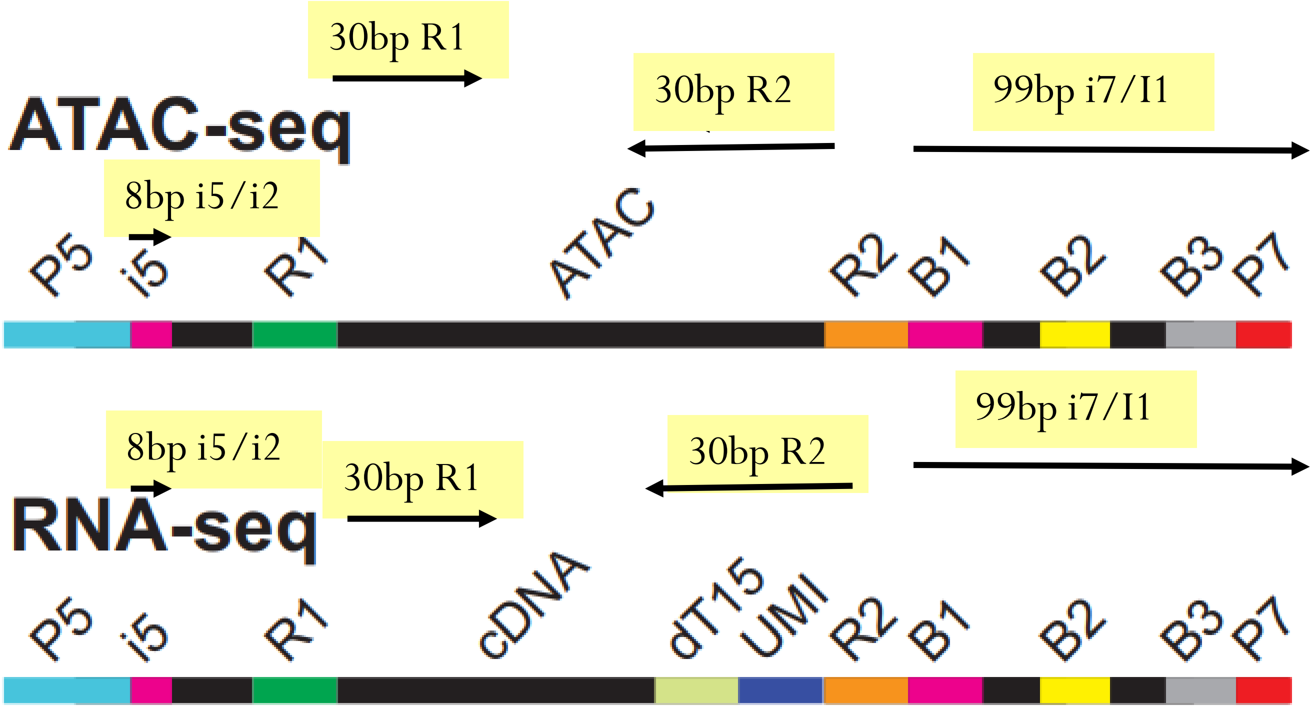
Expected library structure:



B1, B2 and B3: ligation barcodes

Dataset stats ATAC

Species	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio
mm10	**2x30**	Undetermined	228,010,414	100,398,992		0.23	3,780,568	0.04		12.61
hg38	**2x30**	Undetermined	228,010,414	63,553,452		0.22	2,568,418	0.04		4.79

After within-barcode dedupping:

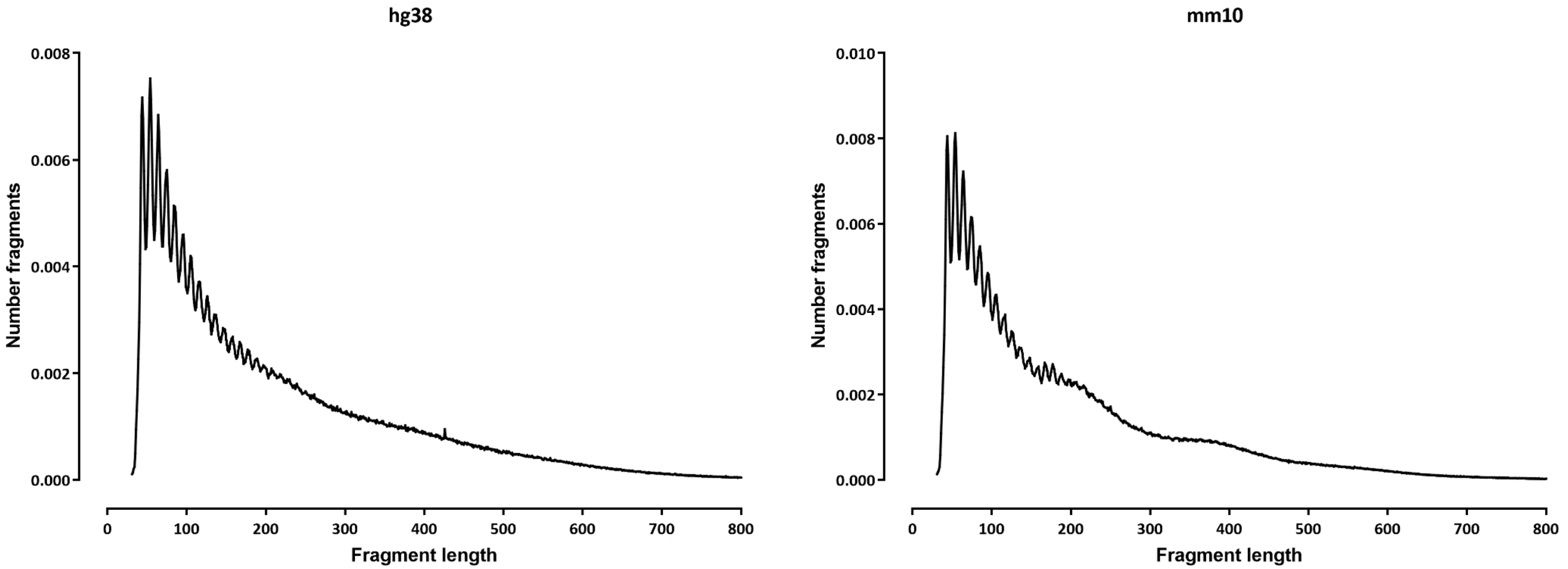
hg38:

Unique:	14,769,090
Complexity:	0.84

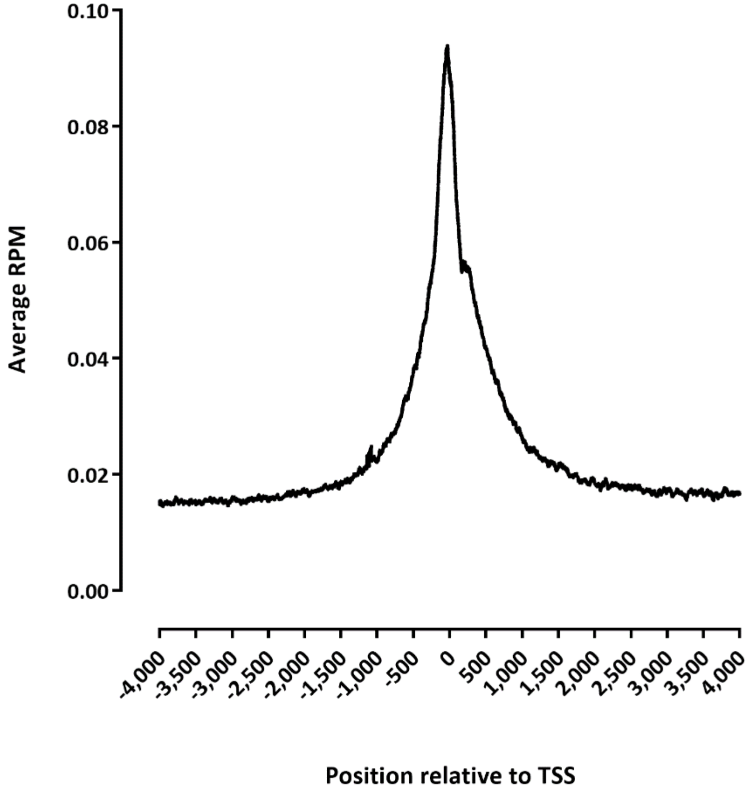
mm10:

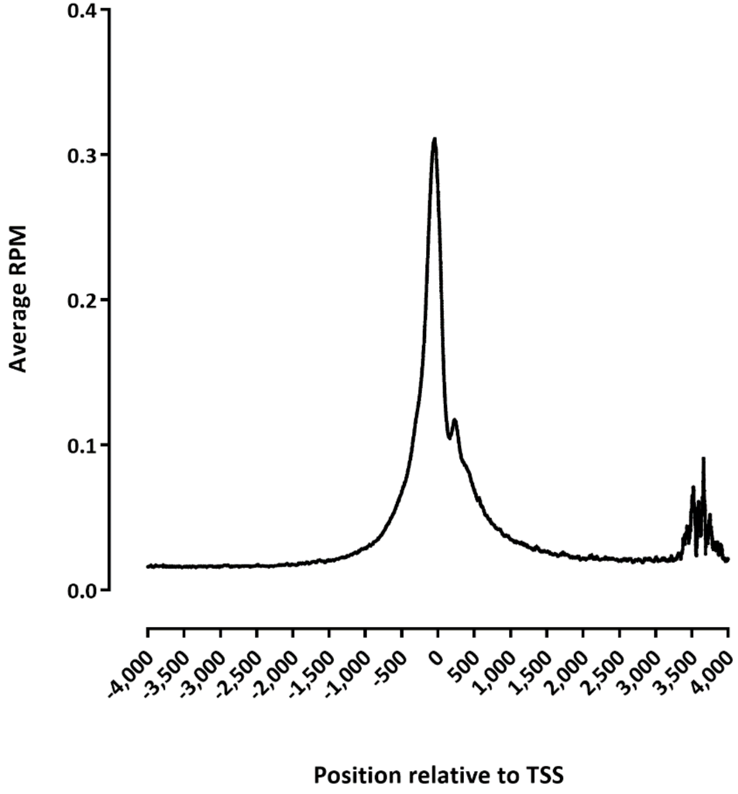
Unique:	26,671,864
Complexity:	0.78

Fragment length distribution



TSS profile


hg38


mm10

Dataset stats ATAC

Species	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio
mm10	**2x30**	Undetermined	228,010,414	100,398,992		0.23	3,780,568	0.04		12.61
hg38	**2x30**	Undetermined	228,010,414	63,553,452		0.22	2,568,418	0.04		4.79

Dataset stats RNA

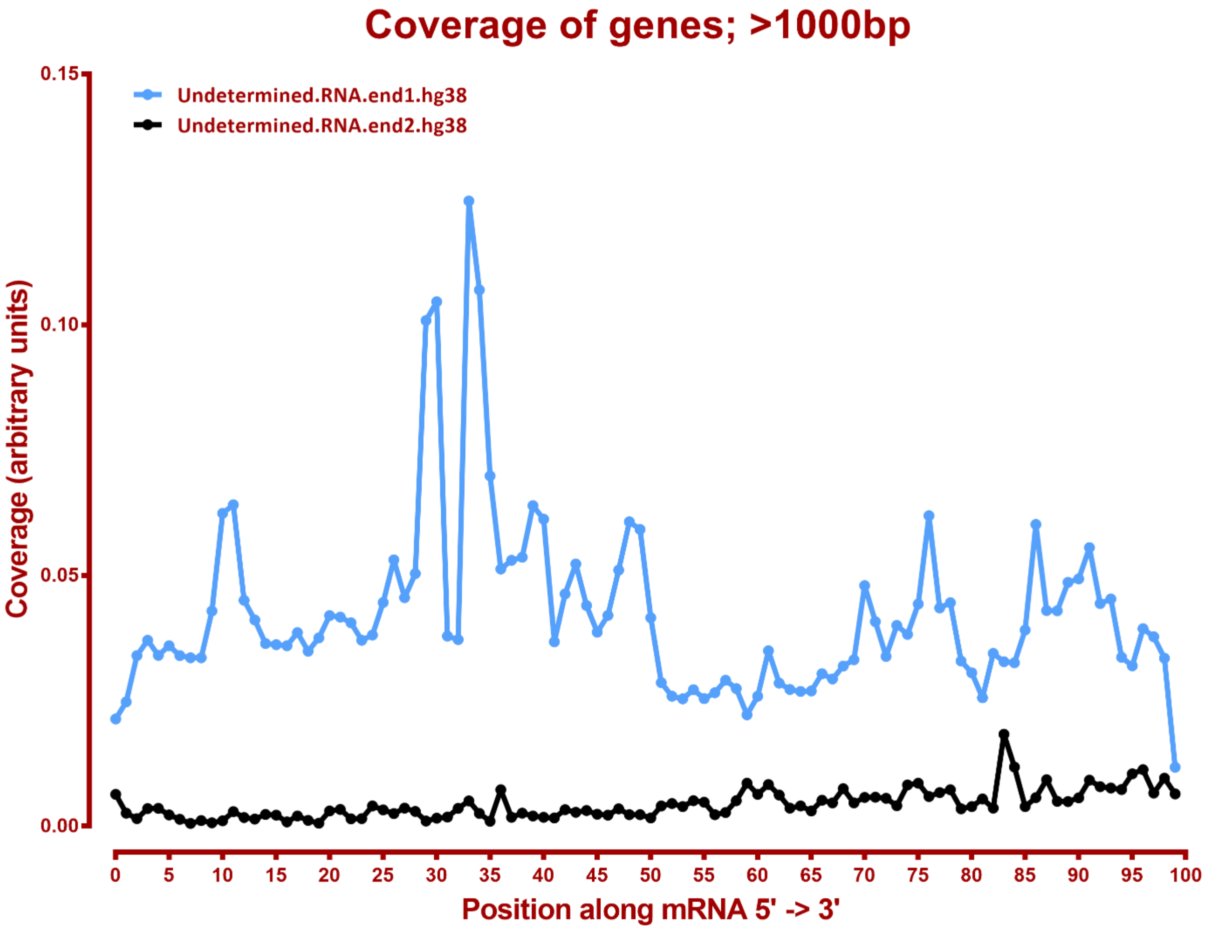
Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
Undetermined.unmapped.end1	**1x30**	STAR-2.5.3a	**hg38**	147,354,159	0.25	31,550,876	600,966	21,255,859	1,367,096	0.19
Undetermined.unmapped.end1	**1x30**	STAR-2.5.3a	**mm10**	147,354,159	0.22	63,908,564	1,699,430	20,565,978	1,765,113	0.30
Undetermined.unmapped.end2	**1x30**	STAR-2.5.3a	**hg38**	147,354,159	0.05	27,396,146	6,215,608	66,374,348	9,821,014	0.37
Undetermined.unmapped.end2	**1x30**	STAR-2.5.3a	**mm10**	147,354,159	0.05	20,819,217	4,422,982	58,913,793	8,054,903	0.31

Note: the second end should really not align at all, it's 10bp UMI + 15bp oligo-dT + 5bp of actual sequence

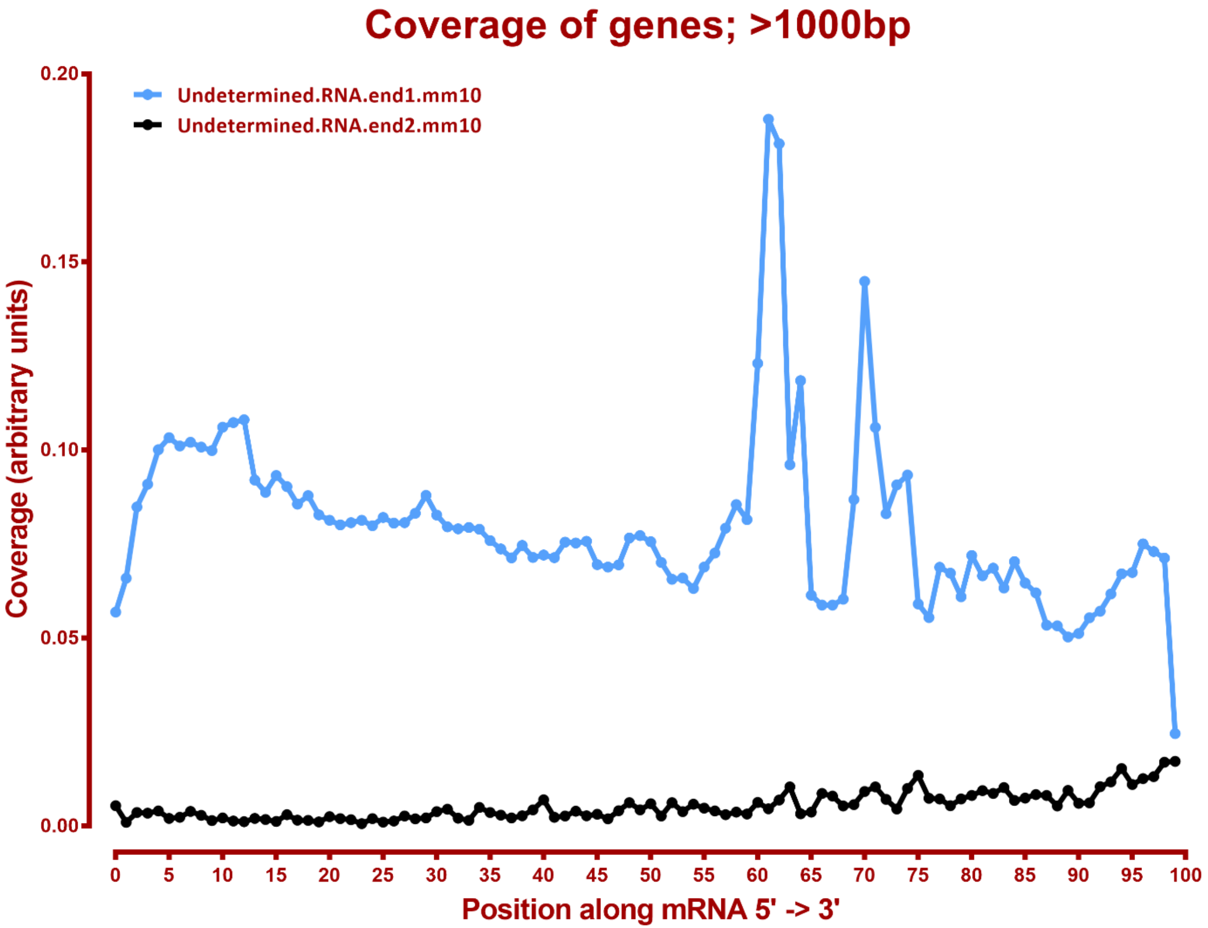
- average alignment length for end1 is 29bp
- average alignment length for end2 is 24bp

#	Exonic:	Intergenic:	Intronic:
Undetermined.RNA.end1.hg38	0.14	0.10	0.76
Undetermined.RNA.end1.mm10	0.21	0.10	0.69
Undetermined.RNA.end2.hg38	0.02	0.34	0.64
Undetermined.RNA.end2.mm10	0.02	0.51	0.47

5’-3’ mRNA coverage

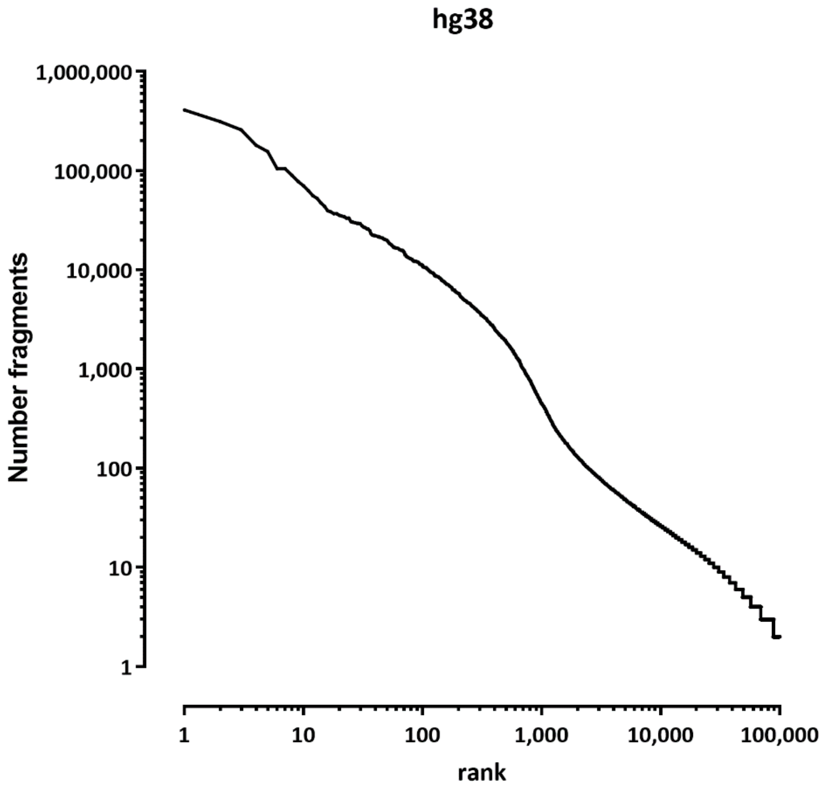


5’-3’ mRNA coverage

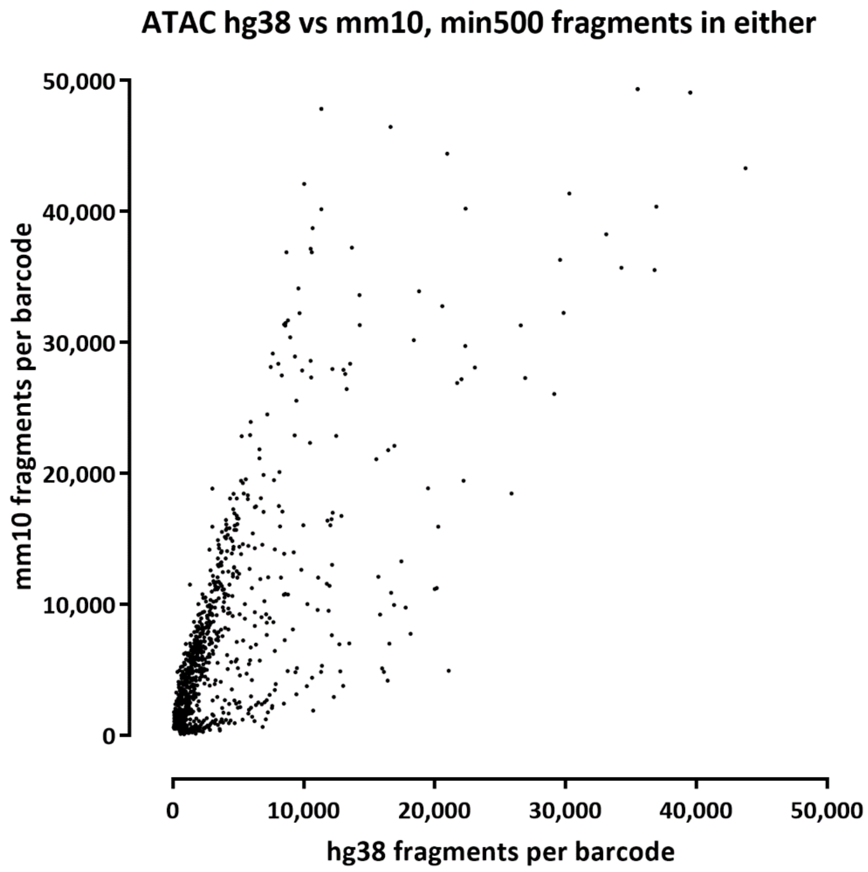


ATAC single-cell level summary:

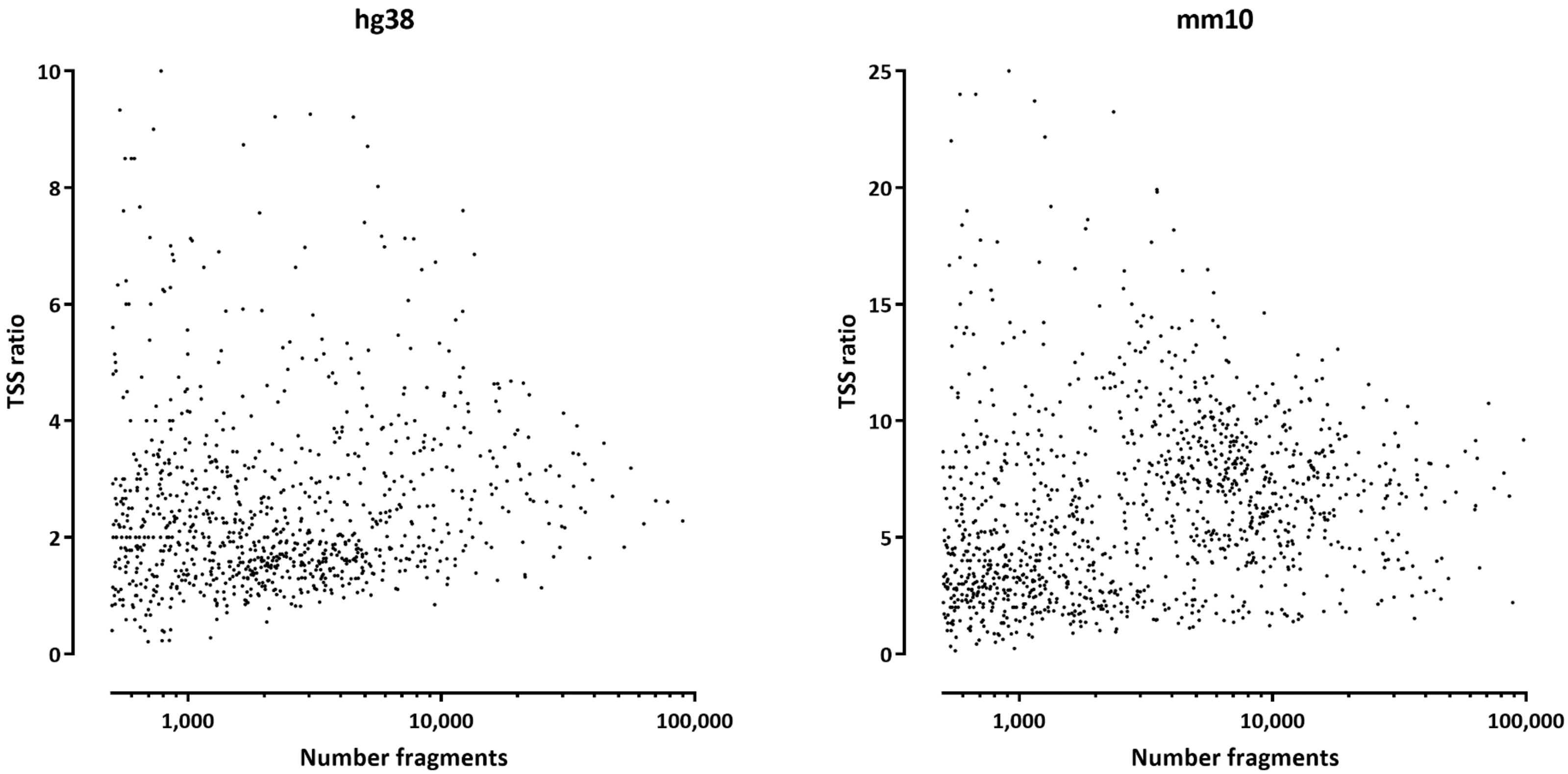
# fragments	**hg38**	**mm10**
<10	223,510	288,179
10-100	28,192	48,020
100-500	1,521	2,937
500-1,000	259	306
1,000-5,000	476	451
5,000-10,000	112	242
>10,000	110	236



ATAC single-cell level summary:

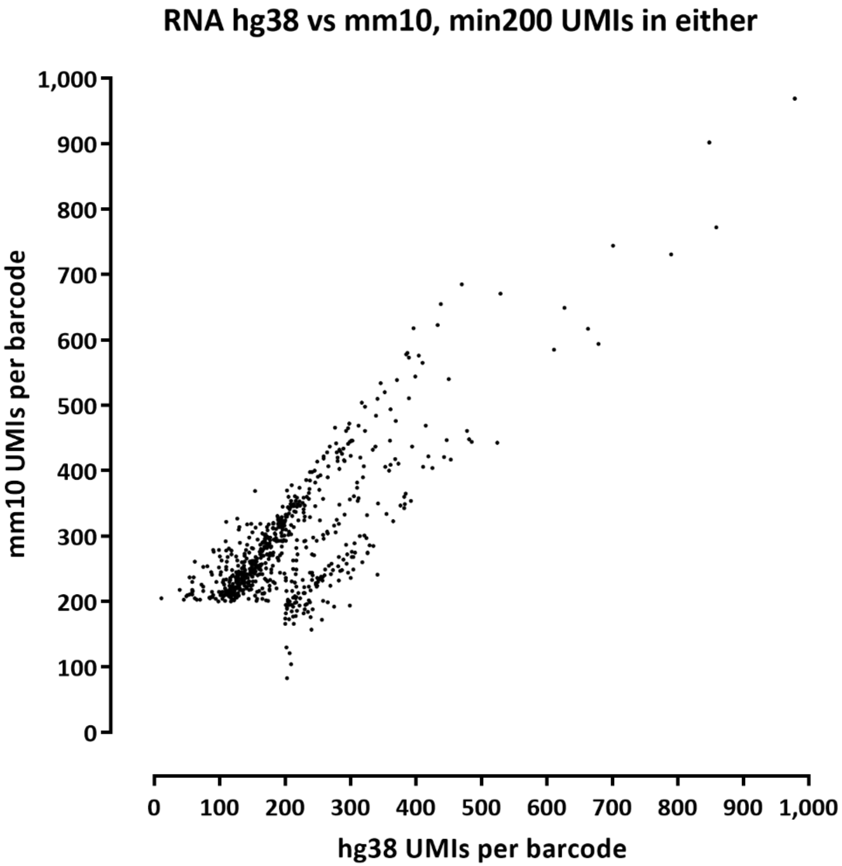


ATAC single-cell level summary:

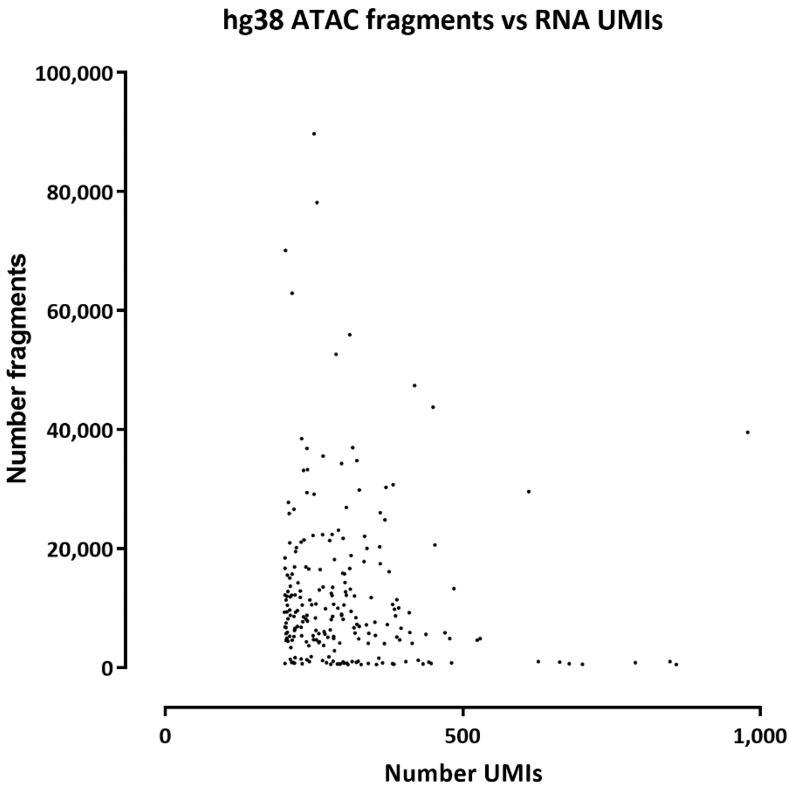


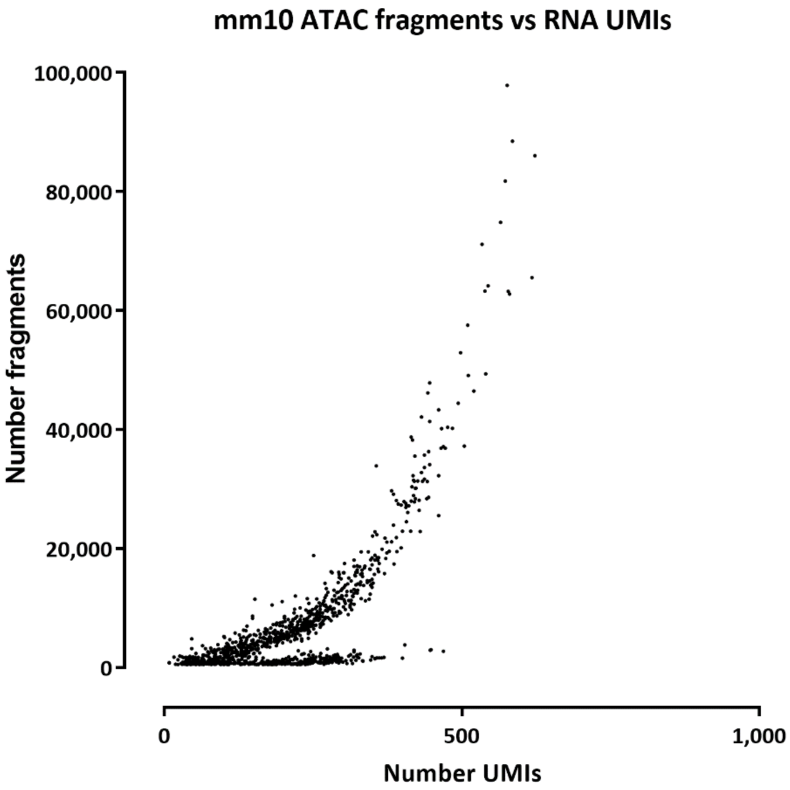
RNA single-cell level summary:

	read1	read2	read1	read2
#UMIs	**hg38**		**mm10**	
0-10	204,389	179,891	339,373	142,732
10-20	9,288	6,417	26,804	3,996
20-50	4,985	2,759	14,694	1,709
50-100	1,737	833	3,447	610
100-200	949	546	1,172	435
200-500	293	241	633	192
500-1000	11	12	27	11
>1000	0	0	0	0



RNA vs ATAC single-cell level summary:





ATAC single-cell level summary: