Table S1. Processing statistics for each sequenced library

Processing statistics are shown for the three fetal and lamb H3K27me3 nucleosomal libraries, as well as the two corresponding input nucleosome libraries. The latter represented pools of the three animals for each developmental state. ChIP-Seq, immunoprecipitated H3K27me3 nucleosomal DNA; Input, nucleosomal input DNA; Cumulative total sequence represented by the sequence reads, total sequence; Reads, total number of sequence reads returned; Clipped reads, number of reads with ≥ 50 bp of unmasked sequence after repeat masking; Mapped reads, number of reads mapped to the bovine genome; Uniquely mapped, number of reads where a single best match position on the bovine genome was identified; Multiple mapped, number of reads with more than one best match position; Final mapped, number of uniquely mapped reads with match length ≥ 50 bp and > 75% identity.

Biological State	Animal identity	DNA	Total sequence[3] (Mb)	Read length (bp)	Reads[4]	Clipped reads[5]	Mapped reads[6]	Uniquely mapped[7]	Multiple mapped[8]	Final mapped[9]
Fetal	**5011**	**ChIP-Seq[1]**	**705**	**65**	**10,844,945**	**7,008,076**	**4,609,462**	**4,489,106**	**120,356**	**4,006,092**
	5012	**ChIP-Seq**	**649**	**65**	**9,989,993**	**6,528,810**	**4,397,430**	**3,985,689**	**411,741**	**3,637,174**
	5015	**ChIP-Seq**	**622**	**65**	**9,566,151**	**6,539,802**	**4,571,301**	**4,175,258**	**396,043**	**3,972,559**
		Input[2]	**691**	**65**	**10,630,644**	**6,122,422**	**4,848,194**	**3,862,641**	**397,887**	**3,847,318**
Adult	**4531**	**ChIP-Seq**	**749**	**65**	**11,529,595**	**6,850,373**	**4,451,004**	**4,044,896**	**406,108**	**3,777,951**
	4577	**ChIP-Seq**	**699**	**65**	**10,747,932**	**6,758,549**	**4,087,111**	**3,714,896**	**372,215**	**3,419,886**
	4572	**ChIP-Seq**	**772**	**65**	**11,873,483**	**6,705,139**	**3,178,731**	**2,889,202**	**289,529**	**2,685,656**
		Input	**1341**	**65**	**20,632,072**	**10,497,190**	**7,073,899**	**6,390,629**	**683,270**	**5,966,574**

[1] ChIP-Seq: H3K27me3 nucleosome immunoprecipitated DNA

[2] Input: control input nucleosomal DNA

[3] Total sequence: total sequence represented by sequence reads for each sample

[4] Reads: total number of sequence reads returned from sequencing

[5] Clipped reads: number of reads with >= 50 bp of unmasked sequence after repeat masking

[6] Mapped reads: number of reads mapped to the bovine genome with at least 75% identity

[7] Uniquely mapped: number of reads where a single best match position was identified

[8] Multiple mapped: number of reads where more than one equivalent best match position was identified

[9] Final mapped: number of uniquely mapped reads with match length >= 50 bp and >= 75% identity (indel size <= 5 bp)