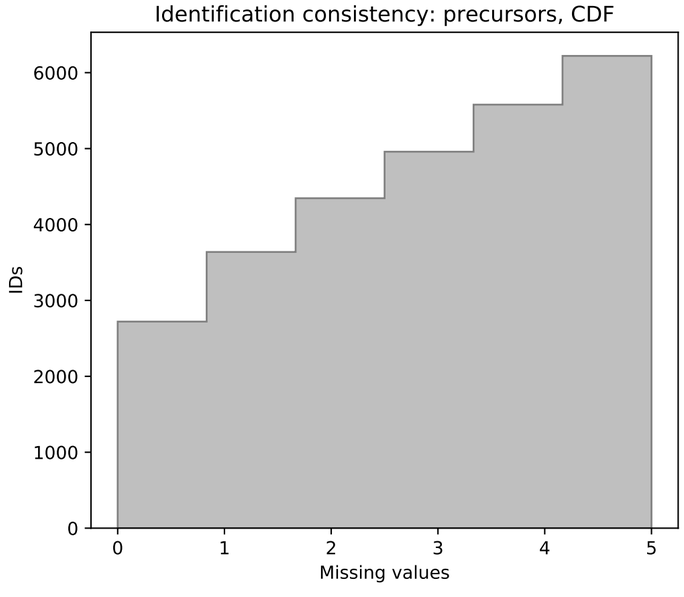
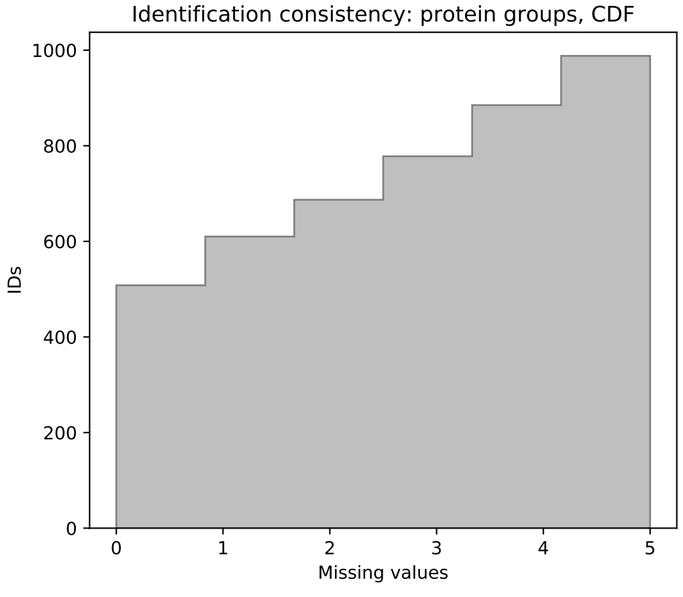
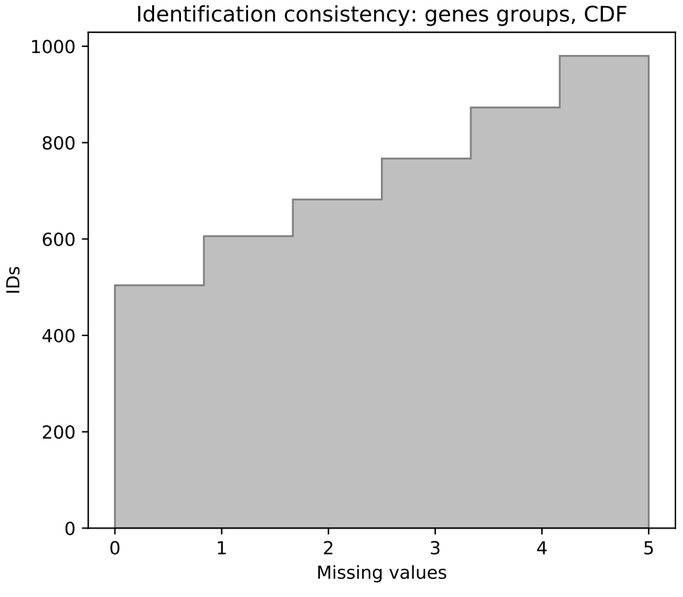
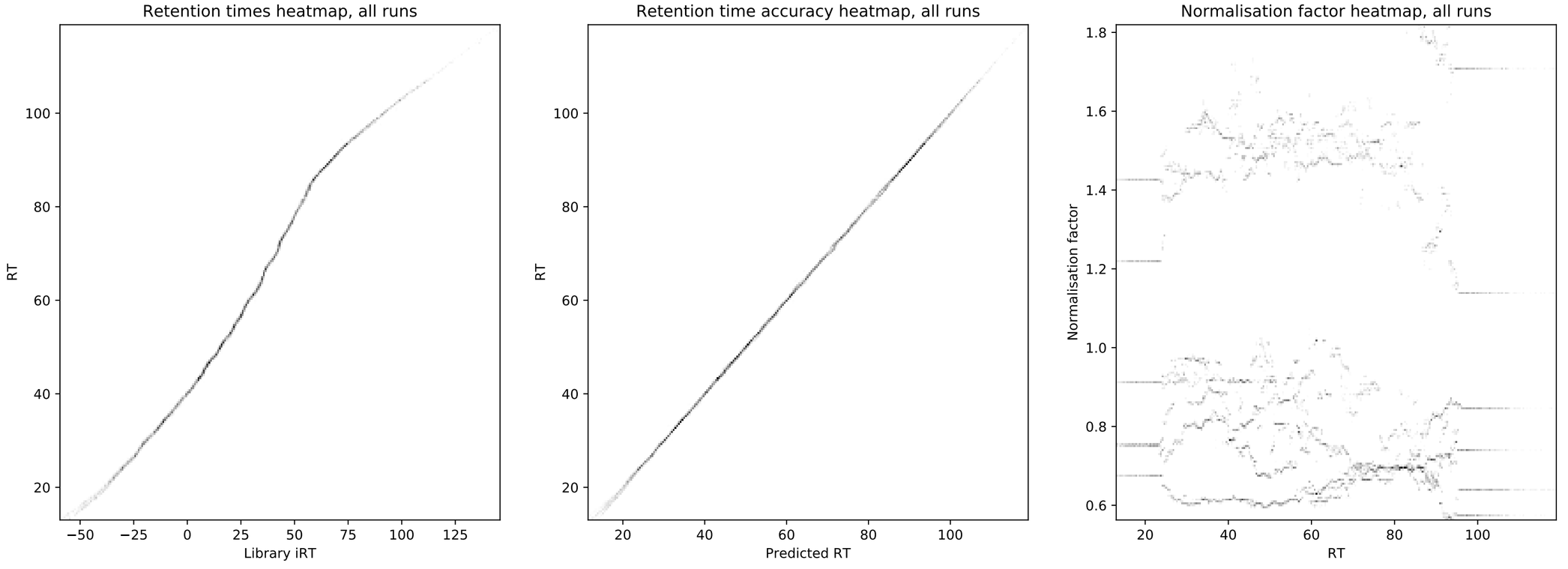
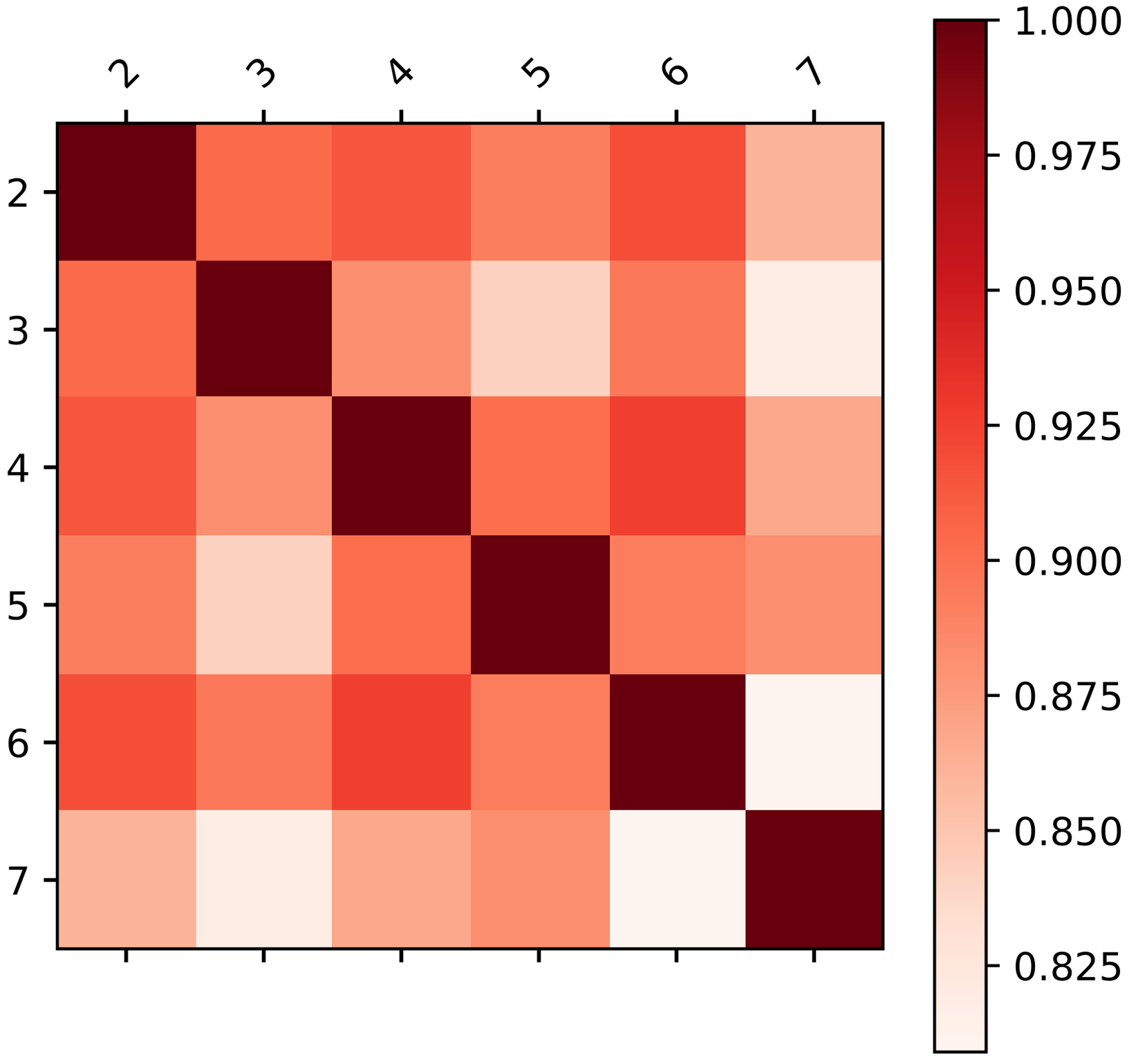
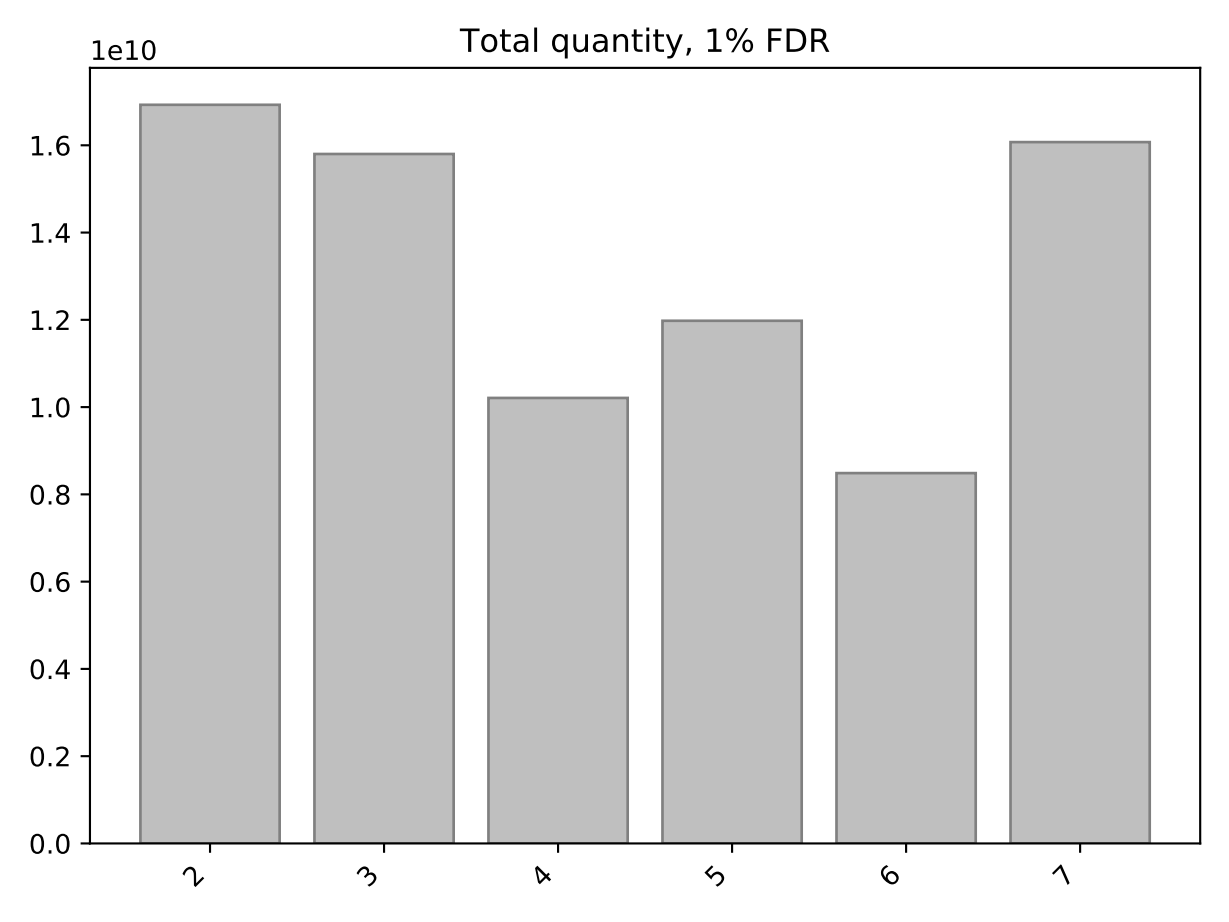

Identification consistency: precursors, CDF
IDs
Missing values
0
1000
2000
3000
4000
5000
6000
0
1
2
3
4
5

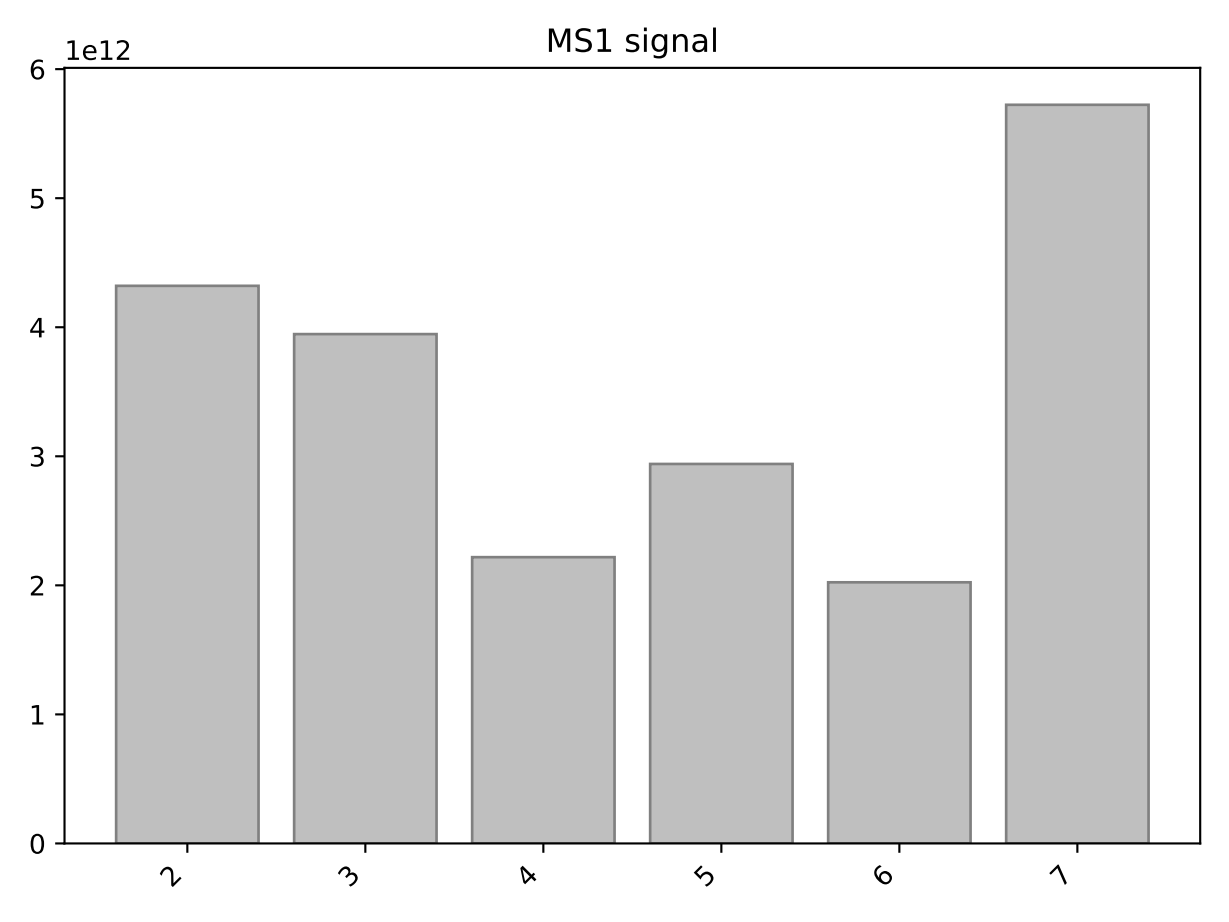

Identification consistency: protein groups, CDF
IDs
Missing values
0
200
400
600
800
1000
0
1
2
3
4
5

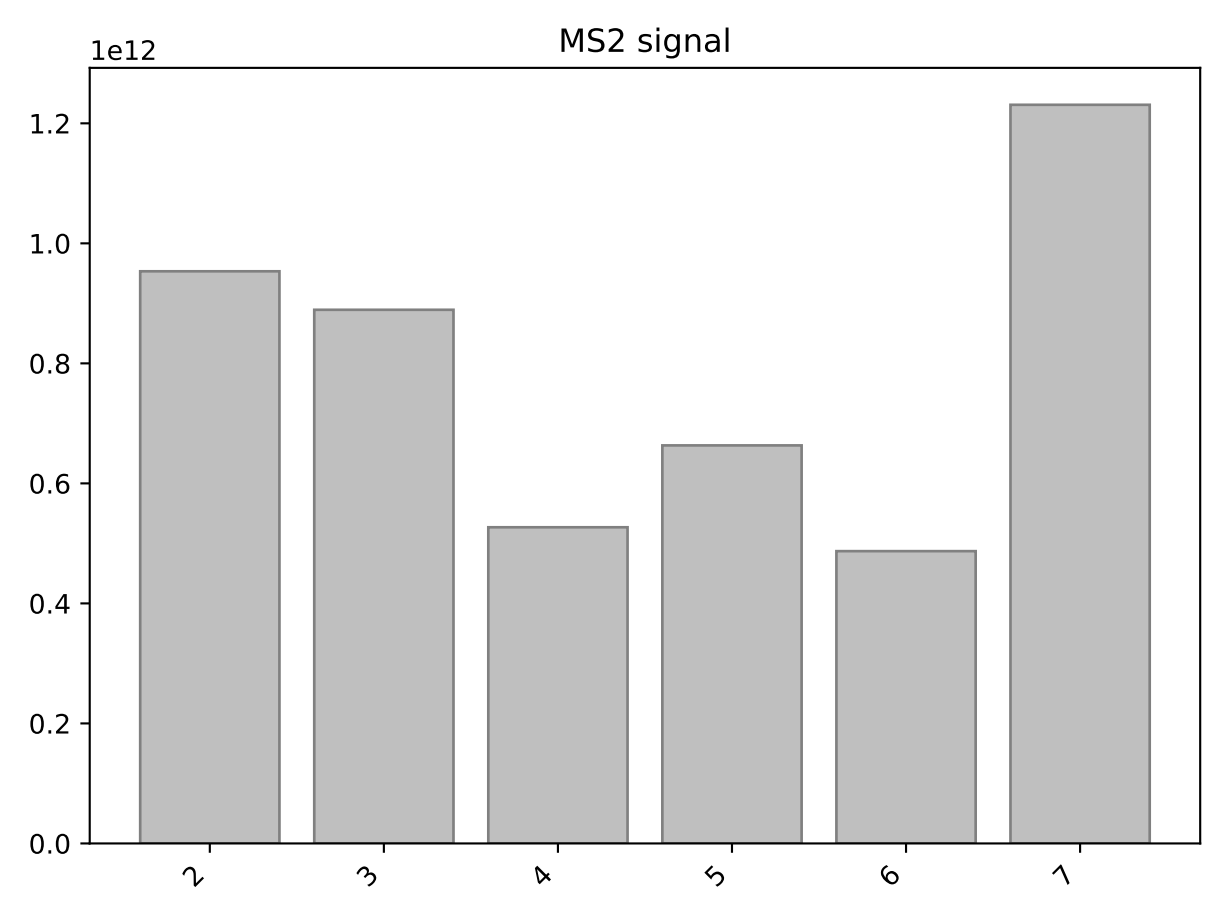

Identification consistency: genes groups, CDF
IDs
Missing values
0
200
400
600
800
1000
0
1
2
3
4
5

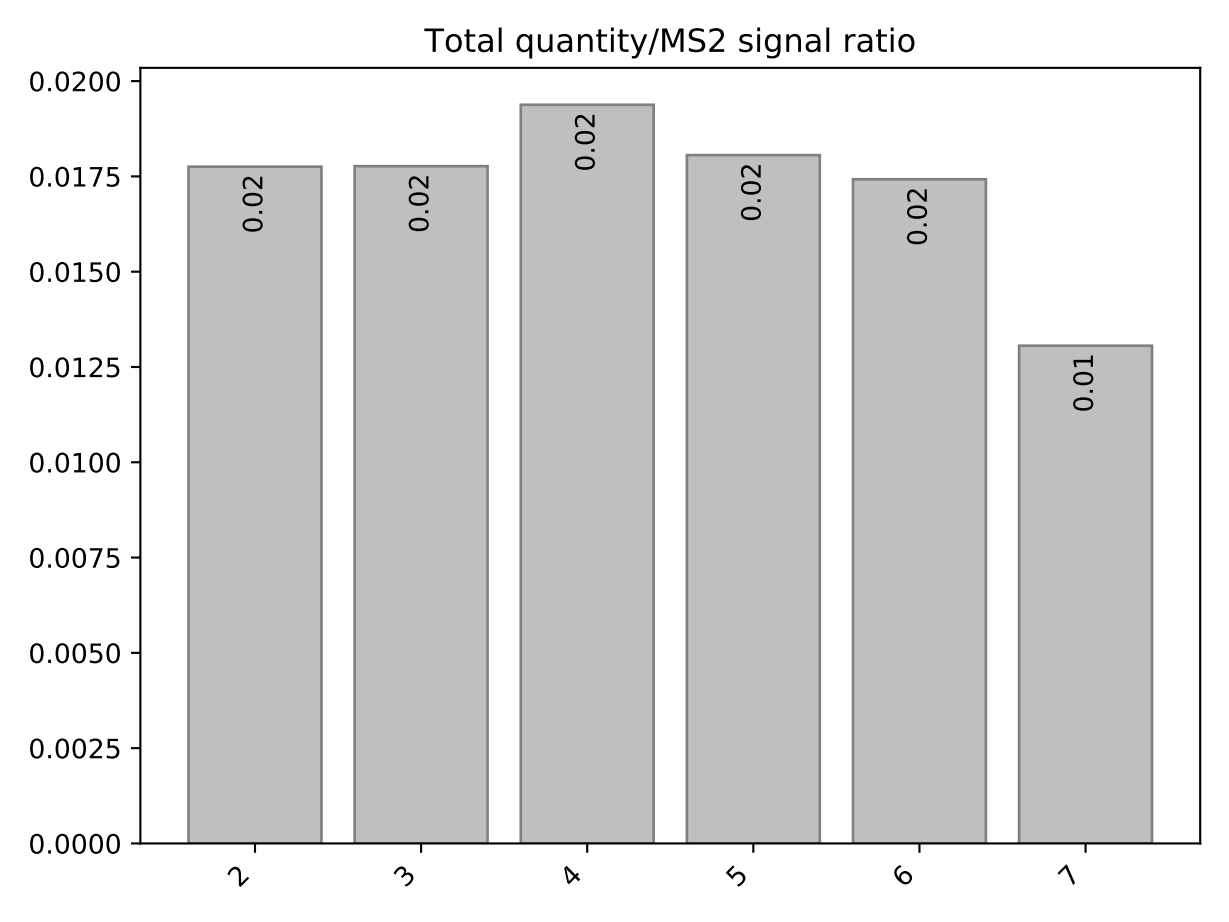

Retention times heatmap, all runs
RT
Library iRT
Retention time accuracy heatmap, all runs
RT
Predicted RT
Normalisation factor heatmap, all runs
Normalisation factor
RT

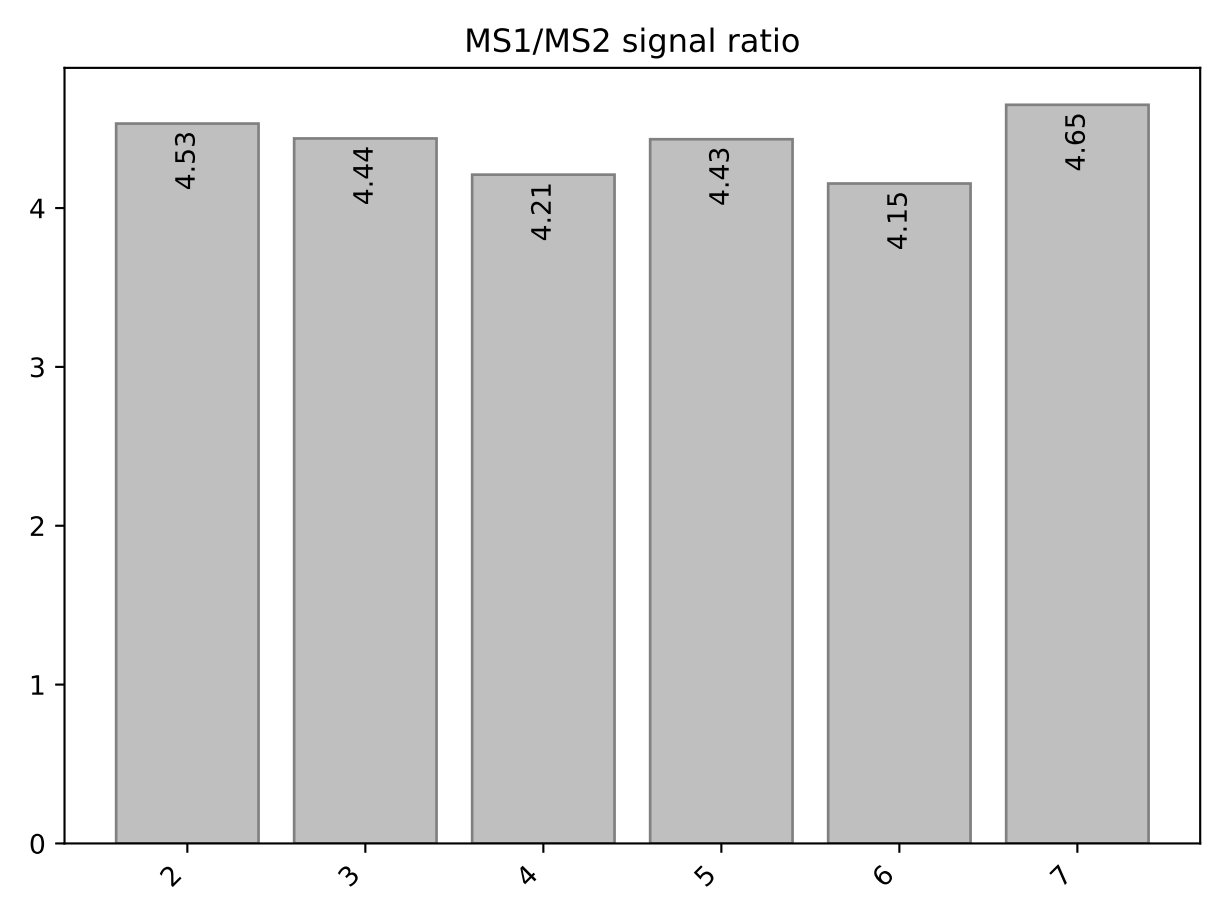

2
3
4
5
6
7
2
3
4
5
6
7
1.000
0.975
0.950
0.925
0.900
0.875
0.850
0.825

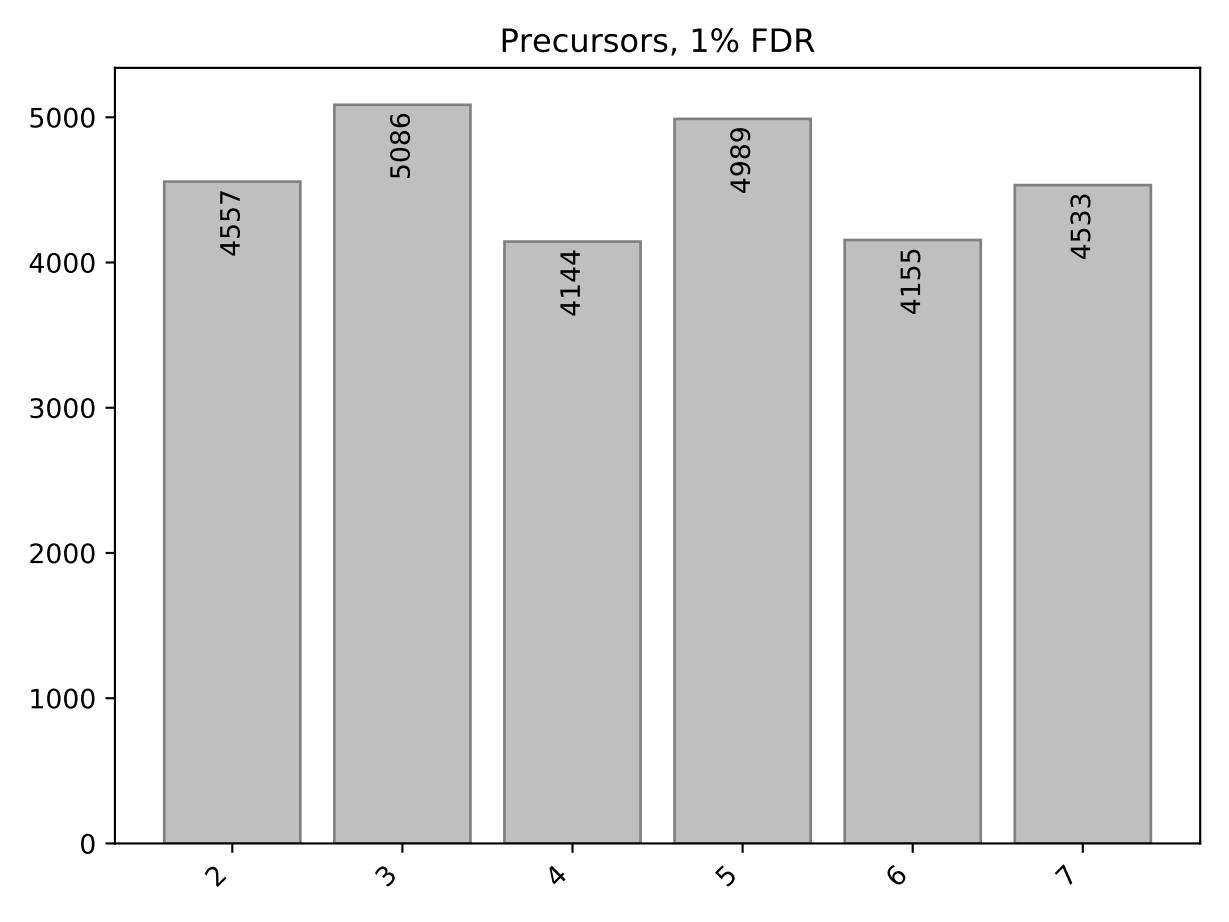

Total quantity, 1% FDR
1e10
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
2
3
4
5
6
7

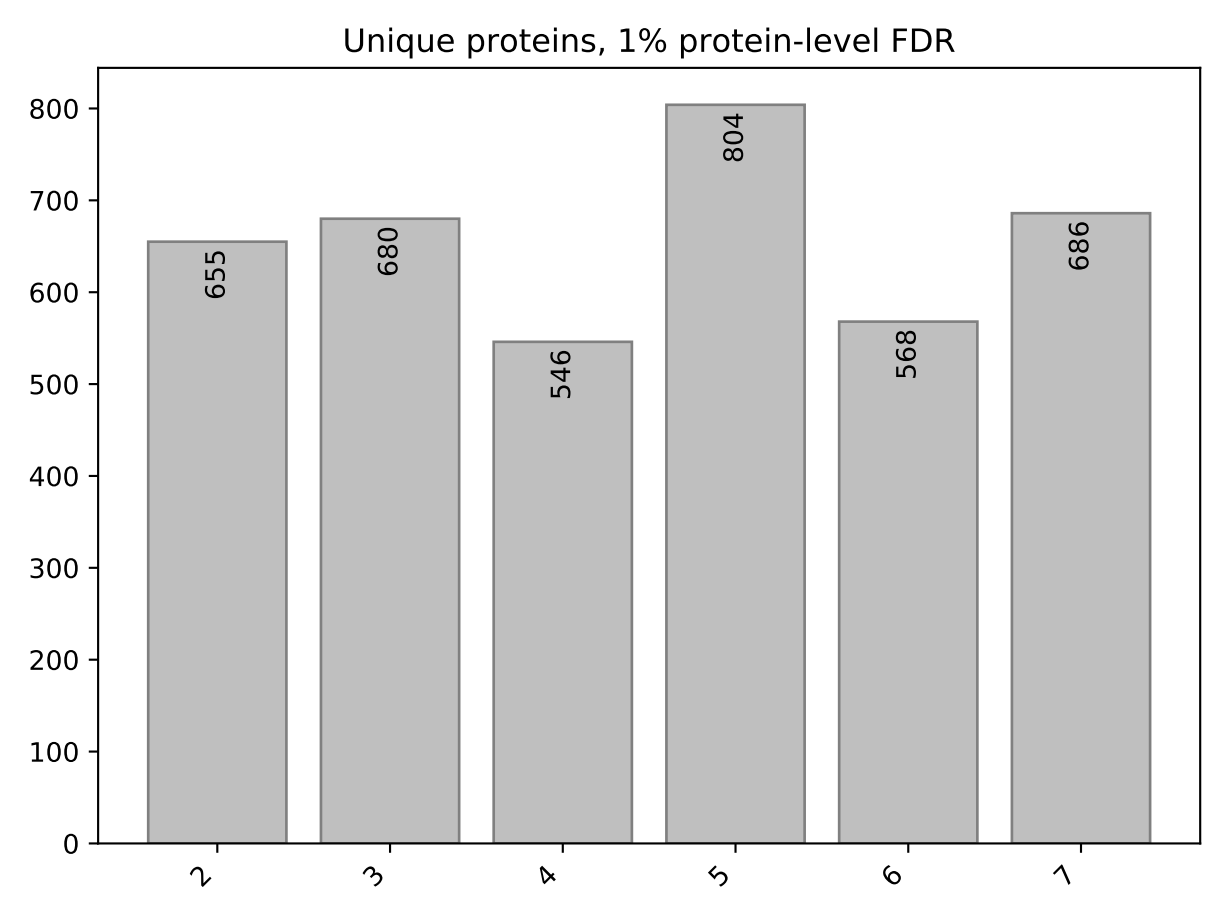

MS1 signal
1e12
6
5
4
3
2
1
0
2
3
4
5
6
7

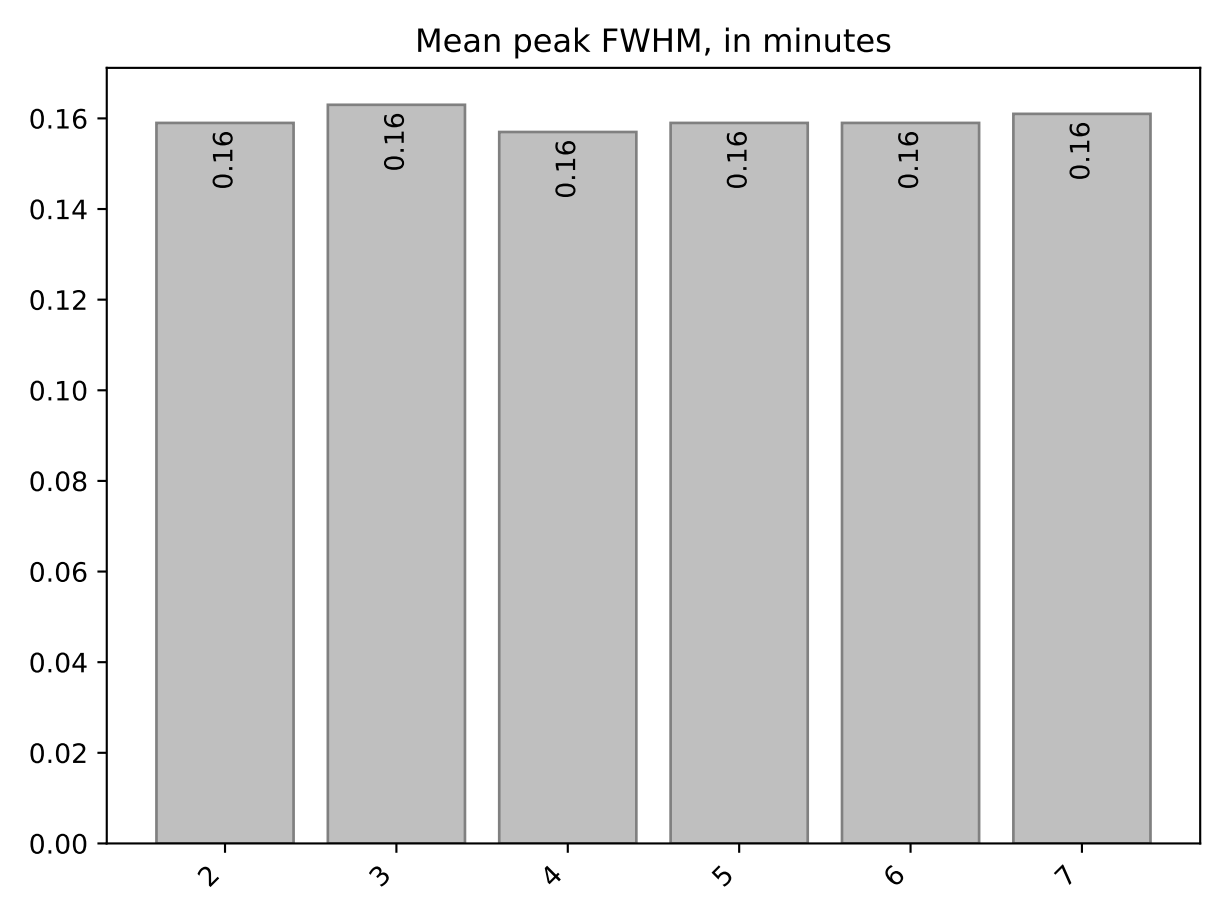

MS2 signal
1e12
1.2
1.0
0.8
0.6
0.4
0.2
0.0
2
3
4
5
6
7

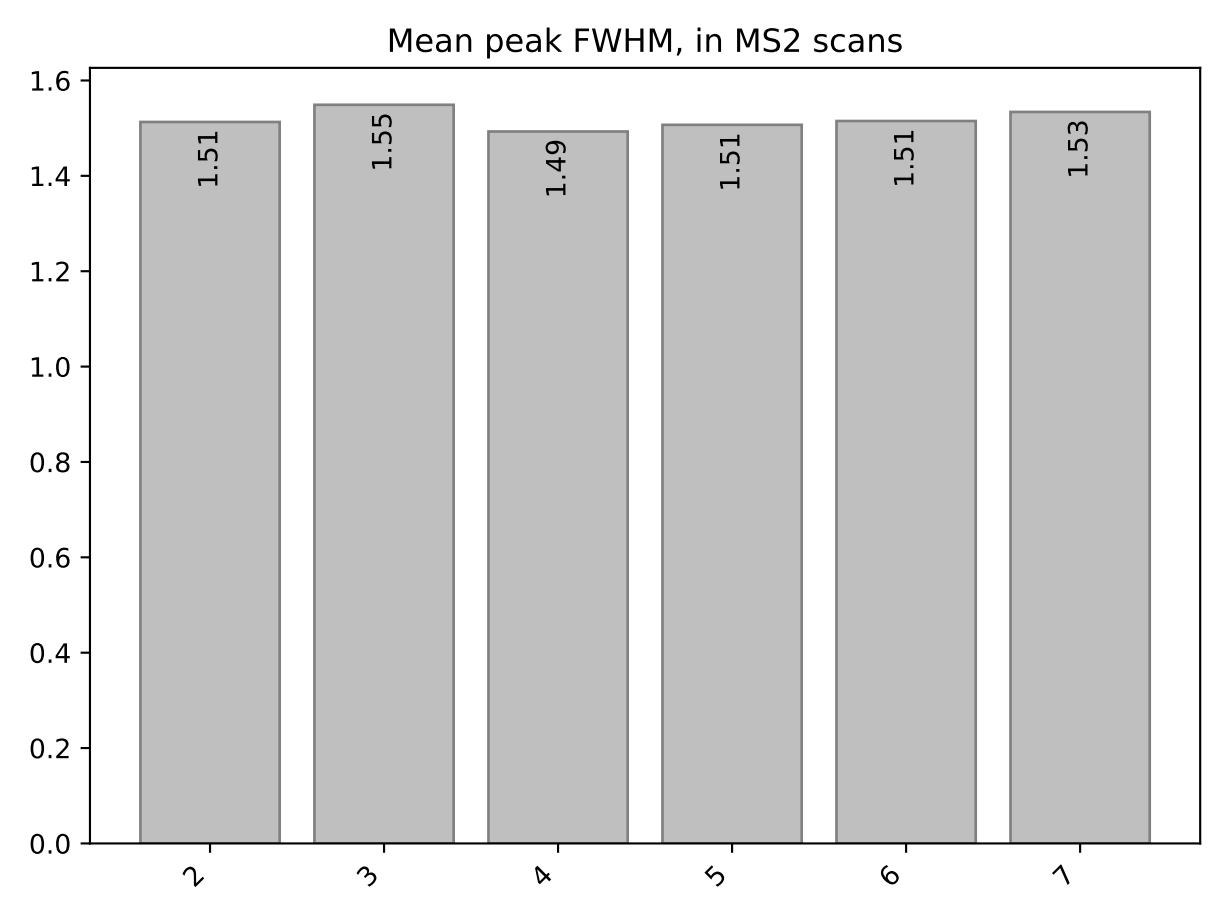

Total quantity/MS2 signal ratio
0.0200
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050
0.0025
0.0000
0.02
0.02
0.02
0.02
0.02
0.01
2
3
4
5
6
7

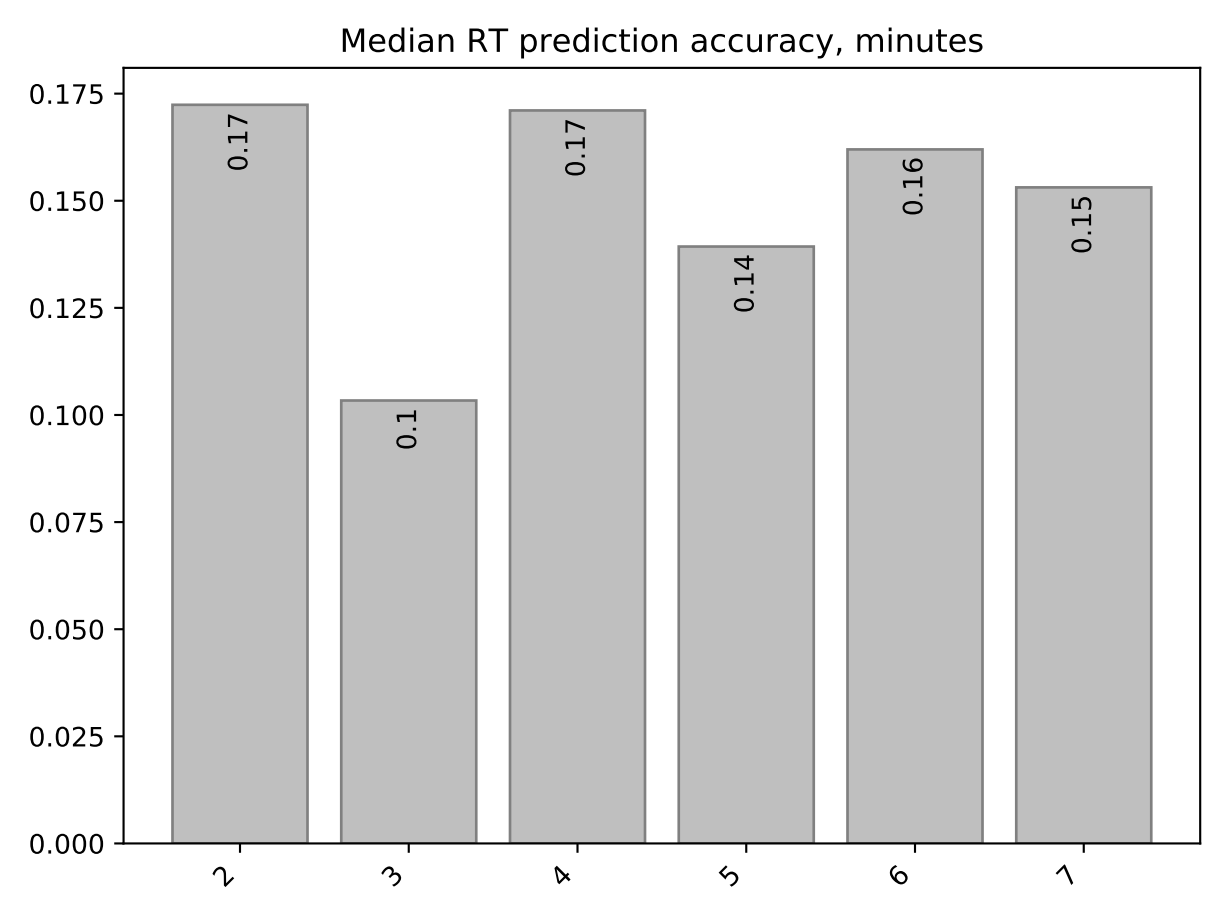

MS1/MS2 signal ratio
4.53
4.44
4.21
4.43
4.15
4.65
0
1
2
3
4
2
3
4
5
6
7

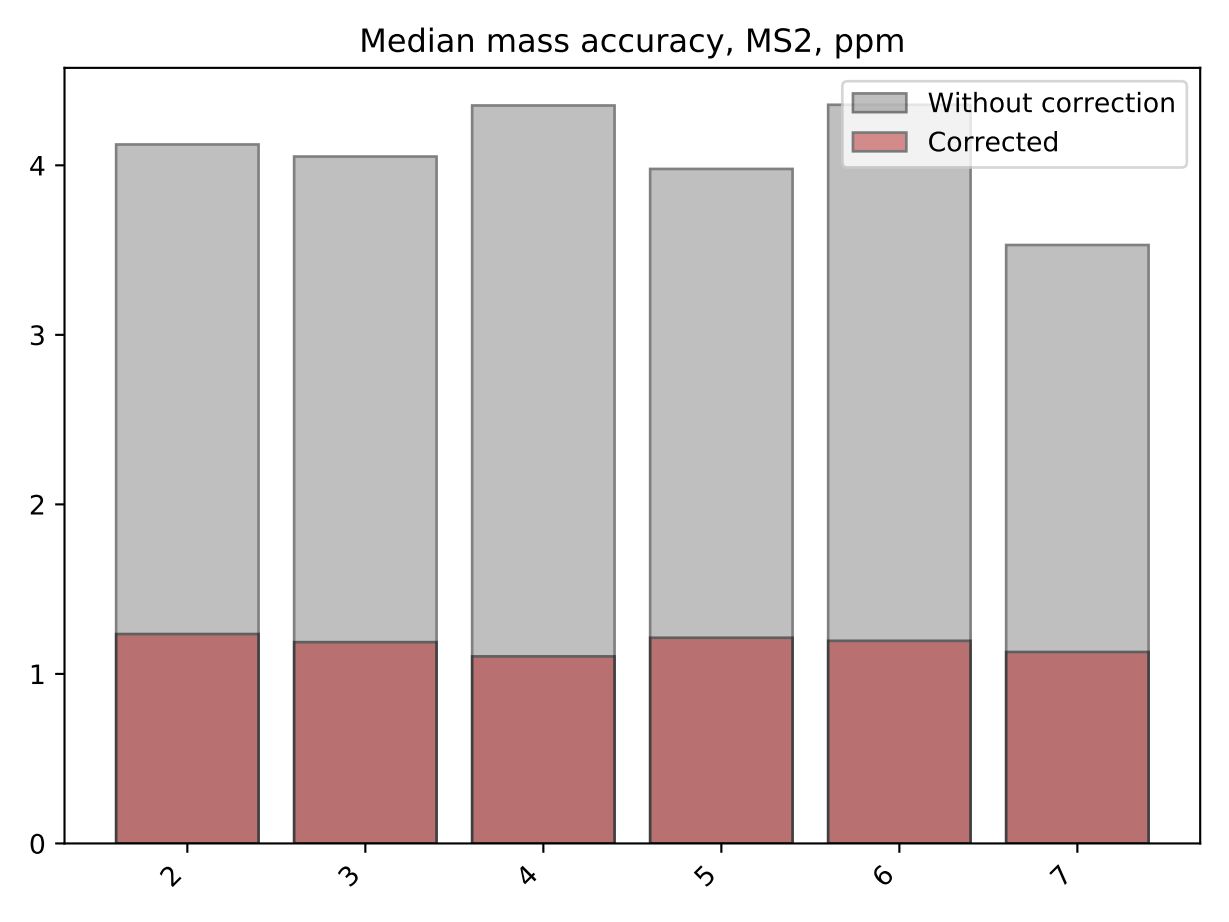

Precursors, 1% FDR
5000
4000
3000
2000
1000
0
4557
5086
4144
4989
4155
4533
2
3
4
5
6
7

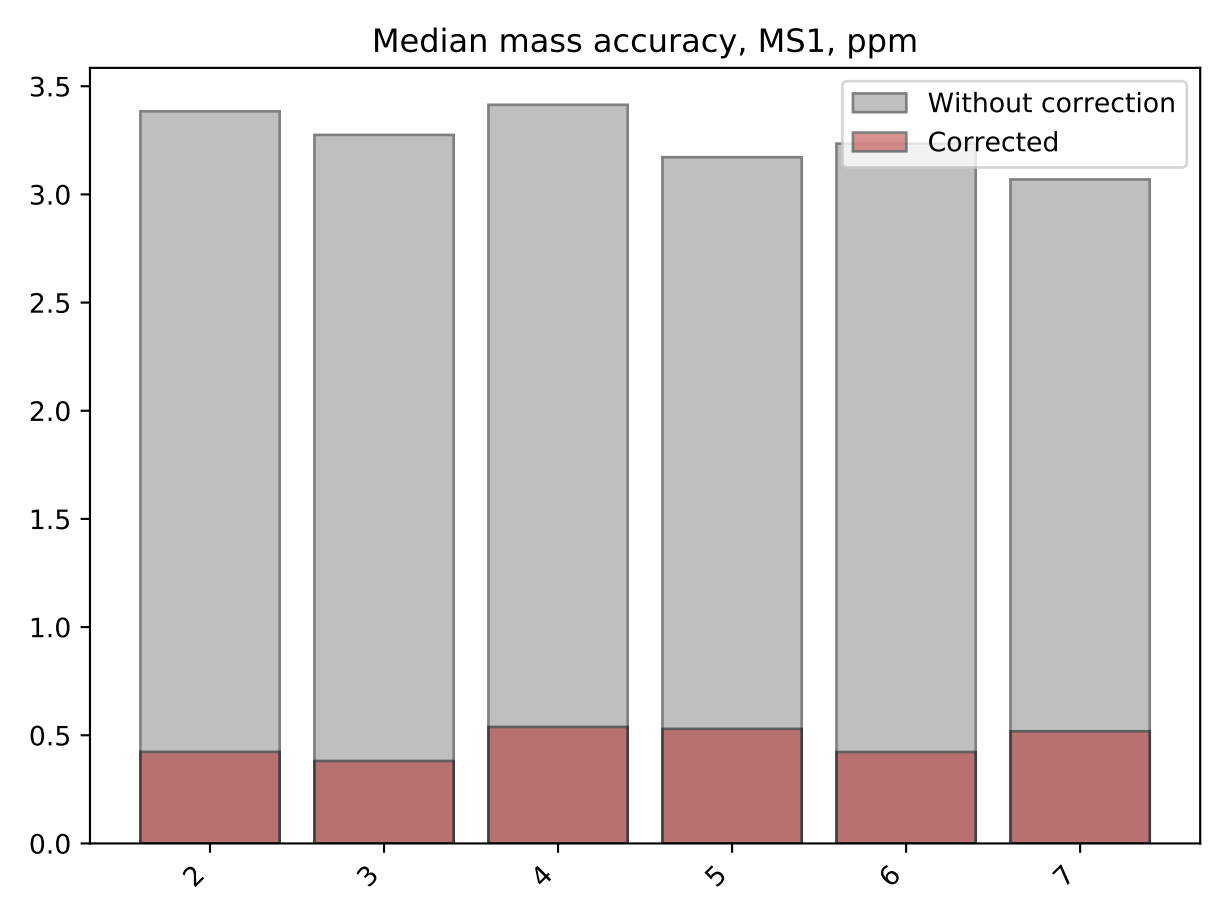

Unique proteins, 1% protein-level FDR
800
700
600
500
400
300
200
100
0
655
680
546
804
568
686
2
3
4
5
6
7

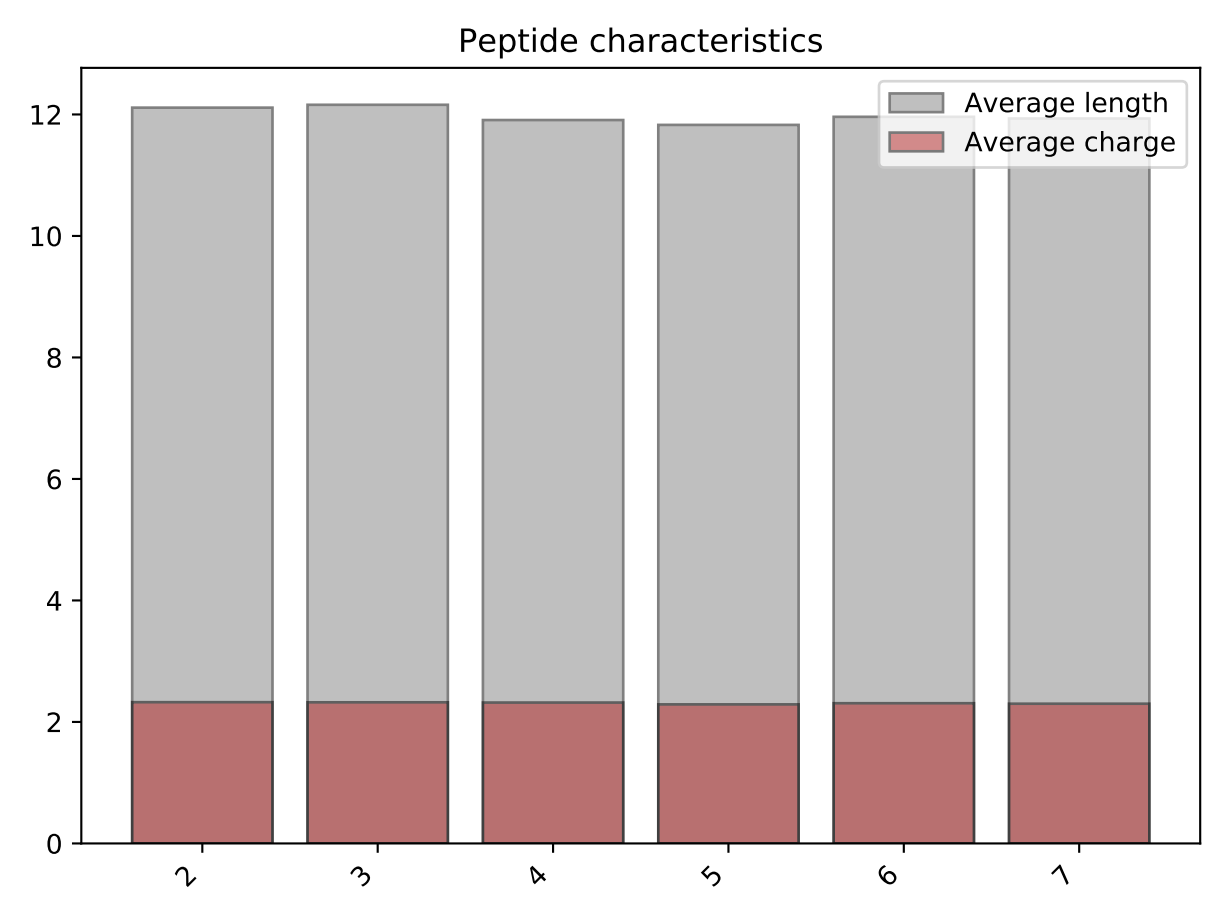

Mean peak FWHM, in minutes
0.16
0.16
0.16
0.16
0.16
0.16
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14
0.16
2
3
4
5
6
7

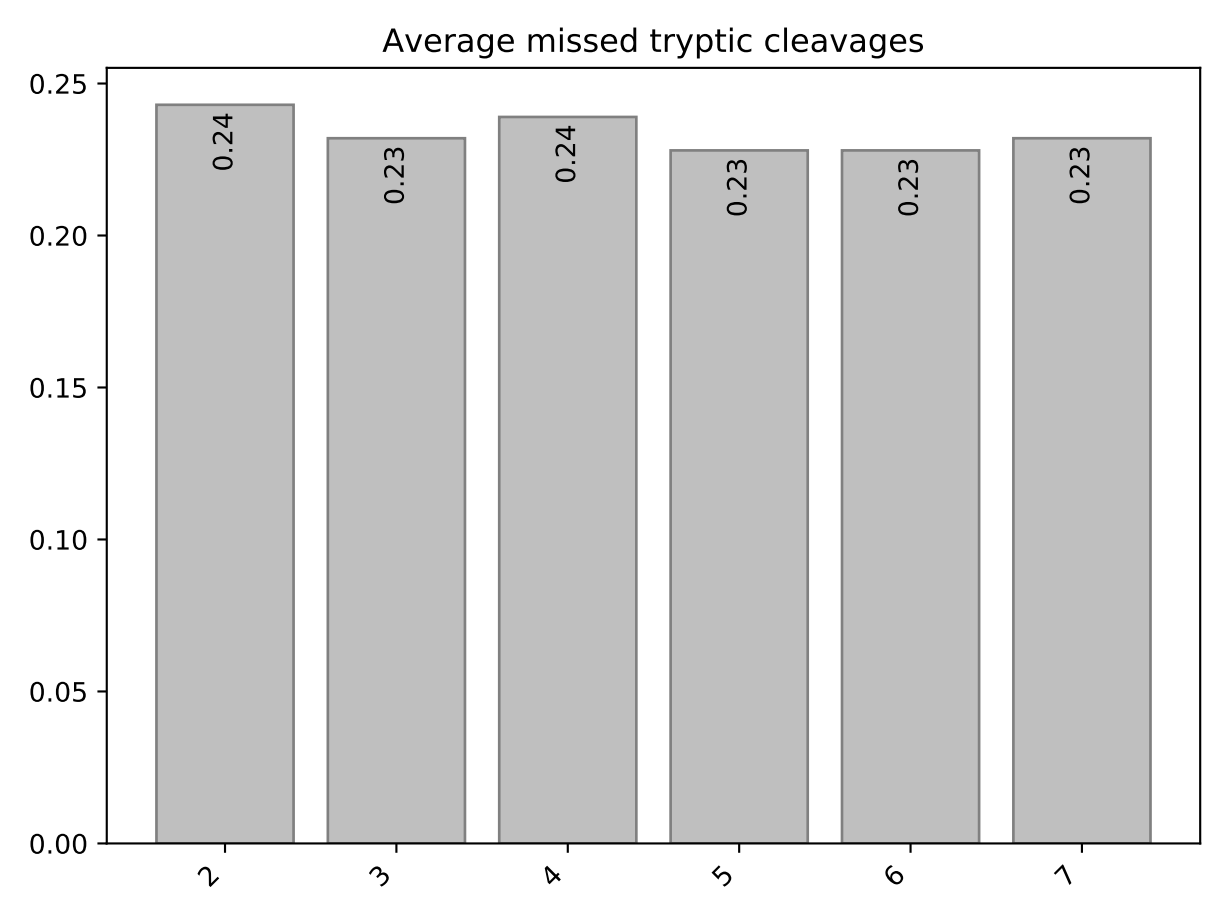

Mean peak FWHM, in MS2 scans
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1.51
1.55
1.49
1.51
1.51
1.53
2
3
4
5
6
7

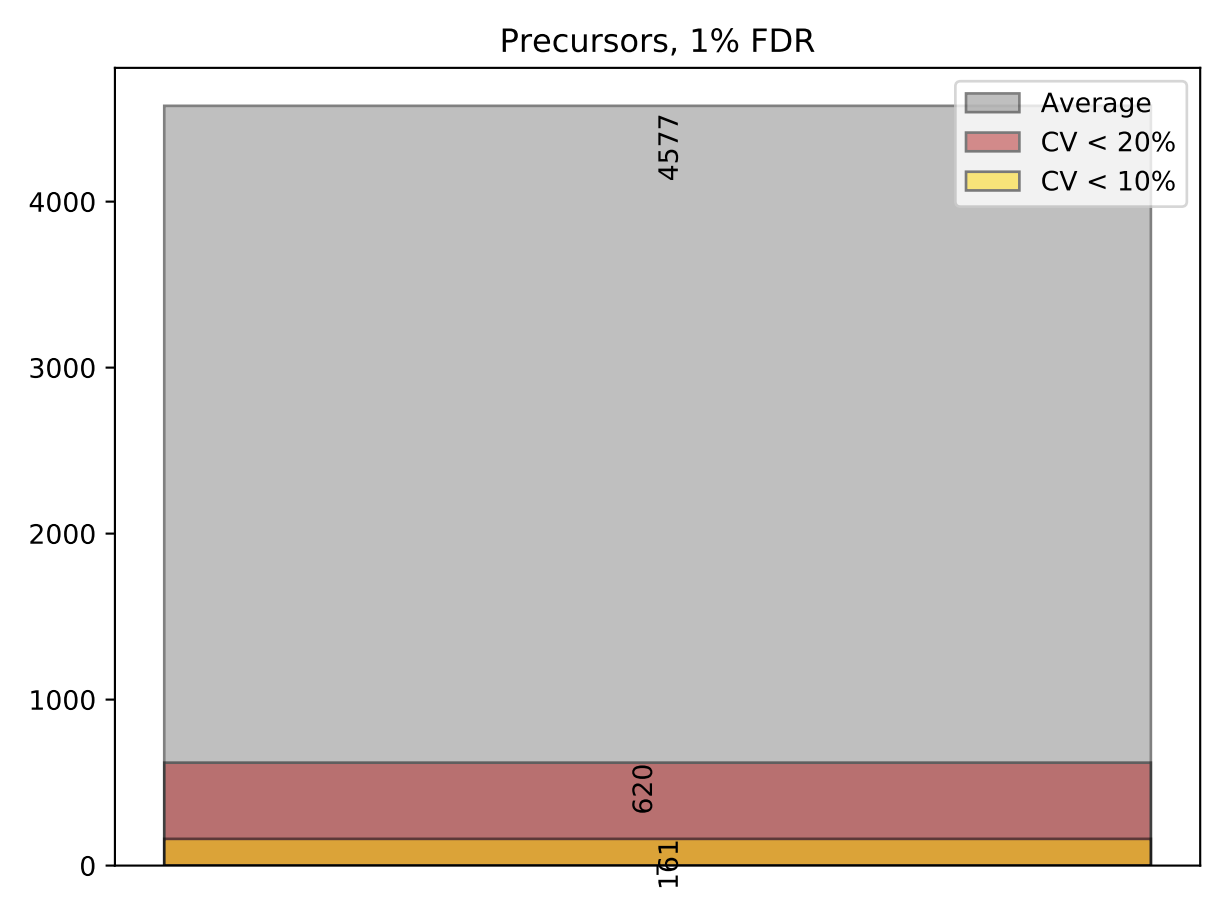

Median RT prediction accuracy, minutes
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0.17
0.1
0.17
0.14
0.16
0.15
2
3
4
5
6
7

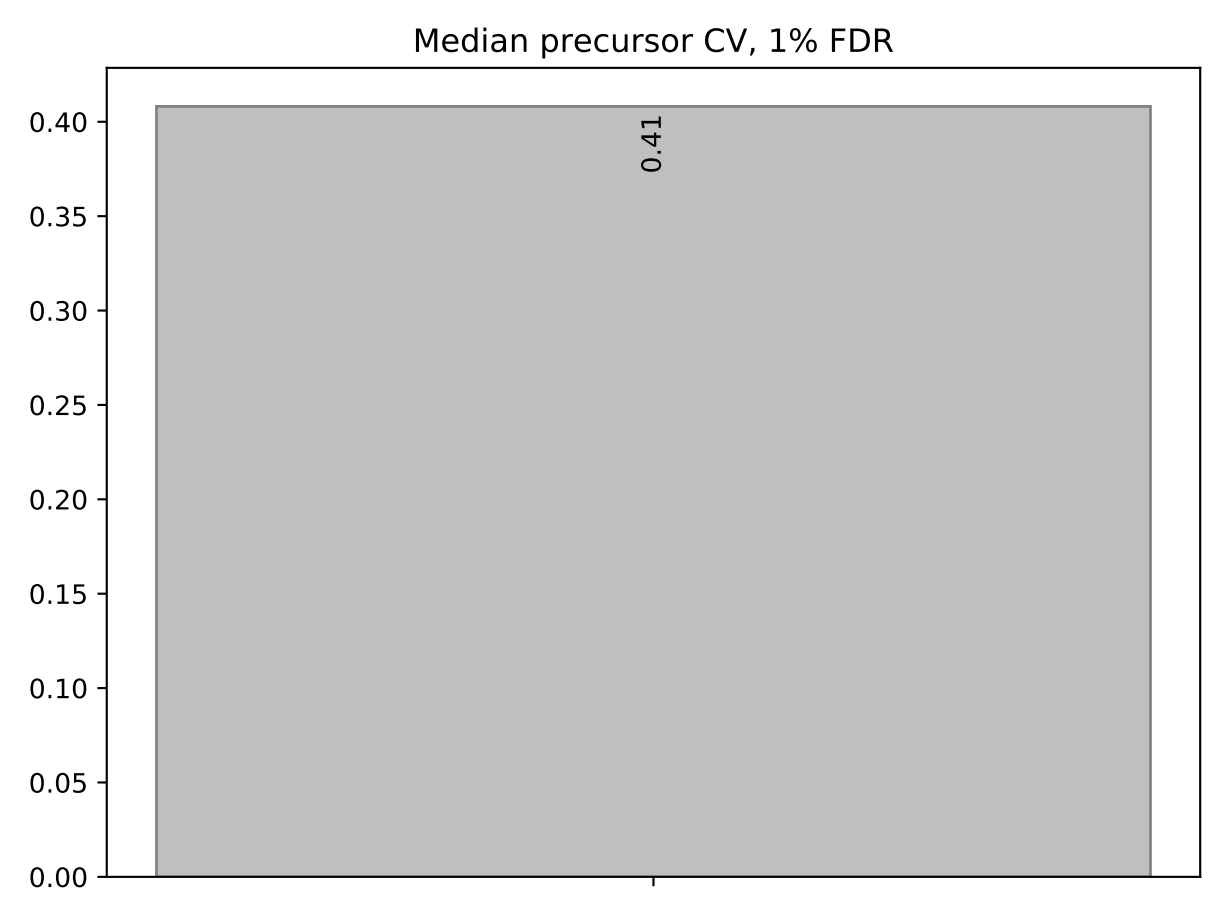

Median mass accuracy, MS2, ppm
Without correction
Corrected
0
1
2
3
4
2
3
4
5
6
7

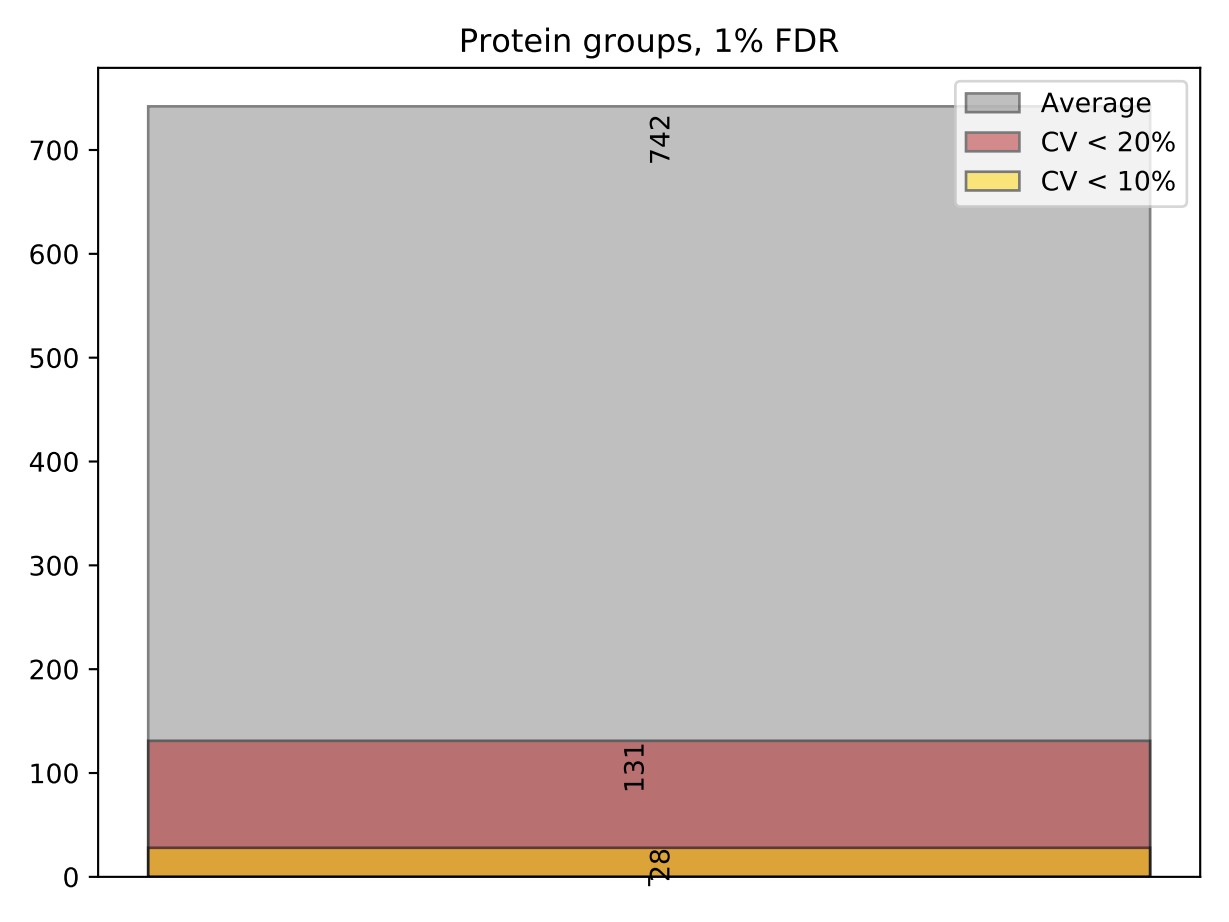

Median mass accuracy, MS1, ppm
Without correction
Corrected
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
2
3
4
5
6
7

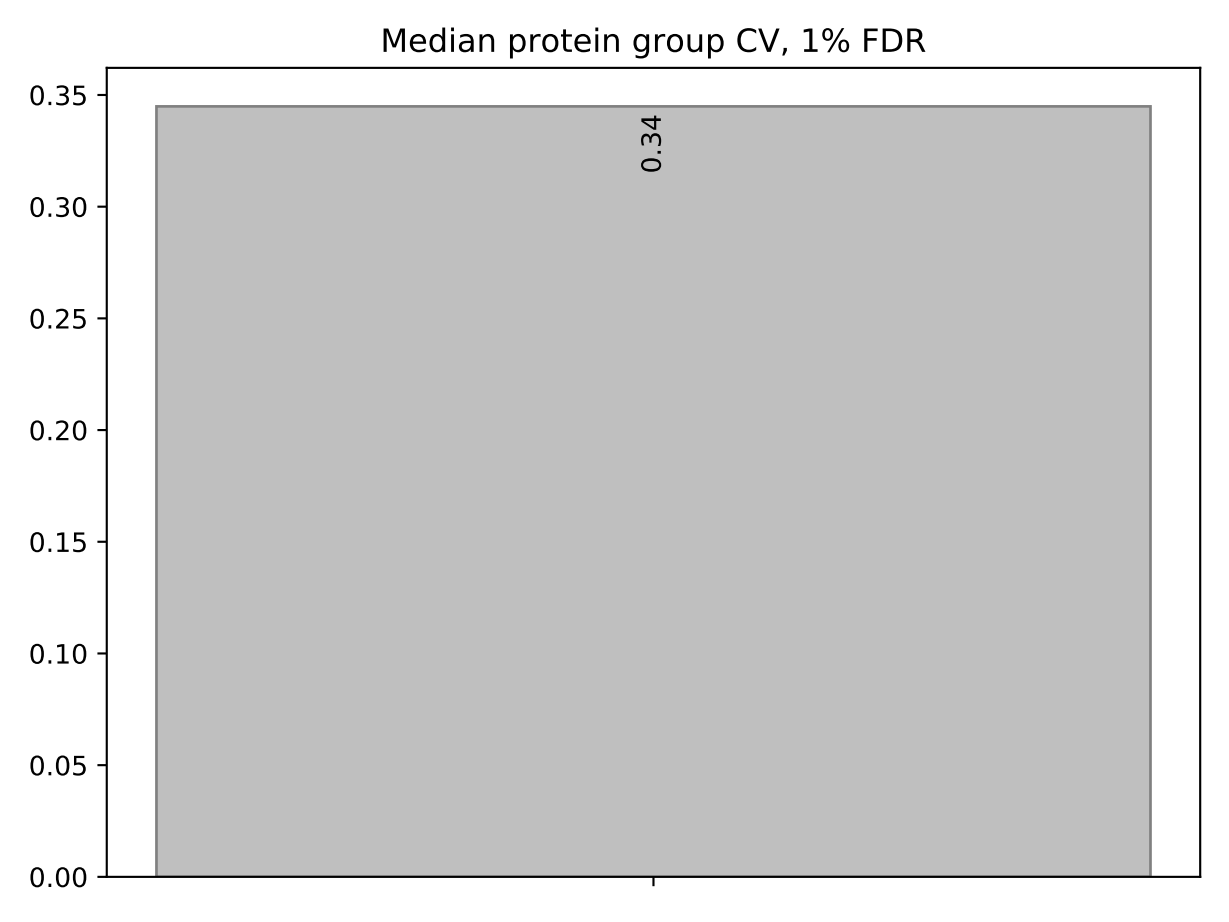

Peptide characteristics
Average length
Average charge
0
2
4
6
8
10
12
2
3
4
5
6
7

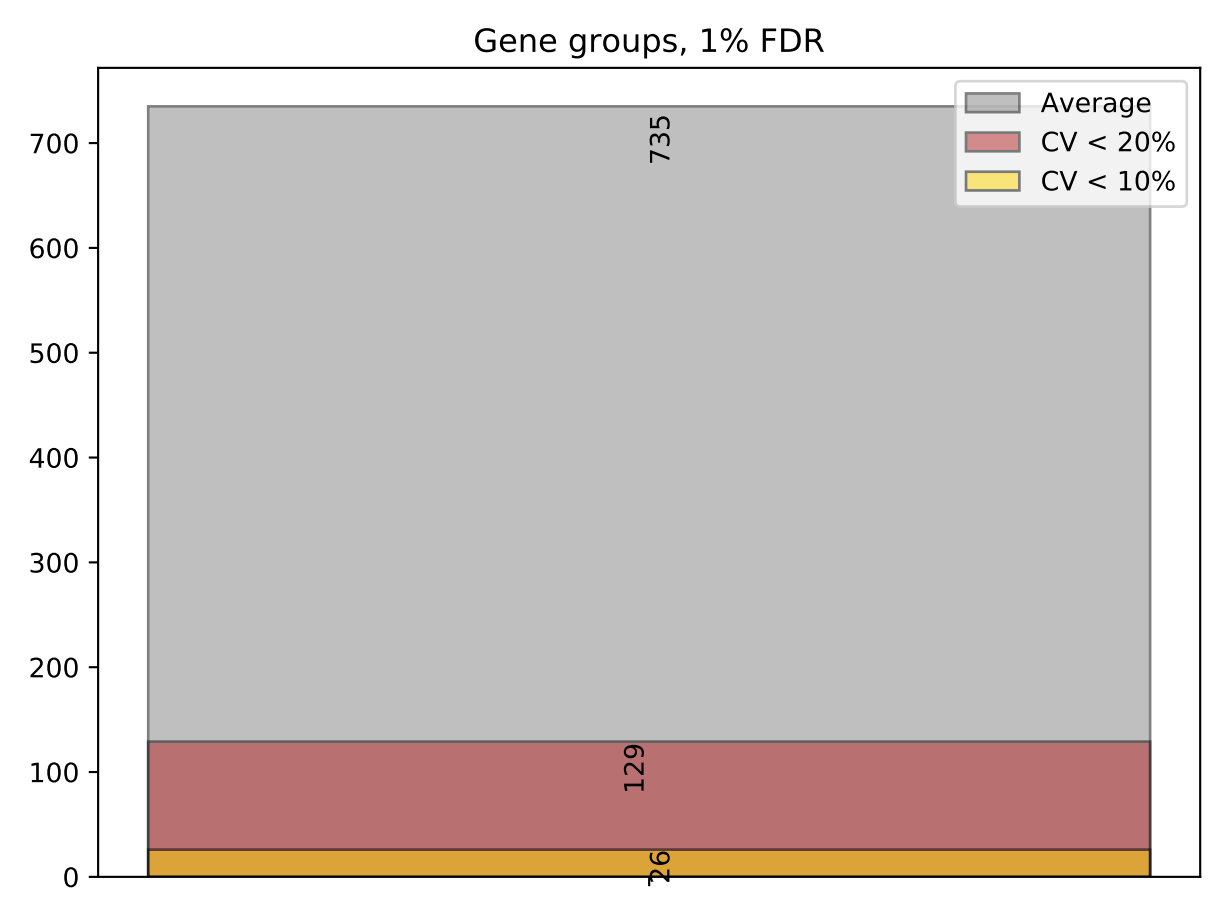

Average missed tryptic cleavages
0.25
0.20
0.15
0.10
0.05
0.00
0.24
0.23
0.24
0.23
0.23
0.23
2
3
4
5
6
7

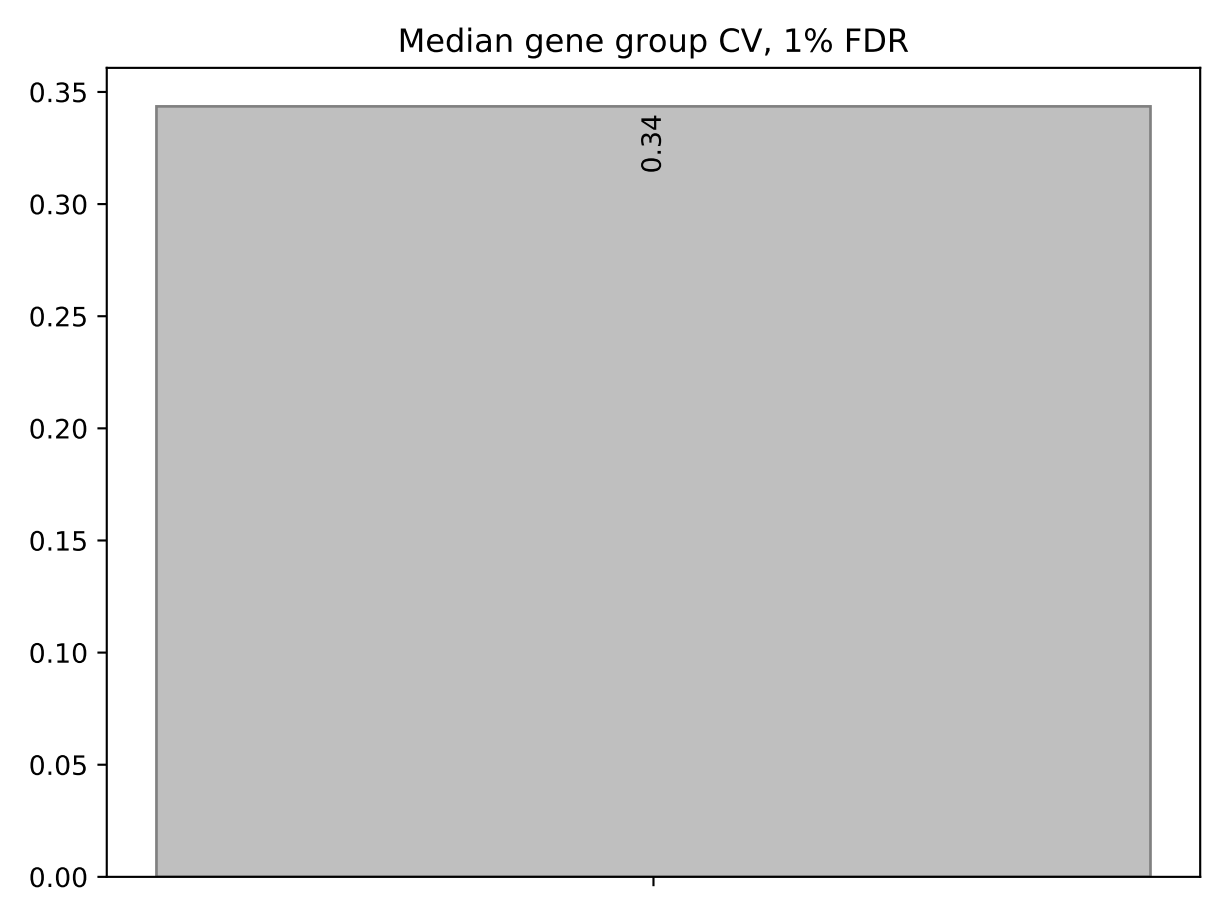

Precursors, 1% FDR
Average
CV < 20%
CV < 10%
4577
620
161
0
1000
2000
3000
4000


Median precursor CV, 1% FDR
0.41
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00


Protein groups, 1% FDR
Average
CV < 20%
CV < 10%
742
131
28
0
100
200
300
400
500
600
700


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


Gene groups, 1% FDR
Average
CV < 20%
CV < 10%
735
129
26
0
100
200
300
400
500
600
700


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