

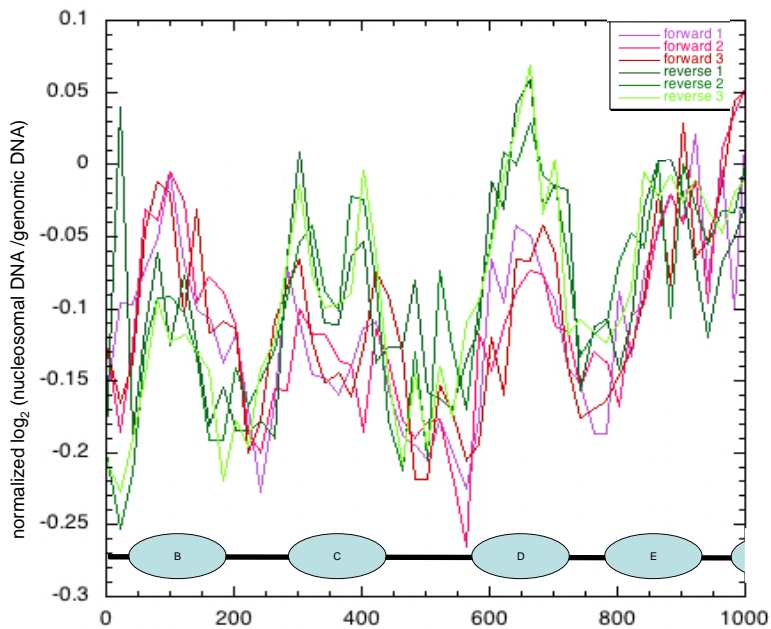
Supplementary Table 1

Name	Sequence (5'-3')	MMTV Position
Extension	GGAAAACCTTTCCCCAAAAG	328-347
Amplification	TTCCTGTTCCCTAGATAAATATAATCAT	352-378
Detection	ATATAATCATGTACCTGTTGTTTCATGTCTG	369-398
Extension	ATATAATCATGTACCTGTTGTTTCATGTCTG	369-398
Amplification	ATACACCAAGGAGGTCTAGCTCTGGC	420-445
Detection	TCTGTATAACACTTTATAGCCGTTGATTGT	470-499
Extension	TGTGACCCACCTATCCCAAT	497-517
Amplification	TAAGTCATATCTTCCTGTATATGGTAA	518-544
Detection	TCTGTAGATGTAAGGTCCCCTATAAGTCc	559-588
Extension	TGCGGCTTGTAAGAGGAAGT	1085-1104
Amplification	ATTCTCTGCTGCAAACCTGGCATAGC	1050-1075
Detection	CCCTTGATTCTTTCAATAATAACTCTTCTG	964- 993
Extension	TTCCTCTTACAAGCCGCATC	875-896
Amplification	TTTTTACCAATAAGACCAATCCAATAG	802-828
Detection	CTCAAATTCAGAAGTTAGAAATGGGAATAG	715- 744
Extension	GGTGGCAACCAGGGACTTAT	581-600
Amplification	ATGCCCCCTTACCATATACAGGAAGA	527-552
Detection	AGGAAGATATGACTTAAATTGGGATAGGTG	504- 533
Name	Sequence (5'-3')	LCMT2 Position
Extension	AAATAATGGGCGCACTTCAG	1124-1105
Amplification	GCGGGAAGAAAGCAGTGATA	1046-1027
Detection	CGGTCCAGCCAGCTTGAAGGAAG	997-975
Name	Sequence (5'-3')	
Linker_A	GCGGTGATTTAAAAGATCTGAATTC	
Linker_B	GAATTCAGATC	

Supplementary Table 1

Primers used in the LM-PCR primer extension experiments of MMTV-LTR and LCMT2. Numbers in bold represent the primer position as referred to in Figure 6A. Positions of the LCMT2 primers were designed using LCMT2 sequence (accession number NM_014793.3) base position numbering reflects the numbering of this sequence.

Supplementary Fig. 1.



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Hybridization of Cot enriched mononucleosomal DNA fragments to a tiling microarray. Gel-purified Cot enriched mononucleosomal DNA was labeled with Cy3 and sonicated Cot enriched bare genomic DNA was labeled with Cy5 and both were hybridized to a tiling microarray containing the MMTV LTR. Probes were 50 bases long and spaced 20 bases apart. Each probe was spotted in triplicate on both the forward and reverse strands. Each probe from the six replicate data sets (three from the forward strand and three from the reverse strand), was log-transformed, normalized, and plotted as log ratios.