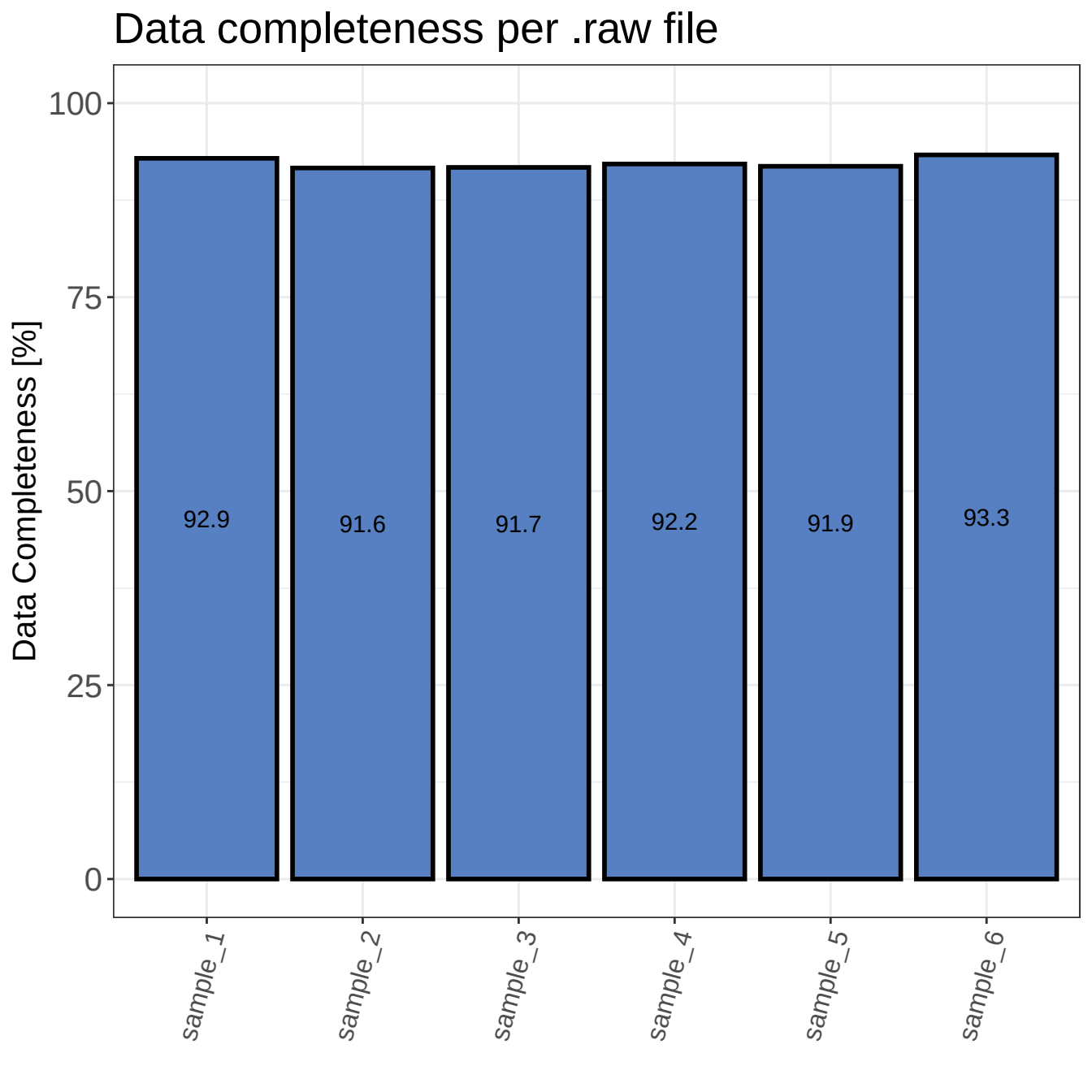
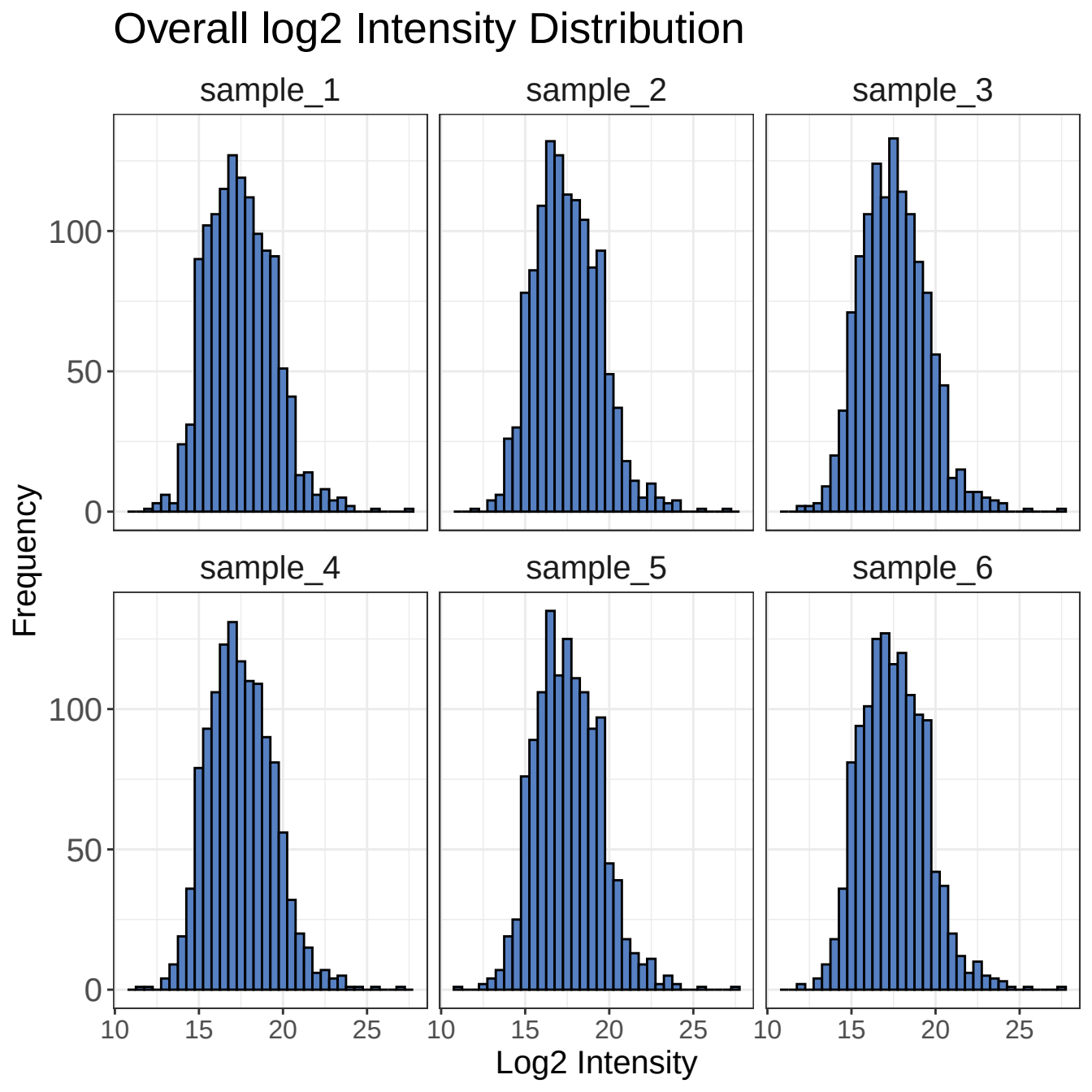
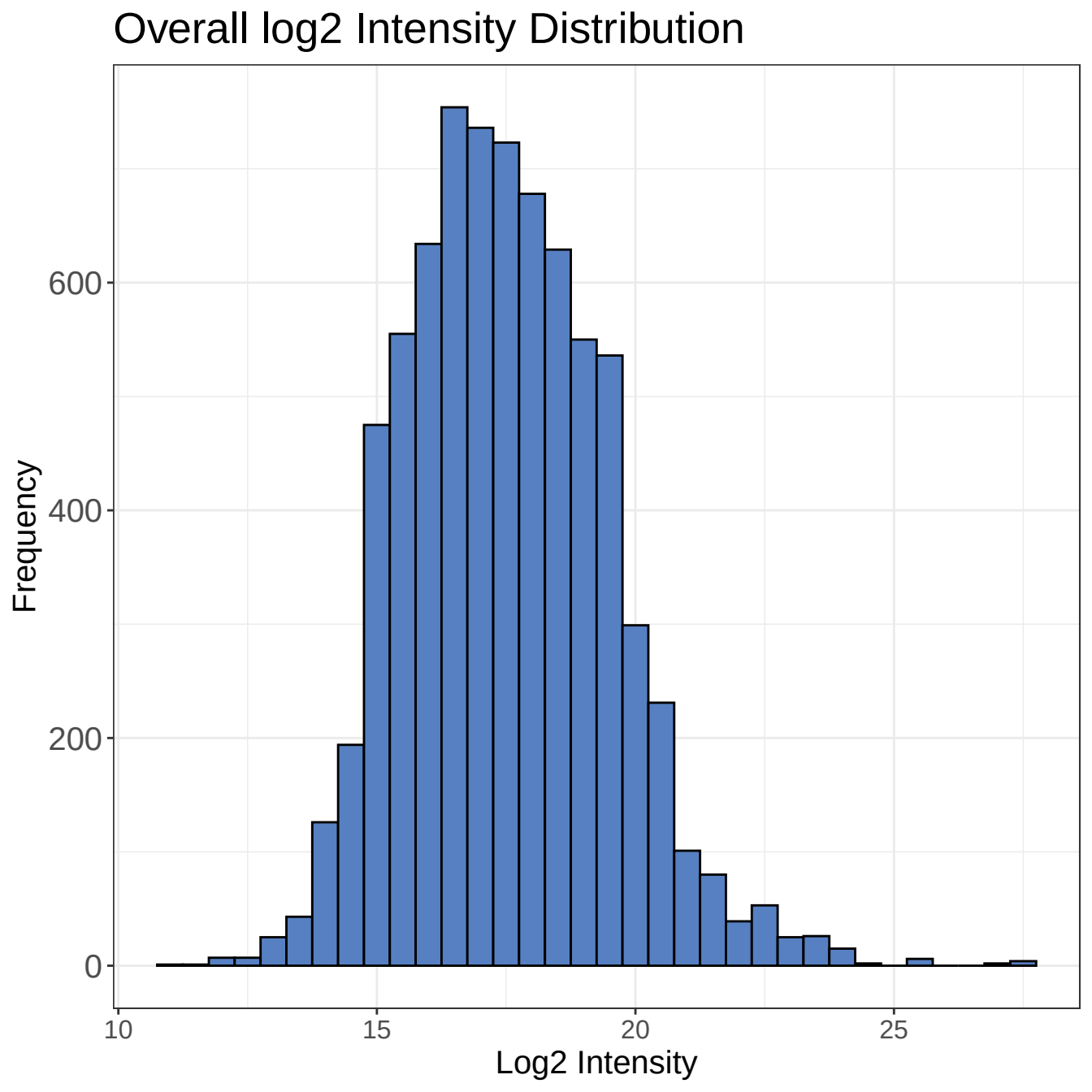
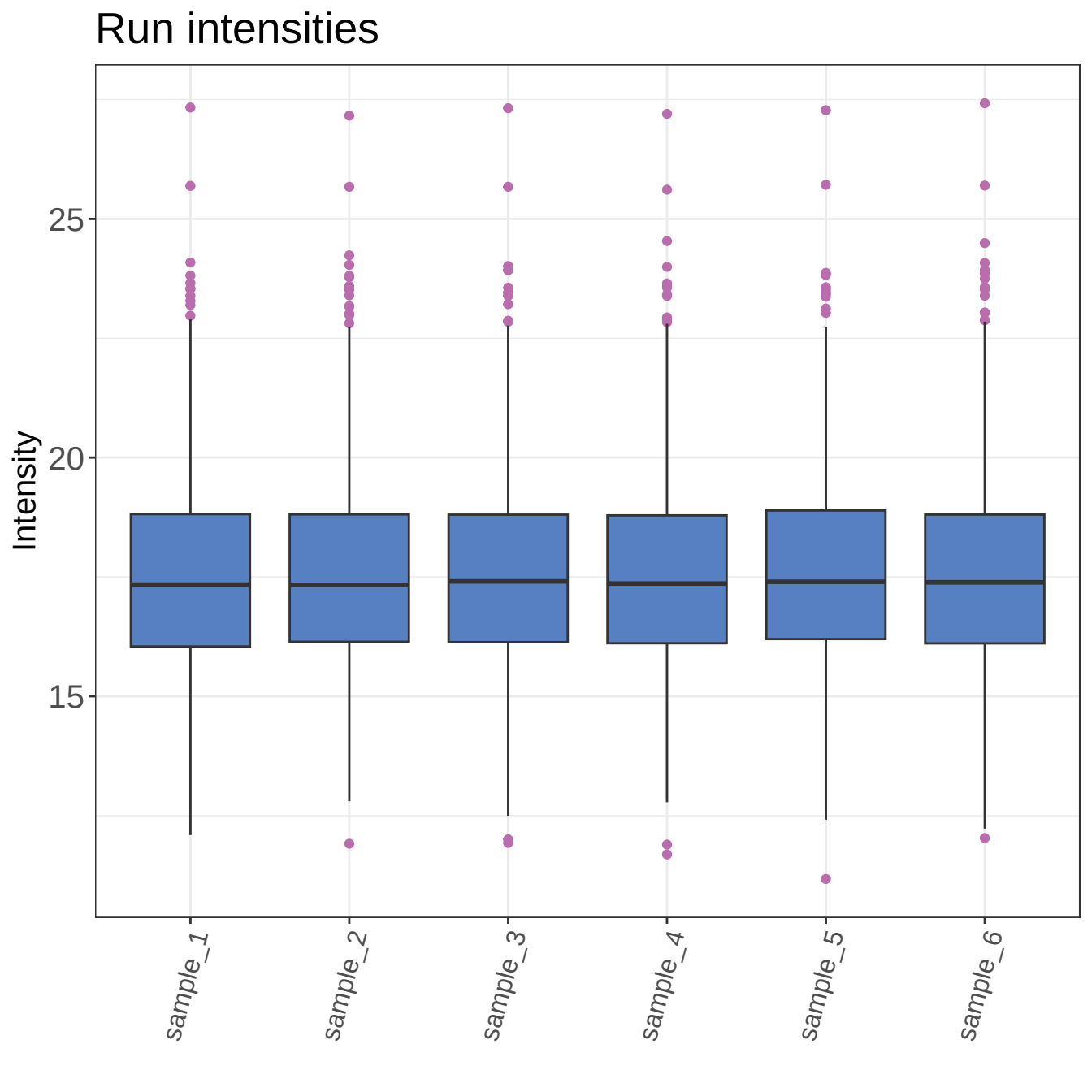
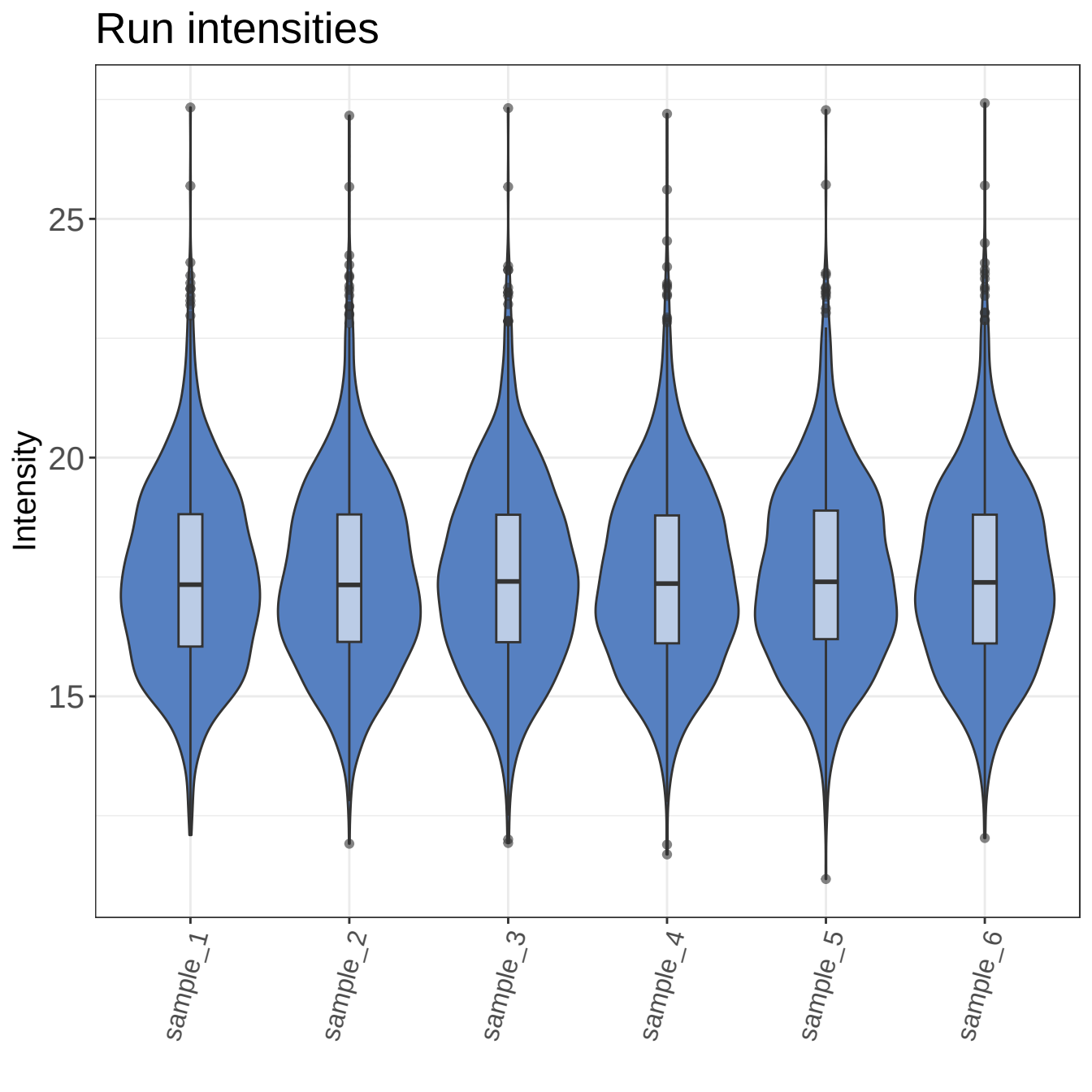
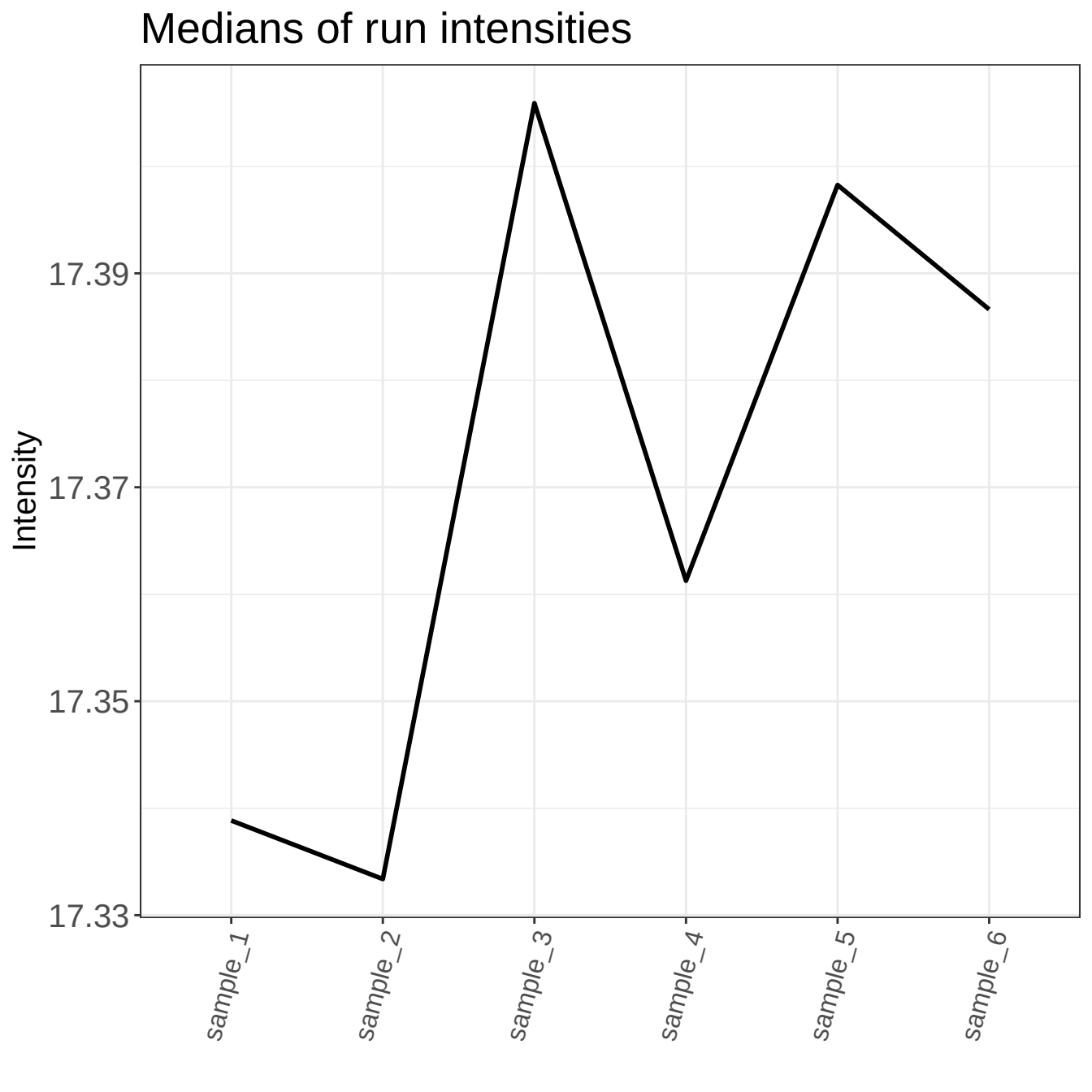

Data completeness per .raw file
Data Completeness [%]
100
75
50
25
0
92.9
91.6
91.7
92.2
91.9
93.3
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6

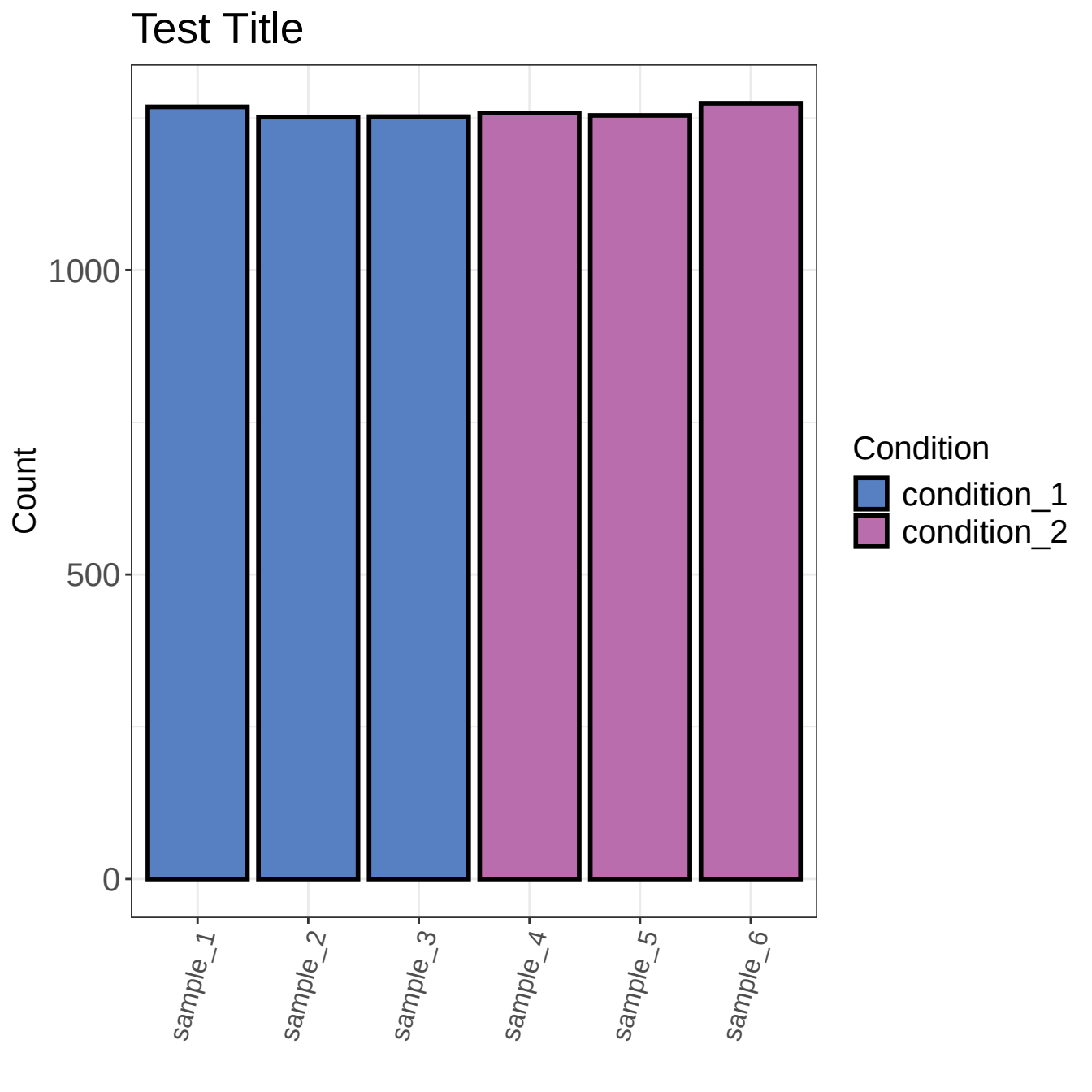

Overall log2 Intensity Distribution
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Frequency
0
50
100
10
15
20
25
Log2 Intensity

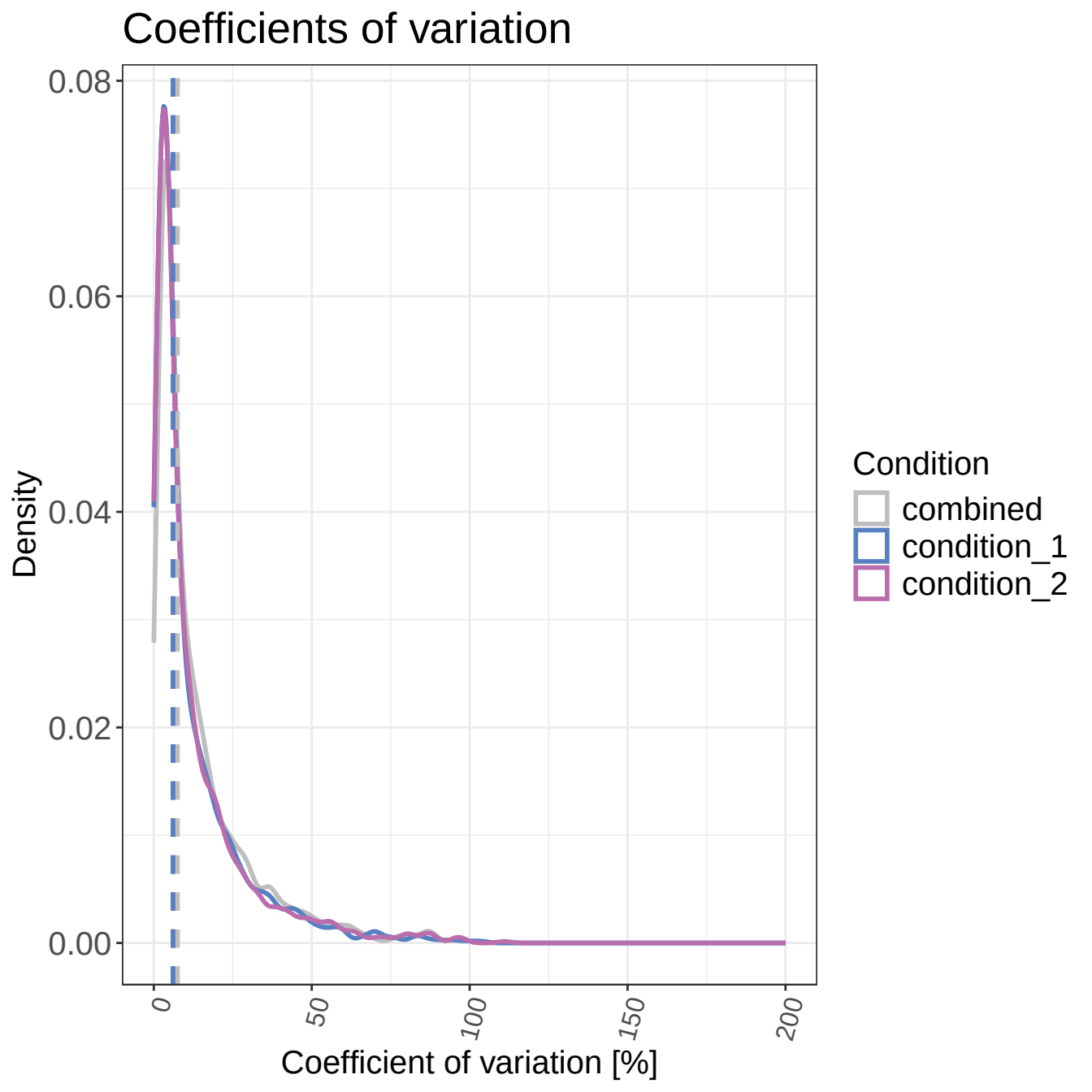

Overall log2 Intensity Distribution
Frequency
600
400
200
0
10
15
20
25
Log2 Intensity

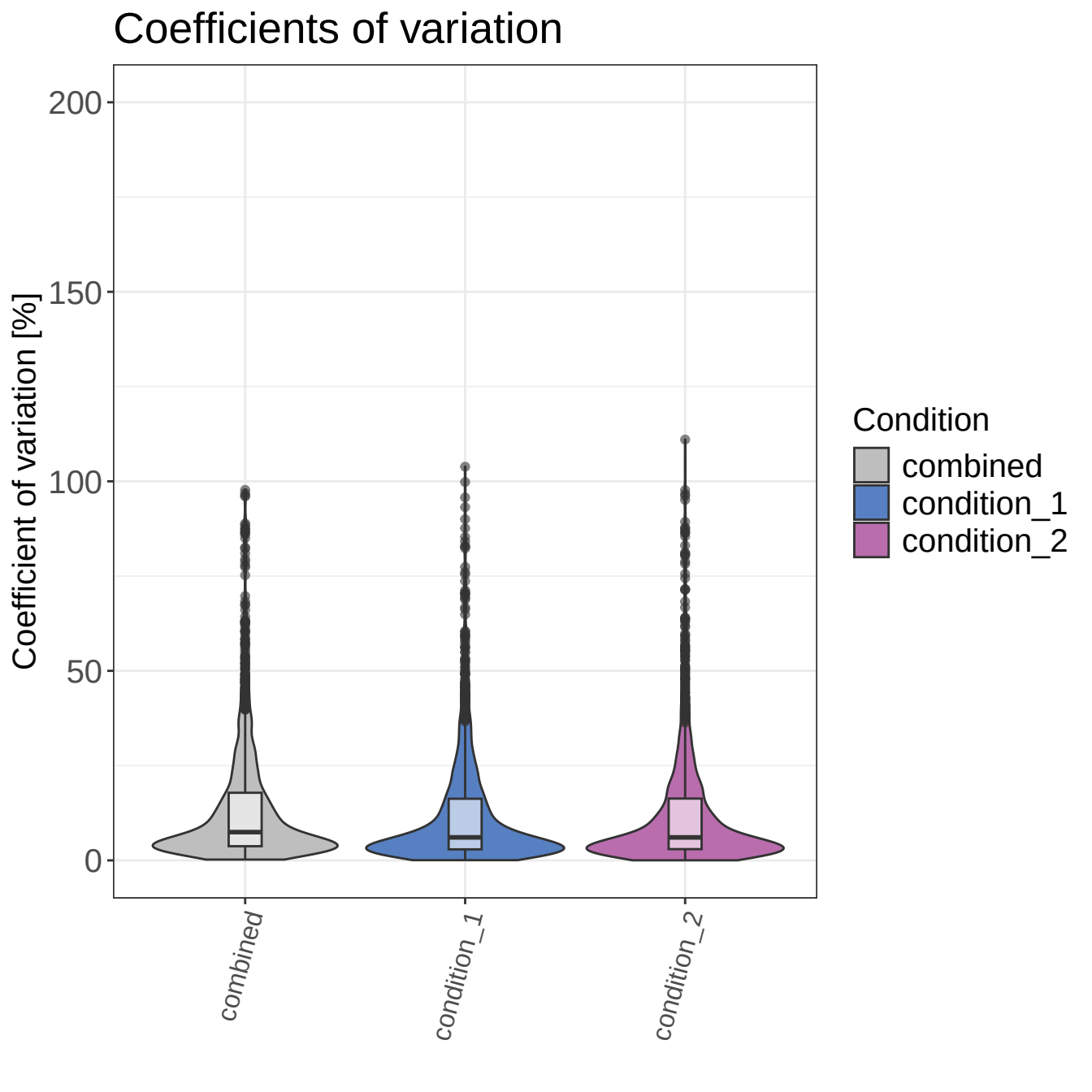

Run intensities
Intensity
25
20
15
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6

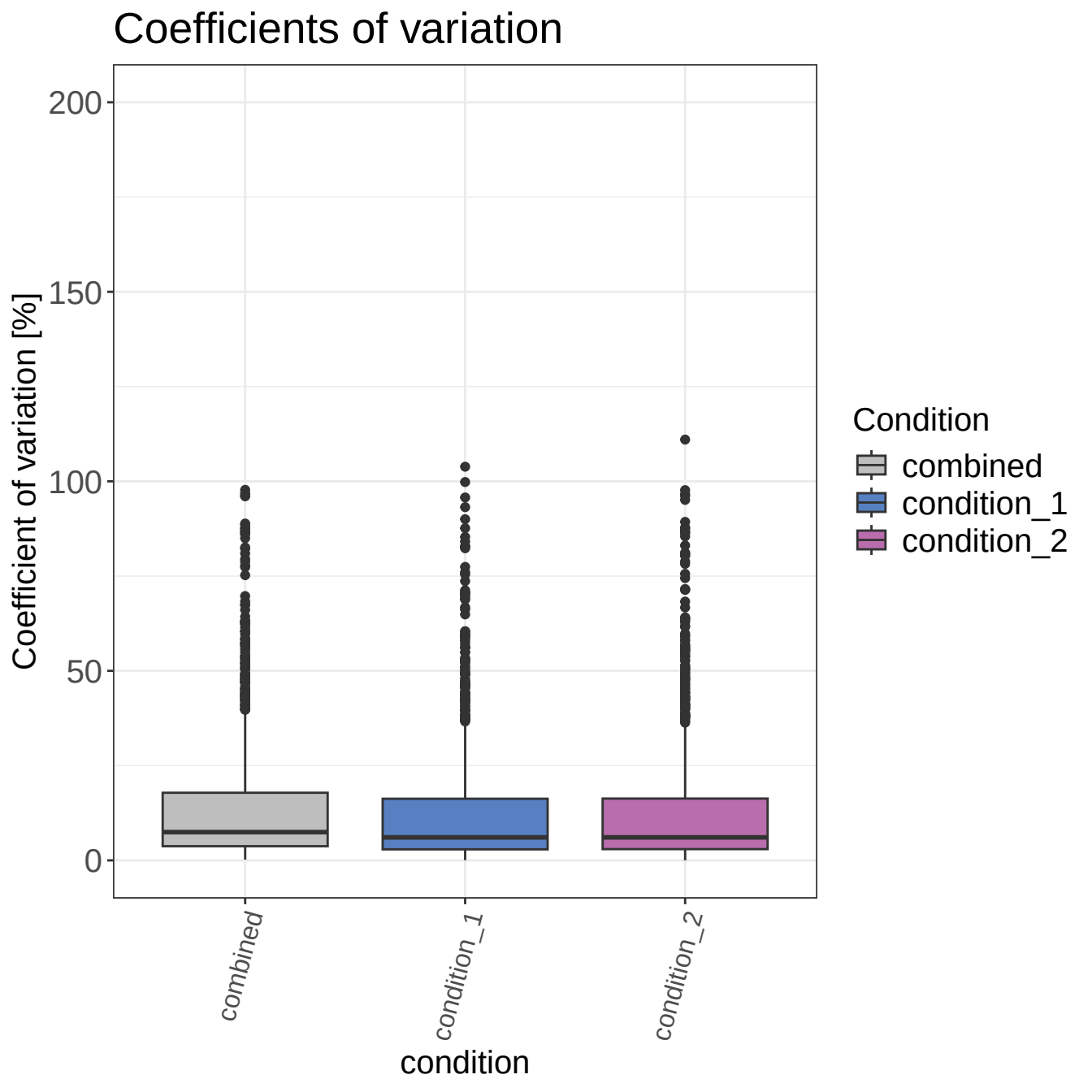

Run intensities
Intensity
25
20
15
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6

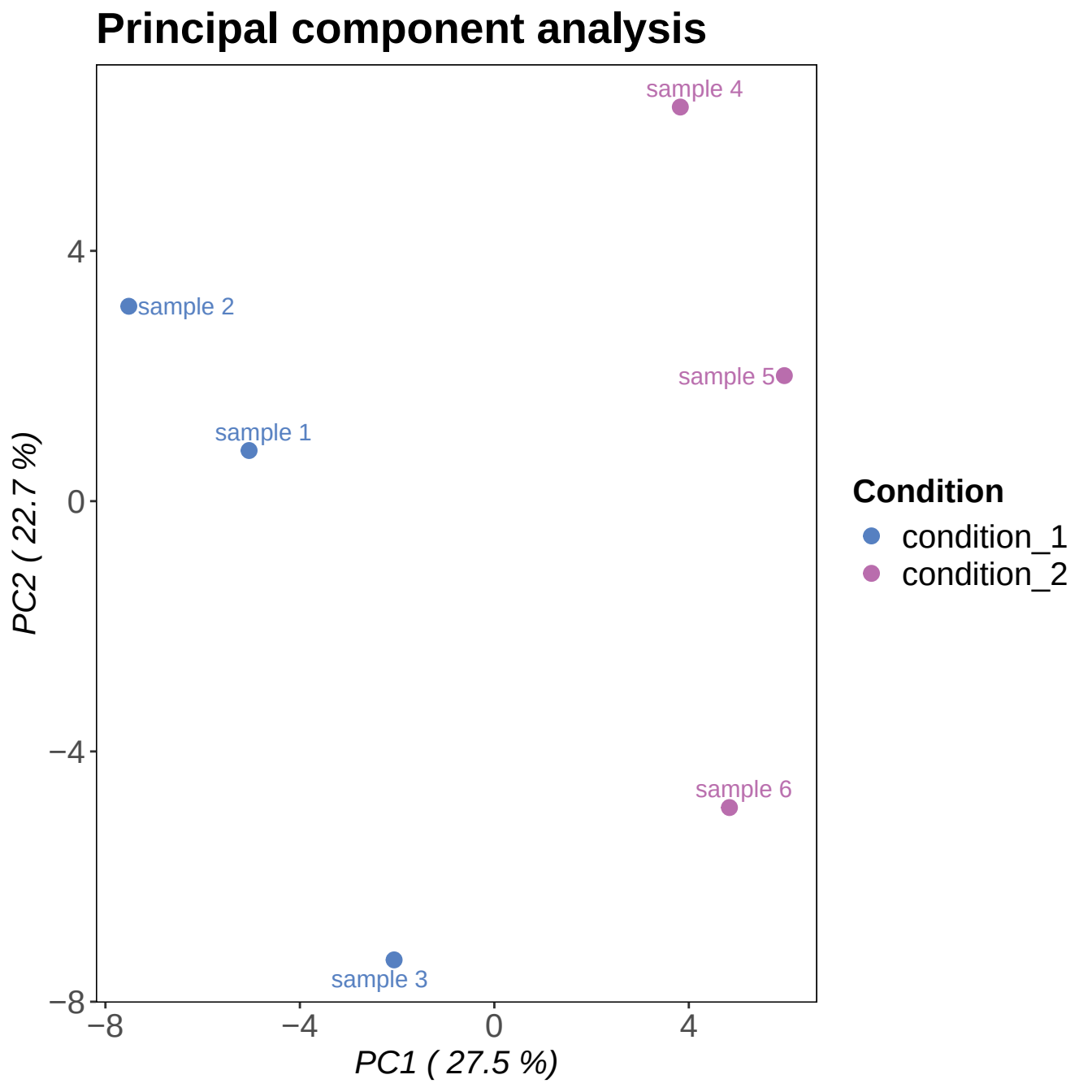

Medians of run intensities
Intensity
17.39
17.37
17.35
17.33
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6

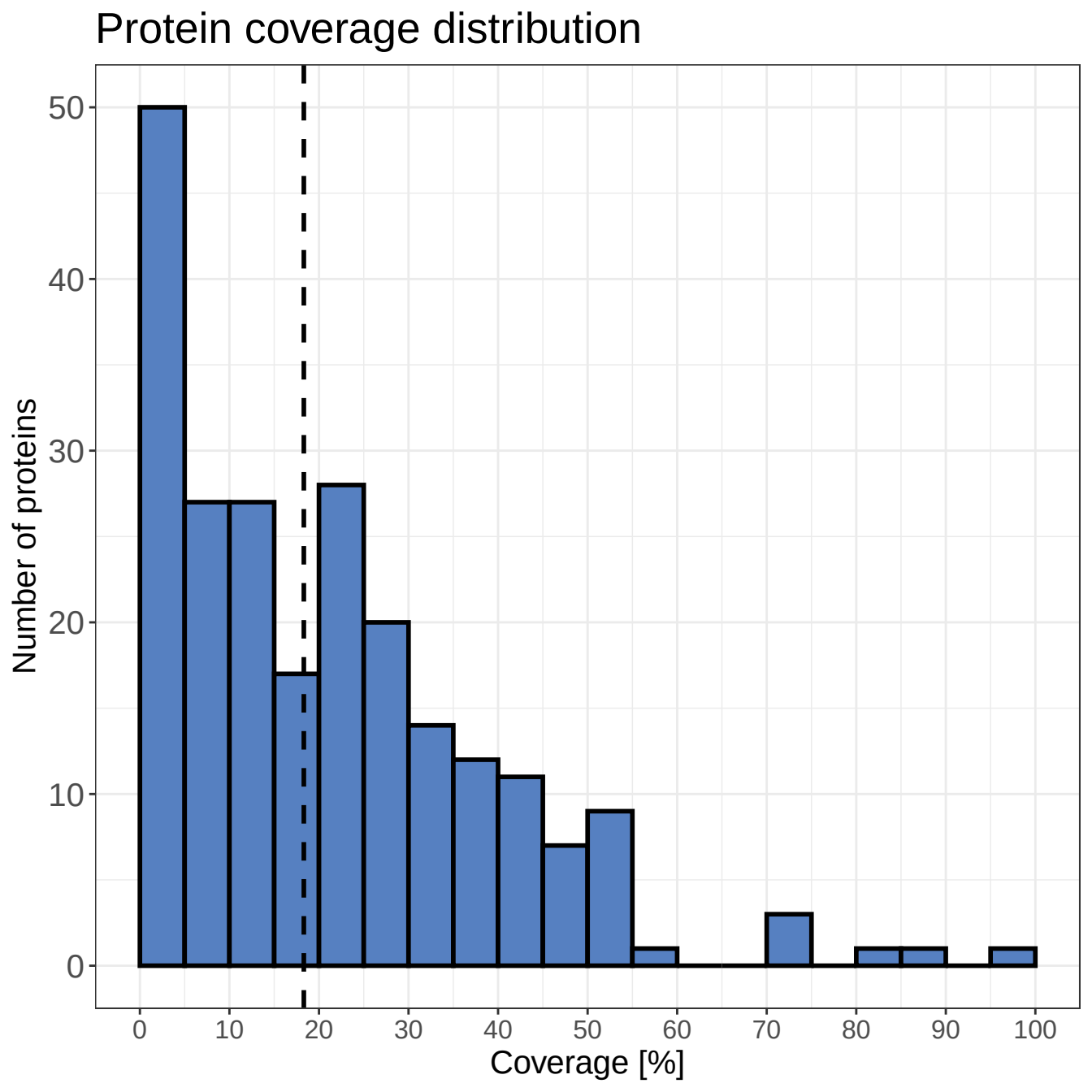

Test Title
Count
1000
500
0
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Condition
condition_1
condition_2

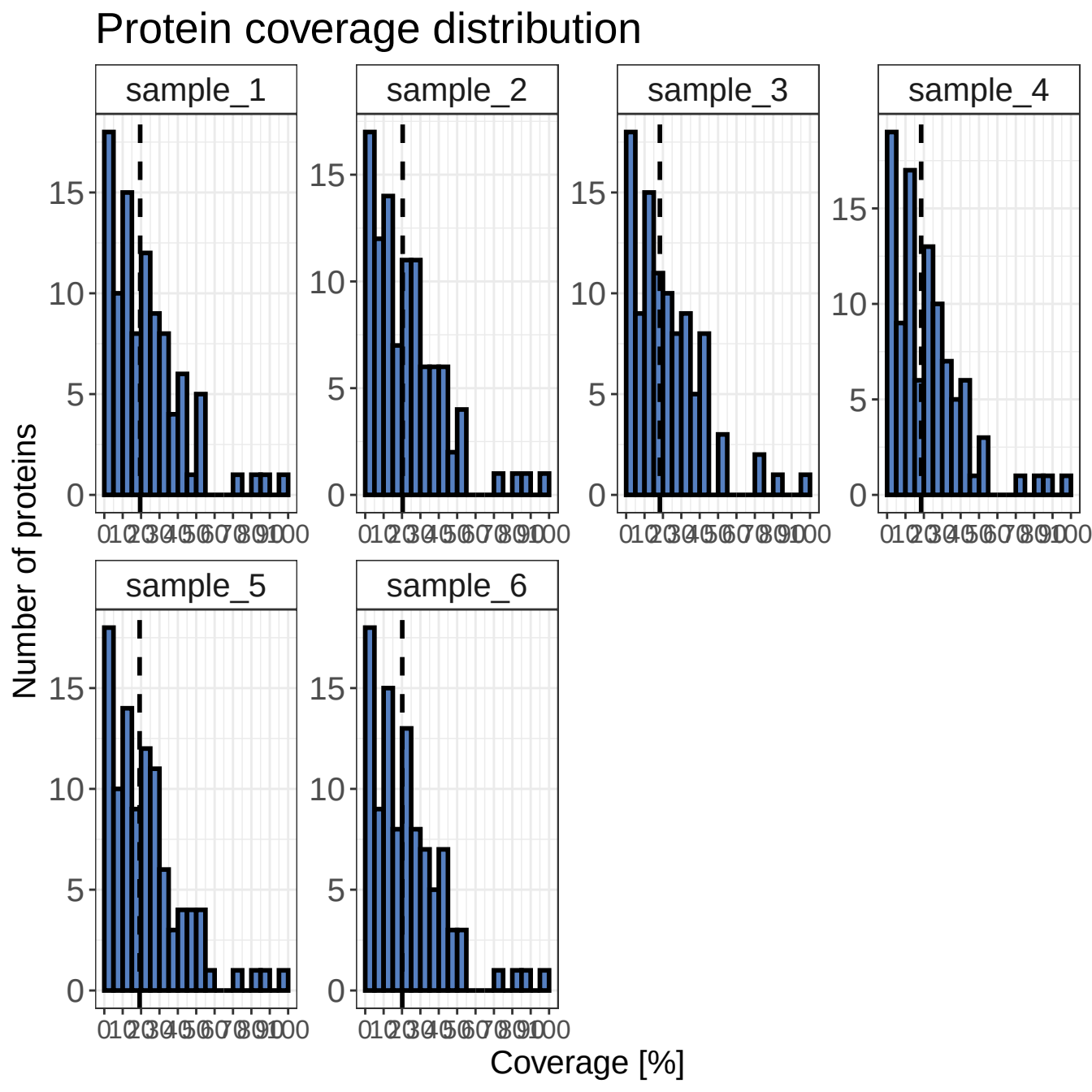

Coefficients of variation
0.08
0.06
0.04
0.02
0.00
Density
0
50
100
150
200
Coefficient of variation [%]
Condition
combined
condition_1
condition_2

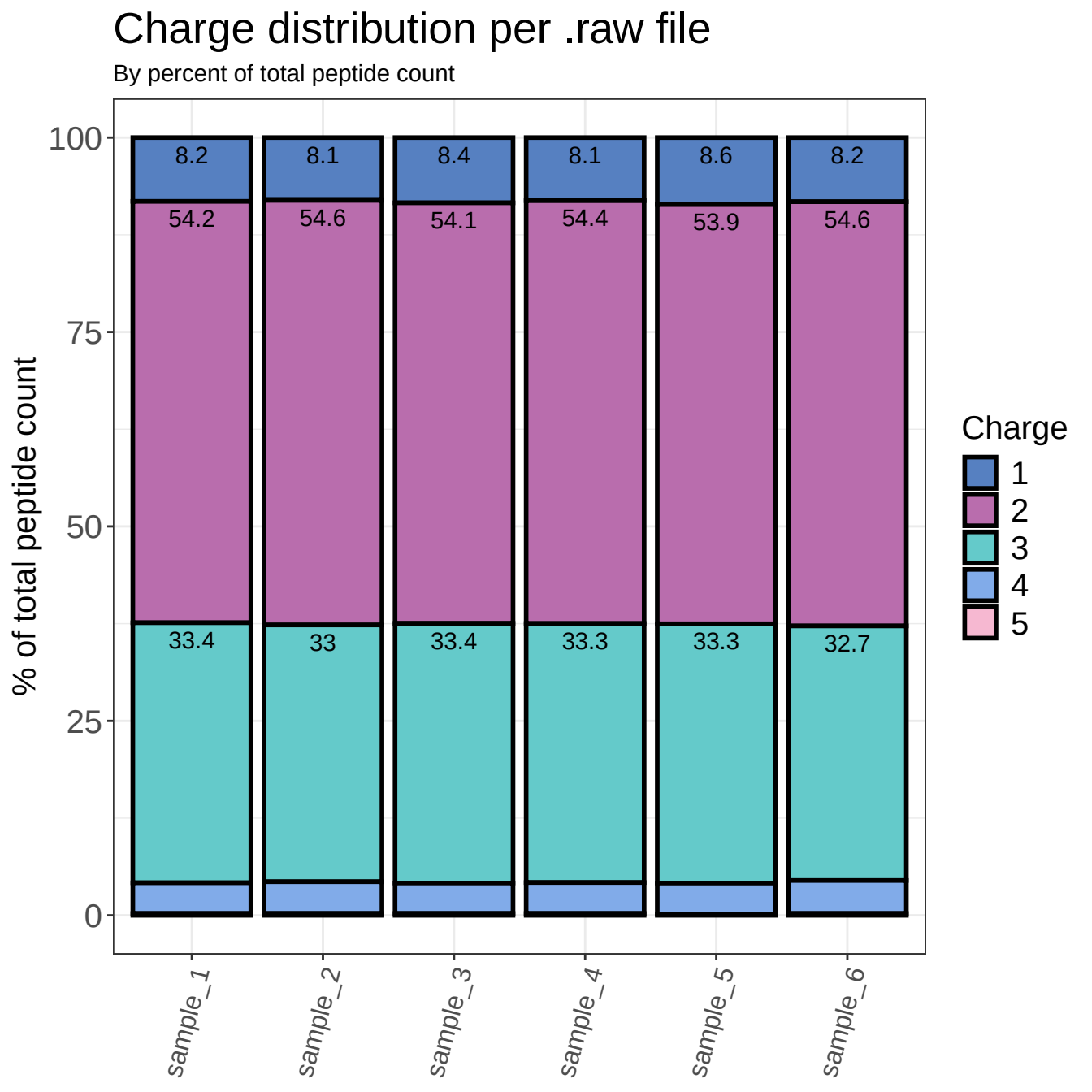

Coefficients of variation
Coefficient of variation [%]
200
150
100
50
0
combined
condition_1
condition_2
Condition
combined
condition_1
condition_2

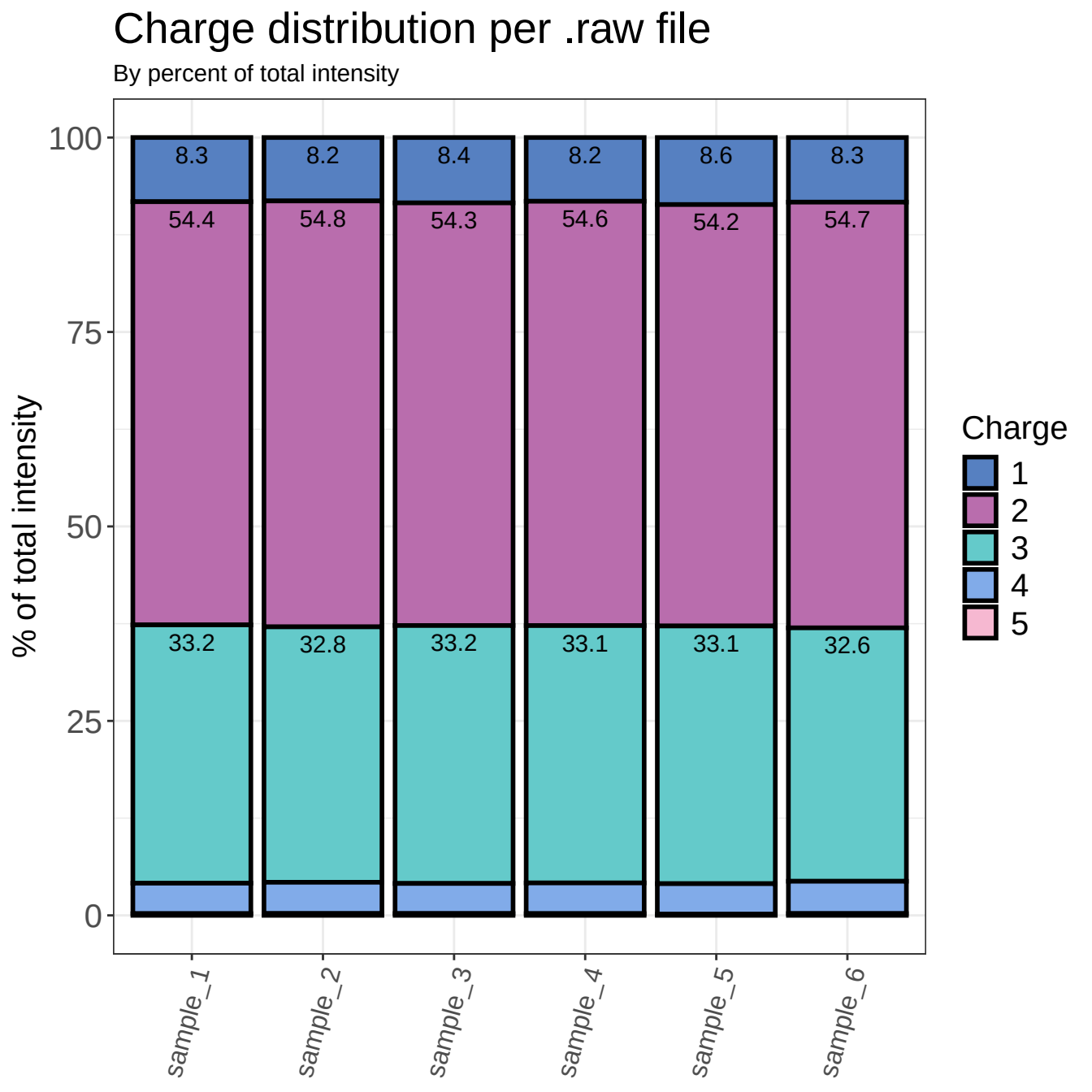

Coefficients of variation
Coefficient of variation [%]
200
150
100
50
0
combined
condition_1
condition_2
condition
Condition
combined
condition_1
condition_2

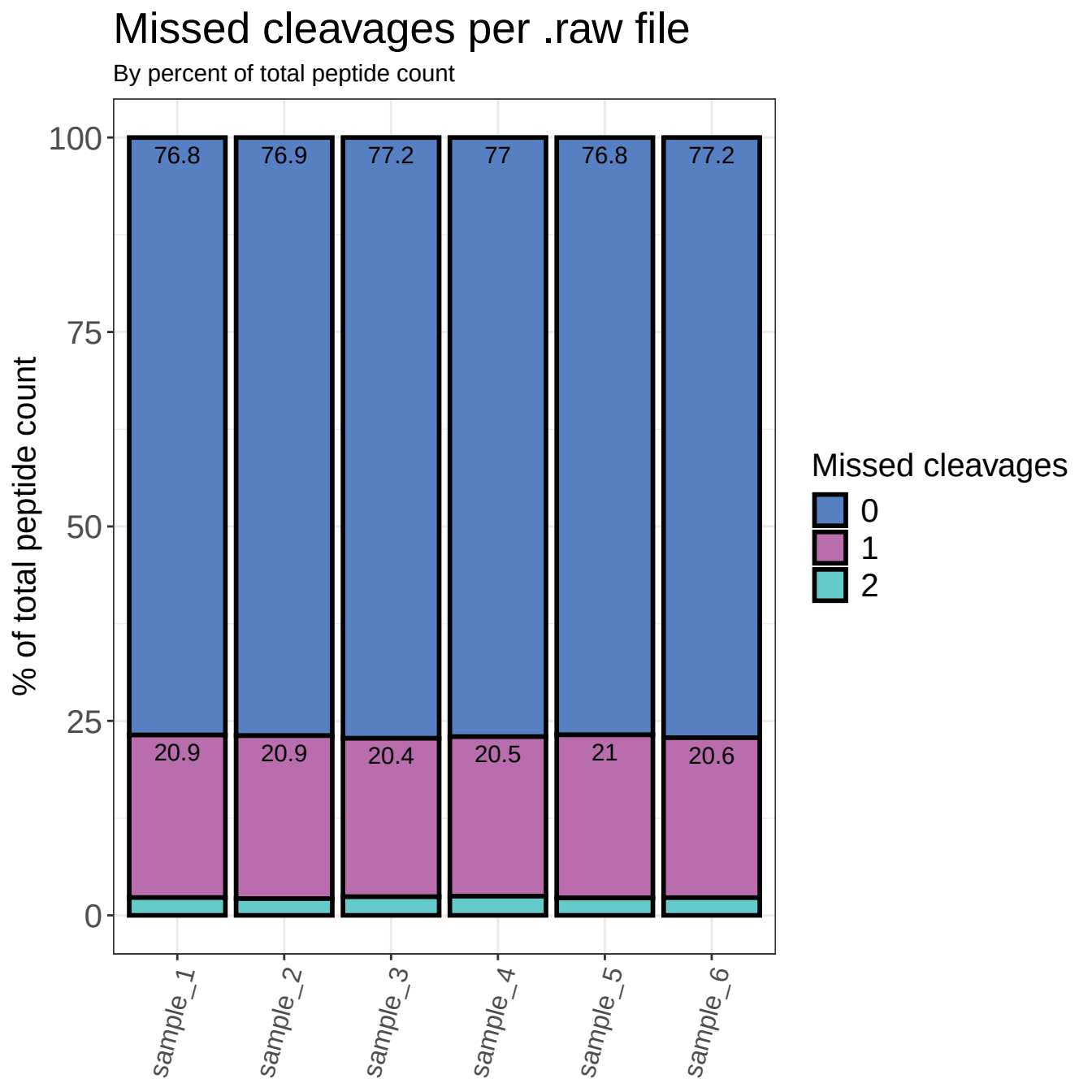

Principal component analysis
sample 4
sample 2
sample 5
sample 1
sample 6
sample 3
4
0
−4
−8
−8
−4
0
4
PC2 (22.7 %)
PC1 (27.5 %)
Condition
condition_1
condition_2

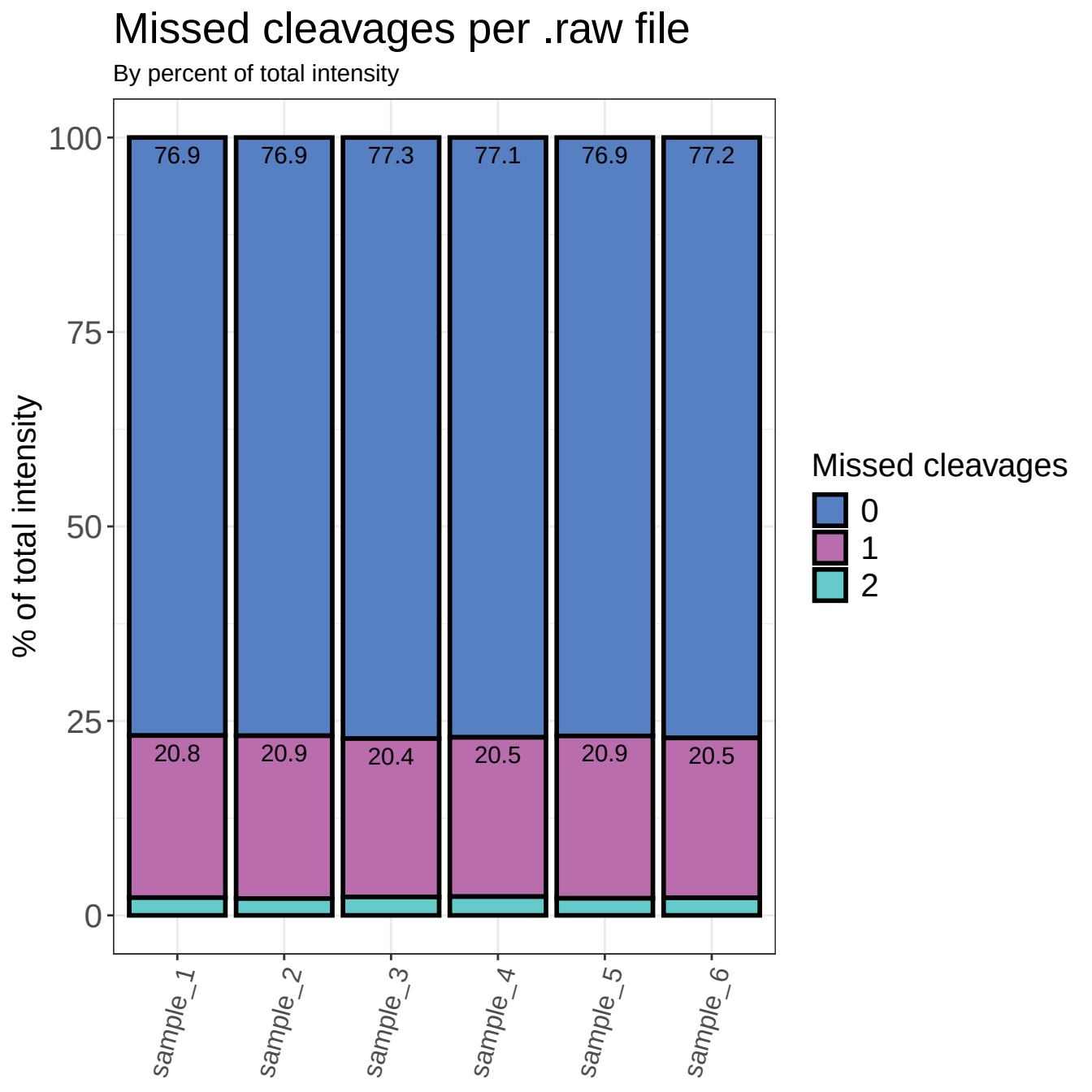

Protein coverage distribution
Number of proteins
Coverage [%]
0
10
20
30
40
50
60
70
80
90
100

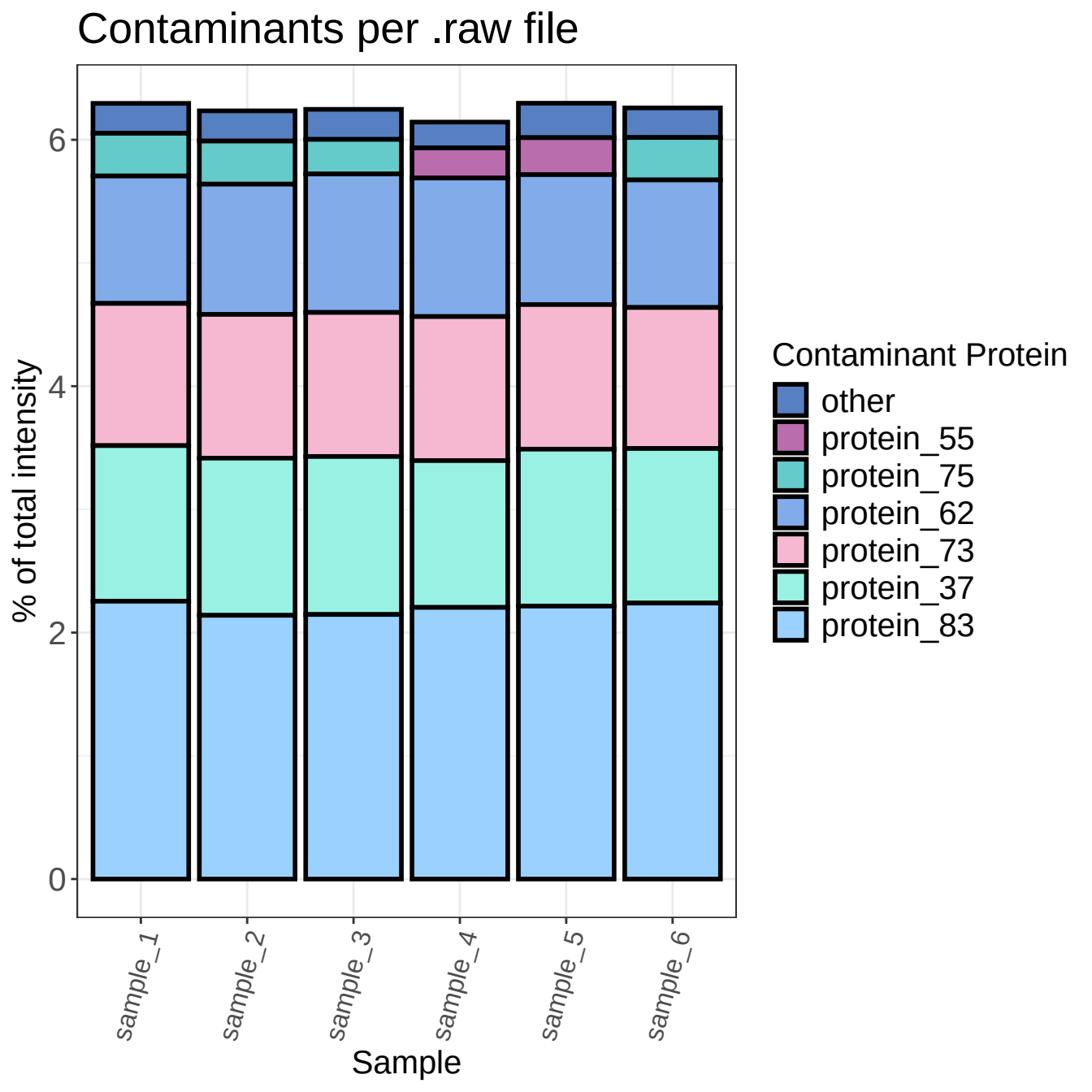

Protein coverage distribution
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Number of proteins
Coverage [%]
0
5
10
15

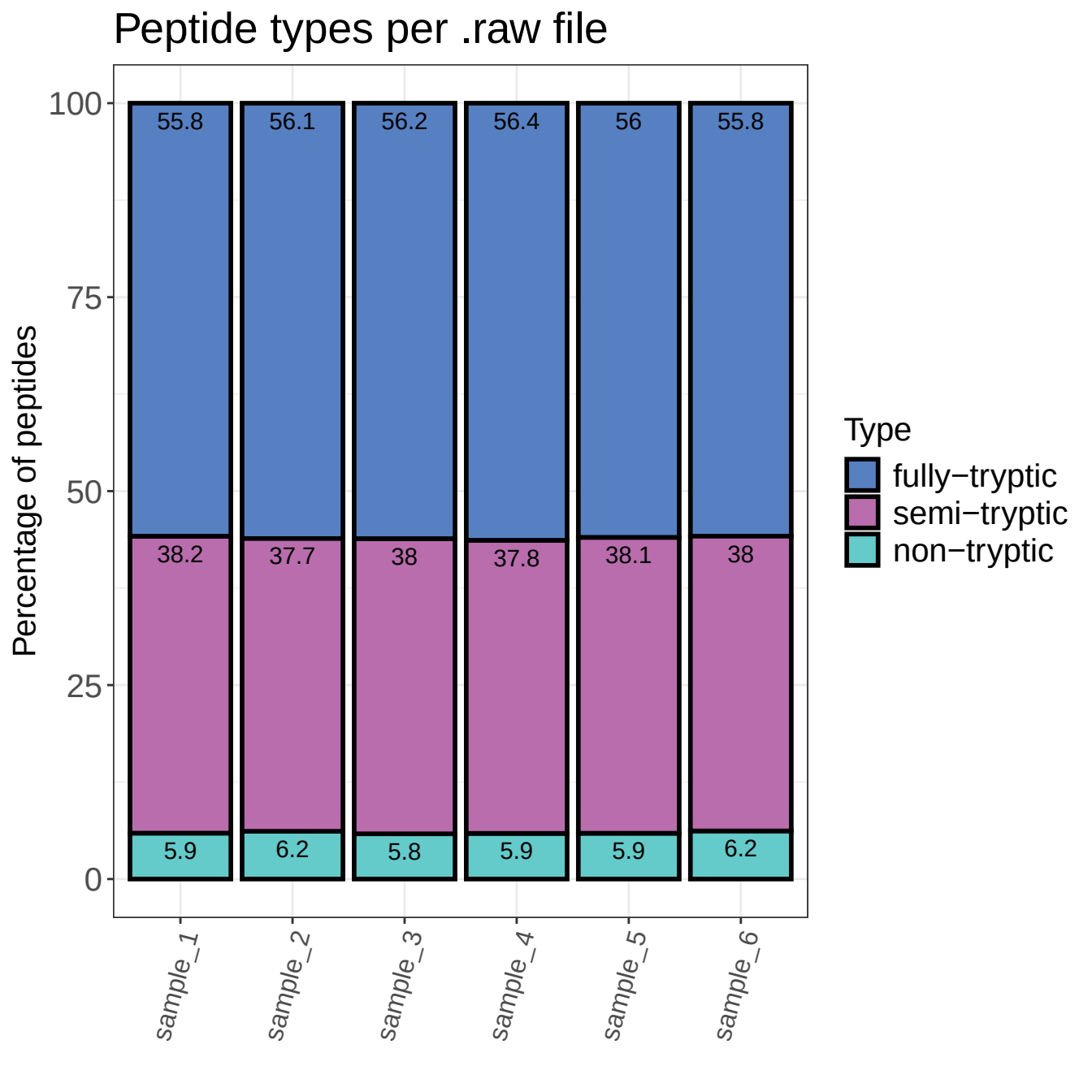

Charge distribution per .raw file
By percent of total peptide count
% of total peptide count
100
75
50
25
0
8.2
8.1
8.4
8.1
8.6
8.2
54.2
54.6
54.1
54.4
53.9
54.6
33.4
33
33.4
33.3
33.3
32.7
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Charge
1
2
3
4
5

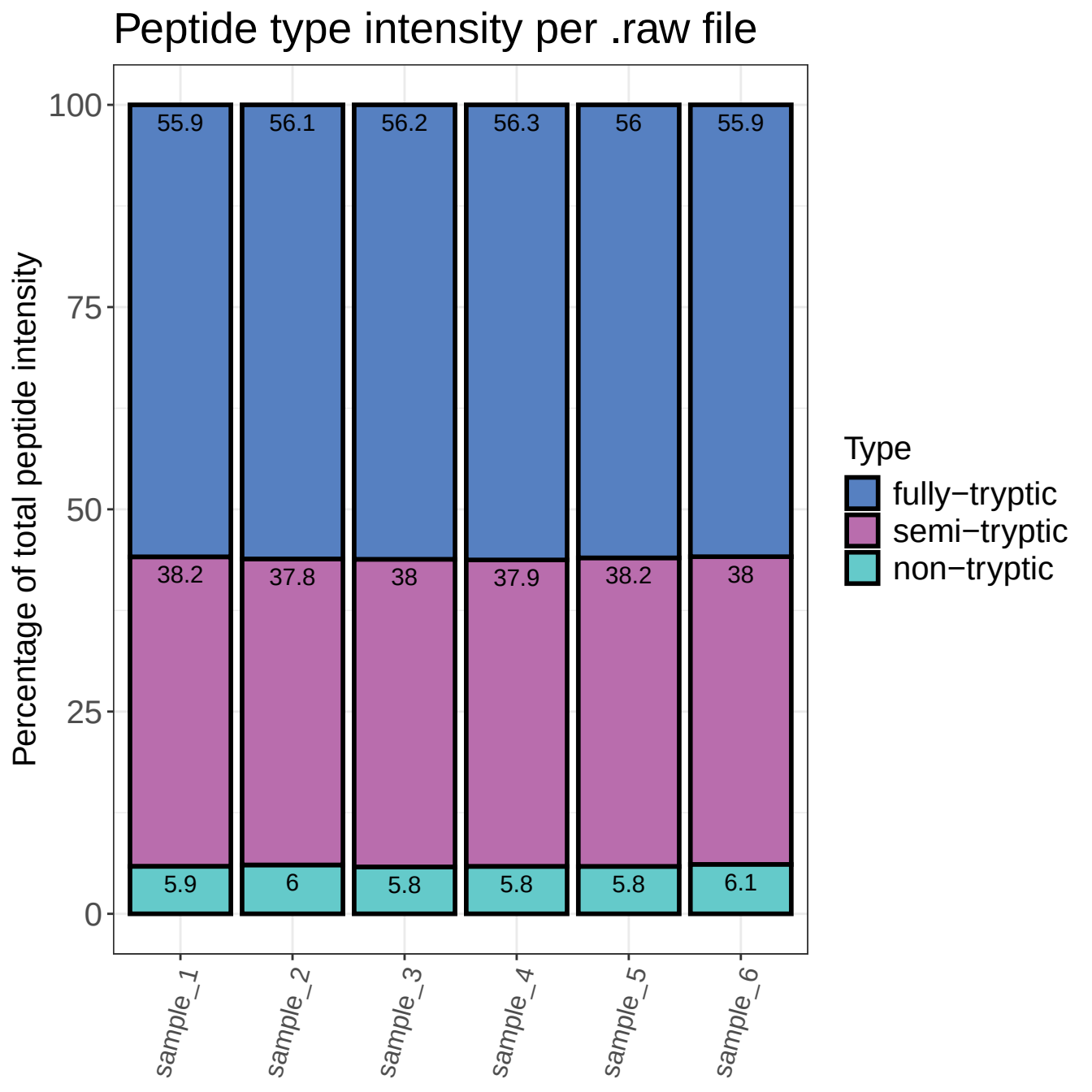

Charge distribution per .raw file
By percent of total intensity
% of total intensity
100
75
50
25
0
8.3
8.2
8.4
8.2
8.6
8.3
54.4
54.8
54.3
54.6
54.2
54.7
33.2
32.8
33.2
33.1
33.1
32.6
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Charge
1
2
3
4
5

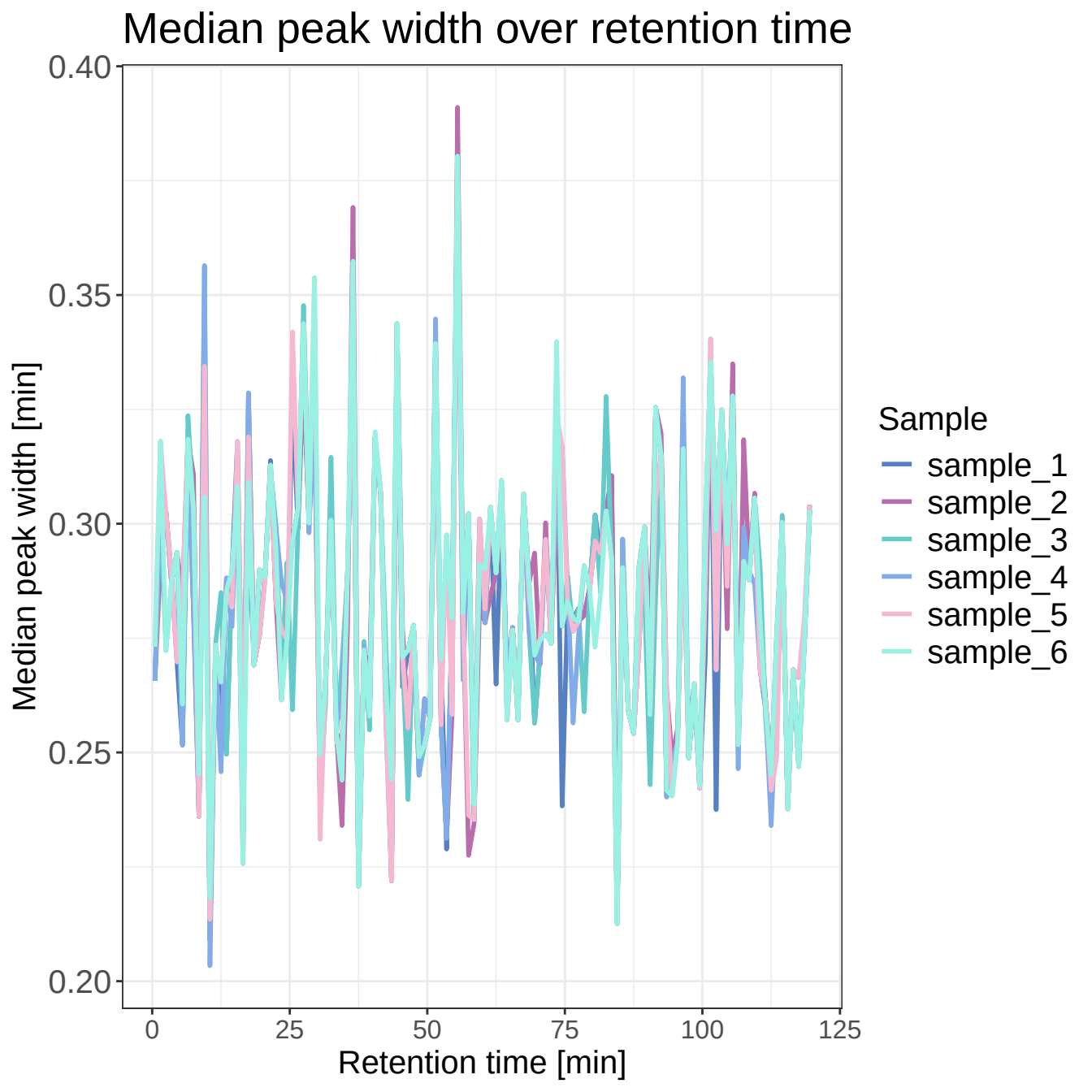

Missed cleavages per .raw file
By percent of total peptide count
% of total peptide count
100
75
50
25
0
76.8
76.9
77.2
77
76.8
77.2
20.9
20.9
20.4
20.5
21
20.6
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Missed cleavages
0
1
2

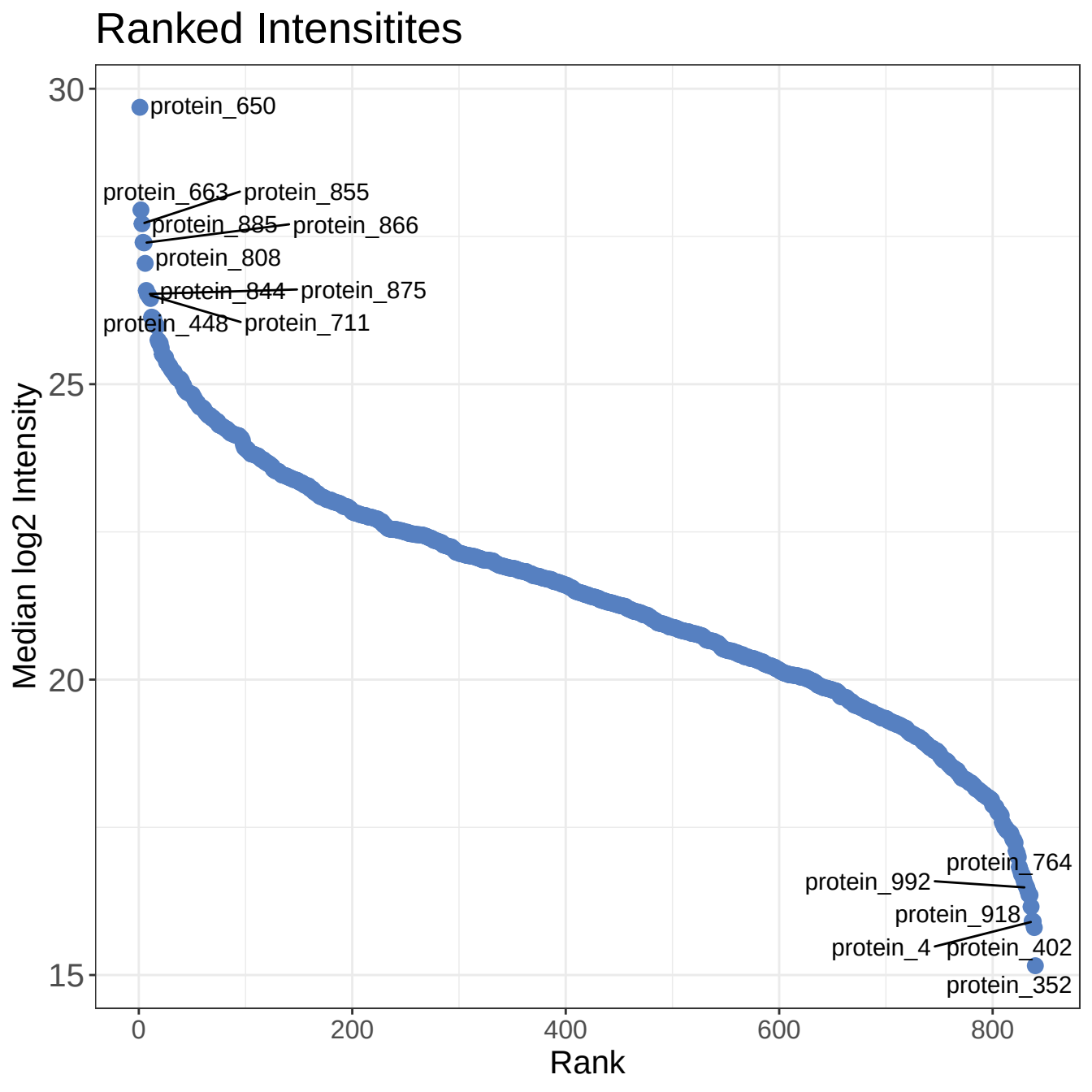

Missed cleavages per .raw file
By percent of total intensity
% of total intensity
100
75
50
25
0
76.9
76.9
77.3
77.1
76.9
77.2
20.8
20.9
20.4
20.5
20.9
20.5
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Missed cleavages
0
1
2

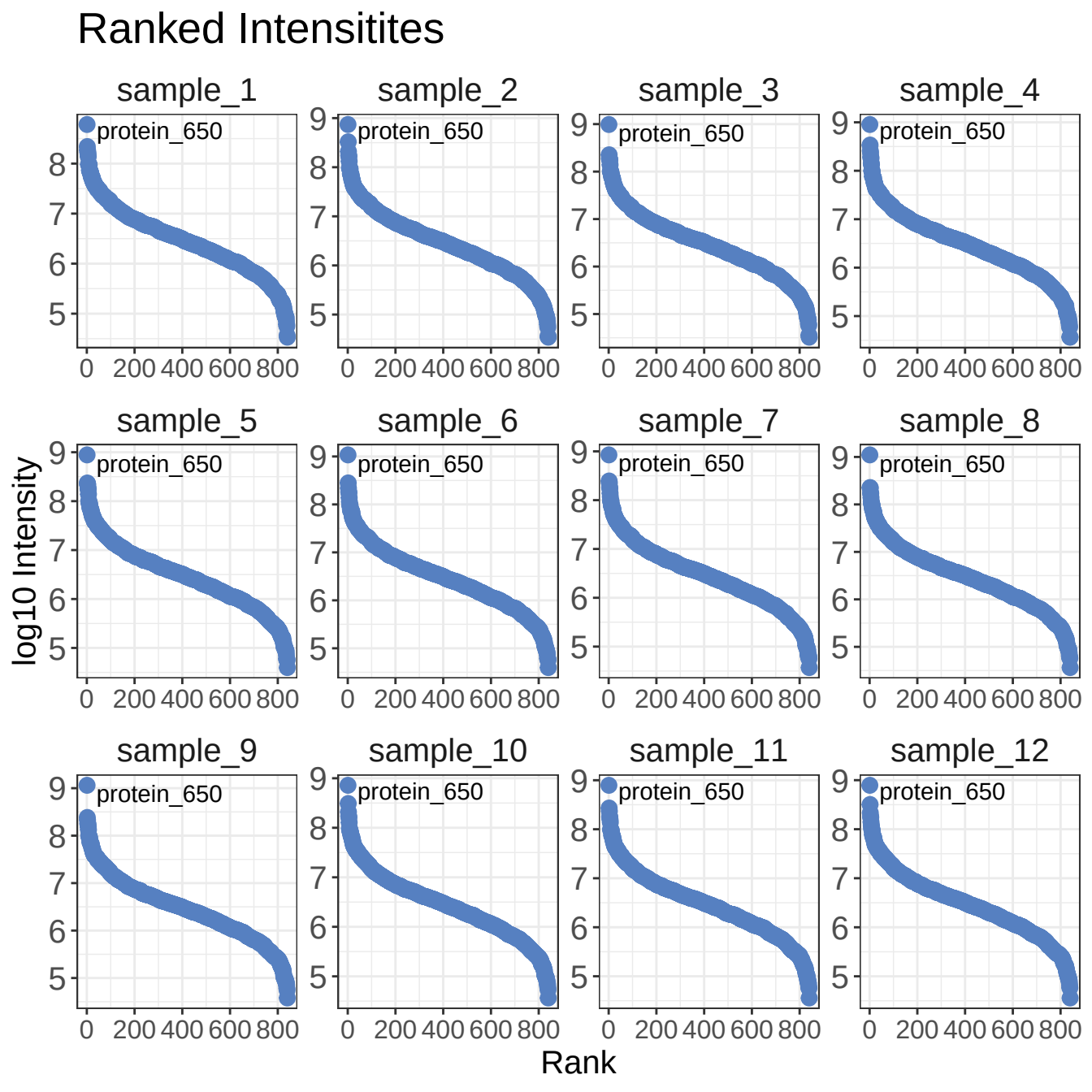

Contaminants per .raw file
% of total intensity
0
2
4
6
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Sample
Contaminant Protein
other
protein_55
protein_75
protein_62
protein_73
protein_37
protein_83

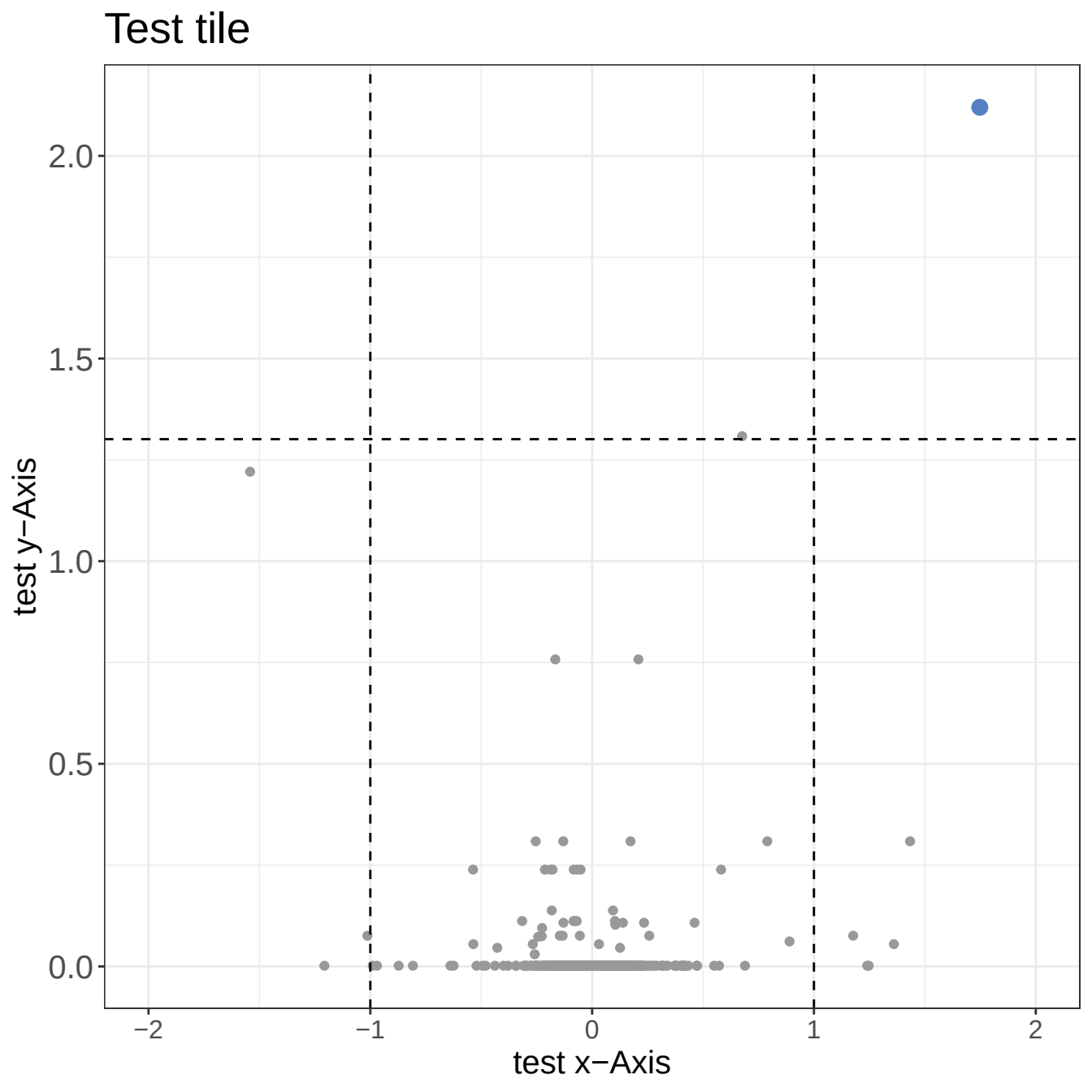

Peptide types per .raw file
Percentage of peptides
100
75
50
25
0
55.8
56.1
56.2
56.4
56
55.8
38.2
37.7
38
37.8
38.1
38
5.9
6.2
5.8
5.9
5.9
6.2
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Type
fully−tryptic
semi−tryptic
non−tryptic

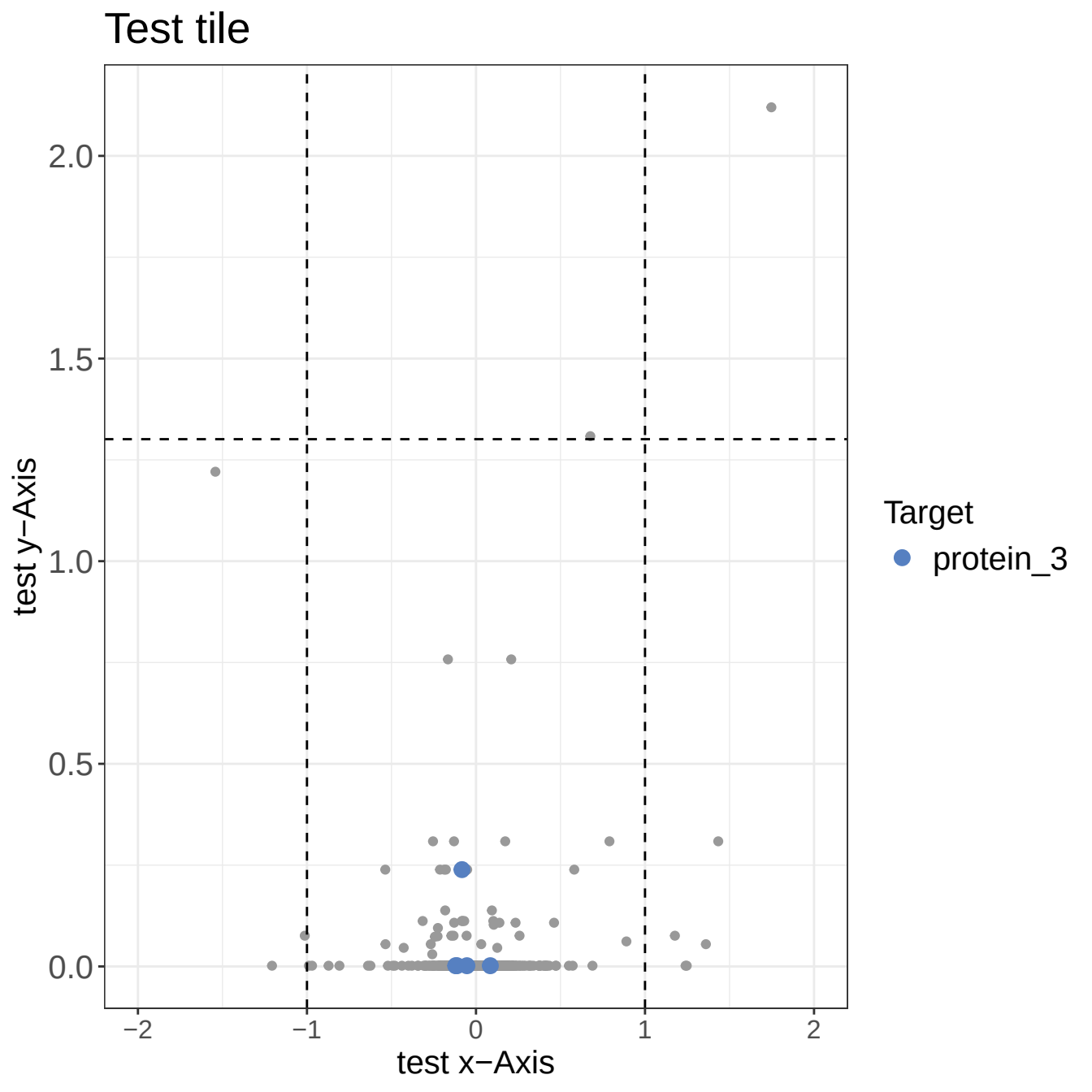

Peptide type intensity per .raw file
Percentage of total peptide intensity
100
75
50
25
0
55.9
56.1
56.2
56.3
56
55.9
38.2
37.8
38
37.9
38.2
38
5.9
6
5.8
5.8
5.8
6.1
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
Type
fully−tryptic
semi−tryptic
non−tryptic


Median peak width over retention time
Median peak width [min]
0.40
0.35
0.30
0.25
0.20
0
25
50
75
100
125
Retention time [min]
Sample
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6


Ranked Intensitites
Median log2 Intensity
Rank
30
25
20
15
0
200
400
600
800
protein_650
protein_663
protein_855
protein_885
protein_866
protein_808
protein_844
protein_875
protein_448
protein_711
protein_764
protein_992
protein_918
protein_4
protein_402
protein_352


Ranked Intensitites
sample_1
sample_2
sample_3
sample_4
sample_5
sample_6
sample_7
sample_8
sample_9
sample_10
sample_11
sample_12
protein_650
log10 Intensity
Rank
0
200
400
600
800
5
6
7
8
9


Test tile
2.0
1.5
1.0
0.5
0.0
test y−Axis
−2
−1
0
1
2
test x−Axis


Test tile
2.0
1.5
1.0
0.5
0.0
test y−Axis
−2
−1
0
1
2
test x−Axis
Target
protein_3