DNA methylation and hydroxymethylation analyses of the active LINE-1 subfamilies in mice

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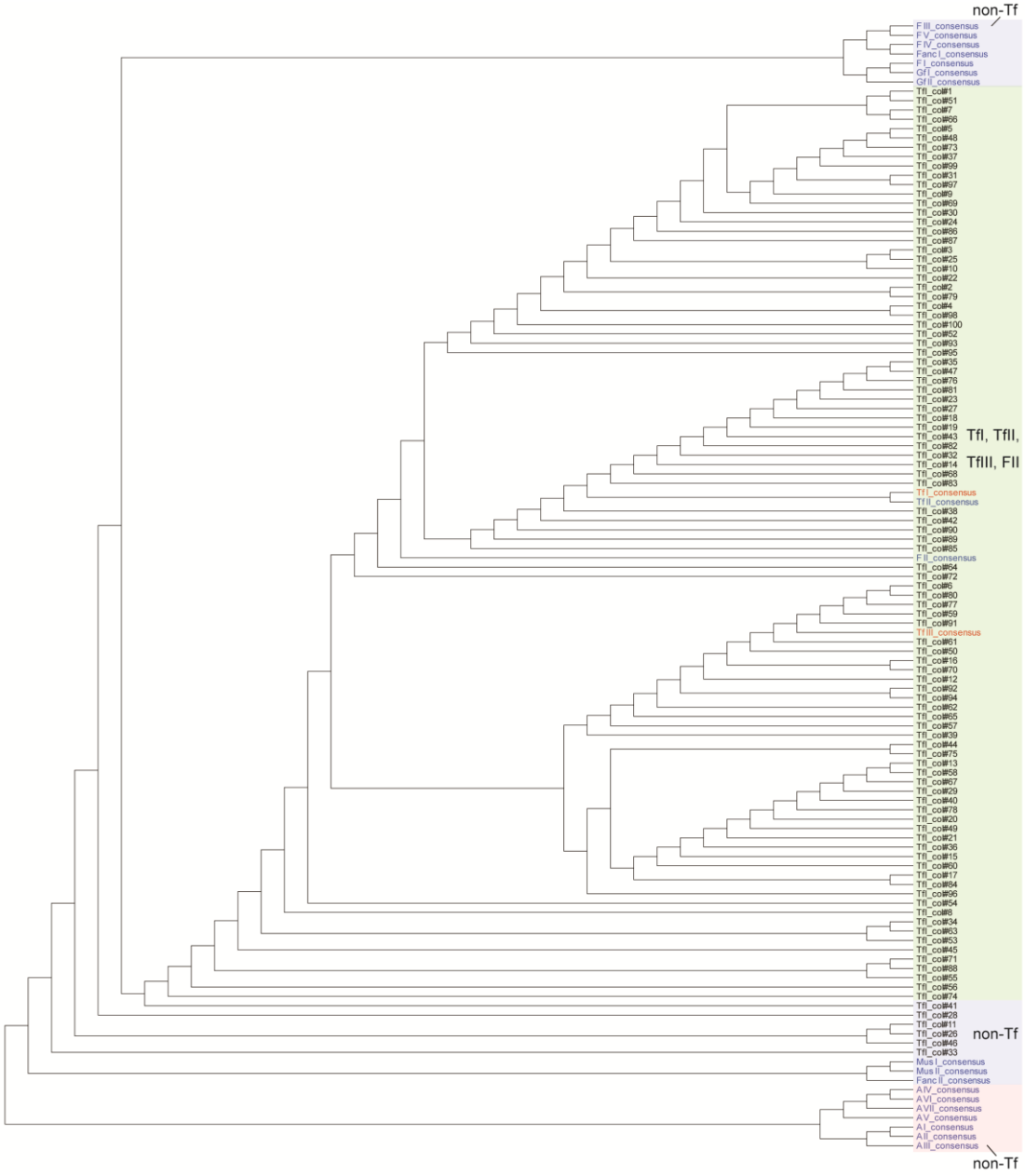
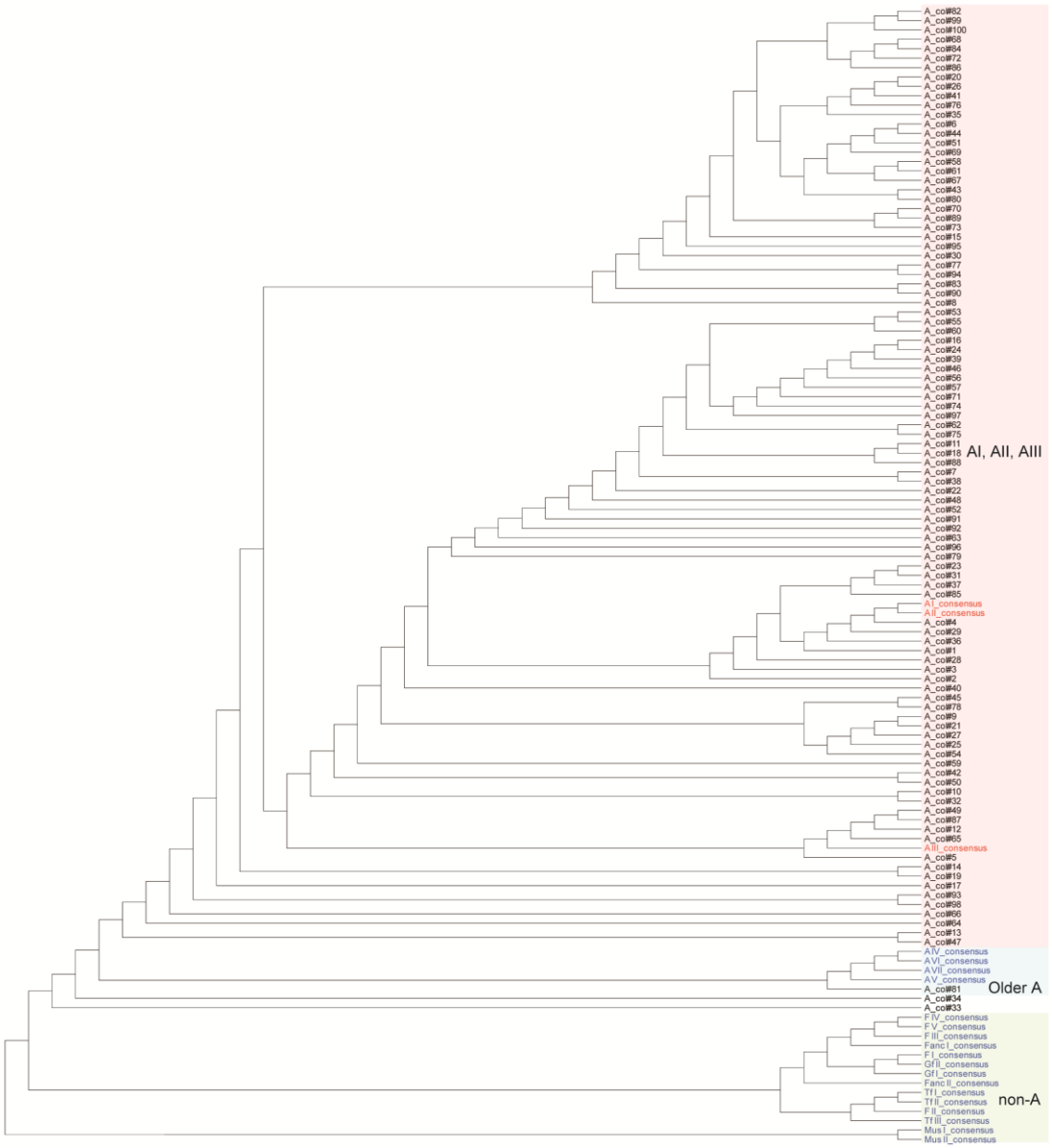
Supplementary Information



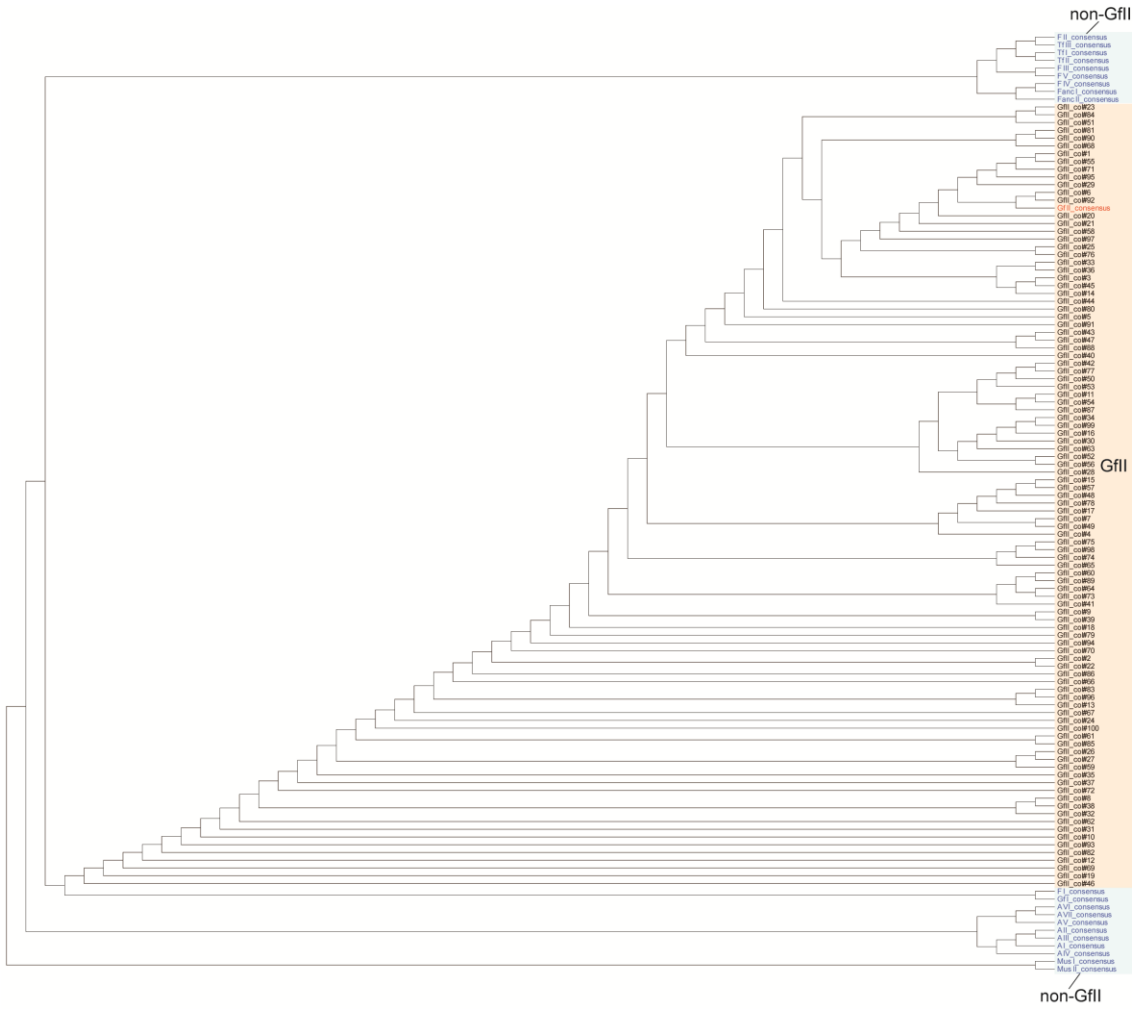
Supplementary Figure S1. Phylogenetic analysis for sequences derived from colonies with bisulfite-PCR product amplified for TfI. Bisulfite converted 5'-UTR regions of

LINE-1 consensus sequences were analyzed together. Out of 100 colonies, 95 were clustered with Tf or FII subfamilies. Close inspection of the sequences derived from colonies showed that all had TfI and TfIII-type variations. Sequencing primer for TfI further discriminates TfI from TfIII in the subsequent pyrosequecing reaction. Note that older subfamilies Lx, V, and nonhomologous subfamily, type N were not included. Samples in red are the target subfamilies, and those in blue are subfamilies not targeted by the assay.

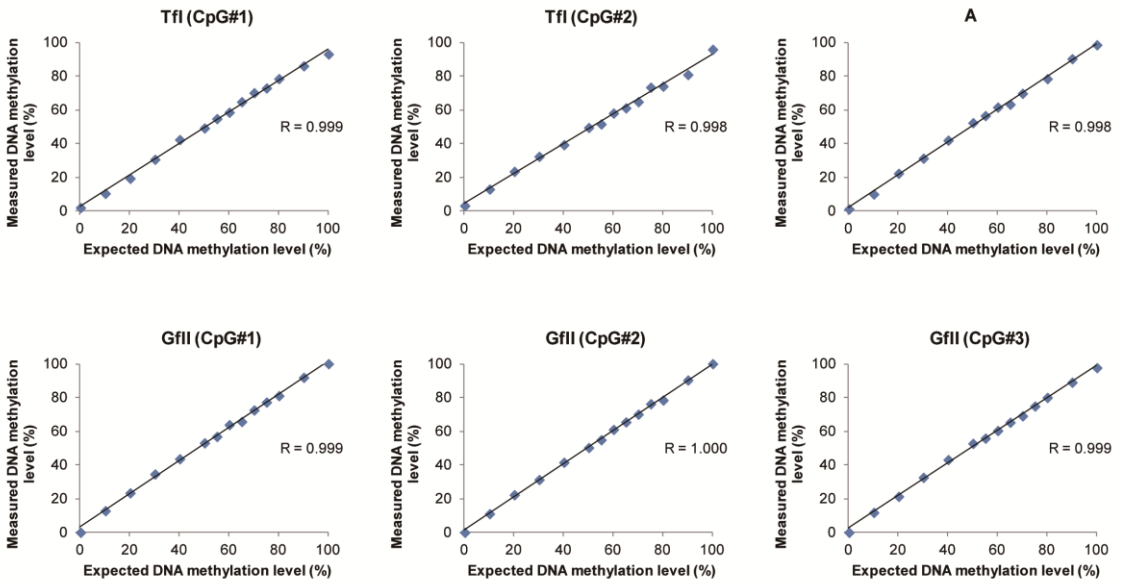


Supplementary Figure S2. Phylogenetic analysis for sequences derived from colonies with bisulfite-PCR product amplified for A (AI, AII and AIII). Bisulfite converted 5'-UTR regions of LINE-1 consensus sequences were analyzed together. Out of 100 colonies, 97 were clustered with types AI, AII or AIII. Note that older subfamilies Lx, V, and nonhomologous subfamily, type N were not included. Samples in red are the target

subfamilies, and those in blue are subfamilies not targeted by the assay.



Supplementary Figure S3. Phylogenetic analysis for sequences derived from colonies with bisulfite-PCR product amplified for GfII. Bisulfite converted 5'-UTR regions of LINE-1 consensus sequences were analyzed together. All of the 100 colonies were clustered with GfII subfamilies. Note that older subfamilies Lx, V, and nonhomologous subfamily, type N were not included. Samples in red are the target subfamilies, and those in blue are subfamilies not targeted by the assay.



Supplementary Figure S4. Correlation between DNA methylation levels of synthetic DNA sequences. All of the CpG sites measured in the assays showed high correlations ($R > 0.998$).

Supplementary Table S1. Sequences of synthetic DNA.

Subfamily	Sample name	Sequence
A	AI_methylated	5’-gtgagtggaatataatttttgttaggagtttggtt**cg**aatattagatatttgggtatttgttttgtaagaagagagtttgtttgtagagaatattttgtttattgaaattaaggagagtgttatttttt-3’
	AI_unmethylated	5’-gtgagtggaatataatttttgttaggagtttggtt**tg**aatattagatatttgggtatttgttttgtaagaagagagtttgtttgtagagaatattttgtttattgaaattaaggagagtgttatttttt-3’
GfII	GfII_methylated	5’-gggggttattttgattttgggattt**cg**tag**cg**ggtagtttgtaggttaaagtaatatagtttttgggaaagattttgttttgggttttttatttt**cg**gttaggaggaggtttaaatattagataattgtgtatttttttgaaagaggagagtttgtttgtagagattgttttgattattgaaatttagggaagagagttagttttttggtttgttgatatagtgtaataaaattattagaggaa-3’
	GfII_unmethylated	5’-gggggttattttgattttgggattt**tg**tag**tg**ggtagtttgtaggttaaagtaatatagtttttgggaaagattttgttttgggttttttatttt**tg**gttaggaggaggtttaaatattagataattgtgtatttttttgaaagaggagagtttgtttgtagagattgttttgattattgaaatttagggaagagagttagttttttggtttgttgatatagtgtaataaaattattagaggaa-3’
TfI	TfI_methylated	5’-tttgggaattgttaaagtaatatagtgtttgagaaaggttttgttttgggttttttttttt**cg**gttaggaggaggtttaaatataagatatttg**cg**tatttttttttgtaagagagtttgttagtagagagtgttttgagtattgaaatttagaggagagaatttgttttttaggtttgttgataga**cg**gtaatagaattattagaagaataatttttaaatagagttaattataattattaattttagagattattagatgg-3’
	TfI_unmethylated	5’-tttgggaattgttaaagtaatatagtgtttgagaaaggttttgttttgggttttttttttt**tg**gttaggaggaggtttaaatataagatatttg**tg**tatttttttttgtaagagagtttgttagtagagagtgttttgagtattgaaatttagaggagagaatttgttttttaggtttgttgataga**tg**gtaatagaattattagaagaataatttttaaatagagttaattataattattaattttagagattattagatgg-3’