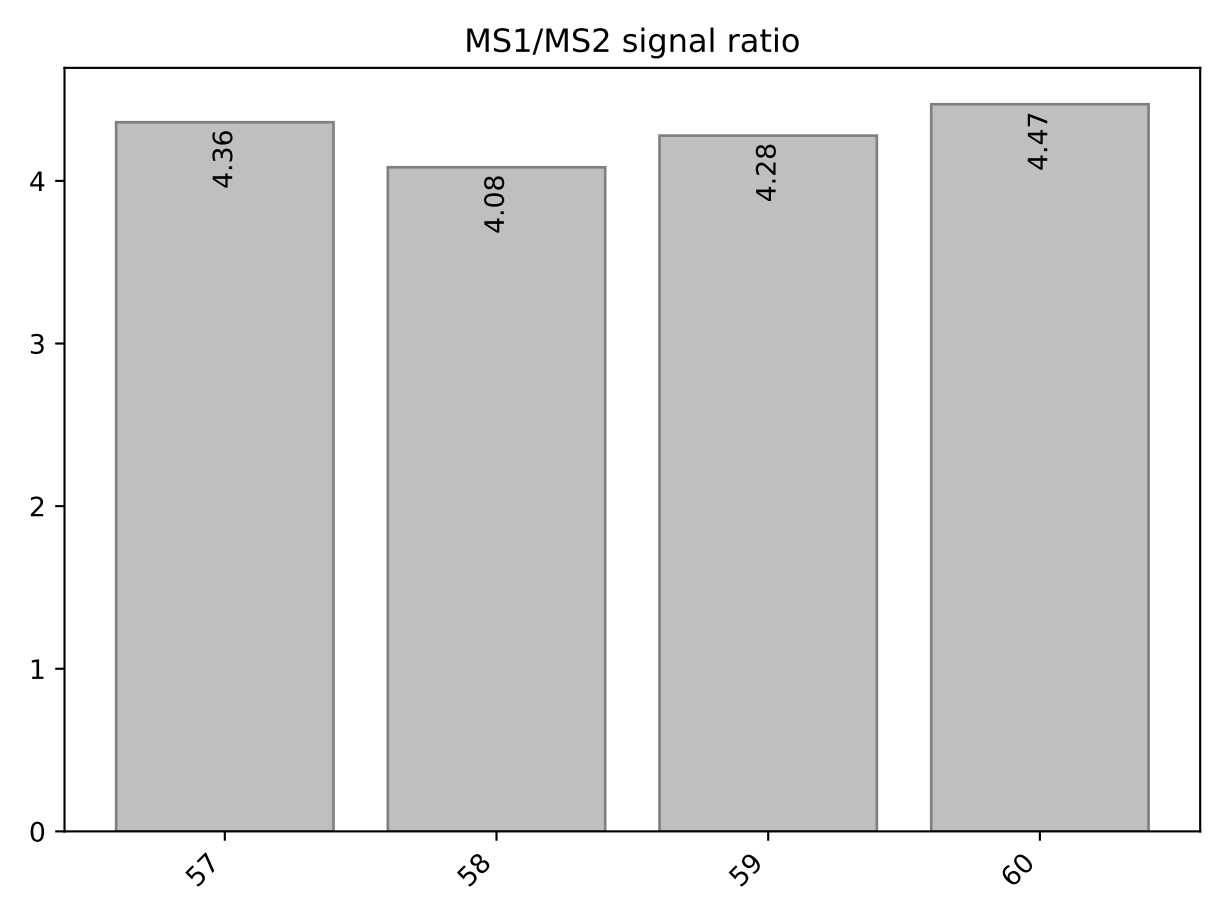

57
58
59
60
57
58
59
60
1.00
0.98
0.96
0.94
0.92
0.90
0.88
0.86
0.84

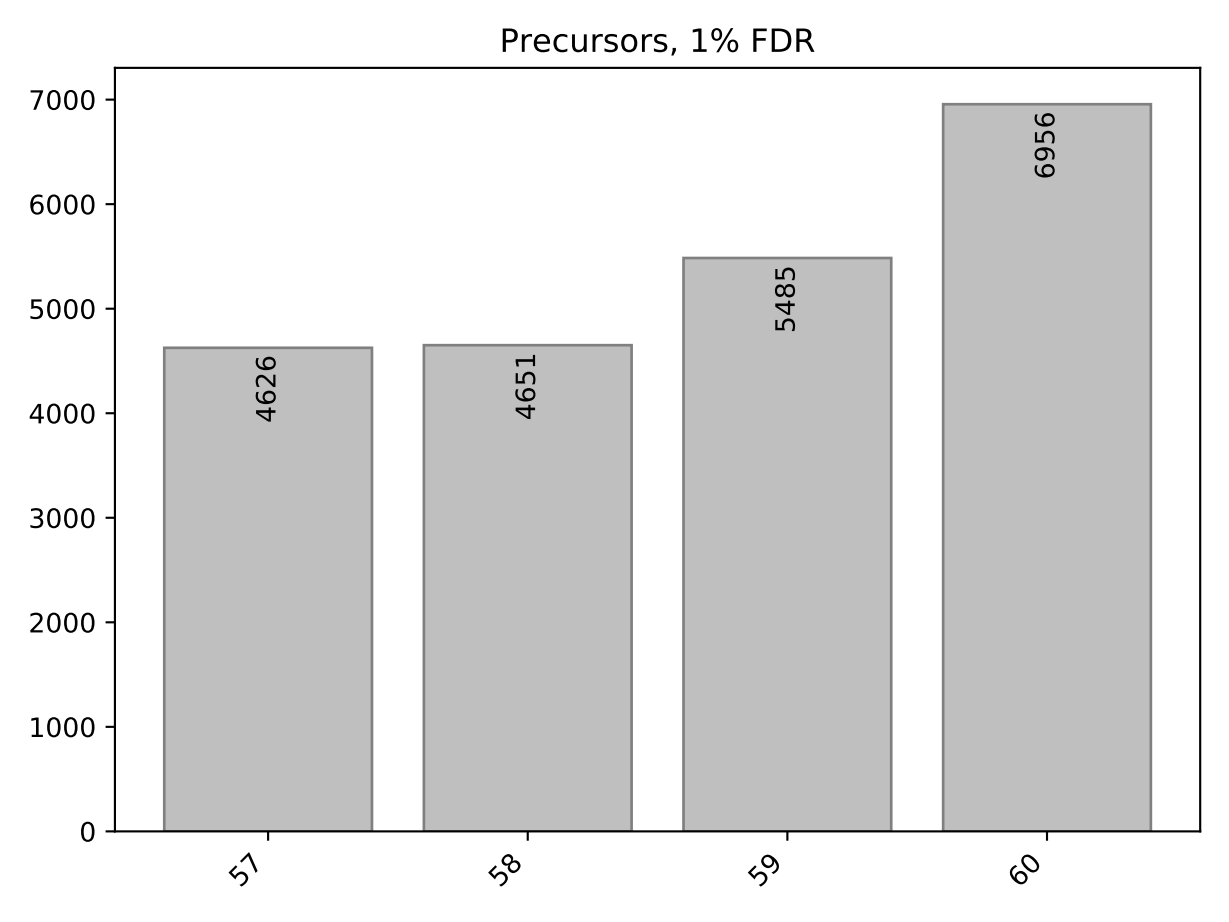

Total quantity, 1% FDR
1e10
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
57
58
59
60

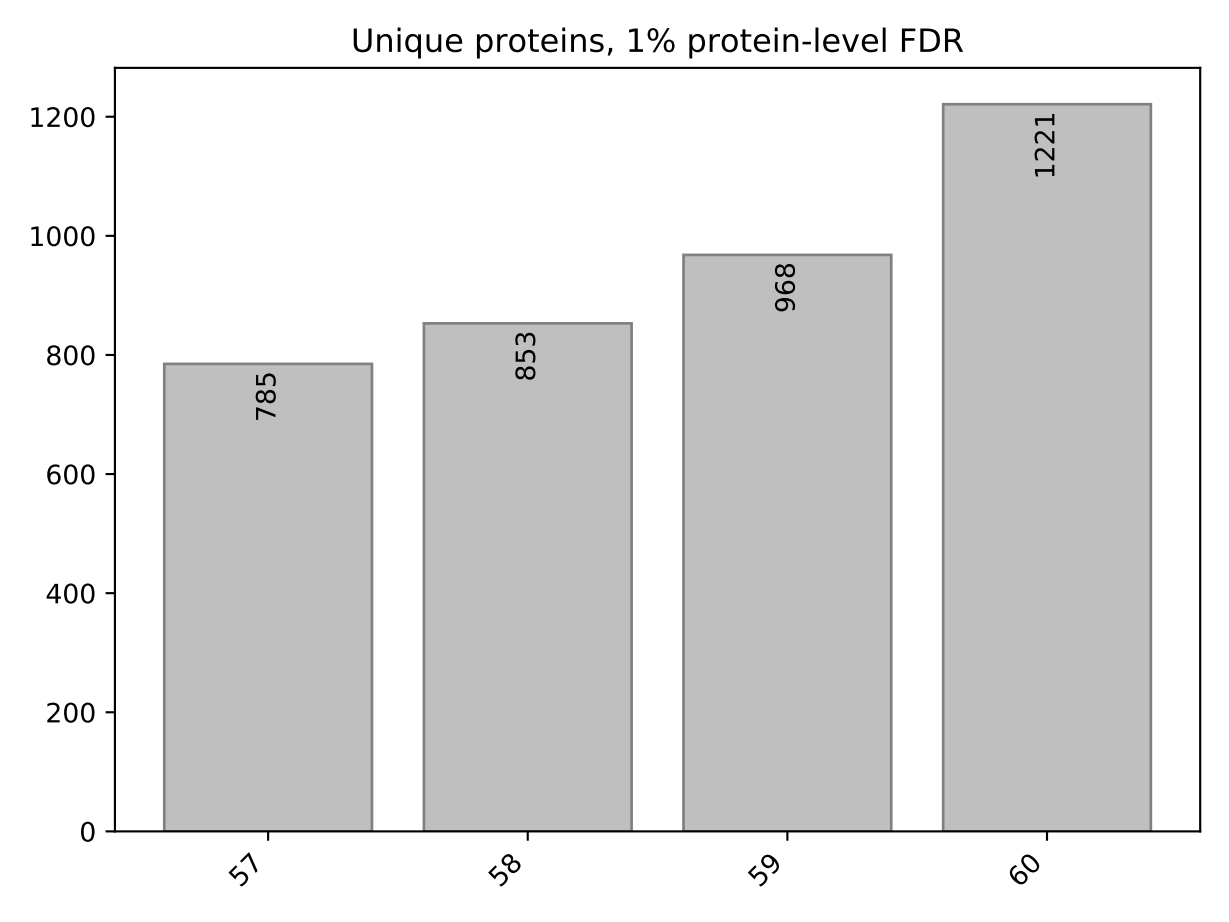

MS1 signal
1e12
2.5
2.0
1.5
1.0
0.5
0.0
57
58
59
60

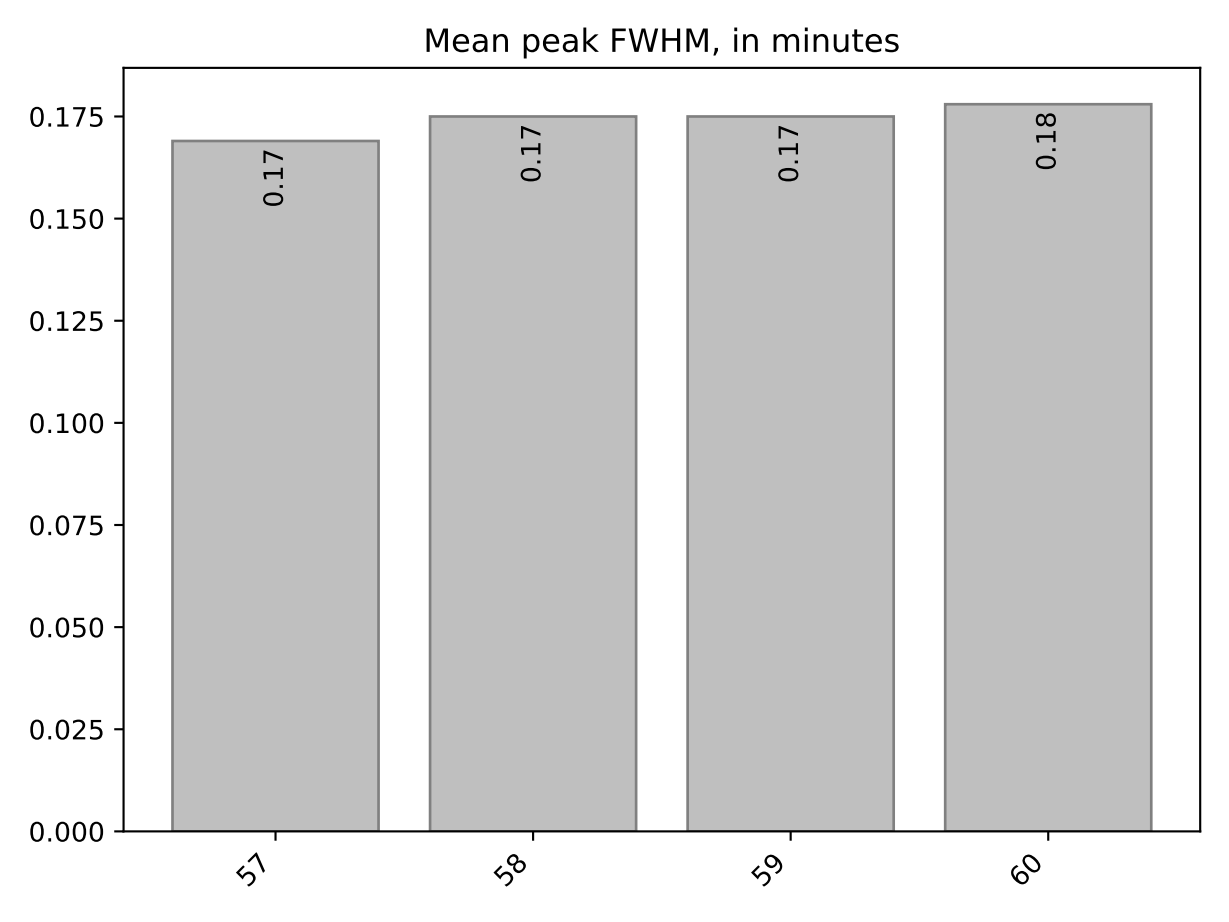

MS2 signal
1e11
0
1
2
3
4
5
57
58
59
60

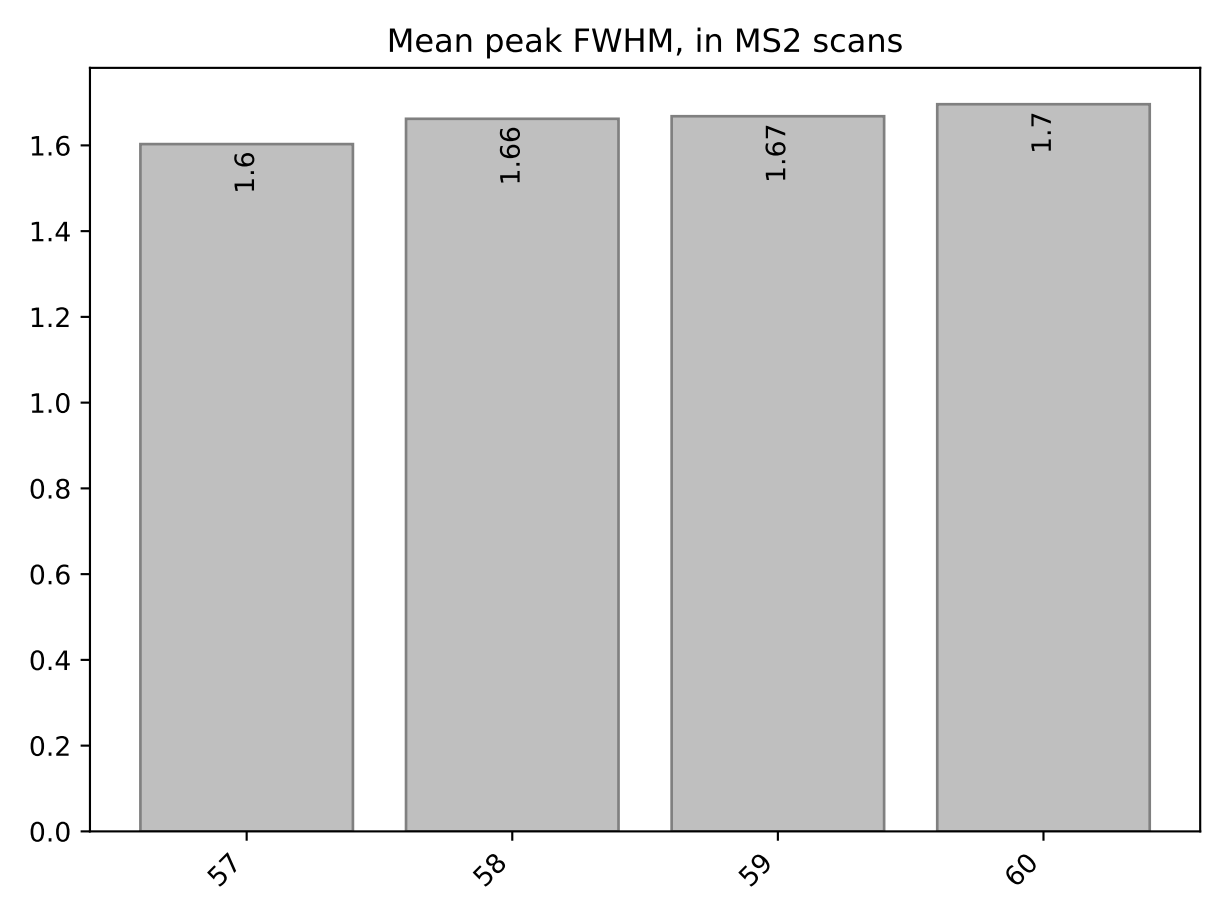

Total quantity/MS2 signal ratio
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0.01
0.01
0.02
0.03
57
58
59
60

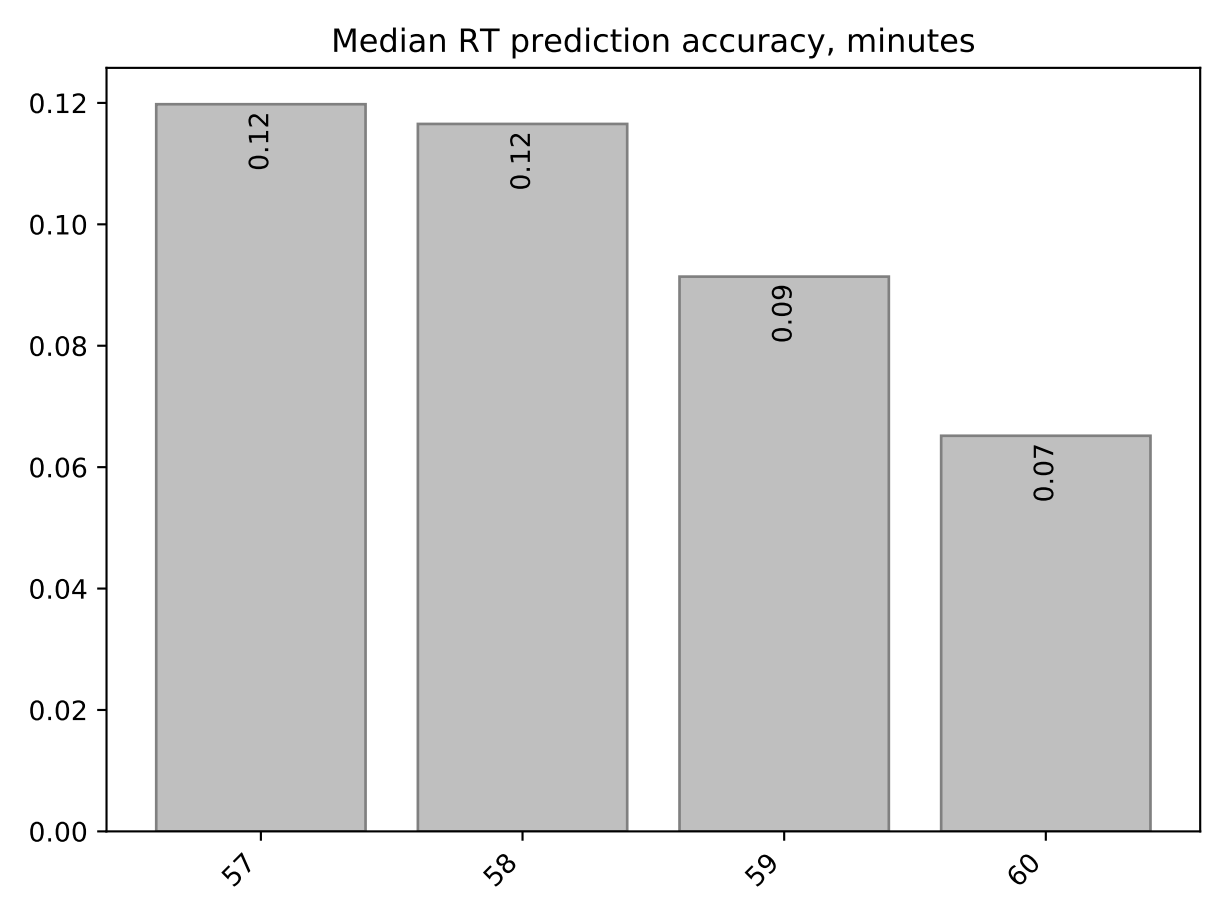

MS1/MS2 signal ratio
4.36
4.08
4.28
4.47
0
1
2
3
4
57
58
59
60

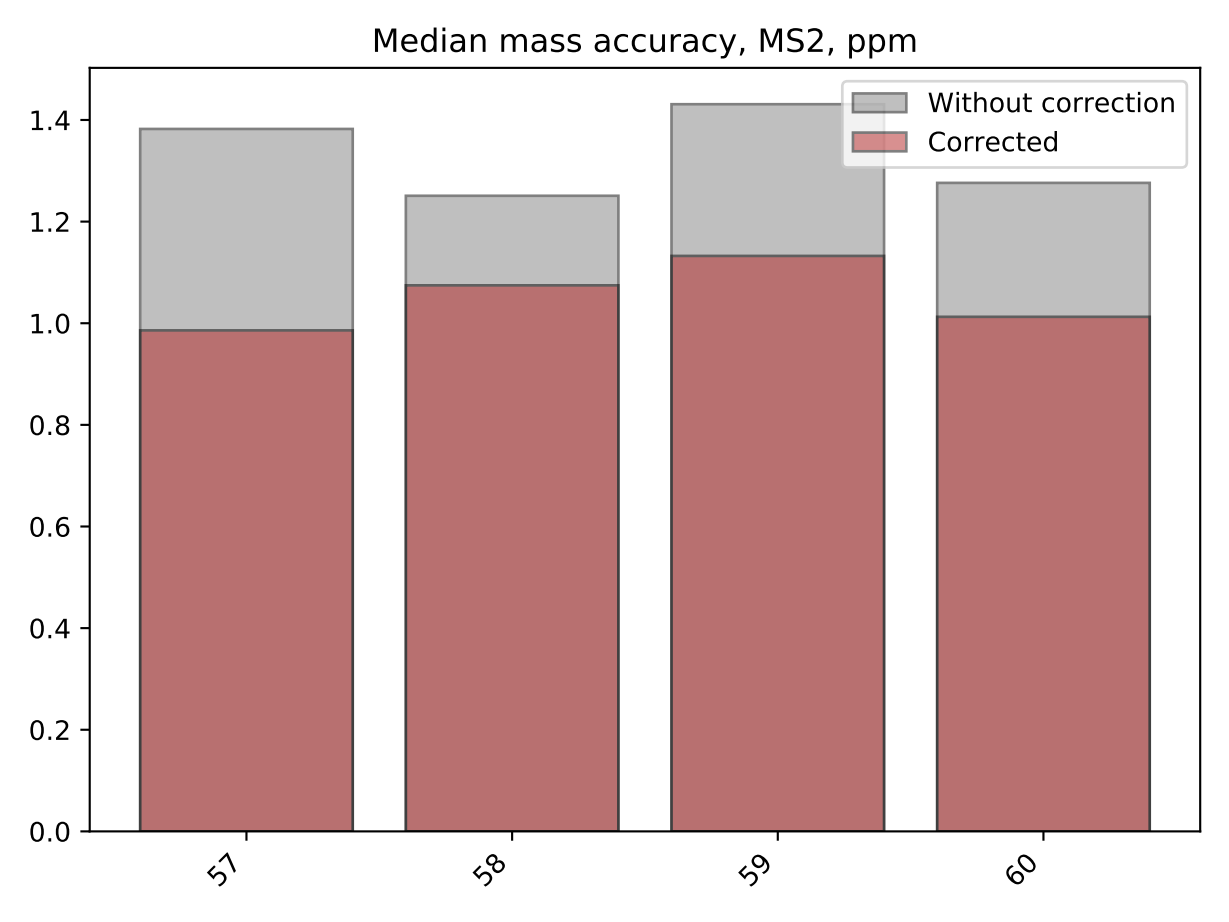

Precursors, 1% FDR
7000
6000
5000
4000
3000
2000
1000
0
4626
4651
5485
6956
57
58
59
60

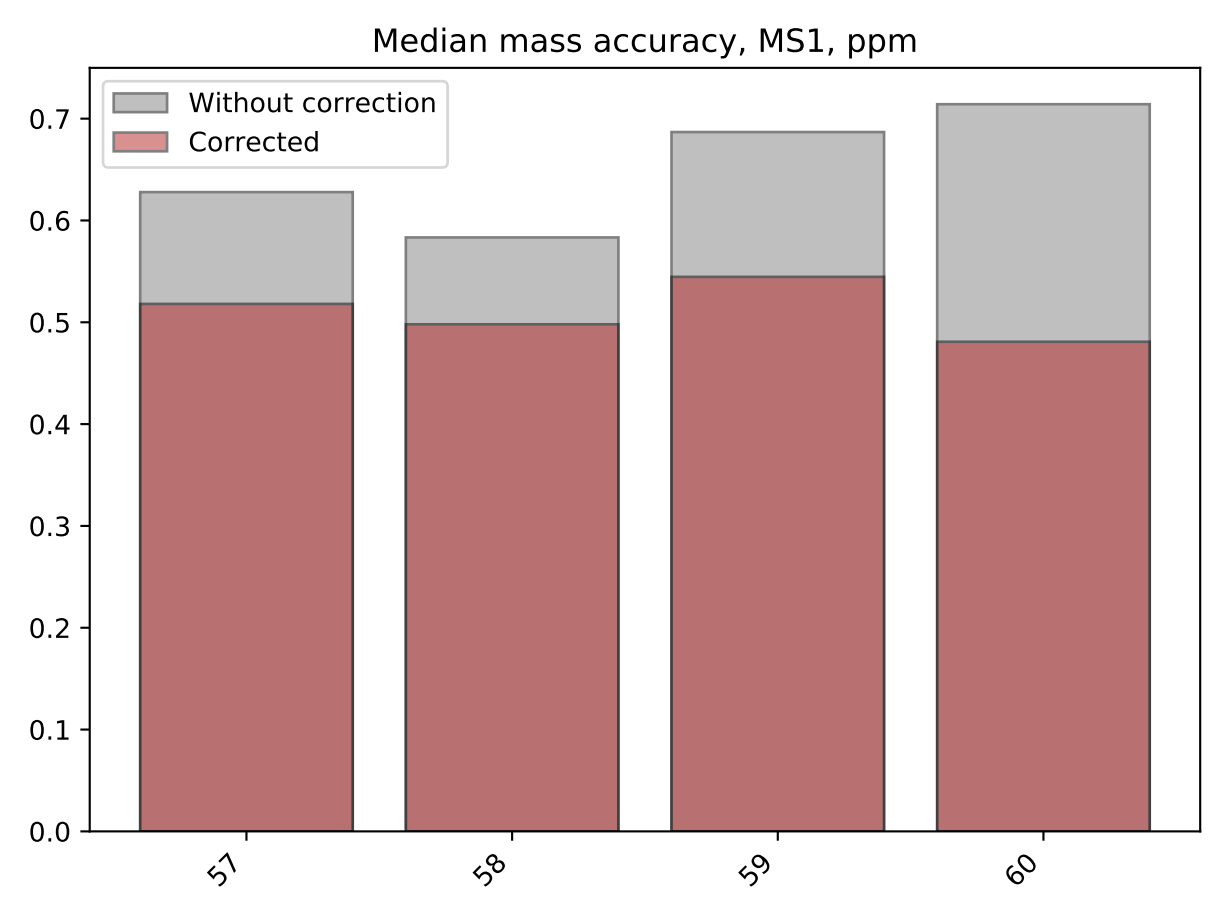

Unique proteins, 1% protein-level FDR
1200
1000
800
600
400
200
0
785
853
968
1221
57
58
59
60

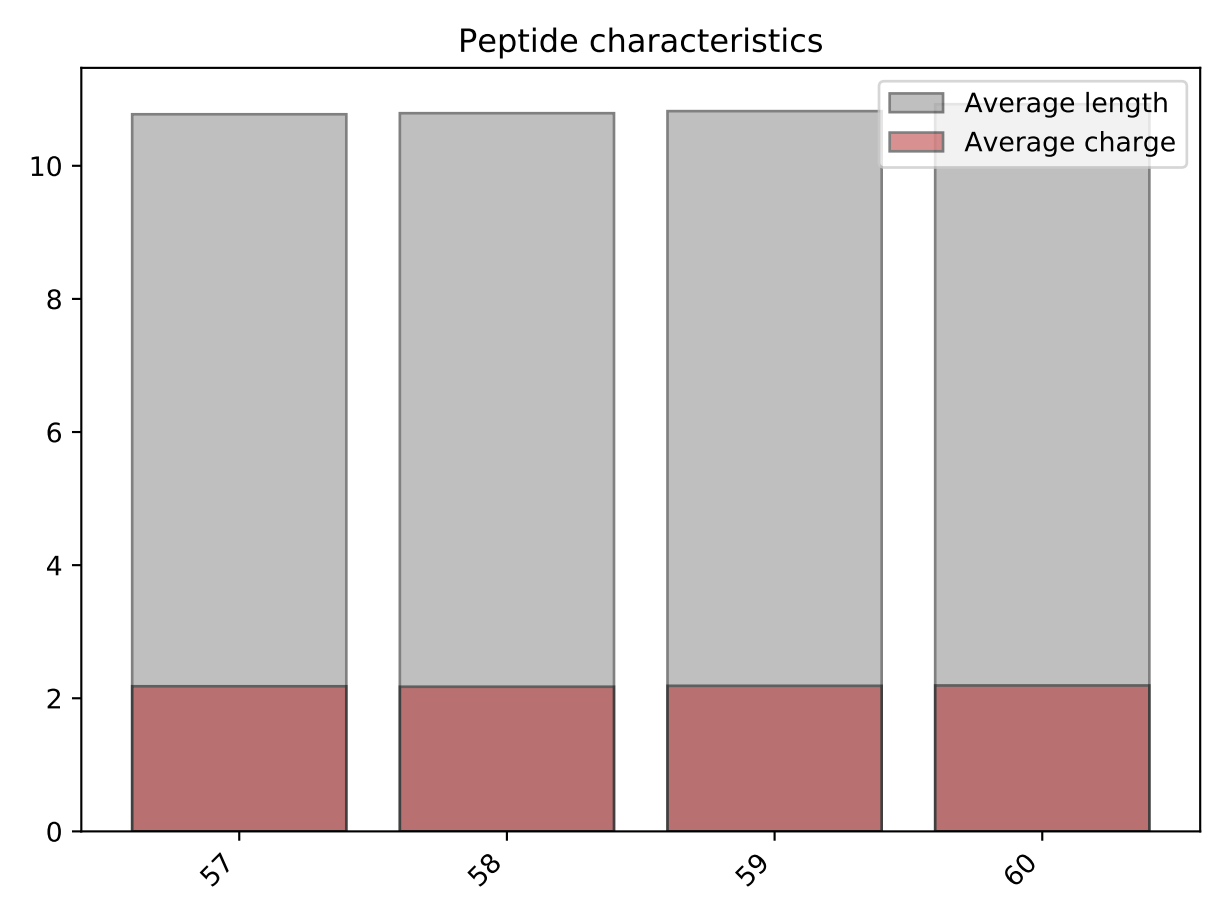

Mean peak FWHM, in minutes
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0.17
0.17
0.17
0.18
57
58
59
60

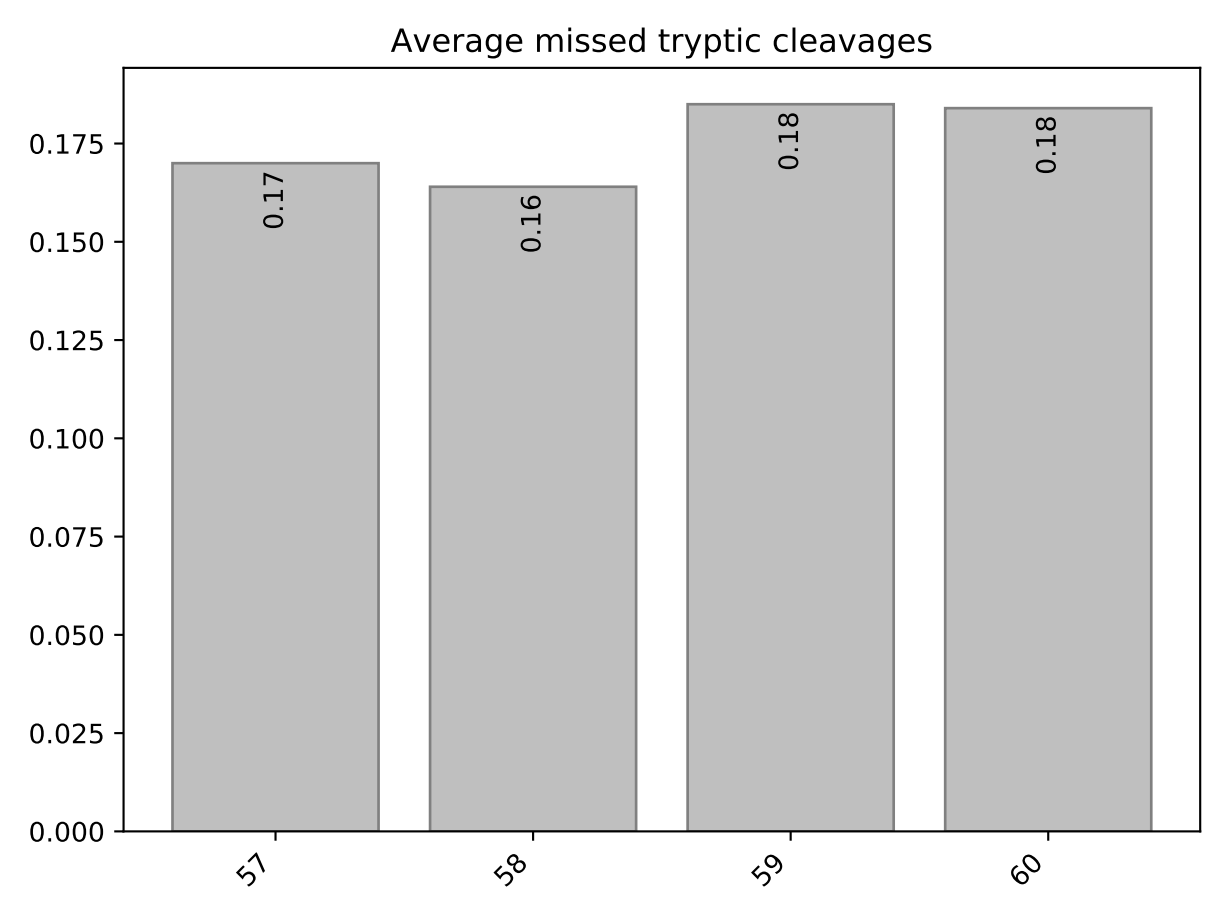

Mean peak FWHM, in MS2 scans
1.6
1.66
1.67
1.7
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
57
58
59
60

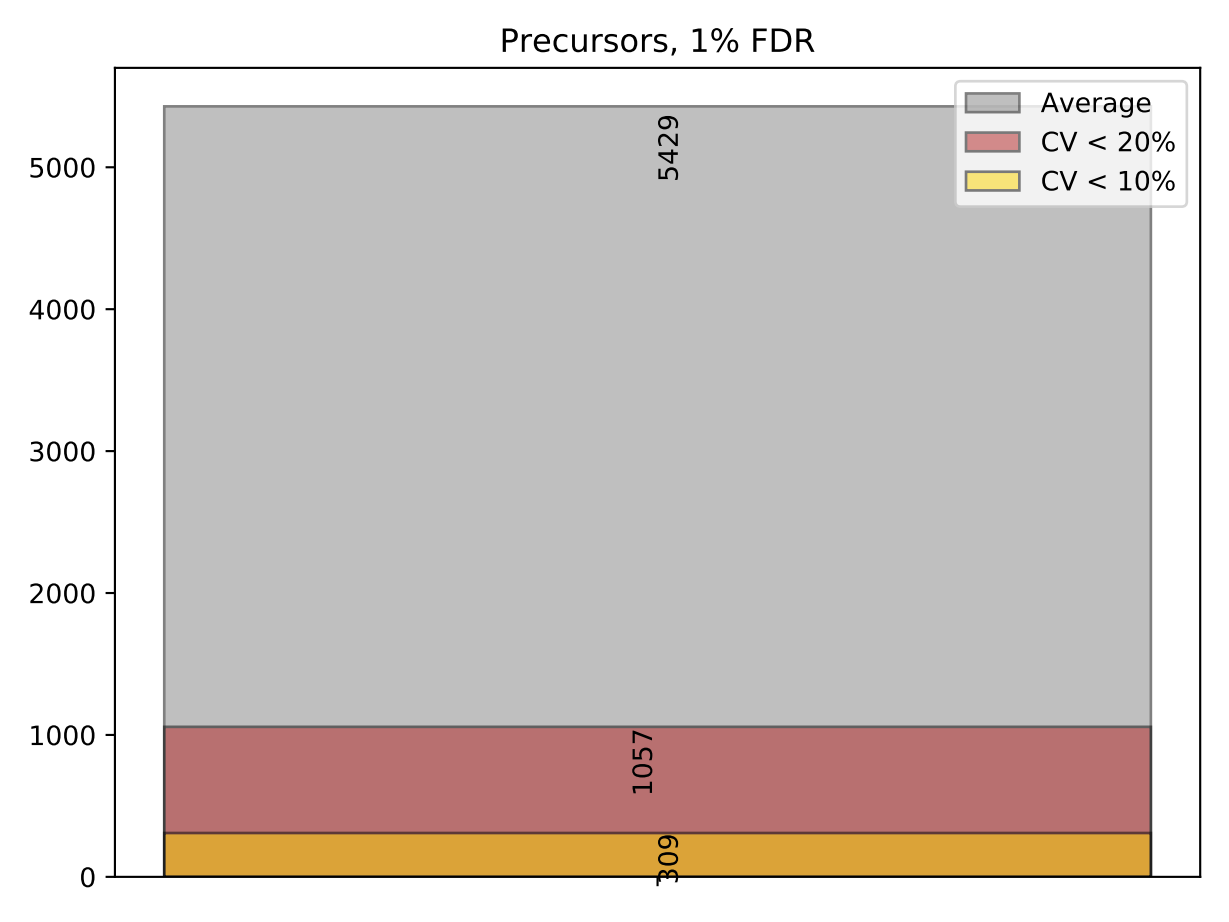

Median RT prediction accuracy, minutes
0.12
0.10
0.08
0.06
0.04
0.02
0.00
0.12
0.12
0.09
0.07
57
58
59
60

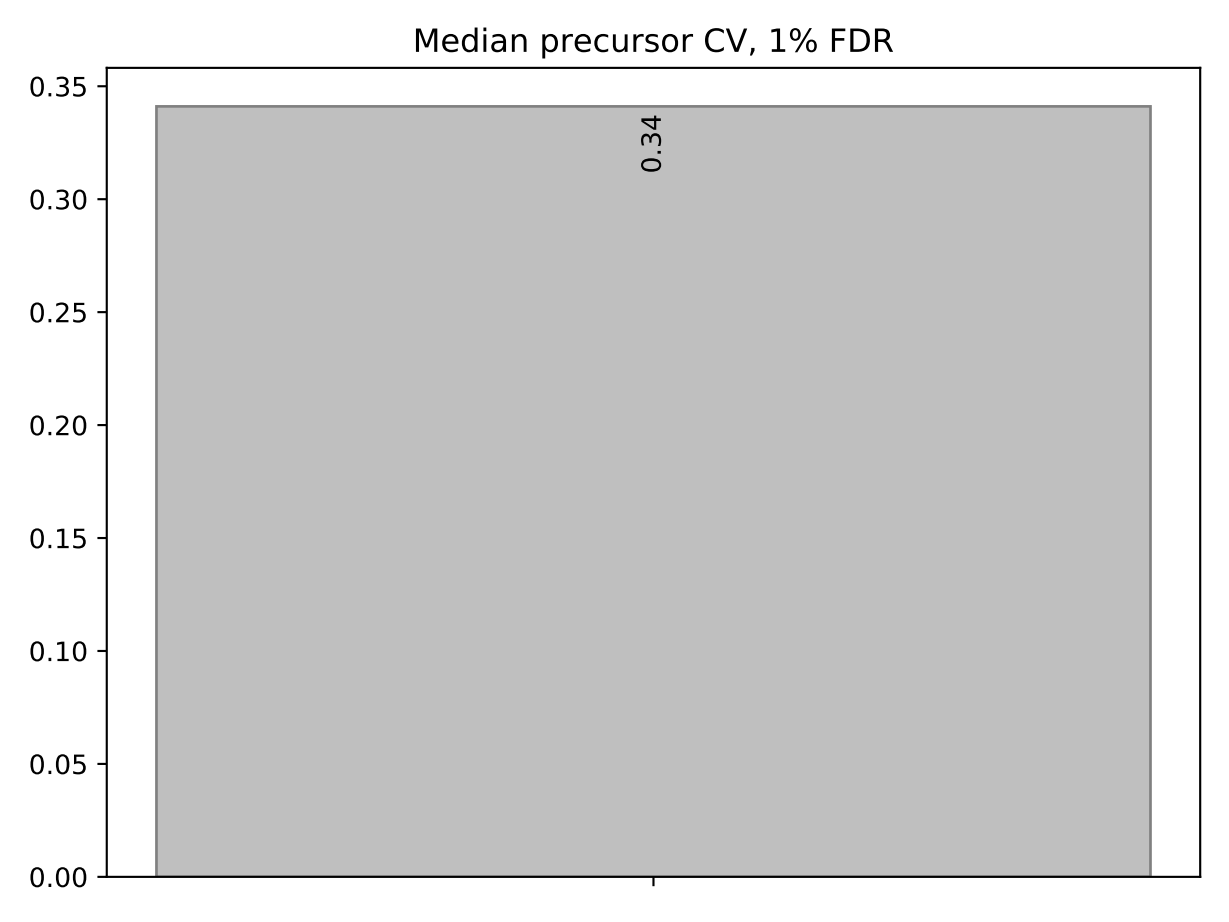

Median mass accuracy, MS2, ppm
Without correction
Corrected
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
57
58
59
60

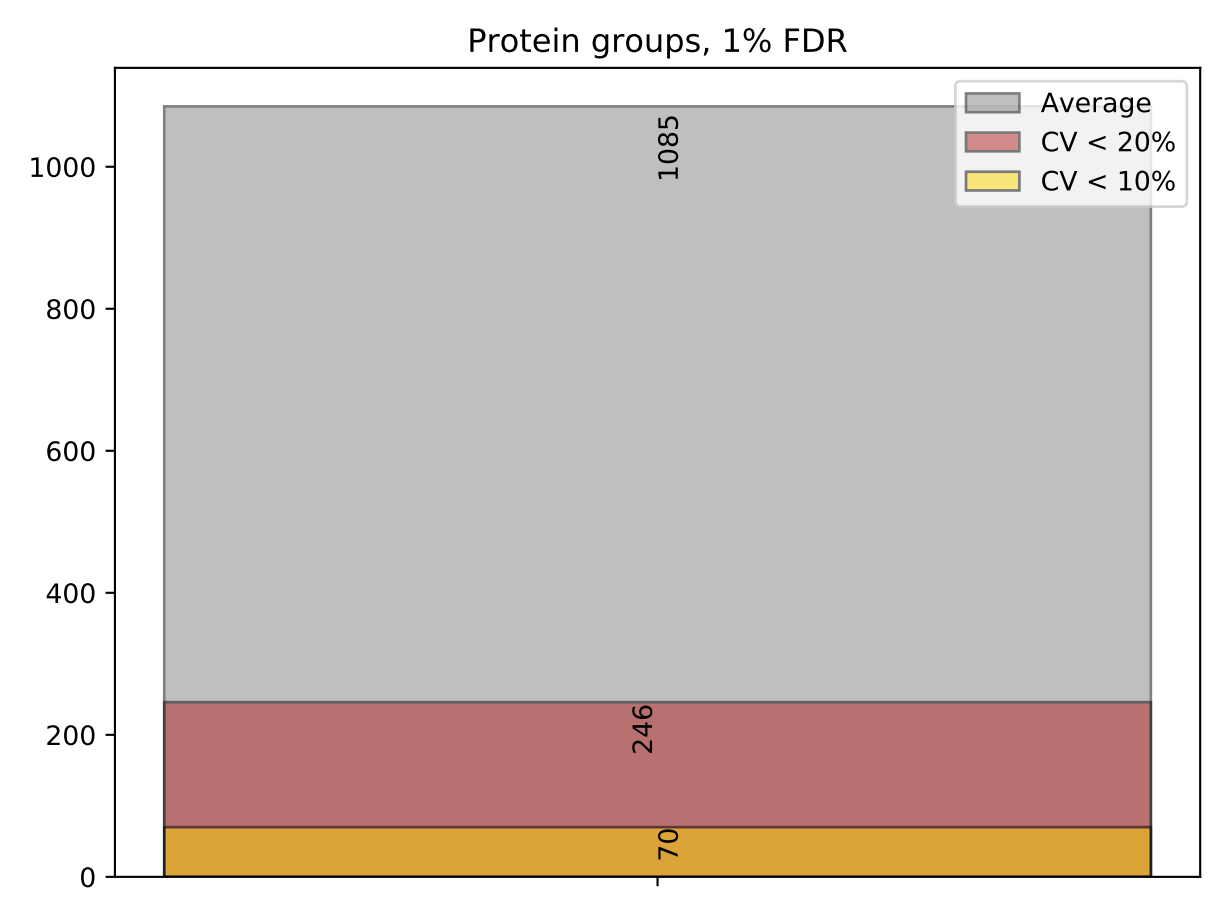

Median mass accuracy, MS1, ppm
Without correction
Corrected
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
57
58
59
60

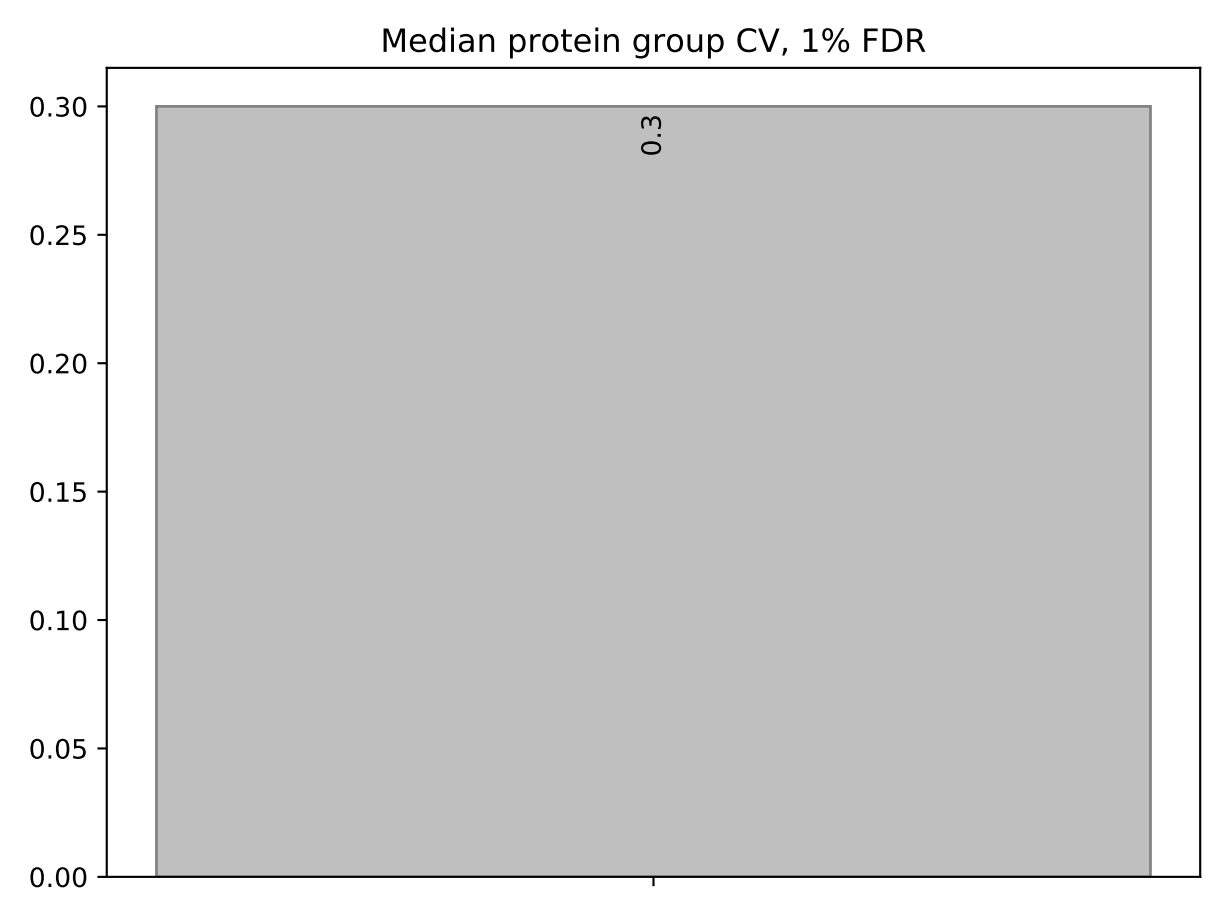

Peptide characteristics
Average length
Average charge
0
2
4
6
8
10
57
58
59
60

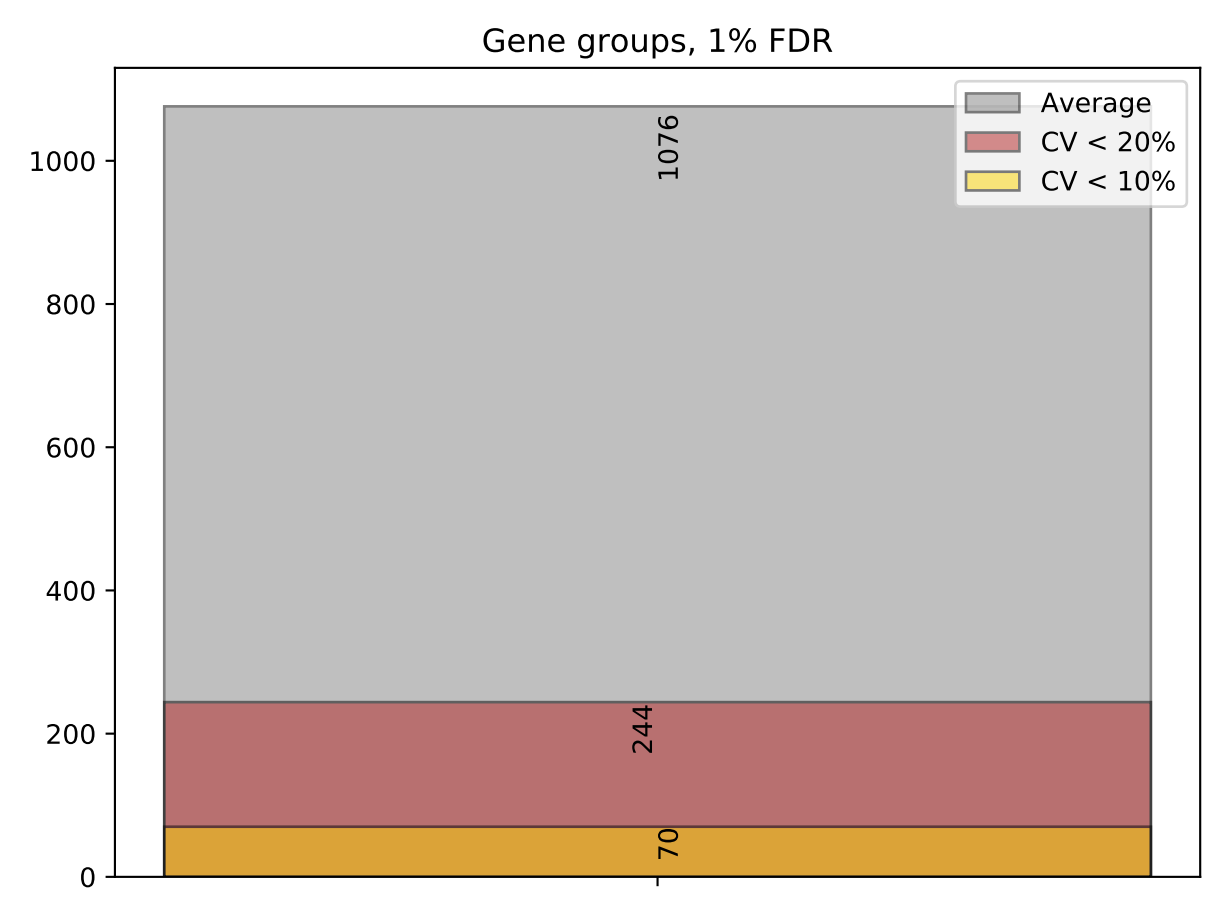

Average missed tryptic cleavages
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0.17
0.16
0.18
0.18
57
58
59
60

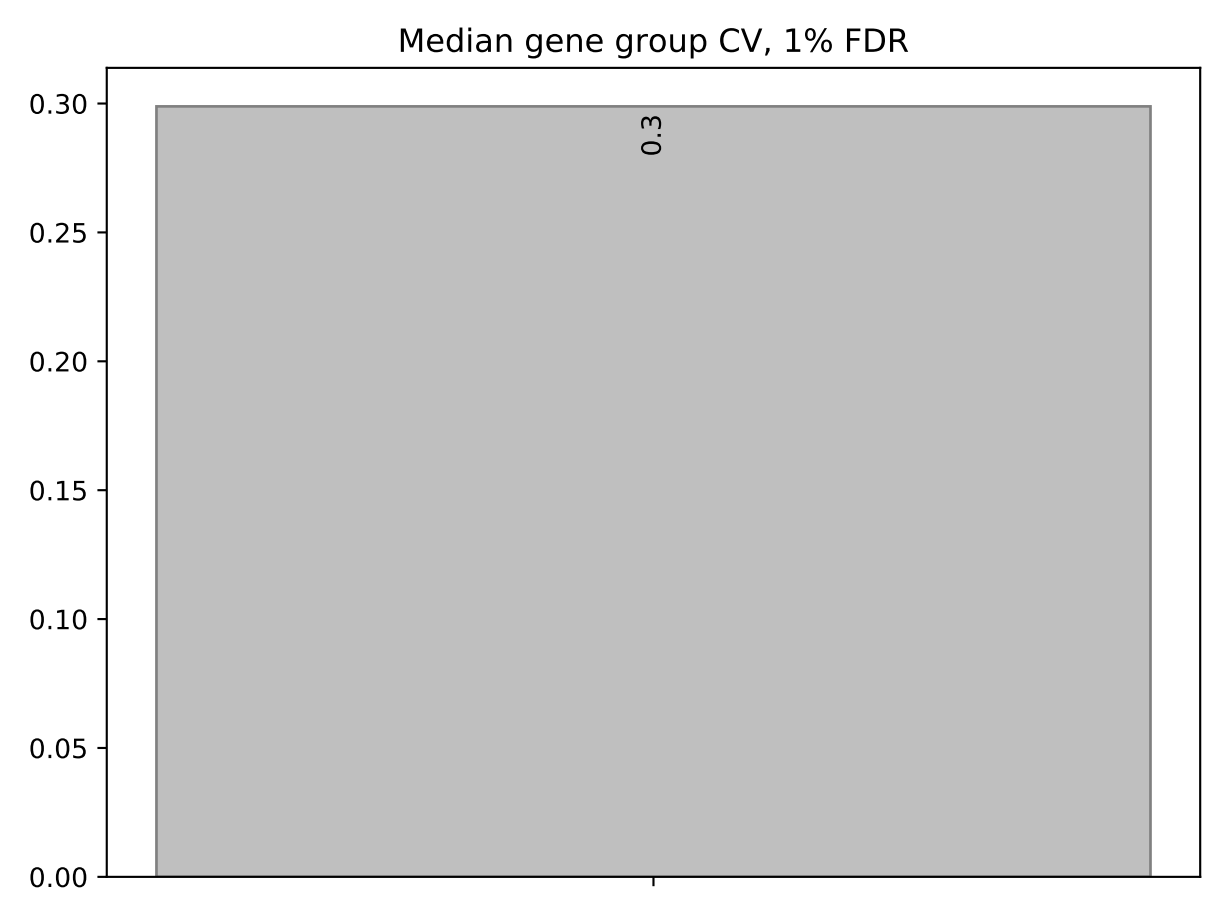

Precursors, 1% FDR
Average
CV < 20%
CV < 10%
5429
1057
309
0
1000
2000
3000
4000
5000


Median precursor CV, 1% FDR
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.34


Protein groups, 1% FDR
Average
CV < 20%
CV < 10%
1085
246
70
0
200
400
600
800
1000


Median protein group CV, 1% FDR
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.3


Gene groups, 1% FDR
Average
CV < 20%
CV < 10%
1076
244
70
0
200
400
600
800
1000


Median gene group CV, 1% FDR
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.3