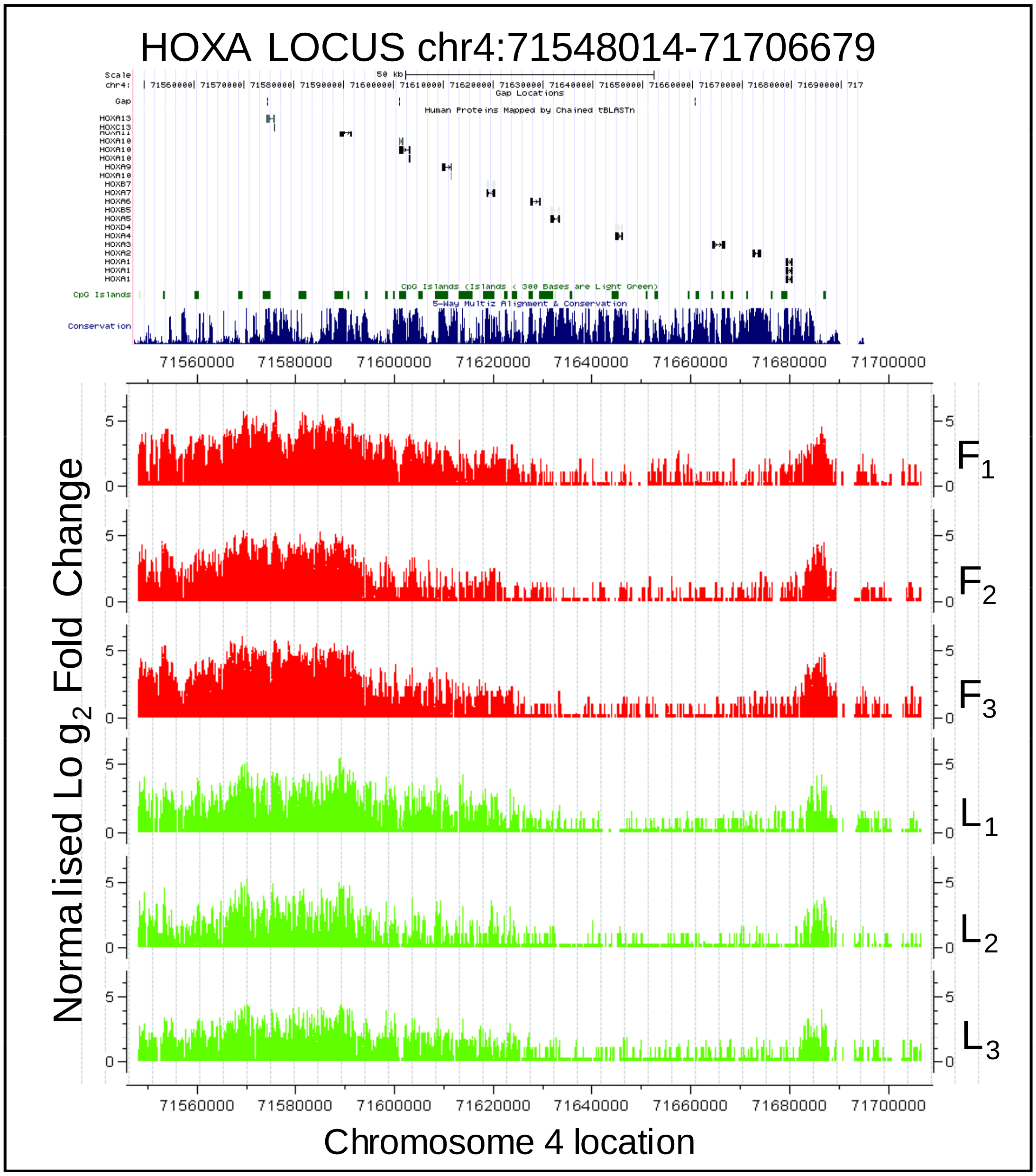
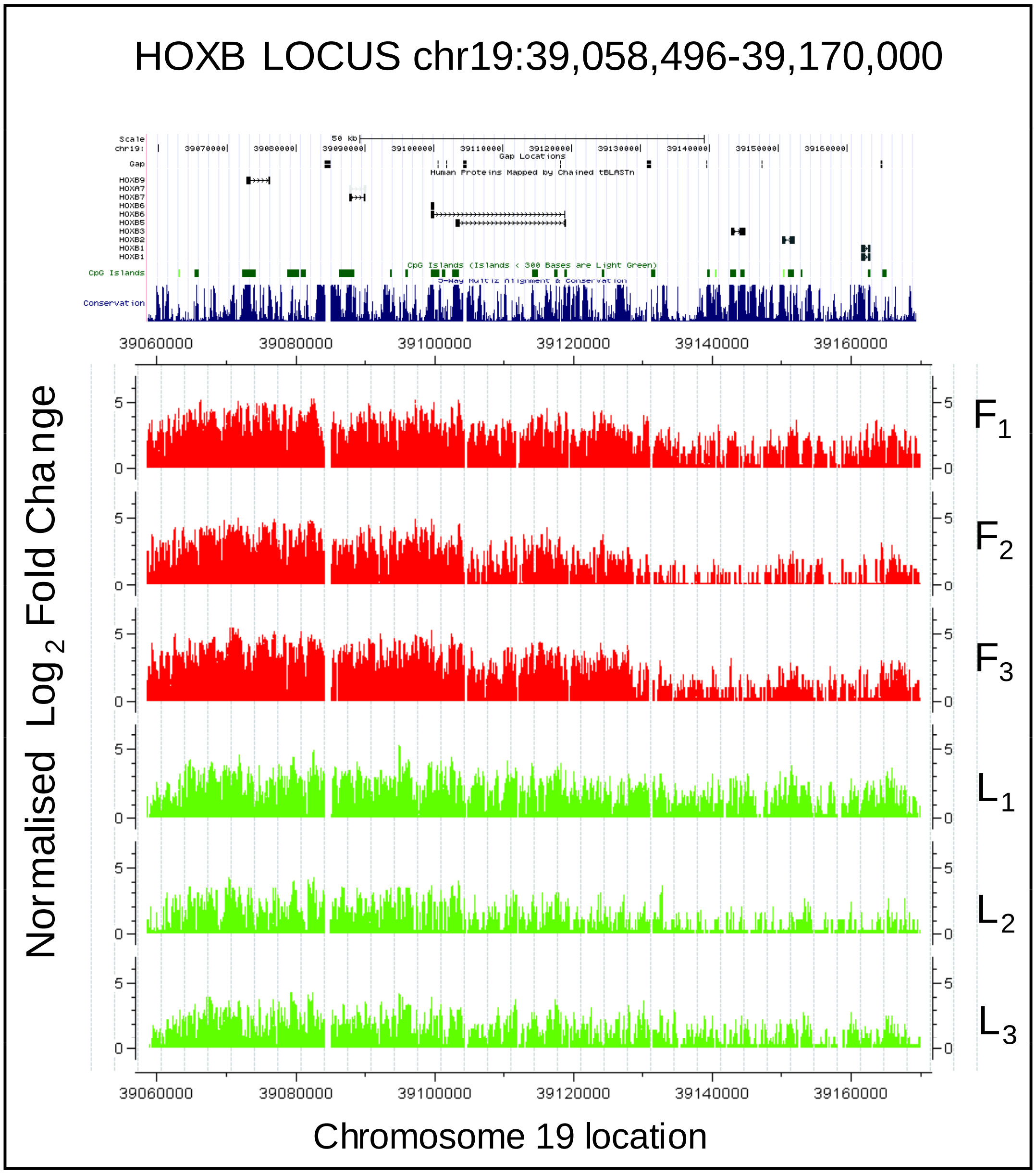
Figure S2. Regional H3K27me3 enrichment at four *HOX* gene loci

The UCSC Genome Browser was employed to highlight H3K27me3 regional enrichment at four *HOX* gene loci for the fetal and lamb samples. (a) *HOXA* locus (BTA4); (b) *HOXB* locus (BTA19); (c) *HOXC* locus (BTA5), and; (d) *HOXD* locus (BTA2:21373648-21541479). In each panel the top track shows RefSeq *HOX* genes and below are tracks for CpG islands (green bars) and UCSC evolutionary conservation. H3K27me3 nucleosome data are displayed for individual animals (fetal (F1-F3), red; lamb (L1-L3), green). The ordinate shows the $\log_2$ normalised fold change for the uniquely mapped reads when the H3K27me3 nucleosomal data was compared to input nucleosomal DNA data using CisGenome (Ji *et al*. 2008). Panel (e) shows a summary of H3K27me3 read counts (normalised for library size and corrected for normalised input control) in the promoters of *HOX* genes in the four loci using pooled data for the lamb. *HOX* genes are presented in chromosomal order; some *HOX* genes are absent or unannotated in the bovine genome assembly. Promoters were defined as 2 kb 5' and 500 bp 3' of the first nucleotide of RefSeq genes. Very similar results were obtained using the fetal data.

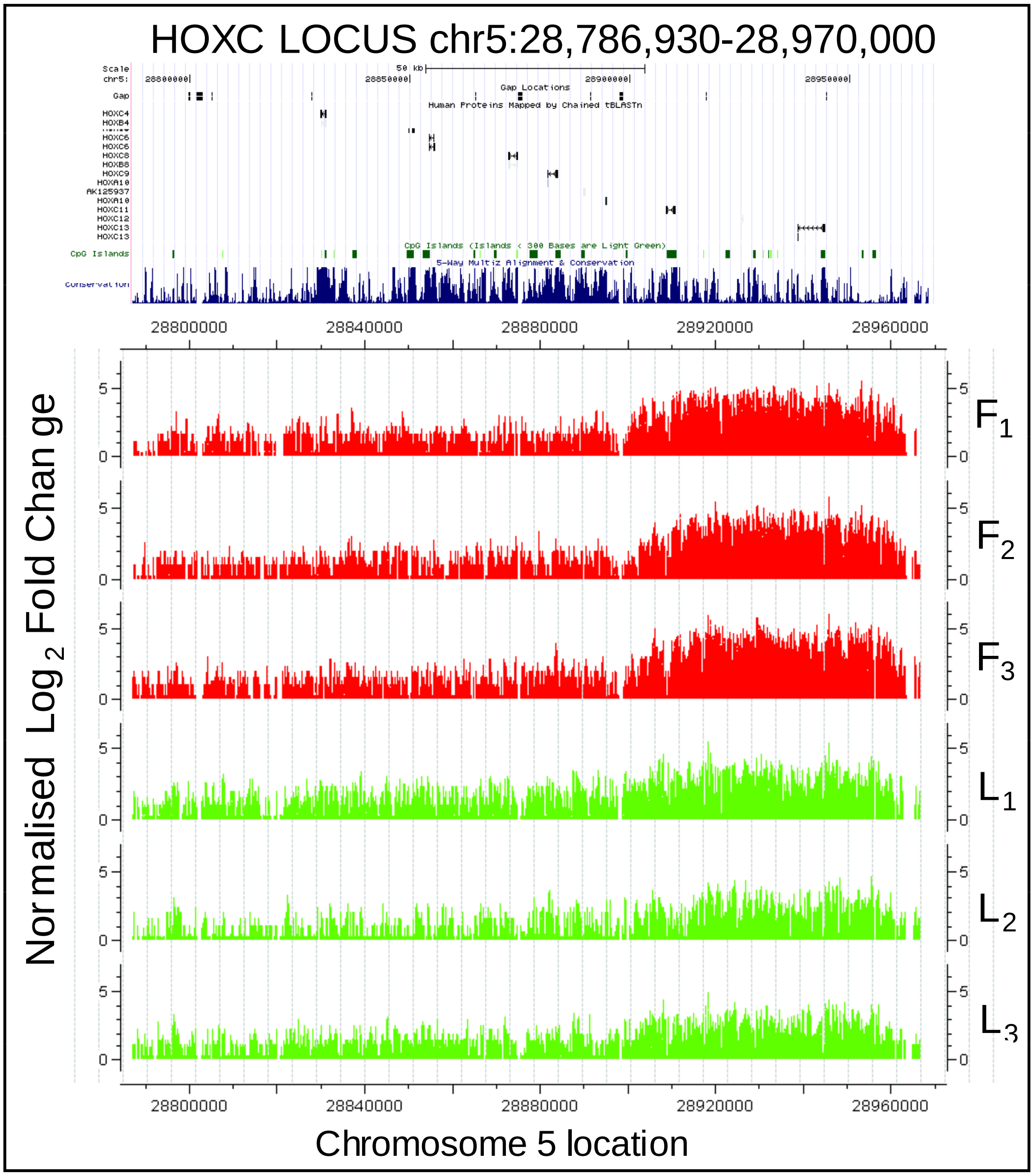
(a)



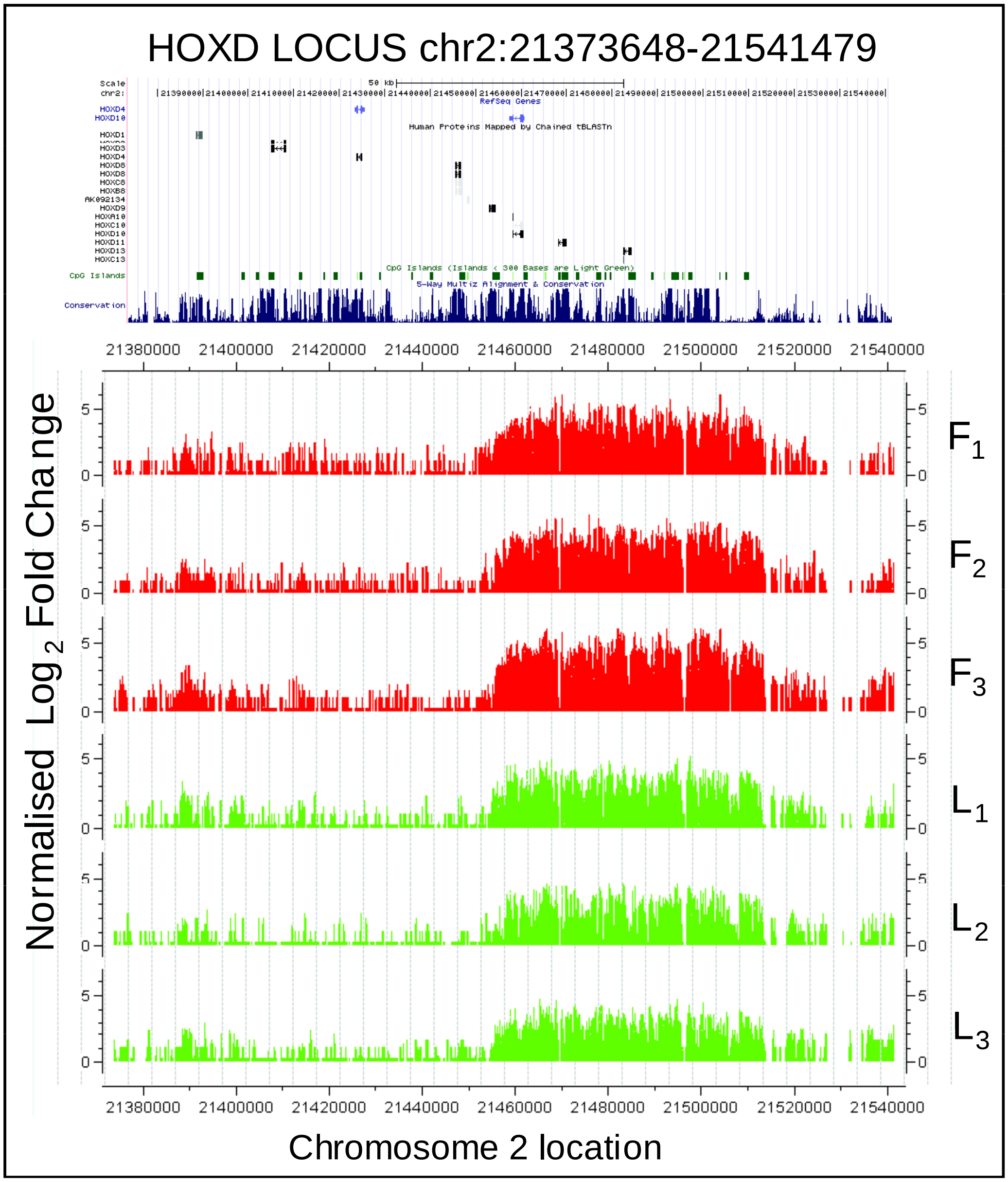
(b)


HOXB LOCUS chr19:39,058,496-39,170,000
Scale
chr19:
50 kb
39070000
39080000
39090000
39100000
39110000
39120000
39130000
39140000
39150000
39160000
Gap
Gap Locations
Human Proteins Mapped by Chained tBLASTn
HOXB9
HOXA7
HOXB7
HOXB6
HOXB6
HOXB5
HOXB3
HOXB2
HOXB1
HOXB1
CpG Islands
CpG Islands (Islands < 300 Bases are Light Green)
5-Way Multiz Alignment & Conservation
Conservation
39060000
39080000
39100000
39120000
39140000
39160000
Normalised Log 2 Fold Change
5
0
F1
F2
F3
L1
L2
L3
Chromosome 19 location

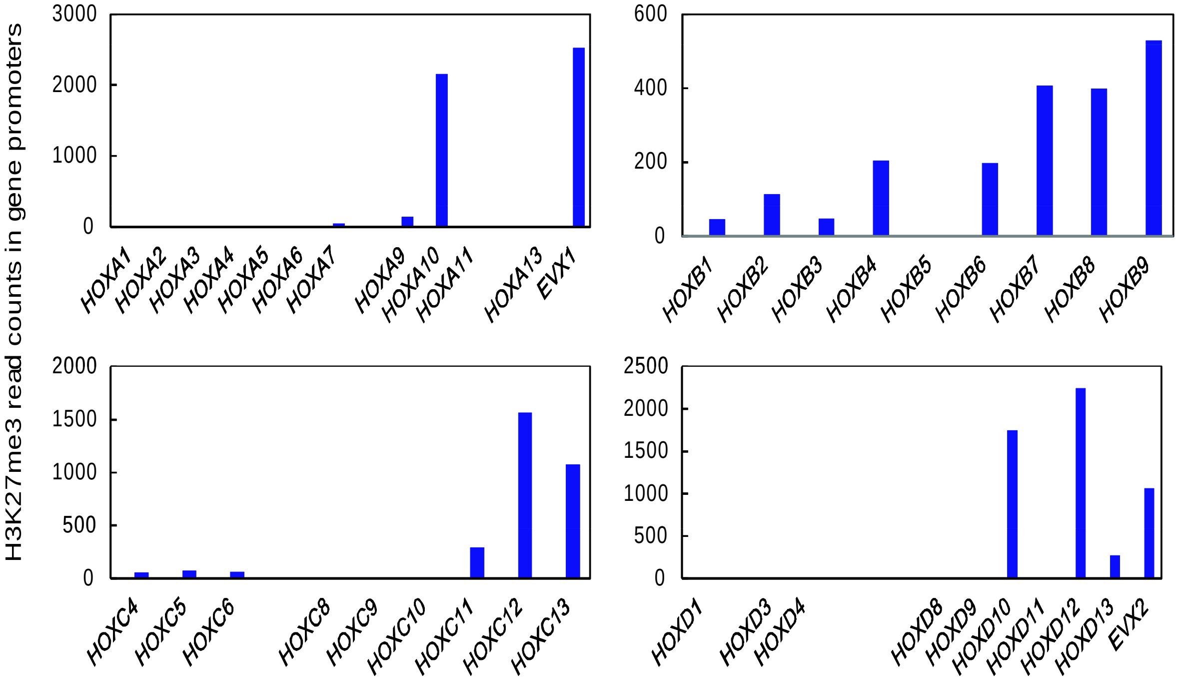
(c)


HOXC LOCUS chr5:28,786,930-28,970,000
Scale
50 kb
chr5:
28800000
28850000
28900000
28950000
Gap Locations
Gap
Human Proteins Mapped by Chained tBLASTn
HOXC4
HOXB4
HOXC6
HOXC6
HOXC8
HOXB8
HOXC9
HOXA10
AK125937
HOXA10
HOXC11
HOXC12
HOXC13
HOXC13
CpG Islands (Islands < 300 Bases are Light Green)
CpG Islands
5-Way Multiz Alignment & Conservation
Conservation
28800000
28840000
28880000
28920000
28960000
Normalised Log 2 Fold Change
5
0
F_1
F_2
F_3
L_1
L_2
L_3
Chromosome 5 location

(d)


HOXD LOCUS chr2:21373648-21541479
Scale
50 kb
chr2:
RefSeq Genes
HOXD4
HOXD10
Human Proteins Mapped by Chained tBLASTn
HOXD1
HOXD3
HOXD4
HOXD8
HOXD8
HOXC8
HOXB8
AK092134
HOXD9
HOXA10
HOXC10
HOXD10
HOXD11
HOXD13
HOXC13
CpG Islands (Islands < 300 Bases are Light Green)
CpG Islands
5-Way Multiz Alignment & Conservation
Conservation
21380000
21400000
21420000
21440000
21460000
21480000
21500000
21520000
21540000
Normalised Log 2 Fold Change
0
5
F1
F2
F3
L1
L2
L3
Chromosome 2 location

(e)


H3K27me3 read counts in gene promoters
3000
2000
1000
0
HOXA1
HOXA2
HOXA3
HOXA4
HOXA5
HOXA6
HOXA7
HOXA9
HOXA10
HOXA11
HOXA13
EVX1
600
400
200
0
HOXB1
HOXB2
HOXB3
HOXB4
HOXB5
HOXB6
HOXB7
HOXB8
HOXB9
2000
1500
1000
500
0
HOXC4
HOXC5
HOXC6
HOXC8
HOXC9
HOXC10
HOXC11
HOXC12
HOXC13
2500
2000
1500
1000
500
0
HOXD1
HOXD3
HOXD4
HOXD8
HOXD9
HOXD10
HOXD11
HOXD12
HOXD13
EVX2