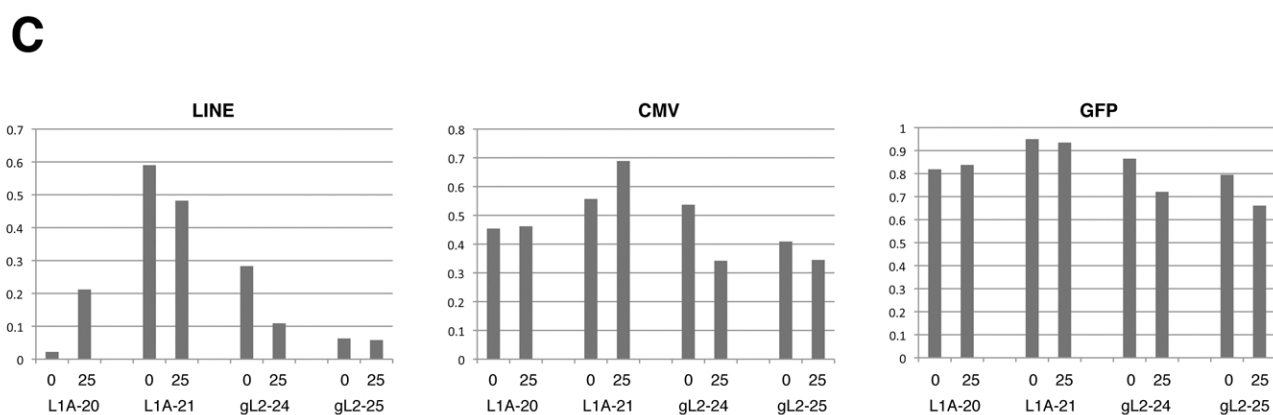
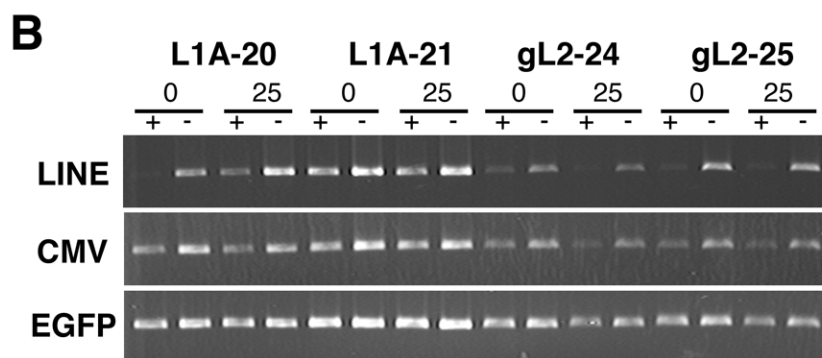
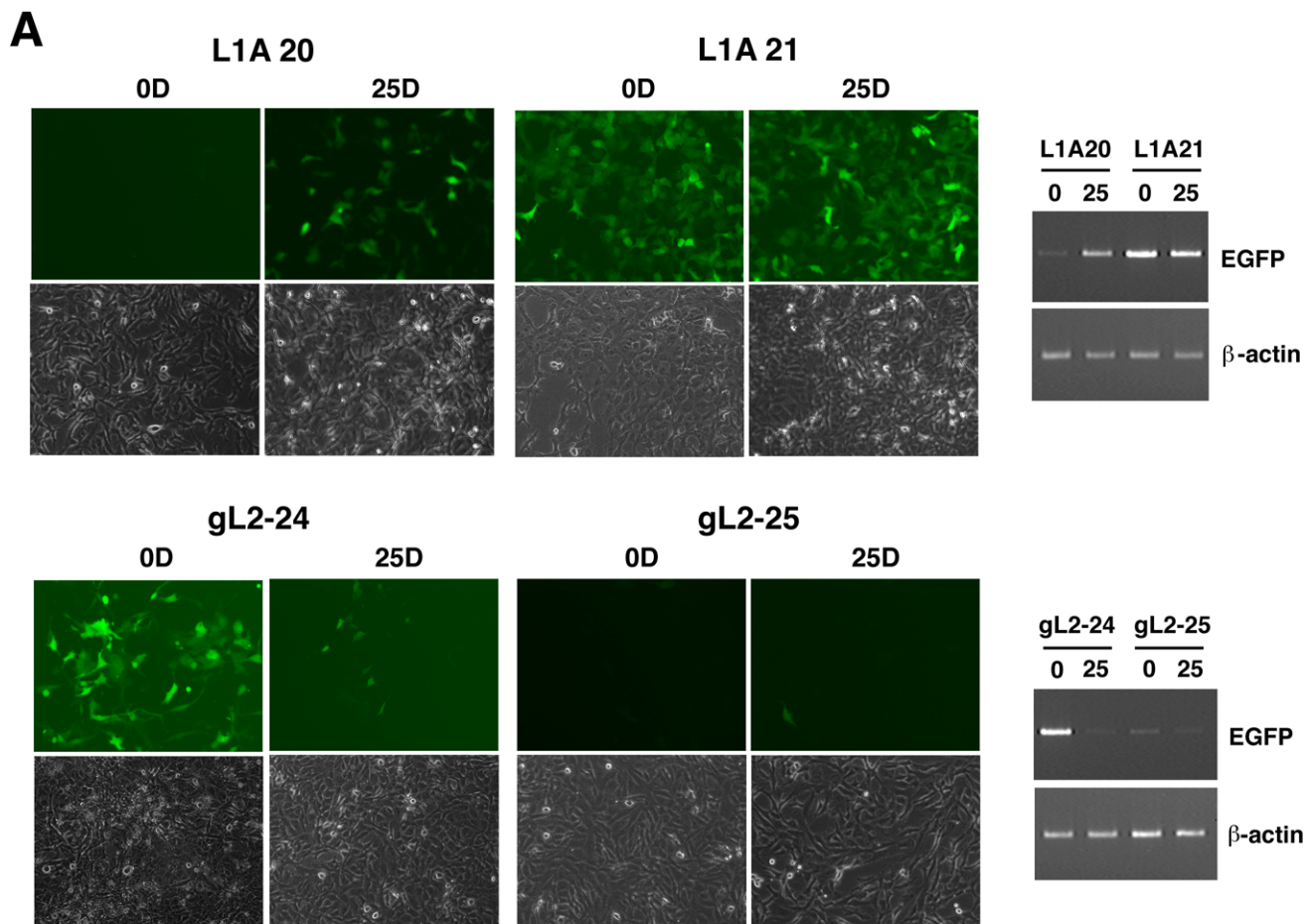


L1RE1	1	AAGTACCAATGACTTTC	CAAGAAATTC	CAAAAAA	CTA	TTTAAA	TT	CATATGGA	59	L1RE1	834	CCCTA	FGAGATA	EA	CTCTCA	CCAGT	FGAATGGCAAT	L	TTTTAAAAGTCA	CA	AAAAA	892		
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	267	CACAA	FGAGATACCAT	TT	TTG	CCAGT	CAGAATGGCAAT	T	TTTTAAA	AGT	CAAGAAACA	326		
gL	1	-----	CAAGAAATTC	CAAAAAA	CTA	TTTAAA	TT	CATATGGA	41	gL	812	TCAA	FGAGATACCAT	CT	CTG	CCAGT	CAGAATGGCAAT	T	TTTTAAA	CT	CAAGAAACA	869		
L1RE1	60	CAAAAAAGAGC	CT	CAAT	GC	CAAG	AT	CCCTAAGC	119	L1RE1	893	ACAGT	FGCTGG	CAAGG	TTG	CGG	GAAATAGGA	CA	TTTTACACT	TT	GGTGG	952		
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	387	AA	FGTTT	CAAT	TTG	GGA	AGACAGT	CA	TTTTACACT	TT	GGTGG	386		
gL	42	CAAAAAAGAGC	CT	CAAT	GC	CAAG	AT	CCCTAAGC	101	gL	870	ACAGAT	GCTGG	CAAGG	TTG	CGG	GAAATAGGA	CA	TTTTACACT	TT	GGTGG	929		
L1RE1	120	CACTACCTGACTT	AACTATACT	CAAGGCT	CAGTAA	CA	AAACAGCA	GGTACTG	179	L1RE1	953	AACT	TTCA	CAACT	TTG	GGA	AGT	CA	TTTCA	CA	GGAT	TT	1006	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	446	AA	FGTTT	CAAT	TTG	GGA	AGACAGT	CA	TTTTACACT	TT	GGTGG	445		
gL	102	GGGCTACCTGACTT	AACTATACT	CAAGGCT	CAGTAA	CA	AAACAGCA	GGTACTG	161	gL	930	AA	FGTTT	CAAT	TTG	GGA	AGACAGT	CA	TTTTACACT	TT	GGTGG	983		
L1RE1	180	GTAC	AAAACAG	ATAGAT	CAAT	GGAA	CAGAA	AGAG	CT	CAGAAATAA	TC	CA	239	L1RE1	1007	TG	AAATACCAT	TTG	ACC	CAAT	CCCAT	TTA	1066	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	446	C	AGAAAT	CCAT	TTG	ACC	CAAT	CCCAT	TTA	TTA	AAAT	505		
gL	162	GTAC	AAAACAG	ATAGAT	CAAT	GGAA	CAGAA	AGAG	CT	CAGAAATAA	TC	CA	221	gL	984	C	AGAAAT	CCAT	TTG	ACC	CAAT	CCCAT	1043	
L1RE1	240	TATCTA	AACTA	ATAGAT	CAAT	GGAA	CAGAA	AGAG	CT	CAGAAATAA	TC	CA	299	L1RE1	1067	CAT	CTE	CA	ATAA	GACA	CT	AT	1126	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	506	C	ATTCT	TATAA	AGACAT	GCAT	GT	TT	CA	TT	CA	565		
gL	222	CATCTA	AACTA	ATAGAT	CAAT	GGAA	CAGAA	AGAG	CT	CAGAAATAA	TC	CA	281	gL	1044	C	ATTCT	TATAA	AGACAT	GCAT	GT	TT	1103	
L1RE1	300	CTATT	TAA	AAATGG	TCTGG	GA	AACTGG	TAG	CT	AT	AG	AAA	CT	GAA	AACT	GGA	359	L1RE1	1127	AG	AC	TT	1186	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	566	AG	AC	TT	GA	AACT	GGA	625	L1RE1	1127	AG	AC	TT	1186
gL	282	CTATT	TAA	AAATGG	TCTGG	GA	AACTGG	TAG	CT	AT	AG	AAA	CT	GAA	AACT	GGA	341	gL	1104	AG	AC	TT	1163	
L1RE1	360	TCCTT	CCTAC	ACTT	TA	CAAAA	AA	TT	AGAT	GGAT	TAA	GA	TT	AAA	TT	AAA	419	L1RE1	1187	F	A	T	1246	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	626	F	A	T	AC	CA	T	745	L1RE1	1187	F	A	T	1246
gL	342	CTCTT	CCTAC	ACTT	TA	CAAAA	AA	TT	AGAT	GGAT	TAA	GA	TT	AAA	TT	AAA	401	gL	1164	F	A	T	1223	
L1RE1	420	AC	CA	AAA	CT	TA	AAAA	CC	TT	GA	AAAA	CT	AG	CA	TT	AC	CA	479	L1RE1	1247	C	T	1306	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	686	F	A	T	AG	GA	AG	745	L1RE1	1247	C	T	1306	
gL	402	TC	CA	AAA	CT	TA	AAAA	CC	TT	GA	AAAA	CT	AG	CA	TT	AC	CA	461	gL	1224	F	A	1283	
L1RE1	480	GGC	AA	GA	TT	AT	GC	AAAA	CT	CA	AAAG	CA	AA	TT	G	CA	AA	539	L1RE1	1307	A	C	1366	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	746	A	C	CA	AT	GT	T	805	L1RE1	1307	A	C	1366	
gL	462	GGC	AA	GA	TT	AT	GC	AAAA	CT	CA	AAAG	CA	AA	TT	G	CA	AA	521	gL	1284	A	C	1343	
L1RE1	540	ATGG	GAT	CTA	AT	TAA	CT	AAAG	AG	CT	T	CT	GC	AC	AG	AA	AA	595	L1RE1	1367	G	G	1424	
aL	1	-----	-----	-----	-----	-----	-----	-----	1	aL	806	G	G	AA	CA	CA	CA	865	L1RE1	1367	G	G	1424	
gL	522	ATGG	GAT	CTA	AT	TAA	CT	AAAG	AG	CT	T	CT	GC	AC	AG	AA	AA	577	gL	1344	G	G	1403	
L1RE1	596	TG	AAC	AG	CA	CT	TA	CA	AT	GG	GA	AA	AA	TT	T	T	GC	655	L1RE1	1425	G	G	1473	
aL	36	TG	AAC	AG	CA	CT	TA	CA	AT	GG	GA	AA	AA	TT	T	T	GC	149	L1RE1	1425	G	G	1473	
gL	578	TG	AAC	AG	CA	CT	TA	CA	AT	GG	GA	AA	AA	TT	T	T	GC	637	aL	866	A	T	925	
L1RE1	656	AA	T	A	T	A	GA	A	T	C	A	A	A	A	A	A	A	715	L1RE1	1474	C	A	1533	
aL	96	AA	T	A	GA	A	T	C	A	A	A	A	A	A	A	A	A	149	aL	926	C	A	985	
gL	638	AA	T	A	GA	A	T	C	A	A	A	A	A	A	A	A	A	693	gL	1464	C	A	1523	
L1RE1	716	TT	AAAA	AG	TGG	CA	AA	AG	CA	T	GA	AG	CA	CT	TT	CA	AAAA	775	L1RE1	1534	CA	CA	1570	
aL	150	TT	AAAA	AG	TGG	CA	AA	AG	CA	T	GA	AG	CA	CT	TT	CA	AAAA	207	aL	986	CA	CA	1005	
gL	694	TT	AAAA	AG	TGG	CA	AA	AG	CA	T	GA	AG	CA	CT	TT	CA	AAAA	753	gL	1524	CA	CA	1553	
L1RE1	776	AA	AA	CA	AT	GA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	833	L1RE1	1534	CA	CA	1570	
aL	208	AA	AA	CA	AT	GA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	266	aL	986	CA	CA	1005	
gL	754	AA	AA	CA	AT	GA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	811	gL	1524	CA	CA	1553	

Supplementary Figure 1. Sequence alignment of LINE1 segments.

Alignment of a segment of the L1RE1 (1570 bp), gL (1553 bp), and aL (1005 bp) sequences. Homologous bases are enclosed by frames. Potential hairpin loops (probability above 80%) are shown as bars (black: stem, gray:loop). CpG sequences are shown as small black circles. Small arrows are position for distinguishing Ta and non-Ta subfamilies.



Supplementary Figure 2. Correlation of EGFP expression and MBN score after cell culturing.

(A) EGFP expression levels (imaging of fluorescence, left; RT-PCR, right) were compared before and after 25 days of culturing cell lines L1A-20, L1A-21, gL2-24, and gL2-25. (B) Genomic DNA harvested before or after 25 days of cell culture (lines L1A-20, L1A-21, gL2-24, and gL2-25) was cleaved with MBN (+), then amplified with primers targeting the LINE elements (gL2 and L1A), the CMV promoter, and the EGFP sequence. (C) Histograms of the ratios (MBN +/-) of PCR products.