Zymo-seq ATAC
QC report

Sample Arrival

The following checklist details the steps performed on your samples:

SERVICE	
Sample Received & Visual inspection	✓
Sample measurements (cell count/ viability)	✓
DNA quantification by nanodrop	✓
Tagmentation efficiency	✓

Sample Received & Visual inspection:

Samples were received on XX/XX/20XX and immediately stored at – 80 °C after visual inspection:

Samples consist of:

SAMPLES		
A	Cell suspension frozen _____	__ vials
B	Cell suspension frozen _____	__ vials

Samples were fully covered by dry ice? ☐

If not, provide detail: _____

When removed from dry ice, samples inside the vials appeared frozen?☐

If not, provide details:

1) Which vials (label specifications) seemed thawed?
   _____
2) Were samples completely thawed or what approximate percentage was still frozen?
   _____

Sample measurement (cell count/viability):

Upon thawing, cells were counted, and values are below as appropriate:

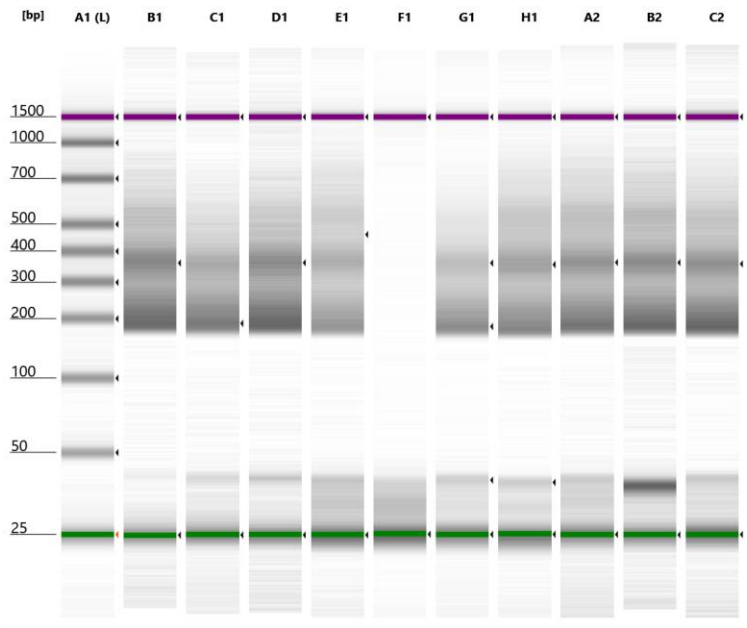
SAMPLES		
A	Total number cells/ mL	
	Percent cells alive (alive cells/ mL)	
	Percent cells dead (dead cells/ mL)	
	Volume cell suspension	

DNA quantification (after tagmentation) using nanodrop:

SAMPLES		Concentration (ng/uL)
A	Replicate 1	
	Replicate 2	
	Replicate 3	
B	Replicate 1	
	Replicate 2	
	Replicate 3	

**nanodrop concentrations are a very rough approximation of true concentration since the tagmented DNA presents fragments of multiple sizes. This control is performed to ensure that DNA is present (even if in low quantity) prior to adaptor ligation*

Tagmentation efficiency:



A1: Ladder

B1: Sample A replicate 1

C1: Sample A replicate 2

D1: Sample A replicate 3

E1: Sample C replicate 1

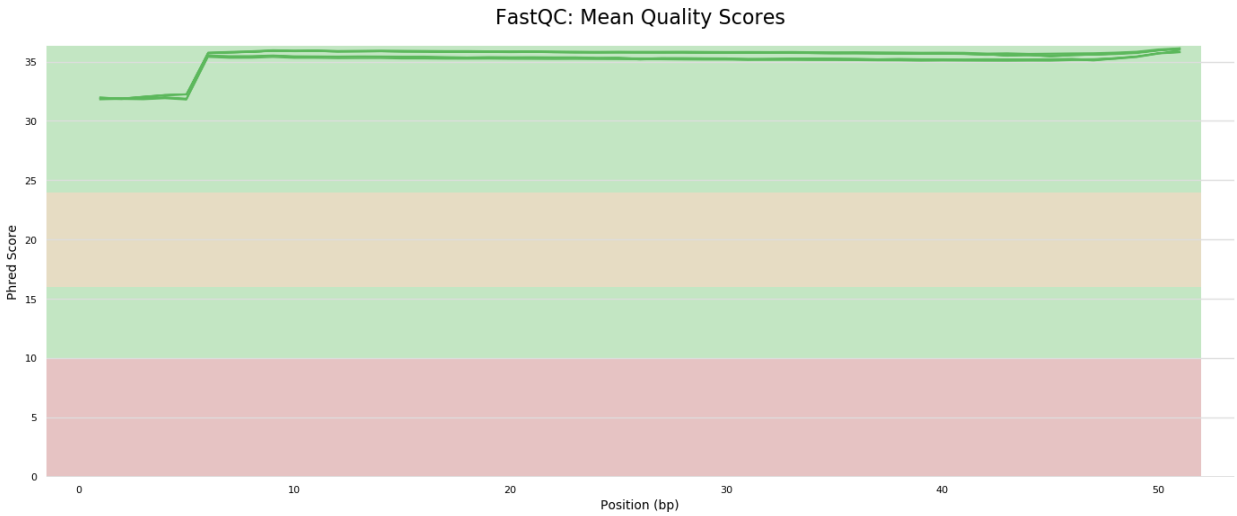
Etc

F1: failed – no amplification seen

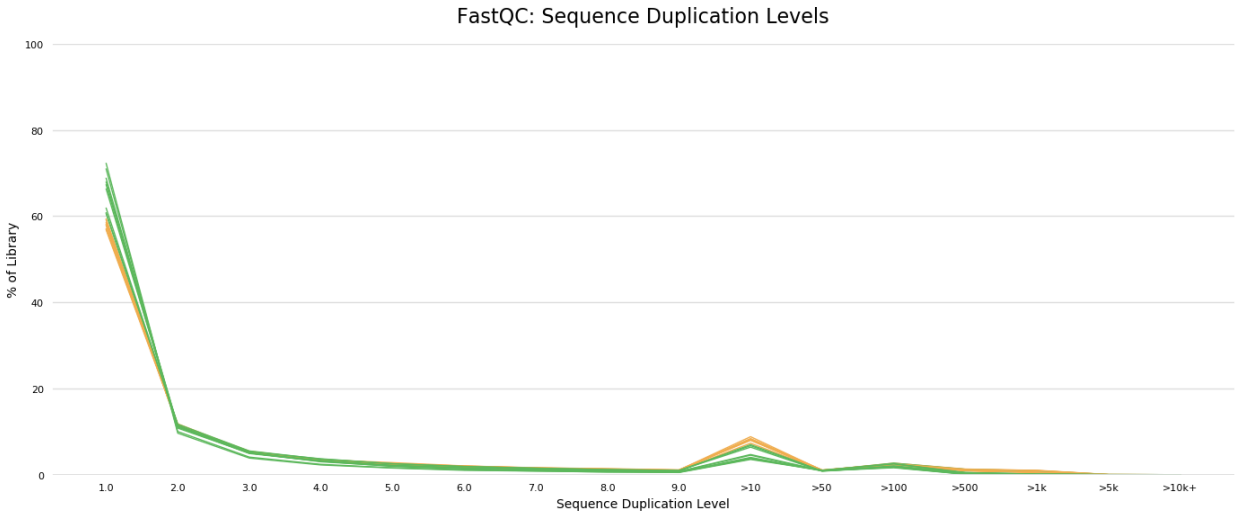
Samples should show fragments on the regions 200-1000 bp, with more intense marks around 200, 400 and sometimes also visible at 600 bp. These stronger bands represent the nucleosome-free, the mononucleosome and dinucleosome fragments plus the adaptor sizes.

Sequencing Results

FastQC (library; trimmed)

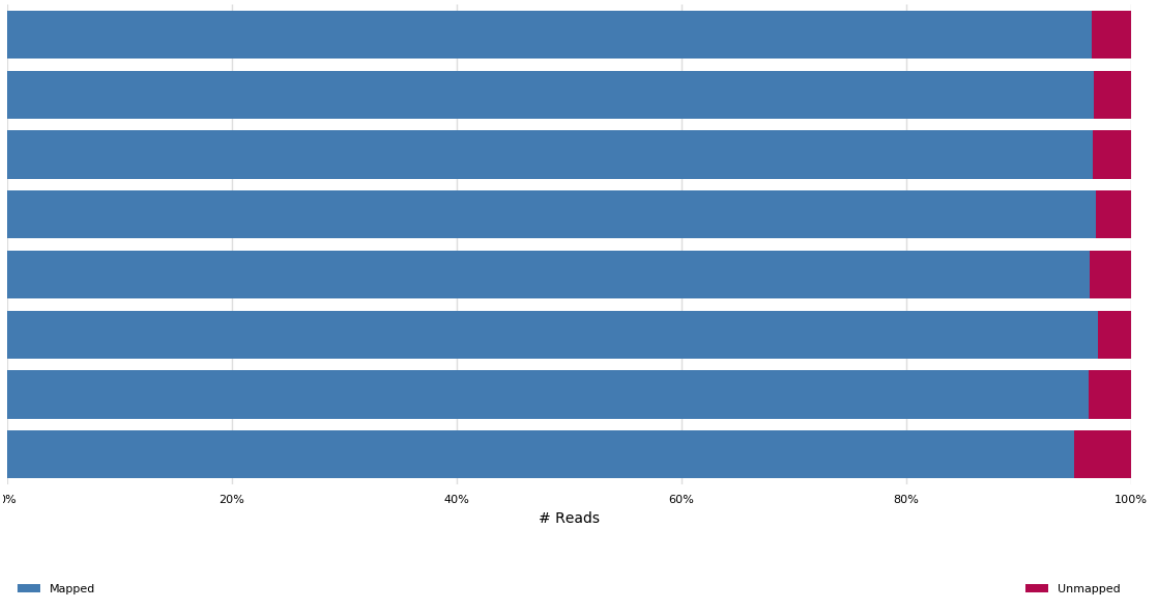


Sequence Duplication Levels



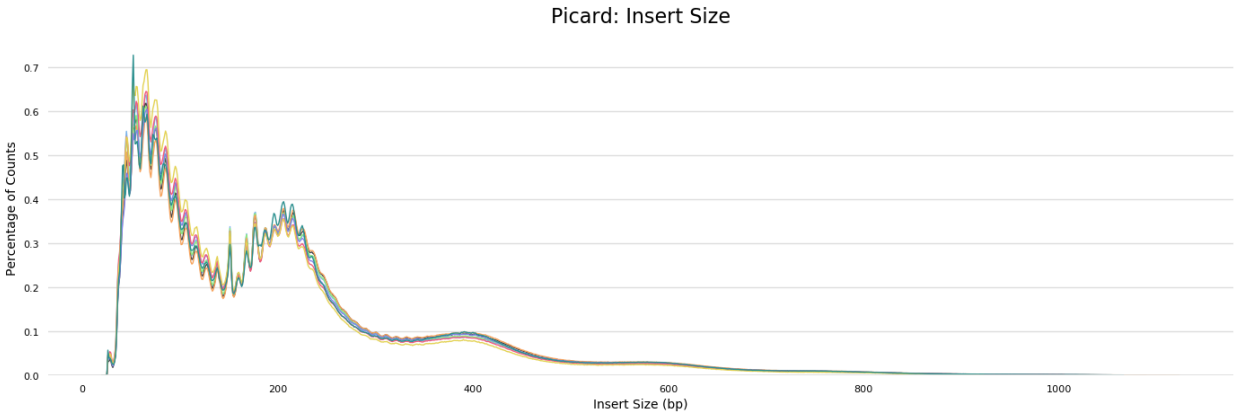
SAMTools (library)

Percent Mapped



Picard (merged library; filtered)

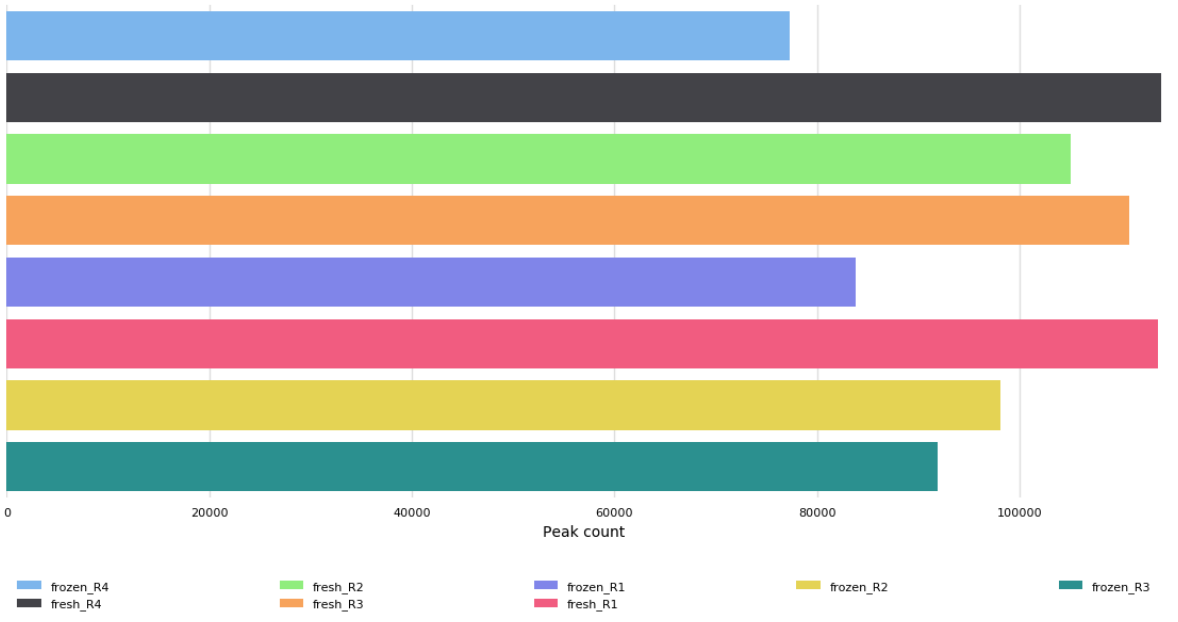
Insert Size



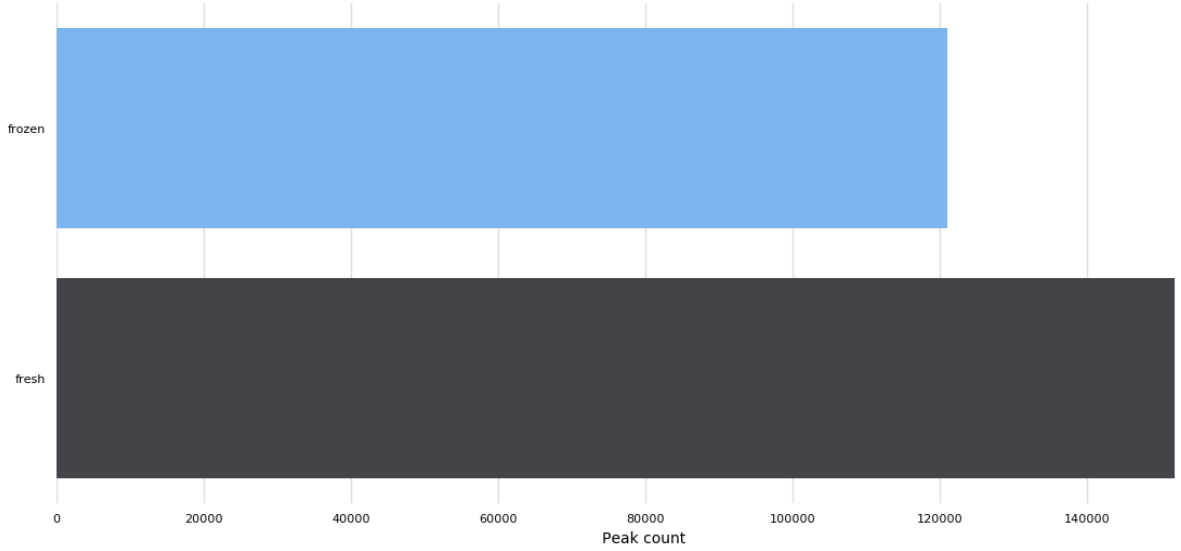
ATAQV: Read count (merged library)

Sample	Total reads	Properly paired and mapped	Autosomal reads	Duplicate in autosomal reads	Total mitochondrial reads
fresh_R4	184 651 124	168 572 350	155 207 040	11 178 055	8 366 553
fresh_R2	156 702 422	142 672 578	130 650 637	8 151 831	7 782 849
fresh_R3	180 896 314	164 579 870	153 065 494	10 847 140	6 663 605
fresh_R1	159 044 040	144 549 711	133 875 273	9 540 636	6 519 106
frozen_R2	128 816 868	117 647 674	110 235 058	6 564 911	3 909 577
frozen_R4	81 491 584	72 386 198	66 628 031	2 250 398	3 275 324
frozen_R3	84 052 294	75 907 143	71 169 150	2 995 712	2 383 854
frozen_R1	71 549 412	64 977 605	60 959 900	2 240 308	2 032 012

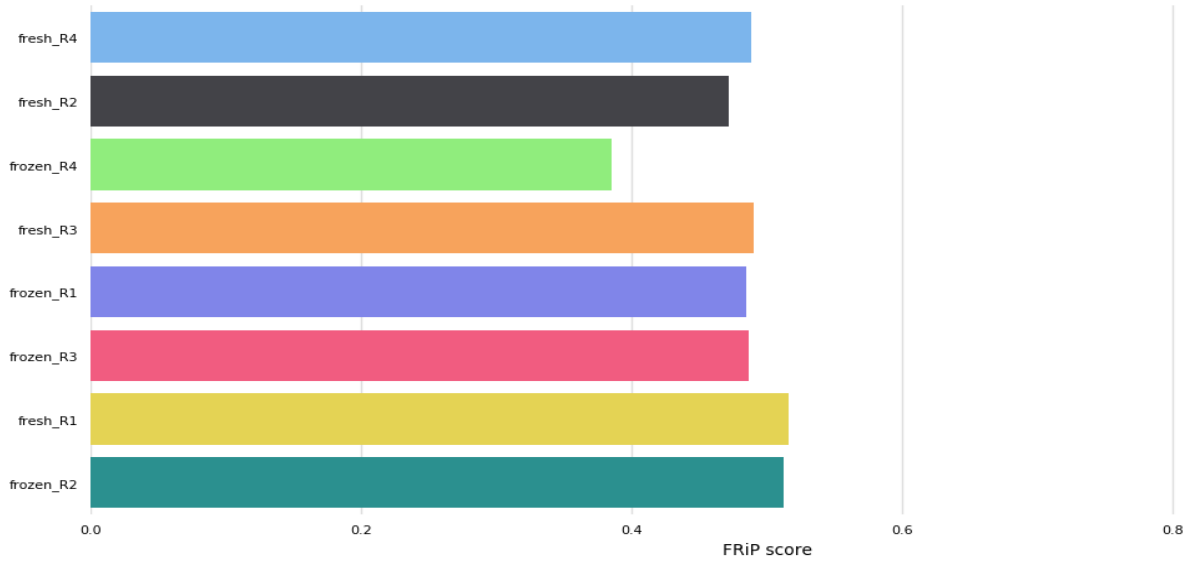
MACS2: Peak count (merged library)



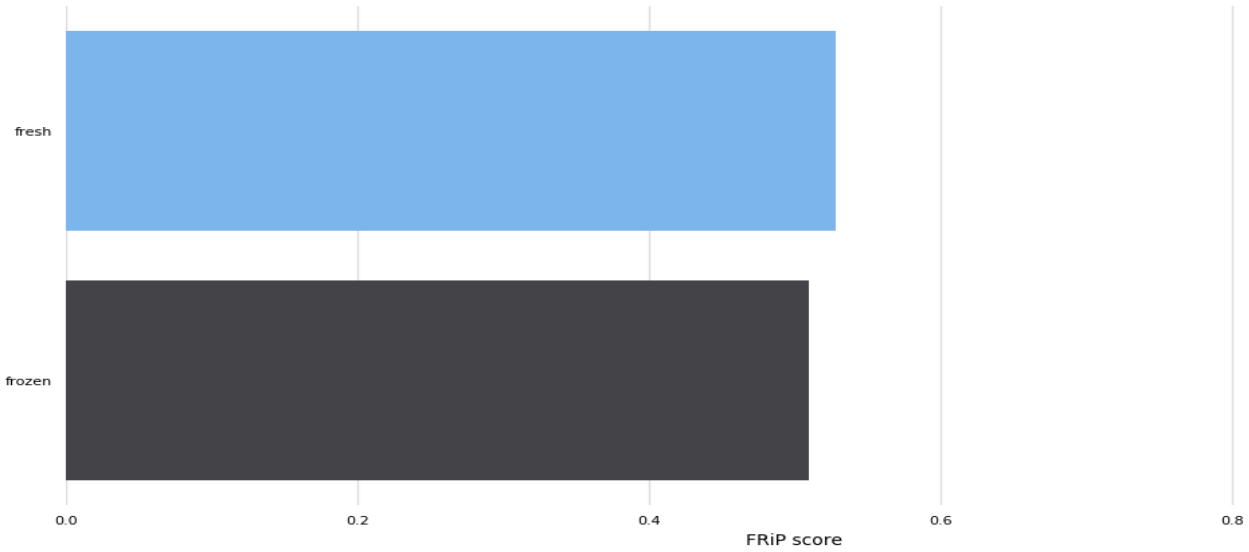
MACS2: Peak count (merged replicate)



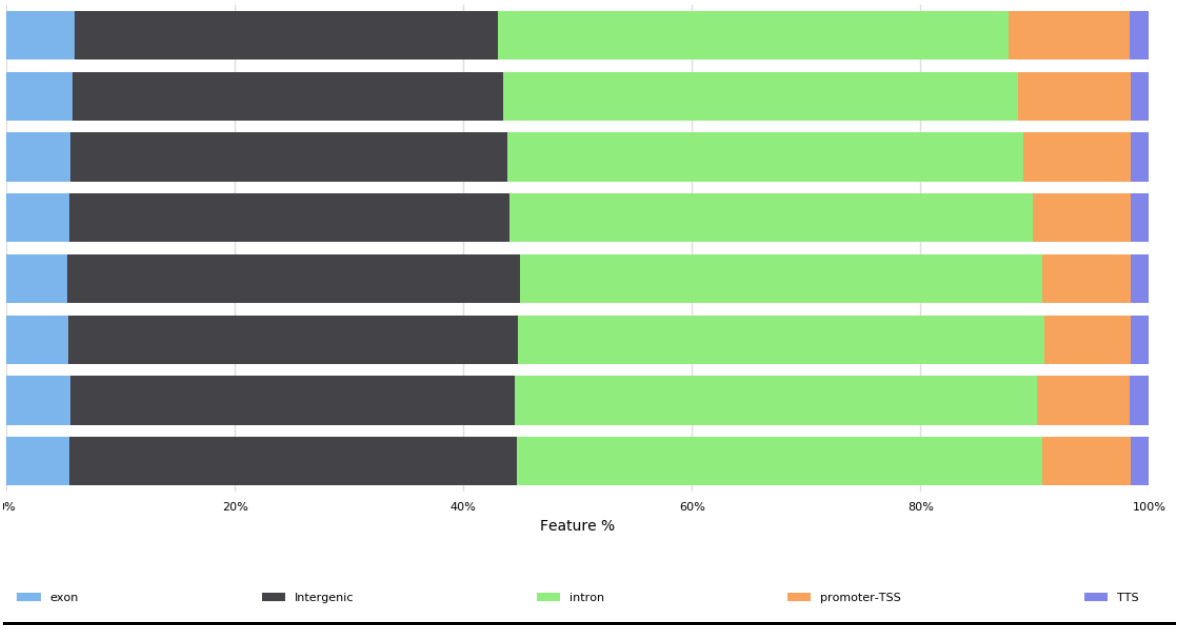
MACS2: Peak FRiP score (merged library)



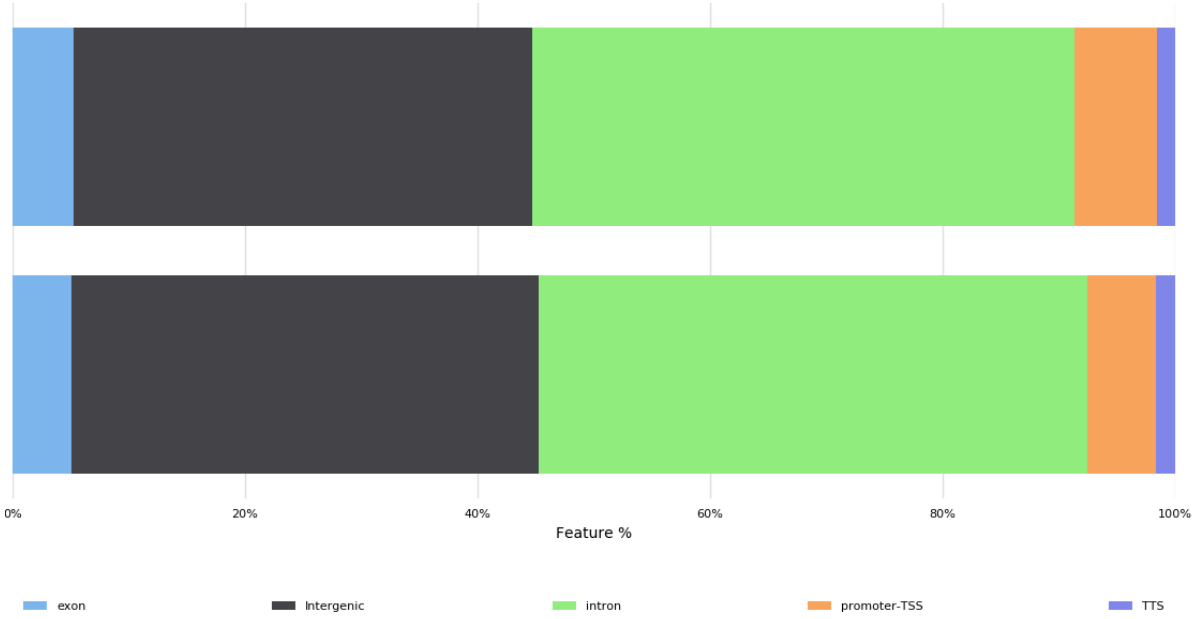
MACS2: Peak FRiP score (merged replicate)



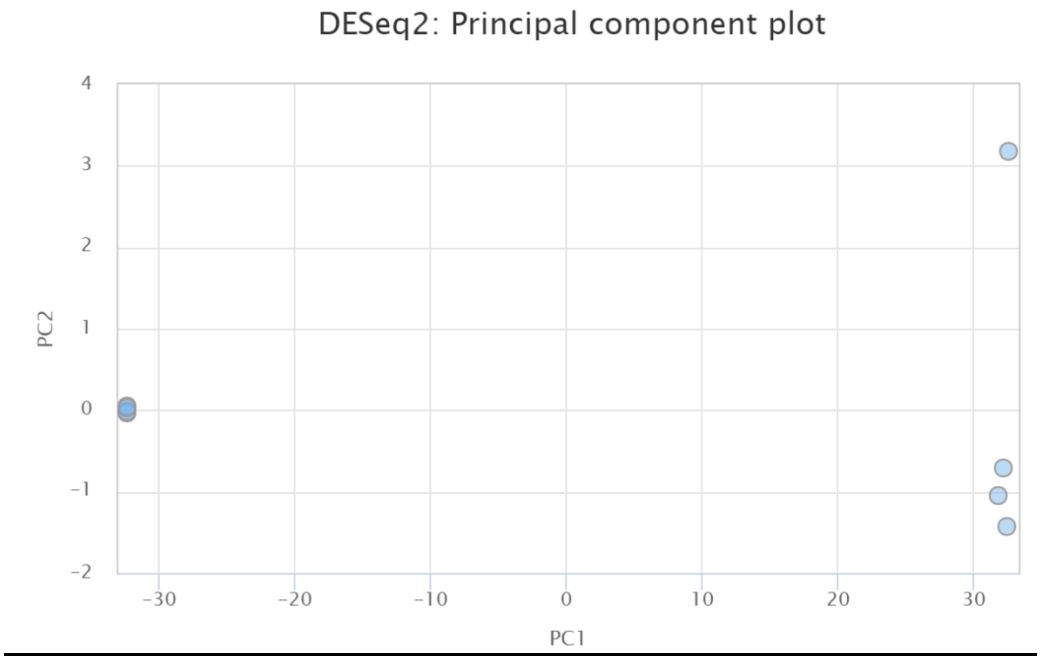
HOMER: Peak annotation (merged library)



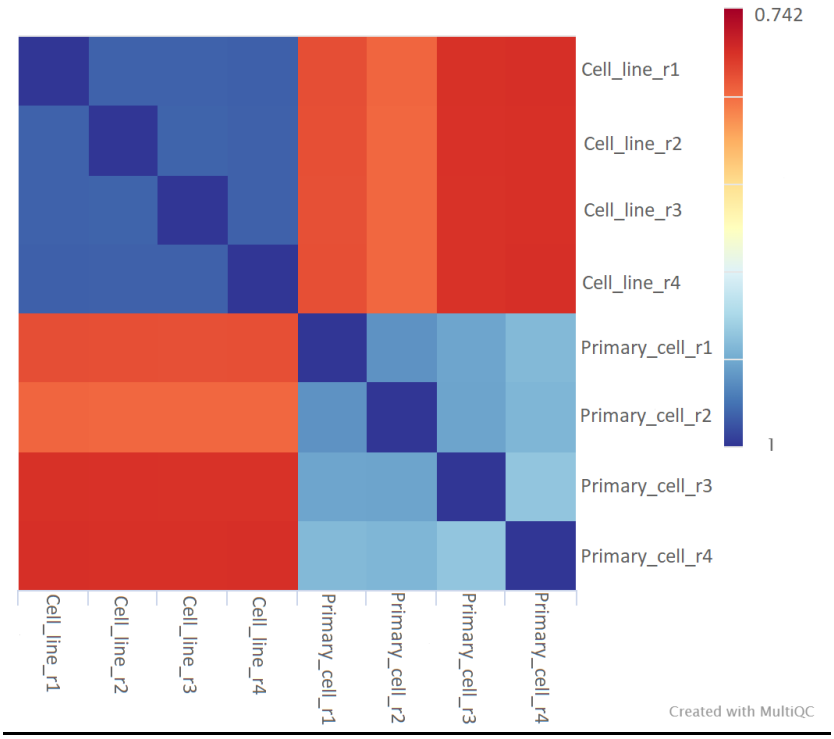
HOMER: Peak annotation (merged replicate)



DESeq2: PCA plot (merged replicate)



DESeq2: Sample similarity (merged replicate)



Fastq (trimmed)

`*.fq.gz` files after quality and adapter trimming.

Copy table | Configure Columns | Plot | Showing 8/8 rows and 2/2 columns.

Sample Name	Read1	Read2
Cell_line_r1	Download	Download
Cell_line_r2	Download	Download
Cell_line_r3	Download	Download
Cell_line_r4	Download	Download
Primary_cell_r1	Download	Download
Primary_cell_r2	Download	Download
Primary_cell_r3	Download	Download
Primary_cell_r4	Download	Download

Bam (merged library; filtered)

Merged library-level, coordinate sorted `*.bam` files after the marking of duplicates, and filtering based on various criteria.

Copy table | Configure Columns | Plot | Showing 8/8 rows and 2/2 columns.

Sample Name	Bam	Index
Cell_line_r1	Download	Download
Cell_line_r2	Download	Download
Cell_line_r3	Download	Download
Cell_line_r4	Download	Download
Primary_cell_r1	Download	Download
Primary_cell_r2	Download	Download
Primary_cell_r3	Download	Download
Primary_cell_r4	Download	Download

BigWig (merged library; filtered)

Normalised `*.bigWig` files scaled to 1 million mapped reads.

Copy table | Showing 8/8 rows and 1/1 columns.

Sample Name	BigWig
Cell_line_r1	Download
Cell_line_r2	Download
Cell_line_r3	Download
Cell_line_r4	Download
Primary_cell_r1	Download
Primary_cell_r2	Download
Primary_cell_r3	Download
Primary_cell_r4	Download

Peak (merged library)

MACS2 output files `.narrowPeak` or `.broadPeak` depend on whether MACS2 has been run in narrowPeak or broadPeak mode.

Copy table | Showing 8/8 rows and 1/1 columns.

Sample Name	Peak
Cell_line_r1	Download
Cell_line_r2	Download
Cell_line_r3	Download
Cell_line_r4	Download
Primary_cell_r1	Download
Primary_cell_r2	Download
Primary_cell_r3	Download
Primary_cell_r4	Download