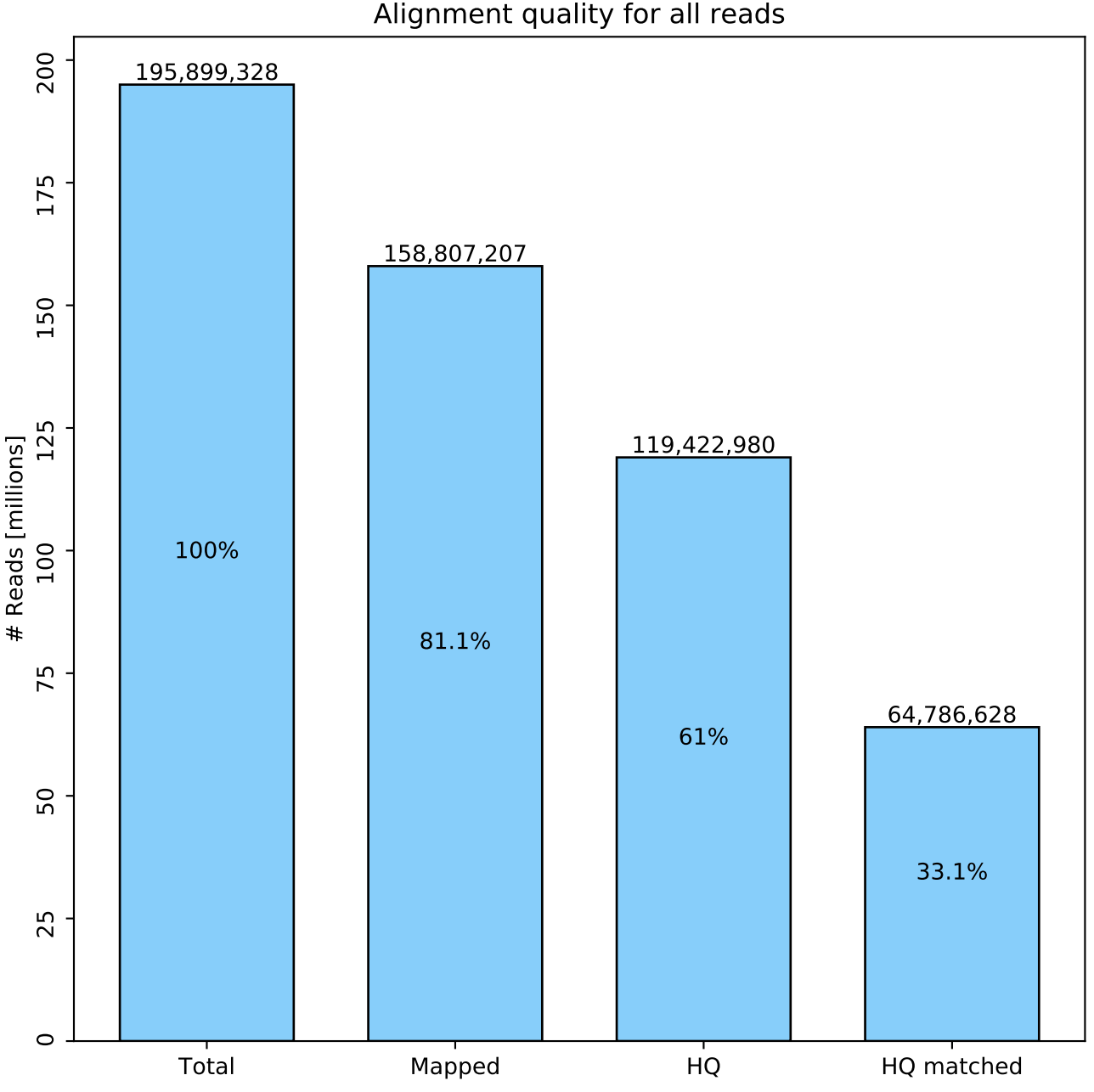
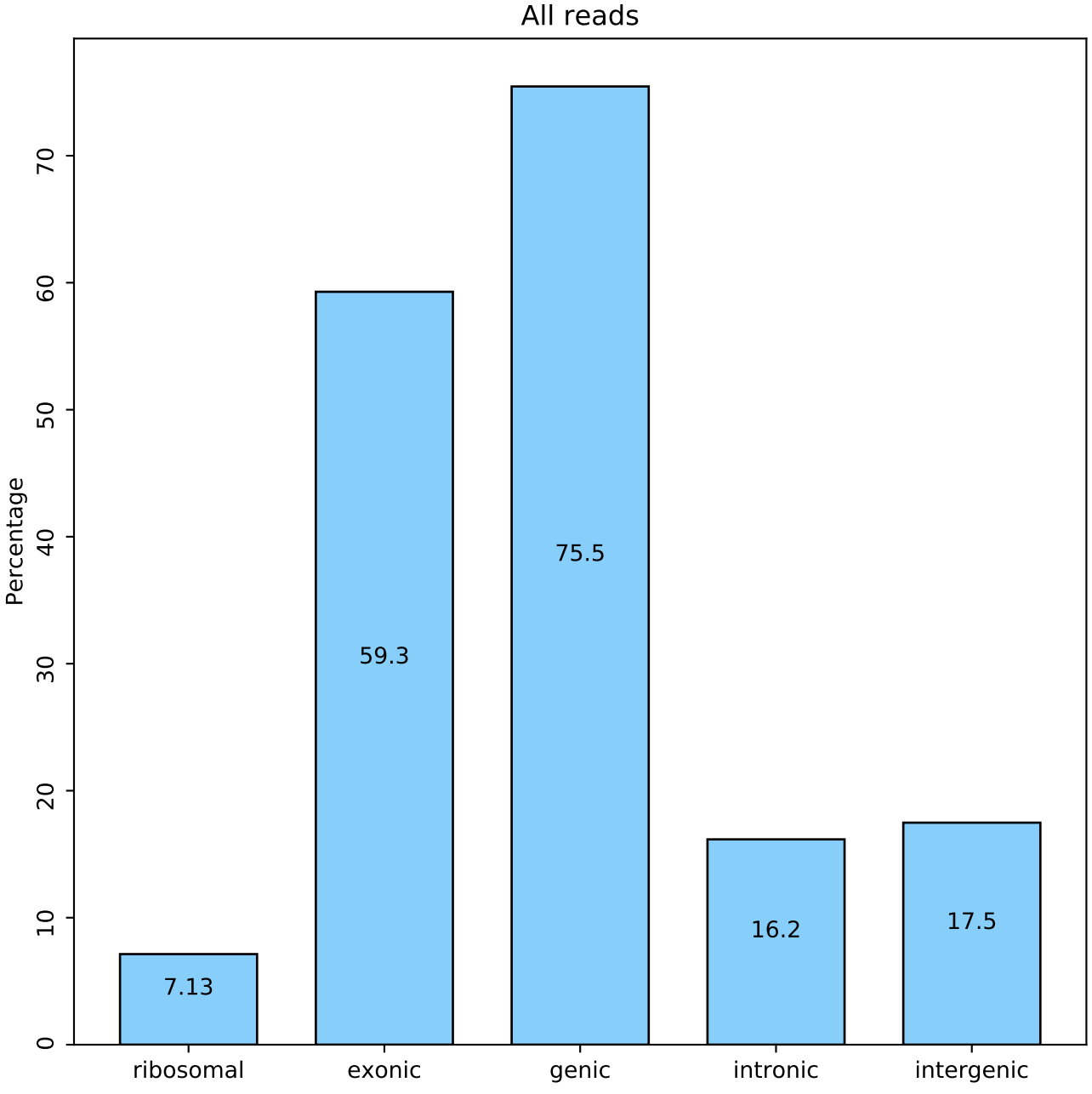
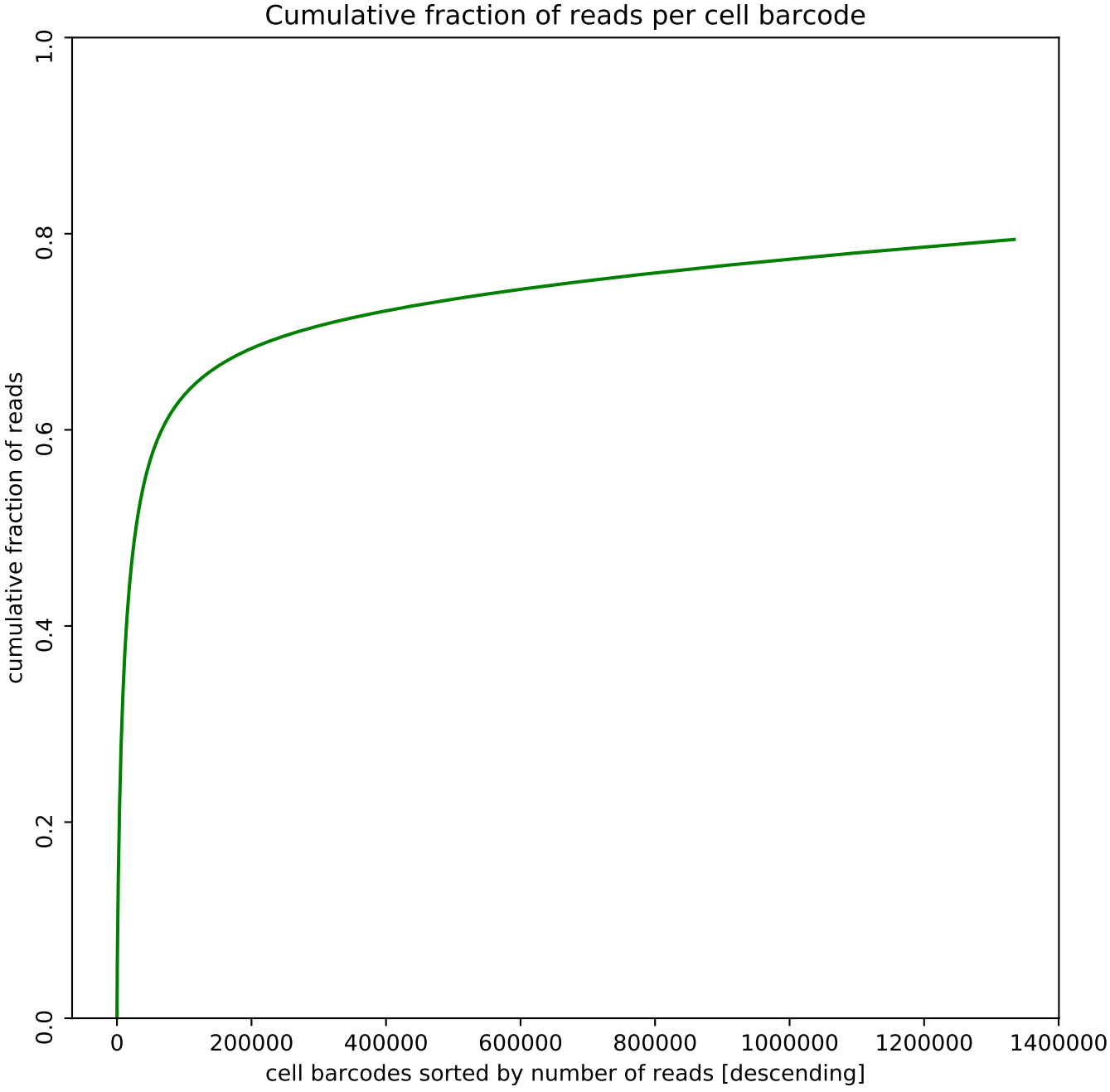
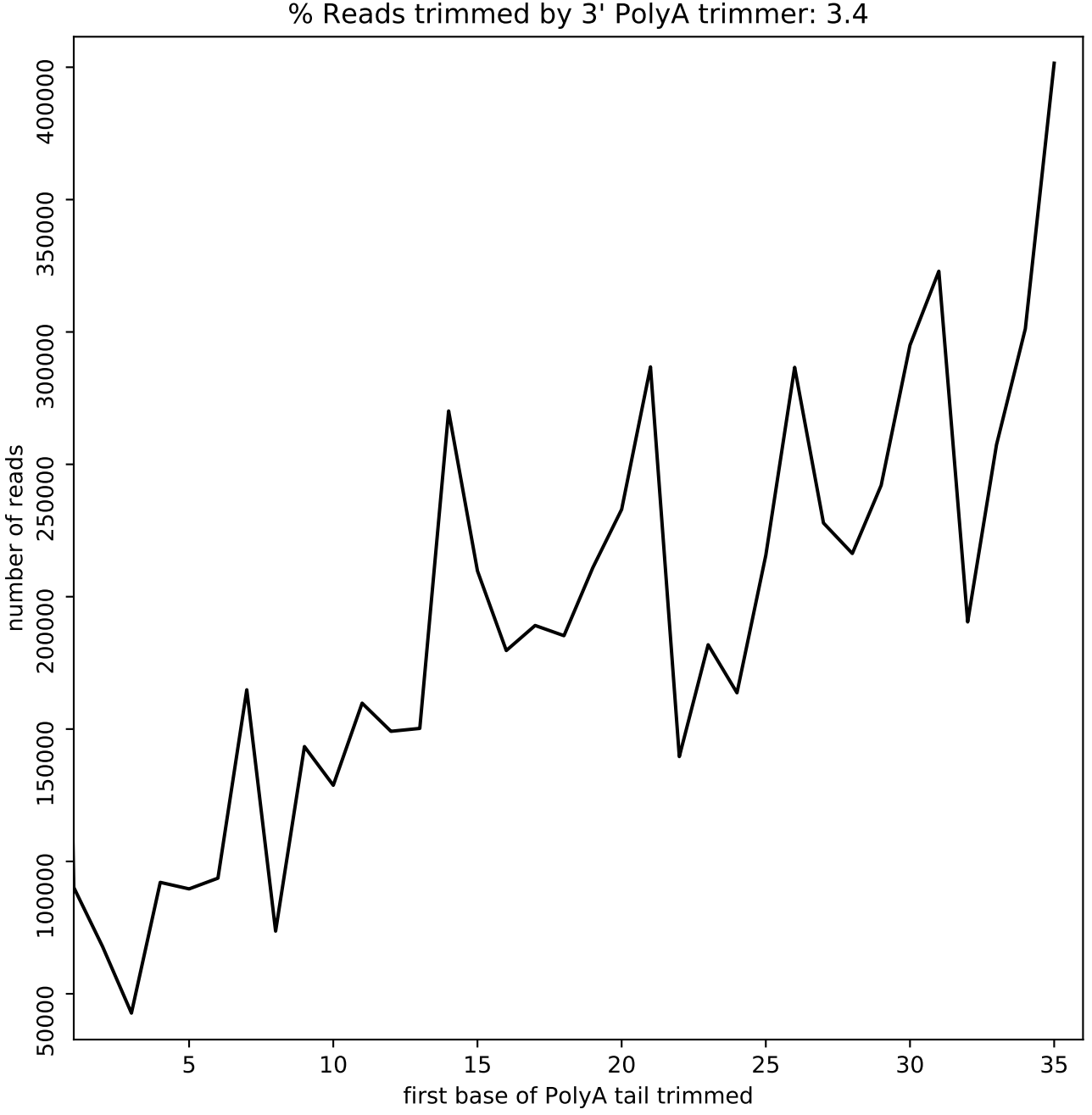
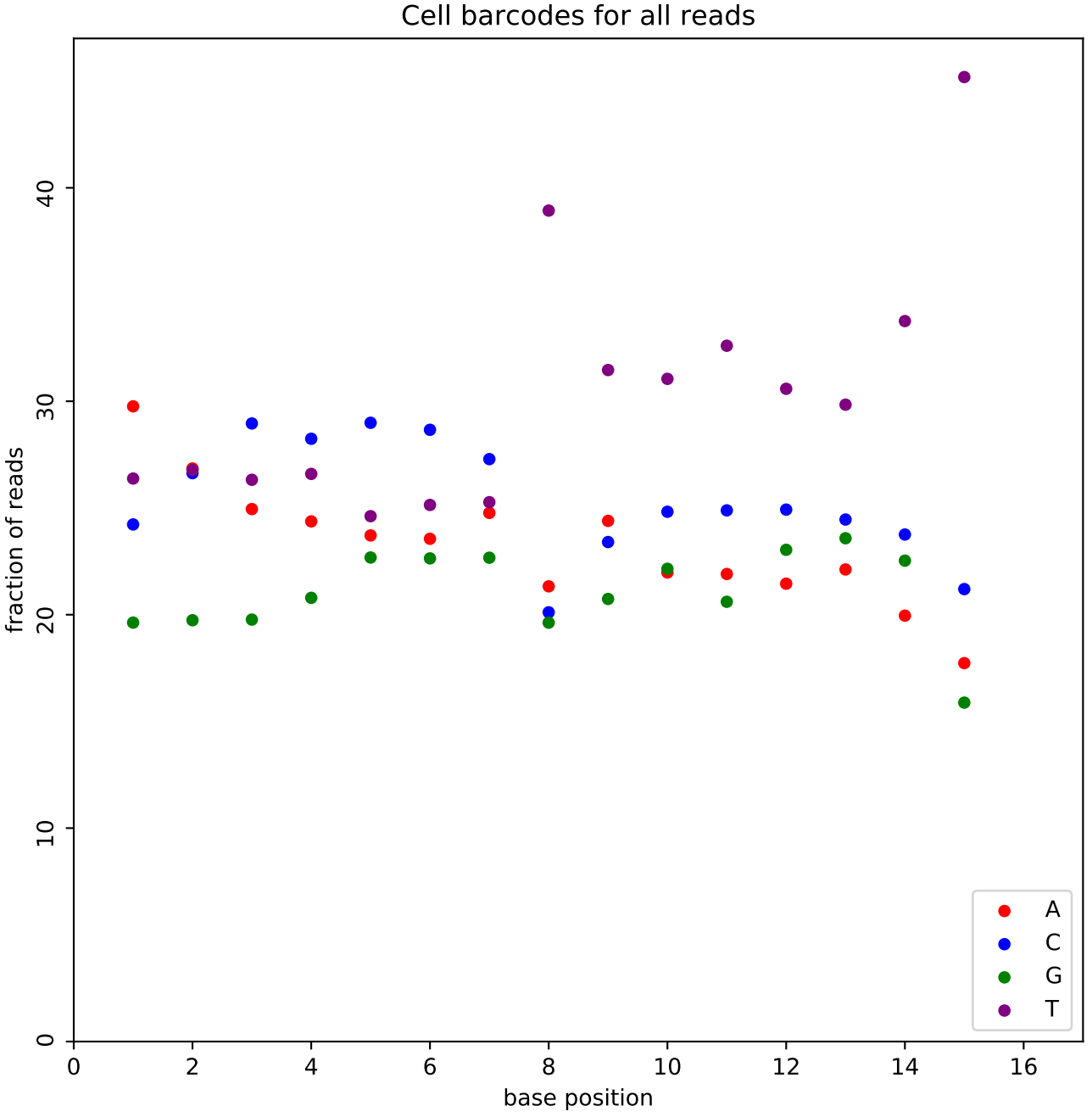
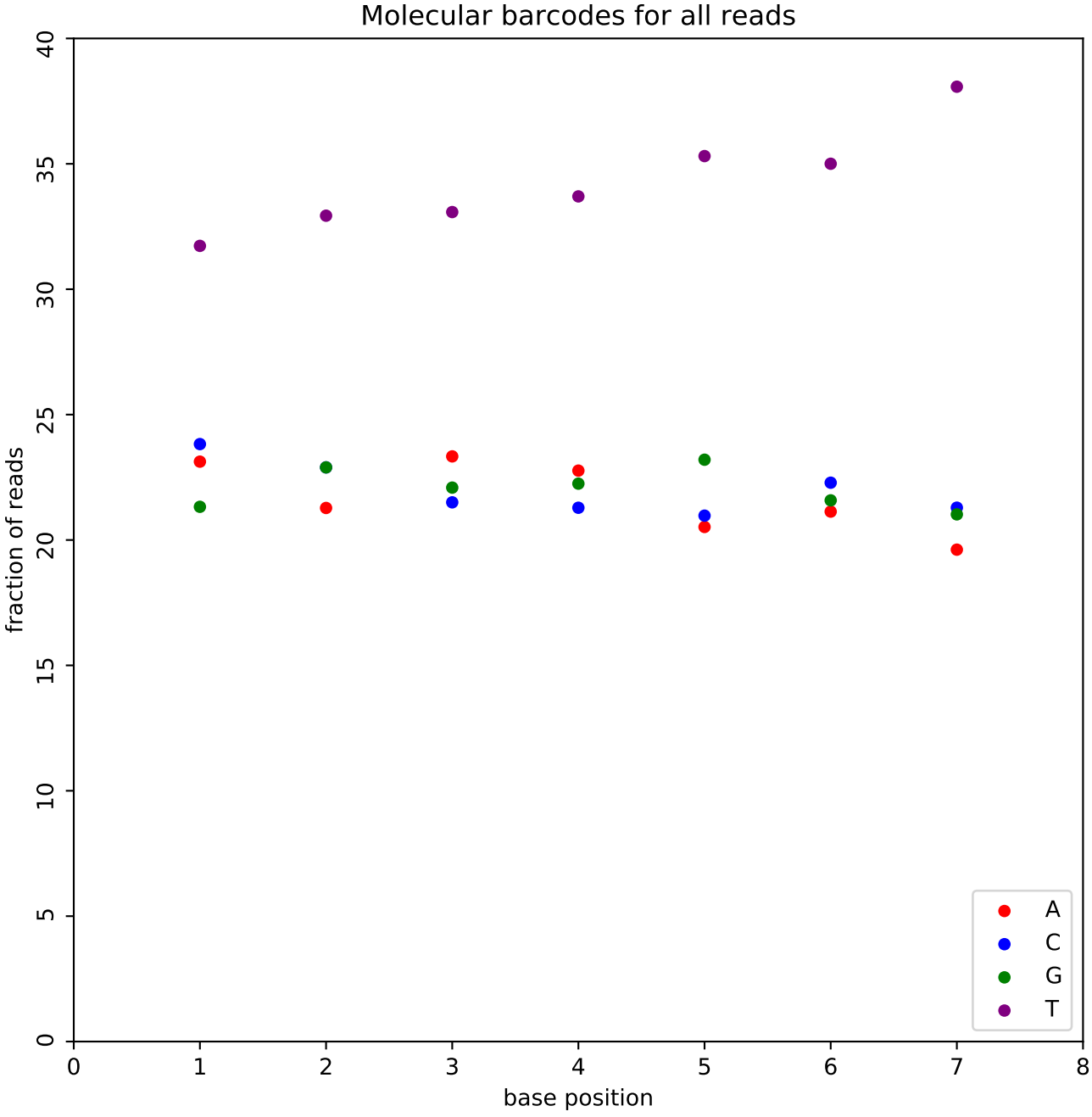

Alignment quality for all reads
# Reads [millions]
0
25
50
75
100
125
150
175
200
195,899,328
158,807,207
119,422,980
64,786,628
100%
81.1%
61%
33.1%
Total
Mapped
HQ
HQ matched

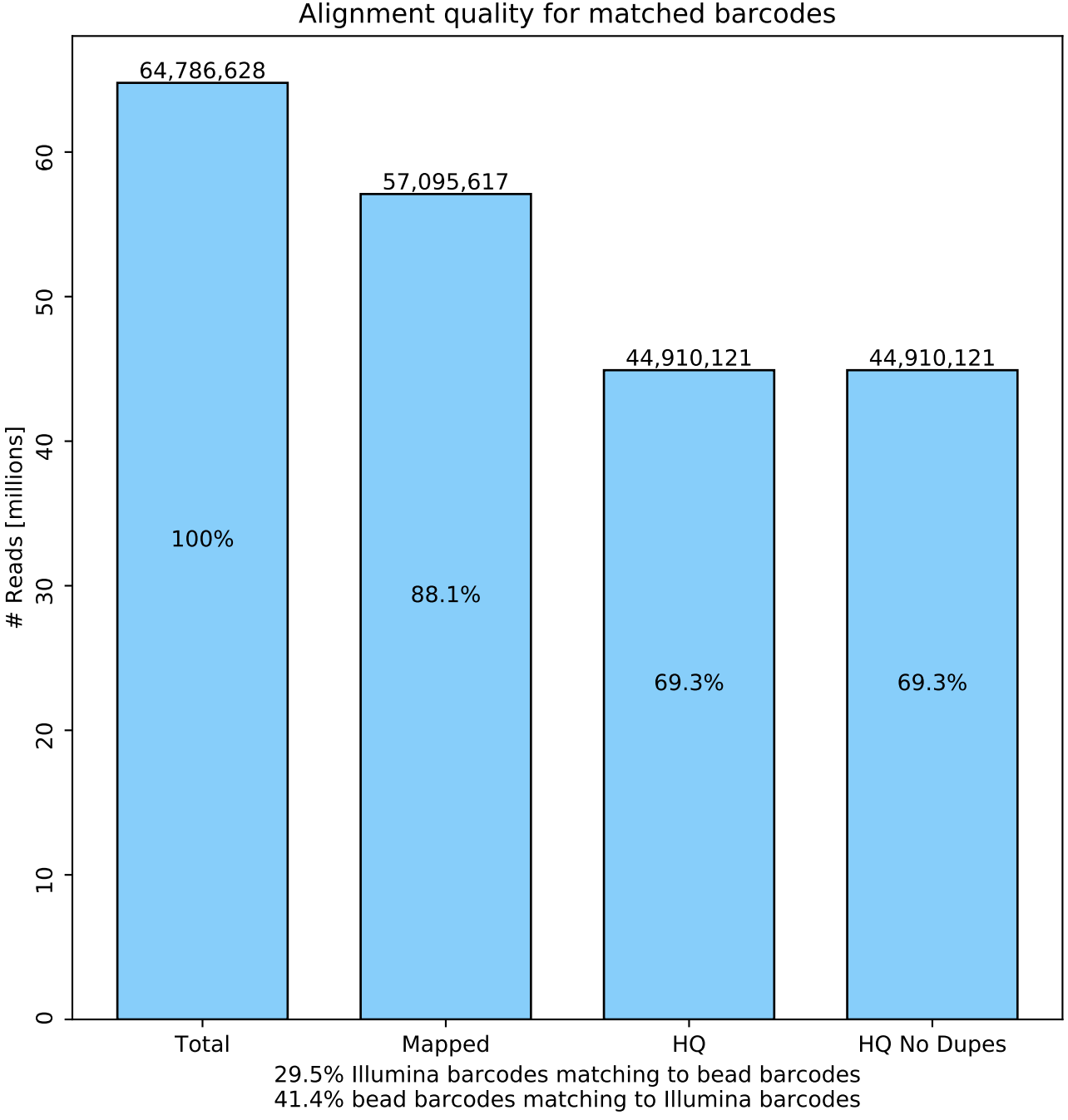

All reads
Percentage
0
10
20
30
40
50
60
70
7.13
59.3
75.5
16.2
17.5
ribosomal
exonic
genic
intronic
intergenic

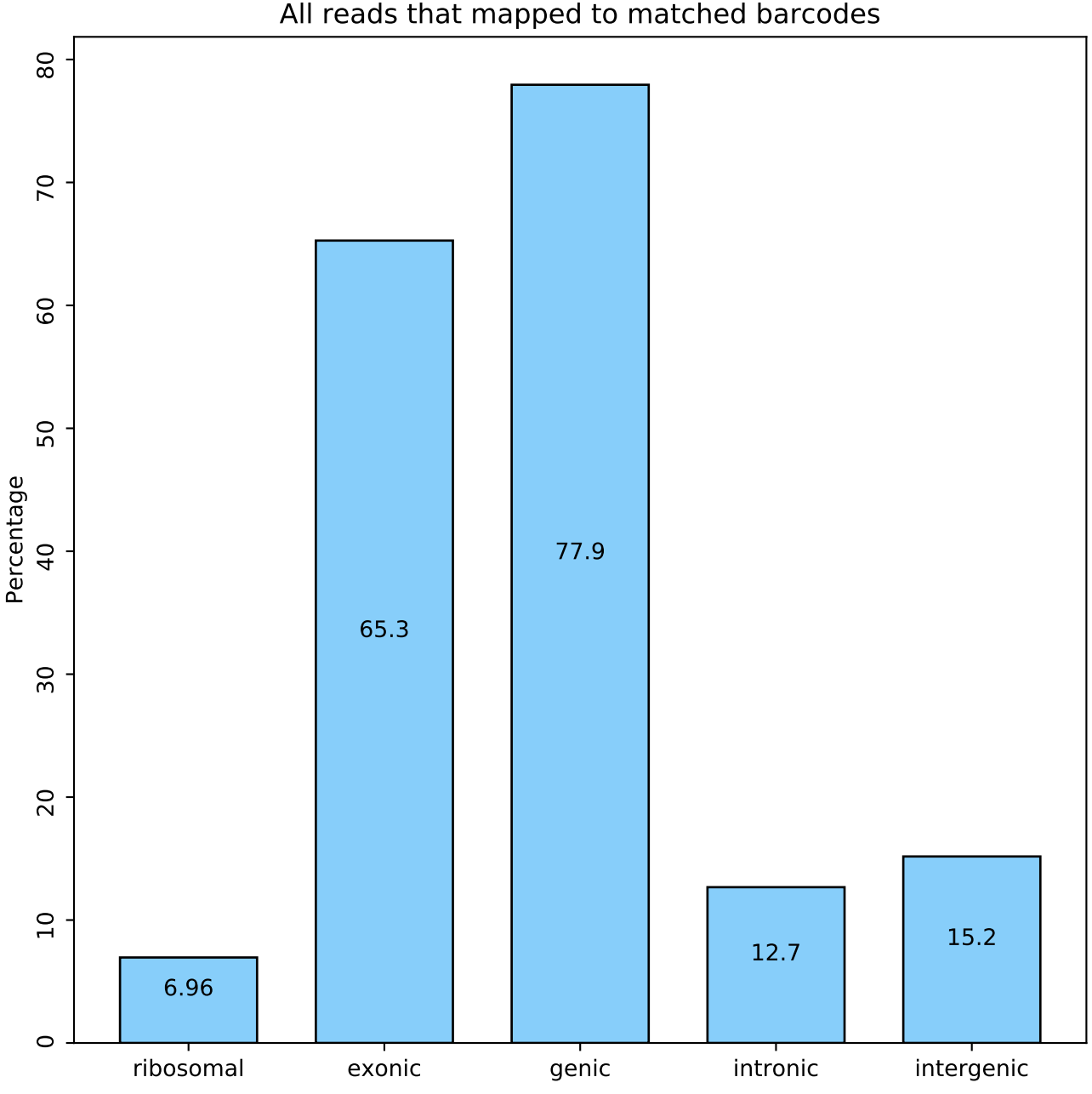

Cumulative fraction of reads per cell barcode
cumulative fraction of reads
0.0
0.2
0.4
0.6
0.8
1.0
0
200000
400000
600000
800000
1000000
1200000
1400000
cell barcodes sorted by number of reads [descending]

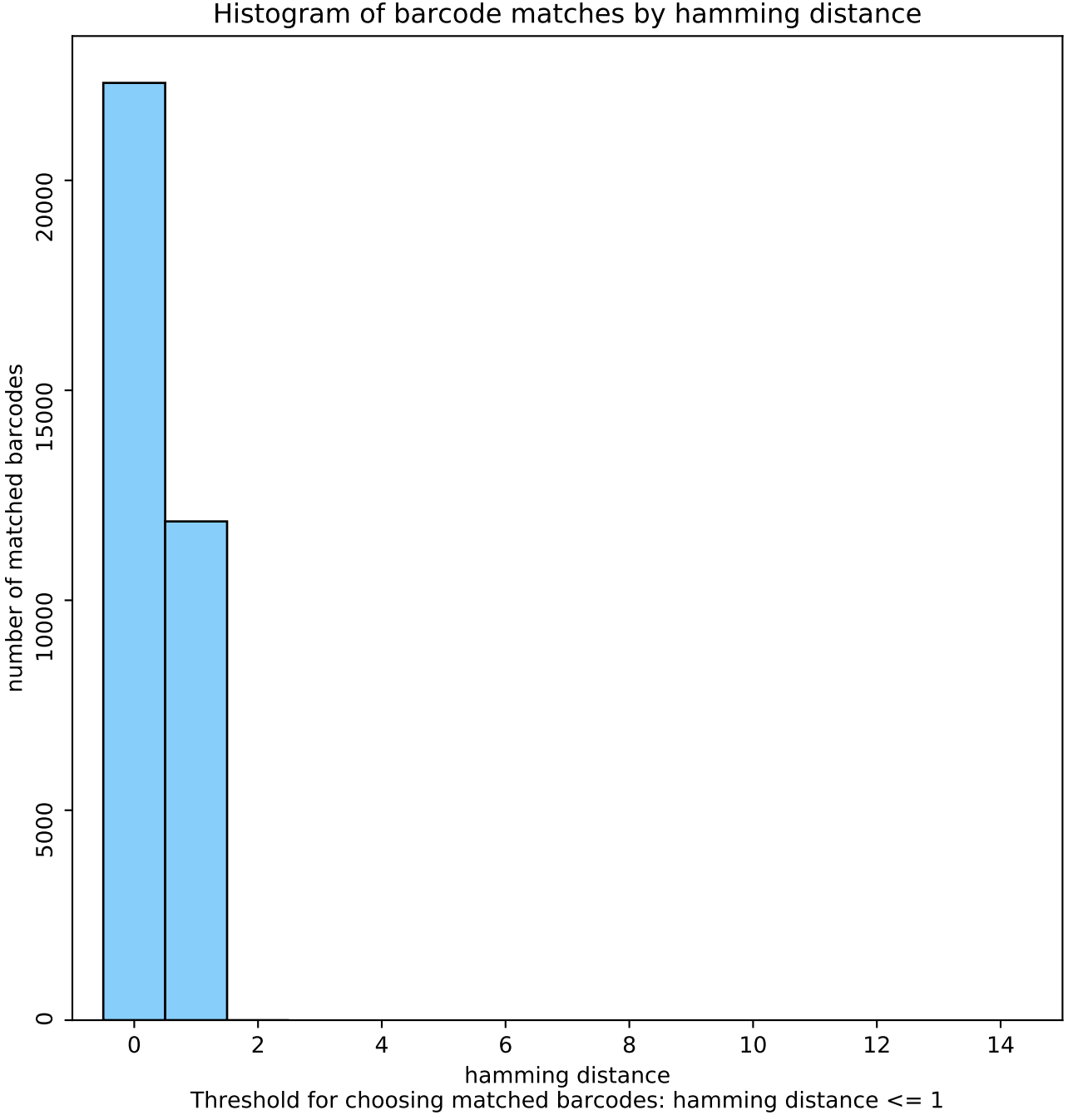

% Reads trimmed by 3' PolyA trimmer: 3.4
number of reads
50000
100000
150000
200000
250000
300000
350000
400000
5
10
15
20
25
30
35
first base of PolyA tail trimmed

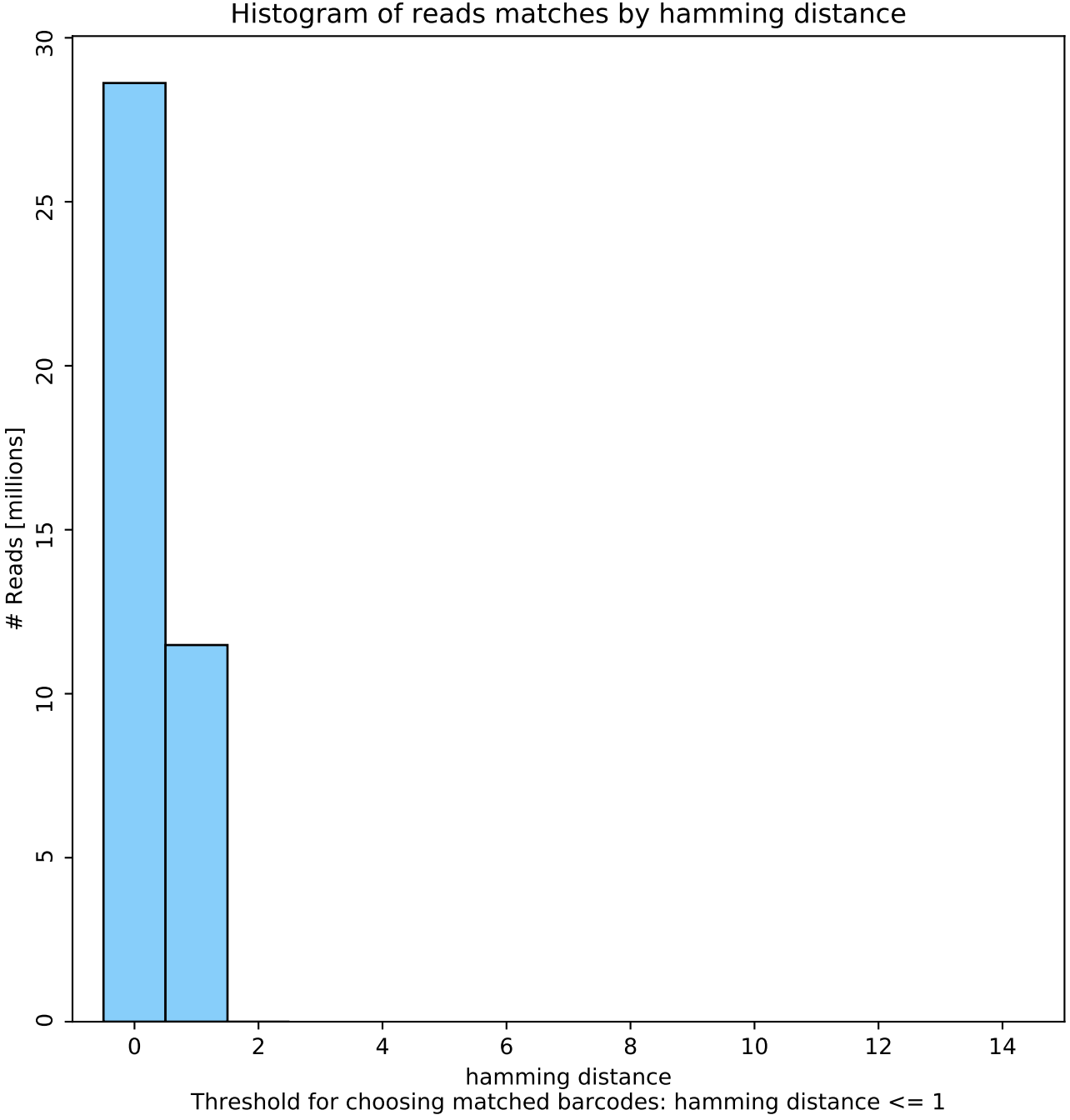

Cell barcodes for all reads
fraction of reads
base position
0
10
20
30
40
0
2
4
6
8
10
12
14
16
A
C
G
T

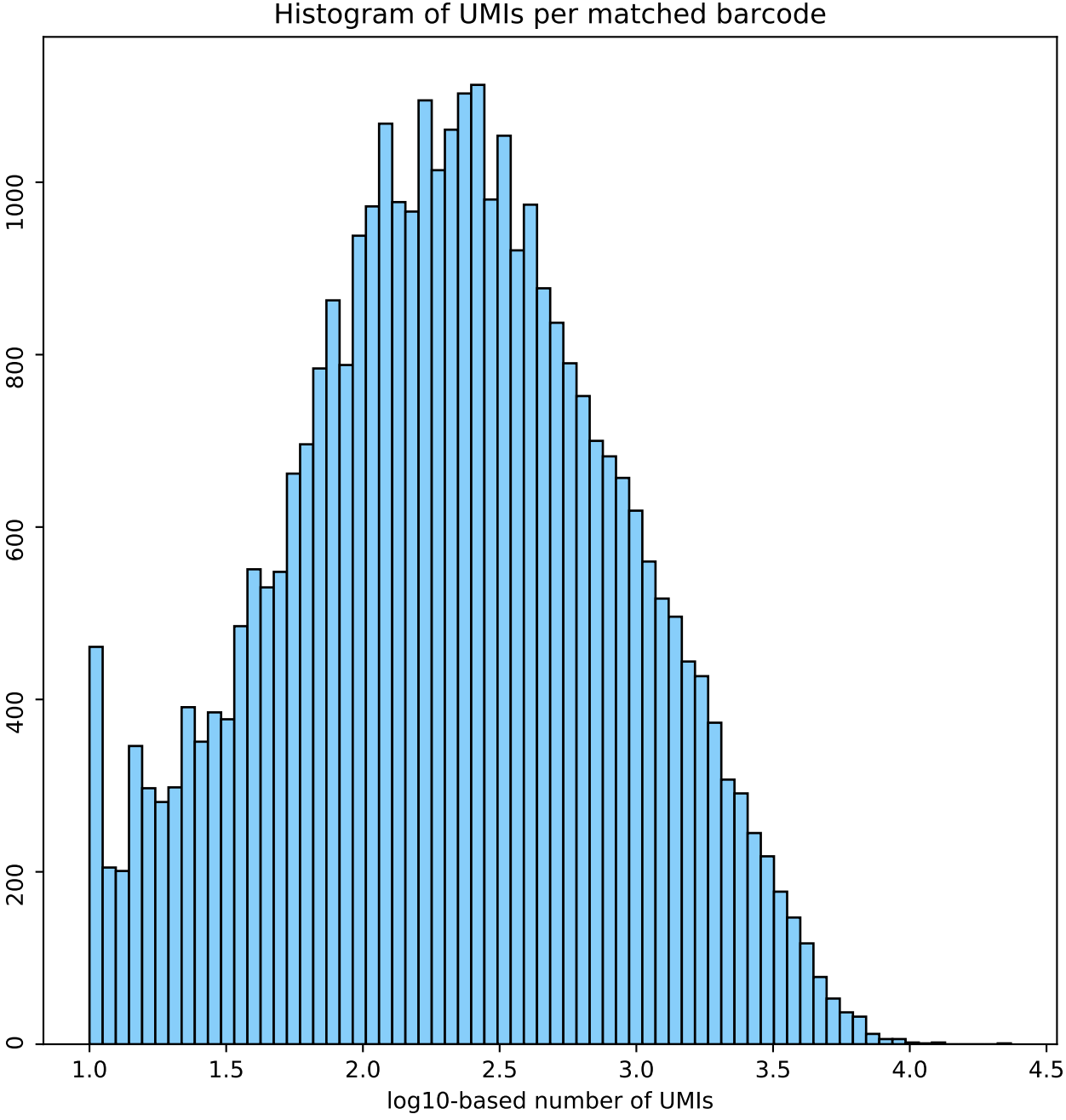

Molecular barcodes for all reads
fraction of reads
base position
0
5
10
15
20
25
30
35
40
0
1
2
3
4
5
6
7
8
A
C
G
T

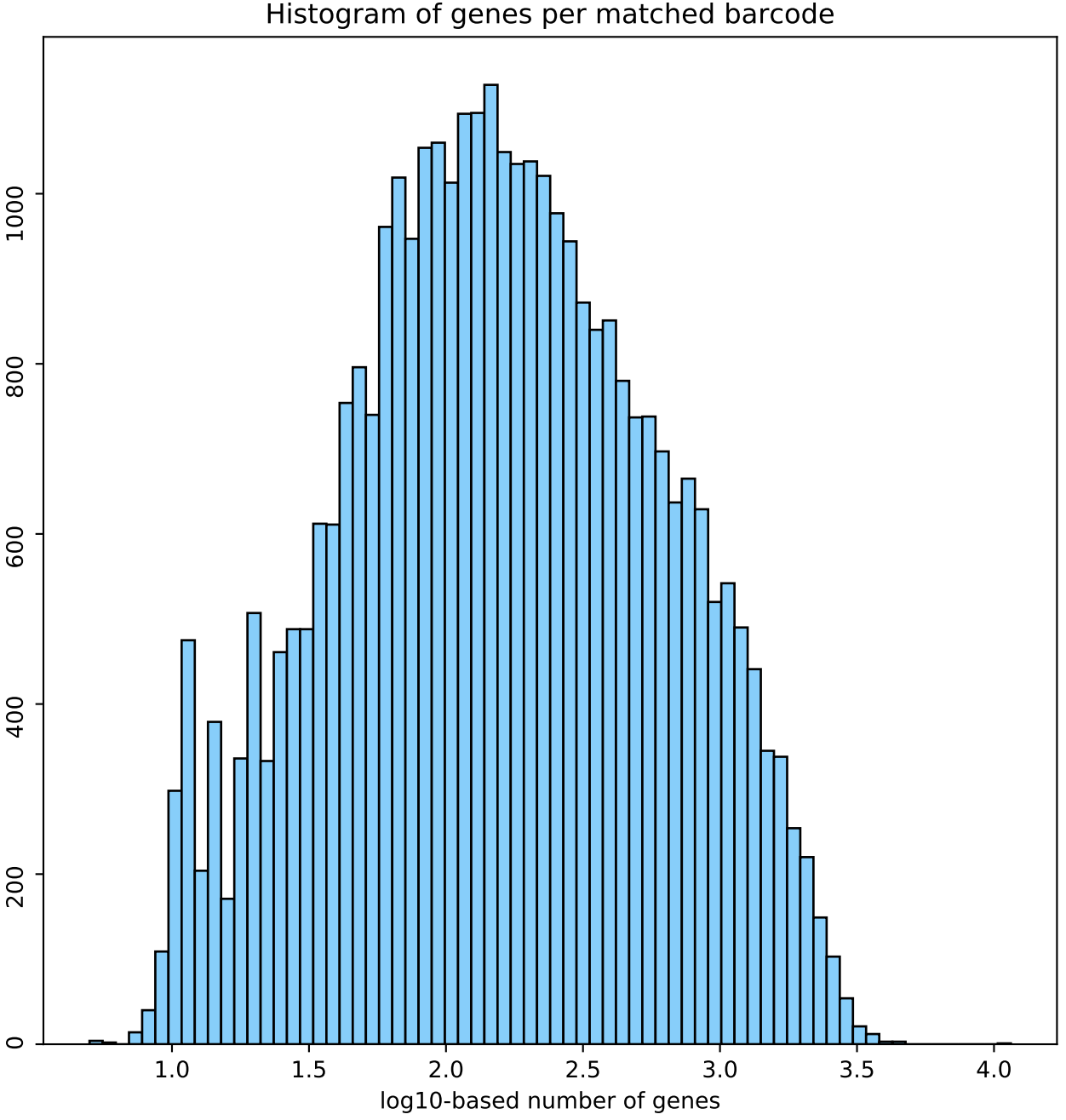

Alignment quality for matched barcodes
64,786,628
57,095,617
44,910,121
44,910,121
100%
88.1%
69.3%
69.3%
# Reads [millions]
0
10
20
30
40
50
60
Total
Mapped
HQ
HQ No Dupes
29.5% Illumina barcodes matching to bead barcodes
41.4% bead barcodes matching to Illumina barcodes

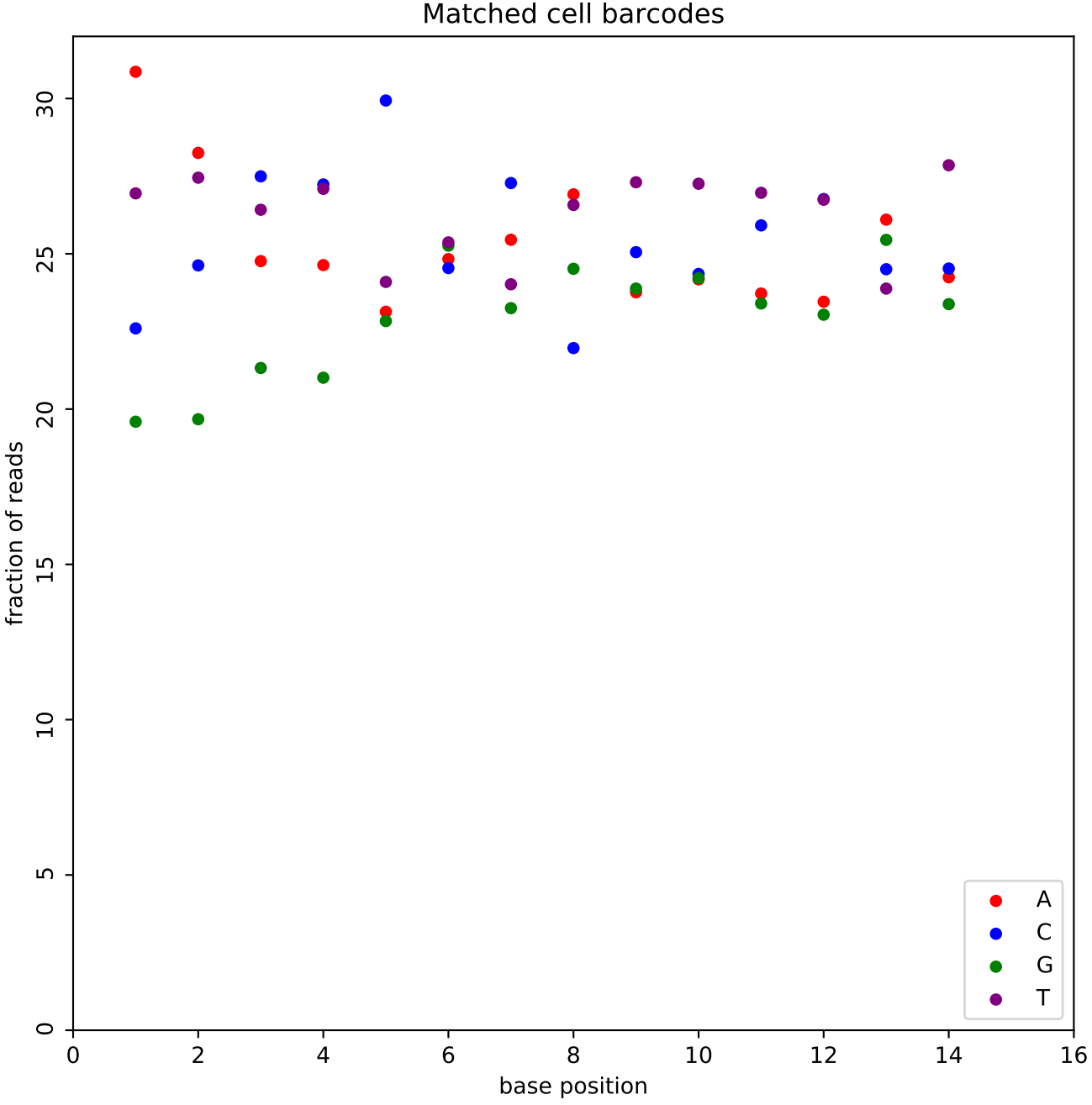

All reads that mapped to matched barcodes
Percentage
0
10
20
30
40
50
60
70
80
6.96
65.3
77.9
12.7
15.2
ribosomal
exonic
genic
intronic
intergenic

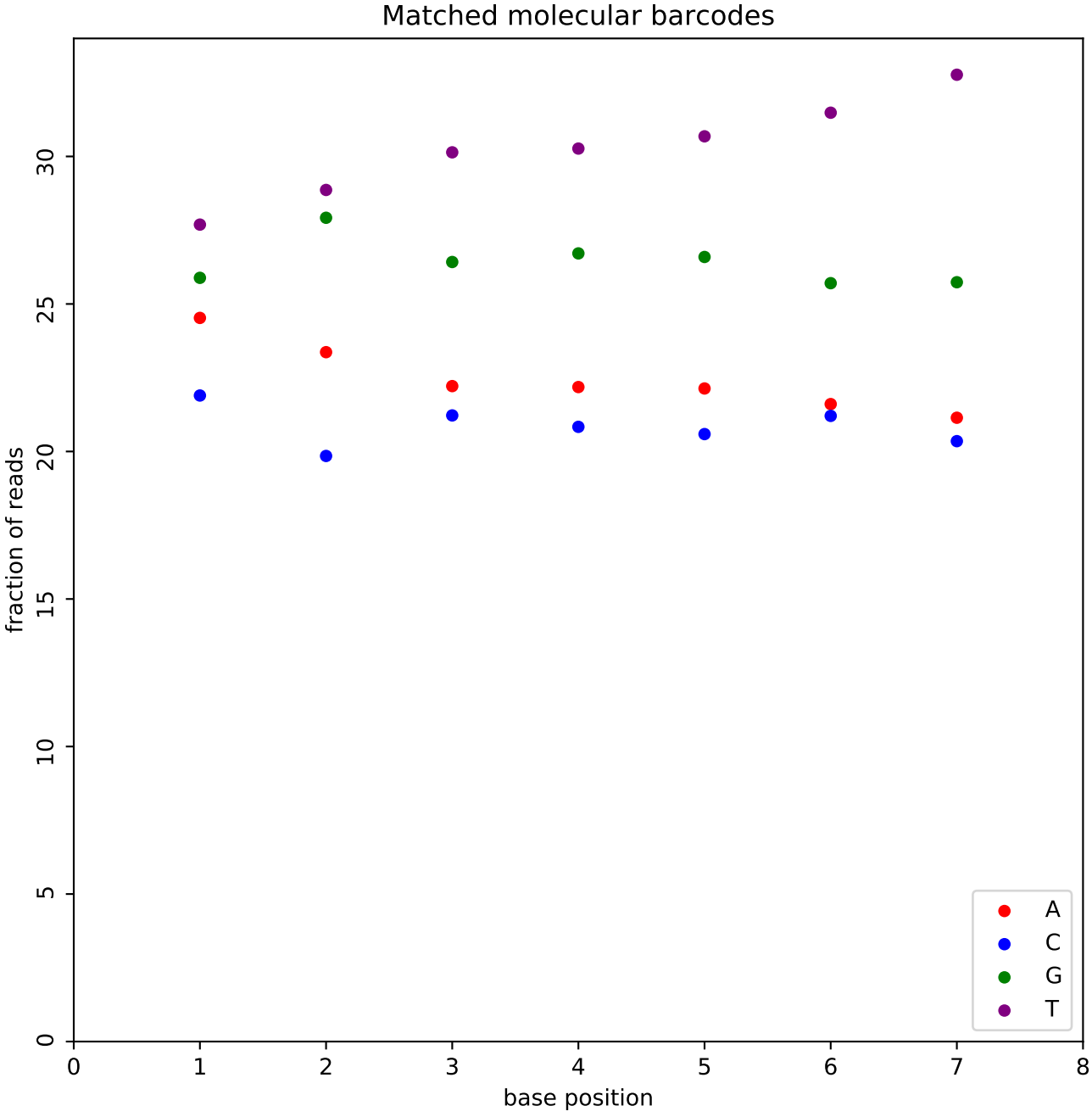

Histogram of barcode matches by hamming distance
number of matched barcodes
0
5000
10000
15000
20000
0
2
4
6
8
10
12
14
hamming distance
Threshold for choosing matched barcodes: hamming distance <= 1

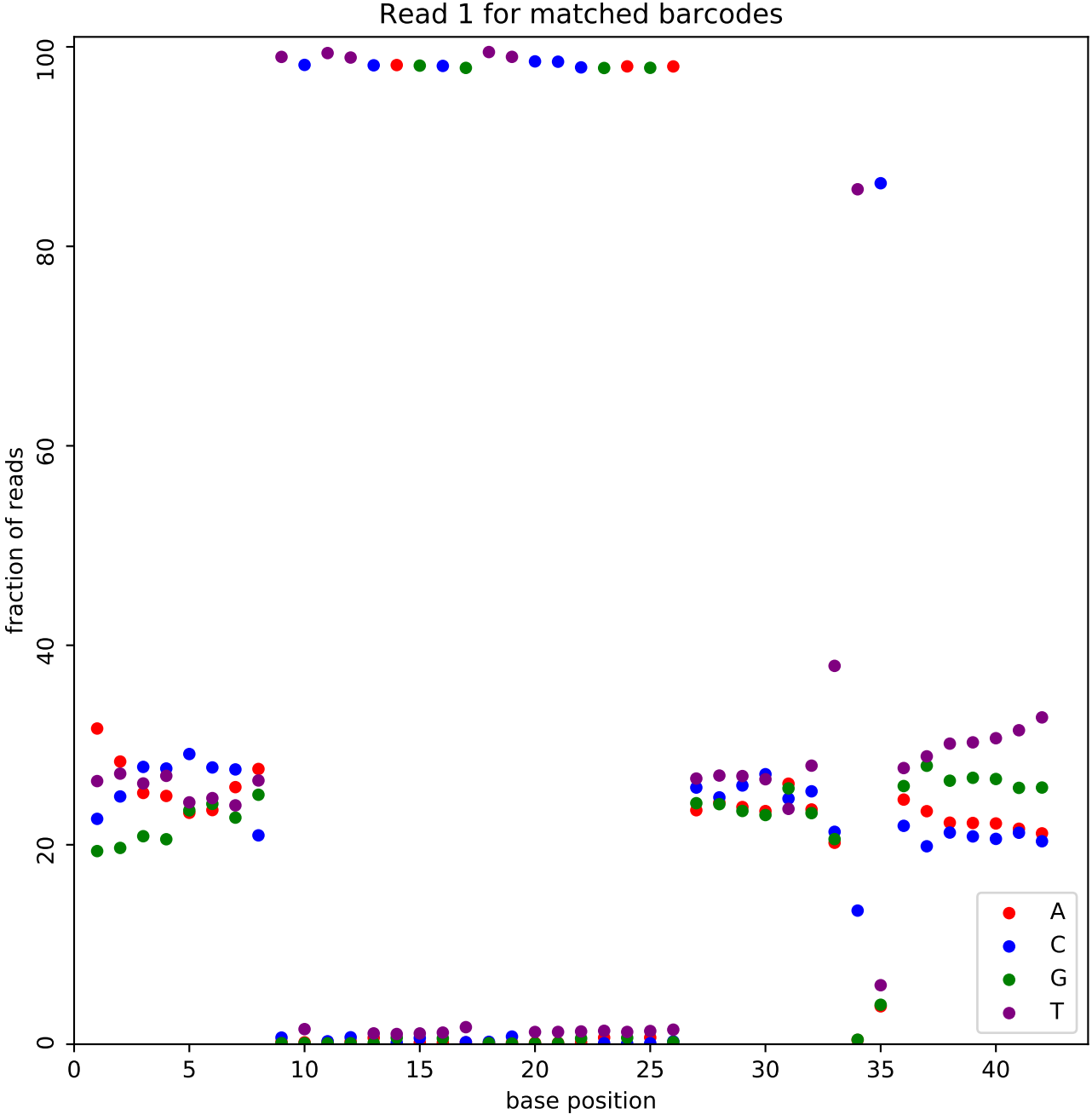

Histogram of reads matches by hamming distance
# Reads [millions]
0
5
10
15
20
25
30
0
2
4
6
8
10
12
14
hamming distance
Threshold for choosing matched barcodes: hamming distance <= 1

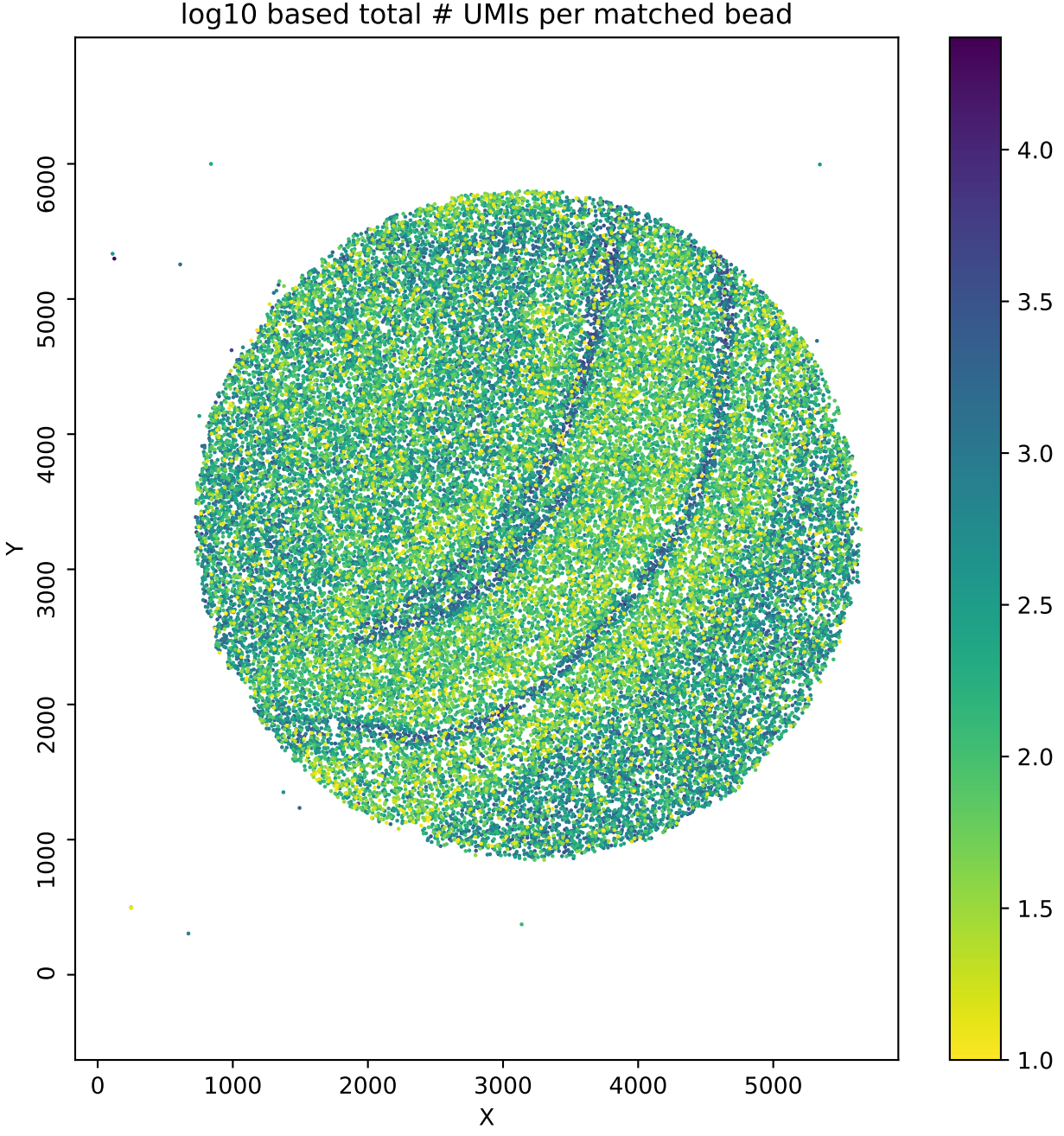

Histogram of UMIs per matched barcode
0
200
400
600
800
1000
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
log10-based number of UMIs

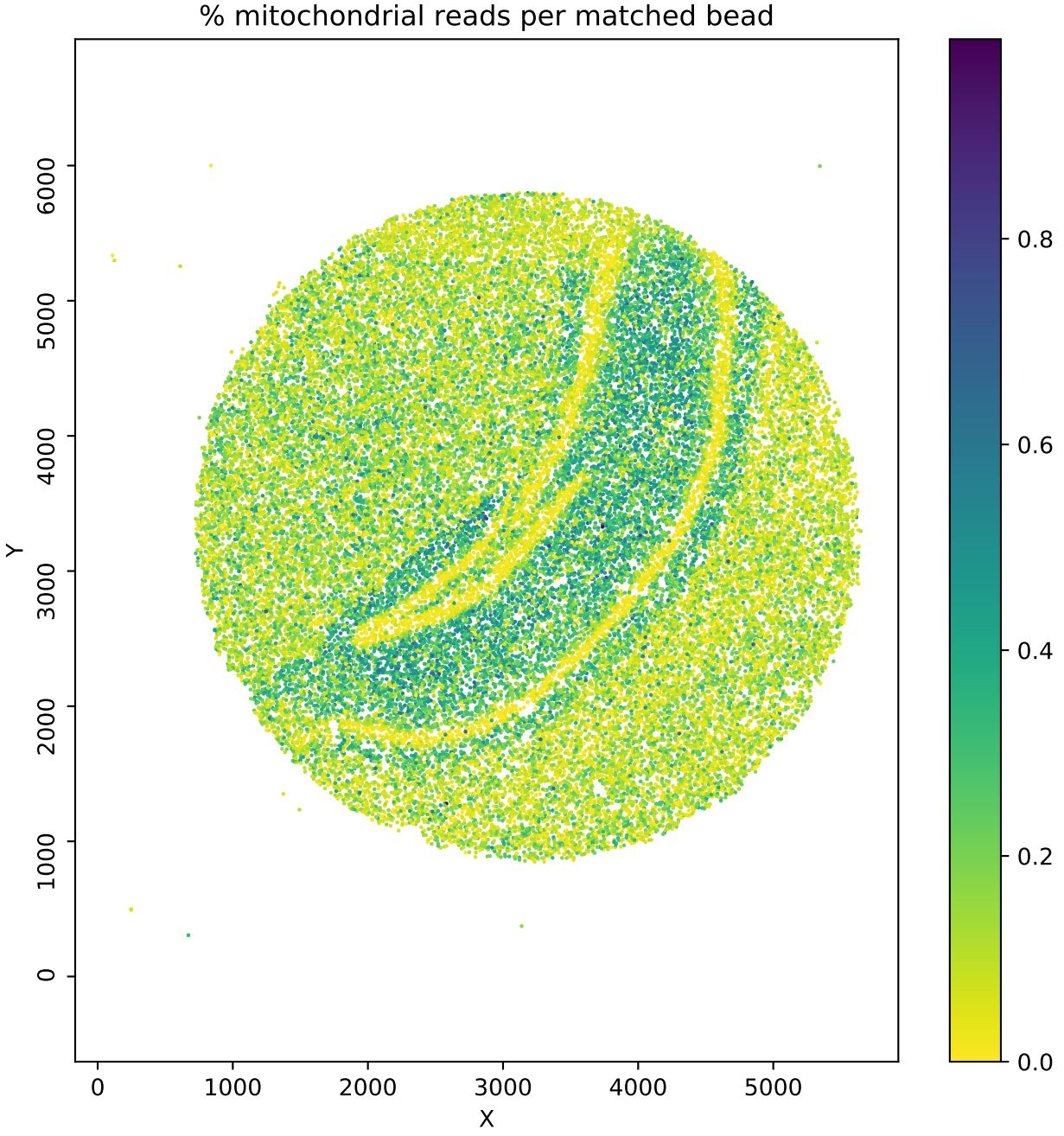

Histogram of genes per matched barcode
0
200
400
600
800
1000
1.0
1.5
2.0
2.5
3.0
3.5
4.0
log10-based number of genes

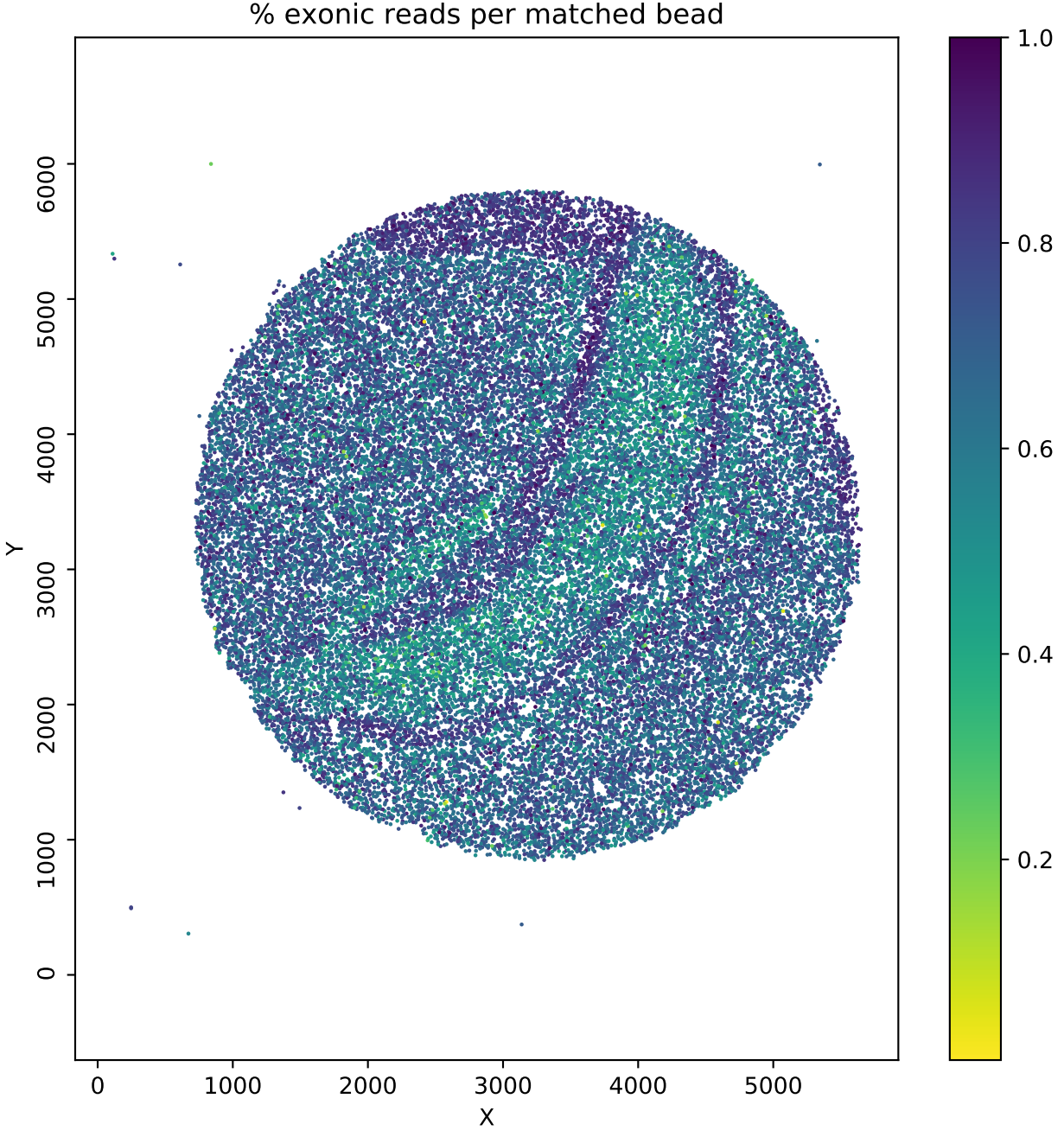

Matched cell barcodes
fraction of reads
base position
0
5
10
15
20
25
30
0
2
4
6
8
10
12
14
16
A
C
G
T

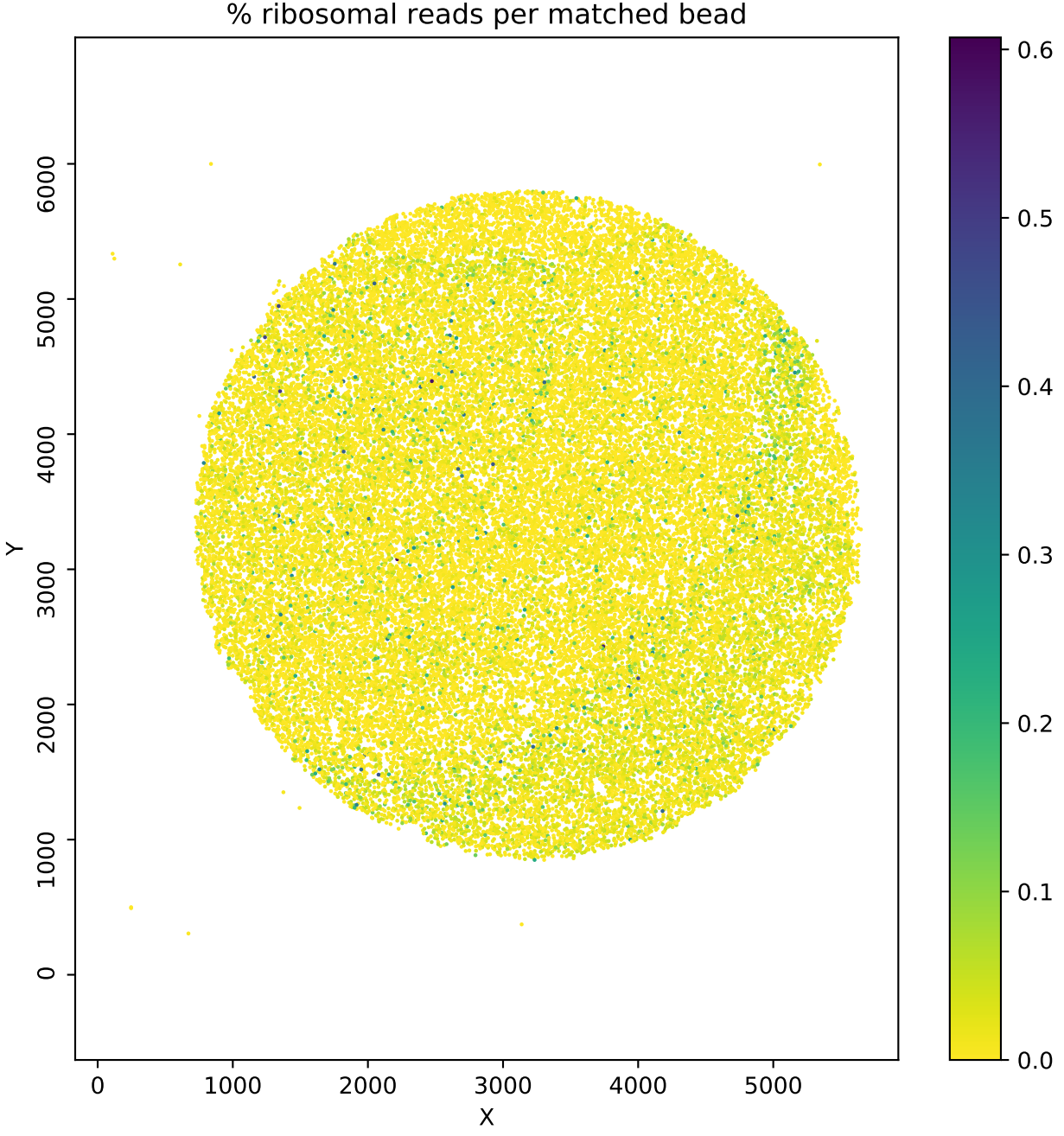

Matched molecular barcodes
fraction of reads
base position
0
5
10
15
20
25
30
0
1
2
3
4
5
6
7
8
A
C
G
T


Read 1 for matched barcodes
fraction of reads
base position
0
20
40
60
80
100
0
5
10
15
20
25
30
35
40
A
C
G
T


log10 based total # UMIs per matched bead
Y
X
0
1000
2000
3000
4000
5000
6000
1.0
1.5
2.0
2.5
3.0
3.5
4.0


% mitochondrial reads per matched bead
Y
X
0
1000
2000
3000
4000
5000
6000
0.0
0.2
0.4
0.6
0.8


% exonic reads per matched bead
Y
X
0
1000
2000
3000
4000
5000
6000
1.0
0.8
0.6
0.4
0.2


% ribosomal reads per matched bead
Y
X
0
1000
2000
3000
4000
5000
6000
0.0
0.1
0.2
0.3
0.4
0.5
0.6