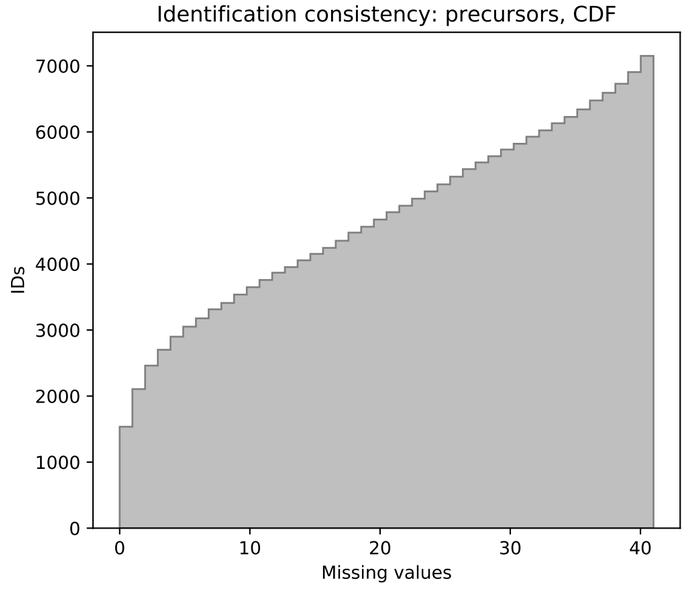
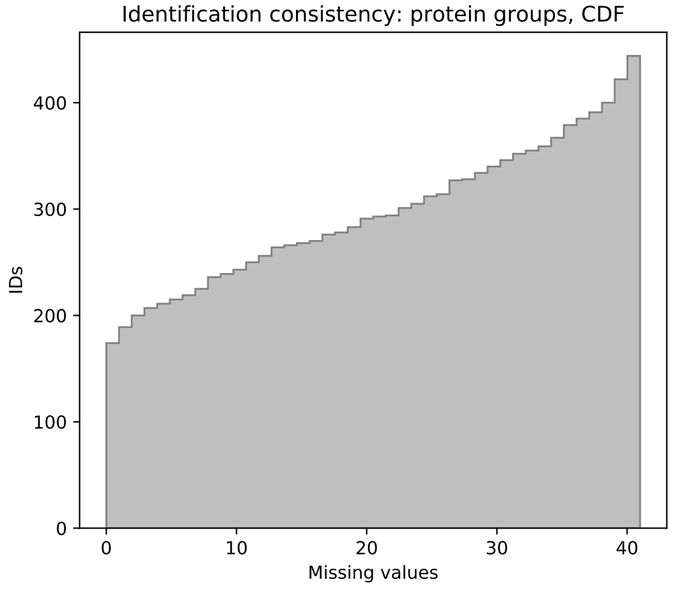
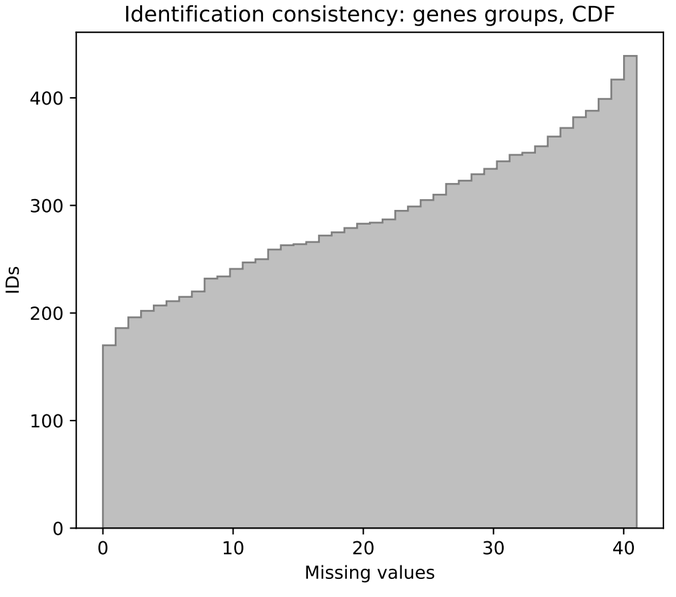
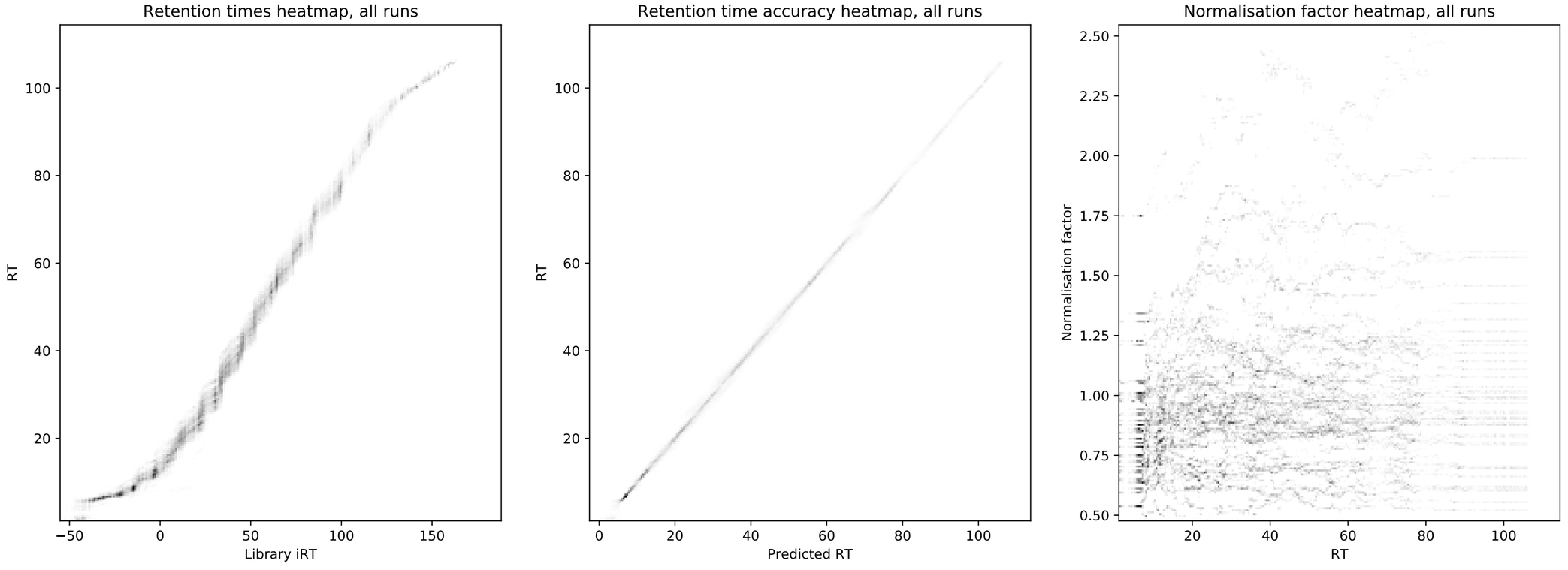
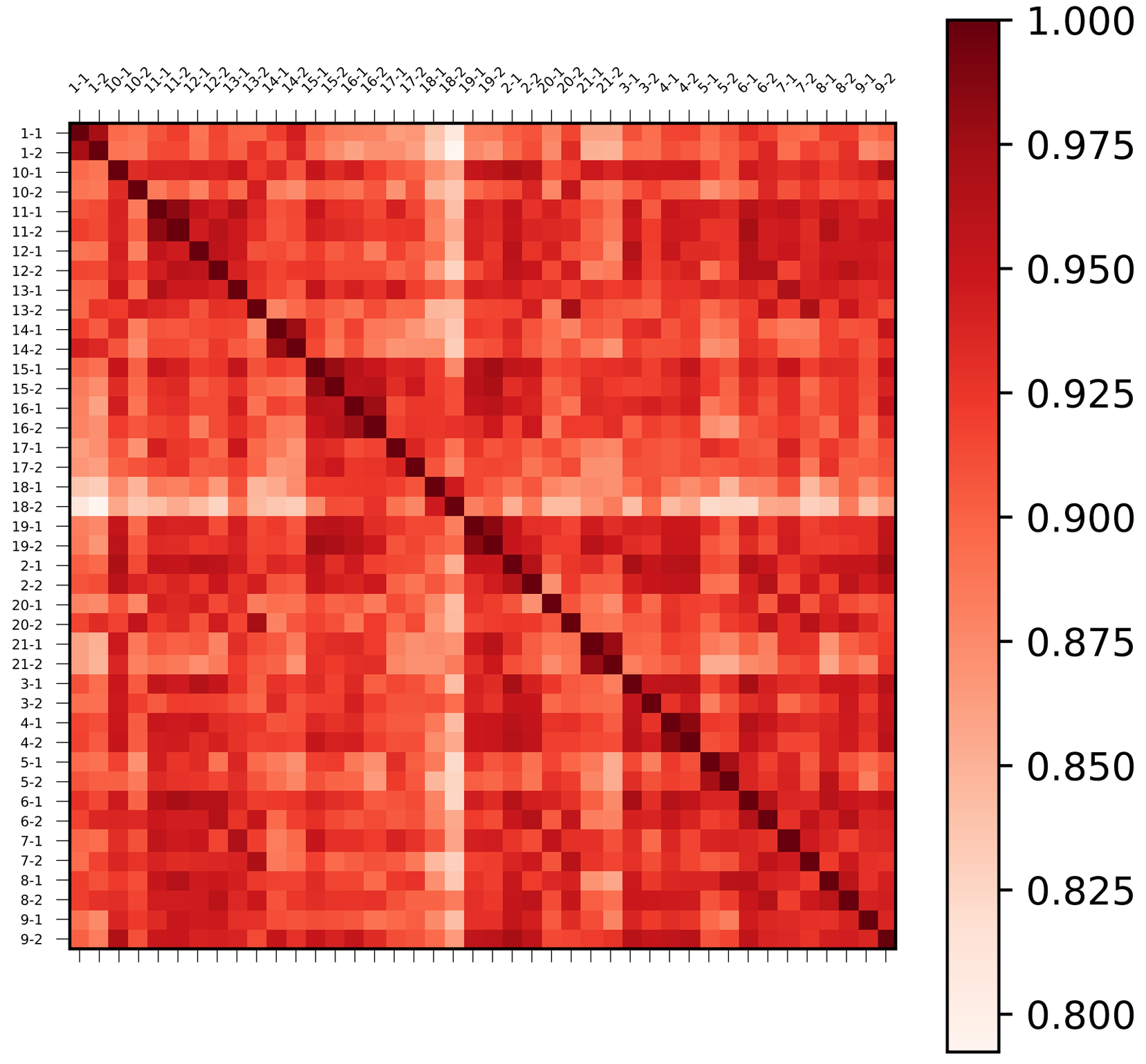
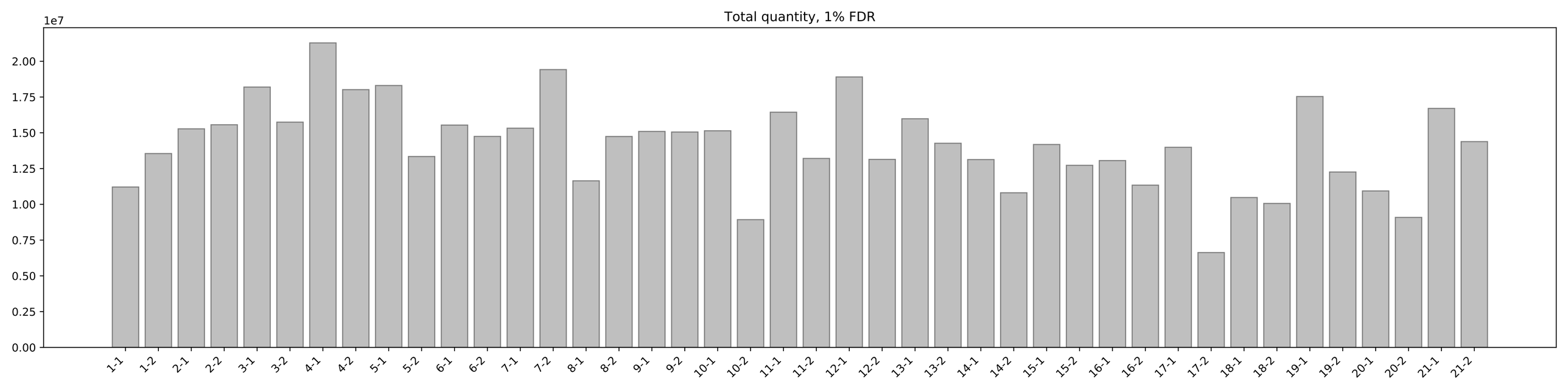

Identification consistency: precursors, CDF
IDs
Missing values
0
1000
2000
3000
4000
5000
6000
7000
0
10
20
30
40

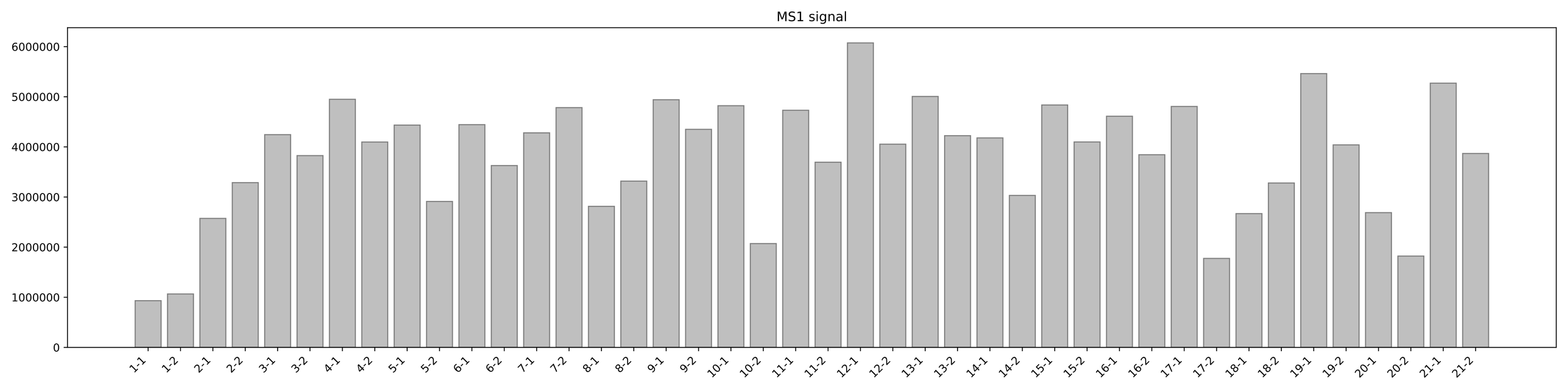

Identification consistency: protein groups, CDF
IDs
Missing values
0
100
200
300
400
0
10
20
30
40

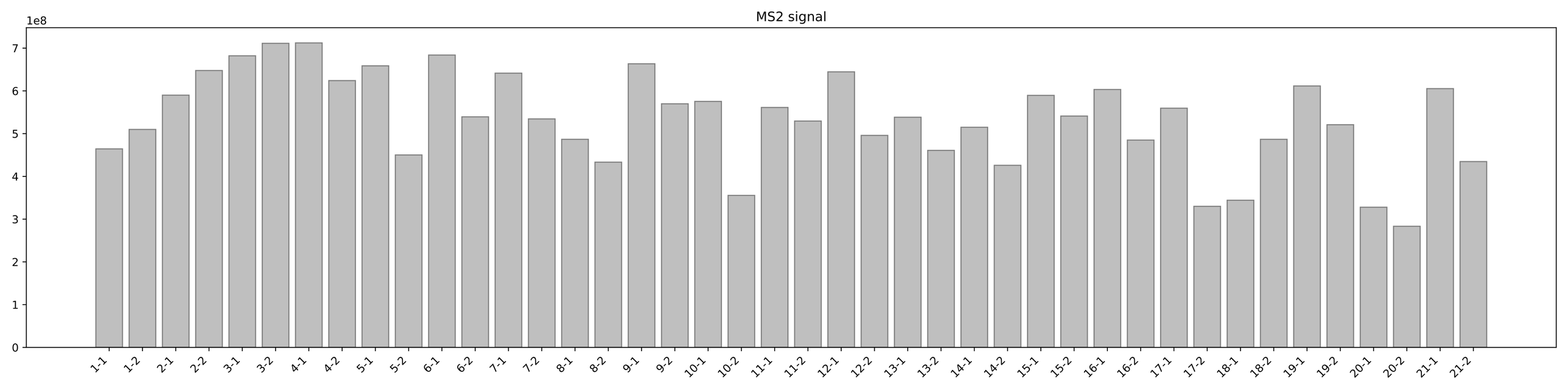

Identification consistency: genes groups, CDF
IDs
Missing values
0
100
200
300
400
0
10
20
30
40


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


1-1
1-2
10-1
10-2
11-1
11-2
12-1
12-2
13-1
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
2-1
2-2
20-1
20-2
21-1
21-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
1.000
0.975
0.950
0.925
0.900
0.875
0.850
0.825
0.800


Total quantity, 1% FDR
1e7
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
13-1
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


MS1 signal
6000000
5000000
4000000
3000000
2000000
1000000
0
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
13-1
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


MS2 signal
1e8
0
1
2
3
4
5
6
7
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
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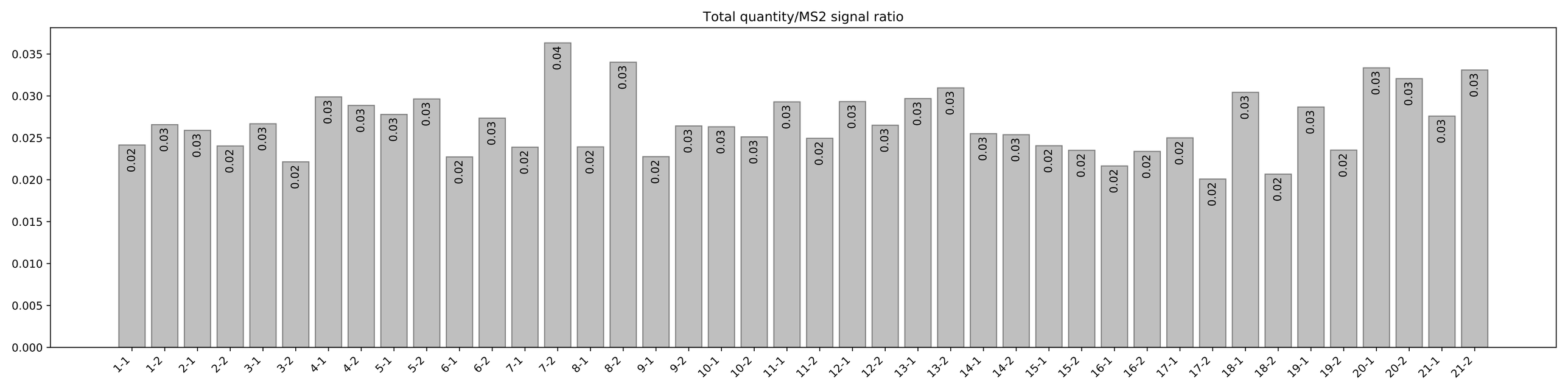
13-1
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Total quantity/MS2 signal ratio
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0.02
0.03
0.03
0.02
0.03
0.02
0.03
0.03
0.03
0.03
0.02
0.03
0.02
0.04
0.02
0.03
0.02
0.03
0.03
0.03
0.03
0.02
0.03
0.03
0.03
0.03
0.03
0.03
0.02
0.02
0.02
0.02
0.02
0.02
0.03
0.02
0.03
0.02
0.03
0.03
0.02
0.03
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
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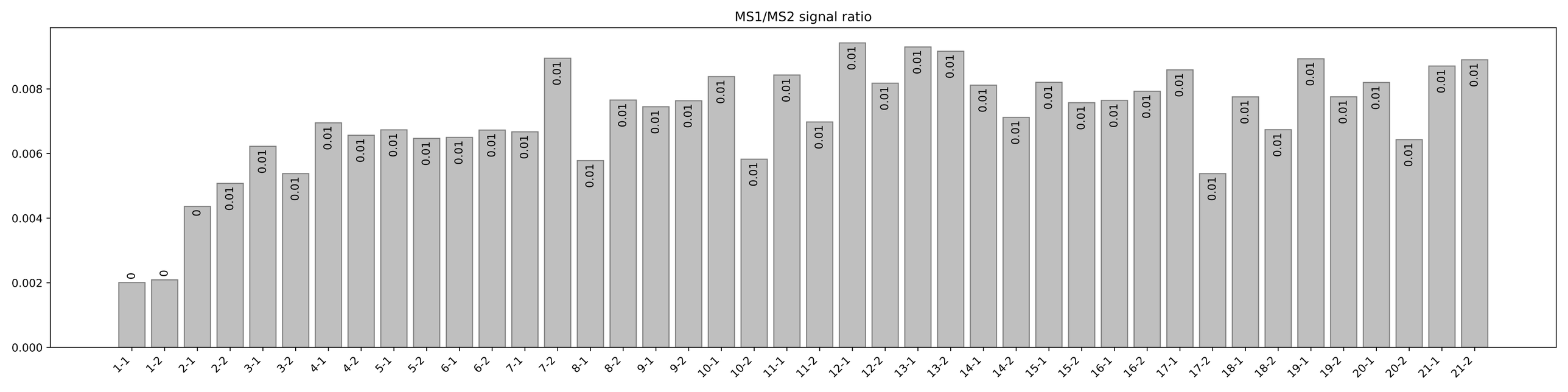
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


MS1/MS2 signal ratio
0.000
0.002
0.004
0.006
0.008
0
0
0
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
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0.01
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0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
0.01
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
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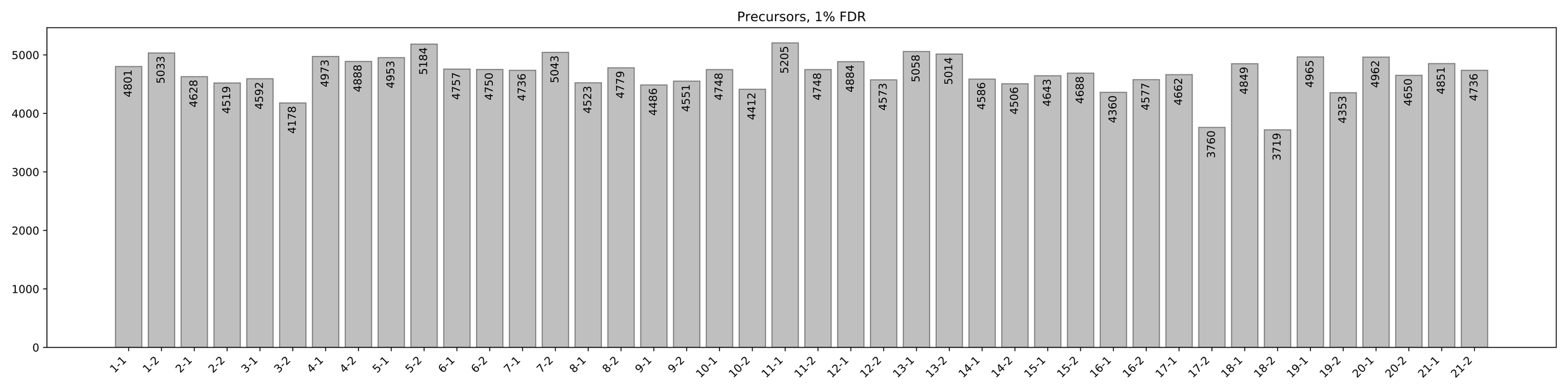
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Precursors, 1% FDR
0
1000
2000
3000
4000
5000
4801
5033
4628
4519
4592
4178
4973
4888
4953
5184
4757
4750
4736
5043
4523
4779
4486
4551
4748
4412
5205
4748
4884
4573
5058
5014
4586
4506
4643
4688
4360
4577
4662
3760
4849
3719
4965
4353
4962
4650
4851
4736
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
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6-2
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8-2
9-1
9-2
10-1
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15-1
15-2
16-1
16-2
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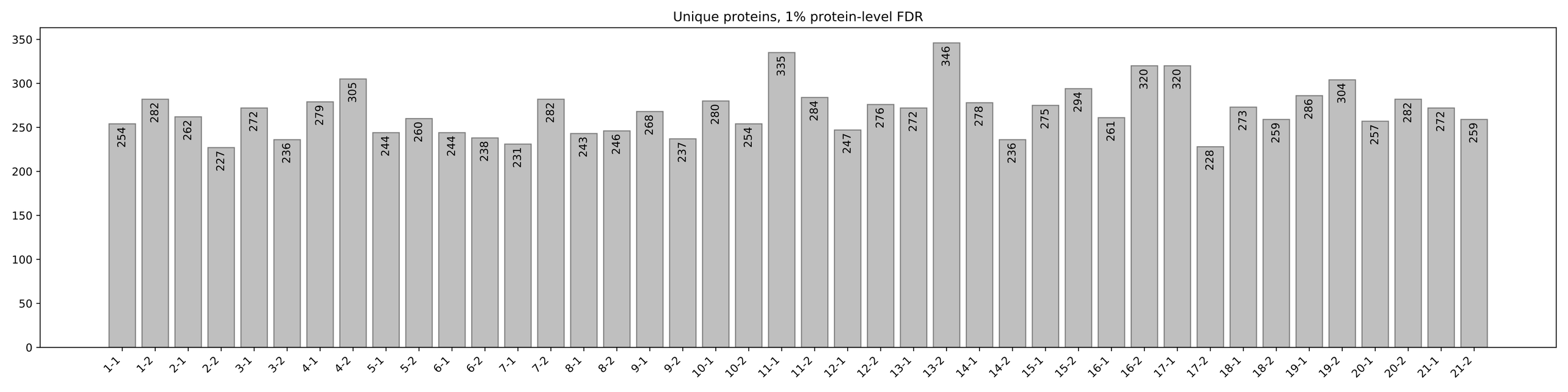
19-2
20-1
20-2
21-1
21-2


Unique proteins, 1% protein-level FDR
0
50
100
150
200
250
300
350
254
282
262
227
272
236
279
305
244
260
244
238
231
282
243
246
268
237
280
254
335
284
247
276
272
346
278
236
275
294
261
320
320
228
273
259
286
304
257
282
272
259
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
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10-2
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11-2
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14-2
15-1
15-2
16-1
16-2
17-1
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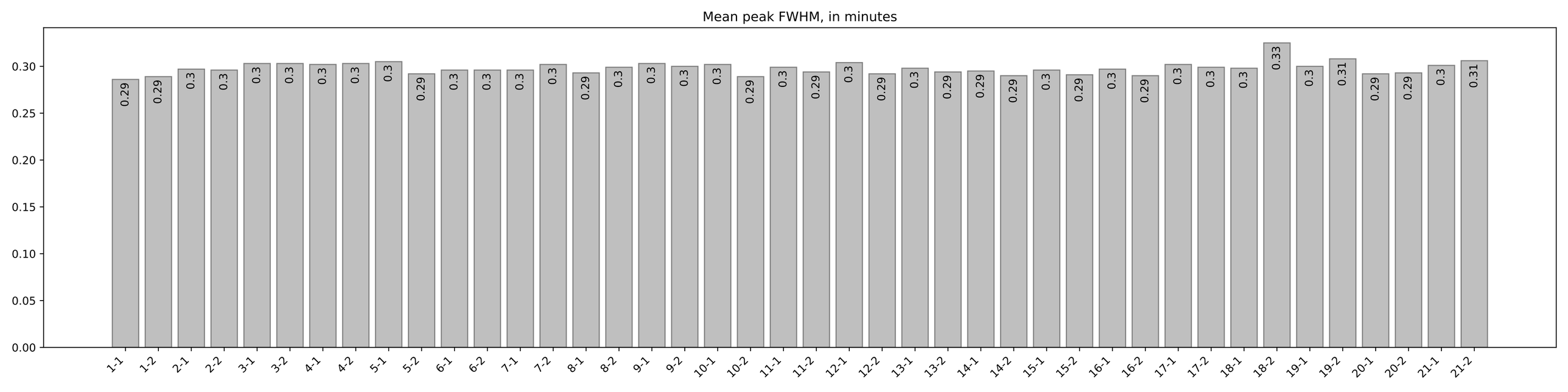
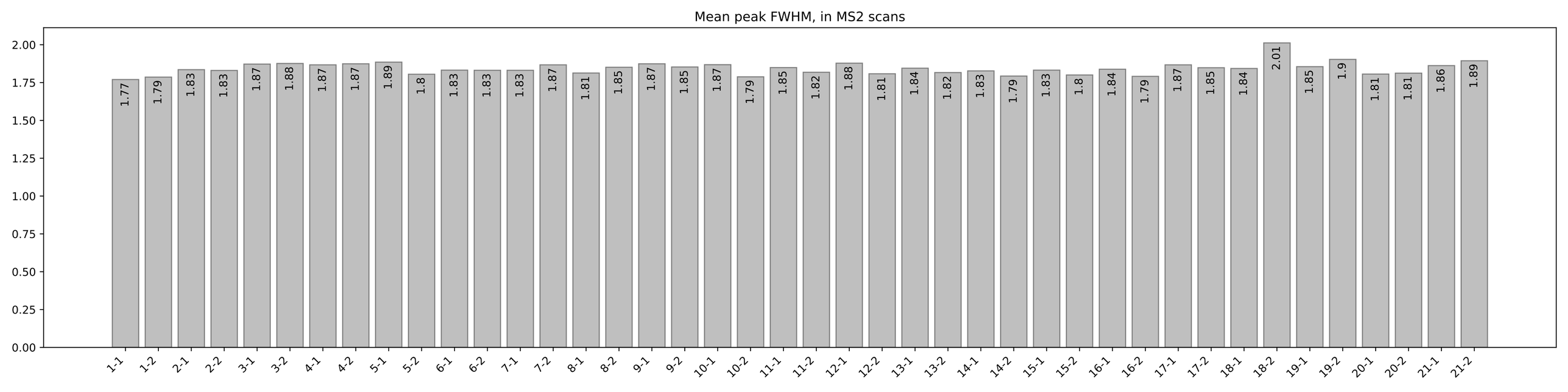
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Mean peak FWHM, in minutes
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.29
0.29
0.3
0.3
0.3
0.3
0.3
0.3
0.3
0.29
0.3
0.3
0.3
0.3
0.29
0.3
0.3
0.3
0.3
0.29
0.3
0.29
0.3
0.29
0.3
0.29
0.29
0.29
0.3
0.29
0.3
0.29
0.3
0.29
0.3
0.3
0.3
0.33
0.3
0.31
0.29
0.29
0.3
0.31
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
13-1
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Mean peak FWHM, in MS2 scans
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00
1.77
1.79
1.83
1.83
1.87
1.88
1.87
1.87
1.89
1.8
1.83
1.83
1.83
1.87
1.81
1.85
1.87
1.85
1.87
1.79
1.85
1.82
1.88
1.81
1.84
1.82
1.83
1.79
1.83
1.8
1.84
1.79
1.87
1.85
1.84
2.01
1.85
1.9
1.81
1.81
1.86
1.89
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
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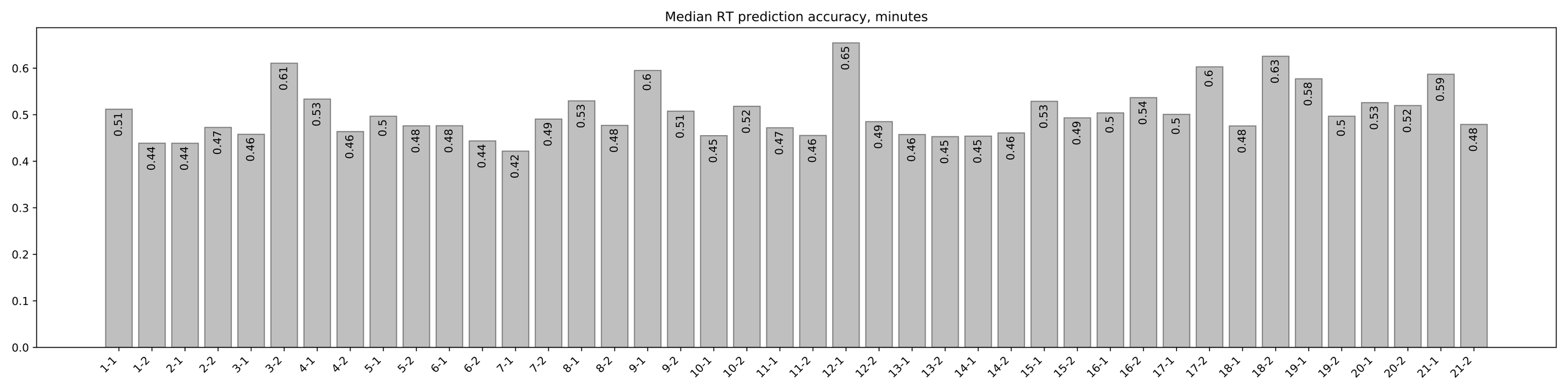
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Median RT prediction accuracy, minutes
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.51
0.44
0.44
0.47
0.46
0.61
0.53
0.46
0.5
0.48
0.48
0.44
0.42
0.49
0.53
0.48
0.6
0.51
0.45
0.52
0.47
0.46
0.65
0.49
0.46
0.45
0.45
0.46
0.53
0.49
0.5
0.54
0.5
0.6
0.48
0.63
0.58
0.5
0.53
0.52
0.59
0.48
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
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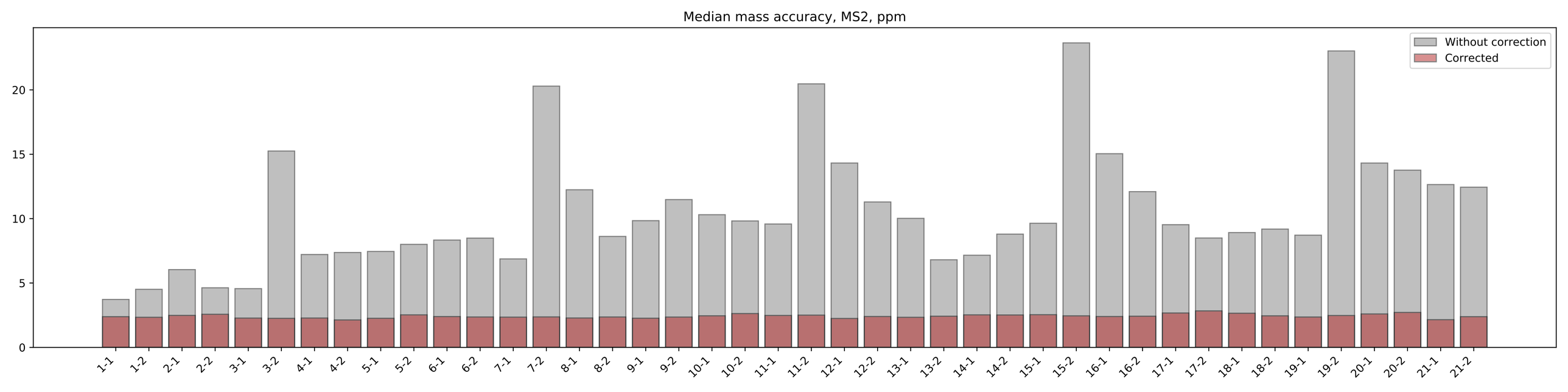
13-2
14-1
14-2
15-1
15-2
16-1
16-2
17-1
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Median mass accuracy, MS2, ppm
Without correction
Corrected
0
5
10
15
20
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
11-2
12-1
12-2
13-1
13-2
14-1
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15-1
15-2
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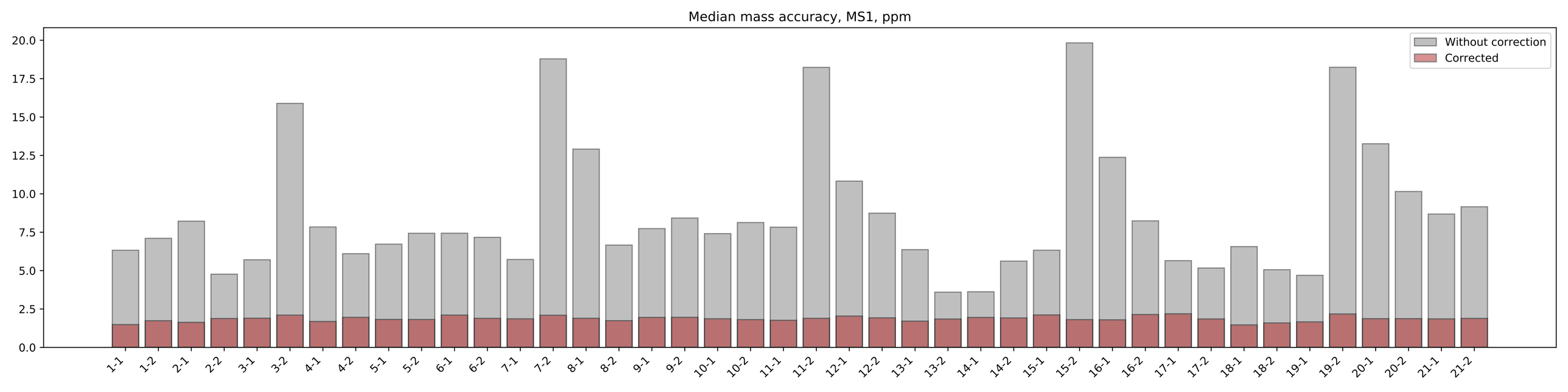
17-2
18-1
18-2
19-1
19-2
20-1
20-2
21-1
21-2


Median mass accuracy, MS1, ppm
Without correction
Corrected
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
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11-1
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15-1
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18-2
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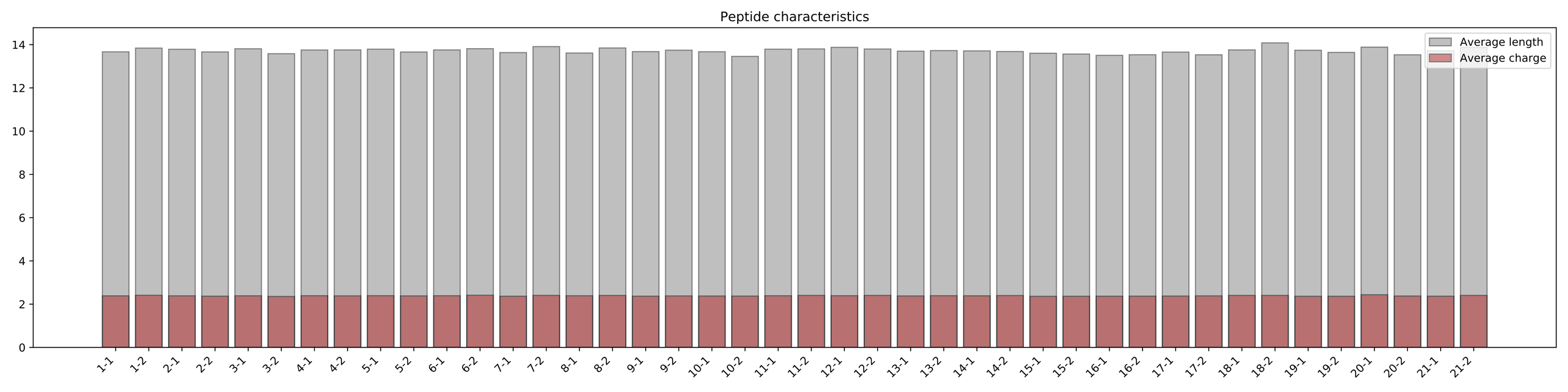
19-2
20-1
20-2
21-1
21-2


Peptide characteristics
Average length
Average charge
0
2
4
6
8
10
12
14
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
8-1
8-2
9-1
9-2
10-1
10-2
11-1
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13-2
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14-2
15-1
15-2
16-1
16-2
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17-2
18-1
18-2
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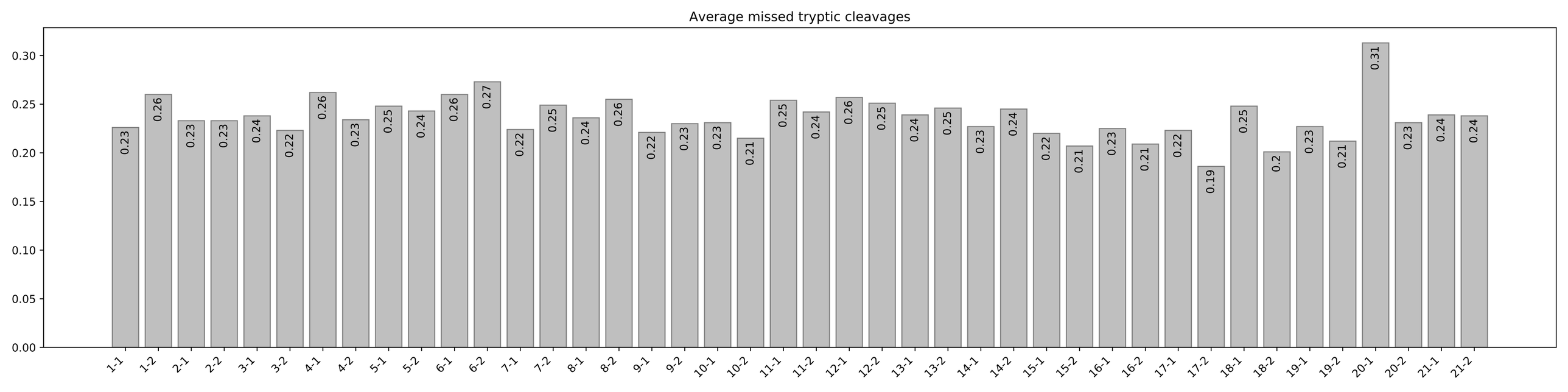
20-1
20-2
21-1
21-2


Average missed tryptic cleavages
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.23
0.26
0.23
0.23
0.24
0.22
0.26
0.23
0.25
0.24
0.26
0.27
0.22
0.25
0.24
0.26
0.22
0.23
0.23
0.21
0.25
0.24
0.26
0.25
0.24
0.25
0.23
0.24
0.22
0.21
0.23
0.21
0.22
0.19
0.25
0.2
0.23
0.21
0.31
0.23
0.24
0.24
1-1
1-2
2-1
2-2
3-1
3-2
4-1
4-2
5-1
5-2
6-1
6-2
7-1
7-2
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8-2
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19-2
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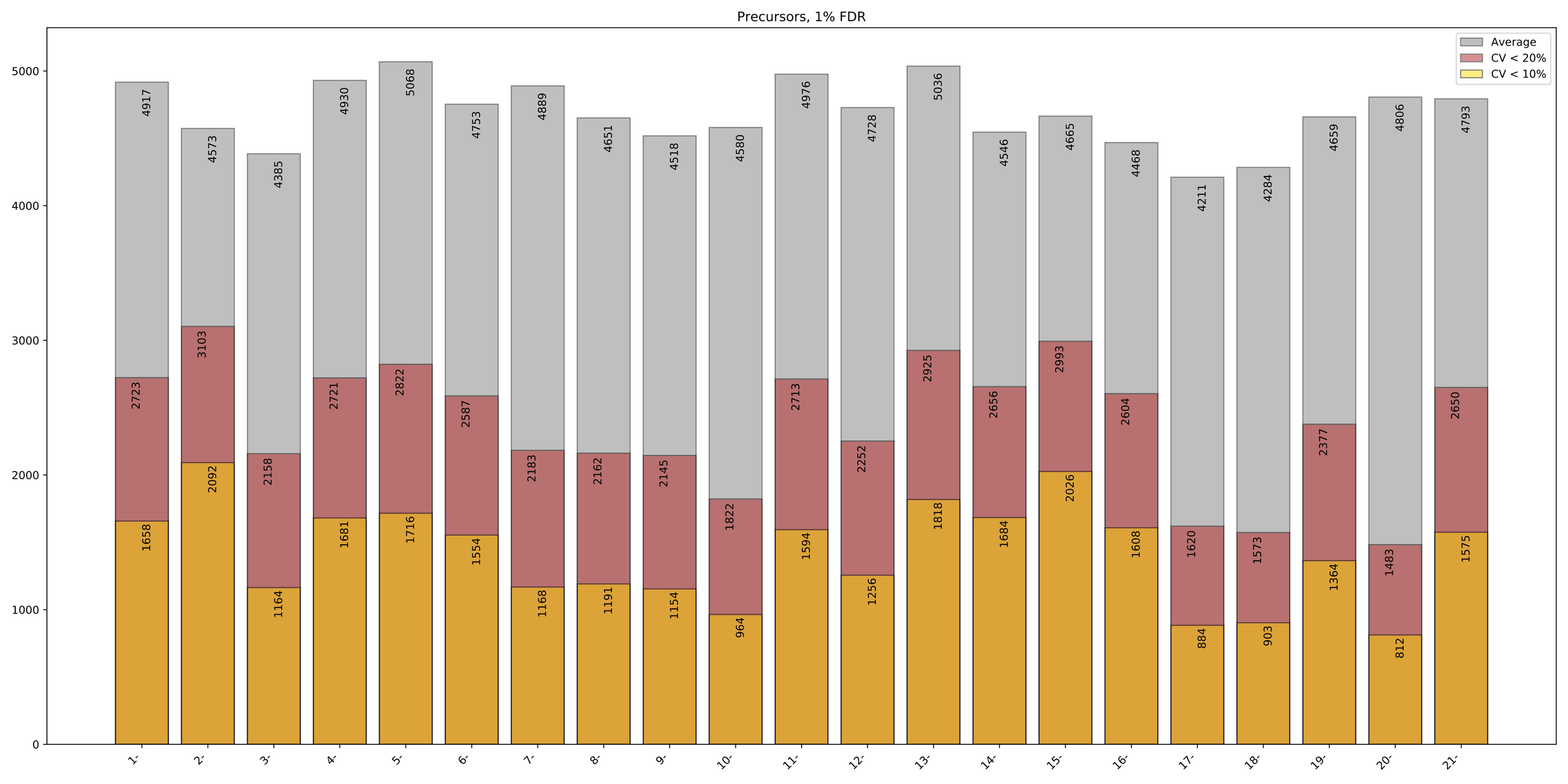
20-2
21-1
21-2


Precursors, 1% FDR
Average
CV < 20%
CV < 10%
0
1000
2000
3000
4000
5000
1-
2-
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2162
1191
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2145
1154
4580
1822
964
4976
2713
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4728
2252
1256
5036
2925
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4546
2656
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4665
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2604
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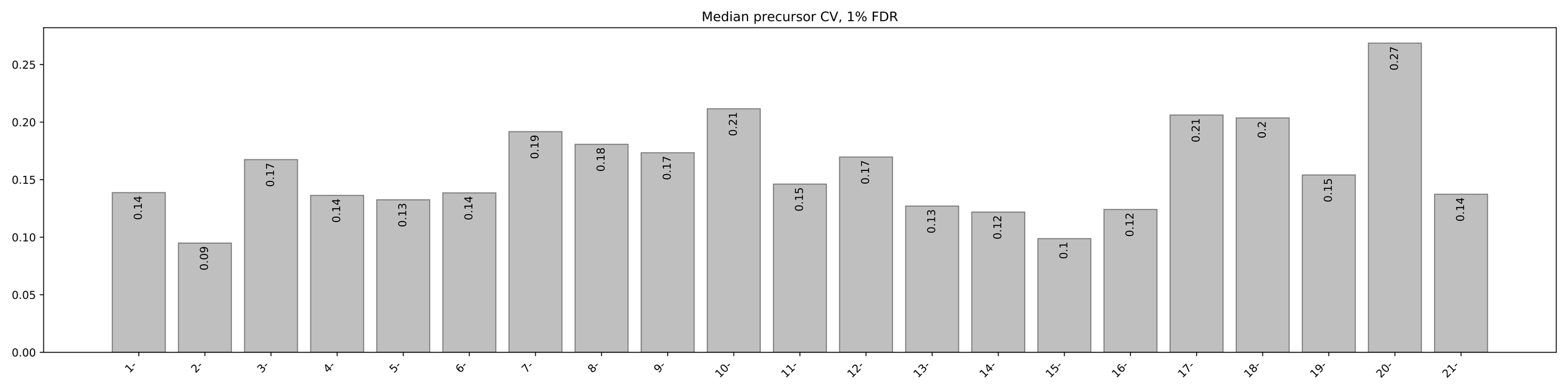
Median precursor CV, 1% FDR
0.00
0.05
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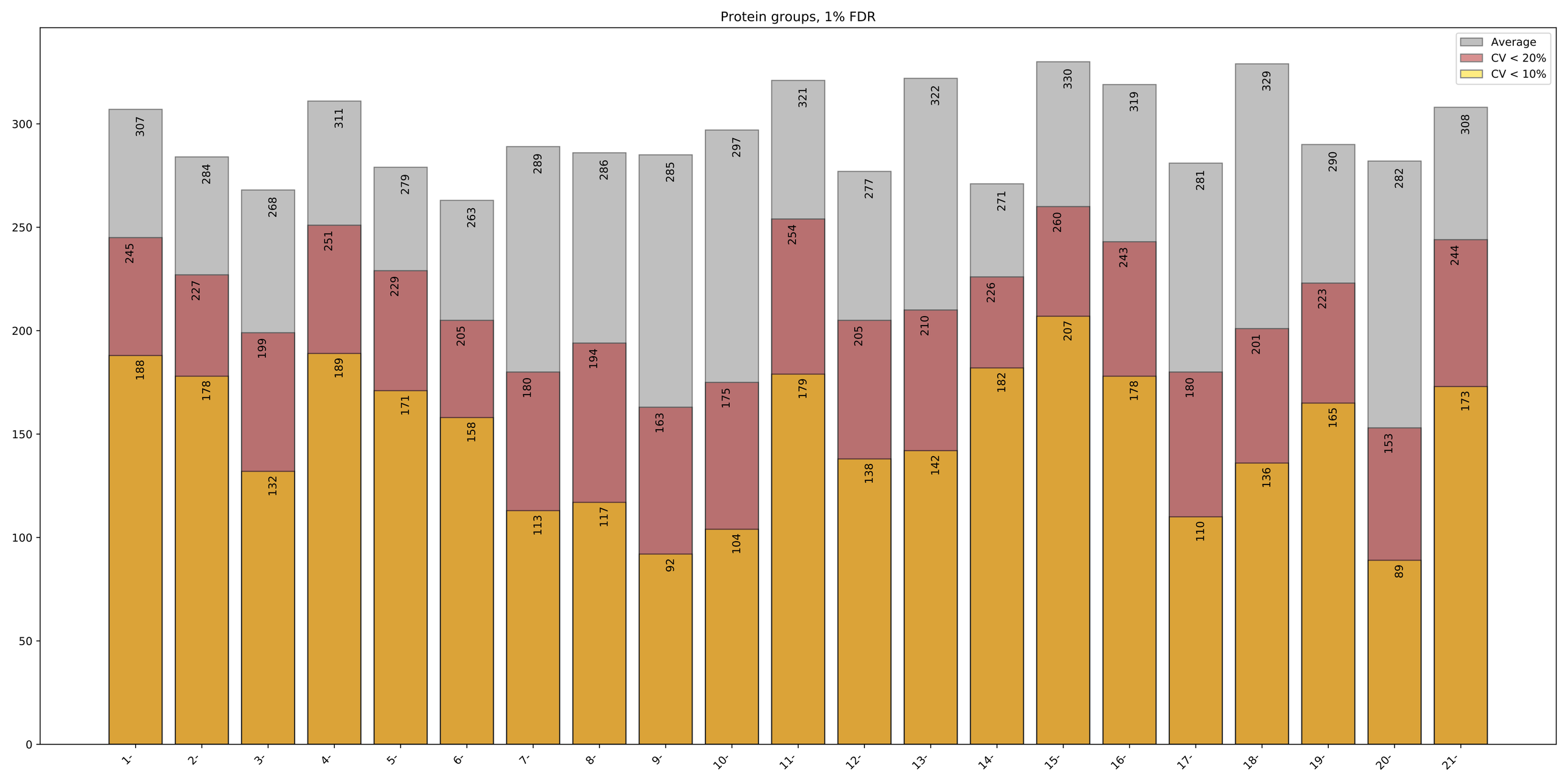
Protein groups, 1% FDR
Average
CV < 20%
CV < 10%
0
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311
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189
279
229
171
263
205
158
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194
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163
92
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175
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321
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179
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205
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322
210
142
271
226
182
330
260
207
319
243
178
281
180
110
329
201
136
290
223
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244
173
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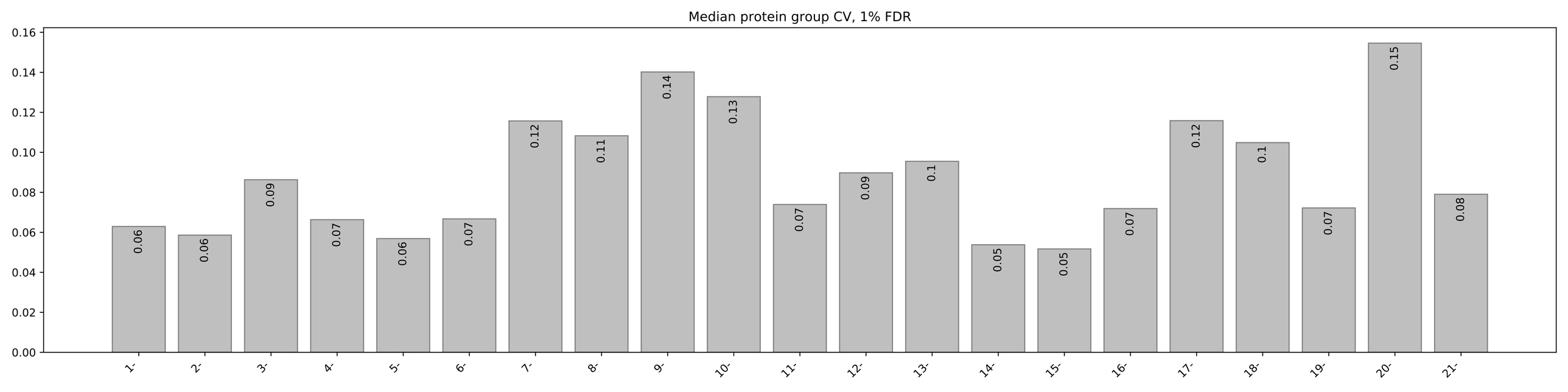
Median protein group CV, 1% FDR
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0.06
0.04
0.02
0.00
0.06
0.06
0.09
0.07
0.06
0.07
0.12
0.11
0.14
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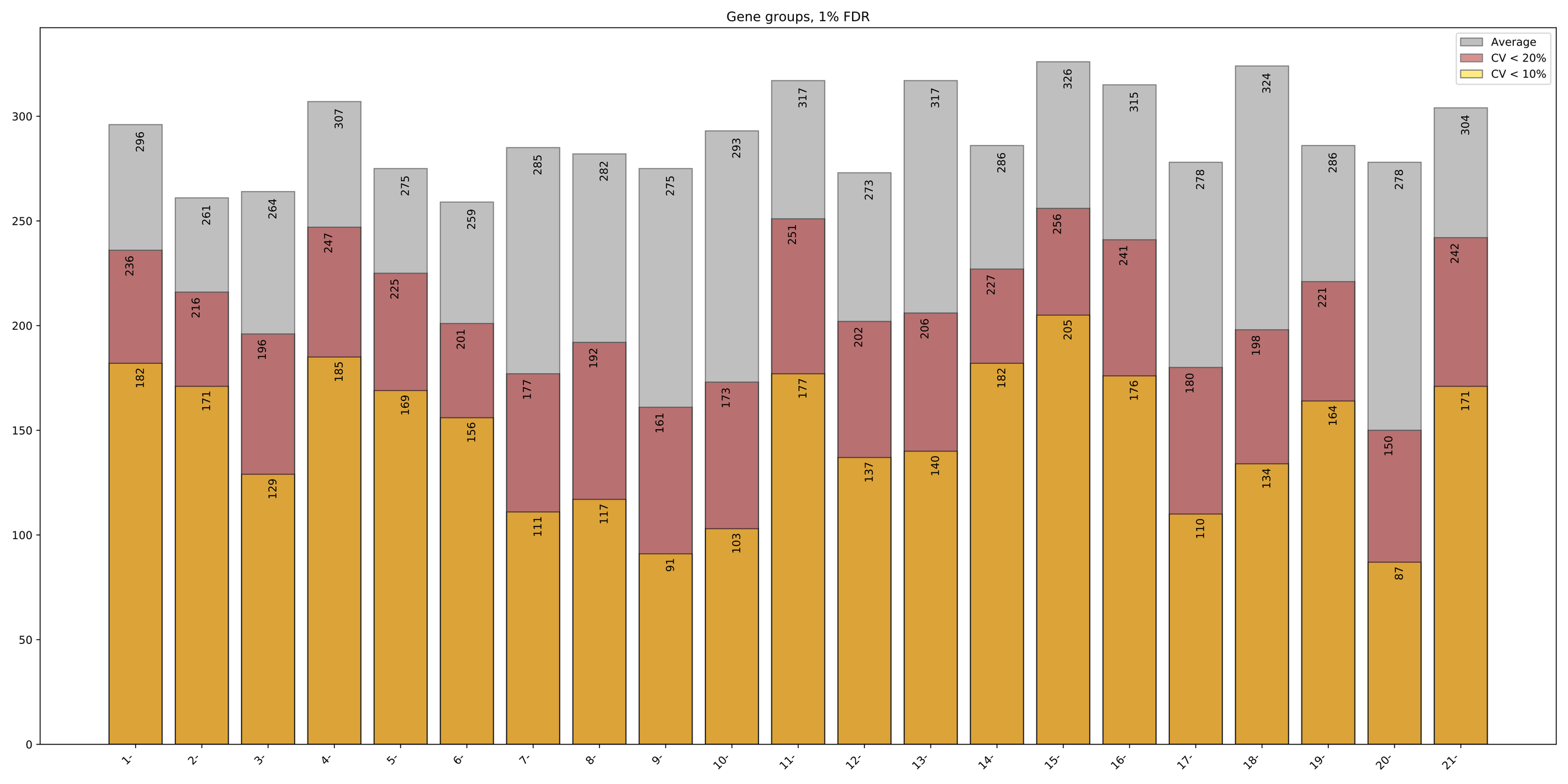
Gene groups, 1% FDR
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CV < 20%
CV < 10%
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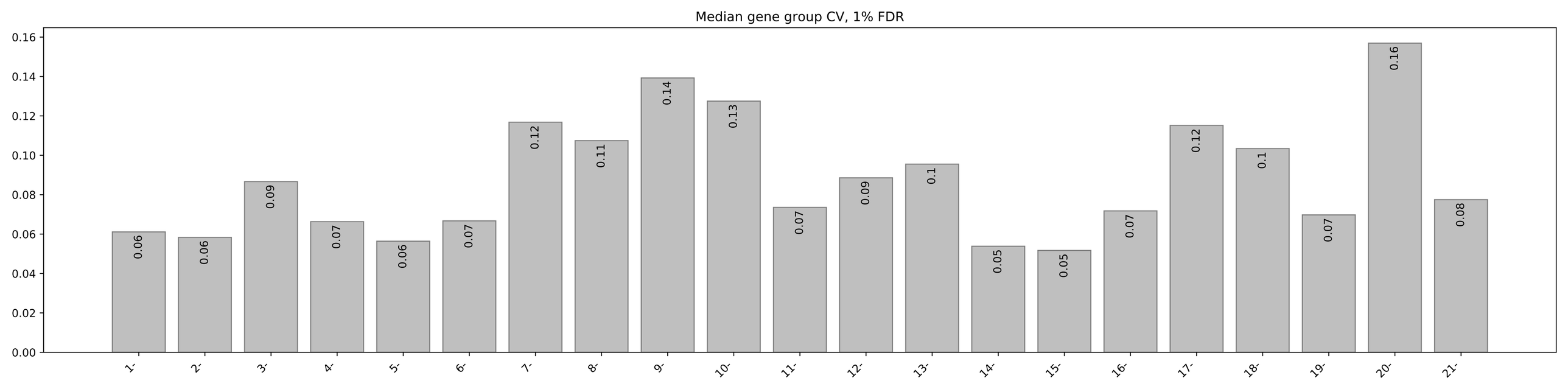
Median gene group CV, 1% FDR
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