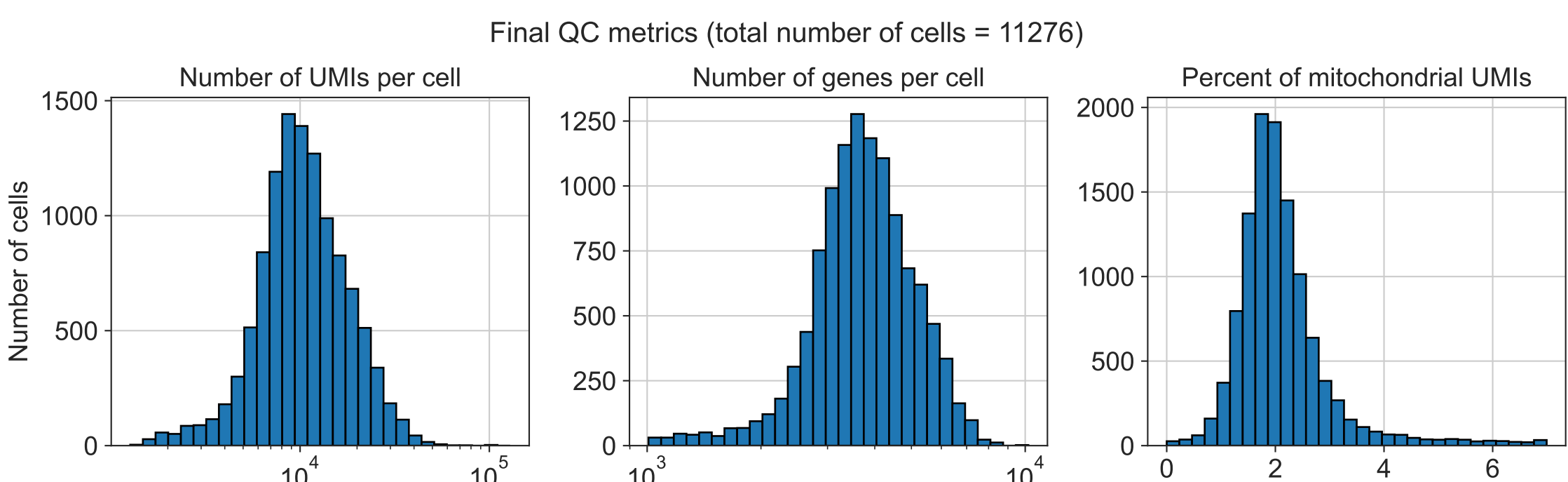


Total number of cells before QC = 12357



min UMI of cloneIDs ≥ 2

min UMI of cloneIDs ≥ 3

min UMI of cloneIDs ≥ 4

Figure 1 displays five bar charts, each representing a different clone (clone_96, clone_392, clone_1022, clone_45, and clone_1). The y-axis for all charts represents the number of cells, ranging from 0 to 20. The x-axis for each chart shows the gene name and the number of cells in that clone. The data is as follows:

Clone	Gene	Number of Cells
clone_96	nan	22
	Acvr2a-2	3
clone_392	nan	16
	Acvr2a-2	3
clone_1022	nan	13
	EGFP-1	5
clone_45	Fzd2-1	9
	nan	9
clone_1	nan	12
	Fzd2-1	5

The figure consists of three pie charts illustrating the distribution of gRNA calling methods and the number of gRNAs per cell.

Left Chart: TOMbc cloneID and gRNA calling

Category	Percentage
CloneID	50%
CloneID + gRNA	16%
None	29%
gRNA	4%

Middle Chart: Different gRNAs calling

Category	Percentage
None	78%
EGFP-1	10%
Acvr2a-2	2%
Fzd2-1	2%
Fgfr1-1	2%
Acvr2a-1	2%
Fgfr1-2	2%
Fgfr2-1	2%
Fgfr3-1	2%
Lepr-1	2%

Right Chart: Number of gRNAs per cell

Number of gRNAs	Percentage
0	80%
1	19%
2	1%

Figure 2 consists of two panels. The left panel is a box plot showing the distribution of Scrublet scores for four categories: Unknown, Single, Multiple in few, and Multiple in single. The y-axis is labeled 'Scrublet score' and ranges from 0.0 to 0.3. The 'Multiple in single' category shows a significantly higher median score and a larger spread compared to the other categories. The right panel displays three t-SNE plots illustrating TOMbc identification. The first plot, 'Single TOMbc (4785 out of 11276 cells)', shows a large cluster of green points. The second plot, 'Multiple TOMbc in few (903 out of 11276 cells)', shows a smaller cluster of blue points. The third plot, 'Multiple TOMbc in single (1828 out of 11276 cells)', shows a cluster of red points. The points are colored based on their TOMbc identification status.

Figure 1 consists of three panels. The left panel, titled 'Clone size distribution', is a histogram showing the frequency of clones across different size bins. The y-axis is on a logarithmic scale from 10^0 to 10^2 . The distribution is right-skewed, with the highest frequency in the smallest size bin (around 300 clones) and decreasing as size increases. The middle panel, titled 'clone_96', shows a map of the study area with 96 orange dots representing the spatial distribution of a specific clone. The right panel, titled 'clone_392', shows a map of the same area with 392 orange dots representing the spatial distribution of another clone. Both maps show a higher density of clones in the central and southern parts of the study area.