Double-stranded methylation patterns of a 104-bp L1 promoter in DNAs from male and female fibroblasts, male leukocytes and female lymphoblastoid cells using hairpin-bisulfite PCR. Fifteen L1 sequences were analyzed for DNAs from the first three sources; twelve L1 sequences were analyzed from the fourth source. (Posted on the Laird Lab website 11-03-06)

**MALE ADULT FIBROBLAST LINE (82-6hTERT)**

<table>
<thead>
<tr>
<th>L1 Sequence</th>
<th>Male Adult Fibroblast Line (82-6hTERT)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MFIB_NM241 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA CGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GTTTAGTTTTTTTTTTTATT GTTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM243 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM246 (99%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTATT GCTTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM247 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM249 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM250 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM251 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
<tr>
<td>MFIB_NM253 (100%)</td>
<td>CGAGTTAAAGAAAGGGGTGA CGGGA TGTTTTTATTATTTGAAAAT CGGGTTATTTTTATT CGAATATTG CGTTTTTTAGAT CGGTTTAAGAAA CGG CGT ATTAAGTGATGTGTT GATTAGTTTTTTTTTTTATT GCTT GTTGGATTTTTTA GCTTAGTGAGGGTGG GCTTATAAT GC GAAAAGTTTG GCTGAATTTTTT GCT GCGTGGT TTGTTATGAGT</td>
</tr>
</tbody>
</table>
MFIB_NM254 (99%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

MFIB_NM255 (99%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

MFIB_NM257 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

MFIB_NM258 (99%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

MFIB_NM259 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FEMALE ADULT FIBROBLAST LINE (81-58A)  

FFIB_NM78 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FFIB_NM80 (98%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FFIB_NM81 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FFIB_NM82 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FFIB_NM83 (100%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT

FFIB_NM84 (98%)  
GGCTTAGTTTTTTTTTTATTATTATTTTTGGAAAATCGGTTTAAGAAAATCGGTTTATTTTTATT
Double-stranded methylation patterns in L1 promoter sequences from DNA of male and female fibroblasts, male leukocytes and female lymphoblastoid cells, using hairpin-bisulfite PCR. The full set of sequences from which data were derived for Table I in Burden et al., 2005 are presented here. Methylation states were inferred using hairpin-bisulfite PCR, as described in Materials and Methods. Methylated CpG sites are highlighted in red and non-methylated CpG sites in blue. The hairpin linker is gray. Evolutionary divergences both within genomic consensus CpG dyads and at sites not within CpG dyads are also highlighted in yellow. For both examples of evolutionary divergence, information on the complementary strands of individual DNA duplexes distinguishes evolutionary changes from PCR errors, which are highlighted in green. Conversion efficiency of each sequence follows the sequence-identification number above each sequence; non-converted non-CpG cytosines, highlighted in magenta, were observed, but only sequences with ≥ 98.2% conversion of non-CpG cytosines (representing one or zero non-conversion events per sequence) were used for analysis. Dashes within the sequence indicate sequencing errors resulting from uncalled bases.