

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

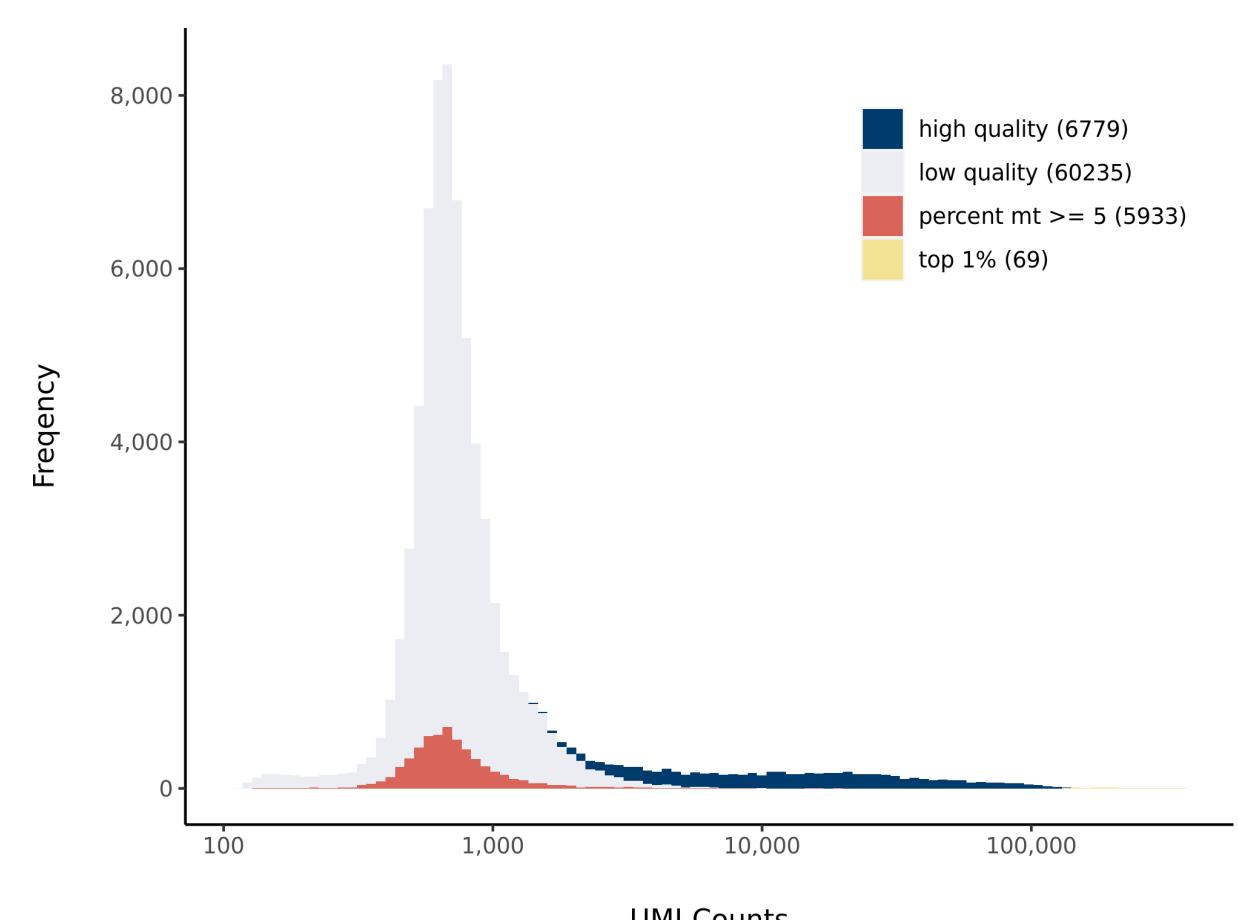
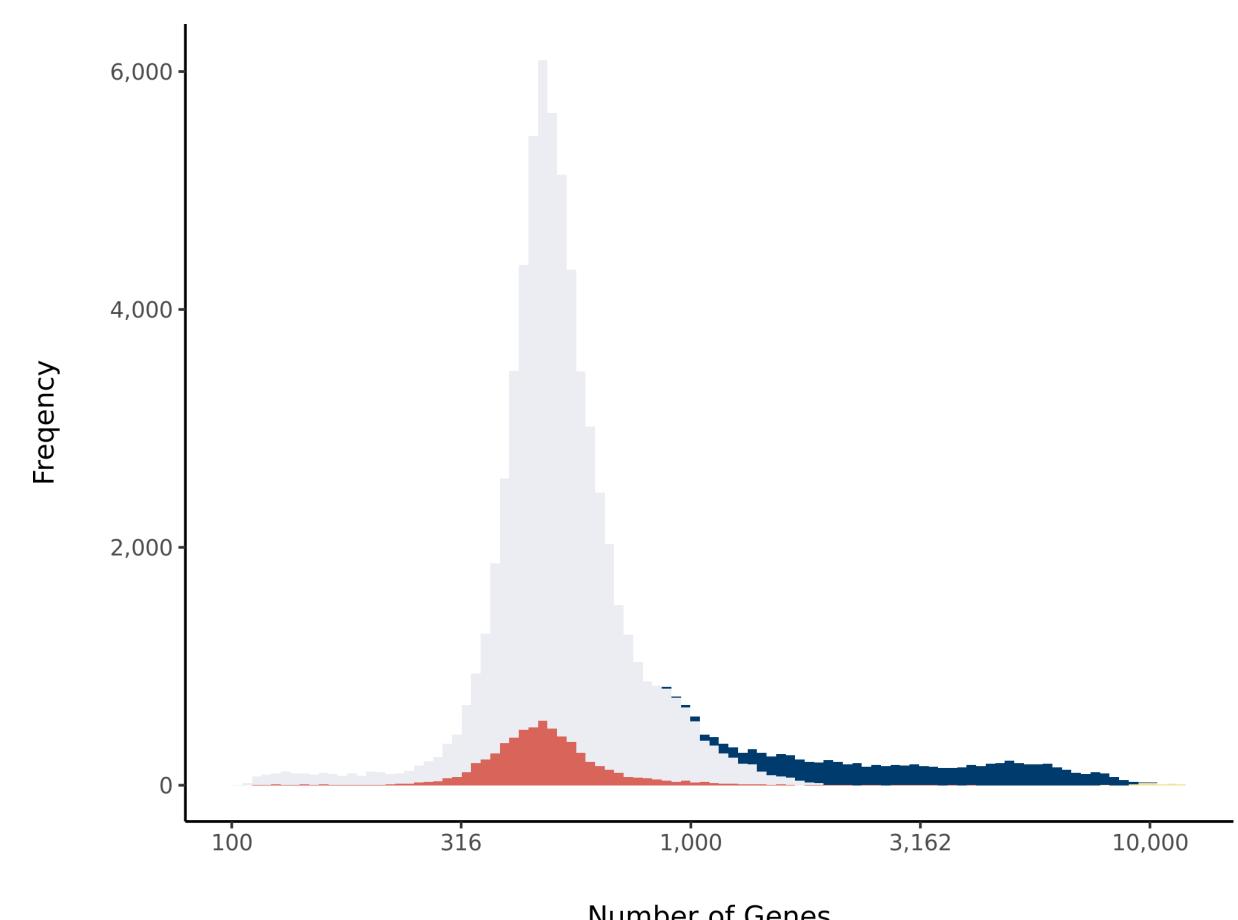
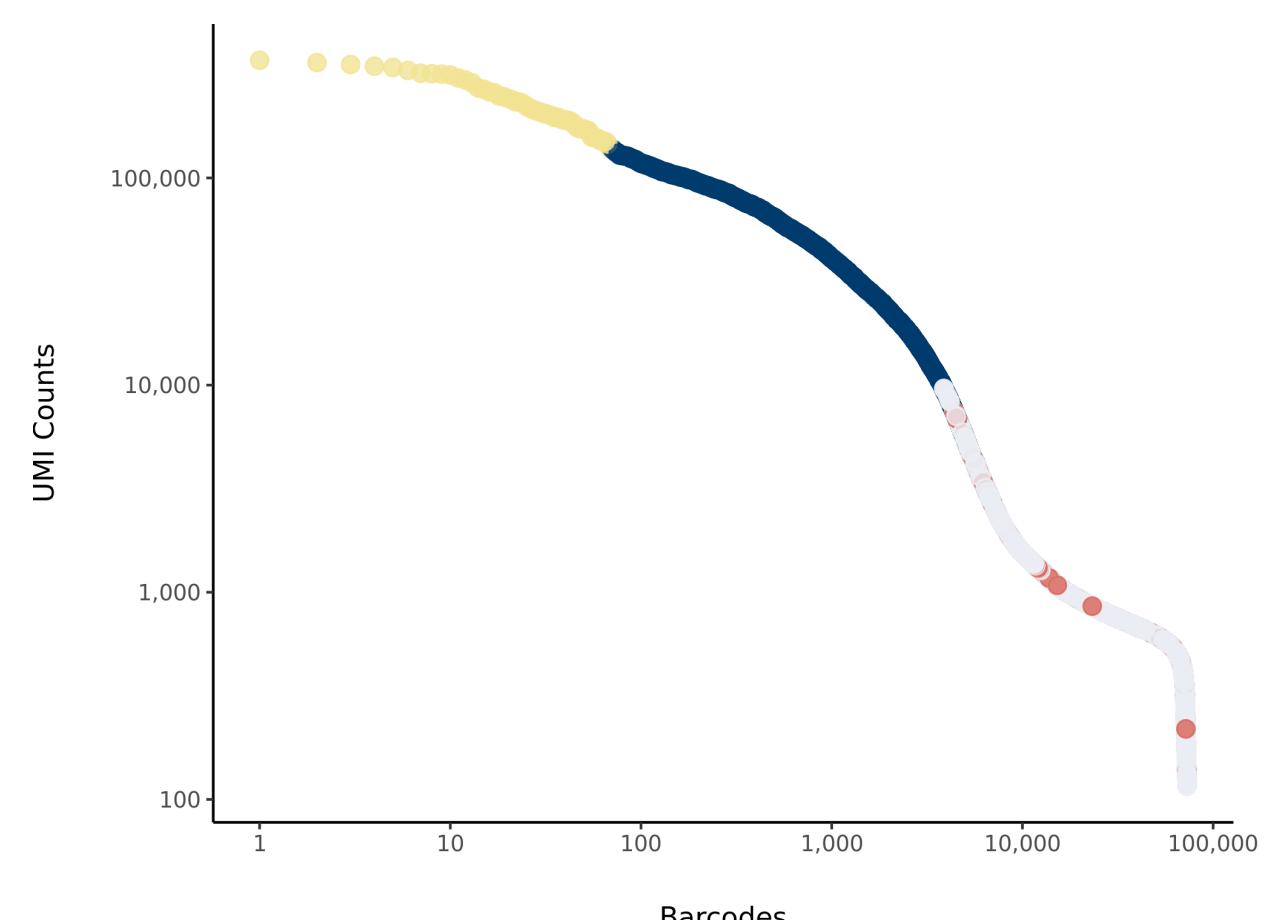
Estimated Number of High Quality Cell	6,779
High Quality Cell	9.28 %
Total UMI Counts in High Quality Cell	136,642,155
UMI Counts in High Quality Cell	66.94 %
Median UMI Counts per High Quality Cell	11,648
Median Genes per High Quality Cell	2,994
Total Genes Detected in High Quality Cell	24,854
Cell above Mitochondrial Expression Threshold	8.13 %
Estimated Doublet Rate in High Quality Cell	5.11 %

**Sequencing Stats**

Number of Reads Processed	385,741,789
Reads Pseudoaligned	88.9 %
Reads on Whitelist	94.66 %
Total UMI Counts	204,120,352
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	col0
Name	WT Col-0
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	5,000
Date	NA
Seq Run	NA

**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

# dc1 Summary

Processed by COPILOT

Summary Analysis

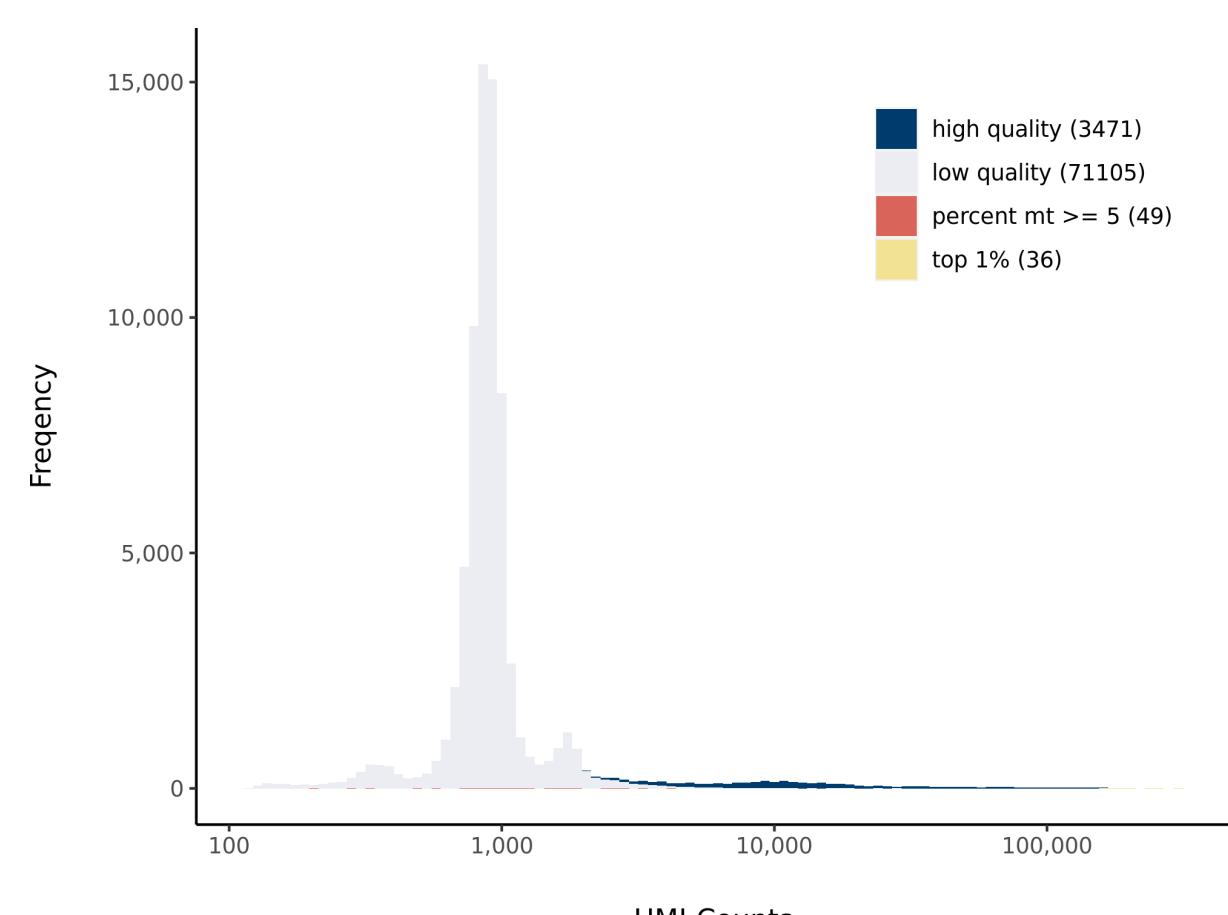
## Parameters

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

## Cell Stats

Estimated Number of High Quality Cell	3,471
High Quality Cell	4.65 %
Total UMI Counts in High Quality Cell	68,731,526
UMI Counts in High Quality Cell	48.3 %
Median UMI Counts per High Quality Cell	10,673
Median Genes per High Quality Cell	3,482
Total Genes Detected in High Quality Cell	25,036
Cell above Mitochondrial Expression Threshold	0.07 %
Estimated Doublet Rate in High Quality Cell	2.68 %

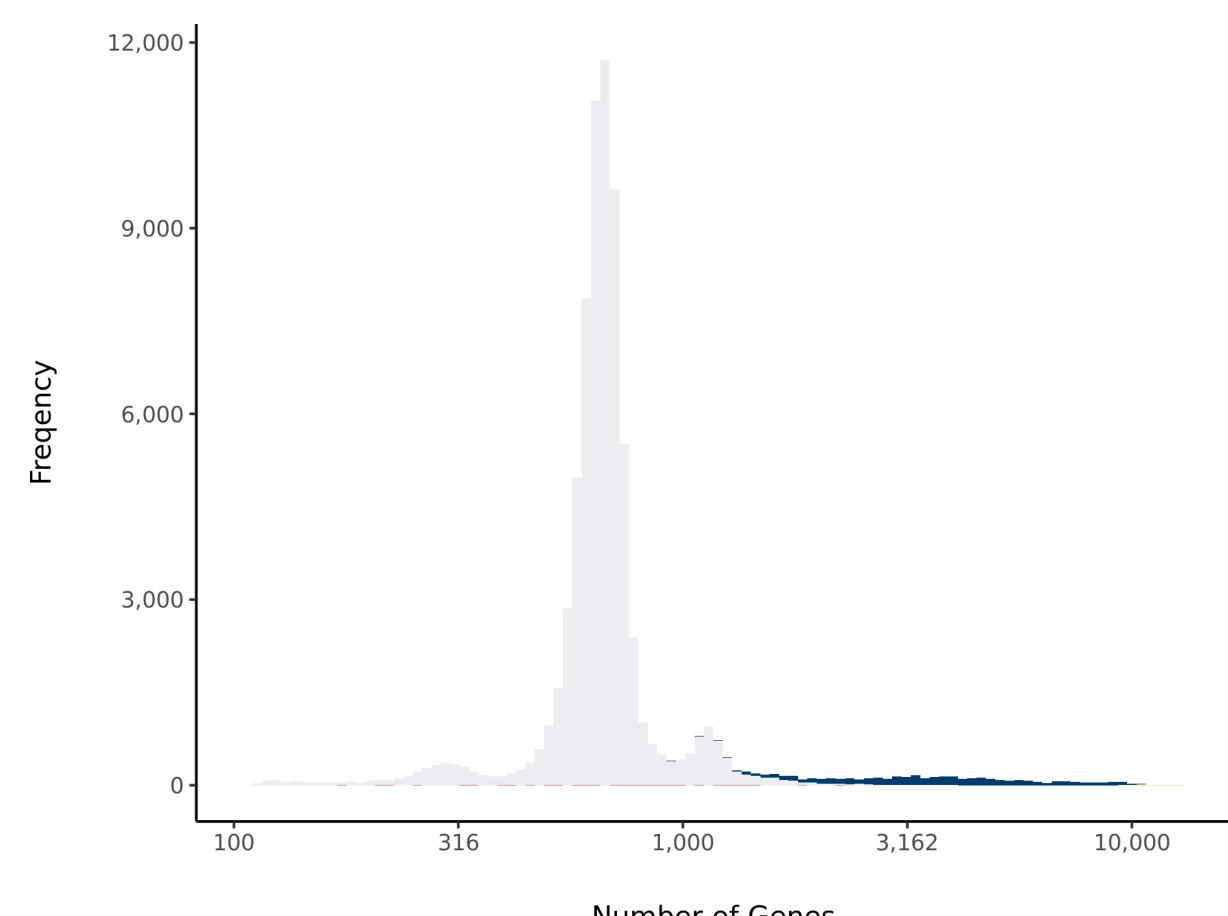
## UMI Counts Histogram



## Sequencing Stats

Number of Reads Processed	261,013,034
Reads Pseudoaligned	90.1 %
Reads on Whitelist	95.61 %
Total UMI Counts	142,313,355
Sequencing Technology	10xv2
Species	Arabidopsis thaliana
Transcriptome	TAIR10

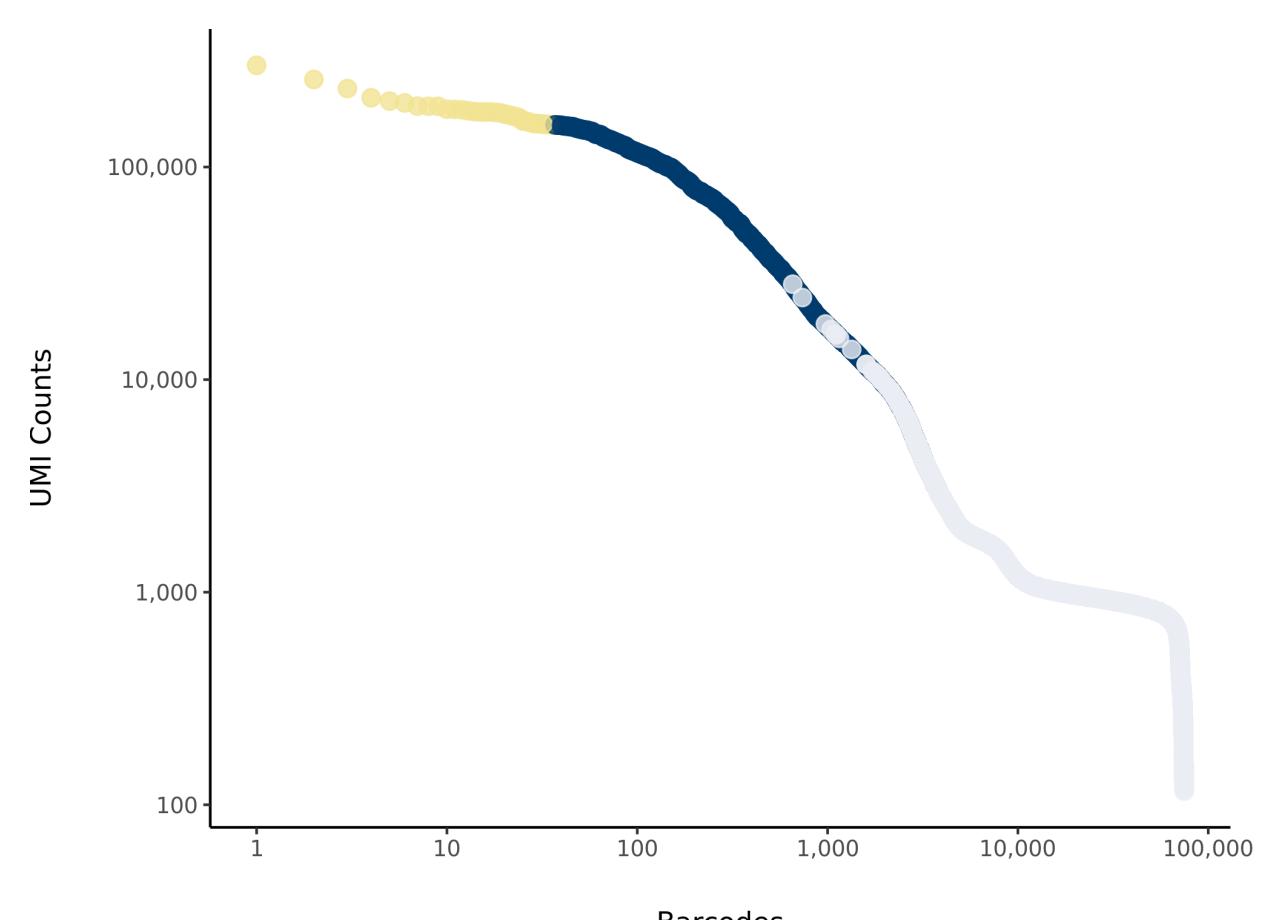
## Number of Genes Histogram



## Sample Stats

Sample	dc1
Name	WT Developmental Cell 1
Source	Denyer et al. 2019, Developmental Cell
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	6_day
Timepoint	NA
Rep	1
Target Cells	NA
Date	NA
Seq Run	NA

## Barcode Rank Plot



**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

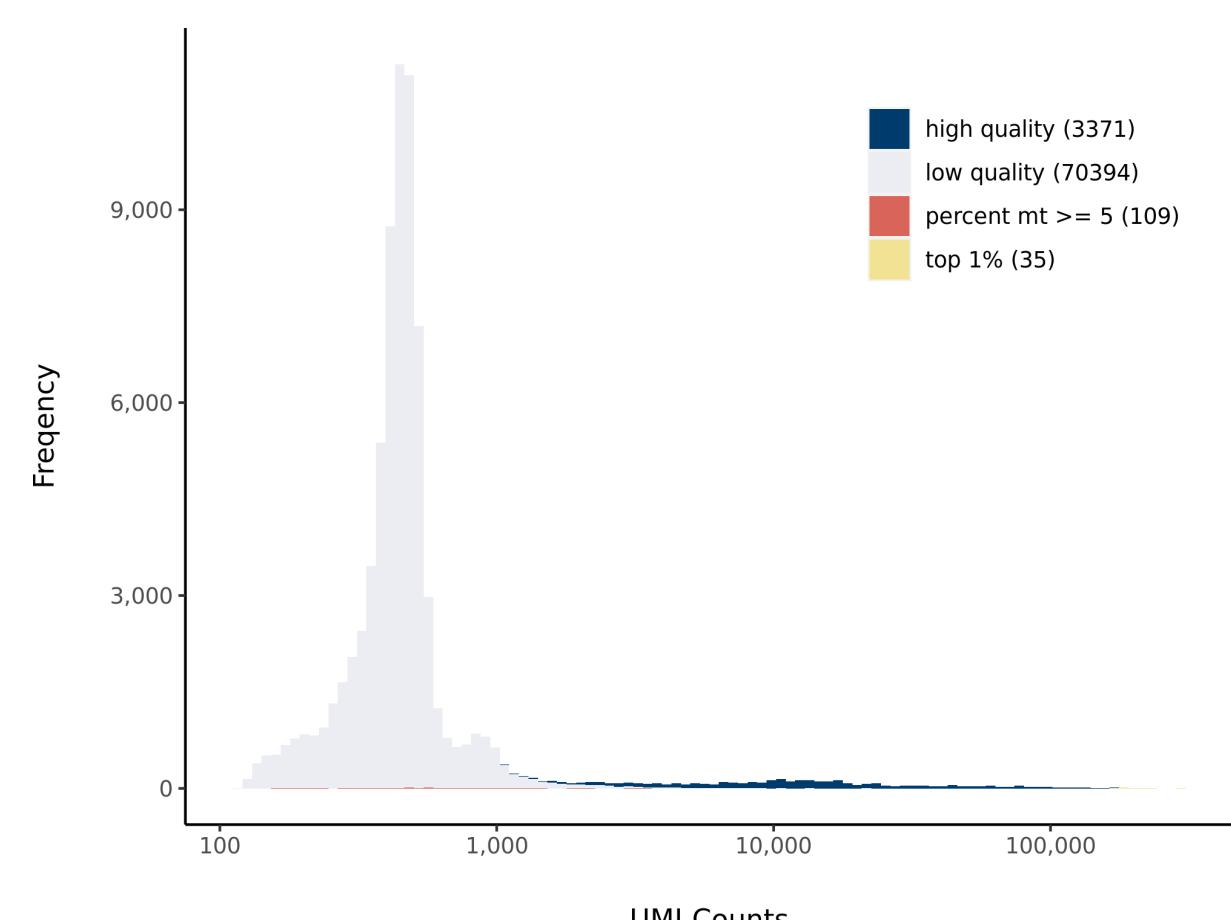
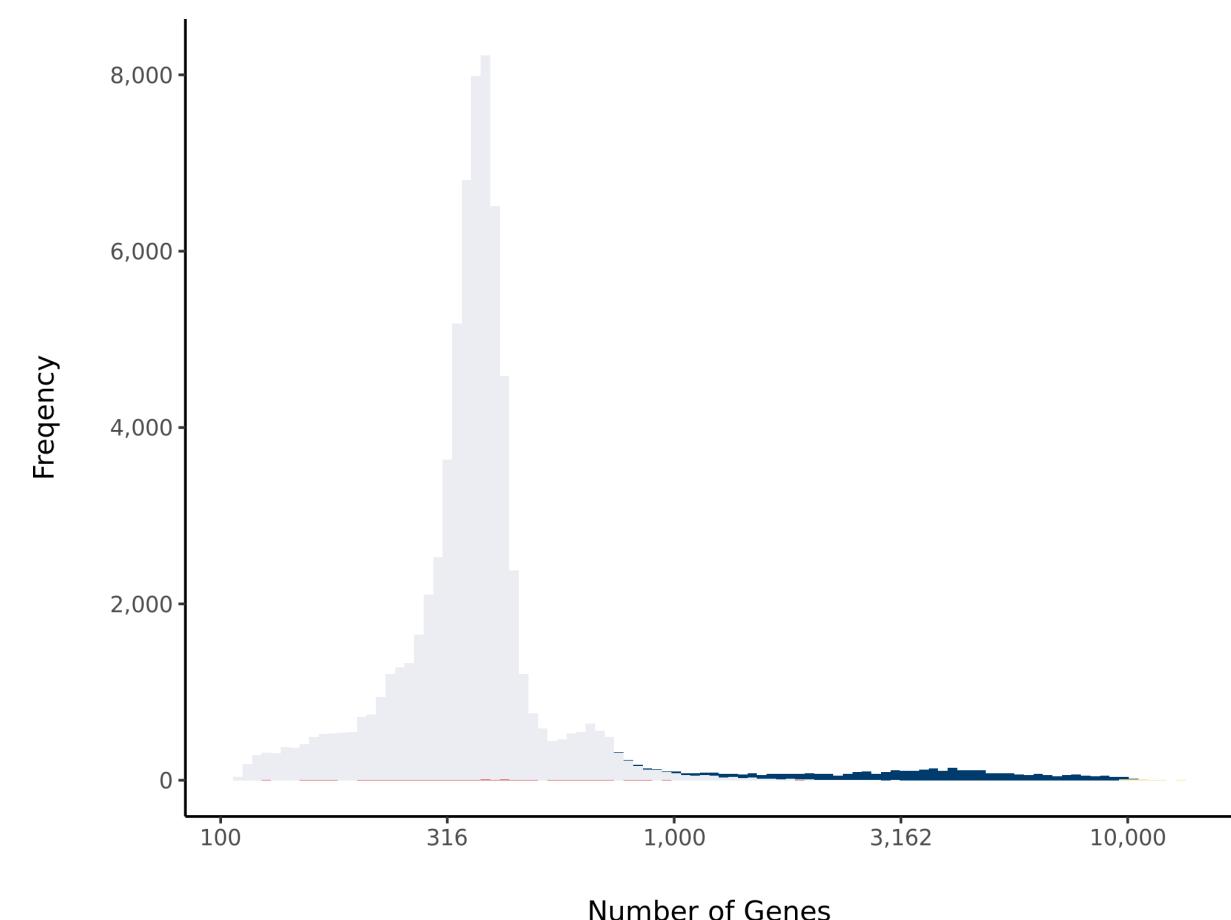
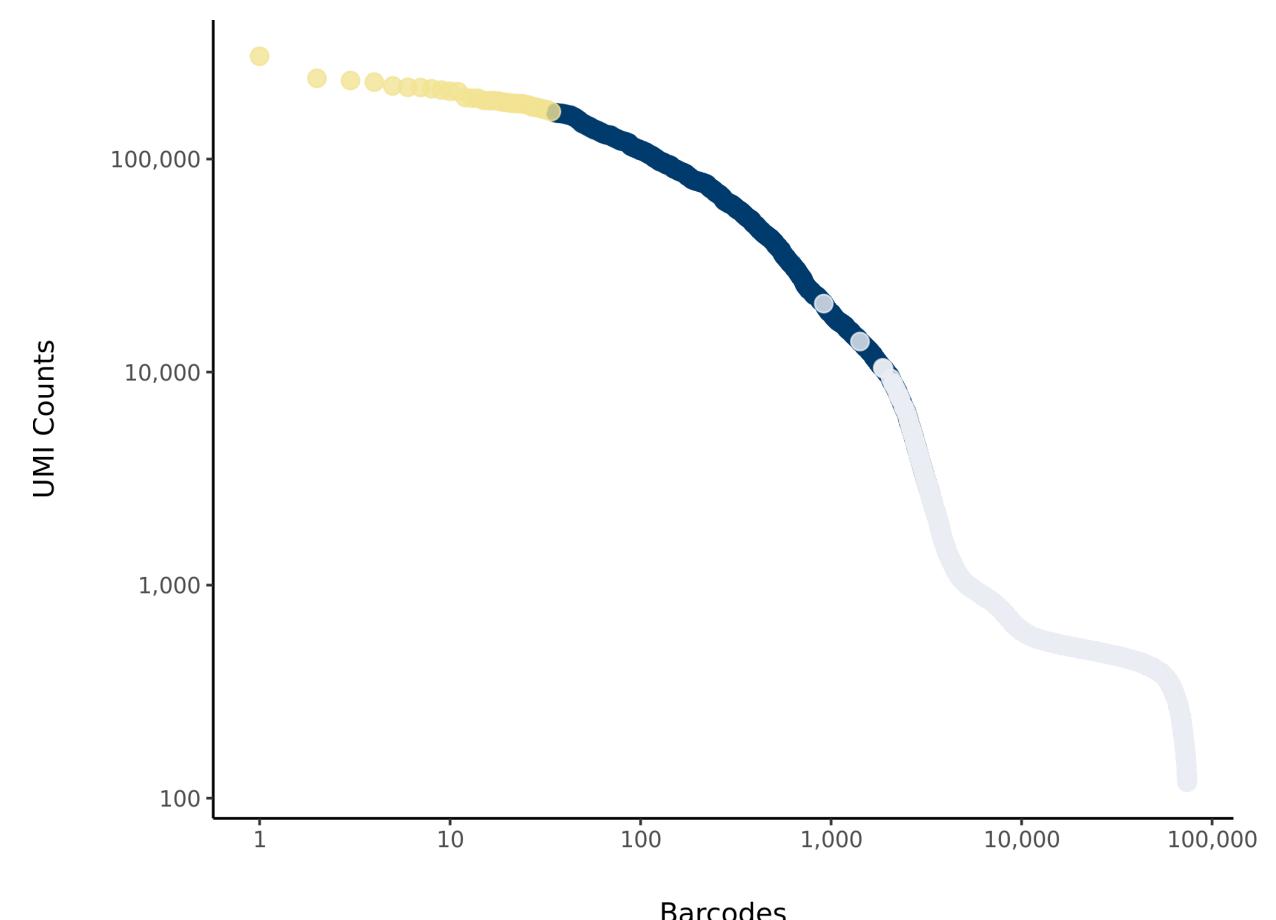
Estimated Number of High Quality Cell	3,371
High Quality Cell	4.56 %
Total UMI Counts in High Quality Cell	68,781,391
UMI Counts in High Quality Cell	63.21 %
Median UMI Counts per High Quality Cell	11,439
Median Genes per High Quality Cell	3,508
Total Genes Detected in High Quality Cell	25,100
Cell above Mitochondrial Expression Threshold	0.15 %
Estimated Doublet Rate in High Quality Cell	2.61 %

**Sequencing Stats**

Number of Reads Processed	235,863,595
Reads Pseudoaligned	89.6 %
Reads on Whitelist	95.56 %
Total UMI Counts	108,819,006
Sequencing Technology	10xv2
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	dc2
Name	WT Developmental Cell 2
Source	Denyer et al. 2019, Developmental Cell
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	6_day
Timepoint	NA
Rep	2
Target Cells	NA
Date	NA
Seq Run	NA

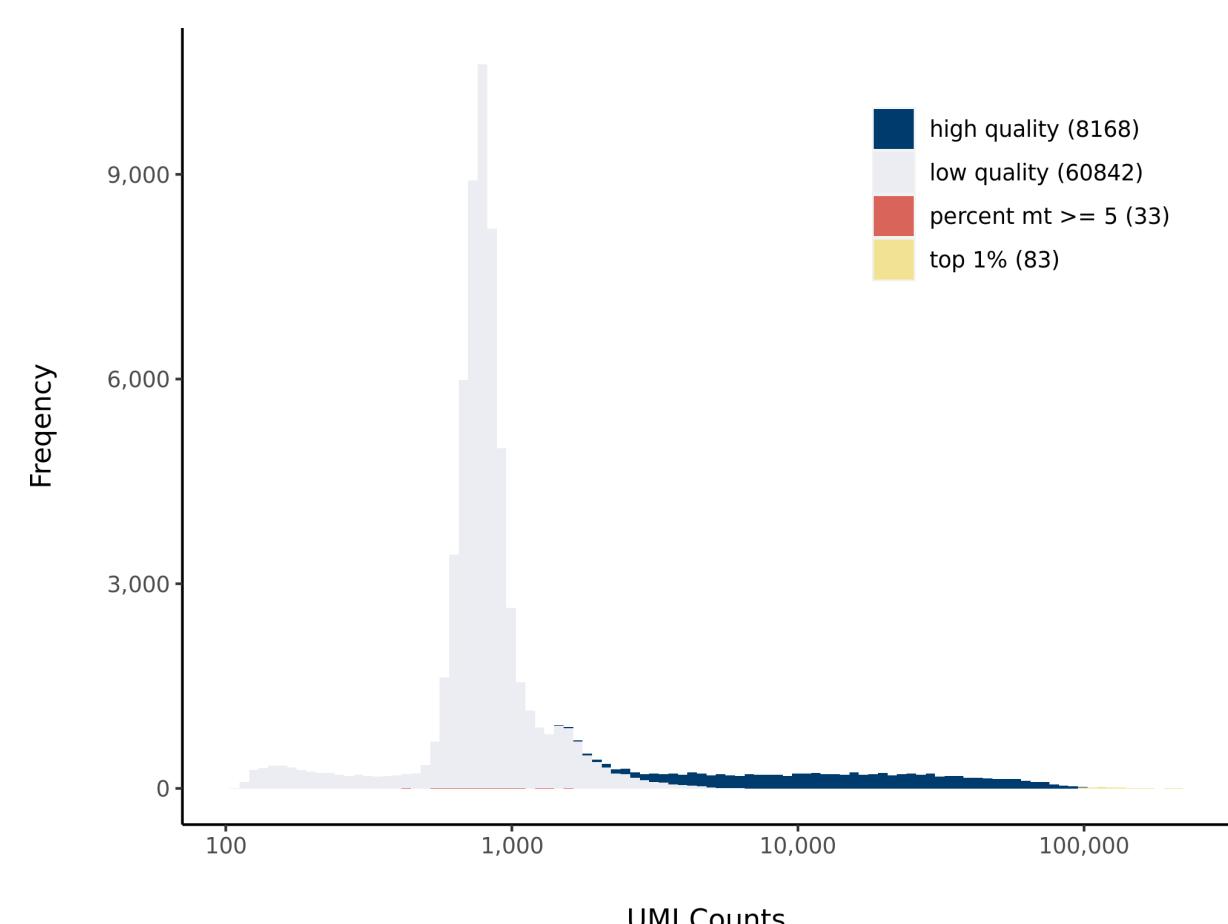
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

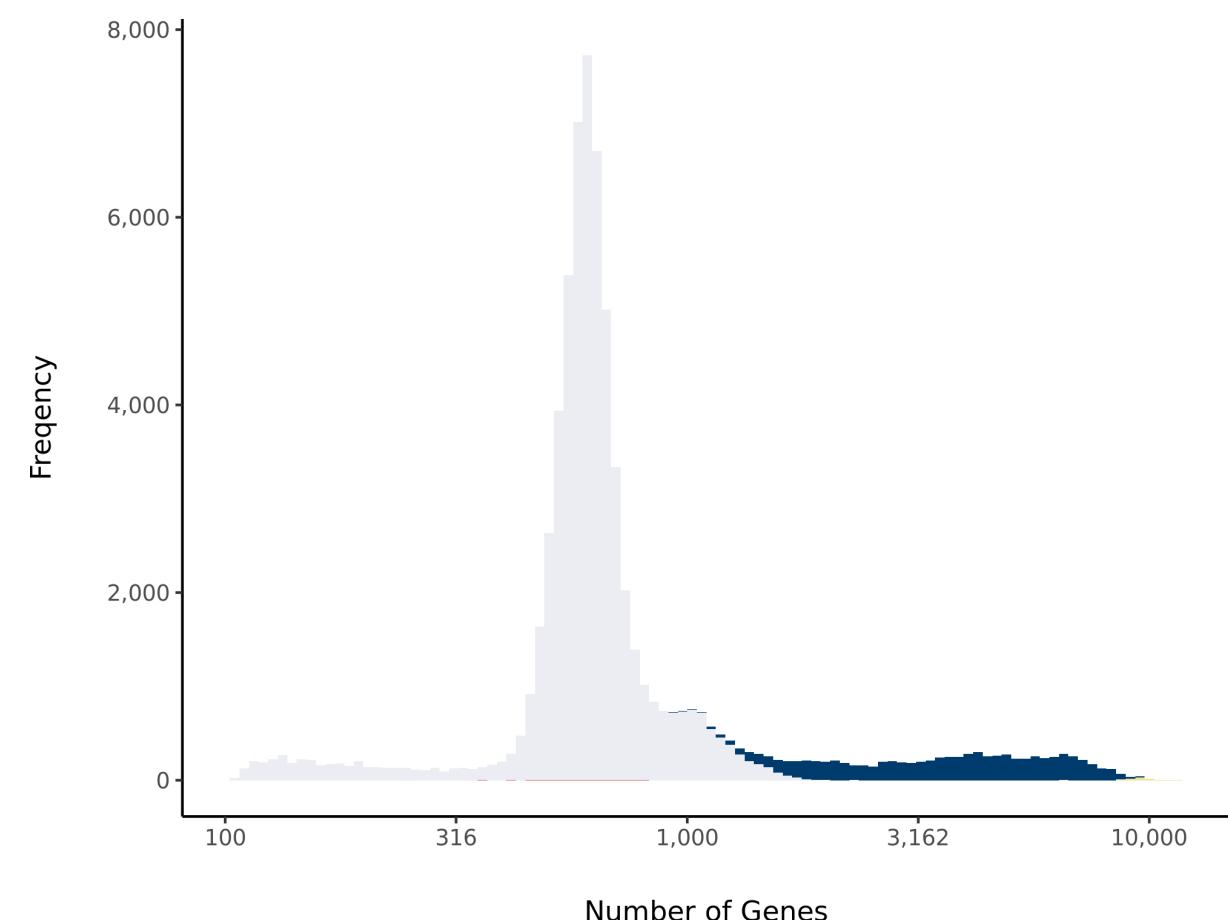
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

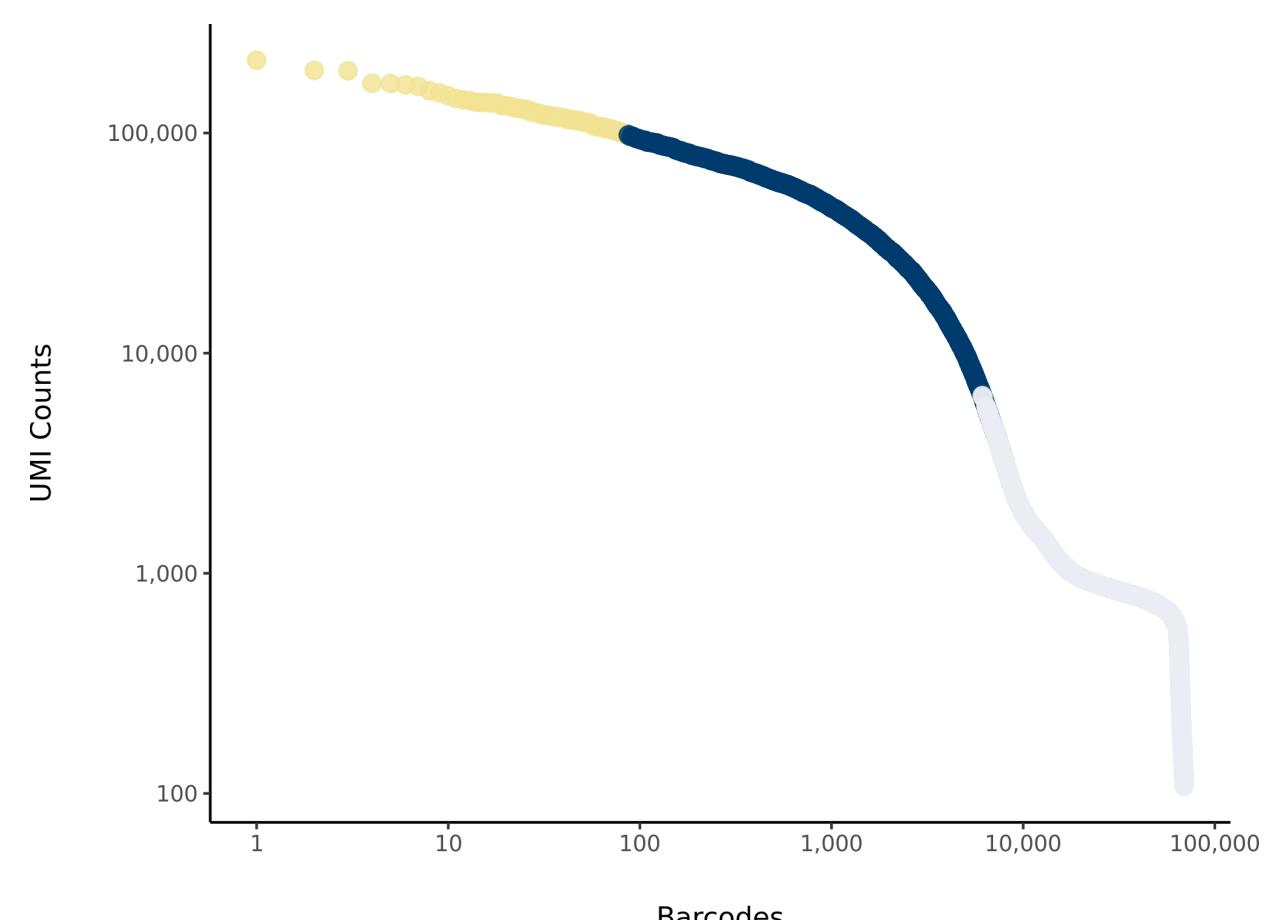
Estimated Number of High Quality Cell	8,168
High Quality Cell	11.82 %
Total UMI Counts in High Quality Cell	165,283,937
UMI Counts in High Quality Cell	72.54 %
Median UMI Counts per High Quality Cell	13,299.5
Median Genes per High Quality Cell	3,777.5
Total Genes Detected in High Quality Cell	25,625
Cell above Mitochondrial Expression Threshold	0.05 %
Estimated Doublet Rate in High Quality Cell	6.13 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	377,721,321
Reads Pseudoaligned	93.6 %
Reads on Whitelist	96.53 %
Total UMI Counts	227,847,045
Sequencing Technology	10xv2
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	pp1
Name	WT Plant Physiology 1
Source	Ryu et al. 2019, Plant Physiology
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	1
Target Cells	NA
Date	NA
Seq Run	NA

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

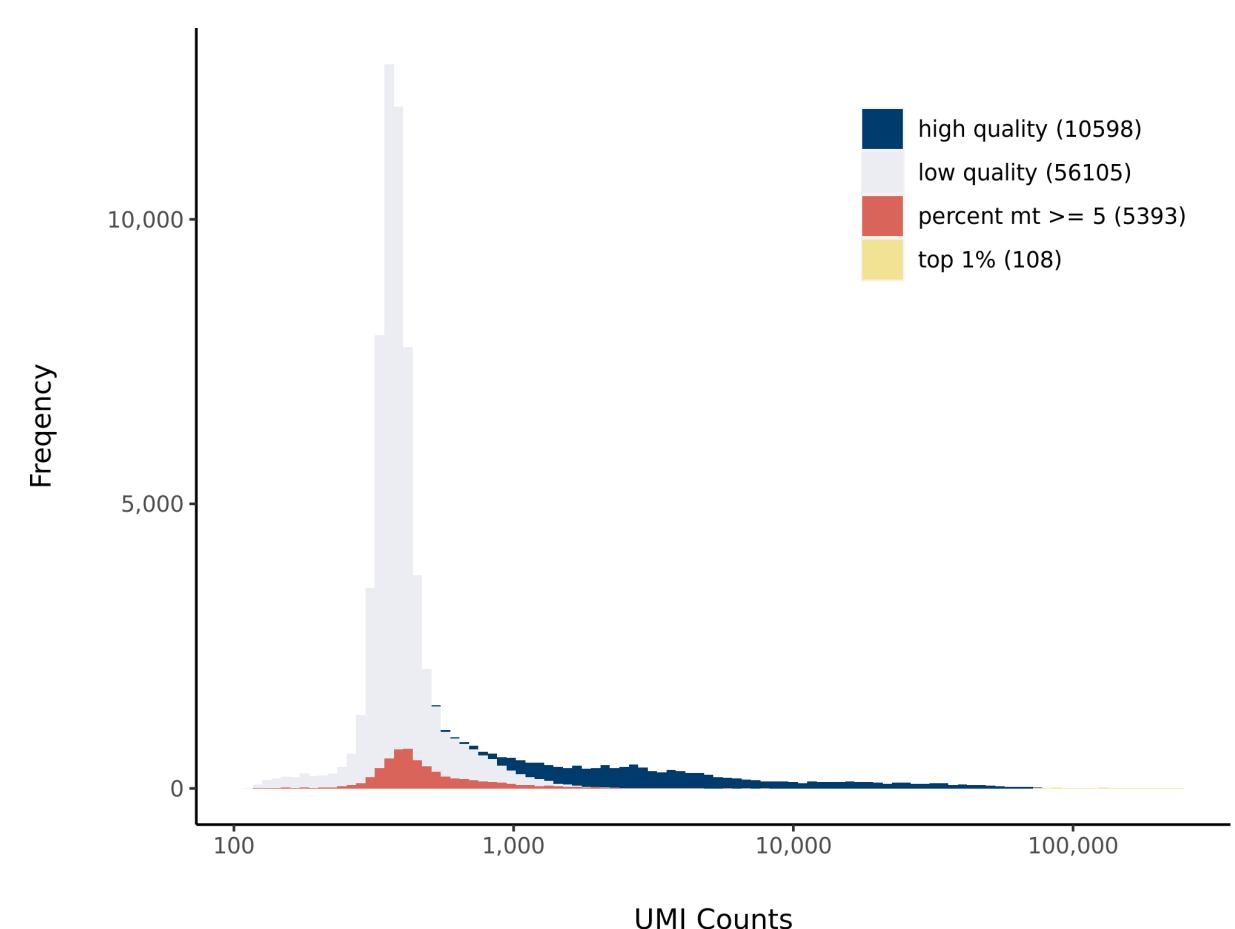
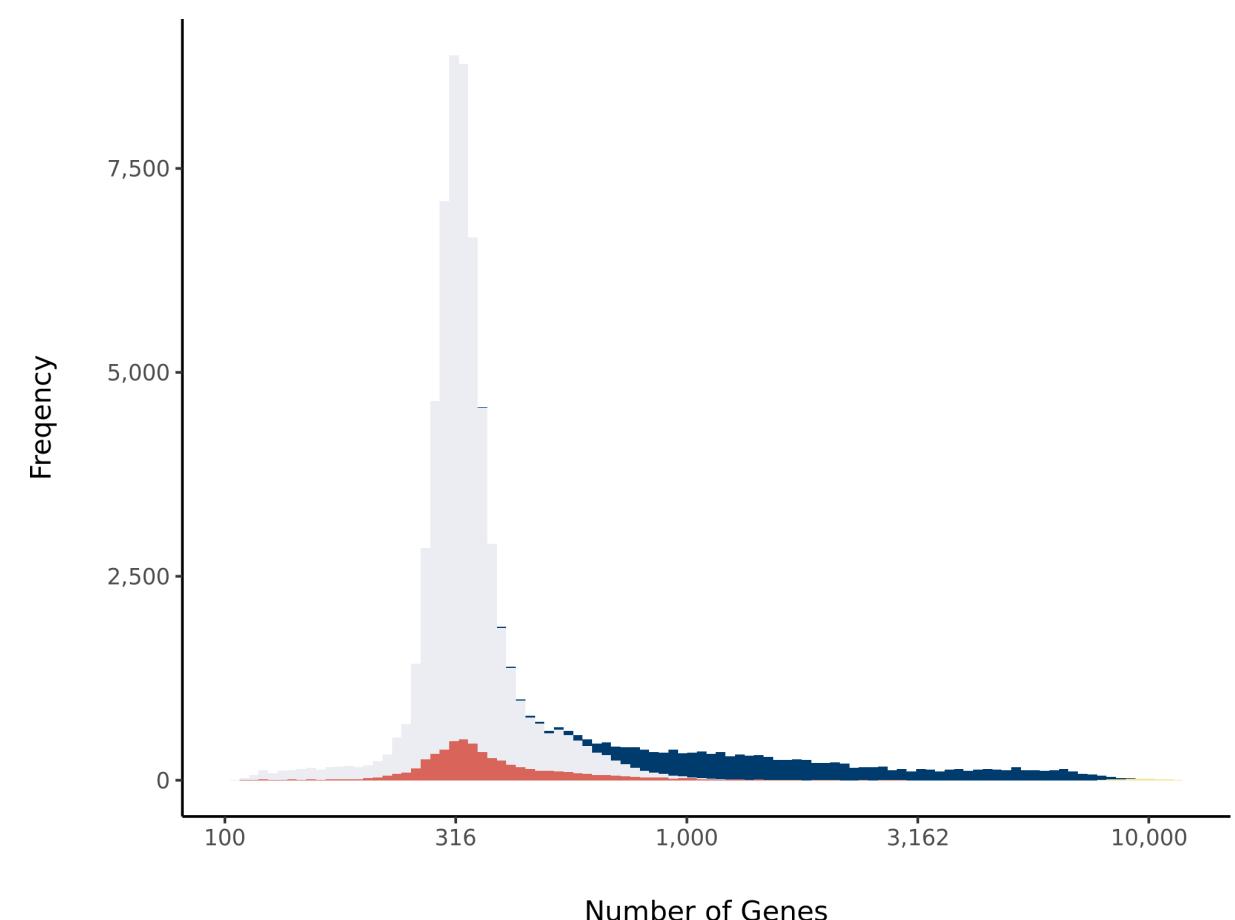
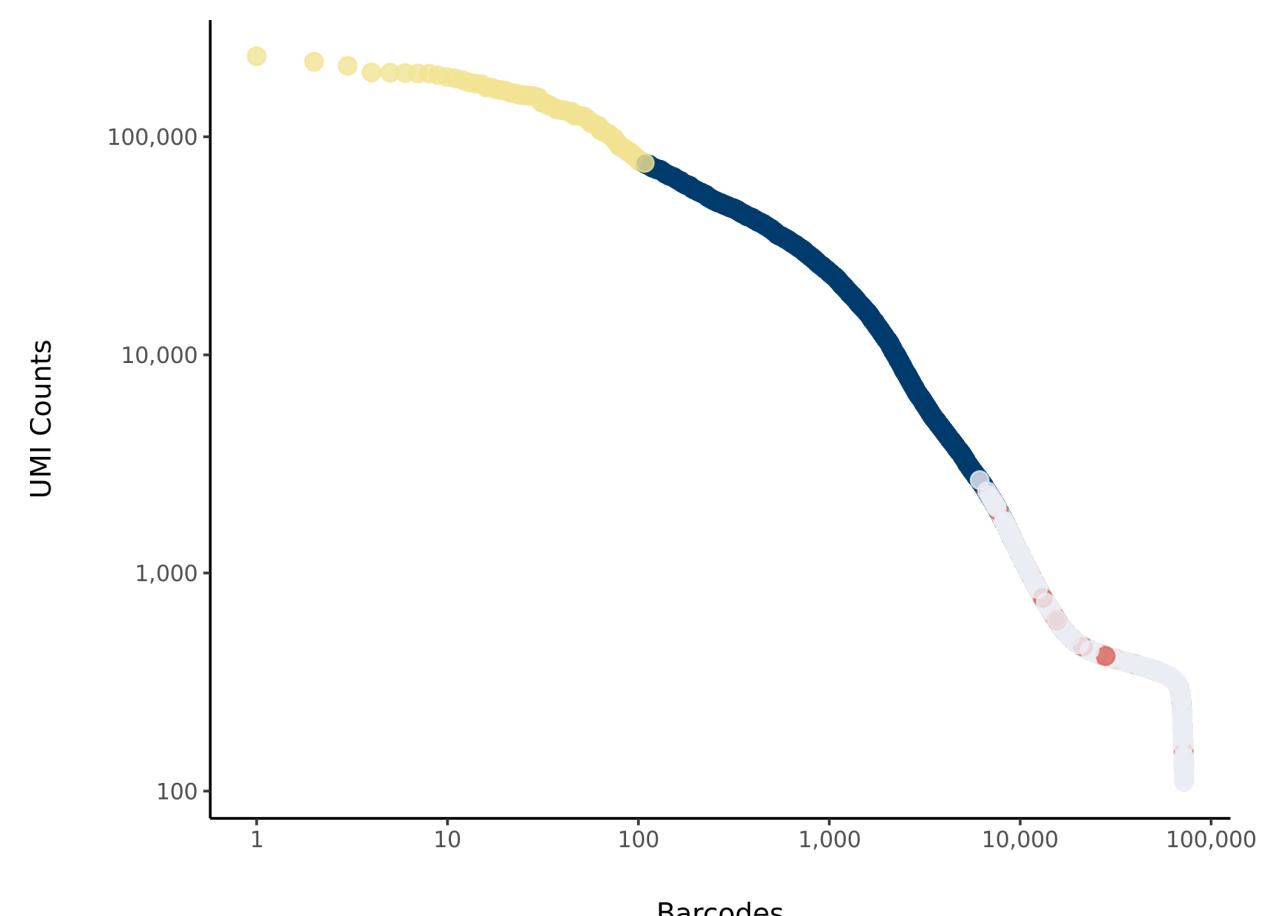
Estimated Number of High Quality Cell	10,598
High Quality Cell	14.68 %
Total UMI Counts in High Quality Cell	79,958,429
UMI Counts in High Quality Cell	67.1 %
Median UMI Counts per High Quality Cell	3,079
Median Genes per High Quality Cell	1,526
Total Genes Detected in High Quality Cell	24,624
Cell above Mitochondrial Expression Threshold	7.47 %
Estimated Doublet Rate in High Quality Cell	7.92 %

**Sequencing Stats**

Number of Reads Processed	255,953,705
Reads Pseudoaligned	92.4 %
Reads on Whitelist	95.01 %
Total UMI Counts	119,154,816
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	sc_1
Name	WT control
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	7_day
Timepoint	0
Rep	1
Target Cells	10,000
Date	2019-12-14
Seq Run	Nolan_6131

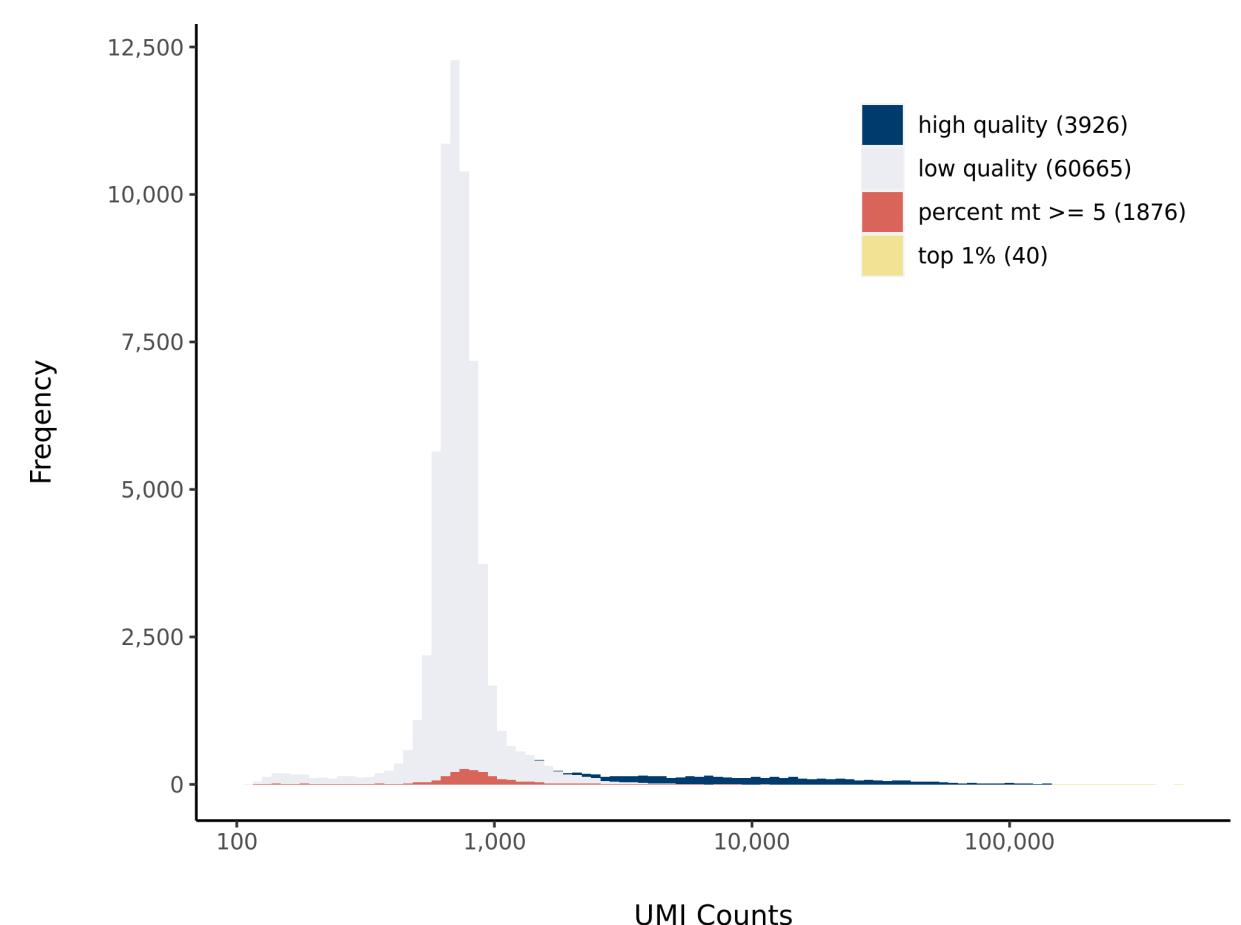
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

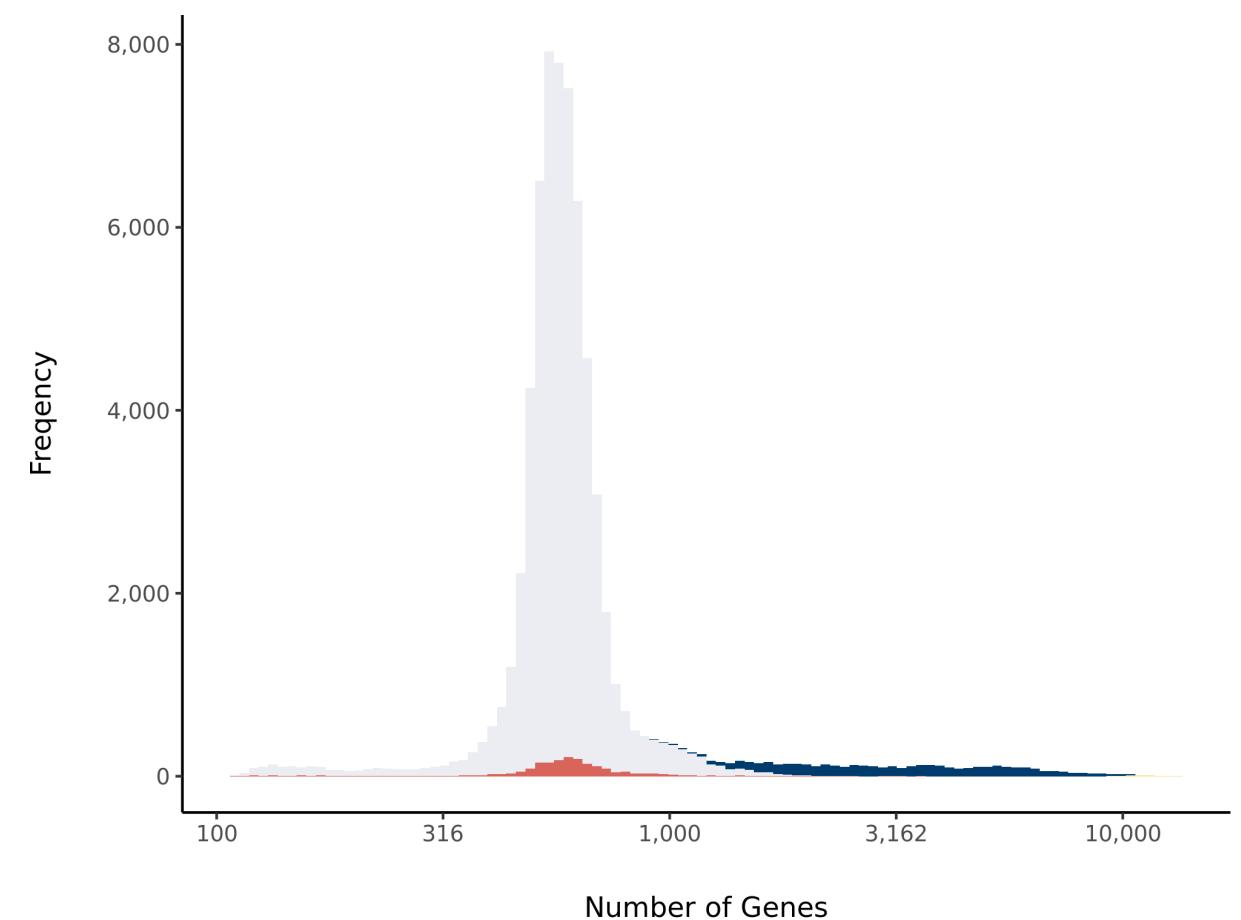
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

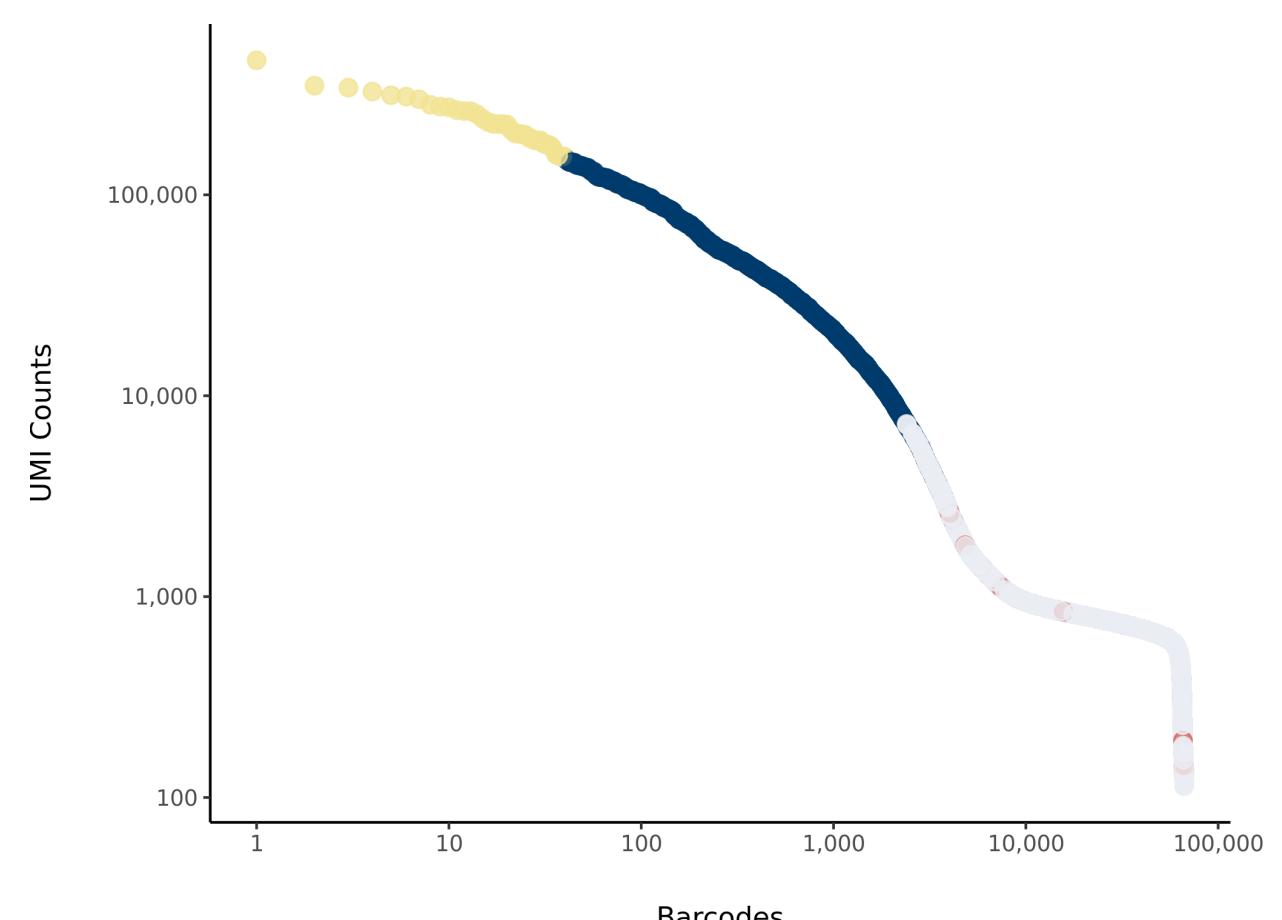
Estimated Number of High Quality Cell	3,926
High Quality Cell	5.9 %
Total UMI Counts in High Quality Cell	67,227,229
UMI Counts in High Quality Cell	54.25 %
Median UMI Counts per High Quality Cell	9,539
Median Genes per High Quality Cell	3,046
Total Genes Detected in High Quality Cell	24,999
Cell above Mitochondrial Expression Threshold	2.82 %
Estimated Doublet Rate in High Quality Cell	3.01 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	271,063,644
Reads Pseudoaligned	91.8 %
Reads on Whitelist	93.83 %
Total UMI Counts	123,926,323
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_9
Name	Rice 1 cm and Arabidopsis
Source	Benfey lab
Genotype	X.Kitaake; WT Col-0
Transgene	NA
Treatment	Untreated
Age	2_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2019-12-18
Seq Run	Nolan_6131

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

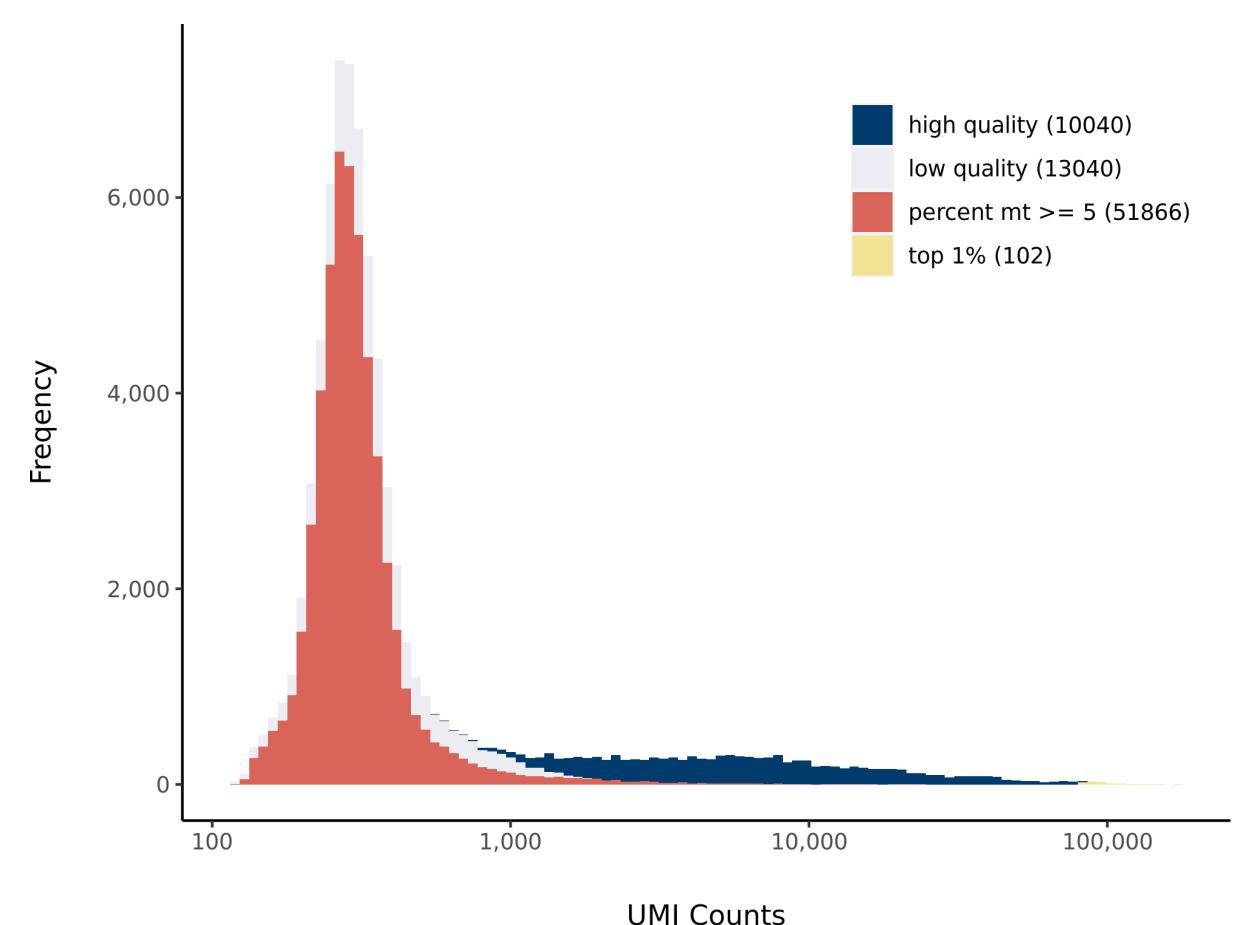
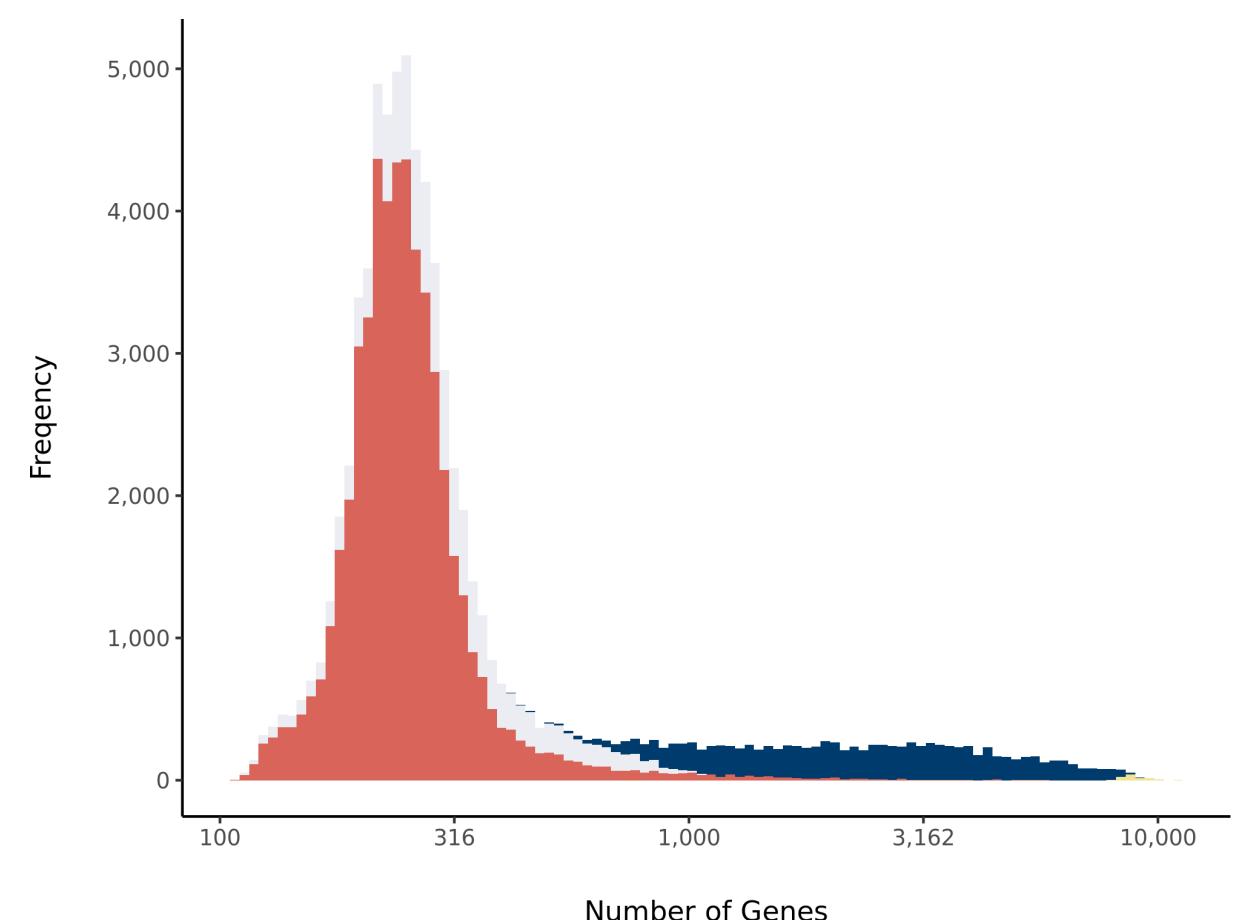
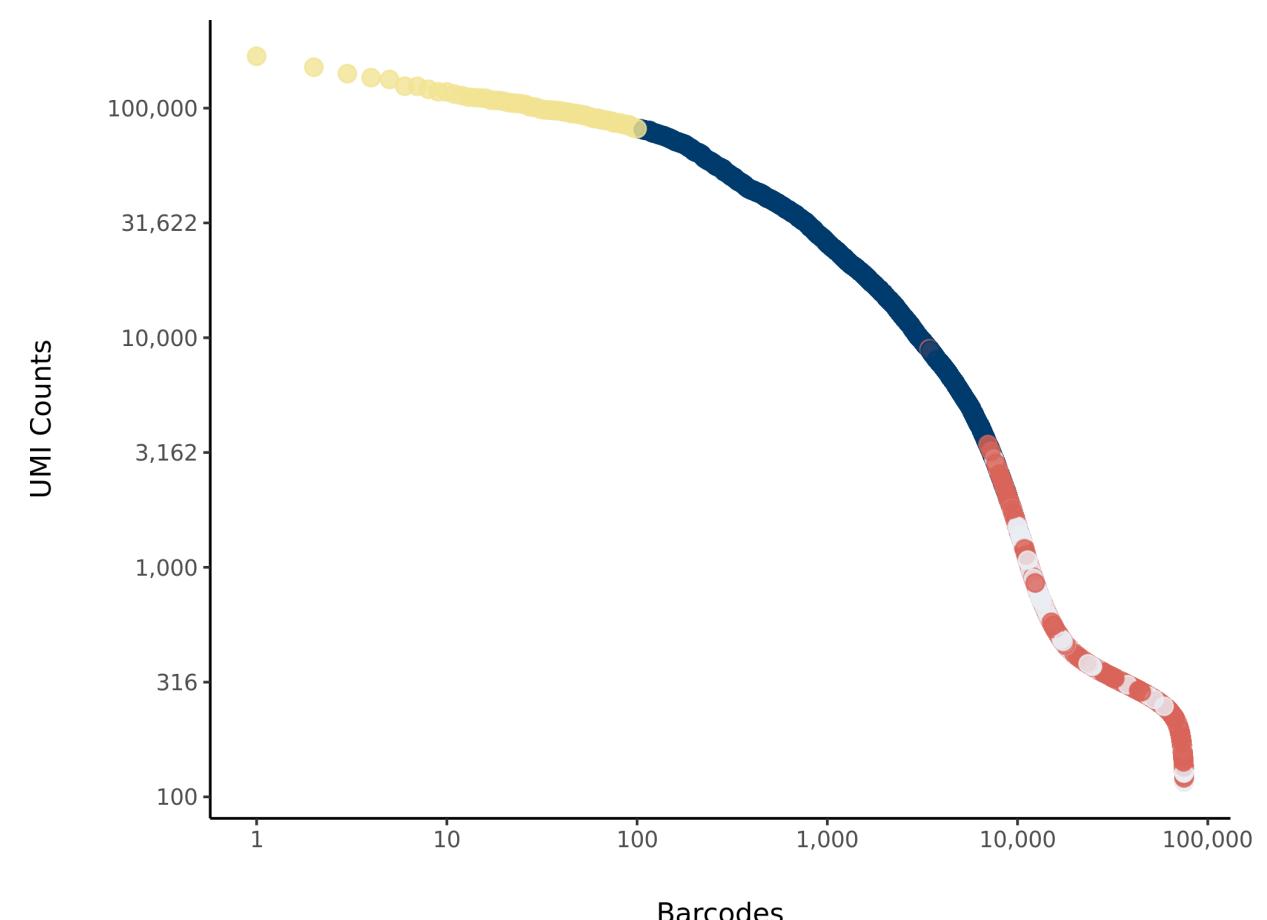
Estimated Number of High Quality Cell	10,040
High Quality Cell	13.38 %
Total UMI Counts in High Quality Cell	100,751,671
UMI Counts in High Quality Cell	75.06 %
Median UMI Counts per High Quality Cell	5,553
Median Genes per High Quality Cell	2,279
Total Genes Detected in High Quality Cell	25,502
Cell above Mitochondrial Expression Threshold	69.11 %
Estimated Doublet Rate in High Quality Cell	7.51 %

**Sequencing Stats**

Number of Reads Processed	300,927,223
Reads Pseudoaligned	90.4 %
Reads on Whitelist	92.36 %
Total UMI Counts	134,231,998
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	sc_10
Name	Rice 1 cm and Arabidopsis
Source	Benfey lab
Genotype	X.Kitaake; WT Col-0
Transgene	NA
Treatment	Untreated
Age	2_day
Timepoint	NA
Rep	NA
Target Cells	20,000
Date	2019-12-18
Seq Run	Nolan_6131

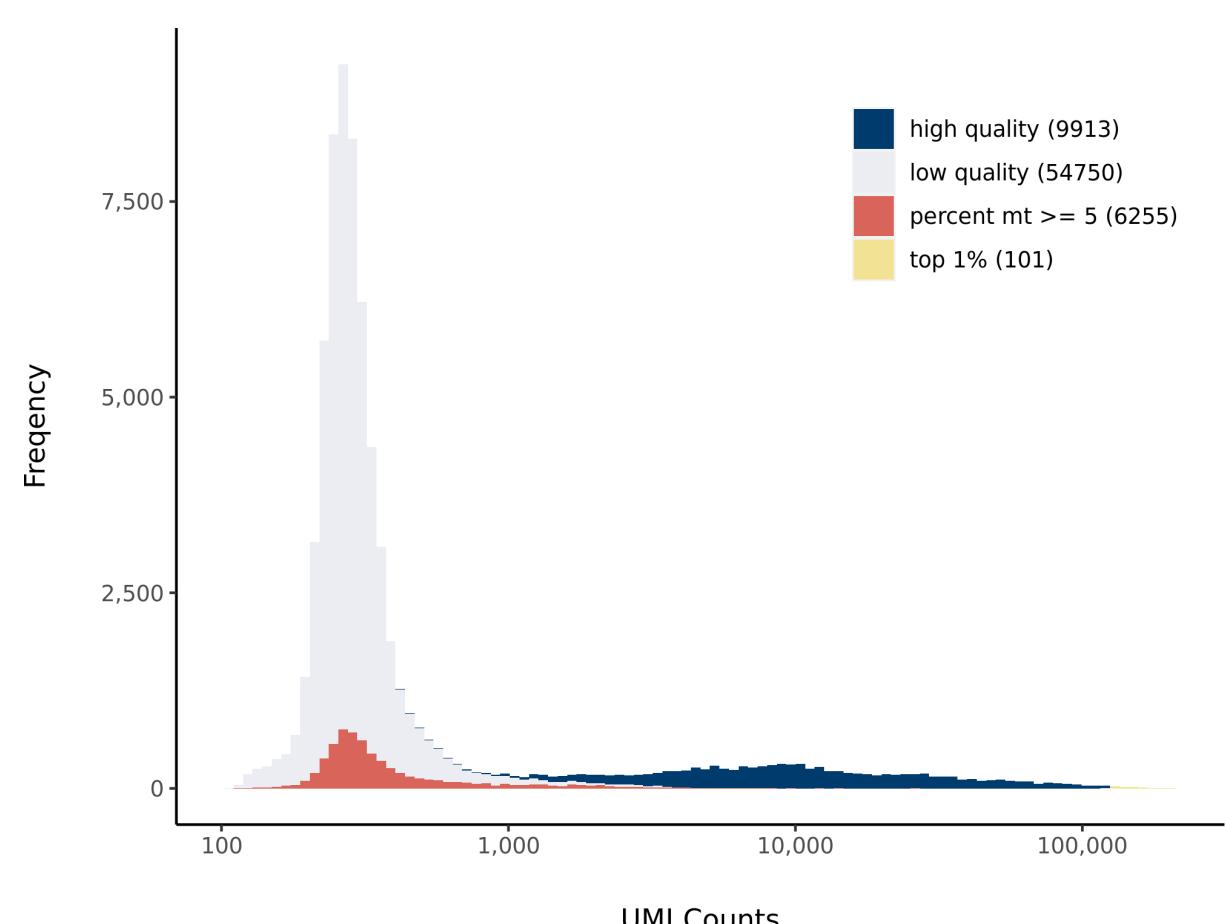
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

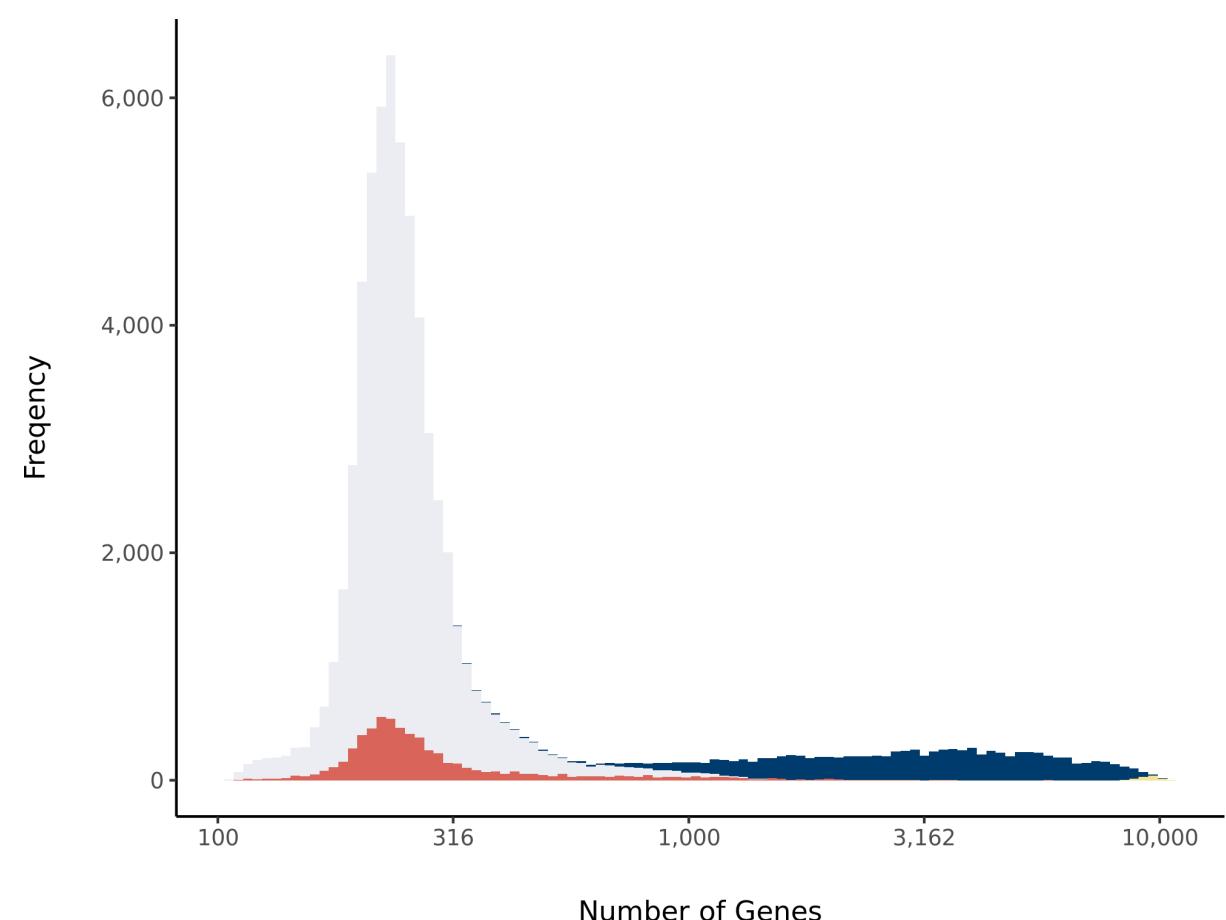
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

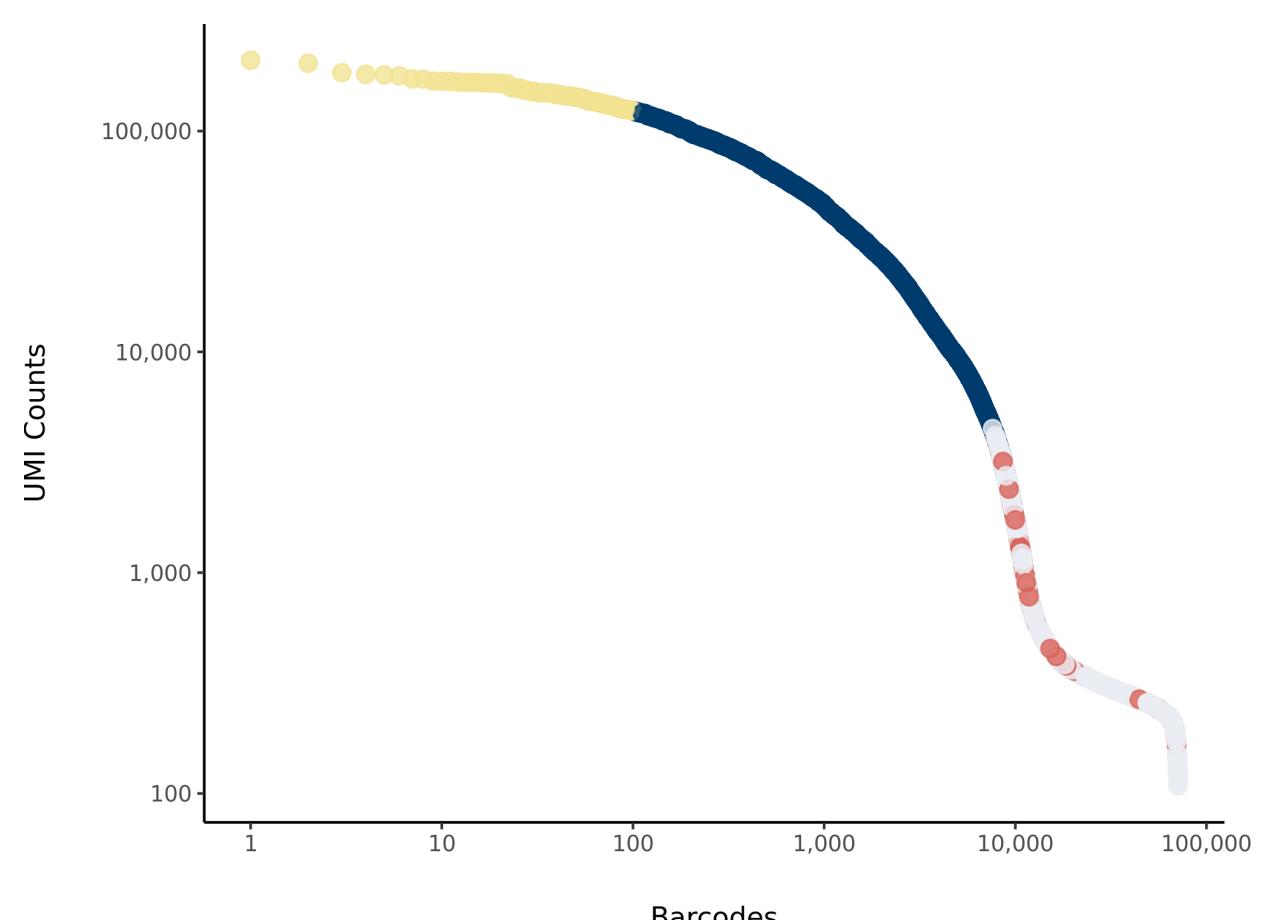
Estimated Number of High Quality Cell	9,913
High Quality Cell	13.96 %
Total UMI Counts in High Quality Cell	168,126,295
UMI Counts in High Quality Cell	82.76 %
Median UMI Counts per High Quality Cell	9,146
Median Genes per High Quality Cell	3,050
Total Genes Detected in High Quality Cell	25,040
Cell above Mitochondrial Expression Threshold	8.81 %
Estimated Doublet Rate in High Quality Cell	7.42 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	329,949,998
Reads Pseudoaligned	93.6 %
Reads on Whitelist	95.21 %
Total UMI Counts	203,138,562
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_11
Name	WT Col-0 untreated
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2019-12-20
Seq Run	Nolan_6131

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

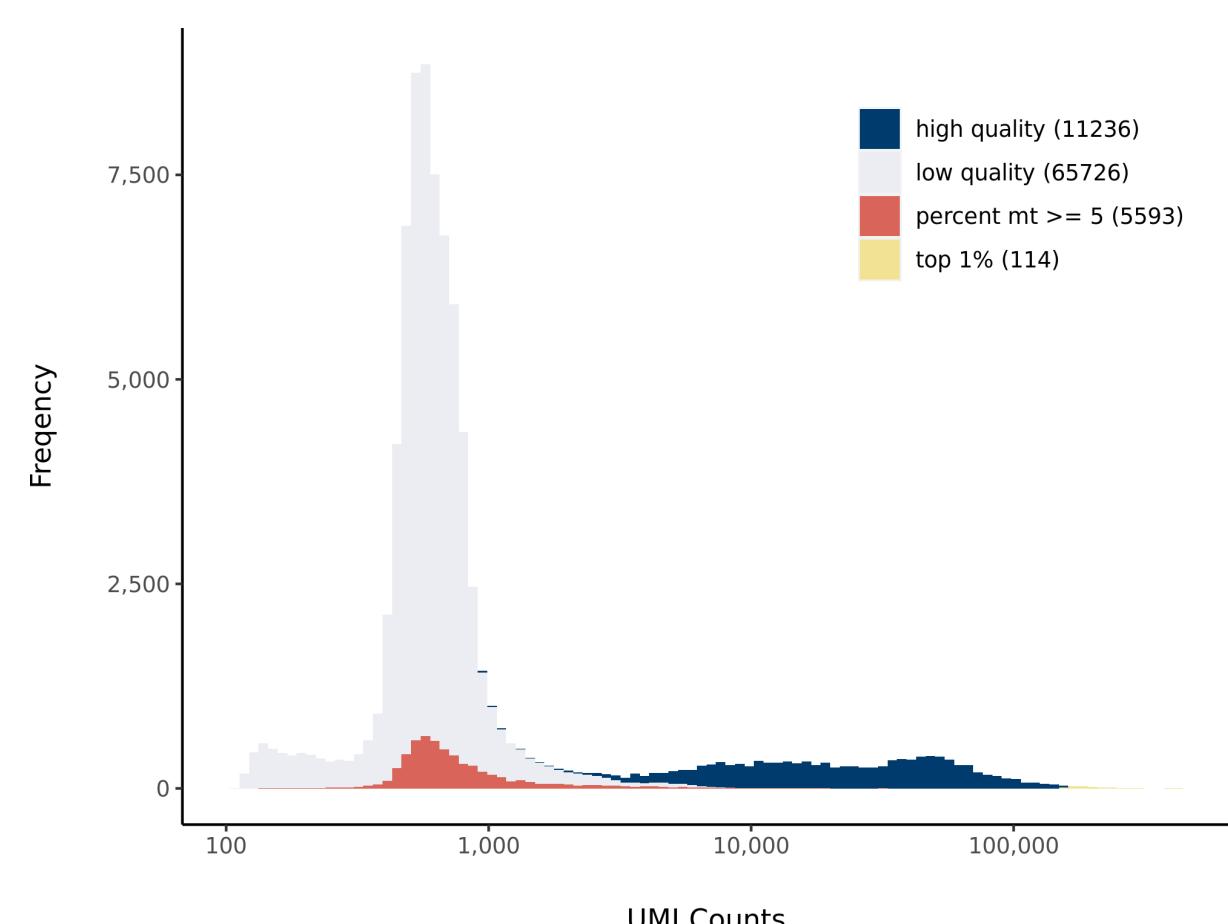
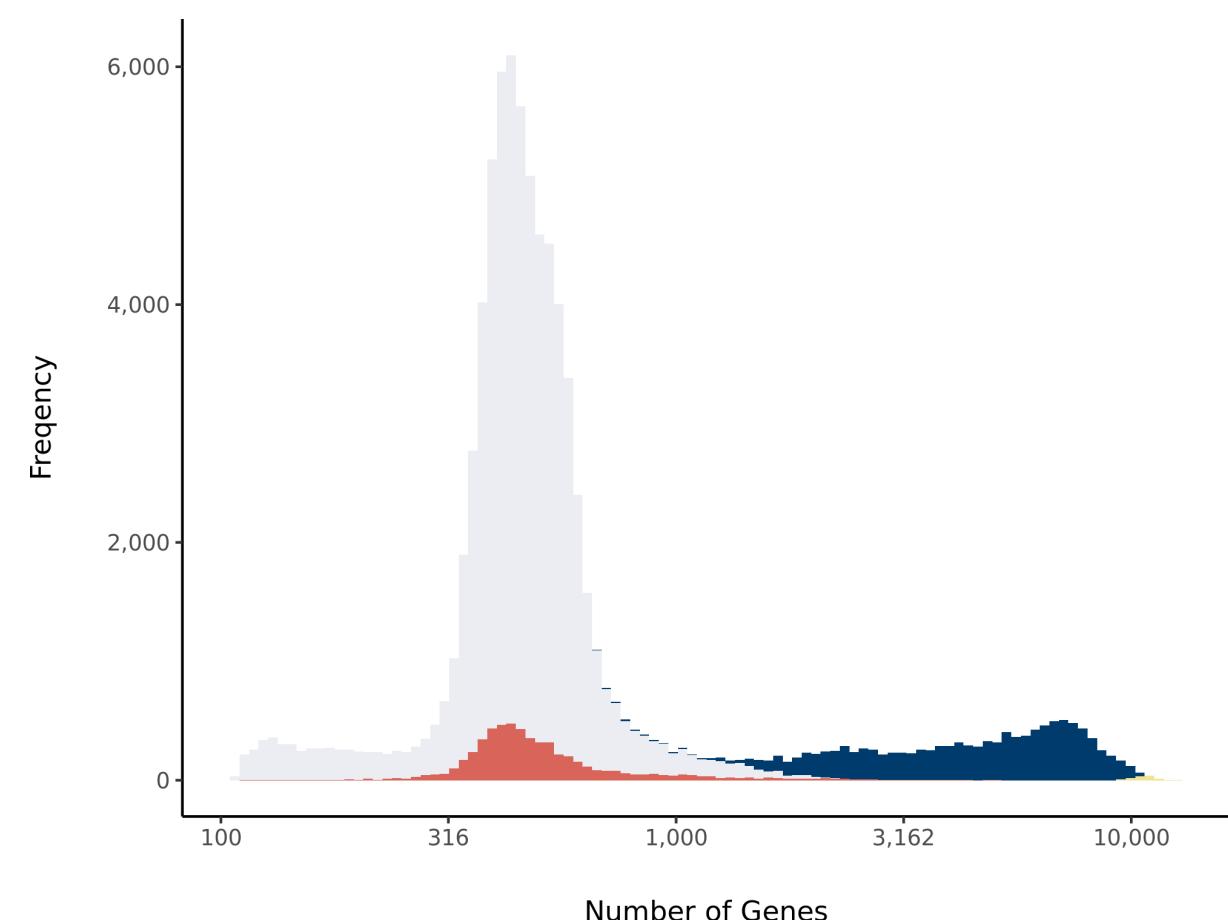
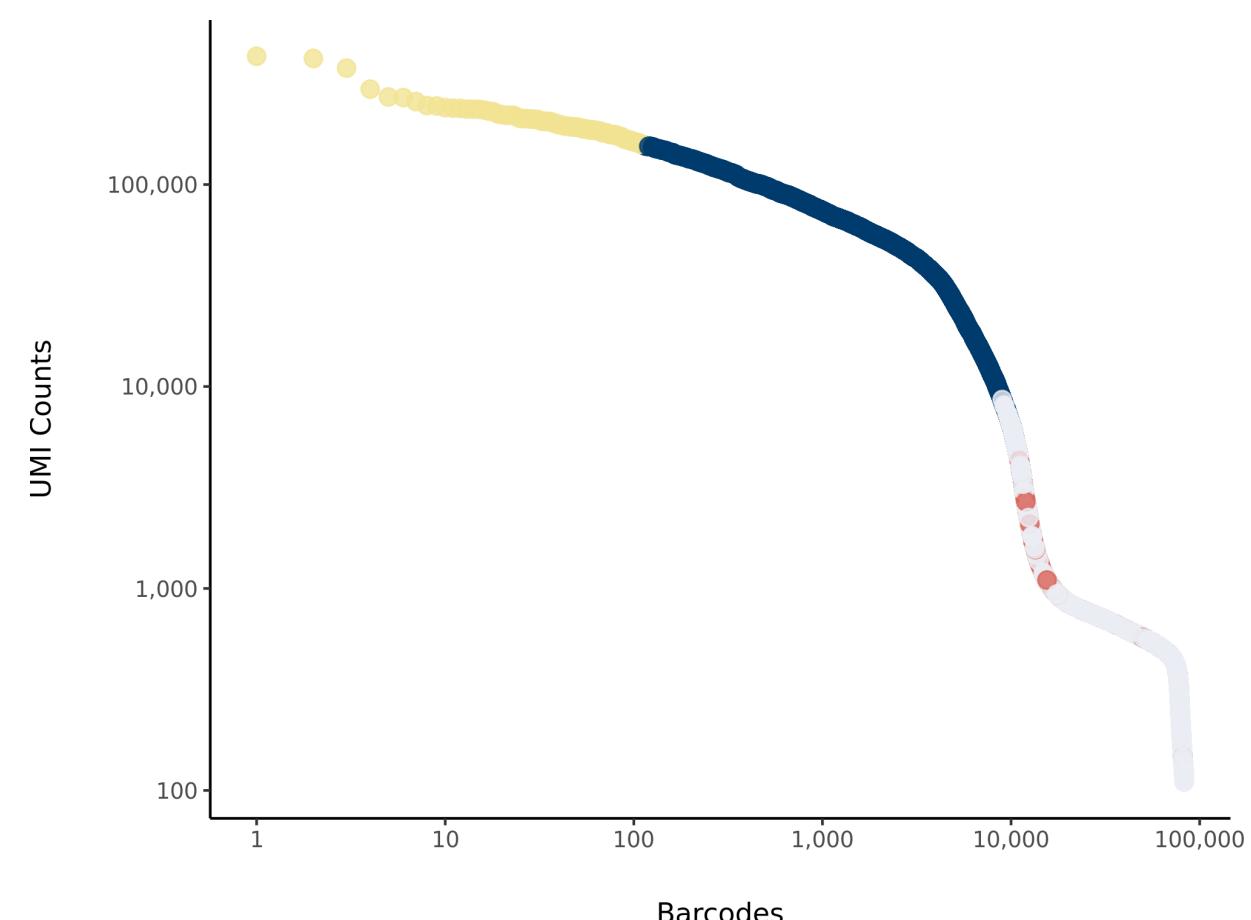
Estimated Number of High Quality Cell	11,236
High Quality Cell	13.59 %
Total UMI Counts in High Quality Cell	346,882,014
UMI Counts in High Quality Cell	83.04 %
Median UMI Counts per High Quality Cell	20,788.5
Median Genes per High Quality Cell	4,774
Total Genes Detected in High Quality Cell	26,018
Cell above Mitochondrial Expression Threshold	6.77 %
Estimated Doublet Rate in High Quality Cell	8.39 %

**Sequencing Stats**

Number of Reads Processed	841,129,261
Reads Pseudoaligned	93.7 %
Reads on Whitelist	96.04 %
Total UMI Counts	417,731,033
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	sc_12
Name	WT Col-0 untreated
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2019-12-20
Seq Run	Nolan_6131;Shahan_6158

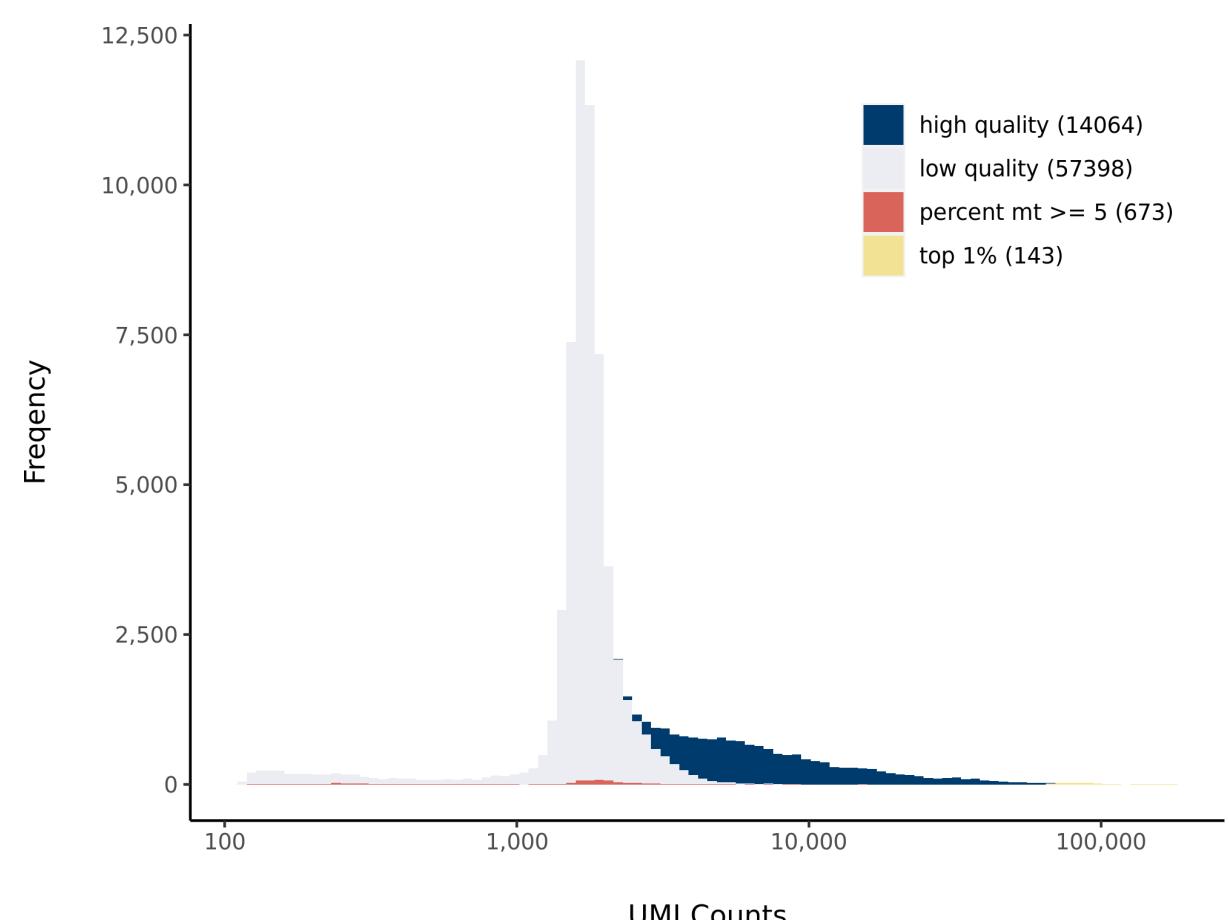
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

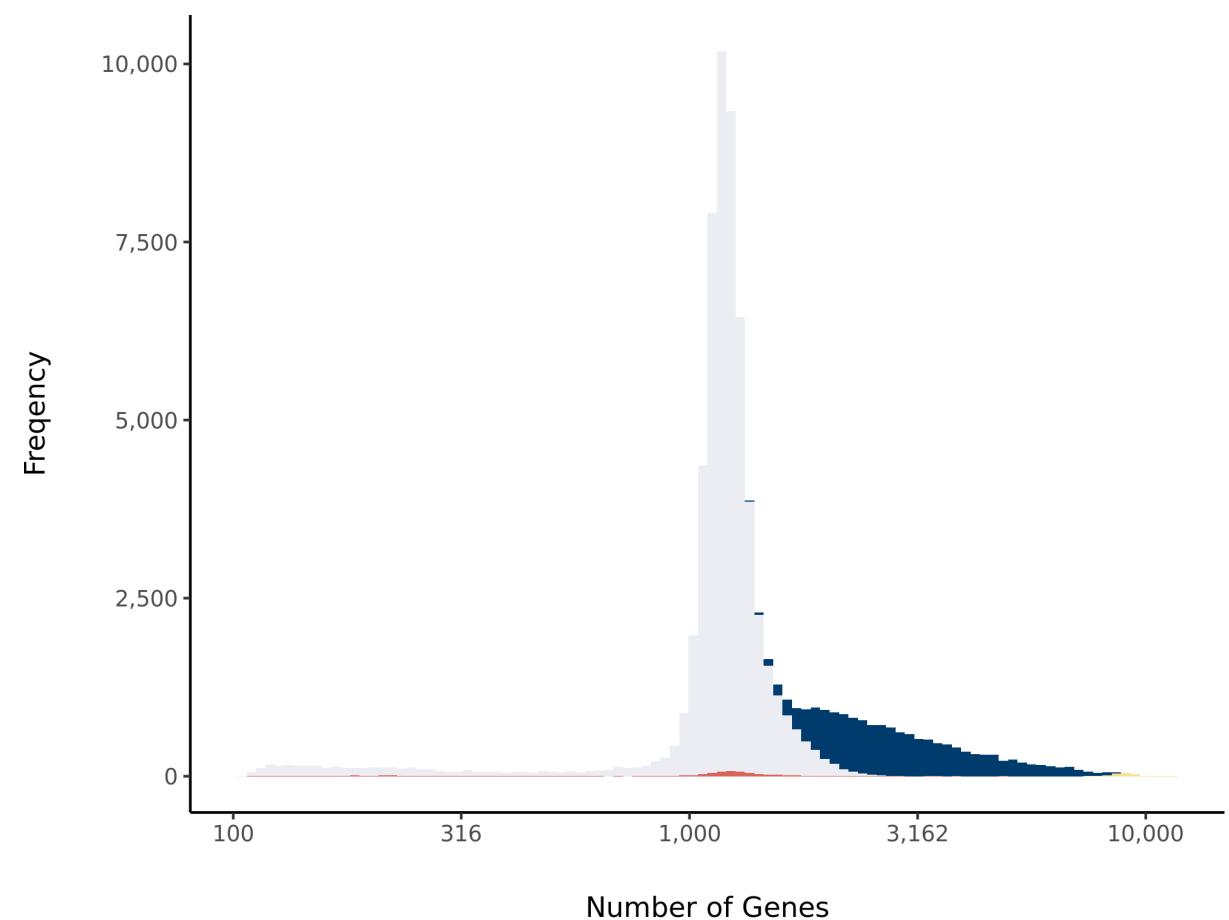
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

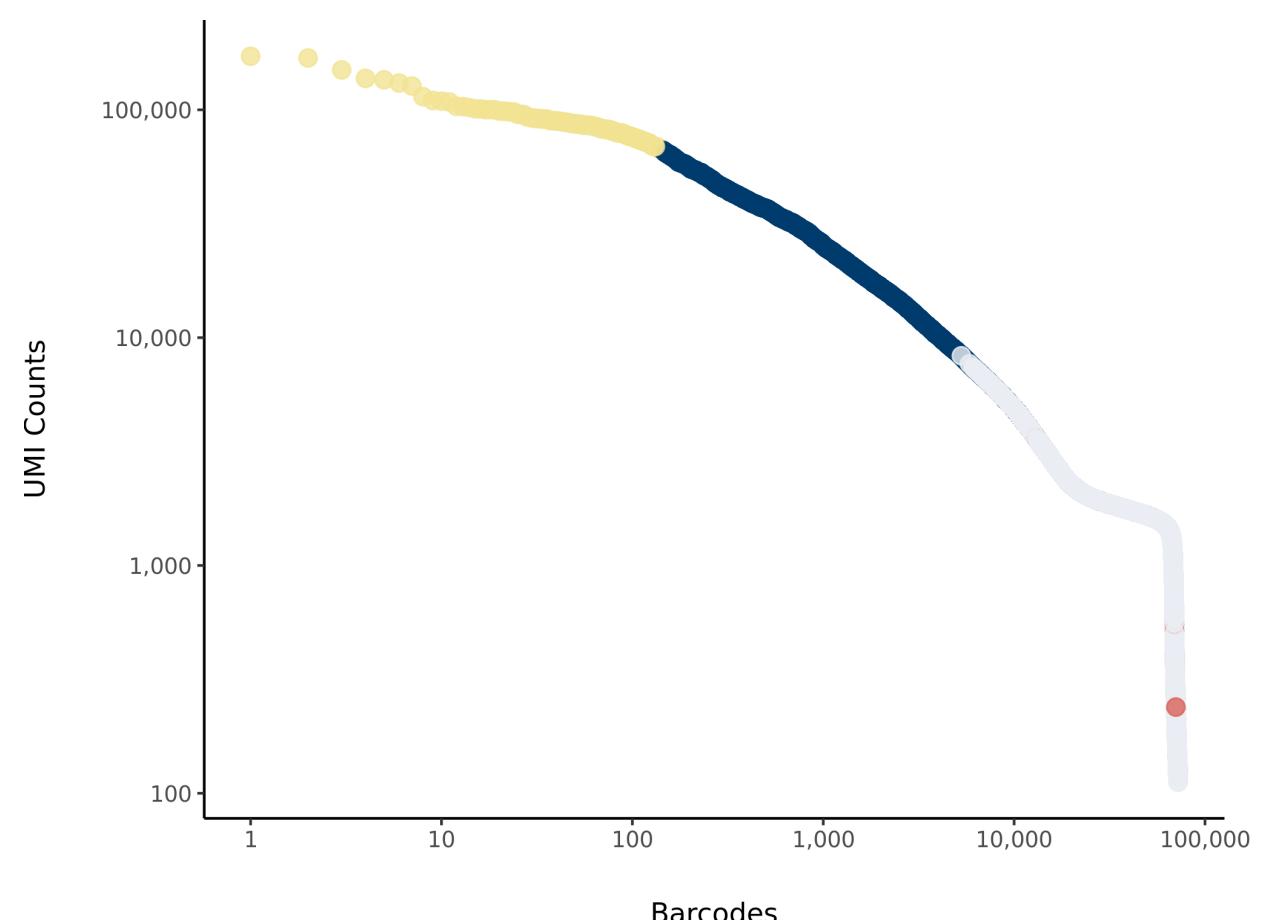
Estimated Number of High Quality Cell	14,064
High Quality Cell	19.46 %
Total UMI Counts in High Quality Cell	135,176,770
UMI Counts in High Quality Cell	54.36 %
Median UMI Counts per High Quality Cell	6,497
Median Genes per High Quality Cell	2,711
Total Genes Detected in High Quality Cell	25,325
Cell above Mitochondrial Expression Threshold	0.93 %
Estimated Doublet Rate in High Quality Cell	10.47 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	327,662,124
Reads Pseudoaligned	94.7 %
Reads on Whitelist	96.89 %
Total UMI Counts	248,691,560
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_20
Name	WT Col-0_RS1
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Shahan_6177

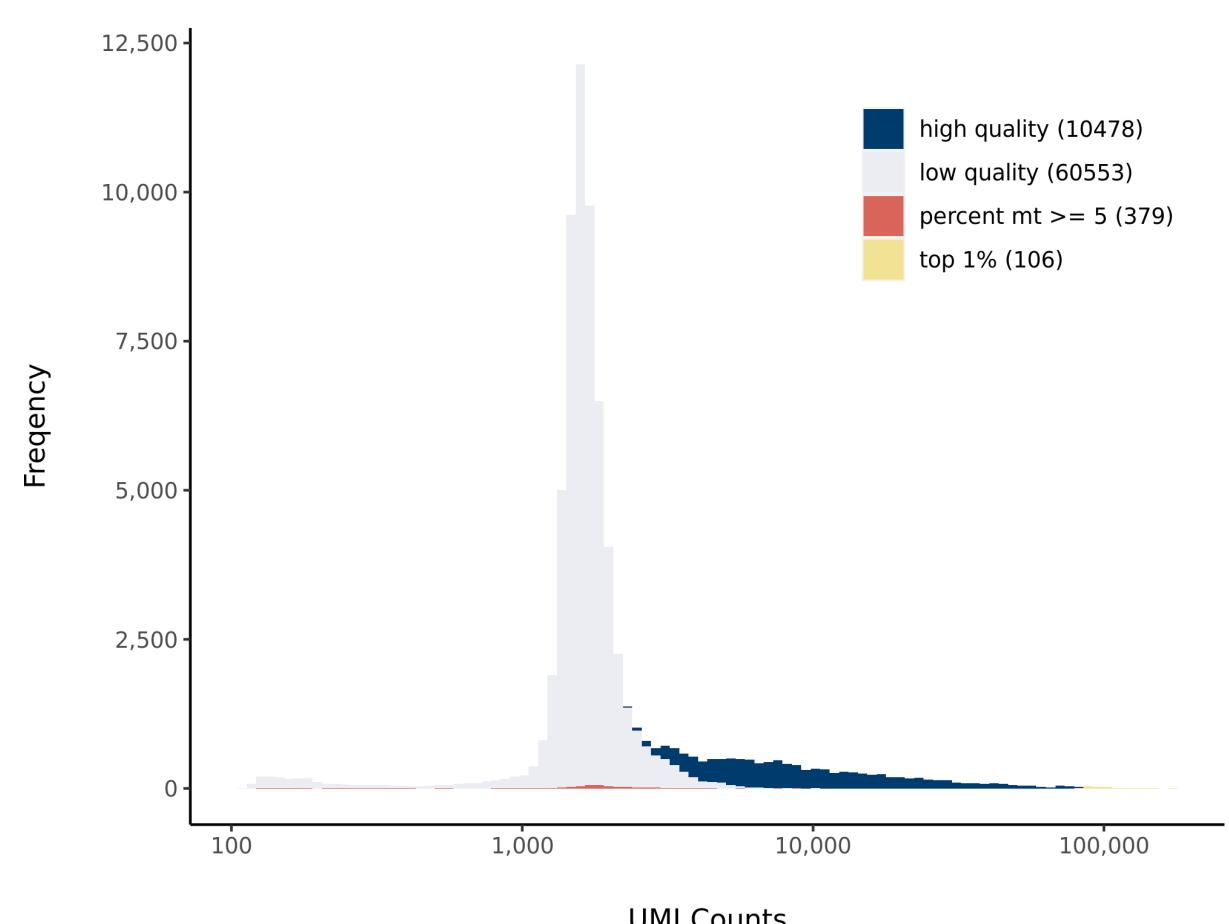
**Barcode Rank Plot**

**Parameters**

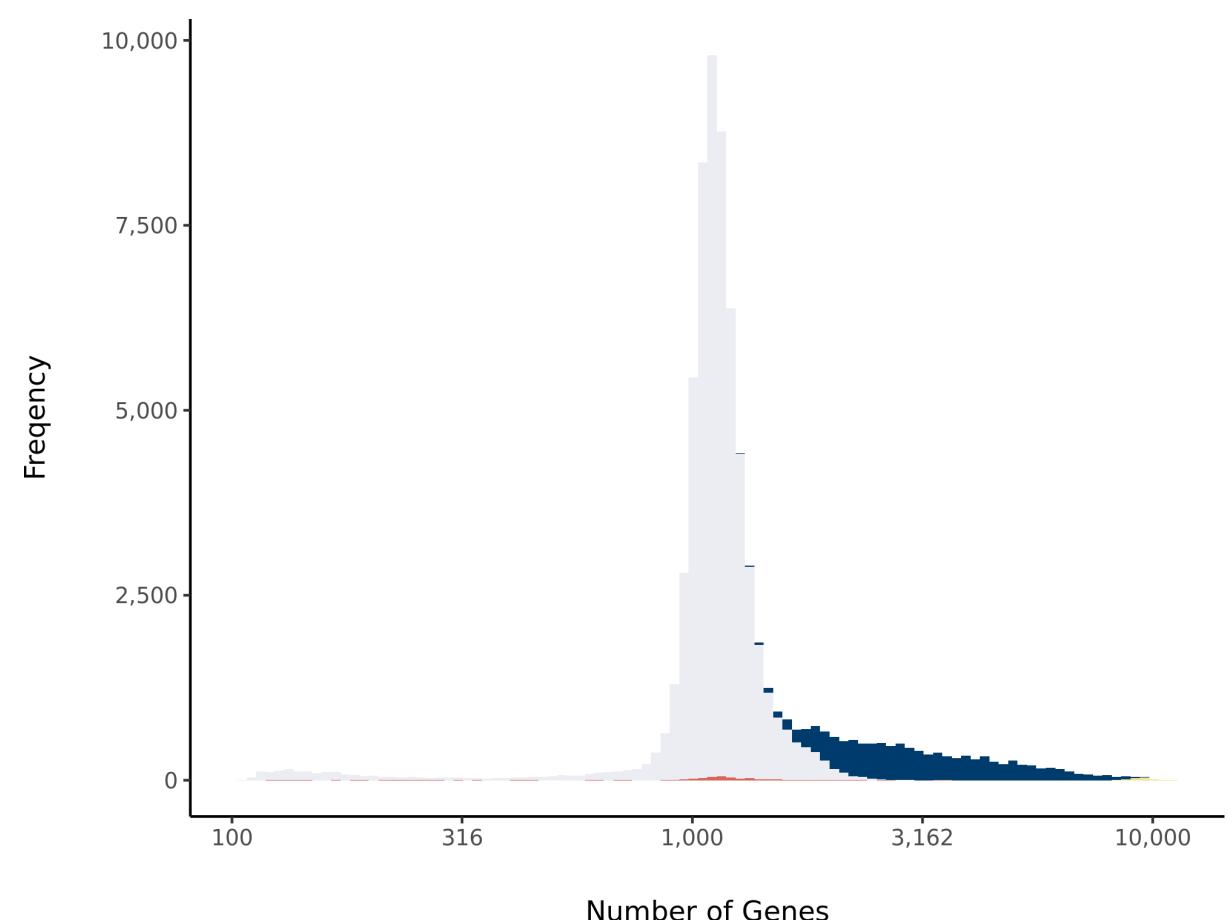
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

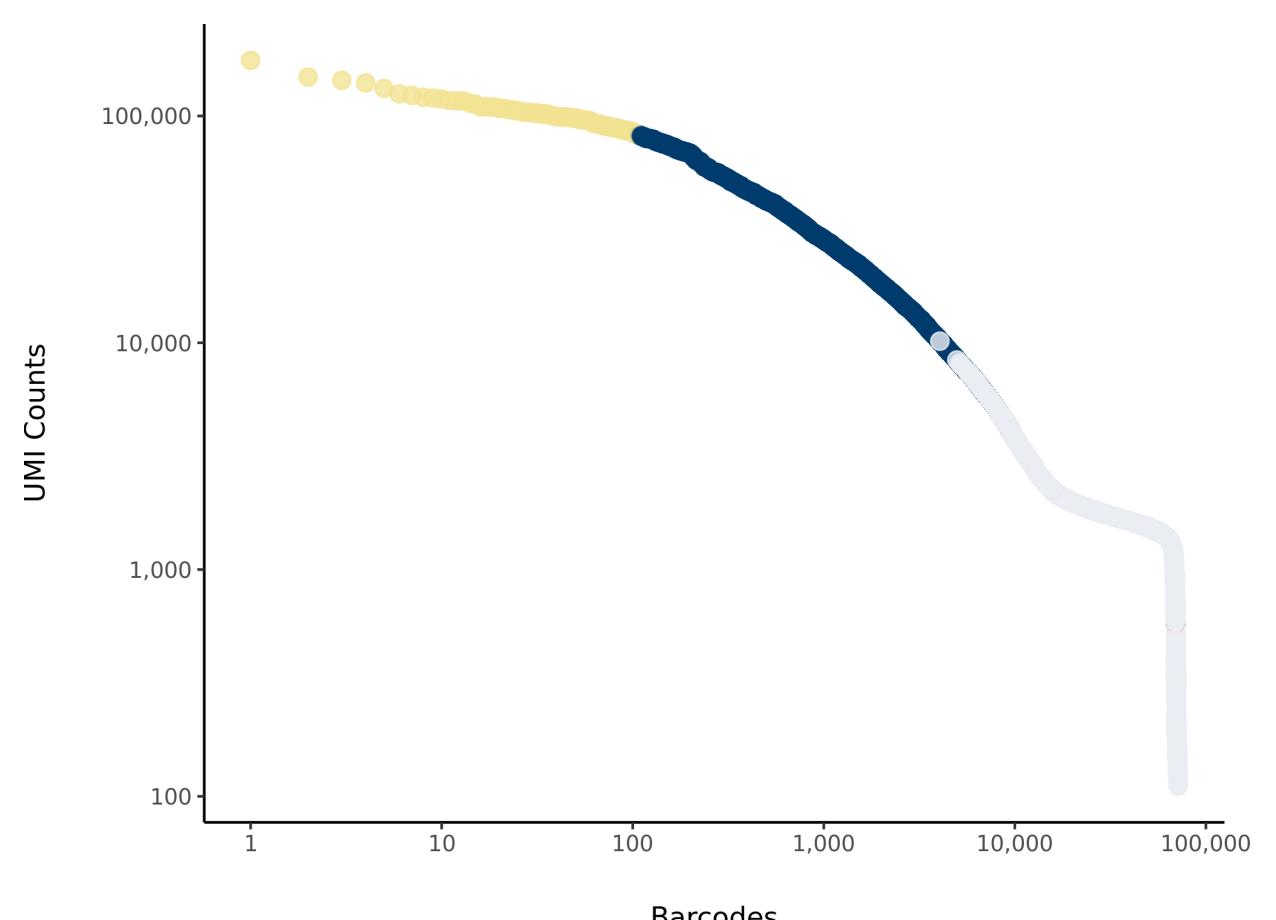
Estimated Number of High Quality Cell	10,478
High Quality Cell	14.65 %
Total UMI Counts in High Quality Cell	128,289,748
UMI Counts in High Quality Cell	53.13 %
Median UMI Counts per High Quality Cell	7,833.5
Median Genes per High Quality Cell	2,899
Total Genes Detected in High Quality Cell	25,296
Cell above Mitochondrial Expression Threshold	0.53 %
Estimated Doublet Rate in High Quality Cell	7.83 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	318,494,791
Reads Pseudoaligned	95.2 %
Reads on Whitelist	96.95 %
Total UMI Counts	241,458,602
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_21
Name	WT Col-0_RS2
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Shahan_6177

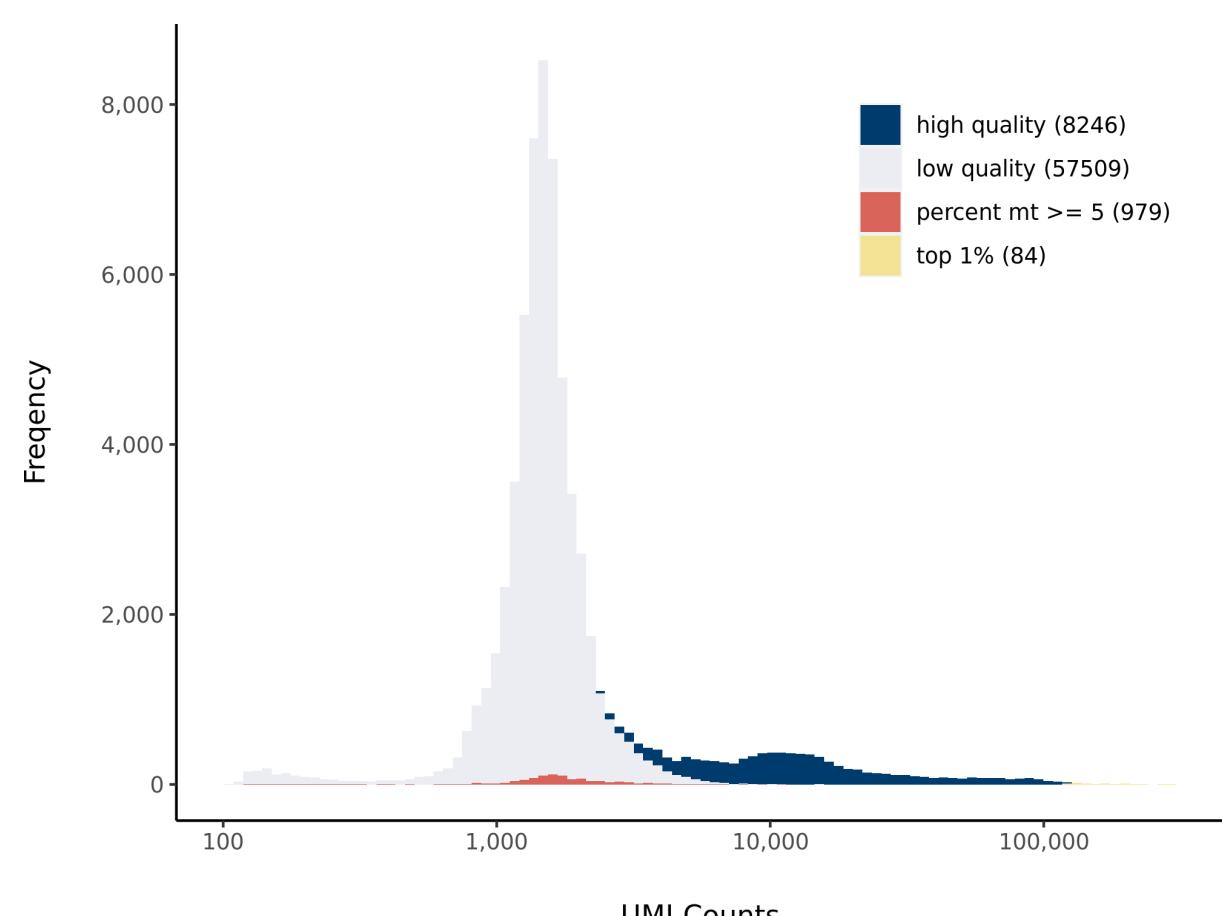
**Barcode Rank Plot**

**Parameters**

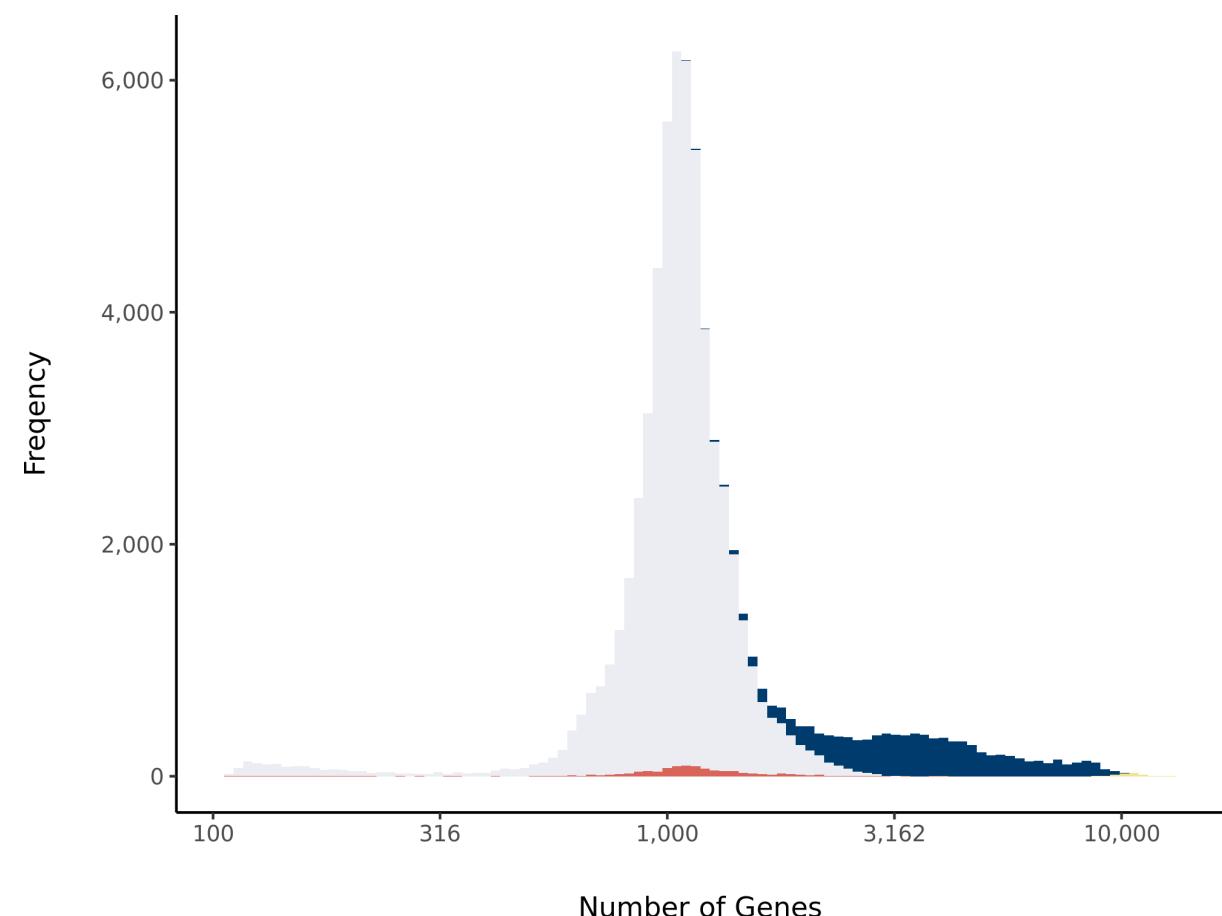
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

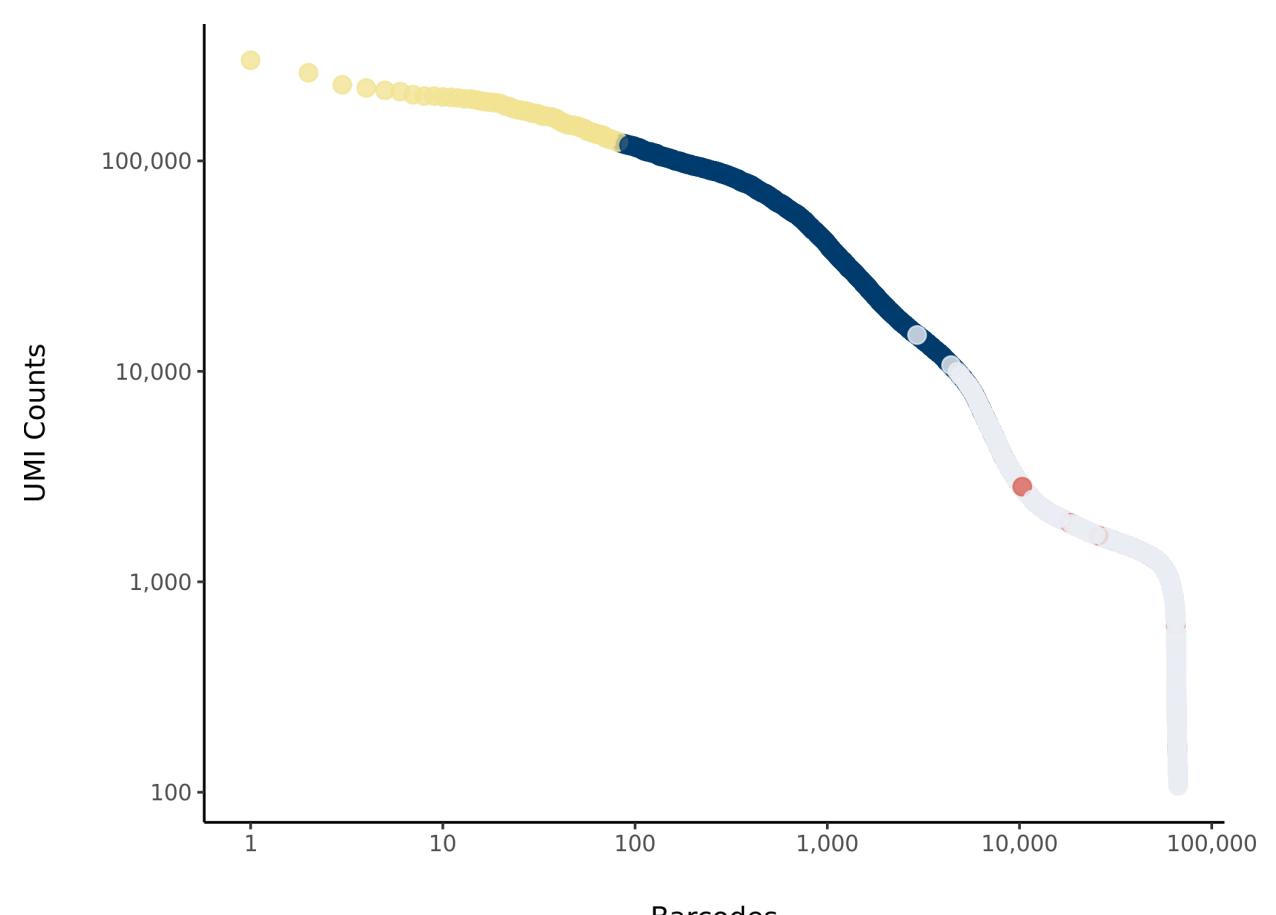
Estimated Number of High Quality Cell	8,246
High Quality Cell	12.34 %
Total UMI Counts in High Quality Cell	151,165,418
UMI Counts in High Quality Cell	59.19 %
Median UMI Counts per High Quality Cell	11,167
Median Genes per High Quality Cell	3,465
Total Genes Detected in High Quality Cell	25,744
Cell above Mitochondrial Expression Threshold	1.47 %
Estimated Doublet Rate in High Quality Cell	6.19 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	357,488,578
Reads Pseudoaligned	94.6 %
Reads on Whitelist	97.17 %
Total UMI Counts	255,403,407
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_25
Name	scr-4_1
Source	Benfey lab
Genotype	scr-4 (Ws backcrossed to Col?)
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Shahan_6177

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

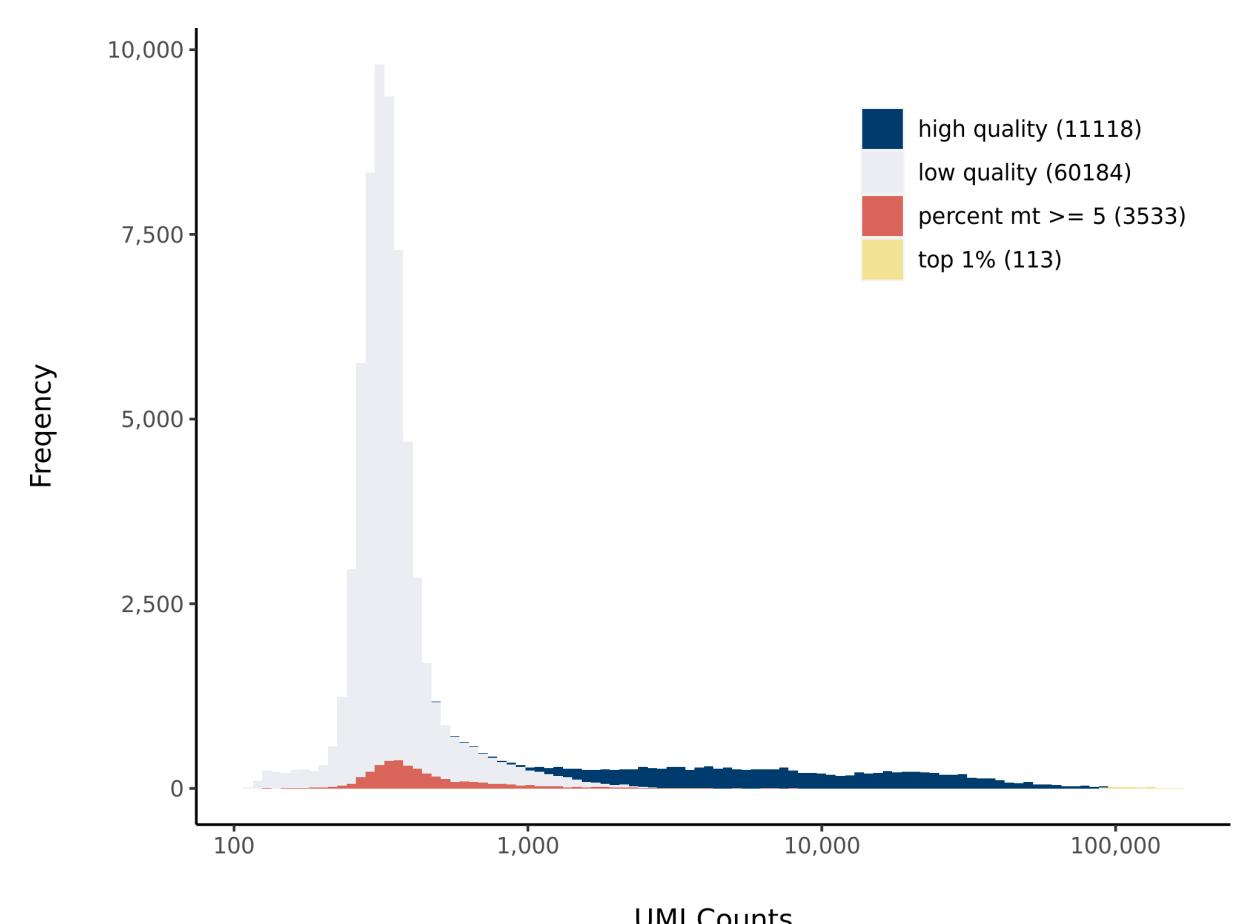
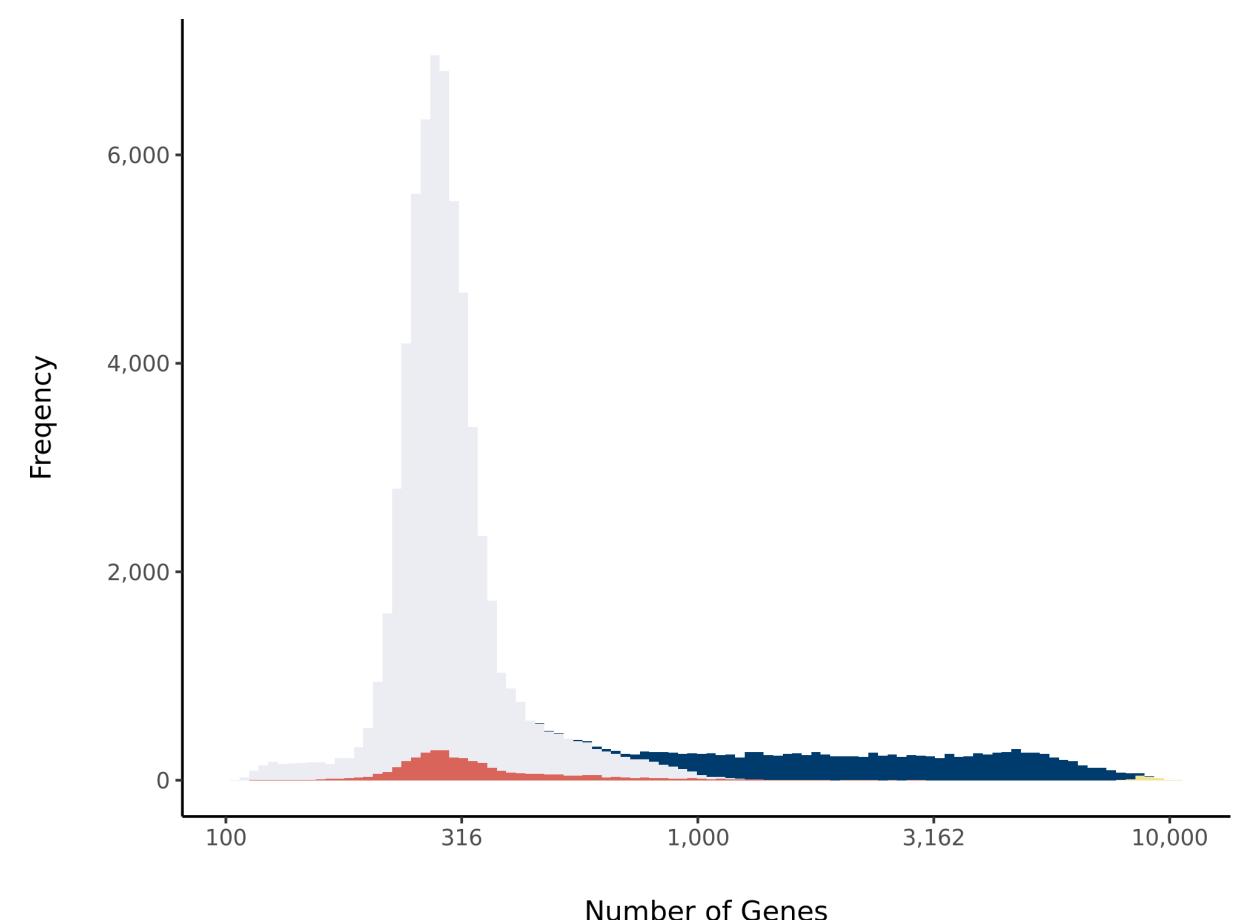
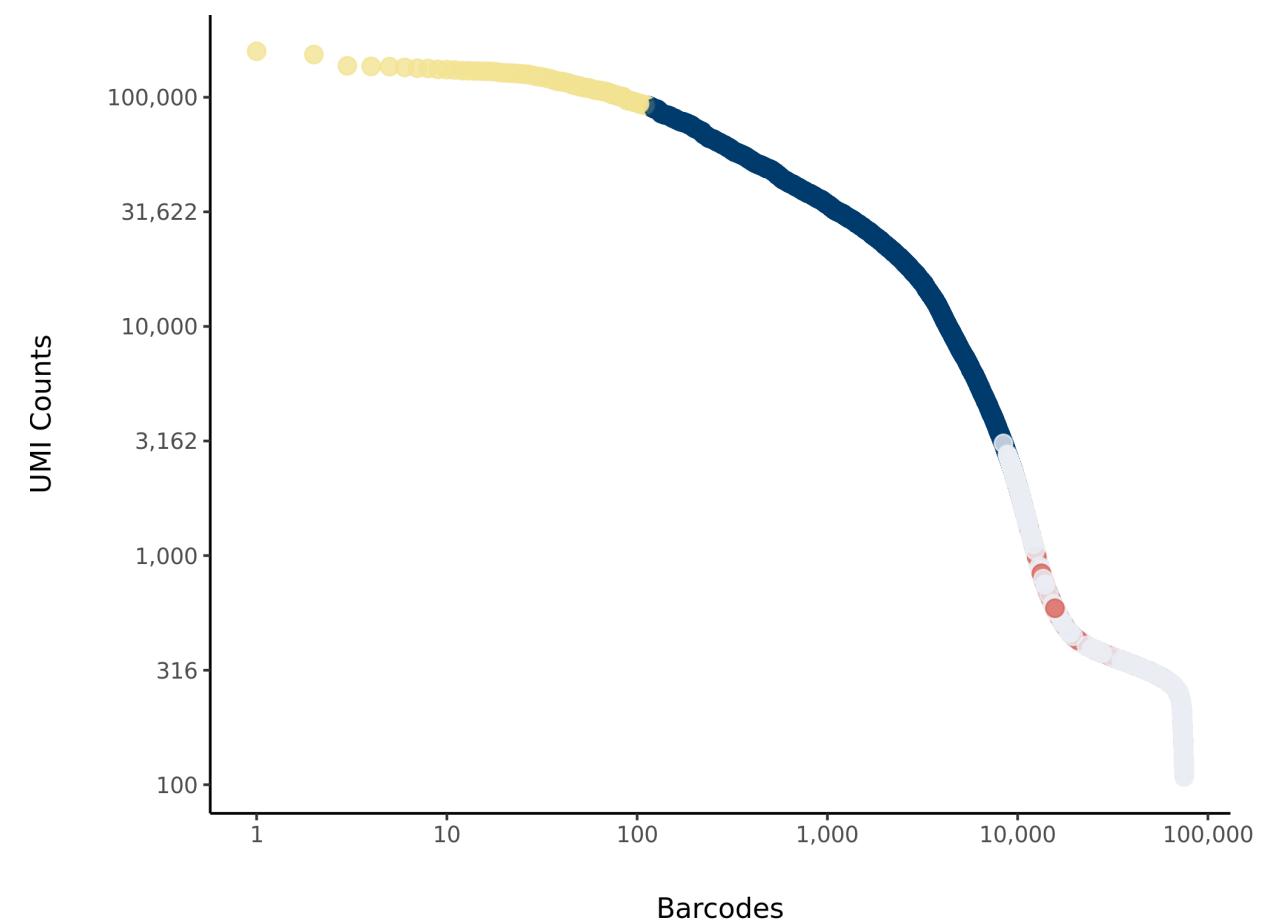
Estimated Number of High Quality Cell	11,118
High Quality Cell	14.83 %
Total UMI Counts in High Quality Cell	137,632,134
UMI Counts in High Quality Cell	79.01 %
Median UMI Counts per High Quality Cell	6,495
Median Genes per High Quality Cell	2,466.5
Total Genes Detected in High Quality Cell	24,739
Cell above Mitochondrial Expression Threshold	4.71 %
Estimated Doublet Rate in High Quality Cell	8.3 %

**Sequencing Stats**

Number of Reads Processed	263,408,174
Reads Pseudoaligned	93.5 %
Reads on Whitelist	96.22 %
Total UMI Counts	174,187,605
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	sc_30
Name	WT Col-0_RS3
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Nolan_6199 (NextSeq); Nolan_6226 (NovaSeq S4)

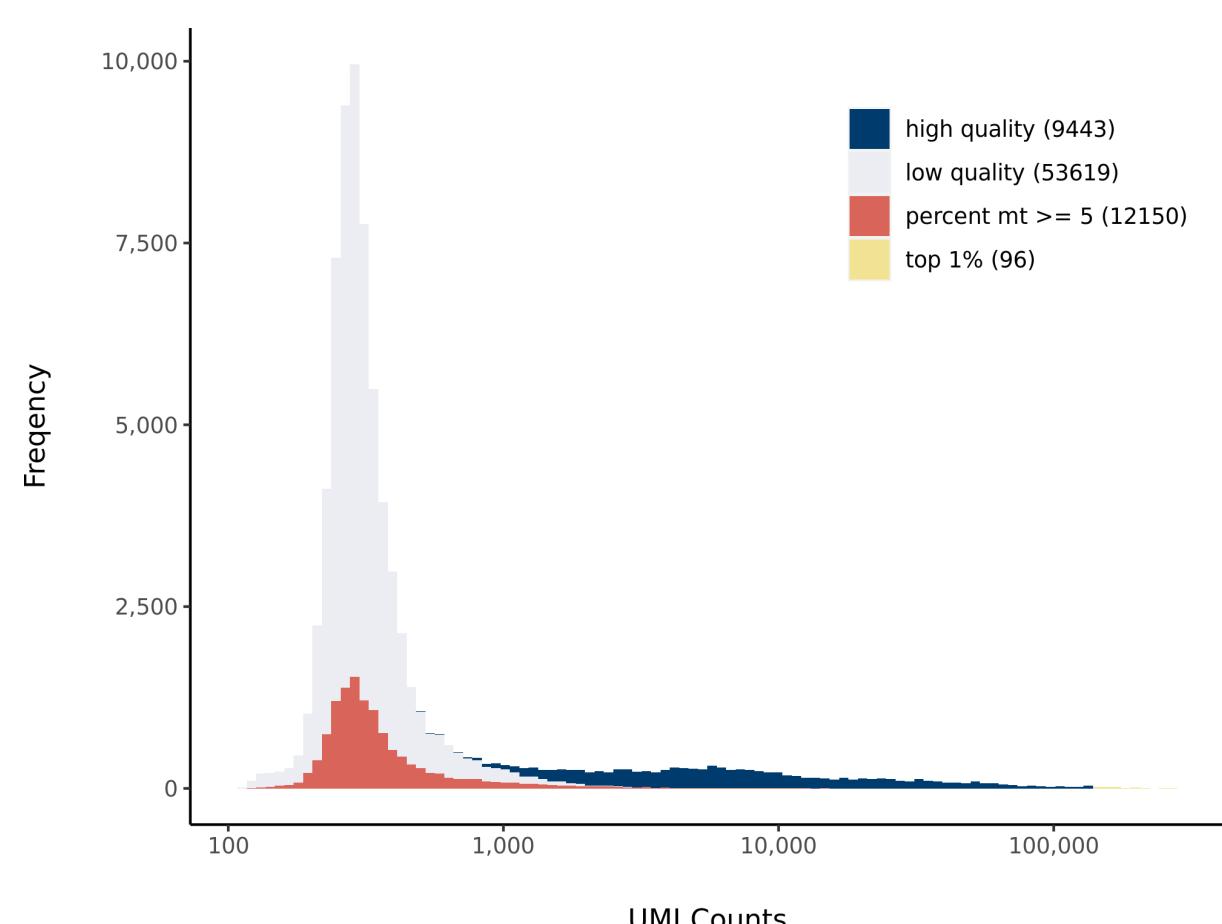
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

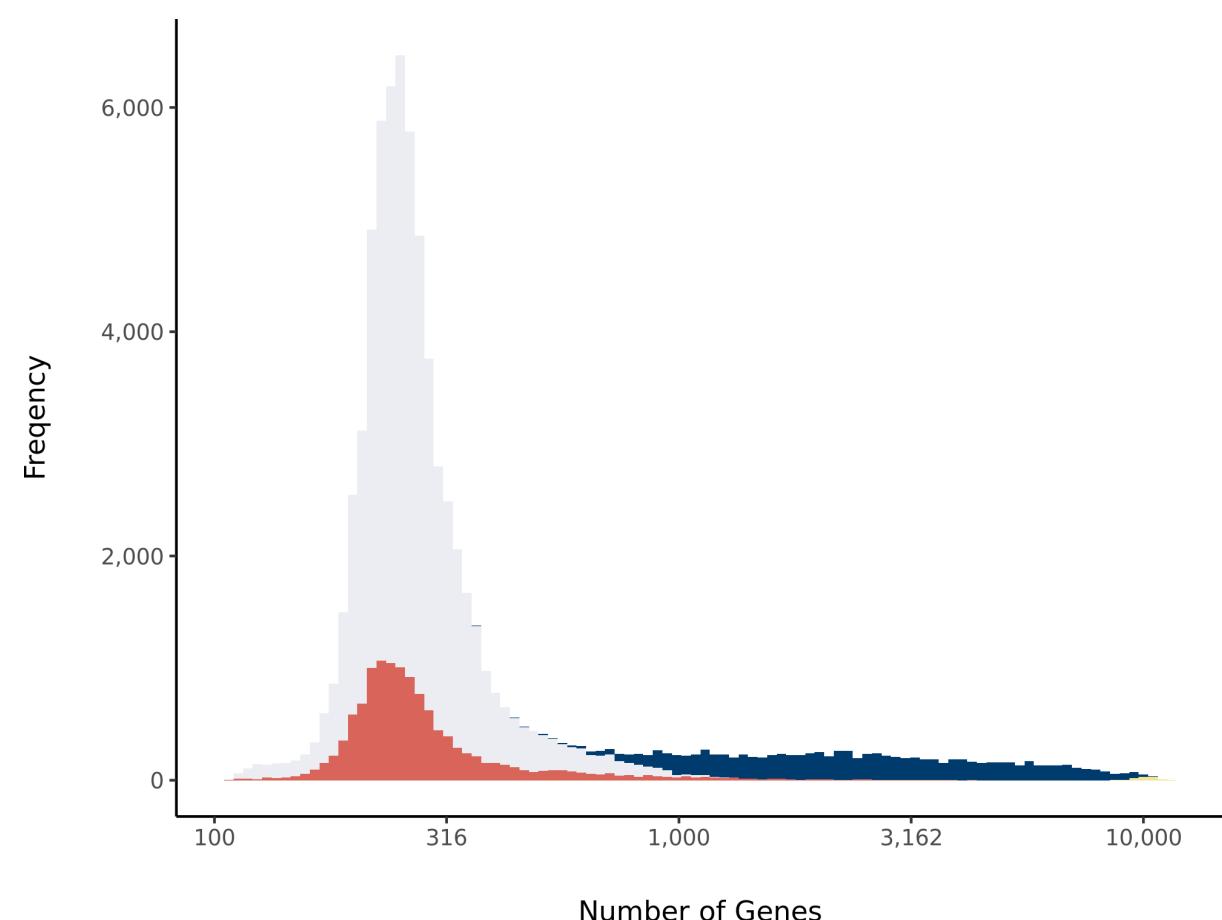
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

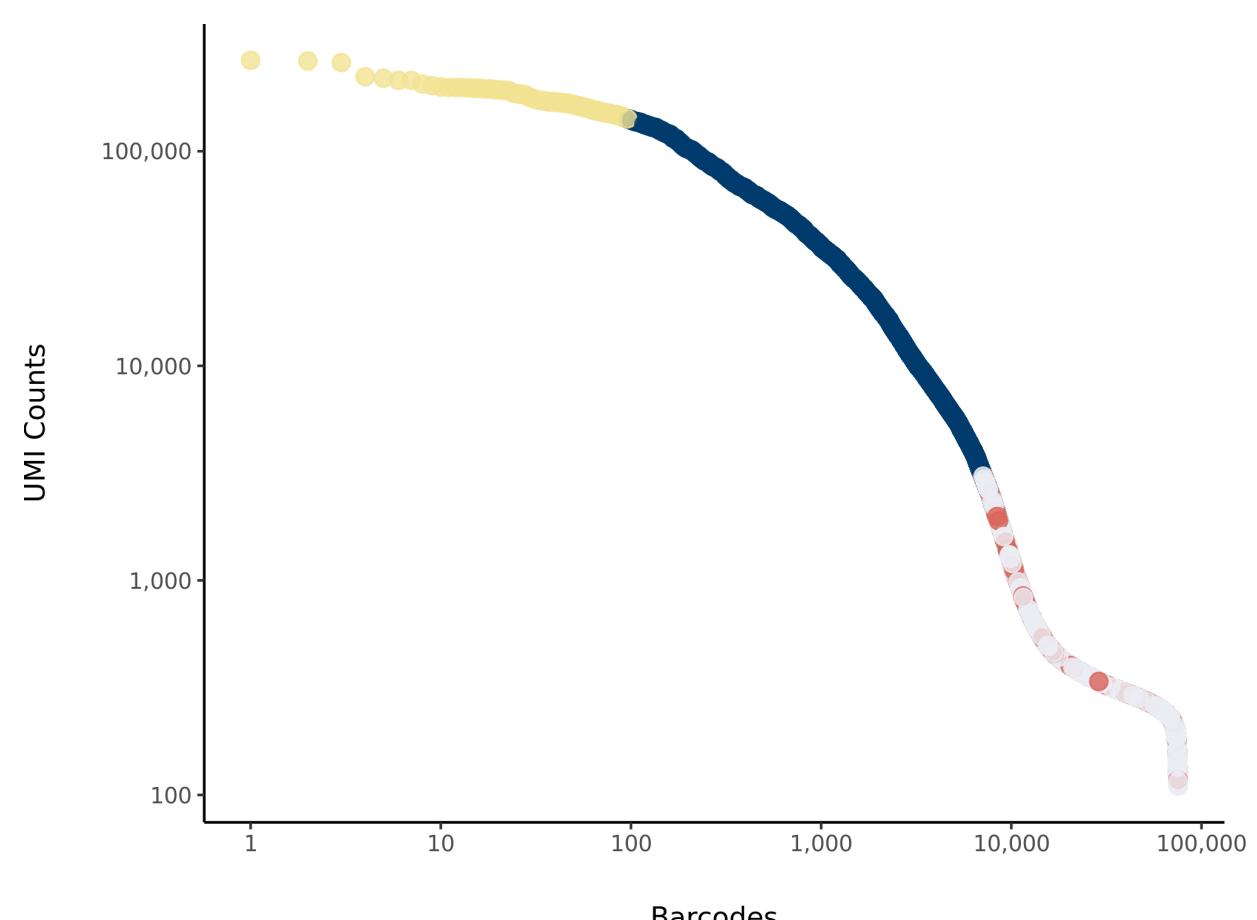
Estimated Number of High Quality Cell	9,443
High Quality Cell	12.54 %
Total UMI Counts in High Quality Cell	128,218,174
UMI Counts in High Quality Cell	76.36 %
Median UMI Counts per High Quality Cell	6,034
Median Genes per High Quality Cell	2,308
Total Genes Detected in High Quality Cell	24,826
Cell above Mitochondrial Expression Threshold	16.13 %
Estimated Doublet Rate in High Quality Cell	7.07 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	266,362,743
Reads Pseudoaligned	92.5 %
Reads on Whitelist	95.91 %
Total UMI Counts	167,906,304
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_31
Name	WT Col-0_RS4
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Nolan_6199 (NextSeq); Nolan_6226 (NovaSeq S4)

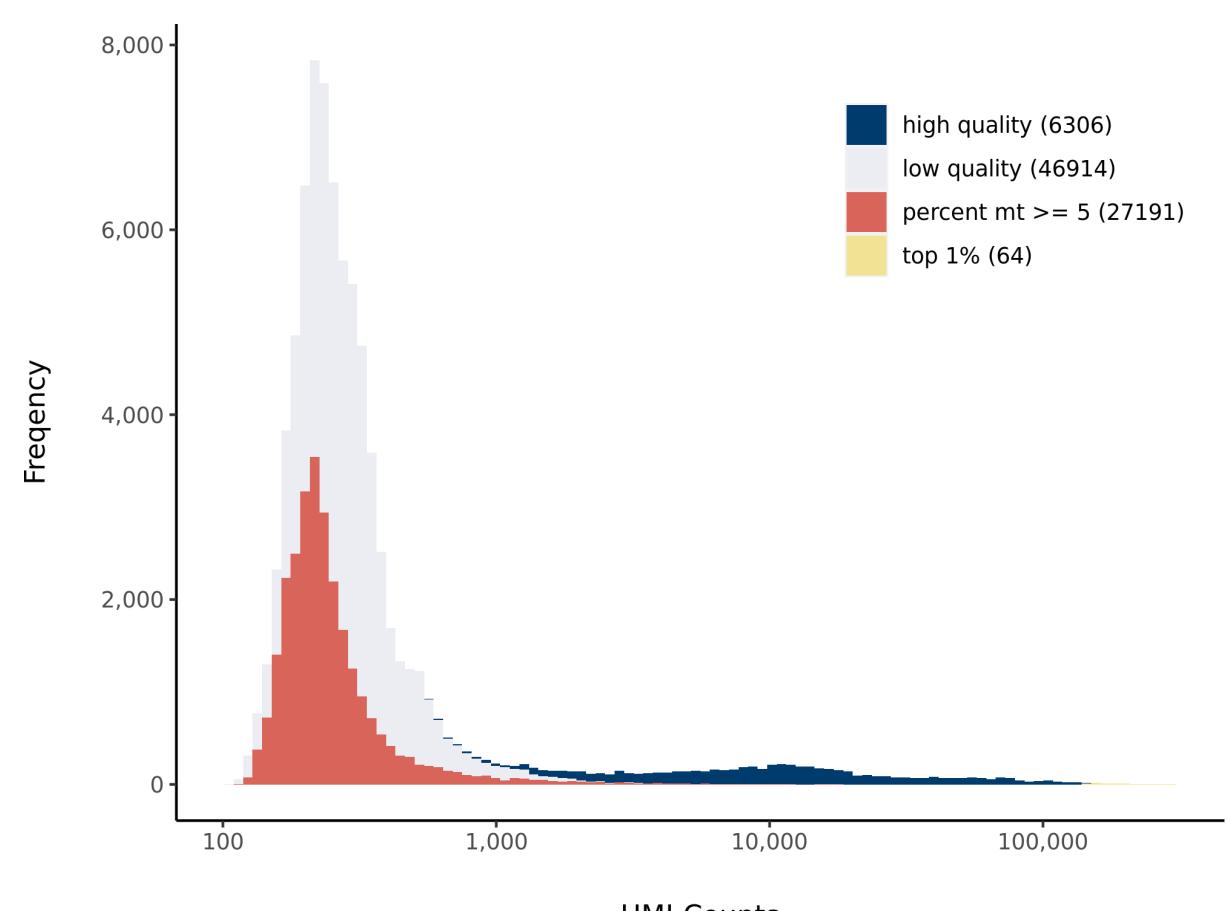
**Barcode Rank Plot**

**Parameters**

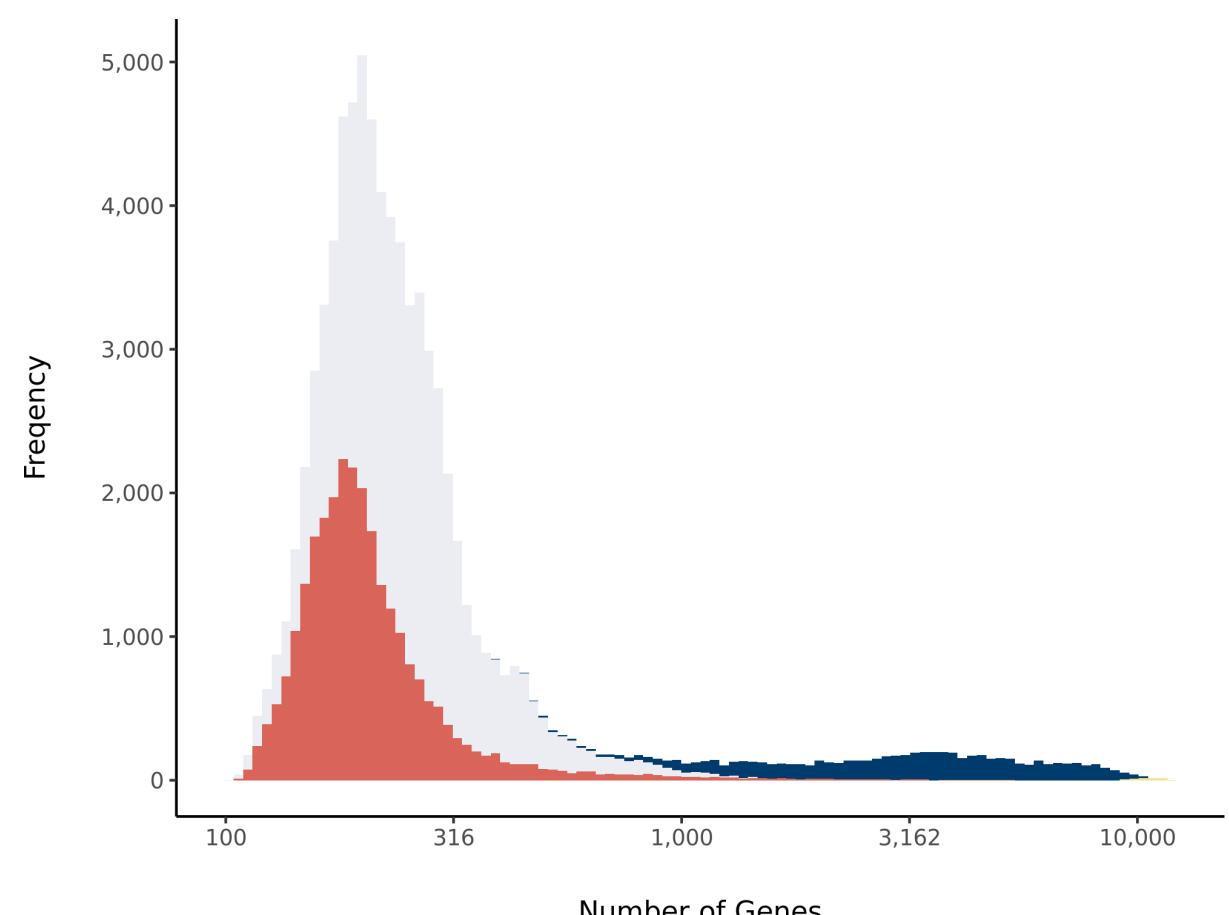
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

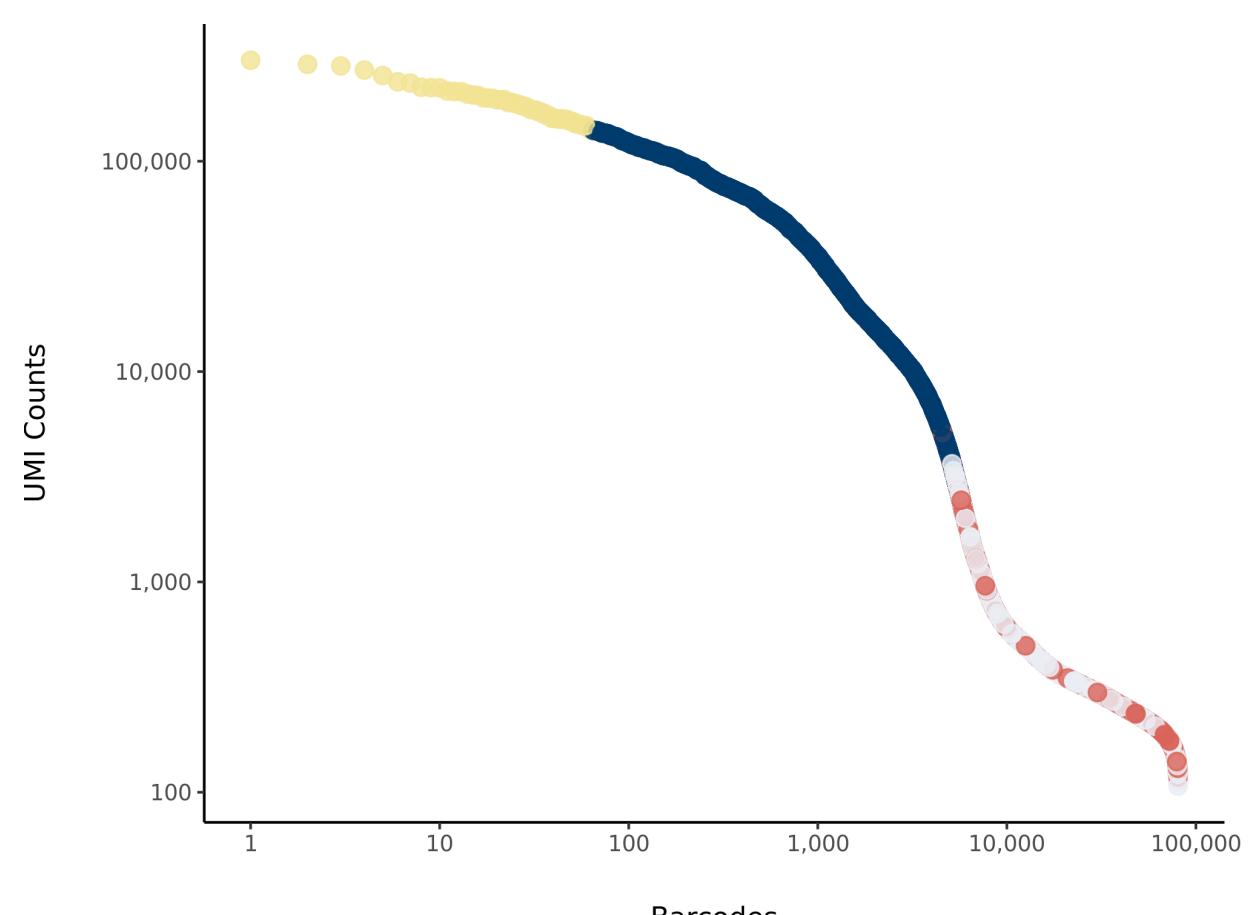
Estimated Number of High Quality Cell	6,306
High Quality Cell	7.84 %
Total UMI Counts in High Quality Cell	114,638,530
UMI Counts in High Quality Cell	76.67 %
Median UMI Counts per High Quality Cell	9,849
Median Genes per High Quality Cell	3,209
Total Genes Detected in High Quality Cell	25,147
Cell above Mitochondrial Expression Threshold	33.79 %
Estimated Doublet Rate in High Quality Cell	4.76 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	280,421,300
Reads Pseudoaligned	91.3 %
Reads on Whitelist	95.85 %
Total UMI Counts	149,515,088
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_36
Name	scr_4_2
Source	Benfey lab
Genotype	scr-4
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	NA
Seq Run	Nolan_6199 (NextSeq); Nolan_6226 (NovaSeq S4)

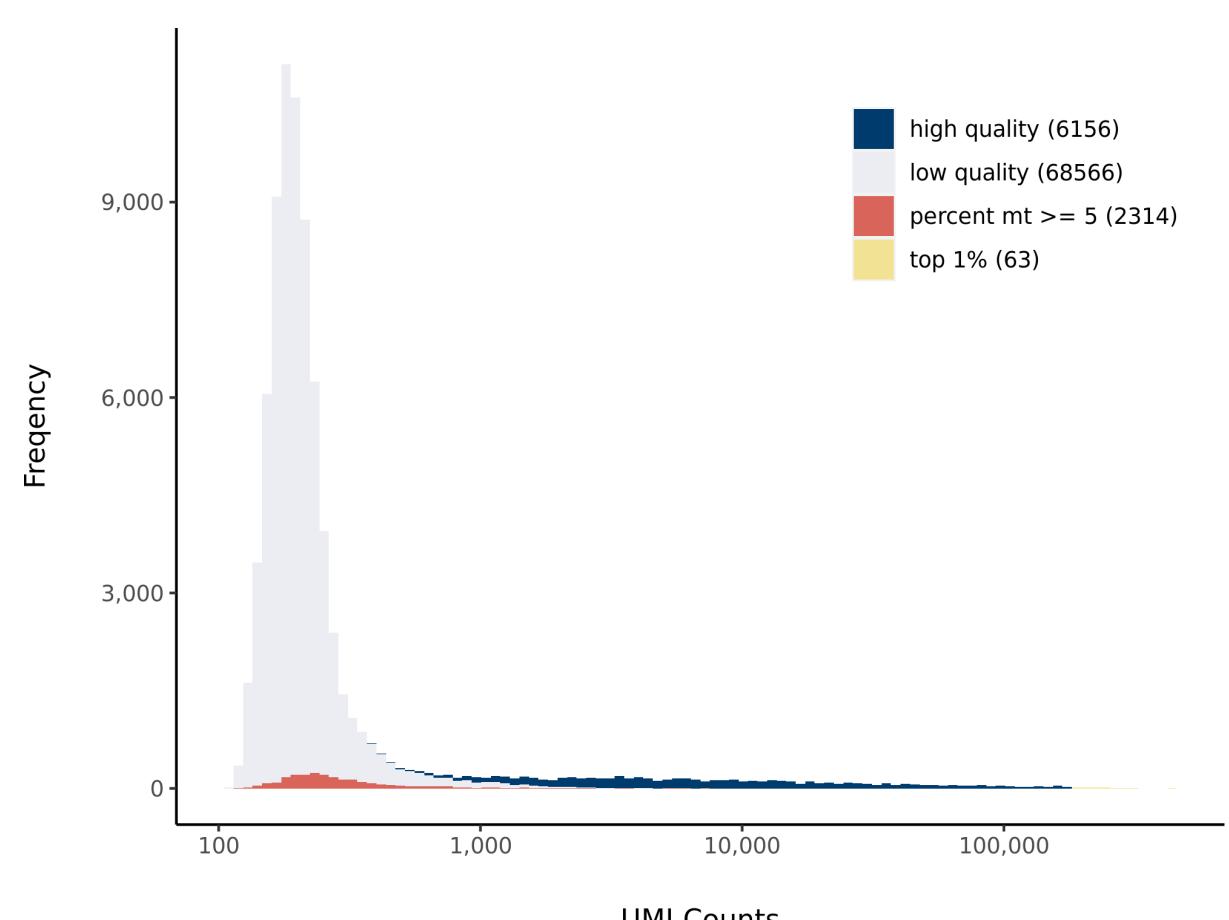
**Barcode Rank Plot**

**Parameters**

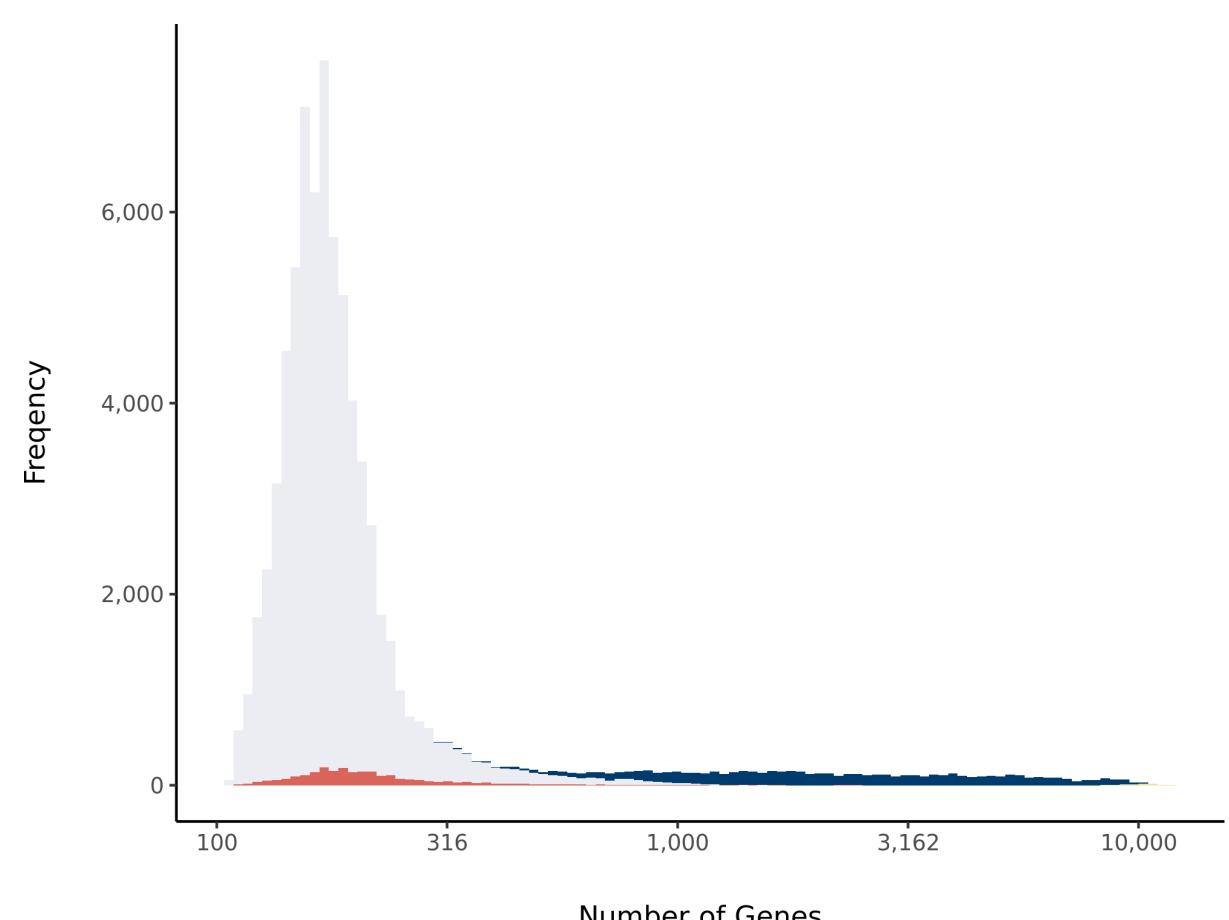
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

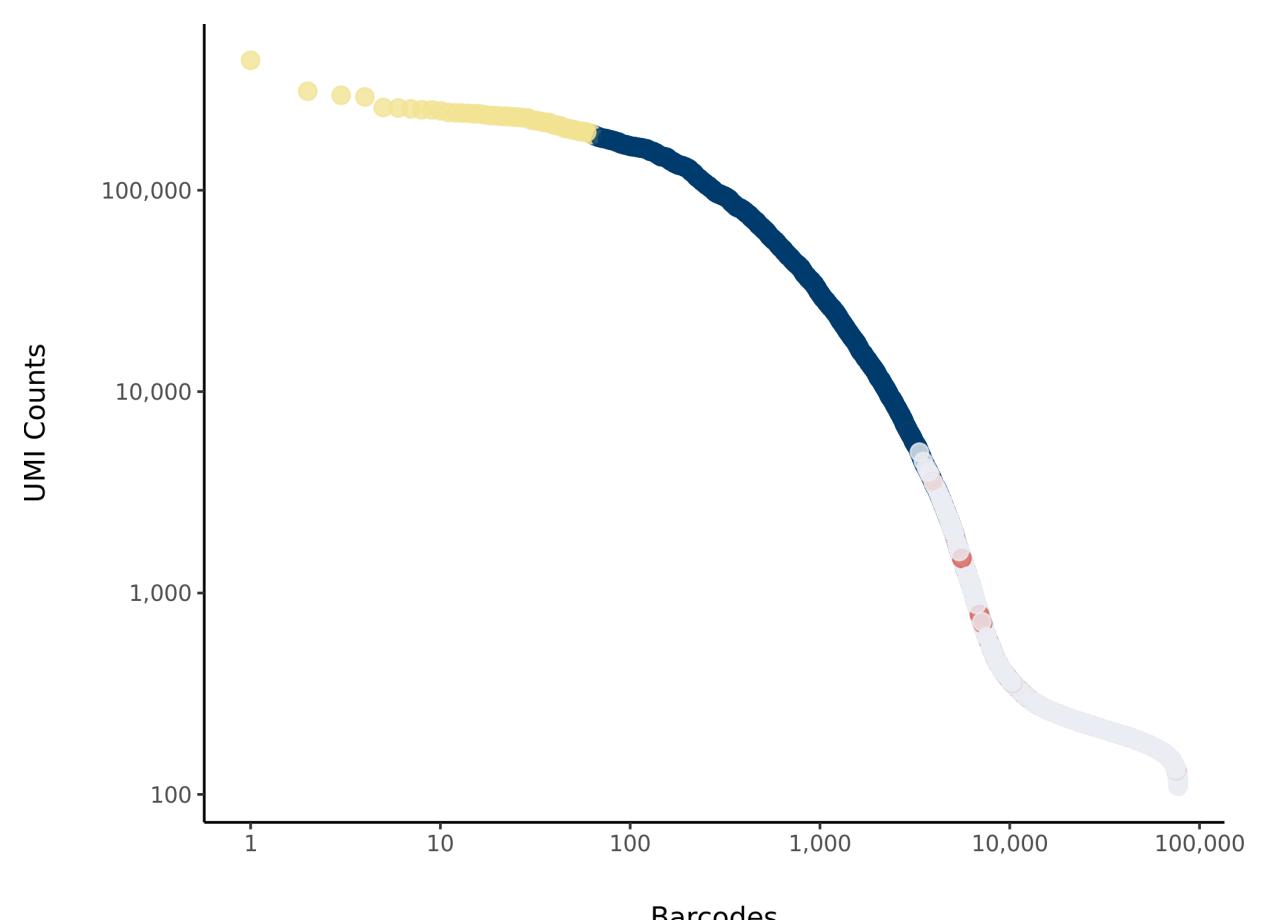
Estimated Number of High Quality Cell	6,156
High Quality Cell	7.98 %
Total UMI Counts in High Quality Cell	106,794,708
UMI Counts in High Quality Cell	77.91 %
Median UMI Counts per High Quality Cell	5,611
Median Genes per High Quality Cell	1,984
Total Genes Detected in High Quality Cell	25,262
Cell above Mitochondrial Expression Threshold	3 %
Estimated Doublet Rate in High Quality Cell	4.65 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	286,251,558
Reads Pseudoaligned	94.3 %
Reads on Whitelist	96.52 %
Total UMI Counts	137,082,512
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_37
Name	WT Col-0 untreated
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	6_day
Timepoint	0
Rep	NA
Target Cells	10,000
Date	2020-02-11
Seq Run	Nolan_6199 (NextSeq); Nolan_6226 (NovaSeq S4)

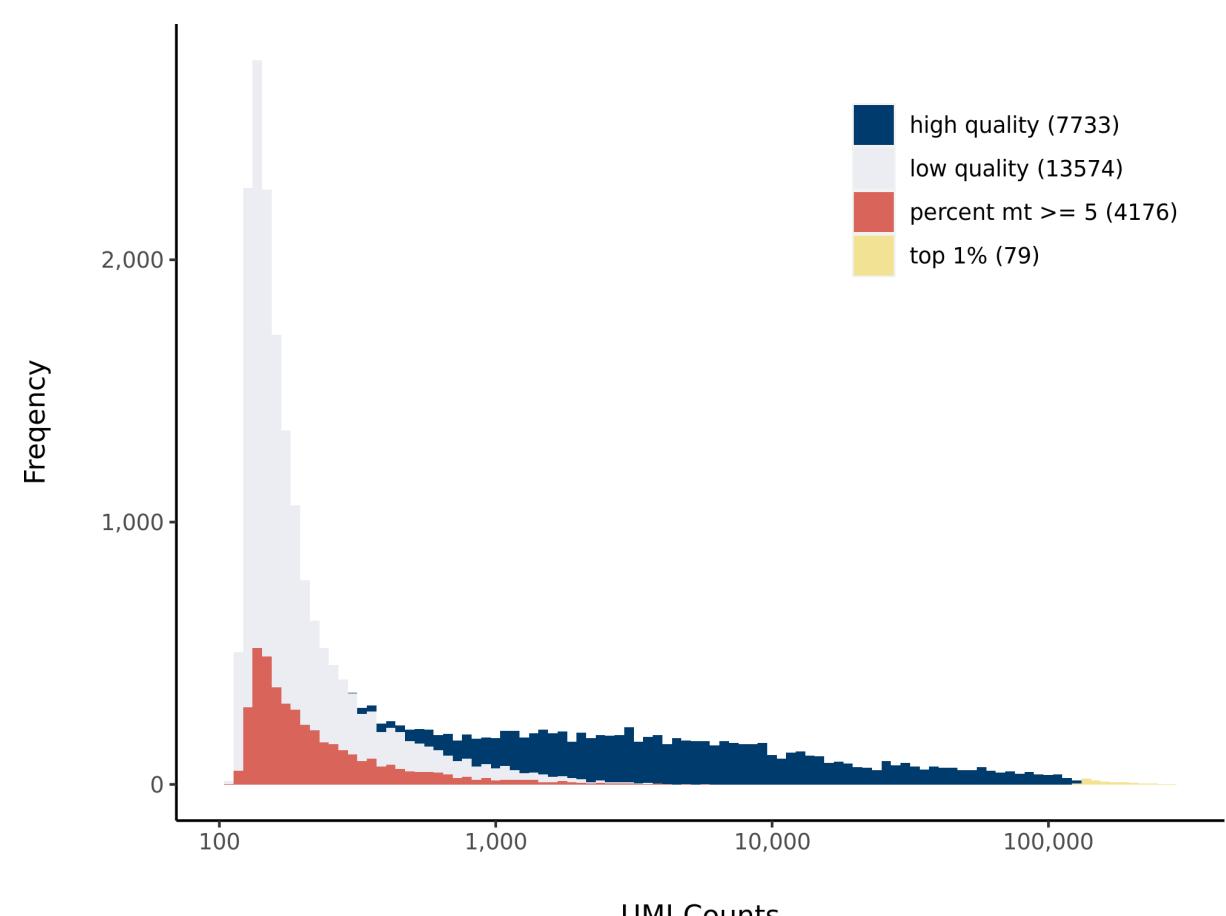
**Barcode Rank Plot**

**Parameters**

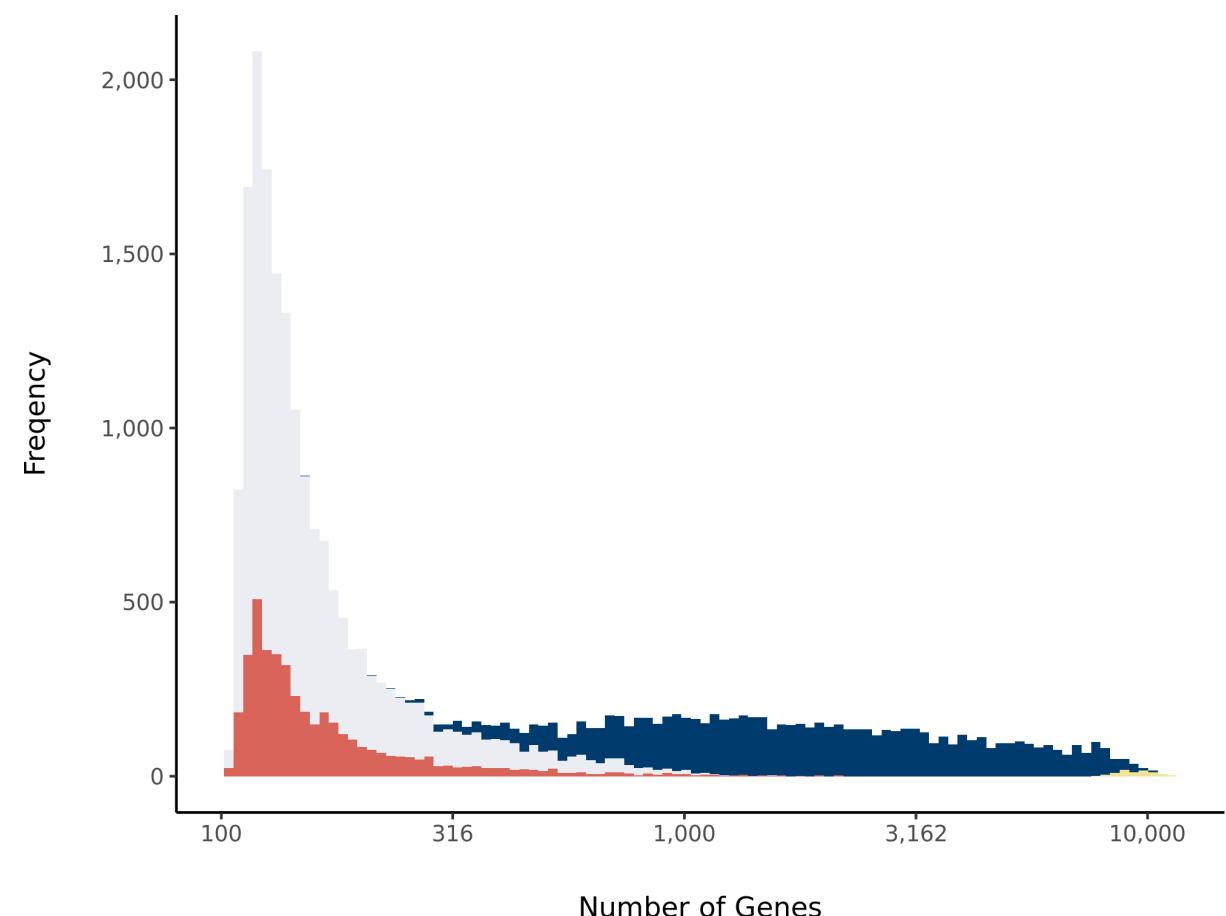
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

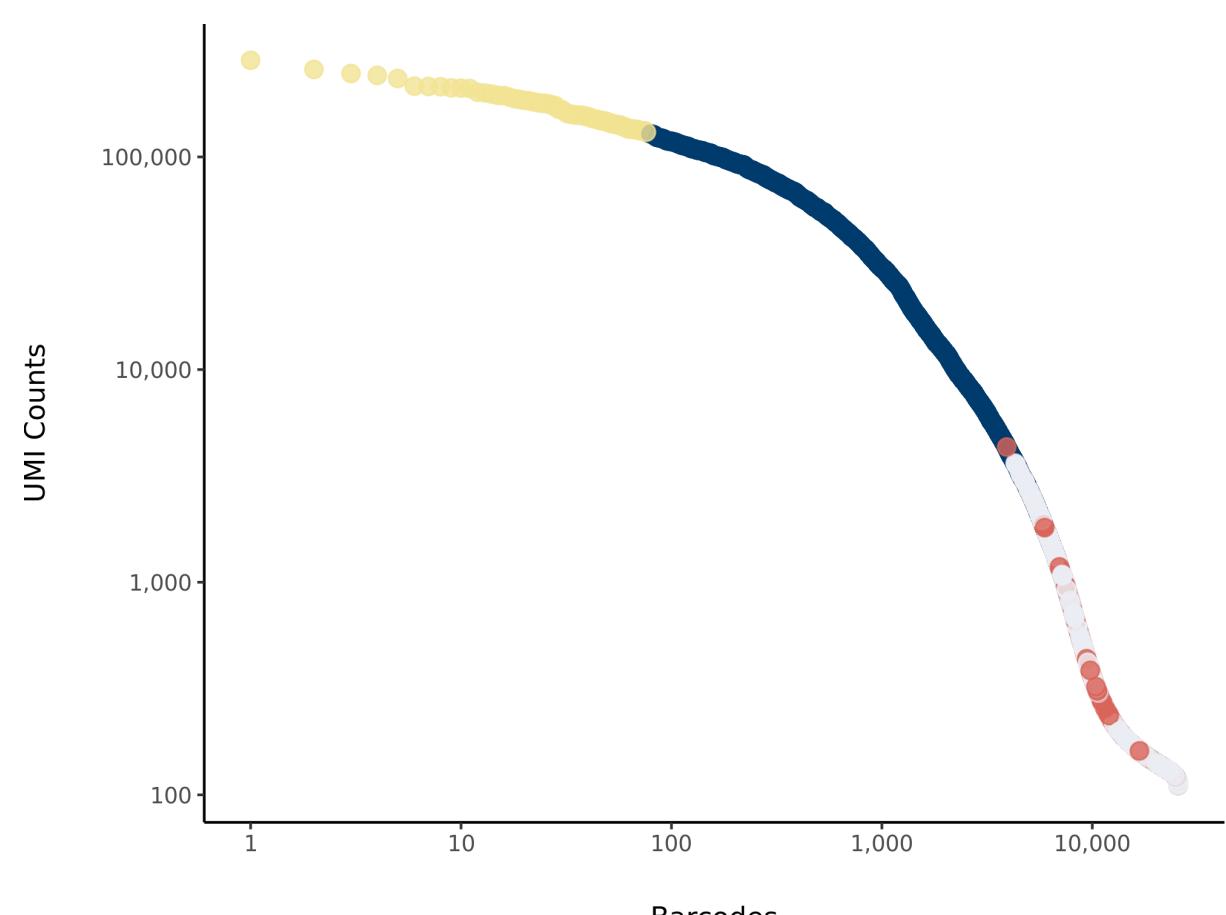
Estimated Number of High Quality Cell	7,733
High Quality Cell	30.25 %
Total UMI Counts in High Quality Cell	95,968,452
UMI Counts in High Quality Cell	84.61 %
Median UMI Counts per High Quality Cell	4,244
Median Genes per High Quality Cell	1,681
Total Genes Detected in High Quality Cell	25,693
Cell above Mitochondrial Expression Threshold	16.34 %
Estimated Doublet Rate in High Quality Cell	5.81 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	276,614,617
Reads Pseudoaligned	93 %
Reads on Whitelist	96.28 %
Total UMI Counts	113,425,205
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_40
Name	WT Col-0 untreated
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	6_day
Timepoint	0
Rep	NA
Target Cells	10,000
Date	2020-02-11
Seq Run	Nolan_6199 (NextSeq); Nolan_6226 (NovaSeq S4)

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

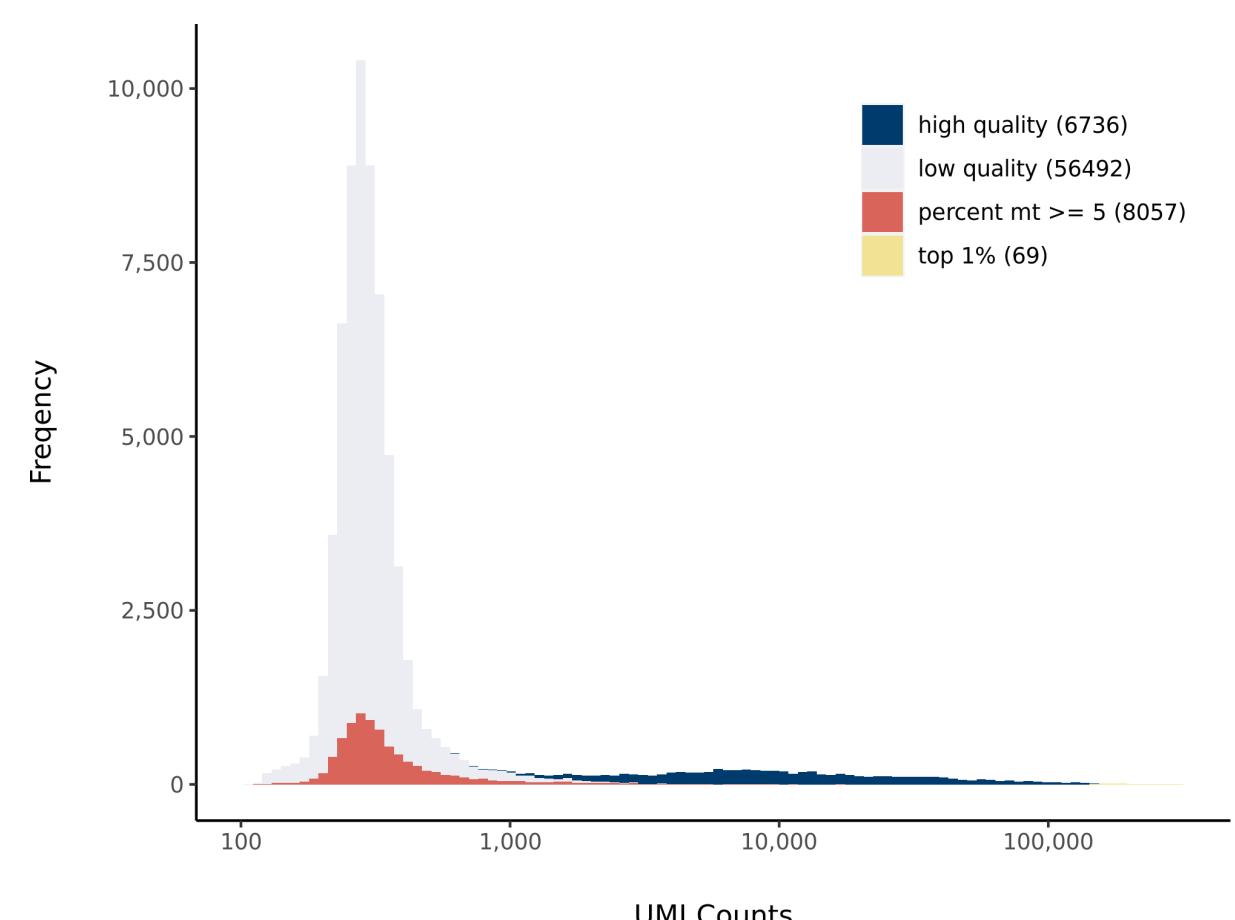
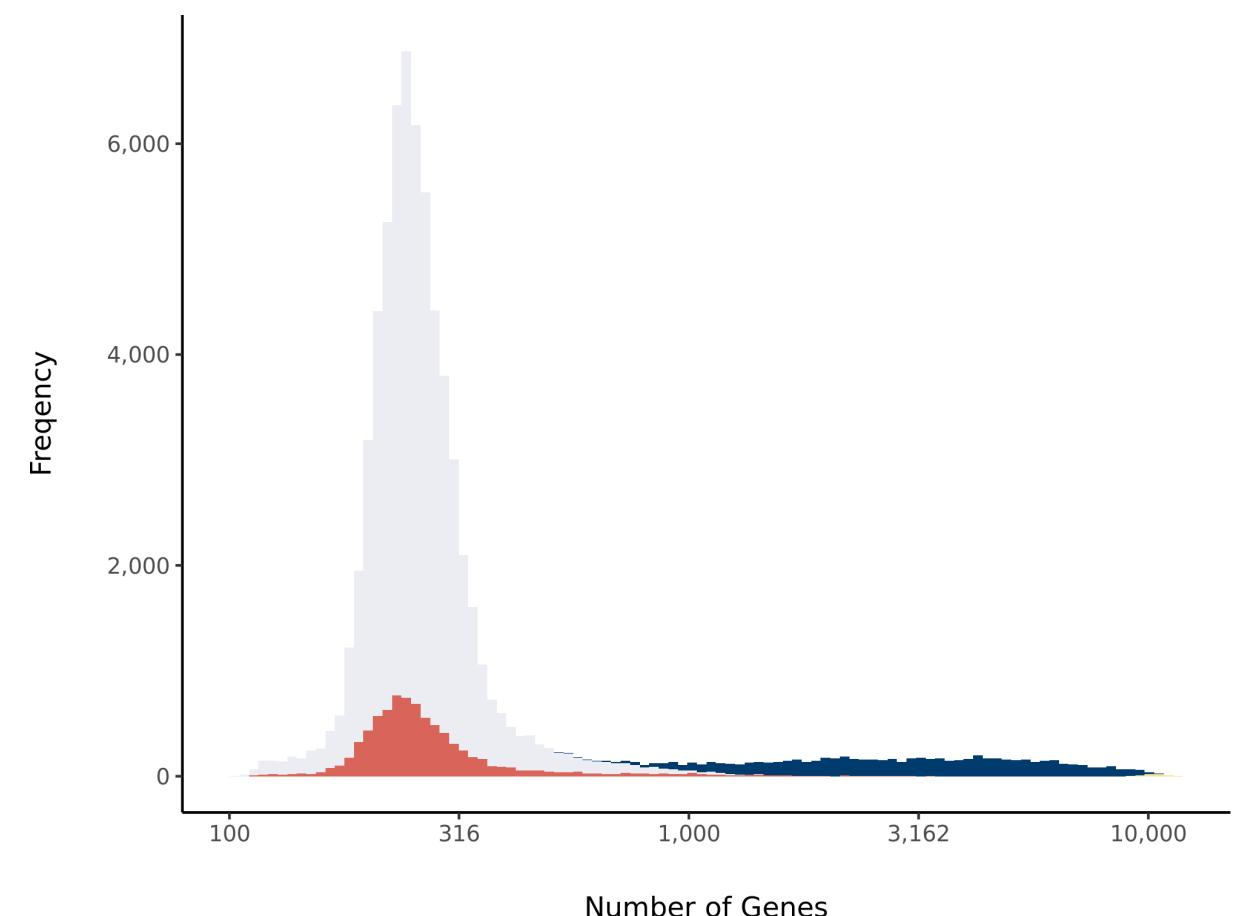
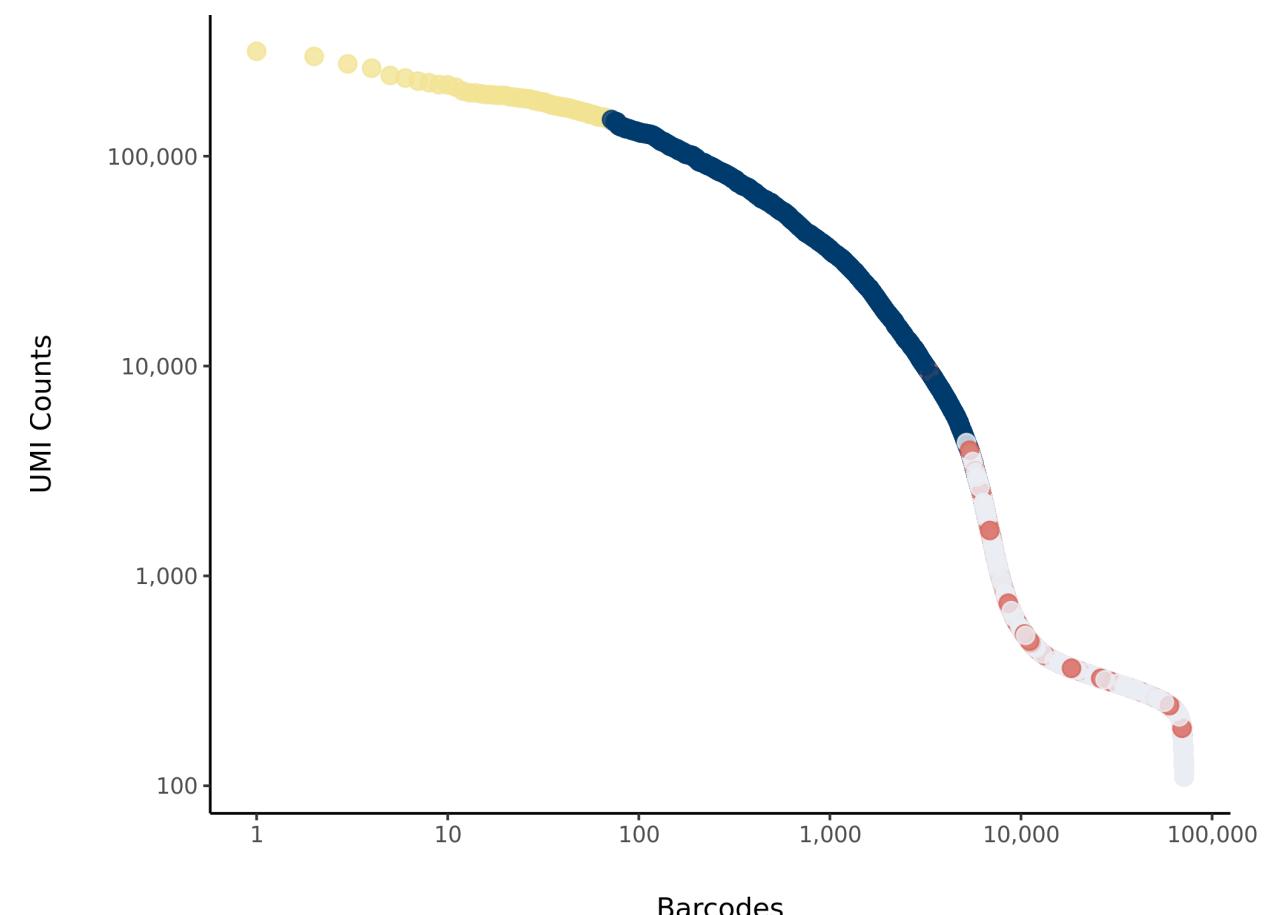
Estimated Number of High Quality Cell	6,736
High Quality Cell	9.44 %
Total UMI Counts in High Quality Cell	119,520,842
UMI Counts in High Quality Cell	77.74 %
Median UMI Counts per High Quality Cell	8,893.5
Median Genes per High Quality Cell	2,997.5
Total Genes Detected in High Quality Cell	24,754
Cell above Mitochondrial Expression Threshold	11.29 %
Estimated Doublet Rate in High Quality Cell	5.08 %

**Sequencing Stats**

Number of Reads Processed	246,772,773
Reads Pseudoaligned	94 %
Reads on Whitelist	96.29 %
Total UMI Counts	153,752,550
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	sc_51
Name	WT Col (RS_5)
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2020-02-24
Seq Run	Nolan_6226

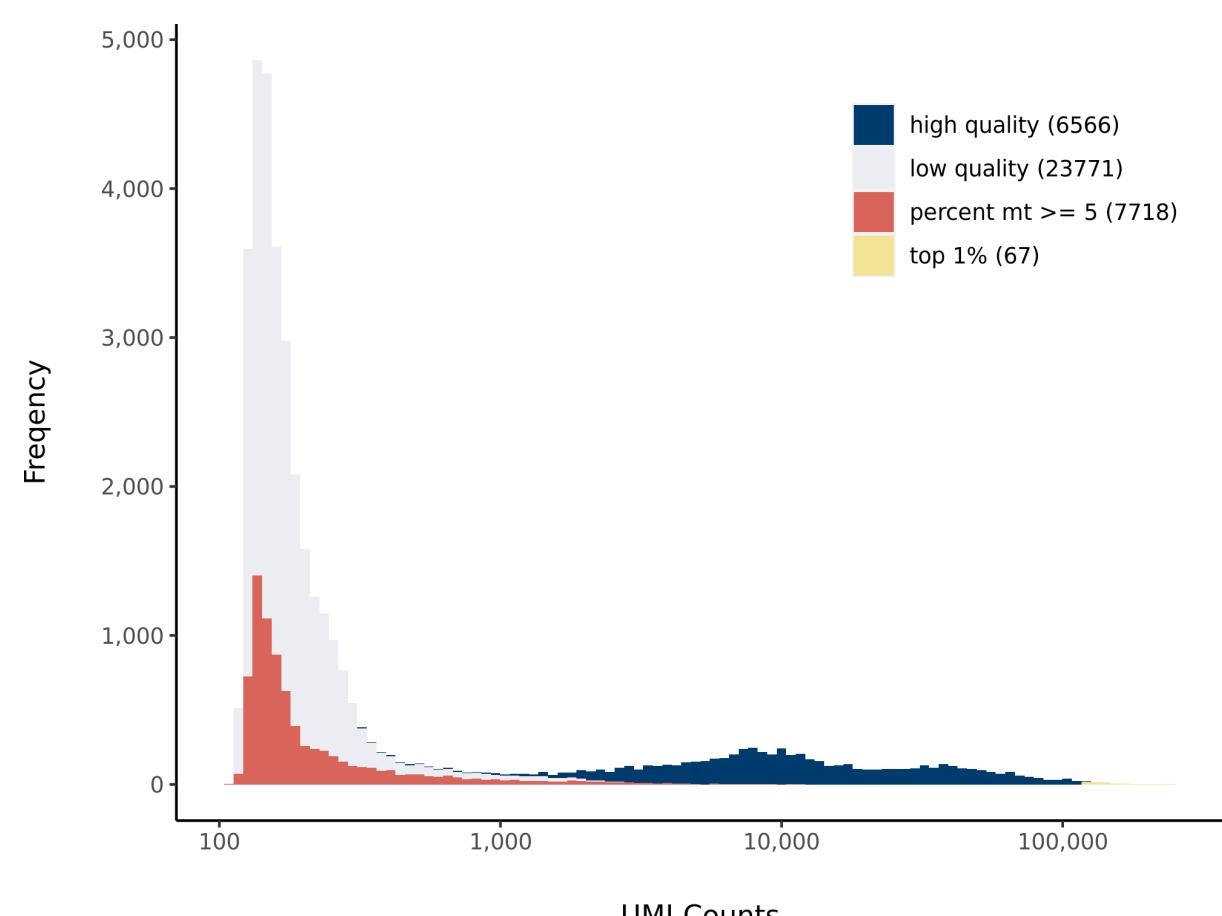
**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**

**Parameters**

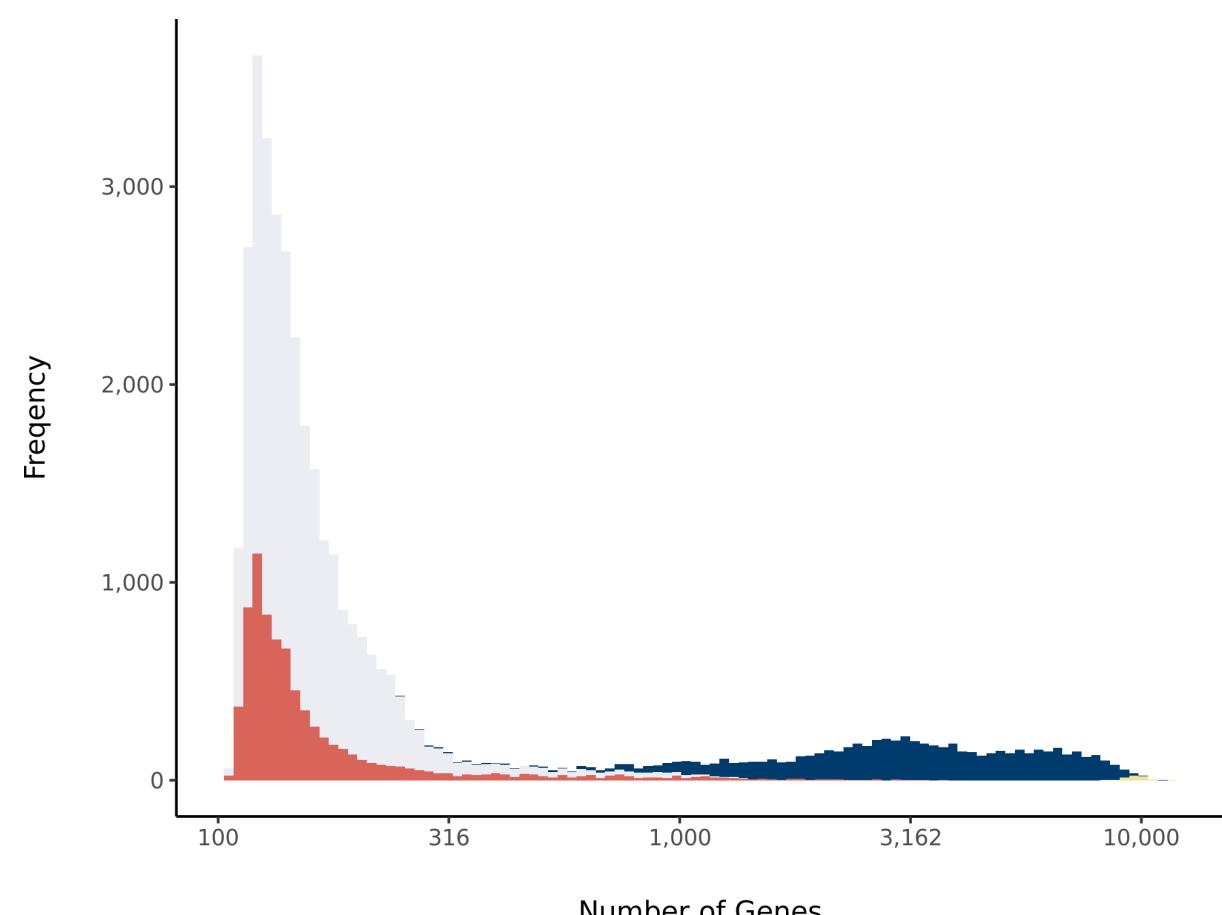
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

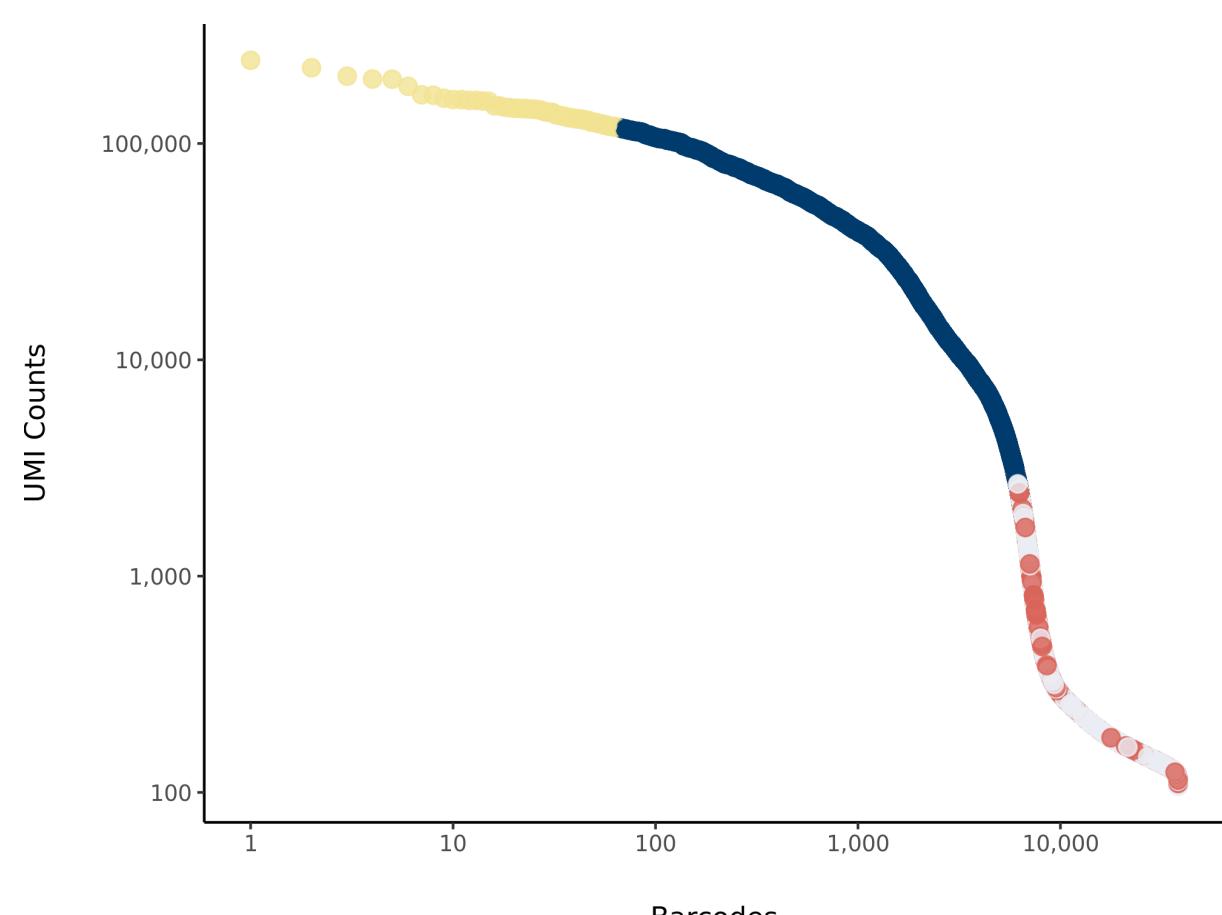
Estimated Number of High Quality Cell	6,566
High Quality Cell	17.22 %
Total UMI Counts in High Quality Cell	122,323,546
UMI Counts in High Quality Cell	87.97 %
Median UMI Counts per High Quality Cell	9,925.5
Median Genes per High Quality Cell	3,122.5
Total Genes Detected in High Quality Cell	24,747
Cell above Mitochondrial Expression Threshold	20.25 %
Estimated Doublet Rate in High Quality Cell	4.95 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	239,215,784
Reads Pseudoaligned	94.1 %
Reads on Whitelist	96.37 %
Total UMI Counts	139,046,144
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_52
Name	shr-2
Source	Benfey lab
Genotype	shr-2
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2020-02-24
Seq Run	Nolan_6226

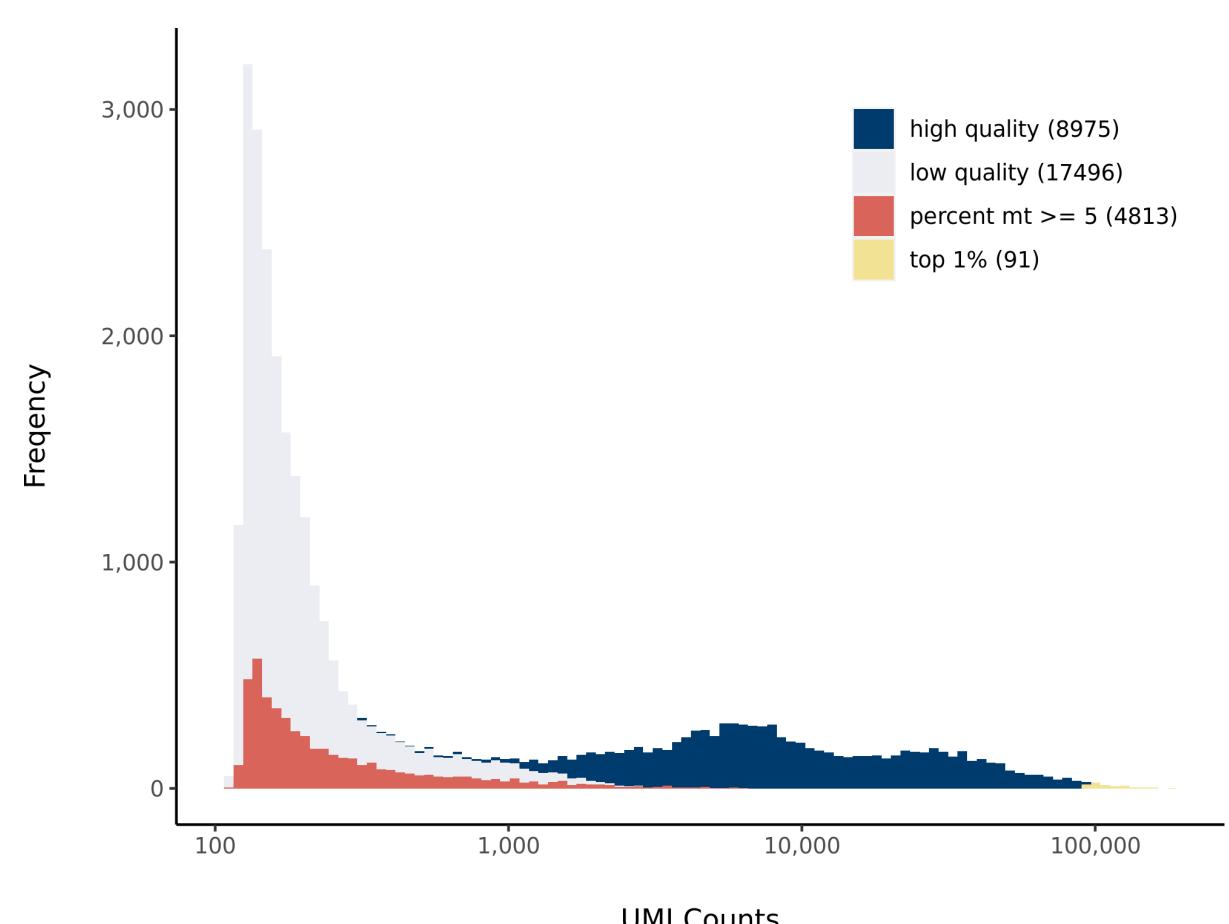
**Barcode Rank Plot**

**Parameters**

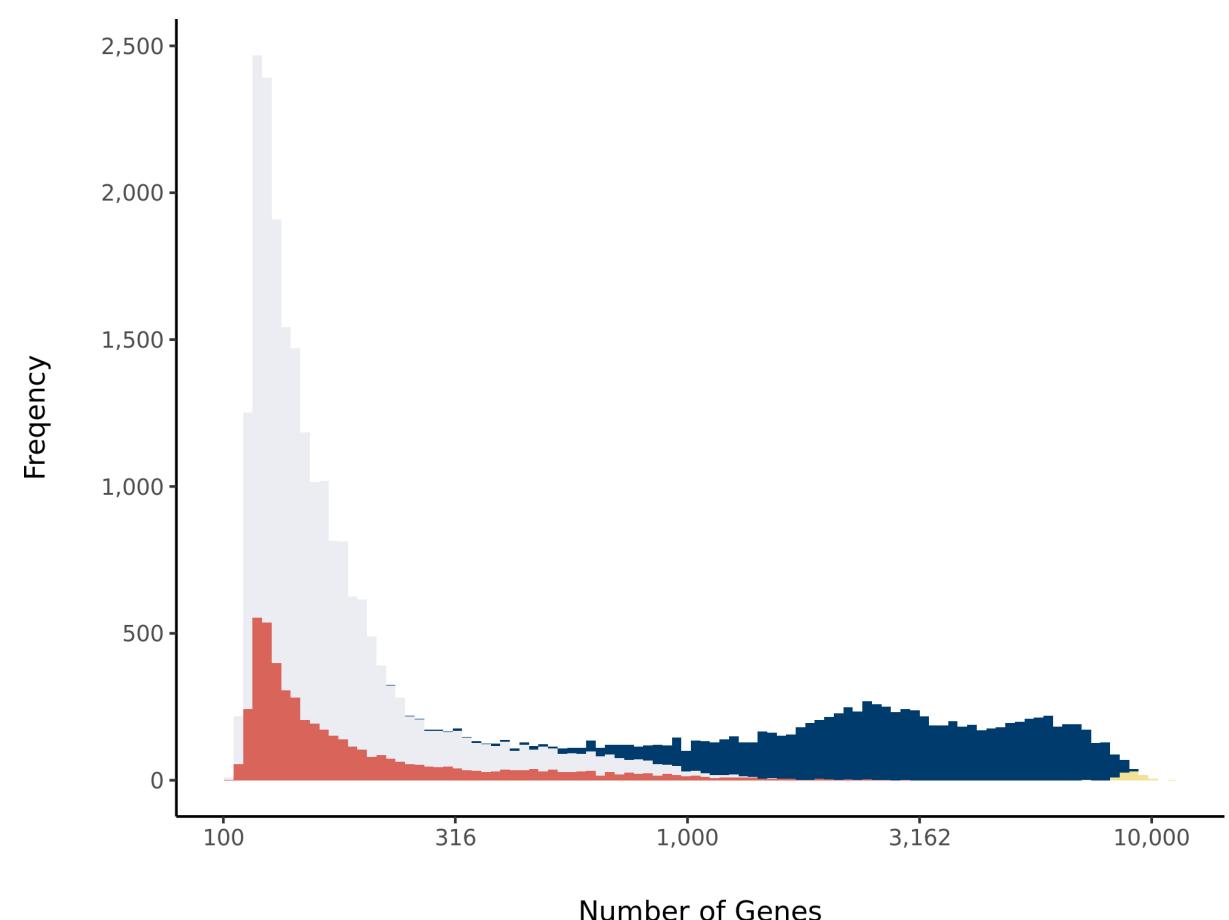
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

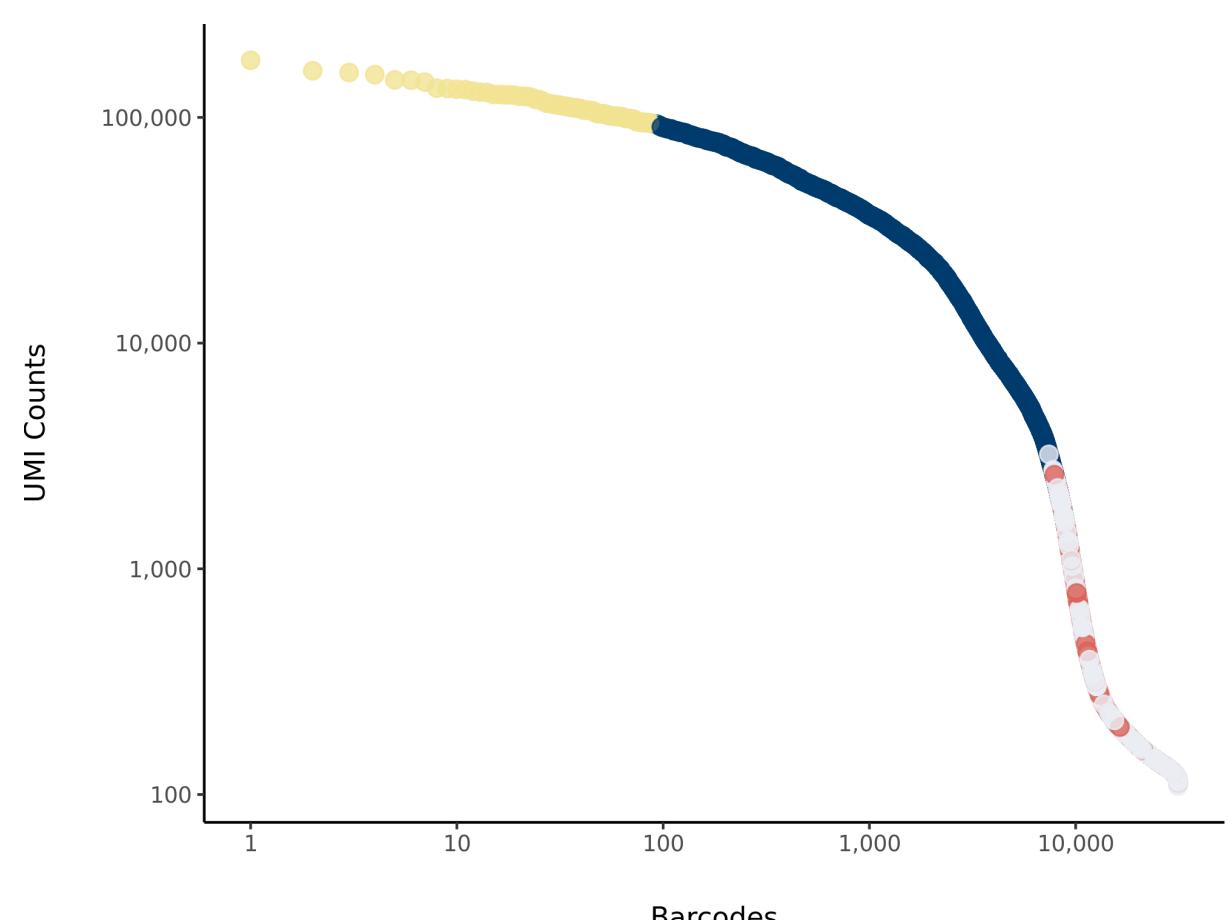
Estimated Number of High Quality Cell	8,975
High Quality Cell	28.61 %
Total UMI Counts in High Quality Cell	130,874,774
UMI Counts in High Quality Cell	89.12 %
Median UMI Counts per High Quality Cell	7,585
Median Genes per High Quality Cell	2,784
Total Genes Detected in High Quality Cell	24,809
Cell above Mitochondrial Expression Threshold	15.34 %
Estimated Doublet Rate in High Quality Cell	6.73 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	244,261,968
Reads Pseudoaligned	93.9 %
Reads on Whitelist	96.36 %
Total UMI Counts	146,853,427
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	sc_53
Name	shr-2
Source	Benfey lab
Genotype	shr-2
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	NA
Rep	NA
Target Cells	10,000
Date	2020-02-24
Seq Run	Nolan_6226

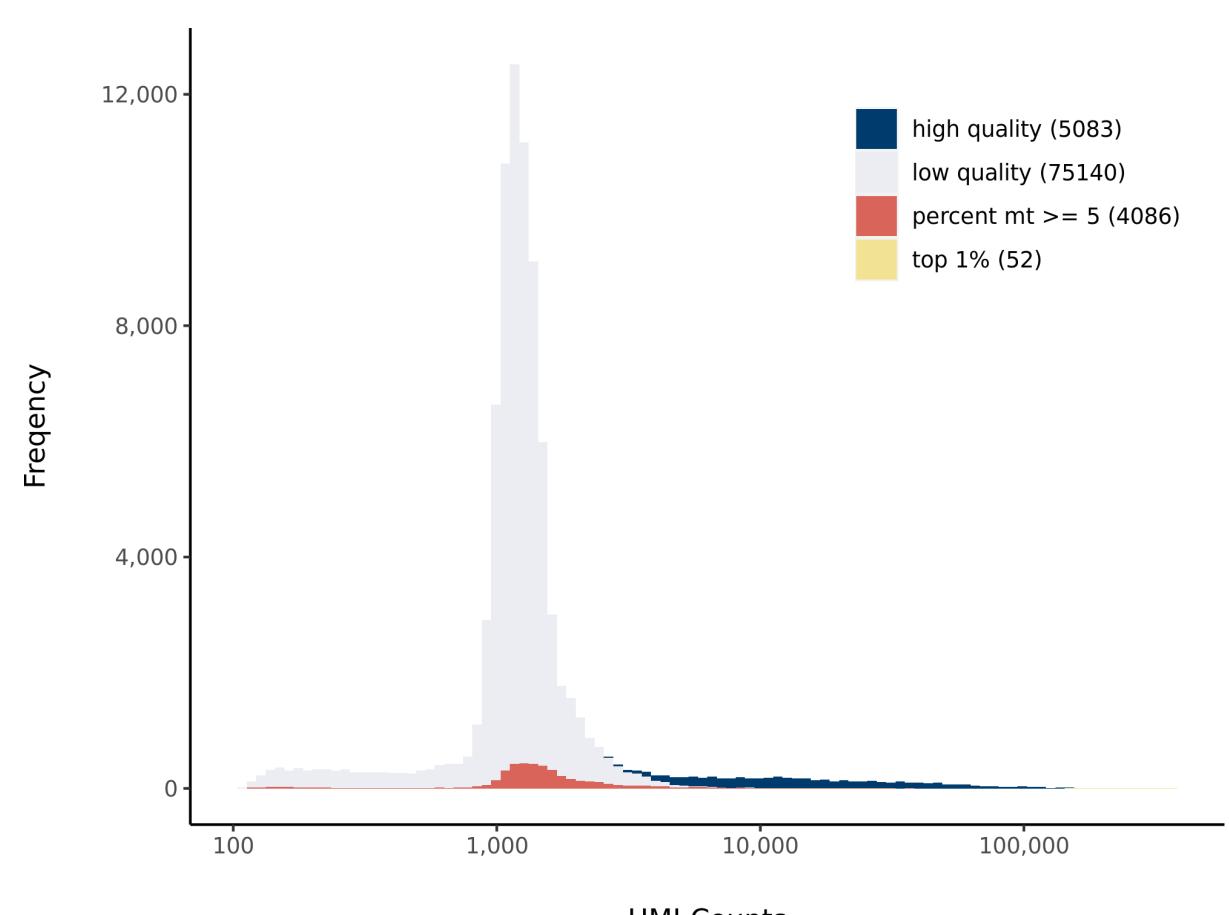
**Barcode Rank Plot**

**Parameters**

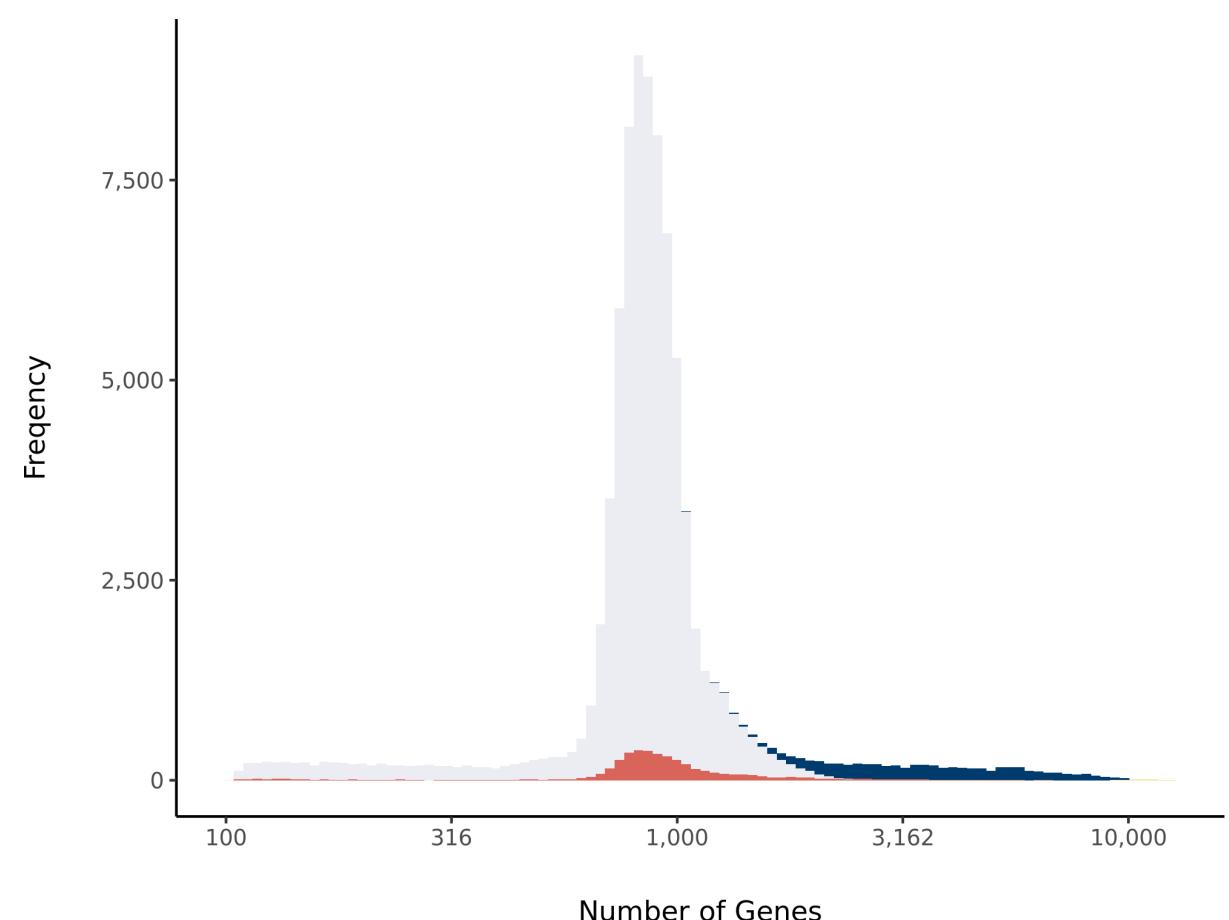
Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

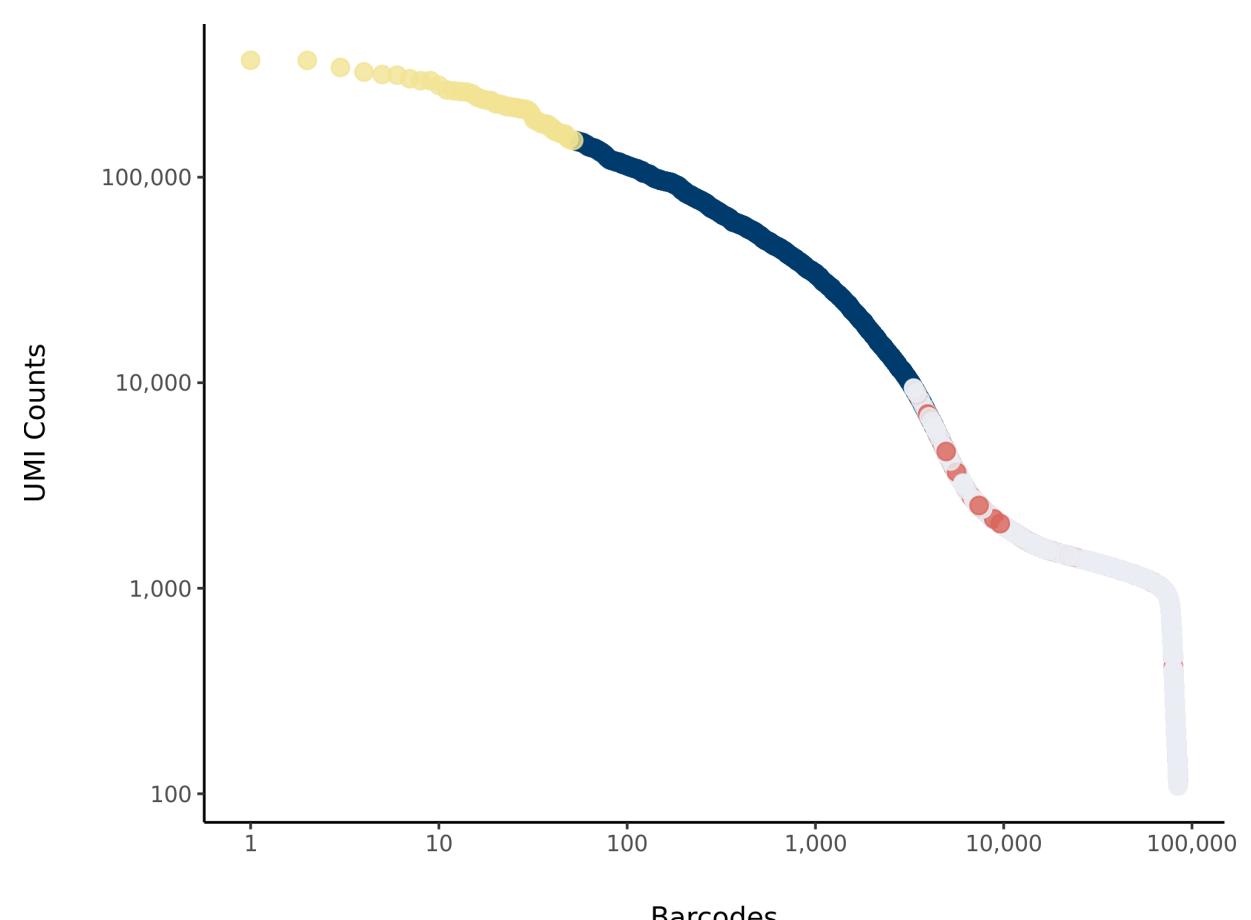
Estimated Number of High Quality Cell	5,083
High Quality Cell	6.03 %
Total UMI Counts in High Quality Cell	108,012,603
UMI Counts in High Quality Cell	49.04 %
Median UMI Counts per High Quality Cell	12,798
Median Genes per High Quality Cell	3,426
Total Genes Detected in High Quality Cell	24,940
Cell above Mitochondrial Expression Threshold	4.84 %
Estimated Doublet Rate in High Quality Cell	3.86 %

**UMI Counts Histogram****Sequencing Stats**

Number of Reads Processed	487,124,902
Reads Pseudoaligned	91.5 %
Reads on Whitelist	95.99 %
Total UMI Counts	220,259,890
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Number of Genes Histogram****Sample Stats**

Sample	tnw1
Name	WT control1
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	4
Rep	1
Target Cells	5,000
Date	2019-10-17
Seq Run	Nolan_6013

**Barcode Rank Plot**

**Parameters**

Iteration of Filtering	1
Mitochondrial Expression Threshold	5 %
Top High Quality Cell Filtered	1 %
Doublet Removed	Yes

**Cell Stats**

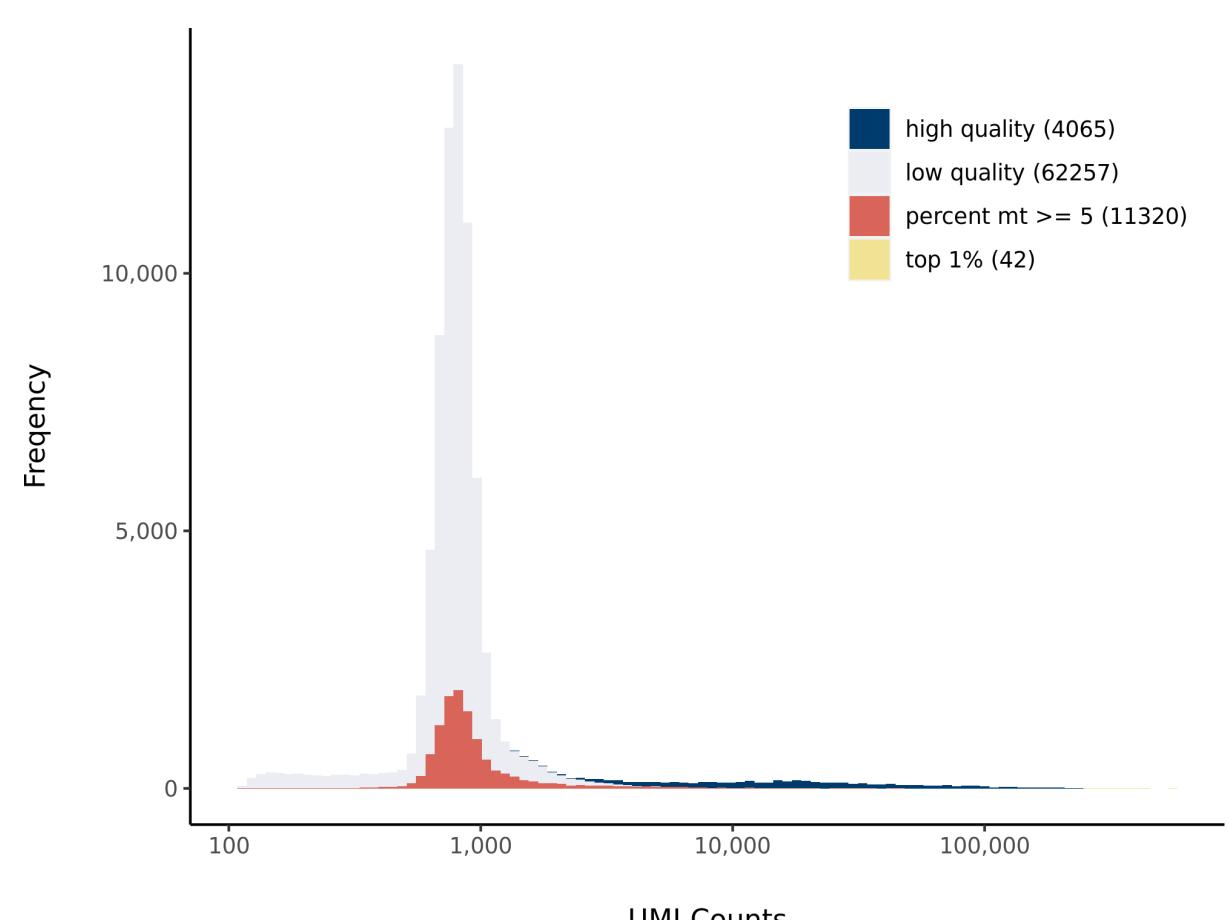
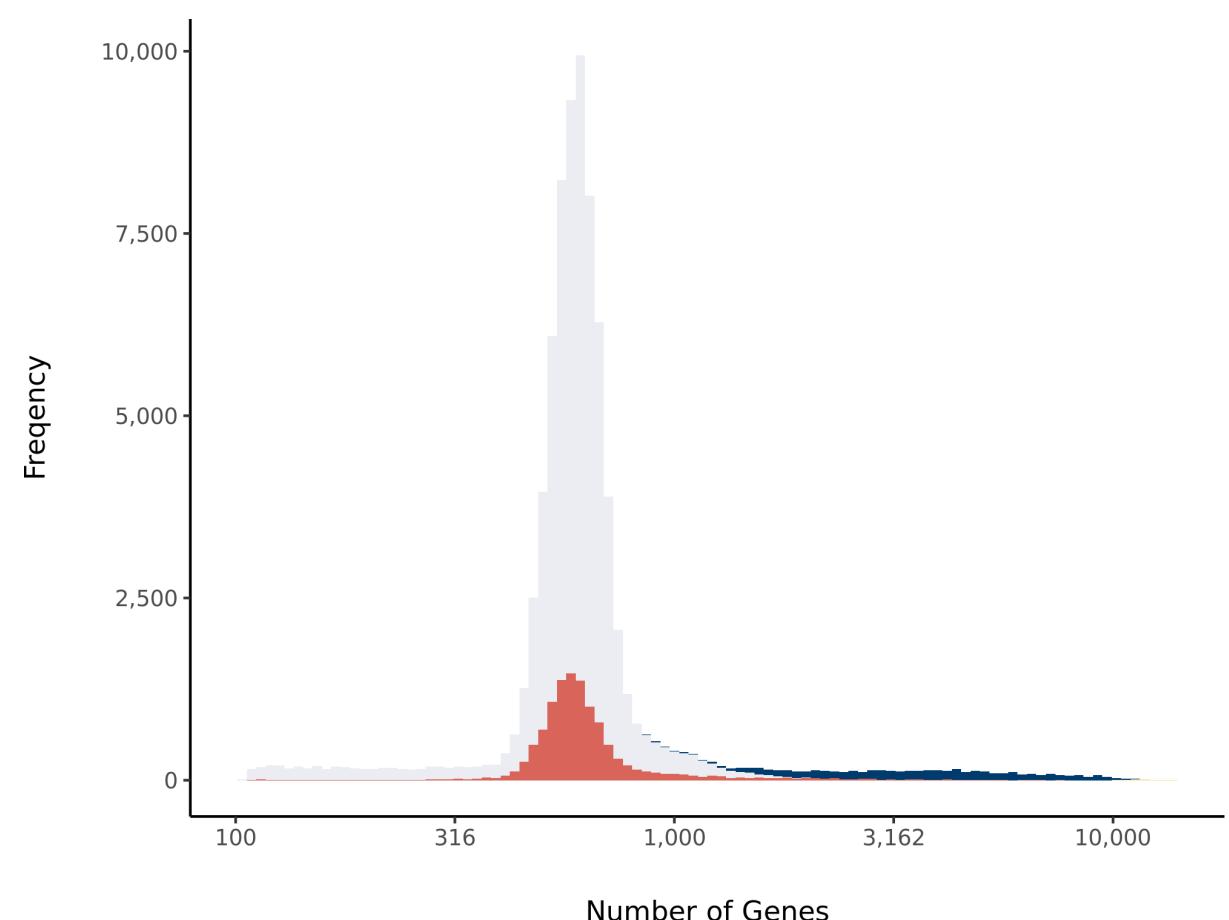
Estimated Number of High Quality Cell	4,065
High Quality Cell	5.23 %
Total UMI Counts in High Quality Cell	114,947,259
UMI Counts in High Quality Cell	59.81 %
Median UMI Counts per High Quality Cell	15,794
Median Genes per High Quality Cell	3,557
Total Genes Detected in High Quality Cell	25,145
Cell above Mitochondrial Expression Threshold	14.57 %
Estimated Doublet Rate in High Quality Cell	3.12 %

**Sequencing Stats**

Number of Reads Processed	481,231,001
Reads Pseudoaligned	93.1 %
Reads on Whitelist	96.28 %
Total UMI Counts	192,190,179
Sequencing Technology	10xv3
Species	Arabidopsis thaliana
Transcriptome	TAIR10

**Sample Stats**

Sample	tnw2
Name	WT control2
Source	Benfey lab
Genotype	WT Col-0
Transgene	NA
Treatment	Untreated
Age	5_day
Timepoint	4
Rep	2
Target Cells	5,000
Date	2019-10-17
Seq Run	Nolan_6013

**UMI Counts Histogram****Number of Genes Histogram****Barcode Rank Plot**