

Summary of snRNA-seq

Sample	Number of Nuclei	Number of Reads	Mean Reads/Nucleus	Mean Genes/Nucleus	Reads Mapped to Genome	Uniquely mapped reads (%)
Seedling-Repl1	1,269	313 M	255 K	3,174	90%	68.52%
Seedling-Repl2	973	223 M	240 K	2,308	95%	73.91%
Seedling-Repl3	1,106	205 M	188 K	2,926	96%	72.71%
Seedling-Fixed	1,209	245 M	177 K	2,270	86%	82.11%
Flower	996	250 M	267 K	3,309	90%	78.18%

Summary of Bulk RNA-seq

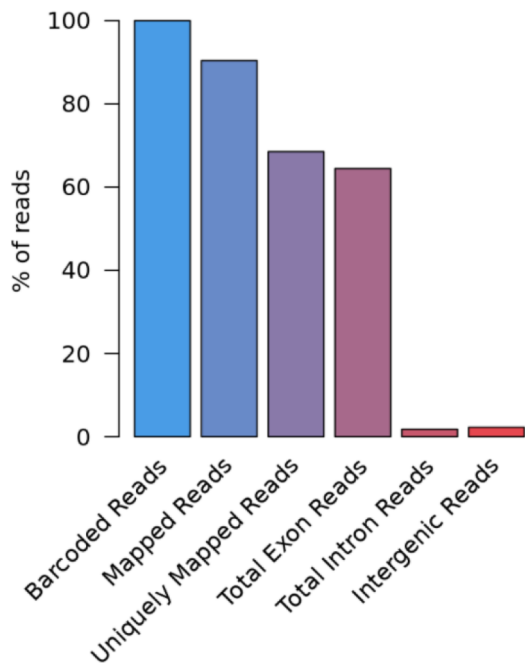
Sample	Number of reads	Reads mapped to Genome	Uniquely mapped reads (%)
bulk-Rep1	61 M	91.31%	86.46%
bulk-Rep2	60 M	96.17%	90.94%
bulk-Rep3	53 M	93.36%	89.38%

Detailed report of snRNA-seq

Experimental Overview

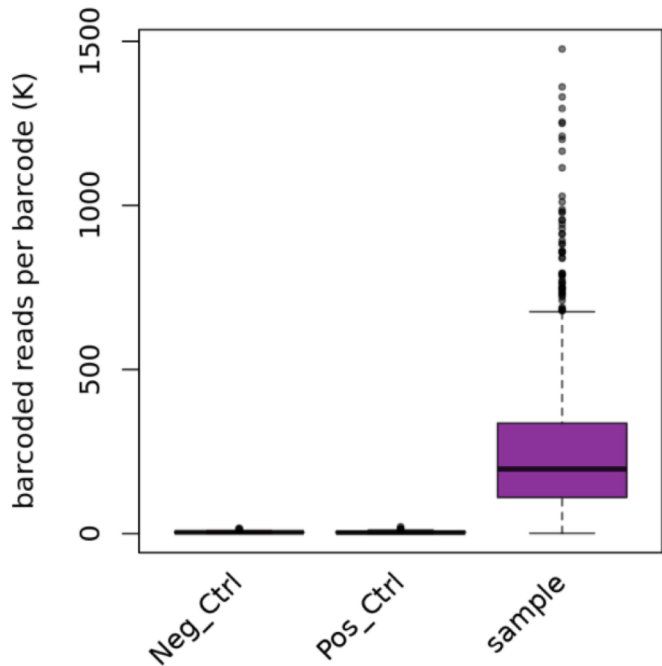
Sample Types	Neg_Ctrl (48) Pos_Ctrl (48) sample (1,173)
Total Reads	313.67 M
Barcoded Reads	299.85 M
Fraction Barcoded Reads	0.96
Barcodes Identified	1,269
Reads per Barcode	236.29 K

Read Statistics



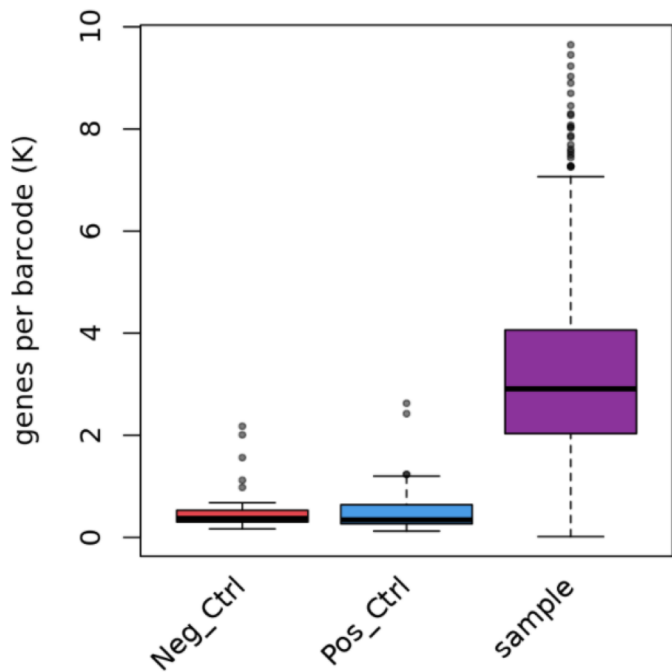
	Read Count	% of Barcoded Reads
Barcoded Reads	299,854,718	100.00
Trimmed Reads	289,379,784	96.51
Unmapped Reads	18,318,765	6.11
Mapped Reads	271,061,019	90.40
Uniquely Mapped Reads	205,452,448	68.52
Multimapped Reads	65,608,571	21.88
Total Exon Reads	193,263,409	64.45
Unique Exon Reads	182,430,105	60.84
Ambiguous Exon Reads	10,833,304	3.61
Total Intron Reads	5,375,695	1.79
Unique Intron Reads	5,322,651	1.78
Ambiguous Intron Reads	53,044	0.02
Intergenic Reads	6,813,344	2.27
Additional Information		
Mitochondrial Reads	2,782,453	0.93
Ribosomal Reads	2,945,187	0.98

Reads by Sample Type



	Reads per Barcode (Mean)	Reads per Barcode (Median)
Neg_Ctrl	4,698.96	3,675.50
Pos_Ctrl	4,943.50	2,940.00
sample	255,236.04	196,529.00

Genes by Sample Type

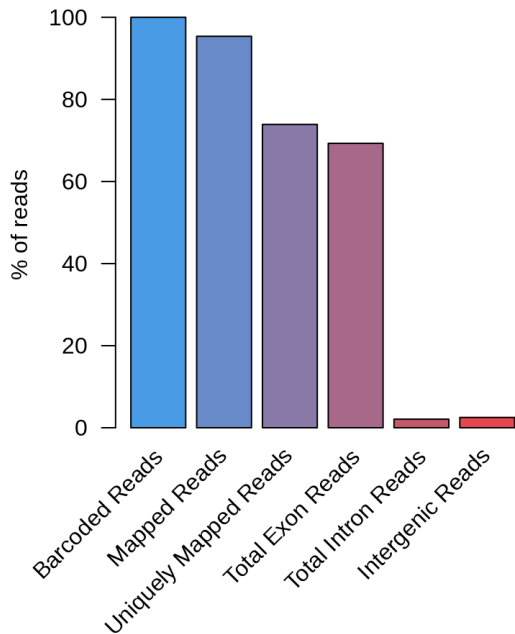


	Genes per Barcode (Mean)	Genes per Barcode (Median)
Neg_Ctrl	500.88	369.50
RPK 10000 > 0.1	500.85	369.50
RPK 10000 > 1.0	445.62	369.50
Pos_Ctrl	530.85	343.00
RPK 10000 > 0.1	530.79	343.00
RPK 10000 > 1.0	471.06	343.00
sample	3,174.58	2,909.00
RPK 10000 > 0.1	1,495.55	1,399.00
RPK 10000 > 1.0	664.22	632.00

Experimental Overview

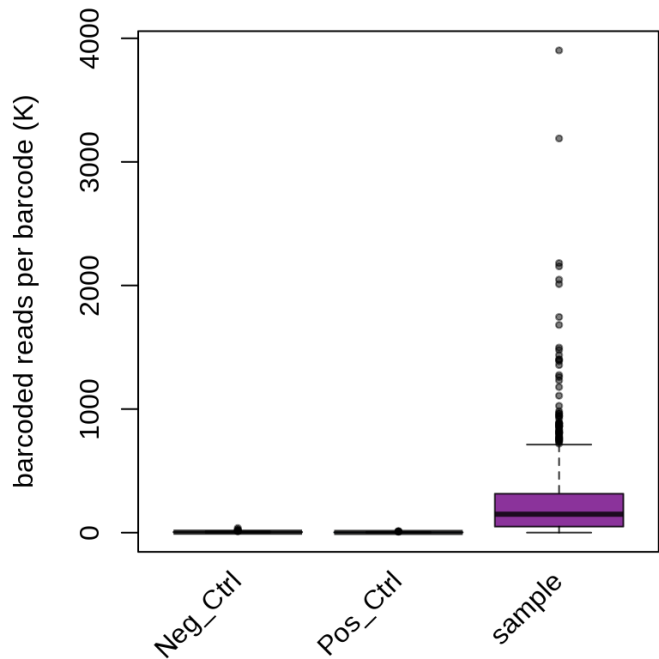
Sample Types	Neg_Ctrl (47) Pos_Ctrl (47) sample (879)
Total Reads	223.14 M
Barcoded Reads	211.74 M
Fraction Barcoded Reads	0.95
Barcodes Identified	973
Reads per Barcode	217.62 K

Read Statistics



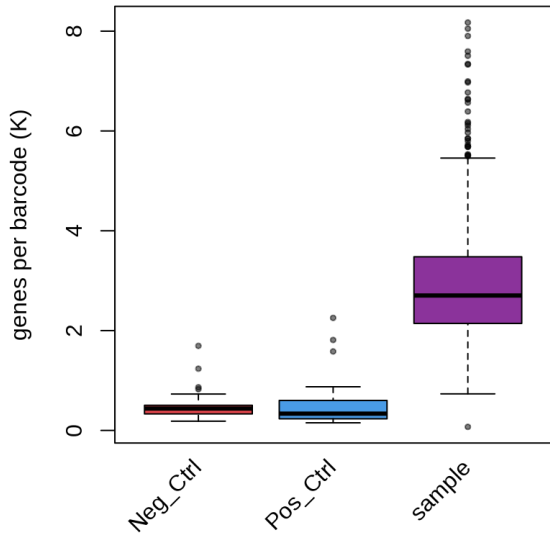
	Read Count	% of Barcoded Reads
Barcoded Reads	211,743,056	100.00
Trimmed Reads	207,173,647	97.84
Unmapped Reads	5,221,717	2.47
Mapped Reads	201,951,930	95.38
Uniquely Mapped Reads	156,500,615	73.91
Multimapped Reads	45,451,315	21.47
Total Exon Reads	146,729,979	69.30
Unique Exon Reads	139,064,104	65.68
Ambiguous Exon Reads	7,665,875	3.62
Total Intron Reads	4,432,812	2.09
Unique Intron Reads	4,396,736	2.08
Ambiguous Intron Reads	36,076	0.02
Intergenic Reads	5,337,824	2.52
Additional Information		
Mitochondrial Reads	1,894,463	0.89
Ribosomal Reads	2,477,563	1.17

Reads by Sample Type



	Reads per Barcode (Mean)	Reads per Barcode (Median)
Neg_Ctrl	5,868.94	3,731.00
Pos_Ctrl	2,722.45	1,784.00
sample	240,431.47	149,274.00

Genes by Sample Type

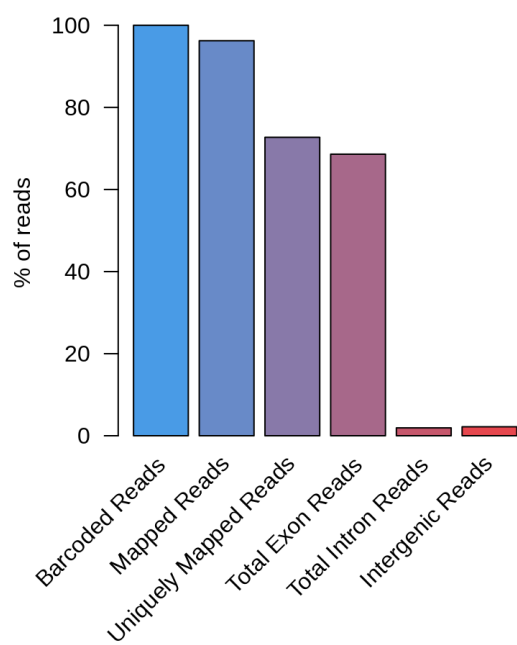


	Genes per Barcode (Mean)	Genes per Barcode (Median)
Neg_Ctrl	473.06	377.00
RPK 10000 > 0.1	473.06	377.00
RPK 10000 > 1.0	462.60	377.00
Pos_Ctrl	375.70	296.00
RPK 10000 > 0.1	375.70	296.00
RPK 10000 > 1.0	372.13	296.00
sample	2,308.36	2,147.00
RPK 10000 > 0.1	1,210.40	1,185.00
RPK 10000 > 1.0	596.03	567.00

Experimental Overview

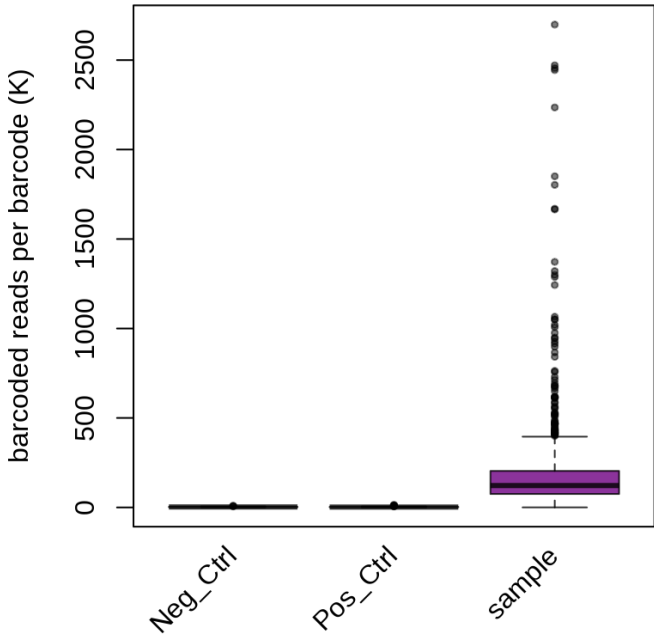
Sample Types	Neg_Ctrl (48) Pos_Ctrl (47) sample (1,011)
Total Reads	205.52 M
Barcoded Reads	191.33 M
Fraction Barcoded Reads	0.93
Barcodes Identified	1,106
Reads per Barcode	173.00 K

Read Statistics



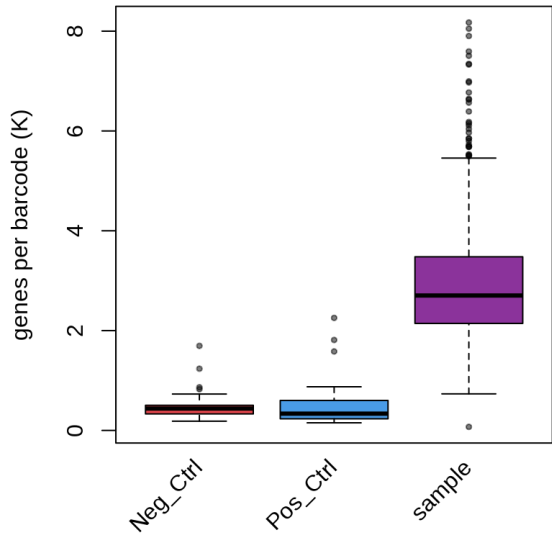
	Read Count	% of Barcoded Reads
Barcoded Reads	191,333,789	100.00
Trimmed Reads	186,940,462	97.70
Unmapped Reads	2,797,928	1.46
Mapped Reads	184,142,534	96.24
Uniquely Mapped Reads	139,124,356	72.71
Multimapped Reads	45,018,178	23.53
Total Exon Reads	131,251,219	68.60
Unique Exon Reads	124,316,795	64.97
Ambiguous Exon Reads	6,934,424	3.62
Total Intron Reads	3,688,398	1.93
Unique Intron Reads	3,642,567	1.90
Ambiguous Intron Reads	45,831	0.02
Intergenic Reads	4,184,739	2.19
Additional Information		
Mitochondrial Reads	1,216,283	0.64
Ribosomal Reads	2,417,577	1.26

Reads by Sample Type



	Reads per Barcode (Mean)	Reads per Barcode (Median)
Neg_Ctrl	2,803.00	2,396.50
Pos_Ctrl	3,112.57	1,939.00
sample	188,974.24	122,326.00

Genes by Sample Type

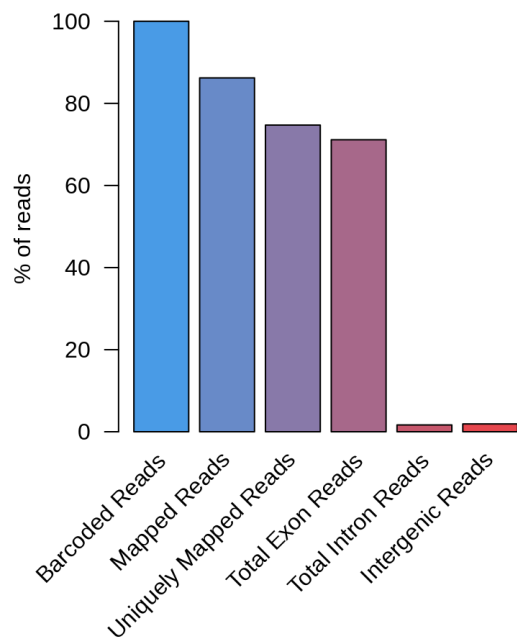


	Genes per Barcode (Mean)	Genes per Barcode (Median)
Neg_Ctrl	476.81	438.00
RPK 10000 > 0.1	476.81	438.00
RPK 10000 > 1.0	467.31	438.00
Pos_Ctrl	470.60	336.00
RPK 10000 > 0.1	470.60	336.00
RPK 10000 > 1.0	447.06	336.00
sample	2,926.01	2,703.00
RPK 10000 > 0.1	1,968.94	1,895.00
RPK 10000 > 1.0	879.87	855.00

Experimental Overview

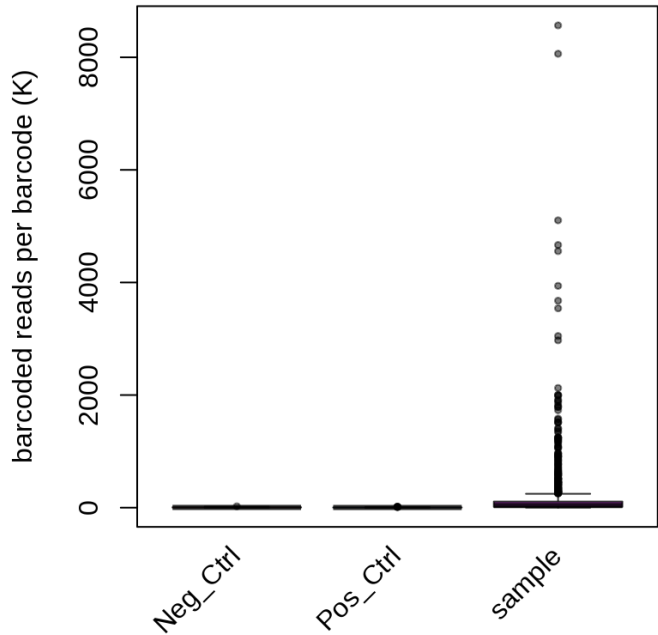
Sample Types	Neg_Ctrl (45) Pos_Ctrl (45) sample (1,119)
Total Reads	245.19 M
Barcoded Reads	199.64 M
Fraction Barcoded Reads	0.81
Barcodes Identified	1,209
Reads per Barcode	165.13 K

Read Statistics



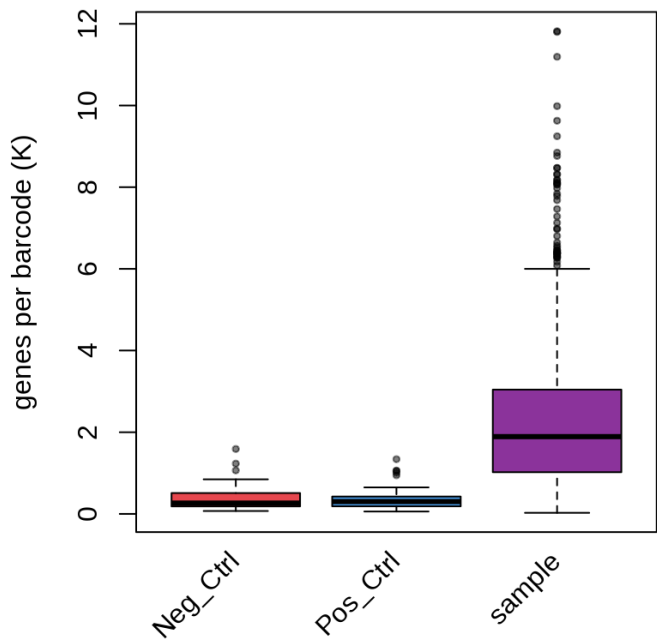
	Read Count	% of Barcoded Reads
Barcoded Reads	199,644,423	100.00
Trimmed Reads	181,669,195	91.00
Unmapped Reads	9,553,769	4.79
Mapped Reads	172,115,426	86.21
Uniquely Mapped Reads	149,160,816	74.71
Multimapped Reads	22,954,610	11.50
Total Exon Reads	142,028,753	71.14
Unique Exon Reads	134,859,300	67.55
Ambiguous Exon Reads	7,169,453	3.59
Total Intron Reads	3,321,079	1.66
Unique Intron Reads	3,301,467	1.65
Ambiguous Intron Reads	19,612	0.01
Intergenic Reads	3,810,984	1.91
Additional Information		
Mitochondrial Reads	1,919,081	0.96
Ribosomal Reads	1,506,199	0.75

Reads by Sample Type



	Reads per Barcode (Mean)	Reads per Barcode (Median)
Neg_Ctrl	5,897.60	4,138.00
Pos_Ctrl	4,544.73	3,540.00
sample	177,993.31	37,876.00

Genes by Sample Type

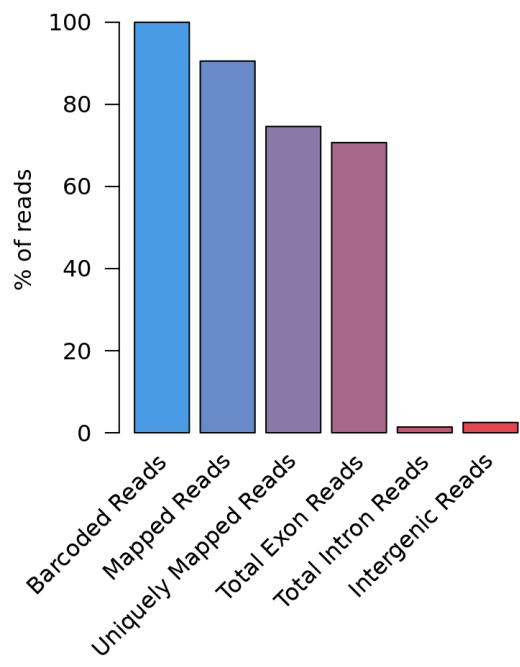


	Genes per Barcode (Mean)	Genes per Barcode (Median)
Neg_Ctrl	403.42	264.00
RPK 10000 > 0.1	403.42	264.00
RPK 10000 > 1.0	401.07	264.00
Pos_Ctrl	377.76	302.00
RPK 10000 > 0.1	377.76	302.00
RPK 10000 > 1.0	376.51	302.00
sample	2,270.27	1,892.00
RPK 10000 > 0.1	1,628.91	1,608.00
RPK 10000 > 1.0	794.85	796.00

Experimental Overview

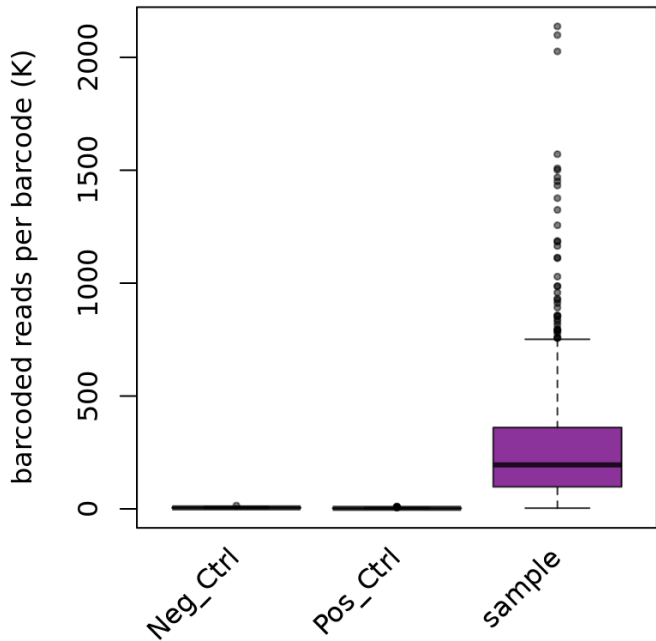
Sample Types	Neg_Ctrl (48) Pos_Ctrl (48) sample (900)
Total Reads	250.87 M
Barcoded Reads	241.60 M
Fraction Barcoded Reads	0.96
Barcodes Identified	996
Reads per Barcode	242.57 K

Read Statistics



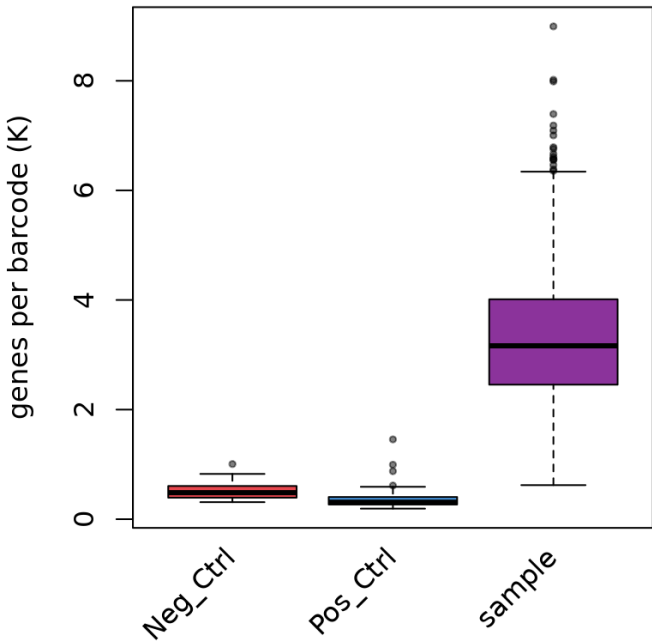
	Read Count	% of Barcoded Reads
Barcoded Reads	241,604,100	100.00
Trimmed Reads	230,595,698	95.44
Unmapped Reads	11,814,320	4.89
Mapped Reads	218,781,378	90.55
Uniquely Mapped Reads	180,275,535	74.62
Multimapped Reads	38,505,843	15.94
Total Exon Reads	170,801,636	70.69
Unique Exon Reads	160,471,912	66.42
Ambiguous Exon Reads	10,329,724	4.28
Total Intron Reads	3,416,113	1.41
Unique Intron Reads	3,396,512	1.41
Ambiguous Intron Reads	19,601	0.01
Intergenic Reads	6,057,786	2.51
Additional Information		
Mitochondrial Reads	4,793,657	1.98
Ribosomal Reads	2,729,610	1.13

Reads by Sample Type



	Reads per Barcode (Mean)	Reads per Barcode (Median)
Neg_Ctrl	5,381.25	4,761.00
Pos_Ctrl	3,129.08	2,524.50
sample	267,995.12	195,046.00

Genes by Sample Type



	Genes per Barcode (Mean)	Genes per Barcode (Median)
Neg_Ctrl	515.81	483.50
RPK 10000 > 0.1	515.81	483.50
RPK 10000 > 1.0	515.02	483.50
Pos_Ctrl	378.90	310.50
RPK 10000 > 0.1	378.90	310.50
RPK 10000 > 1.0	377.48	310.50
sample	3,309.21	3,164.50
RPK 10000 > 0.1	2,127.41	2,047.50
RPK 10000 > 1.0	1,143.84	1,126.00