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Article

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Multimodal chromatin profiling using nanobody-based single-cell CUT&Tag

In the format provided by the authors and unedited

Supplementary sequence 1. Anti-mouse nanobody-Tn5 fusion protein sequence

>anti-Mouse-Tn5_protein_sequence
MHHHHHHSSGVDLGTENLYFQSGDYKDHDGDYKDHDIDYKDDDDKGGGSQVQLVESGGGWVQPGGSLR
LSCAASGFTFSDTAMMWVRQAPGKGREWVAAIDTGGGYTYYADSVKGRFTISRDNAKNTLYLQMNSLK
PEDTARYYCAKTYSGNYYSNYTVANYGTTGRGTLVTVSSGGGGSGGGGSGGGGSGGGGSHMITSALHR
AADWAKSVFSSAALGDPRRTARLVNVAAQLAKYSGKSITISSEGSKAMQEGAYRFIRNPNVSAEAIRK
AGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEATTFRTVGLLH
QEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDKLAHNERFVVRSK
HPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRSGRITLKQGNITLN
AVLAEEINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDN
LERMVSILSFVAVRLLQLRESFTPPQALRAQGLLKEAEHVESQSAETVLTPDECQLLGYLDKGKRKRK
EKAGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKDLMAQGIKI

6x HIS tag
TEV cleavage site
3xFLAG tag
Anti-mouse nanobody
4x GGGGS linker
Tn5 transposase

>anti-Mouse-Tn5_DNA_Sequence
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ACAAGGGCGGTGGTTCACAAGTCCAATTGGTTGAGAGTGGCGGTGGTTGGGTTCAACCGGGTGGT
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TCAAGCTCCGGGCAAGGGGCGTGAGTGGGTGGCTGCCATCGACACTGGTGGCGGCTATACTTACT
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CTAA

Supplementary sequence 2. Anti-mouse nanobody-Tn5 fusion protein sequence

>anti-Rabbit-Tn5_protein_sequence

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MAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKDLMAQGIKI

6x HIS tag
TEV cleavage site
3xFLAG tag
Anti-rabbit nanobody
4x GGGGS linker
Tn5 transposase

>anti-Rabbit-Tn5_DNA_Sequence

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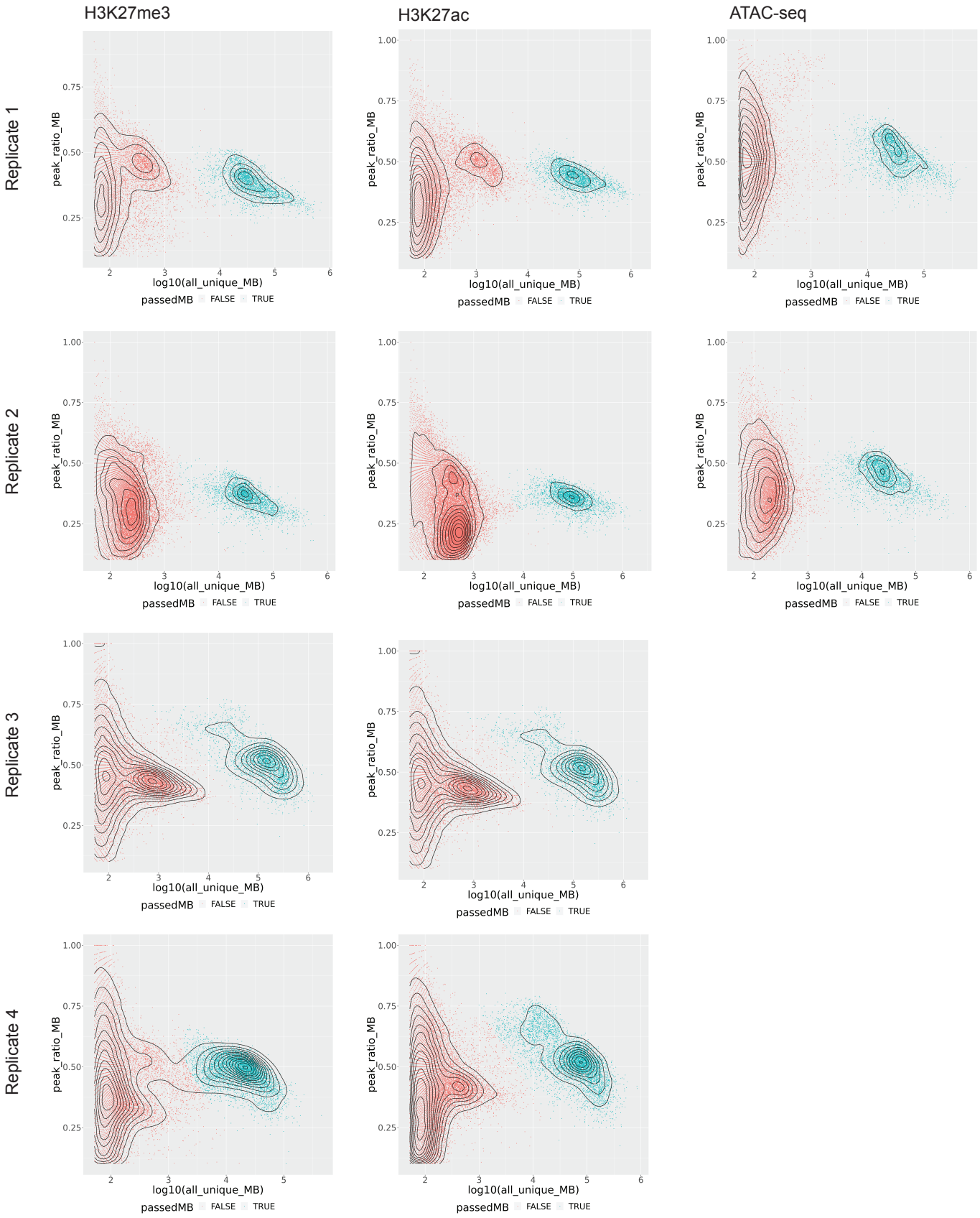
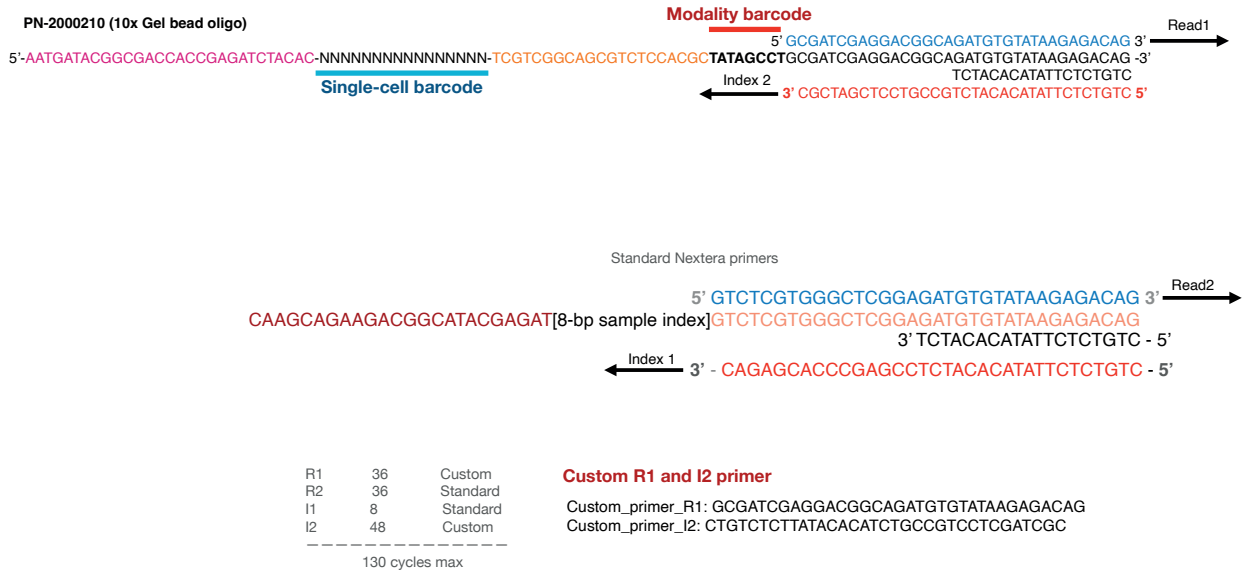
Supplementary figure 1



Supplementary data figure 1. a. Scatter plot showing number of reads per cell (x-axis) versus fraction of reads in peak regions (y-axis). Gaussian mixed model clustering was used to identify clusters of cells and cluster with the highest median of number of reads was selected as valid cells. Valid cells are labeled with cyan, while cells that do not pass QC are red. Contour lines depict density of points withing regions.

Supplementary figure 2

a



Supplementary data figure 2

a. Structure of the nano-CT library with highlighted barcode regions.