

Supplementary Table 1: Regions exhibiting DNA modification levels that are significantly associated with *LCT* mRNA levels in development and adulthood

Chromosome-wide investigation				
Locus	Region*	Species	−log₁₀(<i>q</i>)[†]	Association
<i>LCT</i> exon–intron 1	chr2: 136,594,004–136,594,148	Human	1.78	↑5-mC = ↓ <i>LCT</i> mRNA
<i>Lct</i> exon 10	chr1: 128,295,240–128,295,278	Mouse	2.14	↑5-mC with ↑age
<i>Lct</i> intron 8–exon 9	chr1: 128,298,461–128,298,810	Mouse	3.05	↑5-mC with ↑age
<i>Lct</i> intron 2–exon 3	chr1: 128,312,912–128,313,561	Mouse	3.20	↑5-mC with ↑age
Fine-mapping investigation: Human				
Locus	Region*		−log₁₀(<i>p</i>)[‡]	Association
<i>LCT</i> intron 5 (LncRNA promoter)	chr2: 136,577,792–136,578,051		10.10	Cell-type specific; ↑5-mC = ↑ <i>LCT</i> mRNA
<i>LCT</i> intron 3	chr2: 136,583,097–136,583,652		5.33	Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
<i>LCT</i> intron 2	chr2: 136,589,129–136,589,405		11.48	Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
<i>LCT</i> exon 1	chr2: 136,594,396–136,594,421		10.56	Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
<i>MCM6</i> exon 17 (3'-UTR)	chr2: 136,597,453–136,597,614		4.07	Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
<i>MCM6</i> exon 16	chr2: 136,602,097–136,602,294		4.27	Inter-individual variation & Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
<i>MCM6</i> intron 13–exon 13	chr2: 136,608,430–136,609,013		10.96	Inter-individual variation & Cell-type specific; ↑5-mC = ↓ <i>LCT</i> mRNA
			2.42	↑5-mC = ↓ <i>LCT</i> mRNA

Fine-mapping investigation: Mouse

Locus	Region*		−log₁₀(<i>p</i>)[§]	Association
<i>Lct</i> intron 8	chr1: 128,298,854		3.51	↑5-mC with ↑age
<i>Lct</i> intron 2	chr1: 128,313,221		3.81	↑5-mC with ↑age

*Human regions are GRCh37/hg19, mouse regions are GRCm38/mm10; †, ‡, §Significance values correspond to the most significant site in each region; †FDR $q < 0.05$ after Benjamini-Hochberg multiple testing correction; ‡ $p < 0.01$ after Bonferroni correction for multiple testing; §FDR $q < 0.05$.

Supplementary Table 2: Roadmap Epigenomics Project and ENCODE data sets used for chromatin accessibility and histone modification analysis

Sample code	Sources	Tissue	Age	Sex	Data sets
H-23769	Roadmap Epigenomics Project	Fetal small intestine, human	108 days	Male	DNase I HS
H-24595	Roadmap Epigenomics Project	Fetal small intestine, human	108 days	Male	H3K4me1 H3K4me3 H3K27ac
ENCBS157ENC	ENCODE	Small intestine, mouse Strain: C57BL/6NCrl	8 weeks (60 days)	Male	POLR2A H3K4me1 H3K4me3 H3K27ac