

Supplementary Table 1. Parameters for ChIP Extraction and Shearing

	Adipose	Brain	Heart	Lamina	Liver	Lung	Muscle	Testis
Starting Tissue (mg)	208	109	103	95	55	53	106	105
Homogenization Time (min)	8	5	5	5	5	5	5	5
Fixation Time (min)	10	9	9	9	9	9	9	12
Shearing Volume (μL)	400	1500	1800	1800	1500	1500	1500	1300
Shearing Cycles	5 x 8 ¹	10	10	10	8	10	10	8
Chromatin per IP (ng)	200	700	800	900	1500	1500	280	1500

¹Chromatin from adipose was sheared five times for 8 cycles

Supplementary Table 2. Chromatin and Antibody Amounts Used for ChIP of Stallion Tissues

Tissue	Chromatin IP (ng)	Antibody Amount (μg)			
		H3K27ac	H3K4me1	H3K4me3	H3K27me3
Adipose	200	1	0.5	0.5	1
Brain	700	0.5	0.5	0.5	1
Heart	800	0.5	0.5	0.5	1
Lamina	900	1	0.5	0.5	1
Liver	1500	2	1	1	2
Lung	1500	2	1	1	1
Muscle	280	1	0.5	0.5	0.5
Testis	1500	2	1	1	2

Supplementary Table 3. Software Parameters for ChIP-seq Peak Calling in MACS2 and SICER

Software	Parameter	H3K27ac	H3K4me1	H3K4me3	H3K27me3
MACS2	Size	Narrow	Narrow/ Intermediate	Narrow	Broad
	Size Flag	n/a			--broad
	FDR ¹	0.01	0.05	0.01	0.05
	Broad Cutoff	n/a			0.1
	Genome size	2,409,159,894 bp			
SICERpy ²	Gap Size	n/a			4
	Window Size	n/a			200
	Genome Fraction	n/a			0.973

¹The false discovery rate (FDR) cutoff dictates both peak number and peak width in MACS2, so histone marks with broader peaks have looser FDR cutoffs (<https://github.com/hbctraining/Intro-to-ChIPseq>). H3K4me1 was at one point considered to have broad peaks but has since been determined to have an intermediate peak width (Kingsley et al., 2020).

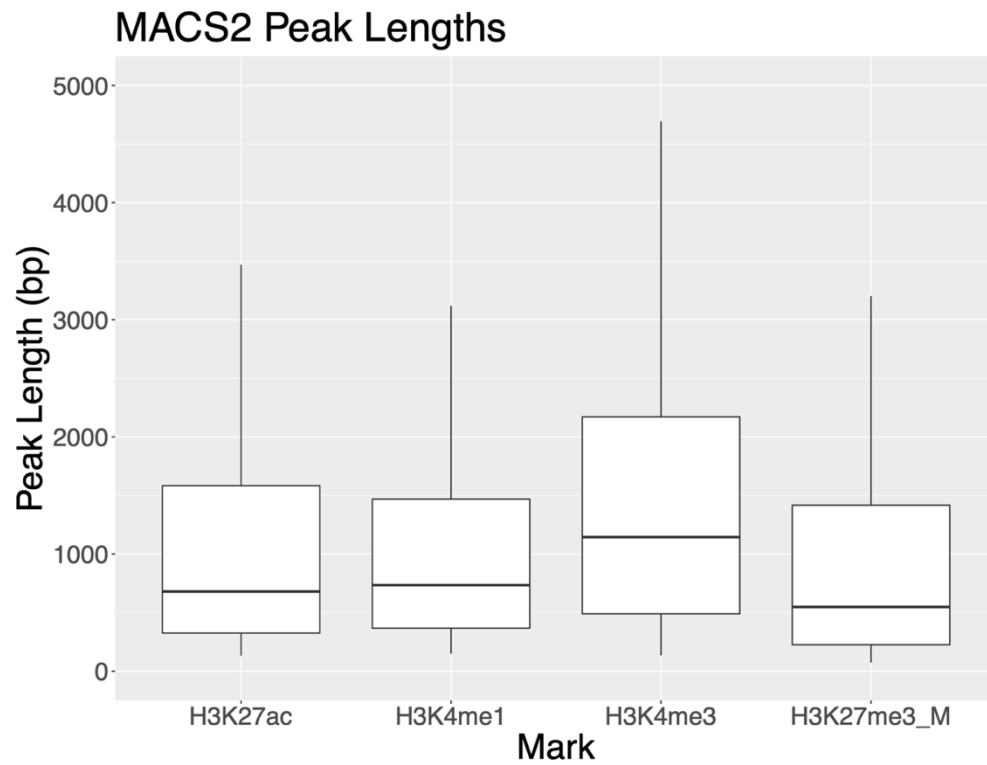
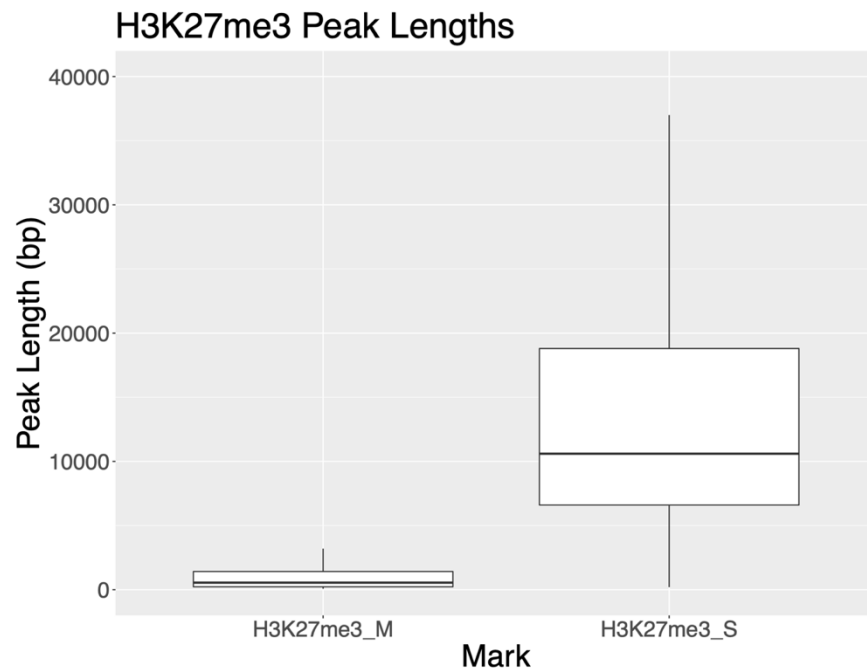
²SICER was only used to call peaks for the broad mark, H3K27me3.

Supplementary Table 4. The Number of Raw Read Pairs Generated and Usable Read Pairs Remaining After Filtering for Stallion Samples

[illegible]

Supplementary Table 5. Overlap of MACS2 H3K27me3 Peaks with SICERpy H3K27me3 Peaks

	Total MACS2 Peaks	Overlapping MACS2 Peaks	Percentage of Overlapping Peaks
Adipose	137,696	119,044	86%
Brain	87,453	74,844	86%
Heart	104,207	89,129	86%
Lamina	190,940	149,917	79%
Liver	265,202	212,970	80%
Lung	249,506	206,519	83%
Muscle	103,055	96,847	94%
Testis	129,784	95,889	74%

A**B**

Supplementary Figure 1. Peak Length Distribution by Histone Mark. The distribution of peak length called by MACS2 was similar across all four histone marks (A), yet the distribution of peak lengths for H3K27me3 varied drastically between peaks called by MACS2 and SICERpy (B).